



(86) Date de dépôt PCT/PCT Filing Date: 2004/11/16
(87) Date publication PCT/PCT Publication Date: 2005/06/02
(45) Date de délivrance/Issue Date: 2015/12/29
(85) Entrée phase nationale/National Entry: 2006/05/16
(86) N° demande PCT/PCT Application No.: US 2004/038262
(87) N° publication PCT/PCT Publication No.: 2005/049075
(30) Priorités/Priorities: 2003/11/17 (US60/520,842);
2003/12/24 (US60/532,426)

(51) Cl.Int./Int.Cl. *A61K 47/48* (2006.01),
A61P 35/00 (2006.01), *C07K 16/30* (2006.01),
C07K 14/705 (2006.01)

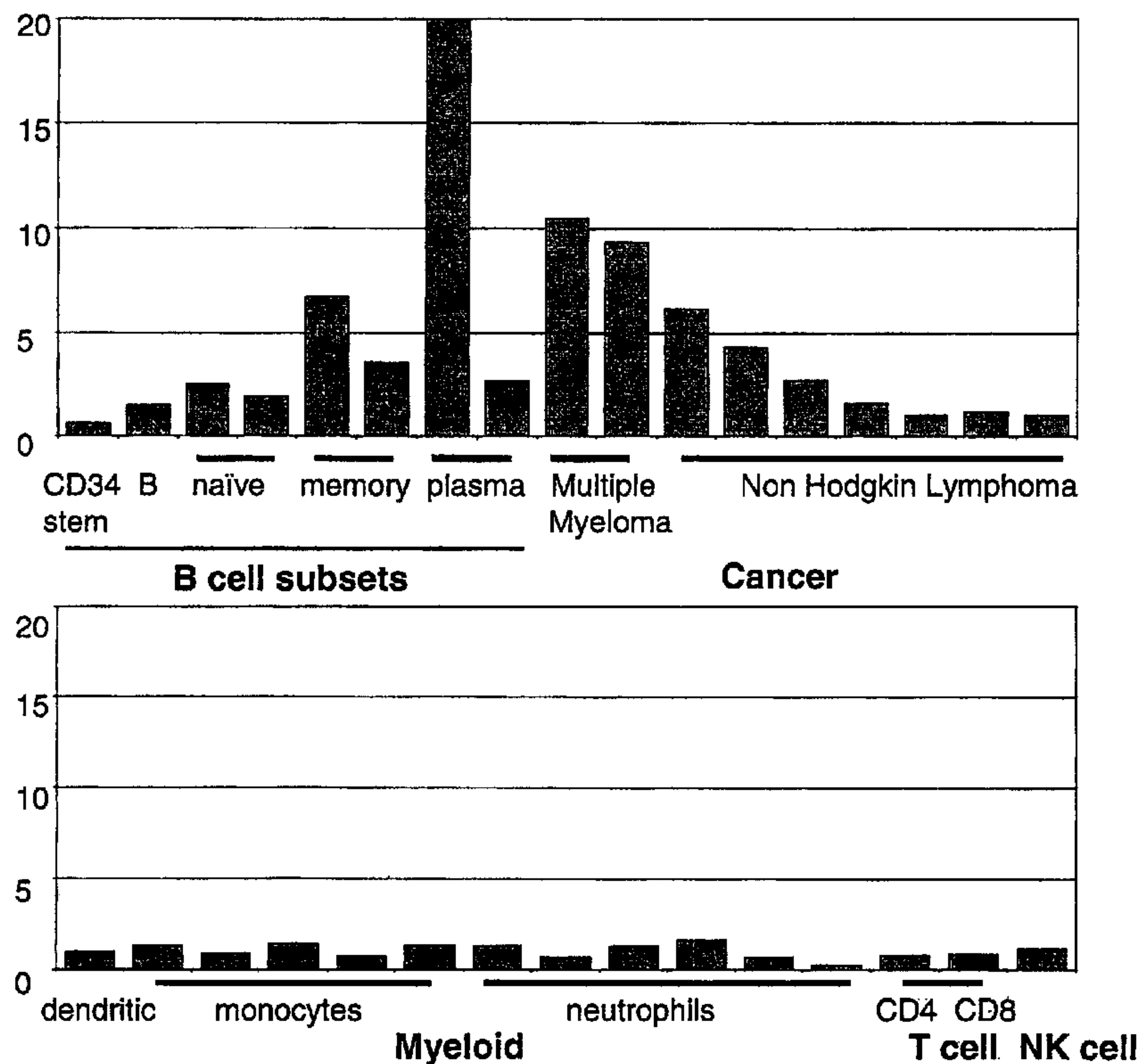
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(54) Titre : COMPOSITIONS ET METHODES DE TRAITEMENT D'UNE TUMEUR D'ORIGINE HEMATOPOIETIQUE
(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR OF HEMATOPOIETIC ORIGIN

TAH015/DNA58721/NAG14



(57) Abrégé/Abstract:

The present invention is directed to compositions of matter useful for the treatment of hematopoietic tumor in mammals and to methods of using those compositions of matter for the same.

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

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
2 June 2005 (02.06.2005)

PCT

(10) International Publication Number
WO 2005/049075 A3

(51) International Patent Classification⁷: **A61K 39/00**,
C07K 14/705

(21) International Application Number:
PCT/US2004/038262

(22) International Filing Date:
16 November 2004 (16.11.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/520,842 17 November 2003 (17.11.2003) US
60/532,426 24 December 2003 (24.12.2003) US

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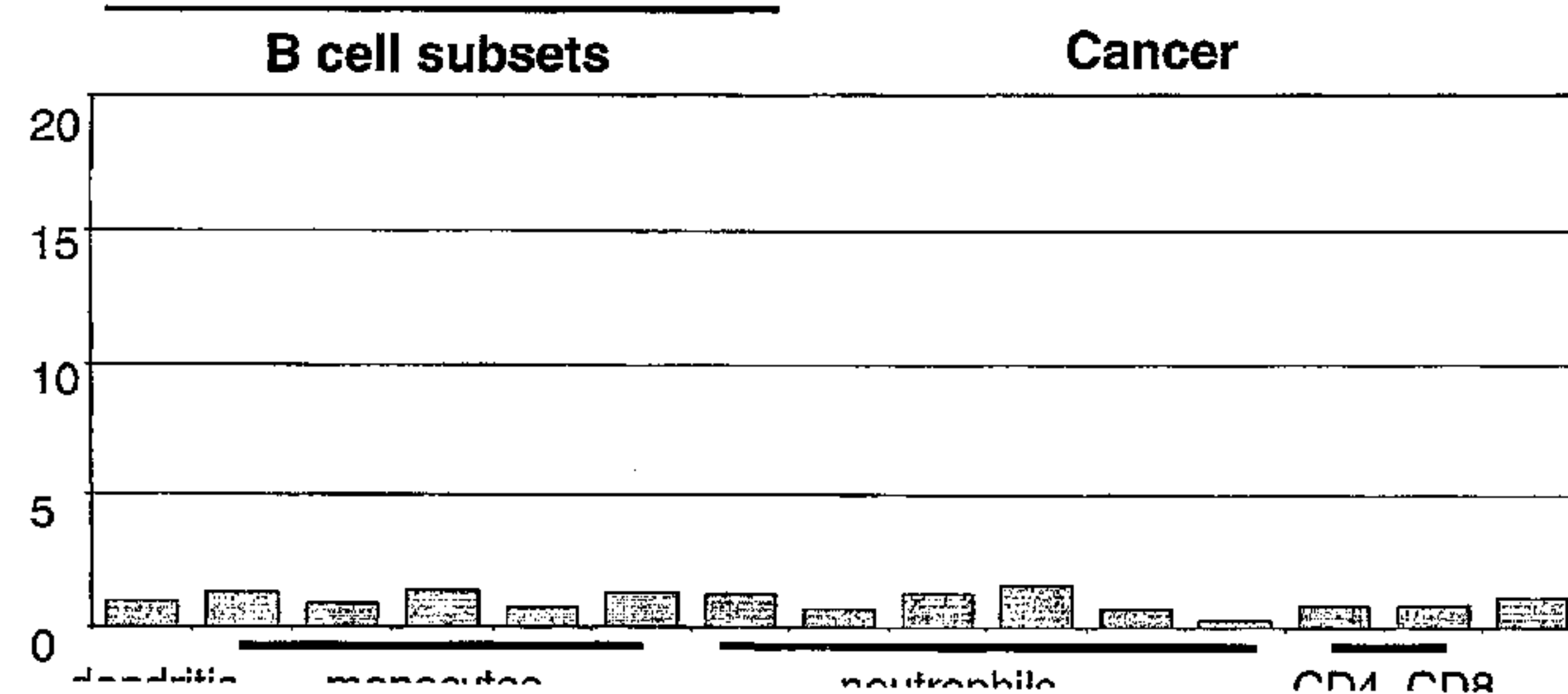
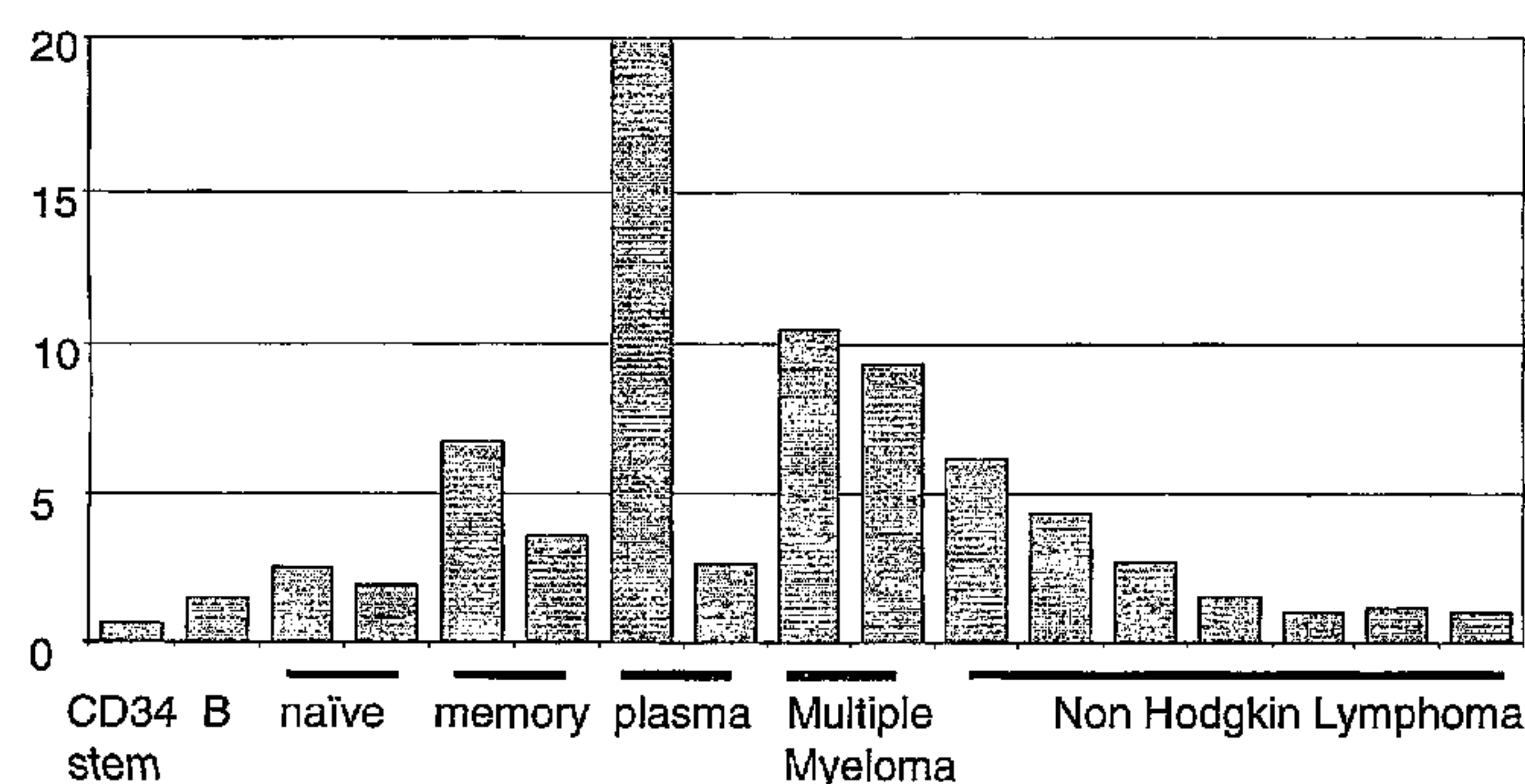
(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,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

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR OF HEMATOPOIETIC ORIGIN

TAHO15/DNA58721/NAG14



(57) Abstract: The present invention is directed to compositions of matter useful for the treatment of hematopoietic tumor in mammals and to methods of using those compositions of matter for the same.

WO 2005/049075 A3

WO 2005/049075 A3



Published:

— *with international search report*

(88) Date of publication of the international search report:

10 November 2005

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WHAT IS CLAIMED IS:

1. An isolated antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:10, with or without its associated signal peptide, wherein said antibody is internalized by a follicular lymphoma cell, a mantle cell lymphoma cell, or a diffuse large cell lymphoma cell expressing said polypeptide and wherein said antibody is conjugated to a growth inhibitory agent or cytotoxic agent, for use to inhibit the growth of the cell that expresses said polypeptide.
2. An isolated antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:10, with or without its associated signal peptide, wherein said antibody is internalized by a follicular lymphoma cell, a mantle cell lymphoma cell, or a diffuse large cell lymphoma cell expressing said polypeptide and wherein said antibody is conjugated to a growth inhibitory agent or cytotoxic agent, for use to formulate a medicament for inhibiting the growth of the cell that expresses said polypeptide.
3. The antibody of claim 1 or 2, wherein the antibody is conjugated to the growth inhibitory agent or cytotoxic agent via a linker.
4. An isolated antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:10, with or without its associated signal peptide, wherein said antibody is internalized by a cell expressing said polypeptide and wherein said antibody is conjugated via a peptidase-sensitive linker to a growth inhibitory agent or cytotoxic agent, for use to inhibit the growth of the cell that expresses said polypeptide.
5. An isolated antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:10, with or without its associated signal peptide, wherein said antibody is internalized by a cell expressing said polypeptide and wherein said antibody is conjugated via a peptidase-sensitive linker to a growth inhibitory agent or cytotoxic agent, for use to formulate a medicament for inhibiting the growth of the cell that expresses said polypeptide.
6. The antibody of any one of claims 1 to 5, wherein said antibody is a monoclonal antibody, or is an antibody fragment, or is a chimeric antibody.

7. The antibody of any one of Claims 1 to 6, wherein the antibody is conjugated to a growth inhibitory agent.
8. The antibody of any one of Claims 1 to 6, wherein the antibody is conjugated to a cytotoxic agent.
9. The antibody of Claim 8, wherein the cytotoxic agent is a toxin, antibiotics, radioactive isotope or nucleolytic enzyme.
10. The antibody of Claim 9, wherein the toxin is a monomethylauristatin (MMAE), maytansinoid or calicheamicin.
11. The antibody of any one of claims 1 to 10, which is produced in bacteria, or which is produced in CHO cells.
12. The antibody of claim 1 or 2, wherein the use is for killing the cell.
13. Use of an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO: 10, with or without its associated signal peptide, for the manufacture of a medicament for inhibiting the growth of a follicular lymphoma cell, a mantle cell lymphoma cell, or a diffuse large cell lymphoma that expresses said polypeptide, wherein said antibody is conjugated to a growth inhibitory agent or cytotoxic agent and is internalized by the cell expressing said polypeptide.
14. Use of an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO: 10, with or without its associated signal peptide, for inhibiting the growth of a follicular lymphoma cell, a mantle cell lymphoma cell, or a diffuse large cell lymphoma that expresses said polypeptide, wherein said antibody is conjugated to a growth inhibitory agent or cytotoxic agent and is internalized by the cell expressing said polypeptide.
15. The use of claim 13 or 14, wherein the antibody is conjugated to the growth inhibitory agent or cytotoxic agent via a linker.

16. Use of an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO: 10, with or without its associated signal peptide, for the manufacture of a medicament for inhibiting the growth of a cell that expresses said polypeptide, wherein said antibody is conjugated via a peptidase-sensitive linker to a growth inhibitory agent or cytotoxic agent and is internalized by the cell expressing said polypeptide.
17. Use of an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO: 10, with or without its associated signal peptide, for inhibiting the growth of a cell that expresses said polypeptide, wherein said antibody is conjugated via a peptidase-sensitive linker to a growth inhibitory agent or cytotoxic agent and is internalized by the cell expressing said polypeptide.
18. The use according to any one of Claims 13 to 17, wherein said antibody is a monoclonal antibody, or is an antibody fragment, or is a chimeric antibody.
19. The use according to any one of Claims 13 to 18, wherein the antibody is conjugated to a growth inhibitory agent.
20. The use according to any one of Claims 13 to 18, wherein the antibody is conjugated to a cytotoxic agent.
21. The use according to Claim 20, wherein the cytotoxic agent is a toxin, antibiotics, radioactive isotope or nucleolytic enzyme.
22. The use according to Claim 21, wherein the toxin is a monomethylauristatin (MMAE), maytansinoid or calicheamicin.
23. The use according to any one of claims 13 to 22, wherein the antibody is produced in bacteria.
24. The use according to any one of claims 13 to 22, wherein the antibody is produced in CHO cells.

25. The use according to claim 13 or 14, wherein the use is for killing the cell.
26. The antibody of claim 10, wherein the toxin is MMAE.
27. The use of claim 22, wherein the toxin is MMAE.
28. The antibody of claim 3, wherein the linker is selected from the group consisting of sulfosuccinimidyl maleimidomethyl cyclohexane carboxylate (SMCC) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP).
29. The use of claim 15, wherein the linker is selected from the group consisting of sulfosuccinimidyl maleimidomethyl cyclohexane carboxylate (SMCC) and N-succinimidyl-4-(2-pyridylthio)pentanoate (SPP).
30. The antibody of claim 28, wherein the linker is SMCC.
31. The use of claim 29, wherein the linker is SMCC.
32. The antibody of claim 28, wherein the linker is SPP.
33. The use of claim 29, wherein the linker is SPP.
34. The antibody of claim 4 or 5, wherein the peptidase-sensitive linker is a valine-citrulline (vc) dipeptide linker.
35. The use of claim 16 or 17, wherein the peptidase-sensitive linker is a valine-citrulline (vc) dipeptide linker.
36. The antibody of claim 34, wherein the antibody is conjugated to monomethylauristatin (MMAE) via the valine-citrulline (vc) dipeptide linker.
37. The use of claim 35, wherein the antibody is conjugated to monomethylauristatin

(MMAE) via the valine-citrulline (vc) dipeptide linker.

38. The antibody of claim 4 or 5, wherein the peptidase-sensitive linker comprises a valine-citrulline (vc) dipeptide linker reagent having a maleimide component and a para-aminobenzylcarbamoyl (PAB) self-immolative component (MC-vc-PAB).

39. The use of claim 16 or 17, wherein the peptidase-sensitive linker comprises a valine-citrulline (vc) dipeptide linker reagent having a maleimide component and a para-aminobenzylcarbamoyl (PAB) self-immolative component (MC-vc-PAB).

40. The antibody claim 38, wherein the antibody is conjugated to monomethylauristatin (MMAE) via the MC-vc-PAB linker.

41. The use of claim 39, wherein the antibody is conjugated to monomethylauristatin (MMAE) via the MC-vc-PAB linker.

FIGURE 1

DNA105250

AGTGTGATGGATATCTGCAGAATTCGCCCTT ATGGCGTTTGACGTCAGCTGCTTCTTTTG
GGTGGTGCTGTTTTCTGCCGGCTGTAAAGTCATCACCTCCTGGGATCAGATGTGCATTGA
GAAAGAAGCCAACAAAACATATAACTGTGAAAATTTAGGTCTCAGTGAAATCCCTGACAC
TCTACCAAACACAACAGAATTTTTGGAATTCAGCTTTAATTTTTTGCCTACAATTCACAA
TAGAACCTTCAGCAGACTCATGAATCTTACCTTTTTGGATTAACTAGGTGCCAGATTAA
CTGGATACATGAAGACACTTTTCAAAGCCATCATCAATTAAGCACACTTGTGTAACTGG
AAATCCCCTGATATTCATGGCAGAAACATCGCTTAATGGGCCCAAGTCACTGAAGCATCT
TTTCTTAATCCAAACGGGAATATCCAATCTCGAGTTTATTCCAGTGCACAATCTGGAAAA
CTTGGAAGCTTGTATCTTGGAAGCAACCATAATTCCTCCATTAAGTTCCCCAAAGACTT
CCCAGCACGGAATCTGAAAGTACTGGATTTTCAGAATAATGCTATACACTACATCTCTAG
AGAAGACATGAGGTCTCTGGAGCAGGCCATCAACCTAAGCCTGAACCTCAATGGCAATAA
TGTTAAAGGTATTGAGCTTGGGGCTTTTGATTCAACGGTCTTCCAAAGTTTGAACCTTGG
AGGAACTCCAAATTTGTCTGTTATATTCAATGGTCTGCAGAACTCTACTACTCAGTCTCT
CTGGCTGGGAACATTTGAGGACATTGATGACGAAGATATTAGTTCAGCCATGCTCAAGGG
ACTCTGTGAAATGTCTGTTGAGAGCCTCAACCTGCAGGAACACCGCTTCTCTGACATCTC
ATCCACCACATTTTCAGTGCTTCACCCAACTCCAAGAATTGGATCTGACAGCAACTCACTT
GAAAGGGTTACCTCTGGGATGAAGGGTCTGAACCTTGCTCAAGAAATTAGTTCTCAGTGT
AAATCATTTTCGATCAATTGTGTCAAATCAGTGCTGCCAATTTCCCCTCCCTTACACACCT
CTACATCAGAGGCAACGTGAAGAACTTCACCTTGGTGTGGCTGCTTGGAGAACTAGG
AAACCTTCAGACACTTGATTAAAGCCATAATGACATAGAGGCTTCTGACTGCTGCAGTCT
GCAACTCAAAAACCTGTCCCCTTGCAAACCTTAAACCTGAGCCACAATGAGCCTCTTGG
TCTCCAGAGTCAGGCATTCAAAGAATGTCCTCAGCTAGAACTCCTCGATTTGGCATTAC
CCGCTTACACATTAATGCTCCACAAAGTCCCTTCCAAAACCTCCATTTCCCTTCAGGTTCT
GAATCTCACTTACTGCTTCCTTGATACCAGCAATCAGCATCTTCTAGCAGGCCTACCAGT
TCTCCGGCATCTCAACTTAAAAGGGAATCACTTTCAAGATGGGACTATCACGAAGACCAA
CCTACTTCAGACCGTGGGCAGCTTGGAGGTTCTGATTTTGTCTCTTGTGGTCTCCTCTC
TATAGACCAGCAAGCATTCACAGCTTGGGAAAAATGAGCCATGTAGACTTAAGCCACAA
CAGCCTGACATGCGACAGCATTGATTCTCTTAGCCATCTTAAGGGAATCTACCTCAATCT
GGCTGCCAACAGCATTAACATCATCTCACCCCGTCTCCTCCCTATCTTGTCCCAGCAGAG
CACCATTAAATTTAAGTCATAACCCCTGGACTGCACTTGCTCGAATATTCATTTCTTAAC
ATGGTACAAAGAAAACCTGCACAACTTGAAGGCTCGGAGGAGACCACGTGTGCAAACCC
GCCATCTCTAAGGGGAGTTAAGCTATCTGATGTCAAGCTTTCCTGTGGGATTACAGCCAT
AGGCATTTTCTTTCTCATAGTATTTCTATTATTGTTGGCTATTCTGCTATTTTTTGCAGT
TAAATACCTTCTCAGGTGGAATACCAACACATTTAGTGCTGAAGGTTTCCAGAGAA

FIGURE 2A

DNA105250

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105250

><subunit 1 of 1, 661 aa, 1 stop

><MW: 74165, pI: 6.34, NX(S/T): 11

MAFDVSCFFWVVLFSAGCKVITSWDQMCIEKEANKTYNCENLGLSEIPDTLPNTTEFLEF
SFNFLPTIHNRTFSRLMNLTFDLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETS
LNGPKSLKHLFLIQTGISNLEFIPVHNLENLESYLGSNHISSIKFPKDFPARNLKVLDF
QNNAIHYISREDMRSLEQAINLSLNFNGNNVKGIELGAFDSTVFQSLNFGGTPNLSVIFN
GLQNSTTQSLWLGTFFEDIDDEDISSAMLKGLCEMSVESLNLQEHFSDISSSTTFQCFTQL
QELDLTATHLKGLPSGMKGLNLLKKLVLSVNHFDQLCQISAANFPSLTHLYIRGNVKKLH
LGVGCLEKLGNLQTLDSLHNDIEASDCCSLQLKNLSHLQTLNLSHNEPLGLQSQAFKECP
QLELLDLAFTRLHINAPQSPFQNLHFLQVLNLTYCFLDTSNQHLLAGLPVLRHLNLKGNH
FQDGTITKTNLLQTVGSLEVLILSSCGLLSIDQQAFHSLGKMSHVLDLSHNSLTCDSDSL
SHLKGIYLNLAANSINIISPRLLPILSQQSTINLSHNPLDCTCSNIHFLTWYKENLHKLE
GSEETTCANPPSLRGVKLSDVKLSCGITAIGIFFLIVFLLLLAILLFFAVKYLLRWKYQH
I

Signal sequence.

amino acids 1-18

Transmembrane domain.

amino acids 489-509, 628-648

Leucine Rich Repeat.

amino acids 54-77, 78-101, 102-125, 126-149, 150-171, 174-197, 275-298, 299-321, 322-348, 371-396, 397-420, 421-445, 446-469, 470-493, 497-520, 521-544

Leucine Rich Repeat C-terminal Domain.

amino acids 577-626

N-glycosylation site.

amino acids 34-37, 53-56, 70-73, 78-81, 201-204, 234-237, 244-247, 394-397, 401-405, 451-454, 573-576

Protein kinase C phosphorylation site.

amino acids 126-128, 163-165, 559-561, 612-614

Casein kinase II phosphorylation site.

amino acids 22-25, 80-83, 138-141, 189-192, 254-257, 378-381, 404-407, 523-526

N-myristoylation site.

amino acids 213-218, 217-222, 230-235, 241-246, 312-317, 370-375, 545-560, 601-606, 615-620

FIGURE 2B

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 8-18

Leucine zipper pattern.
amino acids 44-65, 450-471

CAGCAGTAGGCCCTTGCCCTCAGATCCAAGGTCACTCGGAAGAGGCCATGTCTACCCCTCAAT
GACACTCATGGAGGAAATGCTGAGAGAAGCATTGAGATGCATGACACAAGGTAAGACTGC
CAAAAATCTTGTTCTTGCTCTCCTCATTTTGTATTTGTTTTATTTTTAGGAGTTTTGAG
AGCAAAATGACAACACCCAGAAATTCAGTAAATGGGACTTTCCCGGCAGAGCCAATGAAA
GGCCCTATTGCTATGCAATCTGGTCCAAAACCACTCTTCAGGAGGATGTCTTCACTGGTG
GGCCCCACGCAAAGCTTCTTCATGAGGGAATCTAAGACTTTGGGGGCTGTCCAGATTATG
AATGGGCTCTTCCACATTGCCCTGGGGGGTCTTCTGATGATCCCAGCAGGGATCTATGCA
CCCATCTGTGTGACTGTGTGGTACCCTCTCTGGGGAGGCATTATGTATATTATTTCCGGA
TCACTCCTGGCAGCAACGGAGAAAACTCCAGGAAGTGTTTGGTCAAAGGAAAAATGATA
ATGAATTCATTGAGCCTCTTTGCTGCCATTTCTGGAATGATTCTTTCAATCATGGACATA
CTTAATATTAAAATTTCCCATTTTTTTAAAAATGGAGAGTCTGAATTTTATTAGAGCTCAC
ACACCATATATTAAACATATACAACCTGTGAACCAGCTAATCCCTCTGAGAAAACTCCCCA
TCTACCCAATACTGTTACAGCATACAATCTCTGTTCTTGGGCATTTTGTGAGTGATGCTG
ATCTTTGCCTTCTTCCAGGAACCTGTAAATAGCTGGCATCGTTGAGAATGAATGGAAAAGA
ACGTGCTCCAGACCCAAATCTAACATAGTTCTCCTGTCAGCAGAAGAAAAAAGAACAG
ACTATTGAAATAAAAGAAGAAGTGGTTGGGCTAACTGAAACATCTTCCCAACCAAAGAAT
GAAGAAGACATTGAAATTATTCCAATCCAAGAAGAGGAAGAAGAAGAAACAGAGACGAAC
TTTCCAGAACCTCCCCAAGATCAGGAATCCTCACCAATAGAAAATGACAGCTCTCCT TAA
GTGATTTCTTCTGTTTTCTGTTTCCTTTTTTAAACATTAGTGTTTCATAGCTTCCAAGAGA
CATGCTGACTTTCATTTCTTGAGGTACTCTGCACATACGCACCACATCTCTATCTGGCCT
TTGCATGGAGTGACCATAGCTCCTTCTCTCTTACATTGAATGTAGAGAATGTAGCCATTG
TAGCAGCTTGTGTTGTACGCTTCTTCTTTTGAGCAACTTCTTACACTGAAGAAAGGCA
GAATGAGTGCTTCAGAATGTGATTTCTACTAACCTGTTTCTTGGATAGGCTTTTTTAGTA
TAGTATTTTTTTTTTGTCATTTTCTCCATCAACAACCAGGGAGACTGCACCTGATGGAAAA
GATATATGACTGCTTCATGACATTCCTAAACTATCTTTTTTTTTTATTCCACATCTACGTTT
TTGGTGAGTCCCTTTTGCATCATTGTTTTAAGGATGATAAAAAAAAAATAACAACCTAGGG
ACAATACAGAACCCATTCCATTTATCTTTCTACAGGGCTGACATTGTGGCACATTCTTAG
AGTTACCACACCCCATGAGGGAAGCTCTAAATAGCCAACACCCATCTGTTTTTTGTAAAA
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AGAAAATGCCACCATGAGGTGCCCAAATTTCAAATAATAATTAACATTTAGTTATATTTA
TAATTTCCAGATGACAAAGTATTTTCATCAAATAACTTCATTTGATGTTCCATGATCAAGA
AAGAATCCCTATCTCTATTTTACAAGTAATTCAAAGAGGCCAAATAACTTGTAACAAGA
AAAGGTAACCTGTCAACAGTCATAACTAGTAATTATGAGAGCCTTGTTTTATAACCAGGT
CTTCTTACTCAAATCCTGTGATGTTTGAATAACCAAATTGTCTCTCCAATGTCTGCATA
AACTGTGAGAGCCAAGTCAACAGCTTTTATCAAGAATTTACTCTCTGACCAGCAATAAAC
AAGCACTGAGAGACACAGAGAGCCAGATTCAGATTTTACCCATGGGGATAAAAAGACTCA
GACTTTCACCACATTTGGAAAACCTACTTGTCATCATAAATATATAATAACTGGTAGTTTAT
ATGAAGCAGACACTAAGTGCTATAGACACTCTCAGAATATCATACTTGGAACAATGTAA
TTAAAATGCCGAATCTGAGTCAACAGCTGCCCTACTTTTCAATTGAGATATACTAGTACC
TTACCTAGAAATAATGTTAACCTAGGGTGAAGTCACTATAATCTGTAGTCTATTATTTGG
GCATTTGCTACATGATGAGTGCTGCCAGATTGTGGCAGGTAAAGAGACAATGTAATTTGC
ACTCCCTATGATATTTCTACATTTTTTAGCGACCACTAGTGGAAGACATTCCCCAAAATTA
GAAAAAAGGAGATAGAAGATTTCTGTCTATGTAAAGTTCTCAAAATTTGTTCTAAATTA

FIGURE 4

DNA150004

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150004

><subunit 1 of 1, 297 aa, 1 stop

><MW: 33077, pI: 5.10, NX(S/T): 3

MTTPRNSVNGTFPAEPMKGPIAMQSGPKPLFRMSSLVGPTQSFFMRESKTLGAVQIMNG
LFHIALGGLLMIPAGIYAPICVTWYPLWGGIMYIISGSLLAATEKNSRKCLVKGKMIMN
SLSLFAAISGMILSIMDILNIKISHFLKMESLNFIRAHTPYINIYNCEPANPSEKNPST
QYCYSIQSLFLGILSVMLIFAFFQELVIAGIVENEWKRTCSPKSNIVLLSABEEKKEQTI
EIKKEEVVGLTETSSQPKNEEDIEIIPIQEEEEETETNFPEPPQDQESSPIENDSSP

Transmembrane domain.

amino acids 56-76, 82-102, 118-138, 187-207

CD 20/IgE Fc Receptor Beta Subunit Family.

amino acids 58-224.

N-glycosylation site.

amino acids 9-12, 293-296

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 32-35

Protein kinase C phosphorylation site.

amino acids 3-5, 104-106, 108-110, 173-175

Casein kinase II phosphorylation site.

amino acids 134-137, 231-234, 289-292

N-myristoylation site.

amino acids 10-15, 98-103, 130-135, 210-215, 248-253

FIGURE 5

DNA 182432

GTTGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGGTCCTC ATGCTGCTGTG
GTCATTGCTGGTCATCTTTGATGCAGTCACTGAACAGGCAGATTCGCTGACCCTTGTGGC
GCCCTCTTCTGTCTTCGAAGGAGACAGCATCGTTCTGAAATGCCAGGGAGAACAGAACTG
GAAAATTGAGAAGATGGCTTACCATAAGGATAACAAAGAGTTATCTGTTTTCAAAAAATT
CTCAGATTTCTTATCCAAAGTGCAGTTTTAAGTGACAGTGGTAACTATTTCTGTAGTAC
CAAAGGACAACTCTTTCTCTGGGATAAACTTCAAATATAGTAAAGATAAAAGTCCAAGA
GCTCTTTCAACGTCCTGTGCTGACTGCCAGCTCCTTCCAGCCCATCGAAGGGGGTCCAGT
GAGCCTGAAATGTGAGACCCGGCTCTCTCCACAGAGGTTGGATGTTCAACTCCAGTTCTG
CTTCTTCAGAGAAAACCAGGTCCTGGGGTCAGGCTGGAGCAGCTCTCCGGAGCTCCAGAT
TTCTGCCGTGTGGAGTGAAGACACAGGGTCTTACTGGTGCAAGGCAGAAACGGTGACTCA
CAGGATCAGAAAACAGAGCCTCCAATCCCAGATTCACGTGCAGAGAATCCCCATCTCTAA
TGTAAGCTTGGAGATCCGGGCCCCCGGGGGACAGGTGACTGAAGGACAAAACTGATCCT
GCTCTGCTCAGTGGCTGGGGGTACAGGAAATGTCACATTCTCCTGGTACAGAGAGGCCAC
AGGAACCAGTATGGGAAAGAAAACCCAGCGTTCCCTGTCAGCAGAGCTGGAGATCCCAGC
TGTGAAAGAGAGTGATGCCGGCAAATATTACTGTAGAGCTGACAACGGCCATGTGCCTAT
CCAGAGCAAGGTGGTGAATATCCCTGTGAGAATTCCAGTGTCTCGCCCTGTCCTCACCT
CAGGTCTCCTGGGGCCCAGGCTGCAGTGGGGGACCTGCTGGAGCTTCACTGTGAGGCCCT
GAGAGGCTCTCCCCCAATCTTGTACCAATTTTATCATGAGGATGTCACCCTTGGGAACAG
CTCGGCCCCCTCTGGAGGAGGGGCCTCCTTCAACCTCTCTTTGACTGCAGAACATTCTGG
AACTACTCCTGTGAGGCCAACAACGGCCTGGGGGCCAGTGCAGTGAGGCAGTGCCAGT
CTCCATCTCAGGACCTGATGGCTATAGAAGAGACCTCATGACAGCTGGAGTTCTCTGGGG
ACTGTTTGGTGTCTTGGTTTCACTGGTGTGCTTTGCTGTTGTATGCCTTGTTCCACAA
GATATCAGGAGAAAGTTCTGCCACTAATGAACCCAGAGGGGCTTCCAGGCCAAATCCTCA
AGAGTTCACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAGTGTATGTCAA
TGTGGGCTCTGTAGATGTGGATGTGGTTTATTCTCAGGTCTGGAGCATGCAGCAGCCAGA
AAGCTCAGCAAACATCAGGACACTTCTGGAGAACAAGGACTCCCAAGTCATCTACTCTTC
TGTGAAGAAATCA TAACACTTGGAGGAATCAGAAGGGAAGATCAACAGCAAGGATGGGGC
ATCATTAAGACTTGCTATAAAACCTTATGAAAATGCTTGAGGCTTATCACCTGCCACAGC
CAGAACGTGCCTCAGGAGGCACCTCCTGTCATTTTTGTCTGATGATGTTTCTTCTCCAA
TATCTTCTTTTACCTATCAATATTCATTGAACTGCTGCTACATCCAGACACTGTGCAAAT
AAATTATTTCTGCTACCTTCAAAAAAAAAAAAAAAAAAAAAATGCAG

FIGURE 6A

DNA 182432

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA182432
><subunit 1 of 1, 508 aa, 1 stop
><MW: 55542, pI: 6.30, NX(S/T): 5

MLLWSLLVIFDAVTEQADSLTLVAPSSVFEGDSIVLKCQGEQNWKIQKMAYHKDNKELSV
FKKFSDFLIQSAVLSDSGNYFCSTKGQLFLWDKTSNIVKIKVQELFQRPVLTASSFQPIE
GGPVSLKCETRLSPQRLDVQLQFCFFRENQVLGSGWSSSPQLISAVWSED TGSYWCKAE
TVTHRIRKQSLQSQIHVQRIPISNVSLERAPGGQVTEGQKLILLCSVAGGTGNVTFSWY
REATGTSMGKKTQRSLSAELEIPAVKESDAGKYICRADNGHVPIQSKVVNIPVRIPVSRP
VLTLRSPGAQAQAAVGDLLLELHCEALRGSPPILYQFYHEDVTLGNSSAPSGGGASFNLSLTA
EHSGNYSCEANGLGAQCSEAVPVSISGPDGYRRDLMTAGVLWGLFGVLGFTGVALLLYA
LFHKISGESSATNEPRGASRPNPQEFTYSSPTPDMEELQPVYVNVGSVDVDVVYSQVWSM
QQPESSANIRTLLENKDSQVIYSSVKKS

Signal sequence.

amino acids 1-14.

Transmembrane domain.

amino acids 400-420.

Immunoglobulin domain.

amino acids 17-84, 121-179, 219-277, 314-370.

N-glycosylation site.

amino acids 204-207, 234-237, 343-346, 355-358, 365-368

Glycosaminoglycan attachment site.

amino acids 348-351

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 62-65, 187-190

Protein kinase C phosphorylation site.

amino acids 83-85, 125-127, 183-185, 252-254, 303-305, 504-506

Casein kinase II phosphorylation site.

amino acids 27-30, 158-161, 387-390, 491-494

Tyrosine kinase phosphorylation site.

amino acids 266-273

N-myristoylation site.

amino acids 78-83, 121-126, 153-158, 173-178, 213-218, 230-235, 245-250, 308-313, 349-354, 351-356, 364-369, 375-360, 400-405

FIGURE 6B

Amidation site.

amino acids 248-251

FIGURE 7

DNA225785

TGCTGCAACTCAAAC TAACCAACCCACTGGGAGAAG ATG CCTGGGGGTCCAGGAGTCCTC
CAAGCTCTGCCTGCCACCATCTTCCTCCTCTTCCTGCTGTCTGCTGTCTACCTGGGCCCT
GGGTGCCAGGCCCTGTGGATGCACAAGGTCCCAGCATCATTGATGGTGAGCCTGGGGGAA
GACGCCCACCTTCCAATGCCCCGCACAATAGCAGCAACAACGCCAACGTCACCTGGTGGCGC
GTCCTCCATGGCAACTACACGTGGCCCCCTGAGTTCTTGGGCCCGGGCGAGGACCCCAAT
GGTACGCTGATCATCCAGAATGTGAACAAGAGCCATGGGGGCATATACGTGTGCCGGGTC
CAGGAGGGCAACGAGTCATAACCAGCAGTCCTGCGGCACCTACCTCCGCGTGCGCCAGCCG
CCCCCAGGCCCTTCCTGGACATGGGGGAGGGCACCAAGAACCGAATCATCACAGCCGAG
GGGATCATCCTCCTGTTCTGCGCGGTGGTGCCTGGGACGCTGCTGCTGTTTCAGGAAACGA
TGGCAGAACGAGAAGCTCGGGTTGGATGCCGGGGATGAATATGAAGATGAAAACCTTTAT
GAAGGCCTGAACCTGGACGACTGCTCCATGTATGAGGACATCTCCCGGGGCCTCCAGGGC
ACCTACCAGGATGTGGGCAGCCTCAACATAGGAGATGTCCAGCTGGAGAAGCCG TGA CAC
CCCTACTCCTGCCAGGCTGCCCCCGCCTGCTGTGCACCCAGCTCCAGTGTCTCAGCTCAC
TTCCCTGGGACATTCTCCTTTCAGCCCTTCTGGGGGCTTCCTTAGTCATATTCCCCCAGT
GGGGGGTGGGAGGGTAACCTCACTCTTCTCCAGGCCAGGCCTCCTTGGACTCCCCTGGGG
GTGTCCCACCTCTTCTTCCCTCTAAACTGCCCCACCTCCTAACCTAATCCCCACGCCCCGC
TGCCTTTCCAGGCTCCCCCTACCCAGCGGGTAATGAGCCCTTAATCGCTGCCTCTAGGG
GAGCTGATTGTAGCAGCCTCGTTAGTGTACCCCCCTCCTCCCTGATCTGTCAGGGCCACT
TAGTGATAATAAATTCTTCCCAACTGC

FIGURE 8

DNA225785

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA225785
><subunit 1 of 1, 226 aa, 1 stop
><MW: 25038, pI: 4.91, NX(S/T): 6

MPGGPGVLQALPATIFLLFLLSAVYLGPGCQALWMHKVPASLMVSLGEDAHFQCPHNSSN
NANVTWWRVLHGNYTWPPEFLGPGEDPNGTLIIQNVNKSHPGGIYVCRVQEGNESYQQSCG
TYLRVRQPPPRPFLDMGEGTKNRIITAEGIILLFCVVPGTLLLFRKRWQNEKLGLDAGD
EYEDENLYEGLNLDDCSMYEDISRGLQGTQDVGSLNIGDVQLEKP

Signal sequence.

amino acids 1-29.

Transmembrane domain.

amino acids 143-163.

Immunoreceptor tyrosine-based activation motif.

amino acids 185-205.

N-glycosylation site.

amino acids 57-60, 63-66, 73-76, 88-91, 97-100, 112-115

Casein kinase II phosphorylation site.

amino acids 45-48, 197-200, 209-212.

N-myristoylation site.

amino acids 6-11, 102-107, 175-180, 205-210.

Ribosomal protein S2 signature 1.

amino acids 16-27.

FIGURE 9

DNA225786

CAGGGGACAGGCTGCAGCCGGTGCAGTTACACGTTTTCTCCAAGGAGCCTCGGACGTTG
TCACGGGTTTGGGGTCGGGGACAGAGCAGTGACCATGGCCAGGCTGGCGTTGTCTCCTGT
GCCCAGCCACTGGATGGTGGCGTTGCTGCTGCTCTCAGCTGAGCCAGTACCAGCAGC
CAGATCGGAGGACCGGTACCGGAATCCCAAAGGTAGTGCTTGTTGCGGGATCTGGCAGAG
CCCACGTTTTCATAGCCAGGAAACGGGGCTTCACGGTGAAAATGCACTGCTACATGAACAG
CGCCTCCGGCAATGTGAGCTGGCTCTGGAAGCAGGAGATGGACGAGAATCCCCAGCAGCT
GAAGCTGGAAAAGGGCCGCATGGAAGAGTCCCAGAACGAATCTCTCGCCACCCTCACCAT
CCAAGGCATCCGGTTTGAGGACAATGGCATCTACTTCTGTGTCAGCAGAAGTGCAACAACAC
CTCGGAGGTCTACCAGGGCTGCGGCACAGAGCTGCGAGTCATGGGATTCAGCACCTTGGC
ACAGCTGAAGCAGAGGAACACGCTGAAGGATGGTATCATCATGATCCAGACGCTGCTGAT
CATCCTCTTCATCATCGTGCCTATCTTCCTGCTGCTGGACAAGGATGACAGCAAGGCTGG
CATGGAGGAAGATCACACCTACGAGGGCCTGGACATTGACCAGACAGCCACCTATGAGGA
CATAGTGACGCTGCGGACAGGGGAAGTGAAGTGGTCTGTAGGTGAGCACCAGGCCAGGA
GTGAGAGCCAGGTGCGCCCATGACCTGGGTGCAGGCTCCCTGGCCTCAGTGACTGCTTCG
GAGCTGCCTGGCTCATGGCCCAACCCCTTTCCTGGACCCCCCAGCTGGCCTCTGAAGCTG
GCCACCCAGAGCTGCCATTTGTCTCCAGCCCCTGGTCCCCAGCTCTTGCCAAAGGGCCTG
GAGTAGAAGGACAACAGGGCAGCAACTTGGAGGGAGTTCTCTGGGGATGGACGGGACCCA
GCCTTCTGGGGGTGCTATGAGGTGATCCGTCCCCACACATGGGATGGGGGAGGCAGAGAC
TGGTCCAGAGCCCGCAAATGGACTCGGAGCCGAGGGCCTCCAGCAGAGCTTGGGAAGGG
CCATGGACCCAACTGGGCCCCAGAAGAGCCACAGGAACATCATTCCTCTCCCGCAACCAC
TCCCACCCAGGGAGGCCCTGGCCTCCAGTGCCTTCCCCCGTGGAATAAACGGTGTGTCC
TGAGAAACCA

FIGURE 10

DNA225786

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA225786

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26048, pI: 5.86, NX(S/T): 4

MARLALSPVPSHWMVALLLLLSAEPVPAARSEDYRNPKGSA CSRIWQSPRFIARKRGFT
VKMH CYMNSASGNVSWLWKQEMDENPQQLKLEKGRMEESQNESLATLTIQGIRFEDNGIY
FCQQKCNNTSEVYQGCGTEL RVMGFSTLAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLL
LDKDDSKAGMEEDHTYEGLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE

Signal sequence.

amino acids 1-28.

Transmembrane domain.

amino acids 5-25, 159-179.

Immunoglobulin domain.

amino acids 58-124.

Immunoreceptor tyrosine-based activation motif.

amino acids 193-213.

N-glycosylation site.

amino acids 73-76, 101-104, 127-130, 128-131.

Protein kinase C phosphorylation site.

amino acids 49-51, 60-62, 156-158, 212-214.

Casein kinase II phosphorylation site.

amino acids 99-102, 156-159, 206-209, 221-224.

Tyrosine kinase phosphorylation site.

amino acids 113-120.

N-myristoylation site.

amino acids 40-45, 118-123.

