(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
31 July 2014 (31.07.2014)

WIPO | PCT

(10) International Publication Number
WO 2014/114800 A1

(51) International Patent Classification:
C07K 16/28 (2006.01) ***A61K 39/395*** (2006.01)
C07K 16/30 (2006.01) ***A61P 35/00*** (2006.01)
A61K 47/48 (2006.01) ***C07K 16/46*** (2006.01)

(21) International Application Number:
PCT/EP2014/051550

(22) International Filing Date:
27 January 2014 (27.01.2014)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/756,991 25 January 2013 (25.01.2013) US
61/785,147 14 March 2013 (14.03.2013) US

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(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

(54) Title: ANTIBODY CONSTRUCTS FOR CDH19 AND CD3

(57) Abstract: The present invention provides to a antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell. Moreover, the invention relates to a nucleic acid sequence encoding the antibody construct, a vector comprising said nucleic acid sequence and a host cell transformed or transfected with said vector. Furthermore, the invention relates a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

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Antibody constructs for CDH19 and CD3

Related Applications

This application is related to a U.S. provisional application entitled “Antibodies targeting CDH19 for melanoma”, filed on March 15, 2013, the same day as the present application is filed. This related application is incorporated in its entirety by reference.

Field of the Invention

The present invention relates to an antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell. Moreover, the invention provides a nucleic acid sequence encoding the antibody construct, a vector comprising said nucleic acid sequence and a host cell transformed or transfected with said vector. Furthermore, the invention provides a process for the production of the antibody construct of the invention, a medical use of said antibody construct and a kit comprising said antibody construct.

Background of the Invention

Melanoma is a skin cancer that is caused by the oncogenic transformation of melanocytes, which are pigment producing skin cells. As of 2009, Melanoma had a prevalence of more than 870,000 cases in the US alone (US National Institutes of Health). Each year, over 75,000 new cases of melanoma are diagnosed in the US, and approximately 25% of patients have advanced disease at the time of diagnosis. Despite the fact that cases of primary melanoma can be cured by surgery if they are detected early enough, melanoma is the leading cause of death from skin disease in the US, responsible for about 10,000 deaths per year in the US. Once the disease has spread and became metastatic, the prognosis is poor, with a 5 year relative survival of 15%.

There are four basic types of melanomas. Three types are found in the top layers of the skin and the fourth one is invasive and has penetrated deeper into the skin and may have spread to other areas of the body.

Superficial spreading melanoma is the most common type of melanoma which accounts for about 70% of all cases. It grows along the top layer of the skin for a fairly long time before penetrating more deeply. It first appears as a flat or slightly raised discolored patch that has irregular borders and may be somewhat asymmetrical in form. The color varies, and you may see areas of tan, brown, black, red, blue or white. This type of melanoma can occur in a previously benign mole and is found most often in young people.

Lentigo maligna is similar to the superficial spreading type, as it also remains close to the skin surface for quite a while, and usually appears as a flat or mildly elevated mottled tan, brown or dark brown discoloration. It is found most often in the elderly. When this cancer becomes invasive, it is referred to as lentigo maligna melanoma.

Acral lentiginous melanoma also spreads superficially before penetrating more deeply. It is quite different from the others, though, as it usually appears as a black or brown discoloration under the nails or on the soles of the feet or palms of the hands. This type of melanoma is sometimes found on dark-skinned people, and can often advance more quickly than superficial spreading melanoma and lentigo maligna.

Nodular melanoma is usually invasive at the time it is first diagnosed. The malignancy is recognized when it becomes a bump. It is usually black, but occasionally is blue, gray, white, brown, tan, red or skin tone. This is the most aggressive of the melanomas, and is found in 10 to 15 percent of cases.

Common treatments for metastatic melanoma include chemotherapy, targeted therapies for eligible patients (e.g. BRAF inhibitor treatment for patients with BRAF mutations) and immunotherapy. Metastatic melanoma is a tumor type where immunotherapy has been demonstrated to not only slow disease progression, but to lead to cures in late stage patients. Interleukin-2 was approved for the use in metastatic melanoma in 1998, and in 2011 an antibody targeting CTLA4, a member of a new generation of immune checkpoint inhibitors, gained approval by the FDA.

CDH19 is a type II cadherin transmembrane protein of unknown function. The human gene was cloned in 2000 based on its sequence similarity to CDH7 (Kools, P. et al. Genomics. 2000). Expressed Sequence Tags (ESTs) for CDH19 were isolated from melanocyte cDNA libraries, indicating that expression of CDH19 may be limited to cells of neural crest origin (Kools, P. et al. Genomics. 2000). In support of this notion, rat CDH19 was found to be expressed primarily in nerve ganglia and in Schwann cells during rat embryonic development (Takahashi, M. and Osumi, O. Devl Dynamics. 2005.).

Diagnostic antibodies detecting CDH19 in Western Blot, immunohistochemitstry or flow cytometry are known in the art and commercially available. Those antibodies comprise poly- and monoclonal antibodies generated in animal hosts.

Summary of the Invention

The present invention provides an isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.

In one embodiment the antibody construct of the invention the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

(a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,
CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,
CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131,
CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID

NO: 1170,

CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335, CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337, CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID NO: 1339,

CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348, CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350, CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID NO: 1352,

CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361, CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363, CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID NO: 1365,

CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426, CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428, CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID NO: 1430,

CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439, CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441, CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168, CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170, CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID NO: 2172;

(b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 928, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 929, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 942, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 943, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 937, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 919, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143,

CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936, CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933, CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 934, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932, CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010, CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012, CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID NO: 1014,

CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023, CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025, CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID NO: 1027,

CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036, CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038, CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID NO: 1040,

CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075, CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077,

CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID NO: 1079,

CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101, CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103, CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID NO: 1105,

CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114, CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116, CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID NO: 1118,

CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244, CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246, CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID NO: 1248,

CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257, CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259, CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID NO: 1261,

CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270, CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,

CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285, CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287,

CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID NO: 1300,

CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID NO: 1652,

CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID

NO: 1665,

CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895, CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897, CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID NO: 1899,

CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908, CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910, CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID NO: 1912,

CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID NO: 1934, CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936, CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID NO: 1938,

CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947, CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949, CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960, CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962, CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973, CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975, CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986, CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988, CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999, CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001, CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012, CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014, CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055;

(c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288, CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119,

CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,

CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997, CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999, CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID NO: 1001,

CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049, CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051, CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID NO: 1053,

CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088, CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090, CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID NO: 1092,

CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609, CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611, CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID NO: 1613,

CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622, CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624, CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID NO: 1626,

CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635, CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637, CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID NO: 1639,

CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674, CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676, CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID NO: 1678,

CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687,

CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689, CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID NO: 1691,

CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700, CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702, CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID NO: 1704,

CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713, CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715, CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID NO: 1717,

CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726, CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728, CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID NO: 1730,

CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739, CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741, CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,

CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754, CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,

CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID NO: 1769, and

CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID NO: 1925;

(d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174, CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11, CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198, CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907,

CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 940, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971, CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973, CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975, CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062, CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064,

CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID NO: 1066,

CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140, CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142, CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID NO: 1144,

CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153, CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155, CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID NO: 1157,

CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179, CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181, CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID NO: 1183,

CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID NO: 1313,

CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID

NO: 1326,

CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374, CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376, CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID NO: 1378,

CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387, CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389, CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID NO: 1391,

CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID NO: 1400, CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402, CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413, CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415, CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID NO: 1417,

CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778, CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780, CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID NO: 1782,

CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791, CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793, CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID NO: 1795,

CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804, CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806, CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817, CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819, CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID NO: 1821,

CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830, CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832, CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID NO: 1834,

CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843, CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845, CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID NO: 1847,

CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856, CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858, CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID NO: 1860,

CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869, CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in SEQ ID NO: 1871, CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID NO: 1873,

CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882, CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884, CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066, CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID NO: 2081,

CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID NO: 2094,

CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129,

CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as depicted in SEQ ID NO: 2159,

CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194, CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196, CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207, CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209, CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID NO: 2211; and

(e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2 as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246, CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2 as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113, CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280, CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984, CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986, CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988,

CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583, CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585, CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID NO: 1587, and

CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596, CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598, CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID NO: 1600.

In a further embodiment of the antibody construct of the invention the first binding domain comprises a VH region selected from the group consisting of VH regions

(a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174;

(b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057;

(c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID

NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003, SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID NO: 1628, SEQ ID NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID NO: 1771, and SEQ ID NO: 1927;

(d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386, SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213; and

(e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350, SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602.

In another embodiment of the antibody construct of the invention the first binding domain comprises a VL region selected from the group consisting of VL regions

(a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356, SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176;

(b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059;

(c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929;

(d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID

NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786, SEQ ID NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215; and

(e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406, SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604.

The invention further provides an embodiment of the antibody construct of the invention, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of:

(1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID NOs: 2174+2176;

(2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID

NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059;

(3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929;

(4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380,+1382 SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID

NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215; and

(5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID NOs: 1602+1604.

In a further embodiment of the invention the antibody construct is in a format selected from the group consisting of $(scFv)_2$, $(\text{single domain mAb})_2$, scFv-single domain mAb, diabodies and oligomers thereof.

In a preferred embodiment the first binding domain comprises an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449 and SEQ ID NO: 2178;

(b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID NO: 2048, and SEQ ID NO: 2061;

(c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931;

(d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID

NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID NO: 2217; and

(e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606.

In another embodiment of the antibody construct of the invention the second binding domain is capable of binding to human and Callithrix jacchus, Saguinus Oedipus or Saimiri sciureus CD3 epsilon.

In a preferred embodiment the antibody construct of the invention has an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 14501450 and SEQ ID NO: 2179;

(b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID NO: 2049, and SEQ ID NO: 2062;

(c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;

(d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID

NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID NO: 1841, SEQ ID NO: 1854, SEQ ID NO: 1867, SEQ ID NO: 1880, SEQ ID NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and

(e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

The invention further provides a nucleic acid sequence encoding an antibody construct of the invention.

Furthermore, the invention provides a vector comprising a nucleic acid sequence of the invention. Moreover, the invention provides a host cell transformed or transfected with the nucleic acid sequence of the invention.

In a further embodiment the invention provides a process for the production of a antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

Moreover, the invention provides a pharmaceutical composition comprising an antibody construct of the invention or produced according to the process of the invention

In one embodiment the invention provides the antibody construct of the invention or produced according to the process of the invention for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

The invention also provides a method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject in need thereof the antibody construct of the invention or produced according to the process of the invention.

In a preferred embodiment method of use of the invention the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.

In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, or produced according to the process of the invention, a vector of the invention, and/or a host cell of the invention.

Brief description of the drawings

Figure 1:

FIG. 1 depicts cell viability data of Colo-699 cells that have been treated with fully human anti-CDH19 antibodies and a high concentration of a goat anti-human Fc monovalent Fab conjugated with DM1 (DM1-Fab) at a drug-antibody ratio (DAR) (~1.3).

Figure 2:

FIG. 2 depicts the average cell viability data from a CHL-1 assay plotted against the average cell viability data from the Colo-699 assay.

Figure 3:

FIG. 3 shows the relative expression of CDH19 mRNA in metastatic and primary melanoma samples.

Figure 4:

FIG. 4 shows the expression of CDH19 protein in human tumor samples by IHC.

Figure 5:

FIG. 5 shows the results of the analysis of tumor cell lines by flow cytometry and IHC to identify model systems with CDH19 expression similar to human tumors based on the number of CDH19 receptors present on the cell surface.

Figure 6:

FACS analysis of CDH19/CD3 bispecific antibodies on indicated cell lines:

1) untransfected L1.2. 2) L1.2 cells stably transfected with human CDH19, 3) melanoma cell line CHL-1, 4) melanoma cell line A2058, 5) human CD3 positive human T cell line HBP-

ALL, 6) macaque T cell line 4119 LnPx. Negative controls [1) to 6)]: detection antibodies without prior CDH19/CD3 bispecific antibody.

Figure 7:

Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in a 48-hour FACS-based cytotoxicity assay. Effector cells: unstimulated human PBMC. Target cells: as indicated. Effector to target cell (E:T)-ratio: 10:1.

Figure 8:

Tumor growth *in vivo* inhibition of Colo699 cells by administration of CDH19 BiTE 2G6. The bispecific antibody construct inhibits growth of tumors at 0.5 mg/kg dose.

Figure 9:

Tumor growth *in vivo* inhibition of CHL-1 cells by administration of CDH19 BiTE 2G6. The bispecific antibody construct inhibits growth of tumors at 0.5 mg/kg dose.

Figure 10:

Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in a 48-hour imaging-based cytotoxicity assay. Effector cells: unstimulated human T cells. Target cells: as indicated. Effector to target cell (E:T)-ratio: 10:1.

Figure 11:

Chromatogram IMAC capture and elution CH19 2G6 302 x I2C SA21

Typical IMAC elution profile obtained during purification of an CDH19 BiTE antibody. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. 1 – Capture. 2 – Pre-Elution 50 mM Imidazole. 3. BiTE Elution 500 mM Imidazole

Figure 12:

Chromatogram Protein_A capture and elution CH19 2G6 302 x F12Q

Typical Protein_A elution profile obtained during purification of an CDH19 BiTE antibody. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. Green line indicates the applied gradient percentage. 1 – Capture. 2 – BiTE Elution

Figure 13:

SEC elution profile of CDH19 BiTE antibody 2G6 302 x I2C SA21
Typical SEC elution profile obtained during purification of an CDH19 BiTE antibody. Protein peaks corresponding to the monomeric and dimeric BiTE antibody isoforms are indicated. LMW = low molecular weight. The red line indicates absorption at 254 nm, the blue line indicates absorption at 280 nm. Brown line indicates conductivity. 1 – non BiTE aggregates in SEC exclusion volume. 2. BiTE dimer. 3. BiTE monomer. 4. Low molecular weight contaminants and salts

Figure 14:
Reduced SDS PAGE analytics of CDH19 BiTE Monomer CH19 2G6 302 x I2C SA21 (left) and molecular weight marker Novex Sharp Protein Standard (Life Technologies).

Figure 15:
HP-SEC chromatogram showing the elution of CDH19 BiTE CH19 2G6 302 x I2C SA21 after seven day of storage at 37°C. Pink line indicationg optical absorption at 210 nm wavelength. Brown line indicating conductivity.
1 BiTE Dimer. 2. BiTE Monomer

Figure 16:
HP-SEC chromatogram showing the elution of CDH19 BiTE CH19 2G6 302 x I2C SA21 after three freeze/thaw cycles. Pink line indicationg optical absorption at 210 nm wavelength. Brown line indicating conductivity. 1. BiTE Monomer

Figure 17:
CatIEX chromatogramm of elution of CDH19 BiTE CH19 2G6 302 x I2C SA21. Blue line indicating optical absorption at 280 nm. Red line indicating optical absorption at 254 nm.

Figure 18:
HIC elution profil of CDH19 BiTE CH19 2G6 302 x I2C SA21. Blue line indicating optical absorption at 280 nm. Red line indicating optical absorption at 254 nm. Brown line indicating conductivity.

Figure 19:
FACS analysis of CDH19/CD3 bispecific antibodies on indicated cell lines: 1) HEK293 cells stably transfected with human CDH19, 2) human CD3 positive human T cell line HBP-ALL; Negative controls [1) and 2)]: detection antibodies without prior CDH19/CD3 bispecific antibody cell culture supernatant.

Figure 20:

Cytotoxic activity of CDH19/CD3 bispecific antibodies as measured in an 18-hour Chromium release-based cytotoxicity assay. Effector cells: stimulated human CD8+ T-cells. Target cells: HEK293 transfected with human CDH19. Effector to target cell (E:T)-ratio: 10:1.

Detailed Description of the Invention

Definitions:

It must be noted that as used herein, the singular forms “a”, “an”, and “the”, include plural references unless the context clearly indicates otherwise. Thus, for example, reference to “a reagent” includes one or more of such different reagents and reference to “the method” includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the present invention.

The term "and/or" wherever used herein includes the meaning of "and", "or" and "all or any other combination of the elements connected by said term".

The term "about" or "approximately" as used herein means within ±20%, preferably within ±15%, more preferably within ±10%, and most preferably within ±5% of a given value or range.

Throughout this specification and the claims which follow, unless the context requires otherwise, the word “comprise”, and variations such as “comprises” and “comprising”, will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. When used herein the term “comprising” can be substituted with the term “containing” or “including” or sometimes when used herein with the term “having”.

When used herein “consisting of" excludes any element, step, or ingredient not specified in the claim element. When used herein, "consisting essentially of" does not exclude materials or steps that do not materially affect the basic and novel characteristics of the claim.

In each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms.

The definition of the term “antibody” includes embodiments such as monoclonal, chimeric, single chain, humanized and human antibodies, as well as antibody fragments, like, inter alia, Fab fragments. Antibody fragments or derivatives further comprise $F(ab')_2$, Fv, scFv fragments or single domain antibodies such as domain antibodies or nanobodies, single variable domain antibodies or immunoglobulin single variable domain comprising merely one variable domain, which might be VHH, VH or VL, that specifically bind an antigen or epitope independently of other V regions or domains; see, for example, Harlow and Lane (1988) and (1999), loc. cit.; Kontermann and Dübel, Antibody Engineering, Springer, 2nd ed. 2010 and Little, Recombinant Antibodies for Immunotherapy, Cambridge University Press 2009. Such immunoglobulin single variable domain encompasses not only an isolated antibody single variable domain polypeptide, but also larger polypeptides that comprise one or more monomers of an antibody single variable domain polypeptide sequence.

In line with this definition all above described embodiments of the term antibody can be subsumed under the term “antibody construct”. Said term also includes diabodies or Dual-Affinity Re-Targeting (DART) antibodies. Further envisaged are (bispecific) single chain diabodies, tandem diabodies (Tandab’s), „minibodies“ exemplified by a structure which is as follows: $(VH\text{-}VL\text{-}CH3)_2$, $(scFv\text{-}CH3)_2$ or $(scFv\text{-}CH3\text{-}scFv)_2$, „Fc DART“ antibodies and „IgG DART“ antibodies, and multibodies such as triabodies. Immunoglobulin single variable domains encompass not only an isolated antibody single variable domain polypeptide, but also larger polypeptides that comprise one or more monomers of an antibody single variable domain polypeptide sequence.

Various procedures are known in the art and may be used for the production of such antibody constructs (antibodies and/or fragments). Thus, (antibody) derivatives can be produced by peptidomimetics. Further, techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778, Kontermann and Dübel (2010), loc. cit. and Little(2009), loc. cit.) can be adapted to produce single chain antibodies specific for elected polypeptide(s). Also, transgenic animals may be used to express humanized antibodies specific for polypeptides and fusion proteins of this invention. For the preparation of monoclonal antibodies, any technique, providing antibodies produced by continuous cell line cultures can be used. Examples for such techniques include the hybridoma technique (Köhler and Milstein Nature 256 (1975), 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96). Surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of a target polypeptide, such as CD3 epsilon (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). It is also envisaged in the context of this invention that the term “antibody” comprises antibody constructs, which may be expressed in a host as described herein below, e.g. antibody constructs which may be transfected and/or transduced via, inter alia, viruses or plasmid vectors.

Furthermore, the term "antibody" as employed in the invention also relates to derivatives or variants of the antibodies described herein which display the same specificity as the described antibodies.

The terms "antigen-binding domain", "antigen-binding fragment" and “antibody binding region” when used herein refer to a part of an antibody molecule that comprises amino acids responsible for the specific binding between antibody and antigen. The part of the antigen that is specifically recognized and bound by the antibody is referred to as the "epitope" as described herein above. As mentioned above, an antigen-binding domain may typically comprise an antibody light chain variable region (VL) and an antibody heavy chain variable region (VH); however, it does not have to comprise both. Fd fragments, for example, have two VH regions and often retain some antigen-binding function of the intact antigen-binding domain. Examples of antigen-binding fragments of an antibody include (1) a Fab fragment, a monovalent fragment having the VL, VH, CL and CH1 domains; (2) a F(ab')2 fragment, a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region; (3) a Fd fragment having the two VH and CH1 domains; (4) a Fv fragment having the VL and VH domains of a single arm of an antibody, (5) a dAb fragment (Ward et al., (1989) Nature 341 :544-546), which has a VH domain; (6) an isolated complementarity determining region (CDR), and (7) a single chain Fv (scFv). Although the two domains of the Fv fragment, VL and VH are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the VL and VH regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Huston et al. (1988) Proc. Natl. Acad. Sci USA 85:5879-5883). These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are evaluated for function in the same manner as are intact antibodies.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post- translation modifications (e.g., isomerizations, amidations) that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler *et al.*, Nature, 256: 495 (1975), or may be made by recombinant DNA methods (see, e.g., U. S. Patent No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson *et al.*, Nature, 352: 624-628 (1991) and Marks *et al.*, J. Mol. Biol., 222: 581-597 (1991), for example.

The term "human antibody" includes antibodies having variable and constant regions corresponding substantially to human germline immunoglobulin sequences known in the art, including, for example, those described by Kabat *et al.* (See Kabat *et al.* (1991) loc. cit.). The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*), for example in the CDRs, and in particular, CDR3. The human antibody can have at least one, two, three, four, five, or more positions replaced with an amino acid residue that is not encoded by the human germline immunoglobulin sequence. It is emphasized that the definition of human antibodies as used herein also contemplates fully human antibodies, which include only non-artificially and/or genetically altered human sequences of antibodies as those can be derived by using technologies using systems such as the Xenomice.

Examples of "antibody variants" include humanized variants of non- human antibodies, "affinity matured" antibodies (see, e.g. Hawkins et al. J. Mol. Biol. 254, 889-896 (1992) and Lowman et al., Biochemistry 30, 10832- 10837 (1991)) and antibody mutants with altered effector function (s) (see, e.g., US Patent 5, 648, 260, Kontermann and Dübel (2010), loc. cit. and Little(2009), loc. cit.).

As used herein, "*in vitro* generated antibody" refers to an antibody where all or part of the variable region (e.g., at least one CDR) is generated in a non-immune cell selection (e.g., an in vitro phage display, protein chip or any other method in which candidate sequences can be tested for their ability to bind to an antigen). This term thus preferably excludes sequences generated by genomic rearrangement in an immune cell.

The pairing of a VH and VL together forms a single antigen-binding site. The CH domain most proximal to VH is designated as CH1. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. The VH and VL domains consist of four regions of relatively conserved sequences called framework regions (FR1, FR2, FR3, and FR4), which form a scaffold for three regions of hypervariable sequences (complementarity determining regions, CDRs). The CDRs contain most of the residues responsible for specific interactions of the antibody with the antigen. CDRs are referred to as CDR 1, CDR2, and CDR3. Accordingly, CDR constituents on the heavy chain are referred to as H1, H2, and H3, while CDR constituents on the light chain are referred to as L1, L2, and L3.

The term "variable" refers to the portions of the immunoglobulin domains that exhibit variability in their sequence and that are involved in determining the specificity and binding affinity of a particular antibody (i.e., the "variable domain(s)"). Variability is not evenly distributed throughout the variable domains of antibodies; it is concentrated in sub-domains of each of the heavy and light chain variable regions. These sub-domains are called "hypervariable" regions or "complementarity determining regions" (CDRs). The more conserved (i.e., non-hypervariable) portions of the variable domains are called the "framework" regions (FRM). The variable domains of naturally occurring heavy and light chains each comprise four FRM regions, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRM and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site (see Kabat *et al.*, loc. cit.). The constant domains are not directly involved in antigen binding, but exhibit various effector functions, such as, for example, antibody-dependent, cell-mediated cytotoxicity and complement activation.

The terms "CDR", and its plural "CDRs", refer to a complementarity determining region (CDR) of which three make up the binding character of a light chain variable region (CDRL1, CDRL2 and CDRL3) and three make up the binding character of a heavy chain variable region (CDRH1, CDRH2 and CDRH3). CDRs contribute to the functional activity of an antibody molecule and are separated by amino acid sequences that comprise scaffolding or framework regions. The exact definitional CDR boundaries and lengths are subject to different classification and numbering systems. CDRs may therefore be referred to by Kabat, Chothia, contact or any other boundary definitions, including the numbering system described herein. Despite differing boundaries, each of these systems has some degree of overlap in what constitutes the so called "hypervariable regions" within the variable sequences. CDR definitions according to these systems may therefore differ in length and boundary areas with respect to the adjacent framework region. See for example Kabat, Chothia, and/or MacCallum (Kabat *et al.*, loc. cit.; Chothia *et al.*, J. Mol. Biol, 1987, 196: 901; and MacCallum *et al.*, J. Mol. Biol, 1996, 262: 732). However, the numbering in accordance with the so-called Kabat system is preferred. The CDR3 of the light chain and, particularly, CDR3 of the heavy chain may constitute the most important determinants in antigen binding within the light and heavy chain variable regions. In some antibody constructs, the heavy chain CDR3 appears to constitute the major area of contact between the antigen and the antibody. In vitro selection schemes in which CDR3 alone is varied can be used to vary the binding properties of an antibody or determine which residues contribute to the binding of an antigen.

“Consisting essentially of” means that the amino acid sequence can vary by about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15% relative to the recited SEQ ID NO: sequence and still retain biological activity, as described herein.

In some embodiments, the antibody constructs of the invention are isolated proteins or substantially pure proteins. An “isolated” protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, for example constituting at least about 5%, or at least about 50% by weight of the total protein in a given sample. It is understood that the isolated protein may constitute from 5 to 99.9% by weight of the total protein content depending on the circumstances. For example, the protein may be made at a significantly higher concentration through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. The definition includes the production of an antigen binding protein in a wide variety of organisms and/or host cells that are known in the art.

For amino acid sequences, sequence identity and/or similarity is determined by using standard techniques known in the art, including, but not limited to, the local sequence identity algorithm of Smith and Waterman, 1981, *Adv. Appl. Math.* 2:482, the sequence identity alignment algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443, the search for similarity method of Pearson and Lipman, 1988, *Proc. Nat. Acad. Sci. U.S.A.* 85:2444, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.), the Best Fit sequence program described by Devereux *et al.*, 1984, *Nucl. Acid Res.* 12:387-395, preferably using the default settings, or by inspection. Preferably, percent identity is calculated by FastDB based upon the following parameters: mismatch penalty of 1; gap penalty of 1; gap size penalty of 0.33; and joining penalty of 30, "Current Methods in Sequence Comparison and Analysis," Macromolecule Sequencing and Synthesis, Selected Methods and Applications, pp 127-149 (1988), Alan R. Liss, Inc.

An example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, 1987, *J. Mol. Evol.* 35:351-360; the method is similar to that described by Higgins and Sharp, 1989, *CABIOS* 5:151-153. Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

Another example of a useful algorithm is the BLAST algorithm, described in: Altschul *et al.*, 1990, *J. Mol. Biol.* 215:403-410; Altschul *et al.*, 1997, *Nucleic Acids Res.* 25:3389-3402; and Karin *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90:5873-5787. A particularly useful BLAST program is the WU-BLAST-2 program which was obtained from Altschul *et al.*, 1996, *Methods in Enzymology* 266:460-480. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=II. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity.

An additional useful algorithm is gapped BLAST as reported by Altschul *et al.*, 1993, *Nucl. Acids Res.* 25:3389-3402. Gapped BLAST uses BLOSUM-62 substitution scores; threshold T parameter set to 9; the two-hit method to trigger ungapped extensions, charges gap lengths of k a cost of 10+k; Xu set to 16, and Xg set to 40 for database search stage and to 67 for the output stage of the algorithms. Gapped alignments are triggered by a score corresponding to about 22 bits.

Generally, the amino acid homology, similarity, or identity between individual variant CDRs are at least 80% to the sequences depicted herein, and more typically with preferably increasing homologies or identities of at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, and almost 100%. In a similar manner, "percent (%) nucleic acid sequence identity" with respect to the nucleic acid sequence of the binding proteins identified herein is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues in the coding sequence of the antigen binding protein. A specific method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

Generally, the nucleic acid sequence homology, similarity, or identity between the nucleotide sequences encoding individual variant CDRs and the nucleotide sequences depicted herein are at least 80%, and more typically with preferably increasing homologies or identities of at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%, and almost 100%.
Thus, a “variant CDR” is one with the specified homology, similarity, or identity to the parent CDR of the invention, and shares biological function, including, but not limited to, at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the specificity and/or activity of the parent CDR.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation *per se* need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed antigen binding protein CDR variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of antigen binding protein activities, such as CDH19 binding.

The term "amino acid" or "amino acid residue" typically refers to an amino acid having its art recognized definition such as an amino acid selected from the group consisting of: alanine (Ala or A); arginine (Arg or R); asparagine (Asn or N); aspartic acid (Asp or D); cysteine (Cys or C); glutamine (Gln or Q); glutamic acid (Glu or E); glycine (Gly or G); histidine (His or H);

isoleucine (He or I): leucine (Leu or L); lysine (Lys or K); methionine (Met or M); phenylalanine (Phe or F); pro line (Pro or P); serine (Ser or S); threonine (Thr or T); tryptophan (Trp or W); tyrosine (Tyr or Y); and valine (Val or V), although modified, synthetic, or rare amino acids may be used as desired. Generally, amino acids can be grouped as having a nonpolar side chain (e.g., Ala, Cys, He, Leu, Met, Phe, Pro, Val); a negatively charged side chain (e.g., Asp, Glu); a positively charged sidechain (e.g., Arg, His, Lys); or an uncharged polar side chain (e.g., Asn, Cys, Gln, Gly, His, Met, Phe, Ser, Thr, Trp, and Tyr).

The term "hypervariable region" (also known as "complementarity determining regions" or CDRs) when used herein refers to the amino acid residues of an antibody which are (usually three or four short regions of extreme sequence variability) within the V-region domain of an immunoglobulin which form the antigen-binding site and are the main determinants of antigen specificity. There are at least two methods for identifying the CDR residues: (1) An approach based on cross-species sequence variability (i. e., Kabat *et al.*, loc. cit.); and (2) An approach based on crystallographic studies of antigen-antibody complexes (Chothia, C. *et al.*, J. Mol. Biol. 196: 901-917 (1987)). However, to the extent that two residue identification techniques define regions of overlapping, but not identical regions, they can be combined to define a hybrid CDR. However, in general, the CDR residues are preferably identified in accordance with the so-called Kabat (numbering) system.

The term "framework region" refers to the art-recognized portions of an antibody variable region that exist between the more divergent (i.e., hypervariable) CDRs. Such framework regions are typically referred to as frameworks 1 through 4 (FR1, FR2, FR3, and FR4) and provide a scaffold for the presentation of the six CDRs (three from the heavy chain and three from the light chain) in three dimensional space, to form an antigen-binding surface.

Typically, CDRs form a loop structure that can be classified as a canonical structure. The term "canonical structure" refers to the main chain conformation that is adopted by the antigen binding (CDR) loops. From comparative structural studies, it has been found that five of the six antigen binding loops have only a limited repertoire of available conformations. Each canonical structure can be characterized by the torsion angles of the polypeptide backbone. Correspondent loops between antibodies may, therefore, have very similar three dimensional structures, despite high amino acid sequence variability in most parts of the loops (Chothia and Lesk, J. Mol. Biol., 1987, 196: 901; Chothia *et al.*, Nature, 1989, 342: 877; Martin and Thornton, J. Mol. Biol, 1996, 263: 800, each of which is incorporated by reference in its entirety). Furthermore, there is a relationship between the adopted loop structure and the amino acid sequences surrounding it. The conformation of a particular canonical class is determined by the length of the loop and the amino acid residues residing at key positions within the loop, as well as within the conserved framework (i.e., outside of the loop). Assignment to a particular canonical class can therefore be made based on the presence of these key amino acid residues. The term "canonical structure" may also include considerations as to the linear sequence of the antibody, for example, as catalogued by Kabat (Kabat *et al.*, loc. cit.). The Kabat numbering scheme (system) is a widely adopted standard for numbering the amino acid residues of an antibody variable domain in a consistent manner and is the preferred scheme applied in the present invention as also mentioned elsewhere herein. Additional structural considerations can also be used to determine the canonical structure of an antibody. For example, those differences not fully reflected by Kabat numbering can be described by the numbering system of Chothia et al and/or revealed by other techniques, for example, crystallography and two or three-dimensional computational modeling. Accordingly, a given antibody sequence may be placed into a canonical class which allows for, among other things, identifying appropriate chassis sequences (e.g., based on a desire to include a variety of canonical structures in a library). Kabat numbering of antibody amino acid sequences and structural considerations as described by Chothia *et al.*, loc. cit. and their implications for construing canonical aspects of antibody structure, are described in the literature.

CDR3 is typically the greatest source of molecular diversity within the antibody-binding site. H3, for example, can be as short as two amino acid residues or greater than 26 amino acids. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known in the art. For a review of the antibody structure, see Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, eds. Harlow *et al.*, 1988. One of skill in the art will recognize that each subunit structure, e.g., a CH, VH, CL, VL, CDR, FR structure, comprises active fragments, e.g., the portion of the VH, VL, or CDR subunit the binds to the antigen, i.e., the antigen-binding fragment, or, e.g., the portion of the CH subunit that binds to and/or activates, e.g., an Fc receptor and/or complement. The CDRs typically refer to the Kabat CDRs, as described in Sequences of Proteins of immunological Interest, US Department of Health and Human Services (1991), eds. Kabat *et al.* Another standard for characterizing the antigen binding site is to refer to the hypervariable loops as described by Chothia. See, e.g., Chothia, *et al.* (1987; J. Mol. Biol. 227:799-817); and Tomlinson et al. (1995) EMBO J. 14: 4628-4638. Still another standard is the AbM definition used by Oxford Molecular's AbM antibody modeling software. See, generally, e.g., Protein Sequence and Structure Analysis of Antibody Variable Domains. In: Antibody Engineering Lab Manual (Ed.: Duebel, S. and Kontermann, R., Springer-Verlag, Heidelberg).

Embodiments described with respect to Kabat CDRs can alternatively be implemented using similar described relationships with respect to Chothia hypervariable loops or to the AbM-defined loops.

The sequence of antibody genes after assembly and somatic mutation is highly varied, and these varied genes are estimated to encode 10^{10} different antibody molecules (Immunoglobulin Genes, 2nd ed., eds. Jonio et al., Academic Press, San Diego, CA, 1995). Accordingly, the immune system provides a repertoire of immunoglobulins. The term "repertoire" refers to at least one nucleotide sequence derived wholly or partially from at least one sequence encoding at least one immunoglobulin. The sequence(s) may be generated by rearrangement in vivo of the V, D, and J segments of heavy chains, and the V and J segments of light chains. Alternatively, the sequence(s) can be generated from a cell in response to which rearrangement occurs, e.g., in vitro stimulation. Alternatively, part or all of the sequence(s) may be obtained by DNA splicing, nucleotide synthesis, mutagenesis, and other methods, see, e.g., U.S. Patent 5,565,332. A repertoire may include only one sequence or may include a plurality of sequences, including ones in a genetically diverse collection.

The term “binding molecule” or “antibody construct” in the sense of the present disclosure indicates any molecule capable of (specifically) binding to, interacting with or recognizing the target molecules CDH19 and CD3. Such molecules or constructs may include proteinaceous parts and non-proteinaceous parts (e.g. chemical linkers or chemical cross-linking agents such as glutaraldehyde).

In the event that a linker is used, this linker is preferably of a length and sequence sufficient to ensure that each of the first and second domains can, independently from one another, retain their differential binding specificities. Most preferably and as documented in the appended examples, the antibody construct of the invention is a “bispecific single chain antibody construct”, more prefereably a bispecific single chain Fv (scFv). Bispecific single chain molecules are known in the art and are described in WO 99/54440, Mack, J. Immunol. (1997), 158, 3965-3970, Mack, PNAS, (1995), 92, 7021-7025, Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197, Löffler, Blood, (2000), 95, 6, 2098-2103, Brühl, Immunol., (2001), 166, 2420-2426, Kipriyanov, J. Mol. Biol., (1999), 293, 41-56.

The said variable domains comprised in the herein described antibody constructs may be connected by additional linker sequences. The term “peptide linker” defines in accordance with the present invention an amino acid sequence by which the amino acid sequences of the first domain and the second domain of the antibody construct of the invention are linked with each other. An essential technical feature of such peptide linker is that said peptide linker does not comprise any polymerization activity. Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344. A preferred embodiment of a peptide linker is characterized by the amino acid sequence Gly-Gly-Gly-Gly-Ser, i.e. Gly_4Ser, or polymers thereof, i.e. $(Gly_4Ser)x$, where x is an integer 1 or greater. The characteristics of said peptide linker, which comprise the absence of the promotion of secondary structures are known in the art and described e.g. in Dall'Acqua et al. (Biochem. (1998) 37, 9266-9273), Cheadle et al. (Mol Immunol (1992) 29, 21-30) and Raag and Whitlow (FASEB (1995) 9(1), 73-80). Peptide linkers which also do not promote any secondary structures are preferred. The linkage of said domains to each other can be provided by, e.g. genetic engineering, as described in the examples. Methods for preparing fused and operatively linked bispecific single chain constructs and expressing them in mammalian cells or bacteria are well-known in the art (e.g. WO 99/54440 or Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 2001).

For peptide linkers, which connect the at least two binding domains in the antibody construct of the invention peptide linkers are preferred which comprise only a few number of amino acid residues, e.g. 12 amino acid residues or less. Thus, peptide linker of 12, 11, 10, 9, 8, 7, 6 or 5 amino acid residues are preferred. An envisaged peptide linker with less than 5 amino acids comprises 4, 3, 2 or one amino acid(s) wherein Gly-rich linkers are preferred. A particularly preferred "single" amino acid in context of said "peptide linker" is Gly. Accordingly, said peptide linker may consist of the single amino acid Gly.

The term "multispecific" as used herein refers to a binding molecule which is an antibody construct and comprises at least a first and a second binding domain, wherein the first binding domain is capable of binding to one antigen or target, and the second binding domain is capable of binding to another antigen or target. Accordingly, antibody constructs according to the invention comprise at least specificities for two different antigens or targets and are at least bispecific. The "antibody construct" of the invention also comprises multispecific binding molecules such as e.g. trispecific binding molecules, the latter ones including three binding domains.

It is also envisaged that the antibody construct of the invention has, in addition to its function to bind to the target molecules CDH19 and CD3, a further function. In this format, the antibody construct is a tri-or multifunctional antibody construct by targeting plasma cells through binding to CDH19, mediating cytotoxic T cell activity through CD3 binding and providing a further function such as a fully functional Fc constant domain mediating antibody-dependent cellular cytotoxicity through recruitment of effector cells like NK cells, a label (fluorescent etc.), a therapeutic agent such as, e.g. a toxin or radionuclide, and/or means to enhance serum half-life, etc.

The term "binding domain" characterizes in connection with the present invention a domain which is capable of specifically binding to / interacting with a given target epitope or a given target site on the target molecules CDH19 and CD3.
Binding domains can be derived from a binding domain donor such as for example an antibody. It is envisaged that a binding domain of the present invention comprises at least said part of any of the aforementioned binding domains that is required for binding to/interacting with a given target epitope or a given target site on the target molecules CDH19 and CD3.

It is envisaged that the binding domain of the aforementioned binding domain donors is characterized by that part of these donors that is responsible for binding the respective target, i.e. when that part is removed from the binding domain donor, said donor loses its binding capability. “Loses” means a reduction of at least 50% of the binding capability when compared with the binding donor. Methods to map these binding sites are well known in the art – it is therefore within the standard knowledge of the skilled person to locate/map the binding site of a binding domain donor and, thereby, to “derive” said binding domain from the respective binding domain donors.

The term "epitope" refers to a site on an antigen to which a binding domain, such as an antibody or immunoglobulin or derivative or fragment of an antibody or of an immunoglobulin, specifically binds. An “epitope” is antigenic and thus the term epitope is sometimes also referred to herein as “antigenic structure” or “antigenic determinant”. Thus, the binding domain is an "antigen-interaction-site". Said binding/interaction is also understood to define a "specific recognition". In one example, said binding domain which (specifically) binds to / interacts with a given target epitope or a given target site on the target molecules CDH19 and CD3 is an antibody or immunoglobulin, and said binding domain is a VH and/or VL region of an antibody or of an immunoglobulin.

“Epitopes” can be formed both by contiguous amino acids or non-contiguous amino acids juxtaposed by tertiary folding of a protein. A "linear epitope" is an epitope where an amino acid primary sequence comprises the recognized epitope. A linear epitope typically includes at least 3 or at least 4, and more usually, at least 5 or at least 6 or at least 7, for example, about 8 to about 10 amino acids in a unique sequence.

A "conformational epitope", in contrast to a linear epitope, is an epitope wherein the primary sequence of the amino acids comprising the epitope is not the sole defining component of the epitope recognized (e.g., an epitope wherein the primary sequence of amino acids is not necessarily recognized by the binding domain). Typically a conformational epitope comprises an increased number of amino acids relative to a linear epitope. With regard to recognition of conformational epitopes, the binding domain recognizes a three-dimensional structure of the antigen, preferably a peptide or protein or fragment thereof (in the context of the present invention, the antigen for one of the binding domains is comprised within the CDH19 protein). For example, when a protein molecule folds to form a three-dimensional structure, certain amino acids and/or the polypeptide backbone forming the conformational epitope become juxtaposed enabling the antibody to recognize the epitope. Methods of determining the conformation of epitopes include, but are not limited to, x-ray crystallography, two-dimensional nuclear magnetic resonance (2D-NMR) spectroscopy and site-directed spin labelling and electron paramagnetic resonance (EPR) spectroscopy. Moreover, the provided examples describe a further method to characterize a given binding domain by way of binning, which includes a test whether the given binding domain binds to one or more epitope cluster(s) of a given protein, in particular CDH19.

As used herein, the term “epitope cluster” denotes the entirety of epitopes lying in a defined contiguous stretch of an antigen. An epitope cluster can comprise one, two or more epitopes. The concept of epitope cluster is also used in the characterization of the features of the antibody constructs of the invention.

The terms “(capable of) binding to”, "specifically recognizing", “directed to” and “reacting with” mean in accordance with this invention that a binding domain is capable of specifically interacting with one or more, preferably at least two, more preferably at least three and most preferably at least four amino acids of an epitope.

As used herein, the terms "specifically interacting", “specifically binding” or “specifically bind(s)” mean that a binding domain exhibits appreciable affinity for a particular protein or antigen and, generally, does not exhibit significant reactivity with proteins or antigens other than CDH19 or CD3. “Appreciable affinity” includes binding with an affinity of about 10^{-6}M (KD) or stronger. Preferably, binding is considered specific when binding affinity is about 10^{-12} to 10^{-8} M, 10^{-12} to 10^{-9} M, 10^{-12} to 10^{-10} M, 10^{-11} to 10^{-8} M, preferably of about 10^{-11} to 10^{-}

^{9} M. Whether a binding domain specifically reacts with or binds to a target can be tested readily by, *inter alia*, comparing the reaction of said binding domain with a target protein or antigen with the reaction of said binding domain with proteins or antigens other than CDH19 or CD3. Preferably, a binding domain of the invention does not essentially bind or is not capable of binding to proteins or antigens other than CDH19 or CD3 (i.e. the first binding domain is not capable of binding to proteins other than CDH19 and the second binding domain is not capable of binding to proteins other than CD3).

The term “does not essentially bind”, or “is not capable of binding” means that a binding domain of the present invention does not bind another protein or antigen other than CDH19 or CD3, i.e., does not show reactivity of more than 30%, preferably not more than 20%, more preferably not more than 10%, particularly preferably not more than 9%, 8%, 7%, 6% or 5% with proteins or antigens other than CDH19 or CD3, whereby binding to CDH19 or CD3, respectively, is set to be 100%.

Specific binding is believed to be effected by specific motifs in the amino acid sequence of the binding domain and the antigen. Thus, binding is achieved as a result of their primary, secondary and/or tertiary structure as well as the result of secondary modifications of said structures. The specific interaction of the antigen-interaction-site with its specific antigen may result in a simple binding of said site to the antigen. Moreover, the specific interaction of the antigen-interaction-site with its specific antigen may alternatively or additionally result in the initiation of a signal, e.g. due to the induction of a change of the conformation of the antigen, an oligomerization of the antigen, etc.

Proteins (including fragments thereof, preferably biologically active fragments, and peptides, usually having less than 30 amino acids) comprise one or more amino acids coupled to each other via a covalent peptide bond (resulting in a chain of amino acids). The term "polypeptide" as used herein describes a group of molecules, which consist of more than 30 amino acids. Polypeptides may further form multimers such as dimers, trimers and higher oligomers, i.e. consisting of more than one polypeptide molecule. Polypeptide molecules forming such dimers, trimers etc. may be identical or non-identical. The corresponding higher order structures of such multimers are, consequently, termed homo- or heterodimers, homo- or heterotrimers etc. An example for a hereteromultimer is an antibody molecule, which, in its naturally occurring form, consists of two identical light polypeptide chains and two identical heavy polypeptide chains. The terms "polypeptide" and "protein" also refer to naturally modified polypeptides/proteins wherein the modification is effected e.g. by post-translational modifications like glycosylation, acetylation, phosphorylation and the like. A “polypeptide” when referred to herein may also be chemically modified such as pegylated. Such modifications are well known in the art.

"Isolated" when used to describe the antibody construct disclosed herein, means a antibody construct that has been identified, separated and/or recovered from a component of its production environment. Preferably, the isolated antibody construct is free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the antibody construct will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Ordinarily, however, an isolated antibody will be prepared by at least one purification step.

Amino acid sequence modifications of the antibody constructs described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of the antibody constructs are prepared by introducing appropriate nucleotide changes into the antibody constructs nucleic acid, or by peptide synthesis.

Such modifications include, for example, deletions from, and/or insertions into, and/or substitutions of, residues within the amino acid sequences of the antibody constructs. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antibody constructs, such as changing the number or position of glycosylation sites. Preferably, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids may be substituted in a CDR, while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be substituted in the framework regions (FRs). The substitutions are preferably conservative substitutions as described herein. Additionally or alternatively, 1, 2, 3, 4, 5, or 6 amino acids may be inserted or deleted in each of the CDRs (of course, dependent on their length), while 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or 25 amino acids may be inserted or deleted in each of the FRs.

A useful method for identification of certain residues or regions of the antibody constructs that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells in Science, 244: 1081-1085 (1989). Here, a residue or group of target residues within the antibody construct is/are identified (e.g. charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the epitope.

Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation *per se* needs not to be predetermined. For example, to analyze the performance of a mutation at a given site, ala scanning or random mutagenesis is conducted at a target codon or region and the expressed antibody construct variants are screened for the desired activity.

Preferably, amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 residues to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. An insertional variant of the antibody construct includes the fusion to the N-or C-terminus of the antibody to an enzyme or a fusion to a polypeptide which increases the serum half-life of the antibody.

Another type of variant is an amino acid substitution variant. These variants have preferably at least 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid residues in the antibody construct replaced by a different residue. The sites of greatest interest for substitutional mutagenesis include the CDRs of the heavy and/or light chain, in particular the hypervariable regions, but FR alterations in the heavy and/or light chain are also contemplated.

For example, if a CDR sequence encompasses 6 amino acids, it is envisaged that one, two or three of these amino acids are substituted. Similarly, if a CDR sequence encompasses 15 amino acids it is envisaged that one, two, three, four, five or six of these amino acids are substituted.

Generally, if amino acids are substituted in one or more or all of the CDRs of the heavy and/or light chain, it is preferred that the then-obtained “substituted” sequence is at least 60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the “original” CDR sequence. This means that it is dependent of the length of the CDR to which degree it is identical to the “substituted” sequence. For example, a CDR having 5 amino acids is preferably 80% identical to its substituted sequence in order to have at least one amino acid substituted. Accordingly, the CDRs of the antibody construct may have different degrees of identity to their substituted sequences, e.g., CDRL1 may have 80%, while CDRL3 may have 90%.

Preferred substitutions (or replacements) are conservative substitutions. However, any substitution (including non-conservative substitution or one or more from the “exemplary substitutions” listed in Table 1, below) is envisaged as long as the antibody construct retains its capability to bind to CDH19 via the first binding domain and to CD3 epsilon via the second binding domain and/or its CDRs have an identity to the then substituted sequence (at least 60%, more preferably 65%, even more preferably 70%, particularly preferably 75%, more particularly preferably 80% identical to the “original” CDR sequence).

Conservative substitutions are shown in Table 1under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 1, or as further described below in reference to amino acid classes, may be introduced and the products screened for a desired characteristic.

Table 1: Amino Acid Substitutions

Original	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val, leu, ile	val
Arg (R)	lys, gln, asn	lys
Asn (N)	gln, his, asp, lys, arg	gln
Asp (D)	glu, asn	glu
Cys (C)	ser, ala	ser
Gln (Q)	asn, glu	asn
Glu (E)	asp, gln	asp
Gly (G)	ala	ala
His (H)	asn, gln, lys, arg	arg
Ile (I)	leu, val, met, ala, phe	leu
Leu (L)	norleucine, ile, val, met, ala	ile
Lys (K)	arg, gln, asn	arg
Met (M)	leu, phe, ile	leu
Phe (F)	leu, val, ile, ala, tyr	tyr
Pro (P)	ala	ala

Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr, phe	tyr
Tyr (Y)	trp, phe, thr, ser	phe
Val (V)	ile, leu, met, phe, ala	leu

Substantial modifications in the biological properties of the antibody construct of the present invention are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties: (1) hydrophobic: norleucine, met, ala, val, leu, ile; (2) neutral hydrophilic: cys, ser, thr; (3) acidic: asp, glu; (4) basic: asn, gin, his, lys, arg; (5) residues that influence chain orientation: gly, pro; and (6) aromatic : trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Any cysteine residue not involved in maintaining the proper conformation of the antibody construct may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (e. g. a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (e. g. 6-7 sites) are mutated to generate all possible amino acid substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (e. g. binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the binding domain and, e.g., human CDH19. Such contact residues and neighbouring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

Other modifications of the antibody construct are contemplated herein. For example, the antibody construct may be linked to one of a variety of non-proteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol. The antibody construct may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatine-microcapsules and poly (methylmethacylate) microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, 16th edition, Oslo, A., Ed., (1980).

The antibody constructs disclosed herein may also be formulated as immuno-liposomes. A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.* , Proc. Natl Acad. Sci. USA, 77: 4030 (1980); US Pat. Nos. 4,485,045 and 4,544,545; and W0 97/38731 published October 23, 1997. Liposomes with enhanced circulation time are disclosed in US Patent No. 5,013, 556. Particularly useful liposomes can be generated by the reverse phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.* J. Biol. Chem. 257: 286-288 (1982) via a disulfide interchange reaction. A chemotherapeutic agent is optionally contained within the liposome. See Gabizon *et al.* J. National Cancer Inst. 81 (19) 1484 (1989).

When using recombinant techniques, the antibody construct can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli.*

The antibody construct composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique.

The term “nucleic acid” is well known to the skilled person and encompasses DNA (such as cDNA) and RNA (such as mRNA). The nucleic acid can be double stranded and single stranded, linear and circular. Said nucleic acid molecule is preferably comprised in a vector which is preferably comprised in a host cell. Said host cell is, e.g. after transformation or transfection with the nucleic acid sequence of the invention, capable of expressing the antibody construct. For that purpose the nucleic acid molecule is operatively linked with control sequences.

A vector is a nucleic acid molecule used as a vehicle to transfer (foreign) genetic material into a cell. The term “vector” encompasses – but is not restricted to – plasmids, viruses, cosmids and artificial chromosomes. In general, engineered vectors comprise an origin of replication, a multicloning site and a selectable marker. The vector itself is generally a nucleotide sequence, commonly a DNA sequence, that comprises an insert (transgene) and a larger sequence that serves as the "backbone" of the vector. Modern vectors may encompass additional features besides the transgene insert and a backbone: promoter, genetic marker, antibiotic resistance, reporter gene, targeting sequence, protein purification tag. Vectors called expression vectors (expression constructs) specifically are for the expression of the transgene in the target cell, and generally have control sequences such as a promoter sequence that drives expression of the transgene. Insertion of a vector into the target cell is usually called “transformation” for bacteria, “transfection” for eukaryotic cells, although insertion of a viral vector is also called “transduction”.

As used herein, the term "host cell" is intended to refer to a cell into which a nucleic acid encoding the antibody construct of the invention is introduced by way of transformation, transfection and the like. It should be understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

As used herein, the term "expression" includes any step involved in the production of a antibody construct of the invention including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

A nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The terms "host cell," "target cell" or "recipient cell" are intended to include any individual cell or cell culture that can be or has/have been recipients for vectors or the incorporation of exogenous nucleic acid molecules, polynucleotides and/or proteins. It also is intended to include progeny of a single cell, and the progeny may not necessarily be completely identical (in morphology or in genomic or total DNA complement) to the original parent cell due to natural, accidental, or deliberate mutation. The cells may be prokaryotic or eukaryotic, and include but are not limited to bacteria, yeast cells, animal cells, and mammalian cells, e.g., murine, rat, macaque or human.

Suitable host cells include prokaryotes and eukaryotic host cells including yeasts, fungi, insect cells and mammalian cells.

The antibody construct of the invention can be produced in bacteria. After expression, the antibody construct of the invention, preferably the antibody construct is isolated from the *E. coli* cell paste in a soluble fraction and can be purified through, e.g., affinity chromatography and/or size exclusion. Final purification can be carried out similar to the process for purifying antibody expressed e. g, in CHO cells.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for the antibody construct of the invention. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Schizosaccharomyces pombe*, Kluyveromyces hosts such as, e.g., *K. lactis, K. fragilis* (ATCC 12424), *K. bulgaricus* (ATCC 16045), *K. wickeramii* (ATCC 24178), *K. waltii* (ATCC 56500), *K. drosophilarum* (ATCC 36906), *K. thermotolerans*, and *K. marxianus*; yarrowia (EP 402 226); *Pichia pastoris* (EP 183 070); Candida; *Trichoderma reesia* (EP 244 234); *Neurospora crassa*; Schwanniomyces such as *Schwanniomyces occidentalis*; and filamentous fungi such as, e.g., Neurospora, Penicillium, Tolypocladium, and Aspergillus hosts such as *A. nidulans* and *A. niger*.

Suitable host cells for the expression of glycosylated antibody construct of the invention, preferably antibody derived antibody constructs are derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruit fly), and *Bombyx mori* have been identified. A variety of viral strains for transfection are publicly available, e. g. , the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV, and such viruses may be used as the virus herein according to the present invention, particularly for transfection of *Spodoptera frugiperda* cells.

Plant cell cultures of cotton, corn, potato, soybean, petunia, tomato, Arabidopsis and tobacco can also be utilized as hosts. Cloning and expression vectors useful in the production of proteins in plant cell culture are known to those of skill in the art. See e.g. Hiatt *et al.*, Nature (1989) 342: 76-78, Owen *et al.* (1992) Bio/Technology 10: 790-794, Artsaenko *et al.* (1995) The Plant J 8: 745-750, and Fecker *et al.* (1996) Plant Mol Biol 32: 979-986.

However, interest has been greatest in vertebrate cells, and propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al. , J. Gen Virol. 36 : 59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al.* , Proc. Natl. Acad. Sci. USA 77: 4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23: 243-251 (1980)); monkey kidney cells (CVI ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL1587) ; human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2,1413 8065); mouse mammary tumor (MMT 060562, ATCC CCL5 1); TRI cells (Mather *et al.*, Annals N. Y Acad. Sci. 383 : 44-68 (1982)) ; MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

When using recombinant techniques, the antibody construct of the invention can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antibody construct is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, Bio/Technology 10: 163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

The antibody construct of the invention prepared from the host cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique.

The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly (styrenedivinyl) benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the antibody construct of the invention comprises a CH3 domain, the Bakerbond ABXMresin (J. T. Baker, Phillipsburg, NJ) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE^{TM} chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromato-focusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the antibody to be recovered.

The term "culturing" refers to the in vitro maintenance, differentiation, growth, proliferation and/or propagation of cells under suitable conditions in a medium.

As used herein, the term “pharmaceutical composition” relates to a composition for administration to a patient, preferably a human patient. The particular preferred pharmaceutical composition of this invention comprises the antibody construct of the invention. Preferably, the pharmaceutical composition comprises suitable formulations of carriers, stabilizers and/or excipients. In a preferred embodiment, the pharmaceutical composition comprises a composition for parenteral, transdermal, intraluminal, intraarterial, intrathecal and/or intranasal administration or by direct injection into tissue. It is in particular envisaged that said composition is administered to a patient via infusion or injection. Administration of the suitable compositions may be effected by different ways, e.g., by intravenous, intraperitoneal, subcutaneous, intramuscular, topical or intradermal administration. In particular, the present invention provides for an uninterrupted administration of the suitable composition. As a non-limiting example, uninterrupted, i.e. continuous administration may be realized by a small pump system worn by the patient for metering the influx of therapeutic agent into the body of the patient. The pharmaceutical composition comprising the antibody construct of the invention can be administered by using said pump systems. Such pump systems are generally known in the art, and commonly rely on periodic exchange of cartridges containing the therapeutic agent to be infused. When exchanging the cartridge in such a pump system, a temporary interruption of the otherwise uninterrupted flow of therapeutic agent into the body of the patient may ensue. In such a case, the phase of administration prior to cartridge replacement and the phase of administration following cartridge replacement would still be considered within the meaning of the pharmaceutical means and methods of the invention together make up one “uninterrupted administration” of such therapeutic agent.

The continuous or uninterrupted administration of these antibody constructs of the invention may be intravenous or subcutaneous by way of a fluid delivery device or small pump system including a fluid driving mechanism for driving fluid out of a reservoir and an actuating mechanism for actuating the driving mechanism. Pump systems for subcutaneous administration may include a needle or a cannula for penetrating the skin of a patient and delivering the suitable composition into the patient's body. Said pump systems may be directly fixed or attached to the skin of the patient independently of a vein, artery or blood vessel, thereby allowing a direct contact between the pump system and the skin of the patient. The pump system can be attached to the skin of the patient for 24 hours up to several days. The pump system may be of small size with a reservoir for small volumes. As a non-limiting example, the volume of the reservoir for the suitable pharmaceutical composition to be administered can be between 0.1 and 50 ml.

The continuous administration may be transdermal by way of a patch worn on the skin and replaced at intervals. One of skill in the art is aware of patch systems for drug delivery suitable for this purpose. It is of note that transdermal administration is especially amenable to uninterrupted administration, as exchange of a first exhausted patch can advantageously be accomplished simultaneously with the placement of a new, second patch, for example on the surface of the skin immediately adjacent to the first exhausted patch and immediately prior to removal of the first exhausted patch. Issues of flow interruption or power cell failure do not arise.

The inventive compositions may further comprise a pharmaceutically acceptable carrier. Examples of suitable pharmaceutical carriers are well known in the art and include solutions, e.g. phosphate buffered saline solutions, water, emulsions, such as oil/water emulsions, various types of wetting agents, sterile solutions, liposomes, etc. Compositions comprising such carriers can be formulated by well known conventional methods. Formulations can comprise carbohydrates, buffer solutions, amino acids and/or surfactants. Carbohydrates may be non-reducing sugars, preferably trehalose, sucrose, octasulfate, sorbitol or xylitol. In general, as used herein, "pharmaceutically acceptable carrier" means any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, compatible with pharmaceutical administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed and include: additional buffering agents; preservatives; co-solvents; antioxidants, including ascorbic acid and methionine; chelating agents such as EDTA; metal complexes (e.g., Zn-protein complexes); biodegradable polymers, such as polyesters; salt-forming counter-ions, such as sodium, polyhydric sugar alcohols; amino acids, such as alanine, glycine, asparagine, 2-phenylalanine, and threonine; sugars or sugar alcohols, such as trehalose, sucrose, octasulfate, sorbitol or xylitol stachyose, mannose, sorbose, xylose, ribose, myoinisitose, galactose, lactitol, ribitol, myoinisitol, galactitol, glycerol, cyclitols (e.g., inositol), polyethylene glycol; sulfur containing reducing agents, such as glutathione, thioctic acid, sodium thioglycolate, thioglycerol, [alpha]-monothioglycerol, and sodium thio sulfate; low molecular weight proteins, such as human serum albumin, bovine serum albumin, gelatin, or other immunoglobulins; and hydrophilic polymers, such as polyvinylpyrrolidone. Such formulations may be used for continuous administrations which may be intravenuous or subcutaneous with and/or without pump systems. Amino acids may be charged amino acids, preferably lysine, lysine acetate, arginine, glutamate and/or histidine. Surfactants may be detergents, preferably with a molecular weight of >1.2 KD and/or a polyether, preferably with a molecular weight of >3 KD. Non-limiting examples for preferred detergents are Tween 20, Tween 40, Tween 60, Tween 80 or Tween 85. Non-limiting examples for preferred polyethers are PEG 3000, PEG 3350, PEG 4000 or PEG 5000. Buffer systems used in the present invention can have a preferred pH of 5-9 and may comprise citrate, succinate, phosphate, histidine and acetate.

The compositions of the present invention can be administered to the subject at a suitable dose which can be determined e.g. by dose escalating studies by administration of increasing doses of the polypeptide of the invention exhibiting cross-species specificity described herein to non-chimpanzee primates, for instance macaques. As set forth above, the antibody construct of the invention exhibiting cross-species specificity described herein can be advantageously used in identical form in preclinical testing in non-chimpanzee primates and as drug in humans. These compositions can also be administered in combination with other proteinaceous and non-proteinaceous drugs. These drugs may be administered simultaneously with the composition comprising the polypeptide of the invention as defined herein or separately before or after administration of said polypeptide in timely defined intervals and doses. The dosage regimen will be determined by the attending physician and clinical factors. As is well known in the medical arts, dosages for any one patient depend upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently.

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases and the like. In addition, the composition of the present invention might comprise proteinaceous carriers, like, e.g., serum albumin or immunoglobulin, preferably of human origin. It is envisaged that the composition of the invention might comprise, in addition to the polypeptide of the invention defined herein, further biologically active agents, depending on the intended use of the composition. Such agents might be drugs acting on the gastro-intestinal system, drugs acting as cytostatica, drugs preventing hyperurikemia, drugs inhibiting immunoreactions (e.g. corticosteroids), drugs modulating the inflammatory response, drugs acting on the circulatory system and/or agents such as cytokines known in the art. It is also envisaged that the antibody construct of the present invention is applied in a co-therapy, i.e., in combination with another anti-cancer medicament.

The biological activity of the pharmaceutical composition defined herein can be determined for instance by cytotoxicity assays, as described in the following examples, in WO 99/54440 or by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12). “Efficacy” or “*in vivo* efficacy“ as used herein refers to the response to therapy by the pharmaceutical composition of the invention, using e.g. standardized NCI response criteria. The success or *in vivo* efficacy of the therapy using a pharmaceutical composition of the invention refers to the effectiveness of the composition for its intended purpose, i.e. the ability of the composition to cause its desired effect, i.e. depletion of pathologic cells, e.g. tumor cells. The *in vivo* efficacy may be monitored by established standard methods for the respective disease entities including, but not limited to white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration. In addition, various disease specific clinical chemistry parameters and other established standard methods may be used. Furthermore, computer-aided tomography, X-ray, nuclear magnetic resonance tomography (e.g. for National Cancer Institute-criteria based response assessment [Cheson BD, Horning SJ, Coiffier B, Shipp MA, Fisher RI, Connors JM, Lister TA, Vose J, Grillo-Lopez A, Hagenbeek A, Cabanillas F, Klippensten D, Hiddemann W, Castellino R, Harris NL, Armitage JO, Carter W, Hoppe R, Canellos GP. Report of an international workshop to standardize response criteria for non-Hodgkin's lymphomas. NCI Sponsored International Working Group. J Clin Oncol. 1999 Apr;17(4):1244]), positron-emission tomography scanning, white blood cell counts, differentials, Fluorescence Activated Cell Sorting, bone marrow aspiration, lymph node biopsies/histologies, and various lymphoma specific clinical chemistry parameters (e.g. lactate dehydrogenase) and other established standard methods may be used.

Another major challenge in the development of drugs such as the pharmaceutical composition of the invention is the predictable modulation of pharmacokinetic properties. To this end, a pharmacokinetic profile of the drug candidate, i.e. a profile of the pharmacokinetic parameters that affect the ability of a particular drug to treat a given condition, can be established. Pharmacokinetic parameters of the drug influencing the ability of a drug for treating a certain disease entity include, but are not limited to: half-life, volume of distribution, hepatic first-pass metabolism and the degree of blood serum binding. The efficacy of a given drug agent can be influenced by each of the parameters mentioned above.

“Half-life" means the time where 50% of an administered drug are eliminated through biological processes, e.g. metabolism, excretion, etc.

By "hepatic first-pass metabolism" is meant the propensity of a drug to be metabolized upon first contact with the liver, i.e. during its first pass through the liver.

“Volume of distribution" means the degree of retention of a drug throughout the various compartments of the body, like e.g. intracellular and extracellular spaces, tissues and organs, etc. and the distribution of the drug within these compartments.

“Degree of blood serum binding" means the propensity of a drug to interact with and bind to blood serum proteins, such as albumin, leading to a reduction or loss of biological activity of the drug.

Pharmacokinetic parameters also include bioavailability, lag time (Tlag), Tmax, absorption rates, more onset and/or Cmax for a given amount of drug administered. “Bioavailability” means the amount of a drug in the blood compartment. “Lag time" means the time delay between the administration of the drug and its detection and measurability in blood or plasma.

“Tmax” is the time after which maximal blood concentration of the drug is reached, and “Cmax” is the blood concentration maximally obtained with a given drug. The time to reach a blood or tissue concentration of the drug which is required for its biological effect is influenced by all parameters. Pharmacokinetic parameters of bispecific single chain antibodies exhibiting cross-species specificity, which may be determined in preclinical animal testing in non-chimpanzee primates as outlined above, are also set forth e.g. in the publication by Schlereth *et al.* (Cancer Immunol. Immunother. 20 (2005), 1-12).

The term “toxicity” as used herein refers to the toxic effects of a drug manifested in adverse events or severe adverse events. These side events might refer to a lack of tolerability of the drug in general and/or a lack of local tolerance after administration. Toxicity could also include teratogenic or carcinogenic effects caused by the drug.

The term “safety”, “*in vivo* safety” or “tolerability” as used herein defines the administration of a drug without inducing severe adverse events directly after administration (local tolerance) and during a longer period of application of the drug. “Safety”, “*in vivo* safety” or “tolerability” can be evaluated e.g. at regular intervals during the treatment and follow-up period. Measurements include clinical evaluation, e.g. organ manifestations, and screening of laboratory abnormalities. Clinical evaluation may be carried out and deviations to normal findings recorded/coded according to NCI-CTC and/or MedDRA standards. Organ manifestations may include criteria such as allergy/immunology, blood/bone marrow, cardiac arrhythmia, coagulation and the like, as set forth e.g. in the Common Terminology Criteria for adverse events v3.0 (CTCAE). Laboratory parameters which may be tested include for instance hematology, clinical chemistry, coagulation profile and urine analysis and examination of other body fluids such as serum, plasma, lymphoid or spinal fluid, liquor and the like. Safety can thus be assessed e.g. by physical examination, imaging techniques (i.e. ultrasound, x-ray, CT scans, Magnetic Resonance Imaging (MRI), other measures with technical devices (i.e. electrocardiogram), vital signs, by measuring laboratory parameters and recording adverse events. For example, adverse events in non-chimpanzee primates in the uses and methods according to the invention may be examined by histopathological and/or histochemical methods.

The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts effective for this use will depend upon the severity of the infection and the general state of the subject's own immune system. The term "patient" includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

The term “effective and non-toxic dose” as used herein refers to a tolerable dose of an inventive antibody construct which is high enough to cause depletion of pathologic cells, tumor elimination, tumor shrinkage or stabilization of disease without or essentially without major toxic effects. Such effective and non-toxic doses may be determined e.g. by dose escalation studies described in the art and should be below the dose inducing severe adverse side events (dose limiting toxicity, DLT).

The above terms are also referred to e.g. in the Preclinical safety evaluation of biotechnology-derived pharmaceuticals S6; ICH Harmonised Tripartite Guideline; ICH Steering Committee meeting on July 16, 1997.

The appropriate dosage, or therapeutically effective amount, of the antibody construct of the invention will depend on the condition to be treated, the severity of the condition, prior therapy, and the patient's clinical history and response to the therapeutic agent. The proper dose can be adjusted according to the judgment of the attending physician such that it can be administered to the patient one time or over a series of administrations. The pharmaceutical composition can be administered as a sole therapeutic or in combination with additional therapies such as anti-cancer therapies as needed.

The pharmaceutical compositions of this invention are particularly useful for parenteral administration, i.e., subcutaneously, intramuscularly, intravenously, intra-articular and/or intra-synovial. Parenteral administration can be by bolus injection or continuous infusion.

If the pharmaceutical composition has been lyophilized, the lyophilized material is first reconstituted in an appropriate liquid prior to administration. The lyophilized material may be reconstituted in, e.g., bacteriostatic water for injection (BWFI), physiological saline, phosphate buffered saline (PBS), or the same formulation the protein had been in prior to lyophilization.

In an internal analysis of proprietary mRNA expression data it has been surprisingly found that CDH19 expression is elevated in both primary and metastatic melanoma tumors compared to normal, untransformed tissues. Internal analysis also confirmed that expression of CDH19 in normal tissues is limited to neural crest derived peripheral nerve ganglia and nerve fibers. The differential CDH19 expression in normal and tumor tissues makes this protein attractive for cell-surface targeting therapeutics. Although CDH 19 was discussed as one marker as part of long lists of markers associated with some cancer types (see e.g.

WO2009/055937) or Parkinson's disease (see e.g. WO2005/067391) CDH19 was never discussed as a prognostic marker or a drug target in connection with melanoma tumors.

As stated above, the present invention provides an isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.

The "CDH19 extracellular domain" or "CDH19 ECD" refers to a form of CDH19 which is essentially free of transmembrane and cytoplasmic domains of CDH19. It will be understood by the skilled artisan that the transmembrane domain identified for the CDH19 polypeptide of the present invention is identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain specifically mentioned herein. A preferred human CDH19 ECD is shown in SEQ ID NO: 948. In this context it is understood that the CDH19 ECD represents the part of CDH19 on the surface of a target cell.

The T cell CD3 receptor complex is a protein complex and is composed of four distinct chains. In mammals, the complex contains a CD3γ chain, a CD3δ chain, and two CD3ε (epsilon) chains. These chains associate with a molecule known as the T cell receptor (TCR) and the ζ chain to generate an activation signal in T lymphocytes.

The redirected lysis of target cells via the recruitment of T cells by a multispecific, at least bispecific, antibody construct involves cytolytic synapse formation and delivery of perforin and granzymes. The engaged T cells are capable of serial target cell lysis, and are not affected by immune escape mechanisms interfering with peptide antigen processing and presentation, or clonal T cell differentiation; see, for example, WO 2007/042261.

The affinity of the first binding domain for human CDH19 is preferably ≤15 nM, more preferably ≤10 nM, even more preferably ≤5 nM, even more preferably ≤1 nM, even more preferably ≤0.5 nM, even more preferably ≤0.1 nM, and most preferably ≤0.05 nM. The affinity of the first binding domain for macaque CDH19 is preferably ≤15 nM, more preferably ≤10 nM, even more preferably ≤5 nM, even more preferably ≤1 nM, even more preferably ≤0.5 nM, even more preferably ≤0.1 nM, and most preferably ≤0.05 nM or even ≤0.01 nM. The affinity can be measured for example in a Biacore assay or in a Scatchard assay, e.g. as described in the Examples. The affinity gap for binding to macaque CDH19 versus human

CDH19 is preferably [1:10-1:5] or [5:1-10:1], more preferably [1:5-5:1], and most preferably [1:2-3:1] or even [1:1-3:1]. Other methods of determining the affinity are well-known to the skilled person.

Human antibodies, respectively human antibody constructs, avoid some of the problems associated with antibodies/antibody constructs that possess murine or rat variable and/or constant regions. The presence of such murine or rat derived proteins can lead to the rapid clearance of the antibodies/antibody constructs or can lead to the generation of an immune response against the antibody/antibody construct by a patient. In order to avoid the utilization of murine or rat derived antibodies/antibody constructs, human or fully human antibodies can be generated through the introduction of human antibody function into a rodent so that the rodent produces fully human antibodies.

The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci as well as generating useful models of human disease. Furthermore, the utilization of such technology for substitution of mouse loci with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression.

An important practical application of such a strategy is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the mechanisms underlying programmed expression and assembly of antibodies as well as their role in B-cell development. Furthermore, such a strategy could provide an ideal source for production of fully human monoclonal antibodies (mAbs)--an important milestone towards fulfilling the promise of antibody therapy in human disease. Fully human antibodies/antibody constructs are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized mAbs and thus to increase the efficacy and safety of the administered antibodies/antibody constructs. The use of fully human antibodies/antibody constructs can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as inflammation, autoimmunity, and cancer, which require repeated compound administrations.

One approach towards this goal was to engineer mouse strains deficient in mouse antibody production with large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human mAbs with the desired specificity could be readily produced and selected. This general strategy was demonstrated in connection with our generation of the first XenoMouse mouse strains, as published in 1994. (See Green et al. Nature Genetics 7:13-21 (1994)) The XenoMouse strains were engineered with yeast artificial chromosomes (YACs) containing 245 kb and 190 kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. Id. The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B-cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human mAbs. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through introduction of megabase sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively. See Mendez et al. Nature Genetics 15:146-156 (1997) and U.S. patent application Ser. No. 08/759,620, filed Dec. 3, 1996, the disclosures of which are hereby incorporated by reference.

The production of the XenoMouse mice is further discussed and delineated in U.S. patent application Ser. No. 07/466,008, filed Jan. 12, 1990, Ser. No. 07/610,515, filed Nov. 8, 1990, Ser. No. 07/919,297, filed Jul. 24, 1992, Ser. No. 07/922,649, filed Jul. 30, 1992, filed Ser. No. 08/031,801, filed Mar. 15, 1993, Ser. No. 08/112,848, filed Aug. 27, 1993, Ser. No. 08/234,145, filed Apr. 28, 1994, Ser. No. 08/376,279, filed Jan. 20, 1995, Ser. No. 08/430,938, Apr. 27, 1995, Ser. No. 08/464,584, filed Jun. 5, 1995, Ser. No. 08/464,582, filed Jun. 5, 1995, Ser. No. 08/463,191, filed Jun. 5, 1995, Ser. No. 08/462,837, filed Jun. 5, 1995, Ser. No. 08/486,853, filed Jun. 5, 1995, Ser. No. 08/486,857, filed Jun. 5, 1995, Ser. No. 08/486,859, filed Jun. 5, 1995, Ser. No. 08/462,513, filed Jun. 5, 1995, Ser. No. 08/724,752, filed Oct. 2, 1996, and Ser. No. 08/759,620, filed Dec. 3, 1996 and U.S. Pat.

Nos. 6,162,963, 6,150,584, 6,114,598, 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. See also Mendez et al. Nature Genetics 15:146-156 (1997) and Green and Jakobovits J. Exp. Med. 188:483-495 (1998). See also European Patent No., EP 0 463151 B1, grant published Jun. 12, 1996, International Patent Application No., WO 94/02602, published Feb. 3, 1994, International Patent Application No., WO 96/34096, published Oct. 31, 1996, WO 98/24893, published Jun. 11, 1998, WO 00/76310, published Dec. 21, 2000, WO 03/47336. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.

In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more V.sub.H genes, one or more D.sub.H genes, one or more J.sub.H genes, a mu constant region, and a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Pat. No. 5,545,807 to Surani et al. and U.S. Pat. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299, and 6,255,458 each to Lonberg and Kay, U.S. Pat. Nos. 5,591,669 and 6,023.010 to Krimpenfort and Berns, U.S. Pat. Nos. 5,612,205, 5,721,367, and 5,789,215 to Berns et al., and U.S. Pat. No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. patent application Ser. No. 07/574,748, filed Aug. 29, 1990, Ser. No. 07/575,962, filed Aug. 31, 1990, Ser. No. 07/810,279, filed Dec. 17, 1991, Ser. No. 07/853,408, filed Mar. 18, 1992, Ser. No. 07/904,068, filed Jun. 23, 1992, Ser. No. 07/990,860, filed Dec. 16, 1992, Ser. No. 08/053,131, filed Apr. 26, 1993, Ser. No. 08/096,762, filed Jul. 22, 1993, Ser. No. 08/155,301, filed Nov. 18, 1993, Ser. No. 08/161,739, filed Dec. 3, 1993, Ser. No. 08/165,699, filed Dec. 10, 1993, Ser. No. 08/209,741, filed Mar. 9, 1994, the disclosures of which are hereby incorporated by reference. See also European Patent No. 0 546 073 B 1, International Patent Application Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Pat. No. 5,981,175, the disclosures of which are hereby incorporated by reference in their entirety. See further Taylor et al., 1992, Chen et al., 1993, Tuaillon et al., 1993, Choi et al., 1993, Lonberg et al., (1994), Taylor et al., (1994), and Tuaillon et al., (1995), Fishwild et al., (1996), the disclosures of which are hereby incorporated by reference in their entirety.

Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. See European Patent Application Nos. 773 288 and 843 961, the disclosures of which are hereby incorporated by reference.Xenerex Biosciences is developing a technology for the potential generation of human antibodies. In this technology, SCID mice are reconstituted with human lymphatic cells, e.g., B and/or T cells. Mice are then immunized with an antigen and can generate an immune response against the antigen. See U.S. Pat. Nos. 5,476,996, 5,698,767, and 5,958,765.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. While chimeric antibodies have a human constant region and a murine variable region, it is expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in chronic or multi-dose utilizations of the antibody. Thus, it would be desirable to provide fully human antibodies against EGFRvIII in order to vitiate concerns and/or effects of HAMA or HACA response.

Cytotoxicity mediated by CDH19/CD3 bispecific antibody constructs can be measured in various ways. Effector cells can be e.g. stimulated enriched (human) CD8 positive T cells or unstimulated (human) peripheral blood mononuclear cells (PBMC). If the target cells are of macaque origin or express or are transfected with macaque CDH19, the effector cells should also be of macaque origin such as a macaque T cell line, e.g. 4119LnPx. The target cells should express (at least the extracellular domain of) CDH19, e.g. human or macaque CDH19. Target cells can be a cell line (such as CHO) which is stably or transiently transfected with CDH19, e.g. human or macaque CDH19. Alternatively, the target cells can be a CDH19 positive natural expresser cell line, such as the human myeloma cell line CHL-1 or Colo-699. Usually EC50-values are expected to be lower with target cell lines expressing higher levels of CDH19on the cell surface. The effector to target cell (E:T) ratio is usually about 10:1, but can also vary. Cytotoxic activity of CDH19/CD3 bispecific antibody constructs can be measured in an 51-chromium release assay (incubation time of about 18 hours) or in a in a FACS-based cytotoxicity assay (incubation time of about 48 hours). Modifications of the assay incubation time (cytotoxic reaction) are also possible. Other methods of measuring cytotoxicity are well-known to the skilled person and comprise MTT or MTS assays, ATP-based assays including bioluminescent assays, the sulforhodamine B (SRB) assay, WST assay, clonogenic assay and the ECIS technology.