FIGURE 11A

DNA225875

GCCCTCCCAGAGCTGCCGGACGCTCGCGGGTCTCGGAACGCATCCCGCCGCGGGGGCTTC
GGCCGTGGCATGGGCGCCGCGGGCCTGCTCGGGGTTTTCTTGGCTCTCGTCGCACCGGGG
GTCCTCGGGATTTCTTGTGGCTCTCCTCCGCCTATCCTAAATGGCCGGATTAGTTATTAT
TCTACCCCCATTGCTGTTGGTACCGTGATAAGGTACAGTTGTTTCAGGTACCTTCCGCCTC
ATTGGAGAAAAAGTCTATTATGCATAACTAAAGACAAAGTGGATGGAACCTGGGATAAA
CCTGCTCCTAAATGTGAATATTTCAATAAATATTCTTCTTGCCCTGAGCCCATAGTACCA
GGAGGATACAAAATTAGAGGCTCTACACCCTACAGACATGGTGATTCTGTGACATTTGCC
TGTA AAACCAACTTCTCCATGAACGGAAACAAGTCTGTTTGGTGTCAAGCAAATAATATG
TGGGGGCCGACACGACTACCAACCTGTGTAAGTGTTTTCCCTCTCGAGTGTCCAGCACTT
CCTATGATCCACAATGGACATCACACAAGTGAGAATGTTGGCTCCATTGCTCCAGGATTG
TCTGTGACTTACAGCTGTGAATCTGGTTACTTGCTTGTGAGAAAAGATCATTAACTGT
TTGTCTTCGGGAAAATGGAGTGCTGTCCCCCCCACATGTGAAGAGGCACGCTGTAAATCT
CTAGGACGATTTCCCAATGGGAAGGTAAAGGAGCCTCCAATTCTCCGGGTTGGTGTA ACT
GCAA ACTTTTTCTGTGATGAAGGGTATCGACTGCAAGGCCACCTTCTAGTCGGTGTGTA
ATTGCTGGACAGGGAGTTGCTTGGACCAAAATGCCAGTATGTGAAGAAATTTTTTGCCCA
TCACCTCCCCCTATTCTCAATGGAAGACATATAGGCAACTCACTAGCAAATGTCTCATAT
GGAAGCATAGTCACTTACACTTGTGACCCGGACCCAGAGGAAGGAGTGA ACTTCATCCTT
ATTGGAGAGAGCACTCTCCGTTGTACAGTTGATAGTCAGAAGACTGGGACCTGGAGTGGC
CCTGCCCCACGCTGTGA ACTTTCTACTTCTGCGGTTCA GTGTCCACATCCCCAGATCCTA
AGAGGCCGAATGGTATCTGGGCAGAAAGATCGATATACTATAACGACACTGTGATATTT
GCTTGCATGTTTGGCTTCACCTTGAAGGGCAGCAAGCAAATCCGATGCAATGCCCAAGGC
ACATGGGAGCCATCTGCACCAGTCTGTGAAAAGGAATGCCAGGCCCTCCTAACATCCTC
AATGGGCAAAAGGAAGATAGACACATGGTCCGCTTTGACCCTGGAACATCTATAAAATAT
AGCTGTAACCTGGCTATGTGCTGGTGGGAGAAGAATCCATACAGTGTACCTCTGAGGGG
GTGTGGACACCCCCCTGTACCCCAATGCAAAGTGGCAGCGTGTGAAGCTACAGGAAGGCAA
CTCTTGACAAAACCCAGACCAATTTGTTAGACCAGATGTCAACTCTTCTTGTGGTGAA
GGGTACAAGTTAAGTGGGAGTGTTTATCAGGAGTGTCAAGGCACAATTCCTTGGTTTATG
GAGATTCGTCTTTGTAAAGAAATCACCTGCCACCACCCCCCTGTTATCTACAATGGGGCA
CACACCGGGAGTTCTTAGAAGATTTTCCATATGGAACACGGTCACTTACACATGTAAC
CCTGGGCCAGAAAGAGGAGTGGAATTCAGCCTCATTTGGAGAGAGCACCATCCGTTGTACA
AGCAATGATCAAGAAAGAGGCACCTGGAGTGGCCCTGCTCCCCTATGTAAACTTTCCCTC
CTTGCTGTCCAGTGCTCACATGTCCATATTGCAAATGGATAACAAGATATCTGGCAAGGAA
GCCCCATATTTCTACAATGACACTGTGACATTCAAGTGTTATAGTGGATTTACTTTGAAG
GGCAGTAGTCAGATTCGTTGCAAAGCTGATAACACCTGGGATCCTGAAATACCAGTTTGT
GAAAAGAAACATGCCAGCATGTGAGACAGAGTCTTCAAGAACTTCCAGCTGGTTACGT
GTGGAGCTAGTTAATACGTCCTGCCAAGATGGGTACCAGTTGACTGGACATGCTTATCAG
ATGTGTCAAGATGCTGAAAATGGAATTTGGTTCAAAAAGATTCCACTTTGTAAAGTTATT
CACTGTCACCCCTCCACCAGTGATTGTCAATGGGAAGCACACAGGGATGATGGCAGAAAAC
TTTCTATATGGAATGAAGTCTCTTATGAATGTGACCAAGGATTCTATCTCCTGGGAGAG
AAAAAATTGCAGTGCAGAAAGTGATTCTAAAGGACATGGATCTTGGAGCGGGCCTTCCCCA
CAGTGCTTACGATCTCCTCCTGTGACTCGCTGCCCTAATCCAGAAGTCAAACATGGGTAC
AAGCTCAATAAAACACATTCTGCATATTTCCACAATGACATAGTGTATGTTGACTGCAAT

FIGURE 11B

CCAGGTGTGCCAACTTGTATGAAAAAGCCTTCATAGGGTGTCCACCTCCGCCTAAGACC
CCTAACGGGAACCATACTGGTGGAAACATAGCTCGATTTTCTCCTGGAATGTCAATCCTG
TACAGCTGTGACCAAGGCTACCTGCTGGTGGGAGAGGCACTCCTTCTTTGCACACATGAG
GGAACCTGGAGCCAACCTGCCCCCTCATTGTAAAGAGGTAAACTGTAGCTCACCAGCAGAT
ATGGATGGAATCCAGAAAGGGCTGGAACCAAGGAAAATGTATCAGTATGGAGCTGTTGTA
ACTCTGGAGTGTGAAGATGGGTATATGCTGGAAGGCAGTCCCCAGAGCCAGTGCCAATCG
GATCACCAATGGAACCCTCCCCTGGCGGTTTGCAGATCCCGTTCACTTGCTCCTGTCCTT
TGTGGTATTGCTGCAGGTTTGATACTTCTTACCTTCTTGATTGTCATTACCTTATACGTG
ATATCAAAACACAGAGAACGCAATTATTATACAGATACAAGCCAGAAAGAAGCTTTTCAT
TTAGAAGCACGAGAAGTATATTCTGTTGATCCATAACAACCCAGCCAGC TGATCAGAAGAC
AAACTGGTGTGTGCCTCATTTGCTTGGAAATTCAGCGGAATATTGATTAGAAAGAACTGCT
CTAATATCAGCAAGTCTCTTTATATGGCCTCAAGATCAATGAAATGATGTCATAAGCGAT
CACTTCCTATATGCACTTATTCTCAAGAAGAACATCTTTATGGTAAAGATGGGAGCCCAG
TTTCACTGCCATATACTCTTCAAGGACTTTCTGAAGCCTCACTTATGAGATGCCTGAAGC
CAGGCCATGGCTATAAACAATTACATGGCTCTAAAAAGTTTTGCCCTTTTAAAGGAAGGC
ACTAAAAGAGCTGTCCTGGTATCTAGACCCATCTTCTTTTGGAAATCAGCATACTCAAT
GTACTATCTGCTTTTGGTTATAATGTGTTTTTAATTATCTAAAGTATGAAGCATTTTCT
GGGGTTATGATGGCCTTACCTTTATTAGGAAGTATGGTTTTATTTTGATAGTAGCTTCCT
CCTCTGGTGGTGTAAATCATTTTCACTTTTACCTTACTGTTTGAGTTTCTCTCACATTAC
TGTATATACTTTGCCTTTCCATAATCACTCAGTGATTGCAATTTGCACAAGTTTTTTTAA
ATTATGGGAATCAAGATTTAATCCTAGAGATTTGGTGTACAATTCAGGCTTTGGATGTTT
CTTTAGCAGTTTTGTGATAAGTTCTAGTTGCTTGTAATAATTTCACTTAATAATGTGTACA
TTAGTCATTCAATAAATTGTAATTGTAAAGAAAA

FIGURE 12A

DNA225875

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA225875
><subunit 1 of 1, 1033 aa, 1 stop
><MW: 112992, pI: 7.78, NX(S/T): 11
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MGAAGLLGVFLALVAPGVLGISCGSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLIGE
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NFSMNGNKSVMWCQANNMWGPTRLPTCVSVFPLECPALPMIHNGHHTSENVGSIAPGLSVT
YSCESGYLLVGEKIINCLSSGKWSAVPPTCEEARCKSLGRFPNGKVKEPPILRVGV TANF
FCDEGYRLQGPPSSRCVIAQGQVAWTKMPVCEEIFCPSPPPIILNGRHIGNSLANVSYGSI
VTYTCDDPDPEEGVNFILIGESTLRCTVDSQKTGTWSGPAPRCELSTSAVQCPHPQILRGR
MVSGQKDRYTYNDTVIFACMFGFTLKGSQKQIRCNAQGTWEPSAPVCEKECQAPPNINLNGQ
KEDRHMVRFDPGTSIKYSCNPGYVLVGEESIQTSEGVTWTPVPQCKVAACEATGRQLLT
KPQHQQFVRPDVNSSCGEGYKLSGSVYQECQGTIPWFMEIRLCKEITCPIPPVVIYNGAHTG
SSLEDFPYGTTVTYTCNPGPERGVEFSLIGESTIRCTSNDQERGTWSGPAPLCKLSLLAV
QCSHVHIANGYKISGKEAPYFYNDTVTFKCYSGFTLKGSQIRCKADNTWDPEIPVCEKE
TCQHVRQSLQELPAGSRVELVNTSCQDGYQLTG HAYQMCQDAENGIWFKKIPLCKVIHCH
PPPVIIVNGKHTGMAENFLYGNEVSYECDQGFYLLGEKKLQCRSDSKGHGSWSGSPQCL
RSPPVTRCPNPEVKHGYKLNKTHSAYSHNDIVYVDCNPGFIMNGSRVIRCHTDNTWVPGV
PTCMKKAFIGCPPPKTPNGNHTGGNIARFSPGMSILYSCDQGYLLVGEALLLCTHEGTW
SQPAPHCKEVCNCS PADMDGIQKGLEPRKMYQYGAVVTLECEDGYMLEGSPQSQCQSDHQ
WNPPLAVCRSRSLAPVLCGIAAGLILLTFLIVITLYVISKHRERNYYTDTSQKEAFHLEA
REVYSVDPYNPAS

Signal sequence.

amino acids 1-20.

Transmembrane domain.

amino acids 973-993.

Sushi domain (SCR repeat).

amino acids 23-82, 91-146, 154-210, 215-271, 276-342, 351-406, 410-466, 471-522, 527-593, 602-657, 662-714, 719-779, 788-843, 851-907, 912-968.

N-glycosylation site.

amino acids 121-124, 127-130, 294-297, 372-375, 492-495, 623-626, 682-685, 800-803, 823-826, 861-864, 911-914.

Protein kinase C phosphorylation site.

amino acids 54-56, 200-202, 253-255, 322-324, 329-331, 384-386, 434-436, 474-476, 573-575, 614-616, 627-629, 635-637, 1011-1013.

FIGURE 12B

Casein kinase II phosphorylation site.

amino acids 90-93, 209-212, 370-373, 494-497, 541-544, 542-545, 577-560, 614-617, 668-671, 676-679, 684-687, 807-810, 914-917, 1011-1014.

Tyrosine kinase phosphorylation site.

amino acids 1000-1006, 1000-1007.

N-myristoylation site.

amino acids 8-13, 20-25, 176-181, 235-240, 260-265, 262-267, 289-294, 298-303, 536-541, 549-554, 563-568, 741-746, 839-844, 860-865, 864-869, 920-925, 934-939, 949-954, 979-984.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 13-23, 173-183, 870-880.

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 538-548.

Cereal trypsin/alpha-amylase inhibitors family signature.

amino acids 132-154.

FIGURE 13A

DNA226179

CAAACGTTCCCAAATCTTCCCAGTCGGCTTGCGAGAGACTCCTTGCTCCCAGGAGATAACC
AGAAGCTGCATCTTATTGACAGATGGTCATCACATTGGTGAGCTGGAGTCATCAGATTGT
GGGGCCCGGAGTGAGGCTGAAGGGAGTGGATCAGAGCACTGCCTGAGAGTCACCTCTACT
TTCCTGCTACCGCTGCCTGTGAGCTGAAGGGGCTGAACCATACTCCTTTTTTCTACAAC
CAGCTTGCATTTTTTCTGCCCACAATGAGCGGGGAATCAATGAATTTTCAGCGATGTTTTTC
GACTCCAGTGAAGATTATTTTGTGTGAGTCAATACTTCATATTACTCAGTTGATTCTGAG
ATGTTACTGTGCTCCTTGCGAGGAGGTCAGGCAGTTCTCCAGGCTATTTGTACCGATTGCC
TACTCCTTGATCTGTGTCTTTGGCCTCCTGGGGAATATTCTGGTGGTGATCACCTTTGCT
TTTTATAAGAAGGCCAGGTCTATGACAGACGTCTATCTCTTGAACATGGCCATTGCAGAC
ATCCTCTTTGTTCTTACTCTCCCATTCTGGGCAGTGAGTCATGCCACTGGTGCGTGGGTT
TTCAGCAATGCCACGTGCAAGTTGCTAAAAGGCATCTATGCCATCAACTTTAACTGCGGG
ATGCTGCTCCTGACTTGCAATTAGCATGGACCGGTACATCGCCATTGTACAGGCGACTAAG
TCATTCCGGCTCCGATCCAGAACACTACCGCGCACGAAAATCATCTGCCTTGTTGTGTGG
GGGCTGTCAGTCATCATCTCCAGCTCAACTTTTGTCTTCAACCAAAAATACAACACCCAA
GGCAGCGATGTCTGTGAACCCAAGTACCAGACTGTCTCGGAGCCCATCAGGTGGAAGCTG
CTGATGTTGGGGCTTGAGCTACTCTTTGGTTTCTTTATCCCTTTGATGTTTCATGATATTT
TGTTACACGTTTCAATTGTCAAAACCTTGGTGCAAGCTCAGAATTCTAAAAGGCACAAAGCC
ATCCGTGTAATCATAGCTGTGGTGCTTGTGTTTCTGGCTTGTGAGATTCTCATAACATG
GTCCTGCTTGTGACGGCTGCAAATTTGGGTAAAATGAACCGATCCTGCCAGAGCGAAAAG
CTAATTGGCTATACGAAAACGTGTCACAGAAGTCCTGGCTTTCTGCACTGCTGCCTGAAC
CCTGTGCTCTACGCTTTTATTGGGCAGAAGTTGAGAACTACTTTCTGAAGATCTTGAAG
GACCTGTGGTGTGTGAGAAGGAAGTACAAGTCCTCAGGCTTCTCCTGTGCCGGGAGGTAC
TCAGAAAACATTTCTCGGCAGACCAGTGAGACCGCAGATAACGACAATGCGTCGTCCTTC
ACTATGATAGATAAGCTGAGTCTCCCTAAGGCATGTGTGAAACATACTCATAGATGTTA
TGCAAAAAAAGTCTATGGCCAGGTATGCATGGAAAATGTGGGAATTAAGCAAAATCAAG
CAAGCCTCTCTCCTGCCGGGACTTAACGTGCTCATGGGCTGTGTGATCTCTTCAGGGTGGG
GTGGTCTCTGATAGGTAGCATTTTCCAGCACTTTGCAAGGAATGTTTTGTAGCTCTAGGG
TATATATCCGCCTGGCATTTCACAAAACAGCCTTTGGGAAATGCTGAATTAAAGTGAATT
GTTGACAAATGTAAACATTTTCAGAAATATTCATGAAGCGGTCACAGATCACAGTGTCTT
TTGGTTACAGCACAAAATGATGGCAGTGGTTTGAAAACTAAAACAGAAAAAAAATGGA
AGCCAACACATCACTCATTTTAGGCAAATGTTTAAACATTTTTATCTATCAGAATGTTTA
TTGTTGCTGGTTATAAGCAGCAGGATTGGCCGGCTAGTGTTTCTCTCATTTCCCTTTGA
TACAGTCAACAAGCCTGACCCTGTAAAATGGAGGTGGAAAGACAAGCTCAAGTGTTTACA
ACCTGGAAGTGCTTCGGGAAGAAGGGGACAATGGCAGAACAGGTGTTGGTGACAATTGTC
ACCAATTGGATAAAGCAGCTCAGGTTGTAGTGGGCCATTAGGAACTGTCGGTTTGCTTT
GATTTCCCTGGGAGCTGTTCTCTGTGCTGAGTGTCTCTTGTCTAAACGTCCATTAAGCTG
AGAGTGCTATGAAGACAGGATCTAGAATAATCTTGCTCACAGCTGTGCTCTGAGTGCCTA
GCGGAGTTCCAGCAAACAAAATGGACTCAAGAGAGATTTGATTAATGAATCGTAATGAAG
TTGGGGTTTATGTACAGTTTAAAATGTTAGATGTTTTTAATTTTTTAAATAAATGGAAT
ACTTTTTTTTTTTTTTAAAGAAAGCAACTTTACTGAGACAATGTAGAAAGAAGTTTTGTTC
CGTTTCTTTAATGTGGTTGAAGAGCAATGTGTGGCTGAAGACTTTTGTTATGAGGAGCTG
CAGATTAGCTAGGGGACAGCTGGAATTATGCTGGCTTCTGATAATTATTTTAAAGGGGTC
TGAAATTTGTGATGGAATCAGATTTTAAACAGCTCTCTTCAATGACATAGAAAGTTTCATGG

FIGURE 13B

TACAAAATACAAACACATGTTAGGAAGGTACTGTCATGGGCTAGGCATGGTGGCTCACA
CCTGTAATCCCAGCATTTTGGGAAGCTAAGATGGGTGGATCACTTGAGGTCAGGAGTTTG
AGACCAGCCTGGCCAACATGGCGAAACCCCTCTCTACTAAAAATACAAAAATTTGCCAGG
CGTGGTGGCGGGTGCCTGTAATCCCAGCTACTTGGGAGGCTGAGGCAAGAGAATCGCTTG
AACCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCGTGCCATTGCACTCCAGCCTGGGTG
ACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

DNA226179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA226179
><subunit 1 of 1, 374 aa, 1 stop
><MW: 42508, pI: 9.34, NX(S/T): 6

MSGESMNFSDVFDSSSEDYFVSVNTSYYSVDSEMLLCSLQEVQRQFSRLFVPIAYSLICVFG
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LKGIYAINFNCGMLLLTCISM DRYIAIVQATKSFRLRSRTLPRTKIICLVVWGLSVIIS
STFVFNQKYNTQGS DVC EPKYQTVSEPIRWKLLMLGLELLFGFFIPLMFMIFCYTFIVKT
LVQAQNSKRHKAIRVIIAVVLVFLACQIPHNMVLLVTAANLGKMNRSCQSEKLIGYTKTV
TEVLAF' LHCCCLNPVLYAFIGQKFRNYFLKILKDLWCVRRKYKSSGFSCAGRYSENISRQT
SETADNDNASSFTM

Signal sequence.

amino acids 1-43.

Transmembrane domain.

amino acids 48-68, 84-104, 123-143, 164-184, 204-224, 220-240, 245-265, 261-281, 298-318.

N-glycosylation site.

amino acids 7-10, 23-26, 115-118, 285-288, 355-358, 368-371.

Protein kinase C phosphorylation site.

amino acids 117-119, 153-155, 247-249, 290-292.

Casein kinase II phosphorylation site.

amino acids 14-17, 37-40, 79-82, 203-206, 299-302.

N-myristoylation site.

amino acids 60-65, 193-198.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 256-266.

7 transmembrane receptor (rhodopsin family).

amino acids 63-316.

FIGURE 15

DNA226239

AGTCACAGAGGGAACACAGAGCCTAGTTGTAAACGGACAGAGACGAGAGGGGCAAGGGAG
GACAGTGGATGACAGGGAAGACGAGTGGGGGCAGAGCTGCTCAGGACC ATGGCTGAGGCC
ATCACCTATGCAGATCTGAGGTTTGTGAAGGCTCCCCTGAAGAAGAGCATCTCCAGCCGG
TTAGGACAGGACCCAGGGGCTGATGATGATGGGGAAATCACCTACGAGAATGTTCAAGTG
CCCGCAGTCCTAGGGGTGCCCTCAAGCTTGGCTTCTTCTGTACTAGGGGACAAAGCAGCG
GTCAAGTCGGAGCAGCCAACCTGCGTCCTGGAGAGCCGTGACGTCACCAGCTGTCGGGCGG
ATTCTCCCCTGCCGCACAACCTGCCTGCGATACCTCCTGCTCGGCCTGCTCCTCACCTGC
CTGCTGTTAGGAGTGACCGCCATCTGCCTGGGAGTGCGCTATCTGCAGGTGTCTCAGCAG
CTCCAGCAGACGAACAGGGTTCTGGAAGTCACTAACAGCAGCCTGAGGCAGCAGCTCCGC
CTCAAGATAACGCAGCTGGGACAGAGTGCAGAGGATCTGCAGGGGTCCAGGAGAGAGCTG
GCGCAGAGTCAGGAAGCACTACAGGTGGAACAGAGGGCTCATCAGGCGGCCGAAGGGCAG
CTACAGGCCTGCCAGGCAGACAGACAGAAGACGAAGGAGACCTTGCAAAGTGAGGAGCAA
CAGAGGAGGGCCTTGGAGCAGAAGCTGAGCAACATGGAGAACAGACTGAAGCCCTTCTTC
ACATGCGGCTCAGCAGACACCTGCTGTCCGTGCGGATGGATAATGCATCAGAAAAGCTGC
TTTTACATCTCACTTACTTCAAAAAATTGGCAGGAGAGCCAAAAACAATGTGAAACTCTG
TCTTCCAAGCTGGCCACATTCAGTGAAATTTATCCACAATCACACTCTTACTACTTCTTA
AATTCAGTGTTGCCAAATGGTGGTTCAGGGAATTCATATTGGACTGGCCTCAGCTCTAAC
AAGGATTGGAAGTTGACTGATGATACACAACGCACTAGGACTTATGCTCAAAGCTCAAAA
TGTAACAAGGTACATAAACTTGGTCATGGTGGACACTGGAGTCAGAGTCATGTAGAAGT
TCTCTTCCCTACATCTGTGAGATGACAGCTTTTCAGGTTTCCAGAT TAGGACAGTCCTTTG
CACTGAGTTGACACTCATGCCAACAAGAACCTGTGCCCCCTCCTTCCTAACCTGAGGCCTG
GGGTTCTCAGACCATCTCCTTCATTCTGGGCAGTGCCAGCCACCGGCTGACCCACACCT
GACACTTCCAGCCAGTCTGCTGCCTGCTCCCTCTTCCTGAAACTGGACTGTTCTCTGGGAA
AAGGGTGAAGCCACCTCTAGAAGGGACTTTGGCCTCCCCCAAGAACTTCCCATGGTAGA
ATGGGGTGGGGGAGGAGGGCGCACGGGCTGAGCGGATAGGGGCGGCCCGGAGCCAGCCAG
GCAGTTTTATTGAAATCTTTTTAAATAATTG

FIGURE 16

DNA226239

><subunit 1 of 1, 359 aa, 1 stop

><MW: 40220, pI: 8.70, NX(S/T): 1

MAEAITYADLR FVKAPLKKSIS SRLGQDPGADDDGEITYENVQVPAVLGVPSSLASSVLG
DKAAVKSEQPTASWRAVTSPAVGRILPCRTTCLRYLLLGLLLTCLLLGVTAICLGVRYLQ
VSQQLQQTNRVLEV TNSSLRQQLRLKITQLGQSAEDLQGSRRELAQSQEALQVEQRAHQQA
AEGQLQACQADRQKTKETLQSEEQRRRALEQKLSNMENRLKPFFTCGSADTCCPSGWIMH
QKSCFYISLT'SKNWQESQKQCETLSSKLATFSEIYPQSHSYFFLN SLLPNGGSGNSYWTG
LSSNKDWKLTDDTQRTRTYAQSSKCNKVHKTWSWWTLESESCRSSLPYICEMTAFRFPD

Signal sequence.

amino acids 1-22.

Transmembrane domain.

amino acids 91-111.

N-glycosylation site.

amino acids 136-139.

Protein kinase C phosphorylation site.

amino acids 22-24, 73-75, 128-130, 138-140, 160-162, 250-252, 257-259, 265-267, 303-305, 313-315, 322-324, 341-343.

Casein kinase II phosphorylation site.

amino acids 6-9, 153-156, 160-163, 214-217, 270-273, 303-306.

N-myristoylation site.

amino acids 26-31, 49-54, 99-104, 183-188, 227-232, 291-296, 292-297, 300-305.

Leucine zipper pattern.

amino acids 86-107, 93-114, 143-164, 150-171.

Lectin C-type domain.

amino acids 250-352.

FIGURE 17

DNA226394

GGCACGAGGGTCCGCAAGCCCGGCTGAGAGCGCGCC ATGGGGCAGGCGGGCTGCAAGGGG
CTCTGCCTGTCGCTGTTTCGACTACAAGACCGAGAAGTATGTCATCGCCAAGAACAAGAAG
GTGGGCCTGCTGTACCGGCTGCTGCAGGCCTCCATCCTGGCGTACCTGGTCGTATGGGTG
TTCCTGATAAAGAAGGGTTACCAAGACGTCGACACCTCCCTGCAGAGTGCTGTCATCACC
AAAGTCAAGGGCGTGGCCTTCACCAACACCTCGGATCCTTGGGCAGCGGATCTGGGATGTC
GCCGACTACGTCAATTCAGCCCAGGGAGAGAACGTCTTTTTTGTGGTCACCAACCTGATT
GTGACCCCCAACCAGCGGCAGAACGTCTGTGCTGAGAATGAAGGCATTCCTGATGGCGCG
TGCTCCAAGGACAGCGACTGCCACGCTGGGGAAGCGGTTACAGCTGGAAACGGAGTGAAG
ACCGGCCGCTGCCTGCGGAGAGGGAACCTTGGCCAGGGGCACCTGTGAGATCTTTGCCTGG
TGCCCGTTGGAGACAAGCTCCAGGCCGGAGGAGCCATTCCTGAAGGAGGCCGAAGACTTC
ACCATTTTTCATAAAGAACCACATCCGTTTCCCCAAATTCAACTTCTCCAAAAACAATGTG
ATGGACGTCAAGGACAGATCTTTCCTGAAATCATGCCACTTTGGCCCCAAGAACCCTAC
TGCCCATCTTCCGACTGGGCTCCATCGTCCGCTGGGCCGGGAGCGACTTCCAGGATATA
GCCCTGCGAGGTGGCGTGATAGGAATTAATATTGAATGGAACGTGATCTTGATAAAGCT
GCCTCTGAGTGCCACCCTCACTATTCTTTTAGCCGTCTGGACAATAAACTTTCAAAGTCT
GTCTCCTCCGGGTACAACCTTCAGATTTGCCAGATATTACCGAGACGCAGCCGGGGTGGAG
TTCCGCACCCCTGATGAAAGCCTACGGGATCCGCTTTGACGTGATGGTGAACGGCAAGGGT
GCTTTCTTCTGCGACCTGGTACTCATCTACCTCATCAAAAAGAGAGAGTTTTACCGTGAC
AAGAAGTACGAGGAAGTGAGGGGCCTAGAAGACAGTTCCAGGAGGCCGAGGACGAGGCA
TCGGGGCTGGGGCTATCTGAGCAGCTCACATCTGGGCCAGGGCTGCTGGGGATGCCGGAG
CAGCAGGAGCTGCAGGAGCCACCCGAGGCGAAGCGTGGAAGCAGCAGTCAGAAGGGGAAC
GGATCTGTGTGCCACAGCTCCTGGAGCCCCACAGGAGCACG TGAATTGCCTCTGCTTAC
GTTCAAGGCCCTGTCTAAACCCAGCCGTCTAGCACCCAGTGATCCCATGCCTTTGGGAAT
CCCAGGATGCTGCCCAACGGGAAATTTGTACATTGGGTGCTATCAATGCCACATCACAGG
GACCAGCCATCACAGAGCAAAGTGACCTCCACGTCTGATGCTGGGGTCATCAGGACGGAC
CCATCATGGCTGTCTTTTTGCCCCACCCCTGCCGTGAGTTCTTCCTTTCTCCGTGGCTG
GCTTCCCGCACTAGGGAACGGGTTGTAAATGGGGAACATGACTTCCTTCCGGAGTCCTTG
AGCACCTCAGCTAAGGACCGCAGTGCCCTGTAGAGTTCTTAGATTACCTCACTGGGAATA
GCATTGTGCGTGTCCGGAAAAGGGCTCCATTTGGTTCCAGCCCACTCCCCTCTGCAAGTG
CCACAGCTTCCCTCAGAGCATACTCTCCAGTGGATCCAAGTACTCTCTCTCCTAAAGACA
CCACCTTCTGCCAGCTGTTTGCCCTTAGGCCAGTACACAGAATTAAAGTGGGGGAGATG
GCAGACGCTTTCTGGGACCTGCCCAAGATATGTATTCTCTGACACTCTTATTTGGTCATA
AAACAATAAATGGTGTCAATTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

DNA226394

><subunit 1 of 1, 422 aa, 1 stop
><MW: 47187, pI: 8.40, NX(S/T): 3

MGQAGCKGLCLSLFDYKTEKYVIAKNKKVGLLYRLLQASILAYLVVWVFLIKKGYQDVDT
SLQSAVITKVKGVAFTNTSDLGQRIWDVADYVIPAQGENVFFVVTNLIVTPNQQRQNVCAE
NEGIPDGACSKDSDCHAGEAVTAGNGVKTGRCLRRGNLARGTCEIFAWCPLETSSRPEEP
FLKEAEDFTIFIKNHIRFPKFNFSSKNNVMDVKDRSFLKSCHFGPKNHYCPIFRLGSIVRW
AGSDFQDIALRGGVIGINIEWNCDLDKAASECHPHYSFSRLDNKLSKSVSSGYNFRFARY
YRDAAGVEFRTLKAYGIRFDVMVNGKGAFCDLVLIYLIKKREFYRDKKYEEVRGLED
SQEAEDASGLGLSEQLTSGPGLLGMPQQELQEPPEAKRGSSSQKGNGSVCPQLLEPHR
ST

N-glycosylation site.

amino acids 77-80, 202-205, 408-411.

Glycosaminoglycan attachment site.

amino acids 369-372, 379-382.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 399-402.

Protein kinase C phosphorylation site.

amino acids 18-20, 149-151, 174-176, 404-406.

Casein kinase II phosphorylation site.

amino acids 12-15, 175-178, 279-282, 360-363.

Tyrosine kinase phosphorylation site.

amino acids 84-91.

N-myristoylation site.amino acids 2-7, 8-13, 72-77, 123-128, 146-151, 252-257, 328-333, 356-361,
370-375.**ATP P2X receptor.**

amino acids 14-364.

FIGURE 19

DNA226423

AACTCATTTCTGAAGAGGCTGACGATTTTACTGTCTCATTTTTTTTCTTTCTCCAGA ATGG
GTTCTGGGTGGGTCCCCCTGGGTGGTGGCTCTGCTAGTGAATCTGACCCGACTGGATTCTT
CCATGACTCAAGGCACAGACTCTCCAGAAGATTTTGTGATTTCAGGCAAAGGCTGACTGTT
ACTTCACCAACGGGACAGAAAAGGTGCAGTTTGTGGTCAGATTCATCTTTAACTTGGAGG
AGTATGTACGTTTCGACAGTGATGTGGGGATGTTTGTGGCATTGACCAAGCTGGGGCAGC
CAGATGCTGAGCAGTGGAACAGCCGGCTGGATCTCTTGGAGAGGAGCAGACAGGCCGTGG
ATGGGGTCTGTAGACACAACCTACAGGCTGGGCGCACCCCTTCACTGTGGGGAGAAAAGTGC
AACCAGAGGTGACAGTGTACCCAGAGAGGACCCCACTCCTGCACCAGCATAATCTGCTGC
ACTGCTCTGTGACAGGCTTCTATCCAGGGGATATCAAGATCAAGTGGTTCCTGAATGGGC
AGGAGGAGAGAGCTGGGGTCATGTCCACTGGCCCTATCAGGAATGGAGACTGGACCTTTC
AGACTGTGGTGATGCTAGAAATGACTCCTGAACTTGGACATGTCTACACCTGCCTTGTCG
ATCACTCCAGCCTGCTGAGCCCTGTTTCTGTGGAGTGGAGAGCTCAGTCTGAATATTCTT
GGAGAAAGATGCTGAGTGGCATTGCAGCCTTCCTACTTGGGCTAATCTTCCTTCTGGTGG
GAATCGTCATCCAGCTAAGGGCTCAGAAAGGATATGTGAGGACGCAGATGTCTGGTAATG
AGGTCTCAAGAGCTGTTCTGCTCCCTCAGTCATGC TAAGGTCTCACTAAGCTTGCTCTC
TCTGGAGCCTGAAGTAGTGATGAGTAGTCTGGGCCCTGGGTGAGGTAAAGGACATTCATG
AGGTCAATGTTCTGGGAATAACTCTCTTCCCTGATCCTTGGAGGAGCCCGAACTGATTCT
GGAGCTCTGTGTTCTGAGATCATGCATCTCCACCCATCTGCCCTTCTCCCTTCTACGTG
TACATCATTAATCCCCATTGCCAAGGGCATTGTCCAGAACTCCCCTGAGACCTTACTCC
TTCCAGCCCCAAATCATTTACTTTTCTGTGGTCCAGCCCTACTCCTATAAGTCATGATCT
CCAAAGCTTTCCTGTTCTTCCAAGTGCAGTCTCCACAGTCTTCAGAAGACAAATGCTCAGGT
AGTCACTGTTTCCTTTTCACTGTTTTTAAAAACCTTTTATTGTCAAATAAAATGGAGATA
CA

FIGURE 20

DNA226423

><subunit 1 of 1, 273 aa, 1 stop
><MW: 30822, pI: 6.72, NX(S/T): 2
MGSQWVPWVVALLVNLTRLDSMTQGTDSPEDFVIQAKADCYFTNGTEKVQFVVRFFIFNL
EEYVRFDSDVGMFVALTKLGQPDAEQWNSRLDLLERSRQAVDGVCRHNYRLGAPFTVGRK
VQPEVTVYPERTPLLHQHNLLHCSVTFYFPGDIKIKWFLNGQEERAGVMSTGPIRNGDWT
FQTVVMLEMTPELGHVYTCLVDHSSLLSPVSVEWRAQSEYSWRKMLSGIAAFLLGLIFLL
VGIVIQLRQKGYVRTQMSGNEVSRAVLLPQSC

Signal sequence.

amino acids 1-21.

Transmembrane domain.

amino acids 225-245.

N-glycosylation site.

amino acids 15-18, 45-48.

Protein kinase C phosphorylation site.

amino acids 47-49, 221-223.

Casein kinase II phosphorylation site.

amino acids 17-20, 29-32, 89-92, 259-262.

Tyrosine kinase phosphorylation site.

amino acids 120-128.

N-myristoylation site.

amino acids 71-76, 80-85, 112-117, 167-172, 260-265.

Amidation site.

amino acids 117-120.

Leucine zipper pattern.

amino acids 226-247.

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 197-203.

Class II histocompatibility antigen, beta.

amino acids 39-116.

Immunoglobulin domain.

amino acids 136-201.

FIGURE 21A

DNA227781

GCTGCCACCTCTCTAGAGGCACCTGGCGGGGAGCCTCTCAACATAAGACAGTGACCAGTC
TGGTGACTCACAGCCGGGCACAGCCATGAACTACCCGCTAACGCTGGAAATGGACCTCGAG
AACCTGGAGGACCTGTTCTGGGAACTGGACAGATTGGACAACTATAACGACACCTCCCTG
GTGGAAAATCATCTCTGCCCTGCCACAGAGGGTCCCCTCATGGCCTCCTTCAAGGCCGTG
TTCGTGCCCCGTGGCCTACAGCCTCATCTTCCTCCTGGGCGTGATCGGCAACGTCCTGGTG
CTGGTGATCCTGGAGCGGCACCGGCAGACACGCAGTTCCACGGAGACCTTCCTGTTCCAC
CTGGCCGTGGCCGACCTCCTGCTGGTCTTCATCTTGCCCTTTGCCGTGGCCGAGGGCTCT
GTGGGCTGGGTCTGGGACCTTCCTCTGCAAACTGTGATTGCCCTGCACAAAGTCAAC
TTCTACTGCAGCAGCCTGCTCCTGGCCTGCATCGCCGTGGACCGCTACCTGGCCATTGTC
CACGCCGTCCATGCCCTACCGCCACCGCCGCCTCCTCTCCATCCACATCACCTGTGGGACC
ATCTGGCTGGTGGGCTTCCTCCTTGCCCTTGCCAGAGATTCTCTTCGCCAAAGTCAGCCAA
GGCCATCACAACTCCCTGCCACGTTGCACCTTCTCCCAAGAGAACCAAGCAGAAACG
CATGCCTGGTTACCTCCCGATTCTCTACCATGTGGCGGGATTCTGCTGCCCATGCTG
GTGATGGGCTGGTGCTACGTGGGGGTAGTGACAGGTTGCGCCAGGCCAGCGGCGCCCT
CAGCGGCAGAAGGCAGTCAGGGTGGCCATCCTGGTGACAAGCATCTTCTTCCTCTGCTGG
TCACCCTACCACATCGTCATCTTCCTGGACACCCTGGCGAGGCTGAAGGCCGTGGACAAT
ACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAGTTCCTGGGCCTG
GCCACTGCTGCCTCAACCCCATGCTCTACACTTTCGCCGGCGTGAAGTTCGCAGTGAC
CTGTGCGGGCTCCTGACCAAGCTGGGCTGTACCGGCCCTGCCTCCCTGTGCCAGCTCTTC
CCTAGCTGGCGCAGGAGCAGTCTCTCTGAGTCAGAGAATGCCACCTCTCTCACCACGTTT
TAGGTCCCAGTGTCCTCTTTATTGCTGCTTTTCCTTGGGGCAGGCAGTGATGCTGGATG
CTCCTTCCAACAGGAGCTGGGATCCTAAGGGCTCACCGTGGCTAAGAGTGTCTAGGAGT
ATCCTCATTTGGGGTAGCTAGAGGAACCAACCCCATTTCTAGAACATCCCTGCCAGCTCT
TCTGCCGGCCCTGGGGCTAGGCTGGAGCCCAGGGAGCGGAAAGCAGCTCGAAGGCACAGT
GAAGGCTGTCCTTACCCATCTGCACCCCCCTGGGCTGAGAGAACCTCACGCACCTCCCAT
CCTAATCATCCAATGCTCAAGAAACAATTCTACTTCTGCCCTTGCCAACGGAGAGCGCC
TGCCCCCTCCCAGAACACACTCCATCAGCTTAGGGGGCTGCTGACCTCCACAGCTTCCCCTC
TCTCCTCCTGCCACCTGTCAAACAAAGCCAGAAGCTGAGCACCAGGGGATGAGTGGAGG
TTAAGGCTGAGGAAAGGCCAGCTGGCAGCAGAGTGTGGCTTCGGACAACCTCAGTCCCTAA
AAACACAGACATTC TGCCAGGCCCCCAAGCCTGCAGTCATCTTGACCAAGCAGGAAGCTC
AGACTGGTTGAGTTCAGGTAGCTGCCCCCTGGCTCTGACCGAAACAGCGCTGGGTCCACCC
CATGTCACCGGATCTTGGGTGGTCTGCAGGCAGGGCTGACTCTAGGTGCCCTTGAGGGCC
AGCCAGTGACCTGAGGAAGCGTGAAGGCCGAGAAGCAAGAAAGAAACCCGACAGAGGGAA
GAAAAGAGCTTTCTTCCCCGAACCCCAAGGAGGGAGATGGATCAATCAAACCCGGCTGTCC
CCTCCGCCCAGGCGAGATGGGGTGGGGGGAGAACTCCTAGGGTGGCTGGGTCCAGGGGAT
GGGAGGTTGTGGGCATTGATGGGGAAGGAGGCTGGCTTGTCCCCTCCTCACTCCCTTCCC
ATAAGCTATAGACCCGAGGAAACTCAGAGTCGGAACGGAGAAAGGTGGACTGGAAGGGGC
CCGTGGGAGTCATCTCAACCATCCCCTCCGTGGCATCACCTTAGGCAGGGAAGTGTAAG
AAACACACTGAGGCAGGAACCTCCAGGCCCAGGAAGCCGTGCCCTGCCCCCGTGAGGATG
TCACTCAGATGGAAACCGCAGGAAGCTGCTCCGTGCTTGTCTTGTCTCACCTGGGGTGTGGGA
GGCCCGTCCGGCAGTTCTGGGTGCTCCCTACCACCTCCCCAGCCTTTGATCAGGTGGGGA
GTCAGGGACCCCTGCCCTTGTCCCACTCAAGCCAAGCAGCCAAGCTCCTTGGGAGGCCCC
ACTGGGGAAATAACAGCTGTGGCTCACGTGAGAGTGTCTTCACGGCAGGACAACGAGAAA
GCCCTAAGACGTCCCTTTTTTCTCTGAGTATCTCCTCGCAAGCTGGGTAATCGATGGGGA
CTCTCAAGCAGATCTCTAAGCCGACAGGATCGATTTTCTCAATTTCTTTTAAATAAAGCC

FIGURE 21B

CACCTATAAAACAGGTCAATACAGTACAGGCAGCACAGAGACCCCCGGAACAAGCCTAAA
AATTGTTTCAAAATAAAAACCAAGAAGATGTCTTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

DNA227781

><subunit 1 of 1, 372 aa, 1 stop

><MW: 41955, pI: 8.58, NX(S/T): 4

MNYPLTLEMDLENLEDLFWELDRLDNYNDTSLVENHLCPATEGPLMASFKAVFVPVAYSL
IFLLGVIGNVLVLVILERHRQTRSSTETFLFHLAVADLLLVFILPFAVAEGSVGWVLGTF
LCKTVIALHKVNFYCSSLLLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL
ALPEILFAKVSQGHNNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG
VVHRLRQAQRRPQRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL
PVAITMCEFLGLAHCCLNPMLYTFAGVKFRSDLSRLLTKLGCTGPASLCQLFPSWRRSSL
SESENATSLTTF

Transmembrane domain.

amino acids 52-72, 90-110, 129-149, 166-186, 219-239, 259-279, 299-319.

N-glycosylation site.

amino acids 28-31, 196-199, 297-300, 365-368.

cAMP- and cGMP-dependent protein kinase.

amino acids 356-359.

Protein kinase C phosphorylation site.

amino acids 48-50, 217-219, 293-295, 354-356.

Casein kinase II phosphorylation site.

amino acids 31-34, 84-87, 305-308, 359-362, 361-364.

N-myristoylation site.

amino acids 65-70, 118-123, 311-316.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 132-142.

FIGURE 23

DNA 227879

AGTGGCTCTACTTTCAGAAGAAAGTGTCTCTCTTCCTGCTTAAACCTCTGTCTCTGACGG
TCCCTGCCAATCGCTCTGGTCGACCCCAACACACTAGGAGGACAGACACAGGCTCCAAAC
TCCACTAACCAGAGCTGTGATTGTGCCCCTGAGTGGACTGCGTTGTCAGGGAGTGAGTG
CTCCATCATCGGGAGAATCCAAGCAGGACCGCCATGGAGGAAGGTCAATATTCAGAGATC
GAGGAGCTTCCCAGGAGGCGGTGTTGCAGGCGTGGGACTCAGATCGTGCTGCTGGGGCTG
GTGACCGCCGCTCTGTGGGCTGGGCTGCTGACTCTGCTTCTCCTGTGGCACTGGGACACC
ACACAGAGTCTAAAACAGCTGGAAGAGAGGGCTGCCCGGAACGTCTCTCAAGTTTCCAAG
AACTTGGAAGCCACCACGGTGACCAGATGGCGCAGAAATCCCAGTCCACGCAGATTTCA
CAGGAACTGGAGGAACTTCGAGCTGAACAGCAGAGATTGAAATCTCAGGACTTGAGCTG
TCCTGGAACCTGAACGGGCTTCAAGCAGATCTGAGCAGCTTCAAGTCCCAGGAATTGAAC
GAGAGGAACGAAGCTTCAGATTTGCTGGAAAGACTCCGGGAGGAGGTGACAAAGCTAAGG
ATGGAGTTGCAGGTGTCCAGCGGCTTTGTGTGCAACACGTGCCCTGAAAAGTGGATCAAC
TTCCAACGGAAGTGCTACTACTTCGGCAAGGGCACCAAGCAGTGGGTCCACGCCCGGTAT
GCCTGTGACGACATGGAAGGGCAGCTGGTCAGCATCCACAGCCCGGAGGAGCAGGACTTC
CTGACCAAGCATGCCAGCCACACCGGCTCCTGGATTGGCCTTCGGAACCTTGACCTGAAG
GGAGAGTTTATCTGGGTGGATGGGAGCCATGTGGACTACAGCAACTGGGCTCCAGGGGAG
CCCACCAGCCGGAGCCAGGGCGAGGACTGCGTGATGATGCGGGGCTCCGGTCGCTGGACC
GACGCCTTCTGCGACCGTAAGCTGGGCGCCTGGGTGTGCGACCGGCTGGCCACATGCACG
CCGCCAGCCAGCGAAGGTTCCGCGGAGTCCATGGGACCTGATTCAAGACCAGACCCTGAC
GGCCGCCTGCCCACCCCTCTGCCCCCTCTCCACTCTTGAGCATGGATACAGCCAGGCCCA
GAGCAAGACCCTGAAGACCCCAACCACGGCCTAAAAGCCTCTTTGTGGCTGAAAGGTCC
CTGTGACATTTTCTGCCACCCAAACGGAGGCAGCTGACACATCTCCCGCTCCTCTATGGC
CCCTGCCTTCCCAGGAGTACACCCCAACAGCACCTCTCCAGATGGGAGTGCCCCCAACA
GCACCCTCTCCAGATGAGAGTTACACCCCAACAGCACCTCTCCAGATGCAGCCCCATCT
CCTCAGCACCCCAGGACCTGAGTATCCCCAGCTCAGGGTGGTGAGTCCTCCTGTCCAGCC
TGCATCAATAAAATGGGGCAGTGATGGCC

FIGURE 24

DNA 227879

><subunit 1 of 1, 321 aa, 1 stop

><MW: 36456, pI: 5.52, NX(S/T): 1

MEEGQYSEIEELPRRRCCRRGTQIVLLGLVTAALWAGLLTLLLLWHWDTTQSLKQLEERA
ARNVSQVSKNLESHHGDQMAQKSQSTQISQELEELRAEQQRLKSQDLELSWNLNGLQADL
SSFKSQELNERNEASDLLERLREEVTKLRMELQVSSGFVCNTCPEKWINFQRKCYFYGKG
TKQVHARYACDDMEGQLVSIHSPEEQDFLTKHASHTGSWIGLRNLDLKGEFIWVDGSHV
DYSNWAPGEPTSRSQGEDCVMMRGSGRWTDAFCDRKLGAWVCDRLATCTPPASEGSAESM
GPDSRPDPDGRLPTPSAPLHS

Signal sequence.

amino acids 1-36.

Transmembrane domain.

amino acids 23-43.

N-glycosylation site.

amino acids 63-66.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 19-22.

Protein kinase C phosphorylation site.

amino acids 52-54, 122-124, 251-253, 265-267.

Casein kinase II phosphorylation site.

amino acids 7-10, 162-165, 203-206, 238-241, 254-257, 304-307.

FIGURE 25

getseq sst.DNA256363

AGAGATG GGGACGGAGGCCACAGAGCAGGTTTCCTGGGGCCATTACTCTGGGGATGAAGA
GGACGCATACTCGGCTGAGCCACTGCCGGAGCTTTGCTACAAGGCCGATGTCCAGGCCTT
CAGCCGGGCCTTCCAACCCAGTGTCTCCCTGACCGTGGCTGCGCTGGGTCTGGCCGGCAA
TGGCCTGGTCTG GGCACCCACCTGGCAGCCCGACGCGCAGCGCGCTCGCCACCTCTGC
CCACCTGCTCCAGCTGGCCCTGGCCGACCTCTTGCTGGCCCTGACTCTGCCCTTCGCGGC
AGCAGGGGGCTCTTCAGGGCTGGAGTCTGGGAAGTGCCACCTGCCGCACCATCTCTGGCCT
CTACTCGGCCTCCTTCCACGCCGGCTTCCTCTTCCTGGCCTGTATCAGCGCCGACCGCTA
CGTGGCCATCGCGCGAGCGCTCCAGCCGGGCGCGGCCCTCCACTCCCGGCCGCGCACA
CTTGGTCTCCGTCATCGTGTGGCTGCTGTCACTGCTCCTGGCGCTGCCTGCGCTGCTCTT
CAGCCAGGATGGGCAGCGGGAAGGCCAACGACGCTGTCGCCTCATCTTCCCCGAGGGCCT
CACGCAGACGGTGAAGGGGGCGAGCGCCGTGGCGCAGGTGGCCCTGGGCTTCGCGCTGCC
GCTGGGCGTTCATGGTAGCCTGCTACGCGCTTCTGGGCCGACGCTGCTGGCCGCCAGGGG
GCCCCGAGCGCCGGCGTGCGCTGCGCGTCGTGGTGGCTCTGGTGGCGGCCTTCGTGGTGCT
GCAGCTGCCCTACAGCCTCGCCCTGCTGCTGGATACTGCCGATCTACTGGCTGCGCGCGA
GCGGAGCTGCCCTGCCAGCAAACGCAAGGATGTCGCACTGCTGGTGACCAGCGGCTTGGC
CCTCGCCCCGCTGTGGCCTCAATCCCGTTCTCTACGCCTTCCTGGGCCTGCGCTTCCGCCA
GGACCTGCGGAGGCTGCTACGGGGTGGGAGCTCGCCCTCAGGGCCTCAACCCCGCCGCGG
CTGCCCCCGCCGGCCCCGCTTTCTTCCTGCTCAGCTCCACGGAGACCCACAGTCTCTC
CTGGGACAACTAGGGCTGCGAATCTAGAGGAGGGGGCAGGCTGAGGGTCGTGGGAAAGGG
GAGTAGGTGGGGGAACACTGAGAAAGAGGCAGGGACCTAAAGGGACTACCTCTGTGCCTT
GCCACATTAAATTGATAACATGGAAATGAAAAAAAAAAAAAAAAA

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA256363
><subunit 1 of 1, 362 aa, 1 stop
><MW: 38400, pI: 10.04, NX(S/T): 0
MGTEATEQVSWGHHYSGDEEDAYS AEPLPELCYKADVQAFSRAFPQPSVSLTVAALGLAGNG
LVLATHLAARRAARSPTS A HLLQLALADLLLALTLPFAAAGALQGWSLGSATCRTISGLY
SASFHAGFLFLACISADRYVAIARALPAGPRPSTPGRAHLVSVIVWLLSLLLALPALLFS
QDGQREGQRRCLIFPEGLTQTVKGASAVAQVALGFALPLGVMVACYALLGRTL LAARGP
ERRRALRVVVALVAAFVVLQLPYSLALLLD TADLLAARERSCPASKRKDVALLVT SGLAL
ARCGLNPVLYAFLGLRFRQDLRRLLRGGSSPSGPQPRRGCPRRPRLSSCSAPTETHSLSW
DN

Transmembrane domain.

Amino acids 43-63, 80-100, 119-139, 158-178, 209-229, 249-269, 291-311.

Seven-transmembrane receptor domain.

Amino acids 58-310.

Protein kinase C phosphorylation site.

Amino acids 112-114, 202-204, 285-287.

Casein kinase II phosphorylation site.

Amino acids 15-18.

N-myristoylation site.

Amino acids 2-7, 55-60, 60-65, 101-106, 109-114, 118-123, 183-188, 187-192,
198-203, 221-226, 297-302, 328-333.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 123-133, 216-226.

FIGURE 27

DNA332467

CCTCGGTTCTATCGATTGAATTCATGAAAGACATTGCCTGCCATGCTTGGAAGTGGGAAAT
TATTTTGGGTCTTCTTCTTAATCCCATATCTGGACATCTGGAACATCCATGGGAAAGAAT
CATGTGATGTACAGCTTTATATAAAGAGACAATCTGAACACTCCATCTTAGCAGGAGATC
CCTTTGAACTAGAATGCCCTGTGAAATACTGTGCTAACAGGCCTCATGTGACTTGGTGCA
AGCTCAATGGAACAACATGTGTAAAACCTTGAAGATAGACAAACAAGTTGGAAGGAAGAGA
AGAACATTTTCATTTTTTCATTCTACATTTTGAACCAGTGCTTCCTAATGACAATGGGTCAT
ACCGCTGTCTGCAAATTTTCAGTCTAATCTCATTGAAAGCCACTCAACAACCTCTTTATG
TGACAGATGTAAAAAGTGCTTCAGAACGACCCTCCAAGGACGAAATGGCAAGCAGACCCT
GGCTCCTGTATAGTTTACTTCCTTTGGGGGGGATTGCCTCTACTCATCACTACCTGTTTCT
GCCTGTTCTGCTGCCTGAGAAGGCACCAAGGAAAGCAAAATGAACTCTCTGACACAGCAG
GAAGGGAAATTAACTGGTTGATGCTCACCTTAAGAGTGAGCAAACAGAAGCAAGCACCA
GGCAAAATTTCCCAAGTACTGCTATCAGAAACTGGAATTTATGATAATGACCCTGACCTTT
GTTTCAGAATGCAGGAAGGGTCTGAAGTTTATTCTAATCCATGCCTGGAAGAAAACAAAC
CAGGCATTGTTTATGCTTCCCTGAACCATTCTGTTCATTGGACTGAACTCAAGACTGGCAA
GAAATGTAAAAGAAGCACCAACAGAATATGCATCCATATGTGTGAGGAGTTAAGGATCCT
CTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAA
GTGTTACAAATAACAAATAATATTTCTCAATTTGAGAATTTTACTTTAGAAATGTTCA
TGTTAGTGCTTGGGTCTGAAGGGTCCATAGGACAAATGATTAAAAT

FIGURE 28

DNA332467

><subunit 1 of 1, 289 aa, 1 stop
><MW: 32781, pI: 6.27, NX(S/T): 4
MKTLPAMLG TGKLFWVFFLI PYLDIWN IHGKESCDVQLYIKRQSEHSILAGDPFELECPV
KYCANRPHV TWCKLNGTTCVKLEDRQTSWKEEKNISFFILHFEPVLPNDNGSYRCSANFQ
SNLIESHSTTLYVTDVKSASERPSKDEMASRPWLLYSLLPLGGLPLLITTCFCLFCCLRR
HQGKQNELSDTAGREINLVDAHLKSEQTEASTRQNSQVLLSETGIYDNDPDLCFRMQEGS
EVYSNPCL EENKPGIVYASLNH SVIGLNSRLARNVKEAPTEYASICVRS

Transmembrane domain.

amino acids 153-173.

N-glycosylation site.

amino acids 75-78, 94-97, 110-113, 261-264.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 41-44.

Protein kinase C phosphorylation site.

amino acids 10-12, 88-90, 112-114, 140-142, 211-213.

Casein kinase II phosphorylation site.

amino acids 88-91, 138-141, 144-147.

Tyrosine kinase phosphorylation site.

amino acids 31-39.

N-myristoylation site.

amino acids 111-116, 224-229, 254-259.

Immunoglobulin domain.

amino acids 51-117.

FIGURE 29

DNA335922

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC ATGA
AGCTCTTGTTGGCAGGTAACGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCG
TCTACCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCG
GGCCCCAGAAGTGTCCCTCCGTTTGCTCGTGCAGTAACCAGTTCAGCAAGGTGGTGTGCA
CGCGCCGGGGCCTCTCCGAGGTCCCGCAGGGTATTCCTCGAACACCCGGTACCTCAACC
TCATGGAGAACAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGG
AGGTCCTGCAGTTGGGCAGGAAGTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCC
TGGCCAGCCTCAACACCTGGAGCTGTTGACAACTGGCTGACAGTCATCCCTAGCGGGG
CCTTTGAATACCTGTCCAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCA
TCCCCTCTTACGCCTTCAACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCA
AGAAGCTGGAGTATATCTCTGAGGGAGCTTTTGAGGGGCTGTTCAACCTCAAGTATCTGA
ACTTGGGCATGTGCAACATTAAAGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGG
AGCTGGAGATGTCAGGGAACCACTTCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGA
GCTCCCTCAAGAAGCTCTGGGTGATGAACTCACAGGTCAGCCTGATTGAGCGGAATGCTT
TTGACGGGCTGGCTTCACTTGTGGAAGTCAACTTGGCCCACAATAACCTCTCTTCTTTGC
CCCATGACCTCTTTACCCCGCTGAGGTACCTGGTGGAGTTGCATCTACACCACAACCTT
GGAAGTGTGATTGTGACATTCTGTGGCTAGCCTGGTGGCTTCGAGAGTATATACCCACCA
ATTCCACCTGCTGTGGCCGCTGTCATGCTCCCATGCACATGCGAGGCCGCTACCTCGTGG
AGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCTTCATCATGGACGCACCTCGAGACC
TCAACATTCTCTGAGGGTCGGATGGCAGAACTTAAGTGTGCGGACTCCCCCTATGTCCTCCG
TGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGCCTCCCGCCACCCAAGGATCT
CTGTCCTCAACGACGGCACCTTGAACTTTTCCACGTGCTGCTTTTCAGACACTGGGGTGT
ACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCGGCCTACCTCAATGTGA
GCACGGCTGAGCTTAACACCTCCAAGTACAGCTTCTTACCACAGTAACAGTGGAGACCA
CGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTACCACGTCCACTG
GTTACCAGCCGGCATATAACCACTCTACCACGGTGCTCATTCAGACTACCCGTGTGCCCA
AGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCTGGATGAAG
TCATGAAGACCACCAAGATCATCATTGGCTGCTTTGTGGCAGTGACTCTGCTAGCTGCCG
CCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTCACAG
CCGCCCCGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCGCAG
CAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCACAATTC
ATGACCATATTAACTACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACA
GCCTGGGGAACTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTTCAGA
CCCATAACCAAGGACAAGGTACAGGAACTCAAATA TGACTCCCCTCCCCCAAAAACTTA
TAAATGCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTT
TTCTTGTAATATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAACAGATTATATTAA
AATTTAAAGACAAAAGTCAAAACA

FIGURE 30A

DNA58721

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58721
><subunit 1 of 1, 653 aa, 1 stop
><MW: 72717, pI: 6.99, NX(S/T): 10
MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVV
CTRRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFN
GLASLNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGE
LKKLEYISEGAFEGLFNLKYLNLGMCNIKDMPNLTPLVGLEELEMMSGNHFPFPIRPGSFHG
LSSLKKLWVMNSQVSLIERNAFDGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHN
PWNCDCDILWLAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPR
DLNISEGRMAELKCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTG
VYTCMVTNVAGNSNASAYLNVSTAE LN TSNYSFFT VTVETTEISPEDTTRKYKPVPTTS
TGYQPAYTTSTTVLIQTTRVPKQVAVPATD TTDKMQTS LDEV MKT TKIIIGCFVAVTLLA
AAMLIVFYKLRKRHQQRSTVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPT
IHDHINYNTYKPAHGAHW TENS LGNSLHPTVTTISEPYIIQTHTKDKVQETQI
```

Signal sequence.

amino acids 1-41.

Transmembrane domain.

amino acids 12-32, 526-546.

N-glycosylation site.

amino acids 277-280, 322-325, 363-366, 388-391, 410-413, 434-437, 440-443, 447-450, 450-453.

Glycosaminoglycan attachment site.

amino acids 591-594.

Protein kinase C phosphorylation site.

amino acids 62-63, 94-96, 110-112, 243-245, 381-383, 469-471, 470-472, 497-499, 512-514, 525-527, 609-611.

Casein kinase II phosphorylation site.

amino acids 255-258, 267-270, 442-445, 465-468, 517-520, 518-521, 600-603, 633-636.

N-myristoylation site.

amino acids 72-77, 117-122, 190-195, 236-241, 389-394, 420-425, 431-436, 531-536, 615-620.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 42-52.

FIGURE 30B

Leucine zipper pattern.

amino acids 271-292.

Leucine Rich Repeat.

amino acids 76-99, 100-123, 124-147, 148-171, 172-196, 197-218, 219-242, 243-266, 267-290.

Leucine rich repeat C-terminal domain.

amino acids 300-351.

Leucine rich repeat N-terminal domain.

amino acids 45-74.

FIGURE 31

DNA335924

GCTGAAAGGGCCACGTTTGTTTTCATTACAAATAAGACCACCGAGTGGGCTCCTGGCGTG
GGGGCGGGAGCAGCCGCGCGCAGTCTTTCAGAGGCAGCCCCCAGGCTGTCTCTGGAGGGT
GTGTCTCTGCTTCCCTTTCCCCGTGTTTATTTTCAGACGAAGCCAAGTGGCCCCGGGGGA
CCCTCCGGACTCCCAGCCTTCAGAGAGGAGGGCAGCTCGGGCTTTCGCCGCAGTGCTTCC
TGCCCGTACAGTGTGTGCTCCTAGCCGGGGTCTGGGGGAGCTGGTATCTTGGCCCTTCTGG
GAGGACGCGCACAGCCCGAGGAGGCAGAGCCCCAGACGGGAATGGGCTTTTCAGAGGTGG
GGTGCGGGCGAGGGGACGATGCATTATTTTAAATATTTGATTTATTTTCCAACCTGGACT
TCTTCCCCGGGGCTCTTTCTGGGCCAGCTGCCTTTGTGATCCCGCGCCCCGGTCTCTGGC
CTCTCACCTCCAGCGCCGGGGCGCCCCCTGCTGTCTCGGAAGCGGCTGTGACCGGGCAGAGG
TGCTATCTGGGACTCTGGGTTCTCAGCCCCGGGGACAGCGAACCGAGGGGCAGATGATCCA
TCAGAAAAGAGCCGGCACTGCCAGCCCCGCGCCCCCTGCCCTTCTTCCGGGAGCG
CGCCGCGCCGCACCCGCTACGGCCGCTTGACCCCATCTTTGAGCCCGGCCCCAAGCTCTG
GGACCGTCGTGCCCCCTCATCAAGGAAGAGCCAAGGACCCCAAGGAGAAGGTCAGGAGCGG
CGGTGTGGATGTCCTTGGCTGCAGGCCCCGCGCGCACTCCCTTCAGTCCTTCCCTTCT
CTAGGGACCAGGTAGCATCAGTGCCCTGGATCTCGGCCTTGTGTGCCCTGCTCCCTGCCCC
ACCTACTAAGAACCAAGTCTGGTTCACCGGCTCCCAAGAGCTGGAACCCATTCTCAGCTA
GCTGGGGGCCCAGGCCACCCCTTCCCTCCAGACCTGTGTGCCTTCTGCCCTGGCTCCAGG
GCCCCCACACCGTGACCAGGGCGGGATCCCTATGGGGCTGGCCAGTCGGCACCGTGCCA
GGCCCACAGTGCCCTGGGCGTCCATGGAAGTCGTTCTGTGTCTT TAAAATCAGAAGGAAG
ACATTAACCTTTAGGCTGAAGAAAA TGTTTTAGTACACAGCAATAACTTATTTGTCTTTA
TCCAACAGCCATAAAATATAACTTTAAATATTCTATTGATAGAGAAAGGAGTTCATGAAG
GCAGAAATGCCTGGGGCCACGAACATCCAGTGTGGCCCTGGACGGGACATCATGCTGG
GCAACACAGCTAAAATGCGGGTGAA GACCAGATTTCTTGACATGGCGGTGACGGGATGC
TCCCTAGAGAGCTTCAAGTGGATTCTTTGCTTTTTATTTCTCTCTTAATAAAAAATGTAT
GATGTTTACATTGTCAGAGAACAAA CAGAAAAAAAAAAAAAAAAAAAAA

FIGURE 32

DNA335924

><subunit 1 of 1, 112 aa, 1 stop

><MW: 12158, pI: 11.55, NX(S/T): 0

MSLGCRPRRALPSVLPFSRDQVASVPGSRPCVPCSLPHLLRTKSGSPAPKSWNPFSASWG

PRPPLPSRPVCLLPWLQGPPHRDQGGIPMGLASRHRARPTVPWASMEVVLCL

N-myristoylation site.

amino acids 27-32, 86-91.

FIGURE 33

DNA340394

ATATATCGATATGCTGCCGAGGCTGTTGCTGTTGATCTGTGCTCCACTCTGTGAACCTGC
CGAGCTGTTTTTGATAGCCAGCCCCCTCCCATCCCACAGAGGGGAGCCCAGTGACCCTGAC
GTGTAAGATGCCCTTTCTACAGAGTTCAGATGCCAGTTCAGTTCTGCTTTTTCAGAGA
CACCCGGGCCTTGGGCCCAGGCTGGAGCAGCTCCCCAAGCTCCAGATCGCTGCCATGTG
GAAAGAAGACACAGGGTCATACTGGTGCGAGGCACAGACAATGGCGTCCAAAGTCTTGAG
GAGCAGGAGATCCCAGATAAATGTGCACAGGGTCCCTGTCGCTGATGTGAGCTTGGAGAC
TCAGCCCCCAGGAGGACAGGTGATGGAGGGAGACAGGCTGGTCCTCATCTGCTCAGTTGC
TATGGGCACAGGAGACATCACCTTCCTTTGGTACAAAGGGGCTGTAGGTTTAAACCTTCA
GTCAAAGACCCAGCGTTCCTGACAGCAGAGTATGAGATTCCCTTCAGTGAGGGAGAGTGA
TGCTGAGCAATATTACTGTGTAGCTGAAAATGGCTATGGTCCCAGCCCCAGTGGGCTGGT
GAGCATCACTGTCAGAATCCCGGTGTCTCGCCCAATCCTCATGCTCAGGGCTCCCAGGGC
CCAGGCTGCAGTGGAGGATGTGCTGGAGCTTCACTGTGAGGCCCTGAGAGGCTCTCCTCC
GATCCTGTACTGGTTTTATCACGAGGATATCACCTGGGGAGCAGGTCGGCCCCCTCTGG
AGGAGGAGCCTCCTTCAACCTTTCCTGACTGAAGAACATTCTGGAACTACTCCTGTGA
GGCCAACAATGGCCTGGGGGCCAGCGCAGTGAGGCGGTGACACTCAACTTCACAGTGCC
TACTGGGGCCAGAAGCAATCATCTTACCTCAGGAGTCATTGAGGGGCTGCTCAGCACCCCT
TGGTCCAGCCACCGTGGCCTTATTATTTTGCTACGGCCTCAAAGAAAAATAGGAAGACG
TTCAGCCAGGGATCCACTCAGGAGCCTTCCCAGCCCTTACCCCAAGAGTTCACGTACCT
CAACTCACCTACCCAGGGCAGCTACAGCCTATATATGAAAATGTGAATGTTGTAAGTGG
GGATGAGGTTTATTCACTGGCGTACTATAACCAGCCGGAGCAGGAATCAGTAGCAGCAGA
AACCCTGGGGACACATATGGAGGACAAGGTTTCCTTAGACATCTATTCCAGGCTGAGGAA
AGCAAACATTACAGATGTGGACTATGAAGATGCTATGTAAGGTTATGGAAGATTCTGCTC
TT

FIGURE 34

DNA340394

><subunit 1 of 1, 429 aa, 1 stop

><MW: 46936, pI: 5.42, NX(S/T): 4

MLPRLLLLLICAPLCEPAELFLIASPSHPTEGSPVTLTCKMPFLQSSDAQFQFCFFRDTRA
LGPGWSSSPKLQIAAMWKEDTGSYWCEAQTMASKVLRSSRSQINVHRVPVADVSLQTPP
GGQVMEGDRVLICSVAMGTGDITFLWYKGAVGLNLQSKTQRSLTAEYEIPSVRESDAEQ
YYCVAENGYGPPSPGLVSITVRIPVSRPILMLRAPRAQAAVEDVLELHCEALRGSPPILY
WFYHEDITLGSRSAPSGGGASFNLSTEEHSGNYSCEANGLGAQRSEAVTLNFTVPTGA
RSNHLTSGVIEGLLSTLGPATVALLFCYGLKRKIGRRSARDPLRSLPSPLPQEFTYLNSP
TPGQLQPIYENVNVVSGDEVYSLAYYNQPEQESVAAETLGTHMEDKVSLDIYSRLRKANI
TDVDYEDAM

Signal sequence.

amino acids 1-16.

N-glycosylation site.

amino acids 263-266, 273-276, 293-296, 419-422.

Glycosaminoglycan attachment site.

amino acids 256-259.

Protein kinase C phosphorylation site.

amino acids 37-39, 68-70, 98-100, 160-162, 172-174, 200-202, 338-340.

Casein kinase II phosphorylation site.

amino acids 172-175, 176-179, 265-268, 338-341, 376-379, 401-404, 421-424.

Tyrosine kinase phosphorylation site.

amino acids 174-181.

N-myristoylation site.

amino acids 31-36, 82-87, 257-262, 259-264, 272-277, 283-288, 299-304, 308-313, 312-317.

Amidation site.

amino acids 334-337.

Immunoglobulin.

amino acids 31-88, 127-185, 222-278.

FIGURE 35

DNA56041

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTT
TTGGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTC ATGCTG
CTGTGGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGG
CCCATTAATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTC
ACTTGCAAGGGATTTTCGCTTCTACTCACCACAGAAAAAAAATGGTACCATCGGTACCTT
GGGAAAGAAATACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAG
TACAGATGCCAGGCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCA
GAGATGGGATTTCTCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTG
CTCACCTTAGGCCTCTCAAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTT
TCTGTGTTTGAAGGAGACTCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTG
AATAATACTATTTACAAGAATGATAATGTCCTGGCATTCCTTAATAAAAGAACTGACTTC
CAAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

DNA56041

><subunit 1 of 1, 124 aa, 1 stop

><MW: 14080, pI: 7.48, NX(S/T): 0

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHR
YLGKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEMGFPHAAQANVELLGSS
DLLT

Signal sequence.

amino acids 1-15.

Protein kinase C phosphorylation site.

amino acids 20-22, 43-45.

N-myristoylation site.

amino acids 89-94.

FIGURE 37

DNA59607

GGATTTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCC
AGGACAGGCCCACCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAG
ACGCAGAGAGGCCAAGCCCCTTGCCCTTGGGTCA CACAGCCAAAGGAGGCAGAGCCAGAAC
TCACAACCAGATCCAGAGGCAACAGGGAC ATGGCCACCTGGGACGAAAAGGCAGTCACCC
GCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGG
AGGAGGAGGAGGAGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAG
CCCCTGACGTTGCCCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCA
TGTTGAGGAAACTGTTGAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTC
TGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTA
TGATGGAGATCATCTTTAAATTATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGA
GATCCTGGATGCCCCGTCGTGGTGGTGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCC
AGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCC
GGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTCAGAACGGCAACTCTTAAGGT
TAAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTG
AGAAGCCCCTGGAC TGATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGAT
GGCTATGGGAATGAAAGAATCCGACTTCTACTCTCACACAGCCACCGTGAAAGTCCTGGA
GTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGCATGTTCACTGGGCTG
GTGTTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAAATCTATAAAGATATTCT
GAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTAAAAA AAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 38

DNA59607

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59607

><subunit 1 of 1, 255 aa, 1 stop

><MW: 29405, pI: 7.64, NX(S/T): 0

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYYKKWENEEEEEEEEEQPPPT
PVSGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAEL
ILDLKIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSWMPVVVVV
SFILDIVLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVQLAA
KIQHLEFSCSEKPLD

Transmembrane domain.

amino acids 101-121, 141-161, 168-188, 195-215.

Protein kinase C phosphorylation site.

amino acids 20-22, 43-45.

N-myristoylation site.

amino acids 89-94.

FIGURE 39A

DNA257955

AGTGAAGGGGTTTCCCATATGAAAAATACAGAAAGAATTATTTGAA TACTAGCAAATACA
CAACTTGATATTTCTAGAGAACCCAGGCACAGTCTTGAGACATTACTCCTGAGAGACTG
CAGCTGATGGAAGATGAGCCCCAACTTCTAAAAATGTATCACTACCGGGATTGAGATACA
AACAGCATTTAGGAAGGTCTCATCTGAGTAGCAGCTTCCTGCCCTCCTTCTTGAGATAA
GTCGGGCTTTTGGTGAGACAGACTTTCCCAACCCTCTGCCCGGCCGGTGCCC ATGCTTCT
GTGGCTGCTGCTGCTGATCCTGACTCCTGGAAGAGAACAATCAGGGGTGGCCCCAAAAGC
TGTACTTCTCCTCAATCCTCCATGGTCCACAGCCTTCAAAGGAGAAAAGTGGCTCTCAT
ATGCAGCAGCATATCACATTCCTAGCCCAGGGAGACACATATTGGTATCACGATGAGAA
GTTGTTGAAAATAAAACATGACAAGATCCAAATTACAGAGCCTGGA AATTACCAATGTAA
GACCCGAGGATCCTCCCTCAGTGATGCCGTGCATGTGGAATTTTCA CCTGACTGGCTGAT
CCTGCAGGCTTTACATCCTGTCTTTGAAGGAGACAATGTCATTCTGAGATGTCAGGGGAA
AGACAACAAAAACACTCATCAAAAGGTTTACTACAAGGATGGAAAACAGCTTCCTAATAG
TTATAATTTAGAGAAGATCACAGTGAATTCAGTCTCCAGGGATAATAGCAAATATCATTG
TACTGCTTATAGGAAGTTTTACATACTTGACATTGAAGTAACTTCAAAACCCCTAAATAT
CCAAGTTCAAGAGCTGTTTCTACATCCTGTGCTGAGAGCCAGCTCTTCCACGCCCATAGA
GGGGAGTCCCATGACCCTGACCTGTGAGACCCAGCTCTCTCCACAGAGGCCAGATGTCCA
GCTGCAATTCTCCCTCTTCAGAGATAGCCAGACCCTCGGATTGGGCTGGAGCAGGTCCCC
CAGACTCCAGATCCCTGCCATGTGGACTGAAGACTCAGGGTCTTACTGGTGTGAGGTGGA
GACAGTGACTCACAGCATCAAAAAAAGGAGCCTGAGATCTCAGATACGTGTACAGAGAGT
CCCTGTGTCTAATGTGAATCTAGAGATCCGGCCACCGGAGGGCAGCTGATTGAAGGAGA
AAATATGGTCCTTATTTGCTCAGTAGCCCAGGGTTCAGGGACTGTCACATTCTCCTGGCA
CAAAGAAGGAAGAGTAAGAAGCCTGGGTAGAAAGACCCAGCGTTCCTGTTGGCAGAGCT
GCATGTTCTCACCGTGAAGGAGAGTGATGCAGGGAGATACTACTGTGCAGCTGATAACGT
TCACAGCCCCATCCTCAGCACGTGGATTTCGAGTCACCGTGAGAATTCCGGTATCTCACCC
TGTCTCACCTTCAGGGCTCCCAGGGGCCACACTGTGGTGGGGGACCTGCTGGAGCTTCA
CTGTGAGTCCCTGAGAGGCTCTCCCCCGATCCTGTACCGATTTTATCATGAGGATGTCAC
CCTGGGGAACAGCTCAGCCCCCTCTGGAGGAGGAGCCTCCTTCAACCTCTCTCTGACTGC
AGAACATTCTGGAAACTACTCCTGTGATGCAGACAATGGCCTGGGGGGCCAGCACAGTCA
TGGAGTGAGTCTCAGGGTCACAGTTCCGGTGTCTCGCCCCGTCTCACCCTCAGGGCTCC
CGGGGCCAGGCTGTGGTGGGGGACCTGCTGGAGCTTCACTGTGAGTCCCTGAGAGGCTC
CTTCCCGATCCTGTACTGGTTTTATCACGAGGATGACACCTTGGGGGAACATCTCGGCCCA
CTCTGGAGGAGGGGCATCCTTCAACCTCTCTCTGACTACAGAACA TTTCTGGAACTACTC
ATGTGAGGCTGACAATGGCCTGGGGGCCAGCACAGTAAAGTGGTGACACTCAATGTTAC
AGGAACTTCCAGGAACAGAACAGGCCTTACCGCTGCGGGAATCACGGGGCTGGTGCTCAG
CATCCTCGTCCTTGCTGCTGCTGCTGCTCTGCTGCATTACGCCAGGGCCCCGAAGGAAACC
AGGAGGACTTTCTGCCACTGGAACATCTAGTCACAGTCCTAGTGAGTGTGAGGAGCCTTC
CTCGTCCAGGCCTTCCAGGATAGACCCTCAAGAGCCCACTCACTCTAAACCACTAGCCCC
AATGGAGCTGGAGCCAATGTACAGCAATGTAAATCCTGGAGATAGCAACCCGATTTATTC
CCAGATCTGGAGCATCCAGCATACAAAAGAAAACCTCAGCTAATTGTCCAATGATGCATCA
AGAGCATGAGGAACTTACAGTCCTCTATTGAGAACTGAAGAAGACACACCCAGACGACTC
TGCAGGGGAGGCTAGCAGCAGAGGCAGGGCCCATGAAGAAGATGATGAAGAAAACCTATGA
GAATGTACCACGTGTATTACTGGCCTCAGACCAC TAGCCCCCTTACCAGAGTGGCCCACA
GGAAACAGCCTGCACCATTTTTTTTTTCTGTTCTCTCCAACCACACATCATCCATCTCTCC
AGACTCTGCCTCCTACGAGGCTGGGCTGCAGGGTATGTGAGGCTGAGCAAAAGGTCTGCA

FIGURE 39B

AATCTCCCCTGTGCCTGATCTGTGTGTTCCCCAGGAAGAGAGCAGGCAGCCTCTGAGCAA
GCACTGTGTTATTTTCACAGTGGAGACACGTGGCAAGGCAGGAGGGCCCTCAGCTCCTAG
GGCTGTCGAATAGAGGAGGAGAGAGAAATGGTCTAGCCAGGGTTACAAGGGCACAATCAT
GACCATTGATCCAAGTGTGATCGAAAGCTGTTAATGTGCTCTCTGTATAAACAATTTGC
TCCAAATATTTTGTTTCCCTTTTTTGTGTGGCTGGTAGTGGCATTGCTGATGTTTTGGTG
TATATGCTGTATCCTTGCTACCATATTGGG

FIGURE 40A

DNA257955

><subunit 1 of 1, 734 aa, 1 stop
><MW: 80856, pI: 6.97, NX(S/T): 8
MLLWLLLLLILTPGREQSGVAPKAVLLLLNPPWSTAFKGEKVALICSSISHSLAQGDTYWYH
DEKLLKIKHDKIQITEPGNYQCKTRGSSLSDAVHVEFSPDWLILQALHPVFEGDNVILRC
QGKDNKNTHQKVYYKDQKQLPNSYNLEKITVNSVSRDNSKYHCTAYRKFYILDI EVTSKP
LNIQVQELFLHPVLRASSSTPIEGSPMTLTCETQLSPQRPDVQLQFSLFRDSQTLGLGWS
RSPRLQIPAMWTEDSGSYWCEVETVTHSIKKRSLRSQIRVQRPVPSNVNLEIRPTGGQLI
EGENMVLICSV AQSGTVTF SWHKEGRVRS LGRKTQRSL LAELHVLTVKESDAGRYYCAA
DNVHSPILSTWIRVTVRIPVSHPVLTFRAPRAHTVVGDLLELHCESLRGSPPILYRFYHE
DVTLGNSSAPSGGGASFNL SLTAEHSGNYSCDADNGLGAQHSHGVSLRVTPVSRPVLT
RAPGAQAVVGDLLELHCESLRGSPPILYW FYHEDDTLGNISAHSGGGASFNL SLTTEHSG
NYSCEADNGLGAQH SKVVT LNVTGT SRNRTGLTAAGITGLVLSILVLA AAAALLHYARAR
RKPGGLSATGTSSHSPSECQEPSSSRPSRIDPQEP THSKPLAPMELEPMYSNVNPGDSNP
IYSQIWSIQHTKENSANCPMMHQEHEELTVLYSELKKTHPDD SAGEASSRGRAHEEDDEE
NYENVPRVLLASDH

Signal sequence.

amino acids 1-13.

Transmembrane domain.

amino acids 574-594.

N-glycosylation site.

amino acids 426-429, 438-441, 448-451, 519-522, 531-534, 541-544, 561-564, 568-571.

Glycosaminoglycan attachment site.

amino acids 431-434, 524-527.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-273.

Protein kinase C phosphorylation site.

amino acids 177-179, 242-244, 268-270, 273-275, 335-337, 347-349, 375-377, 386-388, 406-408, 466-468, 479-481, 499-501, 565-567, 624-626, 708-710.

Casein kinase II phosphorylation site.

amino acids 88-91, 200-203, 347-350, 615-618, 628-631, 698-701, 703-706.

Tyrosine kinase phosphorylation site.

amino acids 349-356.

FIGURE 40B

N-myristoylation site.

amino acids 78-83, 86-91, 204-209, 236-241, 256-261, 432-437, 434-439, 447-452, 458-463, 518-523, 525-530, 527-532, 540-545, 551-556, 564-569, 571-576, 579-584, 604-609, 605-610.

Amidation site.

amino acids 331-334.

N-6 Adenine-specific DNA methylases signature.

amino acids 25-31.

Immunoglobulin domain.

amino acids 37-84, 113-165, 204-262, 302-360, 397-453, 490-546.

FIGURE 41A

DNA329863

CTCAATCAGCTTTATGCAGAGAAGAAGCTTACTGAGCTCACTGCTGGTGCTGGTGTAGGC
AAGTGCTGCTTTGGCAATCTGGGCTGACCTGGCTTGTCTCCTCAGAACTCCTTCTCCAAC
CCTGGAGCAGGCTTCCATGCTGCTGTGGGCGTCCTTGCTGGCCTTTGCTCCAGTCTGTGG
ACAATCTGCAGCTGCACACAAACCTGTGATTTCCGTCCATCCTCCATGGACCACATTCTT
CAAAGGAGAGAGAGTGACTCTGACTTGCAATGGATTTTCAGTTCTATGCAACAGAGAAAAC
AACATGGTATCATCGGCACTACTGGGGAGAAAAGTTGACCCTGACCCAGGAAACACCCT
CGAGGTTTCGGGAATCTGGACTGTACAGATGCCAGGCCCGGGGCTCCCCACGAAGTAACCC
TGTGCGCTTGCTCTTTTCTTCAGACTCCTTAATCCTGCAGGCACCATATTCTGTGTTTGA
AGGTGACACATTGGTTCTGAGATGCCACAGAAGAAGGAAAGAGAAATTGACTGCTGTGAA
ATATACTTGGAATGGAAACATTCTTTCCATTTCTAATAAAAGCTGGGATCTTCTTATCCC
ACAAGCAAGTTCAAATAACAATGGCAATTATCGATGCATTGGATATGGAGATGAGAATGA
TGTATTTAGATCAAATTTCAAATAAATTAAAATTCAAGAACTATTTCCACATCCAGAGCT
GAAAGCTACAGACTCTCAGCCTACAGAGGGGAATTCTGTAAACCTGAGCTGTGAAACACA
GCTTCCTCCAGAGCGGTCAGACACCCCACTTCACTTCAACTTCTTCAGAGATGGCGAGGT
CATCCTGTCAGACTGGAGCACGTACCCGGAACCTCCAGCTCCCAACCGTCTGGAGAGAAAA
CTCAGGATCCTATTGGTGTGGTGCTGAAACAGTGAGGGGTAACATCCACAAGCACAGTCC
CTCGCTACAGATCCATGTGCAGCGGATCCCTGTGTCTGGGGTGCTCCTGGAGACCCAGCC
CTCAGGGGGCCAGGCTGTTGAAGGGGAGATGCTGGTCCTTGTCTGCTCCGTGGCTGAAGG
CACAGGGGATACCACATTCTCCTGGCACCGAGAGGACATGCAGGAGAGTCTGGGGAGGAA
AACTCAGCGTTCCCTGAGAGCAGAGCTGGAGCTCCCTGCCATCAGACAGAGCCATGCAGG
GGGATACTACTGTACAGCAGACAACAGCTACGGCCCTGTCCAGAGCATGGTGCTGAATGT
CACTGTGAGAGAGACCCCAAGCAACAGAGATGGCCTTGTTCGCCGCGGGAGCCACTGGAGG
GCTGCTCAGTGCTCTTCTCCTGGCTGTGGCCCTGCTGTTTCACTGCTGGCGTCGGAGGAA
GTCAGGAGTTGGTTTCTTGGGAGACGAAACCAGGCTCCCTCCCGCTCCAGGCCAGGAGA
GTCCTCCCATTTCCATCTGCCCTGCCAGGTGGAGCTTCAGTCGTTGTATGTTGATGTACA
CCCCAAAAGGGAGATTTGGTATACTCTGAGATCCAGACTACTCAGCTGGGAGAAGAAGA
GGAAGCTAATACCTCCAGGACACTTCTAGAGGATAAGGATGTCTCAGTTGTCTACTCTGA
GGTAAAGACACAACACCCAGATAACTCAGCTGGAAAGATCAGCTCTAAGGATGAAGAAAG
TTAAGGAGAATGAAAAGTTACGGGAACGTCCTACTCATGTGATTTCTCCCTTGTCCAAAGT
CCCAGGCCCAGTGCACTCCTTGCGGCACCTGGAATGATCAACTCATTCCAGCTTTCTAAT
TCTTCTCATGCATATGCATTCCTCCAGGAATACTCATTCGTCTACTCTGATGTTGGGA
TGGAATGGCCTCTGAAAGACTTCACTAAAATGACCAGGATCCACAGTTAAGAGAAGACCC
TGTAATATTTGCTGTGGGCTGACCTAATGCATTCCTAGGGTCTGCTTTAGAGAAGGGG
GATAAAGAGAGAGAAGGACTGTTATGAAAAACAGAAGCACAAATTTTGGTGAATTGGGAT
TTGCAGAGATGAAAAGACTGGGTGACCTGGATCTCTGCTTAATACATCTACAACCATTG
TCTCACTGGAGACTCACTTGCATCAGTTTGTTTAACTGTGAGTGGCTGCACAGGCACTGT
GCAAACAATGAAAAGCCCTTCACTTCTGCCTGCACAGCTTACACTGTCAGGATTCAGTT
GCAGATTAAAGAACCCATCTGGAATGGTTTACAGAGAGAGGAATTTAAAAGAGGACATCA
GAAGAGCTGGAGATGCAAGCTCTAGGCTGCGCTTCCAAAAGCAAATGATAATTATGTTAA
TGTCATTAGTGACAAAGATTTGCAACATTAGAGAAAAGAGACACAAATATAAAATTAAAA
ACTTAAGTACCAACTCTCCAAAACATAAATTTGAACTTAAAATATTAGTATAAACTCATAA
TAAACTCTGCCTTTAAAAAAGATAAATATTTCTACGTCTGTTCACTGAAATAATTACC
AACCCCTTAGCAATAAGCACTCCTTGCAGAGAGGTTTTATTCTCTAAATACCATTCCTTT

FIGURE 41B

CTCAAAGGAAATAAGGTTGCTTTTCTTGTAGGAACTGTGTCTTTGAGTTACTAATTAGTT
TATATGAGAATAATTCTTGCAATAAATGAAGAAGGAATAAAAGAAATAGGAAGCCACAAA
TTTGTATGGATATTTTCATGATACACCTACTGGTTAAATAATTGACAAAAACCAGCAGCCA
AATATTAGAGGTCTCCTGATGGAAGTGTACAATACCACCTACAAATTATCCATGCCCCAA
GTGTTAAACTGAATCCATTCAAGTCTTTCTAACTGAATACTTGT'TTTATAGAAAATGCA
TGGAGAAAAGGAATTTGTTTAAATAACATTATGGGATTGCAACCAGCAAAACATAAACTG
AGAAAAAGTTCTATAGGGCAAATCACCTGGCTTCTATAACAAATAAATGGGAAAAAAATG
AAATAAAAAGAAGAGAGGGGAGGAAGAAAGGGAGAGAGAAGAAAAGAAAAATGAAGAAAAG
TAATTAGAATATTTTCAACATAAAGAAAAGACGAATATTTAAGGTGACAGATATCCCAAC
TACGCTGATTTGATCTTTACAAATTATATGAGTGTATGAATTTGTACATGTATCACCCC
CAAAAAAGAGAAAAAGAAAAATAGAAGACATATAAATTAAATGAGACGAGACATGTCGA
CCAAAAGGAATGTGTGGGTCTTGT'TTGGATCCTGACTCAAATTAAGAAAAAATAAACTA
CCTACGAAATACTAAGAAAAATTTGTATACTAATATTAAGAAATTGTTGTGTGT'TTTGGA
TATAAGTGATAGTTTATTGTAGTGATGTTTTTATAAAAGCAAAGGATATTCAC'TTTCAG
CGCTTATACTGAAGTATTAGATTAAAGCTTATTAACGTA

FIGURE 42A

DNA329863

><subunit 1 of 1, 515 aa, 1 stop

><MW: 57224, pI: 6.45, NX(S/T): 4

MLLWASLLAFAPVCGQSAAAHKPVISVHPPWTTFFKGERVTLTTCNGFQFYATEKTTWYHR
HYWGEKLTLTTPGNTLEVRESGLYRCQARGSPRSNPVRLLFSSDSLILQAPYSVFEGDTLV
LRCHRRRKEKLTAVKYTWNGNLSISNKSVDLLIPQASSNNNGNYRCIGYGDENDVFRSN
FKIIKIQELFPHPKATDSQPTGNSVNLSCETQLPPERSDTPLHFNFRRDGEVILSDW
STYPELQLPTVWRENSGSYWCGAETVRGNIHKHSPSLQIHVQRIPVSGVLLETQPSGGQA
VEGEMLVLCVSAEGTGDTTFSWHREDMQESLGRKTQORSLRAELELPAIRQSHAGGYCT
ADNSYGPVQSMVLNVTVRETTPGNRDGLVAAGATGGLLSALLLAVALLFHCWRRRKSGVGF
LGDETRLPPAPGPGESSHSICPAQVELQSLYVDVHPKKGDLVYSEIQTTQLGEEEEANTS
RTLLEDKDVSVVYSEVKTQHPDNSAGKISSKDEES

Signal Sequence.

amino acids 1-16.

Transmembrane domain.

amino acids 387-407.

N-glycosylation site.

amino acids 147-150, 209-212, 374-377, 478-481.

Glycosaminoglycan attachment site.

amino acids 416-419.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-416.

Protein kinase C phosphorylation site.

amino acids 52-54, 90-92, 146-148, 265-267, 336-338, 339-341, 376-378, 479-481, 509-511.

Casein kinase II phosphorylation site.

amino acids 112-115, 242-245, 311-314, 376-379, 482-485, 509-512, 510-513.

Tyrosine kinase phosphorylation site.

amino acids 457-463.

N-myristoylation site.

amino acids 15-20, 81-86, 89-94, 140-145, 163-168, 205-210, 257-262, 315-320, 355-360, 382-387, 386-391, 391-396, 394-399, 395-400.

Amidation site.

amino acids 332-335.

FIGURE 42B

Immunoglobulin domain.

amino acids 37-87, 116-169, 205-263, 303-361.

FIGURE 43

DNA346528

ACACACCCACAGGACCTGCAGCTGAACGAAGTTGAAGACAACTCAGGAGATCTGTTGGAA
AGAGAACGATAGAGGAAAATATATGAATGTTGCCATCTTTAGTTCCCTGTGTTGGGAAAA
CTGTCTGGCTGTACCTCCAAGCCTGGCCAAACCCTGTGTTTGAAGGAGATGCCCTGACTC
TGCGATGTCAGGGATGGAAGAATACACCACTGTCTCAGGTGAAGTTCTACAGAGATGGAA
AATTCCTTCATTTCTCTAAGGAAAACCAGACTCTGTCCATGGGAGCAGCAACAGTGCAGA
GCCGTGGCCAGTACAGCTGCTCTGGGCAGGTGATGTATATTCACAGACATTCACACAAA
CTTCAGAGACTGCCATGGTTCAAGTCCAAGAGCTGTTTCCACCTCCTGTGCTGAGTGCCA
TCCCCTCTCCTGAGCCCCGAGAGGGTAGCCTGGTGACCCTGAGATGTCAGACAAAGCTGC
ACCCCCTGAGGTGAGCCTTGAGGCTCCTTTTCTCCTTCCACAAGGACGGCCACACCTTGC
AGGACAGGGGCCCTCACCCAGAACTCTGCATCCCGGGAGCCAAGGAGGGAGACTCTGGGC
TTTACTGGTGTGAGGTGGCCCCTGAGGGTGGCCAGGTCCAGAAGCAGAGCCCCCAGCTGG
AGGTCAGAGTGCAGGCTCCTGTATCCCGTCCTGTGCTCACTCTGCACCACGGGCCTGCTG
ACCCTGCTGTGGGGGACATGGTGCAGCTCCTCTGTGAGGCACAGAGGGGCTCCCCTCCGA
TCCTGTATTCTTCTACCTTGATGAGAAGATTGTGGGGAACCACTCAGCTCCCTGTGGTG
GAACCACCTCCCTCCTCTTCCCAGTGAAGTCAGAACAGGATGCTGGGAACTACTCCTGCG
AGGCTGAGAACAGTGTCTCCAGAGAGAGGAGTGAGCCCAAGAAGCTGTCTCTGAAGGGTT
CTCAAGTCTTGTTCACTCCCGCCAGCAACTGGCTGGTTCCCTTGGCTTCCTGCGAGCCTGC
TTGGCCTGATGGTTATTGCTGCTGCACTTCTGGTTTATGTGAGATCCTGGAGAAAAGCTG
GGCCCCTTCCATCCCAGATACCACCCACAGCTCCAGGTGGAGAGCAGTGCCCACTATATG
CCAACGTGCATCACAGAAAGGGAAAGATGAAGGTGTTGTCTACTCTGTGGTGCATAGAA
CCTCAAAGAGGAGTGAAGGACAGTTCTATCATCTGTGCGGAGGTGAGATGCCTGCAGCCC
AGTGAGGTTTCATCCACGGAGGTGAATATGAGAAGCAGGACTCTCCAAGAACCCCTTAGC
GACTGTGAGGAGGTTCCTCTGCTAGTGATGGTGTTCCTATCAACACACGCCCACCCCA
GTCTCCAGTGCTCCTCAGGAAGACAGTGGGGTCCTCAACTCTTTCTGTGGGTCCCTCAGT
TCCCAAGCCCAGCATCACAGAGCCCCCTGAGCCCTTGTCTGGTCAGGAGCACCTGAACC
CTGGGTTCTTTTCTTAGCAGAAGACCAACCAATGGAATGGGAAGGGAGATGCTCCCACCA
ACACACACACTTAGGTTCAATCAGTGACACTGGACACATAAGCCACAGATGTCTTCTTTC
CATACAAGCATGTTAGTTCGCCCCAATATACATATATATATGAAATAGTCATGTGCCGCA
TAACAACATTTTCAGTCAGTGATAGACTGCATACACAACAGTGGTCCCATAAGACTGTAAT
GGAGTTTAAAAATTCTACTGCCTAGTGATATCATAGTTGCCTTAACATCATAACACAAC
ACATTTCTCACGCGTTTGTGGTGATGCTGGTACAAACAAGCTACAGCGCCGCTAGTCATA
TACAAATATAGCACATACAATTATGTACAGTACACTATACTTGATAATGATAATAAACA
CTATGTTACTGGT

FIGURE 44

DNA346528

><subunit 1 of 1, 392 aa, 1 stop
><MW: 42948, pI: 8.37, NX(S/T): 3
MLPSLVPCVGKTVWLYLQAWPNPVFEGDALTLRCQGWKNTPLSQVKFYRDGKFLHFSKEN
QTLSMGAATVQSRGQYSCSGQVMYIPQTFTQTSETAMVQVQELFPPPVLSAIPSPEPREG
SLVTLRCQTKLHPLRSALRLLFSFHKDGHTLQDRGPHPELCIPGAKEGDSGLYWCEVAPE
GGQVQKQSPQLEVRVQAPVSRPVLTLHHGPADPAVGDMVQLLCEAQRGSPPILYSFYLDE
KIVGNHSAPCGGTTSLLFVKSEQDAGNYSCEAENSVSRERSEPKKLSLKGSQVLFTPAS
NWLVPWLPASLLGLMVIAAALLVYVRSWRKAGPLPSQIPPTAPGGEQCPLYANVHHQKGK
DEGVVYSVVHRTSKRSEGQFYHLCCGEMPAAQ

Transmembrane domain.

amino acids 302-322.

N-glycosylation site.

amino acids 60-63, 245-248, 268-271.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 285-288.

Protein kinase C phosphorylation site.

amino acids 31-33, 124-126, 288-290, 327-329, 372-374, 373-375.

Casein kinase II phosphorylation site.

amino acids 150-153, 262-265.

Tyrosine kinase phosphorylation site.

amino acids 166-173, 261-269, 358-366, 374-381.

N-myristoylation site.

amino acids 74-79, 120-125, 164-169, 171-176, 251-256, 267-272, 363-368.

Immunoglobulin domain.

amino acids 27-80, 120-177, 216-273.

FIGURE 45

DNA212930

CCATTGTTCTCAACATTCTAGCTGCTCTTGCTGCATTTGCTCTGGAATTCTTGTAGAGAT
ATTACTTGTCTTCCAGGCTGTTCTTTCTGTAGCTCCCTTGTTTTCTTTTGTGATC ATG
TTGCAGATGGCTGGGCAGTGCTCCCAAATGAATATTTTGACAGTTTGTTCATGCTTGC
ATACCTTGTCAACTTCGATGTTCTTCTAATACTCCTCCTCTAACATGTCAGCGTTATTGT
AATGCAAGTGTGACCAATTCAGTGAAAGGAACGAATGCGATTCTCTGGACCTGTTTGGGA
CTGAGCTTAATAATTTCTTTGGCAGTTTTCGTGCTAATGTTTTTGTCTAAGGAAGATAAGC
TCTGAACCATTAAAGGACGAGTTTAAAAACACAGGATCAGGTCTCCTGGGCATGGCTAAC
ATTGACCTGGAAAAGAGCAGGACTGGTGATGAAATTATTCTTCCGAGAGGCCTCGAGTAC
ACGGTGGAAGAATGCACCTGTGAAGACTGCATCAAGAGCAAACCGAAGGTCGACTCTGAC
CATTGCTTTCCACTCCCAGCTATGGAGGAAGGCGCAACCATTTCTTGTCAACACGAAAACG
AATGACTATTGCAAGAGCCTGCCAGCTGCTTTGAGTGCTACGGAGATAGAGAAATCAATT
TCTGCTAGGTAATTAACCATTTGCACTCGAGCAGTGCCACTTTAAAAATCTTTTGTGAGA
ATAGATGATGTGTCAGATCTTTTAGGATGACTGTATTTTTCAGTTGCCGATACAGCTTT
TTGTCCTCTAACTGTGGAACTCTTTATGTTAGATATATTTCTCTAGGTTACTGTTGGGA
GCTTAATGGTAGAACTTCCTTGTTTCATGATTAAAGTCTTTTTTTTCTGAAAAAA

FIGURE 46

DNA212930

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA212930
><subunit 1 of 1, 184 aa, 1 stop
><MW: 20138, pI: 5.30, NX(S/T): 1
MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
YTVEECTCEDCIKSKPKVDSDFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
ISAR
```

Signal sequence.

amino acids 1-28.