The cytotoxic activity mediated by CDH19/CD3 bispecific antibody constructs of the present invention is preferably measured in a cell-based cytotoxicity assay. It is represented by the EC_{50} value, which corresponds to the half maximal effective concentration (concentration of the antibody construct which induces a cytotoxic response halfway between the baseline and maximum). Preferably, the EC_{50} value of the CDH19/CD3 bispecific antibody constructs is ≤20.000 pg/ml, more preferably ≤5000 pg/ml, even more preferably ≤1000 pg/ml, even more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml.

Any of the above given EC_{50} values can be combined with any one of the indicated scenarios of a cell-based cytotoxicity assay. For example, when (human) CD8 positive T cells or a macaque T cell line are used as effector cells, the EC_{50} value of the CDH19/CD3 bispecific antibody construct is preferably ≤1000 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml. If in this assay the target cells are (human or macaque) CDH19 transfected cells such as CHO cells, the EC_{50} value of the CDH19/CD3 bispecific antibody construct is preferably ≤150 pg/ml, more preferably ≤100 pg/ml, even more preferably ≤50 pg/ml, even more preferably ≤30 pg/ml, even more preferably ≤10 pg/ml, and most preferably ≤5 pg/ml.
If the target cells are a CDH19positive natural expresser cell line, then the EC_{50} value is preferably ≤350 pg/ml, more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤200 pg/ml, even more preferably ≤100 pg/ml, even more preferably ≤150 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower.
When (human) PBMCs are used as effector cells, the EC_{50} value of the CDH19/CD3 bispecific antibody construct is preferably ≤1000 pg/ml, more preferably ≤750 pg/ml, more preferably ≤500 pg/ml, even more preferably ≤350 pg/ml, even more preferably ≤320 pg/ml, even more preferably ≤250 pg/ml, even more preferably ≤100 pg/ml, and most preferably ≤50 pg/ml, or lower.

The difference in cytotoxic activity between the monomeric and the dimeric isoform of individual CDH19/CD3 bispecific antibody constructs is referred to as "potency gap". This potency gap can e.g. be calculated as ratio between EC_{50} values of the molecule's monomeric and dimeric form. Potency gaps of the CDH19/CD3 bispecific antibody constructs of the present invention are preferably ≤5, more preferably ≤4, even more preferably ≤3, even more preferably ≤2 and most preferably ≤1.

The antibody construct of the invention is a fusion protein comprising at least two binding domains, with or without peptide linkers (spacer peptides). Among the suitable peptide linkers are those described in U.S. Patents 4,751,180 and 4,935,233 or WO 88/09344.

Another method for preparing oligomeric antibody constuct derivatives involves use of a leucine zipper. Leucine zipper domains are peptides that promote oligomerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz *et al.*, 1988, *Science* 240:1759), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble oligomeric proteins are described in PCT application WO 94/10308, and the leucine zipper derived from lung surfactant protein D (SPD) described in Hoppe *et al.*, 1994, *FEBS Letters* 344:191, hereby incorporated by reference. The use of a modified leucine zipper that allows for stable trimerization of a heterologous protein fused thereto is described in Fanslow *et al.*, 1994, *Semin. Immunol.* 6:267-78. In one approach, recombinant fusion proteins comprising CDH19 antibody fragment or derivative fused to a leucine zipper peptide are expressed in suitable host cells, and the soluble oligomeric CDH19 antibody fragments or derivatives that form are recovered from the culture supernatant.

Covalent modifications of antigen binding proteins are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antigen binding protein are introduced into the molecule by reacting specific amino acid residues of the antigen binding protein with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.
Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues

include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using ^{125}I or ^{131}I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

Derivatization with bifunctional agents is useful for crosslinking antigen binding proteins to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, 1983, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the antigen binding protein included within the scope of this invention comprises altering the glycosylation pattern of the protein. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (*e.g.*, the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

Addition of glycosylation sites to the antigen binding protein is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the antigen binding protein is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, 1981, *CRC Crit. Rev. Biochem.*, pp. 259-306.

Removal of carbohydrate moieties present on the starting antigen binding protein may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin *et al.*, 1987, *Arch. Biochem. Biophys.* 259:52 and by Edge *et al.*, 1981, *Anal. Biochem.* 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura *et al.*, 1987, *Meth. Enzymol.* 138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin *et al.*, 1982, *J. Biol. Chem.* 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

Another type of covalent modification of the antigen binding protein comprises linking the antigen binding protein to various non-proteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antigen binding protein to facilitate the addition of polymers such as PEG.

In some embodiments, the covalent modification of the antigen binding proteins of the invention comprises the addition of one or more labels.

The term "labelling group" means any detectable label. Examples of suitable labelling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{89}Zr, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent groups (*e.g.*, FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labelling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b) magnetic labels (*e.g.,* magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (*e.g.* horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*, leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labelling group is coupled to the antigen binding protein *via* spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

Specific labels include optical dyes, including, but not limited to, chromophores, phosphors and fluorophores, with the latter being specific in many instances. Fluorophores can be either “small molecule” fluores, or proteinaceous fluores.

By “fluorescent label” is meant any molecule that may be detected *via* its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland, hereby expressly incorporated by reference.

Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie *et al.*, 1994, *Science* 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession

Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, *Biotechniques* 24:462-471; Heim *et al.*, 1996, *Curr. Biol.* 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki *et al.*, 1993, *J. Immunol.* 150:5408-5417), β galactosidase (Nolan *et al.*, 1988, *Proc. Natl. Acad. Sci. U.S.A.* 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5292658, 5418155, 5683888, 5741668, 5777079, 5804387, 5874304, 5876995, 5925558). All of the above-cited references are expressly incorporated herein by reference.

The antibody construct of the invention may also comprise additional domains, which e.g. are helpful in the isolation of the molecule or relate to an adapted pharmacokinetic profile of the molecule.

Domains helpful for the isolation of an antibody construct may be elected from peptide motives or secondarily introduced moieties, which can be captured in an isolation method, e.g. an isolation column. A non-limiting embodiments of such additional domains comprise peptide motives known as Myc-tag, HAT-tag, HA-tag, TAP-tag, GST-tag, chitin binding domain (CBD-tag), maltose binding protein (MBP-tag), Flag-tag, Strep-tag and variants thereof (e.g. StrepII-tag) and His-tag. All herein disclosed antibody constructs characterized by the identified CDRs are preferred to comprise a His-tag domain, which is generally known as a repeat of consecutive His residues in the amino acid sequence of a molecule, preferably of six His residues.

As described in appended example 2 a broad number of CDH19 specific binder has been characterized with respect to identified binding characteristics and those binders were grouped into five different bins, which refers to five different subgroups of CDH19 specific binding domains. Accordingly, in one embodiment the antibody construct of the invention the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

(a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222, CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252, CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-

H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,

CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,

CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,

CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,

CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131,

CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID NO: 1170,

CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335, CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337, CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID NO: 1339,

CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348, CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350, CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID NO: 1352, and

CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361, CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363, CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID NO: 1365,

CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426, CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428, CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID NO: 1430,

CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439, CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441, CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168, CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170, CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID NO: 2172,

which all characterize binding domains for CDH19 grouped into bin 1;

(b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300, CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 928, CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 929, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 942, CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 943, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 937, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938, CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 919, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935, CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936, CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933, CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 934, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930, CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131,

CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932,

CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010, CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012, CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID NO: 1014,

CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023, CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025, CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID NO: 1027,

CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036, CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038, CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID NO: 1040,

CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075, CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077, CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID NO: 1079,

CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101, CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103, CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID NO: 1105,

CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114, CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116, CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID NO: 1118,

CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244, CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246, CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID NO: 1248,

CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257, CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259, CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID NO: 1261,

CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270, CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,

CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285, CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287, and

CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID NO: 1300,

CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID NO: 1652,

CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID NO: 1665,

CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895, CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897, CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID NO: 1899,

CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908, CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910, CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID NO: 1912,

CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID NO: 1934, CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936, CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID NO: 1938,

CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947, CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949, CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960,

CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962, CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973, CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975, CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986, CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988, CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999, CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001, CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012, CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014, CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055,

which all characterize binding domains for CDH19 grouped into bin 2;

(c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288, CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288, CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,

CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997, CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999, CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID NO: 1001,

CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049, CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051, CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID NO: 1053,

CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088,

CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090, CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID NO: 1092,

CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609, CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611, CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID NO: 1613,

CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622, CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624, CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID NO: 1626,

CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635, CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637, CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID NO: 1639,

CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674, CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676, CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID NO: 1678,

CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687, CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689, CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID NO: 1691,

CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700, CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702, CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID NO: 1704,

CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713, CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715, CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID NO: 1717,

CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726, CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728, CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID NO: 1730,

CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739, CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741,

CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,
CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754, CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,
CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID NO: 1769, and
CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID NO: 1925,
which all characterize binding domains for CDH19 grouped into bin 3;

(d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174, CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11, CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198, CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-

H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240, CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330, CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939,

CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 940,
CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,
CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,
CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971, CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973, CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975,

CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062, CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064, CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID NO: 1066,
CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140, CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142, CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID NO: 1144,
CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153, CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155, CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID NO: 1157,
CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179, CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181, CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID NO: 1183,

CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID NO: 1313,

CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID NO: 1326,

CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374, CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376, CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID NO: 1378,

CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387, CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389, CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID NO: 1391,

CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID NO: 1400, CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402, CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413,

CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415, CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID NO: 1417,

CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778, CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780, CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID NO: 1782,

CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791, CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793, CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID NO: 1795,

CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804, CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806, CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817, CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819, CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID NO: 1821,

CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830, CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832, CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID NO: 1834,

CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843, CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845, CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID NO: 1847,

CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856, CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858, CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID NO: 1860,

CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869, CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in SEQ ID NO: 1871, CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID NO: 1873,

CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882, CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884,

CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066, CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID NO: 2081,

CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID NO: 2094,

CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129, CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as depicted in SEQ ID NO: 2159,

CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID

NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194, CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196, CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207, CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209, CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID NO: 2211

which all characterize binding domains for CDH19 grouped into bin 4; and

(e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2 as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246, CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2 as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113, CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280, CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282, CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276, CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984, CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986, CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988, CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583, CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585, CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID NO: 1587, and

CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596, CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598, CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID NO: 1600,

which all characterize binding domains for CDH19 grouped into bin 5.

In a further embodiment of the antibody construct of the invention the first binding domain comprises a VH region selected from the group consisting of VH regions

(a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174,
grouped into bin 1;

(b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057,
grouped into bin 2;

(c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003, SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID NO: 1628, SEQ ID NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID NO: 1771, and SEQ ID NO: 1927,
grouped into bin 3;

(d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386, SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466,

SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213,
grouped into bin 4; and

(e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350, SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602,
grouped into bin 5.

In another embodiment of the antibody construct of the invention the first binding domain comprises a VL region selected from the group consisting of VL regions

(a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356, SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176,
grouped into bin 1;

(b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592, SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID

NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059,

grouped into bin 2;

(c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929,

grouped into bin 3;

(d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786, SEQ ID NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID

NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215,
grouped into bin 4; and

(e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406, SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604,
grouped into bin 5.

The invention further provides an embodiment of the antibody construct of the invention, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of:

(1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID NOs: 2174+2176,
all pairs grouped into bin 1;

(2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID

NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059, all pairs grouped into bin 2;

(3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929, all pairs grouped into bin 3;

(4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380,+1382 SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID

NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215,
all pairs grouped into bin 4; and

(5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID NOs: 1602+1604,
all pairs grouped into bin 5.

In a further embodiment of the invention the antibody construct is in a format selected from the group consisting of $(scFv)_2$, $(single\ domain\ mAb)_2$, scFv-single domain mAb, diabodies and oligomers thereof.

In a preferred embodiment the first binding domain comprises an amino acid selected from the group consisting of

(a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449 and SEQ ID NO: 2178,
all binders grouped into bin 1;

(b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID NO: 2048, and SEQ ID NO: 2061,
all binders grouped into bin 2;

(c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931,
all binders grouped into bin 3;

(d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID NO: 2217,
all binders grouped into bin 4; and

(e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606, grouped into bin 5;.

In one aspect of the invention, the second binding domain is capable of binding to to human CD3 and to macaque CD3, preferably to human CD3 epsilon and to macaque CD3 epsilon. Additionally or alternatively, the second binding domain is capable of binding to *Callithrix jacchus*, *Saguinus oedipus* and/or *Saimiri sciureus* CD3 epsilon. According to these embodiments, one or both binding domains of the antibody construct of the invention are preferably cross-species specific for members of the mammalian order of primates. Cross-species specific CD3 binding domains are, for example, described in WO 2008/119567.

It is particularly preferred for the antibody construct of the present invention that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from:

(a) CDR-L1 as depicted in SEQ ID NO: 27 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 28 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 29 of WO 2008/119567;

(b) CDR-L1 as depicted in SEQ ID NO: 117 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 118 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 119 of WO 2008/119567; and

(c) CDR-L1 as depicted in SEQ ID NO: 153 of WO 2008/119567, CDR-L2 as depicted in SEQ ID NO: 154 of WO 2008/119567 and CDR-L3 as depicted in SEQ ID NO: 155 of WO 2008/119567.

In an alternatively preferred embodiment of the antibody construct of the present invention, the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VH region comprising CDR-H 1, CDR-H2 and CDR-H3 selected from:

(a) CDR-H1 as depicted in SEQ ID NO: 12 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 13 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 14 of WO 2008/119567;

(b) CDR-H1 as depicted in SEQ ID NO: 30 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 31 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 32 of WO 2008/119567;

(c) CDR-H1 as depicted in SEQ ID NO: 48 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 49 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 50 of WO 2008/119567;

(d) CDR-H1 as depicted in SEQ ID NO: 66 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 67 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 68 of WO 2008/119567;

(e) CDR-H1 as depicted in SEQ ID NO: 84 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 85 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 86 of WO 2008/119567;

(f) CDR-H1 as depicted in SEQ ID NO: 102 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 103 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 104 of WO 2008/119567;

(g) CDR-H1 as depicted in SEQ ID NO: 120 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 121 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 122 of WO 2008/119567;

(h) CDR-H1 as depicted in SEQ ID NO: 138 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 139 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 140 of WO 2008/119567;

(i) CDR-H1 as depicted in SEQ ID NO: 156 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 157 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 158 of WO 2008/119567; and

(j) CDR-H1 as depicted in SEQ ID NO: 174 of WO 2008/119567, CDR-H2 as depicted in SEQ ID NO: 175 of WO 2008/119567 and CDR-H3 as depicted in SEQ ID NO: 176 of WO 2008/119567.

It is further preferred for the antibody construct of the present invention that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VL region selected from the group consisting of a VL region as depicted in SEQ ID NO: 35, 39, 125, 129, 161 or 165 of WO 2008/119567.

It is alternatively preferred that the second binding domain capable of binding to the T cell CD3 receptor complex comprises a VH region selected from the group consisting of a VH region as depicted in SEQ ID NO: 15, 19, 33, 37, 51, 55, 69, 73, 87, 91, 105, 109, 123, 127, 141, 145, 159, 163, 177 or 181 of WO 2008/119567.

More preferably, the antibody construct of the present invention is characterized by the second binding domain capable of binding to the T cell CD3 receptor complex comprising a VL region and a VH region selected from the group consisting of:

(a) a VL region as depicted in SEQ ID NO: 17 or 21 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 15 or 19 of WO 2008/119567;

(b) a VL region as depicted in SEQ ID NO: 35 or 39 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 33 or 37 of WO 2008/119567;

(c) a VL region as depicted in SEQ ID NO: 53 or 57 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 51 or 55 of WO 2008/119567;

(d) a VL region as depicted in SEQ ID NO: 71 or 75 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 69 or 73 of WO 2008/119567;

(e) a VL region as depicted in SEQ ID NO: 89 or 93 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 87 or 91 of WO 2008/119567;

(f) a VL region as depicted in SEQ ID NO: 107 or 111 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 105 or 109 of WO 2008/119567;

(g) a VL region as depicted in SEQ ID NO: 125 or 129 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 123 or 127 of WO 2008/119567;

(h) a VL region as depicted in SEQ ID NO: 143 or 147 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 141 or 145 of WO 2008/119567;

(i) a VL region as depicted in SEQ ID NO: 161 or 165 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 159 or 163 of WO 2008/119567; and

(j) a VL region as depicted in SEQ ID NO: 179 or 183 of WO 2008/119567 and a VH region as depicted in SEQ ID NO: 177 or 181 of WO 2008/119567.

According to a preferred embodiment of the antibody construct of the present invention, in particular the second binding domain capable of binding to the T cell CD3 receptor complex, the pairs of VH-regions and VL-regions are in the format of a single chain antibody (scFv). The VH and VL regions are arranged in the order VH-VL or VL-VH. It is preferred that the

VH-region is positioned N-terminally to a linker sequence. The VL-region is positioned C-terminally of the linker sequence.

A preferred embodiment of the above described antibody construct of the present invention is characterized by the second binding domain capable of binding to the T cell CD3 receptor complex comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 23, 25, 41, 43, 59, 61, 77, 79, 95, 97, 113, 115, 131, 133, 149, 151, 167, 169, 185 or 187 of WO 2008/119567.

In a preferred embodiment the antibody construct of the invention has an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 1450 and SEQ ID NO: 2179;

(b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID NO: 2049, and SEQ ID NO: 2062;

(c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;

(d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID NO: 1841, SEQ ID NO: 1854, SEQ ID

NO: 1867, SEQ ID NO: 1880, SEQ ID NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and

(e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

The invention further provides a nucleic acid sequence encoding an antibody construct of the invention.

Furthermore, the invention provides a vector comprising a nucleic acid sequence of the invention. Moreover, the invention provides a host cell transformed or transfected with the nucleic acid sequence of the invention.

In a further embodiment the invention provides a process for the production of a antibody construct of the invention, said process comprising culturing a host cell of the invention under conditions allowing the expression of the antibody construct of the invention and recovering the produced antibody construct from the culture.

Moreover, the invention provides a pharmaceutical composition comprising an antibody construct of the invention or produced according to the process of the invention

The formulations described herein are useful as pharmaceutical compositions in the treatment, amelioration and/or prevention of the pathological medical condition as described herein in a patient in need thereof. The term "treatment" refers to both therapeutic treatment and prophylactic or preventative measures. Treatment includes the application or administration of the formulation to the body, an isolated tissue, or cell from a patient who has a disease/disorder, a symptom of a disease/disorder, or a predisposition toward a disease/disorder, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve, or affect the disease, the symptom of the disease, or the predisposition toward the disease.

Those "in need of treatment" include those already with the disorder, as well as those in which the disorder is to be prevented. The term "disease" is any condition that would benefit from treatment with the protein formulation described herein. This includes chronic and acute disorders or diseases including those pathological conditions that predispose the mammal to the disease in question. Non-limiting examples of diseases/disorders to be treated herein include proliferative disease, a tumorous disease, or an immunological disorder.

In some embodiments, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of one or a plurality of the antibody construct of the invention together with a pharmaceutically effective diluents, carrier, solubilizer, emulsifier, preservative, and/or adjuvant. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

Preferably, formulation materials are nontoxic to recipients at the dosages and concentrations employed. In specific embodiments, pharmaceutical compositions comprising a therapeutically effective amount of an antibody construct of the invention.

In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine, proline, or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrins); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, preferably sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. See, REMINGTON'S PHARMACEUTICAL SCIENCES, 18" Edition, (A. R. Genrmo, ed.), 1990, Mack Publishing Company.

In certain embodiments, the optimal pharmaceutical composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format and desired dosage. See, for example, REMINGTON'S PHARMACEUTICAL SCIENCES, supra. In certain embodiments, such compositions may influence the physical state, stability, rate of in vivo release and rate of in vivo clearance of the antigen binding proteins of the invention. In certain embodiments, the primary vehicle or carrier in a pharmaceutical composition may be either aqueous or non-aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution or artificial cerebrospinal fluid, possibly supplemented with other materials common in compositions for parenteral administration. Neutral buffered saline or saline mixed with serum albumin are further exemplary vehicles. In specific embodiments, pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, and may further include sorbitol or a suitable substitute therefore. In certain embodiments of the invention, human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention compositions may be prepared for storage by mixing the selected composition having the desired degree of purity with optional formulation agents (REMINGTON'S PHARMACEUTICAL SCIENCES, supra) in the form of a lyophilized cake or an aqueous solution. Further, in certain embodiments, the human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention may be formulated as a lyophilizate using appropriate excipients such as sucrose.

The pharmaceutical compositions of the invention can be selected for parenteral delivery. Alternatively, the compositions may be selected for inhalation or for delivery through the digestive tract, such as orally. Preparation of such pharmaceutically acceptable compositions is within the skill of the art. The formulation components are present preferably in concentrations that are acceptable to the site of administration. In certain embodiments, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 8.

When parenteral administration is contemplated, the therapeutic compositions for use in this invention may be provided in the form of a pyrogen-free, parenterally acceptable aqueous solution comprising the desired human antibody or antigen binding fragment thereof of the invention or the antibody construct of the invention in a pharmaceutically acceptable vehicle. A particularly suitable vehicle for parenteral injection is sterile distilled water in which the antibody construct of the invention is formulated as a sterile, isotonic solution, properly preserved. In certain embodiments, the preparation can involve the formulation of the desired molecule with an agent, such as injectable microspheres, bio-erodible particles, polymeric compounds (such as polylactic acid or polyglycolic acid), beads or liposomes, that may provide controlled or sustained release of the product which can be delivered via depot injection. In certain embodiments, hyaluronic acid may also be used, having the effect of promoting sustained duration in the circulation. In certain embodiments, implantable drug delivery devices may be used to introduce the desired antigen binding protein.

Additional pharmaceutical compositions will be evident to those skilled in the art, including formulations involving h the antibody construct of the invention in sustained- or controlled-delivery formulations. Techniques for formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. See, for example, International Patent Application No. PCT/US93/00829, which is incorporated by reference and describes controlled release of porous polymeric microparticles for delivery of pharmaceutical compositions. Sustained-release preparations may include semipermeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides (as disclosed in U.S. Pat. No. 3,773,919 and European Patent Application Publication No. EP 058481, each of which is incorporated by reference), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman et al., 1983, Biopolymers 2:547-556), poly (2-hydroxyethyl-methacrylate) (Langer et al., 1981, J. Biomed. Mater. Res. 15:167-277 and Langer, 1982, Chem. Tech. 12:98-105), ethylene vinyl acetate (Langer et al., 1981, supra) or poly-D(-)-3-hydroxybutyric acid (European Patent Application Publication No. EP 133,988). Sustained release compositions may also include liposomes that can be prepared by any of several methods known in the art. See, e.g., Eppstein et al., 1985, Proc. Natl. Acad. Sci. U.S.A. 82:3688-3692; European Patent Application Publication Nos. EP 036,676; EP 088,046 and EP 143,949, incorporated by reference.

Pharmaceutical compositions used for in vivo administration are typically provided as sterile preparations. Sterilization can be accomplished by filtration through sterile filtration membranes. When the composition is lyophilized, sterilization using this method may be conducted either prior to or following lyophilization and reconstitution. Compositions for parenteral administration can be stored in lyophilized form or in a solution. Parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Aspects of the invention includes self-buffering antibody construct of the invention formulations, which can be used as pharmaceutical compositions, as described in international patent application WO 06138181A2 (PCT/US2006/022599), which is incorporated by reference in its entirety herein.

As discussed above, certain embodiments provide antibody construct of the invention protein compositions, particularly pharmaceutical compositions of the invention, that comprise, in addition to the antibody construct of the invention, one or more excipients such as those illustratively described in this section and elsewhere herein. Excipients can be used in the invention in this regard for a wide variety of purposes, such as adjusting physical, chemical, or biological properties of formulations, such as adjustment of viscosity, and or processes of the invention to improve effectiveness and or to stabilize such formulations and processes against degradation and spoilage due to, for instance, stresses that occur during manufacturing, shipping, storage, pre-use preparation, administration, and thereafter. A variety of expositions are available on protein stabilization and formulation materials and methods useful in this regard, such as Arakawa et al., "Solvent interactions in pharmaceutical formulations," Pharm Res. 8(3): 285-91 (1991); Kendrick et al., "Physical stabilization of proteins in aqueous solution," in: RATIONAL DESIGN OF STABLE PROTEIN FORMULATIONS: THEORY AND PRACTICE, Carpenter and Manning, eds. Pharmaceutical Biotechnology. 13: 61-84 (2002), and Randolph et al., "Surfactant-protein interactions," Pharm Biotechnol. 13: 159-75 (2002), each of which is herein incorporated by reference in its entirety, particularly in parts pertinent to excipients and processes of the same for self-buffering protein formulations in accordance with the current invention, especially as to protein pharmaceutical products and processes for veterinary and/or human medical uses.

Salts may be used in accordance with certain embodiments of the invention to, for example, adjust the ionic strength and/or the isotonicity of a formulation and/or to improve the solubility and/or physical stability of a protein or other ingredient of a composition in accordance with the invention.

As is well known, ions can stabilize the native state of proteins by binding to charged residues on the protein's surface and by shielding charged and polar groups in the protein and reducing the strength of their electrostatic interactions, attractive, and repulsive interactions. Ions also can stabilize the denatured state of a protein by binding to, in particular, the denatured peptide linkages (--CONH) of the protein. Furthermore, ionic interaction with charged and polar groups in a protein also can reduce intermolecular electrostatic interactions and, thereby, prevent or reduce protein aggregation and insolubility.

Ionic species differ significantly in their effects on proteins. A number of categorical rankings of ions and their effects on proteins have been developed that can be used in formulating pharmaceutical compositions in accordance with the invention. One example is the Hofmeister series, which ranks ionic and polar non-ionic solutes by their effect on the conformational stability of proteins in solution. Stabilizing solutes are referred to as "kosmotropic." Destabilizing solutes are referred to as “chaotropic.” Kosmotropes commonly are used at high concentrations (e.g., >1 molar ammonium sulfate) to precipitate proteins from solution ("salting-out"). Chaotropes commonly are used to denture and/or to solubilize proteins ("salting-in"). The relative effectiveness of ions to "salt-in" and "salt-out" defines their position in the Hofmeister series.

Free amino acids can be used in the antibody construct of the invention formulations in accordance with various embodiments of the invention as bulking agents, stabilizers, and antioxidants, as well as other standard uses. Lysine, proline, serine, and alanine can be used for stabilizing proteins in a formulation. Glycine is useful in lyophilization to ensure correct cake structure and properties. Arginine may be useful to inhibit protein aggregation, in both liquid and lyophilized formulations. Methionine is useful as an antioxidant.

Polyols include sugars, e.g., mannitol, sucrose, and sorbitol and polyhydric alcohols such as, for instance, glycerol and propylene glycol, and, for purposes of discussion herein, polyethylene glycol (PEG) and related substances. Polyols are kosmotropic. They are useful stabilizing agents in both liquid and lyophilized formulations to protect proteins from physical and chemical degradation processes. Polyols also are useful for adjusting the tonicity of formulations.

Among polyols useful in select embodiments of the invention is mannitol, commonly used to ensure structural stability of the cake in lyophilized formulations. It ensures structural stability to the cake. It is generally used with a lyoprotectant, e.g., sucrose. Sorbitol and sucrose are among preferred agents for adjusting tonicity and as stabilizers to protect against freeze-thaw stresses during transport or the preparation of bulks during the manufacturing process. Reducing sugars (which contain free aldehyde or ketone groups), such as glucose and lactose, can glycate surface lysine and arginine residues. Therefore, they generally are not among preferred polyols for use in accordance with the invention. In addition, sugars that form such reactive species, such as sucrose, which is hydrolyzed to fructose and glucose under acidic conditions, and consequently engenders glycation, also is not among preferred polyols of the invention in this regard. PEG is useful to stabilize proteins and as a cryoprotectant and can be used in the invention in this regard.

Embodiments of the antibody construct of the invention formulations further comprise surfactants. Protein molecules may be susceptible to adsorption on surfaces and to denaturation and consequent aggregation at air-liquid, solid-liquid, and liquid-liquid interfaces. These effects generally scale inversely with protein concentration. These deleterious interactions generally scale inversely with protein concentration and typically are exacerbated by physical agitation, such as that generated during the shipping and handling of a product.

Surfactants routinely are used to prevent, minimize, or reduce surface adsorption. Useful surfactants in the invention in this regard include polysorbate 20, polysorbate 80, other fatty acid esters of sorbitan polyethoxylates, and poloxamer 188.

Surfactants also are commonly used to control protein conformational stability. The use of surfactants in this regard is protein-specific since, any given surfactant typically will stabilize some proteins and destabilize others.

Polysorbates are susceptible to oxidative degradation and often, as supplied, contain sufficient quantities of peroxides to cause oxidation of protein residue side-chains, especially methionine. Consequently, polysorbates should be used carefully, and when used, should be employed at their lowest effective concentration. In this regard, polysorbates exemplify the general rule that excipients should be used in their lowest effective concentrations.

Embodiments of the antibody construct of the invention formulations further comprise one or more antioxidants. To some extent deleterious oxidation of proteins can be prevented in pharmaceutical formulations by maintaining proper levels of ambient oxygen and temperature and by avoiding exposure to light. Antioxidant excipients can be used as well to prevent oxidative degradation of proteins. Among useful antioxidants in this regard are reducing agents, oxygen/free-radical scavengers, and chelating agents. Antioxidants for use in therapeutic protein formulations in accordance with the invention preferably are water-soluble and maintain their activity throughout the shelf life of a product. EDTA is a preferred antioxidant in accordance with the invention in this regard.

Antioxidants can damage proteins. For instance, reducing agents, such as glutathione in particular, can disrupt intramolecular disulfide linkages. Thus, antioxidants for use in the invention are selected to, among other things, eliminate or sufficiently reduce the possibility of themselves damaging proteins in the formulation.

Formulations in accordance with the invention may include metal ions that are protein co-factors and that are necessary to form protein coordination complexes, such as zinc necessary to form certain insulin suspensions. Metal ions also can inhibit some processes that degrade proteins. However, metal ions also catalyze physical and chemical processes that degrade proteins.

Magnesium ions (10-120 mM) can be used to inhibit isomerization of aspartic acid to isoaspartic acid. Ca^{+2} ions (up to 100 mM) can increase the stability of human deoxyribonuclease. Mg^{+2}, Mn^{+2}, and Zn^{+2}, however, can destabilize rhDNase. Similarly, Ca^{+2} and Sr^{+2} can stabilize Factor VIII, it can be destabilized by Mg^{+2}, Mn^{+2} and Zn^{+2}, Cu^{+2} and Fe^{+2}, and its aggregation can be increased by Al^{+3} ions.

Embodiments of the antibody construct of the invention formulations further comprise one or more preservatives. Preservatives are necessary when developing multi-dose parenteral formulations that involve more than one extraction from the same container. Their primary function is to inhibit microbial growth and ensure product sterility throughout the shelf-life or term of use of the drug product. Commonly used preservatives include benzyl alcohol, phenol and m-cresol. Although preservatives have a long history of use with small-molecule parenterals, the development of protein formulations that includes preservatives can be challenging. Preservatives almost always have a destabilizing effect (aggregation) on proteins, and this has become a major factor in limiting their use in multi-dose protein formulations. To date, most protein drugs have been formulated for single-use only. However, when multi-dose formulations are possible, they have the added advantage of enabling patient convenience, and increased marketability. A good example is that of human growth hormone (hGH) where the development of preserved formulations has led to commercialization of more convenient, multi-use injection pen presentations. At least four such pen devices containing preserved formulations of hGH are currently available on the market. Norditropin (liquid, Novo Nordisk), Nutropin AQ (liquid, Genentech) & Genotropin (lyophilized--dual chamber cartridge, Pharmacia & Upjohn) contain phenol while Somatrope (Eli Lilly) is formulated with m-cresol. Several aspects need to be considered during the formulation and development of preserved dosage forms. The effective preservative concentration in the drug product must be optimized. This requires testing a given preservative in the dosage form with concentration ranges that confer anti-microbial effectiveness without compromising protein stability.

As might be expected, development of liquid formulations containing preservatives are more challenging than lyophilized formulations. Freeze-dried products can be lyophilized without the preservative and reconstituted with a preservative containing diluent at the time of use. This shortens the time for which a preservative is in contact with the protein, significantly minimizing the associated stability risks. With liquid formulations, preservative effectiveness and stability should be maintained over the entire product shelf-life (about 18 to 24 months). An important point to note is that preservative effectiveness should be demonstrated in the final formulation containing the active drug and all excipient components.

The antibody construct of the invention generally will be designed for specific routes and methods of administration, for specific administration dosages and frequencies of administration, for specific treatments of specific diseases, with ranges of bio-availability and persistence, among other things. Formulations thus may be designed in accordance with the invention for delivery by any suitable route, including but not limited to orally, aurally, opthalmically, rectally, and vaginally, and by parenteral routes, including intravenous and intraarterial injection, intramuscular injection, and subcutaneous injection.

Once the pharmaceutical composition has been formulated, it may be stored in sterile vials as a solution, suspension, gel, emulsion, solid, crystal, or as a dehydrated or lyophilized powder. Such formulations may be stored either in a ready-to-use form or in a form (e.g., lyophilized) that is reconstituted prior to administration. The invention also provides kits for producing a single-dose administration unit. The kits of the invention may each contain both a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments of this invention, kits containing single and multi-chambered pre-filled syringes (e.g., liquid syringes and lyosyringes) are provided. The therapeutically effective amount of an antibody construct of the invention protein-containing pharmaceutical composition to be employed will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment will vary depending, in part, upon the molecule delivered, the indication for which the antibody construct of the invention is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician may titer the dosage and modify the route of administration to obtain the optimal therapeutic effect. A typical dosage may range from about 0.1 μg/kg to up to about 30 mg/kg or more, depending on the factors mentioned above. In specific embodiments, the dosage may range from 1.0 µg/kg up to about 20 mg/kg, optionally from 10 µg/kg up to about 10 mg/kg or from 100 µg/kg up to about 5 mg/kg.

A therapeutic effective amount of an antibody construct of the invention preferably results in a decrease in severity of disease symptoms, in increase in frequency or duration of disease symptom-free periods or a prevention of impairment or disability due to the disease affliction. For treating CDH19-expressing tumors, a therapeutically effective amount of the antibody construct of the invention, e.g. an anti-CDH19/CD3 antibody construct, preferably inhibits cell growth or tumor growth by at least about 20%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90% relative to untreated patients. The ability of a compound to inhibit tumor growth may be evaluated in an animal model predictive of efficacy in human tumors.

Pharmaceutical compositions may be administered using a medical device. Examples of medical devices for administering pharmaceutical compositions are described in U.S. Patent Nos. 4,475,196; 4,439,196; 4,447,224; 4,447, 233; 4,486,194; 4,487,603; 4,596,556; 4,790,824; 4,941,880; 5,064,413; 5,312,335; 5,312,335; 5,383,851; and 5,399,163, all incorporated by reference herein.

In one embodiment the invention provides the antibody construct of the invention or produced according to the process of the invention for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

The invention also provides a method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject in need thereof the antibody construct of the invention or produced according to the process of the invention.

In a preferred embodiment method of use of the invention the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.

In a further embodiment, the invention provides a kit comprising an antibody construct of the invention, or produced according to the process of the invention, a vector of the invention, and/or a host cell of the invention.

It should be understood that the inventions herein are not limited to particular methodology, protocols, or reagents, as such can vary. The discussion and examples provided herein are presented for the purpose of describing particular embodiments only and are not intended to limit the scope of the present invention, which is defined solely by the claims.

All publications and patents cited throughout the text of this specification (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention. To the extent the material incorporated by reference contradicts or is inconsistent with this specification, the specification will supersede any such material.

Examples:

The following examples are provided for the purpose of illustrating specific embodiments or features of the present invention. These examples should not be construed as to limit the scope of this invention. The examples are included for purposes of illustration, and the present invention is limited only by the claims.

Example 1 – Fully human monoclonal antibodies against CDH19

1.1 Immunization:

Fully human antibodies to Cadherin-19 (CDH19) were generated using XENOMOUSE® technology, transgenic mice engineered to express diverse repertoires of fully human IgGκ and IgGλ antibodies of the corresponding isotype. (United States Patent Nos. 6,114,598; 6,162,963; 6,833,268; 7,049,426; 7,064,244, which are incorporated herein by reference in their entirety; Green *et al.*, 1994, *Nature Genetics* 7:13-21; Mendez *et al.*, 1997, *Nature Genetics* 15:146-156; Green and Jakobovitis, 1998, *J. Ex. Med.* 188:483-495; Kellermann and Green, *Current Opinion in Biotechnology* 13, 593-597, 2002).

Mice were immunized with multiple forms of Cadherin-19 immunogen, including: (1) full length human and cynomologous ("cyno") monkey cadherin-19, (2) secreted Cadherin-19 ecto-domain (amino acids 1-596), and (3) a truncated membrane bound form of human cadherin-19 (amino acids 1-624). Mice were immunized over a period of 8 to 10 weeks with a range of 16-18 boosts.

Sera were collected at approximately 5 and 9 weeks after the first injection and specific titers were determined by FACs staining of recombinant Cadherin-19 receptor transiently expressed on CHO-S cells. A total of 37 animals were identified with specific immune responses, these animals were pooled into 3 groups and advanced to antibody generation.

1.2 Preparation of Monoclonal Antibodies

Animals exhibiting suitable titers were identified, and lymphocytes were obtained from draining lymph nodes and, if necessary, pooled for each cohort. Lymphocytes were dissociated from lymphoid tissue by grinding in a suitable medium (for example, Dulbecco's Modified Eagle Medium (DMEM); obtainable from Invitrogen, Carlsbad, CA) to release the cells from the tissues, and suspended in DMEM. B cells were selected and/or expanded using standard methods, and fused with suitable fusion partner using techniques that were known in the art.

After several days of culture, the hybridoma supernatants were collected and subjected to screening assays as detailed in the examples below, including confirmation of binding to human and cynomologous monkey as well as the ability to kill cell lines in secondary antibody-drug conjugate Bioassays. Hybridoma lines that were identified to have the binding and functional properties of interest were then further selected and subjected to standard cloning and subcloning techniques. Clonal lines were expanded in vitro, and the secreted human antibodies obtained for analysis and V gene sequencing was performed.

1.3 Selection of Cadherin-19 receptor specific binding antibodies by FMAT

After 14 days of culture, hybridoma supernatants were screened for CDH19-specific monoclonal antibodies by Fluorometric Microvolume Assay Technology (FMAT) (Applied Biosystems, Foster City, CA). The supernatants were screened against adherent CHO cells transiently transfected with human Cadherin-19 and counter screened against CHO cells transiently transfected with the same expression plasmid that did not contain the Cadherin-19 gene.

After multiple screening campaigns, a panel of 1570 anti-Cadherin-19 binding hybridoma lines were identified and advanced to further characterization assays.

Example 2 – Assessment of Fully human monoclonal antibodies against CDH19

2.1 Additional Binding Characterization by Flow Cytometry (FACs)

FACS binding assays were performed to evaluate the binding of the anti-Cadherin-19 receptor specific antibodies to endogenous Cadherin-19 receptor expressed on the CHL-1 tumor cell lines. In addition, cross-reactive binding to murine and cynomologous monkey Cadherin-19 orthologues was also evaluated by FACs using recombinant forms of the various receptors transiently expressed on 293T cells.

FACs assays were performed by incubating hybridoma supernatants with 10,000 to 25,000 cells in PBS/2%Fetal bovine serum/2mM Calcium Chloride at 4°C for one hour followed by two washes with PBS/2%Fetal bovine serum/2mM Calcium Chloride. Cells were then treated with florochrome-labeled secondary antibodies at 4°C followed by one wash. The cells were resuspended in 50µl of PBS/2%FBS and antibody binding was analyzed using a FACSCalibur™ instrument.

2.2 Antibody drug conjugate screening of fully human antibodies derived from XenoMouse® hybridomas

Cell killing through antibody drug conjugates requires the delivery of the conjugate into a cell through internalization and the catabolism of the drug-conjugate into a form that it is toxic to the cell. To identify antibodies with these properties, CDH19-positive cell lines (Colo-699 or CHL-1) were seeded at low cell densities and allowed to adhere overnight in a 384 well plate. XENOMOUSE® hybridoma samples containing fully human anti-CDH19 antibodies were then added to these cells in the presence of a high concentration of a goat anti-human Fc monovalent Fab conjugated with DM1 (DM1-Fab) at a relatively low drug-antibody ratio (DAR) (~1.3). The cells were incubated for 96 hours at 37°C and 5% CO_2 in the presence of the antibody samples and the DM1-Fab. At the end of this time, the cell viability was assessed using the CellTiter-Glo® Luminescent Cell Viability reagent (Promega) according to manufacturer's recommendations.

An example of the cell viability data with the Colo-699 cells is shown in Figure 1 and Figure 2. The antibodies capable of delivering the DM1-Fab to the cells and inhibiting the cell growth read out with a lower luminescent signal (RLU). The top antibodies of interest from this screen are observed in the lower left corner of Fig. 1 and are denoted as open circles. These antibodies were taken forward into a cell viability assay on CHL-1 cells. The average cell viability data from the CHL-1 assay is plotted against the average cell viability data from the Colo-699 assay (Fig. 2). The antibodies that had activity on both the Colo-699 and the CHL-1 cells are denoted as open circles on the left-hand side of the Figure 2.

This assay was run concurrently with the FACs antibody binding assay above (2.2), and the results from these two studies were used to select the antibodies for further characterization. In total, 1570 antibodies were run through these cell based viability assays and approximately 44 antibodies were selected on the bases of *in vitro* cell killing and/or antibody binding for sub-cloning,V gene sequencing and expressed in recombinant form for further characterization assays as described below.

These 44 antibodies were again assayed as in Example 2 and 19 antibodies were selected that contained unique sequences. Of these 19 antibodies, 18 antibodies were analyzed and their properties characterized in Table 2 below. The data in this table was generated using FACs binding on recombinant human and cynomologous CDH-19, +/- Calcium ($Ca^{+2)}$ binding data on 293/CDH-19 transfectants, binding to endogenous CDH-19 on CHL-1 and Colo699 tumor cells and competition with the antibody designated as 4A9 in the table. These experiments provided the further characterizations for the grouping of these antibodies into 5 groups or bins.

Table 2 –Binning of Lead panel using Antibody Binding Information

Bin ID	LMR Sequence/ Ab ID	Clone ID	Bin Characteristics
1	13589	4A9	High Endogenous binding, Calcium insensitive, sequence clustered, moderate cyno complete 4A9 competitor
	13591	4F7	
2	13885	19B5	High Endogenous binding, Calcium insensitive, sequence clustered, Good cyno, partial 4A9 competitor
	13880	25F8	
	13882	26D1	
	13881	26F12=27B3	
	13878	16H2=20D3=23E7	
	13879	22D1	
3	13877	22G10	High Endogenous binding, moderate 293 binding, Calcium insensitive, 2 sequence clusters, moderate cyno, partial 4A9 competitor, 22G10 best binder in bin.
	13874	17H8=23B6=28D10	
	13883	25G10	
	13875	16C1	
4	13590	4B10	Low Endogenous and recombinant binding, Calcium sensitive, sequence diverse group, comparable cyno, No 4A9 competition
	13586	4F3	
	13592	4A2	
	13884	23A10	
	13588	2G6	
5	13876	16A4	Best endogenous binder, moderate recombinant binder, calcium insensitive, very weak cyno, No 4A9 competition.

Of these 18 antibodies. 8 antibodies were selected for further analysis of their epitope binding as described below. At least one representative antibody from each bin was selected for further analysis.

Example 3 – Epitope Prediction

Epitope Prediction by 4A9 Antibody Competition and by Human/Mouse Cadherin-19 Chimeras

A 4A9 binding competition method was developed to identify antibodies that compete with 4A9 binding. In 96-well V-bottom plates (Sarstedt #82.1583.001), 50,000 transiently transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by one wash with PBS/2%FBS. 25µl of 5µg/ml Alexa647-labelled 4A9 was then added to each well and the plates incubated for 1 hour at 4°C. Cells were then washed two times and the amount of cell associated Alexa647-labelled 4A9 was quantitated by flow cytometry.

The experiments included negative controls consisting of PBS/2%FBS only. The average signal observed in these negative control experiments was adopted as the maximum possible signal for the assay. Antibodies were compared to this maximum signal and a percent inhibition was calculated for each well (% Inhibition = (1-(FL4 Geomean with the anti-CDH19 antibodies/Maximum FL4 Geomean signal)).

Domain binding was determined by flow cytometry as above on 293T cells transiently transfected with plasmids consisting of single or dual human CDH19 cadherin repeat domain replacements into the mouse Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native human or murine CDH19 leader sequences and a Flag tag (SEQ ID NO: 968). The experiment included assaying the anti-CDH19 antibodies against mouse Cadherin19 to determine suitability for binning on these human/mouse chimeras.

The data from these experiments are presented in the Table below entitled as follows:

Table 3 – Calcium Sensitive Binding and Epitope Prediction Summary

					Hu EC1-5	Hu EC1	Hu EC1-2	Hu EC2	Hu EC2-3	Hu EC3	Hu EC4-5	Hu EC5	Mu EC1-5	
Clone ID	Ab ID	Bin	Ca2+ Sensitive Binding	Competes with 4A9 (13589)	A	B	C	D	E	F	G	H	I	Predicted Epitope Region
4A9	13589	1	No	Yes	+	+	+	-	-	-	-	-	-	44-141
	14056	1	No	Yes	+	+	+	-	-	-	-	-	-	
	14057	1	No	Yes	+	+	+	-	-	-	-	-	-	
25F8	13880	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14094	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14096	2	No	Yes	+	+	+	-	-	-	-	-	-	
26D1	13882	2	No	Yes	+	+	+	-	-	-	-	-	-	
	14088	2	No	Yes	+	+	+	-	-	-	-	-	-	
17H8	13874	3	No	Yes	+	+	+	-	-	-	-	-	-	
	14045	3	No	Yes	+	+	+	-	-	-	-	-	-	
	14048	3	No	Yes	+	+	+	-	-	-	-	-	-	
4A2	13592	4	Yes	No	+	-	-	-	+	+	-	-	-	250-364
	14026	4	Yes	No	+	-	-	-	+	+	-	-	-	
4B10	13590	4	Yes	No	+	-	-	-	+	+	-	-	-	
	14055	4	Yes	No	+	-	-	-	+	+	-	-	-	
	14054	4	Yes	No	+	-	-	-	+	+	-	-	-	
2G6	13588	4	Yes	No	+	+	+	+	+	+	+	+	+	un-assignable
	14304	4	Yes	No	+	+	+	+	+	+	+	+	+	
	14039	4	Yes	No	+	+	+	+	+	+	+	+	+	
16A4	13876	5	No	No	+	+	+	-	-	-	-	-	-	Unassigned complex epitope
	14071	5	No	No	+	+	+	-	-	-	-	-	-	
Rat anti-FLAG					+	+	+	+	+	+	+	+	+	

Legend Table 3

Human and/or murine chimera constructs

A = huCDH19(44-772) (see SEQ ID NO: 944)
B = huCDH19(44-141)::muCDH19(140-770) (see SEQ ID NO: 952)
C = huCDH19(44-249)::muCDH19(248-770) (see SEQ ID NO: 954)
D = muCDH19(44-139)::huCDH19(142-249)::muCDH19(248-770) (see SEQ ID NO: 956)
E = muCDH19(44-139)::huCDH19(142-364)::muCDH19(363-770) (see SEQ ID NO: 958)
F = muCDH19(44-247)::huCDH19(250-364)::muCDH19(363-770) (see SEQ ID NO: 960)
G = muCDH19(44-362)::huCDH19(365-772) (see SEQ ID NO: 962)
H = muCDH19(44-461)::huCDH19(464-772) (see SEQ ID NO: 964)
I = muCDH19(44-770) (see SEQ ID NO: 966)

Epitope Prediction by Human/Chicken Cadherin-19 Chimeras

Domain binding was determined by flow cytometry on 293T cells transiently transfected with plasmids consisting of single human CDH19 cadherin repeat domain replacements into the chicken Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native human or chicken CDH19 leader sequences and a Flag tag. The experiment included assaying a subset of anti-CDH19 antibodies against chicken Cadherin19 to determine suitability for binning on these human/chicken chimeras.

The following binding assay was completed in presence of 2mM CaCl2. In 96-well V-bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The experiments included mock transfected controls. The data from these experiments are presented in the Table below, n.d. = not determined.

Table4 – Antibody Bin C Epitope Prediction Summary

			Hu EC1-5	Ck EC1-5	Hu EC1	Hu EC2	Hu EC3	Hu EC5	
Clone ID	**Ab. ID**	**Bin**	**A**	**J**	**K**	**L**	**M**	**O**	**Predicted Epitope Region**
4A9	**13589**	**1**	+	-	+	-	-	-	**44-141 Bin A**
26F12	**13881**	**2**	+	-	+	-	-	-	
25F8	**14096**	**2**	+	-	+	-	-	-	
26D1	**13882**	**2**	+	-	+	-	-	-	
17H8	**13874**	**3**	+	-	+	-	-	-	
16A4	**14071**	**5**	+	-	+	-	-	-	
4A2	**13592**	**4**	+	-	-	-	+	-	**250-364 Bin B**
4B10	**13590**	**4**	+	-	-	-	+	-	
2G6	**13588**	**4**	+	-	-	-	+	-	
23A10	**14077**	**4**	+	-	-	-	+	-	
Rat anti-FLAG			+	+	+	+	+	+	**control**
Positive Binding (+) **Negative Binding (-)**									

Legend Table 4

Human and/or chicken chimera constructs

A = huCDH19(44-772) (see SEQ ID NO: 944)
J = ckCDH19(44-776) (see SEQ ID NO: 1451)
K = huCDH19(44-141)::ckCDH19(142-776) (see SEQ ID NO: 1452)
L = ckCDH19(44-141)::huCDH19(142-249)::ckCDH19(250-776) (see SEQ ID NO: 1453)
M = ckCDH19(44-249)::huCDH19(250-364)::ckCDH19(365-776) (see SEQ ID NO: 1454)
N = ckCDH19(44-364)::huCDH19(365-463)::ckCDH19(469-776) (see SEQ ID NO: 1455)
O = ckCDH19(44-468)::huCDH19(464-772) (see SEQ ID NO: 1456)

Epitope Prediction by macaque/dog or rat/macaque Cadherin-19 Chimeras

Domain binding was determined by flow cytometry on 293T cells transiently transfected with plasmids consisting of rhesus macaque CDH19 cadherin repeat domain 1 or segments domain 1 (designated EC1a, EC1b, EC1c) replacements into the dog Cadherin19 backbone, or rat CDH19 cadherin repeat domain 2 replacement into the rhesus Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native rhesus or canine CDH19 leader sequences and a Flag tag. The experiment included assaying a subset of anti-CDH19 antibodies against dog, rat and macaque Cadherin19 to determine suitability for binning on these macaque/dog and rat/rhesus chimeras.

The following binding assay was completed in presence of 2mM CaCl2. In 96-well V-bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The experiments included mock transfected controls. The data from these experiments are presented in the Table below, n.d. = not determined.

Table 5 – Antibody BinA Epitope prediction Summary

			Rh EC1-5	Ca EC1-5	rh EC1	rh EC1a	rh EC1b	ra EC2	Ra EC1-5	
Clone ID	**Ab. ID**	**Bin**	**P**	**Q**	**R**	**S**	**T**	**V**	**W**	**Predicted Epitope Region**
4A9	13589	1	+	-	+	-	-	-	-	44-141 Bin A.1
26F12	13881	2	+	-	+	+	+	-	-	44-141 Bin A.2 (44-114)
25F8	14096	2	+	-	+	+	+	-	-	
26D1	13882	2	+	-	+	+	+	-	-	
17H8	13874	3	+	-	+	+	-	-	-	44-141 Bin A.3 (44-65)
16A4	14071	5	+	-	+	+	-	n.d.	+	
4A2	13592	4	+	-	n.d.	n.d.	n.d.	n.d.	+	250-364 Bin B
4B10	13590	4	+	+	n.d.	n.d.	n.d.	n.d.	+	
2G6	13588	4	+	+	n.d.	n.d.	n.d.	n.d.	+	
23A10	14077	4	+	+	n.d.	n.d.	n.d.	n.d.	+	
Rat anti-FLAG			+	+	+	+	+	+	+	
Positive Binding (+) Negative Binding (-) Not Determined (n.d.)										

Legend Table 5

Rhesus macaque, dog, and/or rat chimera constructs

P = rhCDH19(44-772) (see SEQ ID NO: 1457)

Q = caCDH19(44-770) (see SEQ ID NO: 1458)

R = rhCDH19(44-141)::caCDH19(141-770) (see SEQ ID NO: 1459)

S = rhCDH19(44-65)::caCDH19(65-770) (see SEQ ID NO: 1460)

T = caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770) (see SEQ ID NO: 1461)

U = caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770) (see SEQ ID NO: 1462)

V = rhCDH19(44-141)::raCDH19(140-247)::rhCDH19(250-772) (see SEQ ID NO: 1463)

W = raCDH19(44-770) (see SEQ ID NO: 1464)

The data summarized in table 5 allowed for segregating the binder of Bin A 44-141 into the following subgroups:

Bin A.1 44-141
Bin A.2 44-141 (44-114)
Bin A.3 44-141 (44-65)

Epitope Prediction by rat/mouse or human/mouse Cadherin-19 Chimeras

Domain binding was determined by flow cytometry on 293T cells transiently transfected with plasmids consisting of rat CDH19 cadherin repeat domain 3 substitutions (designated EC3a, EC3b) or human CDH19 cadherin repeat domain 3 substitution (designated EC3c) into the mouse Cadherin19 backbone cloned into the pTT5 expression vector immediately preceded by native mouse CDH19 leader sequence and a Flag tag. The experiment included assaying a subset of anti-CDH19 antibodies against human, rat and mouse Cadherin19 to determine suitability for binning on these rat/mouse and human/mouse chimeras.

The following binding assay was completed in presence of 2mM CaCl2. In 96-well V-bottom plates (Costar 3897), 50,000 transiently transfected 293T cells were incubated with 5ug/ml of purified anti-CDH19 antibodies for 1hr at 4oC followed by two washes with PBS/2%FBS. 50µl of 5µg/ml Alexa647-labelled anti-human IgG secondary antibody (Jackson Immuno 109-605-098) and 2ug/ml 7AAD (Sigma A9400) was then added to each well and the plates incubated for 15 minutes at 4oC. Cells were then washed one time and the amount of cell associated Alexa647-labelled Ab was quantitated by flow cytometry. The experiments included mock transfected controls. The data from these experiments are presented in the Table below, n.d. = not determined.

Table 6 – Antibody Bin B Epitope Prediction Summary

			Hu EC1-5	Mo EC1-5	Ra EC1-5	Ra EC3c	Ra EC3b	Hu EC3a	
Clone ID	**Ab. ID**	**Bin**	**A**	**I**	**W**	**X**	**Y**	**Z**	**Predicted Epitope Region**
4A9	**13589**	**1**	+	-	-	n.d.	n.d.	n.d.	**44-141 Bin A**
26F12	**13881**	**2**	+	-	-	n.d.	n.d.	n.d.	
25F8	**14096**	**2**	+	-	-	n.d.	n.d.	n.d.	
26D1	**13882**	**2**	+	-	-	n.d.	n.d.	n.d.	
17H8	**13874**	**3**	+	-	-	n.d.	n.d.	n.d.	
16A4	**14071**	**5**	+	-	+	n.d.	n.d.	n.d.	
4A2	**13592**	**4**	+	-	+	+	-	-	**250-364 (324-327) Bin B.2**
4B10	**13590**	**4**	+	-	+	+	-	-	
2G6	**13588**	**4**	+	+	+	+	+	+	**250-364 Bin B.1**
23A10	**14077**	**4**	+	+	+	n.d.	n.d.	n.d.	
Rat anti-FLAG			+	+	+	+	+	+	**control**
Positive Binding (+) **Negative Binding (-)** **Not Determined (n.d.)**									

Legend Table 6

Rat/mouse or human/mouse chimera constructs

A = huCDH19(44-772) (see SEQ ID NO: 944)

I = muCDH19(44-770) (see SEQ ID NO: 966)

W = raCDH19(44-770) (see SEQ ID NO: 1464)

X = muCDH19(44-323)::raCDH19(324-327)::muCDH19(328-770) (see SEQ ID NO: 1465)

Y = muCDH19(44-770)::raCDH19(290,299,308) (see SEQ ID NO: 1466)

Z = muCDH19(44-770)::huCDH19(271) (see SEQ ID NO: 1467)

The data summarized in table 6 allowed for segregating the binder of Bin B 250-364 into the following subgroups:

Bin B.1 250-364

Bin B.2 250-364 (324-327)) by rodent numeration as referenced in table 6, corresponding to residues (326-329) within human and macaque CDH19.

Example 4 - Hotspot/Covariant Mutants

A total of 18 antibodies were analyzed for potential hotspots and covariance violations. The designed variants (shown below) outline amino acid substitutions capable of reducing and/or avoiding isomerization, deamidation, oxidation, covariance violations, and the like. The 80 engineered variants together with the 15 parental antibodies, thus totaling 95 sequences, were taken forward to the cloning, expression, and purification processes. Site-directed mutagenesis was performed on the engineered variants in a 96-well format. The parental antibodies and engineered variants were expressed by high throughput transient transfection in HEK 293-6E cells, purified using a modified AKTA auto-sampler and assayed for activity and biophysical characteristics. The 3 parental antibodies that had either free (unpaired) Cys or N-glycosylation site were not taken forward in this process. Those were replaced with the engineered version of the parental antibodies. The designed variants outline amino acid substitutions capable of reducing and/or avoiding isomerization, deamidation, oxidation, covariance violations, immunogenicity and the like. It will be appreciated that these variant sequences are examples of engineered antibodies within the meaning of the present application but single point and/or multiple point mutations can be combined in any combinatorial manner in order to arrive at a final desired antigen binding molecule or antibody.

Example 5 – CDH19 mRNA expression pattern

RNA was extracted from individual patient tissues representing tumor (>70% tumor content by cell count) or normal (0% tumor content by cell count). Individual tissues were homogenized using TisssueLyzer (Qiagen, Valencia, CA) and total RNA extracted and purified by the *mir*Vana total RNA extraction kit (Life Technologies, Foster City, CA). RNA quality and quantity checked by NanoDrop (NanoDrop, Wilmington, DE) spectrophotometer readings and Bioanalyzer RNA profiling (Agilient Technologies, Santa Clara, CA). RNA was DNAse treated with DNA-*free* kit (Life Technologies, Foster City, CA) and reverse transcribed according to manufacturer's specifications using random hexamers in the High Capacity cDNA Reverse Transcription Kit (Life Technologies, Foster City, CA). Quantitative Real Time Polymerase Chain Reaction (qRT-PCR) was performed on cDNA using primers to CDH19, probeset Hs00253534_m1, (Life Technologies, Foster City, CA) or the housekeeping gene human *ACTB* (primers CCT GGC ACC CAG CAC AA; GCC GAT CCA CAC GGA GTA CT; probe ATC AAG ATC ATT GCT CCT CCT GAG CG). 10 µL qRT-PCR reaction components; 1.0 ng/µL cDNA, 2xUniversal PCR Master Mix (Life Technologies, Foster City, CA), gene expression assay (ACTB; 75 nM primers, 150 nM probe. EPOR; 300 nM primers, 250 nM probe) Following the qRT-PCR amplification program: (1) activation at 50°C for 2 min; (2) denaturation at 95°C for 10 min; (3) amplification 40 cycles at 95°C for 15 s and 60°C for 1 min with fluorescence capture at each step (ABI PRISM 7900HT Sequence Detection Systems, Applied Biosystems). Threshold cycle values (C_T) were determined, using Sequence Detector software version 2.3 (Applied Biosystems) and transformed to $2^{-\Delta CT}$ for relative expression of CDH19 specific transcript to ACTB. The results are shown in

Figure 3. Of 54 unique metastatic and primary melanoma samples, the majority can be seen to overexpress CDH19 mRNA relative to the expression in samples from normal tissue.

Example 6 – CDH19 protein expression

Expression of CDH19 protein was analyzed in human tumor samples by IHC and the results are shown in Figure 4. Samples were fixed in 10% neutral buffered formalin for 24 hours, dehydrated and paraffin embedded. 4 µm sections were cut. Sections were deparaffinized first and then heated in DIVA Decloaker solution (Biocare) for 40 minutes for antigen retrieval. Remaining IHC steps were performed at room temperature in a DAKO Autostainer. Sections were incubated for 10 minutes with Peroxidazed 1 (Biocare) to block endogenous peroxidase, followed by incubation for 10 minutes with background sniper (Biocare) to reduce nonspecific background. Section were incubated for 60 minutes with CDH19 antibody (Novo Biologicals, Catalog #H00028513-B01P) at 5 µg/ml, then incubated for 30 minutes with Envision+ HRP anti-mouse polymer (DAKO), followed by DAB+ (DAKO) for 5 minutes. Sections were counterstained with hematoxylin (DAKO) approximately for 1 minute. CDH19 expression could be detected in 62% of tumors examined (staining intensity ≥1+ in 101 of 162 samples). 51% of the tumor samples demonstrated medium to high expression (staining intensity of 2+ to 3+ in 83 of162 samples). CDH19 showed dense and distinct membrane staining in many samples, although in some tumors heterogeneity was noted.

Example 7 – Selection of model cell lines

Tumor cell lines were analyzed by flow cytometry and IHC to identify model systems with CDH19 expression similar to human tumors. . Human anti-huCDH19 IgG4 antibody 4A2 was purified directly from hybridoma conditioned media. For flow cytometry, $2x10^5$ cells were incubated with 200 nM of the CDH19 4A2 antibody that was conjugated to PE at a 1:1 ratio. The incubation and subsequent wash steps were performed in the presence of 1.2 mM calcium. A tube of QuantiBRITE PE lyophilized beads with four levels of PE (BD, cat# 340495) was simultaneously prepared according to the manufacturer’s instructions. The beads were analyzed by flow cytometry to generate a standard curve. The PE median values obtained from the melanoma lines after FACS analysis were then calibrated against the standard curve to calculate the antibodies bound per cell (ABC), which provides an estimate of the number of receptors on each cell. IHC was performed as described in Example 6 and the results are provided in Figure 5. The melanoma cell line CHL-1 expresses about 10,000 CDH19 molecules on the cell surface, while Colo699 cells express about 5,000 receptors.

Both cell lines represent tumors with medium to high expression levels based on IHC. Expression in A2058 is very low, while LOX cells do not express any detectable CDH19 protein.

Example 8

Bispecific binding and interspecies cross-reactivity

For confirmation of binding to human CDH19 and to human and macaque CD3, bispecific antibodies were tested by flow cytometry using indicated cell lines. L1.2 transfected with human CDH19, the human melanoma cell lines CHL-1 and A2058 expressing native human CDH19, CD3-expressing human T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) and the CD3-expressing macaque T cell line 4119LnPx (Knappe A, et al., Blood, 2000, 95, 3256-3261) were used as antigen positive cell lines. Moreover, untransfected L1.2 cells were used as negative control.

For flow cytometry 200,000 cells of the respective cell lines were incubated for 30 min on ice with 50 µl of purified bispecific antibody at a concentration of 5 µg/ml. The cells were washed twice in PBS/2% FCS and binding of the constructs was detected with a murine PentaHis antibody (Qiagen; diluted 1:20 in 50 µl PBS/2% FCS). After washing, bound PentaHis antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS/2% FCS. Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

The CDH19/CD3 bispecific antibodies stained L1.2 cells transfected with human CDH19, the human CDH19-expressing melanoma cell lines CHL-1 and A2058 as well as human and macaque T cells. Moreover, there was no staining of untransfected L1.2 cells (see Figure 6).

Example 9

Cytotoxic activity

FACS-based cytotoxicity assay with unstimulated human PBMC

Isolation of effector cells

Human peripheral blood mononuclear cells (PBMC) were prepared by Ficoll density gradient centrifugation from enriched lymphocyte preparations (e.g. buffy coats), a side product of blood banks collecting blood for transfusions. Buffy coats were supplied by a local blood bank and PBMC were prepared on the same day of blood collection. After Ficoll density centrifugation and extensive washes with Dulbecco's PBS (Gibco), remaining erythrocytes were removed from PBMC via incubation with erythrocyte lysis buffer (155 mM NH_4Cl, 10 mM $KHCO_3$, 100 µM EDTA). Platelets were removed via the supernatant upon centrifugation of PBMC at 100 x g. Remaining lymphocytes mainly encompass B and T lymphocytes, NK cells and monocytes. PBMC were kept in culture at 37°C/5% CO_2 in RPMI medium (Gibco) with 10% FCS (Gibco).

Depletion of $CD14^+$ and $CD56^+$ cells

For depletion of $CD14^+$ cells, human CD14 MicroBeads (Milteny Biotec, MACS, #130-050-201) were used, for depletion of NK cells human CD56 MicroBeads (MACS, #130-050-401). PBMC were counted and centrifuged for 10 min at room temperature with 300 x g. The supernatant was discarded and the cell pellet resuspended in MACS isolation buffer [80 µL/ 10^7 cells; PBS (Invitrogen, #20012-043), 0.5% (v/v) FBS (Gibco, #10270-106), 2 mM EDTA (Sigma-Aldrich, #E-6511)]. CD14 MicroBeads and CD56 MicroBeads (20 µL/10^7 cells) were added and incubated for 15 min at 4 - 8°C. The cells were washed with MACS isolation buffer (1 - 2 mL/10^7 cells). After centrifugation (see above), supernatant was discarded and cells resuspended in MACS isolation buffer (500 µL/10^8 cells). CD14/CD56 negative cells were then isolated using LS Columns (Miltenyi Biotec, #130-042-401). PBMC w/o CD14+/CD56+ cells were cultured in RPMI complete medium i.e. RPMI1640 (Biochrom AG, #FG1215) supplemented with 10% FBS (Biochrom AG, #S0115), 1x non-essential amino acids (Biochrom AG, #K0293), 10 mM Hepes buffer (Biochrom AG, #L1613), 1 mM sodium pyruvate (Biochrom AG, #L0473) and 100 U/mL penicillin/streptomycin (Biochrom AG, #A2213) at 37°C in an incubator until needed.

Target cell labeling

For the analysis of cell lysis in flow cytometry assays, the fluorescent membrane dye $DiOC_{18}$ (DiO) (Molecular Probes, #V22886) was used to label human CDH19- as target cells and distinguish them from effector cells. Briefly, cells were harvested, washed once with PBS and adjusted to 10^6 cell/mL in PBS containing 2 % (v/v) FBS and the membrane dye DiO (5 µL/10^6 cells). After incubation for 3 min at 37°C, cells were washed twice in complete RPMI medium and the cell number adjusted to 1.25 x 10^5 cells/mL. The vitality of cells was determined using 0.5 % (v/v) isotonic EosinG solution (Roth, #45380).

Flow cytometry based analysis

This assay was designed to quantify the lysis of human CDH19-transfected CHO cells in the presence of serial dilutions of CDH19 bispecific antibodies.

Equal volumes of DiO-labeled target cells and effector cells (i.e., PBMC w/o $CD14^+$ cells) were mixed, resulting in an E:T cell ratio of 10:1. 160 µL of this suspension were transferred to each well of a 96-well plate. 40 µL of serial dilutions of the CDH19 bispecific antibodies and a negative control bispecific (an CD3-based bispecific antibody recognizing an irrelevant target antigen) or RPMI complete medium as an additional negative control were added. The bispecific antibody-mediated cytotoxic reaction proceeded for 48 hours in a 7% CO_2 humidified incubator. Then cells were transferred to a new 96-well plate and loss of target cell membrane integrity was monitored by adding propidium iodide (PI) at a final concentration of 1 µg/mL. PI is a membrane impermeable dye that normally is excluded from viable cells, whereas dead cells take it up and become identifiable by fluorescent emission.

Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

Target cells were identified as DiO-positive cells. PI-negative target cells were classified as living target cells. Percentage of cytotoxicity was calculated according to the following formula:

$$\text{Cytotoxicity}\,[\%] = \frac{n_{\text{dead target cells}}}{n_{\text{target cells}}} \times 100$$

n = number of events

Using GraphPad Prism 5 software (Graph Pad Software, San Diego), the percentage of cytotoxicity was plotted against the corresponding bispecific antibody concentrations. Dose response curves were analyzed with the four parametric logistic regression models for evaluation of sigmoid dose response curves with fixed hill slope and EC50 values were calculated. The results are shown in Figure 7.

Example 10

In vivo tumor growth inhibition experiments

5 million Colo699 or CHL-1 tumor cells were admixed with 2.5 million freshly isolated peripheral blood mononuclear cells (PBMC) and injected subcutaneously in the left flank of female athymic nude mice on Day 0. The same day, mice were treated intraperitoneally with either CDH19 BiTE 2G6 or non-specific control BiTE (MEC14) at the indicated doses. Dosing continued daily for the first 10 days post-tumor inoculation.

Tumor volumes and body weights were measured twice per week using calipers and an analytical scale, respectively.

The results of experiments with Colo699 or CHL-1 tumor cells are shown in Figures 8 and 9.

Example 11

Cytotoxic activity

Imaging-based cytotoxicity assay with unstimulated human T-cells

Effector cells

Purified, naïve human T cells were obtained from AllCells LLC, Alameda, USA.

Image based analysis

This assay measures the T cell mediated lysis of melanoma cells. 3000 A2058 cells (CDH19 positive) or 2500 LOX IMVI cells (CDH19 negative) are combined with naïve human T cells in a 1:10 ratio in the wells of 384 well plates. After addition of a serial dilution of CDH19 targeting BiTE molecules as well as a negative control bispecific (a CD3-based bispecific antibody recognizing an irrelevant target antigen), the cells are incubated for 48 h at 37°C. Next, the samples are treated for 2 h with 30 µM Hoechst 33342 to stain the nuclei of all cells and 2 µM propidium iodide (PI) to identify dead cells.

Image acquisition and analysis is performed on a ThermoFisher ArrayScan with a 10x objective. Data for two channels is collected, at 386nm (Hoechst 33342) and at 549nm (propidium iodide).

Live cells are identified as Hoechst positive, PI negative events, dead cells as Hoechst positive, PI positive.

Percentage of cytotoxicity is determined as described in example 7. Representative results are shown in figure 10.

Example 12

Domain specificity and biochemical affinity determination of bi-specific binders

Purification of CDH19 sub-domains lacking post-translational modifications

A methionine initiation codon followed by nucleotide sequences encoding CDH19 sub-domain protein A= huCDH19(140-367 of SEQ ID NO:944), immediately preceding a G_4S linker and poly-Histidine tag was cloned into a suitable pET vector; whereas, nucleotides sequences encoding sub-domain proteins B= huCDH19(44-367 of SEQ ID NO:944) and C= rhCDH19(44-367 of SEQ ID NO:1457) were cloned into the pET-SUMO vector (Life Technologies, Invitrogen) by methods known in the art. Each was expressed in E coli, isolated from the soluble fraction and purified to homogeneity by metal chelate affinity chromatography, followed by anion exchange, and size exclusion chromatography in HEPES buffered saline, 3mM CaCl2, pH 8. Sub-domain protein A retained its linker and C terminal polyhistidine tag, but His-SUMO tags constituent to the N termini of proteins B and C were removed by digestion with SUMO protease (Life Technologies, Invitrogen) prior to anion exchange. All proteins were determined to have their expected molecular weight by ESI LC/MS. Proteins used in binding experiments described below were randomly biotinylated by typical methods known in the art.

Purification of CDH19 sub-domains with post-translational modifications

CDH19 sub-domain proteins D= huCDH19(44-367 of SEQ ID NO:944), and E= rhCDH19(44-367 of SEQ ID NO:1457) were generated by cloning nucleotide sequences encoding respective amino acid residues 1-367 into the pSURETech235b vector (Selexis) each immediately preceded a G_4S linker and poly-Histidine tag were cloned into the pSURETech235b vector (Selexis), transfected into CHO-S cells (Life Technologies, Invitrogen), and stable pools were generated following hygromycin selection by methods known in the art. Stable pools were expanded and conditioned media was collected after 7 days culture in serum free media. CM was exchanged by UF/DF with 5 diavolumes HEPES buffered saline plus $CaCl_2$ using a 1 sq ft 10K PES Pellicon 2 membrane and purified to homogeneity as described above. CDH19 sub-domain proteins D and E retained constituent linker and C terminal polyhistidine tags. N terminal sequence of each protein was determined to be G44 as expected, while ESI LC/MS of purified proteins as compared with same subjected to PNGase F digestion revealed the presence of both N- and O-linked glycans. Proteins used in binding experiments described below were randomly biotinylated by methods well known in the art.

Methods for binding affinity determination by Octet

The Octet RED384 biosensor was used to characterize kinetics and affinity of protein-protein interactions. Minimally biotinylated CDH19 domain target proteins A-E were bound to streptavidin tips in the machine while serial dilutions of analyte bi-specific binder proteins were made in 96-well or 384-well plates. Empirical target loading conditions were found from assay development to be 10-20 nM target concentration and loading for 600 seconds to give a 2nm signal. Binding experiments were performed by setting up a plate with 6-point (Tables 7-9) or 3-point (Table 10) 1:3 serial dilutions from 30nM starting concentrations of each analyte, with two reference wells per column having buffer alone. Octet Buffer: 10 mM HEPES (pH 7.5), 150 mM NaCl, +/- 1 mM $CaCl_2$, 0.13% Triton X-100 and 0.10 mg/ml BSA. Additional baseline and dissociation wells in the plate also contained buffer alone. The binding method was as follows: ForteBio Octet streptavidin tips were (1) soaked in buffer for 10 minutes; (2) transferred to the plate baseline wells and incubated for 5 minutes; (3) transferred to the target loading wells and incubated for 10 minutes; (4) transferred to the plate baseline wells and incubated for 5 minutes; (5) transferred to the sample wells and incubated for 5 minutes (Table 9) or 20 minutes (Tables 7, 8, 10); (6) transferred to the dissociation wells and incubated for 8.3 minutes (Table 9) or 1.5hr (Tables 7, 8, 10). Raw data was processed in the following manner: (a) reference tip curves were averaged and subtracted from sample curves; (b) the association and dissociation curves were isolated and aligned to the Y axis; (c) the association and dissociation interstep was aligned; (d) Savitzky-

Golay filtering was implemented to reduce the signal noise and (e) the resulting set of association and dissociation curves for each sample-target interaction were fit globally with a single 1:1 binding model to determine the measured values of the association (Ka) and dissociation (Kd) rate constants to calculate the equilibrium dissociation constant, KD.

Table 7 – Domain Specificity and Biochemical Affinity of Bi-specific Binders to Isolated human CDH19 Protein Domains Lacking Post Translational Modifications

		A = huCDH19(140-367) E coli			B = huCDH19(44-367) E coli			
Clone ID	Bispecific binder ID	KD (nM)	ka (M-1s-1)	kd (s-1)	KD (pM)	ka (M-1s-1)	kd (s-1)	Predicted Epitope Region
2G6	65254	< 0.03	3.37E+05	< 1.0E-05	< 0.04	2.31E+05	< 1.0E-05	250-364 Bin B.1
26F12	65251	(-)	(-)	(-)	0.20	3.86E+05	7.56E-05	44-114 Bin A.2
(-) negative binding, 20 min association, 1.5 hr dissociation								

Legend Table 7

Human CDH19 Protein domains lacking post translational modifications

A = E coli expressed huCDH19(140-367 of SEQ ID NO:944)

B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

The data summarized in table 7 confirmed CDH19 epitope region specificity of bi-specific binders and allowed for their relative affinity ranking.

Table 8 – Calcium Modulated Biochemical Affinity of Bi-specific Binders to Isolated Human and Macaque CDH19 Protein Domains Lacking Post Translational Modifications

		B = huCDH19(44-367) E coli			C = rhCDH19(44-367) E coli			
Clone ID, Epitope Bin	Bispecific binder ID	KD (nM)	ka (M-1s-1)	kd (s-1)	KD (nM)	ka (M-1s-1)	kd (s-1)	$CaCl_2$
2G6, Bin B.1	65254	< 0.06	1.66E+05	< 1.0E-05	< 0.03	2.97E+05	< 1.0 E-05	1mM
26F12, Bin A.2	65251	0.31	2.91E+05	9.0E-05	0.17	8.19E+05	1.36E-04	1mM
2G6, Bin B.1	65254	(-)	(-)	(-)	(-)	(-)	(-)	absent
26F12, Bin A.2	65251	2.56	1.21E+05	3.08E-04	1.16	4.68E+05	5.44E-04	absent
(-) negative binding, 20 min association, 1.5 hr dissociation								

Legend Table 8

CDH19 Protein domains lacking post translational modifications

B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

C = E coli expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 8 allowed determination of calcium sensitivity of bi-specific binders and for their relative affinity ranking. Data further suggests conformational epitopes, with Bin B.1 more dependent on CDH19/Ca2+ association than epitope Bin A.2

Table 9 – Biochemical Affinity of Bi-specific Binders to Isolated Human and Macaque CDH19 Protein Domains Lacking Post Translational Modifications

		B = huCDH19(44-367) E coli			C = rhCDH19(44-367) E coli		
Clone ID	Bispecific binder ID	KD (nM)	ka (M-1s-1)	kd (s-1)	KD (nM)	ka (M-1s-1)	kd (s-1)
2G6	65254	< 0.3	3.11E+05	< 1.0E-04	< 0.3	3.69E+05	< 1.0E-04
2G6.001	65254.001	< 0.4	2.21E+05	< 1.0E-04	< 0.4	2.42E+05	< 1.0E-04
2G6.003	65254.003	< 0.5	1.80E+05	< 1.0E-04	< 0.5	1.91E+05	< 1.0E-04
2G6.007	65254.007	0.57	2.95E+05	1.69E-04	0.55	3.53E+05	1.94E-04
4A2.002	65238.002	< 0.2	5.48E+05	< 1.0E-04	< 0.1	9.13E+05	< 1.0E-04
4B10.002	65240.002	< 0.2	5.02E+05	< 1.0E-04	< 0.1	7.48E+05	< 1.0E-04
4B10.003	65240.003	< 0.2	3.87E+05	< 1.0E-04	< 0.2	5.06E+05	< 1.0E-04
4B10.005	65240.005	< 0.2	4.41E+05	< 1.0E-04	< 0.2	6.00E+05	< 1.0E-04
19B5.1.002	65235.002	1.74	3.74E+05	6.49E-04	1.02	4.94E+05	5.02E-04
19B5.1.003	65235.003	2.44	3.09E+05	7.54E-04	1.63	3.97E+05	6.45E-04
23A10.001 (B1)	65237.001	< 0.4	2.55E+05	< 1.0E-04	< 0.3	3.16E+05	< 1.0E-04
23A10.001 (B2)	65237b.001	0.57	2.95E+05	1.69E-04	0.55	3.53E+05	1.94E-04
23A10.002	65237.002	< 0.3	2.86E+05	< 1.0E-04	< 0.3	3.61E+05	< 1.0E-04
26D1.1.003	65250.003	0.66	3.64E+05	2.41E-04	0.50	5.20E+05	2.62E-04
26D1.1.004	65250.004	1.08	3.39E+05	3.67E-04	0.65	4.66E+05	3.02E-04
26D1.1.005	65250.005	2.65	3.19E+05	8.44E-04	1.42	4.42E+05	6.25E-04
26F12.002	65251.002	0.97	3.25E+05	3.16E-04	1.70	4.33E+05	7.36E-04
26F12.004	65251.004	1.04	2.90E+05	3.00E-04	1.85	3.46E+05	6.38E-04
26F12.006	65251.006	3.96	4.10E+05	1.62E-03	5.39	5.95E+05	3.21E-03
26F12.008	65251.008	3.77	4.87E+05	1.84E-03	5.14	7.45E+05	3.83E-03
1mM $CaCl_2$, 5 min association, 8.3 min dissociation							

Legend Table 9

CDH19 Protein domains lacking post translational modifications

B = E coli expressed huCDH19(44-367 of SEQ ID NO:944)

C = E coli expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 9 allowed relative affinity ranking of bi-specific binders to human and non-human primate CDH19 domains lacking glycosylation.