Transmembrane domain.

amino acids 55-75.

N-glycosylation site.

amino acids 42-45.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 78-81.

Protein kinase C phosphorylation site.

amino acids 48-50, 158-160, 182-184.

Casein kinase II phosphorylation site.

amino acids 9-12, 109-112, 122-125, 127-130, 173-176, 175-178.

N-myristoylation site.

amino acids 118-123.

FIGURE 47

DNA335918

CTTCCCAGCCTTCGGAACATATGGAGCCCGCACTCTCCAGTTCATCACCACCCAGCATCC
CTACTCTTGCACTAACAGTTTCCGCTATTTTGCACCACCTGCCTNGNCCTTATGGGCAA
CTCAAGGAAGAAAGGAAAGAAGAGATAGAGGAAAAATGGATTCAACANATGAAAGTGTTT
TTTCTGACTACTGCTGTGTTTACAAACATTTTAATCATCAAAACATGCTTTATTTGATAG
AAAGATCAAATCTGCCTTTGTAAAACAAGAGACTATTTTAATCATTAAGACAACACANAT
GTTTGATTTGGAGGCGTGTTCTCATTCAAAACCTTGC

[illegible]

FIGURE 49A

DNA225820

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA225820
><subunit 1 of 1, 467 aa, 1 stop
><MW: 51818, pI: 10.69, NX(S/T): 7

MPPPRLLFFLLFLTPMEVRPEEPLVVKVEEGDNAVLQCLKGTSDGPTQQLTWSRESPLKP
FLKLSLGLPGLGIHMRPLAIWLFI FNVSQQMGGFYLCQPGPPSEKAWQPGWTVNVEGSGE
LFRWNVSDLGGLGCGLKNRSSSEGPSSPSGKLMSPKLYVWAKDRPEIWEGEPPCVPPRDSL
NQSLSQDLTMAPGSTLWLSCGVPPDSVSRGPLSWTHVHPKGPKSLLSLELKDDRPARDMW
VMETGLLLPRATAQDAGKYCHRGNL TMSFHLEITARPVLWHWLLRTGGWKVSAVTLAYL
IFCLCSLVGILHLQRALVLRKRKRMTDPTRRFFKVTPPPGSGPQNQYGNVLSLPTPTSG
LGRAQRWAAGLGGTAPSYGNPSSDVQADGALGSRSRREWAQKKRKGRAMRNLTVRRT PSS
MRTTPTLGRTSSPRMAAATRTL RMSPWVLRMKTPSPTLSLMRTRMK S

Signal Sequence.

Amino acids 1-20.

Transmembrane Domain.

Amino acids 294-314.

Immunoglobulin Domain.

Amino acids 31-99, 193-263.

N-glycosylation Site.

Amino acids 86-89, 125-128, 138-141, 181-184, 265-268, 411-414.

Glycosaminoglycan attachment site.

Amino acids 359-362.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 324-327.

Protein kinase C phosphorylation site.

Amino acids 103-105, 148-150, 153-155, 275-277, 330-332, 395-397, 413-415, 420-422, 432-434, 441-443.

Casein kinase II phosphorylation site.

Amino acids 14-17, 252-255, 395-398.

Figure 49B

N-myristoylation Site.

Amino acids 130-135, 131-136, 349-354, 360-365, 370-375, 373-378, 379-384, 389-394.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 190-200.

FIGURE 50A

DNA88116

CCATCCCATAGTGAGGGAAGACACGCGGAAACAGGCTTGCACCCAGACACGACACC **ATGC**
ATCTCCTCGGCCCCTGGCTCCTGCTCCTGGTTCTAGAATACTTGGCTTTCTCTGACTCAA
GTAAATGGGTTTTTTGAGCACCCCTGAAACCCCTCTACGCCTGGGAGGGGGCCTGCGTCTGGA
TCCCCTGCACCTACAGAGCCCTAGATGGTGACCTGGAAAGCTTCATCCTGTTCCACAATC
CTGAGTATAACAAGAACACCTCGAAGTTTGATGGGACAAGACTCTATGAAAGCACAAAGG
ATGGGAAGGTTTCCTTCTGAGCAGAAAAGGGTGCAATTCCTGGGAGACAAGAATAAGAACT
GCACACTGAGTATCCACCCGGTGACCTCAATGACAGTGGTCAGCTGGGGCTGAGGATGG
AGTCCAAGACTGAGAAATGGATGGAACGAATACACCTCAATGTCTCTGAAAGGCCTTTTC
CACCTCATATCCAGCTCCCTCCAGAAATTCAAGAGTCCCAGGAAGTCACTCTGACCTGCT
TGCTGAATTTCTCCTGCTATGGGTATCCGATCCAATTGCAGTGGCTCCTAGAGGGGGTTC
CAATGAGGCAGGCTGCTGTCACCTCGACCTCCTTGACCATCAAGTCTGTCTTCACCCGGA
GCGAGCTCAAGTTCTCCCCACAGTGGAGTCACCATGGGAAGATTGTGACCTGCCAGCTTC
AGGATGCAGATGGGAAGTTCTCTCCAATGACACGGTGCAGCTGAACGTGAAGCACACCC
CGAAGTTGGAGATCAAGGTCCTCCAGTGATGCCATAGTGAGGGAGGGGGACTCTGTGA
CCATGACCTGCGAGGTCAGCAGCAGCAACCCGGAGTACACGACGGTATCCTGGCTCAAGG
ATGGGACCTCGCTGAAGAAGCAGAATACATTACGCTAAACCTGCGCGAAGTGACCAAGG
ACCAGAGTGGGAAGTACTGCTGTCAGGTCTCCAATGACGTGGGCCCGGGAAGGTCGGAAG
AAGTGTTCTGCAAGTGCAGTATGCCCCGGAACCTTCCACGGTTCAGATCCTCCACTCAC
CGGCTGTGGAGGGAAGTCAAGTCGAGTTTCTTTGCATGTCACTGGCCAATCCTCTTCCAA
CAAATTACACGTGGTACCACAATGGGAAAGAAATGCAGGGAAGGACAGAGGAGAAAGTCC
ACATCCCAAAGATCCTCCCCTGGCACGCTGGGACTTATTCTGTGTGGCAGAAAACATTC
TTGGTACTGGACAGAGGGGCCCCGGGAGCTGAGCTGGATGTCCAGTATCCTCCCAAGAAGG
TGACCACAGTGATTCAAAACCCCATGCCGATTCGAGAAGGAGACACAGTGACCCTTTCTCT
GTA ACTACAATTCCAGTAACCCAGTGTTACCCGGTATGAATGGAAACCCCATGGCGCCT
GGGAGGAGCCATCGCTTGGGGTGCTGAAGATCCAAAACGTTGGCTGGGACAACACAACCA
TCGCCTGCGCACGTTGTAATAGTTGGTGCTCGTGGGCCTCCCCTGTCGCCCTGAATGTCC
AGTATGCCCCCGAGACGTGAGGGTCCGGAAAATCAAGCCCCTTTCCGAGATTCACCTCTG
GAAACTCGGTCAGCCTCCAATGTGACTTCTCAAGCAGCCACCCCAAAGAAGTCCAGTTCT
TCTGGGAGAAAAATGGCAGGCTTCTGGGGAAAGAAAGCCAGCTGAATTTTGACTCCATCT
CCCCAGAAGATGCTGGGAGTTACAGCTGCTGGGTGAACAACTCCATAGGACAGACAGCGT
CCAAGGCCTGGACACTTGAAGTGCTGTATGCACCCAGGAGGCTGCGTGTGTCCATGAGCC
CGGGGGACCAAGTGATGGAGGGGAAGAGTGCAACCCTGACCTGTGAGAGTGACGCCAACC
CTCCCGTCTCCCACTACACCTGGTTTGACTGGAATAACCAAAGCCTCCCCACACAGCC
AGAAGCTGAGATTGGAGCCGGTGAAGGTCCAGCACTCGGGTGCCTACTGGTGCCAGGGGA
CCAACAGTGTGGGCAAGGGCCGTTTCGCCTCTCAGCACCCCTTACTGTCTACTATAGCCCGG
AGACCATCGGCAGGCGAGTGGCTGTGGGACTCGGGTCCTGCCTCGCCATCCTCATCCTGG
CAATCTGTGGGCTCAAGCTCCAGCGACGTTGGAAGAGGACACAGAGCCAGCAGGGGCTTC
AGGAGAATTCCAGCGGCCAGAGCTTCTTTGTGAGGAATAAAAAGGTTAGAAGGGCCCCC
TCTCTGAAGGCCCCCACTCCCTGGGATGCTACAATCCAATGATGGAAGATGGCATTAGCT
ACACCACCCTGCGCTTTCCCGAGATGAACATAACCAAGTGGAGATGCAGAGTCCTCAG
AGATGCAGAGACCTCCCCGGACCTGCGATGACACGGTCACTTATTAGCATTTGCACAAGC

FIGURE 50B

GCCAAGTGGGCGACTATGAGAACGTCATTCCAGATTTTCCAGAAGATGAGGGGATTCATT
ACTCAGAGCTGATCCAGTTTGGGGTCGGGGAGCGGCCTCAGGCACAAGAAAATGTGGACT
ATGTGATCCTCAAACATTGACACTGGATGGGCTGCAGCAGAGGCACTGGGGGCAGCGGGG
GCCAGGGAAGTCCCCGAGTTTCCCCAGACACCGCCACATGGCTTCCTCCTGCGTGCATGT
GCGCACACACACACACACACGCACACACACACACACACACTCACTGCGGAGAACCTTGTG
CCTGGCTCAGAGCCAGTCTTTTTTGGTGAGGGTAACCCCAAACCTCCAAAACCTCCTGCCCC
TGTTCTCTTCCACTCTCCTTGCTACCCAGAAATCATCTAAATACCTGCCCTGACATGCAC
ACCTCCCCTGCCCCACCAGCCCACTGGCCATCTCCACCCGGAGCTGCTGTGTCCTCTGGA
TCTGCTCGTCATTTTCCTTCCCTTCTCCATCTCTCTGGCCCTCTACCCCTGATCTGACAT
CCCCACTCACGAATATTATGCCCAGTTTCTGCTCTGAGGGAAAGCCCAGAAAAGGACAG
AAACGAAGTAGAAAGGGGCCCAGTCCTGGCCTGGCTTCTCCTTTGGAAGTGAGGCATTGC
ACGGGGAGACGTACGTATCAGCGGCCCCCTTGACTCTGGGGACTCCGGGTTTGAGATGGAC
ACACTGGTGTGGATTAACCTGCCAGGGAGACAGAGCTCACAATAAAAATGGCTCAGATGC
CACTTCAAAGAAAAAAAAAAAA

FIGURE 51A

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA88116

><subunit 1 of 1, 847 aa, 1 stop

><MW: 95452, pI: 6.82, NX(S/T): 13

MHLLGPWLLLLLVLEYLAFSDSSKWVFEHPETLYAWEGACVWIPCTYRALDGDLESFILFH
 NPEYNKNTSKFDGTRLYEESTKDGKVPSEQKRVQFLGDKNKNCTLSIHPVHLNDSGQLGLR
 MESKTEKWMERIHLNVSERPFPFPHIQLPPEIQESQEVTLTCLLNFSCYGYPIQLQWLLEG
 VPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKIVTCQLQDADGKFLSNDTVQLNVKH
 TPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTTVSWLKDGTSLKKQNTFTLNLREVT
 KDQSGKYCCQVSNDVGPGRSEEVFLQVQYAPEPSTVQILHSPAVEGSQVEFLCMSLANPL
 PTNYTWYHNGKEMQGRTEEKVHIPKILPWHAGTYSCVAENILGTGQRGPGAELDVQYPPK
 KVTTVIQNPMPIREGDTVTLSCNYNSSNPSVTRYEWKPHGAWEEPSLGVLKIQNVGWDNT
 TIACARCNSWCSWASPVALNVQYAPRDVRVRKIKPLSEIHSGNSVSLQCDFSSSHPKVQ
 FFWEKNGRLLGKESQLNFDSISPEDAGSYSCWVNNSIGQTASKAWTLEVLYAPRRLRVSM
 SPGDQVMEGKSATLTCESDANPPVSHYTWFDWNNQSLPHHSQKLRLEPVKVQHSGAYWCQ
 GTNSVGKGRSPLSTLTVYYSPETIGRRVAVGLGSLAILILAICGLKLQRRWKRTQSQQG
 LQENSSGQSFFVRNKKVRRAPLSEGPLSLGCYNPMMEDGISYTTLRFPENIIPRTGDAES
 SEMQRPRTCDTDTVTYSALHKRQVGDYENVIPDFPEDEGIHYSELIQFGVGERPQAQENV
 DYVILKH

Signal sequence.

Amino acids 1-19.

Transmembrane domain.

Amino acids 685-705.

Immunoglobulin domain.

Amino acids 154-221, 258-311, 346-398, 435-486, 522-573, 609-611.

N-glycosylation site.

Amino acids 67-70, 101-104, 112-115, 135-138, 164-167, 231-234, 363-366, 445-448, 479-482, 574-577, 634-637, 724-727.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 420-423.

Protein kinase C phosphorylation site.

Amino acids 21-23, 45-47, 68-70, 79-81, 125-127, 137-139, 194-196, 241-243, 285-287, 304-306, 641-643, 764-766.

FIGURE 51B**Casein kinase II phosphorylation site.**

Amino acids 69-72, 79-82, 123-126, 200-203, 249-252, 270-273, 347-350, 452-455, 562-565, 601-604, 628-631, 789-792.

Tyrosine kinase phosphorylation site.

Amino acids 788-796.

N-myristoylation site.

Amino acids 392-397, 522-527, 567-572, 578-583, 655-660, 691-696, 693-698, 720-725, 759-764, 819-824.

Amidation site.

Amino acids 684-687.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 386-396.

FIGURE 52

DNA227752

CCAACCACAAGCACCAAAGCAGAGGGGCAGGCAGCACACCACCCAGCAGCCAGAGCACCA
GCCCAGCCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGACGCCGAGGTTGCCG
CCCTCCTGGAGAACTTCAGCTCTTCCTATGACTATGGAGAAAACGAGAGTGACTCGTGCT
GTACCTCCCCGCCCTGCCACAGGACTTCAGCCTGAACTTCGACCGGGCCTTCCTGCCAG
CCCTCTACAGCCTCCTCTTTCTGCTGGGGCTGCTGGGCAACGGCGCGGTGGCAGCCGTGC
TGCTGAGCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCCTGCTCCACCTAGCTGTAG
CAGACACGCTGCTGGTGCTGACACTGCCGCTCTGGGCAGTGGACGCTGCCGTCCAGTGGG
TCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAG
GAGCCCTCCTGCTGGCCTGCATCAGCTTTGACCGCTACCTGAACATAGTTCATGCCACCC
AGCTCTACCGCCGGGGGGCCCCGGCCCGCGTGACCCCTCACCTGCCTGGCTGTCTGGGGGC
TCTGCCTGCTTTTCGCCCTCCCAGACTTCATCTTCCTGTGCGGCCACCACGACGAGCGCC
TCAACGCCACCCACTGCCAATACTTCCCACAGGTGGGCCGCACGGCTCTGCGGGTGC
TGCAGCTGGTGGCTGGCTTTCTGCTGCCCCCTGCTGGTCATGGCCTACTGCTATGCCACA
TCCTGGCCGTGCTGCTGGTTTCCAGGGGCCAGCGGCGCCTGCGGGCCATGCGGCTGGTGG
TGGTGGTCGTGGTGGCCTTTGCCCTCTGCTGGACCCCTATCACCTGGTGGTGCTGGTGG
ACATCCTCATGGACCTGGGCGCTTTGGCCCGCAACTGTGGCCGAGAAAGCAGGGTAGACG
TGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGCACTGCTGCCTCAACCCGCTGCTCT
ATGCCTTTGTAGGGGTCAAGTTCCGGGAGCGGATGTGGATGCTGCTCTTGCGCCTGGGCT
GCCCCAACCAGAGAGGGCTCCAGAGGCAGCCATCGTCTTCCCGCCGGGATTTCATCCTGGT
CTGAGACCTCAGAGGCCTCCTACTCGGGCTTGTGAGGCGGGAATCCGGGCTCCCCTTTCG
CCCACAGTCTGACTTCCCCGCATTCCAGGCTCCTCCCTCCCTCTGCCGGCTCTGGCTCTC
CCCAATATCCTCGCTCCCGGGACTCACTGGCAGCCCCAGCACACCAGGTCTCCCGGGAA
GCCACCCTCCCAGCTCTGAGGACTGCACCATTGCTGCTCCTTAGCTGCCAAGCCCCATCC
TGCCGCCCCGAGGTGGCTGCCTGGAGCCCCACTGCCCTTCTCATTTGGAACTAAACTTC
ATCTTCCCCAAGTGCGGGGAGTACAAGGCATGGCGTAGAGGGTGCTGCCCCATGAAGCCA
CAGCCCAGGCCTCCAGCTCAGCAGTGACTGTGGCCATGGTCCCCAAGACCTCTATATTTG
CTCTTTTATTTTATGTCTAAAATCCTGCTTAAACTTTTCAATAAACAAGATCGTCAGG
ACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA227752

><subunit 1 of 1, 368 aa, 1 stop

><MW: 40660, pI: 8.10, NX(S/T): 3

MVLEVSDHQVLNDAEVAALLENFSSSYDYGENESDSCCTSPPCPQDFSLNFDRAFLPALY
 SLLFLLGLLGNGAVAVALLSRRTALSSTDTFLLHLAVADTLLVLTPLWAVDAAVQWVFG
 SGLCKVAGALFNINFYAGALLLACISFDRLNIVHATQLYRRGPPARVTLTCLAVWGLCL
 LFALPDFIFLSAHHDERLNATHCQYNFPQVGR TALRVLQLVAGFLLPLLVMAYCYAHILA
 VLLVSRGQRRRLRAMRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESRVDVAK
 SVTSGLGVMHCCLNPLLYAFVGVKFRERMWMLLLRLGCPNQRGLQRQPSSSRDSSWSET
 SEASYSGL

Transmembrane domain.

Amino acids 54-74, 90-110, 129-149, 168-188, 216-236, 260-280, 303-323.

Seven transmembrane receptor domain.

Amino acids 70-318.

N-glycosylation site.

Amino acids 22-25, 32-35, 199-202.

Glycosaminoglycan attachment site.

Amino acids 304-307,

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 352-355.

Protein kinase C phosphorylation site.

Amino acids 80-82, 350-352, 351-353.

Casein kinase II phosphorylation site.

Amino acids 25-28, 86-89, 294-297, 351-354, 356-359.

N-myristoylation site.

Amino acids 67-72, 72-77, 120-125, 128-133.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 134-144.

FIGURE 54

DNA119476

GAGGGAAGAACACAATGGATCTGGTGCTAAAAAGATGCCTTCTTCATTTGGCTGTGATAG
GTGCTTTGCTGGCTGTGGGGGCTACAAAAGTACCCAGAAACCAGGACTGGCTTGGTGTCT
CAAGGCAACTCAGAACCAGCCTGGAACAGGCAGCTGTATCCAGAGTGGACAGAAGCCC
AGAGACTTGACTGCTGGAGAGGTGGTCAAGTGTCCCTCAAGGTCAGTAATGATGGGCCTA
CACTGATTGGTGCAAATGCCTCCTTCTCTATTGCCTTGAAGTCCCTGGAAGCCAAAAGG
TATTGCCAGATGGGCAGGTTATCTGGGTCAACAATACCATCATCAATGGGAGCCAGGTGT
GGGGAGGACAGCCAGTGTATCCCCAGGAACTGACGATGCCTGCATCTTCCCTGATGGTG
GACCTTGCCCATCTGGCTCTTGGTCTCAGAAGAGAAGCTTTGTTTATGTCTGGAAGACCT
GGGGCCAATACTGGCAAGTTCTAGGGGGGCCAGTGTCTGGGCTGAGCATTGGGACAGGCA
GGGCAATGCTGGGCACACACACCATGGAAGTGACTGTCTACCATCGCCGGGGATCCCGGA
GCTATGTGCCTCTTGCTCATTCAGCTCAGCCTTCACCATTAAGTACCAGGTGCCTTTCT
CCGTGAGCGTGTCCAGTTGCGGGCCTTGATGGAGGGAACAAGCACTTCCTGAGAAATC
AGCCTCTGACCTTTGCCCTCCAGCTCCATGACCCAGTGGCTATCTGGCTGAAGCTGACC
TCTCCTACACCTGGGACTTTGGAGACAGTAGTGGAACCCTGATCTCTCGGGCACTTGTGG
TCACTCATACTTACCTGGAGCCTGGCCCAGTCACTGCCAGGTGGTCTGCAGGCTGCCA
TTCTCTCACCTCCTGTGGCTCCTCCCCAGTTCCAGGCACCACAGATGGGCACAGGCCAA
CTGCAGAGGGCCCTAACACCACAGCTGGCCAAGTGCCCTACTACAGAAGTTGTGGGTACTA
CACCTGGTCAGGCGCCAACTGCAGAGCCCTCTGGAACCACATCTGTGCAGGTGCCAACCA
CTGAAGTCATAAGCACTGCACCTGTGCAGATGCCAACTGCAGAGAGCACAGGTATGACAC
CTGAGAAGGTGCCAGTTTCAGAGGTCATGGGTACCACACTGGCAGAGATGTCAACTCCAG
AGGCTACAGGTATGACACCTGCAGAGGTATCAATTGTGGTGCTTTCTGGAACCACAGCTG
CACAGGTAACAACCTACAGAGTGGGTGGAGACCACAGCTAGAGAGCTACCTATCCCTGAGC
CTGAAGGTCCAGATGCCAGCTCAATCATGTCTACGGAAAGTATTACAGGTTCCCTGGGCC
CCCTGCTGGATGGTACAGCCACCTTAAGGCTGGTGAAGAGACAAGTCCCCCTGGATTGTG
TTCTGTATCGATATGGTTCCCTTTCCGTACCCCTGGACATTGTCCAGGGTATTGAAAGTG
CCGAGATCCTGCAGGCTGTGCCGTCCGGTGAGGGGGATGCATTTGAGCTGACTGTGTCT
GCCAAGGCGGGCTGCCCAAGGAAGCCTGCATGGAGATCTCATCGCCAGGGTGCCAGCCCC
CTGCCCAGCGGCTGTGCCAGCCTGTGCTACCCAGCCCAGCCTGCCAGCTGGTTCTGCACC
AGATACTGAAGGGTGGCTCGGGGACATACTGCCTCAATGTGTCTCTGGCTGATACCAACA
GCCTGGCAGTGGTCAGCACCCAGCTTATCATGCCTGGTCAAGAAGCAGGCCTTGGGCAGG
TTCCGCTGATCGTGGGCATCTTGCTGGTGTGATGGCTGTGGTCCTTGATCTCTGATAT
ATAGGCGCAGACTTATGAAGCAAGACTTCTCCGTACCCAGTTGCCACATAGCAGCAGTC
ACTGGCTGCGTCTACCCCGCATCTTCTGCTCTTGTCCATTGGTGAGAACAGCCCCCTCC
TCAGTGGGCAGCAGGTCTTGAGTACTCTCATATGATGCTGTGATTTTCCTGGAGTTGACAG
AAACACCTATATTTCCCCCAGTCTTCCCTGGGAGACTACTATTAAGTAAATAAATACTC
AGAGCCTGA

FIGURE 55A

><Thu Jul 20 10:27:08 2000 DNA119476 [min]
 ></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119476
 ><subunit 1 of 1, 661 aa, 1 stop
 ><MW: 70255, pI: 5.52, NX(S/T): 5

MDLVLRCLLHLAVIGALLAVGATKVPRNQDWLGVSRLRTKAWNRQLYPEWTEAQRLLDC
 WRGGQVSLKVSNDGPTLIGANASFSLNFPQSQKVLDPGQVIWVNNTIINGSQVWGGQP
 VYPQETDDACIFPDGGPCPSGSWSQKRSEFVYVWKTWGQYWQVLGGPVSGLSIGTGRAMLG
 THTMEVTVYHRRGSRSYVPLAHSSSAFTITDQVPFSVSVSQLRALDGGNKHFLRNQPLTF
 ALQLHDPSGYLAELADLSYTWDFGDSSGTLISRALVVHTYLEPGPVTAQVVLQAAIPLTS
 CGSSPVPGTTDGHRTAEAPNTTAGQVPTTEVVGTTPGQAPTAEPSTTSVQVPTTEVIS
 TAPVQMPTAESTGMTPEKVPVSEVMGTTLAEMSTPEATGMTPAEVSIVVLSGTTAAQVTT
 TEWVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGTATLRLVKRQVPLDCVLYRY
 GSFSVTLDIVQGIESAELQAVPSGEGDAFELTVSCQGGLPKEACMEISSPGCQPPAQRLL
 CQPVLPSPACQLVLHQILKGGSGTYCLNVSLADTNSLAVVSTQLIMPGQEAGLGQVPLIV
 GILLVLMVVLASLIYRRRLMKQDFSVLPQLPHSSSHWLRLPRIFCSCPIGENSPLLSGQQ
 V

Signal Sequence.

Amino acids 1-20.

Transmembrane Domain.

Amino acids 594-614.

N-glycosylation site.

Amino acids 81-84, 106-109, 111-114, 321-324, 568-571.

Glycosaminoglycan attachment site.

Amino acids 504-507.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 191-194.

Protein kinase C phosphorylation site.

Amino acids 67-69, 93-95, 144-146, 174-176, 427-429, 463-465.

Casein kinase II phosphorylation site.

Amino acids 208-211, 279-282, 388-391, 401-404, 419-422, 427-430, 570-573.

FIGURE 55B

N-myristoylation site.

Amino acids 16-21, 63-68, 79-84, 164-169, 173-178, 267-272, 308-313, 325-330, 334-339, 338-343, 386-391, 399-404, 412-417, 492-497, 560-565, 588-593.

FIGURE 56A

DNA254890

CAGTCGGCACCGGCGAGGCCGTGCTGGAACCCGGGCCTCAGCCGCAGCCGCAGCGGGGCC
GACATGACGACAGCTCCCCAGGAGCCCCCGCCCGCCCCCTCCAGGCGGGCAGTGGAGCT
GGCCCGGCGCCTGGGCGCGCCATGCGCAGCACACGCTCCTGGCCCTGCTGGCGCTGGTC
TTGCTTTACTTGGTGTCTGGTGCCCTGGTGTTCCGGGCCCTGGAGCAGCCCCACGAGCAG
CAGGCCCAGAGGGAGCTGGGGGAGGTCCGAGAGAAGTTCCTGAGGGCCCATCCGTGTGTG
AGCGACCAGGAGCTGGGCCTCCTCATCAAGGAGGTGGCTGATGCCCTGGGAGGGGGTGCG
GACCCAGAAACCAACTCGACCAGCAACAGCAGCCACTCAGCCTGGGACCTGGGCAGCGCC
TTCTTTTTTCTCAGGGACCATCATCACCACCATCGGCTATGGCAATGTGGCCCTGCGCACA
GATGCCGGGCGCCTCTTCTGCATCTTCTATGCGCTGGTGGGGATTCCGCTGTTTGGGATC
CTACTGGCAGGGGTGCGGGACCGGCTGGGCTCCTCCCTGCGCCATGGCATCGGTACATT
GAAGCCATCTTCTTGAAGTGGCACGTGCCACCGGAGCTAGTAAGAGTGCTGTCGGCGATG
CTTTTCCTGCTGATCGGCTGCCTGCTCTTTGTCTCACGCCACGTTCTGTCTCTGCTAT
ATGGAGGACTGGAGCAAGCTGGAGGCCATCTACTTTGTCTAGTGACGCTTACCACCGTG
GGCTTTGGCGACTATGTGGCCGGCGCGGACCCCAGGCAGGACTCCCCGGCCTATCAGCCG
CTGGTGTGGTTCTGGATCCTGCTCGGCCTGGCTTACTTCGCCTCAGTGCTCACCACCATC
GGAACTGGCTGCGAGTAGTGTCCTCGCCGCACTCGGGCAGAGATGGGCGGCCTCACGGCT
CAGGCTGCCAGCTGGACTGGCACAGTGACAGCGCGCTGACCCAGCGAGCCGGGGCCCGCC
GCCCCGCCGCCGAGAAAGGAGCAGCCACTGCTGCCTCCACCGCCCTGTCCAGCGCAGCCG
CTGGGCAGGCCCCGATCCCCCTTCGCCCCCGAGAAGGCTCAGCTGCCTTCCCCGCCACG
GCCTCGGCCCTGGATTATCCCAGCGAGAACCTGGCCTTCATCGACGAGTCCTCGGATACG
CAGAGCGAGCGCGGCTGCCCCGCTGCCCCGCGCGCCGAGAGGTGCGCCGCCGCCAAATCCC
CCCAGGAAGCCCGTGCGGCCCCCGCGGCCCGGGCGTCCCCGAGACAAAGGCGTGCCGGTG
TAGGGGCAGGATCCCTGGCCGGGCCTCTCAAGGGCTTCGTTTCTGCTCTCCCCGGCATGC
CTGGCTTGTTTGACCAAAGAGCCCTCTTTCCACGAGACTGAAGTCTGGGGAGGAGGCTAC
AGTTGCCTCTCCGCCTCCTCCCTGGCCCCGGCCCTTCCCTCACTTCCATCCATCTCTAGA
CCCCCCCCAAGGCTTTCTGTGTGCTGCCCCGGGCGGGTGTATCCCTCACAGCACCTCACG
ACTGTGCCTCAAAGCCTGCATCAATAAATGAAAACGGTCTGCACCGCTGCGGGCGTGACG
CTCCCCGACGCGAGTGGGTGTGGAATTGCTTTCCTCGGGCCACCGTGGGGGCACCTCTGG
CCTCCCGTGACCCCCAGGCCGAGGGTCCCCGGGCACCCAGGTGCGTCAAGTCTCGGCCCT
CTCAGGCCCCGCTCTCTGCCTGGAGGAGACTGTGTAGGGTCCGGCGTGGGGATCAGCCGG
GATGGGCTGCGCGTCTCCAGCCTCTGCACACACATTGGCGGGTGGGGTGACGGGAGGGAG
AGGCAGGGGAGAGAGAATGGCATCTCGCGTGGAGGGCTGTCGTTTGAAGTCTCCCAGCGC
GAGAGACCCTGCCCCGCCCCCTTCTGGAGCGTTGACTCCCTTCTCGTCTCGAGGCCTGT
GGCGTCTGGGTCCGTTGGGGCAGAACCATGGAGGAAAAGCCTTCGAAAGTGTGCTCAAG
TCTTCCGACCGCCAAGGCTCGGACGAGGAGAGCGTGCATAGCGACACTCGGGACCTGTGG
ACCACGACCACGCTGTCCCAGGCACAGCTGAACATGCCGCTGTCCGAGGTCTGCGAGGGC
TTCGACGAGGAGGGCCGCAACATTAGCAAGACCCGCGGGTGGCACAGCCCGGGGCGGGGC
TCGTTGGACGAGGGGTACAAGGCCAGCCACAAGCCGGAGGAACTGGACGAGCACGCGCTG
GTGGAGCTGGAGTTGCACCGCGGCAGCTCCATGGAAATCAATCTGGGGGAGAAGGACACT
GCATCCCAGATCGAGGCCGAAAAGTCTTCCTCAATGTCACTCAATATTGCGAAGCAC
ATGCCCCATCGAGCCTACTGGGCAGAGCAGCAGAGCAGGCTGCCACTGCCCTGATGGAA
CTCATGGAGAATGAAGCTCTGGAAATCCTCACCAAAGCCCTCCGGAGCTACCAGTTAGGG

FIGURE 56B

CGCCGGAGCAAGAGGCTGTACGTGAATTAAAAACGCCACCTTGGGCTCGAGCAGCGACCC
GAACCAGCCCCGTGCCAGCCCGGTCCCCAGACCCAAGCCTGACCCCATCCGAGTGGAATT
TGAGTCCTAAAGAAATAAAAGAGTCGATGCATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 57

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA254890
><subunit 1 of 1, 419 aa, 1 stop
><MW: 45189, pI: 9.15, NX(S/T): 2

MTTAPQEPPARPLQAGSGAGPAPGRAMRSTTLLALLLVLLYLVS GALVFRALEQPHEQQ
AQRELGEVREKFLRAHPCVSDQELGLLIKEVADALGGGADPETNSTSNSSHSAWDLGSAF
FFSGTIITTIGYGNVALRTDAGRLFCIFYALVGIPLFGILLAGVGDR LGSSLRHGIGHIE
AIFLKWHVPPPELVRLVLSAMLFLIGCLLFVLTPTFVFCYMEDWSKLEAIYFVIVTTLTTVG
FGDYVAGADPRQDSPAYQPLVFWILLGLAYFASVLT TIGNWLRVVSRRTRAEMGGLTAQ
AASWTGTVTARVTQRAGPAAPPPEKEQPLLPPPPCPAQPLGRPRSPSPPEKAQLPSPPTA
SALDYPSENLA FIDESSDTQSERGCPLPRAPRGRRRPNP PRKPVRPRGPGRPRDKGVPV

Signal sequence.

Amino acids 1-46.

Transmembrane domain.

Amino acids 114-134, 145-165, 190-210, 224-244, 259-279.

N-glycosylation site.

Amino acids 104-107, 108-111.

Glycosaminoglycan attachment site.

Amino acids 17-20.

Protein kinase C phosphorylation site.

Amino acids 171-173, 287-289, 309-311, 313-315, 381-383.

Casein kinase II phosphorylation site.

Amino acids 80-83, 112-115, 224-227, 290-293, 347-351, 361-364,
379-382.

N-myristoylation site.

Amino acids 124-129, 158-163, 295-300, 306-311.

Amidation site.

Amino acids 392-395.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 196-206.

FIGURE 58A

getseq sst.DNA219240

GCCAACACTGGCCAAACAGAAGCCTCCGGTCGGCCTGCAGTGCCCAAGTCCCATGGCGAG
GGCAGCCCCGAGTGGCCGTCGCGGCTGTAGGTCCGCATGCCGGGCACCGCACCAGGCGTCT
AGCAGATGGACACAGGAAGATCCAGAAGCTAGTGGCACATCTAGCAACAGAGCCAGATCA
GAACCCAGATGCTAAACTCCTGGTGGACTGCAGAGGAGAGGGATTTCAGTCTTCTCCTGAT
GTCGATTGCGATTTCTGCTGGGAGCTCAAGACGGGCGAGCTGCCCGAGATCTCTTCGAGA
TACCCAGGGGAGGAGGAGATGGGCAGGATTTAGTAGGACAACTCGGTACTAATGACTT
GGCGGCTGGCTGCGACCCCCCGGGAATCAGGTGCAAGCATGTTTGCCTGTAGGTACCTG
AGTTGACACCGAAGGTGCCTAAAGATGCTGAGCGGCGTTTGGTTCCTCAGTGTGTTAACCC
GTGGCCGGGATCTTACAGACAGAGAGTCGAAAACCTGCCAAAGACATTTGCAAGATCCGC
TGTCTGTGCGAAGAAAAGGAAAACGTACTGAATATCAACTGTGAGAACAAGGATTTACA
ACAGTTAGCCTGCTCCAGCCCCCCCAGTATCGAATCTATCAGCTTTTTTCTCAATGGAAAC
CTCTTGACAAGACTGTATCCAAACGAATTTGTCAATTACTCCAACGCGGTGACTCTTCAC
CTAGGTAACAACGGGTACAGGAGATCCGAACGGGGGCATTTCAGTGGCCTGAAAACCTCTC
AAAAGACTGCATCTCAACAACAACAAGCTTGAGATATTGAGGGAGGACACCTTCCTAGGC
CTGGAGAGCCTGGAGTATCTCCAGGCCGACTACAATTACATCAGTGCCATCGAGGCTGGG
GCATTTCAGCAAACCTTAACAAGCTCAAAGTGCTCATCCTGAATGACAACCTTCTGCTTTCA
CTGCCCAGCAATGTGTTCCGCTTTGTCTGCTGACCCACTTAGACCTCAGGGGGAATAGG
CTAAAAGTAATGCCTTTTGTGCTGGCGTCTTGAACATATTGGAGGGATCATGGAGATTCAG
CTGGAGGAAAATCCATGGAATTGCACTTGTGACTTACTTCCTCTCAAGGCCTGGCTAGAC
ACCATAACTGTTTTTGTGGGAGAGATTGTCTGTGAGACTCCCTTTAGGTTGCATGGGAAA
GACGTGACCCAGCTGACCAGGCAAGACCTCTGTCCCAGAAAAAGTGCCAGTGATTCCAGT
CAGAGGGGCAGCCATGCTGACACCCACGTCCAAGGCTGTCACCTACAATGAATCCTGCT
CTCAACCCAACCAGGGCTCCGAAAGCCAGCCGGCCGCCAAAATGAGAAATCGTCCAACCT
CCCCGAGTGACTGTGTCAAAGGACAGGCAAAGTTTTGGACCCATCATGGTGTACCAGACC
AAGTCTCCTGTGCCTCTCACCTGTCCCAGCAGCTGTGTCTGCACCTCTCAGAGCTCAGAC
AATGGTCTGAATGTAAACTGCCAAGAAAGGAAGTTCATAATATCTCTGACCTGCAGCCC
AAACCGACCAGTCCAAGAAACTCTACCTAACAGGGAACCTATCTTCAAACCTGTCTATAAG
AATGACCTCTTAGAATACAGTTCTTTGGACTTACTGCACTTAGGAAACAACAGGATTGCA
GTCATTTCAGGAAGGTGCCTTTACAAACCTGACCAGTTTACGCAGACTTTATCTGAATGGC
AATTACCTTGAAGTGCTGTACCCTTCTATGTTTGATGGACTGCAGAGCTTGCAATATCTC
TATTTAGAGTATAATGTCATTAAGGAAATTAAGCCTCTGACCTTTGATGCTTTGATTAAC
CTACAGCTACTGTTTCTGAACAACAACCTTCTTCGGTCCTTACCTGATAATATATTTGGG
GGGACGGCCCTAACCAGGCTGAATCTGAGAAACAACCATTTTTTCTCACCTGCCCGTGAAA
GGGGTTCTGGATCAGCTCCCGGCTTTCATCCAGATAGATCTGCAGGAGAACCCCTGGGAC
TGTACCTGTGACATCATGGGGCTGAAAGACTGGACAGAACATGCCAATTCCTGTGCATC
ATTAATGAGGTGACTTGCGAATCTCCTGCTAAGCATGCAGGGGAGATACTAAAATTTCTG
GGGAGGGAGGCTATCTGTCCAGACAGCCCAAACCTTGTGAGATGGAACCGTCTTGTCAATG
AATCACAATACAGACACACCTCGGTGCTTAGTGTGTCTCCTAGTTCCTATCCTGAACTA
CACACTGAAGTTCCACTGTCTGTCTTAATTCTGGGATTGCTTGTTGTTTTTCATCTTATCT
GTCTGTTTTTGGGGCTGGTTTATTCTGCTTTTGTCTTGAAACGCCGAAAGGGAGTGCCGAGC
GTTCCCAGGAATACCAACAACCTTAGACGTAAGCTCCTTTCAATTACAGTATGGGTCTTAC
AACACTGAGACTCACGATAAAACAGACGGCCATGTCTACAACCTATATCCCCCACCTGTG
GGTCAGATGTGCCAAAACCCCATCTACATGCAGAAGGAAGGAGACCCAGTAGCCTATTAC
CGAAACCTGCAGGAGTTCAAGACCAGCCTAGAGAACATATGGAGACCCTGTCTTCACAAA

FIGURE 58B

AAATAAAAAAGTCAGCCAAGCGTGGTGGTGTGTGCCTGTAGTTACTTAGGAGGCTGAGGC
AGGACGATCGCTTAAGCCCAGGAGTTTGAGGCTGTGGTGAGCTACAATTGCGCCACTGCA
CGCCAGCCTGGCTACAGAACGAGACCCTGCCTCTCTAAAAAAAAAAAAAAAAAAAAA

FIGURE 59A

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA219240
><subunit 1 of 1, 733 aa, 1 stop
><MW: 82695, pI: 8.37, NX(S/T): 6

MLSGVWFLSVLTVAGILQTESRKTAKDICKIRCLCEEKENVLNINCENKGFTTVSLLQPP
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KLEILREDTFLGLESLEYLQADYNYISAIEAGAFSKLNKLVLIILNDNLLLSLPSNVFRF
VLLTHLDLRGNRLKVMFPFAGVLEHIGGIMEIQLEENPWNCTCDLLPLKAWLDTITVFVGE
IVCETPFRLHKGKDVLTQLTRQDLCPRKSSASDSSQRGSHADTHVQRLSPTMNPALNPTRAPK
ASRPPKMRNRPTPRVTVSKDRQSFPGPIMVYQTKSPVPLTCPSSCVCTSQSSDNGLNVNCQ
ERKFTNISDLQPKPTSPKKLYLTGNYLQTVYKNDLLEYSSLDLLHLGNNRIAVIQEGAF
NLTSRLRLYLNGNYLEVLYPSMFDGLQSLQYLYLEYNVIKEIKPLTFDALINLQLLFLNN
NLLRSLPDNIFGGTALTRLNLRNNHFSHLPVKGVLQDLPAFIQIDLQENPWDCTCDIMGL
KDWTEHANSPIINEVTCESPAKHAGEILKFLGREAI CPDSPNLS DGTVLSMNHNTDTPR
SLSVSPSSYPELHTEVPLSVLILGLLVVFILSVCFGAGLFVFLKRRKGVPSVPRNTNNL
DVSSFQLQYGSYNTETHDKTDGHVYNYIPPPVGQMCQNPIYMQKEGDPVAYYRNLOEFKT
SLENIWRPCLHKK

Signal sequence.

Amino acids 1-18.

Transmembrane domain.

Amino acids 161-181, 466-486, 616-636.

N-glycosylation site.

Amino acids 84-87, 219-222, 366-369, 421-424, 583-586.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 362-365.

Protein kinase C phosphorylation site.

Amino acids 21-23, 24-26, 111-113, 272-274, 312-314, 376-378,
424-426, 598-600.

Casein kinase II phosphorylation site.

Amino acids 24-27, 147-150, 184-187, 258-261, 267-270, 276-279,
399-402, 441-444, 485-488, 608-611, 720-723.

Tyrosine kinase phosphorylation site.

Amino acids 704-711.

FIGURE 59B

N-myristoylation site.

Amino acids 15-20, 71-76, 104-109, 354-359, 417-422, 493-498,
587-592, 670-675.

FIGURE 60A

getseq sst.DNA37151

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGG
CTCAGAAGGACTCTGAAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAA
CACACATGTGCATGTACACACACACATACACACACATACCTTCTCTCTCTTCACTGAA
GACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACACTAAAGCCTTAAGGAC
AGGCTTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
CCAGGCACGGTGACTCACACCTGTAATCCAGCATT'TTGGGAGACCGAGGTGAGCAGATC
ACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTA
AAAATACAAAAATTAGCCAGGAGTGGTGGCAGGTGCCTGTAATCCAGCTACTCAGGTGG
CTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGTCAGCTGAGTGCACCG
CTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGC
CCCTGATGGGGCCTGGCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGG
CATATTGAGGAGGGCAAGAAGTGACGCCCCGGTGTAGAATGACTGCCCTGGGAGGGTGTT
CCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACAAAGAGCAGGACTCCA
GACTCTCCTTGTTGAATGGTCCCCTGCCCTGCAGCTCCACC ATGAGGCTTCTCGTGGCCCC
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCCGTGGTACCCTGGCATGT
TCCCTGCCCCCTCAGTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCCTA
CCGCGAGGCTACCACTGTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGCACT
CCCCGCAGGCACACAGACCCTGCTCCTGCAGAGCAACAGCATTGTCCGTGTGGACCAGAG
TGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAA
CCAGCTGACCCGGCTGGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACTCTA
TCTCAACCACAACCAGCTCTACCGCATCGCCCCAGGGCCTTTTCTGGCCTCAGCAACTT
GCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAGCCGCTGGTTTGAAT
GCTGCCCAACTTGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGA
GATCTCCGACTATGCCCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAA
CCAGCTGGCCCCGGGTGCCAGGCGGGCACTGGAACAGGTGCCCGGGCTCAAGTTCCTAGA
CCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGCCAACATGCTGCACCT
TAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTCATCCA
CCCCGCGCCTTCCACCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCT
CAGTGCCTTGCAACCAGCAGACGGTGGAGTCCCTGCCAACCTGCAGGAGGTAGGTCTCCA
CGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGGCCAATGCCACGGGCACCCGTGT
CCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATCTCCCCACG
AAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGC
ACTGGCCGAACCCGAACCCGAGATCTACTGGGTCACTCCAGCTGGGCTTCGACTGACACC
TGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCCTGGAGCTGCGGAGGGT
GACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACA
GGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTCAC
CCCACCCAAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCTCCCGGGGCA

FIGURE 60B

GGGGGCCACAGCTCTGGCCCGCCTGCCTCGGGGAACCCACAGCTACAACATTACCCGCCT
CCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCCACACCCA
GTTGGCTTGTGTATGGGCCAGGACCAAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGA
TCGTCCTGGGCTCATTTGCCATCCTGGCTCTCGCTGTCCTTCTCCTGGCAGCTGGGCTAGC
GGCCACCTTGGCACAGGCCAACCCAGGAAGGGTGTGGGTGGGAGGCGGCCTCTCCCTCC
AGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTGTGTCTGCTCCCCTCGT
CCTGCCCTGGAATCCAGGGAGGAAGCTGCCCAGATCCTCAGAAGGGGAGACACTGTTGCC
ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGA
CTACTTTTTTACCAAAGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGG
ACCCACGTGCTTGAGGCCTGGCAGCTGGGCCAAGACAGATGGGGCTTTGTGGCCCTGGGG
GTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCACCTCTGCTGCCATTC
TGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
CTCTCTGCCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCTACCTGTGTCCCCGGGCTG
CACCCCTTCCTCTTCTCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCTCCTGGG
CAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGGCTGCCCTCAATGTGGGAGTGA
CCCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCCAGGAACGCCTCATCTCAGCA
GCCTGGGCTCGGCATTCCGAAGCTGACTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
ATGTGTCACCTCCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATA
AATAATAACAATAAAAAAA

FIGURE 61A

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA37151
><subunit 1 of 1, 713 aa, 1 stop
><MW: 78889, pI: 7.49, NX(S/T): 4
MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFL
TAVPPALPAGTQTLTLLQSNSIVRVDQSELGYLANLTDLTSLQNSFSRDARDCDFHALPQLL
SLHLEENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAI
DSRWFEMLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLE
SLSFYDNQLARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVS
IDKFALVNLPELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQTVESLPN
LQEVGLHGNPIRCDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHC
LPLISPRSFPPSLQVASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEG
TLELRRVTAAEEAGLYTCVAQNLVGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYH
ILLSWVTPPNTVSTNLTWSSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVA
FADAHTQLACVWARTKEATSCHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVG
GRRPLPPAWAFWGSAPSVRVVSAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence.

Amino acids 1-18.

Transmembrane domain.

Amino acids 628-648, 667-687.

Leucine rich repeat domain.

Amino acids 94-117, 118-141, 142-165, 166-189, 190-213, 214-237,
238-261, 262-285, 286-310, 311-335, 336-359, 360-407.

Immunoglobulin domain.

Amino acids 438-499.

N-glycosylation site.

Amino acids 94-97, 381-834, 555-558, 583-586.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 485-488.

Protein kinase C phosphorylation site.

Amino acids 42-44, 46-48, 425-427, 563-565, 678-680.

Casein kinase II phosphorylation site.

Amino acids 46-49, 51-54, 96-99, 104-107, 130-133, 142-145, 243-
246, 313-316, 488-491, 700-703.

FIGURE 61B

Tyrosine kinase phosphorylation site.

Amino acids 532-539.

N-myristoylation site.

Amino acids 15-20, 493-498, 566-571.

Amidation site.

Amino acids 470-473, 660-663, 692-695.

FIGURE 62

getseq sst.DNA210233

GGCACGAGCCGGCAAGCCGAGCTAGGGTGAAAAC TGGGGGCGCACCAGG ATGTXXGACAG
AAAAGCAGAAGATGAGACTCTGTTCAATTCAC TTTTCCTAGGCCCATCCTGTGGTCATCTT
TCCCCCTCCCATCATACCTCCTCCTTCCTGGG AGCCTCTGCCGGCTTGGCTGTAATGGTGG
CACTTACCTGGATATTTTCAGTGGGAGGATGAA AGGCGAGACTCACCTACGCGGTGGGAC
AGATGGGGAGAGGAAAAAGGCAGAGATGGCCAG GAGAGGGGTGCAGGACAAACCAGAGAG
GTTGGGTCAGGGGAAAAGGGTGGGGAGAAAGAGG GGTGCAGGCCCTGCAGGCCGGTTAGC
CAGCAGCTGCGGCCTCCCCGGGCCCTTGGCATCC AACTTCGCAGACAGGGTACCAGCCTC
CTGGTGTGTATCATAGGATTTGTTTCACATAGT GTTATGCATGATCTTCGTAAGGTTAAGA
AGCCGTGGTGGTGCACCATGACATCCAACCCGTAT ATATAAAGATAAATATATATATATA
TGTATGTAAATTATGGCACGAGAAATTATAGCACT GAGGGCCCTGCTGCCCTGCTGGACC
AAGCAAAACTAAGCCTTTTGGTTTGGGTATTATGT TTTTCGTTTTGTTATTTGTTTGT
GTGGCTTGTCTTATGTCGTGATAGCACAAGTGCCAG TCGGATTGCTCTGTATTACAGAAT
AGTGTTTTTAATTCATCAATGTTCTAGTTAATGTCT ACCTCAGCACCTCCTCTTAGCCTA
ATTTTAGGAGGTTGCCCAATTTTGTTCCTTCAATTTT TACTGGTTACTTTTTTGTACAAAT
CAATCTCTTTCTCTCTTTCTCTCCTCCCCACCTCTC ACCCTTGCCCTCTCCATCTCCCTC
TCCCGCCCTCCCCTCCTCCCTCTGGCTCCCCGTCTCA TTTCTGTCCACTCCATTCTCTCT
CCCTCTCTCCTGCCTCCTGCTGCCCCCTCCCCAGCCC ACTTCCCCGAGTTGTGCTTGCCG
CTCCTTATCTGTTCTAGTTCCGAAGCAGTTTCACTCGA AGTTGTGCAGTCCTGGTTGCAG
CTTTCGCGCATCTGCCTTCGTTTCGTGTAGATTGACGC GTTTCTTTGTAATTTTCAGTGTTT
CTGACAAGATTTAAAAAAGGAAAAA