Table 10 – Calcium Modulated Biochemical Affinity of Bi-specific Binders to Isolated Glycosylated Human and Macaque CDH19 Protein Domains

		D = huCDH19(44-367) CHO			E = rhCDH19(44-367) CHO			
Clone ID, Epitope Bin	**Bispecific binder ID**	**KD (nM)**	**ka (M-1s-1)**	**kd (s-1)**	**KD (nM)**	**ka (M-1s-1)**	**kd (s-1)**	**$CaCl_2$**
2G6, Bin B.1	**65254**	**< 0.041**	2.44E+05	< 1.0E-05	**< 0.031**	3.19E+05	< 1.0E-05	**1mM**
2G6.003, Bin B.1	**65254.003**	**< 0.099**	1.01E+05	< 1.0E-05	**< 0.09**	1.10E+05	< 1.0E-05	**1mM**
4B10.003, Bin B.2	**65240.003**	**0.24**	2.08E+05	4.91E-05	**0.29**	2.70E+05	7.88E-05	**1mM**
19B5.1.003, Bin A.2	**65235.003**	**1.01**	4.02E+05	4.07E-04	**0.27**	7.12E+05	1.93E-04	**1mM**
23A10.002, Bin B.1	**65237.002**	**< 0.036**	2.75E+05	< 1.0E-05	**< 0.035**	2.82E+05	< 1.0E-05	**1mM**
26D1.1.005, Bin A.2	**65250.005**	**0.97**	3.13E+05	3.04E-04	**0.37**	4.64E+05	1.74E-04	**1mM**
26F12, Bin A.2	**65251**	**0.28**	5.28E+05	1.50E-04	**0.22**	8.72E+05	1.94E-04	**1mM**
26F12.006, Bin A.2	**65251.006**	**1.24**	4.92E+05	6.07E-04	**1.13**	6.94E+05	7.86E-04	**1mM**
2G6, Bin B.1	**65254**	**(-)**	(-)	(-)	**(-)**	(-)	(-)	**absent**
2G6.003, Bin B.1	**65254.003**	**(-)**	(-)	(-)	**(-)**	(-)	(-)	**absent**
4B10.003, Bin B.2	**65240.003**	**(-)**	(-)	(-)	**(-)**	(-)	(-)	**absent**
19B5.1.003, Bin A.2	**65235.003**	**3.49**	2.90E+05	1.01E-03	**3.28**	2.65E+05	8.68E-04	**absent**
23A10.002, Bin B.1	**65237.002**	**(-)**	(-)	(-)	**(-)**	(-)	(-)	**absent**
26D1.1.005, Bin A.2	**65250.005**	**0.86**	4.12E+05	3.56E-04	**2.58**	3.26E+05	8.41E-04	**absent**
26F12, Bin A.2	**65251**	**1.91**	2.66E+05	5.09E-04	**1.09**	5.38E+05	5.88E-04	**absent**
26F12.006, Bin A.2	**65251.006**	**0.79**	6.29E+05	4.95E-04	**18.53**	3.36E+05	6.22E-03	**absent**
(-) negative binding, 20 min association, 1.5 hr dissociation								

Legend Table 10

Glycosylated CDH19 Protein domains

D =CHO expressed huCDH19(44-367 of SEQ ID NO:944)

E = CHO expressed rhCDH19(44-367 of SEQ ID NO:1457)

The data summarized in table 10 allowed determination of calcium sensitivity of bi-specific binders and relative affinity ranking toward glycosylated human and non-human primate CDH19 domain proteins. As compared to data in Table 8, affinities are similar to those with domains lacking post-translational modifications. Data further suggests conformational epitopes, with epitope Bins B.1 and B.2 being more dependent on CDH19/Ca2+ association than epitope Bin A.2

Example 13

Bispecific binding and interspecies cross-reactivity:

For confirmation of binding to human CDH19 and to human CD3, bispecific antibodies were tested by flow cytometry using indicated cell lines. HEK293 transfected with human CDH19 (see example 14) and CD3-expressing human T cell leukemia cell line HPB-ALL (DSMZ, Braunschweig, ACC483) were used as antigen positive cell lines.

For flow cytometry 200,000 cells of the respective cell lines were incubated for 30 min on ice with 100 µl of BiTE containing cell culture supernatant. The cells were washed twice in PBS/2% FCS and binding of the constructs was detected with a murine anti-CD3scFv antibody (3E5.A5, Amgen; diluted to 2 µg/ml PBS/2% FCS). After washing, bound anti-CD3scFv antibodies were detected with an Fc gamma-specific antibody (Dianova) conjugated to phycoerythrin, diluted 1:100 in PBS/2% FCS. Samples were measured by flow cytometry on a FACSCanto II instrument and analyzed by FACSDiva software (both from Becton Dickinson).

The CDH19/CD3 bispecific antibodies stained HEK293 cells transfected with human CDH19 as well as human and macaque T cells (see Figure 19).

Example 14

Cytotoxic activity

Chromium release assay with stimulated human T cells

Isolation of effector cells

A petri dish (145 mm diameter, Greiner bio-one GmbH, Kremsmünster) was coated with a commercially available anti-CD3 specific antibody (OKT3, Orthoclone) in a final concentration of 1 µg/ml for 1 hour at 37°C. Unbound protein was removed by one washing step with PBS. 3 – 5 x 10^7 human PBMC were added to the precoated petri dish in 120 ml of RPMI 1640 with stabilized glutamine / 10% FCS / IL-2 20 U/ml (Proleukin®, Chiron) and stimulated for 2 days. On the third day, the cells were collected and washed once with RPMI 1640. IL-2 was added to a final concentration of 20 U/ml and the cells were cultured again for one day in the same cell culture medium as above.

Depletion of $CD4^+$ and $CD56^+$ cells

$CD8^+$ cytotoxic T lymphocytes (CTLs) were enriched by depletion of $CD4^+$ T cells and $CD56^+$ NK cells using Dynal-Beads according to the manufacturer`s protocol.

^{51}Cr release based analysis

Human CDH19-transfected HEK293 target cells (production see example 14) were washed twice with PBS and labeled with 11.1 MBq ^{51}Cr in a final volume of 50 µl supplemented RPMI for 60 minutes at 37°C. Subsequently, the labeled target cells were washed 3 times with 5 ml RPMI and then used in the cytotoxicity assay. The assay was performed in a 96-well plate in a total volume of 200 µl supplemented RPMI with an E:T ratio of 10:1. A starting concentration of 0.1 – 1 µg/ml of purified bispecific antibody and threefold dilutions thereof were used. Incubation time for the assay was 18 hours. Cytotoxicity was determined as relative values of released chromium in the supernatant relative to the difference of maximum lysis (addition of Triton-X) and spontaneous lysis (without effector cells). All measurements were carried out in quadruplicates. Measurement of chromium activity in the supernatants was performed in a Wizard 3'' gamma counter (Perkin Elmer Life Sciences GmbH, Köln, Germany). Analysis of the results was carried out with Prism 6 for Windows (version 6.02, GraphPad Software Inc., San Diego, California, USA). EC50 values calculated by the analysis program from the sigmoidal dose response curves were used for comparison of cytotoxic activity (see Figure 20).

Example 15

Production and purification of BiTE antibodies

Standardized research scale production of CDH19 BiTE antibodies was performed in roller bottles. Harvested culture supernatant was subjected after filtration to two step BiTE antibody purification based either on immobilized metal affinity chromatography (IMAC) capture and subsequent size exclusion chromatography or Protein_A capture and subsequent size exclusion chromatography (SEC).

15.1 IMAC capture step of BiTE antibodies

Äkta® Explorer Systems (GE Healthcare) controlled by Unicorn® Software were used for chromatography. Immobilized metal affinity chromatography (IMAC) was performed using Fractogel EMD chelate® (Merck, Darmstadt) which was loaded with ZnCl2 according to the protocol provided by the manufacturer. The column was equilibrated with buffer A (20 mM sodium phosphate buffer , 0.1 M NaCl , 10 mM imidazole, pH 7.2) and the cell culture supernatant (1000 ml) applied to the column (10 ml packing volume) at a flow rate of 4 ml/min. The column was washed with buffer A to remove unbound sample. Bound protein was eluted using a two step gradient of buffer B (20 mM sodium phosphate buffer, 0.1 M NaCl, 0.5 M imidazole, pH 7.2) according to the following procedure:

Step 1: 10 % buffer B in 5 column volumes
Step 2: 100% buffer B in 5 column volumes

Eluted protein fractions from step 2 were pooled for further purification and concentrated to 3 ml final volume using Vivaspin (Sartorius-Stedim, Göttingen-Germany) centrifugation units with PES membran and a molecular weight cut-off of 10 kDa. All chemicals were of research grade and purchased from Merck (Darmstadt, Germany). Figure 11

15.2 Protein_A capture of BiTE antibodies

Äkta® Explorer Systems (GE Life Sciences) controlled by Unicorn® Software were used for chromatography. Affinity columns which containin beads with covalently bound Protein_A were used for the capture step. The column was equilibrated with equillibration buffer pH 7.4 and the cell culture supernatant applied. After washing the column with three column volumes of equillibration buffer to wash out unbound sample the bound BiTE antibodies were eluted by application of an elution buffer at pH 3.0. Eluted solution was immediately neutralized in pH by a Trishydroxymethylamine Tris solution pH 8.0 already contained in the fractionation tubes in the fraction collector.

Eluted protein fractions from step 2 were pooled for further purification and concentrated to 3 ml final volume using Vivaspin (Sartorius-Stedim, Göttingen-Germany) centrifugation units with PES membran and a molecular weight cut-off of 10 kDa. All chemicals were of research grade and purchased from Merck (Darmstadt, Germany). Figure 12

15.3 Size Exclusion Chromatography

Size exclusion chromatography was performed on a HiLoad 16/60 Superdex 200 prep grade column (GE Healthcare) equilibrated with SEC buffer (20 mM NaCl, 30 mM NaH2PO4, 100 mM L-Arginin, pH 7.0) at a flow rate of 1 ml/min. BiTE antibody monomer and dimer fractions were pooled and a 24% trehalose stock solution was added to reach a final trehalose concentration of 4%. Eluted protein samples were subjected to reducing SDS-PAGE and Anti His TAG Western Blot for analysis.

Protein pools were measured at 280 nm in polycarbonate cuvettes with 1 cm lightpath (Eppendorf, Hamburg-Germany) and protein concentration was calculated on the base of the Vector NTI sequence analysis software calculated factor for each protein.

BiTE monomer pools were adjusted to 250 µg/ml with additional BiTE formulation buffer (20 mM NaCl, 30 mM NaH2PO4, 100 mM L-Arginin, 4% Trehalose, pH 7.0). An amount of a minimum of 600 µg for each BiTE was taken and transferred for immediate protein analytics as described in example 16.

Remaining protein pools of BiTE antibody monomer and BiTE antibody dimer were aliquoted in 15 and 50 µg protein aliquots and shock frozen in liquid nitrogen. Further storage until usage was done in a -80°C freezer until analysis of biologic activity and affinity measurements. Figure 13.

The purity of isolated BiTE antibody monomer was determined by SDS-PAGE to be >95%. As expected, purified monomeric BiTE antibody appeared as protein bands in the molecular weight range of 54-56 kDa. Figure 14

Example 16

Protein Properties

The freshly prepared BiTE monomer solution generated in example 15 was applied to the following analytical methods

- High Performance Size Exclusion Chromatography (HP-SEC) of initially monomeric CDH19 BiTE antibodies after one week of incubation at 250 µg/ml and 37°C.
- BiTE monomer conversion of BiTE monomer to dimer by three freeze/thaw cycles followed by HP-SEC
- High resolution analytical cation exchange
- Hydrophobic interaction chromatography on a Sepharose Octyl FF matrix.
- Concentration to 2500 µg/ml followed by over night storage and turbidity measurement
- Aggregation temperature TA determination by heated Dynamic Light Scattering measurment

16.1 BiTE monomer conversion into dimer by incubation for 7 days

15 µg of the monomeric CDH19 BiTE antibody at a concentration of 250 µg/ml were incubated at 37°C for 7 days.

A high resolution SEC Column TSK Gel G3000 SWXL (Tosoh,Tokyo-Japan) was connected to an Äkta Purifier 10 FPLC (GE Lifesciences) equipped with an A905 Autosampler. Column equilibration and running buffer consisted of 100 mM KH_2PO_4 – 200 mM Na_2SO_4 adjusted to pH 6.6. After 7 days of incubation, the BiTE antibody solution (15 µg protein) was applied to the equilibrated column and elution was carried out at a flow rate of 0.75 ml/min at a maximum pressure of 7 MPa. The whole run was monitored at 280, 254 and 210 nm optical absorbance. Analysis was done by peak integration of the 210 nm signal recorded in the Äkta Unicorn software run evaluation sheet. Dimer content was calculated by dividing the area of the dimer peak by the total area of monomer plus dimer peak. Figure 15

16.2. BiTE monomer conversion into dimer by three freeze/thaw cycles

15 µg of monomeric BiTE antibody at 250 µg/ml were frozen at -80°C for 30 min followed by thawing for 30 min at room temperature. After three freeze/thaw cycles the dimer content was determined by HP-SEC as described in example 16.1. Figure 16

CDH19 BiTE CH19 2G6 302 x I2C SA21: 0.50 % Dimer content

16.3 High resolution analytical ion exchange chromatography

A 1 ml BioPro SP column manufactured by YMC (YMC Europe GmbH, Dinslaken-Germany) with sulphpropyl groups coupled to solid beads was connected to a Äkta Micro FPLC (GE Healthcare) device.

For column equilibration, sample dilution and washing a buffer consisting of 20 mM sodium dihydrogen phosphate and 30 mM sodium chloride adjusted with sodium hydroxide to a pH of 5.5 was used.

For elution a buffer consisting of 20 mM NaH2PO4 and 1000 mM NaCl adjusted with sodium hydroxide to a pH of 5.5 was used.

50 µg of BiTE antibody monomer were diluted with dilution buffer to 50 ml final volume.

After column equilibration 40 ml of the diluted protein solution was applied to the column followed by a wash step.

Elution was carried out by a steadily increasing gradient with elution buffer from zero to 100% over a total volume corresponding to 200 column volumes. The whole run was monitored at 280 (blue line) and 254 nm (red line) optical absorption.

Percentage of Main Peak was calculated by dividing the peak area of the main peak by the sum of peak area of all detected peaks followed by multiplication with a factor of 100. Figure 17

CDH19 BiTE CH19 2G6 302 x I2C SA21: 89.3 % Main Peak Percentage

16.4 Sepharose Octyl FF

Elution of monomeric BiTE antibodies was evaluated on a hydrophobic interaction chromatography C8 Sepharose Octyl FF column (GE Healthcare) with 1 ml gel volume.

50 µg of BiTE antibody monomeric protein was filled up with buffer (10 mM Citric acid – 75 mM Lysine x HCl – 4% Trehalose – pH 7.2) to a final volume of 300 µl. The column was connected to an Äkta Purifier 10 system (GE Healthcare). A 500 µl sample loop was connected to the system. The system and column were equilibrated with running buffer (10 mM Citric acid – 75 mM Lysine x HCl — 200 mM NaCl – pH 7.2).

The complete sampe was injected into the sample loop and the content of the sample loop was applied to the column. After sample injection a volume of 10 ml running buffer was applied to the column at a flow rate of 0,2 ml/min while recording the optical absorption at 254 and 280 nm together with conductivity. Figure 18

CDH19 BiTE CH19 2G6 302 x I2C SA21: Rapid and complete elution

16.5 Concentration of BiTE monomer to 2500 µg/ml followed by over night storage and turbidity measurement

1000 µl of CDH19 BiTE monomer were concentrated in two Vivaspin 500 centrifugation units with 10 kDa PES membran (Sartorius-Stedim, Göttingen-Germany) to a final volume of 100 µl. This volume as stored over night at 5°C in a cooling cabinet. Turbidity was measured three times at 340 nm optical wavelength absorption. Afterwards the mean value oft he three measurement values was calculated.

OD340 Turbidity of CDH19 BiTE CH19 2G6 302 x I2C SA21: 0.034

16.6 Aggregation temperature TA determination by heated Dynamic Light Scattering measurement

A volume of 40 µl monomeric BiTE antibody at 250 µg/ml was transferred into the inner core of a disposable plastic cuvette. The deeper placed outer core was filled up with generic BiTE formulation buffer. The top of the cuvette was sealed with a rubber top to avoid liquid loss by evaporation in the process of sample heating.

The cuvette was placed in a Nanostar Dynamic Light Scattering device (Wyatt) and heated from 40°C to 70°C at a heating increment of 0.5 °C/min

Aggregation status was permanently monitored and recorded in the whole heating process. Evaluation was was executed with the software package supplied by the device manufacturer.

Aggregation temperature of CDH19 BiTE CH19 2G6 302 x I2C SA21: 52.4°C

16.7 PEGylation of BiTE antibodies with CysLoop

Monomeric BiTE antibody containing an c-terminal CysLoop (see for methodical details WO 2006/008096) was dialyzed against a Tris/NaCl buffer pH 7.4 and reduced by the addition of the reduction agent Tris(2-carboxyethyl)phosphine TCEP (Perbio Pierce) to create two reduced cysteins of the now opened CysLoop.

TCEP was removed by dialysis. PEG Maleimid capable of covalent binding to reduced cystein was added in molar excess and incubated for 3 hours at room temperature.

A Sepharose SP column cation exchange column (GE Healthcare) was connected to an Äkta FPLC system and equillibrated with binding buffer (low molar Phosphat/NaCl buffer of pH 5.0)

The protein solution was diluted with binding buffer adjusted to pH 5.0 to enable binding of the BiTE protein to the cation exchange column. Unbound PEG was removed in the wash step with further binding puffer pH 5.0 over 10 column volumes. Bound protein was eluted by a linear increasing percentage of elution buffer 20 mM phosphat 1 M NaCl.
PEGylated BiTE antibody eluted at lower molarity of the elutionbuffer compared to the unmodified BiTE antibody.

Sequence Table:

TABLE Ia: HEAVY CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
1D10 2C12	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	AGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 1	SEQ ID NO: 2	SEQ ID NO: 3
	AA	SYGMH	VIWYDGSNKYYADSVKG	RAGIIGTTGYYYGMDV
		SEQ ID NO: 4	SEQ ID NO: 5	SEQ ID NO: 6
1F10	NA	AGTGGTGGTTACTACTGGAGC	TACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCACGAGT	GATGGAAGCAGTGGCTGGTACTTCCAGCAC
		SEQ ID NO: 7	SEQ ID NO: 8	SEQ ID NO: 9
	AA	SGGYYWS	YIYYSGSTYYNPSLTS	DGSSGWYFQH
		SEQ ID NO: 10	SEQ ID NO: 11	SEQ ID NO: 12
2C12_LC#1	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	AGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 13	SEQ ID NO: 14	SEQ ID NO: 15
	AA	SYGMH	VIWYDGSNKYYADSVKG	RAGIIGTTGYYYGMDV
		SEQ ID NO: 16	SEQ ID NO: 17	SEQ ID NO: 18
2G6_LC#1	NA	AGCTATGGCATGCAC	TTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGAC	AGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 19	SEQ ID NO: 20	SEQ ID NO: 21
	AA	SYGMH	FIWYDGSNKYYADSVKD	RAGIIGTIGYYYGMDV
		SEQ ID NO: 22	SEQ ID NO: 23	SEQ ID NO: 24
2G6	NA	AGCTATGGCATGCAC	TTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGAC	AGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 25	SEQ ID NO: 26	SEQ ID NO: 27
	AA	SYGMH	FIWYDGSNKYYADSVKD	RAGIIGTIGYYYGMDV
		SEQ ID NO: 28	SEQ ID NO: 29	SEQ ID NO: 30
2H12	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATACAGACTCCGTGAAGGGC	AGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 31	SEQ ID NO: 32	SEQ ID NO: 33
	AA	SYGMH	VIWYDGSNKYYTDSVKG	RAGIIGTTGYYYGMDV
		SEQ ID NO: 34	SEQ ID NO: 35	SEQ ID NO: 36
2H12_LC#2	NA	AGCTATGGCATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATACAGACTCCGTGAAGGGC	AGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTC
		SEQ ID NO: 37	SEQ ID NO: 38	SEQ ID NO: 39
	AA	SYGMH	VIWYDGSNKYYTDSVKG	RAGIIGTTGYYYGMDV
		SEQ ID NO: 40	SEQ ID NO: 41	SEQ ID NO: 42
4A2 5B4 5C5	NA	AGTAGTGGTTACTACTGGAGC	TACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAGAGT	GATGGAAGCAGTGGCTGGTACTTCCAGTAT
		SEQ ID NO: 43	SEQ ID NO: 44	SEQ ID NO: 45
	AA	SSGYYWS	YIYYTGSAYYNPSLKS	DGSSGWYFQY
		SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 48

Ab	Type	CDR 1	CDR 2	CDR 3
4A9	NA	GGTTACTACTGGAGC	TATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT	AACTGGGCCTTCCACTTTGACTTC
		SEQ ID NO: 49	SEQ ID NO: 50	SEQ ID NO: 51
	AA	GYYWS	YFSYSGSTNYNPSLKS	NWAFHFDF
		SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 54
4B10 4C2	NA	AGCTATGACATGCAC	GTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGC	GAACGATATTTTGACTGGTCTTTTGACTAC
		SEQ ID NO: 55	SEQ ID NO: 56	SEQ ID NO: 57
	AA	SYDMH	VISYDGTNEYYADSVKG	ERYFDWSFDY
		SEQ ID NO: 58	SEQ ID NO: 59	SEQ ID NO: 60
4D2	NA	AGTTATGACATGCAC	GTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGC	GAACGATATTTTGACTGGTCTTTTGACTAC
		SEQ ID NO: 61	SEQ ID NO: 62	SEQ ID NO: 63
	AA	SYDMH	VISYDGTNEYYADSVKG	ERYFDWSFDY
		SEQ ID NO: 64	SEQ ID NO: 65	SEQ ID NO: 66
4D3 4F3	NA	AGCTATGACATGGAC	GTTATATGGTATGATGGAAGTAATAAAtacTATGCAGACTCCGTGAGGGGC	GAAACTGGGGAGGgCTGGTACTTCGAtctc
		SEQ ID NO: 67	SEQ ID NO: 68	SEQ ID NO: 69
	AA	SYDMD	VIWYDGSNKYYADSVRG	ETGEGWYFDL
		SEQ ID NO: 70	SEQ ID NO: 71	SEQ ID NO: 72
4E10	NA	AGCTATGACATGCAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	GAGTATAGGTACAGCTGGTACTTTGACTAC
		SEQ ID NO: 73	SEQ ID NO: 74	SEQ ID NO: 75
	AA	SYDMH	VIWYDGSNKYYADSVKG	EYRYSWYFDY
		SEQ ID NO: 76	SEQ ID NO: 77	SEQ ID NO: 78
4F7	NA	AGTTACTCCTGGAGC	TATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT	AACTGGGCCTTCCACTTTGACTAC
		SEQ ID NO: 79	SEQ ID NO: 80	SEQ ID NO: 81
	AA	SYSWS	YIYYSGSTNYNPSLKS	NWAFHFDY
		SEQ ID NO: 82	SEQ ID NO: 83	SEQ ID NO: 84
5E3	NA	AGCTATAGCATGCAC	TCCATTAGTAGTAGTAGTAGTTACATATACTACGCAGACTCAGTGAAGGGC	GGGGAAACTGGAACTAACTACTACTACTACGGTATGGACGTC
		SEQ ID NO: 85	SEQ ID NO: 86	SEQ ID NO: 87
	AA	SYSMH	SISSSSSYIYYADSVKG	GETGTNYYYYGMDV
		SEQ ID NO: 88	SEQ ID NO: 89	SEQ ID NO: 90
17H8 23B6 28D10	NA	AGTTACTACTGGAGC	TATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT	GATTCCCGGTATAGAAGTGGCTGGTACGATGCTTTTGATATC
		SEQ ID NO: 91	SEQ ID NO: 92	SEQ ID NO: 93
	AA	SYYWS	YIYYIGSTNYNPSLKS	DSRYRSGWYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 96
16C1	NA	GGTTACTACTGGAGC	TATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT	GATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCC

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 97	SEQ ID NO: 98	SEQ ID NO: 99
	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGWYRWFDP
		SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 102
16A4	NA	AGTTACTACTGGAGC	TATATCTATTACAGTGGGAGCACCAATTACAACCCCTCCCTCAAGAGT	GATCAAAGGCGGATAGCAGCAGCTGGTACCCACTTCTACGGTATGGACGTC
		SEQ ID NO: 103	SEQ ID NO: 104	SEQ ID NO: 105
	AA	SYYWS	YIYYSGSTNYNPSLKS	DQRRIAAAGTHFYGMDV
		SEQ ID NO: 106	SEQ ID NO: 107	SEQ ID NO: 108
16E2 17E10 20B12	NA	AGCTATGGCATGCAC	GTGATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	GACGGGTGGGAGCTGTCCTTTGACTAC
		SEQ ID NO: 109	SEQ ID NO: 110	SEQ ID NO: 111
	AA	SYGMH	VIWYDGSNKYYADSVKG	DGWELSFDY
		SEQ ID NO: 112	SEQ ID NO: 113	SEQ ID NO: 114
22G10	NA	AGTTATGCCATGAAC	ACTATTAGTGGTGGTGGTGCTAACACATACTACGCAGACTCCGTGAAGGGC	GGGGGAATGGGGGGATACTACTACGGTATGGACGTC
		SEQ ID NO: 115	SEQ ID NO: 116	SEQ ID NO: 117
	AA	SYAMN	TISGGGANTYYADSVKG	GGMGGYYYGMDV
		SEQ ID NO: 118	SEQ ID NO: 119	SEQ ID NO: 120
16H2 20D3 23E7	NA	AGCTACTTTATTCAC	ATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC	GGGGGGATACAGCTATGGTTACATTTTGACTAC
		SEQ ID NO: 121	SEQ ID NO: 122	SEQ ID NO: 123
	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLWLHFDY
		SEQ ID NO: 124	SEQ ID NO: 125	SEQ ID NO: 126
22D1	NA	AGCTACTTTATTCAC	ATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC	GGGGGGATACAGCTATGGTTACATTTGGACTAC
		SEQ ID NO: 127	SEQ ID NO: 128	SEQ ID NO: 129
	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLWLHLDY
		SEQ ID NO: 130	SEQ ID NO: 131	SEQ ID NO: 132
25F8	NA	AGCTACTATATTCAC	ATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGGC	GGGGGAATACAGCTATGGTTACATTttGACTAC
		SEQ ID NO: 133	SEQ ID NO: 134	SEQ ID NO: 135
	AA	SYYIH	IINPSGGSTRYAQKFQG	GGIQLWLHFDY
		SEQ ID NO: 136	SEQ ID NO: 137	SEQ ID NO: 138
26F12 27B3	NA	AACTACTATATGTCC	ATAATCAACCCTAGTGGTGGTGACTCAACCTACGCACAGAAGTTCCAGGGC	GGGGGGATACAACTATGGTTACATTTTGACTAC
		SEQ ID NO: 139	SEQ ID NO: 140	SEQ ID NO: 141
	AA	NYYMS	IINPSGGDSTYAQKFQG	GGIQLWLHFDY
		SEQ ID NO: 142	SEQ ID NO: 143	SEQ ID NO: 144
26D1	NA	AGCTACTATATGTCC	ATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGC	GGGGGGATAAAACTATGGTTACATTTTGACTAT
		SEQ ID NO: 145	SEQ ID NO: 146	SEQ ID NO: 147
	AA	SYYMS	IIHPSGGDTTYAQKFQG	GGIKLWLHFDY

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 148	SEQ ID NO: 149	SEQ ID NO: 150
25G10	NA	GGTTACTACTGGAGC	TATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGT	GATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCC
		SEQ ID NO: 151	SEQ ID NO: 152	SEQ ID NO: 153
	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGWYRWFDP
		SEQ ID NO: 154	SEQ ID NO: 155	SEQ ID NO: 156
23A10	NA	CGCTATGGCATACAC	GTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC	AGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTC
		SEQ ID NO: 157	SEQ ID NO: 158	SEQ ID NO: 159
	AA	RYGIH	VIWYDGSNKYYADSVKG	RAGIPGTTGYYYGMDV
		SEQ ID NO: 160	SEQ ID NO: 161	SEQ ID NO: 162
19B5	NA	AGCTACTTTATTCAC	ATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC	GGGGGGATACAGCTATGGTTACATTTGGACTAC
		SEQ ID NO: 163	SEQ ID NO: 164	SEQ ID NO: 165
	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLWLHLDY
		SEQ ID NO: 166	SEQ ID NO: 167	SEQ ID NO: 168

TABLE Ib: LIGHT CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
1D10 2C12	NA	TCTGGAGATAGATTGGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		SEQ ID NO: 169	SEQ ID NO: 170	SEQ ID NO: 171
	AA	SGDRLGEKYTC	QDTKRPS	QAWDSSTVV
		SEQ ID NO: 172	SEQ ID NO: 173	SEQ ID NO: 174
1F10	NA	AGGGCCAGTCGGAGTATTAGCAGCAGCTACTTAGCC	GGTCCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCATTCACT
		SEQ ID NO: 175	SEQ ID NO: 176	SEQ ID NO: 177
	AA	RASRSISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 178	SEQ ID NO: 179	SEQ ID NO: 180
2C12_LC#1	NA	AGGtCTAGTCAAAGcctcgtaTACAGTGATGGAAACAcctACTTGAAT	AAGGTTTCTAACTGGGactct	ATGCAAGGTATAGTGTGGCCGTGCAGT
		SEQ ID NO: 181	SEQ ID NO: 182	SEQ ID NO: 183
	AA	RSSQSLVYSDGNTYLN	KVSNWDS	MQGIVWPCS
		SEQ ID NO: 184	SEQ ID NO: 185	SEQ ID NO: 186
2G6_LC#1	NA	AGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAAT	CAGGTTTCTAACTGGGACTCT	ATGCAAGATACACTGTGGCCGTGCAGT
		SEQ ID NO: 187	SEQ ID NO: 188	SEQ ID NO: 189
	AA	RSSQSLVYSDGNTYLN	QVSNWDS	MQDTLWPCS
		SEQ ID NO: 190	SEQ ID NO: 191	SEQ ID NO: 192
2G6	NA	TCTGGAGATAGGTTGGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 193	SEQ ID NO: 194	SEQ ID NO: 195
	AA	SGDRLGEKYTC	QDTKRPS	QAWDSSTVV
		SEQ ID NO: 196	SEQ ID NO: 197	SEQ ID NO: 198
2H12	NA	TCTGGAGATAGATTGGGGAAAAATATACTTGC	CAAGATACCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		SEQ ID NO: 199	SEQ ID NO: 200	SEQ ID NO: 201
	AA	SGDRLGEKYTC	QDTKRPS	QAWDSSTVV
		SEQ ID NO: 202	SEQ ID NO: 203	SEQ ID NO: 204
2H12_LC#2	NA	AGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAAT	AAGGTTTCTAACTGGGACTCT	ATGCAAGATACACTGTGGCCGTGCAGT
		SEQ ID NO: 205	SEQ ID NO: 206	SEQ ID NO: 207
	AA	RSSQSLVYSDGNTYLN	KVSNWDS	MQDTLWPCS
		SEQ ID NO: 208	SEQ ID NO: 209	SEQ ID NO: 210
4A2 5B4 5C5	NA	AGGgcCAGTCGGAATATTAGCAGCAGCTACttaGCC	GGTCCATCCAGCAGGGccaCT	CAGCAGTATGGtagctCATTCACT
		SEQ ID NO: 211	SEQ ID NO: 212	SEQ ID NO: 213
	AA	RASRNISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 214	SEQ ID NO: 215	SEQ ID NO: 216
4A9	NA	ACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACAC	GGTAACAACAATCGGCCCTCA	CAGTCCTATGACAGCagACTGAGTGGTTGGGTG
		SEQ ID NO: 217	SEQ ID NO: 218	SEQ ID NO: 219
	AA	TGSSSNIGTGYAVH	GNNNRPS	QSYDSRLSGWV
		SEQ ID NO: 220	SEQ ID NO: 221	SEQ ID NO: 222
4B10 4C2	NA	AGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTACAGTAACTCgtgGACG
		SEQ ID NO: 223	SEQ ID NO: 224	SEQ ID NO: 225
	AA	RASQSVSNTYLA	GASSRAT	QQYSNSWT
		SEQ ID NO: 226	SEQ ID NO: 227	SEQ ID NO: 228
4D2	NA	AGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCC	GGTGCATCCAGCAGGGCCGCT	CagcagTATAGTAacTcgtgGACG
		SEQ ID NO: 229	SEQ ID NO: 230	SEQ ID NO: 231
	AA	RASQSVSNTYLA	GASSRAA	QQYSNSWT
		SEQ ID NO: 232	SEQ ID NO: 233	SEQ ID NO: 234
4D3 4F3	NA	AGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAGCTCGTGGACG
		SEQ ID NO: 235	SEQ ID NO: 236	SEQ ID NO: 237
	AA	RASQSVSSSYLA	GASSRAT	QQYGSSWT
		SEQ ID NO: 238	SEQ ID NO: 239	SEQ ID NO: 240
4E10	NA	AGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGTCACT	CAGCAATATAGTAACTCGTGGACG
		SEQ ID NO: 241	SEQ ID NO: 242	SEQ ID NO: 243

Ab	Type	CDR 1	CDR 2	CDR 3
	AA	RASQSVGSSYLA	GASSRVT	QQYSNSWT
		SEQ ID NO: 244	SEQ ID NO: 245	SEQ ID NO: 246
4F7	NA	ACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACAC	GGTAACAGCAATCGGCCCTCA	CAGTCCTATGACAGCAGTCTGAGTGGTTGGGTG
		SEQ ID NO: 247	SEQ ID NO: 248	SEQ ID NO: 249
	AA	TGSSSNIGTGYDVH	GNSNRPS	QSYDSSLSGWV
		SEQ ID NO: 250	SEQ ID NO: 251	SEQ ID NO: 252
5E3	NA	TCTGGAGATAAATTGGGGGATGAATATGCTTGC	CAAGATAGCAAGCGGCCCTCA	CAGGCGTGGGACAGCAGCACTGTGGTA
		SEQ ID NO: 253	SEQ ID NO: 254	SEQ ID NO: 255
	AA	SGDKLGDEYAC	QDSKRPS	QAWDSSTVV
		SEQ ID NO: 256	SEQ ID NO: 257	SEQ ID NO: 258
17H8 23B6 28D10	NA	AGGGCCAGTCAGAGTGTTGCCGGCAGCTACCTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAAATCACCGATCACC
		SEQ ID NO: 259	SEQ ID NO: 260	SEQ ID NO: 261
	AA	RASQSVAGSYLA	GASSRAT	QQYGKSPIT
		SEQ ID NO: 262	SEQ ID NO: 263	SEQ ID NO: 264
16C1	NA	AGGGCCAGCCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAACTCACCGCTCACT
		SEQ ID NO: 265	SEQ ID NO: 266	SEQ ID NO: 267
	AA	RASQSVSSSYLA	GASSRAT	QQYGNSPLT
		SEQ ID NO: 268	SEQ ID NO: 269	SEQ ID NO: 270
16A4	NA	AGGGCCAGTCAGAGTGTTAGCAGCAGTTATTTAGCC	GGTACATCCAGCAGGGCCACT	CAGCAGTACGGTAGCTCACCTTTCACT
		SEQ ID NO: 271	SEQ ID NO: 272	SEQ ID NO: 273
	AA	RASQSVSSSYLA	GTSSRAT	QQYGSSPFT
		SEQ ID NO: 274	SEQ ID NO: 275	SEQ ID NO: ***276
16E2 17E10 20B12	NA	CGGGCGAGTCAGGGCATTAGCAATTATTTAGCC	GCTGCATCCAGTTTGCAAAGT	CAACACTATTTTACTTACCCTCGGACG
		SEQ ID NO: 277	SEQ ID NO: 278	SEQ ID NO: 279
	AA	RASQGISNYLA	AASSLQS	QHYFTYPRT
		SEQ ID NO: 280	SEQ ID NO: 281	SEQ ID NO: 282
22G10	NA	AGGGCCAGTCAGAGTATTAGCAGCAACTTAGCC	GGTGCATTTACCAGGGCCACT	CAGCAGTATAATTACTGGCCGCTCACT
		SEQ ID NO: 283	SEQ ID NO: 284	SEQ ID NO: 285
	AA	RASQSISSNLA	GAFTRAT	QQYNYWPLT
		SEQ ID NO: 286	SEQ ID NO: 287	SEQ ID NO: 288
16H2 20D3 23E7	NA	TCTGGAAGCAGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGCCTGAATGGTTGGGTG
		SEQ ID NO: 289	SEQ ID NO: 290	SEQ ID NO: 291
	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDDSLNGWV
		SEQ ID NO: 292	SEQ ID NO: 293	SEQ ID NO: 294

Ab	Type	CDR 1	CDR 2	CDR 3
22D1	NA	TCTGGAAGCAGCTCCAACATCGGAAGCAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGTATGAATGGTTGGGTG
		SEQ ID NO: 295	SEQ ID NO: 296	SEQ ID NO: 297
	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDDSMNGWV
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 300
25F8	NA	TCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAGCATGGGATGACAGCCTGAATGGTTGGGTG
		SEQ ID NO: 301	SEQ ID NO: 302	SEQ ID NO: 303
	AA	SGSSSNIGRNFVN	TNNQRPS	AAWDDSLNGWV
		SEQ ID NO: 304	SEQ ID NO: 305	SEQ ID NO: 306
26F12 27B3	NA	TCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATTATCAGCGGCCCTCA	GCAGTATGGGATGACAGCCTGAATGGTTGGGTG
		SEQ ID NO: 307	SEQ ID NO: 308	SEQ ID NO: 309
	AA	SGSRSNIGSNFVN	TNYQRPS	AVWDDSLNGWV
		SEQ ID NO: 310	SEQ ID NO: 311	SEQ ID NO: 312
26D1	NA	TCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAGTATGGGATGACAGCCTGAATGGTTGGGTG
		SEQ ID NO: 313	SEQ ID NO: 314	SEQ ID NO: 315
	AA	SGSRSNIGSNFVN	TNNQRPS	AVWDDSLNGWV
		SEQ ID NO: 316	SEQ ID NO: 317	SEQ ID NO: 318
25G10	NA	AGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCC	GGTGCATCCAGCAGGGCCACT	CAGCAGTATGGTAACTCACCGCTCACT
		SEQ ID NO: 319	SEQ ID NO: 320	SEQ ID NO: 321
	AA	RASQSVSSSYLA	GASSRAT	QQYGNSPLT
		SEQ ID NO: 322	SEQ ID NO: 323	SEQ ID NO: 324
23A10	NA	TCTGGAGATAGATTGGGGGAGAAATATGTTTGC	CAAGATAATAAGTGGCCCTCA	CAGGCGTGGGACAGCAGcacTGTGGTA
		SEQ ID NO: 325	SEQ ID NO: 326	SEQ ID NO: 327
	AA	SGDRLGEKYVC	QDNKWPS	QAWDSSTVV
		SEQ ID NO: 328	SEQ ID NO: 329	SEQ ID NO: 330
19B5	NA	TCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAAC	ACTAATAATCAGCGGCCCTCA	GCAACATGGGATGACAGTATGAATGGTTGGGTG
		SEQ ID NO: 331	SEQ ID NO: 332	SEQ ID NO: 333
	AA	SGSRSNIGSNFVN	TNNQRPS	ATWDDSMNGWV
		SEQ ID NO: 334	SEQ ID NO: 335	SEQ ID NO: 336

Anti-CDH19 Variable Region Amino Acid Sequences and Polynucleotide Sequences

TABLE IIa: Heavy Chain Variable Region Polynucleotide and Amino acid Sequences

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
337	17H8 23B6 28D10	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACGTGCACTGTCTCTGGTGGCTCCATCAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGCGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCCTGTATTACTGTGCGAGAGATTCCCGGTATAGAAGTGGCTGGTACGATGCTTTTGATATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
338	17H8 23B6 28D10	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
339	4A2 5B4 5C5	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA
340	4A2 5B4 5C5	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
341	16H2 20D3 23E7	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
342	16H2 20D3 23E7	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
343	26F12 27B3	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTAGATACACCTTCACCAACTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTGACTCAACCTACGCACAGAAGTTCCAGGGCAGACTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATACAACTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
344	26F12 27B3	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
345	4B10 4C2	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCAGTGTCTCCTCA
346	4B10 4C2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
347	4D3 4F3	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCTCCTTCAGTAGCTATGACATGGACTGGGTCCGCCAGACTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAGGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAACTGGGGAGGGCTGGTACTTCGATCTCTGGGGCCGTGGCACCCTGGTCACTGTCTCCTCA
348	4D3 4F3	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
349	16E2 17E10 20B12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCATCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGACTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTGATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGTGGGAGCTGTCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
350	16E2 17E10 20B12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQTPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDISKNTLYLQMNSLRVEDTAVYYCARDGWELSFDYWGQGTLVTVSS
351	1D10 2C12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGCGCGAGAAGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
352	1D10 2C12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
353	16C1	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTTGTACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATGTCAATAGACACGTCCAAGAACCAGTTCTCCCTGACGCTGAGCTCTTTGACCGCTGCGGACACGGCCGTGTATTTCTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
354	16C1	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSIDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
355	25G10	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCAT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
356	25G10	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
357	16A4	artificial	nt	CAGGTGCAGCTGCAGGAGTCgGGCCCAGGACTGGCGAAgccttcGGAGACcctgtccctcacctgCACTGTCTCTGGTGACTCCATCACTAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAATTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGAGATCAAAGGCGGATAGCAGCAGCTGGTACCCACTTCTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
358	16A4	artificial	aa	QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSS
359	1F10	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTACTACTGGAGCTGGATCCGCCAGCACCCAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCACGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGCACTGGGGCCAGGGCACCCTGGTCACCGTCTCCTCA
360	1F10	artificial	aa	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLTSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQHWGQGTLVTVSS
361	4A9	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGACTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
362	4A9	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
363	4F7	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
364	4F7	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
365	22D1	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAGGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTACGCCAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCA

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
366	22D1	artificial	aa	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
367	19B5	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGcCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
368	19B5	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
369	25F8	artificial	nt	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAAGGACTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCagcctGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGAATACAGCTATGGTTACATTttGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
370	25F8	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
371	26D1	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTAGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
372	26D1	artificial	aa	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
373	4D2	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCAGTGTCTCCTCA
374	4D2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
375	4E10	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCACGAACACGCTGCATCTGCAAATGAACAGCCCG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AGAGCCGAGGACACGGCTGTGTACTACTGTGCGAGAGAGTATAGGTACAGCTGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
376	4E10	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSTNTLHLQMNSPRAEDTAVYYCAREYRYSWYFDYWGQGTLVTVSS
377	22G10	artificial	nt	GAGGTGCAACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGCAGTTATGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACTATTAGTGGTGGTGGTGCTAACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGTGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGCGGACACGGCCGTATATCACTGTGCGAAAGGGGGAATGGGGGGATACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
378	22G10	artificial	aa	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
379	2C12_LC#1	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGTCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGCGCGAGAAGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
380	2C12_LC#1	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVSVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
381	2H12_LC#2	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATACAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
382	2H12_LC#2	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
383	2G6_LC#1	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
384	2G6_LC#1	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
385	2H12	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATACAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTACAGGCTACTACTACGGTATGGACGTCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GGGCCAAGGGACCACGGTCACCGTCTCCTCA
386	2H12	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYTDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTTGYYYGMDVWGQGTTVTVSS
387	2G6	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
388	2G6	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
389	23A10	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
390	23A10	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
391	5E3	artificial	nt	GAGGTGCAGTTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTTACATATACTACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGAAACTGGAACTAACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
392	5E3	artificial	aa	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMHWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARGETGTNYYYYGMDVWGQGTTVTVSS

TABLE IIB: Light Chain Variable Region Polynucleotide and Amino acid Sequences

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
393	17H8 23B6 28D10	artificial	nt	GACATTGTATTGACGCAGtctCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGCCGGCAGCTACCTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTCTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAAATCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATGAAAGGA
394	17H8 23B6	artificial	aa	DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	28D10			
395	4A2 5B4 5C5	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCTTGCAGGGCCAGTCGGAATATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTACAGTGTATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGA
396	4A2 5B4 5C5	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASRNISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKR
397	16H2 20D3 23E7	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACAAACAACTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTGTGCAACATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
398	16H2 20D3 23E7	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLG
399	26F12 27B3	artificial	nt	CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGGCAGAAGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATTATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
400	26F12 27B3	artificial	aa	QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
401	4B10 4C2	artificial	nt	GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAGTGGCAGTGGGTCTGGGACAGACTTCGCTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACAGTAACTCgtgGACGTTCGGCCAAGGGACCAAGGTGGAAATCAaacGA
402	4B10 4C2	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
403	4D3 4F3	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAACCTGAGGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
404	4D3 4F3	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
405	16E2 17E10	artificial	nt	GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTTACAGCAGAAACCAGGGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	20B12			TCCCATCAAAGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACACTATTTTACTTACCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
406	16E2 17E10 20B12	artificial	aa	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQHYFTYPRTFGQGTKVEIKR
407	1D10 2C12	artificial	nt	TCCTATGCGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCCTCACCTGCTCTGGAGATAGATTGGGGAAAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCACCTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
408	1D10 2C12	artificial	aa	SYALTQPPSVSVSPGQTASLTCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSTSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
409	16C1	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGCCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCGGACTGGAGCCTGAAGATTTTGCAGTGTATCACTGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
410	16C1	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
411	25G10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGactTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATCACTGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
412	25G10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
413	16A4	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCtCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGTTATTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTACATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTATTGTCAGCAGTACGGTAGCTCACCTTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGA
414	16A4	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKR
415	1F10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCGGAGTATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGA
416	1F10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASRSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKR

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
417	4A9	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGTTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
418	4A9	artificial	aa	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
419	4F7	artificial	nt	CAGTCTGTgcTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGcttcCAGGAACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTAGGT
420	4F7	artificial	aa	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLG
421	22D1	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTGTGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
422	22D1	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
423	19B5	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAACGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTGCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTAGGT
424	19B5	artificial	aa	QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
425	25F8	artificial	nt	CAGTCTGCGCTGactCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAACTGGTATAAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATTTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTGTGCAGCATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
426	25F8	artificial	aa	QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
427	26D1	artificial	nt	CACTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
428	26D1	artificial	aa	HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
429	4D2	artificial	nt	GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCGCTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
430	4D2	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRAAGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
431	4E10	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGTCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAATATAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGA
432	4E10	artificial	aa	EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGASSRVTGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
433	22G10	artificial	nt	GAAATAGTGATGACGCAGTCTCCAGTCACCCTGTCTCTGTCTCTAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTAGCAGCAACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGACTCCTCATCTATGGTGCATTTACCAGGGCCACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATTACTGGCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAGCGA
434	22G10	artificial	aa	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
435	2C12_LC#1	artificial	nt	GATGTTGTGATGactCAGtCTccActctccctgcCCGTCACCCTTGGACAGCCGGcctCCAtctcctgCAGGtCTAGTCAAAGcctcgtaTACAGTGATGGAAACAcctACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGcgcctaATTTATAAGGTTTCTAACTGGGactctGGGGtCCCAGACAGATTCAGCgGCAGTGGGTCAGGCActGATTTCACactGAAAAtCAGCAGGGTGGaggctgaGGATGTTGGGGTTTATTactgCATGCAAGGTATAGTGTGGCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAaCgA
436	2C12_LC#1	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIVWPCSFGQGTKLEIKR
437	2H12_LC#2	artificial	nt	GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCTTGGACAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACTGGGACTCTGGGGTCCCAGACAGAATCAGCGGCAGTGGGTCAGGCACCGATTTCACACTGAAAATCAGCAGGGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGATACACTGTGGCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
438	2H12_LC#2	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRISGSGSGTDFTLKISRVEAEDVGVYYCMQDTLWPCSFGQGTKLEIKR
439	2G6_LC#1	artificial	nt	GaTGTTGTGATGACTCagtctccACTCTCCCTGCCCGTCACCCttggacaGCCGGCCTccaTCTCCTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAGAGGCCAGGCCAATCTCCACGGCGCCTAATTTATCAGGTTTCTAACTGGGACTCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGTCAGGCACTGATTTCACACTGAAAATCAGCAGGGTGGAGGCTGAGGATGTTGGGATTTATTACTGCATGCAAGATACACTGTGGCCGTGCAGTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGA
440	2G6_LC#1	artificial	aa	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYQVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQDTLWPCSFGQGTKLEIKR

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
441	2H12	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA AAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGCCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCtAGGT
442	2H12	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQPMDEADYY CQAWDSSTVVFGGGTKLTVLG
443	2G6	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGA AAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
444	2G6	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG
445	23A10	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGA GAAATATGTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTAGGT
446	23A10	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG
447	5E3	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGA TGAATATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAGATAGCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGT
448	5E3	artificial	aa	SYELTQPPSVSVSPGQTASITCSGDKLGDEYACWYQQKPGQSPVLVIYQDSKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWDSSTVVFGGGTKLTVLG

TABLE IIc: Heavy Chain Variable Region Polynucleotide and Amino acid Sequences

13586 HC [hu anti-<huCDH19> 4F3 VH]

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS

SEQ ID NO: 449

13589 HC [hu anti-<huCDH19> 4A9 VH]

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS

SEQ ID NO: 450

13590 HC [hu anti-<huCDH19> 4B10 VH]

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS

SEQ ID NO: 451

13874 HC [hu anti-<huCDH19> 17H8.2 VH]

QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS

SEQ ID NO: 452

13875 HC [hu anti-<huCDH19> 16C1.1 VH]

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSIDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS

SEQ ID NO: 453

13876 HC [hu anti-<huCDH19> 16A4.1 VH]

QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSS

SEQ ID NO: 454

13877 HC [hu anti-<huCDH19> 22G10.1 VH]

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS

SEQ ID NO: 455

13878 HC [hu anti-<huCDH19> 20D3.1 VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS

SEQ ID NO: 456

13879 HC [hu anti-<huCDH19> 22D1.1 VH]

QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS

SEQ ID NO: 457

13880 HC [hu anti-<huCDH19> 25F8.1 VH]

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS

SEQ ID NO: 458

13881 HC [hu anti-<huCDH19> 26F12.1 VH]

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS

SEQ ID NO: 459

13882 HC [hu anti-<huCDH19> 26D1.1 VH]

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS

SEQ ID NO: 460

13883 HC [hu anti-<huCDH19> 25G10.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 461

13885 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 462

14022 HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 463

14024 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 464

14025 HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 465

14026 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 466

14027 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 467

14028 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYFQYWGQGTLVTVSS
SEQ ID NO: 468

14029 HC [hu anti-<huCDH19> 4A2 VH]
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
SEQ ID NO: 469

14030 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
SEQ ID NO: 470

14031 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
SEQ ID NO: 471

14032 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
SEQ ID NO: 472

14033 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
SEQ ID NO: 473

14034 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGYYFDLWGQGTLVTVSS
SEQ ID NO: 474

14039 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 475

14040 HC [hu anti-<huCDH19> 16C1.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 476

14041 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 477

14042 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCAREGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 478

14043 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGYYRYFDPWGQGTLVTVSS
SEQ ID NO: 479

14044 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 480

14045 HC [hu anti-<huCDH19> 17H8.2 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 481

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 482

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGYYDAFDIWGQGTMVTVSS
SEQ ID NO: 483

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSS
SEQ ID NO: 484

14049 HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 485

14050 HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 486

14051 HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDYWGQGTLVTVSS
SEQ ID NO: 487

14052 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGTLVSVSS
SEQ ID NO: 488

14053 HC [hu anti-<huCDH19> 4B10 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 489

14054 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKG
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 490

14055 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
SEQ ID NO: 491

14056 HC [hu anti-<huCDH19> 4A9 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 492

14057 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 493

14058 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
SEQ ID NO: 494

14059 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G,W113Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGQGTLVTVSS
SEQ ID NO: 495

14060 HC [hu anti-<huCDH19> 20D3.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 496

14061 HC [hu anti-<huCDH19> 20D3.1 VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 497

14062 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 498

14063 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 499

14064 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 500

14065 HC [hu anti-<huCDH19> 22G10.1 (1-470)(S82R,A99E) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 501

14066 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E,H105Y) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 502

14067 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 503

14068 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 504

14069 HC [hu anti-<huCDH19> 22G10.1 (1-470)(D72E,A99E) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRF
TISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 505

14070 HC [hu anti-<huCDH19> 22G10.1 (1-470)(H105Y) VH]
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 506

14071 HC [hu anti-<huCDH19> 16A4.1 (1-474)(T144L) VH]
QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSS
SEQ ID NO: 507

14072 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 508

14073 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 509

14074 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 510

14075 HC [hu anti-<huCDH19> 19B5.1 VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 511

14076 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 512

14077 HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 513

14078 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 514

14079 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 515

14080 HC [hu anti-<huCDH19> 23A10.3 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 516

14081 HC [hu anti-<huCDH19> 25G10.1 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
SEQ ID NO: 517

14082 HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYRYFDPWGQGTLVTVSS
SEQ ID NO: 518

14083 HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 519

14084 HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 520

14085 HC [hu anti-<huCDH19> 26D1.1 VH]

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 521

14086 HC [hu anti-<huCDH19> 26D1.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 522

14087 HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLYLHFDYWGQGTLVTVSS
SEQ ID NO: 523

14088 HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
SEQ ID NO: 524

14089 HC [hu anti-<huCDH19> 26F12.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 525

14090 HC [hu anti-<huCDH19> 26F12.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 526

14091 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 527

14092 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 528

14093 HC [hu anti-<huCDH19> 25F8.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 529

14094 HC [hu anti-<huCDH19> 25F8.1 VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 530

14095 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 531

14096 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
SEQ ID NO: 532

14097 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSS
SEQ ID NO: 533

14098 HC [hu anti-<huCDH19> 22D1.1 VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 534

14099 HC [hu anti-<huCDH19> 22D1.1 VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 535

14100 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 536

14101 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSS
SEQ ID NO: 537

14102 HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
SEQ ID NO: 538

13591 HC [hu anti-<huCDH19> 4F7 VH]
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
SEQ ID NO: 539

14301 HC [hu anti-<huCDH19> 2G6 VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 540

14302 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 541

14303 HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 542

14304 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
SEQ ID NO: 543

TABLE IId: Light Chain Variable Region Amino acid Sequences

13586 LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 544

13589 LC [hu anti-<huCDH19> 4A9 VL]

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 545

13590 LC [hu anti-<huCDH19> 4B10 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 546

13874 LC [hu anti-<huCDH19> 17H8.2 VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKG
SEQ ID NO: 547

13875 LC [hu anti-<huCDH19> 16C1.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 548

13876 LC [hu anti-<huCDH19> 16A4.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKR
SEQ ID NO: 549

13877 LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 552

13878 LC [hu anti-<huCDH19> 20D3.1 VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 554

13879 LC [hu anti-<huCDH19> 22D1.1 VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 555

13880 LC [hu anti-<huCDH19> 25F8.1 VL]

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 556

13881 LC [hu anti-<huCDH19> 26F12.1 VL]
QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 557

13882 LC [hu anti-<huCDH19> 26D1.1 VL]
HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 555

13883 LC [hu anti-<huCDH19> 25G10.1 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 556

13885 LC [hu anti-<huCDH19> 19B5.1 VL]

QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 557

14022 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 558

14024 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 559

14025 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 560

14026 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 561

14027 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 562

14028 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKR
SEQ ID NO: 563

14029 LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKR
SEQ ID NO: 564

14030 LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 565

14031 LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 566

14032 LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 567

14033 LC [hu anti-<huCDH19> 4F3 VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 568

14034 LC [hu anti-<huCDH19> 4F3 VL]

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKR
SEQ ID NO: 569

14039 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 570

14040 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 571

14041 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 572

14042 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 573

14043 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 574

14044 LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKR
SEQ ID NO: 575

14045 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 576

14046 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 577

14047 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 578

14048 LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKR
SEQ ID NO: 579

14049 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLG
SEQ ID NO: 580

14050 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLG
SEQ ID NO: 581

14051 LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLG
SEQ ID NO: 582

14052 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 583

14053 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 584

14054 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 585

14055 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKR
SEQ ID NO: 586

14056 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 587

14057 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLG
SEQ ID NO: 588

14058 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLG
SEQ ID NO: 589

14059 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLG
SEQ ID NO: 590

14060 LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 591

14061 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 592

14062 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 593

14063 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLG
SEQ ID NO: 594

14064 LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDESDYYCATYDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 595

14065 LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 596

14066 LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 597

14067 LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 598

14068 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 599

14069 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 600

14070 LC [hu anti-<huCDH19> 22G10.1 VL]
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKR
SEQ ID NO: 601

14071 LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD FTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKR
SEQ ID NO: 602

14072 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 603

14073 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 604

14074 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]

QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 605

14075 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
SEQ ID NO: 606

14076 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
SEQ ID NO: 607

14077 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 608

14078 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 609

14079 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 610

14080 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 611

14081 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 612

14082 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKR
SEQ ID NO: 613

14083 LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]

HSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 614

14084 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 615

14085 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 616

14086 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]

QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 617

14087 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 618

14088 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 619

14089 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 620

14090 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 621

14091 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 622

14092 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLG
SEQ ID NO: 623

14093 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 624

14094 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 625

14095 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLG
SEQ ID NO: 626

14096 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLG
SEQ ID NO: 627

14097 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLQGWVFGGGTKLTVLG
SEQ ID NO: 628

14098 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 629

14099 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLG
SEQ ID NO: 630

14100 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLG
SEQ ID NO: 631

14101 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 632

14102 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLG
SEQ ID NO: 633

13591 LC [hu anti-<huCDH19> 4F7 VL]
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLG
SEQ ID NO: 634

14301 LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 635

14302 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 636

14303 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLG
SEQ ID NO: 637

14304 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLG
SEQ ID NO: 638

Anti-CDH19 Variable and Constant Region Polynucleotide and Amino Acid Sequences

TABLE IIIa: Heavy Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

2G6
CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGG
CTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGAC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCT

GAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTAC
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCG
GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCAC
ACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCA
GCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
AAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTC
CTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACC
CCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 639

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 640

4A2
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGACCCTGTCCCTCACCTGC
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AAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAG
AGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACT
GCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGG
GGCCAGGGCACCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
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ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 641

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 642

4B10

4A9
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
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CTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACC
CTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGA
GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG
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GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTGAC
AAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTC
CCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC
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CCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
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CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 643

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 644

4B10
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
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CAGGGAACCCTGGTCAGCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCC
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ATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGT
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GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
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CACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
ACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 645

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
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TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV

KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 646

4F3
CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
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CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAGGGGC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAACAGCCTGAGAGTC
GAGGACACGGCTGTGTATTACTGTGCGAGAGAAACTGGGGAGGGCTGGTACTTCGATCTCTGGGGC
CGTGGCACCCTGGTCACCGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCT
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CGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA
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TCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC
TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
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GCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
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CACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTAC
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SEQ ID NO: 647

QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
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STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 648

4F7
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GTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
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GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
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CAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCC
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CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGA
GCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 649

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 650

16A4
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGCGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
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CTGGAGTGGATTGGGTATATCTATTACAGCGGGAGCACCAATTACAACCCCTCCCTCAAGAGTCGA
GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGTTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGAGATCAAAGGCGGATAGCAGCAGCTGGTACCCACTTCTAC
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACTGTCTCCTCAGCTTCCACCAAGGGCCCATCC
GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCA
CACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
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CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT
CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
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GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 651

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SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 652

16C1
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACTTGT
ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATGTCAATAGACACGTCCAAGAACCAGTTCTCCCTGACGCTGAGCTCTTTGACCGCTGCG
GACACGGCCGTGTATTTCTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCG
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA

AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 653

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 654

17H8

CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACGTGC
ACTGTCTCTGGTGGCTCCATCAATAGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGC
GTCACCATATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCCTGTATTACTGTGCGAGAGATTCCCGGTATAGAAGTGGCTGGTACGATGCTTTTGAT
ATCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCC
CTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC
TTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCG
GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTT
GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCA
CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGT
CAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAA
CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAC
AGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTG
GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAA
CTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA
CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 655

QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 656

19B5

CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGG
CTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG

CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 657

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 658

20D3
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTTGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 659

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 660

22D1
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAGGGTTTCCTGC
AAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTACGCCAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC

CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 661

QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 662

22G10

GAGGTGCAACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGT
GCAGCCTCTGGATTCACCTTTAGCAGTTATGCCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGG
CTGGAGTGGGTCTCAACTATTAGTGGTGGTGGTGCTAACACATACTACGCAGACTCCGTGAAGGGC
CGGTTCACCATCTCCAGTGACAATTCCAAGAGCACGCTGTATCTGCAAATGAACAGCCTGAGAGCC
GCGGACACGGCCGTATATCACTGTGCGAAAGGGGGAATGGGGGGATACTACTACGGTATGGACGT
CTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCT
GGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTT
CCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC
ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGA
GCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACC
GTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA
TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACA
AAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTC
AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA
CAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 663

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 664

23A10

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGT
GCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGG

CTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC
CGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCC
GAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTAT
GGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCC
GTCTTCCCCCTGGCGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCA
CACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCC
AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
CAAGAAAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT
CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCA
AGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCC
CGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGC
CGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCA
AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 665

QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 666

25F8
CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTGGATACACCTTCACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAAGGA
CTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGG
CAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGAT
CTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGAATACAGCTATGGTTACATTTTGACTACT
GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGG
CGCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC
CCGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCA
CCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAG
CCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCG
TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 667

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 668

25G10
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGC
ACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGA
CTGGAGTGGATTGGGTATATCTATTACATTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGA
GTCACCATGTCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCG
GACACGGCCGTGTATTACTGTGCGAGAGATGGGAGCAGTGGCTGGTACCGGTGGTTCGACCCCTGG
GGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCG
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
GAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC
CAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
AGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGA
GGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA
GCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAA
AGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACA
AGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACA
AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACT
ACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 669

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
SEQ ID NO: 670

26D1
CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGT
AAGGCATCTAGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGC
AGAGTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 671

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS

KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 672

26F12
CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGC
AAGGCATCTAGATACACCTTCACCAACTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGG
CTTGAGTGGATGGGAATAATCAACCCTAGTGGTGGTGACTCAACCTACGCACAGAAGTTCCAGGGC
AGACTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATC
TGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATACAACTATGGTTACATTTTGACTACTG
GGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCAAGGGCCCATCCGTCTTCCCCCTGGC
GCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGT
CCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC
CCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC
CCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGT
CAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCA
AAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC
AAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGAC
AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAC
TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA
SEQ ID NO: 673

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 674

TABLE IIIb: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

2G6
TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGC
TCTGGAGATAGGTTGGGGGAAAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTG
CTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCT
GGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAG
GCGTGGGACAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAA
GGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGCCACACT
AGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAGCCC
CGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAAGTACGCGGCCAGCA
GCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCAT
GAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 675

SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 676

4A2
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCGGAATATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTACAGTGTATTAC
TGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGTACGGTG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 677

EIVLTQSPGTLSLSPGERATLSCRASRNISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 678

4A9
CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGC
ACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGTTTCCAGGAACA
GCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCT
CCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATT
ACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCC
TAGGTCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCA
ACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAGG
CAGATGGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAAG
TACGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCTG
CCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 679

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 680

4B10
GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCATCAGAGACCTGGCCAGGCTC
CCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAGTGGCAGTG
GGTCTGGGACAGACTTCGCTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTGTATTACT
GTCAGCAGTACAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTG
GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTG
TGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCC
AATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGC
AGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 681

EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 682

4F3
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT

CCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAACCTGAGGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAGCTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGTACGGT
GGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTT
GTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC
CAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAG
CAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 683

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 684

<u>**4F7**</u>

CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGC
ACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACA
GCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC
TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTAT
TACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTC
CTAGGTCAGCCCAAGGCCAACCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCC
AACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTGGAAG
GCAGATGGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCAAACCCTCCAAACAGAGCAACAACAA
GTACGCGGCCAGCAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCACAGAAGCTACAGCT
GCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 685

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 686

<u>**16A4**</u>

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAGCAGTTATTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTC
CCAGGCTCCTCATCTATGGTACATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTG
GGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTATT
GTCAGCAGTACGGTAGCTCACCTTTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACTG
TGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTGT
TGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
CCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA
GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACC
CATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 687

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 688

<u>**16C1**</u>

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGCCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCGGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
TGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
GTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTG

TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 689

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 690

17H8
GACATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTGCCGGCAGCTACCTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTCTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTAC
TGTCAGCAGTATGGTAAATCACCGATCACCTTCGGCCAAGGGACACGACTGGAGATGAAAGGAAC
TGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCT
GTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC
CTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCT
CAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 691

DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 692

19B5
CAGTCTGCGCTGACTCAGCCACCCTCAACGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
TCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGC
CCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCC
AAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACT
GCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
GGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAAC
AAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCA
GATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTA
CGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCC
AGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 693

QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 694

20D3
CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
TCTGGAAGCAGCTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGCC
CCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTG
TGCAACATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG
ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA

SEQ ID NO: 695

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 696

22D1
CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGCAATTTTGTAAACTGGTACAAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTGTGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 697

QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 698

22G10
GAAATAGTGATGACGCAGTCTCCAGTCACCCTGTCTCTGTCTCTAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTAGCAGCAACTTAGCCTGGTTCCAGCAGAAACCTGGCCAGGCTCCCAGACTCCTCATCTATGGTGCATTTACCAGGGCCACTGGTATCCCAGCCAGGGTCAGTGGCAGTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATTACTGGCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAGCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 699

EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 700

23A10
TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 701

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF

YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 702

25F8
CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGT
TCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAACTGGTATAAGCAGCTCCCAGGAACGGCC
CCCAAAGTCCTCATTTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCA
AGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTATTACTG
TGCAGCATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAG
GTCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACA
AGGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAG
ATAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTAC
GCGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCA
GGTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 703

QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 704

25G10
GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCT
GCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCT
CCCAGGCTCCTCATCTTTGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGT
GGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATCAC
TGTCAGCAGTATGGTAACTCACCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGAACT
GTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGTACCGCCTCTG
TTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCC
TCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTGA
SEQ ID NO: 705

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 706

26D1
CACTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTT
CTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCC
CCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
GTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGT
GCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAA
GGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGA
TAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACG
CGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAG
GTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 707

HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 708

26F12
CAGTCTGTGCTGACTCAGTCACCCTCAGCGTCTGGGACCCCCGGGCAGAAGGTCACCATCTCTTGTT
CTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCC
CCAAACTCCTCATCTATACTAATTATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAA
GTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGT
GCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTAGG
TCAGCCCAAGGCTGCCCCCTCGGTCACTCTGTTCCCACCCTCCTCTGAGGAGCTTCAAGCCAACAA
GGCCACACTGGTGTGTCTCATAAGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGA
TAGCAGCCCCGTCAAGGCGGGAGTGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACG
CGGCCAGCAGCTATCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAG
GTCACGCATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA
SEQ ID NO: 709

QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 710

TABLE IIIc: Heavy Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586 HC [hu anti-<huCDH19> 4F3 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 711

13589 HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 712

13590 HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 713

13874 HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 714

13875 HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 715

13876 HC [hu anti-<huCDH19> 16A4.1 VH]::huIgG1z
QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 716

13877 HC [hu anti-<huCDH19> 22G10.1 VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 717

13878 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 718

13879 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 719

13880 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 720

13881 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 721

13882 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 722

13883 HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 723

13885 HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z

QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 724

14022 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 725

14024 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 726

14025 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 727

14026 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 728

14027 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 729

14028 HC [hu anti-<huCDH19> 4A2 (1-472)(Q17E,H47P,D111E,W134Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 730

14029 HC [hu anti-<huCDH19> 4A2 VH]::huIgG1z
QVQLQESGPGLVKPSQTLSLTCTVSGGSISSSGYYWSWIRQHPGKGLEWIGYIYYTGSAYYNPSLKSRV
TISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 731

14030 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 732

14031 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 733

14032 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 734

14033 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 735

14034 HC [hu anti-<huCDH19> 4F3 (1-471)(R17G,T47A,D61E,D72E,W134Y,R141Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRG
RFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGYYFDLWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 736

14039 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,D61E,D72E,K94N) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 737

14040 HC [hu anti-<huCDH19> 16C1.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLTLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 738

14041 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 739

14042 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCAREGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 740

14043 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K,W132Y,W135Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGYYRYFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 741

14044 HC [hu anti-<huCDH19> 16C1.1 (1-469)(T92K) VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
IDTSKNQFSLKLSSLTAADTAVYFCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 742

14045 HC [hu anti-<huCDH19> 17H8.2 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 743

14046 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 744

14047 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E,W132Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGYYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 745

14048 HC [hu anti-<huCDH19> 17H8.2 (1-471)(D109E) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISV
DTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 746

14049 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 747

14050 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 748

14051 HC [hu anti-<huCDH19> 4F7 (1-468)(W113Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 749

14052 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E,W134Y) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDYSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 750

14053 HC [hu anti-<huCDH19> 4B10 VH]::huIgG1z

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 751

14054 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKG
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 752

14055 HC [hu anti-<huCDH19> 4B10 (1-471)(R17G,D61E,D72E) VH]::huIgG1z

QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGR
FTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 753

14056 HC [hu anti-<huCDH19> 4A9 VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 754

14057 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 755

14058 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G) VH]::huIgG1z

QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 756

14059 HC [hu anti-<huCDH19> 4A9 (1-468)(F55I,A56G,W113Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLS
VDTSKNQFSLKLSSVTAADTAVYYCARNYAFHFDFWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 757

14060 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 758

14061 HC [hu anti-<huCDH19> 20D3.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 759

14062 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 760

14063 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 761

14064 HC [hu anti-<huCDH19> 20D3.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 762

14065 HC [hu anti-<huCDH19> 22G10.1 (1-470)(S82R,A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 763

14066 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E,H105Y) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 764

14067 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 765

14068 HC [hu anti-<huCDH19> 22G10.1 (1-470)(A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 766

14069 HC [hu anti-<huCDH19> 22G10.1 (1-470)(D72E,A99E) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRF
TISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPS
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICN
VNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 767

14070 HC [hu anti-<huCDH19> 22G10.1 (1-470)(H105Y) VH]::huIgG1z
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGR
FTISSDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
NVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF
LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 768

14071 HC [hu anti-<huCDH19> 16A4.1 (1-474)(T144L) VH]::huIgG1z
QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 769

14072 HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 770

14073 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 771

14074 HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 772

14075 HC [hu anti-<huCDH19> 19B5.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 773

14076 HC [hu anti-<huCDH19> 19B5.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 774

14077 HC [hu anti-<huCDH19> 23A10.3 (1-474)(L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 775

14078 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVF
PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ
TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 776

14079 HC [hu anti-<huCDH19> 23A10.3 (1-474)(R17G,D61E,D72E,L92Q) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGR
FTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 777

14080 HC [hu anti-<huCDH19> 23A10.3 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGR
FTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 778

14081 HC [hu anti-<huCDH19> 25G10.1 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH
KPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 779

14082 HC [hu anti-<huCDH19> 25G10.1 (1-469)(D109E,W132Y,W135Y) VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMS
VDTSKNQFSLKLSSVTAADTAVYYCAREGSSGYYRYFDPWGQGTLVTVSSASTKGPSVFPLAPSSKSTS
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 780

14083 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 781

14084 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 782

14085 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 783

14086 HC [hu anti-<huCDH19> 26D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 784

14087 HC [hu anti-<huCDH19> 26D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 785

14088 HC [hu anti-<huCDH19> 26D1.1 (1-469)(R27G,G82R) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 786

14089 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 787

14090 HC [hu anti-<huCDH19> 26F12.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 788

14091 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 789

14092 HC [hu anti-<huCDH19> 26F12.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQG
RLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 790

14093 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 791

14094 HC [hu anti-<huCDH19> 25F8.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 792

14095 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 793

14096 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSASTKGPSVFPLAPSS
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV
NHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 794

14097 HC [hu anti-<huCDH19> 25F8.1 (1-469)(F90Y,W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGR
VTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLYLHFDYWGQGTLVTVSSASTKGPSVFPLAPSSK
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 795

14098 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 796

14099 HC [hu anti-<huCDH19> 22D1.1 VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 797

14100 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 798

14101 HC [hu anti-<huCDH19> 22D1.1 (1-469)(W133Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLYLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 799

14102 HC [hu anti-<huCDH19> 22D1.1 (1-469)(F90Y) VH]::huIgG1z
QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRV
TMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSASTKGPSVFPLAPSSKS
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
HKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 800

13591 HC [hu anti-<huCDH19> 4F7 VH]::huIgG1z
QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISL
DTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 801

14301 HC [hu anti-<huCDH19> 2G6 VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 802

14302 HC [hu anti-<huCDH19> 2G6 (1-477)(R17G,K94N) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 803

14303 HC [hu anti-<huCDH19> 2G6 (1-477)(D61E,D72E) VH]::huIgG1z
QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 804

14304_HC [hu anti-<huCDH19> 2G6 (1-477)(R17G) VH]::huIgG1z
QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKD
RFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
SEQ ID NO: 805

TABLE IIId: Light Chain Variable and Contant Region Polynucleotide and Amino acid Sequences

13586_LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 806

13589_LC [hu anti-<huCDH19> 4A9 VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 807

13590_LC [hu anti-<huCDH19> 4B10 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 808

13874_LC [hu anti-<huCDH19> 17H8.2 VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 809

13875_LC [hu anti-<huCDH19> 16C1.1 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 810

13876_LC [hu anti-<huCDH19> 16A4.1 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 811

13877_LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 812

13878 LC [hu anti-<huCDH19> 20D3.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 813

13879 LC [hu anti-<huCDH19> 22D1.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 814

13880 LC [hu anti-<huCDH19> 25F8.1 VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 815

13881 LC [hu anti-<huCDH19> 26F12.1 VL]::huLLC-C2
QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 816

13882 LC [hu anti-<huCDH19> 26D1.1 VL]::huLLC-C2
HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 817

13883 LC [hu anti-<huCDH19> 25G10.1 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 818

13885 LC [hu anti-<huCDH19> 19B5.1 VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 819

14022 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC
SEQ ID NO: 820

14024 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE
AKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC

SEQ ID NO: 821

14025 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 822

14026 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 823

14027 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 824

14028 LC [hu anti-<huCDH19> 4A2 (1-236)(N30Q,T102A,P141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 825

14029 LC [hu anti-<huCDH19> 4A2 (1-236)(R29Q,N30S) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFTVYYCQQYGSSFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 826

14030 LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 827

14031 LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 828

14032 LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 829

14033 LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 830

14034 LC [hu anti-<huCDH19> 4F3 VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 831

14039 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 832

14040 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 833

14041 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 834

14042 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 835

14043 LC [hu anti-<huCDH19> 16C1.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISGLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 836

14044 LC [hu anti-<huCDH19> 16C1.1 (1-235)(G95R,H105Y,G141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 837

14045 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF

YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 838

14046 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 839

14047 LC [hu anti-<huCDH19> 17H8.2 (1-235)(G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 840

14048 LC [hu anti-<huCDH19> 17H8.2 (1-235)(S57Y,G149R) VL]::huKLC
DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC
SEQ ID NO: 841

14049 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y) VL]::huLLC-C2

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 842

14050 LC [hu anti-<huCDH19> 4F7 (1-239)(H57Y,D110E) VL]::huLLC-C2
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 843

14051 LC [hu anti-<huCDH19> 4F7 (1-239)(D110E) VL]::huLLC-C2
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 844

14052 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 845

14053 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 846

14054 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 847

14055 LC [hu anti-<huCDH19> 4B10 (1-236)(H45Q,A90T) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTD
FTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR
EAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN
RGEC
SEQ ID NO: 848

14056 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 849

14057 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 850

14058 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1

QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 851

14059 LC [hu anti-<huCDH19> 4A9 (1-239)(F47L,D110E) VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYESRLSGWVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 852

14060 LC [hu anti-<huCDH19> 20D3.1 (1-235)(S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 853

14061 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 854

14062 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI

SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 855

14063 LC [hu anti-<huCDH19> 20D3.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 856

14064 LC [hu anti-<huCDH19> 20D3.1 (1-235)(W109Y) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDESDYYCATYDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 857

14065 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 858

14066 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 859

14067 LC [hu anti-<huCDH19> 22G10.1 (1-234)(Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 860

14068 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 861

14069 LC [hu anti-<huCDH19> 22G10.1 (1-234)(V78F,Q97E,S98P) VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEF
TLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 862

14070 LC [hu anti-<huCDH19> 22G10.1 VL]::huKLC
EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEF
TLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 863

14071 LC [hu anti-<huCDH19> 16A4.1 (1-235)(G141Q) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTD
FTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP
REAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
NRGEC
SEQ ID NO: 864

14072 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 865

14073 LC [hu anti-<huCDH19> 19B5.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 866

14074 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 867

14075 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 868

14076 LC [hu anti-<huCDH19> 19B5.1 (1-235)(T11V,K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 869

14077 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 870

14078 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 871

14079 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S,D110E) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF

YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 872

14080 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42Y) VL]::huLLC-C2
SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 873

14081 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC
EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 874

14082 LC [hu anti-<huCDH19> 25G10.1 (1-235)(H105Y) VL]::huKLC

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
SEQ ID NO: 875

14083 LC [hu anti-<huCDH19> 26D1.1 (1-235)(S7P) VL]::huLLC-C2
HSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 876

14084 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 877

14085 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 878

14086 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 879

14087 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
SEQ ID NO: 880

14088 LC [hu anti-<huCDH19> 26D1.1 (1-235)(H1Q,S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 881

14089 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 882

14090 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 883

14091 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,D111E) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 884

14092 LC [hu anti-<huCDH19> 26F12.1 (1-235)(S7P,W109Y,D111E,N135Q) VL]::huLLC-C2
QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 885

14093 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 886

14094 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 887

14095 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDDSLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 888

14096 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS

SEQ ID NO: 889

14097 LC [hu anti-<huCDH19> 25F8.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGT
SASLAISGLQSEDEADYYCAAWDESLQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 890

14098 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 891

14099 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 892

14100 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y,D111E,N135Q) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 893

14101 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A,W109Y) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATYDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLI
SDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAPTECS
SEQ ID NO: 894

14102 LC [hu anti-<huCDH19> 22D1.1 (1-235)(K45Q,S102A) VL]::huLLC-C2
QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTS
ASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCL
ISDFYPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE
KTVAPTECS
SEQ ID NO: 895