FIGURE 63

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA210233
><subunit 1 of 1, 145 aa, 0 stop
><MW: 15963, pI: 10.59, NX(S/T): 1
MSTSAPPLSLILGGCPILFLQFYWLLFCTNQSLSLFLSSPPLTLALSISLSRPPLLPLAP
RLISVHSILSPSLLPPAAPSPAHPFPELCLPLLICSSSEAVSLEVQSWLQLSASAFVSCR
LTRFFVISVFLTRFKKKKRKKKKKK
```

Signal sequence.

Amino acids 1-45.

Transmembrane domain.

Amino acids 54-74, 108-128.

N-glycosylation site.

Amino acids 30-33.

Protein kinase C phosphorylation site.

Amino acids 118-120.

Casein kinase II phosphorylation site.

Amino acids 95-98.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 5-15, 109-119.

FIGURE 64

getseq sst.DNA35918

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCA
ACATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGGATTCAGGCTCGCCAGCGCCC
AGCCAGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGC
TCCTGCTGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCC
AGCCCTGGACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAG
TGAAAGATCACGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACT
TTGGGGAGAAGAGAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACG
AGCTCAGCATCAGCATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAA
TCTTCACTATGCCTGTGCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGA
AGCCCATCATCACTGGTTATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACT
GTCAGTCTTCTGGGAGCAAGCCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAAC
TCCACGGAGAACCAACCCGCATACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCA
GCTCGGTGACATTCCAGGTTACCCGGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGA
ACCATGAATCTCTAAAGGGAGCTGACAGATCCACCTCTCAACGCATTGAAGTTTATACA
CACCAACTGCGATGATTAGGCCAGACCCTCCCCATCCTCGTGAGGGCCAGAAGCTGTTGC
TACACTGTGAGGGTCGCGGCAATCCAGTCCCCCAGCAGTACCTATGGGAGAAGGAGGGCA
GTGTGCCACCCCTGAAGATGACCCAGGAGAGTGCCCTGATCTTCCCTTTCCTCAACAAGA
GTGACAGTGGCACCTACGGCTGCACAGCCACCAGCAACATGGGCAGCTACAAGGCCTACT
ACACCCTCAATGTTAATGACCCCGAGTCCGGTGCCCTCCTCCTCCAGCACCTACCACGCCA
TCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTGCTCATCATGCTCATCTTCCTTG
GCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACATGAGGCAAAAGGCTCCGACG
ATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCGGGCAGTCAGGAGGGGACG
ACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGCGCCCCCCAGGGGCCCT
GTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAACCGCAGGGCCGCCC
CTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGCTTTGGGTGCGGT
TTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGGAGGGGAGGGTTGCCCTCAG
CCCTTTCCGTGGCTTCTCTGCATTTGGGTATTATTATTTTGTAAACAATCCCAAATCAA
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AAACA

FIGURE 65

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><subunit 1 of 1, 398 aa, 1 stop
><MW: 43300, pI: 6.00, NX(S/T): 2
MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSL
QWSNPAQQTLYFG EKRALRDNRIQLVTSTPHELSSISISNVALADEGEYTCSIFTMPVRTA
KSLVTVLGI PQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQ
EDPNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPD
PPHPREGQKLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCT
ATSNMGSYKAYYT LNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLI RHKG
TYLTHEAKGSDDAPDADTAIINAEGGQSGGDDKKEYFI

Signal Sequence

Amino acids 1-20.

Transmembrane domain.

Amino acids 332-352.

Immunoglobulin domain.

Amino acids 43-112, 145-211, 247-301.

N-glycosylation site.

Amino acids 25-28, 290-293, 119-121, 141-143, 164-166, 215-217,
224-226, 307-309.

Casein kinase II phosphorylation site.

Amino acids 27-30, 35-38, 89-92, 141-144, 199-202, 388-391.

N-myristoylation site.

Amino acids 2-7, 23-28, 156-161, 218-223, 295-300, 298-303, 306-
311, 334-339, 360-365, 385-390, 386-391.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 7-17.

FIGURE 66

getseq sst.DNA260038

CTTGGATCTGCCTGCCAGGCCATCCTGGGCGCTGCAGGAAGCAACATGACTTAGGTA
ACTGCCAGAGGTGCACCAGACATGATGCAGCAGCCGCGAGTGGAGACAGATACCATCGGGGC
TGGCGAGGGGCCACAGCAGGCAGTGCCTGGTCAGCCTGGGTCACGAGGCATGGCTGGGTG
CGCTGGTGGGTGAGCCACATGCCCCCGAGCTGGATCCAGTGGTGGAGCACCTCGAACTGG
CGGCAACCGCTGCAGCGCCTGCTGTGGGGTCTGGAGGGGATACTCTACCTGCTGCTGGCA
CTGATGTTGTGCCATGCACTCTTCACCACTGGCTCCACCTGCTGAGCTCCTTGTGGCCT
GTCGTGGC'CGCGGTGTGGCGCCACCTGCTACCGGCTCTCCTGCTGCTGGTGCTCAGTGCT
CTGCCTGCCCTCCTCTTCACGGCCTCCTTCCTGCTGCTCTTCTCCACACTGCTGAGCCTT
GTGGGCCT'CCTCACCTCCATGACTCACCCAGGCGACACTCAGGATTTGGATCAA TAGAAG
GGCAACCCCATCCCACTGCCTGTGTTTGTGAGCCCTGGCCTAGGGCCTGAGACCCACG
GGGAGAGGGAGGGCAATGGGATCAGGGCTCCCTGCCTTGGCAGGGCCCAGACCCCTAGTC
CCTAACAGGTAGGCTGGCCTG

FIGURE 67

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA260038
><subunit 1 of 1, 112 aa, 1 stop
><MW: 12573, pI: 6.85, NX(S/T): 0
MPPSWIQWWSTSNWRQPLQRLLWGLEGILYLLLALMLCHALFTTGSHLLSSLWPVVAHV
RHLLPALLLLVLSPALLFTASFLLLFSTLLSLVGLLTSMTHPGDTQDLQ

Signal sequence.

Amino acids 1-40.

Transmembrane domain.

Amino acids 54-74, 70-90.

N-myristoylation site.

Amino acids 96-101.

Eukaryotic thiol (cysteine) proteases histidine active site.

Amino acids 37-47.

FIGURE 68

getseq sst.DNA334818

ACATGCGCCCTGACAGCCCAACAATGGCGGCGCCCGCGGAGTCGCTGAGGAGGCGGAAGA
CTGGGTACTCGGATCCGGAGCCTGAGTCGCCGCCCGCGCCGGGGCGTGGCCCCGCAGGCT
CTCCGGCCCATCTTCACACGGGCACCTTCTGGCTGACCCGGATCGTGCTCCTGAAGGCCC
TAGCCTTCGTGTACTTCGTGGCATTCTTGGTGGCTTTCCATCAGAACAAGCAGCTCATCG