13591 LC [hu anti-<huCDH19> 4F7 VL]::huLLC-C1
QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSG
TSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLGQPKANPTVTLFPPSSEELQANKATLVC
LISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV
EKTVAPTECS
SEQ ID NO: 896

14301 LC [hu anti-<huCDH19> 2G6 (1-234)(D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 897

14302 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1
SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY

PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 898

14303 LC [hu anti-<huCDH19> 2G6 (1-234)(C42S,D110E) VL]::huLLC-C1

SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTAT
LTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFY
PGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVA
PTECS
SEQ ID NO: 899

14304 LC [hu anti-<huCDH19> 23A10.3 (1-231)(C42S) VL]::huLLC-C2

SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTA
TLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDF
YPGAVTVAWKADSSPVKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTV
APTECS
SEQ ID NO: 900

TABLE IVa: HEAVY CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
14039 14303	AA	SYGMH	FIWYEGSNKYYAESVKD	RAGIIGTIGYYYGMDV
		SEQ ID NO: 28	SEQ ID NO: 901	SEQ ID NO: 30
14027	AA	SSGYYWS	YIYYTGSAYYNPSLKS	EGSSGWYFQY
		SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 902
14028	AA	SSGYYWS	YIYYTGSAYYNPSLKS	EGSSGYYFQY
		SEQ ID NO: 46	SEQ ID NO: 47	SEQ ID NO: 903
14059	AA	GYYWS	YFSYSGSTNYNPSLKS	NYAFHFDF
		SEQ ID NO: 52	SEQ ID NO: 53	SEQ ID NO: 904
14052	AA	SYDMH	VISYEGTNEYYAESVKG	ERYFDYSFDY
		SEQ ID NO: 58	SEQ ID NO: 905	SEQ ID NO: 906
14055	AA	SYDMH	VISYEGTNEYYAESVKG	ERYFDWSFDY
		SEQ ID NO: 58	SEQ ID NO: 905	SEQ ID NO: 60
14033	AA	SYDMD	VIWYEGSNKYYAESVRG	ETGEGWYFDL
		SEQ ID NO: 70	SEQ ID NO: 907	SEQ ID NO: 72
14034	AA	SYDMD	VIWYEGSNKYYAESVRG	ETGEGYYFDL
		SEQ ID NO: 70	SEQ ID NO: 907	SEQ ID NO: 908
14051	AA	SYSWS	YIYYSGSTNYNPSLKS	NYAFHFDY
		SEQ ID NO: 82	SEQ ID NO: 83	SEQ ID NO: 909
14046 14048	AA	SYYWS	YIYYIGSTNYNPSLKS	ESRYRSGWYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 910
14047	AA	SYYWS	YIYYIGSTNYNPSLKS	ESRYRSGYYDAFDI
		SEQ ID NO: 94	SEQ ID NO: 95	SEQ ID NO: 911
14042	AA	GYYWS	YIYYIGSTNYNPSLKS	EGSSGWYRWFDP
		SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 912
14043	AA	GYYWS	YIYYIGSTNYNPSLKS	DGSSGYYRYFDP
		SEQ ID NO: 100	SEQ ID NO: 101	SEQ ID NO: 913
14069	AA	SYAMN	TISGGGANTYYAESVKG	GGMGGYYYGMDV
		SEQ ID NO: 118	SEQ ID NO: 914	SEQ ID NO: 120

Ab	Type	CDR 1	CDR 2	CDR 3
14062 14063 14064	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 124	SEQ ID NO: 125	SEQ ID NO: 915
14100 14101	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHLDY
		SEQ ID NO: 130	SEQ ID NO: 131	SEQ ID NO: 916
14097	AA	SYYIH	IINPSGGSTRYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 136	SEQ ID NO: 137	SEQ ID NO: 917
14091 14092	AA	NYYMS	IINPSGGDSTYAQKFQG	GGIQLYLHFDY
		SEQ ID NO: 142	SEQ ID NO: 143	SEQ ID NO: 918
14087	AA	SYYMS	IIHPSGGDTTYAQKFQG	GGIKLYLHFDY
		SEQ ID NO: 148	SEQ ID NO: 149	SEQ ID NO: 919
14082	AA	GYYWS	YIYYIGSTNYNPSLKS	EGSSGYYRYFDP
		SEQ ID NO: 154	SEQ ID NO: 155	SEQ ID NO: 920
14079	AA	RYGIH	VIWYEGSNKYYAESVKG	RAGIPGTTGYYYGMDV
		SEQ ID NO: 160	SEQ ID NO: 921	SEQ ID NO: 162
14073 14076	AA	SYFIH	IINPISVSTSYAQKFQG	GGIQLYLHLDY
		SEQ ID NO: 1	SEQ ID NO: 2	SEQ ID NO: 3
	AA	SYGMH	VIWYDGSNKYYADSVKG	RAGIIGTTGYYYGMDV
		SEQ ID NO: 4	SEQ ID NO: 5	SEQ ID NO: 6

TABLE IVb: LIGHT CHAIN CDRs

Ab	Type	CDR 1	CDR 2	CDR 3
14039 14302 14303	AA	SGDRLGEKYTS	QDTKRPS	QAWESSTVV
		SEQ ID NO: 922	SEQ ID NO: 197	SEQ ID NO: 923
14301	AA	SGDRLGEKYTC	QDTKRPS	QAWESSTVV
		SEQ ID NO: 196	SEQ ID NO: 197	SEQ ID NO: 923
14022 14024 14025 14026 14027 14028	AA	RASRQISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 924	SEQ ID NO: 215	SEQ ID NO: 216
14029	AA	RASQSISSSYLA	GPSSRAT	QQYGSSFT
		SEQ ID NO: 925	SEQ ID NO: 215	SEQ ID NO: 216
14058 14059	AA	TGSSSNIGTGYAVH	GNNNRPS	QSYESRLSGWV
		SEQ ID NO: 220	SEQ ID NO: 221	SEQ ID NO: 926
14050 14051	AA	TGSSSNIGTGYDVH	GNSNRPS	QSYESSLSGWV
		SEQ ID NO: 250	SEQ ID NO: 251	SEQ ID NO: 927
14063	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDESLQGWV
		SEQ ID NO: 292	SEQ ID NO: 293	SEQ ID NO: 928
14064	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDDSLNGWV
		SEQ ID NO: 292	SEQ ID NO: 293	SEQ ID NO: 929
14099	AA	SGSSSNIGSNFVN	TNNQRPS	ATWDESMQGWV
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 930
14100	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDESMQGWV
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 931
14101	AA	SGSSSNIGSNFVN	TNNQRPS	ATYDDSMNGWV

Ab	Type	CDR 1	CDR 2	CDR 3
		SEQ ID NO: 298	SEQ ID NO: 299	SEQ ID NO: 932
14096	AA	SGSSSNIGRNFVN	TNNQRPS	AAWDESLNGWV
		SEQ ID NO: 304	SEQ ID NO: 305	SEQ ID NO: 933
14097	AA	SGSSSNIGRNFVN	TNNQRPS	AAWDESLQGWV
		SEQ ID NO: 304	SEQ ID NO: 305	SEQ ID NO: 934
14090 14091	AA	SGSRSNIGSNFVN	TNYQRPS	AVWDESLNGWV
		SEQ ID NO: 310	SEQ ID NO: 311	SEQ ID NO: 935
14092	AA	SGSRSNIGSNFVN	TNYQRPS	AVYDESLQGWV
		SEQ ID NO: 310	SEQ ID NO: 311	SEQ ID NO: 936
14085	AA	SGSRSNIGSNFVN	TNNQRPS	AVYDDSLNGWV
		SEQ ID NO: 316	SEQ ID NO: 317	SEQ ID NO: 937
14086 14087	AA	SGSRSNIGSNFVN	TNNQRPS	AVYDESLQGWV
		SEQ ID NO: 316	SEQ ID NO: 317	SEQ ID NO: 938
14077 14078 14304	AA	SGDRLGEKYVS	QDNKWPS	QAWDSSTVV
		SEQ ID NO: 939	SEQ ID NO: 329	SEQ ID NO: 330
14079	AA	SGDRLGEKYVS	QDNKWPS	QAWESSTVV
		SEQ ID NO: 939	SEQ ID NO: 329	SEQ ID NO: 940
14080	AA	SGDRLGEKYVY	QDNKWPS	QAWDSSTVV
		SEQ ID NO: 941	SEQ ID NO: 329	SEQ ID NO: 330
14075	AA	SGSRSNIGSNFVN	TNNQRPS	ATWDESMQGWV
		SEQ ID NO: 334	SEQ ID NO: 335	SEQ ID NO: 942
14076	AA	SGSRSNIGSNFVN	TNNQRPS	ATYDESMQGWV
		SEQ ID NO: 334	SEQ ID NO: 335	SEQ ID NO: 943

human and cynomologous monkey cadherin-19 sequences

TABLE V:

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
944	Human Cadherin-19	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
945	Human Cadherin-19	Human	nt	atgaactgttatttactgctgcgttttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaactctcaaacaaagaaagtcaagcagccagtgcgatctcatttgagagtgaagcgtggctgggtgtggaaccaatttttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagcttttgggagctggagctggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggagcgatccctctacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcctctacagcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaattaaactttcagatgttaatgacaataagcctatatttaaagaaagtttataccgcttgactgtctctgaatctgcacccactgggacttctataggaacaatcatggcatatgataatgacataggagagaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatagttatattaaaaaagaaagtggattttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcagctcatgaagtaccacactgaggcttccaccactttcattaagatccaggtggaagatgttgatgagcctcctcttttcctccttccatattatgtatttgaagtttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaataggaaatctcctatcaggtattctattactaggagcaaagtgttcaatatcaatgataatggtacaatcactacaagtaactcactggatcgtgaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacaatatagaacagatctcttcgatcccactgtatgtgcaagttcttaacatcaatgatcatgctcctgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaattcagactatcagtgcagtggatagagatgaatccatagaagagcaccatttttactttaatctatctgtagaagacactaacaattcaagttttacaatcatagataatcaagataacacagctgtcattttgactaatagaactggttttaaccttcaagaagaacctgtcttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaacacccttaccatccatgtctgtgactgtggtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaagtcatcattgctattctcatttgcattatgatcatatttgggtttatttttttgactttgggtttaaaacaacggagaaaacagattctatttcctgagaaaagtgaagatttcagagagaatatattccaatatgatgatgaagggggtggagaagaagatacagaggcctttgatatagcagagctgaggagtagtaccataatgcgggaacgcaagactcggaaaaccacaagcgctgagatcaggagcctatacaggcagtctttgcaagtt

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				ggccccgacagtgccatattcaggaaattcattctggaaaagctcgaagaagctaatactgatccgtgtgcccctcctttgattc cctccagacctacgcttttgagggaacagggtcattagctggatccctgagctccttagaatcagcagtctctgatcaggatgaaa gctatgattaccttaatgagttgggacctcgctttaaaagattagcatgcatgtttggttctgcagtgcagtcaaataattag
946	Cyno Cadherin-19	Macaca fascicularis	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGA GSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTA SDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKE SLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKVKNHHVDEQ LMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTITTTNSLDR EISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNS SSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFKTEVIIAIL ICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRSLYRQSLQV GPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
947	Cyno Cadherin-19	Macaca fascicularis	nt	ATGAATTGTTATTTACTGCTGCCTTTTATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAA GAAAGTCCAGCAGCCAGTAGGATCTCATCTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTGTACCAGAGGAAATGAATA CGACTAGTCATCACGTTGGCCGGCTAAGATCTGATTTAGACAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCT GGAAGTACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATAGAGAAGCTTGATAGAGAGGAGCGATCCCTCTACATCTT AAGAGCCCAGGTAATAGACATCACTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTCATCAAAGTTTCGGATATCAATGACA ATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTCATCCAGGTGACAGCA AGTGATGCTGATGACCCTTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTATTACAAGGCCAGCCATATTTTTCTGTTGAACC AACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGA TTGGTCAGCCAGGAGCGTTGTCTGGAACAACGAGTGTATTAATTAAACTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAA AGTTTATACCGCCTGACGGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGA GAATGCAGAAATGGATTACAGCATTGAAGAGGATGATTCACAGACATTTGACATTATTACTAATCATGAAACTCAAGAAGGAATAG TTATATTAAAAAAGAAAGTGAATTTTGAGCACCAGAACCACTATGGTATTAGAGCAAAAGTTAAAAACCATCATGTTGATGAGCAG CTCATGAAATACCACACTGAAGCTTCCACCACTTTCATTAAGATCCAGGTGGAAGATGTTGATGAGCCTCCTCTTTTCCTCCTTCC GTATTACATATTTGAAATTTTTGAAGAAACCCCACAAGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCGATGATAATGGTACAATCACTACAACTAACTCACTGGATCGG GAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCACAGAAAAATACAATATAGAGCAGATCTCTTCGATCCCAGTGTATGTGCA AGTTCTTAATATCAATGATCATGCTCCTGAGTTCTCTCAATACTATGAGAGTTATGTTTGTGAAAATGCAGGCTCTGGTCAGGTAA TTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTTACTTTAATCTATCTGTAGAAGACACTAACTCT TCAAGTTTTACAATCATAGACAATCAAGATAACACAGCTGTCATTTTGACTAATAGAACTGGTTTTAACCTTCAAGAAGAGCCCAT CTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTACCATCCATGTCTGTGACTGTG ATGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTATGCTTTCCATGGGATTCAAGACAGAAGTCATCATTGCTATTCTC ATTTGCATTATGGTAATATTTGGGTTTATTTTTTTGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCCTGAGAAAAG TGAAGATTTCAGAGAGAATATATTCCGATATGATGACGAAGGGGGTGGAGAAGAAGATACAGAGGCCTTTGACGTAGCAGCGCTGA GGAGTAGCACCATAATGCGGGAACGCAAGACTCGGAAAACCACCAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GGCCCCGACAGTGCCATATTCAGGAAGTTCATCCTGGAAAAGCTCGAAGAAGCTGATACTGATCCGTGTGCCCCTCCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCAGCTGTCTCTGATCAGGATGAAAGCTATGATTACCTTAACGAGTTGGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAG
948	secreted Cadherin-19 ecto-domain (amino acids 1-596)	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTE
949	secreted Cadherin-19 ecto-domain (amino acids 1-596)	Human	nt	atgaactgttatttactgctgcgttttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaactctcaaacaaagaaagtcaagcagccagtgcgatctcatttgagagtgaagcgtggctgggtgtggaaccaatttttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagcttttgggagctggagctggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggagcgatccctctacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcctctacagcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaattaaactttcagatgttaatgacaataagcctatatttaaagaaagtttataccgcttgactgtctctgaatctgcacccactgggacttctataggaacaatcatggcatatgataatgacataggagagaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatagttatattaaaaaagaaagtggattttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcagctcatgaagtaccacactgaggcttccaccactttcattaagatccaggtggaagatgttgatgagcctcctcttttcctccttccatattatgtatttgaagtttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaataggaaatctcctatcaggtattctattactaggagcaaagtgttcaatatcaatgataatggtacaatcactacaagtaactcactggatcgtgaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacaatatagaacagatctcttcgatcccactgtatgtgcaagttcttaacatcaatgatcatgctcctgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaattcagactatcagtgcagtggatagagatgaatccatagaagagcaccatttttactttaatctatctgtagaagacactaacaattcaagttttacaatcatagataatcaagataacacagctgtcattttgactaatagaactggttttaaccttcaagaagaacctgtcttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaacacccttaccatccatgtctgtgactgtggtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaa
950	truncated membrane bound form of human cadherin-19	Human	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDR

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(amino acids 1-624)			EISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNN SSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAIL ICIMIIFGFIFLTLGLKQRRKQ
951	truncated membrane bound form of human cadherin-19 (amino acids 1-624)	Humanl	nt	atgaactgttatttactgctgcgttttatgttgggaattcctctcctatggccttgtcttggagcaacagaaaactctcaaacaaa gaaagtcaagcagccagtgcgatctcatttgagagtgaagcgtggctgggtgtggaaccaatttttgtaccagaggaaatgaata cgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagcttttgggagctggagct ggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggagcgatccctctacatctt aagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgaca atgaaccaaaattcctagatgaaccttatgaggccattgtaccagagatgtctccagaaggaacattagttatccaggtgacagca agtgatgctgacgatccctcaagtggtaataatgctcgtctcctctacagcttacttcaaggccagccatatttttctgttgaacc aacaacaggagtcataagaatatcttctaaaatggatagagaactgcaagatgagtattgggtaatcattcaagccaaggacatga ttggtcagccaggagcgttgtctggaacaacaagtgtattaattaaactttcagatgttaatgacaataagcctatatttaaagaa agtttataccgcttgactgtctctgaatctgcacccactgggacttctataggaacaatcatggcatatgataatgacataggaga gaatgcagaaatggattacagcattgaagaggatgattcgcaaacatttgacattattactaatcatgaaactcaagaaggaatag ttatattaaaaaagaaagtggatttgagcaccagaaccactacggtattagagcaaaagttaaaaaccatcatgttcctgagcag ctcatgaagtaccacactgaggcttccaccactttcattaagatccaggtggaagatgttgatgagcctcctcttttcctccttcc atattatgtatttgaagtttttgaagaaaccccacagggatcatttgtaggcgtggtgtctgccacagacccagacaataggaaat ctcctatcaggtattctattactaggagcaaagtgttcaatatcaatgataatggtacaatcactacaagtaactcactggatcgt gaaatcagtgcttggtacaacctaagtattacagccacagaaaaatacaatatagaacagatctcttcgatcccactgtatgtgca agttcttaacatcaatgatcatgctcctgagttctctcaatactatgagacttatgtttgtgaaaatgcaggctctggtcaggtaa ttcagactatcagtgcagtggatagagatgaatccatagaagagcaccatttttactttaatctatctgtagaagacactaacaat tcaagttttacaatcatagataatcaagataacacagctgtcattttgactaatagaactggttttaaccttcaagaagaacctgt cttctacatctccatcttaattgccgacaatggaatcccgtcacttacaagtacaaacacccttaccatccatgtctgtgactgtg gtgacagtgggagcacacagacctgccagtaccaggagcttgtgctttccatgggattcaagacagaagtcatcattgctattctc atttgcattatgatcatatttgggtttatttttttgactttgggtttaaaacaacggagaaaacag
952	C137897 huCDH19 (44-141) muCDH19 (140-770)	artificial	aa	GWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVE PESEFVIKVSDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRE LQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSK IFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGT IVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQF YETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPS LTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEG GGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAG SLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
953	C137897 huCDH19	artificial	nt	ggctgggtgtggaaccaatttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaa tggaaacaattctttccagtacaagcttttgggagctggagctggaagtacttttatcattgatgaaagaacaggtgacatatatg

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(44-141) muCDH19 (140-770)			ccatacagaagcttgatagagaggagcgatccctctacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaacctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcctatacaacttagaacgaggtcaaccatacttttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaagatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagctgtcagatattaatgacaacaagccaatattcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaacatcaatagggaaaattatggcatatgatgatgacataggggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatatttgacataatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgattttgagcagcagagctattatggcattagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaagttcaagtagaagatgaagatgaacctcctgttttcctcttaccatattacatacttgaaattcctgaaggaaaaccatatggaacaattgtggggacggtttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatatcaatgacaatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaacatacaatgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccagagttctctcaattctatgagacttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaagatcaccattttttactttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaattctgagtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatctctcacaagcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaacttgtgctaacaaggacttctctttatcatgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggtttttcttttttgattcttgctctgaaacagcgaagaaaggagactctatttccagagaagactgaagactttagggagaatatatttgctatgatgatgaaggcggcggggaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaagagtgcggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagcttgaagaagccaacacagacccatgtgctcccccctttgattcactacagacgtttgcctatgagggaacagggtcatcagctggctctctgagctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcgttttaaaagattagcaagcatgtttggctctgcagtacaacccaacaattag
954	C137896 huCDH19 (44-249) muCDH19 (248-770)	artificial	aa	GWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
955	C137896 huCDH19 (44-249)	artificial	nt	ggctgggtgtggaaccaatttttgtaccagaggaaatgaatacgactagtcatcacatcggccagctaagatctgatttagacaatggaaacaattctttccagtacaagcttttgggagctggagctggaagtacttttatcattgatgaaagaacaggtgacatatatgccatacagaagcttgatagagaggagcgatccctctacatcttaagagcccaggtaatagacatcgctactggaagggctgtggaa

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	muCDH19 (248-770)			cctgagtctgagtttgtcatcaaagtttcggatatcaatgacaatgaaccaaaattcctagatgaaccttatgaggccattgtacc agagatgtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcc tctacagcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaa ctgcaagatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaat taaactttcagatgttaatgacaacaagccaatattcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaa catcaatagggaaaattatggcatatgatgatgacatagggagaatgcagagatggagtacagcattgaagatgatgattcaaaa atatttgacataatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgattttgagcagcagagctatta tggcattagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaag ttcaagtagaagatgaagatgaacctcctgttttcctcttaccatattacatacttgaaattcctgaaggaaaaccatatggaaca attgtggggacggtttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatat caatgacaatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaa catacaatgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccagagttctctcaattc tatgagacttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaaga tcaccattttttactttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaa ttctgagtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatct ctcacaagcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaacttgtgctaacaaggacttct ctttatcatgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggtttttcttttttgattcttg ctctgaaacagcgaagaaaggagactctatttccagagaagactgaagactttagggagaatatatttgctatgatgatgaaggc ggcggggaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaa gagtgcggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagc ttgaagaagccaacacagacccatgtgctcccccctttgattcactacagacgtttgcctatgagggaacagggtcatcagctggc tctctgagctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcgttttaaaagatt agcaagcatgtttggctctgcagtacaacccaacaattag
956	C137913 muCDH19 (44-139) huCDH19 (142-249) muCDH19 (248-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQ DEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIF DIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
957	C137913 muCDH19 (44-139) huCDH19	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatgg aaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac agaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaa tccgagtttgtcatcagagttttggatatcaatgacaatgaaccaaaattcctagatgaaccttatgaggccattgtaccagagat

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	(142-249) muCDH19 (248-770)			gtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcctctaca gcttacttcaaggccagccatatttttctgttgaaccaacaacaggagtcataagaatatcttctaaaatggatagagaactgcaa gatgagtattgggtaatcattcaagccaaggacatgattggtcagccaggagcgttgtctggaacaacaagtgtattaattaaact ttcagatgttaatgacaacaagccaatattcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaacatcaa tagggaaaattatggcatatgatgatgacataggggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatattt gacataatcattgacaatgacacccaagaagggatagttatacttaaaaagaaagttgattttgagcagcagagctattatggcat tagagctaaggttaaaaactgccatgtggatgaagagcttgcacctgcccatgttaacgcttccacaacctacattaaagttcaag tagaagatgaagatgaacctcctgttttcctcttaccatattacatacttgaaattcctgaaggaaaaccatatggaacaattgtg gggacggtttctgccacagacccagatcgaagacaatctcctatgagatattatctcactggaagcaaaatgtttgatatcaatga caatggaacaataatcaccactaacatgcttgacagagaggtcagtgcttggtacaacttgactgtcacagctactgaaacataca atgtacaacagatctcttcagcccatgtttatgtacaagtctttaacattaacgacaatgctccagagttctctcaattctatgag acttatgtttgtgaaaatgctgaatctggtgagatagttcagatcatcagtgcaattgatagagatgagtccatagaagatcacca tttttactttaatcactctctggaagacacaaacaactcaagttttatgctaacagacaatcaagataacacagctgtaattctga gtaatagaactggtttcaatcttaaagaagagcctgtcttctacatgatcatcttgattgctgataacgggatcccatctctcaca agcacaaacactctcactatccaagtctgtgactgtggagacagtagaaacacagaaacttgtgctaacaagggacttctctttat catgggattcagaacagaggcaataattgccatcatgatatgtgttatggtaatatttgggtttttcttttttgattcttgctctga aacagcgaagaaaggagactctatttccagagaagactgaagactttagggagaatatattttgctatgatgatgaaggcggcggg gaagaagactcggaagcctttgacatcgtagagctgagacaaagtacagtaatgagagaaagaaagcctcagagaagcaagagtgc ggagatcaggagcttgtacaggcagtccctgcaggtgggcccagacagtgccatatttcgaaaatttatcctagagaagcttgaag aagccaacacagacccatgtgctcccccctttgattcactacagacgtttgcctatgagggaacagggtcatcagctggctctctg agctccttggcatccagagacactgatcaggaggatgacttcgactaccttaatgacctgggacctcgttttaaaagattagcaag catgtttggctctgcagtacaacccaacaattag
958	C137847 muCDH19 (44-139) huCDH19 (142-364) muCDH19 (363-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETE SEFVIRVLDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQ DEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTF DIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFLLPYYILEIPEGKPYGTIV GTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYE TYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLT STNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGG EEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSL SSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
959	C137847 muCDH19 (44-139) huCDH19 (142-364)	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatgg aaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatac agaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaa tccgagtttgtcatcagagttttggatatcaatgacaatgaaccaaaattcctagatgaaccttatgaggccattgtaccagagat gtctccagaaggaacattagttatccaggtgacagcaagtgatgctgacgatccctcaagtggtaataatgctcgtctcctctaca

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
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960	C137911 muCDH19 (44-247) huCDH19 (250-364) muCDH19 (363-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
961	C137911 muCDH19 (44-247) huCDH19 (250-364) muCDH19	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatggaaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatacagaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaatccgagtttgtcatcagagttttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcctatacaacttagaacgaggtcaaccatacttttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaa

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962	C137917 muCDH19 (44-362) huCDH19 (365-772)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
963	C137917 muCDH19 (44-362) huCDH19 (365-772)	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatggaaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatacagaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaatccgagtttgtcatcagagttttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcctatacaacttagaacgaggtcaaccatacttttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaagatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagct

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
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964	C137915 muCDH19 (44-461) huCDH19 (464-772)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
965	C137915 muCDH19 (44-461) huCDH19 (464-772)	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatggaaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatacagaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaatccgagtttgtcatcagagttttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcctatacaacttagaacgaggtcaaccatacttttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaagatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagctgtcagatattaatgacaacaagccaatattcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaacatcaa

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966	C71144 muCDH19 (44-770)	artificial	aa	AWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
967	C71144 muCDH19 (44-770)	artificial	nt	gcctgggtgtggagaccatttgttgttctagaagaaatggatgatatacaatgtgttggaaagctaagatctgacttagacaatggaaacaactctttccagtacaagctactggggattggcgctggaagctttagcattaatgaaagaacaggtgaaatatgtgccatacagaagcttgatagagaggaaaaatccctctacattctgagagcccaggtaatagacaccactattgggaaggctgtggaaactgaatccgagtttgtcatcagagttttggatatcaatgacaatgaacccagattcctagatgaaccatatgaggccattgtacctgagatgtctccagaaggaacatttgtcatcaaggtgacagccaatgacgcagatgatccttcaactggctatcatgctcgcatcctatacaacttagaacgaggtcaaccatacttttctgttgagccaacaacaggagtcataaggatatcttctaagatggatagagagttgcaagatacatactgtgtaattattcaagccaaggacatgctcggtcagcctggagccttgtctggaacaacaaccgtatcaattaagctgtcagatattaatgacaacaagccaatattcaaagaaagtttctaccgcttcactatatctgaatctgcacccattggaacatcaatagggaaaattatggcatatgatgatgacataggggagaatgcagagatggagtacagcattgaagatgatgattcaaaaatattt

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968	Flag Tag	artificial	aa	DYKDDDDK
969	Flag Tag	artificial	nt	gactacaaagacgatgacgacaag

Bispecific binding molecules

TABLE VI:

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
970	CDR-H1 of CDH19 2G6	artificial	AA	SYGMH
971	CDR-H2 of CDH19 2G6	artificial	AA	FIWYDGSNKYYADSVKD
972	CDR-H3 of CDH19 2G6	artificial	AA	RAGIIGTIGYYYGMDV
973	CDR-L1 of CDH19 2G6	artificial	AA	SGDRLGEKYTC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
974	CDR-L2 of CDH19 2G6	artificial	AA	QDTKRPS
975	CDR-L3 of CDH19 2G6	artificial	AA	QAWDSSTVV
976	VH of CDH19 2G6	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
977	VH of CDH19 2G6	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
978	VL of CDH19 2G6	artificial	NT	TACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCTGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
979	VL of CDH19 2G6	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
980	VH-VL of CDH19 2G6	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCTGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
981	VH-VL of CDH19 2G6	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
982	CDH19 2G6 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
983	CDR-H1 of CDH19 16E2.1	artificial	AA	SYGMH
984	CDR-H2 of CDH19 16E2.1	artificial	AA	VIWYDGSNKYYADSVKG
985	CDR-H3 of CDH19 16E2.1	artificial	AA	DGWELSFDY
986	CDR-L1 of CDH19 16E2.1	artificial	AA	RASQGISNYLA
987	CDR-L2 of CDH19 16E2.1	artificial	AA	AASSLQS
988	CDR-L3 of CDH19 16E2.1	artificial	AA	QHYFTYPRT
989	VH of CDH19 16E2.1	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCATCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACATCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGGGACGGCTGGGAGCTGTCCTTCGATTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
990	VH of CDH19 16E2.1	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQTPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDISKNTLYLQMNSLRVEDTAVYYCARDGWELSFDYWGQGTLVTVSS
991	VL of CDH19 16E2.1	artificial	NT	GACATCCAGATGACCCAGTCCCCCTCCAGCCTGTCCGCCTCCGTGGGCGACAGAGTGACCATCACCTGTCGGGCCTCCCAGGGCATCAGCAACTACCTGGCCTGGCTGCAGCAGAAGCCCGGCAAGGCCCCCAAGTCCCTGATCTACGCCGCCAGCTCCCTGCAGTCCGGCGTGCCCTCCAAGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCTCCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCACTACTTCACCTACCCCCGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAG
992	VL of CDH19 16E2.1	artificial	AA	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQHYFTYPRTFGQGTKVEIK
993	VH-VL of CDH19 16E2.1	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCATCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACATCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGGGACGGCTGGGAGCTGTCCTTCGATTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGACATCCAGATGACCCAGTCCCCCTCCAGCCTGTCCGCCTCCGTGGGCGACAGAGTGACCATCACCTGTCGGGCCTCCCAGGGCATCAGCAACTACCTGGCCTGGCTGCAGCAGAAGCCCGGCAAGGCCCCCAAGTCCCTGATCTACGCCGCCAGCTCCCTGCAGTCCGGCGTGCCCTCCAAGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCTCCAGCCTGCAGCCCGAGGACTTCGCCACCTACTACTGCCAGCACTACTTCACCTACCCCCGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
994	VH-VL of CDH19 16E2.1	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQTPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDISKNTLYLQMNSLRVEDTAVYYCARDGWELSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQHYFTYPRTFGQGTKVEIK
995	CDH19 16E2.1 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQTPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDISKNTLYLQMNSLRVEDTAVYYCARDGWELSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQHYFTYPRTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
996	CDR-H1 of CDH19 17H8.2	artificial	AA	SYYWS
997	CDR-H2 of CDH19 17H8.2	artificial	AA	YIYYIGSTNYNPSLKS
998	CDR-H3 of CDH19 17H8.2	artificial	AA	DSRYRSGWYDAFDI
999	CDR-L1 of CDH19 17H8.2	artificial	AA	RASQSVAGSYLA
1000	CDR-L2 of CDH19 17H8.2	artificial	AA	GASSRAT
1001	CDR-L3 of CDH19 17H8.2	artificial	AA	QQYGKSPIT
1002	VH of CDH19 17H8.2	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCAACTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCCTGTACTACTGCGCCAGAGACTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGGCACCATGGTCACCGTGTCCTCT
1003	VH of CDH19 17H8.2	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
1004	VL of CDH19 17H8.2	artificial	NT	GATATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGTGGCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTCCGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAG
1005	VL of CDH19 17H8.2	artificial	AA	DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMK

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1006	VH-VL of CDH19 17H8.2	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CAACTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCA ACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACC GCCGCTGACACCGCCCTGTACTACTGCGCCAGAGACTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGG CACCATGGTCACCGTGTCCTCTGGTGGCGGAGGCTCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCCGATATCGTGCTGACCCAGT CCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGTGGCCGGCTCCTACCTGGCT TGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTCCGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTC CGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACG GCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAG
1007	VH-VL of CDH19 17H8.2	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLA WYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMK
1008	CDH19 17H8.2 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLA WYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKSGGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1009	CDR-H1 of CDH19 19B5.1	artificial	AA	SYFIH
1010	CDR-H2 of CDH19 19B5.1	artificial	AA	IINPISVSTSYAQKFQG
1011	CDR-H3 of CDH19 19B5.1	artificial	AA	GGIQLWLHLDY
1012	CDR-L1 of CDH19 19B5.1	artificial	AA	SGSRSNIGSNFVN
1013	CDR-L2 of CDH19 19B5.1	artificial	AA	TNNQRPS
1014	CDR-L3 of CDH19 19B5.1	artificial	AA	ATWDDSMNGWV
1015	VH of CDH19 19B5.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTT CACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCA CCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTG CGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCT GGTCACCGTGTCCTCT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1016	VH of CDH19 19B5.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1017	VL of CDH19 19B5.1	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCCTCCACCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1018	VL of CDH19 19B5.1	artificial	AA	QSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVL
1019	VH-VL of CDH19 19B5.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCCCTGACCCAGCCTCCCTCCACCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1020	VH-VL of CDH19 19B5.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVL
1021	CDH19 19B5.1 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSTTGTPGQRVTISCSGSRSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1022	CDH-H1 of CDH19 20D3.1	artificial	AA	SYFIH
1023	CDR-H2 of CDH19 20D3.1	artificial	AA	IINPISVSTSYAQKFQG
1024	CDR-H3 of CDH19 20D3.1	artificial	AA	GGIQLWLHFDY
1025	CDR-L1 of CDH19 20D3.1	artificial	AA	SGSSSNIGSNFVN
1026	CDR-L2 of	artificial	AA	TNNQRPS

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	CDH19 20D3.1			
1027	CDR-L3 of CDH19 20D3.1	artificial	AA	ATWDDSLNGWV
1028	VH of CDH19 20D3.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1029	VH of CDH19 20D3.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1030	VL of CDH19 20D3.1	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1031	VL of CDH19 20D3.1	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVL
1032	VH-VL of CDH19 20D3.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCTCAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1033	VH-VL of CDH19 20D3.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVL
1034	CDH19 20D3.1 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1035	CDR-H1 of	artificial	AA	SYFIH

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	CDH19 22D1.1			
1036	CDR-H2 of CDH19 22D1.1	artificial	AA	IINPISVSTSYAQKFQG
1037	CDR-H3 of CDH19 22D1.1	artificial	AA	GGIQLWLHLDY
1038	CDR-L1 of CDH19 22D1.1	artificial	AA	SGSSSNIGSNFVN
1039	CDR-L2 of CDH19 22D1.1	artificial	AA	TNNQRPS
1040	CDR-L3 of CDH19 22D1.1	artificial	AA	ATWDDSMNGWV
1041	VH of CDH19 22D1.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGCGGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCT
1042	VH of CDH19 22D1.1	artificial	AA	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1043	VL of CDH19 22D1.1	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCTTCCGCTACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1044	VL of CDH19 22D1.1	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVL
1045	VH-VL of CDH19 22D1.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGCGGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCCCTGACCCAGCCTCCTTCCGCTACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1046	VH-VL of	artificial	AA	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWY

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	CDH19 22D1.1			KQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVL
1047	CDH19 22D1.1 x I2C	artificial		QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCATWDDSMNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1048	CDR-H1 of CDH19 22G10.1	artificial	AA	SYAMN
1049	CDR-H2 of CDH19 22G10.1	artificial	AA	TISGGGANTYYADSVKG
1050	CDR-H3 of CDH19 22G10.1	artificial	AA	GGMGGYYYGMDV
1051	CDR-L1 of CDH19 22G10.1	artificial	AA	RASQSISSNLA
1052	CDR-L2 of CDH19 22G10.1	artificial	AA	GAFTRAT
1053	CDR-L3 of CDH19 22G10.1	artificial	AA	QQYNYWPLT
1054	VH of CDH19 22G10.1	artificial	NT	GAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1055	VH of CDH19 22G10.1	artificial	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
1056	VL of CDH19 22G10.1	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCA

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				TCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAG
1057	VL of CDH19 22G10.1	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIK
1058	VH-VL of CDH19 22G10.1	artificial	NT	GAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAG
1059	VH-VL of CDH19 22G10.1	artificial	AA	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIK
1060	CDH19 22G10.1 x I2C	artificial		EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISSDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1061	CDR-H1 of CDH19 23A10.3	artificial	AA	RYGIH
1062	CDR-H2 of CDH19 23A10.3	artificial	AA	VIWYDGSNKYYADSVKG
1063	CDR-H3 of CDH19 23A10.3	artificial	AA	RAGIPGTTGYYYGMDV
1064	CDR-L1 of CDH19 23A10.3	artificial	AA	SGDRLGEKYVC

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1065	CDR-L2 of CDH19 23A10.3	artificial	AA	QDNKWPS
1066	CDR-L3 of CDH19 23A10.3	artificial	AA	QAWDSSTVV
1067	VH of CDH19 23A10.3	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCTGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1068	VH of CDH19 23A10.3	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1069	VL of CDH19 23A10.3	artificial	NT	TACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGTGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1070	VL of CDH19 23A10.3	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1071	VH-VL of CDH19 23A10.3	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCTGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGTGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1072	VH-VL of CDH19 23A10.3	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1073	CDH19 23A10.3 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVCWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED

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				TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1074	CDR-H1 of CDH19 25F8.1	artificial	AA	SYYIH
1075	CDR-H2 of CDH19 25F8.1	artificial	AA	IINPSGGSTRYAQKFQG
1076	CDR-H3 of CDH19 25F8.1	artificial	AA	GGIQLWLHFDY
1077	CDR-L1 of CDH19 25F8.1	artificial	AA	SGSSSNIGRNFVN
1078	CDR-L2 of CDH19 25F8.1	artificial	AA	TNNQRPS
1079	CDR-L3 of CDH19 25F8.1	artificial	AA	AAWDDSLNGWV
1080	VH of CDH19 25F8.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGCTACACCTTCACCAGCTACTACATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCCGGCGGCTCCACCAGATACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1081	VH of CDH19 25F8.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1082	VL of CDH19 25F8.1	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCCGGAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCGCCTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1083	VL of CDH19 25F8.1	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVL
1084	VH-VL of CDH19 25F8.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGCTACACCTTCACCAGCTACTACATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCCGGCGGCTCCACCAGATACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCTCAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCCGGAACTTCGTGAACTGGTACAAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTC

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				CAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGTCCGACTACTACTGTGCCGCCTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1085	VH-VL of CDH19 25F8.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVL
1086	CDH19 25F8.1 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYKQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDESDYYCAAWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1087	CDR-H1 of CDH19 25G10.1	artificial	AA	GYYWS
1088	CDR-H2 of CDH19 25G10.1	artificial	AA	YIYYIGSTNYNPSLKS
1089	CDR-H3 of CDH19 25G10.1	artificial	AA	DGSSGWYRWFDP
1090	CDR-L1 of CDH19 25G10.1	artificial	AA	RASQSVSSSYLA
1091	CDR-L2 of CDH19 25G10.1	artificial	AA	GASSRAT
1092	CDR-L3 of CDH19 25G10.1	artificial	AA	QQYGNSPLT
1093	VH of CDH19 25G10.1	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCTCCGGCTGGTATCGTTGGTTCGACCCTTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC

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1094	VH of CDH19 25G10.1	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
1095	VL of CDH19 25G10.1	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTTCGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCTCCCGGCTGGAACCCGAGGACTTCGCTGTGTACCACTGCCAGCAGTACGGCAACAGCCCCCTGACCTTCGGCGGAGGCACCAAGGTGGAAATCAAG
1096	VL of CDH19 25G10.1	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIK
1097	VH-VL of CDH19 25G10.1	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCTCCGGCTGGTATCGTTGGTTCGACCCTTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTTCGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCTCCCGGCTGGAACCCGAGGACTTCGCTGTGTACCACTGCCAGCAGTACGGCAACAGCCCCCTGACCTTCGGCGGAGGCACCAAGGTGGAAATCAAG
1098	VH-VL of CDH19 25G10.1	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIK
1099	CDH19 25G10.1 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYHCQQYGNSPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1100	CDH19-H1 of CDH19 26D1.1	artificial	AA	SYYMS
1101	CDR-H2 of CDH19 26D1.1	artificial	AA	IIHPSGGDTTYAQKFQG
1102	CDR-H3 of CDH19 26D1.1	artificial	AA	GGIKLWLHFDY
1103	CDR-L1 of CDH19 26D1.1	artificial	AA	SGSRSNIGSNFVN

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1104	CDR-L2 of CDH19 26D1.1	artificial	AA	TNNQRPS
1105	CDR-L3 of CDH19 26D1.1	artificial	AA	AVWDDSLNGWV
1106	VH of CDH19 26D1.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1107	VH of CDH19 26D1.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1108	VL of CDH19 26D1.1	artificial	NT	CATTCCGTGCTGACCCAGTCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1109	VL of CDH19 26D1.1	artificial	AA	HSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1110	VH-VL of CDH19 26D1.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCATTCCGTGCTGACCCAGTCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1111	VH-VL of CDH19 26D1.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSHSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1112	CDH19 26D1.1 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSHSVLTQSPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH

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1113	CDR-H1 of CDH19 26F12.1	artificial	AA	NYYMS
1114	CDR-H2 of CDH19 26F12.1	artificial	AA	IINPSGGDSTYAQKFQG
1115	CDR-H3 of CDH19 26F12.1	artificial	AA	GGIQLWLHFDY
1116	CDR-L1 of CDH19 26F12.1	artificial	AA	SGSRSNIGSNFVN
1117	CDR-L2 of CDH19 26F12.1	artificial	AA	TNYQRPS
1118	CDR-L3 of CDH19 26F12.1	artificial	AA	AVWDDSLNGWV
1119	VH of CDH19 26F12.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1120	VH of CDH19 26F12.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1121	VL of CDH19 26F12.1	artificial	NT	CAGTCTGTGCTGACCCAGTCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1122	VL of CDH19 26F12.1	artificial	AA	QSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1123	VH-VL of CDH19 26F12.1	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGTCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1124	VH-VL of CDH19 26F12.1	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1125	CDH19 26F12.1 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQSPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1126	CDR-H1 of CDH19 4A9	artificial	AA	GYYWS
1127	CDR-H2 of CDH19 4A9	artificial	AA	YFSYSGSTNYNPSLKS
1128	CDR-H3 of CDH19 4A9	artificial	AA	NWAFHFDF
1129	CDR-L1 of CDH19 4A9	artificial	AA	TGSSSNIGTGYAVH
1130	CDR-L2 of CDH19 4A9	artificial	AA	GNNNRPS
1131	CDR-L3 of CDH19 4A9	artificial	AA	QSYDSRLSGWV
1132	VH of CDH19 4A9	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGTTCGCCTACTTCTCCTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCCTGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGATTTCTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1133	VH of CDH19 4A9	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS

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1134	VL of CDH19 4A9	artificial	NT	CAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGAGAGTGACCATCTCCTGCACCGGCTCCTCCAGCAACATCGGCACCGGCTACGCCGTGCACTGGTATCAGCAGTTCCCCGGCACCGCCCCCAAGCTGCTGATCTACGGCAACAACAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGACTCCCGGCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1135	VL of CDH19 4A9	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL
1136	VH-VL of CDH19 4A9	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGTTCGCCTACTTCTCCTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCCTGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGATTTCTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGAGAGTGACCATCTCCTGCACCGGCTCCTCCAGCAACATCGGCACCGGCTACGCCGTGCACTGGTATCAGCAGTTCCCCGGCACCGCCCCCAAGCTGCTGATCTACGGCAACAACAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGACTCCCGGCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTG
1137	VH-VL of CDH19 4A9	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL
1138	CDH19 4A9 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQFPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1139	CDR-H1 of CDH19 4B10	artificial	AA	SYDMH
1140	CDR-H2 of CDH19 4B10	artificial	AA	VISYDGTNEYYADSVKG
1141	CDR-H3 of CDH19 4B10	artificial	AA	ERYFDWSFDY
1142	CDR-L1 of CDH19 4B10	artificial	AA	RASQSVSNTYLA
1143	CDR-L2 of CDH19 4B10	artificial	AA	GASSRAT
1144	CDR-L3 of	artificial	AA	QQYSNSWT

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	CDH19 4B10			
1145	VH of CDH19 4B10	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGC
1146	VH of CDH19 4B10	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
1147	VL of CDH19 4B10	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCACCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCGCCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAG
1148	VL of CDH19 4B10	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIK
1149	VH-VL of CDH19 4B10	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCACCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCGCCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAG
1150	VH-VL of CDH19 4B10	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIK
1151	CDH19 4B10 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYHQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFALTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1152	CDR-H1 of CDH19 4F3	artificial	AA	SYDMD
1153	CDR-H2 of	artificial	AA	VIWYDGSNKYYADSVRG

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	CDH19 4F3			
1154	CDR-H3 of CDH19 4F3	artificial	AA	ETGEGWYFDL
1155	CDR-L1 of CDH19 4F3	artificial	AA	RASQSVSSSYLA
1156	CDR-L2 of CDH19 4F3	artificial	AA	GASSRAT
1157	CDR-L3 of CDH19 4F3	artificial	AA	QQYGSSWT
1158	VH of CDH19 4F3	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGC
1159	VH of CDH19 4F3	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
1160	VL of CDH19 4F3	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAG
1161	VL of CDH19 4F3	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIK
1162	VH-VL of CDH19 4F3	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAG
1163	VH-VL of CDH19 4F3	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIK
1164	CDH19 4F3 x	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSL

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	I2C			RVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1165	CDR-H1 of CDH19 4F7	artificial	AA	SYSWS
1166	CDR-H2 of CDH19 4F7	artificial	AA	YIYYSGSTNYNPSLKS
1167	CDR-H3 of CDH19 4F7	artificial	AA	NWAFHFDY
1168	CDR-L1 of CDH19 4F7	artificial	AA	TGSSSNIGTGYDVH
1169	CDR-L2 of CDH19 4F7	artificial	AA	GNSNRPS
1170	CDR-L3 of CDH19 4F7	artificial	AA	QSYDSSLSGWV
1171	VH of CDH19 4F7	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTACTCTTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1172	VH of CDH19 4F7	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
1173	VL of CDH19 4F7	artificial	NT	CAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGCGCGTGACCATTTCCTGCACCGGCTCCTCCAGCAACATCGGCACCGGCTACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCCACGGCAACTCCAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGACTCCTCCCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAGACTGACCGTGCTG
1174	VL of CDH19 4F7	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1175	VH-VL of CDH19 4F7	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTACTCTTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				TAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGCGCGTGACCATTTCCTGCACCGGCTCCTCCAGCAACATCGGCACCGGCTACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCCACGGCAACTCCAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGACTCCTCCCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAGACTGACCGTGCTG
1176	VH-VL of CDH19 4F7	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1177	CDH19 4F7 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1178	CDR-H1 of CDH19 14039	artificial	AA	SYGMH
1179	CDR-H2 of CDH19 14039	artificial	AA	FIWYEGSNKYYAESVKD
1180	CDR-H3 of CDH19 14039	artificial	AA	RAGIIGTIGYYYGMDV
1181	CDR-L1 of CDH19 14039	artificial	AA	SGDRLGEKYTS
1182	CDR-L2 of CDH19 14039	artificial	AA	QDTKRPS
1183	CDR-L3 of CDH19 14039	artificial	AA	QAWESSTVV
1184	VH of CDH19 14039	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1185	VH of CDH19 14039	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1186	VL of CDH19	artificial	NT	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC

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	14039			CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1187	VL of CDH19 14039	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1188	VH-VL of CDH19 14039	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1189	VH-VL of CDH19 14039	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1190	CDH19 14039 x I2C	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1191	CDR-H1 of CDH19 14304	artificial	AA	SYGMH
1192	CDR-H2 of CDH19 14304	artificial	AA	FIWYDGSNKYYADSVKD
1193	CDR-H3 of CDH19 14304	artificial	AA	RAGIIGTIGYYYGMDV
1194	CDR-L1 of CDH19 14304	artificial	AA	SGDRLGEKYVS
1195	CDR-L2 of CDH19 14304	artificial	AA	QDNKWPS
1196	CDR-L3 of CDH19 14304	artificial	AA	QAWDSSTVV
1197	VH of CDH19	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT

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	14304			CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1198	VH of CDH19 14304	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1199	VL of CDH19 14304	artificial	NT	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1200	VL of CDH19 14304	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1201	VH-VL of CDH19 14304	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1202	VH-VL of CDH19 14304	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1203	CDH19 14304 x I2C	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1204	CDR-H1 of CDH19 14301	artificial	AA	SYGMH
1205	CDR-H2 of CDH19 14301	artificial	AA	FIWYDGSNKYYADSVKD
1206	CDR-H3 of	artificial	AA	RAGIIGTIGYYYGMDV

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	CDH19 14301			
1207	CDR-L1 of CDH19 14301	artificial	AA	SGDRLGEKYTC
1208	CDR-L2 of CDH19 14301	artificial	AA	QDTKRPS
1209	CDR-L3 of CDH19 14301	artificial	AA	QAWESSTVV
1210	VH of CDH19 14301	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1211	VH of CDH19 14301	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1212	VL of CDH19 14301	artificial	NT	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1213	VL of CDH19 14301	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1214	VH-VL of CDH19 14301	artificial	NT	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTTGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1215	VH-VL of CDH19 14301	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1216	CDH19 14301 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTCWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVE

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				SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1217	CDR-H1 of CDH19 14079	artificial	AA	RYGIH
1218	CDR-H2 of CDH19 14079	artificial	AA	VIWYEGSNKYYAESVKG
1219	CDR-H3 of CDH19 14079	artificial	AA	RAGIPGTTGYYYGMDV
1220	CDR-L1 of CDH19 14079	artificial	AA	SGDRLGEKYVS
1221	CDR-L2 of CDH19 14079	artificial	AA	QDNKWPS
1222	CDR-L3 of CDH19 14079	artificial	AA	QAWESSTVV
1223	VH of CDH19 14079	artificial	NT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1224	VH of CDH19 14079	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1225	VL of CDH19 14079	artificial	NT	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1226	VL of CDH19 14079	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1227	VH-VL of CDH19 14079	artificial	NT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTT

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				AGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1228	VH-VL of CDH19 14079	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1229	CDH19 14079 x I2C	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1230	CDR-H1 of CDH19 14077	artificial	AA	RYGIH
1231	CDR-H2 of CDH19 14077	artificial	AA	VIWYDGSNKYYADSVKG
1232	CDR-H3 of CDH19 14077	artificial	AA	RAGIPGTTGYYYGMDV
1233	CDR-L1 of CDH19 14077	artificial	AA	SGDRLGEKYVS
1234	CDR-L2 of CDH19 14077	artificial	AA	QDNKWPS
1235	CDR-L3 of CDH19 14077	artificial	AA	QAWDSSTVV
1236	VH of CDH19 14077	artificial	NT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1237	VH of CDH19 14077	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1238	VL of CDH19 14077	artificial	NT	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1239	VL of CDH19 14077	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1240	VH-VL of CDH19 14077	artificial	NT	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1241	VH-VL of CDH19 14077	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1242	CDH19 14077 x I2C	artificial		QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1243	CDR-H1 of CDH19 14096	artificial	AA	SYYIH
1244	CDR-H2 of CDH19 14096	artificial	AA	IINPSGGSTRYAQKFQG
1245	CDR-H3 of CDH19 14096	artificial	AA	GGIQLWLHFDY
1246	CDR-L1 of CDH19 14096	artificial	AA	SGSSSNIGRNFVN
1247	CDR-L2 of CDH19 14096	artificial	AA	TNNQRPS
1248	CDR-L3 of CDH19 14096	artificial	AA	AAWDESLNGWV
1249	VH of CDH19 14096	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAAGGACTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGAATACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
1250	VH of CDH19 14096	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1251	VL of CDH19 14096	artificial	NT	CAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAACTGGTATCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATTTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGAGAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1252	VL of CDH19	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVL
1253	VH-VL of CDH19 14096	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGCATCTGGATACACCTTCACCAGCTACTATATTCACTGGGTGCGCCAGGCCCCTGGACAAGGACTTGAGTGGATGGGAATAATCAACCCCAGTGGTGGTAGCACAAGGTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGAATACAGCTATGGTTACATTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCGCTGACTCAGCCACCCTCAGCGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGGAATTTTGTAAACTGGTATCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATTTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGCATGGGATGAGAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1254	VH-VL of CDH19 14096	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVL
1255	CDH19 14096 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYIHWVRQAPGQGLEWMGIINPSGGSTRYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGRNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDESLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1256	CDR-H1 of CDH19 14088	artificial	AA	SYYMS
1257	CDR-H2 of CDH19 14088	artificial	AA	IIHPSGGDTTYAQKFQG
1258	CDR-H3 of CDH19 14088	artificial	AA	GGIKLWLHFDY
1259	CDR-L1 of	artificial	AA	SGSRSNIGSNFVN

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	CDH19 14088			
1260	CDR-L2 of CDH19 14088	artificial	AA	TNNQRPS
1261	CDR-L3 of CDH19 14088	artificial	AA	AVWDDSLNGWV
1262	VH of CDH19 14088	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTGGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
1263	VH of CDH19 14088	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1264	VL of CDH19 14088	artificial	NT	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1265	VL of CDH19 14088	artificial	AA	QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1266	VH-VL of CDH19 14088	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTGGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATGGGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1267	VH-VL of CDH19 14088	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVL
1268	CDH19 14088 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1269	CDR-H1 of CDH19 14085	artificial	AA	SYYMS
1270	CDR-H2 of CDH19 14085	artificial	AA	IIHPSGGDTTYAQKFQG
1271	CDR-H3 of CDH19 14085	artificial	AA	GGIKLWLHFDY
1272	CDR-L1 of CDH19 14085	artificial	AA	SGSRSNIGSNFVN
1273	CDR-L2 of CDH19 14085	artificial	AA	TNNQRPS
1274	CDR-L3 of CDH19 14085	artificial	AA	AVYDDSLNGWV
1275	VH of CDH19 14085	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTAGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
1276	VH of CDH19 14085	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1277	VL of CDH19 14085	artificial	NT	CAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATACGATGACAGCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1278	VL of CDH19 14085	artificial	AA	QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVL
1279	VH-VL of CDH19 14085	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGTAAGGCATCTAGATACACCTTCACCAGCTACTATATGTCCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCCACCCTAGTGGTGGTGACACAACCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCGGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAGAGGGGGGATAAAACTATGGTTACATTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACTCAGCCACCCTCAGCGTCTGGGACCCCCGGACAGAGGGTCACCATCTCTTGTTCTGGAAGCCGCTCCAACATCGGAAGTAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGCAGTATACGATGACA

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GCCTGAATGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1280	VH-VL of CDH19 14085	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVL
1281	CDH19 14085 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1282	CDR-H1 of CDH19 14074	artificial	AA	SYFIH
1283	CDR-H2 of CDH19 14074	artificial	AA	IINPISVSTSYAQKFQG
1284	CDR-H3 of CDH19 14074	artificial	AA	GGIQLWLHLDY
1285	CDR-L1 of CDH19 14074	artificial	AA	SGSRSNIGSNFVN
1286	CDR-L2 of CDH19 14074	artificial	AA	TNNQRPS
1287	CDR-L3 of CDH19 14074	artificial	AA	ATWDDSMNGWV
1288	VH of CDH19 14074	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
1289	VH of CDH19 14074	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1290	VL of CDH19 14074	artificial	NT	CAGTCTGCGCTGACTCAGCCACCCTCAGTGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
1291	VL of CDH19	artificial	AA	QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVL

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	14074			
1292	VH-VL of CDH19 14074	artificial	NT	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCGCTGACTCAGCCACCCTCAGTGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGCGCAACATGGGATGACAGTATGAATGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
1293	VH-VL of CDH19 14074	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVL
1294	CDH19 14074 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1295	CDR-H1 of CDH19 14075	artificial	AA	SYFIH
1296	CDR-H2 of CDH19 14075	artificial	AA	IINPISVSTSYAQKFQG
1297	CDR-H3 of CDH19 14075	artificial	AA	GGIQLWLHLDY
1298	CDR-L1 of CDH19 14075	artificial	AA	SGSRSNIGSNFVN
1299	CDR-L2 of CDH19 14075	artificial	AA	TNNQRPS
1300	CDR-L3 of CDH19 14075	artificial	AA	ATWDESMQGWV
1301	VH of CDH19 14075	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				GGTCACCGTCTCCTCA
1302	VH of CDH19 14075	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1303	VL of CDH19 14075	artificial	nt	CAGTCTGCGCTGACTCAGCCACCCTCAGTGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGCGCAACATGGGATGAGAGTATGCAGGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
1304	VL of CDH19 14075	artificial	AA	QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVL
1305	VH-VL of CDH19 14075	artificial	nt	CAGGTGCAGTTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCTCAGTGAAGGTTTCCTGCAAGGTTTCTGGATACACCTTCACCAGCTACTTTATTCACTGGGTGCGCCAGGCCCCTGGACAAGGGCTTGAATGGATGGGAATTATCAACCCTATTAGTGTTAGCACAAGCTACGCACAGAAGTTCCAGGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTTCATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGCGAGGGGGGATACAGCTATGGTTACATTTGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCGCTGACTCAGCCACCCTCAGTGACTGGGACCCCCGGGCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGGTCCAACATCGGAAGCAATTTTGTAAACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAAGTCCTCATCTATACTAATAATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGGCTCCAGTCTGAGGATGAGGCTGATTATTACTGCGCAACATGGGATGAGAGTATGCAGGGTTGGGTGTTCGGCGGAGGGACCAAACTGACCGTCCTA
1306	VH-VL of CDH19 14075	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVL
1307	CDH19 14075 x I2C	artificial		QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1308	CDR-H1 of CDH19 14024	artificial	AA	SSGYY
1309	CDR-H2 of CDH19 14024	artificial	AA	YIYYTGSAYYNPSLKS
1310	CDR-H3 of CDH19 14024	artificial	AA	DGSSGWYFQY
1311	CDR-L1 of CDH19 14024	artificial	AA	RASRQISSSYLA

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1312	CDR-L2 of CDH19 14024	artificial	AA	GPSSRAT
1313	CDR-L3 of CDH19 14024	artificial	AA	QQYGSSFT
1314	VH of CDH19 14024	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCAGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGGGGCCAGGGCACCCTGGTCACCGTCTCTAGT
1315	VH of CDH19 14024	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
1316	VL of CDH19 14024	artificial	nt	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCGGCAGATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCAGGGGACCAAAGTGGATATCAAA
1317	VL of CDH19 14024	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIK
1318	VH-VL of CDH19	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCAGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGCAGTAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGGCCTGGAGTGGATTGGGTACATCTATTACACTGGGAGCGCCTACTACAACCCGTCCCTCAAGAGTCGAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATGGAAGCAGTGGCTGGTACTTCCAGTATTGGGGCCAGGGCACCCTGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCGGCAGATTAGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTCCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCATTCACTTTCGGCCAGGGGACCAAAGTGGATATCAAA
1319	VH-VL of CDH19 14024	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIK
1320	CDH19 14024 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH

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1321	CDR-H1 of CDH19 14054	artificial	AA	SYDMH
1322	CDR-H2 of CDH19 14054	artificial	AA	VISYDGTNEYYADSVKG
1323	CDR-H3 of CDH19 14054	artificial	AA	ERYFDWSFDY
1324	CDR-L1 of CDH19 14054	artificial	AA	RASQSVSNTYLA
1325	CDR-L2 of CDH19 14054	artificial	AA	GASSRAT
1326	CDR-L3 of CDH19 14054	artificial	AA	QQYSNSWT
1327	VH of CDH19 14054	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCAGCGTCTCTAGT
1328	VH of CDH19 14054	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
1329	VL of CDH19 14054	artificial	nt	GAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA
1330	VL of CDH19 14054	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIK
1331	VH-VL of CDH19 14054	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAACTAATGAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGCTGTATTTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTATATTACTGTGCGAGAGAACGATATTTTGACTGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCAGCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTGAAATTGTATTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAACACCTACTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGATTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGTCTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTACAGTAACTCGTGGACGTTCGGCCAAGGGACCAAGGTGGAAATCAAA

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1332	VH-VL of CDH19 14054	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIK
1333	CDH19 14054 x I2C	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1334	CDR-H1 of CDH19 14056	artificial	AA	GYYWS
1335	CDR-H2 of CDH19 14056	artificial	AA	YFSYSGSTNYNPSLKS
1336	CDR-H3 of CDH19 14056	artificial	AA	NWAFHFDF
1337	CDR-L1 of CDH19 14056	artificial	AA	TGSSSNIGTGYAVH
1338	CDR-L2 of CDH19 14056	artificial	AA	GNNNRPS
1339	CDR-L3 of CDH19 14056	artificial	AA	QSYDSRLSGWV
1340	VH of CDH19 14056	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGACTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT
1341	VH of CDH19 14056	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
1342	VL of CDH19 14056	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1343	VL of CDH19 14056	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL

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1344	VH-VL of CDH19 14056	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGACTGGAGTGGTTTGCATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1345	VH-VL of CDH19 14056	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL
1346	CDH19 14056 x I2C	artificial		QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWFAYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1347	CDR-H1 of CDH19 14057	artificial	AA	GYYWS
1348	CDR-H2 of CDH19 14057	artificial	AA	YFSYSGSTNYNPSLKS
1349	CDR-H3 of CDH19 14057	artificial	AA	NWAFHFDF
1350	CDR-L1 of CDH19 14057	artificial	AA	TGSSSNIGTGYAVH
1351	CDR-L2 of CDH19 14057	artificial	AA	GNNNRPS
1352	CDR-L3 of CDH19 14057	artificial	AA	QSYDSRLSGWV
1353	VH of CDH19 14057	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGACTGGAGTGGATTGGATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT

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1354	VH of CDH19 14057	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSS
1355	VL of CDH19 14057	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1356	VL of CDH19 14057	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL
1357	VH-VL of CDH19 14057	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTGGTTACTACTGGAGCTGGATCCGGCAGCCCCCAGGAAAGGGACTGGAGTGGATTGGATATTTCTCTTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCTTATCAGTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGACAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAACATCGGGACAGGTTATGCTGTACACTGGTACCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAACAATCGGCCCTCAGGGGTTCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGACTGAGTGGTTGGGTGTTCGGCGGAGGGACCAAGCTGACCGTCCTA
1358	VH-VL of CDH19 14057	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVL
1359	CDH19 14057 x I2C	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYFSYSGSTNYNPSLKSRVTLSVDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDFWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYAVHWYQQLPGTAPKLLIYGNNNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSRLSGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1360	CDR-H1 of CDH19 14049	artificial	AA	SYSWS
1361	CDR-H2 of CDH19 14049	artificial	AA	YIYYSGSTNYNPSLKS
1362	CDR-H3 of CDH19 14049	artificial	AA	NWAFHFDY
1363	CDR-L1 of CDH19 14049	artificial	AA	TGSSSNIGTGYDVH
1364	CDR-L2 of	artificial	AA	GNSNRPS

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	CDH19 14049			
1365	CDR-L3 of CDH19 14049	artificial	AA	QSYDSSLSGWV
1366	VH of CDH19 14049	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT
1367	VH of CDH19 14049	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
1368	VL of CDH19 14049	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1369	VL of CDH19 14049	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1370	VH-VL of CDH19 14049	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1371	VH-VL of CDH19 14049	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1372	CDH19 14049 x I2C	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1373	CDR-H1 of	artificial	AA	SYGMH

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 14302			
1374	CDR-H2 of CDH19 14302	artificial	AA	FIWYDGSNKYYADSVKD
1375	CDR-H3 of CDH19 14302	artificial	AA	RAGIIGTIGYYYGMDV
1376	CDR-L1 of CDH19 14302	artificial	AA	SGDRLGEKYTS
1377	CDR-L2 of CDH19 14302	artificial	AA	QDTKRPS
1378	CDR-L3 of CDH19 14302	artificial	AA	QAWESSTVV
1379	VH of CDH19 14302	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1380	VH of CDH19 14302	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1381	VL of CDH19 14302	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1382	VL of CDH19 14302	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1383	VH-VL of CDH19 14302	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1384	VH-VL of	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT

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	CDH19 14302			SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1385	CDH19 14302 x I2C	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1386	CDR-H1 of CDH19 14303	artificial	AA	SYGMH
1387	CDR-H2 of CDH19 14303	artificial	AA	FIWYEGSNKYYAESVKD
1388	CDR-H3 of CDH19 14303	artificial	AA	RAGIIGTIGYYYGMDV
1389	CDR-L1 of CDH19 14303	artificial	AA	SGDRLGEKYTS
1390	CDR-L2 of CDH19 14303	artificial	AA	QDTKRPS
1391	CDR-L3 of CDH19 14303	artificial	AA	QAWESSTVV
1392	VH of CDH19 14303	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA AATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTG AGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTG GGGCCAAGGGACCACGGTCACCGTCTCTAGT
1393	VH of CDH19 14303	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSL RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1394	VL of CDH19 14303	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGA AAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCC CTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTAC TGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1395	VL of CDH19 14303	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYY CQAWESSTVVFGGGTKLTVL
1396	VH-VL of CDH19 14303	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTT CAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA

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				AATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1397	VH-VL of CDH19 14303	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1398	CDH19 14303 x I2C	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1399	CDR-H1 of CDH19 14078	artificial	AA	RYGIH
1400	CDR-H2 of CDH19 14078	artificial	AA	VIWYDGSNKYYADSVKG
1401	CDR-H3 of CDH19 14078	artificial	AA	RAGIPGTTGYYYGMDV
1402	CDR-L1 of CDH19 14078	artificial	AA	SGDRLGEKYVS
1403	CDR-L2 of CDH19 14078	artificial	AA	QDNKWPS
1404	CDR-L3 of CDH19 14078	artificial	AA	QAWDSSTVV
1405	VH of CDH19 14078	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1406	VH of CDH19 14078	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS

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1407	VL of CDH19 14078	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1408	VL of CDH19 14078	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1409	VH-VL of CDH19 14078	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTAGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1410	VH-VL of CDH19 14078	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1411	CDH19 14078 x I2C	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1412	CDR-H1 of CDH19 14080	artificial	AA	RYGIH
1413	CDR-H2 of CDH19 14080	artificial	AA	VIWYDGSNKYYADSVKG
1414	CDR-H3 of CDH19 14080	artificial	AA	RAGIPGTTGYYYGMDV
1415	CDR-L1 of CDH19 14080	artificial	AA	SGDRLGEKYVY
1416	CDR-L2 of CDH19 14080	artificial	AA	QDNKWPS
1417	CDR-L3 of	artificial	AA	QAWDSSTVV

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	CDH19 14080			
1418	VH of CDH19 14080	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
1419	VH of CDH19 14080	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1420	VL of CDH19 14080	artificial	nt	TCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTTACTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1421	VL of CDH19 14080	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1422	VH-VL of CDH19 14080	artificial	nt	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCGCTATGGCATACACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCTAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATACCTGGAACTACGGGCTACTACTATGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCAGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAGCTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGATTGGGGGAGAAATATGTTTACTGGTATCAGCAGAAGCCAGGCCAGTCCCCTATACTGGTCATCTATCAAGATAATAAGTGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGACAGCAGCACTGTGGTATTCGGCGGGGGGACCAAGCTGACCGTCCTA
1423	VH-VL of CDH19 14080	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVL
1424	CDH19 14080 x I2C	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLLMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVYWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1425	CDR-H1 of CDH19 13591	artificial	AA	SYSWS
1426	CDR-H2 of	artificial	AA	YIYYSGSTNYNPSLKS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 13591			
1427	CDR-H3 of CDH19 13591	artificial	AA	NWAFHFDY
1428	CDR-L1 of CDH19 13591	artificial	AA	TGSSSNIGTGYDVH
1429	CDR-L2 of CDH19 13591	artificial	AA	GNSNRPS
1430	CDR-L3 of CDH19 13591	artificial	AA	QSYDSSLSGWV
1431	VH of CDH19 13591	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT
1432	VH of CDH19 13591	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
1433	VL of CDH19 13591	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1434	VL of CDH19 13591	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1435	VH-VL of CDH19 1591	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1436	VH-VL of CDH19 13591	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1437	CDH19 13591	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	x I2C			AADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1438	CDR-H1 of CDH19 14299	artificial	AA	SYSWS
1439	CDR-H2 of CDH19 14299	artificial	AA	YIYYSGSTNYNPSLKS
1440	CDR-H3 of CDH19 14299	artificial	AA	NWAFHFDY
1441	CDR-L1 of CDH19 14299	artificial	AA	TGSSSNIGTGYDVH
1442	CDR-L2 of CDH19 14299	artificial	AA	GNSNRPS
1443	CDR-L3 of CDH19 14299	artificial	AA	QSYDSSLSGWV
1444	VH of CDH19 14299	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT
1445	VH of CDH19 14299	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
1446	VL of CDH19 14299	artificial	nt	CAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1447	VL of CDH19 14299	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1448	VH-VL of CDH19 14299	artificial	nt	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTCCTGGAGCTGGATCCGGCAGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACTGTGCGAGGAACTGGGCCTTCCACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				TAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGTGCTGACGCAGCCGCCCTCAGTGTCTGGGGCCCCAGGGCAGAGGGTCACCATCTCCTGCACTGGGAGCAGCTCCAATATCGGGACAGGTTATGATGTACACTGGTATCAGCAGCTTCCAGGAACAGCCCCCAAACTCCTCATCCATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGTCTGAGTGGTTGGGTGTTCGGCGGAGGGACCAGGTTGACCGTCCTA
1449	VH-VL of CDH19 14299	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVL
1450	CDH19 14299 x I2C	artificial	aa	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIHGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGWVFGGGTRLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1451	ckCDH19(1-43)::FLAG::ckCDH19(44-776)	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSLQYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEGTSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVNDNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKAVNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINEHNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQRSTRD
1452	huCDH19(1-43)::FLAG::hu(44-141)::ckCDH19(142-776)	artificial	aa	MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSDINDHEPQFLDGPYVATVPEMSPEGTSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVNDNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKAVNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINEHNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQRSTRD
1453	ckCDH19(1-43)::FLAG::ckC	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSLQYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDNEPKFLDEPYEAIVPEMSPEG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	DH19(44-141)::huCDH19(142-249)::ckCDH19(250-776)			TLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKAVNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINEHNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQRSTRD
1454	ckCDH19(1-43)::FLAG::ckCDH19(44-249)::huCDH19(250-364)::ckCDH19(365-776)	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSLQYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEGTSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINEHNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQRSTRD
1455	ckCDH19(1-43)::FLAG::ckCDH19(44-364)::huCDH19(365-463)::ckCDH19(469-776)	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSLQYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEGTSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVNDNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKAVNRYIDDRFLKEGPFEDITIVQISVVDADEPPLFLLPYYVFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSKYYETFVCENAVPGQLIQNISAVDKDDSAENHRFYFSLAQATNSSHFTVKDNQDNTAGIFTAGSGFSRKEQFYFFLPILILDNGSPPLTSTNTLTVTVCDCDTEVNTLYCRYGAFLYSIGLSTEALVAVLACLLILLVFFLAIIGIRQQRKKTLFSEKVEEFRENIVRYDDEGGGEEDTEAFDISALRTRAVLRTHKPRKKITTEIHSLYRQSLQVGPDSAIFRQFISEKLEEANTDPSVPPYDSLQTYAFEGTGSLAGSLSSLGSNTSDVDQNYEYLVGWGPPFKQLAGMYTSQRSTRD
1456	(1-43)::FLAG::ckCDH19(44-468)::huCDH19(464-772)	artificial	aa	MNCSTFLSLVLALVQLQLCSPTTQIFSAQKTDQSYTTIRRVKRDYKDDDDKGWVWEPLFVTEEETSTMPMYVGQLKSDLDKEDGSLQYILTGEGADSIFFINEHGKIYVRQKLDREKKSFYILRAQVINRKTRHPIEPDSEFIIKVRDINDHEPQFLDGPYVATVPEMSPEGTSVTQVTATDGDDPSYGNNARLLYSLIQGQPYFSVEPKTGVIRMTSQMDRETKDQYLVVIQAKDMVGQAGAFSATATVTINLSDVNDNPPKFQQRLYYLNVSEEAPVGTTVGRLLAEDSDIGENAAMNYFIEEDSSDVFGIITDRETQEGIIILKKRVDYESKRKHSVRVKAVNRYIDDRFLKEGPFEDITIVQISVVDADEPPVFTLESYVMEIAEGVVSGSLVGTVSARDLDNDDSSVRYSIVQGLHLKRLFSINEHNGTIITTEPLDREKASWHNITVTATETRNPEKISEANVYIQVLDVNDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDCGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
1457	rhCDH19(1-43)::FLAG::rhCDH19(44-772)	artificial	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKVKNHHVDEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTITTTNSLDREISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNSSSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFKTEVIIAILICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
1458	caCDH19(1-42)::FLAG::caCDH19(43-770)	artificial	aa	QFFVPEEMNKTDYHIGQLRSDLDNGNNSFQYKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIITTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN
1459	rhCDH19(1-43):FLAG::rhCDH19(44-141)::caCDH19(141-770)	artificial	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIITTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN
1460	rhCDH19(1-43)::FLAG::rhCDH19(44-65)::caCDH19(65-770)	artificial	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTII

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				TTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN
1461	caCDH19(1-43)::FLAG::caCDH19(44-87)::rhCDH19(89-114)::caCDH19(115-770)	artificial	aa	MNYCFLLPLMLGIPLIWPCFTASESSKTEVKHQAGSHLRVKRDYKDDDDKGWMWNQFFVPEEMNKTDYHIGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDSTTGRAVEPESEFVIRVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIITTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN
1462	caCDH19(1-43)::FLAG::caCDH19(44-120)::rhCDH19(122-137)::caCDH19(137-770)	artificial	aa	MNYCFLLPLMLGIPLIWPCFTASESSKTEVKHQAGSHLRVKRDYKDDDDKGWMWNQFFVPEEMNKTDYHIGQLRSDLDNGNNSFQYKLLGAGAGSIFVIDERTGDIYAIQKLDREERSLYTLRAQVIDITTGRAVEPESEFVIKVSDINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTATDADDPASGNNARLLYSLLQGQPYFSIEPTTGVIRISSKMDRELQDEYWVIIQAKDMIGLPGALSGTTSVLIKLSDVNDNKPIFKERLYRLTVSESAPTGTSIGRIMAYDNDIGENAEMDYSIEDDSQTFDIITNNETQEGIVILKKKVDFEHQNHYLIRANVKNRHVAEHLMEYHVEASTTFVRVQVEDEDEPPVFLLPYYLFEILEESPHGSFVGMVSATDPDQRKSPIRYSITRSKVFSIDDNGTIITTNPLDREISAWYNLSITATEKYNVQQISAVPVYVQVLNINDHAPEFSEYYDSYVCENAGSGQVIQTISAVDRDESVEDHHFYFNLSVEDTKNSSFIIIDNEDNTAVILTNRTGFSLQEEPVFYISVLIADNGIPSLTSTNTLTIHICDCDDYGSTQTCRDKDLLLSMGFRTEVILAILISIMIIFGFIFLILGLKQRRKPTLFPEKGEDFRENIFRYDDEGGGEEDTEAFDIVQLRSSTIMRERKTRKTAAAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLGSAVSDQDENYDYLNELGPRFKRLACMFGSAMQSNN
1463	rhCDH19(1-43)::FLAG::rhCDH19(44-141)::raCDH19(140-247)::rhCDH19(250-772)	artificial	aa	MNCYLLLPFMLGIPLLWPCLGATENSQTKKVQQPVGSHLRVKRDYKDDDDKGWVWNQFFVPEEMNTTSHHVGRLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIEKLDREERSLYILRAQVIDITTGRAVEPESEFVIKVSDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPTSGYHARILYNLEQGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTISIKLSDINDNKPIFKESLYRLTVSESAPTGTSIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHETQEGIVILKKKVNFEHQNHYGIRAKVKNHHVDEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYYIFEIFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNIDDNGTITTTNSLDREISAWYNLSITATEKYNIEQISSIPVYVQVLNINDHAPEFSQYYESYVCENAGSGQVIQTISAVDRDESIEEHHFYFNLSVEDTNSSSFTIIDNQDNTAVILTNRTGFNLQEEPIFYISILIADNGIPSLTSTNTLTIHVCDCDDSGSTQTCQYQELMLSMGFKTEVIIAILICIMVIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFRYDDEGGGEEDTEAFDVAALRSSTIMRERKTRKTTSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEADTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYLNELGPRFKRLACMFGSAVQSNN
1464	raCDH19(1-	artificial	aa	MNHYFLKYWILMVPLIWPCLKVAETLKIEKAQRAVPSLGRAKRDYKDDDDKGWVWKQFVVPEEMDTIQHVGRLRSDLDNGNNSFQY

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	43)::FLAG::raCDH19(44-770)			KLLGTGDGSFSIDEKTGDIFAMQKLDREKQSLYILRAQVIDTTIGKAVEPESEFVIRVSDVNDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPTSGYHARILYNLEQGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTISIKLSDINDNKPIFKESFYRFTISESAPSGTTIGKIMAYDDDIGENAEMDYSIEDDESQIFDIVIDNETQEGIVILKKKVDFEHQNHYGIRVKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPTFLLPYYIFEIPEGKPYGTMVGTVSAVDPDRRQSPMRYSLIGSKMFDINGNGTIVTTNLLDREVSAWYNLSVTATETYNVQQISSAHVYVQVLNINDHAPEFSQLYETYVCENAESGEIIQTISAIDRDESIEDHHFYFNHSVEDTNNSSFILTDNQDNTAVILSNRAGFSLKEETVFYMIILIADNGIPPLTSTNTLTIQVCDCGDSRSTETCTSKELLFIMGFKAEAIIAIVICVMVIFGFIFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIIELRQSTVMRERKPRKSRSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDSSAPPFDSLQTFAYEGTGSSAGSLSSLGSSVTDQEDDFDYLNDLGPCFKRLANMFGSAVQPDN
1465	(1-43)::FLAG::muCDH19(44-323)::raCDH19(324-327)::muCDH19(328-770)	artificial	aa	MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEHQNHYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
1466	muCDH19(1-43)::FLAG::muCDH19(44-770)::raCDH19(290,299,308)	artificial	aa	MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPIGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTEAIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
1467	muCDH19(1-43)::FLAG::muCDH19(44-770)::huCDH19(271)	artificial	aa	MNYCFLKHWILMIPLLWPCLKVSETLKAEKARRTVPSTWRAKRDYKDDDDKAWVWRPFVVLEEMDDIQCVGKLRSDLDNGNNSFQYKLLGIGAGSFSINERTGEICAIQKLDREEKSLYILRAQVIDTTIGKAVETESEFVIRVLDINDNEPRFLDEPYEAIVPEMSPEGTFVIKVTANDADDPSTGYHARILYNLERGQPYFSVEPTTGVIRISSKMDRELQDTYCVIIQAKDMLGQPGALSGTTTVSIKLSDINDNKPIFKESFYRFTISESAPTGTSIGKIMAYDDDIGENAEMEYSIEDDDSKIFDIIIDNDTQEGIVILKKKVDFEQQSYYGIRAKVKNCHVDEELAPAHVNASTTYIKVQVEDEDEPPVFLLPYYILEIPEGKPYGTIVGTVSATDPDRRQSPMRYYLTGSKMFDINDNGTIITTNMLDREVSAWYNLTVTATETYNVQQISSAHVYVQVFNINDNAPEFSQFYETYVCENAESGEIVQIISAIDRDESIEDHHFYFNHSLEDTNNSSFMLTDNQDNTAVILSNRTGFNLKEEPVFYMIILIADNGIPSLTSTNTLTIQVCDCGDSRNTETCANKGLLFIMGFRTE