GTGACAGGGGGCTGCTTCCCTGCAGAGTGTTCTGAAGGACTTCCAGCAGTACTTCCAGG
ACAGGACAAGCTGGGAAGTCTTCAGCTACATGCCACCATCCTCTGGCTGATGGACTGGT
CAGACATGAACTCCAACCTGGACTTGCTGGCTCTTCTCGGACTGGGCATCTCGTCTTTCG
TACTGATCACGGGTTGCGCCAACATGCTTCTCATGGCTGCCCTGTGGGGCCTCTACATGT
CCCTGGTTAATGTGGGCCATGTCTGGTACTCTTTCGGATGGGAGTCCCAGCTTCTGGAGA
CGGGATTCTTGGGGATCTTCTGTGCCCTCTGTGGACGCTGTCAAGGCTGCCCCAGCATA
CCCCACATCCCGGATTGTCTGTGGGGCTTCCGGTGGCTGATCTTCAGGATCATGCTTG
GAGCAGGCCTGATCAAGATCCGGGGGGACCGGTGCTGGCGAGACCTCACCTGCATGGACT
TCCACTATGAGACCCAGCCGATGCCCAATCCTGTGGCATACTACCTGCACCACTCACCTT
GGTGGTTCCATCGCTTCGAGACGCTCAGCAACCACTTCATCGAGCTCCTGGTGCCCTTCT
TCCTCTTCTCGGCCGGCGGGCGTGCATCATCCACGGGGTGCTGCAGATCCTGTTCCAGG
CCGTCTTCATCGTCAGCGGGAACCTCAGCTTCTGAACTGGCTGACTATGGTGCCCAGCC
TGGCCTGCTTTGATGACGCCACCCTGGGATTCTTGTTCCTCTGGGCCAGGCAGCCTGA
AGGACCGAGTTCTGCAGATGCAGAGGGACATCCGAGGGGGCCCGGCCCGAGCCAGATTCTG
GCTCCGTGGTGCGGCGTGCAGCCAACGTCTCGCTGGGCGTCTGCTGGCCTGGCTCAGCG
TGCCCGTGGTCCTCAACTTGCTGAGCTCCAGGCAGGTCATGAACACCCACTTCAACTCTC
TTACATCGTCAACACTTACGGGGCCTTCGGAAGCATCACCAAGGAGCGGGCGGAGGTGA
TCCTGCAGGGCACAGCCAGCTCCAACGCCAGCGCCCCCGATGCCATGTGGGAGGACTACG
AGTTCAAGTGCAAGCCAGGTGACCCAGCAGACGGCCCTGCCTCATCTCCCCGTACCACT
ACCGCCTGGACTGGCTGATGTGGTTTCGCGGCCTTCCAGACCTACGAGCACAACGACTGGA
TCATCCACCTGGCTGGCAAGCTCCTGGCCAGCGACGCCGAGGCCTTGTCCCTGCTGGCAC
ACAACCCCTTCGCGGGCAGGCCCCCGCCAGGTGGGTCCGAGGAGAGCACTACAGGTACA
AGTTCAAGCGTCCTGGGGGCAGGCACGCCGCCGAGGGCAAGTGGTGGGTGCGGAAGAGGA
TCGGAGCCTACTTCCCTCCGCTCAGCCTGGAGGAGCTGAGGCCCTACTTCAGGGACCGTG
GGTGGCCTCTGCCCGGGCCCCCTCTAGACGTGCACCAGAAATAAAGGCGAAGACCCAGCCC
CTCGGCGGCTCAGCAACGTTTGGCCTTCCCTGCGCCCAGCCCAAGCTGGGCATCGCCAAG
AGAGACGTGGAGAGGAGAGCGGTGGGACCCAGCCCCCAGCACGGGGGTCCAGGGTGGGGT
CTGTTGTACATACTGTGGCGGCTCCAGGCCCTGCCACCTGGGGCCCCACATCCAGGC
CAACCTTGTCCCAGGCGCCAGGGGCTCTGATCTCCCATCCATCCCACCCTCCTCCCAGA
GGCCAGCCTGGGGCTGTGCCGCCACAGGAGTTGAGACAATGGCAATCCTGACACCTTC
CTCCACTACAGCCCTGACCATAGACCCAGCCAGGTAGCTCTTGGGGTCTCTAGCGTCCCA
GGGCTGGTTTCTGTTCCCTCTTCAATGGTGTGTTCCCAGCCAGGTCCTGACCCTCAGAG
CCAAGTCCCTGTCACGTCTGGGGCAGCCAAACCTCGCCCCACAGGGACCTGGACACGCC
CGGCCAGGATGTGGGGTTGGATGGGCCATTTTCTGTCTTATCCCTCATCTCCACCCCCGC
CACAGCCTACACGCATCCCACACATGCAGGCACACACAGCCTGTGCACACATGTGTTCTT
GGCCCGGTTTTCATCCCCCATGACTGGTGTCTGTGAGGTGCAGATGGACACAGCGCACAC
CCAGACCCTCCACCAGGCTGTGACCTCGCTGCCTCTGAGGCCTTGACAAGGCCCTCAAT
CGGAGGACAGCCGGCCGTGCACACTTTCATCATCGTCGGACAAACAGCGTCTACTGCACA
TTTTTCTTATTCTTATTCTTGAGCCATAGCTATGGCATATTCTTCTACTATTCTATTAT
ACCACTTACAGGCTTACTCG

FIGURE 69A

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 ><MW: 64874, pI: 9.45, NX(S/T): 3

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 DMNSNLDLLALLGLGIS SFVLITGCANMLLMAALWGLYMSLVNVGHVWYSFGWESQLLET
 GFLGIFLCPLWTL SRLPQHTPTSRIVLWGFRWLIFRIMLGAGLIKIRGDRCWRDLTCMDF
 HYETQPMNPVAYYLHH SPWWFHRFETLSNHFIELLVPFFLFLGRRACIIHGVLQILFQA
 VLIVSGNLSFLNWLTMVPSLACFDDATLGFLFPSGPGSLKDRVLQMQRDIRGARPEPRFG
 SVVRRANVSLGVLLAWLSVPVVLNLLSSRQVMNTHFNSLHIVNTYGAFGSITKERA EVI
 LQGTASSNASAPDAMWEDYEFKCKPGDPSRRPCLISPYHYRLDWLMWF AAFQTYEHNDWI
 IHLAGKLLASDAEALSLLAHNPFAGRPPPRWVRGEHYRYKFSRPGGRHAAEGKWWVRKRI
 GAYFPPLSLEELRPYFRDRGWPLPGPL

Transmembrane domain.

Amino acids 51-71, 124-144, 175-195, 205-225, 272-292, 295-315,
 320-340, 365-385.

Protein of unknown function (DUF1222) domain.

Amino acids 362-549.

N-glycosylation site.

Amino acids 307-310, 368-371, 428-431.

Glycosaminoglycan attachment site.

Amino acids 334-337.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Amino acids 17-20.

Protein kinase C phosphorylation site.

Amino acids 14-16, 202-204, 338-340, 388-390, 449-451.

Casein kinase II phosphorylation site.

Amino acids 23-26, 102-105, 124-127, 236-239, 338-341, 430-433,
 490-493, 548-551.

Tyrosine kinase phosphorylation site.

Amino acids 101-109.

FIGURE 69B

N-myristoylation site.

Amino acids 83-88, 133-138, 156-161, 372-377, 407-412, 423-428, 525-530.

Amidation site.

Amino acids 283-286.

Prokaryotic membrane lipoprotein lipid attachment site.

Amino acids 135-145.

Cell attachment sequence.

Amino acids 227-229.

FIGURE 70

getseq sst.DNA257501

GGCACGAGGAGAAGACTTTGGTGGGGTAGTCTCGGGGCAGCTCAGCGGCCCGCTGTGCCC
GTTTCTGGCCTCGCTCGCAGCTTGCACGTCGAGACTCGTAGGCCGCACCGTAGGGCGAGC
GTGCGGGTCGCCGCCGCGGCCGCTCGGGGTCTGGGGCCAGCCGCAGCCTCTTCTACCGC
GGCCGGTTGGGAGTCGCCGCGAGATGCAGCCTCCGGGGCCCGCCCCGGCCTATGCCCCCA
CTAACGGGGACTTCACCTTTGTCTCCTCAGCAGACGCGGAAGATCTCAGTGGTTCAATAG
CATCCCCAGATGTCAAATTAAATCTTGGTGGAGATTTTATCAAAGAATCTACAGCTACTA
CATTTCTGAGACAAAGAGGTATGGCTGGCTTCTGGAAGTTGAAGATGATGATCCTGAAG
ATAACAAGCCACTCTTGGAAGAATTGGACATTGATCTAAAGGATATTTACTACAAAATCC
GATGTGTTTTGATGCCAATGCCATCACTTGGTTTTAATAGACAAGTGGTGAGAGACAATC
CTGACTTTTGGGGTCCTCTGGCTGTTGTTCTTTTCTTTTCCATGATATCATTATATGGAC
AGTTTAGGGTGGTCTCATGGATTATAACCATTTGGATATTTGGTTCACTAACAATTTTCT
TACTGGCCAGAGTTCTTGGTGGAGAAGTTGCATATGGCCAAGTCCTTGGAGTTATAGGAT
ATTCATTACTTCCTCTCATTTGTAATAGCCCCTGTACTTTTGGTGGTTGGATCATTGAAG
TGGTGTCTACACTTATAAACTGTTTGGTGTGTTTTGGGCTGCCTACAGTGCTGCTTCAT
TGTTAGTGGGTGAAGAATTCAAGACCAAAAAGCCTCTTCTGATTTATCCAATCTTTTTAT
TATACATTTATTTTTTGTCTTATATACTGGTGTGTGATCCAAGTTATACATGAATAGAA
AAAGATGGTGTAAATTTGTGTGTAGGCTGGGAATTCCTGCTGAAGGAATTGGAGAAAAC
CTGTTGCTGCAAAATTTTACATGTTCCAGATGGAAAGGGAAGTCTAAGCGCTTTTTTAAAA
CAATTTTTTTTTGTATTTAATTAAGCAATTGCAGTTATCTGGGATTTTTTGGGTCAGAATT
TTAAATTCTGTTTGATTCTCCATATTCCAGTGAATAAAATACAAAAGCATTGTGTTTTTA