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				AIIAIMICVMVIFGFFFLILALKQRRKETLFPEKTEDFRENIFCYDDEGGGEEDSEAFDIVELRQSTVMRERKPQRSKSAEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTFAYEGTGSSAGSLSSLASRDTDQEDDFDYLNDLGPRFKRLASMFGSAVQPNN
1468	VH of CDH19 14302 CC x I2C	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1469	VH of CDH19 14302 CC x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1470	VL of CDH19 14302 CC x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1471	VL of CDH19 14302 CC x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1472	VH-VL of CDH19 14302 CC x I2C	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1473	VH-VL of CDH19 14302 CC x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1474	CDH19 14302 CC x I2C	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1475	CDH19 14302	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSL

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	x F12q0			RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1476	CDH19 14302 CC x F12q0	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1477	VH of CDH19 21-14302 x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1478	VH of CDH19 21-14302 x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1479	VL of CDH19 21-14302 x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1480	VL of CDH19 21-14302 x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1481	VH-VL of CDH19 21-14302 x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGG

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				ACCAAGCTGACCGTCCTA
1482	VH-VL of CDH19 21-14302 x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1483	CDH19 21-14302 x I2C	artificial	aa	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1484	VH of CDH19 21-14302 CC x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1485	VH of CDH19 21-14302 CC x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1486	VL of CDH19 21-14302 CC x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1487	VL of CDH19 21-14302 CC x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1488	VH-VL of CDH19 21-14302 CC x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				TGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1489	VH-VL of CDH19 21-14302 CC x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1490	CDH19 21-14302 CC x I2C	artificial	aa	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1491	CDH19 14302 x I2C-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLWEDDHHHHHH
1492	CDH19 14302 CC x I2C-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLWEDDHHHHHH
1493	VH of CDH19 14302 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1494	VH of CDH19 14302 x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS

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1495	VL of CDH19 14302 x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1496	VL of CDH19 14302 x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1497	VH-VL of CDH19 14302 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1498	VH-VL of CDH19 14302 x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1499	CDH19 14302 x I2C x FcBY	artificial	aa	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1500	VH of CDH19 14302 CC x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1501	VH of CDH19 14302 CC x I2C	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS

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	x FcBY			
1502	VL of CDH19 14302 CC x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1503	VL of CDH19 14302 CC x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1504	VH-VL of CDH19 14302 CC x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1505	VH-VL of CDH19 14302 CC x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1506	CDH19 14302 CC x I2C x FcBY	artificial	aa	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1507	VH of CDH19 14303 CC x I2C	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1508	VH of CDH19	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSL

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	14303 CC x I2C			RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1509	VL of CDH19 14303 CC x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1510	VL of CDH19 14303 CC x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1511	VH-VL of CDH19 14303 CC x I2C	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1512	VH-VL of CDH19 14303 CC x I2C	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1513	CDH19 14303 CC x I2C	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1514	CDH19 14303 x F12q0	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1515	CDH19 14303 CC x F12q0	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTED

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				TAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1516	CDH19 14303 x I2C-21	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLWEDDHHHHHH
1517	CDH19 14303 CC x I2C-21	artificial	aa	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLWEDDHHHHHH
1518	VH of CDH19 14303 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1519	VH of CDH19 14303 x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1520	VL of CDH19 14303 x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1521	VL of CDH19 14303 x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1522	VH-VL of CDH19 14303 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAG

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				GACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1523	VH-VL of CDH19 14303 x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1524	CDH19 14303 x I2C x FcBY	artificial	aa	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1525	VH of CDH19 14303 CC x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1526	VH of CDH19 14303 CC x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1527	VL of CDH19 14303 CC x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1528	VL of CDH19 14303 CC x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1529	VH-VL of	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGG

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	CDH19 14303 CC x I2C x FcBY			GGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAAAAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1530	VH-VL of CDH19 14303 CC x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1531	CDH19 14303 CC x I2C x FcBY	artificial	aa	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1532	VH of CDH19 14039 CC x I2C	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1533	VH of CDH19 14039 CC x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1534	VL of CDH19 14039 CC x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1535	VL of CDH19 14039 CC x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1536	VH-VL of CDH19 14039	artificial	nt	CAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATA

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	CC x I2C			AATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1537	VH-VL of CDH19 14039 CC x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1538	CDH19 14039 CC x I2C	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1539	CDH19 14039 x F12q0	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1540	CDH19 14039 CC x F12q0	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFNSYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCVRHGNFGNSYVSWWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVL
1541	VH of CDH19 21-14039 x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1542	VH of CDH19 21-14039 x	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS

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	I2C			
1543	VL of CDH19 21-14039 x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1544	VL of CDH19 21-14039 x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1545	VH-VL of CDH19 21-14039 x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1546	VH-VL of CDH19 21-14039 x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1547	CDH19 21-14039 x I2C	artificial		RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1548	VH of CDH19 21-14039 CC x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1549	VH of CDH19	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS

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	21-14039 CC x I2C			
1550	VL of CDH19 21-14039 CC x I2C	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1551	VL of CDH19 21-14039 CC x I2C	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1552	VH-VL of CDH19 21-14039 CC x I2C	artificial	nt	CGGCTGATCGAGGACATCTGCCTGCCCAGATGGGGCTGCCTGTGGGAGGACGACCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1553	VH-VL of CDH19 21-14039 CC x I2C	artificial	AA	RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1554	CDH19 21-14039 CC x I2C	artificial		RLIEDICLPRWGCLWEDDQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1555	CDH19 14039 x I2C-21	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLW

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				EDDHHHHHH
1556	CDH19 14039 CC x I2C-21	artificial		QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLRLIEDICLPRWGCLWEDDHHHHHH
1557	VH of CDH19 14039 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1558	VH of CDH19 14039 x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1559	VL of CDH19 14039 x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1560	VL of CDH19 14039 x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1561	VH-VL of CDH19 14039 x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCGGAGGGACCAAGCTGACCGTCCTA
1562	VH-VL of	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVK

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	CDH19 14039 x I2C x FcBY			DRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVL
1563	CDH19 14039 x I2C x FcBY	artificial		QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1564	VH of CDH19 14039 CC x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGT
1565	VH of CDH19 14039 CC x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
1566	VL of CDH19 14039 CC x I2C x FcBY	artificial	nt	TCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTCGGCTGCGGGACCAAGCTGACCGTCCTA
1567	VL of CDH19 14039 CC x I2C x FcBY	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1568	VH-VL of CDH19 14039 CC x I2C x FcBY	artificial	nt	CAACGTTTCTGTACCGGTCACTTCGGTGGTCTGTACCCGTGTAATGGTGGTGGTGGTGGTTCGCAGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGTGTCTGGAGTGGGTGGCATTTATATGGTATGAGGGAAGTAATAAATACTATGCAGAGTCCGTGAAGGACCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAATAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAGGGCCGGTATAATAGGAACTATAGGCTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCTAGTGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCCTATGAACTGACTCAGCCACCCTCAGTGTCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAGGTTGGGGGAAAAATATACTAGCTGGTATCAGCAGAGGCCAGGCCAGTCCCCTTTGCTGGTCATCTATCAAGATACCAAGCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACTCTGGTAACACAGCCACTCTGACCATCAGCGGGACCCAGGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGAGAGCAGCACTGTGGTATTC

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				GGCTGCGGGACCAAGCTGACCGTCCTA
1569	VH-VL of CDH19 14039 CC x I2C x FcBY	artificial	AA	QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVL
1570	CDH19 14039 CC x I2C x FcBY	artificial		QRFCTGHFGGLYPCNGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1571	CDH19 14302 x I2C-156	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH
1572	CDH19 14302 x I2C-LFcBY	artificial	aa	QRFVTGHFGGLYPANGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGSQRFCTGHFGGLHPCNGHHHHHH
1573	CDH19 14302 x I2C-LFcBY-156	artificial	aa	QRFVTGHFGGLYPANGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGS QRFCTGHFGGLHPCNGGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH
1574	CDH19 14302 x I2C-Cys-Loop	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVE

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGCGGGGCHHHHHH
1575	CDH19 14302 x I2C-HALB	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLDYHHHHHH
1576	CDH19 14302 x I2C-GS-D3HSA	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
1577	CDH19 14302 x I2C-3GS-D3HSA	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
1578	CDH19 14302 x I2C-GS-	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	D3HSA-156			SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH
1579	CDH19 14302 x I2C-3GS-D3HSA-156	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRDWDFDVFGGGTPVGGHHHHHH
1580	CDH19 14302 x I2C-GS-D3HSA-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRLIEDICLPRWGCLWEDDHHHHHH
1581	CDH19 14302 x I2C-3GS-D3HSA-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLGGGGSGGGSRLIEDICLPRWGCLWEDDHHHHHH
1582	CDR-H1 of CDH19	artificial	AA	SYYWS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	65231.002			
1583	CDR-H2 of CDH19 65231.002	artificial	AA	YIYYSGSTNYNPSLKS
1584	CDR-H3 of CDH19 65231.002	artificial	AA	DQRRIAAAGTHFYGMDV
1585	CDR-L1 of CDH19 65231.002	artificial	AA	RASQSVSSSYLA
1586	CDR-L2 of CDH19 65231.002	artificial	AA	GTSSRAT
1587	CDR-L3 of CDH19 65231.002	artificial	AA	QQYGSSPFT
1588	VH of CDH19 65231.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGCCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGACTCCATCACCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGGGACCAGCGGAGAATCGCCGCTGCCGGCACCCACTTCTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGC
1589	VH of CDH19 65231.002	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSS
1590	VL of CDH19 65231.002	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCACCTCCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCAGCCCCTTCACCTTCGGCGGAGGCACCAAGGTGGAAATCAAGTCC
1591	VL of CDH19 65231.002	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKS
1592	VH-VL of CDH19 65231.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGCCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGACTCCATCACCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGGGACCAGCGGAGAATCGCCGCTGCCGGCACCCACTTCTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGC

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				TGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCC TACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCACCTCCTCCAGAGCCACCGGCATCCCTGA CCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCC AGCAGTACGGCTCCAGCCCCTTCACCTTCGGCGGAGGCACCAAGGTGGAAATCAAGTCC
1593	VH-VL of CDH19 65231.002	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKS
1594	CDH19 65231.002 x I2C	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGDSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVT AADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSS YLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGGGTKVEIKSGGGGSEVQL VESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKT EDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPN WVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1595	CDR-H1 of CDH19 65231.003	artificial	AA	SYYWS
1596	CDR-H2 of CDH19 65231.003	artificial	AA	YIYYSGSTNYNPSLKS
1597	CDR-H3 of CDH19 65231.003	artificial	AA	DQRRIAAAGTHFYGMDV
1598	CDR-L1 of CDH19 65231.003	artificial	AA	RASQSVSSSYLA
1599	CDR-L2 of CDH19 65231.003	artificial	AA	GTSSRAT
1600	CDR-L3 of CDH19 65231.003	artificial	AA	QQYGSSPFT
1601	VH of CDH19 65231.003	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGCCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CACCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCA ACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACC

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				GCCGCTGACACCGCCGTGTACTACTGCGCCAGGGACCAGCGGAGAATCGCCGCTGCCGGCACCCACTTCTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGC
1602	VH of CDH19 65231.003	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGGSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSS
1603	VL of CDH19 65231.003	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCACCTCCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCAGCCCCTTCACCTTCGGCCAAGGCACCAAGGTGGAAATCAAGTCC
1604	VL of CDH19 65231.003	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKS
1605	VH-VL of CDH19 65231.003	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGCCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCACCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGGGACCAGCGGAGAATCGCCGCTGCCGGCACCCACTTCTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCACCTCCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCAGCCCCTTCACCTTCGGCCAAGGCACCAAGGTGGAAATCAAGTCC
1606	VH-VL of CDH19 65231.003	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGGSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKS
1607	CDH19 65231.003 x I2C	artificial	AA	QVQLQESGPGLAKPSETLSLTCTVSGGSITSYYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDQRRIAAAGTHFYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPFTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1608	CDR-H1 of CDH19 65234.001	artificial	AA	SYYWS
1609	CDR-H2 of CDH19 65234.001	artificial	AA	YIYYIGSTNYNPSLKS
1610	CDR-H3 of	artificial	AA	DSRYRSGWYDAFDI

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	CDH19 65234.001			
1611	CDR-L1 of CDH19 65234.001	artificial	AA	RASQSVAGSYLA
1612	CDR-L2 of CDH19 65234.001	artificial	AA	GASSRAT
1613	CDR-L3 of CDH19 65234.001	artificial	AA	QQYGKSPIT
1614	VH of CDH19 65234.001	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCAACTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCCTGTACTACTGCGCCAGAGACTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGGCACCATGGTCACCGTGTCCTCT
1615	VH of CDH19 65234.001	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSS
1616	VL of CDH19 65234.001	artificial	NT	GATATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGTGGCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAGTCC
1617	VL of CDH19 65234.001	artificial	AA	DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKS
1618	VH-VL of CDH19 65234.001	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCAACTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCCTGTACTACTGCGCCAGAGACTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGGCACCATGGTCACCGTGTCCTCTGGTGGCGGAGGCTCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCCGATATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGTGGCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAGTCC
1619	VH-VL of	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLA

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	CDH19 65234.001			WYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKS
1620	CDH19 65234.001 x I2C	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSINSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARDSRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1621	CDR-H1 of CDH19 65234.004	artificial	AA	SYYWS
1622	CDR-H2 of CDH19 65234.004	artificial	AA	YIYYIGSTNYNPSLKS
1623	CDR-H3 of CDH19 65234.004	artificial	AA	ESRYRSGWYDAFDI
1624	CDR-L1 of CDH19 65234.004	artificial	AA	RASQSVAGSYLA
1625	CDR-L2 of CDH19 65234.004	artificial	AA	GASSRAT
1626	CDR-L3 of CDH19 65234.004	artificial	AA	QQYGKSPIT
1627	VH of CDH19 65234.004	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCAGCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCCTGTACTACTGCGCCAGAGAGTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGGCACCATGGTCACCGTGTCCTCT
1628	VH of CDH19 65234.004	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSS
1629	VL of CDH19	artificial	NT	GATATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGT

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	65234.004			GGCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAGTCC
1630	VL of CDH19 65234.004	artificial	AA	DIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKS
1631	VH-VL of CDH19 65234.004	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCAGCTCCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCCTGTACTACTGCGCCAGAGAGTCCCGGTACAGATCCGGGTGGTACGACGCCTTCGACATCTGGGGCCAGGGCACCATGGTCACCGTGTCCTCTGGTGGCGGAGGCTCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCCGATATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCTCAGTCCGTGGCCGGCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCTAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCAAGTCCCCCATCACCTTCGGCCAGGGAACCCGGCTGGAAATGAAGTCC
1632	VH-VL of CDH19 65234.004	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKS
1633	CDH19 65234.004 x I2C	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTALYYCARESRYRSGWYDAFDIWGQGTMVTVSSGGGGSGGGGSGGGGSDIVLTQSPGTLSLSPGERATLSCRASQSVAGSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGKSPITFGQGTRLEMKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1634	CDR-H1 of CDH19 65235.005	artificial	AA	SYFIH
1635	CDR-H2 of CDH19 65235.005	artificial	AA	IINPISVSTSYAQKFQG
1636	CDR-H3 of CDH19 65235.005	artificial	AA	GGIQLWLHLDY
1637	CDR-L1 of CDH19	artificial	AA	SGSRSNIGSNFVN

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	65235.005			
1638	CDR-L2 of CDH19 65235.005	artificial	AA	TNNQRPS
1639	CDR-L3 of CDH19 65235.005	artificial	AA	ATYDESMQGWV
1640	VH of CDH19 65235.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCT
1641	VH of CDH19 65235.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1642	VL of CDH19 65235.005	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTACGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1643	VL of CDH19 65235.005	artificial	AA	QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLS
1644	VH-VL of CDH19 65234.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGCTCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCCCAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTACGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1645	VH-VL of CDH19 65234.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLS
1646	CDH19 65234.005 x	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLSGGGGSEVQLVES

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	I2C			GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1647	CDR-H1 of CDH19 65235.002	artificial	AA	SYFIH
1648	CDR-H2 of CDH19 65235.002	artificial	AA	IINPISVSTSYAQKFQG
1649	CDR-H3 of CDH19 65235.002	artificial	AA	GGIQLWLHLDY
1650	CDR-L1 of CDH19 65235.002	artificial	AA	SGSRSNIGSNFVN
1651	CDR-L2 of CDH19 65235.002	artificial	AA	TNNQRPS
1652	CDR-L3 of CDH19 65235.002	artificial	AA	ATWDDSMNGWV
1653	VH of CDH19 65235.002	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCT
1654	VH of CDH19 65235.002	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1655	VL of CDH19 65235.002	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1656	VL of CDH19 65235.002	artificial	AA	QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1657	VH-VL of CDH19 65235.002	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGACTCCATGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1658	VH-VL of CDH19 65235.002	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLS
1659	CDH19 65235.002 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDDSMNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1660	CDH19 CDR-H1 of CDH19 65235.003	artificial	AA	SYFIH
1661	CDR-H2 of CDH19 65235.003	artificial	AA	IINPISVSTSYAQKFQG
1662	CDR-H3 of CDH19 65235.003	artificial	AA	GGIQLWLHLDY
1663	CDR-L1 of CDH19 65235.003	artificial	AA	SGSRSNIGSNFVN
1664	CDR-L2 of CDH19 65235.003	artificial	AA	TNNQRPS
1665	CDR-L3 of	artificial	AA	ATWDESMQGWV

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	CDH19 65235.003			
1666	VH of CDH19 65235.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCT
1667	VH of CDH19 65235.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1668	VL of CDH19 65235.003	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1669	VL of CDH19 65235.003	artificial	AA	QSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLS
1670	VH-VL of CDH19 65235.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTTCATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCCCTGACCCAGCCTCCCTCCGTCACCGGCACACCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1671	VH-VL of CDH19 65235.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLS
1672	CDH19 65235.003 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVFMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSVTGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESMQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1673	CDR-H1 of CDH19	artificial	AA	SYAMN

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	65236.001			
1674	CDR-H2 of CDH19 65236.001	artificial	AA	TISGGGANTYYADSVKG
1675	CDR-H3 of CDH19 65236.001	artificial	AA	GGMGGYYYGMDV
1676	CDR-L1 of CDH19 65236.001	artificial	AA	RASQSISSNLA
1677	CDR-L2 of CDH19 65236.001	artificial	AA	GAFTRAT
1678	CDR-L3 of CDH19 65236.001	artificial	AA	QQYNYWPLT
1679	VH of CDH19 65236.001	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1680	VH of CDH19 65236.001	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
1681	VL of CDH19 65236.001	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1682	VL of CDH19 65236.001	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1683	VH-VL of CDH19 65236.001	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCC

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTC CAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTC CGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACT GGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1684	VH-VL of CDH19 65236.001	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSL RAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1685	CDH19 65236.001 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSL RAADTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWF QQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1686	CDR-H1 of CDH19 65236.007	artificial	AA	SYAMN
1687	CDR-H2 of CDH19 65236.007	artificial	AA	TISGGGANTYYAESVKG
1688	CDR-H3 of CDH19 65236.007	artificial	AA	GGMGGYYYGMDV
1689	CDR-L1 of CDH19 65236.007	artificial	AA	RASQSISSNLA
1690	CDR-L2 of CDH19 65236.007	artificial	AA	GAFTRAT
1691	CDR-L3 of CDH19 65236.007	artificial	AA	QQYNYWPLT
1692	VH of CDH19 65236.007	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTT CTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACA CCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTG

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				AGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGC
1693	VH of CDH19 65236.007	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSS
1694	VL of CDH19 65236.007	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1695	VL of CDH19 65236.007	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1696	VH-VL of CDH19 65236.007	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCTCCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1697	VH-VL of CDH19 65236.007	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1698	CDH19 65236.007 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISSDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1699	CDR-H1 of CDH19 65236.009	artificial	AA	SYAMN
1700	CDR-H2 of CDH19 65236.009	artificial	AA	TISGGGANTYYADSVKG
1701	CDR-H3 of	artificial	AA	GGMGGYYYGMDV

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	CDH19 65236.009			
1702	CDR-L1 of CDH19 65236.009	artificial	AA	RASQSISSNLA
1703	CDR-L2 of CDH19 65236.009	artificial	AA	GAFTRAT
1704	CDR-L3 of CDH19 65236.009	artificial	AA	QQYNYWPLT
1705	VH of CDH19 65236.009	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1706	VH of CDH19 65236.009	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
1707	VL of CDH19 65236.009	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1708	VL of CDH19 65236.009	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1709	VH-VL of CDH19 65236.009	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1710	VH-VL of	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWF

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	CDH19 65236.009			QQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1711	CDH19 65236.009 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1712	CDR-H1 of CDH19 65236.010	artificial	AA	SYAMN
1713	CDR-H2 of CDH19 65236.010	artificial	AA	TISGGGANTYYADSVKG
1714	CDR-H3 of CDH19 65236.010	artificial	AA	GGMGGYYYGMDV
1715	CDR-L1 of CDH19 65236.010	artificial	AA	RASQSISSNLA
1716	CDR-L2 of CDH19 65236.010	artificial	AA	GAFTRAT
1717	CDR-L3 of CDH19 65236.010	artificial	AA	QQYNYWPLT
1718	VH of CDH19 65236.010	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1719	VH of CDH19 65236.010	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
1720	VL of CDH19	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCAT

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	65236.010			CTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1721	VL of CDH19 65236.010	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1722	VH-VL of CDH19 65236.010	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1723	VH-VL of CDH19 65236.010	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1724	CDH19 65236.010 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1725	CDR-H1 of CDH19 65236.011	artificial	AA	SYAMN
1726	CDR-H2 of CDH19 65236.011	artificial	AA	TISGGGANTYYADSVKG
1727	CDR-H3 of CDH19 65236.011	artificial	AA	GGMGGYYYGMDV
1728	CDR-L1 of CDH19	artificial	AA	RASQSISSNLA

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	65236.011			
1729	CDR-L2 of CDH19 65236.011	artificial	AA	GAFTRAT
1730	CDR-L3 of CDH19 65236.011	artificial	AA	QQYNYWPLT
1731	VH of CDH19 65236.011	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1732	VH of CDH19 65236.011	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
1733	VL of CDH19 65236.011	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1734	VL of CDH19 65236.011	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1735	VH-VL of CDH19 65236.011	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1736	VH-VL of CDH19 65236.011	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1737	CDH19 65236.011 x	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGG

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	I2C			GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1738	CDR-H1 of CDH19 65236.012	artificial	AA	SYAMN
1739	CDR-H2 of CDH19 65236.012	artificial	AA	TISGGGANTYYAESVKG
1740	CDR-H3 of CDH19 65236.012	artificial	AA	GGMGGYYYGMDV
1741	CDR-L1 of CDH19 65236.012	artificial	AA	RASQSISSNLA
1742	CDR-L2 of CDH19 65236.012	artificial	AA	GAFTRAT
1743	CDR-L3 of CDH19 65236.012	artificial	AA	QQYNYWPLT
1744	VH of CDH19 65236.012	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1745	VH of CDH19 65236.012	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSS
1746	VL of CDH19 65236.012	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1747	VL of CDH19 65236.012	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS

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1748	VH-VL of CDH19 65236.012	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1749	VH-VL of CDH19 65236.012	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1750	CDH19 65236.012 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1751	CDR-H1 of CDH19 65236.013	artificial	AA	SYAMN
1752	CDR-H2 of CDH19 65236.013	artificial	AA	TISGGGANTYYADSVKG
1753	CDR-H3 of CDH19 65236.013	artificial	AA	GGMGGYYYGMDV
1754	CDR-L1 of CDH19 65236.013	artificial	AA	RASQSISSNLA
1755	CDR-L2 of CDH19 65236.013	artificial	AA	GAFTRAT
1756	CDR-L3 of	artificial	AA	QQYNYWPLT

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	CDH19 65236.013			
1757	VH of CDH19 65236.013	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACTACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1758	VH of CDH19 65236.013	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSS
1759	VL of CDH19 65236.013	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1760	VL of CDH19 65236.013	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1761	VH-VL of CDH19 65236.013	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGCCGACACCGCCGTGTACTACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGAGTGTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGCAGTCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1762	VH-VL of CDH19 65236.013	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1763	CDH19 65236.013 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYADSVKGRFTISRDNSKSTLYLQMNSLRAADTAVYYCAKGGMGGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARVSGSGSGTEFTLTISSLQSEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1764	CDR-H1 of CDH19	artificial	AA	SYAMN

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	65236.014			
1765	CDR-H2 of CDH19 65236.014	artificial	AA	TISGGGANTYYAESVKG
1766	CDR-H3 of CDH19 65236.014	artificial	AA	GGMGGYYYGMDV
1767	CDR-L1 of CDH19 65236.014	artificial	AA	RASQSISSNLA
1768	CDR-L2 of CDH19 65236.014	artificial	AA	GAFTRAT
1769	CDR-L3 of CDH19 65236.014	artificial	AA	QQYNYWPLT
1770	VH of CDH19 65236.014	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGC
1771	VH of CDH19 65236.014	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSS
1772	VL of CDH19 65236.014	artificial	NT	GAGATCGTGATGACCCAGTCCCCCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1773	VL of CDH19 65236.014	artificial	AA	EIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1774	VH-VL of CDH19 65236.014	artificial	NT	CAGGTGCAGCTGCTGGAATCCGGCGGAGGACTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGCCATGAACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGTCCACCATCAGCGGCGGAGGCGCCAACACCTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAACTCCAAGTCCACCCTGTACCTGCAGATGAACTCCCTGAGAGCCGAGGACACCGCCGTGTACCACTGTGCTAAGGGCGGCATGGGCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCCTCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGCGGTGGTGGTTCTGGCGGAGGCGGCTCCGAGATCGTGATGACCCAGTCCC

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				CCGTGACCCTGTCCCTGAGCCTGGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCATCTCCAGCAACCTGGCCTGGTTCCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTTTACCCGGGCCACCGGCATCCCTGCCAGATTCTCTGGCTCCGGCTCCGGCACCGAGTTCACCCTGACCATCAGCTCCCTGGAGCCCGAGGACTTTGCCGTGTACTACTGCCAGCAGTACAACTACTGGCCCCTGACCTTCGGAGGCGGCACCAAGGTGGAAATCAAGTCC
1775	VH-VL of CDH19 65236.014	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKS
1776	CDH19 65236.014 x I2C	artificial	AA	QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSTISGGGANTYYAESVKGRFTISRDNSKSTLYLQMNSLRAEDTAVYHCAKGGMGGYYYGMDVWGQGTLVTVSSGGGGSGGGGSGGGGSEIVMTQSPVTLSLSLGERATLSCRASQSISSNLAWFQQKPGQAPRLLIYGAFTRATGIPARFSGSGSGTEFTLTISSLEPEDFAVYYCQQYNYWPLTFGGGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1777	CDR-H1 of CDH19 65237.001	artificial	AA	RYGIH
1778	CDR-H2 of CDH19 65237.001	artificial	AA	VIWYDGSNKYYADSVKG
1779	CDR-H3 of CDH19 65237.001	artificial	AA	RAGIPGTTGYYYGMDV
1780	CDR-L1 of CDH19 65237.001	artificial	AA	SGDRLGEKYVS
1781	CDR-L2 of CDH19 65237.001	artificial	AA	QDNKWPS
1782	CDR-L3 of CDH19 65237.001	artificial	AA	QAWDSSTVV
1783	VH of CDH19 65237.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1784	VH of CDH19 65237.001	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1785	VL of CDH19 65237.001	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1786	VL of CDH19 65237.001	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
1787	VH-VL of CDH19 65237.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1788	VH-VL of CDH19 65237.001	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
1789	CDH19 65237.001 x I2C	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1790	CDH-H1 of CDH19 65237b.001	artificial	AA	RYGIH
1791	CDR-H2 of CDH19 65237b.001	artificial	AA	VIWYEGSNKYYAESVKG
1792	CDR-H3 of	artificial	AA	RAGIPGTTGYYYGMDV

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	CDH19 65237b.001			
1793	CDR-L1 of CDH19 65237b.001	artificial	AA	SGDRLGEKYVS
1794	CDR-L2 of CDH19 65237b.001	artificial	AA	QDNKWPS
1795	CDR-L3 of CDH19 65237b.001	artificial	AA	QAWESSTVV
1796	VH of CDH19 65237b.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1797	VH of CDH19 65237b.001	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1798	VL of CDH19 65237b.001	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGAGTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1799	VL of CDH19 65237b.001	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLS
1800	VH-VL of CDH19 65237b.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGAGTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1801	VH-VL of	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYV

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	CDH19 65237b.001			SWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLS
1802	CDH19 65237b.001 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYEGSNKYYAESVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1803	CDR-H1 of CDH19 65237.002	artificial	AA	RYGIH
1804	CDR-H2 of CDH19 65237.002	artificial	AA	VIWYDGSNKYYADSVKG
1805	CDR-H3 of CDH19 65237.002	artificial	AA	RAGIPGTTGYYYGMDV
1806	CDR-L1 of CDH19 65237.002	artificial	AA	SGDRLGEKYVS
1807	CDR-L2 of CDH19 65237.002	artificial	AA	QDNKWPS
1808	CDR-L3 of CDH19 65237.002	artificial	AA	QAWDSSTVV
1809	VH of CDH19 65237.002	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
1810	VH of CDH19 65237.002	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSS
1811	VL of CDH19	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGA

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	65237.002			GAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1812	VL of CDH19 65237.002	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
1813	VH-VL of CDH19 65237.002	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGATACGGCATCCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACTCCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCCCCGGCACCACCGGCTACTACTACGGCATGGATGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAATACGTGAGCTGGTATCAGCAGAAGCCCGGCCAGTCCCCCATCCTGGTCATCTACCAGGACAACAAGTGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1814	VH-VL of CDH19 65237.002	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
1815	CDH19 65237.002 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSRYGIHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDSAVYYCARRAGIPGTTGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYVSWYQQKPGQSPILVIYQDNKWPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1816	CDR-H1 of CDH19 65238.002	artificial	AA	SSGYYWS
1817	CDR-H2 of CDH19 65238.002	artificial	AA	YIYYTGSAYYNPSLKS
1818	CDR-H3 of CDH19 65238.002	artificial	AA	DGSSGWYFQY
1819	CDR-L1 of CDH19	artificial	AA	RASRQISSSYLA

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	65238.002			
1820	CDR-L2 of CDH19 65238.002	artificial	AA	GPSSRAT
1821	CDR-L3 of CDH19 65238.002	artificial	AA	QQYGSSFT
1822	VH of CDH19 65238.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCCGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACACCGGCTCCGCCTACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1823	VH of CDH19 65238.002	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
1824	VL of CDH19 65238.002	artificial	NT	GAGATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCCGGGCCTCCCGGCAGATCTCCTCCAGCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCTCCTCCTTCACCTTCGGCCAGGGCACCAAGGTGGACATCAAGTCC
1825	VL of CDH19 65238.002	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKS
1826	VH-VL of CDH19 65238.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCCGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACACCGGCTCCGCCTACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCCGGGCCTCCCGGCAGATCTCCTCCAGCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCTCCTCCTTCACCTTCGGCCAGGGCACCAAGGTGGACATCAAGTCC
1827	VH-VL of CDH19 65238.002	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKS
1828	CDH19 65238.002 x	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGQGTKVDIKSGGGGSEVQLVESGGG

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	I2C			LVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1829	CDR-H1 of CDH19 65238.004	artificial	AA	SSGYYWS
1830	CDR-H2 of CDH19 65238.004	artificial	AA	YIYYTGSAYYNPSLKS
1831	CDR-H3 of CDH19 65238.004	artificial	AA	DGSSGWYFQY
1832	CDR-L1 of CDH19 65238.004	artificial	AA	RASRQISSSYLA
1833	CDR-L2 of CDH19 65238.004	artificial	AA	GPSSRAT
1834	CDR-L3 of CDH19 65238.004	artificial	AA	QQYGSSFT
1835	VH of CDH19 65238.004	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCCGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACACCGGCTCCGCCTACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1836	VH of CDH19 65238.004	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSS
1837	VL of CDH19 65238.004	artificial	NT	GAGATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCCGGGCCTCCCGGCAGATCTCCTCCAGCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCTCCTCCTTCACCTTCGGCCCTGGCACCAAGGTGGACATCAAGTCC
1838	VL of CDH19 65238.004	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKS

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1839	VH-VL of CDH19 65238.004	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACCCTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCCGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACACCGGCTCCGCCTACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCAGCGGCTGGTACTTCCAGTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCCGGCACCCTGTCTCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCCGGGCCTCCCGGCAGATCTCCTCCAGCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCCCTAGCTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCCGGCTGGAACCCGAGGACTTCGCCGTGTACTATTGCCAGCAGTACGGCTCCTCCTTCACCTTCGGCCCTGGCACCAAGGTGGACATCAAGTCC
1840	VH-VL of CDH19 65238.004	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKS
1841	CDH19 65238.004 x I2C	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSSGYYWSWIRQPPGKGLEWIGYIYYTGSAYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYFQYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASRQISSSYLAWYQQKPGQAPRLLIYGPSSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSFTFGPGTKVDIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1842	CDR-H1 of CDH19 65240.002	artificial	AA	SYDMH
1843	CDR-H2 of CDH19 65240.002	artificial	AA	VISYDGTNEYYADSVKG
1844	CDR-H3 of CDH19 65240.002	artificial	AA	ERYFDWSFDY
1845	CDR-L1 of CDH19 65240.002	artificial	AA	RASQSVSNTYLA
1846	CDR-L2 of CDH19 65240.002	artificial	AA	GASSRAT
1847	CDR-L3 of	artificial	AA	QQYSNSWT

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	CDH19 65240.002			
1848	VH of CDH19 65240.002	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGC
1849	VH of CDH19 65240.002	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
1850	VL of CDH19 65240.002	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1851	VL of CDH19 65240.002	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1852	VH-VL of CDH19 65240.002	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGACGGCACCAACGAGTACTACGCCGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1853	VH-VL of CDH19 65240.002	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1854	CDH19 65240.002 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYDGTNEYYADSVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1855	CDR-H1 of CDH19	artificial	AA	SYDMH

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	65240.003			
1856	CDR-H2 of CDH19 65240.003	artificial	AA	VISYEGTNEYYAESVKG
1857	CDR-H3 of CDH19 65240.003	artificial	AA	ERYFDWSFDY
1858	CDR-L1 of CDH19 65240.003	artificial	AA	RASQSVSNTYLA
1859	CDR-L2 of CDH19 65240.003	artificial	AA	GASSRAT
1860	CDR-L3 of CDH19 65240.003	artificial	AA	QQYSNSWT
1861	VH of CDH19 65240.003	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGC
1862	VH of CDH19 65240.003	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
1863	VL of CDH19 65240.003	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1864	VL of CDH19 65240.003	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1865	VH-VL of CDH19 65240.003	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCA

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				CCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGCGCCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1866	VH-VL of CDH19 65240.003	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1867	CDH19 65240.003 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1868	CDR-H1 of CDH19 65240.004	artificial	AA	SYDMH
1869	CDR-H2 of CDH19 65240.004	artificial	AA	VISYEGTNEYYAESVKG
1870	CDR-H3 of CDH19 65240.004	artificial	AA	ERYFDWSFDY
1871	CDR-L1 of CDH19 65240.004	artificial	AA	RASQSVSNTYLA
1872	CDR-L2 of CDH19 65240.004	artificial	AA	GASSRAT
1873	CDR-L3 of CDH19 65240.004	artificial	AA	QQYSNSWT
1874	VH of CDH19 65240.004	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTG

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				CGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGC
1875	VH of CDH19 65240.004	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSS
1876	VL of CDH19 65240.004	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGAAGCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1877	VL of CDH19 65240.004	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1878	VH-VL of CDH19 65240.004	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGTCCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGAAGCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1879	VH-VL of CDH19 65240.004	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1880	CDH19 65240.004 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVSVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1881	CDR-H1 of CDH19 65240.005	artificial	AA	SYDMH
1882	CDR-H2 of CDH19 65240.005	artificial	AA	VISYEGTNEYYAESVKG
1883	CDR-H3 of	artificial	AA	ERYFDWSFDY

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	CDH19 65240.005			
1884	CDR-L1 of CDH19 65240.005	artificial	AA	RASQSVSNTYLA
1885	CDR-L2 of CDH19 65240.005	artificial	AA	GASSRAT
1886	CDR-L3 of CDH19 65240.005	artificial	AA	QQYSNSWT
1887	VH of CDH19 65240.005	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGACCGTGTCTAGC
1888	VH of CDH19 65240.005	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVTVSS
1889	VL of CDH19 65240.005	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGAAGCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1890	VL of CDH19 65240.005	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1891	VH-VL of CDH19 65240.005	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGACATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCGTGATCTCCTACGAGGGCACCAACGAGTACTACGCCGAGTCCGTGAAGGGCCGGTTCACCATCTCCCGGGACACCTCCAAGAACACCCTGTACCTGCAGATGAACTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGCGCCAGAGAGCGGTACTTCGACTGGTCCTTCGACTACTGGGGCCAGGGCACCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCTTGCCGGGCCTCCCAGTCCGTGTCCAACACCTACCTGGCCTGGTATCAGCAGAAGCCTGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCTGGCACCGACTTCACCCTGACCATCTCCAGCCTGGAACCCGAGGATTTCGCTGTGTACTATTGCCAGCAGTACTCCAACTCCTGGACCTTCGGACAGGGCACCAAGGTGGAAATCAAGTCC
1892	VH-VL of	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQ

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	CDH19 65240.005			QKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKS
1893	CDH19 65240.005 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVISYEGTNEYYAESVKGRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARERYFDWSFDYWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSNTYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYSNSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1894	CDR-H1 of CDH19 65246.004	artificial	AA	SYFIH
1895	CDR-H2 of CDH19 65246.004	artificial	AA	IINPISVSTSYAQKFQG
1896	CDR-H3 of CDH19 65246.004	artificial	AA	GGIQLWLHFDY
1897	CDR-L1 of CDH19 65246.004	artificial	AA	SGSSSNIGSNFVN
1898	CDR-L2 of CDH19 65246.004	artificial	AA	TNNQRPS
1899	CDR-L3 of CDH19 65246.004	artificial	AA	ATWDESLQGWV
1900	VH of CDH19 65246.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1901	VH of CDH19 65246.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1902	VL of CDH19	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACAT

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	65246.004			CGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1903	VL of CDH19 65246.004	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLS
1904	VH-VL of CDH19 65246.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCTCAGTCTGCCCTGACCCAGCCTCCTTCTGCCACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTGGGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1905	VH-VL of CDH19 65246.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLS
1906	CDH19 65246.004 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATWDESLQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1907	CDR-H1 of CDH19 65247.004	artificial	AA	SYFIH
1908	CDR-H2 of CDH19 65247.004	artificial	AA	IINPISVSTSYAQKFQG
1909	CDR-H3 of CDH19 65247.004	artificial	AA	GGIQLWLHLDY
1910	CDR-L1 of CDH19	artificial	AA	SGSSSNIGSNFVN

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	65247.004			
1911	CDR-L2 of CDH19 65247.004	artificial	AA	TNNQRPS
1912	CDR-L3 of CDH19 65247.004	artificial	AA	ATYDESMQGWV
1913	VH of CDH19 65247.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGCGGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCT
1914	VH of CDH19 65247.004	artificial	AA	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSS
1915	VL of CDH19 65247.004	artificial	NT	CAGTCTGCCCTGACCCAGCCTCCTTCCGCTACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTACGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1916	VL of CDH19 65247.004	artificial	AA	QSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLS
1917	VH-VL of CDH19 65247.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGCGGGTGTCCTGCAAGGTGTCCGGCTACACCTTCACCAGCTACTTCATCCACTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCTATCTCCGTGTCCACCTCCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGGGACACCTCCACCTCCACCGTGTACATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACCTGGACTATTGGGGCCAGGGCACCCTGGTCACCGTGTCCTCTGGTGGCGGAGGATCTGGCGGAGGTGGAAGCGGAGGCGGCGGATCTCAGTCTGCCCTGACCCAGCCTCCTTCCGCTACCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCTCCTCCAACATCGGCTCCAACTTCGTGAACTGGTACCAGCAGCTGCCCGGCACCGCCCCCAAGGTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCCGAGGACGAGGCCGACTACTACTGTGCCACCTACGACGAGTCCATGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1918	VH-VL of CDH19 65247.004	artificial	AA	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLS
1919	CDH19 65247.004 x	artificial	AA	QVQLVQSGAEVKKPGASVRVSCKVSGYTFTSYFIHWVRQAPGQGLEWMGIINPISVSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHLDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSALTQPPSATGTPGQRVTISCSGSSSNIGSNFVNWYQQLPGTAPKVLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCATYDESMQGWVFGGGTKLTVLSGGGGSEVQLVES

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	I2C			GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1920	CDR-H1 of CDH19 65249.002	artificial	AA	GYYWS
1921	CDR-H2 of CDH19 65249.002	artificial	AA	YIYYIGSTNYNPSLKS
1922	CDR-H3 of CDH19 65249.002	artificial	AA	DGSSGWYRWFDP
1923	CDR-L1 of CDH19 65249.002	artificial	AA	RASQSVSSSYLA
1924	CDR-L2 of CDH19 65249.002	artificial	AA	GASSRAT
1925	CDR-L3 of CDH19 65249.002	artificial	AA	QQYGNSPLT
1926	VH of CDH19 65249.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCTCCGGCTGGTATCGTTGGTTCGACCCTTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1927	VH of CDH19 65249.002	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSS
1928	VL of CDH19 65249.002	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCTTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTTCGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCTCCCGGCTGGAACCCGAGGACTTCGCTGTGTACTACTGCCAGCAGTACGGCAACAGCCCCCTGACCTTCGGCCAAGGCACCAAGGTGGAAATCAAGTCC
1929	VL of CDH19 65249.002	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
1930	VH-VL of CDH19 65249.002	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCAT CTCCGGCTACTACTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACATCGGCTCCACCA ACTACAACCCCAGCCTGAAGTCCAGAGTGACCATGTCCGTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACC GCCGCTGACACCGCCGTGTACTACTGCGCCAGAGATGGCTCCTCCGGCTGGTATCGTTGGTTCGACCCTTGGGGCCAGGGCACCCT GGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTG GCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCTTGGTAT CAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTTCGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTC TGGCTCCGGCACCGACTTCACCCTGACCATCTCCCGGCTGGAACCCGAGGACTTCGCTGTGTACTACTGCCAGCAGTACGGCAACA GCCCCCTGACCTTCGGCCAAGGCACCAAGGTGGAAATCAAGTCC
1931	VH-VL of CDH19 65249.002	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVT AADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWY QQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKS
1932	CDH19 65249.002 x I2C	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISGYYWSWIRQPPGKGLEWIGYIYYIGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVT AADTAVYYCARDGSSGWYRWFDPWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWY QQKPGQAPRLLIFGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGNSPLTFGQGTKVEIKSGGGGSEVQLVESGG GLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAV YYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQK PGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1933	CDR-H1 of CDH19 65250.003	artificial	AA	SYYMS
1934	CDR-H2 of CDH19 65250.003	artificial	AA	IIHPSGGDTTYAQKFQG
1935	CDR-H3 of CDH19 65250.003	artificial	AA	GGIKLWLHFDY
1936	CDR-L1 of CDH19 65250.003	artificial	AA	SGSRSNIGSNFVN
1937	CDR-L2 of CDH19 65250.003	artificial	AA	TNNQRPS
1938	CDR-L3 of	artificial	AA	AVYDDSLNGWV

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	CDH19 65250.003			
1939	VH of CDH19 65250.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1940	VH of CDH19 65250.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1941	VL of CDH19 65250.003	artificial	NT	CAGTCCGTGCTGACCCAGCCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1942	VL of CDH19 65250.003	artificial	AA	QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLS
1943	VH-VL of CDH19 65250.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCCGTGCTGACCCAGCCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1944	VH-VL of CDH19 65250.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLS
1945	CDH19 65250.003 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1946	CDR-H1 of CDH19	artificial	AA	SYYMS

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	65250.004			
1947	CDR-H2 of CDH19 65250.004	artificial	AA	IIHPSGGDTTYAQKFQG
1948	CDR-H3 of CDH19 65250.004	artificial	AA	GGIKLWLHFDY
1949	CDR-L1 of CDH19 65250.004	artificial	AA	SGSRSNIGSNFVN
1950	CDR-L2 of CDH19 65250.004	artificial	AA	TNNQRPS
1951	CDR-L3 of CDH19 65250.004	artificial	AA	AVYDESLQGWV
1952	VH of CDH19 65250.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1953	VH of CDH19 65250.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1954	VL of CDH19 65250.004	artificial	NT	CAGTCCGTGCTGACCCAGCCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1955	VL of CDH19 65250.004	artificial	AA	QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
1956	VH-VL of CDH19 65250.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCCGTGCTGACCCAGCCTCCTT

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				CCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1957	VH-VL of CDH19 65250.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
1958	CDH19 65250.004 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1959	CDR-H1 of CDH19 65250.005	artificial	AA	SYYMS
1960	CDR-H2 of CDH19 65250.005	artificial	AA	IIHPSGGDTTYAQKFQG
1961	CDR-H3 of CDH19 65250.005	artificial	AA	GGIKLWLHFDY
1962	CDR-L1 of CDH19 65250.005	artificial	AA	SGSRSNIGSNFVN
1963	CDR-L2 of CDH19 65250.005	artificial	AA	TNNQRPS
1964	CDR-L3 of CDH19 65250.005	artificial	AA	AVYDESLQGWV
1965	VH of CDH19 65250.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTG

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				CGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1966	VH of CDH19 65250.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSS
1967	VL of CDH19 65250.005	artificial	NT	CAGTCCGTGCTGACCCAGCCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1968	VL of CDH19 65250.005	artificial	AA	QSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
1969	VH-VL of CDH19 65250.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAGCTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCCACCCCTCTGGCGGCGACACCACCTACGCCCAGAAATTCCAGGGCAGAGTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCAAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCCGTGCTGACCCAGCCTCCTTCCGCCTCCGGCACCCCTGGCCAGCGCGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACAACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1970	VH-VL of CDH19 65250.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
1971	CDH19 65250.005 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMSWVRQAPGQGLEWMGIIHPSGGDTTYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIKLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQRVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1972	CDH-H1 of CDH19 65251.002	artificial	AA	NYYMS
1973	CDR-H2 of CDH19 65251.002	artificial	AA	IINPSGGDSTYAQKFQG
1974	CDR-H3 of	artificial	AA	GGIQLWLHFDY

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 65251.002			
1975	CDR-L1 of CDH19 65251.002	artificial	AA	SGSRSNIGSNFVN
1976	CDR-L2 of CDH19 65251.002	artificial	AA	TNYQRPS
1977	CDR-L3 of CDH19 65251.002	artificial	AA	AVWDESLNGWV
1978	VH of CDH19 65251.002	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1979	VH of CDH19 65251.002	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1980	VL of CDH19 65251.002	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1981	VL of CDH19 65251.002	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLS
1982	VH-VL of CDH19 65251.002	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1983	VH-VL of	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWY

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	CDH19 65251.002			QQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLS
1984	CDH19 65251.002 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1985	CDR-H1 of CDH19 65251.003	artificial	AA	NYYMS
1986	CDR-H2 of CDH19 65251.003	artificial	AA	IINPSGGDSTYAQKFQG
1987	CDR-H3 of CDH19 65251.003	artificial	AA	GGIQLWLHFDY
1988	CDR-L1 of CDH19 65251.003	artificial	AA	SGSRSNIGSNFVN
1989	CDR-L2 of CDH19 65251.003	artificial	AA	TNYQRPS
1990	CDR-L3 of CDH19 65251.003	artificial	AA	AVWDESLQGWV
1991	VH of CDH19 65251.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
1992	VH of CDH19 65251.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
1993	VL of CDH19	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACAT

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	65251.003			CGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1994	VL of CDH19 65251.003	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLS
1995	VH-VL of CDH19 65251.003	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
1996	VH-VL of CDH19 65251.003	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLS
1997	CDH19 65251.003 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
1998	CDR-H1 of CDH19 65251.004	artificial	AA	NYYMS
1999	CDR-H2 of CDH19 65251.004	artificial	AA	IINPSGGDSTYAQKFQG
2000	CDR-H3 of CDH19 65251.004	artificial	AA	GGIQLWLHFDY
2001	CDR-L1 of CDH19	artificial	AA	SGSRSNIGSNFVN

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	65251.004			
2002	CDR-L2 of CDH19 65251.004	artificial	AA	TNYQRPS
2003	CDR-L3 of CDH19 65251.004	artificial	AA	AVYDESLQGWV
2004	VH of CDH19 65251.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2005	VH of CDH19 65251.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
2006	VL of CDH19 65251.004	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2007	VL of CDH19 65251.004	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
2008	VH-VL of CDH19 65251.004	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCCGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCGGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2009	VH-VL of CDH19 65251.004	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
2010	CDH19 65251.004 x	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASRYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTGDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLSGGGGSEVQLVES

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	I2C			GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2011	CDR-H1 of CDH19 65251.005	artificial	AA	NYYMS
2012	CDR-H2 of CDH19 65251.005	artificial	AA	IINPSGGDSTYAQKFQG
2013	CDR-H3 of CDH19 65251.005	artificial	AA	GGIQLWLHFDY
2014	CDR-L1 of CDH19 65251.005	artificial	AA	SGSRSNIGSNFVN
2015	CDR-L2 of CDH19 65251.005	artificial	AA	TNYQRPS
2016	CDR-L3 of CDH19 65251.005	artificial	AA	AVWDDSLNGWV
2017	VH of CDH19 65251.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2018	VH of CDH19 65251.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
2019	VL of CDH19 65251.005	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2020	VL of CDH19 65251.005	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLS

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2021	VH-VL of CDH19 65251.005	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGACTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2022	VH-VL of CDH19 65251.005	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLS
2023	CDH19 65251.005 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDDSLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2024	CDH-H1 of CDH19 65251.006	artificial	AA	NYYMS
2025	CDR-H2 of CDH19 65251.006	artificial	AA	IINPSGGDSTYAQKFQG
2026	CDR-H3 of CDH19 65251.006	artificial	AA	GGIQLWLHFDY
2027	CDR-L1 of CDH19 65251.006	artificial	AA	SGSRSNIGSNFVN
2028	CDR-L2 of CDH19 65251.006	artificial	AA	TNYQRPS
2029	CDR-L3 of	artificial	AA	AVWDESLNGWV

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	CDH19 65251.006			
2030	VH of CDH19 65251.006	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2031	VH of CDH19 65251.006	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
2032	VL of CDH19 65251.006	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2033	VL of CDH19 65251.006	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLS
2034	VH-VL of CDH19 65251.006	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGAACGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2035	VH-VL of CDH19 65251.006	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLS
2036	CDH19 65251.006 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLNGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2037	CDR-H1 of CDH19	artificial	AA	NYYMS

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	65251.007			
2038	CDR-H2 of CDH19 65251.007	artificial	AA	IINPSGGDSTYAQKFQG
2039	CDR-H3 of CDH19 65251.007	artificial	AA	GGIQLWLHFDY
2040	CDR-L1 of CDH19 65251.007	artificial	AA	SGSRSNIGSNFVN
2041	CDR-L2 of CDH19 65251.007	artificial	AA	TNYQRPS
2042	CDR-L3 of CDH19 65251.007	artificial	AA	AVWDESLQGWV
2043	VH of CDH19 65251.007	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2044	VH of CDH19 65251.007	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
2045	VL of CDH19 65251.007	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2046	VL of CDH19 65251.007	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLS
2047	VH-VL of CDH19 65251.007	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTT

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				CCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTAT CAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTC CAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTGGGACGAGT CCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2048	VH-VL of CDH19 65251.007	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLS
2049	CDH19 65251.007 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSL RSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWY QQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVWDESLQGWVFGGGTKLTVLSGGGGSEVQLVES GGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDT AVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQ QKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2050	CDR-H1 of CDH19 65251.008	artificial	AA	NYYMS
2051	CDR-H2 of CDH19 65251.008	artificial	AA	IINPSGGDSTYAQKFQG
2052	CDR-H3 of CDH19 65251.008	artificial	AA	GGIQLWLHFDY
2053	CDR-L1 of CDH19 65251.008	artificial	AA	SGSRSNIGSNFVN
2054	CDR-L2 of CDH19 65251.008	artificial	AA	TNYQRPS
2055	CDR-L3 of CDH19 65251.008	artificial	AA	AVYDESLQGWV
2056	VH of CDH19 65251.008	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTT CACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACT CCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTG

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				CGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2057	VH of CDH19 65251.008	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSS
2058	VL of CDH19 65251.008	artificial	NT	CAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2059	VL of CDH19 65251.008	artificial	AA	QSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
2060	VH-VL of CDH19 65251.008	artificial	NT	CAGGTGCAGCTGGTGCAGTCTGGCGCCGAAGTGAAGAAACCTGGCGCCTCCGTGAAGGTGTCCTGCAAGGCCTCCGGGTACACCTTCACCAACTACTACATGTCCTGGGTCCGACAGGCCCCAGGCCAGGGCCTGGAATGGATGGGCATCATCAACCCCTCTGGCGGCGACTCCACCTACGCCCAGAAGTTCCAGGGCCGGCTGACCATGACCCGCGACACCTCCACCTCCACCGTGTATATGGAACTGTCCTCCCTGCGGAGCGAGGACACCGCCGTGTACTACTGCGCCAGAGGCGGCATCCAGCTGTGGCTGCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCCCCTTCCGCCTCTGGCACCCCTGGCCAGAAAGTGACCATCTCCTGCTCCGGCTCCCGGTCCAACATCGGCTCCAACTTCGTGAACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACACCAACTACCAGCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCCATCTCCGGCCTGCAGTCTGAGGACGAGGCCGACTACTACTGTGCCGTGTACGACGAGTCCCTGCAGGGCTGGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2061	VH-VL of CDH19 65251.008	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLS
2062	CDH19 65251.008 x I2C	artificial	AA	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMSWVRQAPGQGLEWMGIINPSGGDSTYAQKFQGRLTMTRDTSTSTVYMELSSLRSEDTAVYYCARGGIQLWLHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSASGTPGQKVTISCSGSRSNIGSNFVNWYQQLPGTAPKLLIYTNYQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAVYDESLQGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2063	CDR-H1 of CDH19 65252.005	artificial	AA	SYDMD
2064	CDR-H2 of CDH19 65252.005	artificial	AA	VIWYDGSNKYYADSVRG
2065	CDR-H3 of	artificial	AA	ETGEGWYFDL

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	CDH19 65252.005			
2066	CDR-L1 of CDH19 65252.005	artificial	AA	RASQSVSSSYLA
2067	CDR-L2 of CDH19 65252.005	artificial	AA	GASSRAT
2068	CDR-L3 of CDH19 65252.005	artificial	AA	QQYGSSWT
2069	VH of CDH19 65252.005	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGC
2070	VH of CDH19 65252.005	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
2071	VL of CDH19 65252.005	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2072	VL of CDH19 65252.005	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2073	VH-VL of CDH19 65252.005	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2074	VH-VL of	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ

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	CDH19 65252.005			QKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2075	CDH19 65252.005 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2076	CDR-H1 of CDH19 65252.006	artificial	AA	SYDMD
2077	CDR-H2 of CDH19 65252.006	artificial	AA	VIWYDGSNKYYADSVRG
2078	CDR-H3 of CDH19 65252.006	artificial	AA	ETGEGWYFDL
2079	CDR-L1 of CDH19 65252.006	artificial	AA	RASQSVSSSYLA
2080	CDR-L2 of CDH19 65252.006	artificial	AA	GASSRAT
2081	CDR-L3 of CDH19 65252.006	artificial	AA	QQYGSSWT
2082	VH of CDH19 65252.006	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGC
2083	VH of CDH19 65252.006	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
2084	VL of CDH19	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGT

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	65252.006			GTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2085	VL of CDH19 65252.006	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2086	VH-VL of CDH19 65252.006	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2087	VH-VL of CDH19 65252.006	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2088	CDH19 65252.006 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2089	CDR-H1 of CDH19 65252.007	artificial	AA	SYDMD
2090	CDR-H2 of CDH19 65252.007	artificial	AA	VIWYDGSNKYYADSVRG
2091	CDR-H3 of CDH19 65252.007	artificial	AA	ETGEGWYFDL
2092	CDR-L1 of CDH19	artificial	AA	RASQSVSSSYLA

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	65252.007			
2093	CDR-L2 of CDH19 65252.007	artificial	AA	GASSRAT
2094	CDR-L3 of CDH19 65252.007	artificial	AA	QQYGSSWT
2095	VH of CDH19 65252.007	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGC
2096	VH of CDH19 65252.007	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
2097	VL of CDH19 65252.007	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2098	VL of CDH19 65252.007	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2099	VH-VL of CDH19 65252.007	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2100	VH-VL of CDH19 65252.007	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2101	CDH19 65252.007 x	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGL

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	I2C			VQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2102	CDR-H1 of CDH19 65252.008	artificial	AA	SYDMD
2103	CDR-H2 of CDH19 65252.008	artificial	AA	VIWYEGSNKYYAESVRG
2104	CDR-H3 of CDH19 65252.008	artificial	AA	ETGEGWYFDL
2105	CDR-L1 of CDH19 65252.008	artificial	AA	RASQSVSSSYLA
2106	CDR-L2 of CDH19 65252.008	artificial	AA	GASSRAT
2107	CDR-L3 of CDH19 65252.008	artificial	AA	QQYGSSWT
2108	VH of CDH19 65252.008	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGC
2109	VH of CDH19 65252.008	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
2110	VL of CDH19 65252.008	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2111	VL of CDH19 65252.008	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
2112	VH-VL of CDH19 65252.008	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAAGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2113	VH-VL of CDH19 65252.008	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2114	CDH19 65252.008 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2115	CDR-H1 of CDH19 65252.009	artificial	AA	SYDMD
2116	CDR-H2 of CDH19 65252.009	artificial	AA	VIWYDGSNKYYADSVRG
2117	CDR-H3 of CDH19 65252.009	artificial	AA	ETGEGWYFDL
2118	CDR-L1 of CDH19 65252.009	artificial	AA	RASQSVSSSYLA
2119	CDR-L2 of CDH19 65252.009	artificial	AA	GASSRAT
2120	CDR-L3 of	artificial	AA	QQYGSSWT

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 65252.009			
2121	VH of CDH19 65252.009	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGC
2122	VH of CDH19 65252.009	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
2123	VL of CDH19 65252.009	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2124	VL of CDH19 65252.009	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2125	VH-VL of CDH19 65252.009	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGACCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2126	VH-VL of CDH19 65252.009	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2127	CDH19 65252.009 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQTPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2128	CDR-H1 of CDH19	artificial	AA	SYDMD

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	65252.010			
2129	CDR-H2 of CDH19 65252.010	artificial	AA	VIWYDGSNKYYADSVRG
2130	CDR-H3 of CDH19 65252.010	artificial	AA	ETGEGWYFDL
2131	CDR-L1 of CDH19 65252.010	artificial	AA	RASQSVSSSYLA
2132	CDR-L2 of CDH19 65252.010	artificial	AA	GASSRAT
2133	CDR-L3 of CDH19 65252.010	artificial	AA	QQYGSSWT
2134	VH of CDH19 65252.010	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGC
2135	VH of CDH19 65252.010	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSS
2136	VL of CDH19 65252.010	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2137	VL of CDH19 65252.010	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2138	VH-VL of CDH19 65252.010	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCAGAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCA

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2139	VH-VL of CDH19 65252.010	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2140	CDH19 65252.010 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGRGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2141	CDR-H1 of CDH19 65252.011	artificial	AA	SYDMD
2142	CDR-H2 of CDH19 65252.011	artificial	AA	VIWYDGSNKYYADSVRG
2143	CDR-H3 of CDH19 65252.011	artificial	AA	ETGEGWYFDL
2144	CDR-L1 of CDH19 65252.011	artificial	AA	RASQSVSSSYLA
2145	CDR-L2 of CDH19 65252.011	artificial	AA	GASSRAT
2146	CDR-L3 of CDH19 65252.011	artificial	AA	QQYGSSWT
2147	VH of CDH19 65252.011	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTG

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				CGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGC
2148	VH of CDH19 65252.011	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
2149	VL of CDH19 65252.011	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2150	VL of CDH19 65252.011	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2151	VH-VL of CDH19 65252.011	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2152	VH-VL of CDH19 65252.011	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2153	CDH19 65252.011 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYDGSNKYYADSVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2154	CDR-H1 of CDH19 65252.012	artificial	AA	SYDMD
2155	CDR-H2 of CDH19 65252.012	artificial	AA	VIWYEGSNKYYAESVRG
2156	CDR-H3 of	artificial	AA	ETGEGWYFDL

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 65252.012			
2157	CDR-L1 of CDH19 65252.012	artificial	AA	RASQSVSSSYLA
2158	CDR-L2 of CDH19 65252.012	artificial	AA	GASSRAT
2159	CDR-L3 of CDH19 65252.012	artificial	AA	QQYGSSWT
2160	VH of CDH19 65252.012	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGC
2161	VH of CDH19 65252.012	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSS
2162	VL of CDH19 65252.012	artificial	NT	GAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2163	VL of CDH19 65252.012	artificial	AA	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2164	VH-VL of CDH19 65252.012	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGTGCCGCCTCCGGCTTCAGCTTCTCCTCCTACGACATGGACTGGGTCCGACAGGCCCCCGGCAAGGGCCTGGAATGGGTGGCCGTGATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGCGGGGCAGATTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTTTCTGCAGATGAACTCCCTGCGGGTGGAAGATACCGCCGTGTACTACTGCGCCAGAGAGACAGGCGAGGGCTGGTACTTCGACCTGTGGGGCCAAGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCGAGATCGTGCTGACCCAGTCCCCTGGCACCCTGTCCCTGAGCCCTGGCGAGAGAGCCACCCTGTCCTGCAGAGCCTCCCAGTCCGTGTCCTCCTCCTACCTGGCCTGGTATCAGCAGAGGCCCGGCCAGGCCCCTCGGCTGCTGATCTACGGCGCCTCTTCCAGAGCCACCGGCATCCCTGACCGGTTCTCCGGCTCTGGCTCCGGCACCGACTTCACCCTGACCATCAGCTCGCTGGAACCCGAGGACTTCGCTGTGTACTATTGCCAGCAGTACGGCTCCTCCTGGACCTTCGGCCAGGGCACCAAGGTGGAAATCAAGTCC
2165	VH-VL of	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQ

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
	CDH19 65252.012			QRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKS
2166	CDH19 65252.012 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFSFSSYDMDWVRQAPGKGLEWVAVIWYEGSNKYYAESVRGRFTISRDNSKNTLFLQMNSLRVEDTAVYYCARETGEGWYFDLWGQGTLVTVSSGGGGSGGGGSGGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISSLEPEDFAVYYCQQYGSSWTFGQGTKVEIKSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2167	CDR-H1 of CDH19 65253.003	artificial	AA	SYSWS
2168	CDR-H2 of CDH19 65253.003	artificial	AA	YIYYSGSTNYNPSLKS
2169	CDR-H3 of CDH19 65253.003	artificial	AA	NWAFHFDY
2170	CDR-L1 of CDH19 65253.003	artificial	AA	TGSSSNIGTGYDVH
2171	CDR-L2 of CDH19 65253.003	artificial	AA	GNSNRPS
2172	CDR-L3 of CDH19 65253.003	artificial	AA	QSYESSLSGWV
2173	VH of CDH19 65253.003	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTACTCTTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGC
2174	VH of CDH19 65253.003	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSS
2175	VL of CDH19	artificial	NT	CAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGCGCGTGACCATTTCCTGCACCGGCTCCTCCAGCAACAT

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	65253.003			CGGCACCGGCTACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACGGCAACTCCAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGAGTCCTCCCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAAACTGACCGTGCTGTCC
2176	VL of CDH19 65253.003	artificial	AA	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTKLTVLS
2177	VH-VL of CDH19 65253.003	artificial	NT	CAGGTGCAGCTGCAGGAATCCGGCCCTGGCCTGGTCAAGCCCTCCGAGACACTGTCCCTGACCTGCACCGTGTCCGGCGGCTCCATCTCCTCCTACTCTTGGTCCTGGATCCGGCAGCCCCCTGGCAAGGGCCTGGAATGGATCGGCTACATCTACTACTCCGGCTCCACCAACTACAACCCCAGCCTGAAGTCCAGAGTGACCATCTCCCTGGACACCTCCAAGAACCAGTTCTCCCTGAAGCTGTCCTCCGTGACCGCCGCTGACACCGCCGTGTACTACTGCGCCCGGAACTGGGCCTTCCACTTCGACTACTGGGGCCAGGGCACCCTGGTCACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCCAGTCTGTGCTGACCCAGCCTCCCTCTGTGTCTGGCGCCCCTGGCCAGCGCGTGACCATTTCCTGCACCGGCTCCTCCAGCAACATCGGCACCGGCTACGACGTGCACTGGTATCAGCAGCTGCCCGGCACCGCCCCCAAGCTGCTGATCTACGGCAACTCCAACCGGCCCTCCGGCGTGCCCGACCGGTTCTCTGGCTCCAAGTCTGGCACCTCCGCCTCCCTGGCTATCACCGGCCTGCAGGCTGAGGACGAGGCCGACTACTACTGCCAGTCCTACGAGTCCTCCCTGTCCGGCTGGGTGTTCGGCGGAGGCACCAAACTGACCGTGCTGTCC
2178	VH-VL of CDH19 65253.003	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTKLTVLS
2179	CDH19 65253.003 x I2C	artificial	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYSWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISLDTSKNQFSLKLSSVTAADTAVYYCARNWAFHFDYWGQGTLVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGSSSNIGTGYDVHWYQQLPGTAPKLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYESSLSGWVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2180	CDR-H1 of CDH19 65254.001	artificial	AA	SYGMH
2181	CDR-H2 of CDH19 65254.001	artificial	AA	FIWYDGSNKYYADSVKD
2182	CDR-H3 of CDH19 65254.001	artificial	AA	RAGIIGTIGYYYGMDV
2183	CDR-L1 of CDH19	artificial	AA	SGDRLGEKYTS

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	65254.001			
2184	CDR-L2 of CDH19 65254.001	artificial	AA	QDTKRPS
2185	CDR-L3 of CDH19 65254.001	artificial	AA	QAWDSSTVV
2186	VH of CDH19 65254.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
2187	VH of CDH19 65254.001	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
2188	VL of CDH19 65254.001	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2189	VL of CDH19 65254.001	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
2190	VH-VL of CDH19 65254.001	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCCGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2191	VH-VL of CDH19 65254.001	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
2192	CDH19 65254.001 x	artificial	AA	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVE

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	I2C			SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2193	CDR-H1 of CDH19 65254.003	artificial	AA	SYGMH
2194	CDR-H2 of CDH19 65254.003	artificial	AA	FIWYDGSNKYYADSVKD
2195	CDR-H3 of CDH19 65254.003	artificial	AA	RAGIIGTIGYYYGMDV
2196	CDR-L1 of CDH19 65254.003	artificial	AA	SGDRLGEKYTS
2197	CDR-L2 of CDH19 65254.003	artificial	AA	QDTKRPS
2198	CDR-L3 of CDH19 65254.003	artificial	AA	QAWDSSTVV
2199	VH of CDH19 65254.003	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
2200	VH of CDH19 65254.003	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
2201	VL of CDH19 65254.003	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2202	VL of CDH19 65254.003	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS

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2203	VH-VL of CDH19 65254.003	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGACGGCTCCAACAAGTACTACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAAGTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGACTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2204	VH-VL of CDH19 65254.003	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLS
2205	CDH19 65254.003 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMKSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2206	CDR-H1 of CDH19 65254.007	artificial	AA	SYGMH
2207	CDR-H2 of CDH19 65254.007	artificial	AA	FIWYEGSNKYYAESVKD
2208	CDR-H3 of CDH19 65254.007	artificial	AA	RAGIIGTIGYYYGMDV
2209	CDR-L1 of CDH19 65254.007	artificial	AA	SGDRLGEKYTS
2210	CDR-L2 of CDH19 65254.007	artificial	AA	QDTKRPS
2211	CDR-L3 of	artificial	AA	QAWESSTVV

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	CDH19 65254.007			
2212	VH of CDH19 65254.007	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAATTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGC
2213	VH of CDH19 65254.007	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSS
2214	VL of CDH19 65254.007	artificial	NT	TCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGAGTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2215	VL of CDH19 65254.007	artificial	AA	SYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLS
2216	VH-VL of CDH19 65254.007	artificial	NT	CAGGTGCAGCTGGTGGAATCCGGCGGAGGCGTGGTGCAGCCTGGCGGGTCCCTGAGACTGTCTTGCGCCGCCTCCGGCTTCACCTTCTCCAGCTACGGCATGCACTGGGTCCGACAGGCCCCTGGCAAGGGCCTGGAATGGGTGGCCTTCATTTGGTACGAGGGCTCCAACAAGTACTACGCCGAGTCCGTGAAGGACCGGTTCACCATCTCCCGGGACAACTCCAAGAACACCCTGTACCTGCAGATGAATTCCCTGCGGGCCGAGGACACCGCCGTGTACTACTGTGCCAGAAGGGCCGGCATCATCGGCACCATCGGCTACTACTACGGCATGGACGTGTGGGGCCAGGGCACCACCGTGACCGTGTCTAGCGGAGGCGGAGGATCTGGTGGCGGTGGTTCTGGCGGCGGAGGCTCCTCTTACGAGCTGACCCAGCCCCCCTCCGTGTCCGTGTCTCCTGGCCAGACCGCCTCCATCACCTGTTCTGGCGACCGGCTGGGCGAGAAGTACACCAGTTGGTATCAGCAGCGGCCTGGCCAGTCCCCCCTGCTGGTCATCTACCAGGACACCAAGCGGCCCTCCGGCATCCCTGAGCGGTTCTCCGGCTCCAACTCCGGCAACACCGCCACCCTGACCATCTCCGGCACCCAGGCCATGGACGAGGCCGACTACTACTGCCAGGCCTGGGAGTCCTCCACCGTGGTGTTCGGCGGAGGCACCAAGCTGACCGTGCTGTCC
2217	VH-VL of CDH19 65254.007	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLS
2218	CDH19 65254.007 x I2C	artificial	AA	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIWYEGSNKYYAESVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGGGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLHHHHHH
2219	CDH19 14302 CC x I2C-LFcBY	artificial	aa	QRFVTGHFGGLYPANGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVS

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				VSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGS QRFCTGHFGGLHPCNGHHHHHH
2220	CDH19 14302 CC x I2C-LFcBY-156	artificial	aa	QRFVTGHFGGLYPANGGGGGSQVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGGGGS QRFCTGHFGGLHPCNG GGGGS GGGS RDWDFDVFGGGTPVGGHHHHHH
2221	CDH19 14302 CC x I2C-Cys-Loop	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLGCGGGGCHHHHHH
2222	CDH19 14302 CC x I2C-HALB	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLDYHHHHHH
2223	CDH19 14302 CC x I2C-GS-D3HSA	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWV

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2224	CDH19 14302 CC x I2C-3GS-D3HSA	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGLHHHHHH
2225	CDH19 14302 CC x I2C-GS-D3HSA-156	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL GGGGSGGGS RDWDFDVFGGGTPVGG HHHHHH
2226	CDH19 14302 CC x I2C-3GS-D3HSA-156	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWVQQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGGSEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALGL GGGGSGGGS RDWDFDVFGGGTPVGG HHHHHH
2227	CDH19 14302 CC x I2C-GS-D3HSA-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYTSWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVESGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTEDTAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWV

SEQ ID NO.	DESIGNATION	SOURCE	TYPE	SEQUENCE
				QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSEEPQNLIKQ NCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKC CTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKAD DKETCFAEEGKKLVAASQAALGL GGGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH
2228	CDH19 14302 CC x I2C-3GS-D3HSA-21	artificial	aa	QVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKCLEWVAFIWYDGSNKYYADSVKDRFTISRDNSKNTLYLQMNSL RAEDTAVYYCARRAGIIGTIGYYYGMDVWGQGTTVTVSSGGGGSGGGGSGGGGSSYELTQPPSVSVSPGQTASITCSGDRLGEKYT SWYQQRPGQSPLLVIYQDTKRPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWESSTVVFGCGTKLTVLSGGGGSEVQLVE SGGGLVQPGGSLKLSCAASGFTFNKYAMNWVRQAPGKGLEWVARIRSKYNNYATYYADSVKDRFTISRDDSKNTAYLQMNNLKTED TAVYYCVRHGNFGNSYISYWAYWGQGTLVTVSSGGGGSGGGGSGGGGSQTVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGNYPNWV QQKPGQAPRGLIGGTKFLAPGTPARFSGSLLGGKAALTLSGVQPEDEAEYYCVLWYSNRWVFGGGTKLTVLPGGGGSGGGGSGGGG SEEPQNLIKQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEK TPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFA AFVEKCCKADDKETCFAEEGKKLVAASQAALGL GGGGSGGGS RLIEDICLPRWGCLWEDD HHHHHH

Claims

1. An isolated multispecific antibody construct comprising a first human binding domain capable of binding to human CDH19 on the surface of a target cell and a second domain capable of binding to human CD3 on the surface of a T cell.

2. The antibody construct according to claim 1, wherein the first binding domain comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

   (a) CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 222,

   CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 252,

   CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 84, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,

   CDR-H1 as depicted in SEQ ID NO: 82, CDR-H2 as depicted in SEQ ID NO: 83, CDR-H3 as depicted in SEQ ID NO: 909, CDR-L1 as depicted in SEQ ID NO: 250, CDR-L2 as depicted in SEQ ID NO: 251 and CDR-L3 as depicted in SEQ ID NO: 927,

   CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 54, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,

   CDR-H1 as depicted in SEQ ID NO: 52, CDR-H2 as depicted in SEQ ID NO: 53, CDR-H3 as depicted in SEQ ID NO: 904, CDR-L1 as depicted in SEQ ID NO: 220, CDR-L2 as depicted in SEQ ID NO: 221 and CDR-L3 as depicted in SEQ ID NO: 926,

   CDR-H1 as depicted in SEQ ID NO: 1126, CDR-H2 as depicted in SEQ ID NO: 1127, CDR-H3 as depicted in SEQ ID NO: 1128, CDR-L1 as depicted in SEQ ID NO: 1129, CDR-L2 as depicted in SEQ ID NO: 1130 and CDR-L3 as depicted in SEQ ID NO: 1131,

CDR-H1 as depicted in SEQ ID NO: 1165, CDR-H2 as depicted in SEQ ID NO: 1166, CDR-H3 as depicted in SEQ ID NO: 1167, CDR-L1 as depicted in SEQ ID NO: 1168, CDR-L2 as depicted in SEQ ID NO: 1169 and CDR-L3 as depicted in SEQ ID NO: 1170,

CDR-H1 as depicted in SEQ ID NO: 1334, CDR-H2 as depicted in SEQ ID NO: 1335, CDR-H3 as depicted in SEQ ID NO: 1336, CDR-L1 as depicted in SEQ ID NO: 1337, CDR-L2 as depicted in SEQ ID NO: 1338 and CDR-L3 as depicted in SEQ ID NO: 1339,

CDR-H1 as depicted in SEQ ID NO: 1347, CDR-H2 as depicted in SEQ ID NO: 1348, CDR-H3 as depicted in SEQ ID NO: 1349, CDR-L1 as depicted in SEQ ID NO: 1350, CDR-L2 as depicted in SEQ ID NO: 1351 and CDR-L3 as depicted in SEQ ID NO: 1352,

CDR-H1 as depicted in SEQ ID NO: 1360 CDR-H2 as depicted in SEQ ID NO: 1361, CDR-H3 as depicted in SEQ ID NO: 1362, CDR-L1 as depicted in SEQ ID NO: 1363, CDR-L2 as depicted in SEQ ID NO: 1364 and CDR-L3 as depicted in SEQ ID NO: 1365,

CDR-H1 as depicted in SEQ ID NO: 1425 CDR-H2 as depicted in SEQ ID NO: 1426, CDR-H3 as depicted in SEQ ID NO: 1427, CDR-L1 as depicted in SEQ ID NO: 1428, CDR-L2 as depicted in SEQ ID NO: 1429 and CDR-L3 as depicted in SEQ ID NO: 1430,

CDR-H1 as depicted in SEQ ID NO: 1438 CDR-H2 as depicted in SEQ ID NO: 1439, CDR-H3 as depicted in SEQ ID NO: 1440, CDR-L1 as depicted in SEQ ID NO: 1441, CDR-L2 as depicted in SEQ ID NO: 1442 and CDR-L3 as depicted in SEQ ID NO: 1443, and

CDR-H1 as depicted in SEQ ID NO: 2167 CDR-H2 as depicted in SEQ ID NO: 2168, CDR-H3 as depicted in SEQ ID NO: 2169, CDR-L1 as depicted in SEQ ID NO: 2170, CDR-L2 as depicted in SEQ ID NO: 2171 and CDR-L3 as depicted in SEQ ID NO: 2172;

(b) CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 126, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 300,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID

NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 306,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 312,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 294,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 928,

CDR-H1 as depicted in SEQ ID NO: 124, CDR-H2 as depicted in SEQ ID NO: 125, CDR-H3 as depicted in SEQ ID NO: 915, CDR-L1 as depicted in SEQ ID NO: 292, CDR-L2 as depicted in SEQ ID NO: 293 and CDR-L3 as depicted in SEQ ID NO: 929,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 336,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 942,

CDR-H1 as depicted in SEQ ID NO: 166, CDR-H2 as depicted in SEQ ID NO: 167, CDR-H3 as depicted in SEQ ID NO: 168, CDR-L1 as depicted in

SEQ ID NO: 334, CDR-L2 as depicted in SEQ ID NO: 335 and CDR-L3 as depicted in SEQ ID NO: 943,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 318,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 937,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 150, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,

CDR-H1 as depicted in SEQ ID NO: 148, CDR-H2 as depicted in SEQ ID NO: 149, CDR-H3 as depicted in SEQ ID NO: 919, CDR-L1 as depicted in SEQ ID NO: 316, CDR-L2 as depicted in SEQ ID NO: 317 and CDR-L3 as depicted in SEQ ID NO: 938,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 144, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 935,

CDR-H1 as depicted in SEQ ID NO: 142, CDR-H2 as depicted in SEQ ID NO: 143, CDR-H3 as depicted in SEQ ID NO: 918, CDR-L1 as depicted in SEQ ID NO: 310, CDR-L2 as depicted in SEQ ID NO: 311 and CDR-L3 as depicted in SEQ ID NO: 936,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 138, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as depicted in SEQ ID NO: 933,

CDR-H1 as depicted in SEQ ID NO: 136, CDR-H2 as depicted in SEQ ID NO: 137, CDR-H3 as depicted in SEQ ID NO: 917, CDR-L1 as depicted in SEQ ID NO: 304, CDR-L2 as depicted in SEQ ID NO: 305 and CDR-L3 as

depicted in SEQ ID NO: 934,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 132, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 930,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 931,

CDR-H1 as depicted in SEQ ID NO: 130, CDR-H2 as depicted in SEQ ID NO: 131, CDR-H3 as depicted in SEQ ID NO: 916, CDR-L1 as depicted in SEQ ID NO: 298, CDR-L2 as depicted in SEQ ID NO: 299 and CDR-L3 as depicted in SEQ ID NO: 932,

CDR-H1 as depicted in SEQ ID NO: 1009, CDR-H2 as depicted in SEQ ID NO: 1010, CDR-H3 as depicted in SEQ ID NO: 1011, CDR-L1 as depicted in SEQ ID NO: 1012, CDR-L2 as depicted in SEQ ID NO: 1013 and CDR-L3 as depicted in SEQ ID NO: 1014,

CDR-H1 as depicted in SEQ ID NO: 1022, CDR-H2 as depicted in SEQ ID NO: 1023, CDR-H3 as depicted in SEQ ID NO: 1024, CDR-L1 as depicted in SEQ ID NO: 1025, CDR-L2 as depicted in SEQ ID NO: 1026 and CDR-L3 as depicted in SEQ ID NO: 1027,

CDR-H1 as depicted in SEQ ID NO: 1035, CDR-H2 as depicted in SEQ ID NO: 1036, CDR-H3 as depicted in SEQ ID NO: 1037, CDR-L1 as depicted in SEQ ID NO: 1038, CDR-L2 as depicted in SEQ ID NO: 1039 and CDR-L3 as depicted in SEQ ID NO: 1040,

CDR-H1 as depicted in SEQ ID NO: 1074, CDR-H2 as depicted in SEQ ID NO: 1075, CDR-H3 as depicted in SEQ ID NO: 1076, CDR-L1 as depicted in SEQ ID NO: 1077, CDR-L2 as depicted in SEQ ID NO: 1078 and CDR-L3 as depicted in SEQ ID NO: 1079,

CDR-H1 as depicted in SEQ ID NO: 1100, CDR-H2 as depicted in SEQ ID NO: 1101, CDR-H3 as depicted in SEQ ID NO: 1102, CDR-L1 as depicted in SEQ ID NO: 1103, CDR-L2 as depicted in SEQ ID NO: 1104 and CDR-L3 as depicted in SEQ ID NO: 1105,

CDR-H1 as depicted in SEQ ID NO: 1113, CDR-H2 as depicted in SEQ ID NO: 1114, CDR-H3 as depicted in SEQ ID NO: 1115, CDR-L1 as depicted in SEQ ID NO: 1116, CDR-L2 as depicted in SEQ ID NO: 1117 and CDR-L3 as depicted in SEQ ID NO: 1118,

CDR-H1 as depicted in SEQ ID NO: 1243, CDR-H2 as depicted in SEQ ID NO: 1244, CDR-H3 as depicted in SEQ ID NO: 1245, CDR-L1 as depicted in SEQ ID NO: 1246, CDR-L2 as depicted in SEQ ID NO: 1247 and CDR-L3 as depicted in SEQ ID NO: 1248,
CDR-H1 as depicted in SEQ ID NO: 1256, CDR-H2 as depicted in SEQ ID NO: 1257, CDR-H3 as depicted in SEQ ID NO: 1258, CDR-L1 as depicted in SEQ ID NO: 1259, CDR-L2 as depicted in SEQ ID NO: 1260 and CDR-L3 as depicted in SEQ ID NO: 1261,
CDR-H1 as depicted in SEQ ID NO: 1269, CDR-H2 as depicted in SEQ ID NO: 1270, CDR-H3 as depicted in SEQ ID NO: 1271, CDR-L1 as depicted in SEQ ID NO: 1272, CDR-L2 as depicted in SEQ ID NO: 1273 and CDR-L3 as depicted in SEQ ID NO: 1274,
CDR-H1 as depicted in SEQ ID NO: 1282, CDR-H2 as depicted in SEQ ID NO: 1283, CDR-H3 as depicted in SEQ ID NO: 1284, CDR-L1 as depicted in SEQ ID NO: 1285, CDR-L2 as depicted in SEQ ID NO: 1286 and CDR-L3 as depicted in SEQ ID NO: 1287,
CDR-H1 as depicted in SEQ ID NO: 1295, CDR-H2 as depicted in SEQ ID NO: 1296, CDR-H3 as depicted in SEQ ID NO: 1297, CDR-L1 as depicted in SEQ ID NO: 1298, CDR-L2 as depicted in SEQ ID NO: 1299 and CDR-L3 as depicted in SEQ ID NO: 1300,
CDR-H1 as depicted in SEQ ID NO: 1647, CDR-H2 as depicted in SEQ ID NO: 1648, CDR-H3 as depicted in SEQ ID NO: 1649, CDR-L1 as depicted in SEQ ID NO: 1650, CDR-L2 as depicted in SEQ ID NO: 1651 and CDR-L3 as depicted in SEQ ID NO: 1652,
CDR-H1 as depicted in SEQ ID NO: 1660, CDR-H2 as depicted in SEQ ID NO: 1661, CDR-H3 as depicted in SEQ ID NO: 1662, CDR-L1 as depicted in SEQ ID NO: 1663, CDR-L2 as depicted in SEQ ID NO: 1664 and CDR-L3 as depicted in SEQ ID NO: 1665,
CDR-H1 as depicted in SEQ ID NO: 1894, CDR-H2 as depicted in SEQ ID NO: 1895, CDR-H3 as depicted in SEQ ID NO: 1896, CDR-L1 as depicted in SEQ ID NO: 1897, CDR-L2 as depicted in SEQ ID NO: 1898 and CDR-L3 as depicted in SEQ ID NO: 1899,
CDR-H1 as depicted in SEQ ID NO: 1907, CDR-H2 as depicted in SEQ ID NO: 1908, CDR-H3 as depicted in SEQ ID NO: 1909, CDR-L1 as depicted in SEQ ID NO: 1910, CDR-L2 as depicted in SEQ ID NO: 1911 and CDR-L3 as depicted in SEQ ID NO: 1912,
CDR-H1 as depicted in SEQ ID NO: 1933, CDR-H2 as depicted in SEQ ID

NO: 1934, CDR-H3 as depicted in SEQ ID NO: 1935, CDR-L1 as depicted in SEQ ID NO: 1936, CDR-L2 as depicted in SEQ ID NO: 1937 and CDR-L3 as depicted in SEQ ID NO: 1938,

CDR-H1 as depicted in SEQ ID NO: 1946, CDR-H2 as depicted in SEQ ID NO: 1947, CDR-H3 as depicted in SEQ ID NO: 1948, CDR-L1 as depicted in SEQ ID NO: 1949, CDR-L2 as depicted in SEQ ID NO: 1950 and CDR-L3 as depicted in SEQ ID NO: 1951,

CDR-H1 as depicted in SEQ ID NO: 1959, CDR-H2 as depicted in SEQ ID NO: 1960, CDR-H3 as depicted in SEQ ID NO: 1961, CDR-L1 as depicted in SEQ ID NO: 1962, CDR-L2 as depicted in SEQ ID NO: 1963 and CDR-L3 as depicted in SEQ ID NO: 1964,

CDR-H1 as depicted in SEQ ID NO: 1972, CDR-H2 as depicted in SEQ ID NO: 1973, CDR-H3 as depicted in SEQ ID NO: 1974, CDR-L1 as depicted in SEQ ID NO: 1975, CDR-L2 as depicted in SEQ ID NO: 1976 and CDR-L3 as depicted in SEQ ID NO: 1977,

CDR-H1 as depicted in SEQ ID NO: 1985, CDR-H2 as depicted in SEQ ID NO: 1986, CDR-H3 as depicted in SEQ ID NO: 1987, CDR-L1 as depicted in SEQ ID NO: 1988, CDR-L2 as depicted in SEQ ID NO: 1989 and CDR-L3 as depicted in SEQ ID NO: 1990,

CDR-H1 as depicted in SEQ ID NO: 1998, CDR-H2 as depicted in SEQ ID NO: 1999, CDR-H3 as depicted in SEQ ID NO: 2000, CDR-L1 as depicted in SEQ ID NO: 2001, CDR-L2 as depicted in SEQ ID NO: 2002 and CDR-L3 as depicted in SEQ ID NO: 2003,

CDR-H1 as depicted in SEQ ID NO: 2011, CDR-H2 as depicted in SEQ ID NO: 2012, CDR-H3 as depicted in SEQ ID NO: 2013, CDR-L1 as depicted in SEQ ID NO: 2014, CDR-L2 as depicted in SEQ ID NO: 2015 and CDR-L3 as depicted in SEQ ID NO: 2016,

CDR-H1 as depicted in SEQ ID NO: 2024, CDR-H2 as depicted in SEQ ID NO: 2025, CDR-H3 as depicted in SEQ ID NO: 2026, CDR-L1 as depicted in SEQ ID NO: 2027, CDR-L2 as depicted in SEQ ID NO: 2028 and CDR-L3 as depicted in SEQ ID NO: 2029,

CDR-H1 as depicted in SEQ ID NO: 2037, CDR-H2 as depicted in SEQ ID NO: 2038, CDR-H3 as depicted in SEQ ID NO: 2039, CDR-L1 as depicted in SEQ ID NO: 2040, CDR-L2 as depicted in SEQ ID NO: 2041 and CDR-L3 as depicted in SEQ ID NO: 2042, and

CDR-H1 as depicted in SEQ ID NO: 2050, CDR-H2 as depicted in SEQ ID NO: 2051, CDR-H3 as depicted in SEQ ID NO: 2052, CDR-L1 as depicted in

SEQ ID NO: 2053, CDR-L2 as depicted in SEQ ID NO: 2054 and CDR-L3 as depicted in SEQ ID NO: 2055;

(c) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 102, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 156, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 912, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 100, CDR-H2 as depicted in SEQ ID NO: 101, CDR-H3 as depicted in SEQ ID NO: 913, CDR-L1 as depicted in SEQ ID NO: 268, CDR-L2 as depicted in SEQ ID NO: 269 and CDR-L3 as depicted in SEQ ID NO: 270,

CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 910, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 911, CDR-L1 as depicted in SEQ ID NO: 262, CDR-L2 as depicted in SEQ ID NO: 263 and CDR-L3 as depicted in SEQ ID NO: 264,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 119, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as

depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 118, CDR-H2 as depicted in SEQ ID NO: 914, CDR-H3 as depicted in SEQ ID NO: 120, CDR-L1 as depicted in SEQ ID NO: 286, CDR-L2 as depicted in SEQ ID NO: 287 and CDR-L3 as depicted in SEQ ID NO: 288,

CDR-H1 as depicted in SEQ ID NO: 154, CDR-H2 as depicted in SEQ ID NO: 155, CDR-H3 as depicted in SEQ ID NO: 920, CDR-L1 as depicted in SEQ ID NO: 322, CDR-L2 as depicted in SEQ ID NO: 323 and CDR-L3 as depicted in SEQ ID NO: 324,

CDR-H1 as depicted in SEQ ID NO: 996, CDR-H2 as depicted in SEQ ID NO: 997, CDR-H3 as depicted in SEQ ID NO: 998, CDR-L1 as depicted in SEQ ID NO: 999, CDR-L2 as depicted in SEQ ID NO: 1000 and CDR-L3 as depicted in SEQ ID NO: 1001,

CDR-H1 as depicted in SEQ ID NO: 1048, CDR-H2 as depicted in SEQ ID NO: 1049, CDR-H3 as depicted in SEQ ID NO: 1050, CDR-L1 as depicted in SEQ ID NO: 1051, CDR-L2 as depicted in SEQ ID NO: 1052 and CDR-L3 as depicted in SEQ ID NO: 1053,

CDR-H1 as depicted in SEQ ID NO: 1087, CDR-H2 as depicted in SEQ ID NO: 1088, CDR-H3 as depicted in SEQ ID NO: 1089, CDR-L1 as depicted in SEQ ID NO: 1090, CDR-L2 as depicted in SEQ ID NO: 1091 and CDR-L3 as depicted in SEQ ID NO: 1092,

CDR-H1 as depicted in SEQ ID NO: 1608, CDR-H2 as depicted in SEQ ID NO: 1609, CDR-H3 as depicted in SEQ ID NO: 1610, CDR-L1 as depicted in SEQ ID NO: 1611, CDR-L2 as depicted in SEQ ID NO: 1612 and CDR-L3 as depicted in SEQ ID NO: 1613,

CDR-H1 as depicted in SEQ ID NO: 1621, CDR-H2 as depicted in SEQ ID NO: 1622, CDR-H3 as depicted in SEQ ID NO: 1623, CDR-L1 as depicted in SEQ ID NO: 1624, CDR-L2 as depicted in SEQ ID NO: 1625 and CDR-L3 as depicted in SEQ ID NO: 1626,

CDR-H1 as depicted in SEQ ID NO: 1634, CDR-H2 as depicted in SEQ ID NO: 1635, CDR-H3 as depicted in SEQ ID NO: 1636, CDR-L1 as depicted in SEQ ID NO: 1637, CDR-L2 as depicted in SEQ ID NO: 1638 and CDR-L3 as depicted in SEQ ID NO: 1639,

CDR-H1 as depicted in SEQ ID NO: 1673, CDR-H2 as depicted in SEQ ID NO: 1674, CDR-H3 as depicted in SEQ ID NO: 1675, CDR-L1 as depicted in SEQ ID NO: 1676, CDR-L2 as depicted in SEQ ID NO: 1677 and CDR-L3 as depicted in SEQ ID NO: 1678,

CDR-H1 as depicted in SEQ ID NO: 1686, CDR-H2 as depicted in SEQ ID NO: 1687, CDR-H3 as depicted in SEQ ID NO: 1688, CDR-L1 as depicted in SEQ ID NO: 1689, CDR-L2 as depicted in SEQ ID NO: 1690 and CDR-L3 as depicted in SEQ ID NO: 1691,

CDR-H1 as depicted in SEQ ID NO: 1699, CDR-H2 as depicted in SEQ ID NO: 1700, CDR-H3 as depicted in SEQ ID NO: 1701, CDR-L1 as depicted in SEQ ID NO: 1702, CDR-L2 as depicted in SEQ ID NO: 1703 and CDR-L3 as depicted in SEQ ID NO: 1704,

CDR-H1 as depicted in SEQ ID NO: 1712, CDR-H2 as depicted in SEQ ID NO: 1713, CDR-H3 as depicted in SEQ ID NO: 1714, CDR-L1 as depicted in SEQ ID NO: 1715, CDR-L2 as depicted in SEQ ID NO: 1716 and CDR-L3 as depicted in SEQ ID NO: 1717,

CDR-H1 as depicted in SEQ ID NO: 1725, CDR-H2 as depicted in SEQ ID NO: 1726, CDR-H3 as depicted in SEQ ID NO: 1727, CDR-L1 as depicted in SEQ ID NO: 1728, CDR-L2 as depicted in SEQ ID NO: 1729 and CDR-L3 as depicted in SEQ ID NO: 1730,

CDR-H1 as depicted in SEQ ID NO: 1738, CDR-H2 as depicted in SEQ ID NO: 1739, CDR-H3 as depicted in SEQ ID NO: 1740, CDR-L1 as depicted in SEQ ID NO: 1741, CDR-L2 as depicted in SEQ ID NO: 1742 and CDR-L3 as depicted in SEQ ID NO: 1743,

CDR-H1 as depicted in SEQ ID NO: 1751, CDR-H2 as depicted in SEQ ID NO: 1752, CDR-H3 as depicted in SEQ ID NO: 1753, CDR-L1 as depicted in SEQ ID NO: 1754, CDR-L2 as depicted in SEQ ID NO: 1755 and CDR-L3 as depicted in SEQ ID NO: 1756,

CDR-H1 as depicted in SEQ ID NO: 1764, CDR-H2 as depicted in SEQ ID NO: 1765, CDR-H3 as depicted in SEQ ID NO: 1766, CDR-L1 as depicted in SEQ ID NO: 1767, CDR-L2 as depicted in SEQ ID NO: 1768 and CDR-L3 as depicted in SEQ ID NO: 1769, and

CDR-H1 as depicted in SEQ ID NO: 1920, CDR-H2 as depicted in SEQ ID NO: 1921, CDR-H3 as depicted in SEQ ID NO: 1922, CDR-L1 as depicted in SEQ ID NO: 1923, CDR-L2 as depicted in SEQ ID NO: 1924 and CDR-L3 as depicted in SEQ ID NO: 1925;

(d) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 172, CDR-L2 as depicted in SEQ ID NO: 173 and CDR-L3 as depicted in SEQ ID NO: 174,

CDR-H1 as depicted in SEQ ID NO: 10, CDR-H2 as depicted in SEQ ID NO: 11,

CDR-H3 as depicted in SEQ ID NO: 12, CDR-L1 as depicted in SEQ ID NO: 178, CDR-L2 as depicted in SEQ ID NO: 179 and CDR-L3 as depicted in SEQ ID NO: 180,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 198,

CDR-H1 as depicted in SEQ ID NO: 34, CDR-H2 as depicted in SEQ ID NO: 35, CDR-H3 as depicted in SEQ ID NO: 36, CDR-L1 as depicted in SEQ ID NO: 202, CDR-L2 as depicted in SEQ ID NO: 203 and CDR-L3 as depicted in SEQ ID NO: 204,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 214, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 59, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 64, CDR-H2 as depicted in SEQ ID NO: 65, CDR-H3 as depicted in SEQ ID NO: 66, CDR-L1 as depicted in SEQ ID NO: 232, CDR-L2 as depicted in SEQ ID NO: 233 and CDR-L3 as depicted in SEQ ID NO: 234,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 71, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 328, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 902, CDR-L1 as depicted in SEQ ID

NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 903, CDR-L1 as depicted in SEQ ID NO: 924, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 46, CDR-H2 as depicted in SEQ ID NO: 47, CDR-H3 as depicted in SEQ ID NO: 48, CDR-L1 as depicted in SEQ ID NO: 925, CDR-L2 as depicted in SEQ ID NO: 215 and CDR-L3 as depicted in SEQ ID NO: 216,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 72, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 70, CDR-H2 as depicted in SEQ ID NO: 907, CDR-H3 as depicted in SEQ ID NO: 908, CDR-L1 as depicted in SEQ ID NO: 238, CDR-L2 as depicted in SEQ ID NO: 239 and CDR-L3 as depicted in SEQ ID NO: 240,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 906, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 58, CDR-H2 as depicted in SEQ ID NO: 905, CDR-H3 as depicted in SEQ ID NO: 60, CDR-L1 as depicted in SEQ ID NO: 226, CDR-L2 as depicted in SEQ ID NO: 227 and CDR-L3 as depicted in SEQ ID NO: 228,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 921, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as

depicted in SEQ ID NO: 940,

CDR-H1 as depicted in SEQ ID NO: 160, CDR-H2 as depicted in SEQ ID NO: 161, CDR-H3 as depicted in SEQ ID NO: 162, CDR-L1 as depicted in SEQ ID NO: 941, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 196, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 901, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 922, CDR-L2 as depicted in SEQ ID NO: 197 and CDR-L3 as depicted in SEQ ID NO: 923,

CDR-H1 as depicted in SEQ ID NO: 28, CDR-H2 as depicted in SEQ ID NO: 29, CDR-H3 as depicted in SEQ ID NO: 30, CDR-L1 as depicted in SEQ ID NO: 939, CDR-L2 as depicted in SEQ ID NO: 329 and CDR-L3 as depicted in SEQ ID NO: 330,

CDR-H1 as depicted in SEQ ID NO: 970, CDR-H2 as depicted in SEQ ID NO: 971, CDR-H3 as depicted in SEQ ID NO: 972, CDR-L1 as depicted in SEQ ID NO: 973, CDR-L2 as depicted in SEQ ID NO: 974 and CDR-L3 as depicted in SEQ ID NO: 975,

CDR-H1 as depicted in SEQ ID NO: 1061, CDR-H2 as depicted in SEQ ID NO: 1062, CDR-H3 as depicted in SEQ ID NO: 1063, CDR-L1 as depicted in SEQ ID NO: 1064, CDR-L2 as depicted in SEQ ID NO: 1065 and CDR-L3 as depicted in SEQ ID NO: 1066,

CDR-H1 as depicted in SEQ ID NO: 1139, CDR-H2 as depicted in SEQ ID NO: 1140, CDR-H3 as depicted in SEQ ID NO: 1141, CDR-L1 as depicted in SEQ ID NO: 1142, CDR-L2 as depicted in SEQ ID NO: 1143 and CDR-L3 as depicted in SEQ ID NO: 1144,

CDR-H1 as depicted in SEQ ID NO: 1152, CDR-H2 as depicted in SEQ ID NO: 1153, CDR-H3 as depicted in SEQ ID NO: 1154, CDR-L1 as depicted in SEQ ID NO: 1155, CDR-L2 as depicted in SEQ ID NO: 1156 and CDR-L3 as depicted in SEQ ID NO: 1157,

CDR-H1 as depicted in SEQ ID NO: 1178, CDR-H2 as depicted in SEQ ID NO: 1179, CDR-H3 as depicted in SEQ ID NO: 1180, CDR-L1 as depicted in SEQ ID NO: 1181, CDR-L2 as depicted in SEQ ID NO: 1182 and CDR-L3 as depicted in SEQ ID NO: 1183,

CDR-H1 as depicted in SEQ ID NO: 1191, CDR-H2 as depicted in SEQ ID NO: 1192, CDR-H3 as depicted in SEQ ID NO: 1193, CDR-L1 as depicted in SEQ ID NO: 1194, CDR-L2 as depicted in SEQ ID NO: 1195 and CDR-L3 as depicted in SEQ ID NO: 1196,

CDR-H1 as depicted in SEQ ID NO: 1204, CDR-H2 as depicted in SEQ ID NO: 1205, CDR-H3 as depicted in SEQ ID NO: 1206, CDR-L1 as depicted in SEQ ID NO: 1207, CDR-L2 as depicted in SEQ ID NO: 1208 and CDR-L3 as depicted in SEQ ID NO: 1209,

CDR-H1 as depicted in SEQ ID NO: 1217, CDR-H2 as depicted in SEQ ID NO: 1218, CDR-H3 as depicted in SEQ ID NO: 1219, CDR-L1 as depicted in SEQ ID NO: 1220, CDR-L2 as depicted in SEQ ID NO: 1221 and CDR-L3 as depicted in SEQ ID NO: 1222,

CDR-H1 as depicted in SEQ ID NO: 1230, CDR-H2 as depicted in SEQ ID NO: 1231, CDR-H3 as depicted in SEQ ID NO: 1232, CDR-L1 as depicted in SEQ ID NO: 1233, CDR-L2 as depicted in SEQ ID NO: 1234 and CDR-L3 as depicted in SEQ ID NO: 1235,

CDR-H1 as depicted in SEQ ID NO: 1308, CDR-H2 as depicted in SEQ ID NO: 1309, CDR-H3 as depicted in SEQ ID NO: 1310, CDR-L1 as depicted in SEQ ID NO: 1311, CDR-L2 as depicted in SEQ ID NO: 1312 and CDR-L3 as depicted in SEQ ID NO: 1313,

CDR-H1 as depicted in SEQ ID NO: 1321, CDR-H2 as depicted in SEQ ID NO: 1322, CDR-H3 as depicted in SEQ ID NO: 1323, CDR-L1 as depicted in SEQ ID NO: 1324, CDR-L2 as depicted in SEQ ID NO: 1325 and CDR-L3 as depicted in SEQ ID NO: 1326,

CDR-H1 as depicted in SEQ ID NO: 1373, CDR-H2 as depicted in SEQ ID NO: 1374, CDR-H3 as depicted in SEQ ID NO: 1375, CDR-L1 as depicted in SEQ ID NO: 1376, CDR-L2 as depicted in SEQ ID NO: 1377 and CDR-L3 as depicted in SEQ ID NO: 1378,

CDR-H1 as depicted in SEQ ID NO: 1386, CDR-H2 as depicted in SEQ ID NO: 1387, CDR-H3 as depicted in SEQ ID NO: 1388, CDR-L1 as depicted in SEQ ID NO: 1389, CDR-L2 as depicted in SEQ ID NO: 1390 and CDR-L3 as depicted in SEQ ID NO: 1391,

CDR-H1 as depicted in SEQ ID NO: 1399, CDR-H2 as depicted in SEQ ID

NO: 1400, CDR-H3 as depicted in SEQ ID NO: 1401, CDR-L1 as depicted in SEQ ID NO: 1402, CDR-L2 as depicted in SEQ ID NO: 1403 and CDR-L3 as depicted in SEQ ID NO: 1404,

CDR-H1 as depicted in SEQ ID NO: 1412, CDR-H2 as depicted in SEQ ID NO: 1413, CDR-H3 as depicted in SEQ ID NO: 1414, CDR-L1 as depicted in SEQ ID NO: 1415, CDR-L2 as depicted in SEQ ID NO: 1416 and CDR-L3 as depicted in SEQ ID NO: 1417,

CDR-H1 as depicted in SEQ ID NO: 1777, CDR-H2 as depicted in SEQ ID NO: 1778, CDR-H3 as depicted in SEQ ID NO: 1779, CDR-L1 as depicted in SEQ ID NO: 1780, CDR-L2 as depicted in SEQ ID NO: 1781 and CDR-L3 as depicted in SEQ ID NO: 1782,

CDR-H1 as depicted in SEQ ID NO: 1790, CDR-H2 as depicted in SEQ ID NO: 1791, CDR-H3 as depicted in SEQ ID NO: 1792, CDR-L1 as depicted in SEQ ID NO: 1793, CDR-L2 as depicted in SEQ ID NO: 1794 and CDR-L3 as depicted in SEQ ID NO: 1795,

CDR-H1 as depicted in SEQ ID NO: 1803, CDR-H2 as depicted in SEQ ID NO: 1804, CDR-H3 as depicted in SEQ ID NO: 1805, CDR-L1 as depicted in SEQ ID NO: 1806, CDR-L2 as depicted in SEQ ID NO: 1807 and CDR-L3 as depicted in SEQ ID NO: 1808,

CDR-H1 as depicted in SEQ ID NO: 1816, CDR-H2 as depicted in SEQ ID NO: 1817, CDR-H3 as depicted in SEQ ID NO: 1818, CDR-L1 as depicted in SEQ ID NO: 1819, CDR-L2 as depicted in SEQ ID NO: 1820 and CDR-L3 as depicted in SEQ ID NO: 1821,

CDR-H1 as depicted in SEQ ID NO: 1829, CDR-H2 as depicted in SEQ ID NO: 1830, CDR-H3 as depicted in SEQ ID NO: 1831, CDR-L1 as depicted in SEQ ID NO: 1832, CDR-L2 as depicted in SEQ ID NO: 1833 and CDR-L3 as depicted in SEQ ID NO: 1834,

CDR-H1 as depicted in SEQ ID NO: 1842, CDR-H2 as depicted in SEQ ID NO: 1843, CDR-H3 as depicted in SEQ ID NO: 1844, CDR-L1 as depicted in SEQ ID NO: 1845, CDR-L2 as depicted in SEQ ID NO: 1846 and CDR-L3 as depicted in SEQ ID NO: 1847,

CDR-H1 as depicted in SEQ ID NO: 1855, CDR-H2 as depicted in SEQ ID NO: 1856, CDR-H3 as depicted in SEQ ID NO: 1857, CDR-L1 as depicted in SEQ ID NO: 1858, CDR-L2 as depicted in SEQ ID NO: 1859 and CDR-L3 as depicted in SEQ ID NO: 1860,

CDR-H1 as depicted in SEQ ID NO: 1868, CDR-H2 as depicted in SEQ ID NO: 1869, CDR-H3 as depicted in SEQ ID NO: 1870, CDR-L1 as depicted in

SEQ ID NO: 1871, CDR-L2 as depicted in SEQ ID NO: 1872 and CDR-L3 as depicted in SEQ ID NO: 1873,

CDR-H1 as depicted in SEQ ID NO: 1881, CDR-H2 as depicted in SEQ ID NO: 1882, CDR-H3 as depicted in SEQ ID NO: 1883, CDR-L1 as depicted in SEQ ID NO: 1884, CDR-L2 as depicted in SEQ ID NO: 1885 and CDR-L3 as depicted in SEQ ID NO: 1886,

CDR-H1 as depicted in SEQ ID NO: 2063, CDR-H2 as depicted in SEQ ID NO: 2064, CDR-H3 as depicted in SEQ ID NO: 2065, CDR-L1 as depicted in SEQ ID NO: 2066, CDR-L2 as depicted in SEQ ID NO: 2067 and CDR-L3 as depicted in SEQ ID NO: 2068,

CDR-H1 as depicted in SEQ ID NO: 2076, CDR-H2 as depicted in SEQ ID NO: 2077, CDR-H3 as depicted in SEQ ID NO: 2078, CDR-L1 as depicted in SEQ ID NO: 2079, CDR-L2 as depicted in SEQ ID NO: 2080 and CDR-L3 as depicted in SEQ ID NO: 2081,

CDR-H1 as depicted in SEQ ID NO: 2089, CDR-H2 as depicted in SEQ ID NO: 2090, CDR-H3 as depicted in SEQ ID NO: 2091, CDR-L1 as depicted in SEQ ID NO: 2092, CDR-L2 as depicted in SEQ ID NO: 2093 and CDR-L3 as depicted in SEQ ID NO: 2094,

CDR-H1 as depicted in SEQ ID NO: 2102, CDR-H2 as depicted in SEQ ID NO: 2103, CDR-H3 as depicted in SEQ ID NO: 2104, CDR-L1 as depicted in SEQ ID NO: 2105, CDR-L2 as depicted in SEQ ID NO: 2106 and CDR-L3 as depicted in SEQ ID NO: 2107,

CDR-H1 as depicted in SEQ ID NO: 2115, CDR-H2 as depicted in SEQ ID NO: 2116, CDR-H3 as depicted in SEQ ID NO: 2117, CDR-L1 as depicted in SEQ ID NO: 2118, CDR-L2 as depicted in SEQ ID NO: 2119 and CDR-L3 as depicted in SEQ ID NO: 2120,

CDR-H1 as depicted in SEQ ID NO: 2128, CDR-H2 as depicted in SEQ ID NO: 2129, CDR-H3 as depicted in SEQ ID NO: 2130, CDR-L1 as depicted in SEQ ID NO: 2131, CDR-L2 as depicted in SEQ ID NO: 2132 and CDR-L3 as depicted in SEQ ID NO: 2133,

CDR-H1 as depicted in SEQ ID NO: 2141, CDR-H2 as depicted in SEQ ID NO: 2142, CDR-H3 as depicted in SEQ ID NO: 2143, CDR-L1 as depicted in SEQ ID NO: 2144, CDR-L2 as depicted in SEQ ID NO: 2145 and CDR-L3 as depicted in SEQ ID NO: 2146,

CDR-H1 as depicted in SEQ ID NO: 2154, CDR-H2 as depicted in SEQ ID NO: 2155, CDR-H3 as depicted in SEQ ID NO: 2156, CDR-L1 as depicted in SEQ ID NO: 2157, CDR-L2 as depicted in SEQ ID NO: 2158 and CDR-L3 as

depicted in SEQ ID NO: 2159,

CDR-H1 as depicted in SEQ ID NO: 2180, CDR-H2 as depicted in SEQ ID NO: 2181, CDR-H3 as depicted in SEQ ID NO: 2182, CDR-L1 as depicted in SEQ ID NO: 2183, CDR-L2 as depicted in SEQ ID NO: 2184 and CDR-L3 as depicted in SEQ ID NO: 2185,

CDR-H1 as depicted in SEQ ID NO: 2193, CDR-H2 as depicted in SEQ ID NO: 2194, CDR-H3 as depicted in SEQ ID NO: 2195, CDR-L1 as depicted in SEQ ID NO: 2196, CDR-L2 as depicted in SEQ ID NO: 2197 and CDR-L3 as depicted in SEQ ID NO: 2198, and

CDR-H1 as depicted in SEQ ID NO: 2206, CDR-H2 as depicted in SEQ ID NO: 2207, CDR-H3 as depicted in SEQ ID NO: 2208, CDR-L1 as depicted in SEQ ID NO: 2209, CDR-L2 as depicted in SEQ ID NO: 2210 and CDR-L3 as depicted in SEQ ID NO: 2211; and

(e) CDR-H1 as depicted in SEQ ID NO: 76, CDR-H2 as depicted in SEQ ID NO: 77, CDR-H3 as depicted in SEQ ID NO: 78, CDR-L1 as depicted in SEQ ID NO: 244, CDR-L2 as depicted in SEQ ID NO: 245 and CDR-L3 as depicted in SEQ ID NO: 246,

CDR-H1 as depicted in SEQ ID NO: 88, CDR-H2 as depicted in SEQ ID NO: 89, CDR-H3 as depicted in SEQ ID NO: 90, CDR-L1 as depicted in SEQ ID NO: 256, CDR-L2 as depicted in SEQ ID NO: 257 and CDR-L3 as depicted in SEQ ID NO: 258,

CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276 ,

CDR-H1 as depicted in SEQ ID NO: 112, CDR-H2 as depicted in SEQ ID NO: 113, CDR-H3 as depicted in SEQ ID NO: 114, CDR-L1 as depicted in SEQ ID NO: 280, CDR-L2 as depicted in SEQ ID NO: 281 and CDR-L3 as depicted in SEQ ID NO: 282,

CDR-H1 as depicted in SEQ ID NO: 106, CDR-H2 as depicted in SEQ ID NO: 107, CDR-H3 as depicted in SEQ ID NO: 108, CDR-L1 as depicted in SEQ ID NO: 274, CDR-L2 as depicted in SEQ ID NO: 275 and CDR-L3 as depicted in SEQ ID NO: 276,

CDR-H1 as depicted in SEQ ID NO: 983, CDR-H2 as depicted in SEQ ID NO: 984, CDR-H3 as depicted in SEQ ID NO: 985, CDR-L1 as depicted in SEQ ID NO: 986, CDR-L2 as depicted in SEQ ID NO: 987 and CDR-L3 as depicted in SEQ ID NO: 988,

CDR-H1 as depicted in SEQ ID NO: 1582, CDR-H2 as depicted in SEQ ID NO: 1583, CDR-H3 as depicted in SEQ ID NO: 1584, CDR-L1 as depicted in SEQ ID NO: 1585, CDR-L2 as depicted in SEQ ID NO: 1586 and CDR-L3 as depicted in SEQ ID NO: 1587, and

CDR-H1 as depicted in SEQ ID NO: 1595, CDR-H2 as depicted in SEQ ID NO: 1596, CDR-H3 as depicted in SEQ ID NO: 1597, CDR-L1 as depicted in SEQ ID NO: 1598, CDR-L2 as depicted in SEQ ID NO: 1599 and CDR-L3 as depicted in SEQ ID NO: 1600.

3. The antibody construct according to claim 1 or 2, wherein the first binding domain comprises a VH region selected from the group consisting of VH regions
   (a) as depicted in SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 487, SEQ ID NO: 492, SEQ ID NO: 493, SEQ ID NO: 494, SEQ ID NO: 495, SEQ ID NO: 1133, SEQ ID NO: 1172, SEQ ID NO: 1341, SEQ ID NO: 1354, SEQ ID NO: 1367, SEQ ID NO: 1432, SEQ ID NO: 1445 and SEQ ID NO: 2174;
   (b) as depicted in SEQ ID NO: 342, SEQ ID NO: 366, SEQ ID NO: 370, SEQ ID NO: 344, SEQ ID NO: 372, SEQ ID NO: 368, SEQ ID NO: 496, SEQ ID NO: 497, SEQ ID NO: 498, SEQ ID NO: 499, SEQ ID NO: 500, SEQ ID NO: 508, SEQ ID NO: 509, SEQ ID NO: 510, SEQ ID NO: 511, SEQ ID NO: 512, SEQ ID NO: 519, SEQ ID NO: 520, SEQ ID NO: 521, SEQ ID NO: 522, SEQ ID NO: 523, SEQ ID NO: 524, SEQ ID NO: 525, SEQ ID NO: 526, SEQ ID NO: 527, SEQ ID NO: 528, SEQ ID NO: 529, SEQ ID NO: 530, SEQ ID NO: 531, SEQ ID NO: 532, SEQ ID NO: 533, SEQ ID NO: 534, SEQ ID NO: 535, SEQ ID NO: 536, SEQ ID NO: 537, SEQ ID NO: 538, SEQ ID NO: 1016, SEQ ID NO: 1029, SEQ ID NO: 1042, SEQ ID NO: 1081, SEQ ID NO: 1107, SEQ ID NO: 1120, SEQ ID NO: 1250, SEQ ID NO: 1263, SEQ ID NO: 1276, SEQ ID NO: 1289, SEQ ID NO: 1302, SEQ ID NO: 1654, SEQ ID NO: 1667, SEQ ID NO: 1901, SEQ ID NO: 1914, SEQ ID NO: 1940, SEQ ID NO: 1953, SEQ ID NO: 1966, SEQ ID NO: 1979, SEQ ID NO: 1992, SEQ ID NO: 2005, SEQ ID NO: 2018, SEQ ID NO: 2031, SEQ ID NO: 2044, and SEQ ID NO: 2057;
   (c) as depicted in SEQ ID NO: 338, SEQ ID NO: 354, SEQ ID NO: 378, SEQ ID NO: 356, SEQ ID NO: 476, SEQ ID NO: 477, SEQ ID NO: 478, SEQ ID NO: 479, SEQ ID NO: 480, SEQ ID NO: 481, SEQ ID NO: 482, SEQ ID NO: 483, SEQ ID NO: 484, SEQ ID NO: 501, SEQ ID NO: 502, SEQ ID NO: 503, SEQ ID NO: 504, SEQ ID NO: 505, SEQ ID NO: 506, SEQ ID NO: 517, SEQ ID NO: 518, SEQ ID NO: 1003, SEQ ID NO: 1055, SEQ ID NO: 1094, SEQ ID NO: 1615, SEQ ID

NO: 1628, SEQ ID NO: 1641, SEQ ID NO: 1680, SEQ ID NO: 1693, SEQ ID NO: 1706, SEQ ID NO: 1719, SEQ ID NO: 1732, SEQ ID NO: 1745, SEQ ID NO: 1758, SEQ ID NO: 1771, and SEQ ID NO: 1927;

(d) as depicted in SEQ ID NO: 352, SEQ ID NO: 360, SEQ ID NO: 388, SEQ ID NO: 386, SEQ ID NO: 340, SEQ ID NO: 346, SEQ ID NO: 374, SEQ ID NO: 348, SEQ ID NO: 390, SEQ ID NO: 463, SEQ ID NO: 464, SEQ ID NO: 465, SEQ ID NO: 466, SEQ ID NO: 467, SEQ ID NO: 468, SEQ ID NO: 469, SEQ ID NO: 470, SEQ ID NO: 471, SEQ ID NO: 472, SEQ ID NO: 473, SEQ ID NO: 474, SEQ ID NO: 475, SEQ ID NO: 488, SEQ ID NO: 489, SEQ ID NO: 490, SEQ ID NO: 491, SEQ ID NO: 513, SEQ ID NO: 514, SEQ ID NO: 515, SEQ ID NO: 516, SEQ ID NO: 540, SEQ ID NO: 541, SEQ ID NO: 542, SEQ ID NO: 543, SEQ ID NO: 977, SEQ ID NO: 1068, SEQ ID NO: 1146, SEQ ID NO: 1159, SEQ ID NO: 1185, SEQ ID NO: 1198, SEQ ID NO: 1211, SEQ ID NO: 1224, SEQ ID NO: 1237, SEQ ID NO: 1315, SEQ ID NO: 1328, SEQ ID NO: 1380, SEQ ID NO: 1393, SEQ ID NO: 1406, SEQ ID NO: 1419, SEQ ID NO: 1469, SEQ ID NO: 1478, SEQ ID NO: 1485, SEQ ID NO: 1494, SEQ ID NO: 1501, SEQ ID NO: 1508, SEQ ID NO: 1519, SEQ ID NO: 1526, SEQ ID NO: 1533, SEQ ID NO: 1542, SEQ ID NO: 1549, SEQ ID NO: 1558, SEQ ID NO: 1565, SEQ ID NO: 1784, SEQ ID NO: 1797, SEQ ID NO: 1810, SEQ ID NO: 1823, SEQ ID NO: 1836, SEQ ID NO: 1849, SEQ ID NO: 1862, SEQ ID NO: 1875, SEQ ID NO: 1888, SEQ ID NO: 2070, SEQ ID NO: 2083, SEQ ID NO: 2096, SEQ ID NO: 2109, SEQ ID NO: 2122, SEQ ID NO: 2135, SEQ ID NO: 2148, SEQ ID NO: 2161, SEQ ID NO: 2187, SEQ ID NO: 2200, and SEQ ID NO: 2213; and

(e) as depicted in SEQ ID NO: 376, SEQ ID NO: 392, SEQ ID NO: 358, SEQ ID NO: 350, SEQ ID NO: 507, SEQ ID NO: 990, SEQ ID NO: 1589, and SEQ ID NO: 1602.

4. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VL region selected from the group consisting of VL regions

(a) as depicted in SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 580, SEQ ID NO: 581, SEQ ID NO: 582, SEQ ID NO: 587, SEQ ID NO: 588, SEQ ID NO: 589, SEQ ID NO: 590, SEQ ID NO: 1135, SEQ ID NO: 1174, SEQ ID NO: 1343, SEQ ID NO: 1356, SEQ ID NO: 1369, SEQ ID NO: 1434, SEQ ID NO: 1447 and SEQ ID NO: 2176;

(b) as depicted in SEQ ID NO: 398, SEQ ID NO: 422, SEQ ID NO: 426, SEQ ID NO: 400, SEQ ID NO: 428, SEQ ID NO: 424, SEQ ID NO: 591, SEQ ID NO: 592,

SEQ ID NO: 593, SEQ ID NO: 594, SEQ ID NO: 595, SEQ ID NO: 603, SEQ ID NO: 604, SEQ ID NO: 605, SEQ ID NO: 606, SEQ ID NO: 607, SEQ ID NO: 614, SEQ ID NO: 615, SEQ ID NO: 616, SEQ ID NO: 617, SEQ ID NO: 618, SEQ ID NO: 619, SEQ ID NO: 620, SEQ ID NO: 621, SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624, SEQ ID NO: 625, SEQ ID NO: 626, SEQ ID NO: 627, SEQ ID NO: 628, SEQ ID NO: 629, SEQ ID NO: 630, SEQ ID NO: 631, SEQ ID NO: 632, SEQ ID NO: 633, SEQ ID NO: 1018, SEQ ID NO: 1031, SEQ ID NO: 1044, SEQ ID NO: 1083, SEQ ID NO: 1109, SEQ ID NO: 1122, SEQ ID NO: 1252, SEQ ID NO: 1265, SEQ ID NO: 1278, SEQ ID NO: 1291, SEQ ID NO: 1304, SEQ ID NO: 1656, SEQ ID NO: 1669, SEQ ID NO: 1903, SEQ ID NO: 1916, SEQ ID NO: 1942, SEQ ID NO: 1955, SEQ ID NO: 1968, SEQ ID NO: 1981, SEQ ID NO: 1994, SEQ ID NO: 2007, SEQ ID NO: 2020, SEQ ID NO: 2033, SEQ ID NO: 2046, and SEQ ID NO: 2059;

(c) as depicted in SEQ ID NO: 394, SEQ ID NO: 410, SEQ ID NO: 434, SEQ ID NO: 412, SEQ ID NO: 571, SEQ ID NO: 572, SEQ ID NO: 573, SEQ ID NO: 574, SEQ ID NO: 575, SEQ ID NO: 576, SEQ ID NO: 577, SEQ ID NO: 578, SEQ ID NO: 579, SEQ ID NO: 596, SEQ ID NO: 597, SEQ ID NO: 598, SEQ ID NO: 599, SEQ ID NO: 600, SEQ ID NO: 601, SEQ ID NO: 612, SEQ ID NO: 613, SEQ ID NO: 1005, SEQ ID NO: 1057, SEQ ID NO: 1096, SEQ ID NO: 1617, SEQ ID NO: 1630, SEQ ID NO: 1643, SEQ ID NO: 1682, SEQ ID NO: 1695, SEQ ID NO: 1708, SEQ ID NO: 1721, SEQ ID NO: 1734, SEQ ID NO: 1747, SEQ ID NO: 1760, SEQ ID NO: 1773, and SEQ ID NO: 1929;

(d) as depicted in SEQ ID NO: 408, SEQ ID NO: 416, SEQ ID NO: 444, SEQ ID NO: 442, SEQ ID NO: 396, SEQ ID NO: 402, SEQ ID NO: 430, SEQ ID NO: 404, SEQ ID NO: 446, SEQ ID NO: 558, SEQ ID NO: 559, SEQ ID NO: 560, SEQ ID NO: 561, SEQ ID NO: 562, SEQ ID NO: 563, SEQ ID NO: 564, SEQ ID NO: 565, SEQ ID NO: 566, SEQ ID NO: 567, SEQ ID NO: 568, SEQ ID NO: 569, SEQ ID NO: 570, SEQ ID NO: 583, SEQ ID NO: 584, SEQ ID NO: 585, SEQ ID NO: 586, SEQ ID NO: 608, SEQ ID NO: 609, SEQ ID NO: 610, SEQ ID NO: 611, SEQ ID NO: 635, SEQ ID NO: 636, SEQ ID NO: 637, SEQ ID NO: 638, SEQ ID NO: 979, SEQ ID NO: 1070, SEQ ID NO: 1148, SEQ ID NO: 1161, SEQ ID NO: 1187, SEQ ID NO: 1200, SEQ ID NO: 1213, SEQ ID NO: 1226, SEQ ID NO: 1239, SEQ ID NO: 1317, SEQ ID NO: 1330, SEQ ID NO: 1382, SEQ ID NO: 1395, SEQ ID NO: 1408, SEQ ID NO: 1421, SEQ ID NO: 1471, SEQ ID NO: 1480, SEQ ID NO: 1487, SEQ ID NO: 1496, SEQ ID NO: 1503, SEQ ID NO: 1510, SEQ ID NO: 1521, SEQ ID NO: 1528, SEQ ID NO: 1535, SEQ ID NO: 1544, SEQ ID NO: 1551, SEQ ID NO: 1560, SEQ ID NO: 1567, SEQ ID NO: 1786,

SEQ ID NO: 1799, SEQ ID NO: 1812, SEQ ID NO: 1825, SEQ ID NO: 1838, SEQ ID NO: 1851, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ ID NO: 1890, SEQ ID NO: 2072, SEQ ID NO: 2085, SEQ ID NO: 2098, SEQ ID NO: 2111, SEQ ID NO: 2124, SEQ ID NO: 2137, SEQ ID NO: 2150, SEQ ID NO: 2163, SEQ ID NO: 2189, SEQ ID NO: 2202, and SEQ ID NO: 2215; and

(e) as depicted in SEQ ID NO: 432, SEQ ID NO: 448, SEQ ID NO: 414, SEQ ID NO: 406, SEQ ID NO: 602, SEQ ID NO: 992, SEQ ID NO: 1591, and SEQ ID NO: 1604.

5. The antibody construct according to any one of the preceding claims, wherein the first binding domain comprises a VH region and a VL region selected from the group consisting of:

(1) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 362+418, SEQ ID NOs: 364+420, SEQ ID NOs: 485+580, SEQ ID NOs: 486+581, SEQ ID NOs: 487+582, SEQ ID NOs: 492+587, SEQ ID NOs: 493+588, SEQ ID NOs: 494+589, SEQ ID NOs: 495+590, SEQ ID NOs: 1133+1135, SEQ ID NOs: 1172+1174, SEQ ID NOs: 1341+1343, SEQ ID NOs: 1354+1356, SEQ ID NOs: 1367+1369, SEQ ID NOs: 1432+1434, SEQ ID NOs: 1445+1447, and SEQ ID NOs: 2174+2176;

(2) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 342+398, SEQ ID NOs: 366+422, SEQ ID NOs: 370+426, SEQ ID NOs: 344+400, SEQ ID NOs: 372+428, SEQ ID NOs: 368+424, SEQ ID NOs: 496+591, SEQ ID NOs: 497+592, SEQ ID NOs: 498+593, SEQ ID NOs: 499+594, SEQ ID NOs: 500+595, SEQ ID NOs: 508+603, SEQ ID NOs: 509+604, SEQ ID NOs: 510+605, SEQ ID NOs: 511+606, SEQ ID NOs: 512+607, SEQ ID NOs: 519+614, SEQ ID NOs: 520+615, SEQ ID NOs: 521+616, SEQ ID NOs: 522+617, SEQ ID NOs: 523+618, SEQ ID NOs: 524+619, SEQ ID NOs: 525+620, SEQ ID NOs: 526+621, SEQ ID NOs: 527+622, SEQ ID NOs: 528+623, SEQ ID NOs: 529+624, SEQ ID NOs: 530+625, SEQ ID NOs: 531+626, SEQ ID NOs: 532+627, SEQ ID NOs: 533+628, SEQ ID NOs: 534+629, SEQ ID NOs: 535+630, SEQ ID NOs: 536+631, SEQ ID NOs: 537+632, SEQ ID NOs: 538+633, SEQ ID NOs: 1016+1018, SEQ ID NOs: 1029+1031, SEQ ID NOs: 1042+1044, SEQ ID NOs: 1081+1083, SEQ ID NOs: 1107+1109, SEQ ID NOs: 1120+1122, SEQ ID NOs: 1250+1252, SEQ ID NOs: 1263+1265, SEQ ID NOs: 1276+1278, SEQ ID NOs: 1289+1291, SEQ ID NOs: 1302+1304, SEQ ID NOs: 1654+1656, SEQ ID NOs: 1667+1669, SEQ ID NOs: 1901+1903, SEQ ID NOs: 1914+1916, SEQ ID NOs: 1940+1942, SEQ ID

NOs: 1953+1955, SEQ ID NOs: 1966+1968, SEQ ID NOs: 1979+1981, SEQ ID NOs: 1992+1994, SEQ ID NOs: 2005+2007, SEQ ID NOs: 2018+2020, SEQ ID NOs: 2031+2033, SEQ ID NOs: 2044+2046, and SEQ ID NOs: 2057+2059;

(3) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 338+394, SEQ ID NOs: 354+410, SEQ ID NOs: 378+434, SEQ ID NOs: 356+412, SEQ ID NOs: 476+571, SEQ ID NOs: 477+572, SEQ ID NOs: 478+573, SEQ ID NOs: 479+574, SEQ ID NOs: 480+575, SEQ ID NOs: 481+576, SEQ ID NOs: 482+577, SEQ ID NOs: 483+578, SEQ ID NOs: 484+579, SEQ ID NOs: 501+596, SEQ ID NOs: 502+597, SEQ ID NOs: 503+598, SEQ ID NOs: 504+599, SEQ ID NOs: 505+600, SEQ ID NOs: 506+601, SEQ ID NOs: 517+612, SEQ ID NOs: 518+613, SEQ ID NOs: 1003+1005, SEQ ID NOs: 1055+1057, SEQ ID NOs: 1094+1096, SEQ ID NOs: 1615+1617, SEQ ID NOs: 1628+1630, SEQ ID NOs: 1641+1643, SEQ ID NOs: 1680+1682, SEQ ID NOs: 1693+1695, SEQ ID NOs: 1706+1708, SEQ ID NOs: 1719+1721, SEQ ID NOs: 1732+1734, SEQ ID NOs: 1745+1747, SEQ ID NOs: 1758+1760, SEQ ID NOs: 1771+1773, and SEQ ID NOs: 1927+1929;

(4) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 352+408, SEQ ID NOs: 360+416, SEQ ID NOs: 388+444, SEQ ID NOs: 386+442, SEQ ID NOs: 340+396, SEQ ID NOs: 346+402, SEQ ID NOs: 374+430, SEQ ID NOs: 348+404, SEQ ID NOs: 390+446, SEQ ID NOs: 463+558, SEQ ID NOs: 464+559, SEQ ID NOs: 465+560, SEQ ID NOs: 466+561, SEQ ID NOs: 467+562, SEQ ID NOs: 468+563, SEQ ID NOs: 469+564, SEQ ID NOs: 470+565, SEQ ID NOs: 471+566, SEQ ID NOs: 472+567, SEQ ID NOs: 473+568, SEQ ID NOs: 474+569, SEQ ID NOs: 475+570, SEQ ID NOs: 488+583, SEQ ID NOs: 489+584, SEQ ID NOs: 490+585, SEQ ID NOs: 491+586, SEQ ID NOs: 513+608, SEQ ID NOs: 514+609, SEQ ID NOs: 515+610, SEQ ID NOs: 516+611, SEQ ID NOs: 540+635, SEQ ID NOs: 541+636, SEQ ID NOs: 542+637, SEQ ID NOs: 543+638, SEQ ID NOs: 977+979, SEQ ID NOs: 1068+1070, SEQ ID NOs: 1146+1148, SEQ ID NOs: 1159+1161, SEQ ID NOs: 1185+1187, SEQ ID NOs: 1198+1200, SEQ ID NOs: 1211+1213, SEQ ID NOs: 1224+1226, SEQ ID NOs: 1237+1239, SEQ ID NOs: 1315+1317, SEQ ID NOs: 1328+1330, SEQ ID NOs: 1380+1382 SEQ ID NOs: 1393+1395, SEQ ID NOs: 1406+1408, SEQ ID NOs: 1419+1421, SEQ ID NOs: 1469+1471, SEQ ID NOs: 1478+1480, SEQ ID NOs: 1485+1487, SEQ ID NOs: 1494+1496, SEQ ID NOs: 1501+1503, SEQ ID NOs: 1508+1510, SEQ ID NOs: 1519+1521, SEQ ID NOs: 1526+1528, SEQ ID NOs: 1533+1535, SEQ ID NOs: 1542+1544, SEQ ID NOs: 1549+1551, SEQ ID NOs: 1558+1560, SEQ ID

NOs: 1565+1567, SEQ ID NOs: 1784+1786, SEQ ID NOs: 1797+1799, SEQ ID NOs: 1810+1812, SEQ ID NOs: 1823+1825, SEQ ID NOs: 1836+1838, SEQ ID NOs: 1849+1851, SEQ ID NOs: 1862+1864, SEQ ID NOs: 1875+1877, SEQ ID NOs: 1888+1890, SEQ ID NOs: 2070+2072, SEQ ID NOs: 2083+2085, SEQ ID NOs: 2096+2098, SEQ ID NOs: 2109+2111, SEQ ID NOs: 2122+2124, SEQ ID NOs: 2135+2137, SEQ ID NOs: 2148+2150, SEQ ID NOs: 2161+2163, SEQ ID NOs: 2187+2189, SEQ ID NOs: 2200+2202, and SEQ ID NOs: 2213+2215; and

(5) pairs of a VH region and a VL region as depicted in SEQ ID NOs: 376+432, SEQ ID NOs: 392+448, SEQ ID NOs: 358+414, SEQ ID NOs: 350+406, SEQ ID NOs: 507+602, SEQ ID NOs: 990+992, SEQ ID NOs: 1589+1591, and SEQ ID NOs: 1602+1604.

6. The antibody construct according to any one of the preceding claims, wherein the antibody construct is in a format selected from the group consisting of $(scFv)_2$, $(single domain mAb)_2$, scFv-single domain mAb, diabodies and oligomers thereof.

7. The antibody construct according to claim 6, wherein the first binding domain comprises an amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 117, SEQ ID NO: 1137, SEQ ID NO: 1176, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1371, SEQ ID NO: 1436, SEQ ID NO: 1449 and SEQ ID NO: 2178;

(b) as depicted in SEQ ID NO: 1020, SEQ ID NO: 1033, SEQ ID NO: 1046, SEQ ID NO: 1085, SEQ ID NO: 1111, SEQ ID NO: 1124, SEQ ID NO: 1254, SEQ ID NO: 1267, SEQ ID NO: 1280, SEQ ID NO: 1293, SEQ ID NO: 1306, SEQ ID NO: 1658, SEQ ID NO: 1671, SEQ ID NO: 1905, SEQ ID NO: 1918, SEQ ID NO: 1944, SEQ ID NO: 1957, SEQ ID NO: 1970, SEQ ID NO: 1983, SEQ ID NO: 1996, SEQ ID NO: 2009, SEQ ID NO: 2022, SEQ ID NO: 2035, SEQ ID NO: 2048, and SEQ ID NO: 2061;

(c) as depicted in SEQ ID NO: 1007, SEQ ID NO: 1059, SEQ ID NO: 1098, SEQ ID NO: 1619, SEQ ID NO: 1632, SEQ ID NO: 1645, SEQ ID NO: 1684, SEQ ID NO: 1697, SEQ ID NO: 1710, SEQ ID NO: 1723, SEQ ID NO: 1736, SEQ ID NO: 1749, SEQ ID NO: 1762, SEQ ID NO: 1775, and SEQ ID NO: 1931;

(d) as depicted in SEQ ID NO: 981, SEQ ID NO: 1072, SEQ ID NO: 1150, SEQ ID NO: 1163, SEQ ID NO: 1189, SEQ ID NO: 1202, SEQ ID NO: 1215, SEQ ID NO: 1228, SEQ ID NO: 1241, SEQ ID NO: 1319, SEQ ID NO: 1332, SEQ ID NO: 1384, SEQ ID NO: 1397, SEQ ID NO: 1410, SEQ ID NO: 1423, SEQ ID NO: 1473, SEQ ID NO: 1482, SEQ ID NO: 1489, SEQ ID NO: 1498, SEQ ID

NO: 1505, SEQ ID NO: 1512, SEQ ID NO: 1523, SEQ ID NO: 1530, SEQ ID NO: 1537, SEQ ID NO: 1546, SEQ ID NO: 1553, SEQ ID NO: 1562, SEQ ID NO: 1569, SEQ ID NO: 1788, SEQ ID NO: 1801, SEQ ID NO: 1814, SEQ ID NO: 1827, SEQ ID NO: 1840, SEQ ID NO: 1853, SEQ ID NO: 1866, SEQ ID NO: 1879, SEQ ID NO: 1892, SEQ ID NO: 2074, SEQ ID NO: 2087, SEQ ID NO: 2100, SEQ ID NO: 2113, SEQ ID NO: 2126, SEQ ID NO: 2139, SEQ ID NO: 2152, SEQ ID NO: 2165, SEQ ID NO: 2191, SEQ ID NO: 2204, and SEQ ID NO: 2217; and

(e) as depicted in SEQ ID NO: 994, SEQ ID NO: 1593, and SEQ ID NO: 1606.

8. The antibody construct according to any one of the preceding claims, wherein the second binding domain is capable of binding to human and Callithrix jacchus, Saguinus Oedipus or Saimiri sciureus CD3 epsilon.

9. The antibody construct according claim 8, having the amino acid sequence selected from the group consisting of

(a) as depicted in SEQ ID NO: 1138, SEQ ID NO: 1177, SEQ ID NO: 1346, SEQ ID NO: 1359, SEQ ID NO: 1372, SEQ ID NO: 1437, SEQ ID NO: 1450 and SEQ ID NO: 2179;

(b) as depicted in SEQ ID NO: 1021, SEQ ID NO: 1034, SEQ ID NO: 1047, SEQ ID NO: 1086, SEQ ID NO: 1112, SEQ ID NO: 1125, SEQ ID NO: 1255, SEQ ID NO: 1268, SEQ ID NO: 1281, SEQ ID NO: 1294, SEQ ID NO: 1307, SEQ ID NO: 1659, SEQ ID NO: 1672, SEQ ID NO: 1906, SEQ ID NO: 1919, SEQ ID NO: 1945, SEQ ID NO: 1958, SEQ ID NO: 1971, SEQ ID NO: 1984, SEQ ID NO: 1997, SEQ ID NO: 2010, SEQ ID NO: 2023, SEQ ID NO: 2036, SEQ ID NO: 2049, and SEQ ID NO: 2062;

(c) as depicted in SEQ ID NO: 1008, SEQ ID NO: 1060, SEQ ID NO: 1099, SEQ ID NO: 1620, SEQ ID NO: 1633, SEQ ID NO: 1646, SEQ ID NO: 1685, SEQ ID NO: 1698, SEQ ID NO: 1711, SEQ ID NO: 1724, SEQ ID NO: 1737, SEQ ID NO: 1750, SEQ ID NO: 1763, SEQ ID NO: 1776, and SEQ ID NO: 1932;

(d) as depicted in SEQ ID NO: 982, SEQ ID NO: 1073, SEQ ID NO: 1151, SEQ ID NO: 1164, SEQ ID NO: 1190, SEQ ID NO: 1203, SEQ ID NO: 1216, SEQ ID NO: 1229, SEQ ID NO: 1242, SEQ ID NO: 1320, SEQ ID NO: 1333, SEQ ID NO: 1385, SEQ ID NO: 1398, SEQ ID NO: 1411, SEQ ID NO: 1424, SEQ ID NO: 1474, SEQ ID NO: 1475, SEQ ID NO: 1476, SEQ ID NO: 1483, SEQ ID NO: 1490, SEQ ID NO: 1491, SEQ ID NO: 1492, SEQ ID NO: 1499, SEQ ID NO: 1506, SEQ ID NO: 1513, SEQ ID NO: 1514, SEQ ID NO: 1515, SEQ ID

NO: 1516, SEQ ID NO: 1517, SEQ ID NO: 1524, SEQ ID NO: 1531, SEQ ID NO: 1538, SEQ ID NO: 1539, SEQ ID NO: 1540, SEQ ID NO: 1547, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1556, SEQ ID NO: 1563, SEQ ID NO: 1570, SEQ ID NO: 1571, SEQ ID NO: 1572, SEQ ID NO: 1573, SEQ ID NO: 1574, SEQ ID NO: 1575, SEQ ID NO: 1576, SEQ ID NO: 1577, SEQ ID NO: 1578, SEQ ID NO: 1579, SEQ ID NO: 1580, SEQ ID NO: 1581, SEQ ID NO: 1789, SEQ ID NO: 1802, SEQ ID NO: 1815, SEQ ID NO: 1828, SEQ ID NO: 1841, SEQ ID NO: 1854, SEQ ID NO: 1867, SEQ ID NO: 1880, SEQ ID NO: 1893, SEQ ID NO: 2075, SEQ ID NO: 2088, SEQ ID NO: 2101, SEQ ID NO: 2114, SEQ ID NO: 2127, SEQ ID NO: 2140, SEQ ID NO: 2153, SEQ ID NO: 2166, SEQ ID NO: 2192, SEQ ID NO: 2205, and SEQ ID NO: 2218 to 2228; and

(e) as depicted in SEQ ID NO: 995, SEQ ID NO: 1594, and SEQ ID NO: 1607.

10. A nucleic acid sequence encoding an antibody construct as defined in any one of claims 1 to 9.

11. A vector comprising a nucleic acid sequence as defined in claim 10.

12. A host cell transformed or transfected with the nucleic acid sequence as defined in claim 10 or with the vector as defined in claim 11.

13. A process for the production of a antibody construct according to any one of claims 1 to 9, said process comprising culturing a host cell as defined in claim 12 under conditions allowing the expression of the antibody construct as defined in any one of claims 1 to 9 and recovering the produced antibody construct from the culture.

14. A pharmaceutical composition comprising an antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13.

15. The antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13 for use in the prevention, treatment or amelioration of a melanoma disease or metastatic melanoma disease.

16. A method for the treatment or amelioration of a melanoma disease or metastatic melanoma disease, comprising the step of administering to a subject in need thereof

the antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13.

17. The method according to claim 16, wherein the melanoma disease or metastatic melanoma disease is selected from the group consisting of superficial spreading melanoma, lentigo maligna, lentigo maligna melanoma, acral lentiginous melanoma and nodular melanoma.

18. A kit comprising an antibody construct according to any one of claims 1 to 9, or produced according to the process of claim 13, a vector as defined in claim 11, and/or a host cell as defined in claim 12.

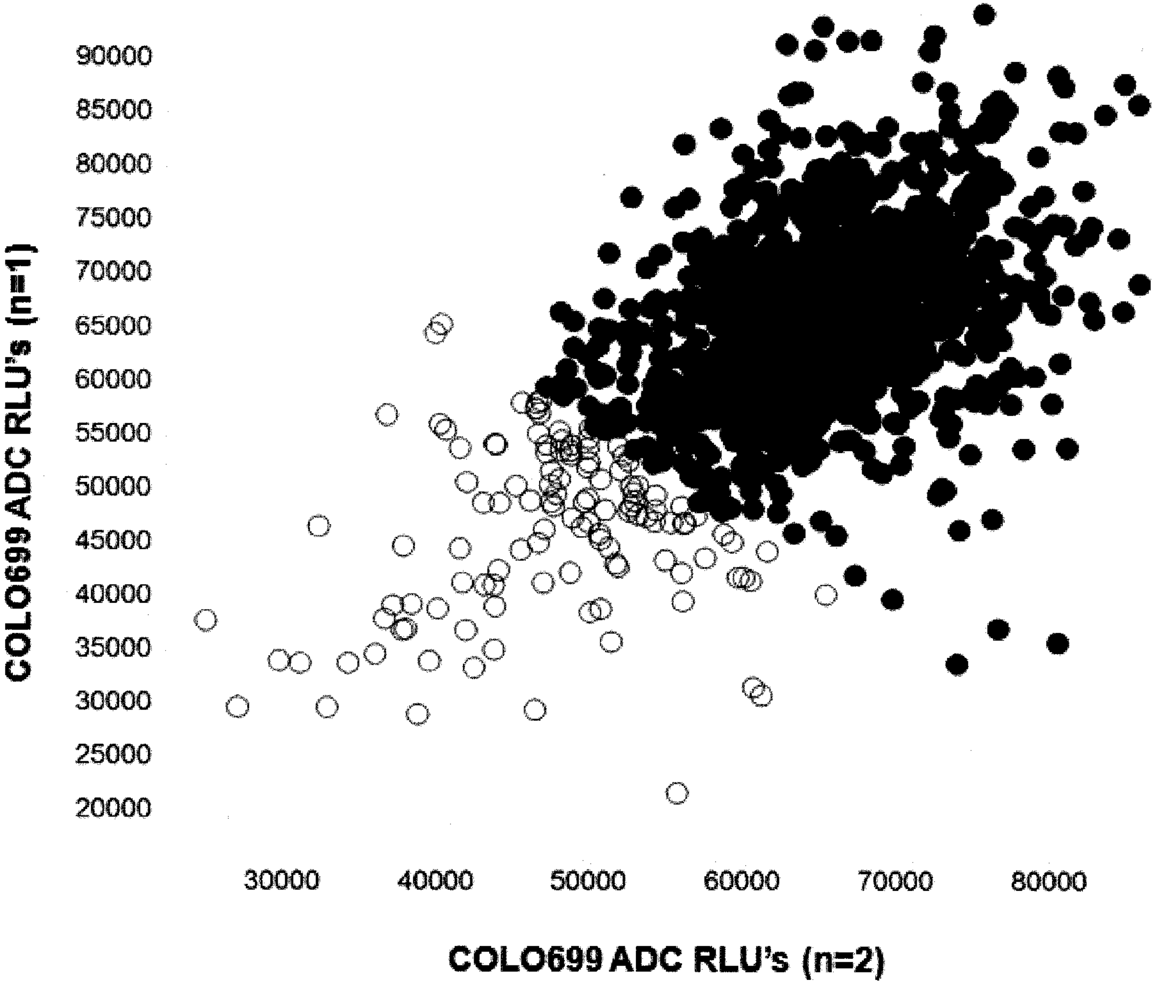

COLO699 ADC RLU's (n=1)
90000
85000
80000
75000
70000
65000
60000
55000
50000
45000
40000
35000
30000
25000
20000
30000
40000
50000
60000
70000
80000
COLO699 ADC RLU's (n=2)

Figure 1

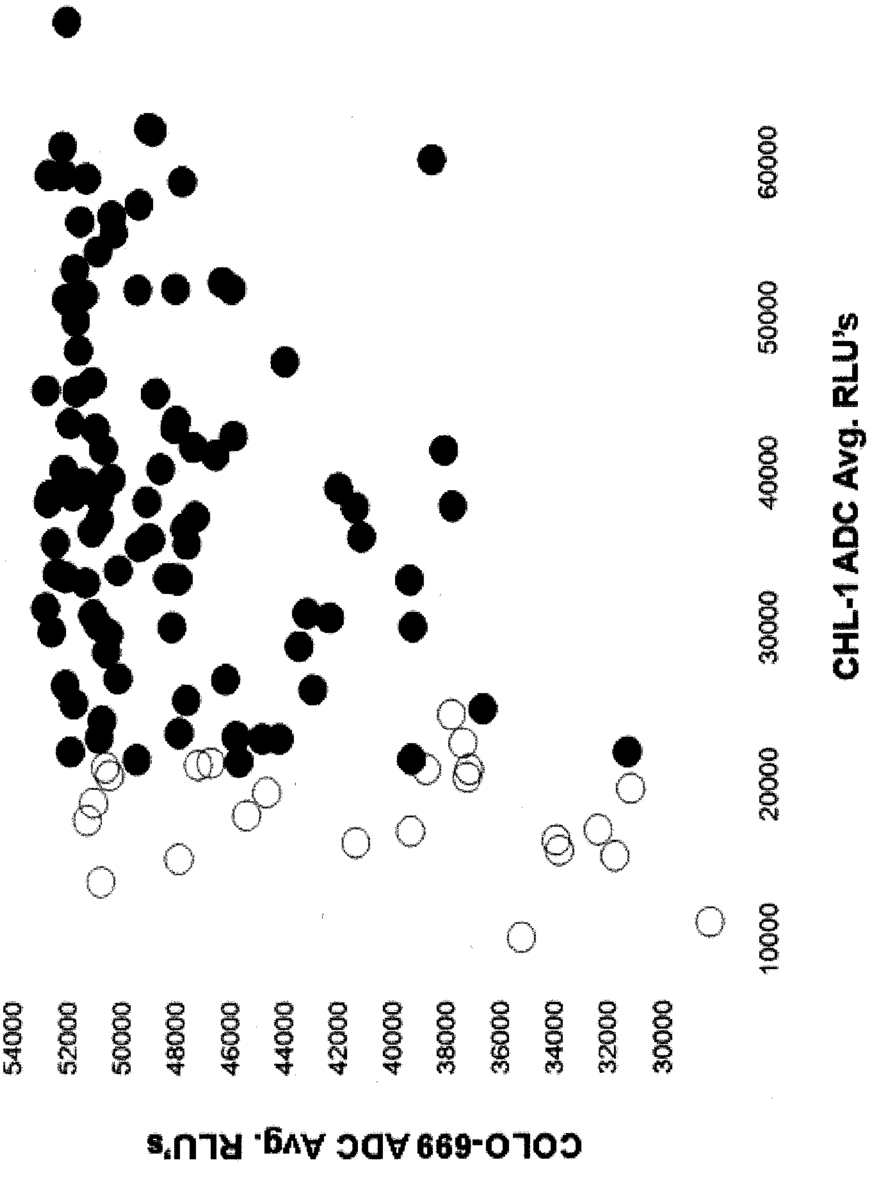
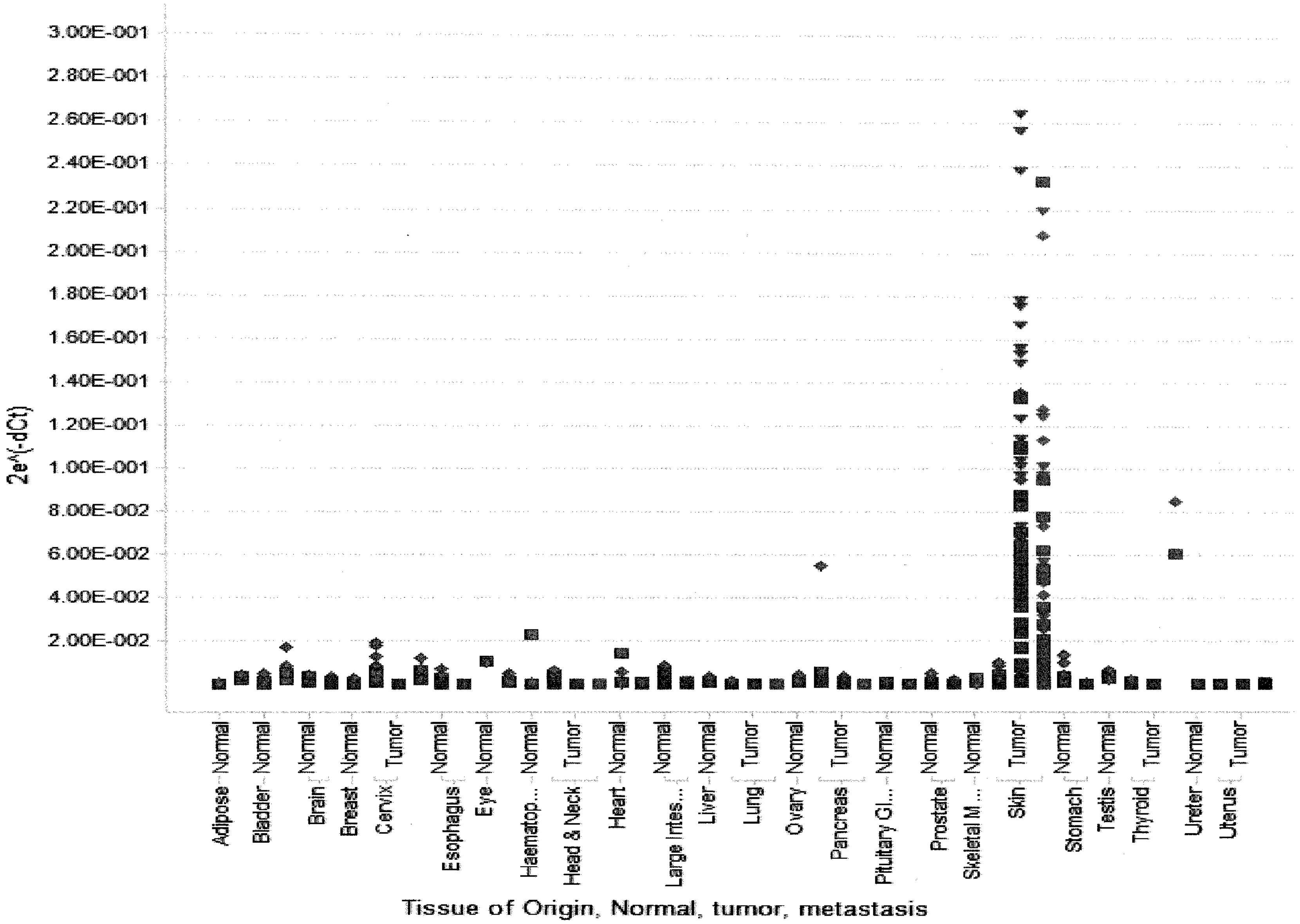
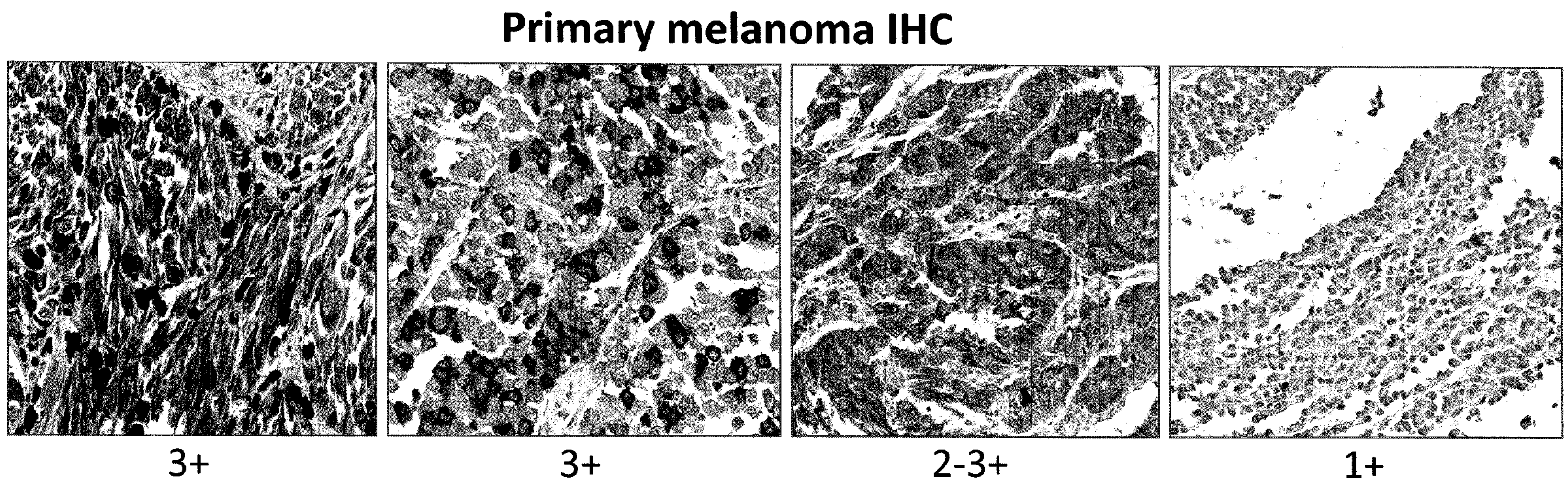

COLO-699 ADC Avg. RLU's
54000
52000
50000
48000
46000
44000
42000
40000
38000
36000
34000
32000
30000
10000
20000
30000
40000
50000
60000
CHL-1 ADC Avg. RLU's

Figure 2

Figure 3


3.00E-001
2.80E-001
2.60E-001
2.40E-001
2.20E-001
2.00E-001
1.80E-001
1.60E-001
1.40E-001
1.20E-001
1.00E-001
8.00E-002
6.00E-002
4.00E-002
2.00E-002
2e^(-dCt)
Adipose Normal
Bladder Normal
Brain Normal
Breast Normal
Cervix Tumor
Esophagus Normal
Eye Normal
Haematop... Normal
Head & Neck Tumor
Heart Normal
Large Intes... Normal
Liver Normal
Lung Tumor
Ovary Normal
Pancreas Tumor
Pituitary Gl... Normal
Prostate Normal
Skeletal M ... Normal
Skin Tumor
Stomach Normal
Testis Normal
Thyroid Tumor
Ureter Normal
Uterus Tumor
Tissue of Origin, Normal, tumor, metastasis



Primary melanoma IHC

Figure 4

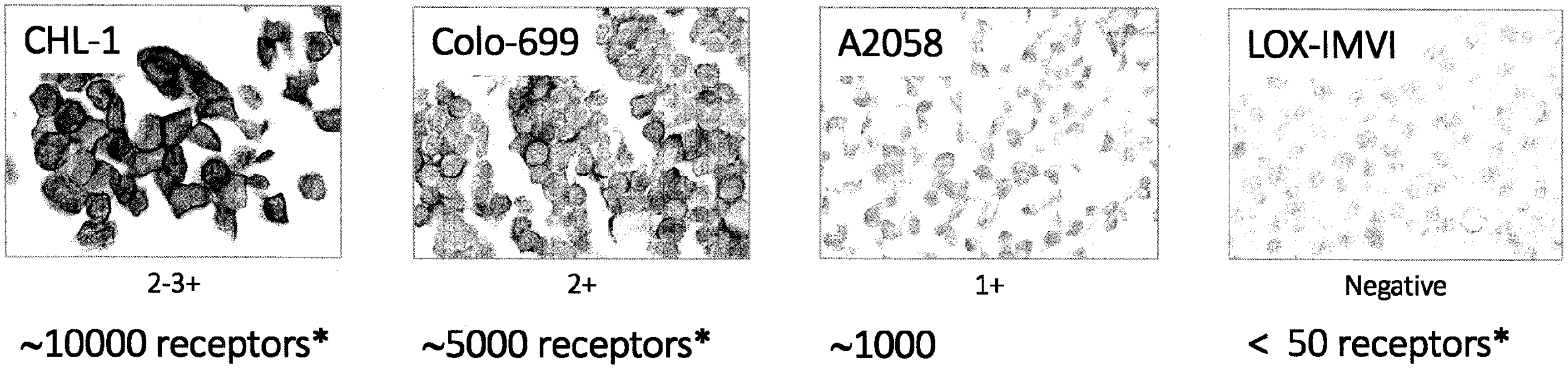

CHL-1
2-3+
~10000 receptors*
Colo-699
2+
~5000 receptors*
A2058
1+
~1000
LOX-IMVI
Negative
< 50 receptors*

Figure 5

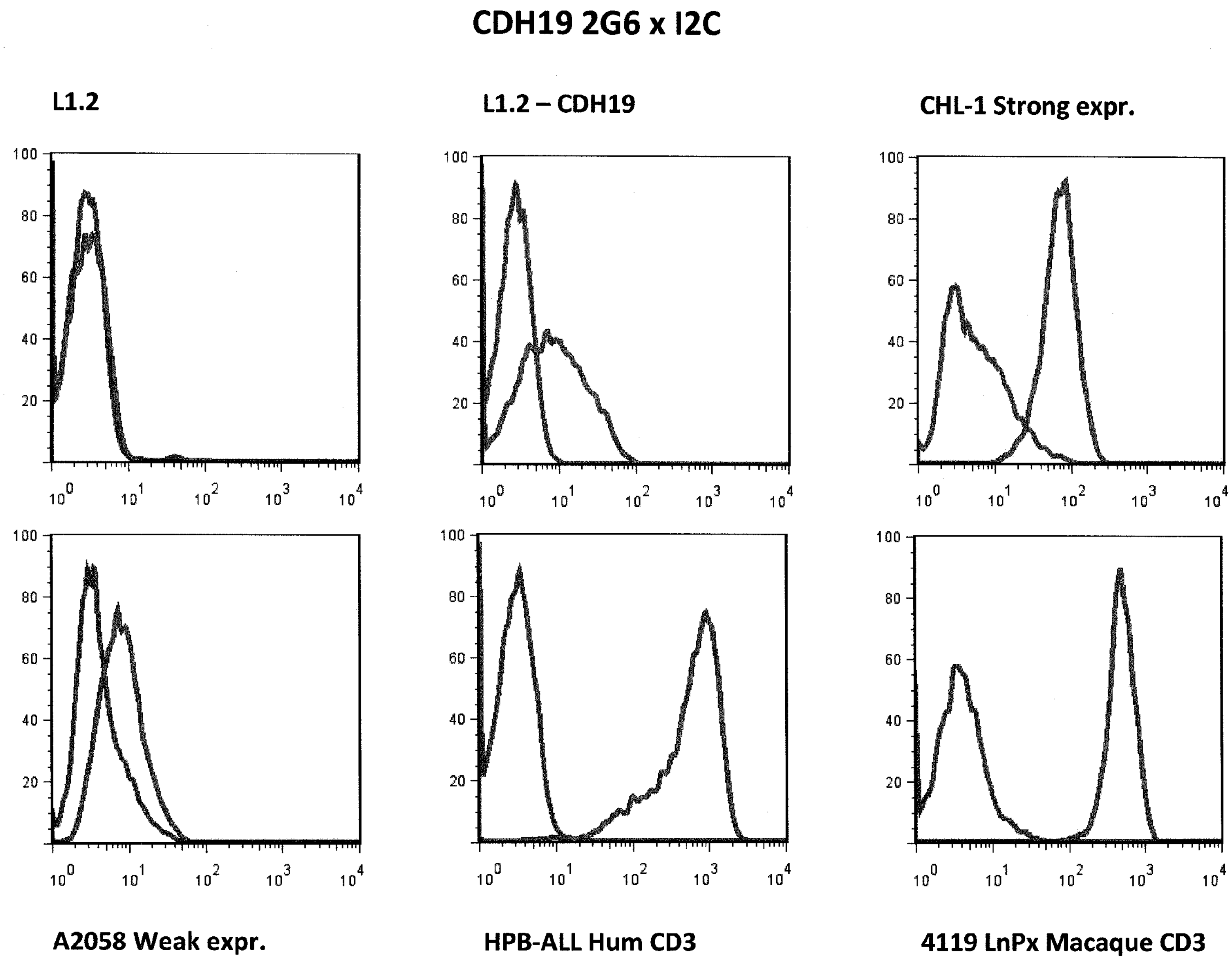

CDH19 2G6 x I2C
L1.2
L1.2 – CDH19
CHL-1 Strong expr.
A2058 Weak expr.
HPB-ALL Hum CD3
4119 LnPx Macaque CD3
100
80
60
40
20
10^0
10^1
10^2
10^3
10^4

Figure 6

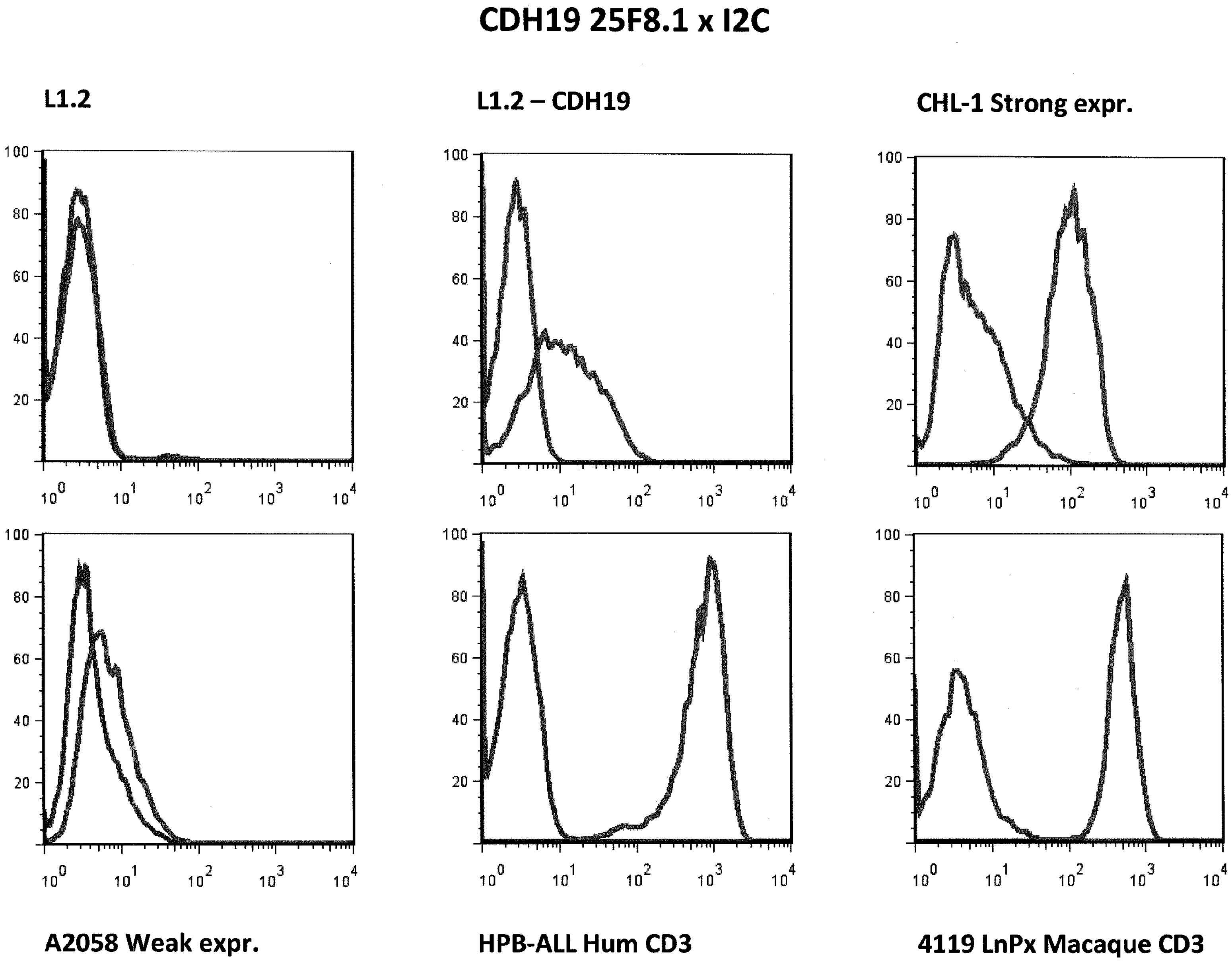


Figure 6 (continued)

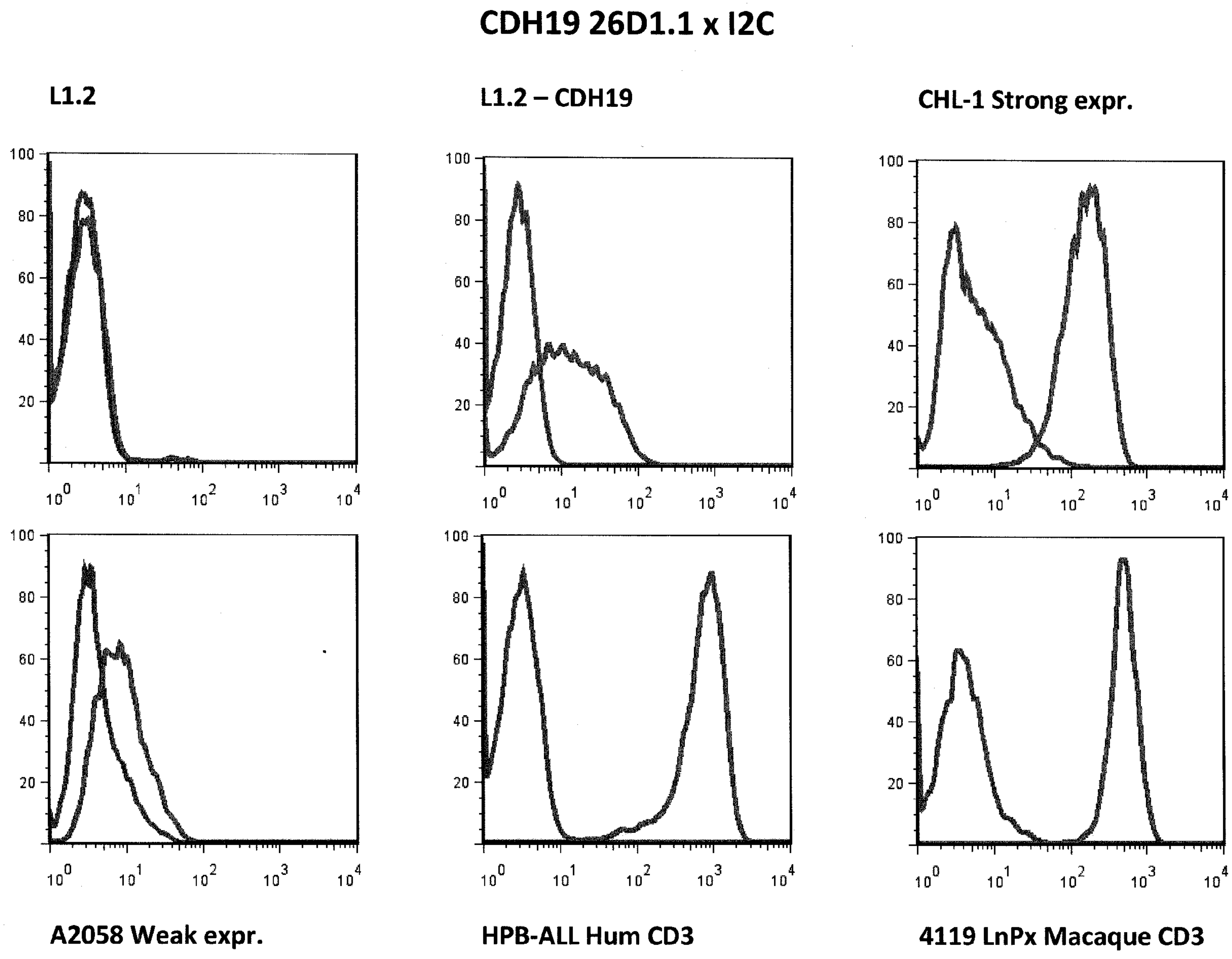
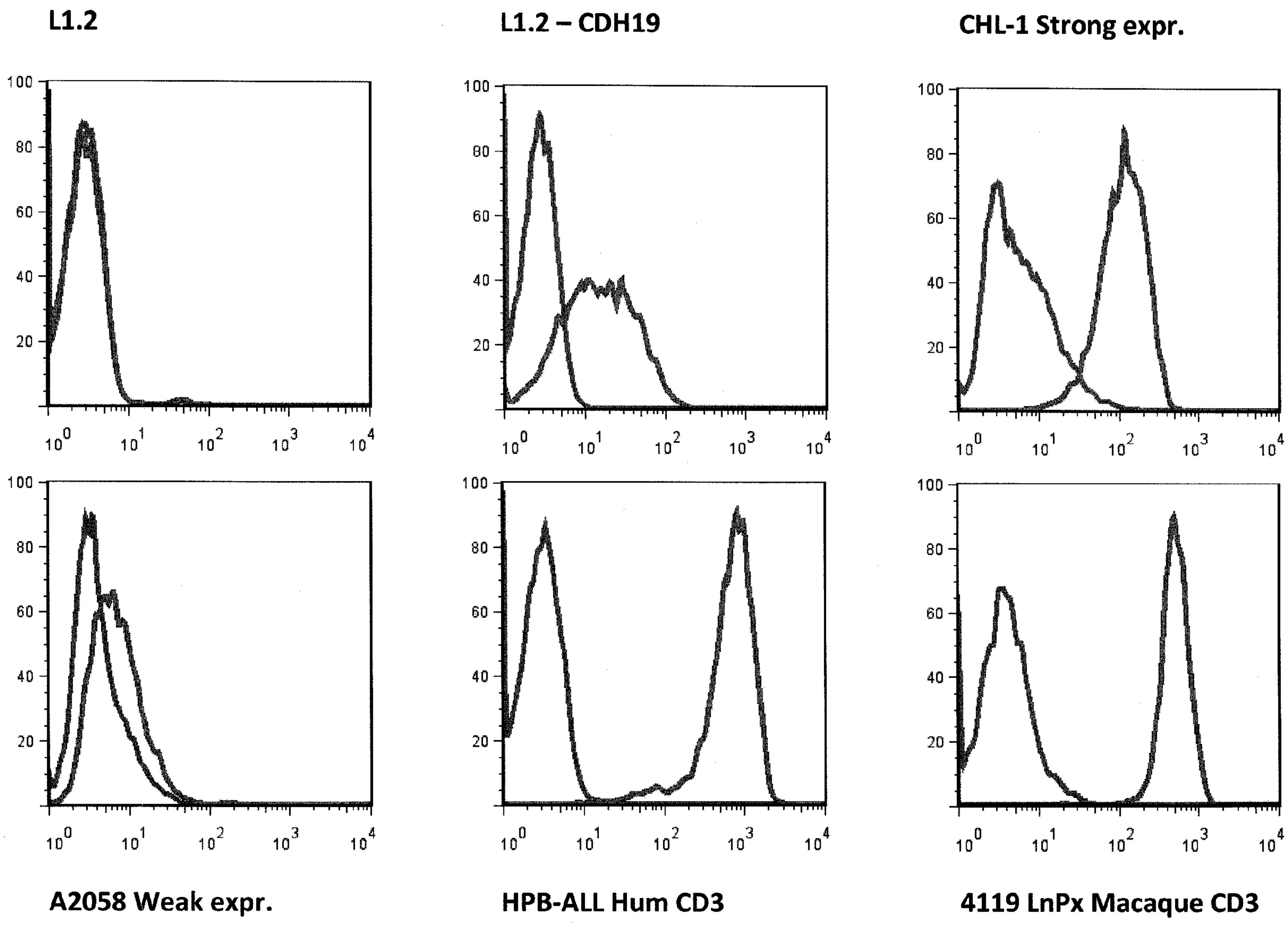


Figure 6 (continued)

CDH19 19B5.1 x I2C


L1.2

L1.2 – CDH19

CHL-1 Strong expr.

A2058 Weak expr.

HPB-ALL Hum CD3

4119 LnPx Macaque CD3

Figure 6 (continued)

CDH19 26F12.1 x I2C

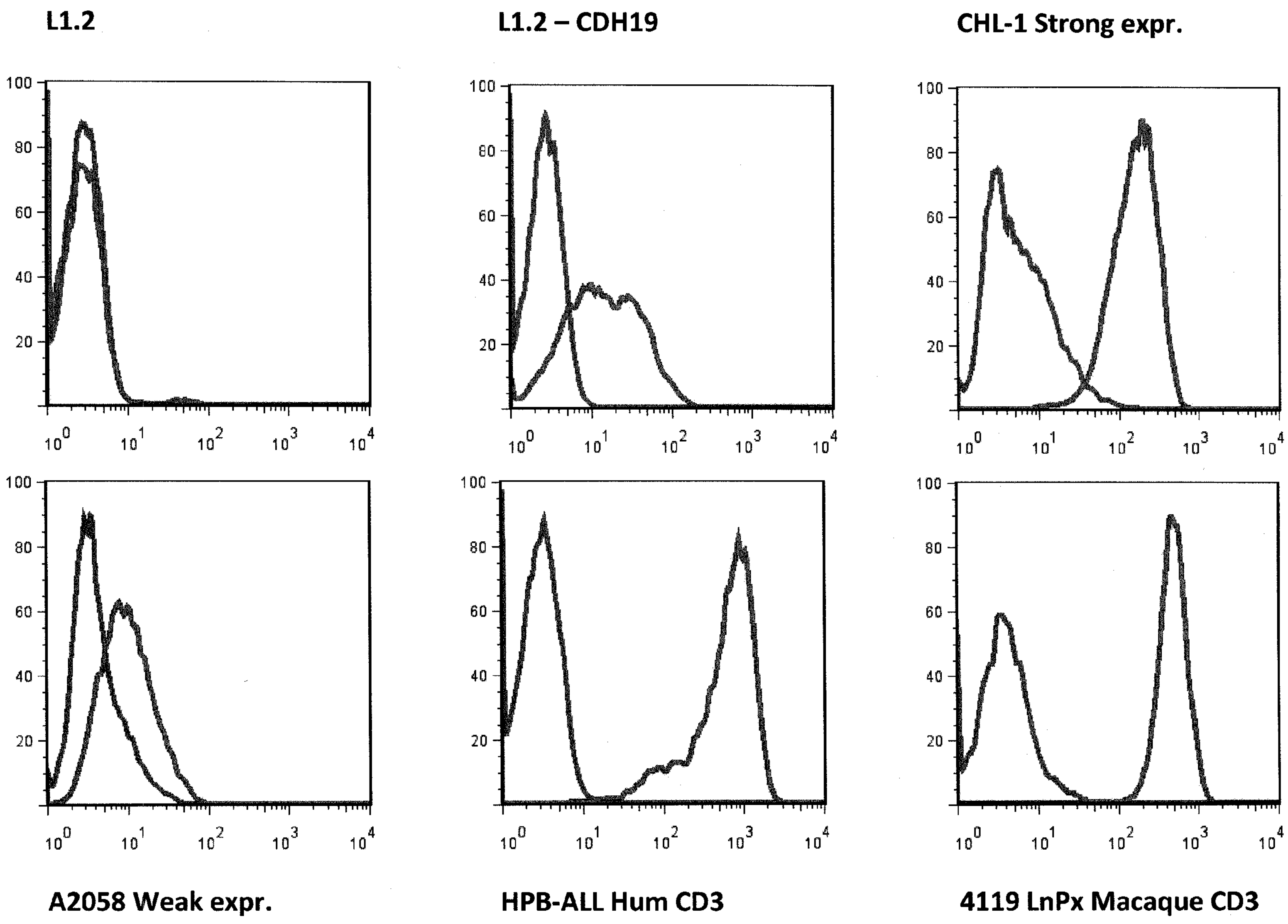


Figure 6 (continued)

CDH19 20D3.1 x I2C

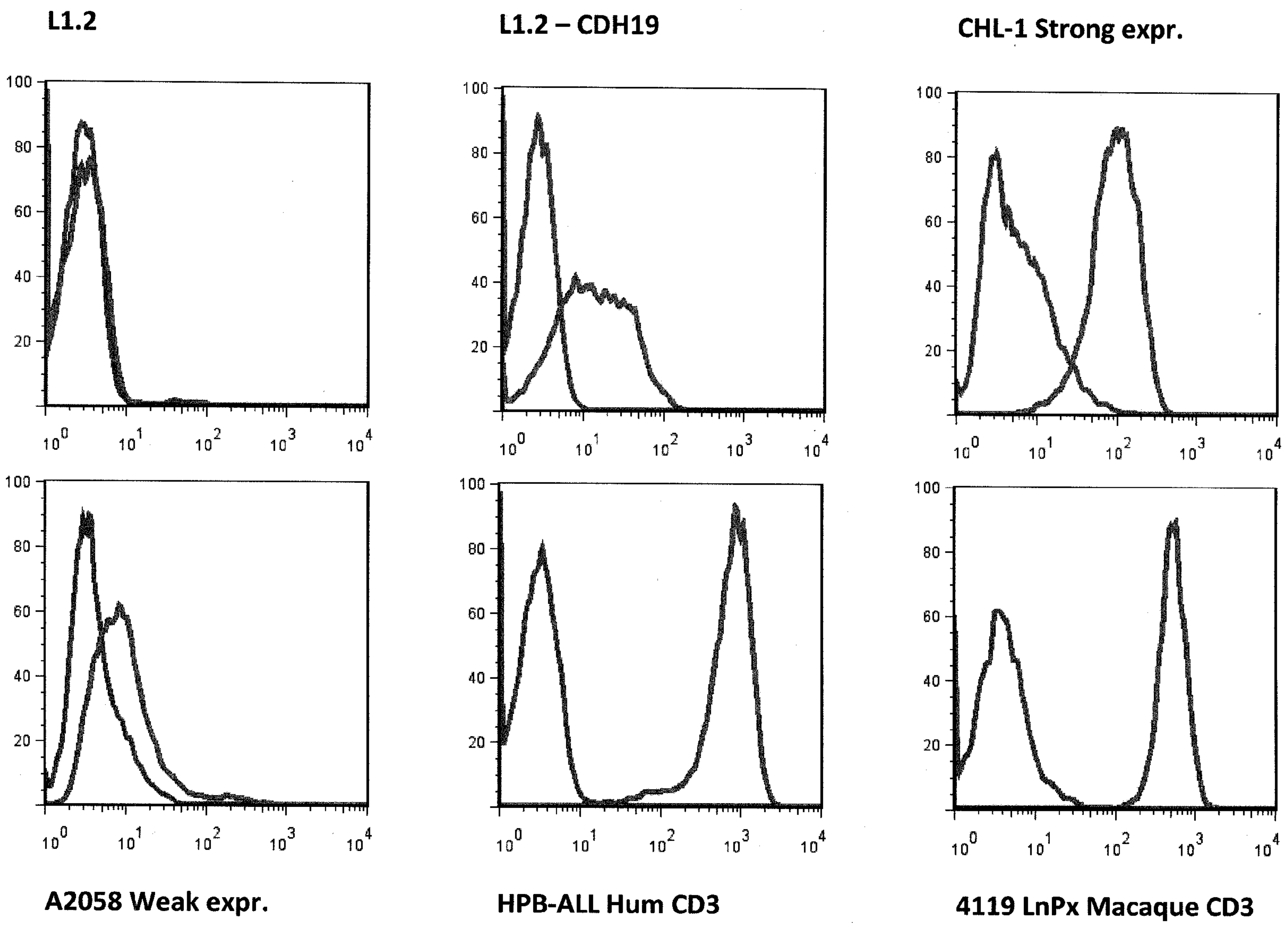
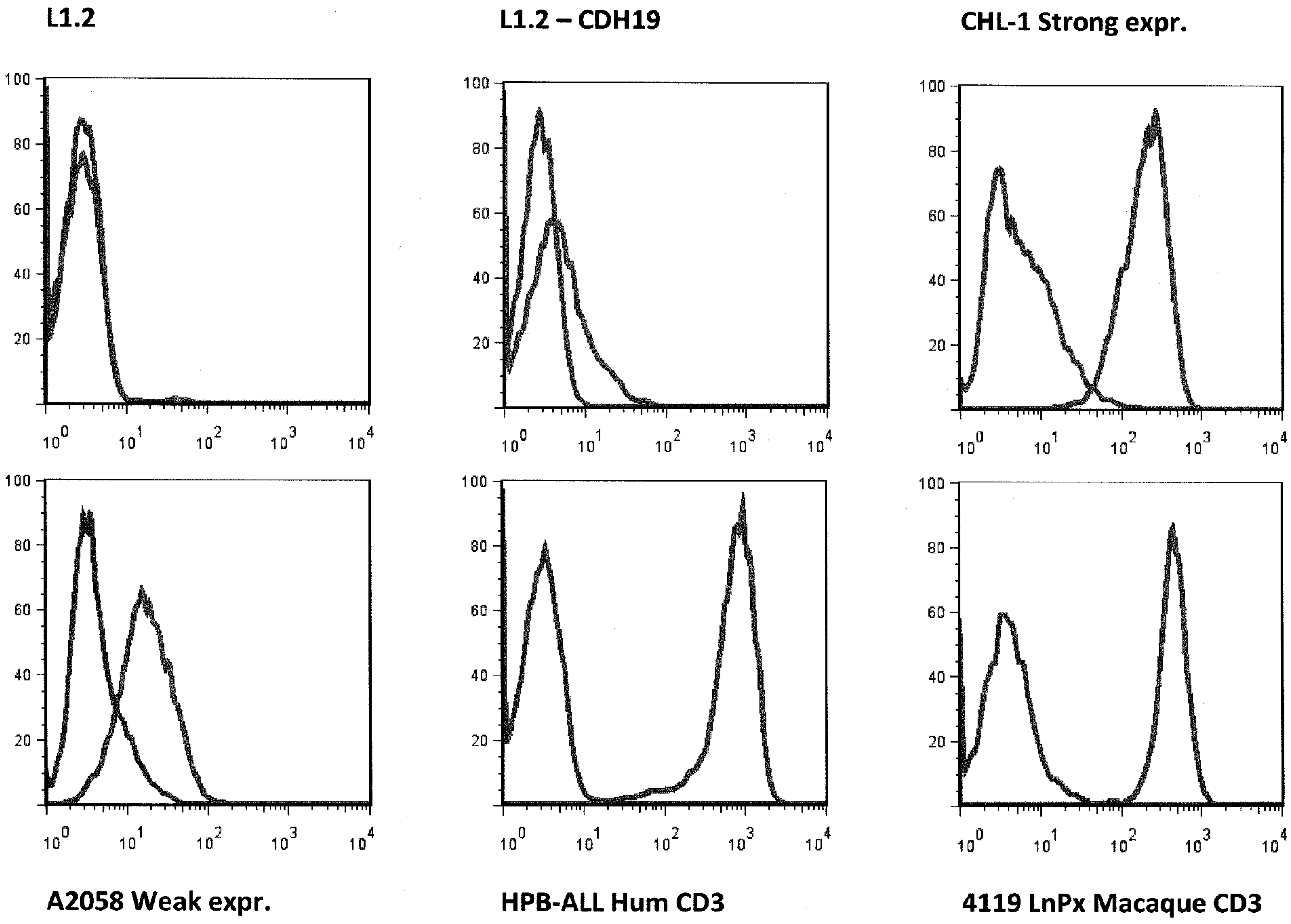


Figure 6 (continued)

CDH19 4F7 x I2C



L1.2

L1.2 – CDH19

CHL-1 Strong expr.

A2058 Weak expr.

HPB-ALL Hum CD3

4119 LnPx Macaque CD3

Figure 6 (continued)

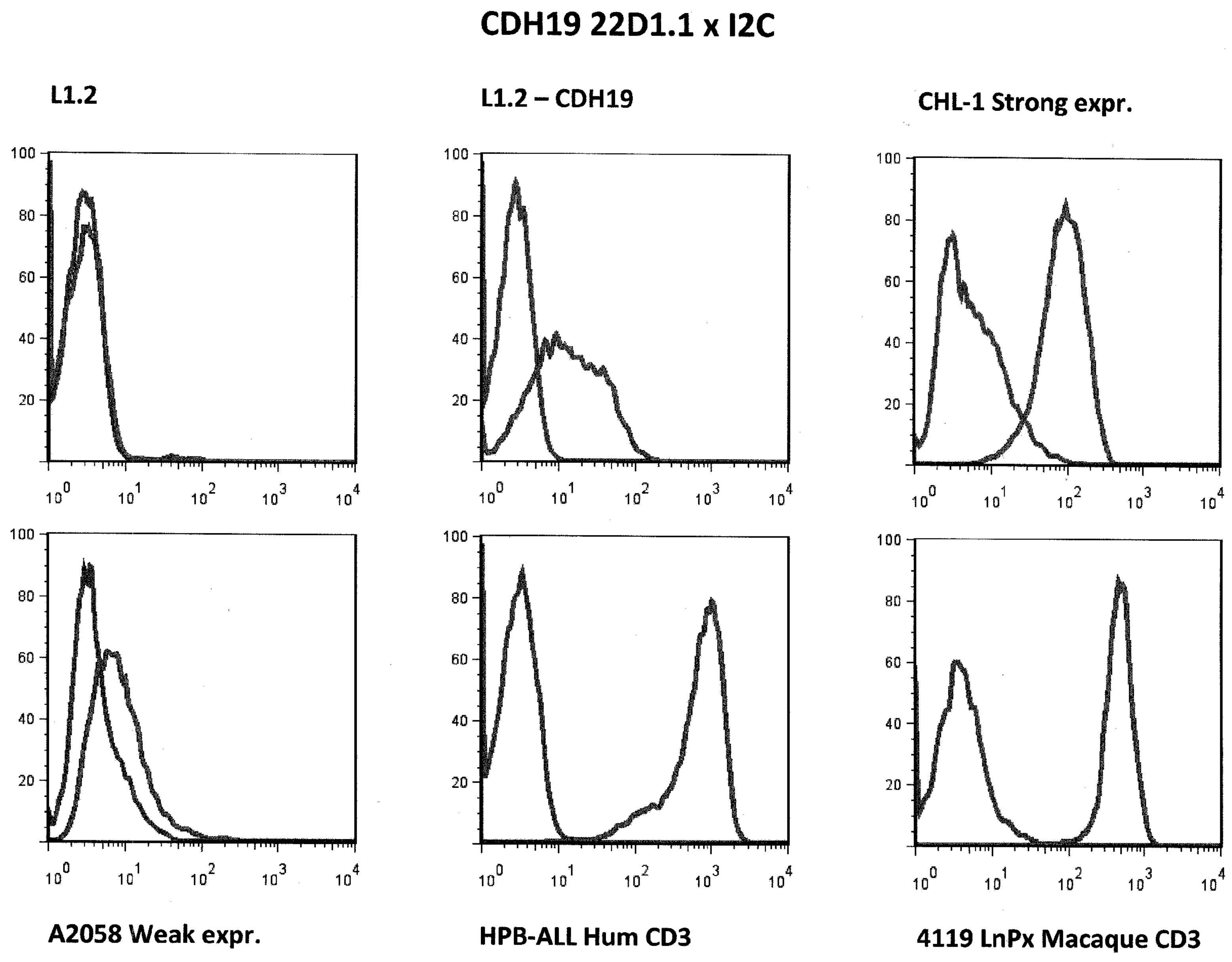


Figure 6 (continued)

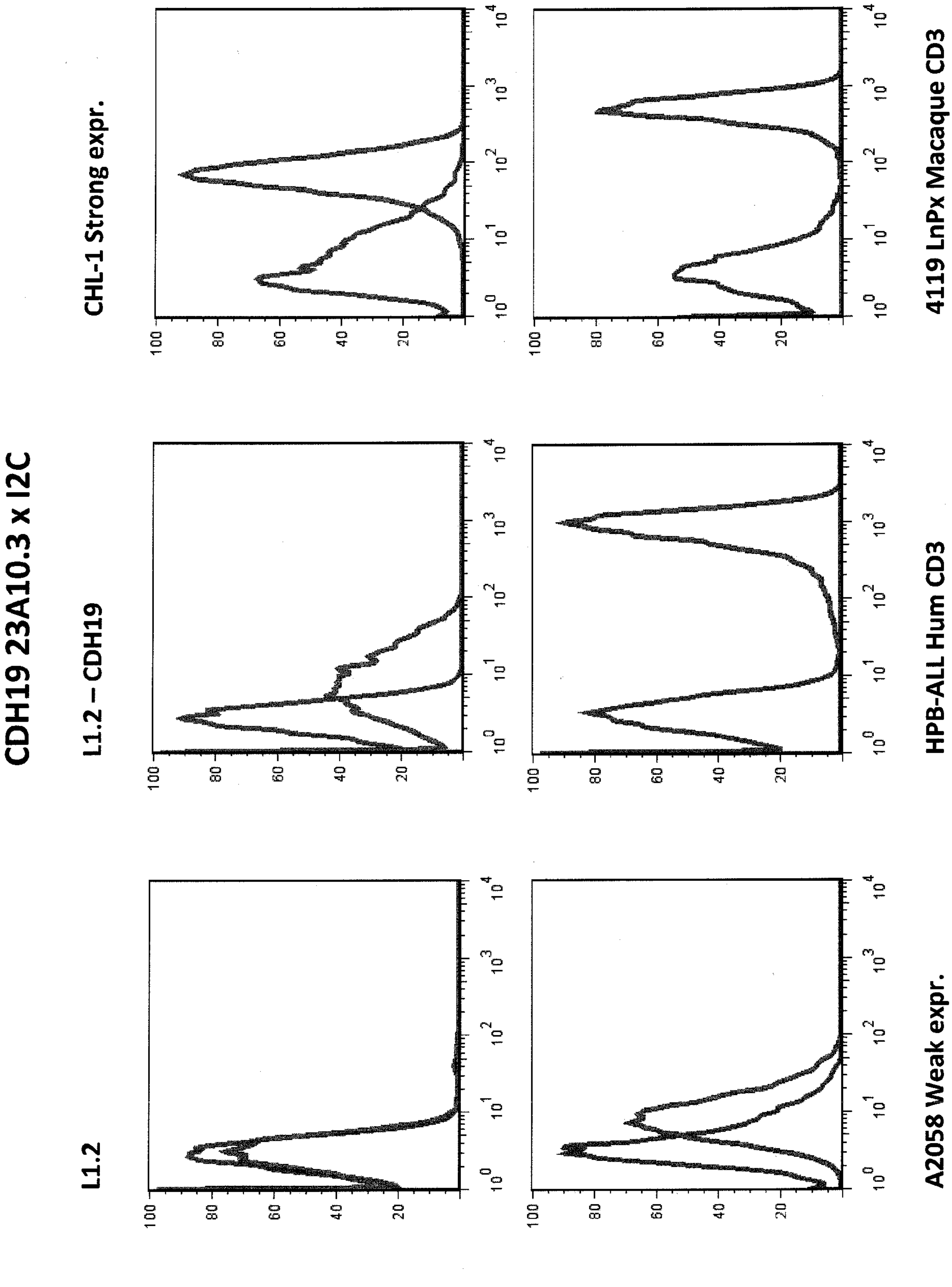


Figure 6 (continued)

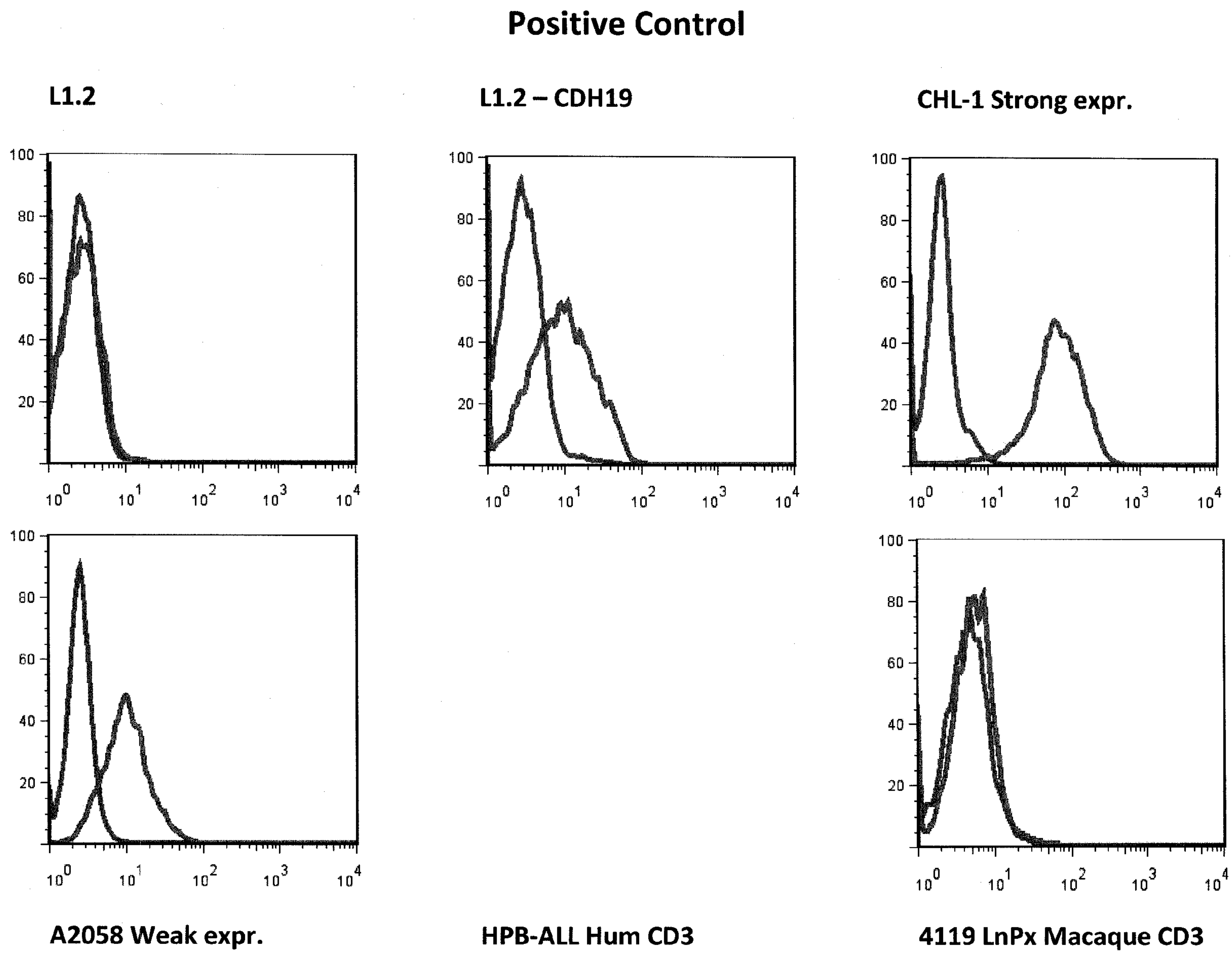
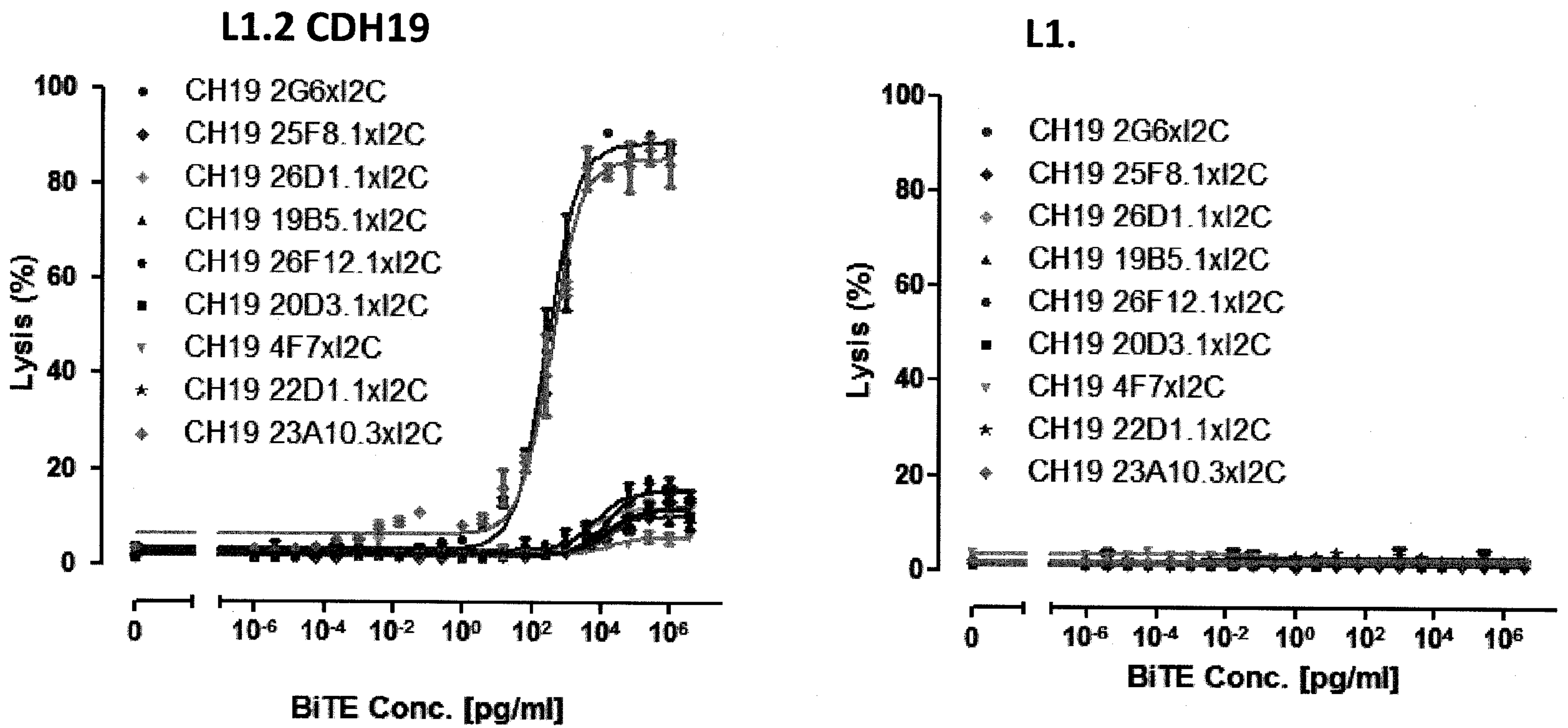
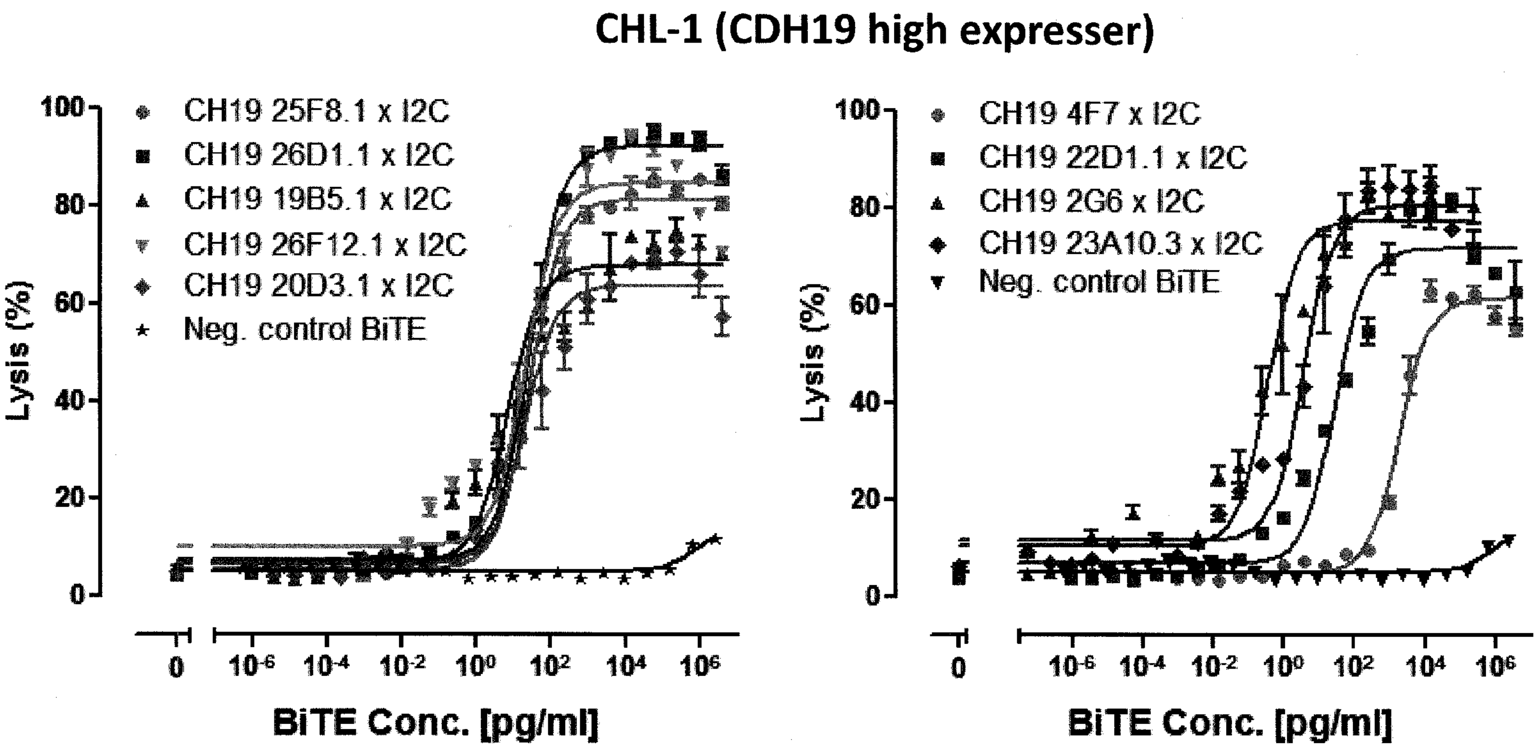


Figure 6 (continued)



EC_{50}	2G6 x I2C	25F8.1 x I2C	26D1.1 x I2C	19B5.1 x I2C	26F12.1 x I2C	20D3.1 x I2C	4F7 x I2C	22D1.1 x I2C	23A10.3 x I2C
[pg/ml]	261	6973	3487	14236	6748	23796	16168	14379	346
pMolar	4.9	131	65.6	268	127	447	304	270	6.5

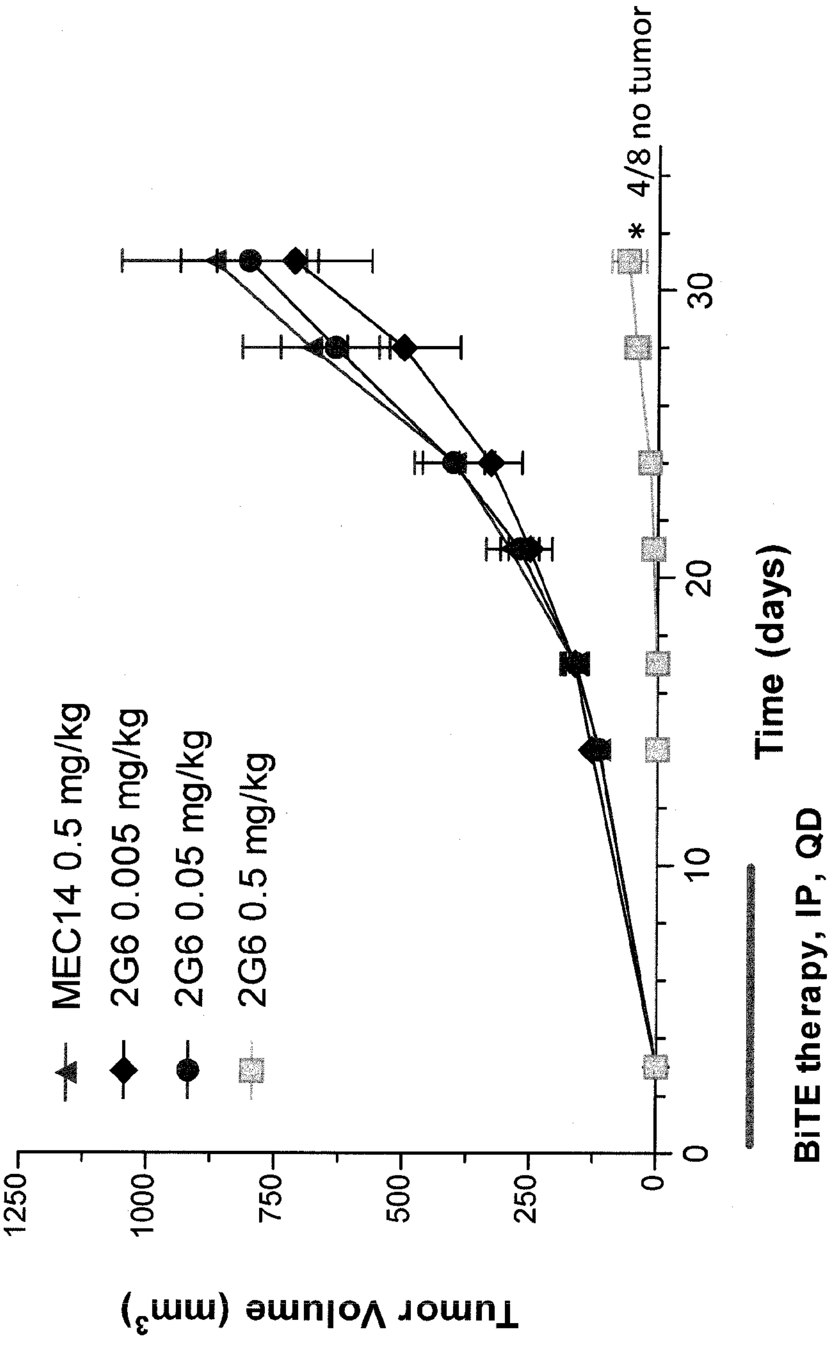
Figure 7



CHL-1 (CDH19 high expresser)

EC_{50}	2G6 x I2C	25F8.1 x I2C	26D1.1 x I2C	19B5.1 x I2C	26F12.1 x I2C	20D3.1 x I2C	4F7 x I2C	22D1.1 x I2C	23A10.3 x I2C
[pg/ml]	0.4	28	27	6.9	21	20	1842	28	3.6
fMolar	7.5	526	508	130	395	376	34630	526	67.7

Figure 7 (continued)



@ Tumors and human PBMC inoculated at a 2:1 ratio on Day 0.

Figure 8

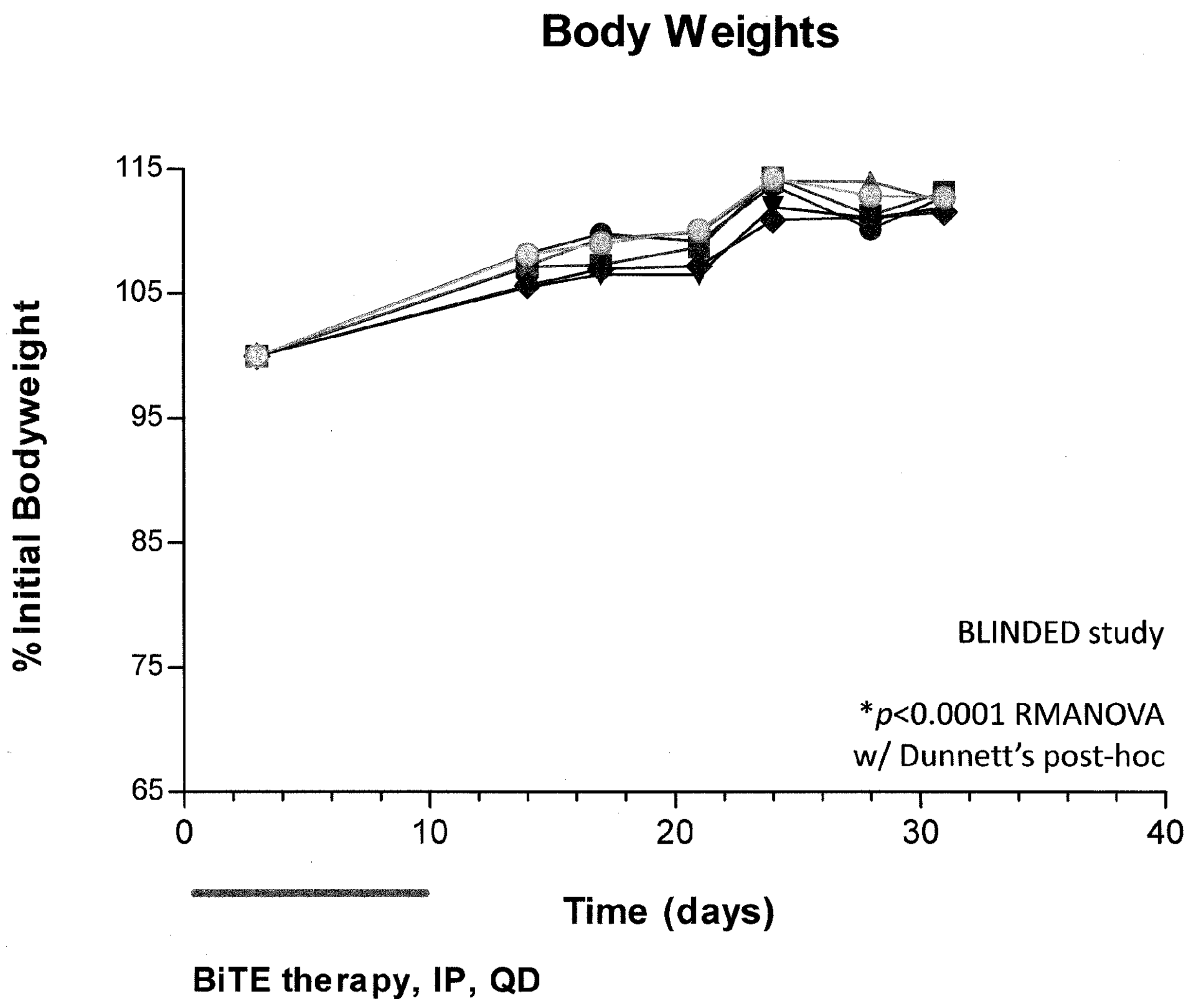
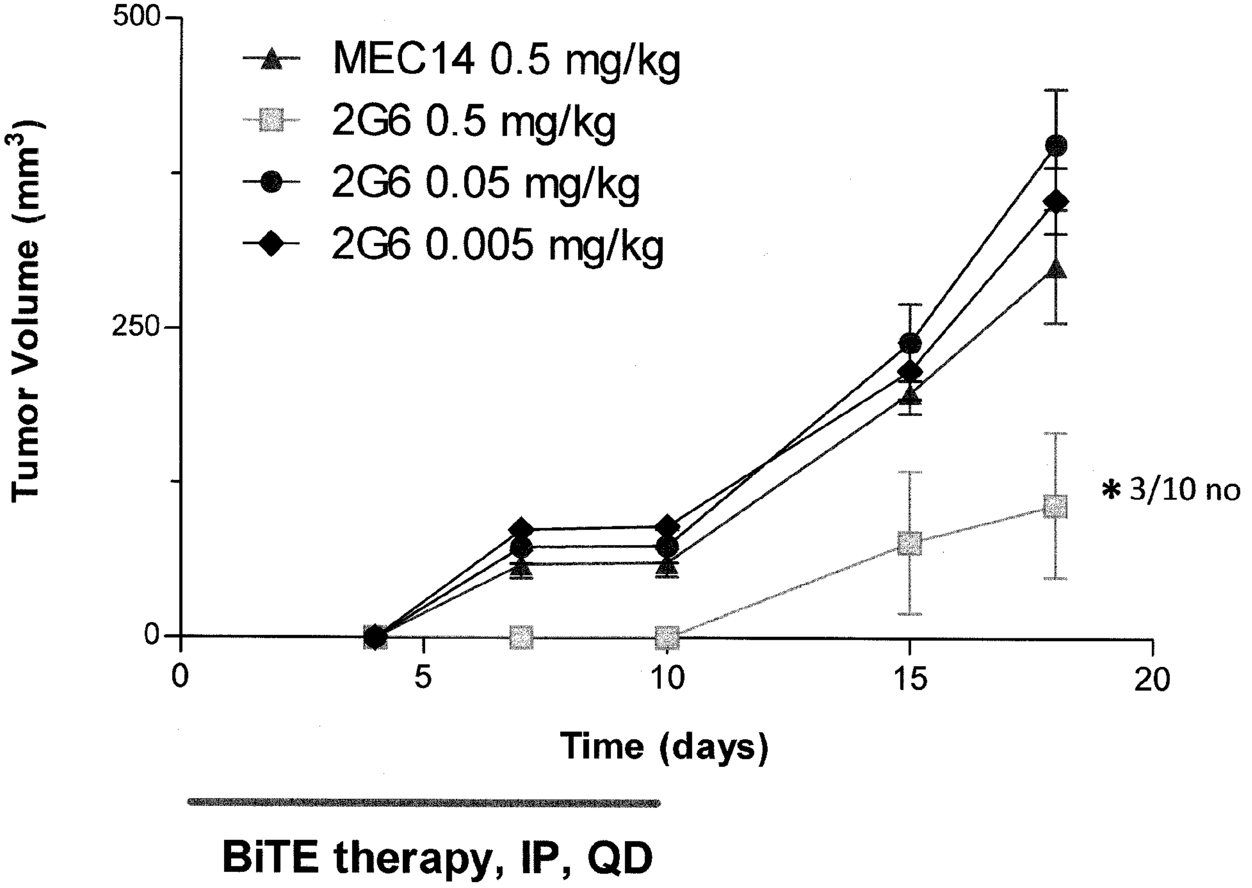


Figure 8 (continued)



@ Tumor cells and human PBMC inoculated at a 2:1 ratio on Day

Figure 9

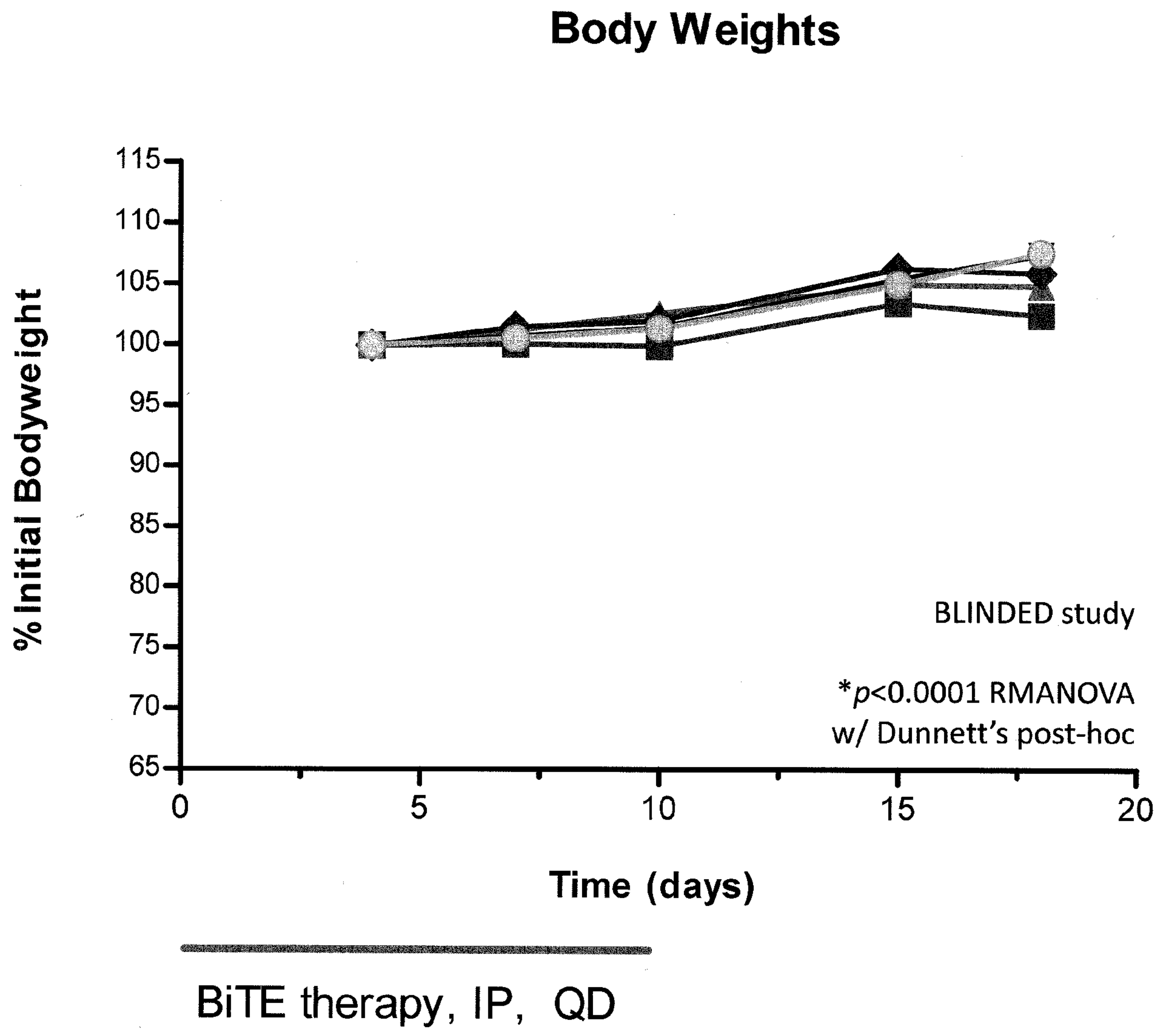


Figure 9 (continued)

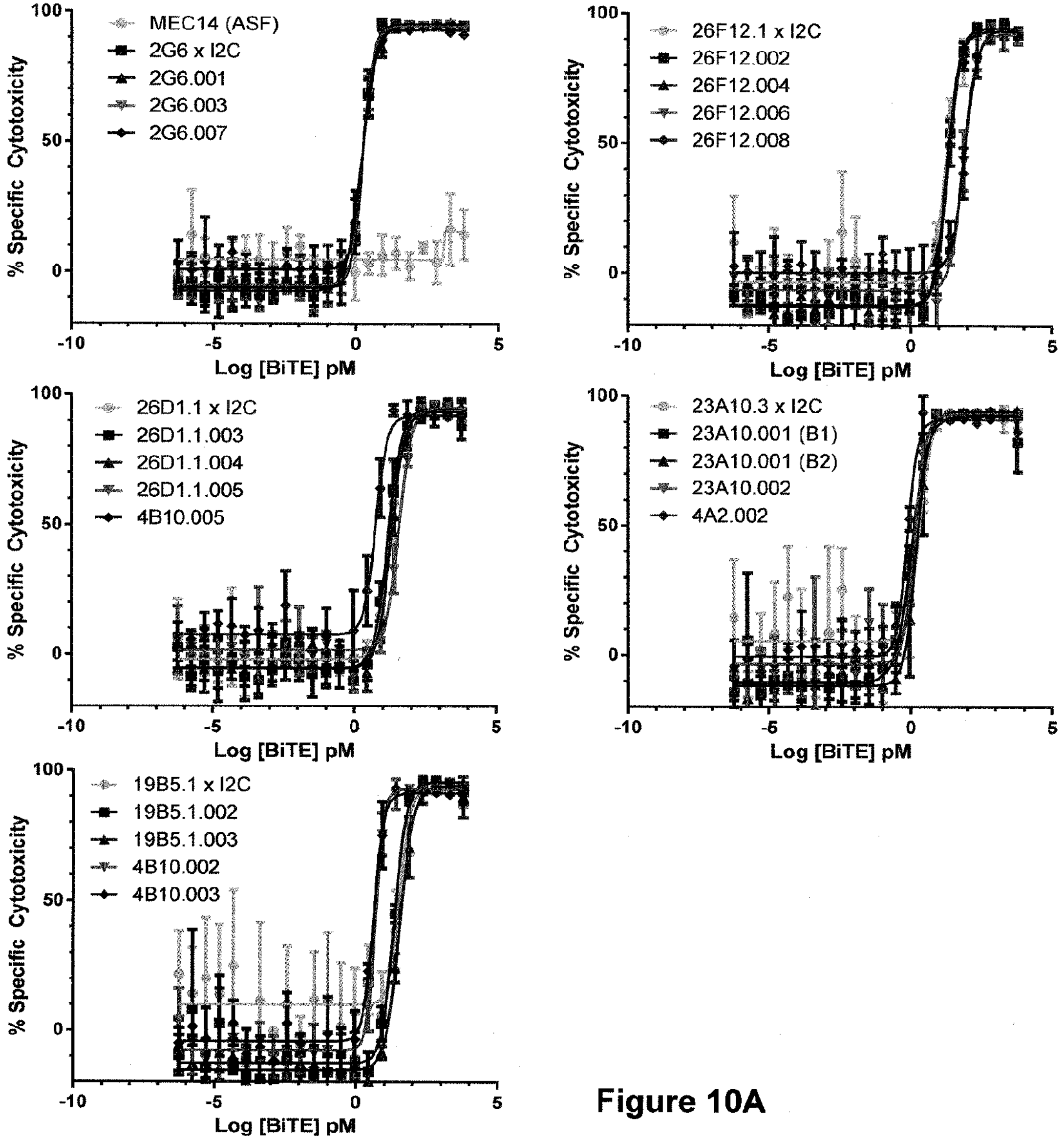
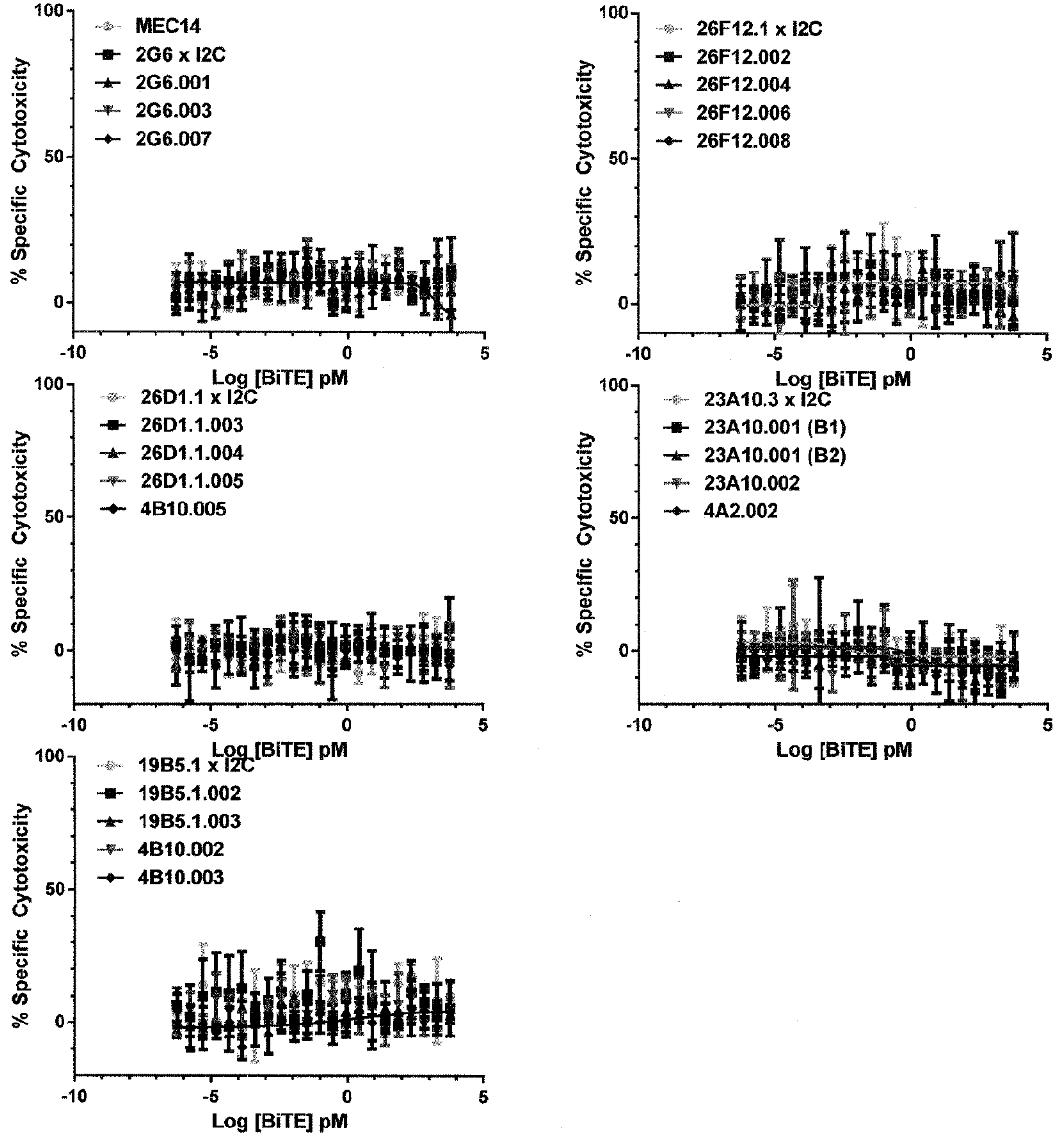


Figure 10A

CDH19 BiTE	*EC50[pM]*
2G6 x I2C	1.729
2G6.001	1.576
2G6.003	1.721
2G6.007	1.783
26F12.1 x I2C	18.48
26F12.002	19.4
26F12.004	20.74
26F12.006	72.22
26F12.008	83.43
19B5.1 x I2C	33.59
19B5.1.002	22.37
19B5.1.003	34.62
4B10.002	4.83
4B10.003	4.088
4B10.005	5.583
26D1.1 x I2C	19.19
26D1.1.003	15.53
26D1.1.004	19.77
26D1.1.005	36.42
23A10.3 x I2C	2.086
23A10.001 (B1)	1.078
23A10.001 (B2)	1.623
23A10.002	1.351
4A2.002	0.7547



CDH19 BiTE	EC50[pM]
2G6 x I2C	no specific activity
2G6.001	no specific activity
2G6.003	no specific activity
2G6.007	no specific activity
26F12.1 x I2C	no specific activity
26F12.002	no specific activity
26F12.004	no specific activity
26F12.006	no specific activity
26F12.008	no specific activity
19B5.1 x I2C	no specific activity
19B5.1.002	no specific activity
19B5.1.003	no specific activity
4B10.002	no specific activity
4B10.003	no specific activity
4B10.005	no specific activity
26D1.1 x I2C	no specific activity
26D1.1.003	no specific activity
26D1.1.004	no specific activity
26D1.1.005	no specific activity
23A10.3 x I2C	no specific activity
23A10.001 (B1)	no specific activity
23A10.001 (B2)	no specific activity
23A10.002	no specific activity
4A2.002	no specific activity

Figure 10B

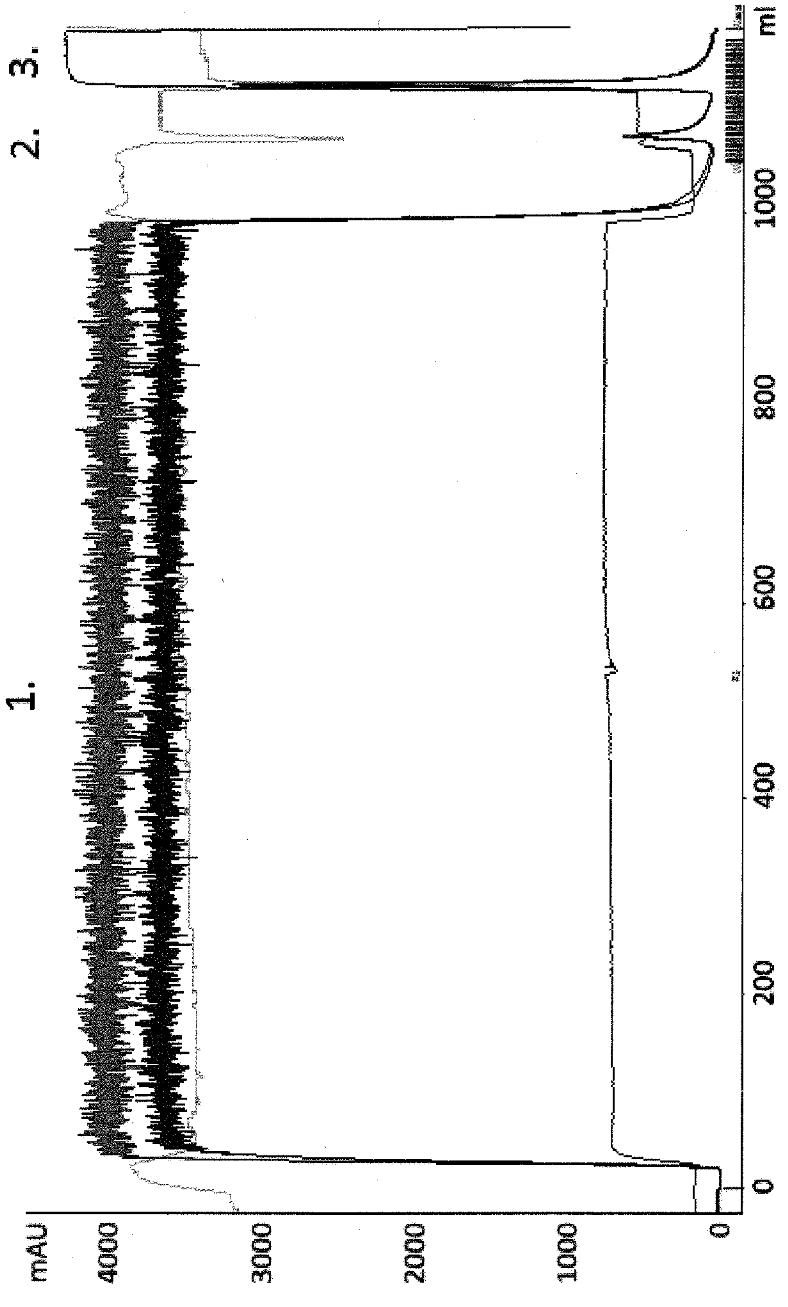


Figure 11

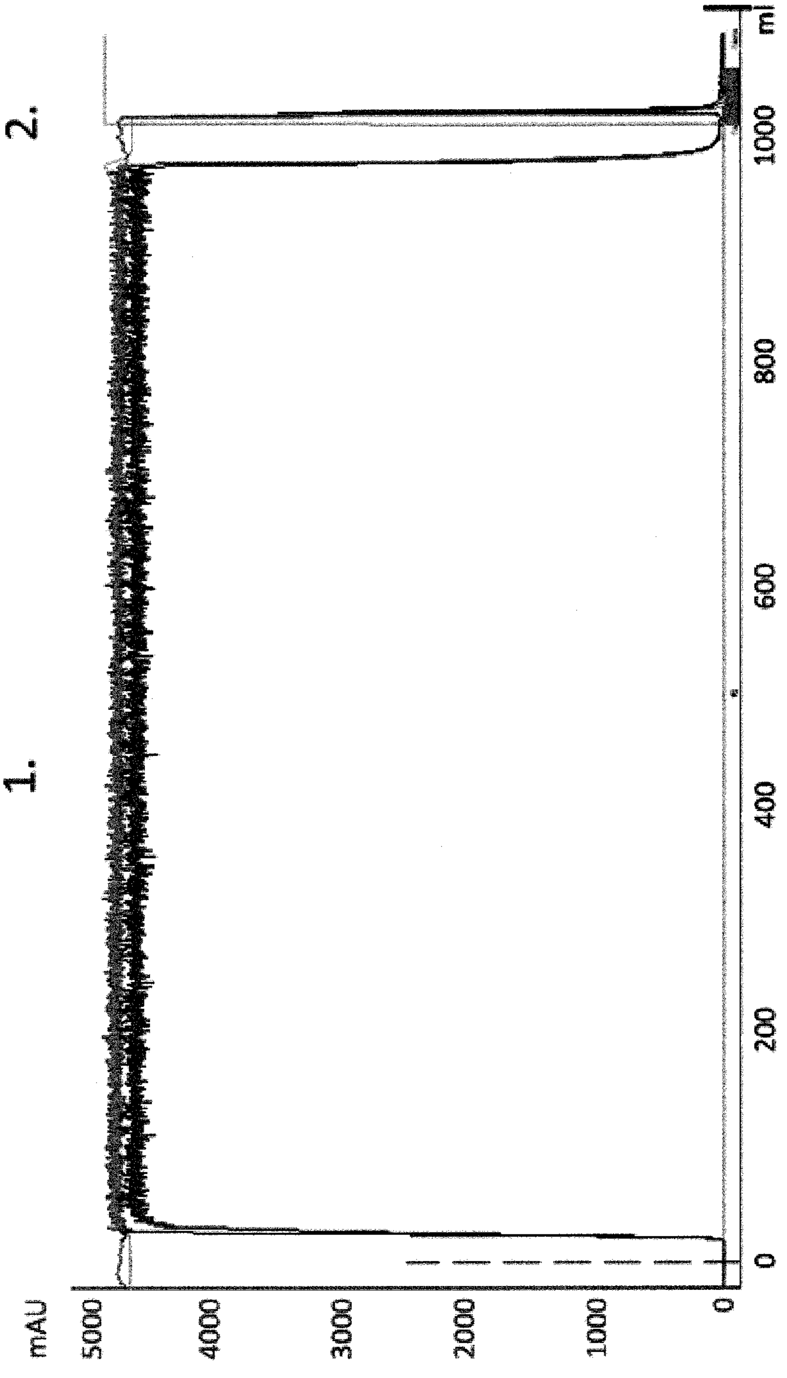


Figure 12

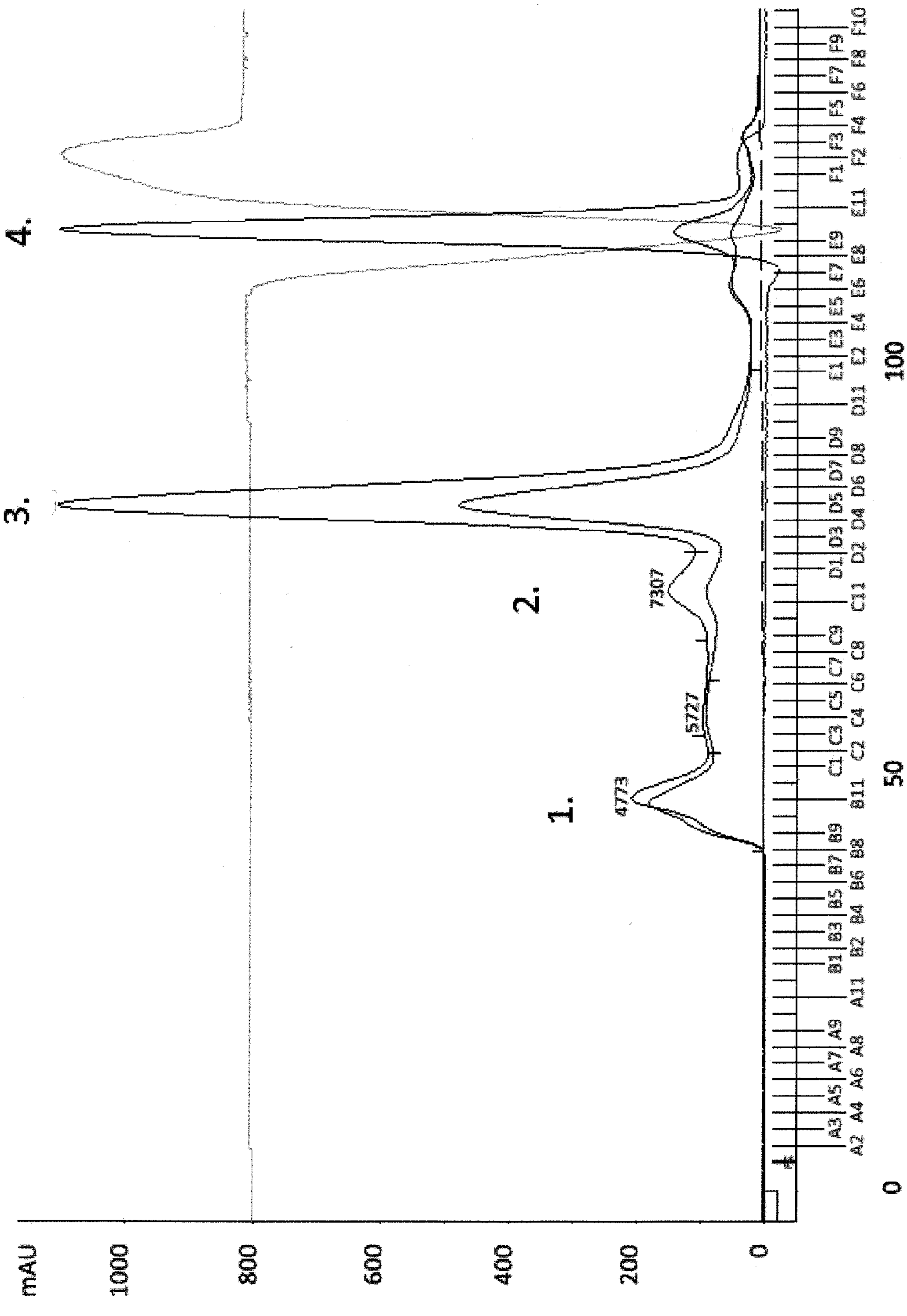


Figure 13

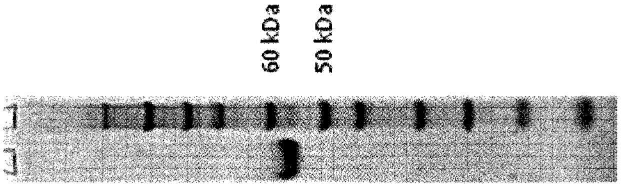


Figure 14

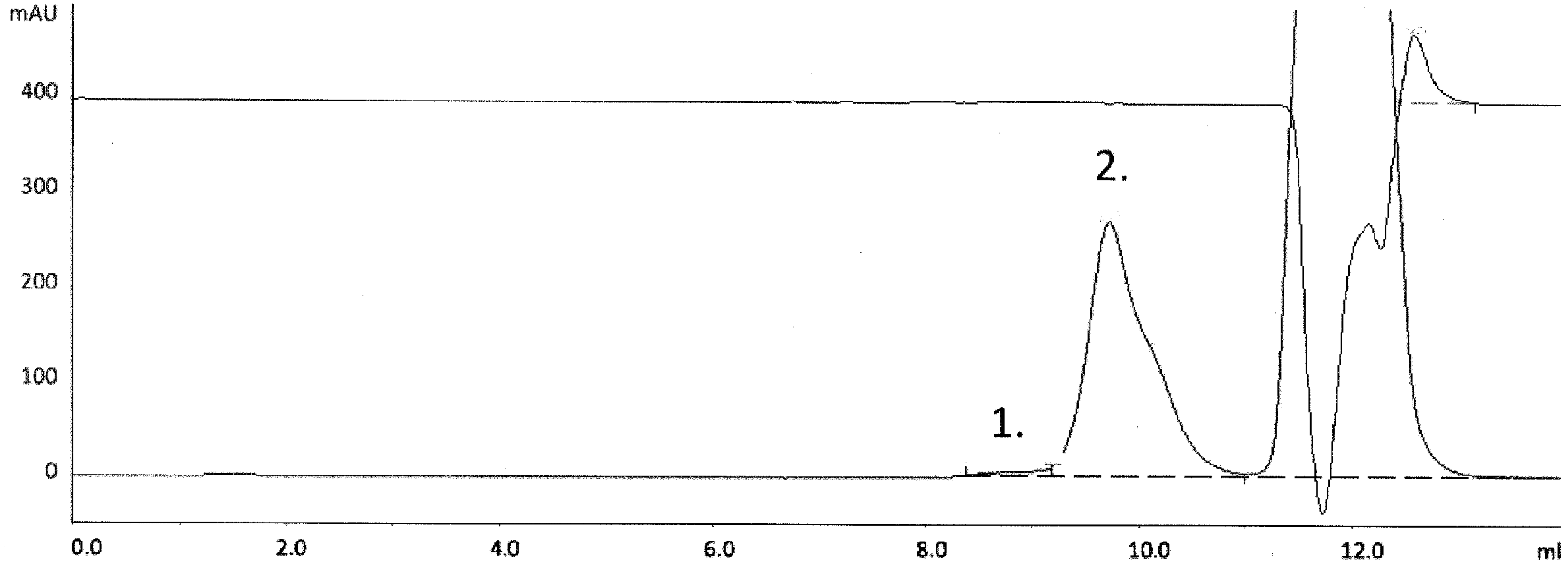


Figure 15

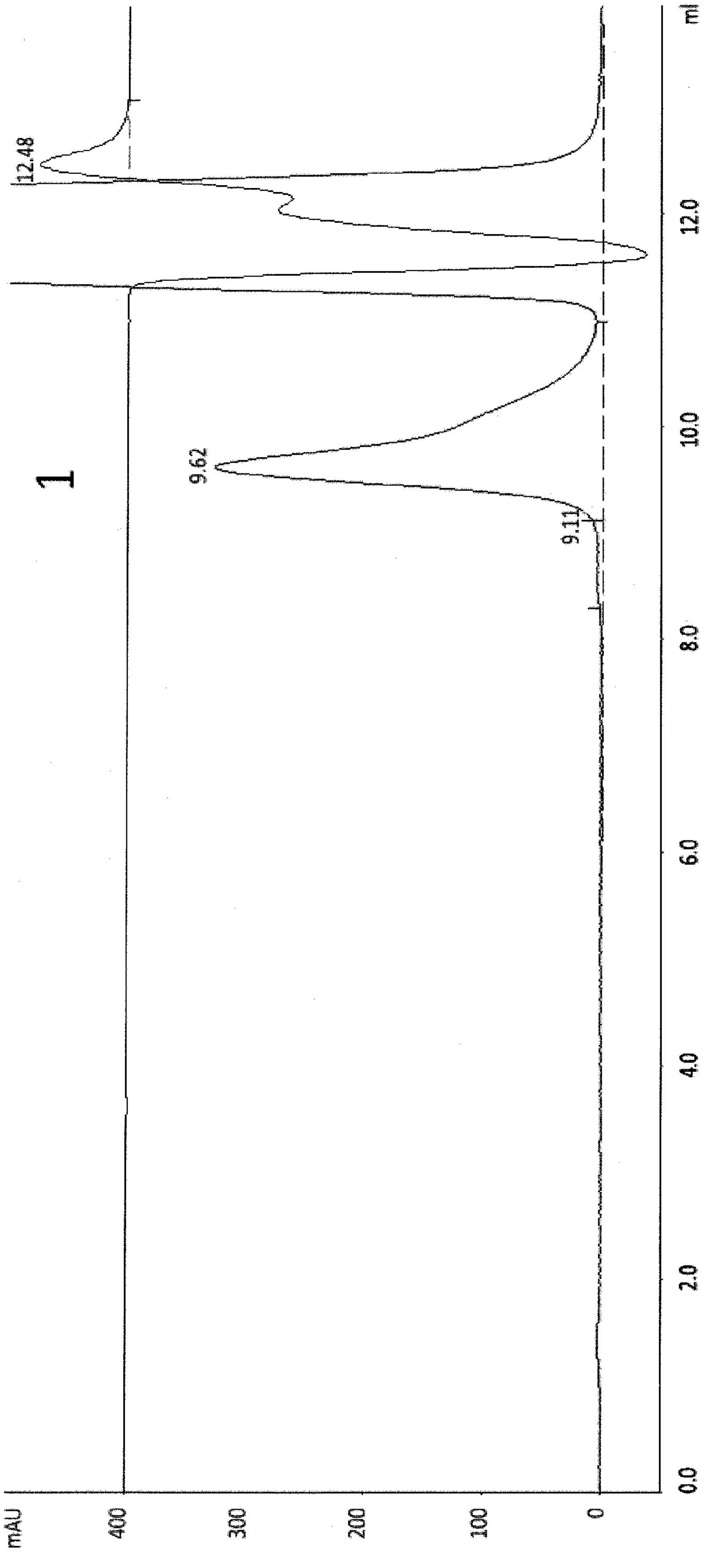


Figure 16

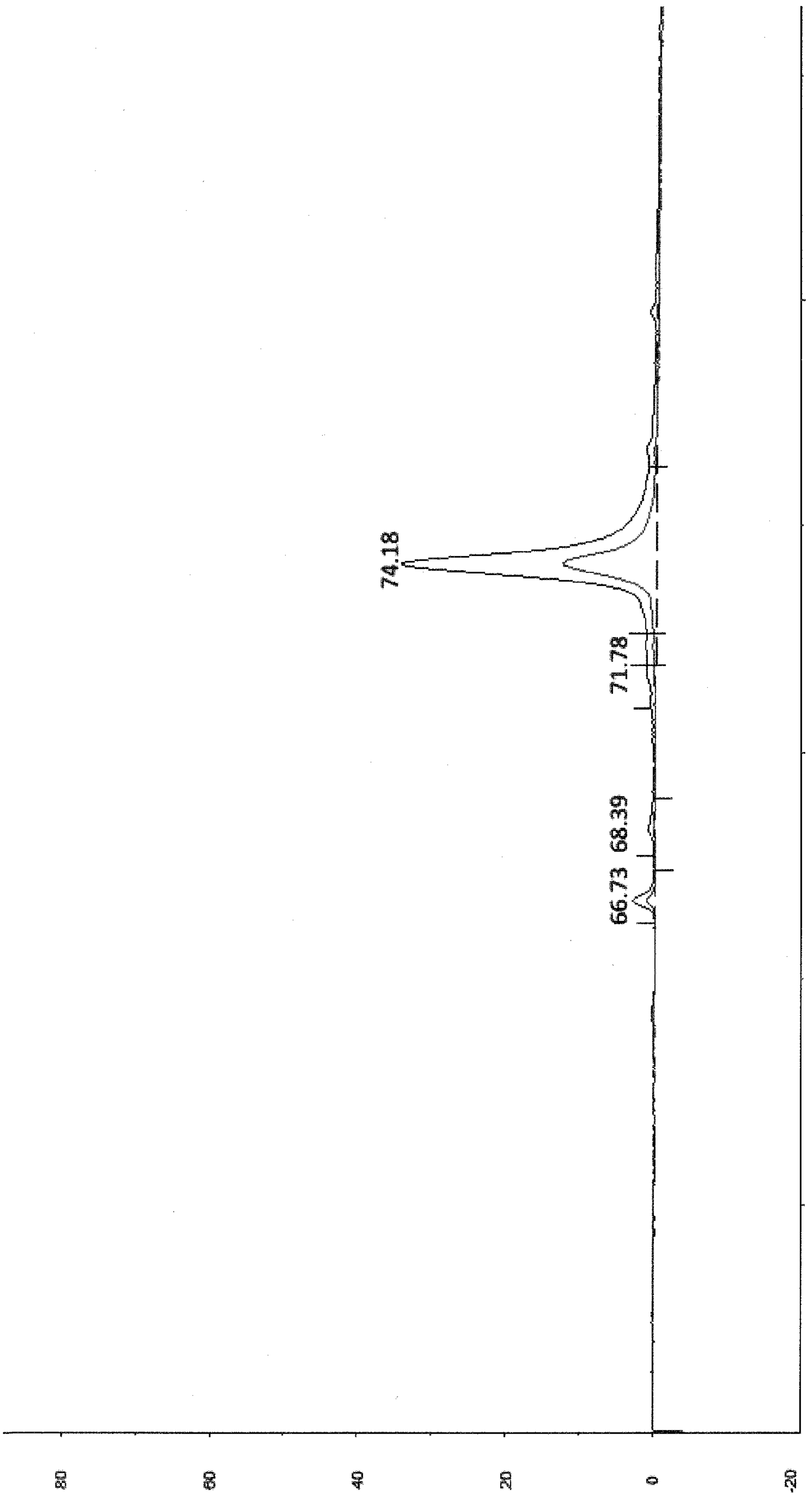


Figure 17

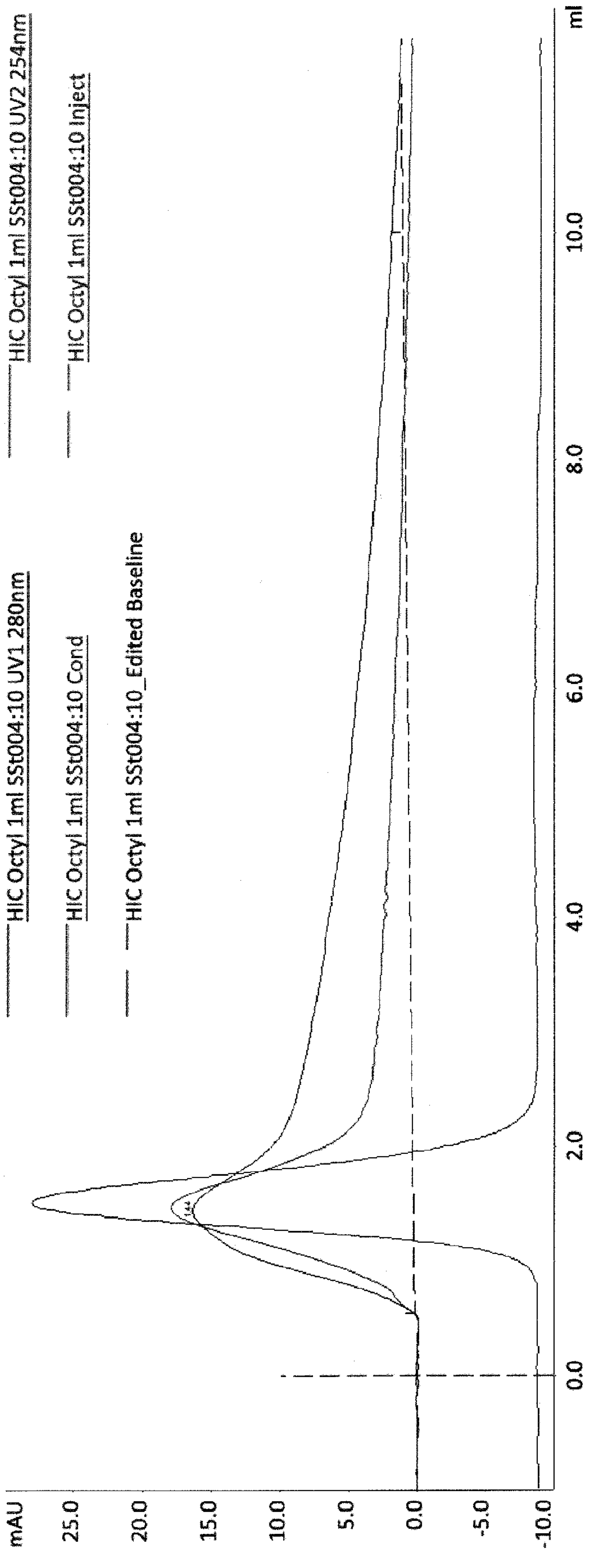

HIC Octyl 1ml SSt004:10 UV1 280nm
HIC Octyl 1ml SSt004:10 Cond
HIC Octyl 1ml SSt004:10_Edited Baseline
HIC Octyl 1ml SSt004:10 UV2 254nm
HIC Octyl 1ml SSt004:10 Inject
mAU
25.0
20.0
15.0
10.0
5.0
0.0
-5.0
-10.0
0.0
2.0
4.0
6.0
8.0
10.0
ml

Figure 18

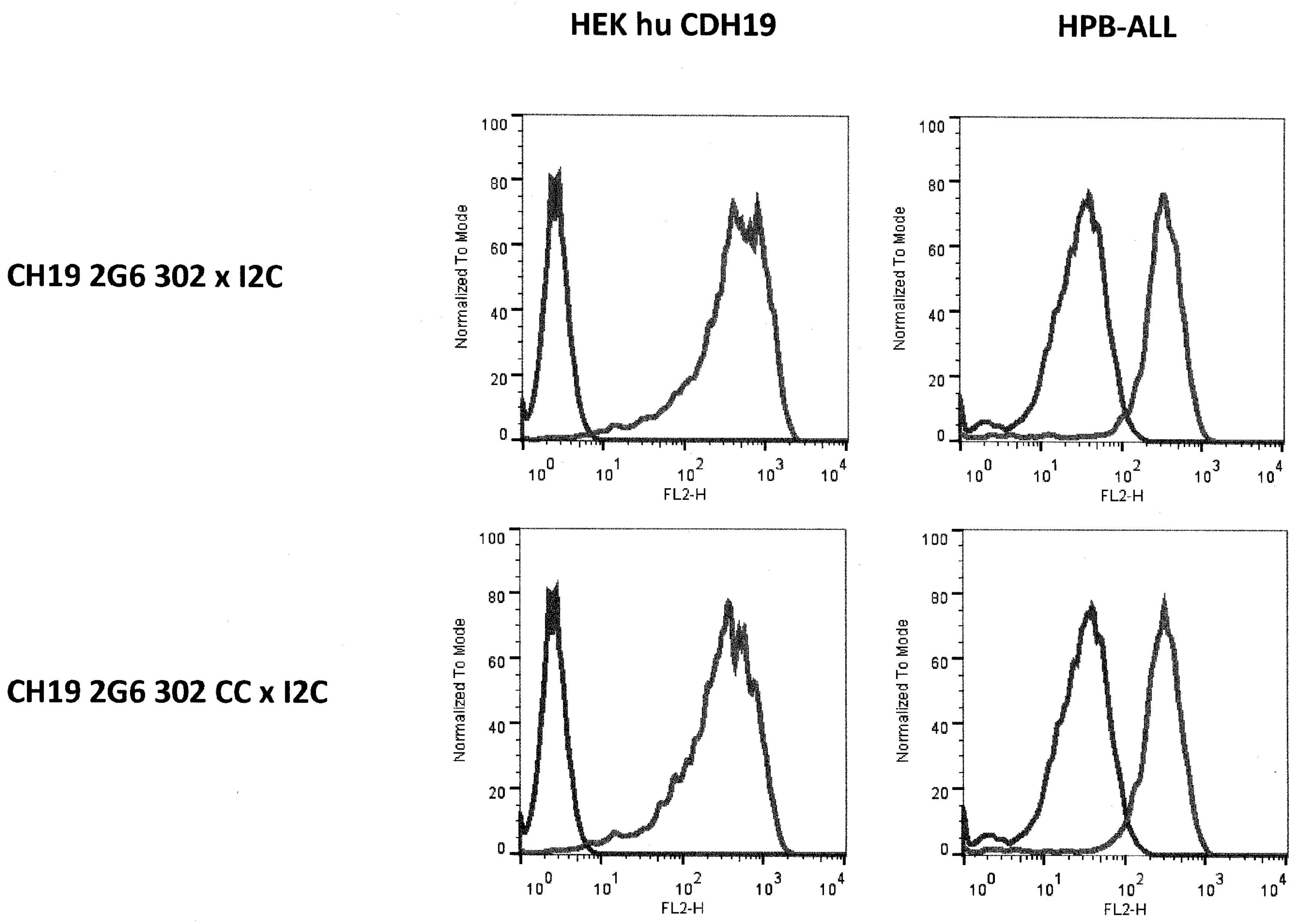

HEK hu CDH19
HPB-ALL
CH19 2G6 302 x I2C
CH19 2G6 302 CC x I2C
Normalized To Mode
0
20
40
60
80
100
10^0
10^1
10^2
10^3
10^4
FL2-H

Figure 19

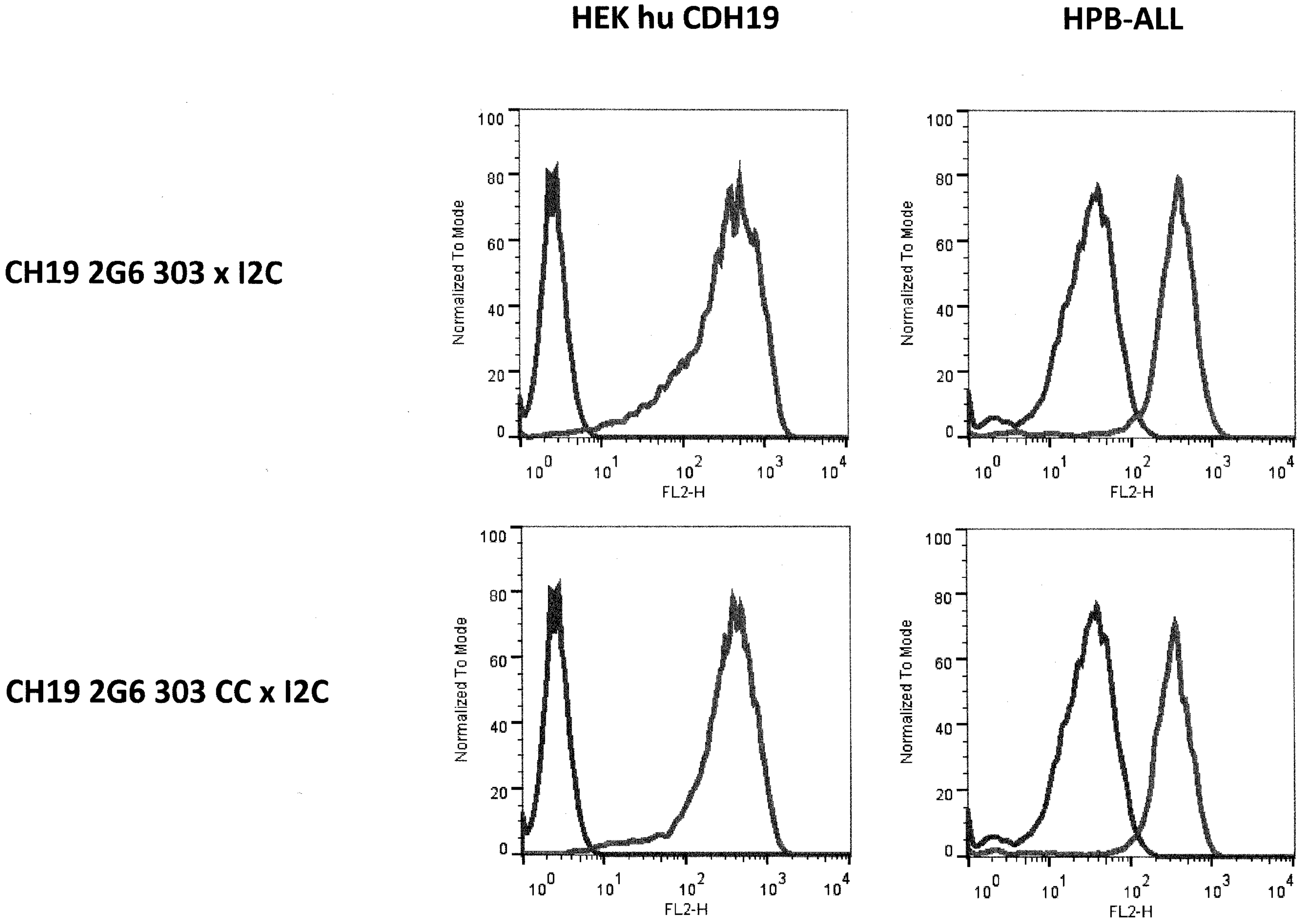


Figure 19 (continued)

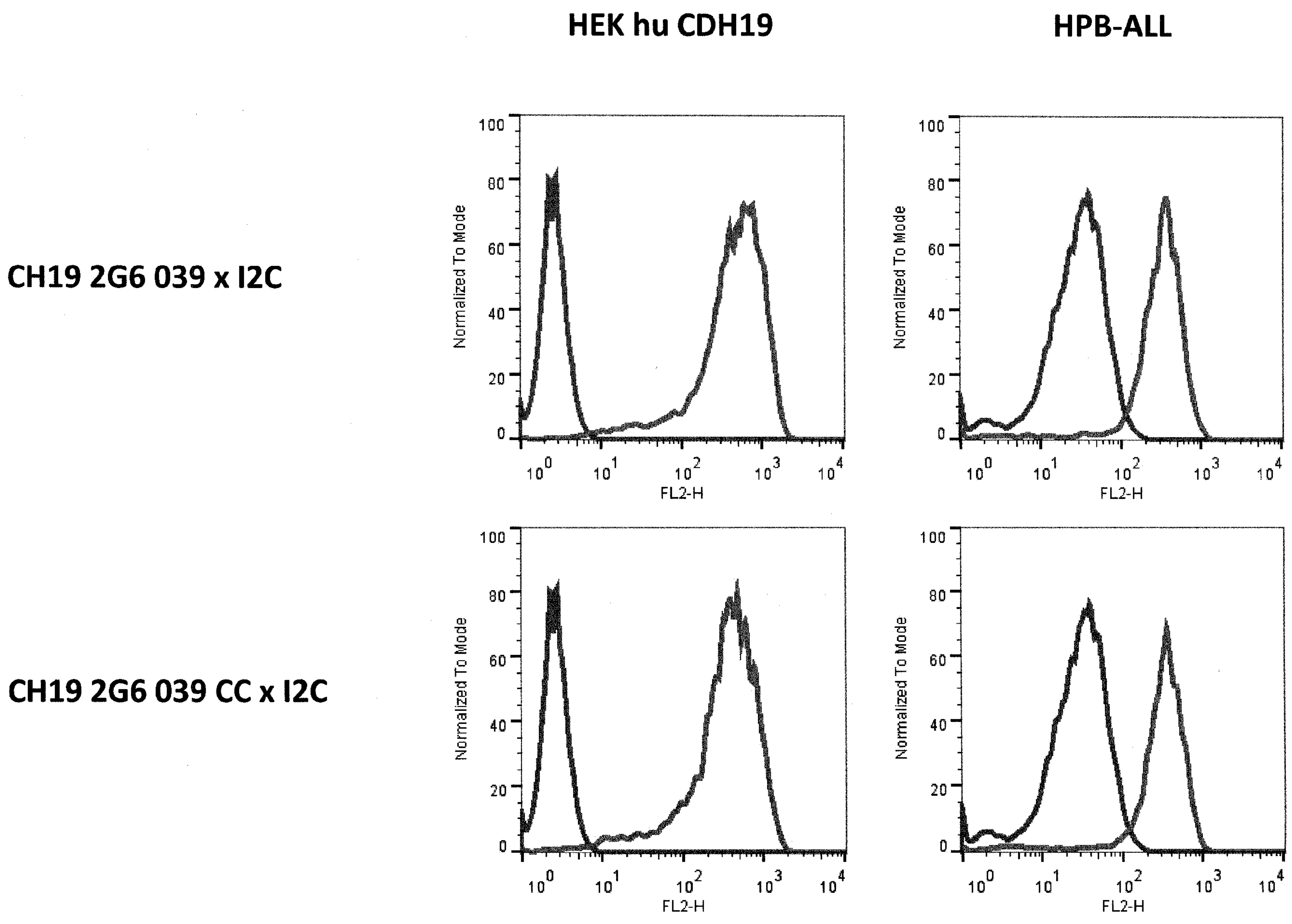


Figure 19 (continued)

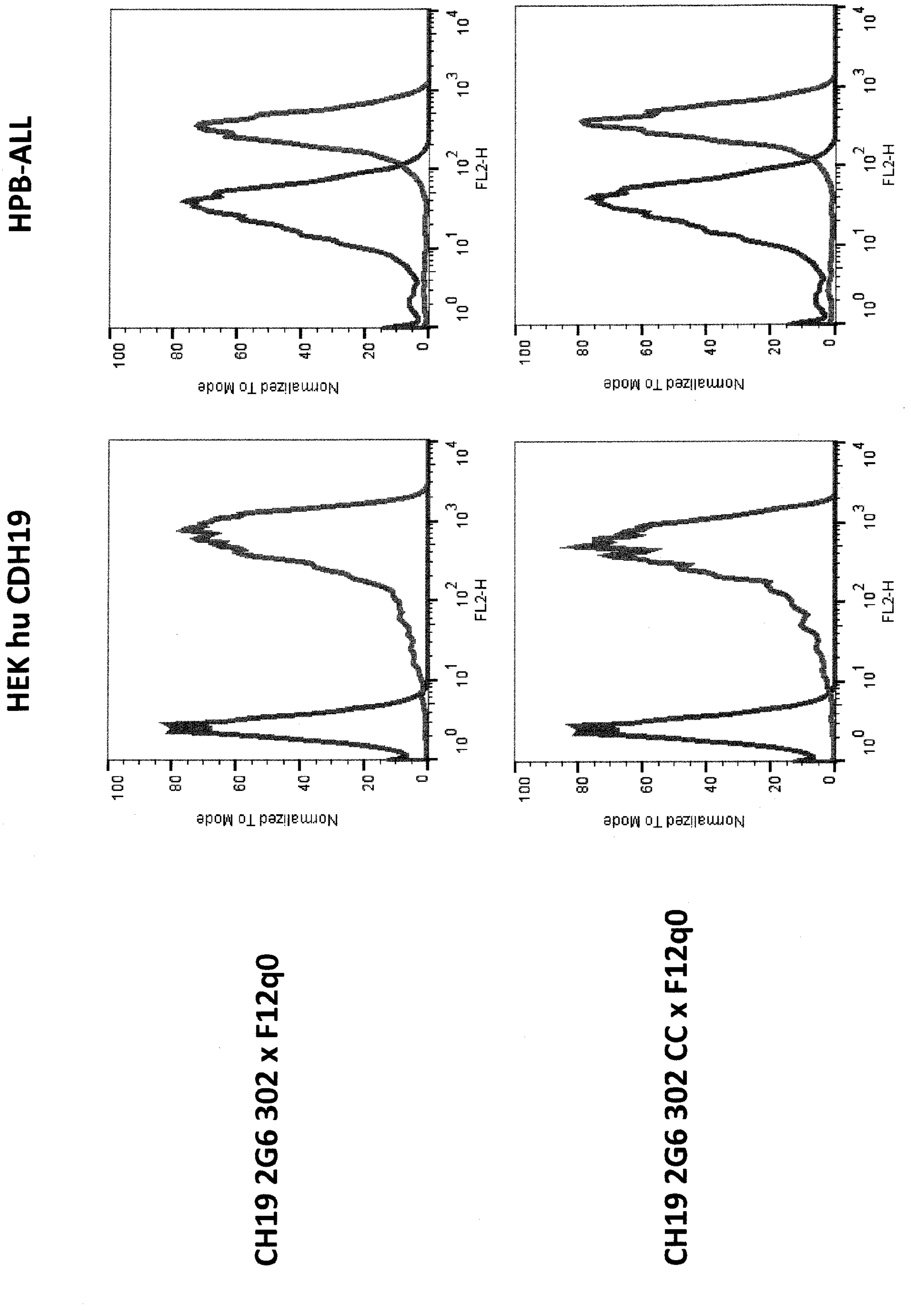


Figure 19 (continued)

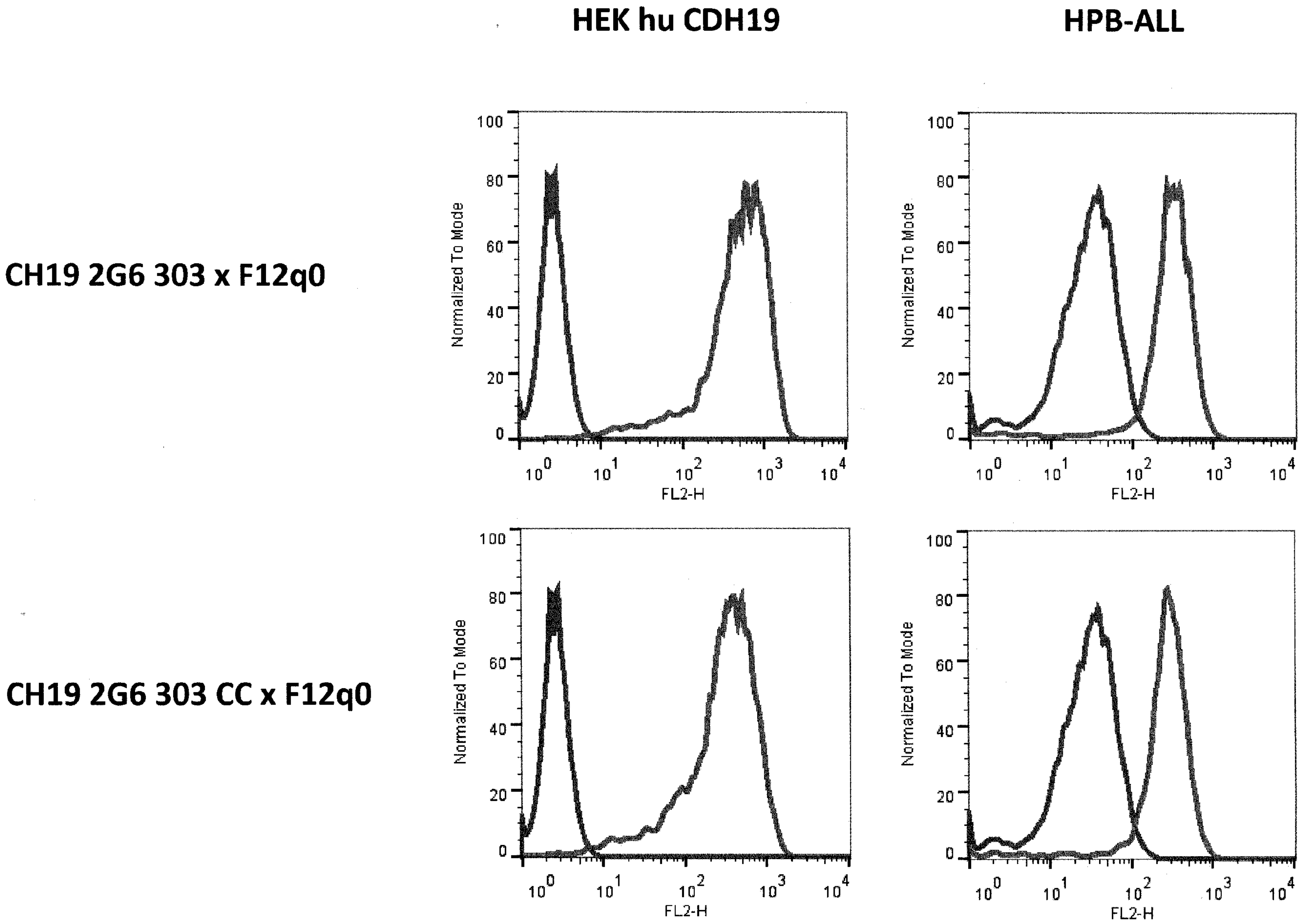
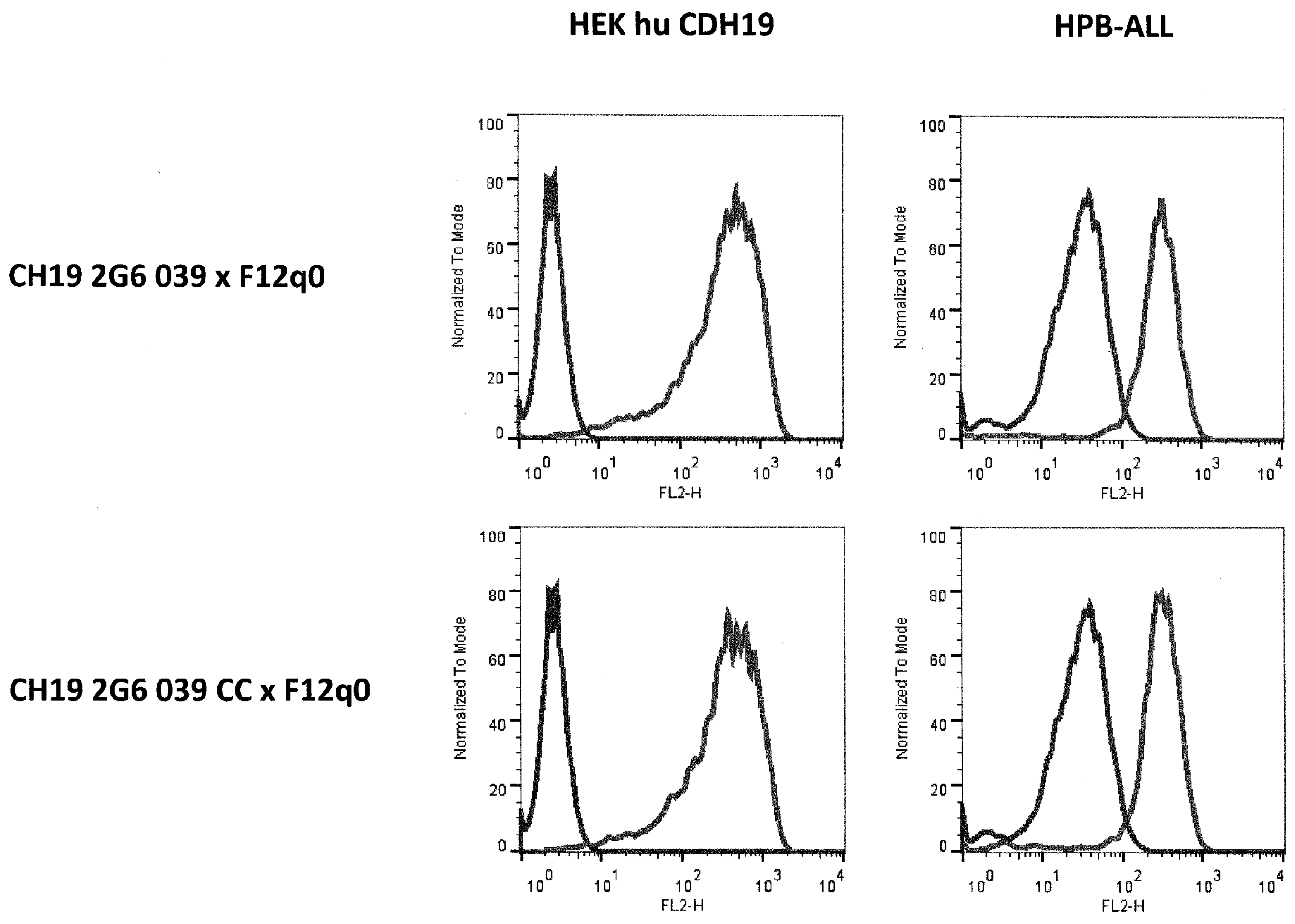


Figure 19 (continued)



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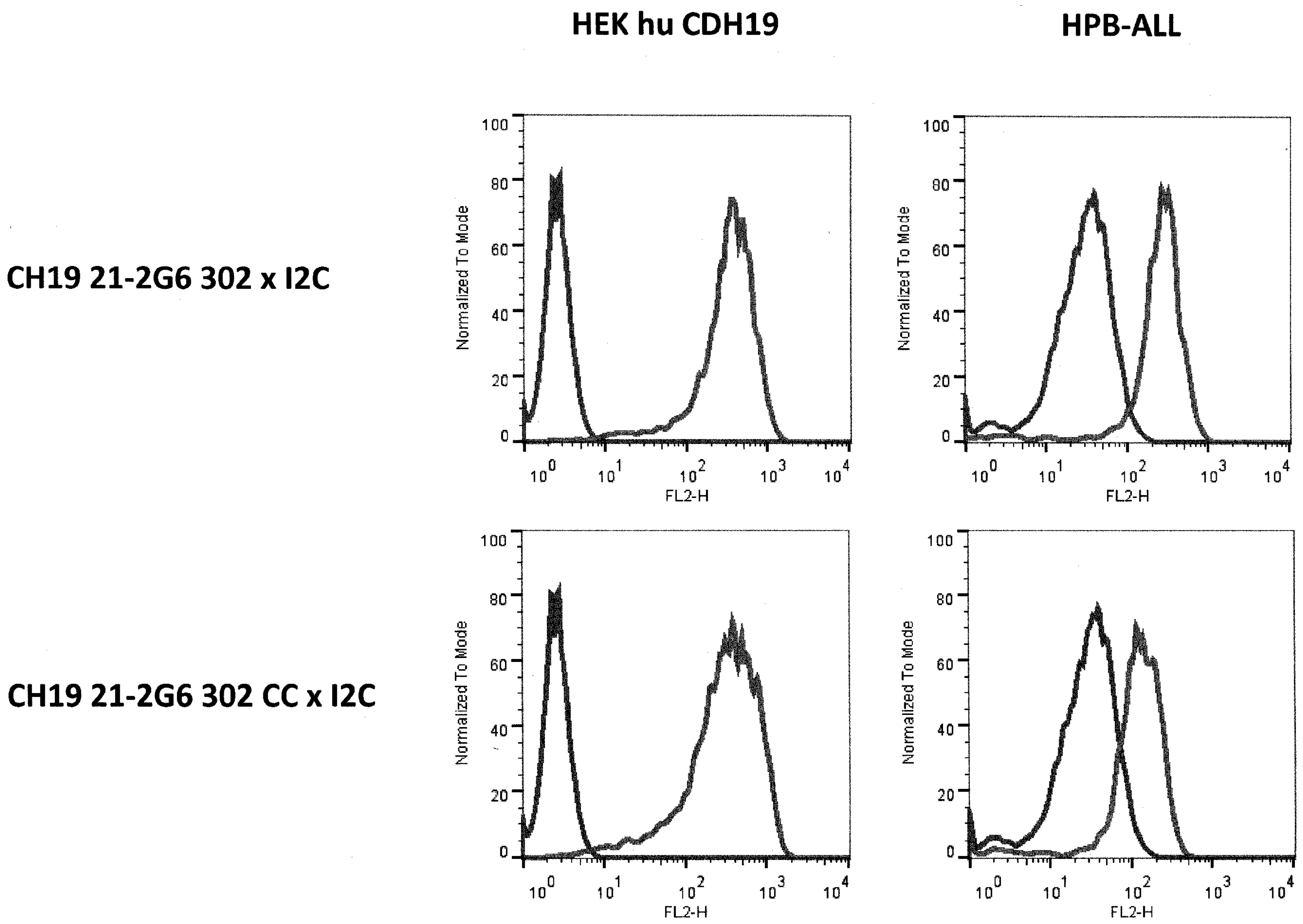

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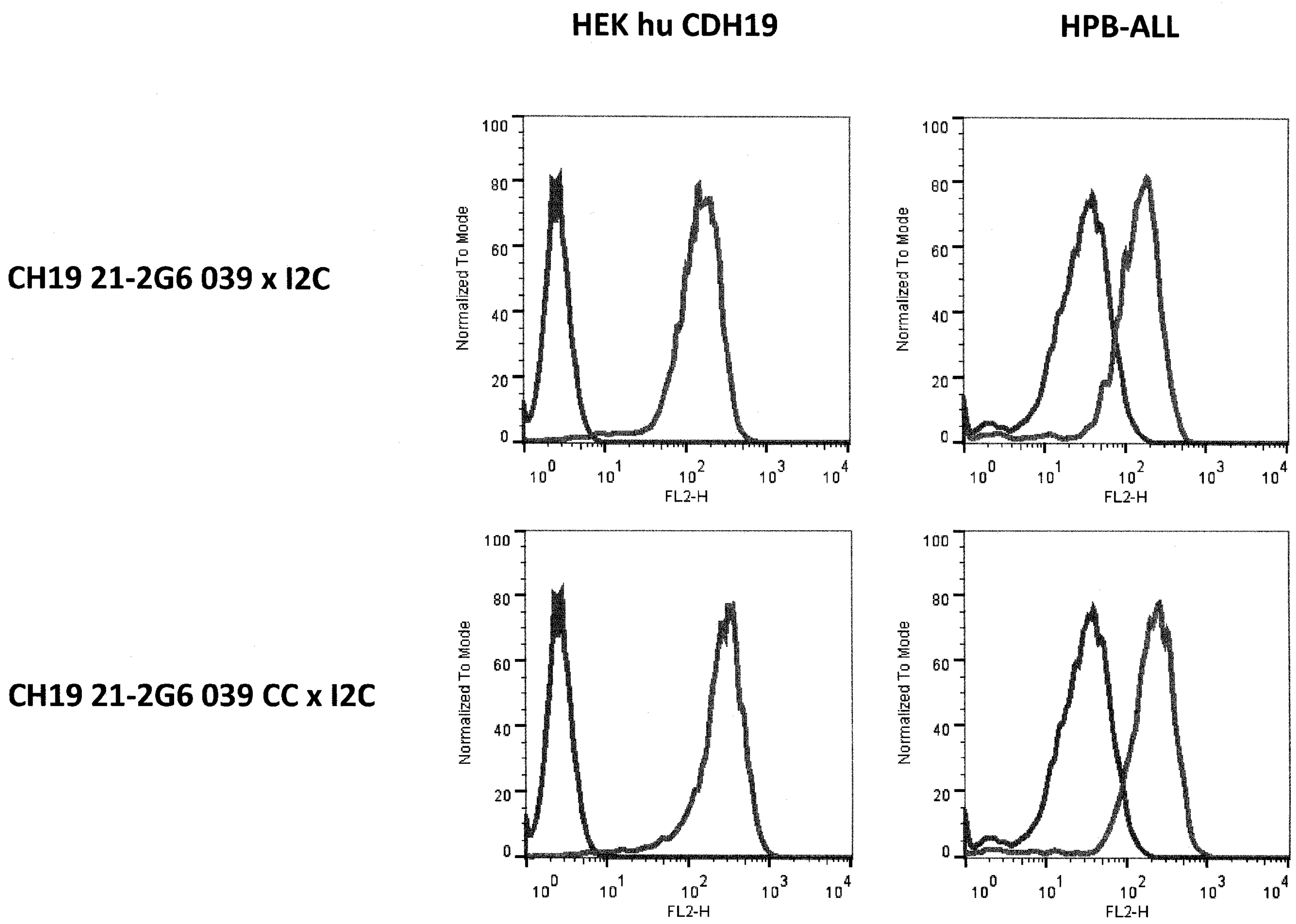

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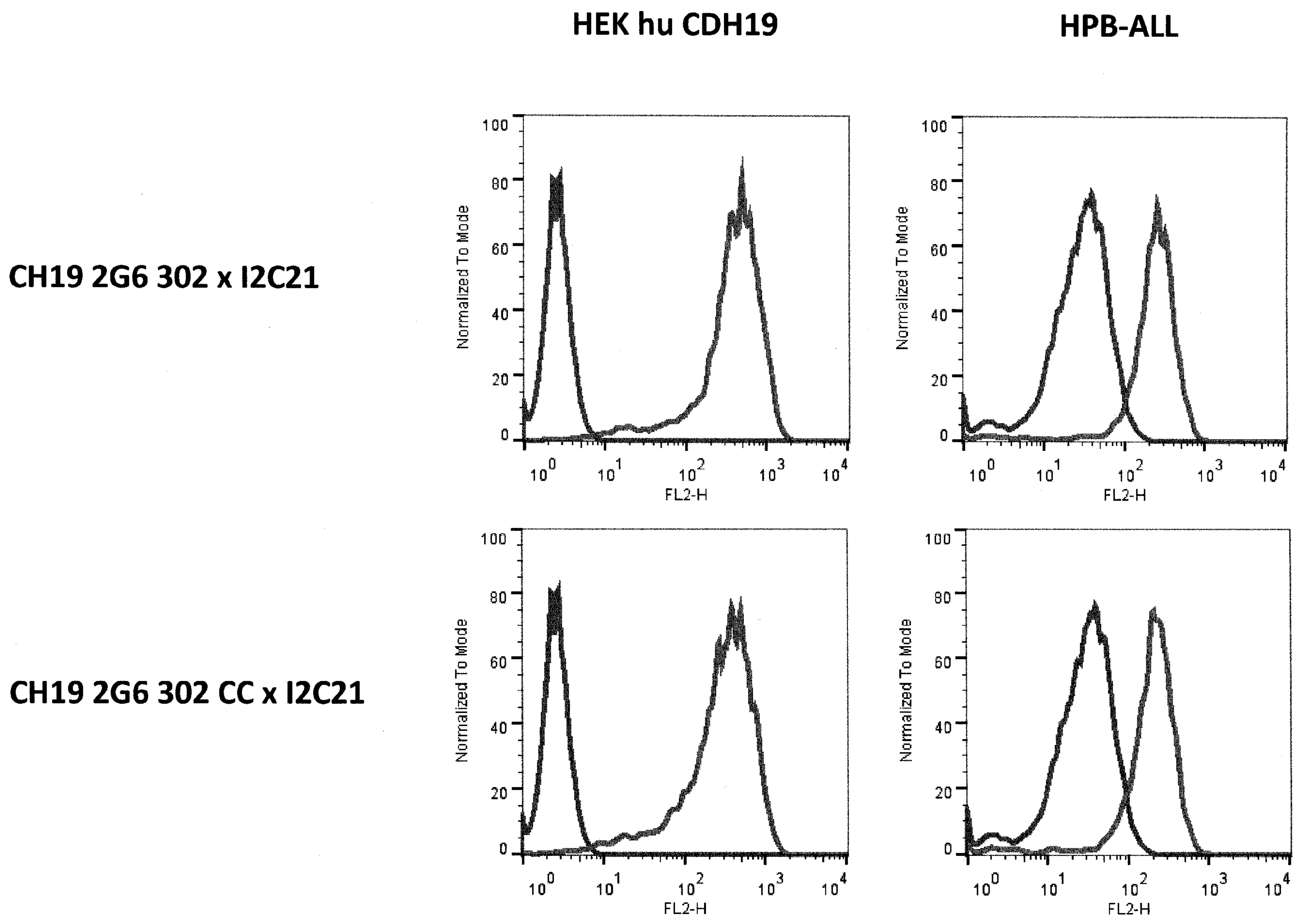

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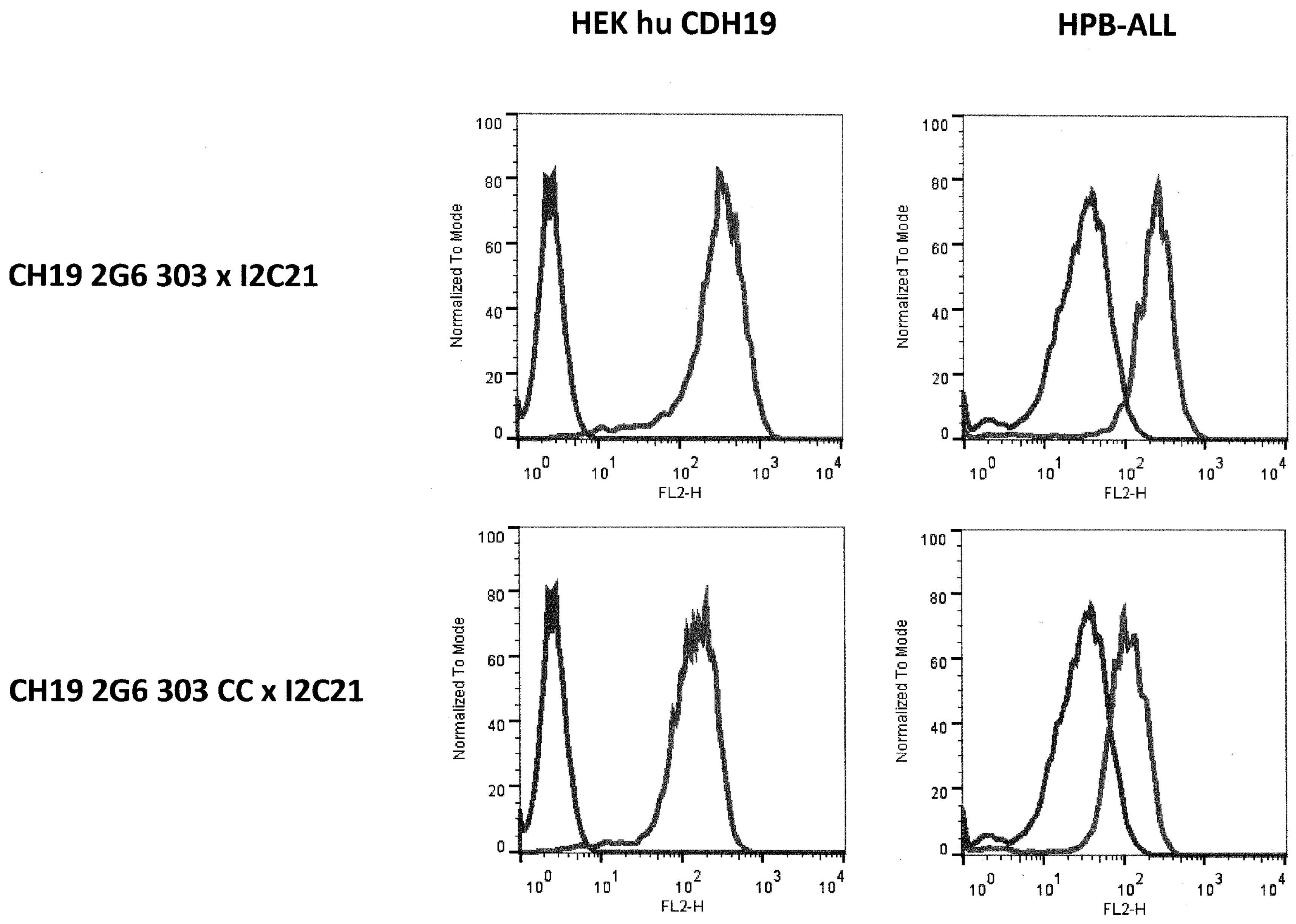

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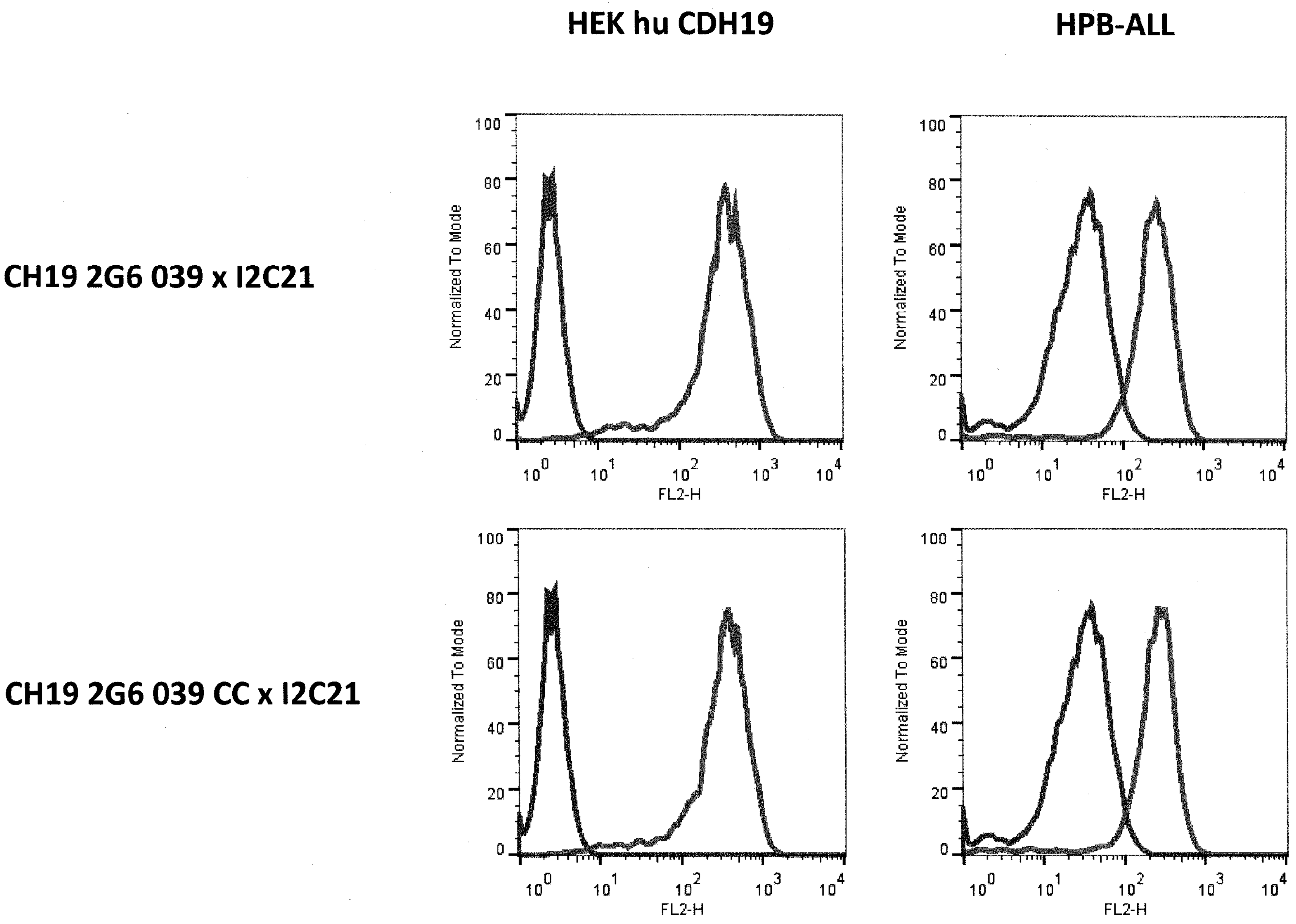

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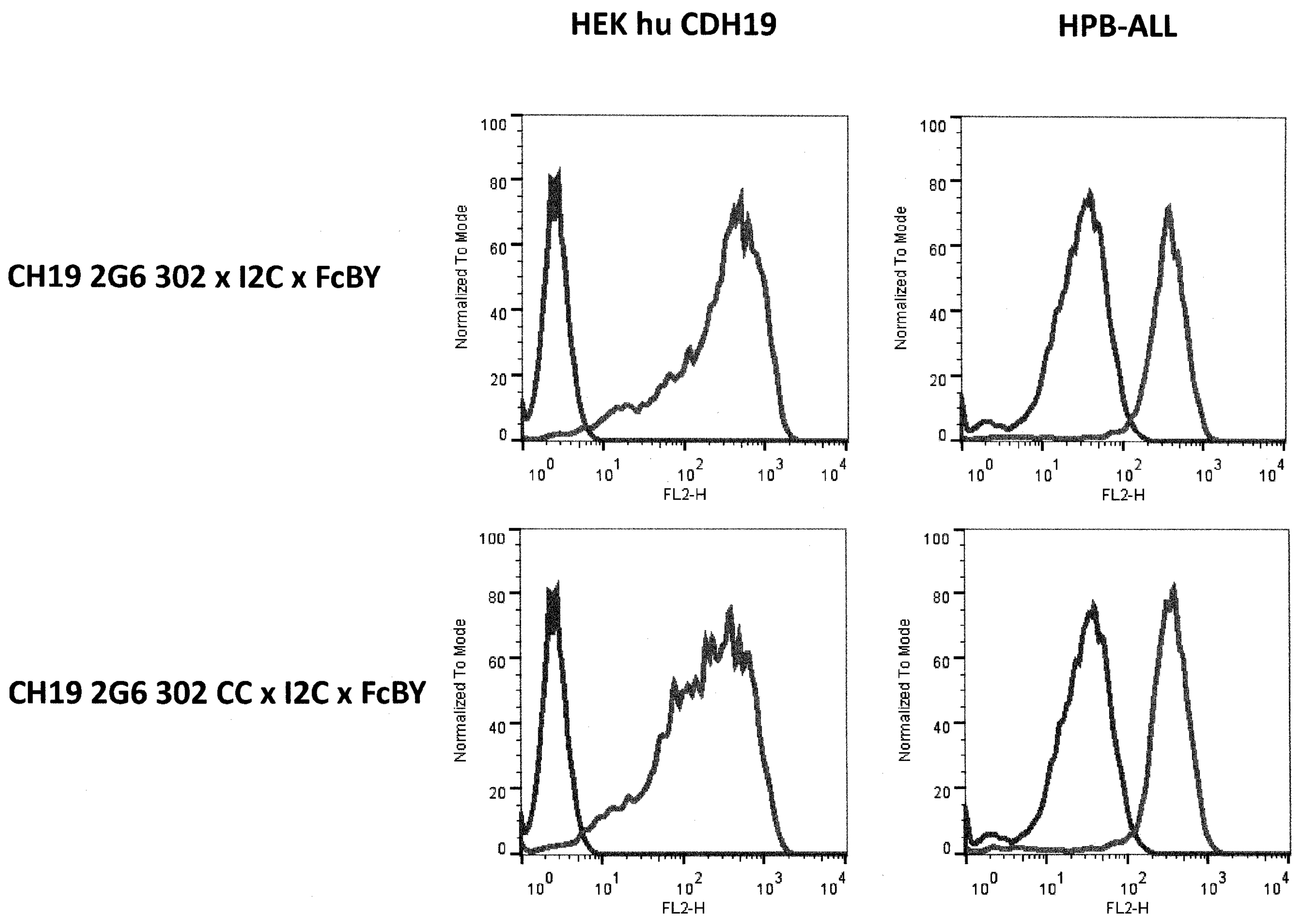
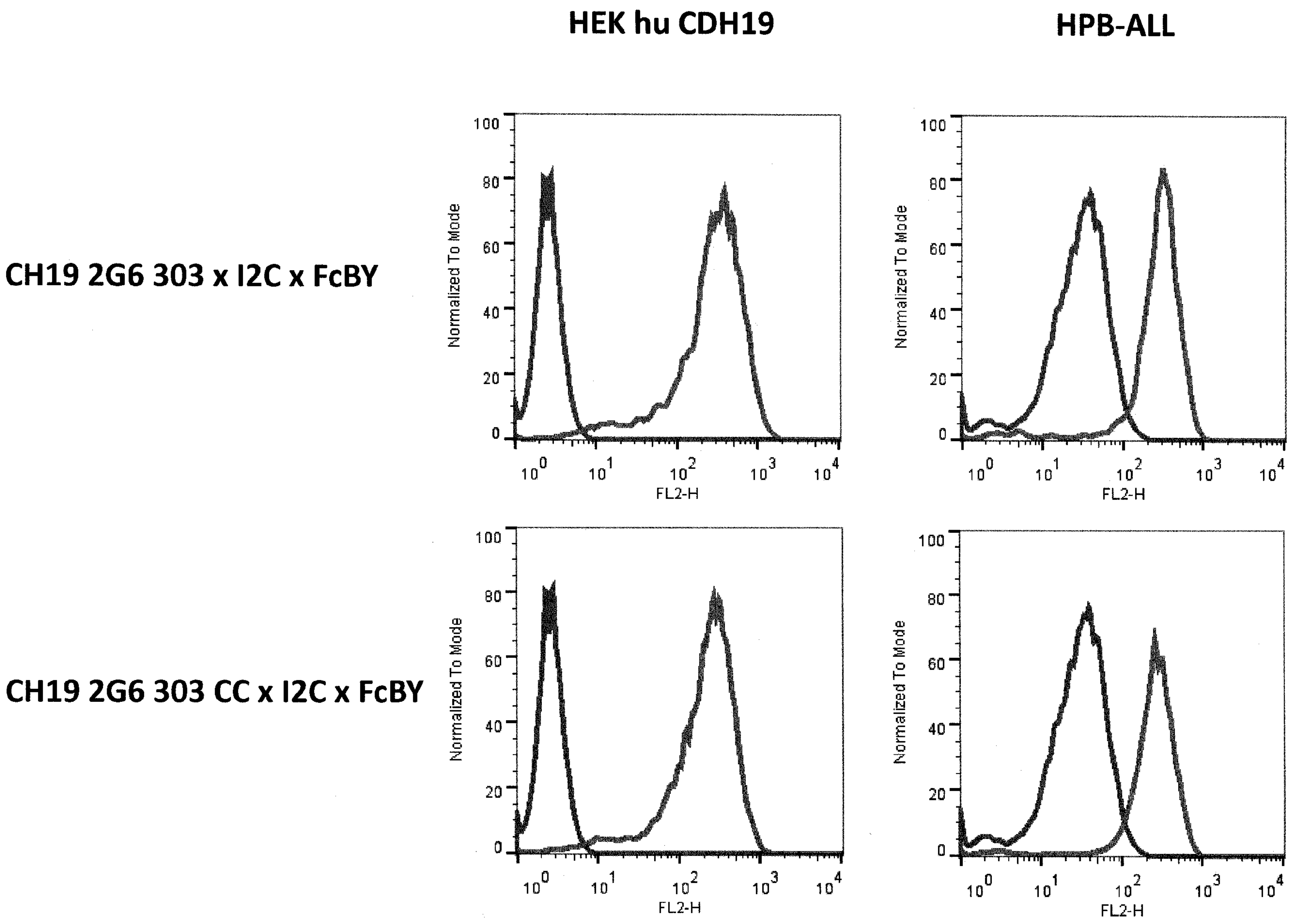


Figure 19 (continued)



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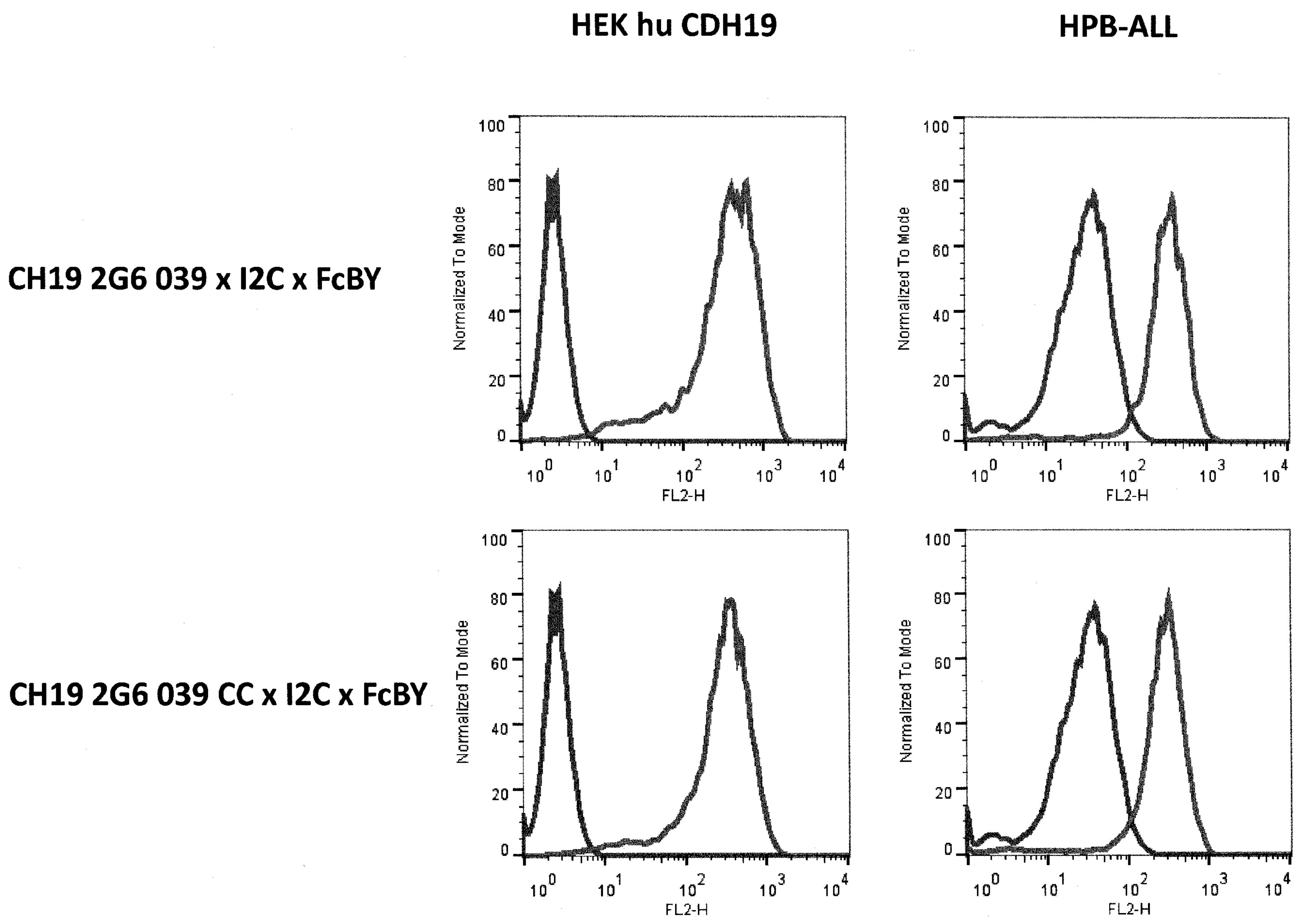

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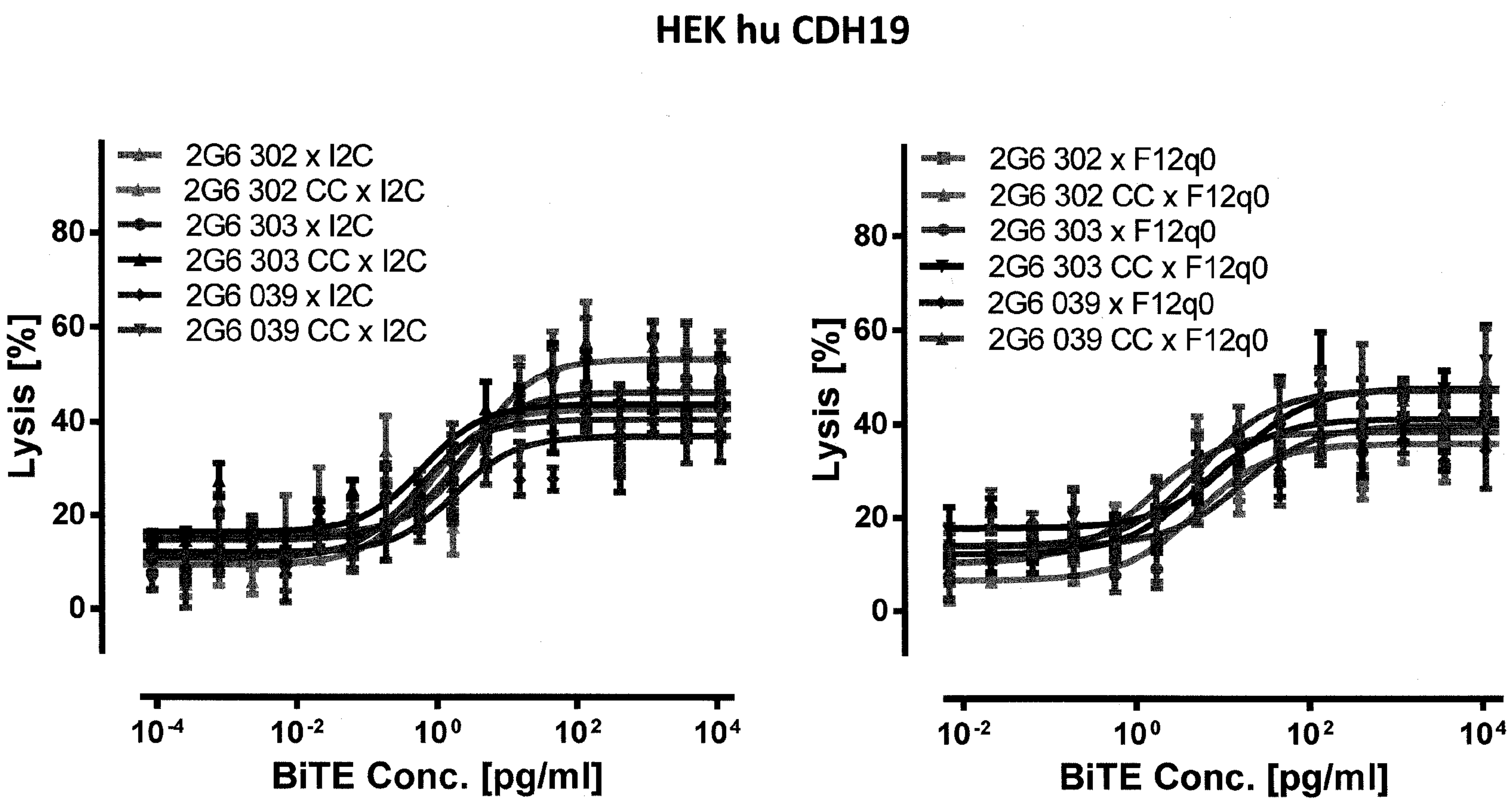

HEK hu CDH19

Figure 20

HEK hu CDH19

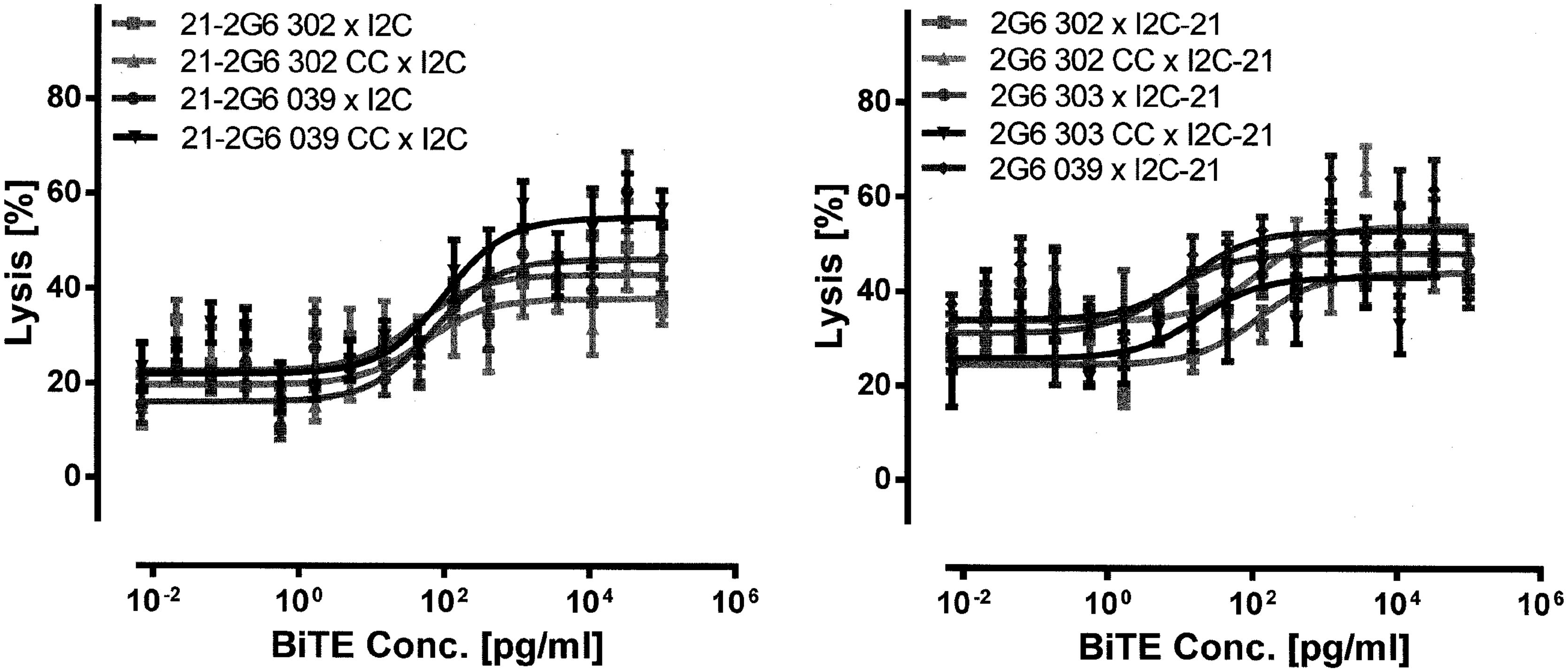

Figure 20 (continued)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2014/051550

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:

   a. (means)

   ☐ on paper
   ☒ in electronic form

   b. (time)

   ☐ in the international application as filed
   ☐ together with the international application in electronic form
   ☒ subsequently to this Authority for the purpose of search

2. ☒ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/051550

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/28 C07K16/30 A61K47/48 A61K39/395 A61P35/00
C07K16/46
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2006/071441 A2 (CURAGEN CORP [US]; ABGENIX INC [US]; XIAO FENG [US]; JIA XIAO-CHI [US]) 6 July 2006 (2006-07-06) whole document, especially Examples 13, 19, 20, 28; Figures 1, 4, 5, 20 ----- -/--	1-18

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 14 May 2014	Date of mailing of the international search report 22/05/2014
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Luyten, Kattie

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KISCHEL ROMAN ET AL: "Characterization of novel CD33-and MCSP-specific BiTE antibodies for the treatment of acute myeloid leukemia and melanoma, respectively, that are fully human in sequence", AMERICAN ASSOCIATION FOR CANCER RESEARCH. PROCEEDINGS OF THE ANNUAL MEETING, AMERICAN ASSOCIATION FOR CANCER RESEARCH, US, vol. 49, 12 April 2008 (2008-04-12), pages 567-568, XP009175475, ISSN: 0197-016X the whole document -----	1-18
Y	WO 2008/119567 A2 (MICROMET AG [DE]; EBERT EVELYN [DE]; MEIER PETRA [DE]; SRISKANDARAJAH) 9 October 2008 (2008-10-09) cited in the application whole document, especially Table 2; Examples 16-18 -----	1-18
Y	BERTUCCI FRANÇOIS ET AL: "Gene expression profiling of human melanoma cell lines with distinct metastatic potential identifies new progression markers", ANTICANCER RESEARCH - INTERNATIONAL JOURNAL OF CANCER RESEARCH AND TREATMENT, INTERNATIONAL INSTITUTE OF ANTICANCER RESEARCH, GR, vol. 27, no. 5A, 1 September 2007 (2007-09-01), pages 3441-3449, XP009154071, ISSN: 0250-7005 whole document, especially the Abstract; Table I; page 3446, left-hand column, lines 44-46 -----	1-18
A	Anonymous: "Anti-CDH19 Product Datasheet", , December 2012 (2012-12), XP055117756, Retrieved from the Internet: URL:https://atlasantibodies.com/print_datasheet/R74953 [retrieved on 2014-05-13] the whole document ----- -/--	1-18

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INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2014/051550

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Anonymous: "CDH19 monoclonal antibody (M01), clone 1G4", , 1 January 2008 (2008-01-01), page 1, XP055117753, Retrieved from the Internet: URL:http://www.abnova.com/protocol_pdf/DS_H00028513-M01.pdf [retrieved on 2014-05-13] the whole document -----	1-18
A	J. NIU ET AL: "Monocyte Chemotactic Protein (MCP)-1 Promotes Angiogenesis via a Novel Transcription Factor, MCP-1-induced Protein (MCPIP)", JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 283, no. 21, 23 May 2008 (2008-05-23), pages 14542-14551, XP055116978, ISSN: 0021-9258, DOI: 10.1074/jbc.M802139200 page 14545, left-hand column, line 15 -----	1-18

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2014/051550

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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		SG 195609 A1	30-12-2013
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