AGATTGTGTCGATATTCACCTAAAACTTGTGCCAAAAGCACCTGGATTGGTAATTATAT
TTCATTAAAGGGTAAATTTGACAATATCTTGATAATCAAAGTGCAATTTTTTTTCTTCA
AAATGTTTTCTCCAGCATCACAGATCCTGCAGATATATATTTATATTTATACATATATAT
TTATGAAATAATTCTTACTCACAAAATATATTTCTGATAAACATTAAGATATTAAATCTG
ATGCACAACTTTAATTTGGCCATTAAATCTTTTTTATTTAAAAATTTAAATTTGTTTTTA
AAATTGTATATAGTTTTTAAAAATCTCACACATGCTTCGATACTTCCTTGTTAAGAATTCT
TAATAACTACTAAACTGATTTTTTAATAGTTGCTGATATATATTTGGTTTGTTTGGGTAT
ACTTTTCAAACCATTTTTTGAATGTCCAAACATCTGATTTAAAGTTTCTGTTTATCTTTC
TGACCAAAGGAGCAAGAGGTATAATGGATATGGCATTCAATTAATCTTTACTATGTACA
AAAACAGTAATATTTACAGCATCAGTAAATATTTTAAAGTGGTACTTCTAAATCATAAAA
GTTGGGGAAAGAGACCTTTAAAAATCTTGTGGTGTGGAACAATGTTATATGAAGTAGAAAA
AATAAAATACTTCCCAGTTGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 71

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA257501
><subunit 1 of 1, 244 aa, 1 stop
><MW: 27083, pI: 4.49, NX(S/T): 0
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VVLFFSMISLYGQFRVVSIIITIWIFGSLTIFLLARVLGGEVAYGQVLGVIGYSLLPLIV
IAPVLLVVGSEFVSTLIKLFVFWAAYSASLLVGEEFKTKKPLLIYPIFLLYIYFLSL

Transmembrane domain.

Amino acids 115-135, 136-156, 170-190, 186-206, 224-243.

Yip1 domain.

Amino acids 81-226.

Protein kinase C phosphorylation site.

Amino acids 221-223.

Casein kinase II phosphorylation site.

Amino acids 13-16, 21-24.

N-myristoylation site.

Amino acids 159-164, 165-170, 202-207.

93/185

FIGURE 72

TAHO15/DNA58721/NAG14

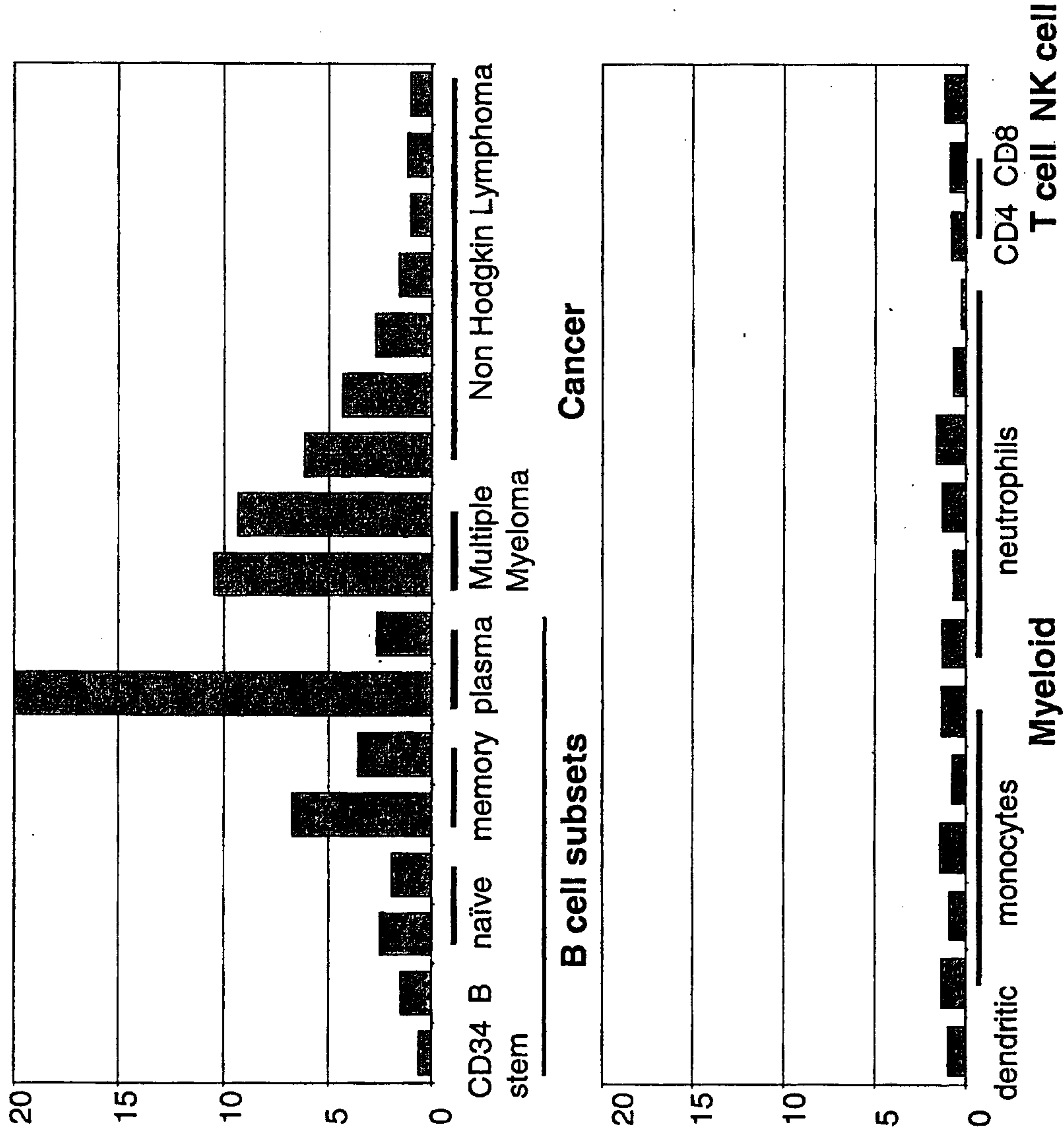


FIGURE 73A

TAHO1/DNA105250/CD180 (LY64)

LY64

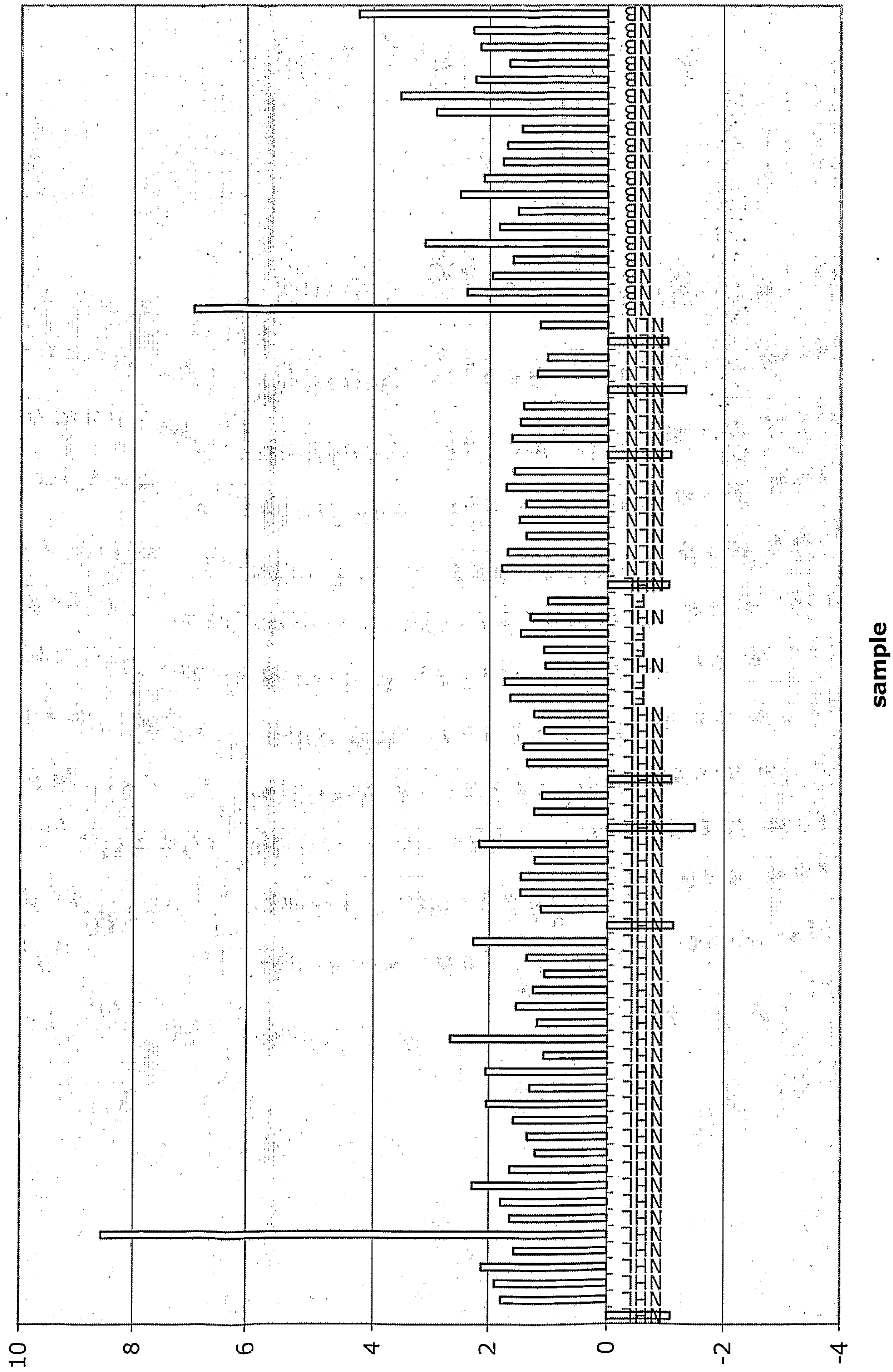


FIGURE 73B

TAHO1/DNA105250/CD180 (LY64)

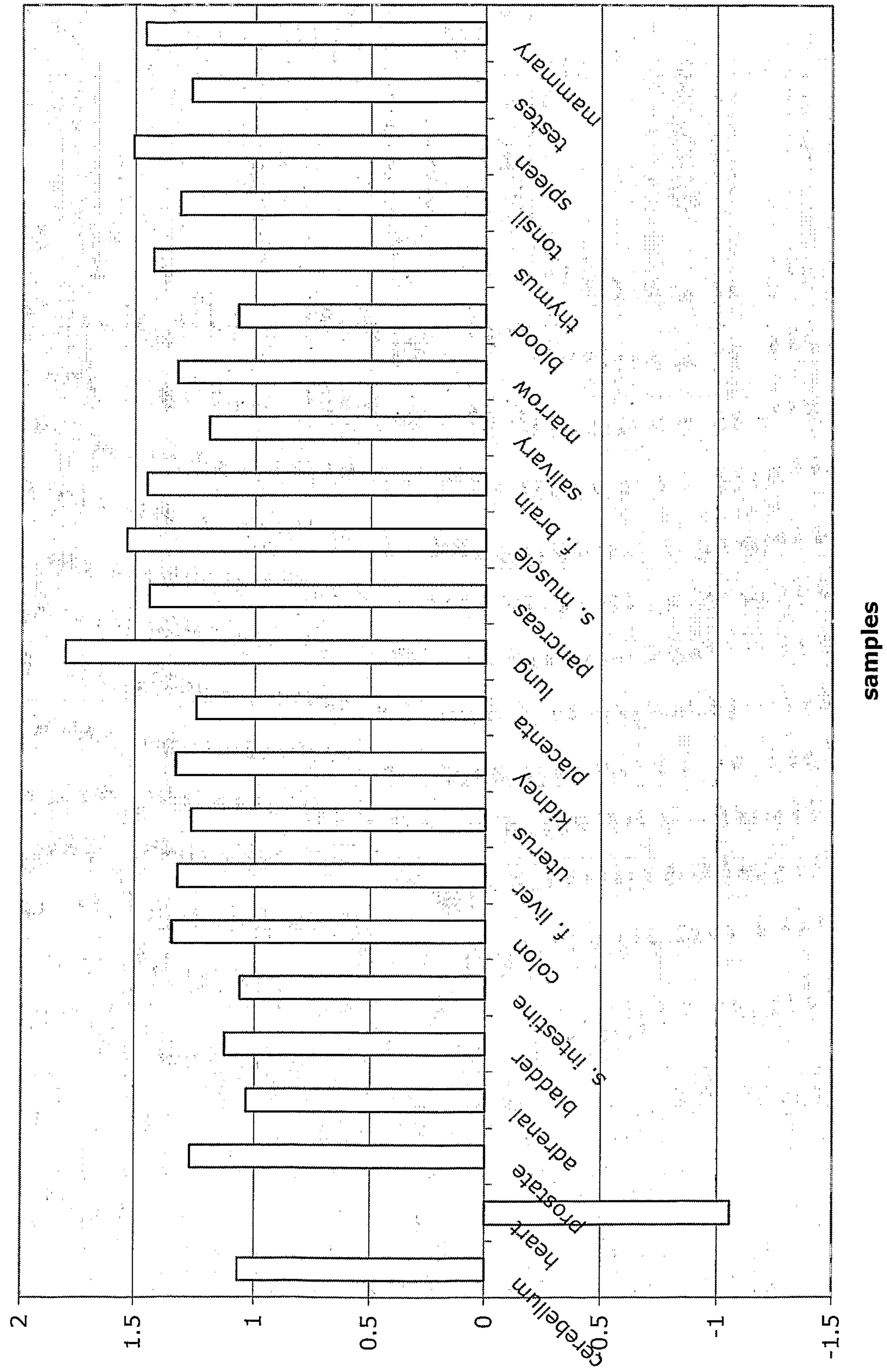
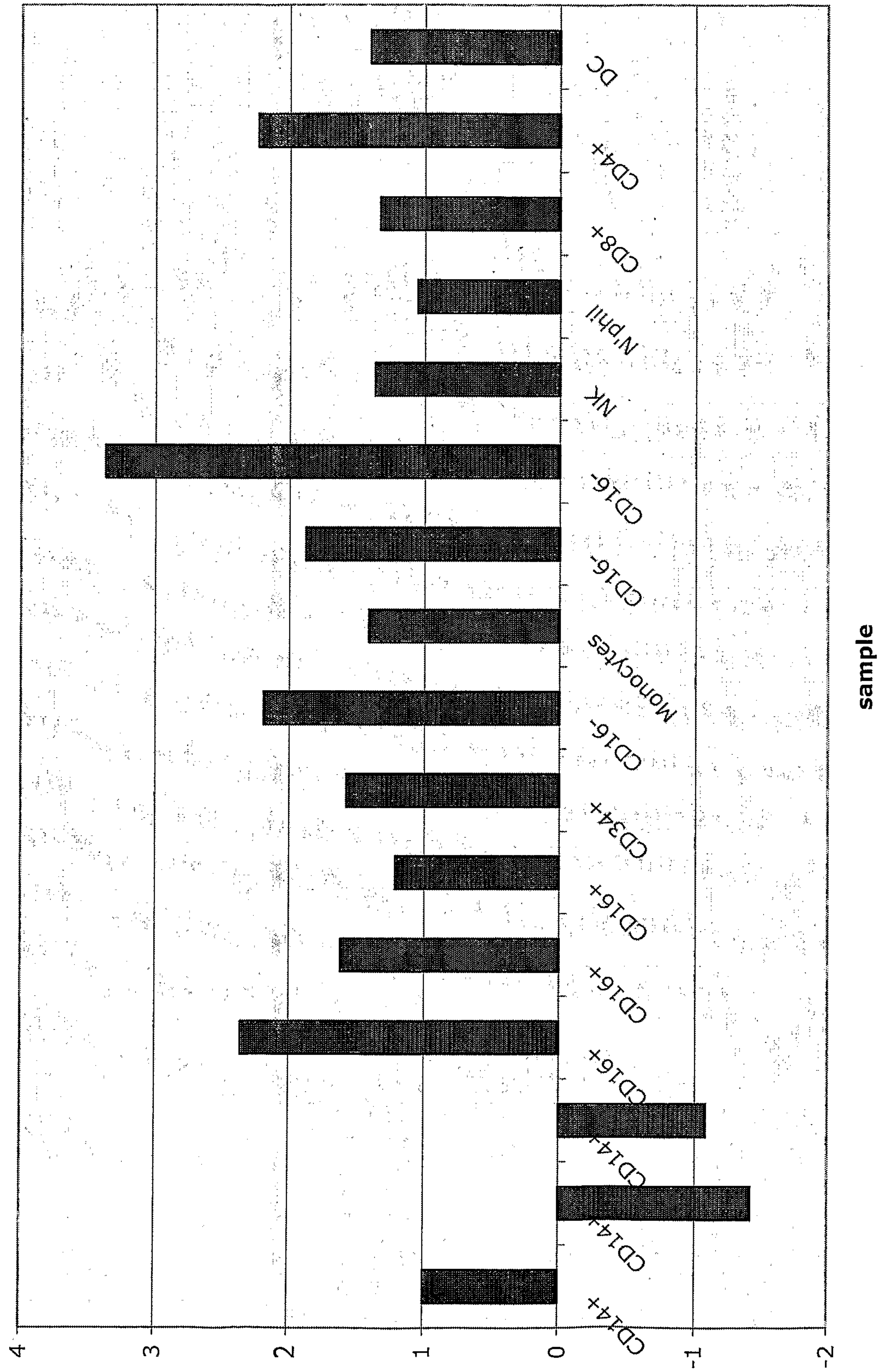
LY64

FIGURE 73C**LY64**

TAHO1/DNA105250/CD180 (LY64)



LY64

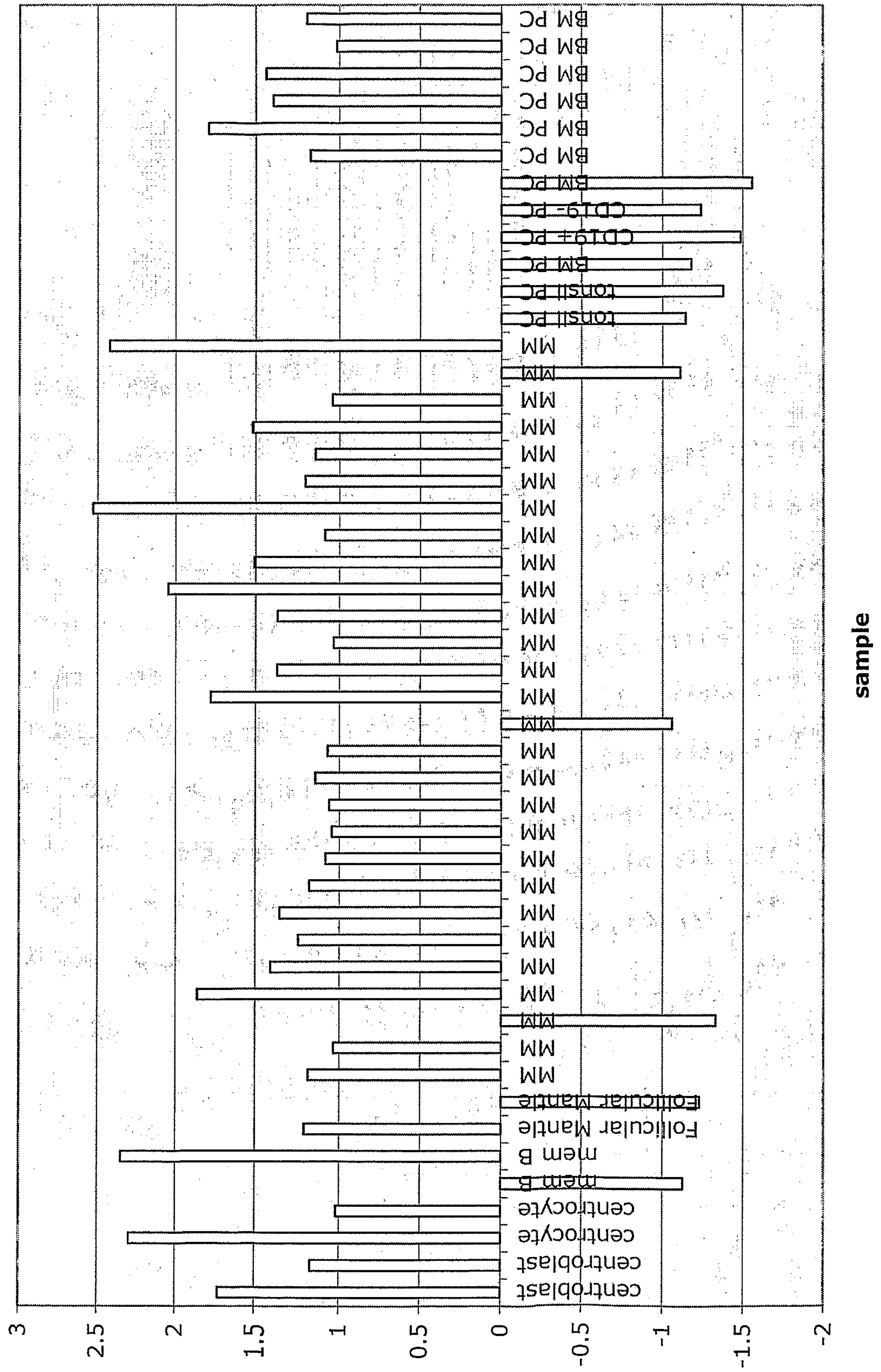


FIGURE 74A

TAHO2/DNA15004/CD20 (MS4A1)

MS4A1

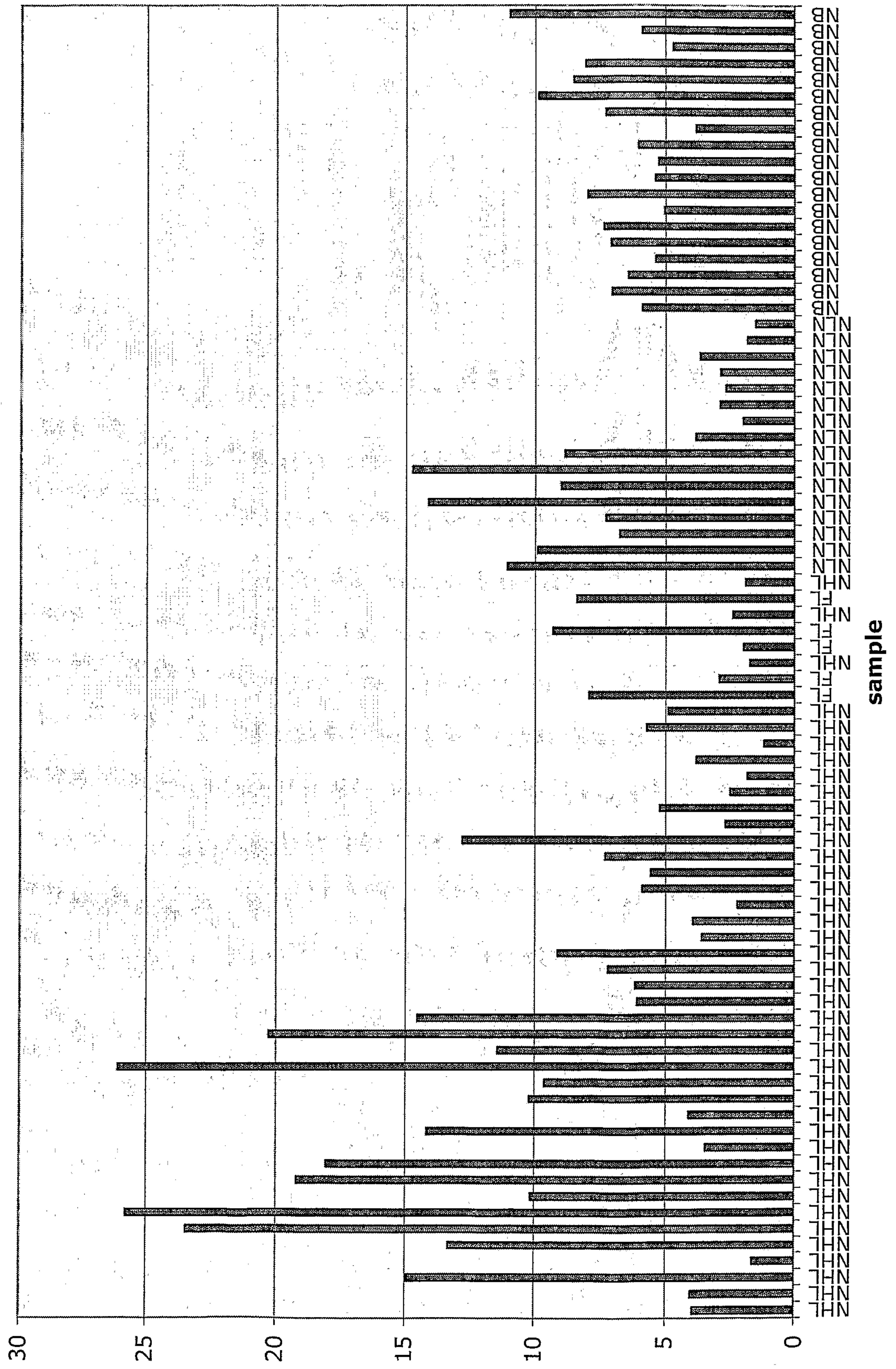


FIGURE 74B**MS4A1**

TAHO2/DNA15004/CD20 (MS4A1)

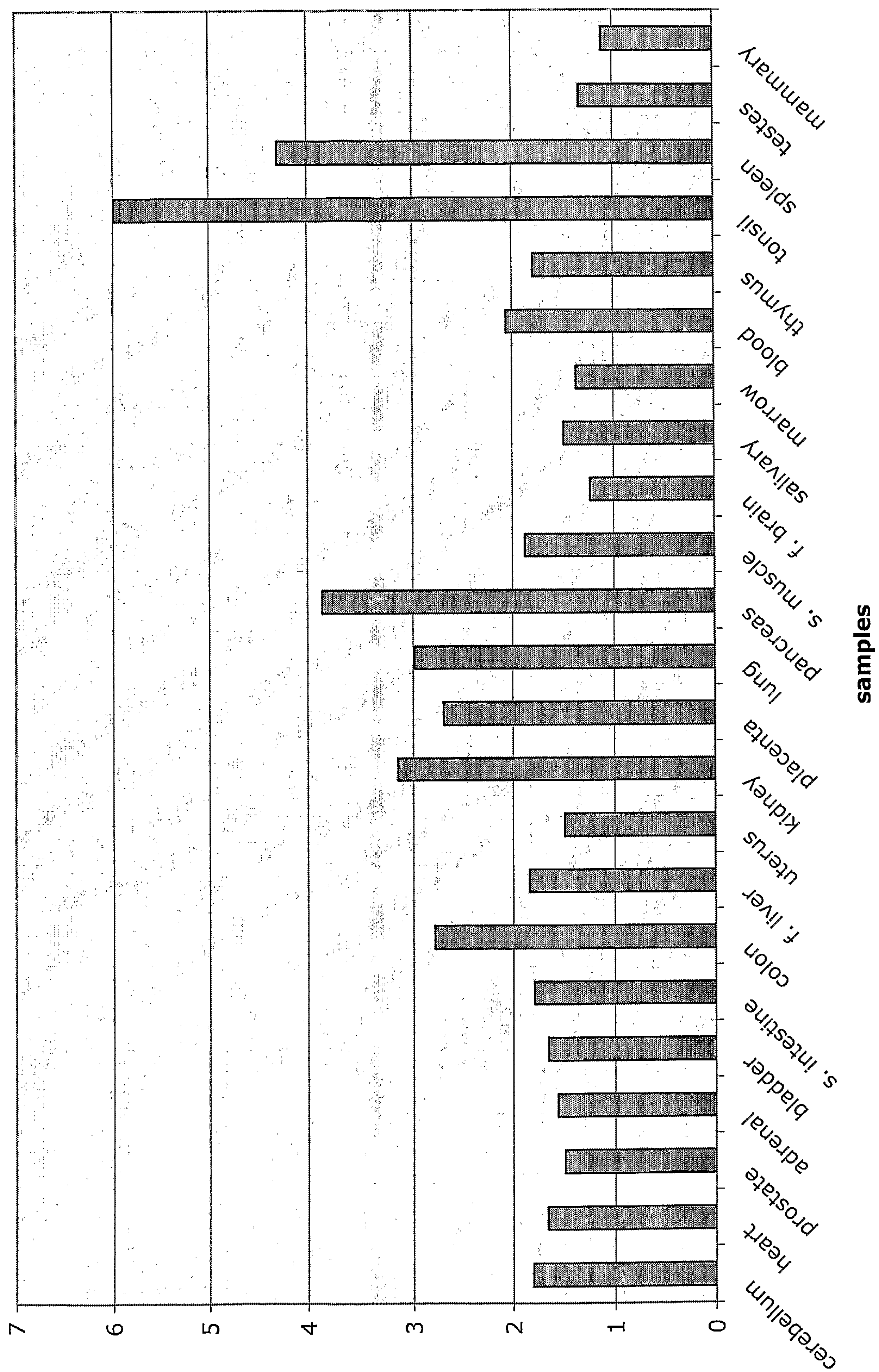


FIGURE 74C**MS4A1**

TAHO2/DNA15004/CD20 (MS4A1)

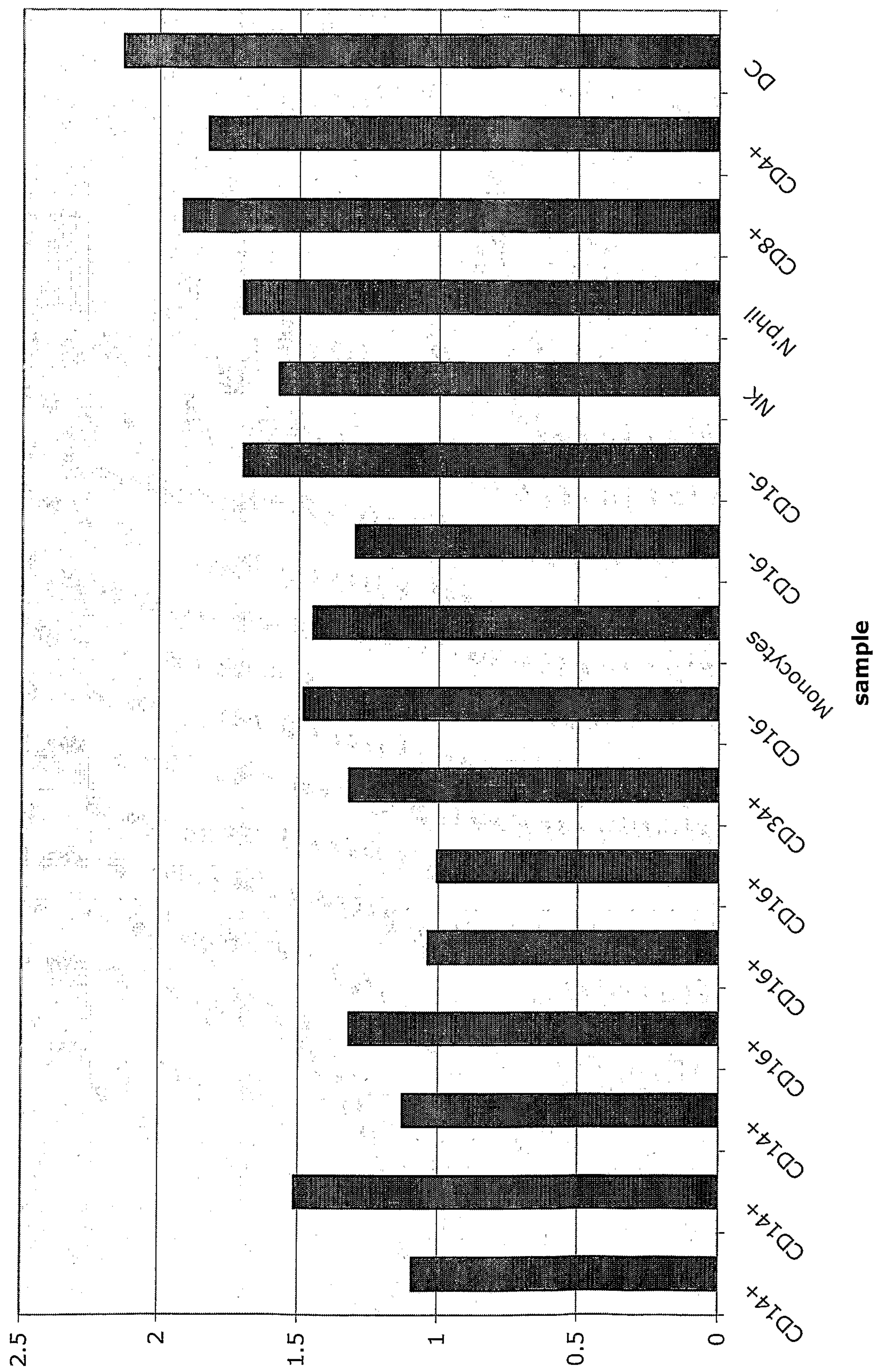


FIGURE 74D

TAHO2/DNA15004/CD20 (MS4A1)

MS4A1

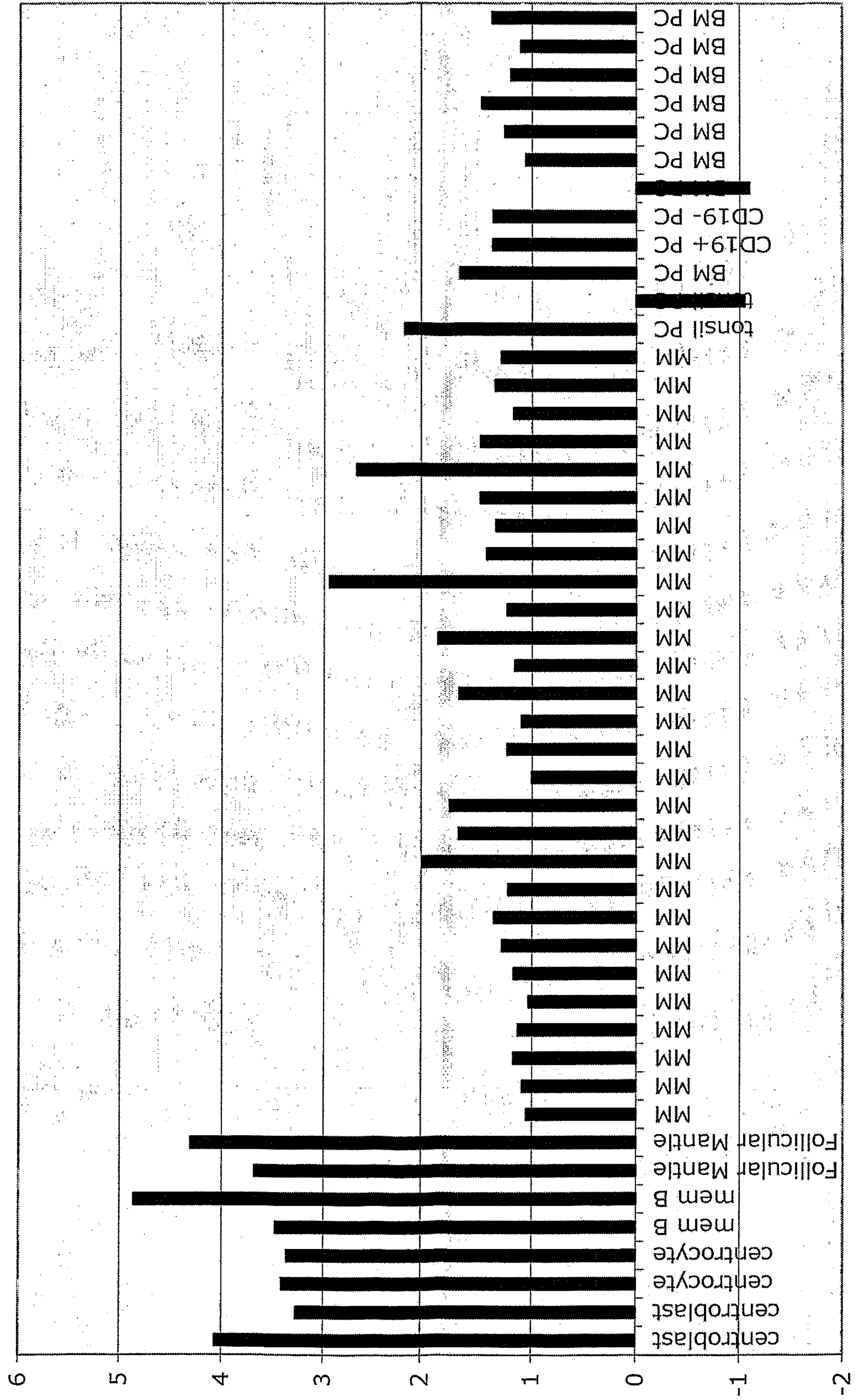


FIGURE 75A

TAHO3/DNA182432/FcRH2 (SPAP1)

SPAP1

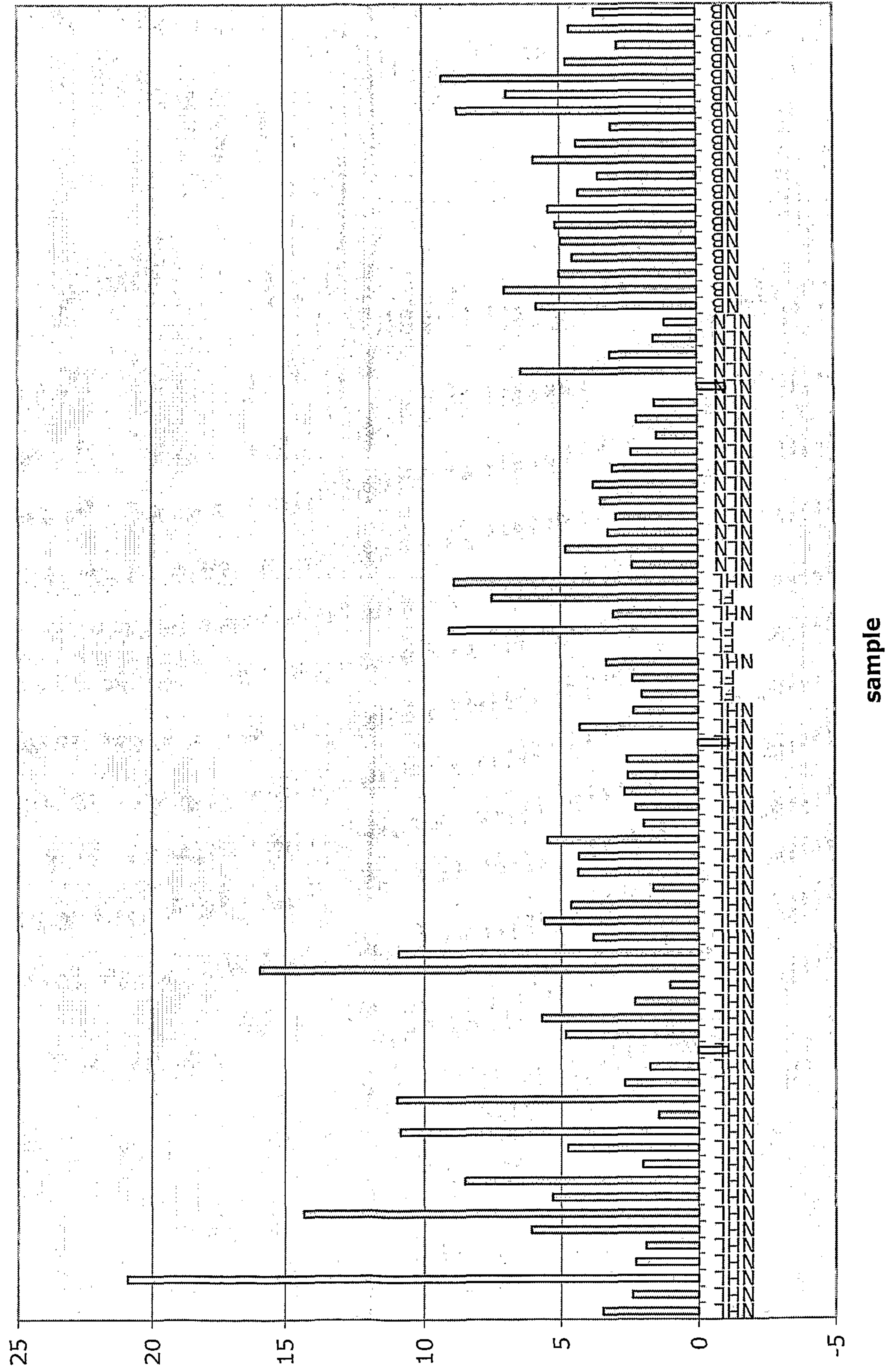


FIGURE 75B

TAHO3/DNA182432/FcRH2 (SPAP1)

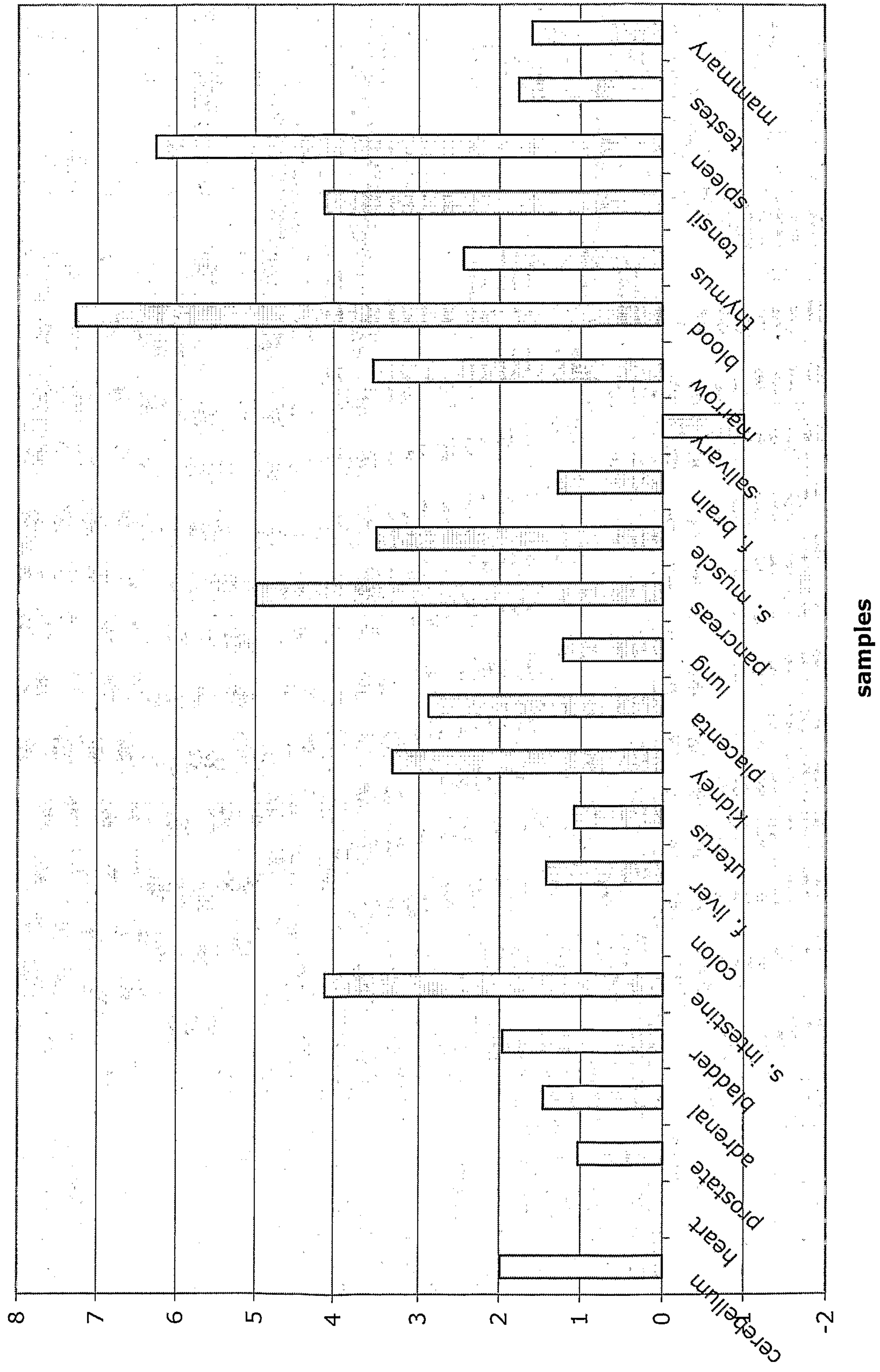
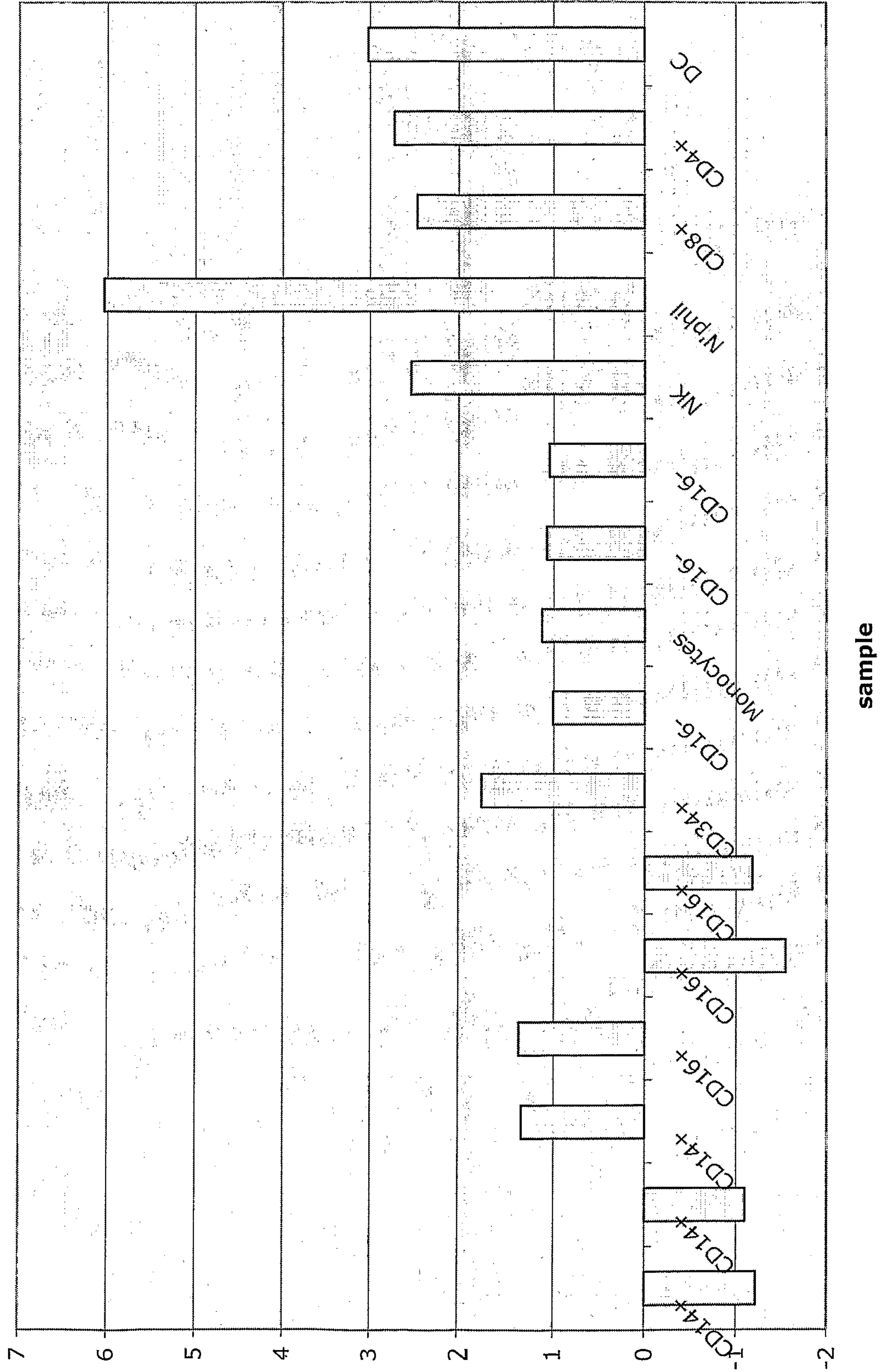
SPAP1

FIGURE 75C

TAHO3/DNA182432/FcRH2 (SPAP1)

SPAP1



TAHO3/DNA182432/FcRH2 (SPAP1)

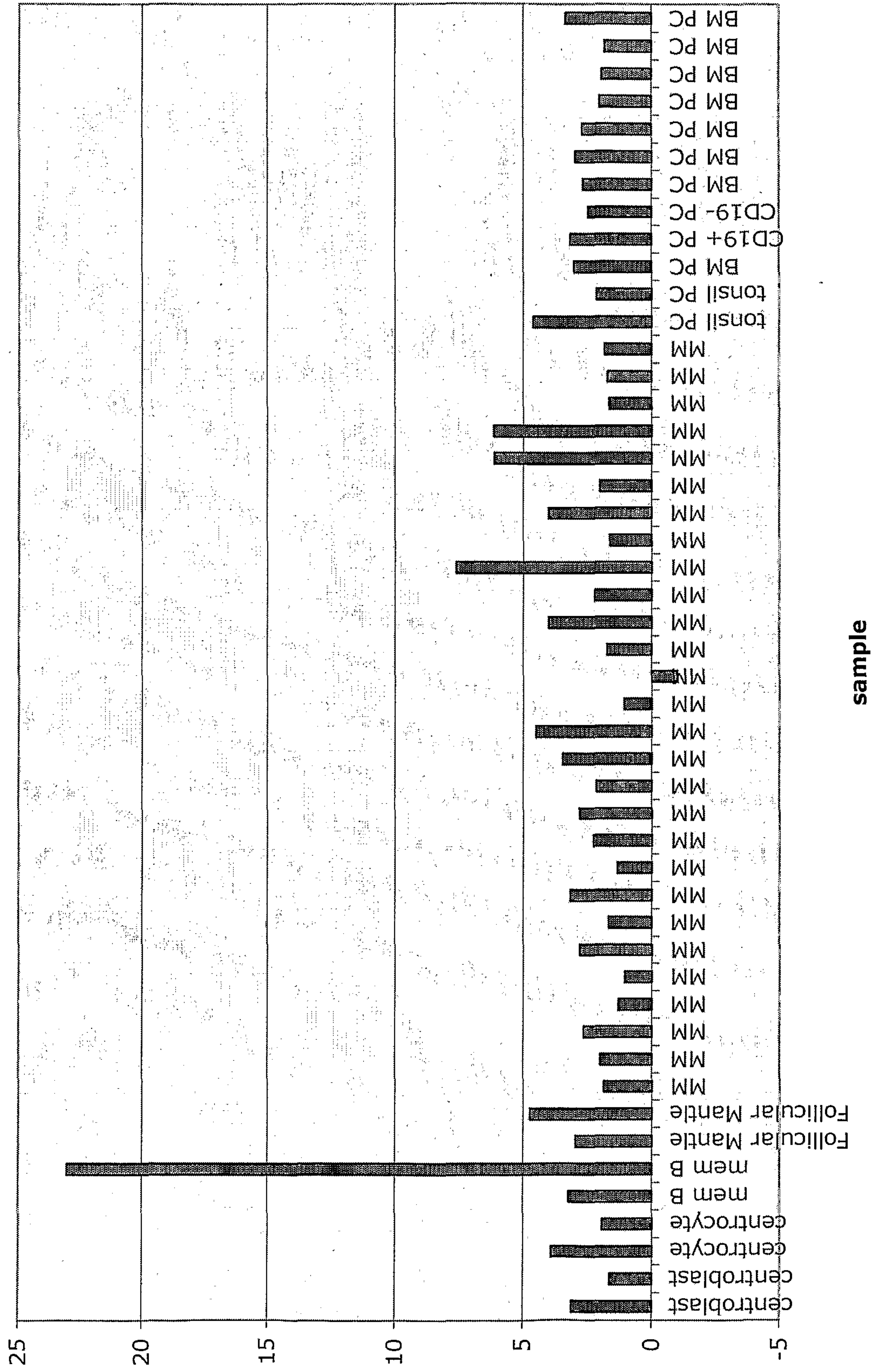


FIGURE 76A

TAHO4/DNA225785/CD79A

CD79A

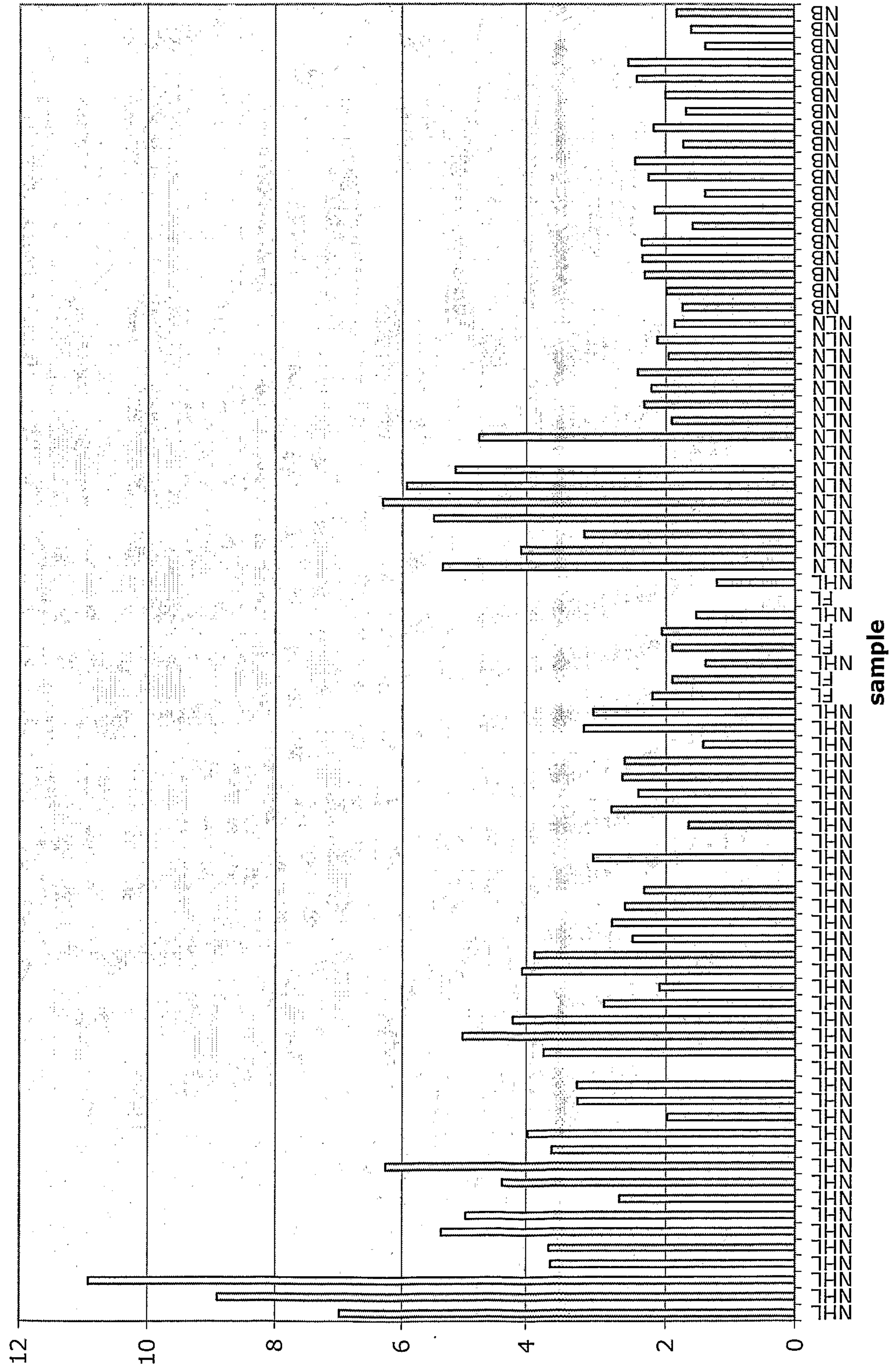


FIGURE 76B**CD79A**

TAHO4/DNA225785/CD79A

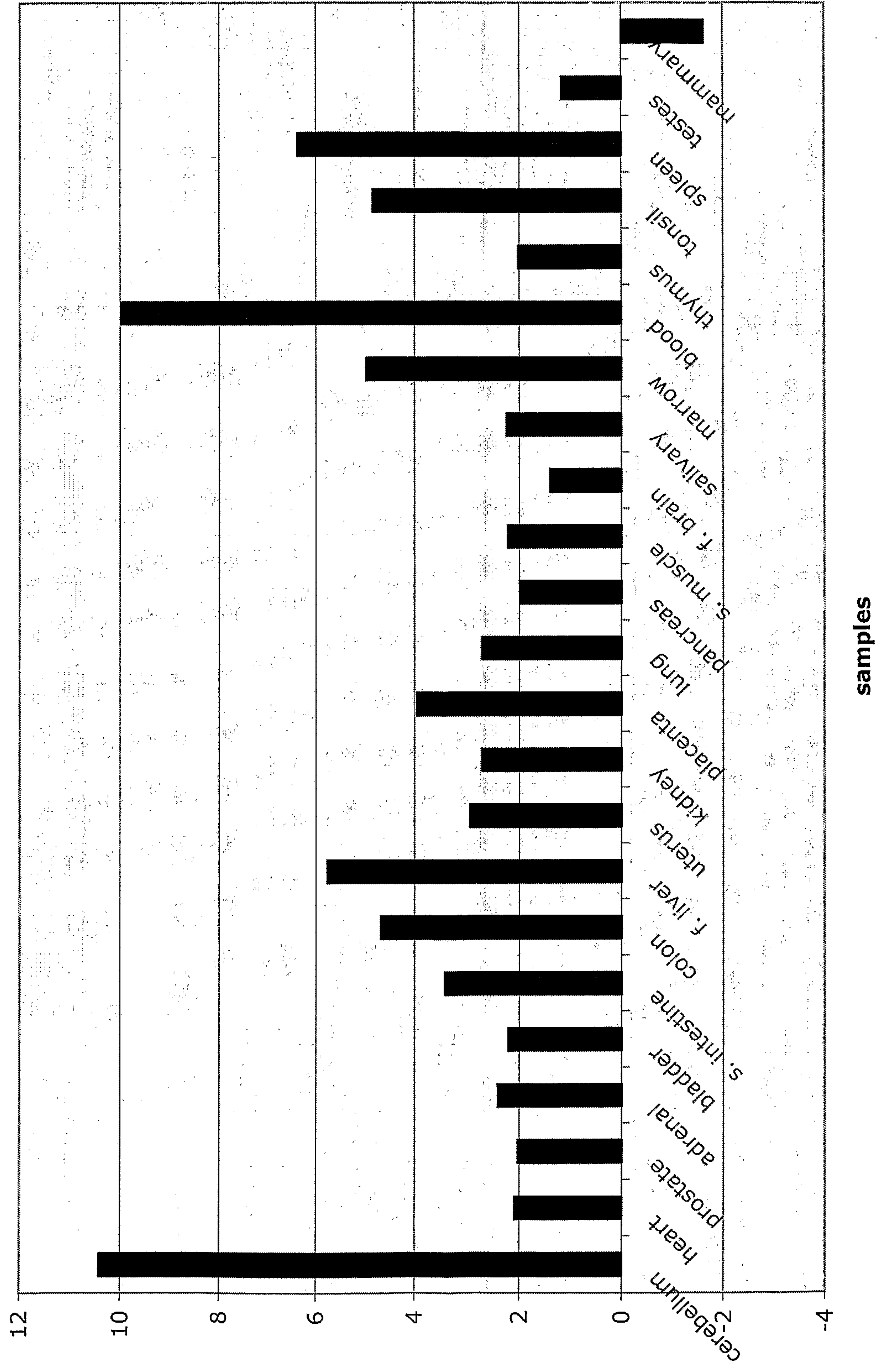


FIGURE 76C

CD79A

TAHO4/DNA225785/CD79A

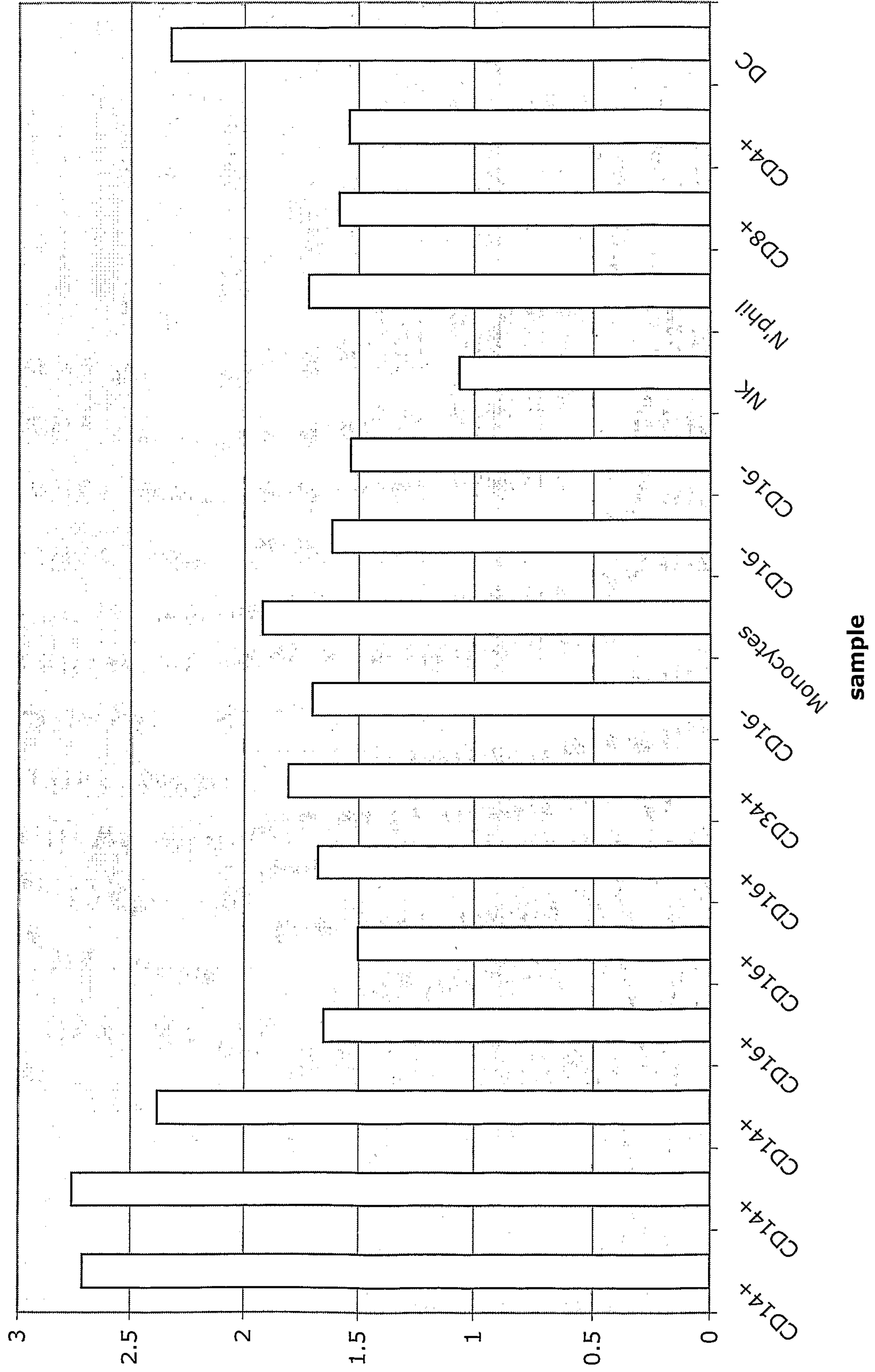


FIGURE 76D

CD79A

TAHO4/DNA25785/CD79A

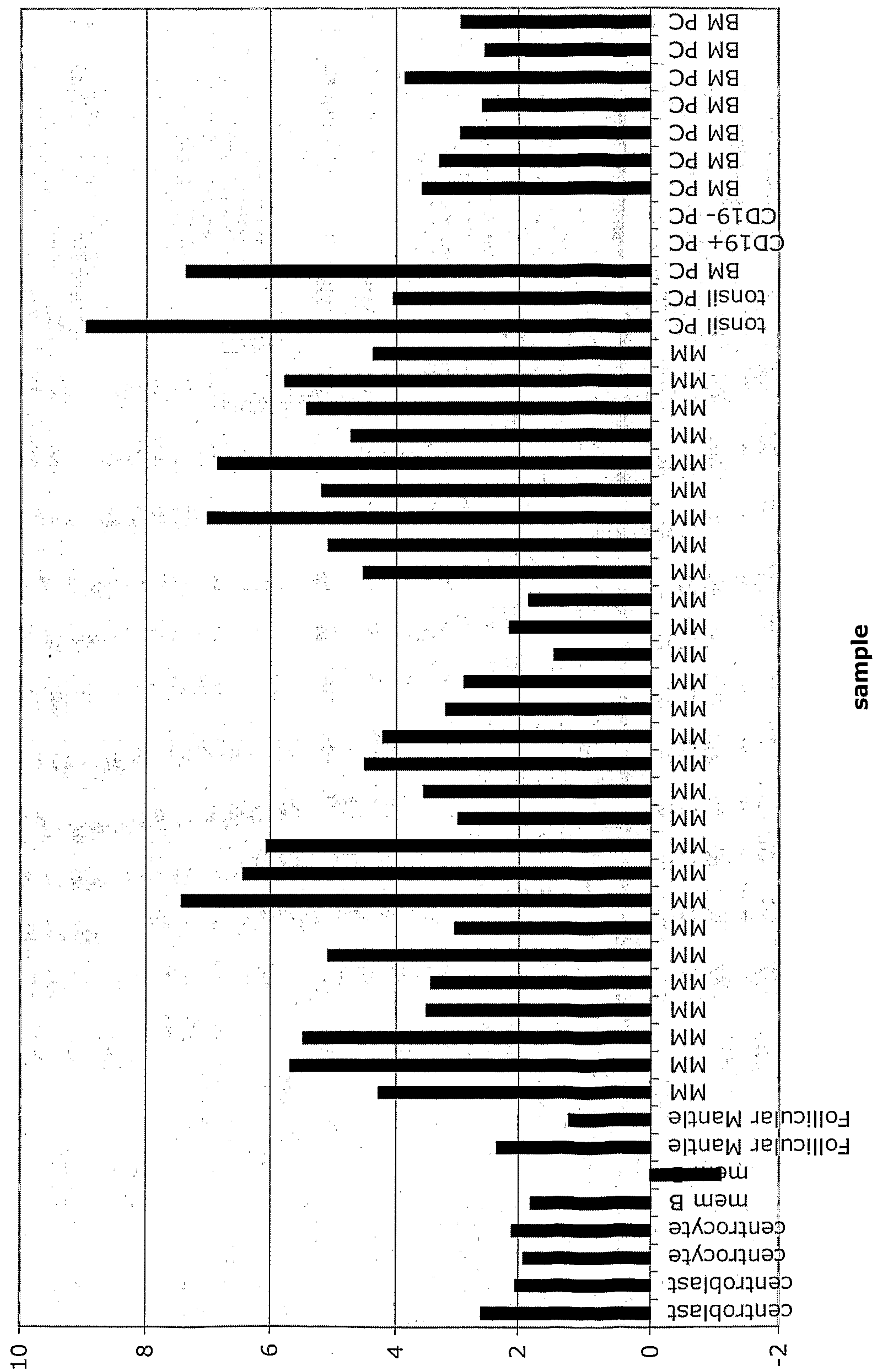


FIGURE 77A

TAHO5/DNA225786/CD79B

CD79B

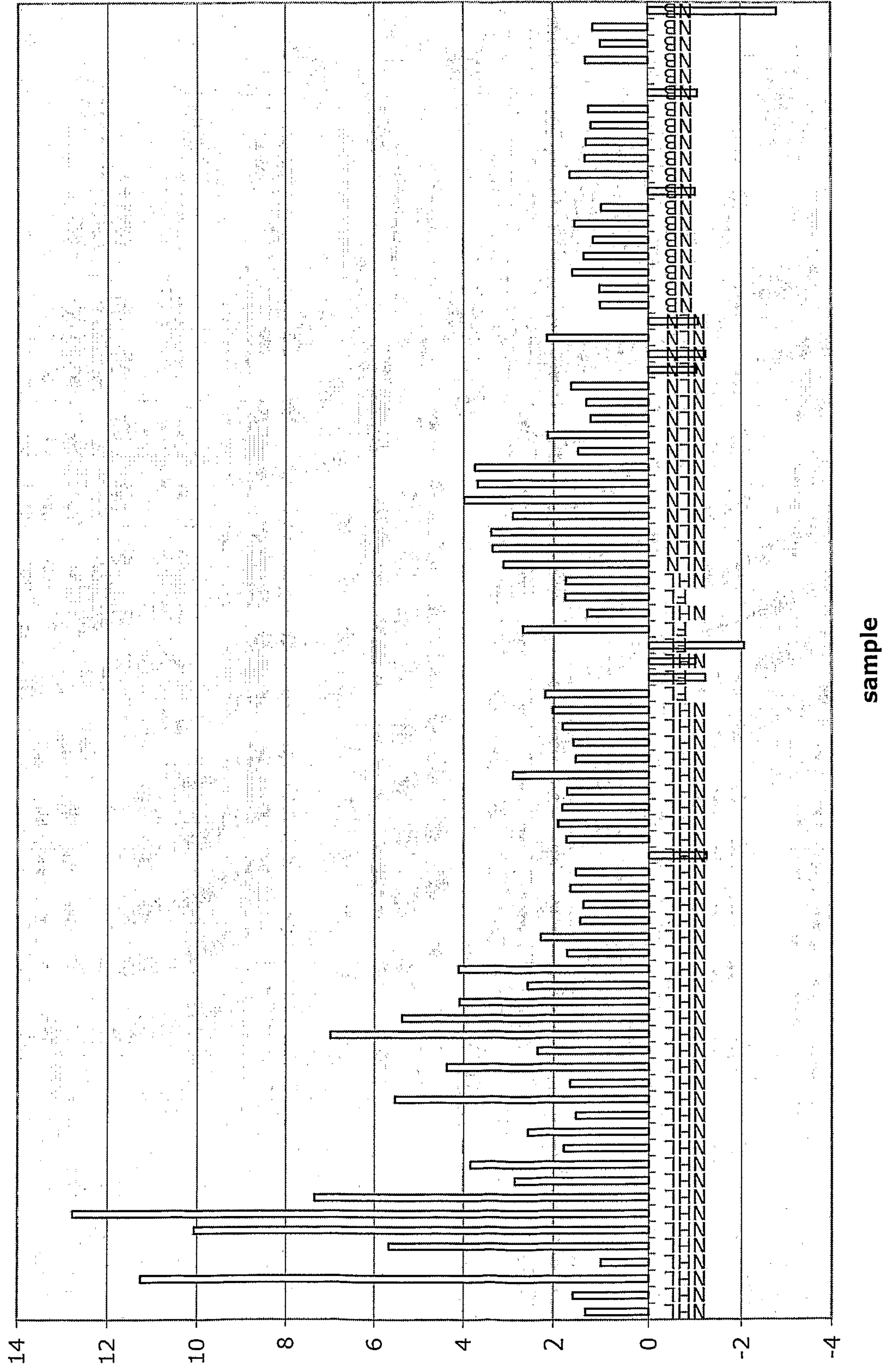


FIGURE 77B**CD79B**

TAHO5/DNA225786/CD79B

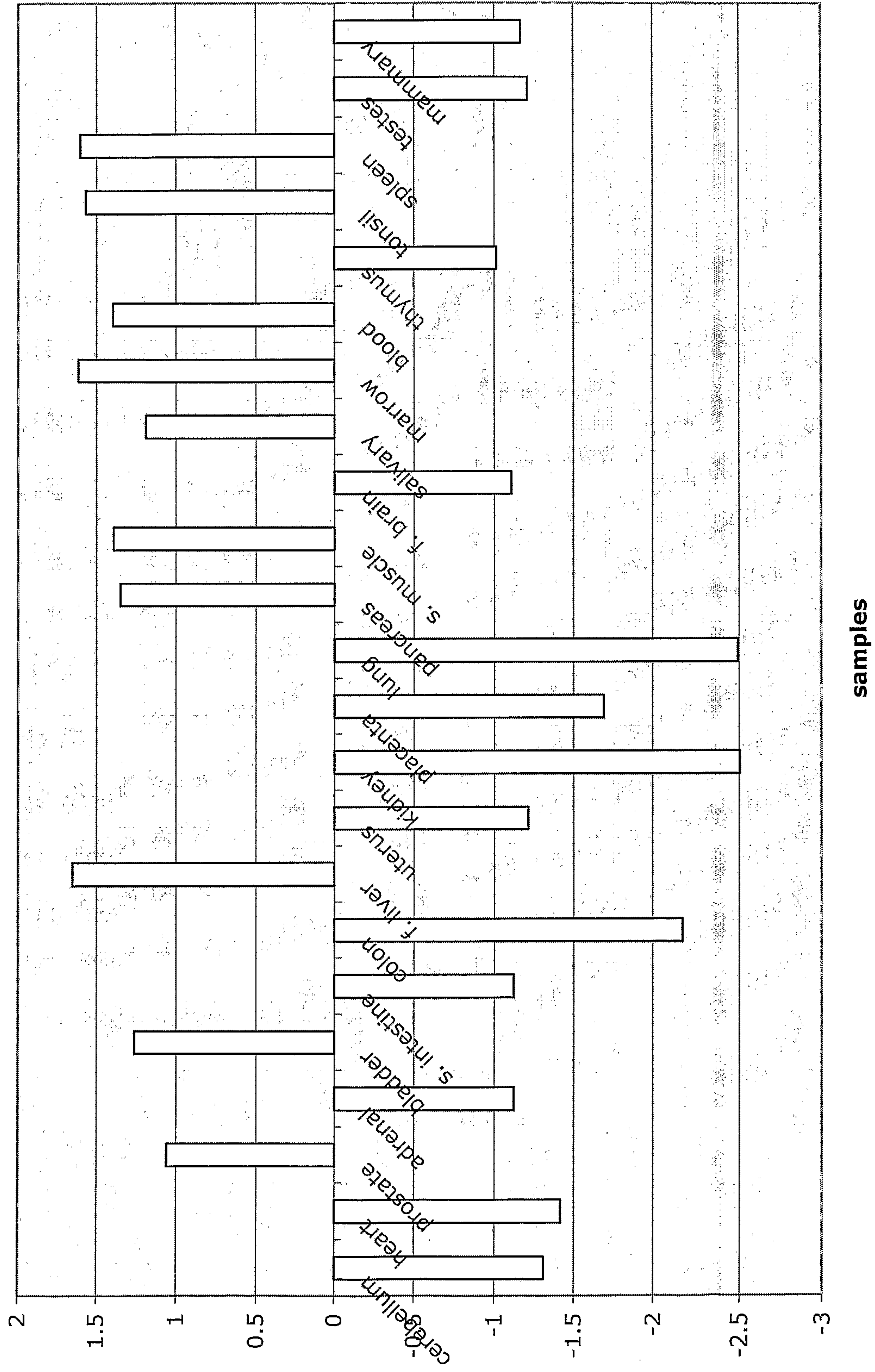


FIGURE 77C

CD79B

TAHO5/DNA225786/CD79B

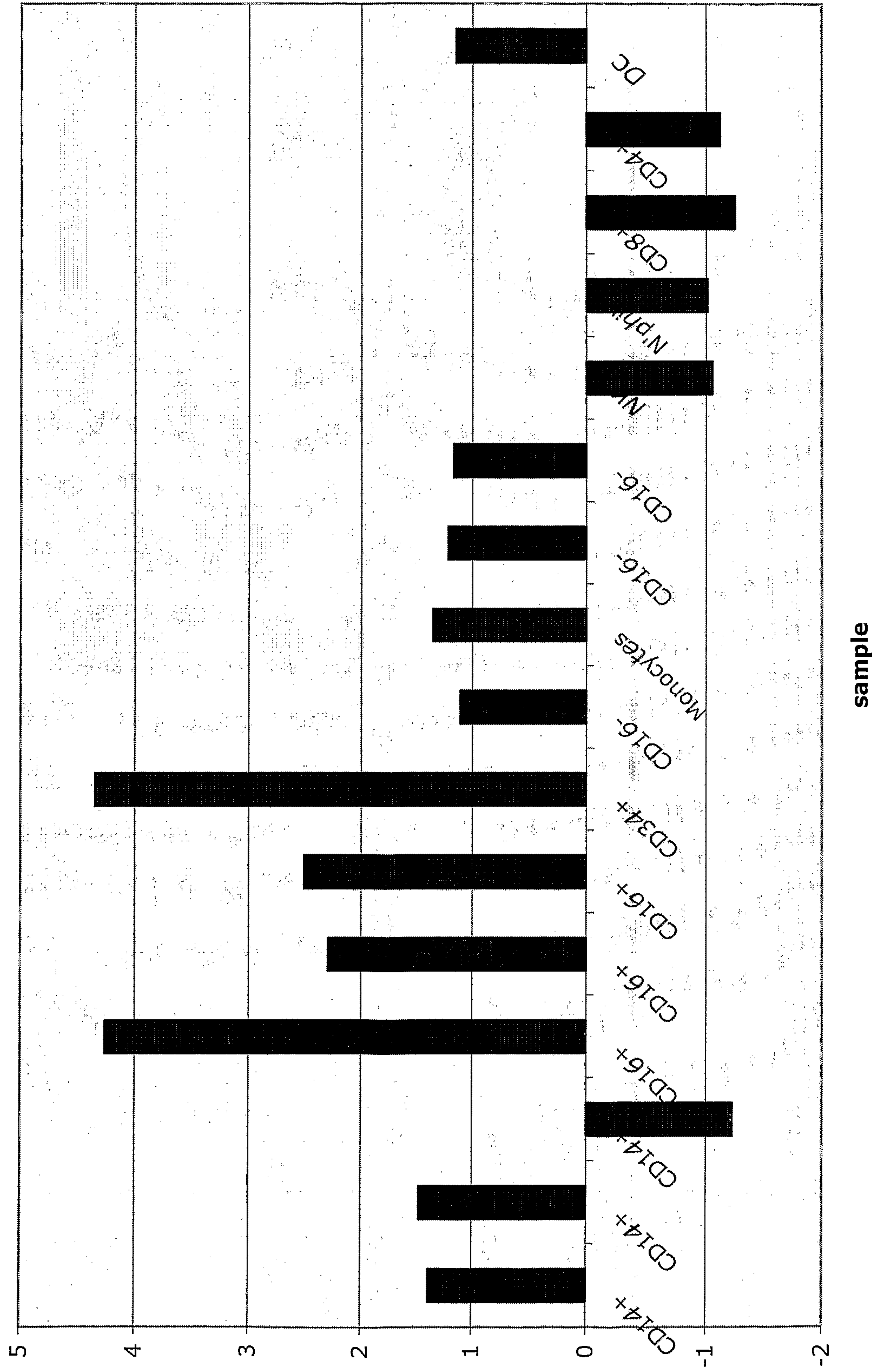


FIGURE 77D

CD79B

TAHO5/DNA225786/CD79B

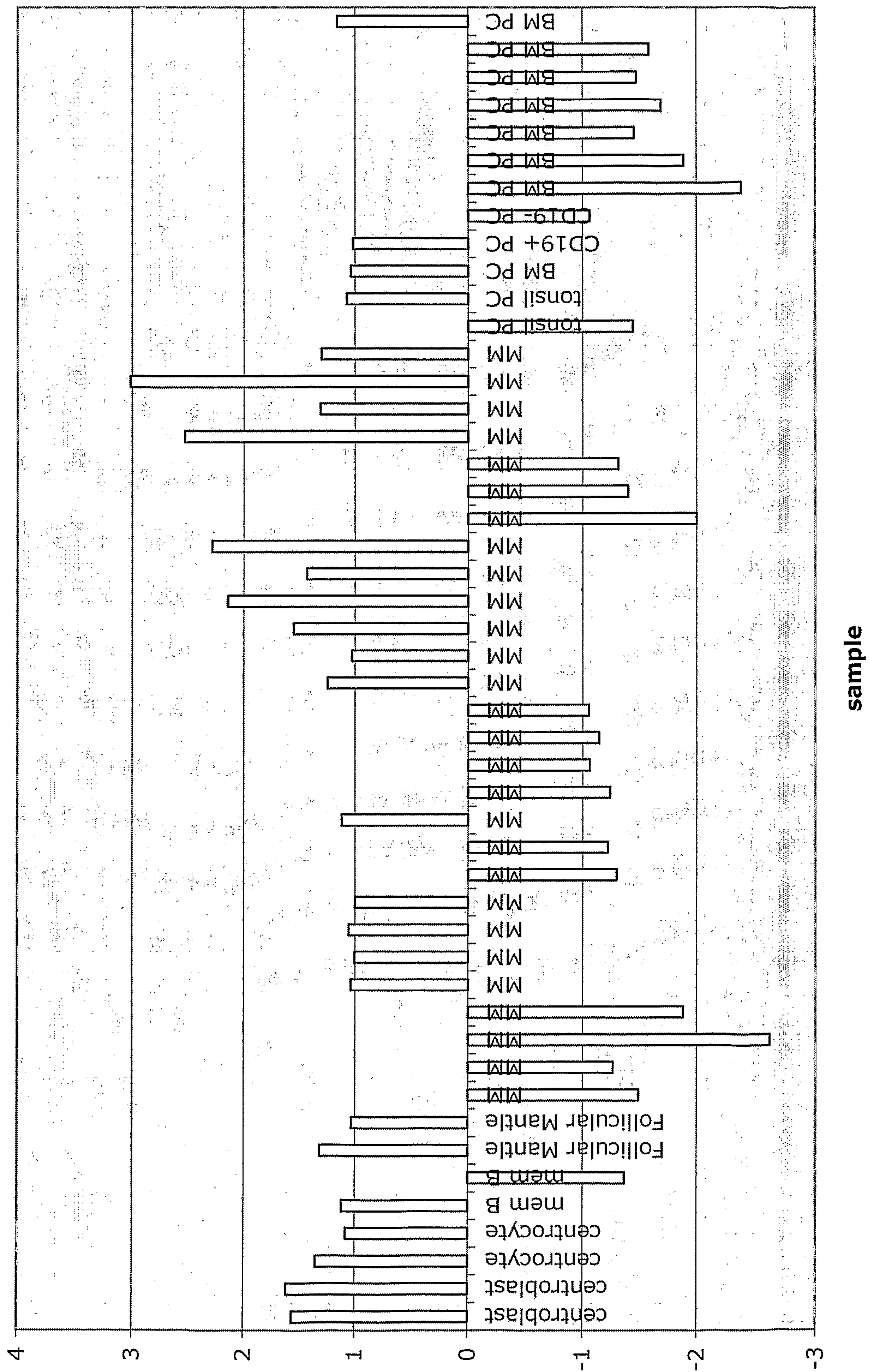
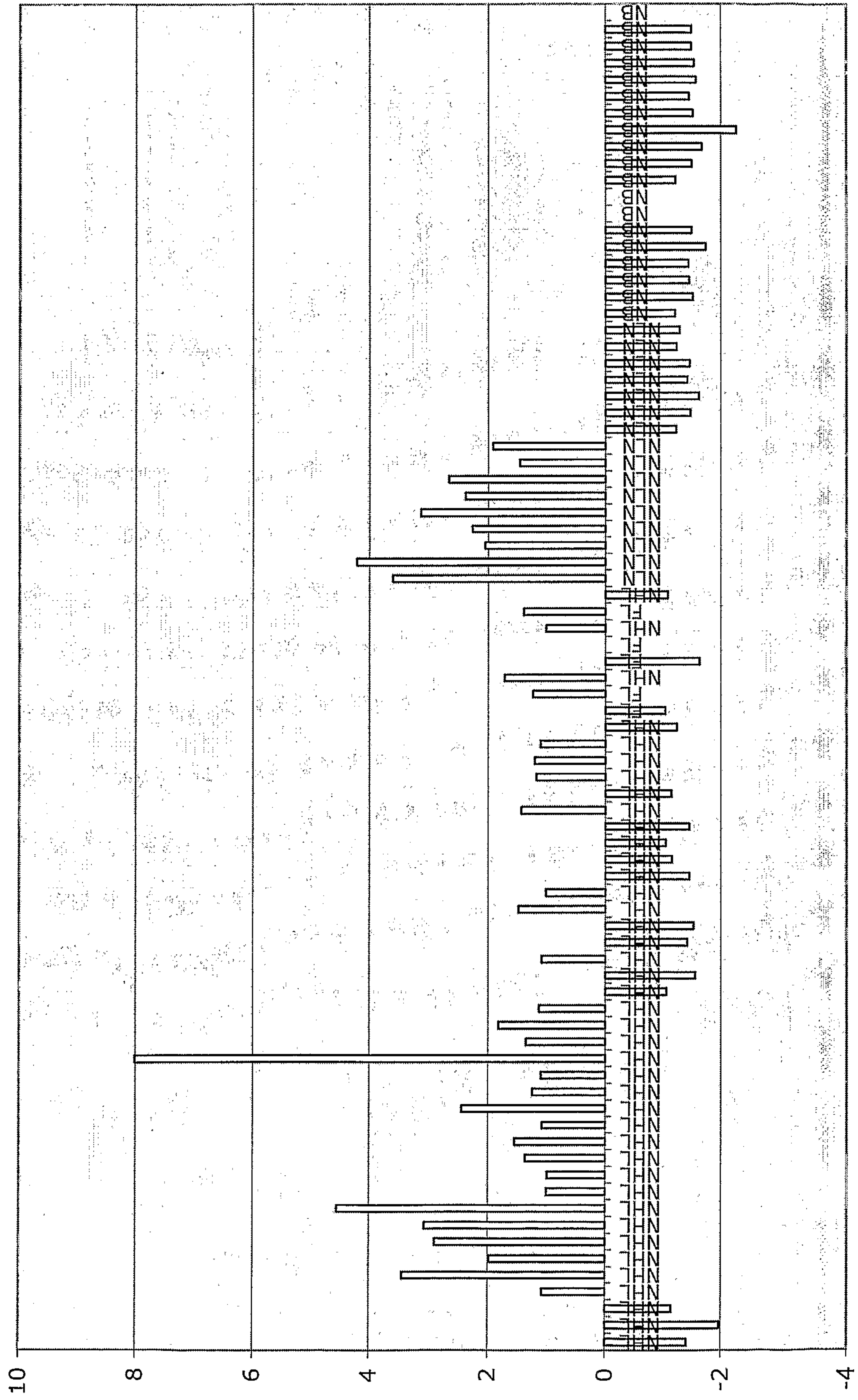


FIGURE 78A

TAHO6/DNA225875/CD21 (CR2)

CR2

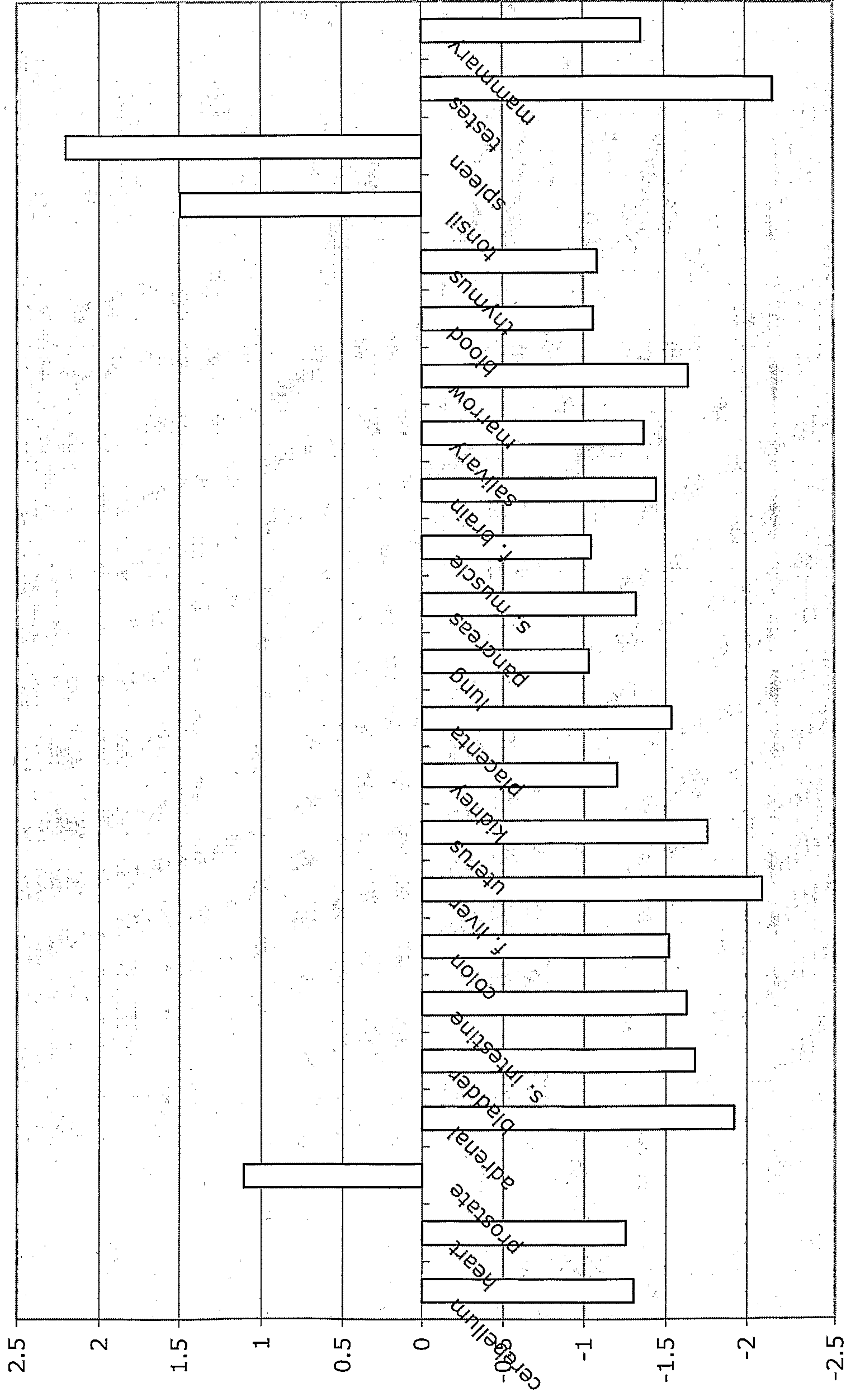


sample

FIGURE 78B

TAHO6/DNA225875/CD21 (CR2)

CR2



samples

TAHO6/DNA225875/CD21 (CR2)

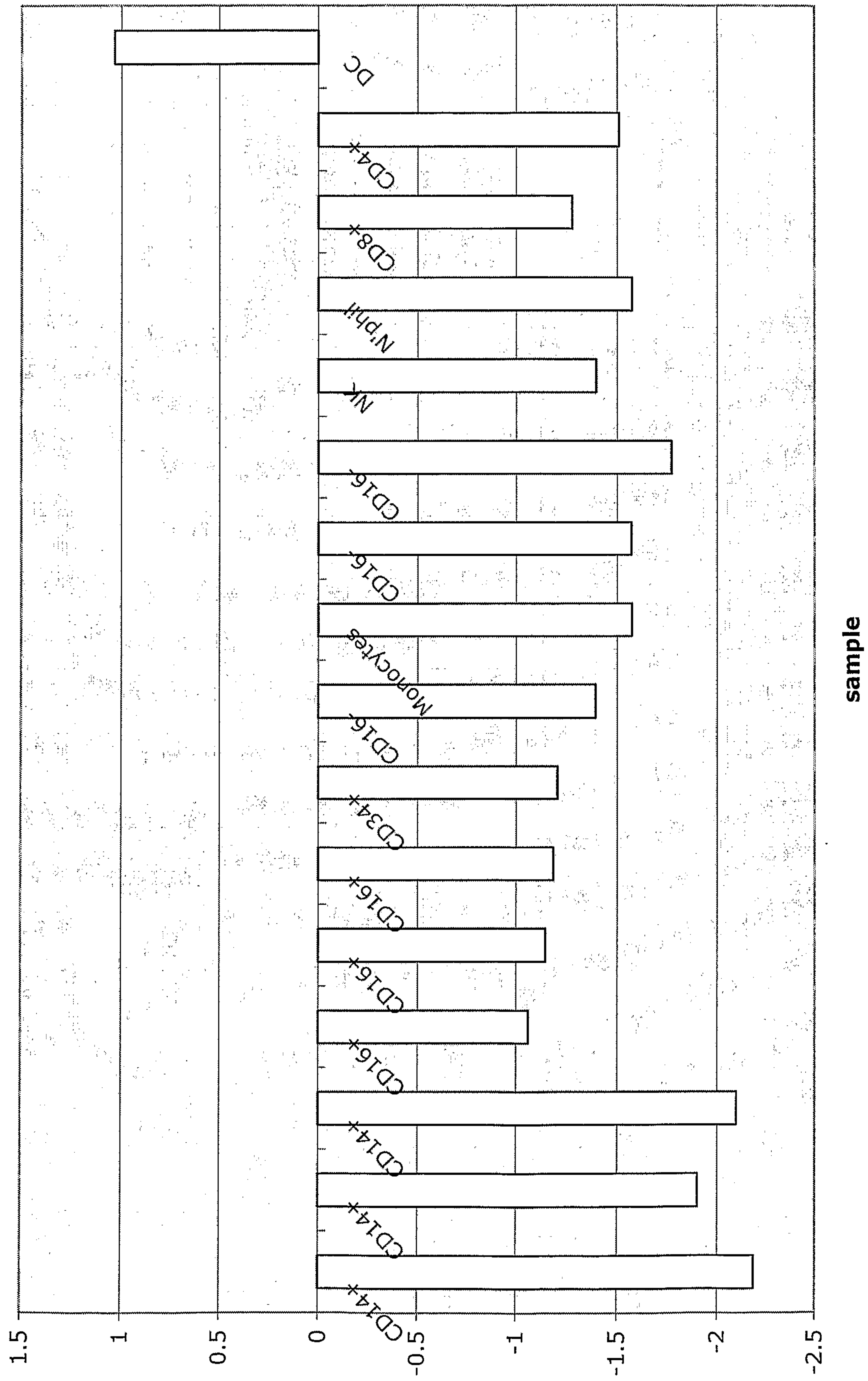


FIGURE 78D

CR2

TAHO6/DNA225875/CD21 (CR2)

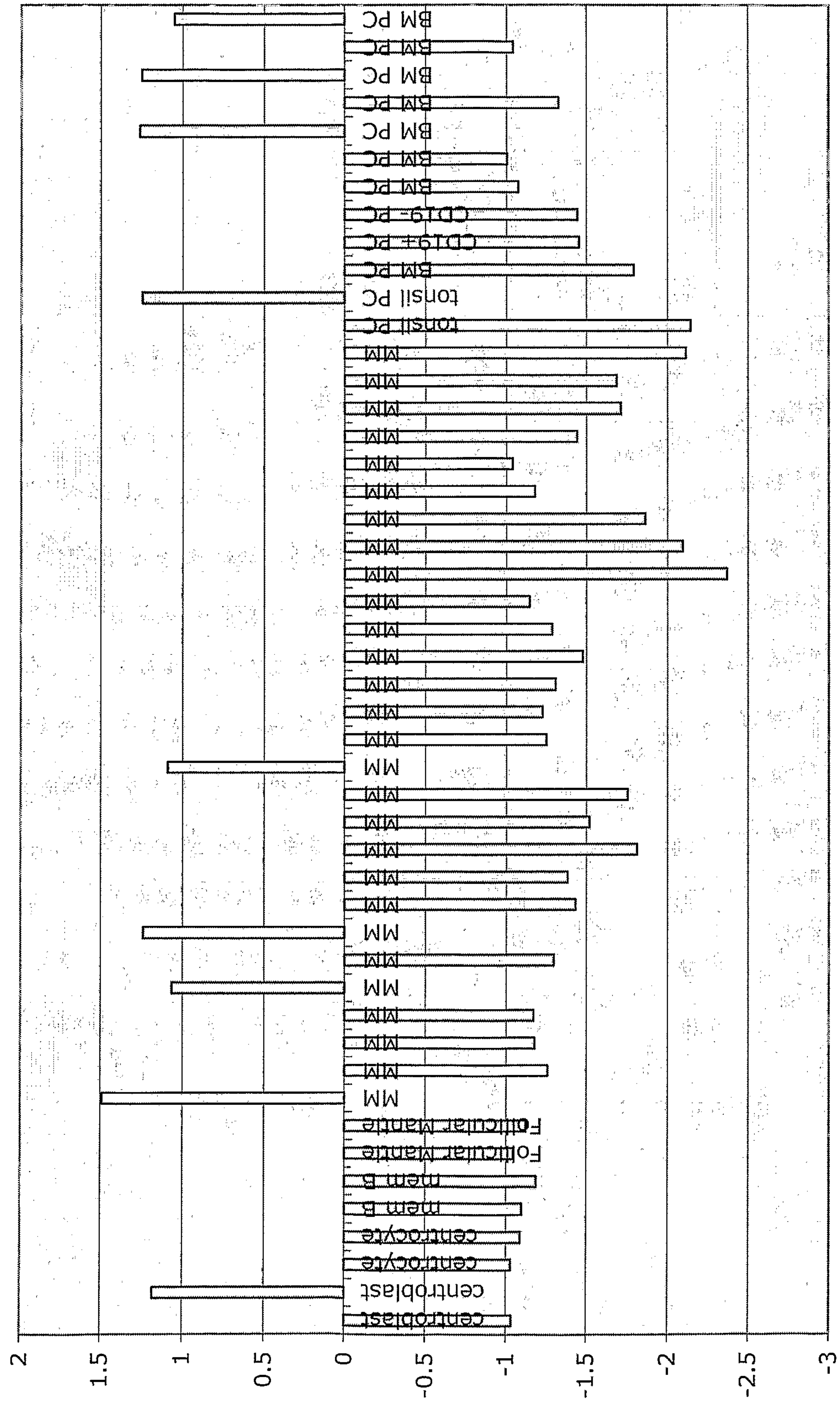


FIGURE 79A

TAHO8/DNA226239/CD72

CD72

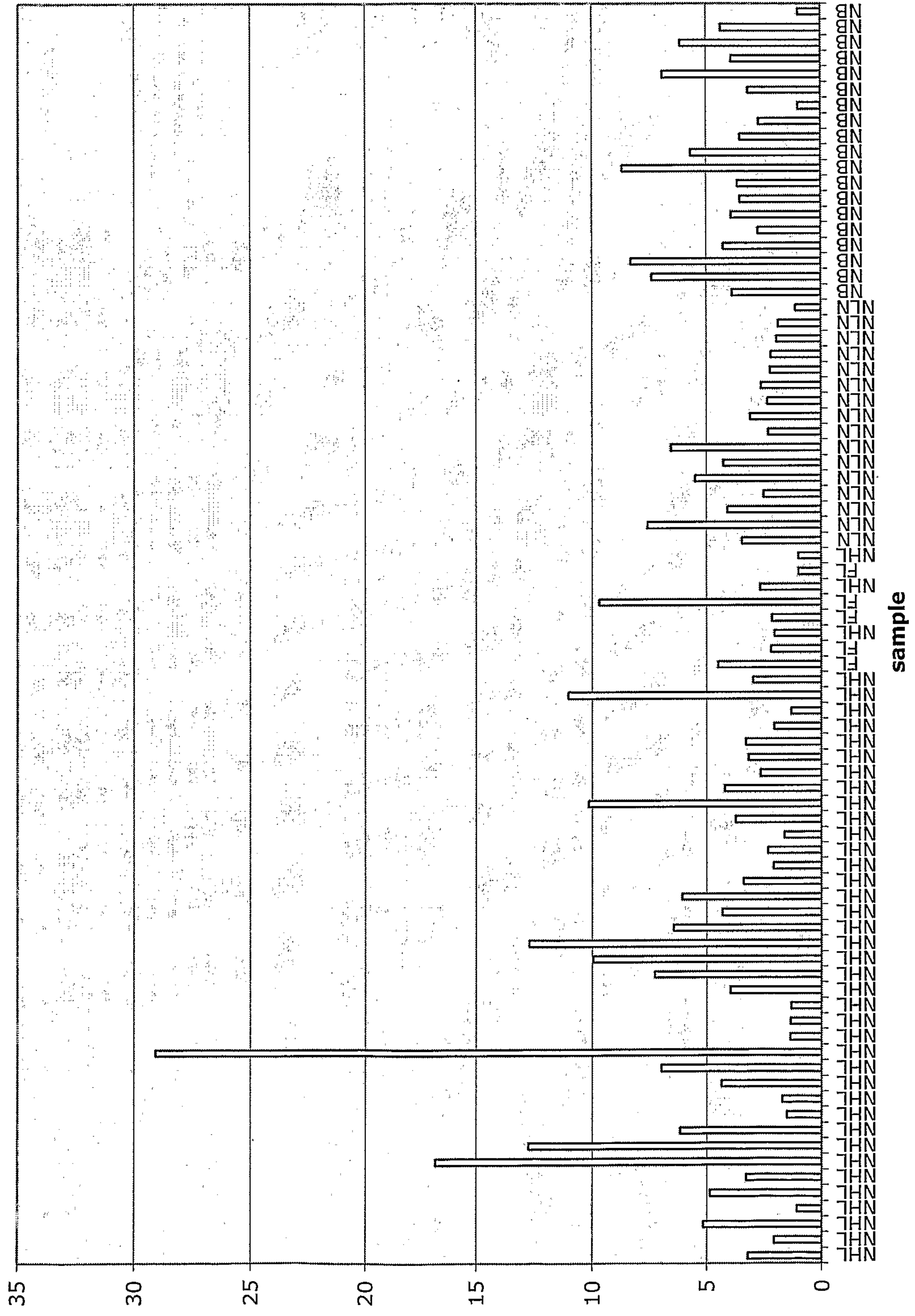


FIGURE 79B**CD72**

TAHO8/DNA226239/CD72

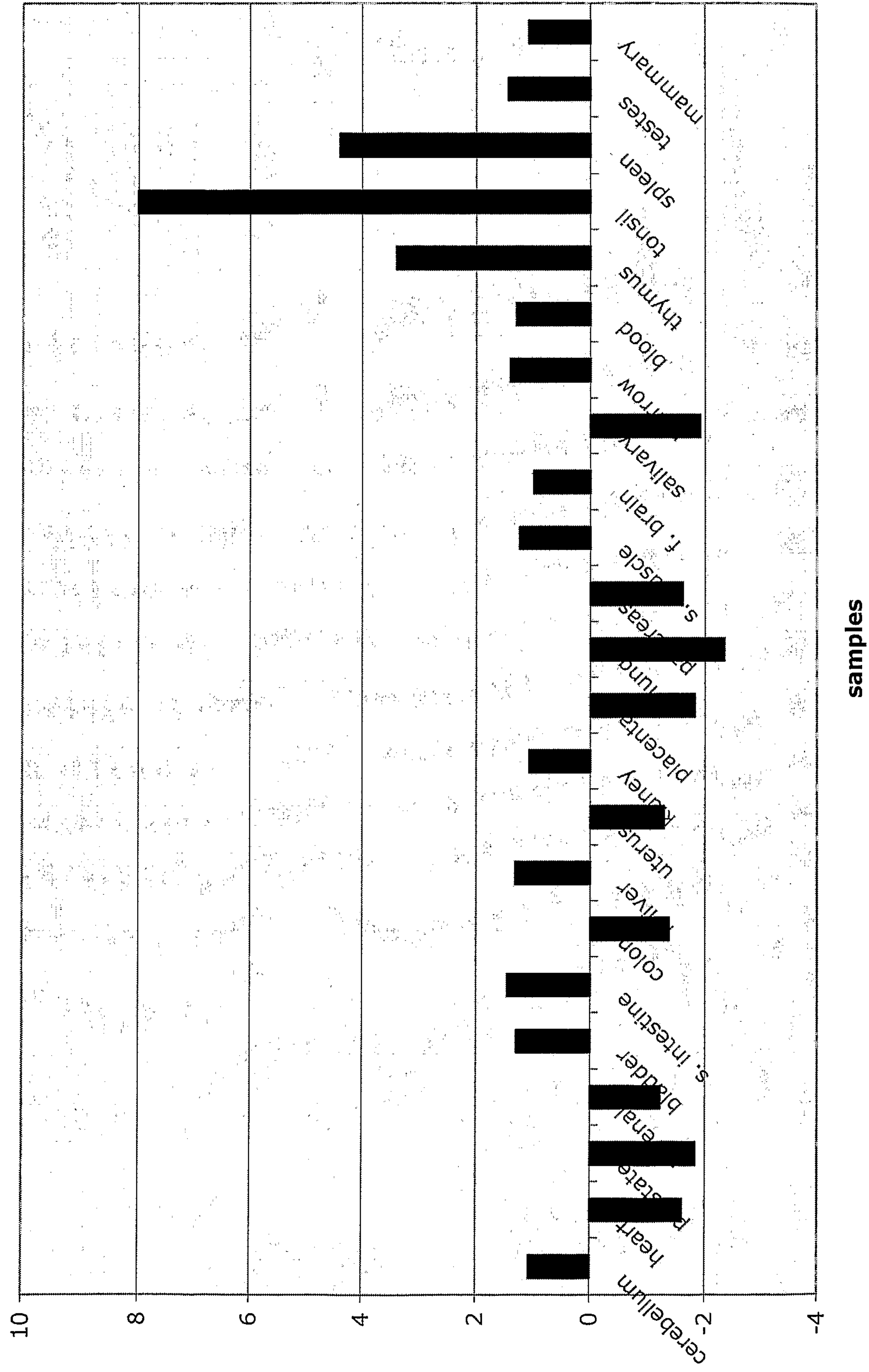


FIGURE 79C**CD72**

TAHO8/DNA226239/CD72

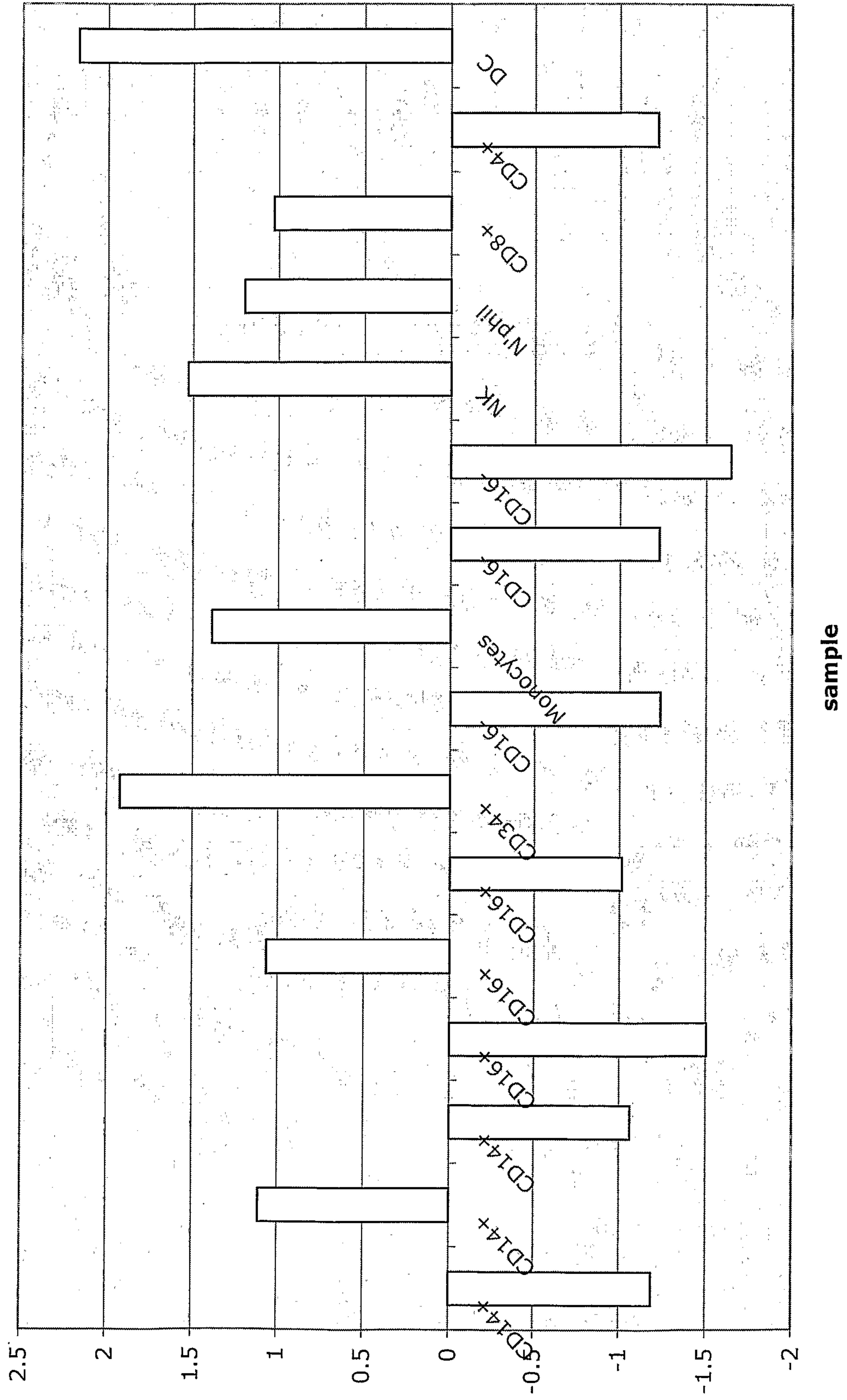


FIGURE 79D

CD72

TAH08/DNA226239/CD72

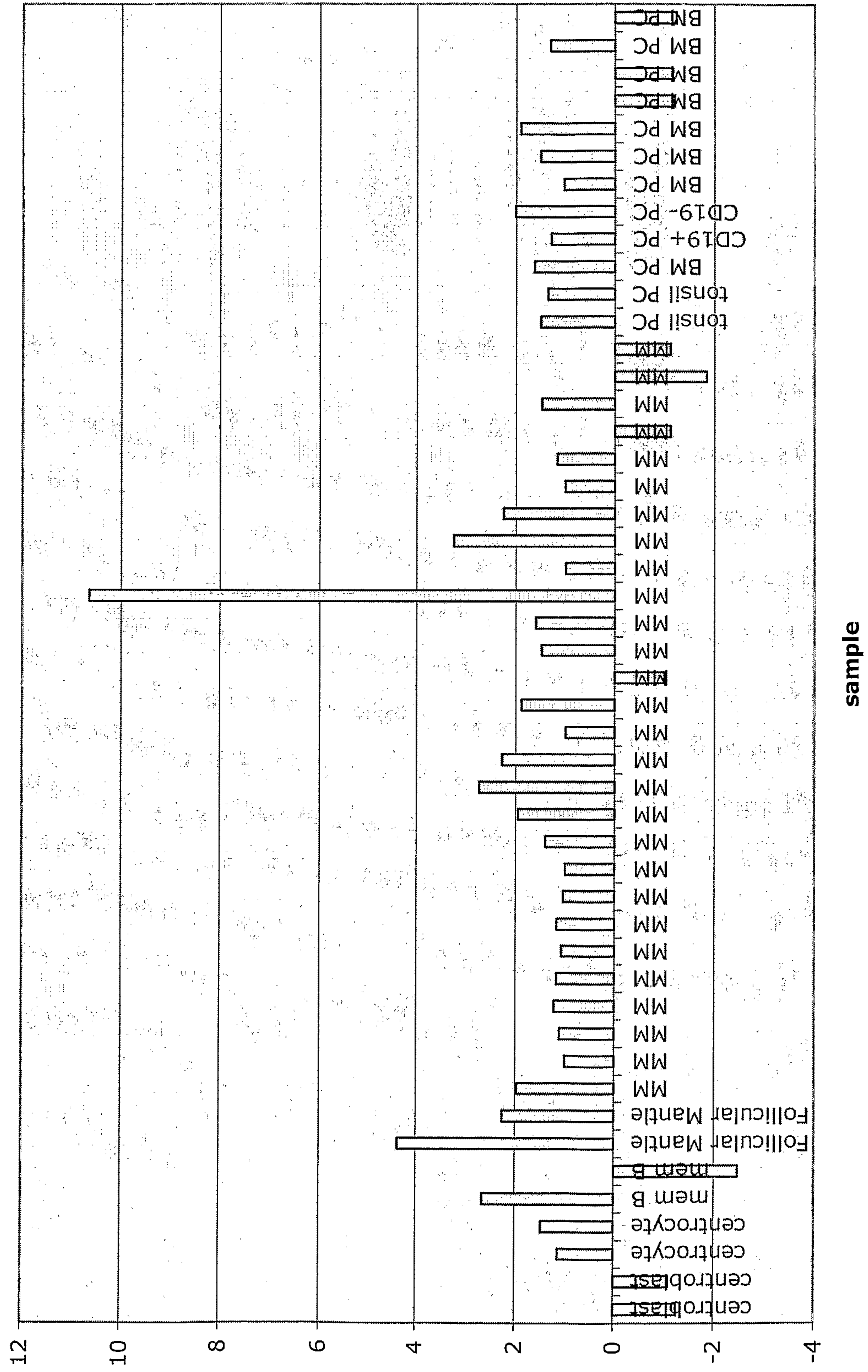


FIGURE 80A

TAHO9/DNA226394/P2XR5

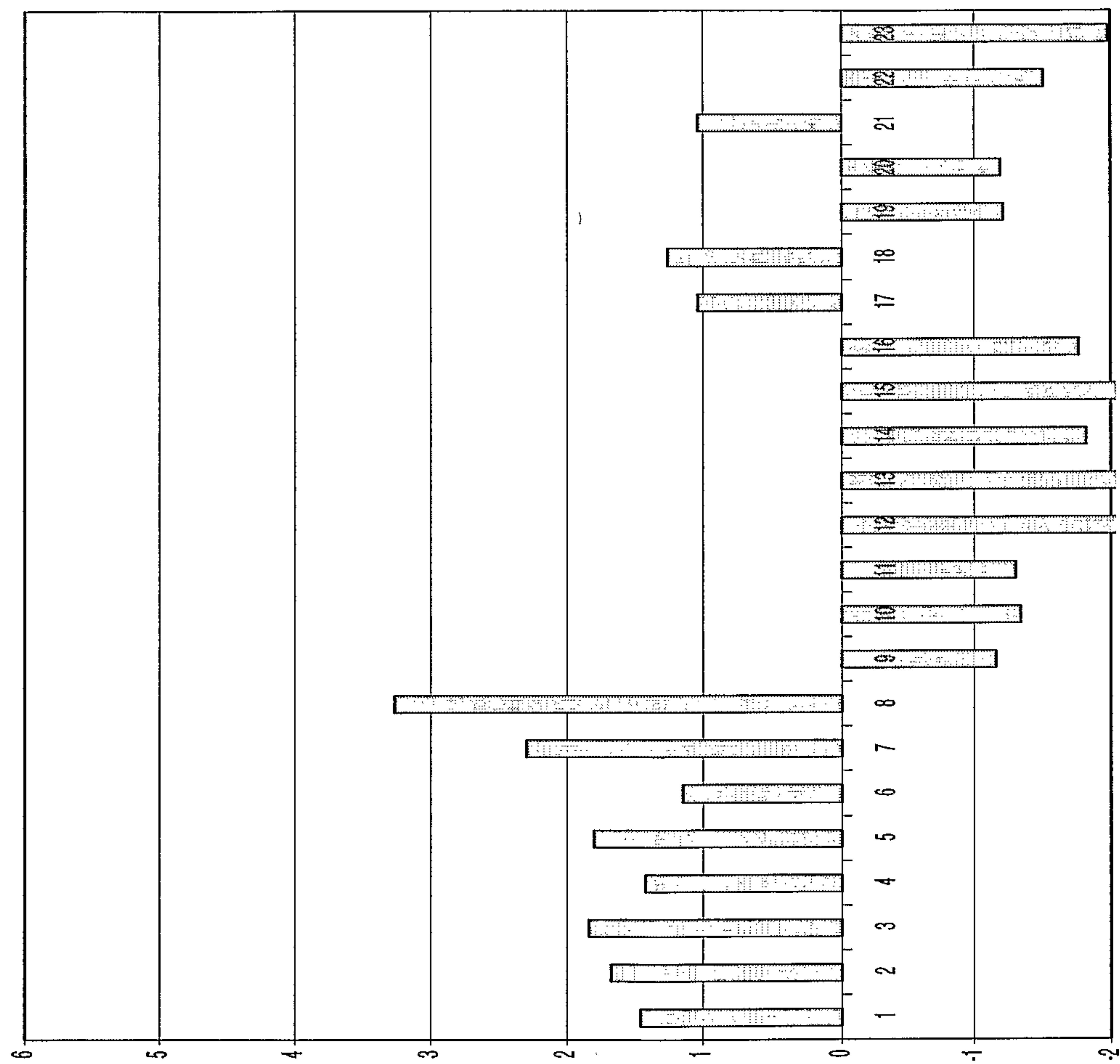
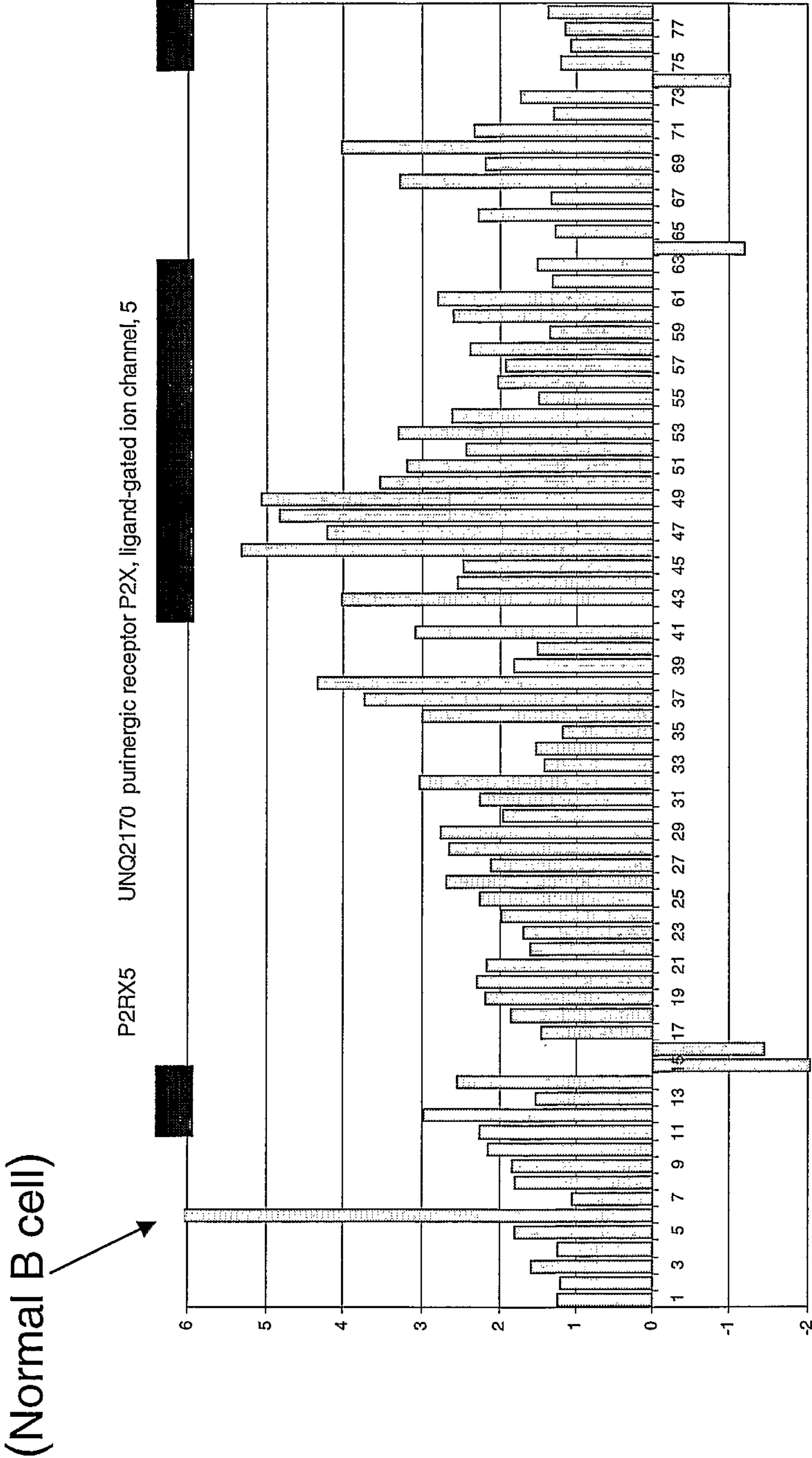
P2RX5 UNC2170 purinergic receptor P2X₁ ligand-gated ion channel, 5

FIGURE 80B

TAHO9/DNA226394/P2XR5



■ = multiple myeloma samples

FIGURE 81A

TAHO10/DNA226423/HLA-DOB

HLA-DOB

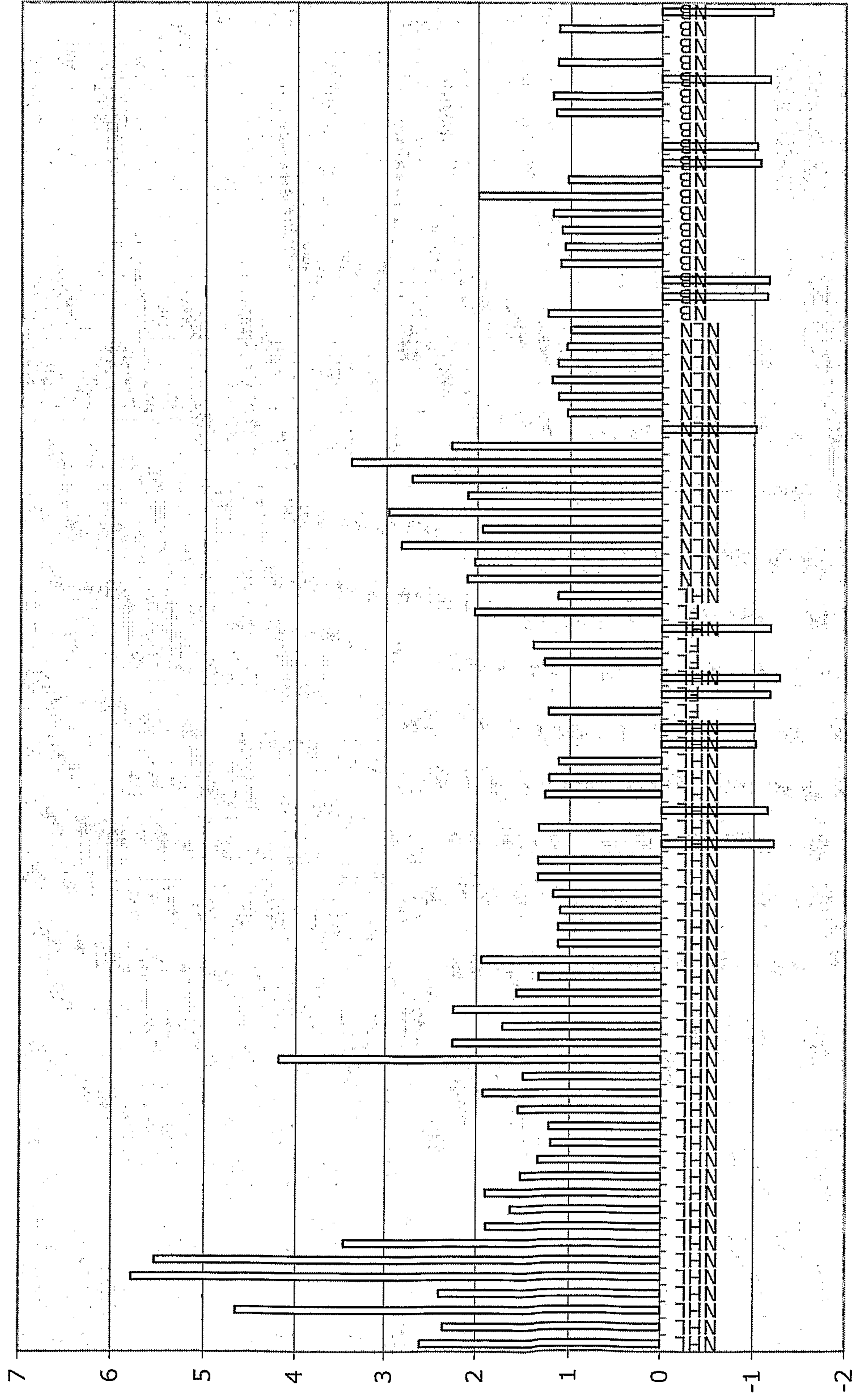
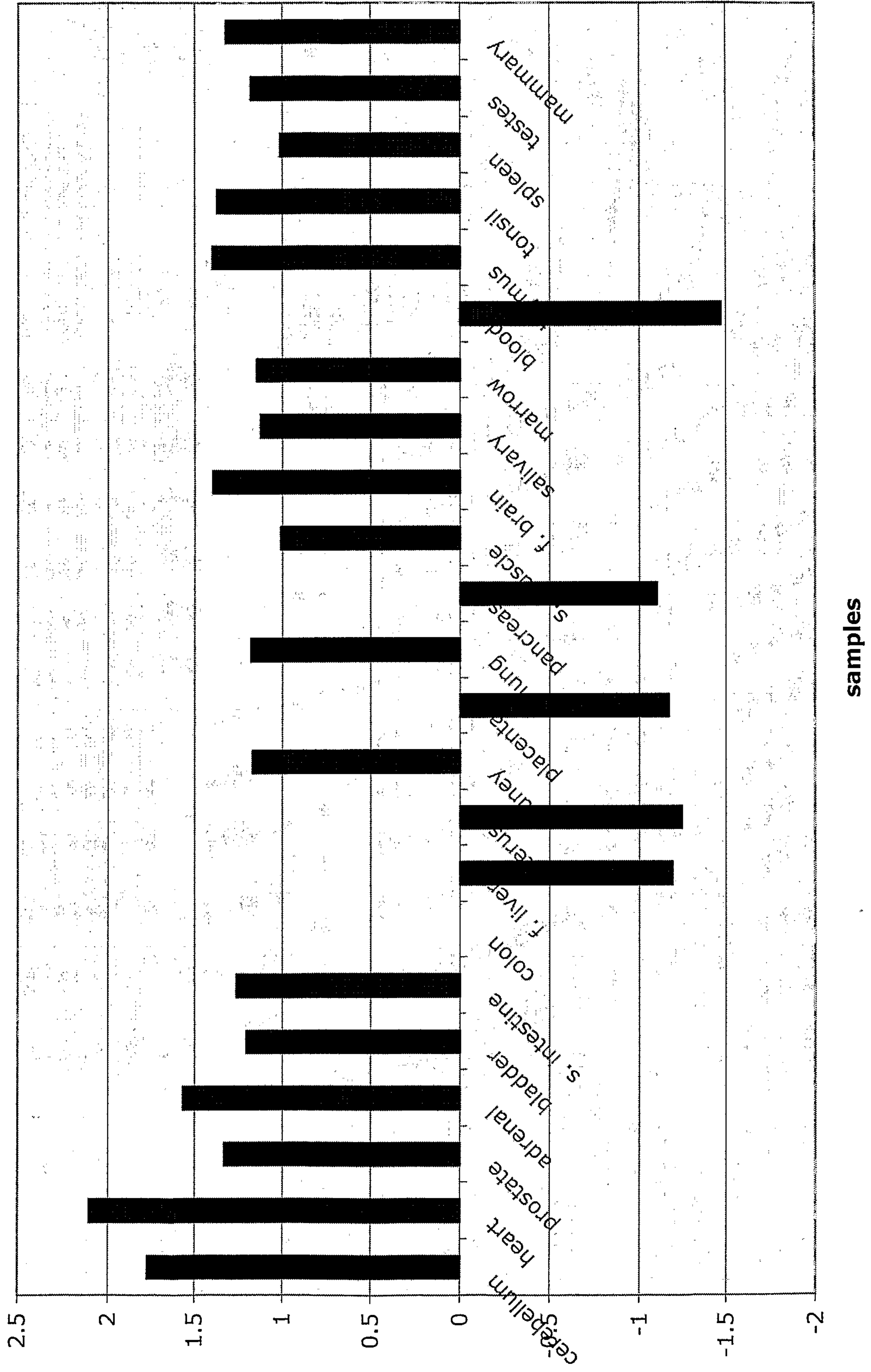


FIGURE 81B

TAHO10/DNA226423/HLA-DOB

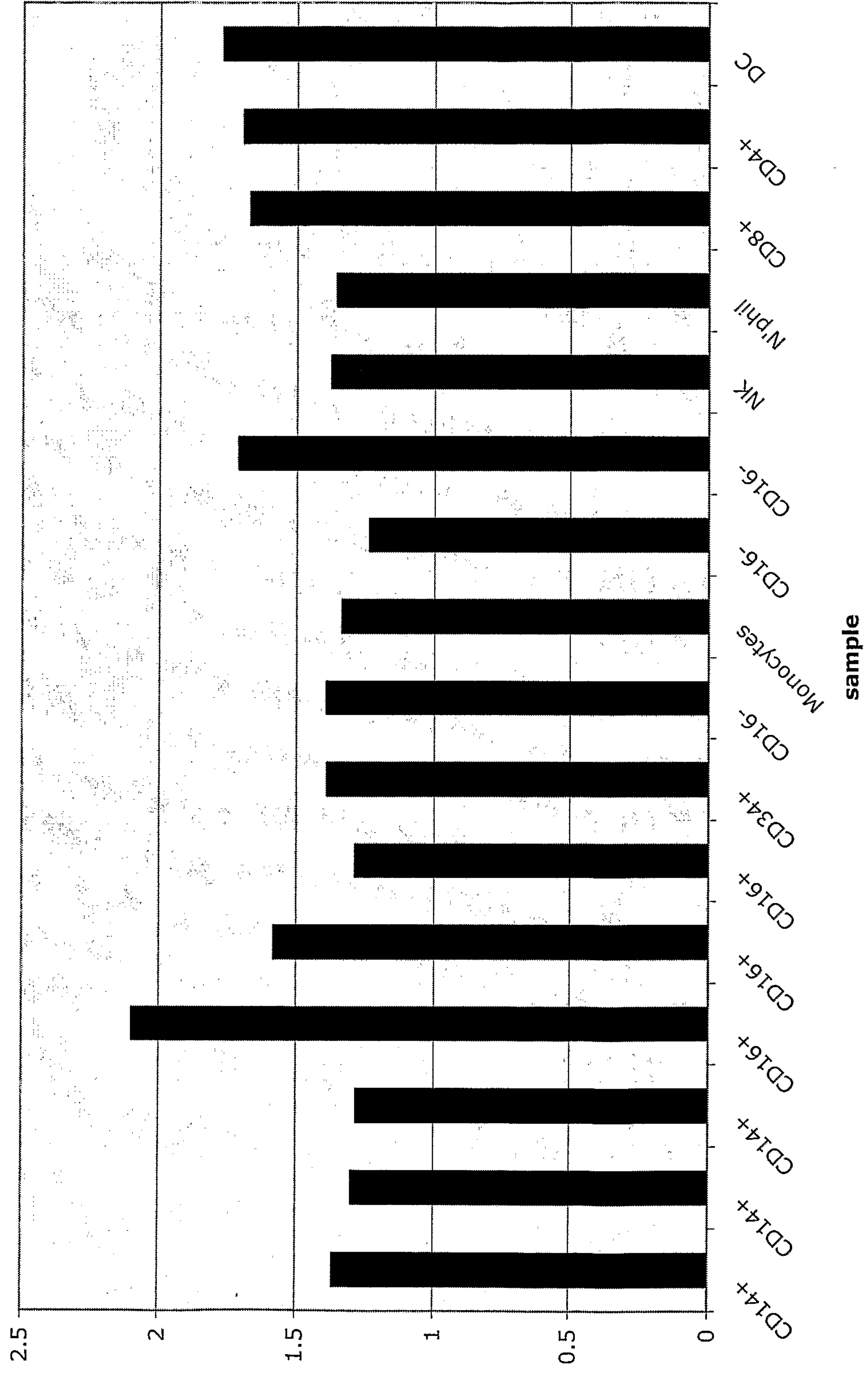
HLA-DOB



samples

FIGURE 81C

TAHO10/DNA226423/HLA-DOB

HLA-DOB

TAHO10/DNA226423/HLA-DOB

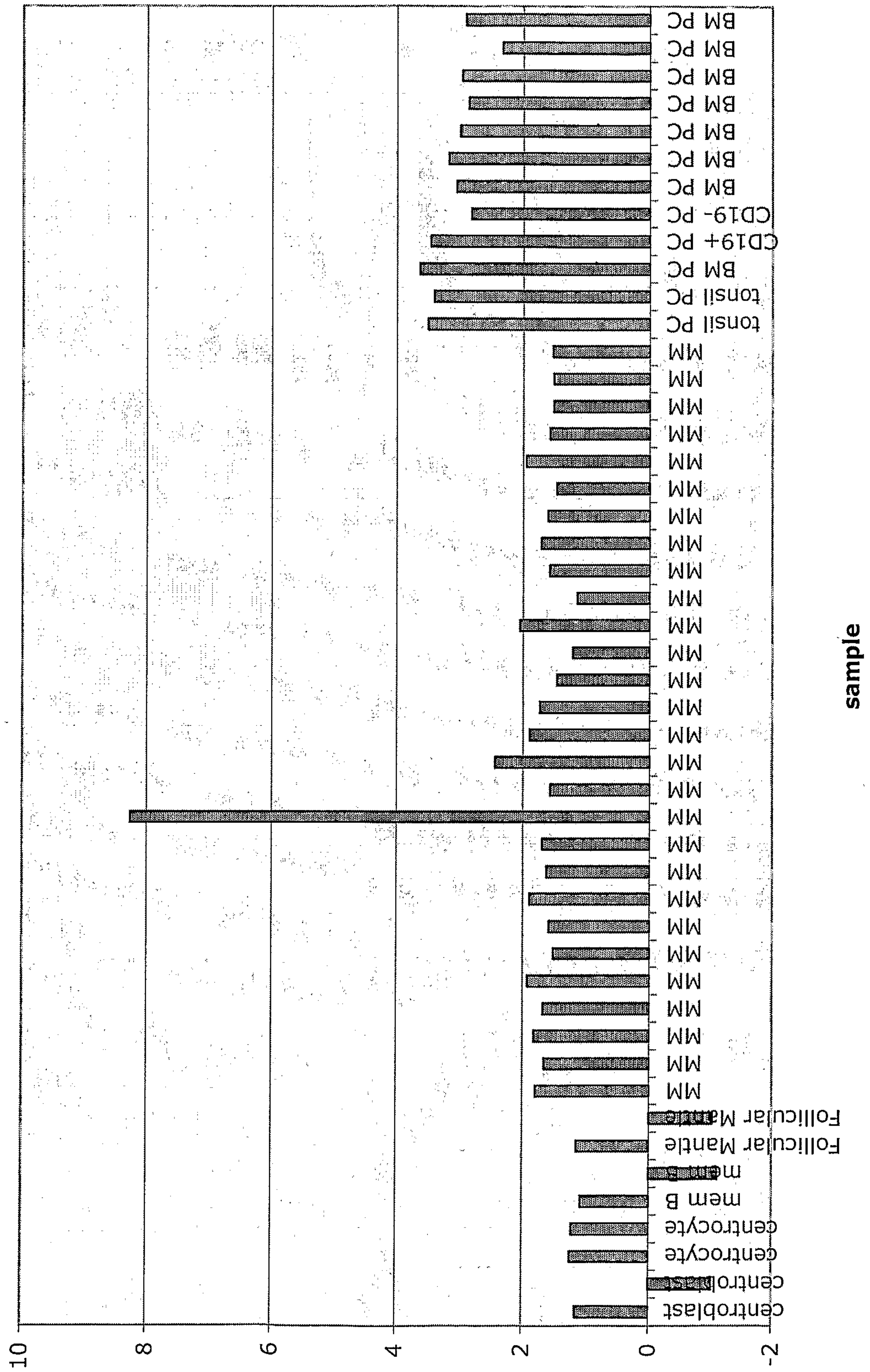
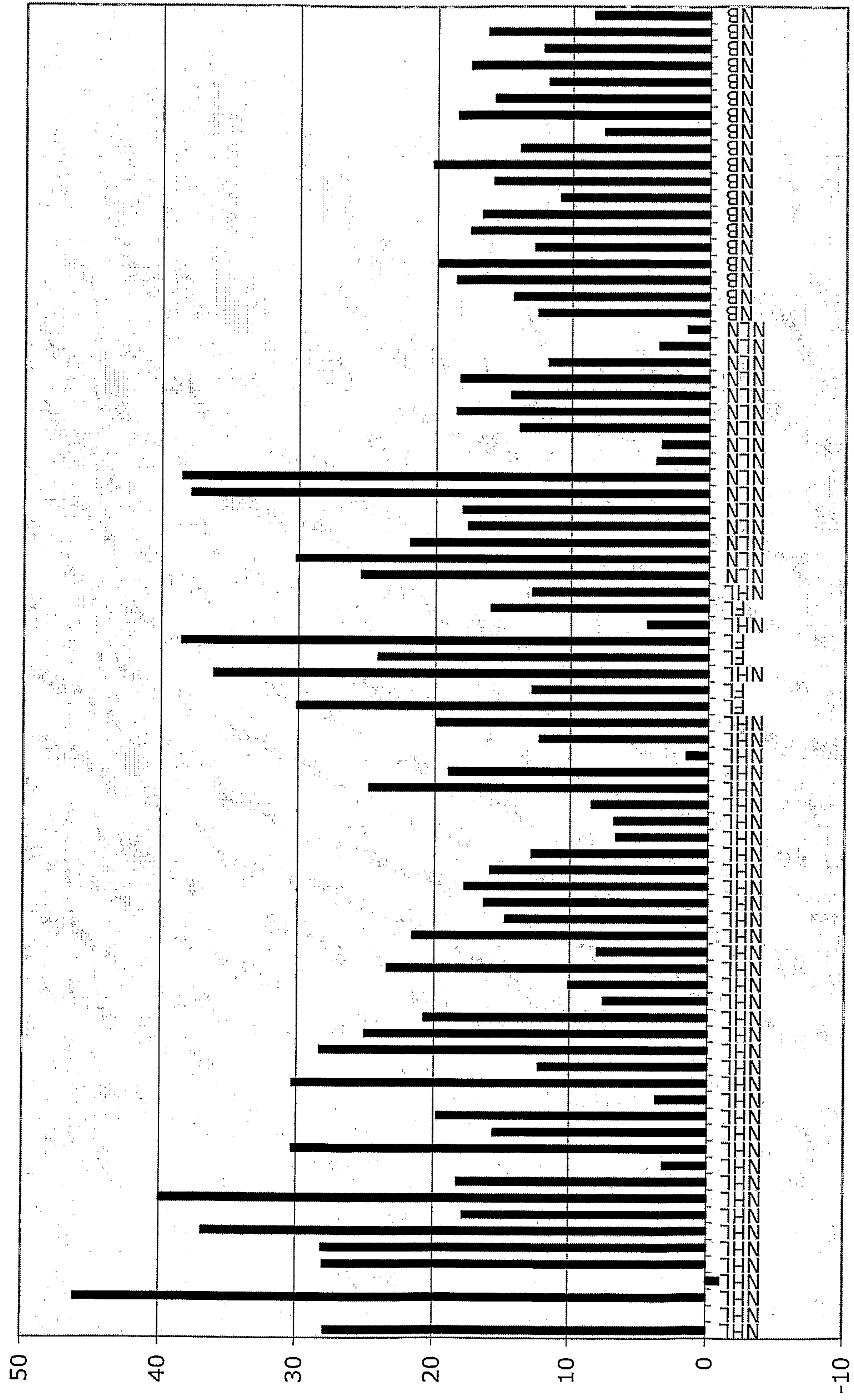


FIGURE 82A

TAHO11/DNA227781/CXCR5 (BLR1)

BLR1



sample

FIGURE 82B

TAHO11/DNA227781/CXCR5 (BLR1)

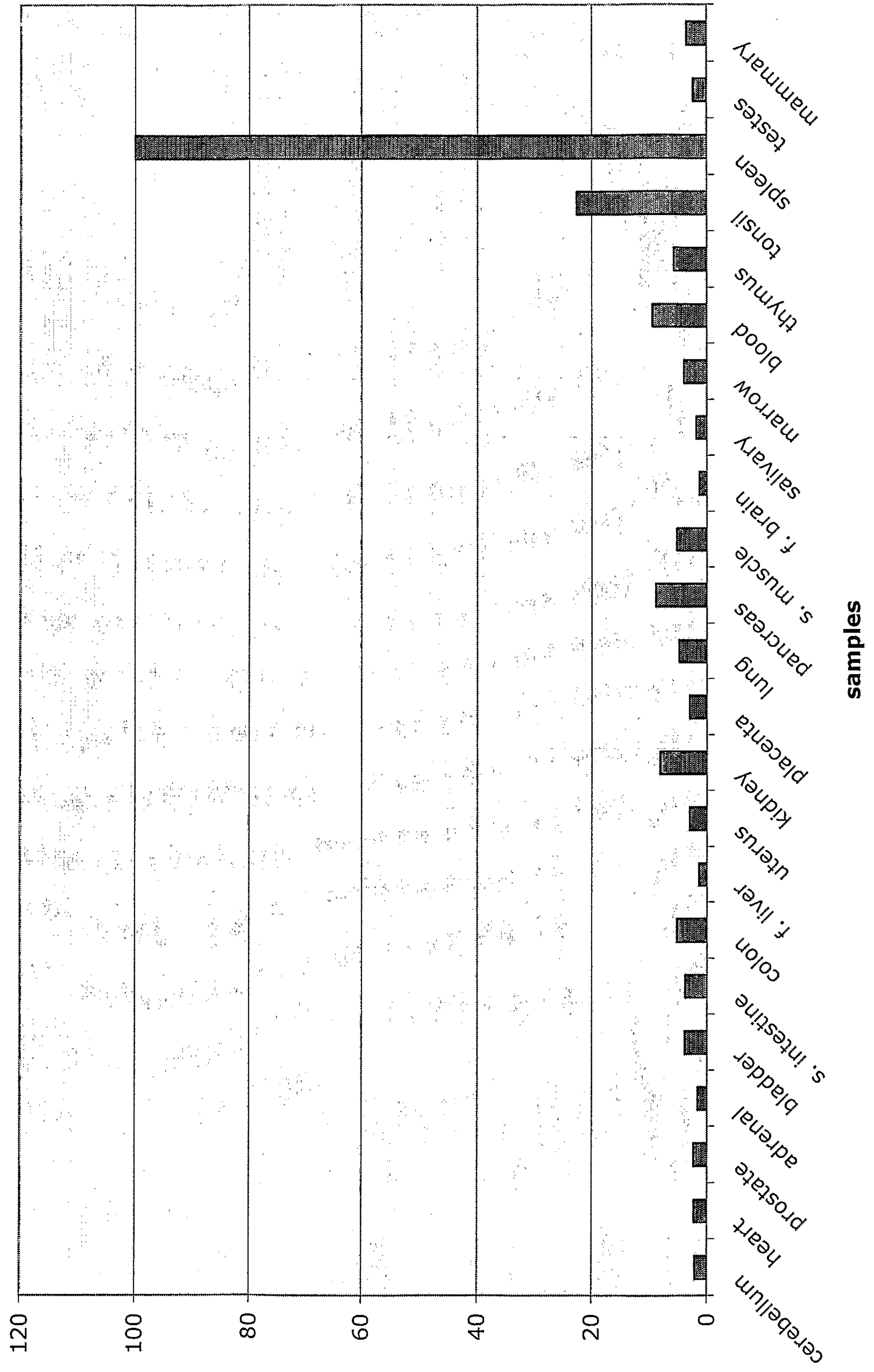
BLR1

FIGURE 82C

TAHO11/DNA227781/CXCR5 (BLR1)

BLR1

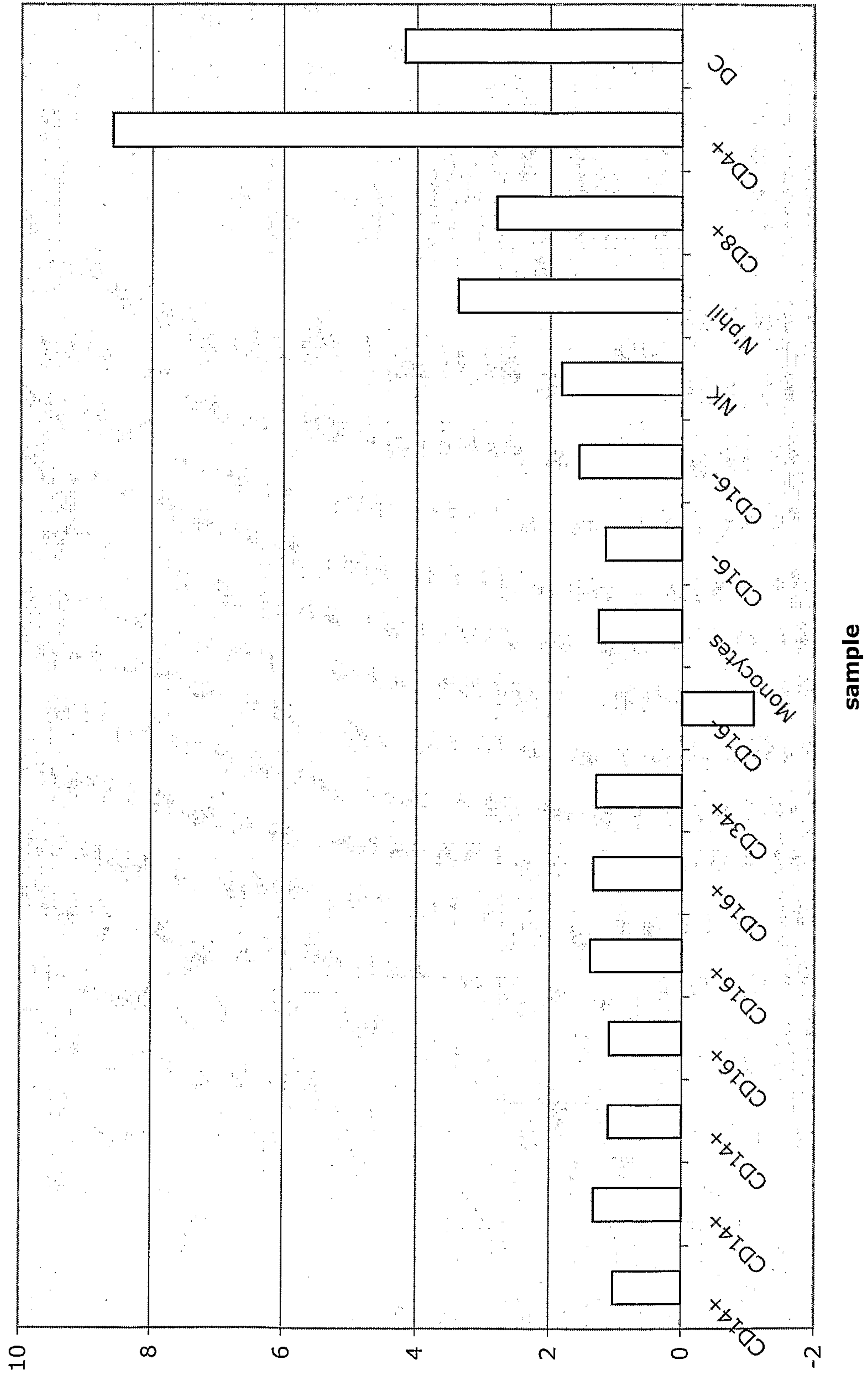


FIGURE 82D

BLR1

TAHO11/DNA227781/CXCR5 (BLR1)

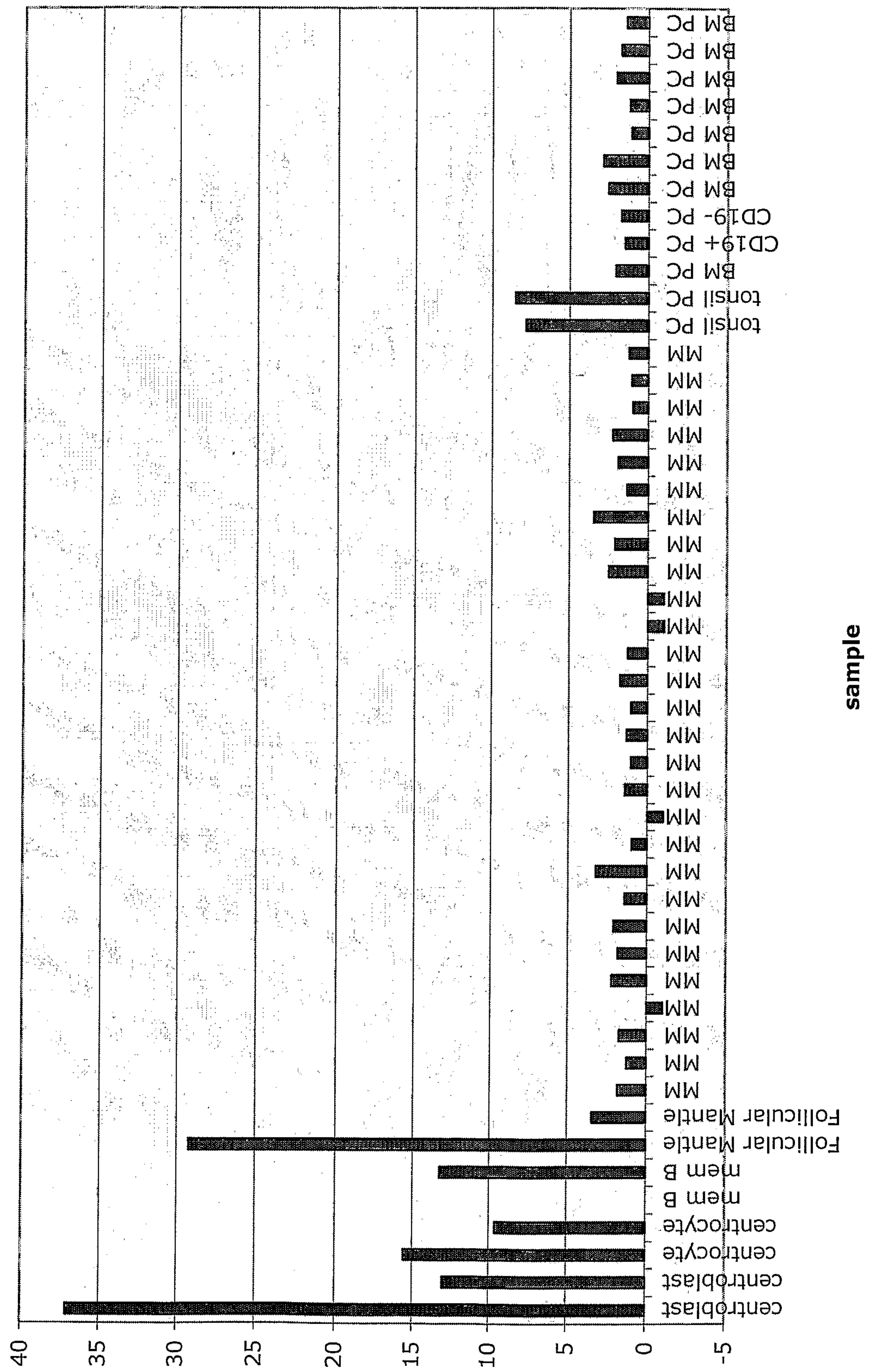


FIGURE 83A

TAHO12/DNA227879/FCER2

FCER2

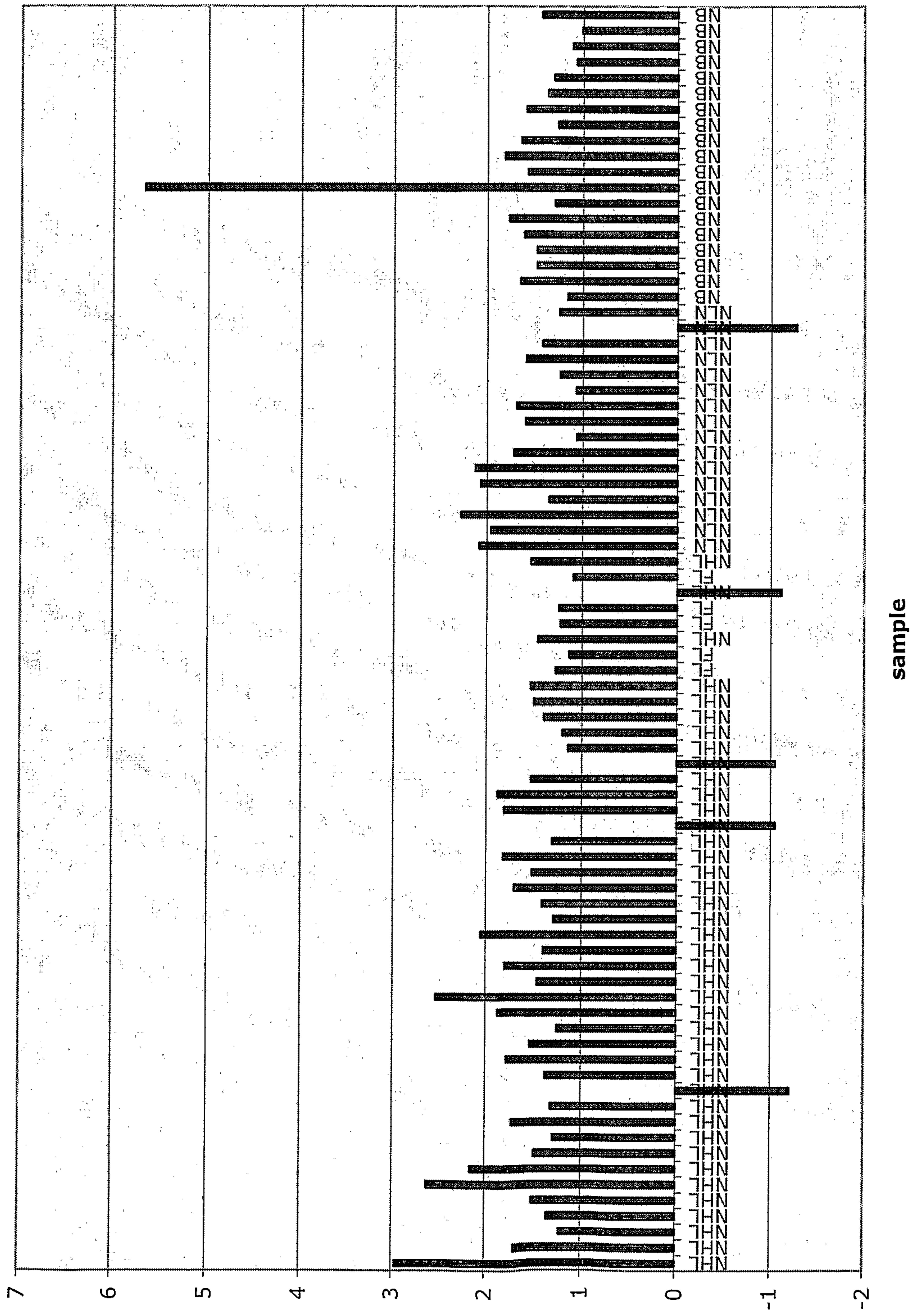


FIGURE 83B**FCER2**

TAHO12/DNA227879/FCER2

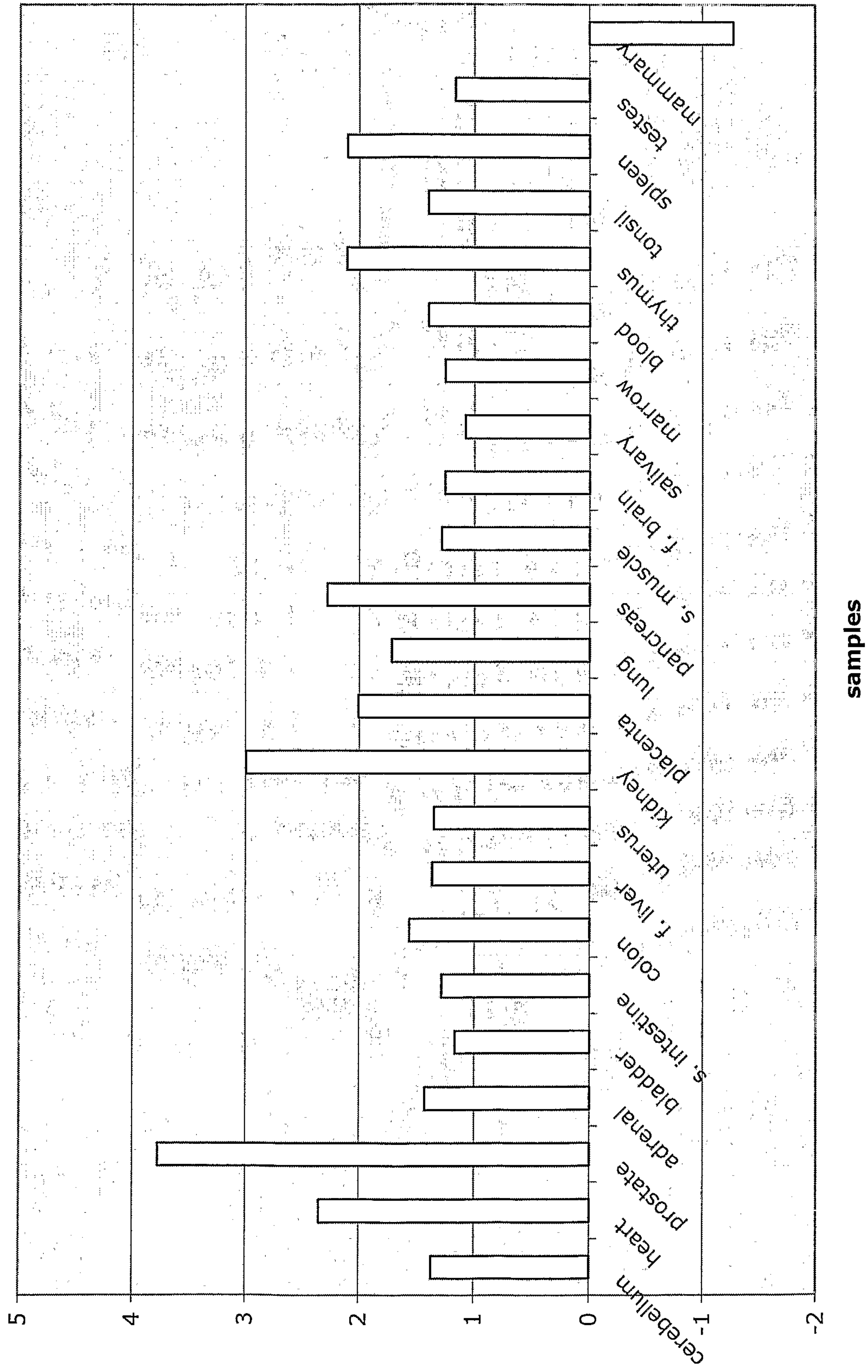


FIGURE 83C

FCER2

TAHO12/DNA227879/FCER2

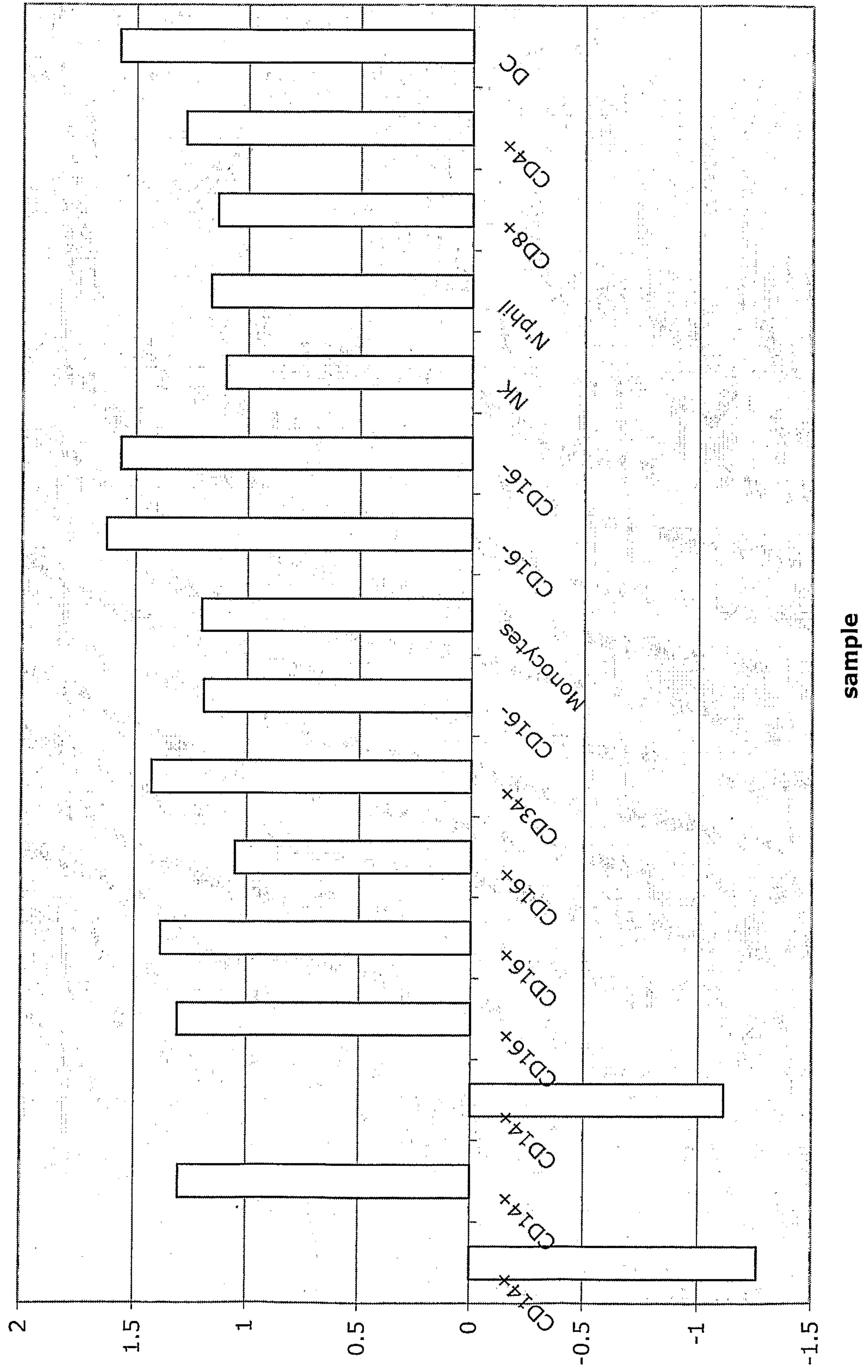


FIGURE 83D

FCER2

TAHO12/DNA27879/FCER2

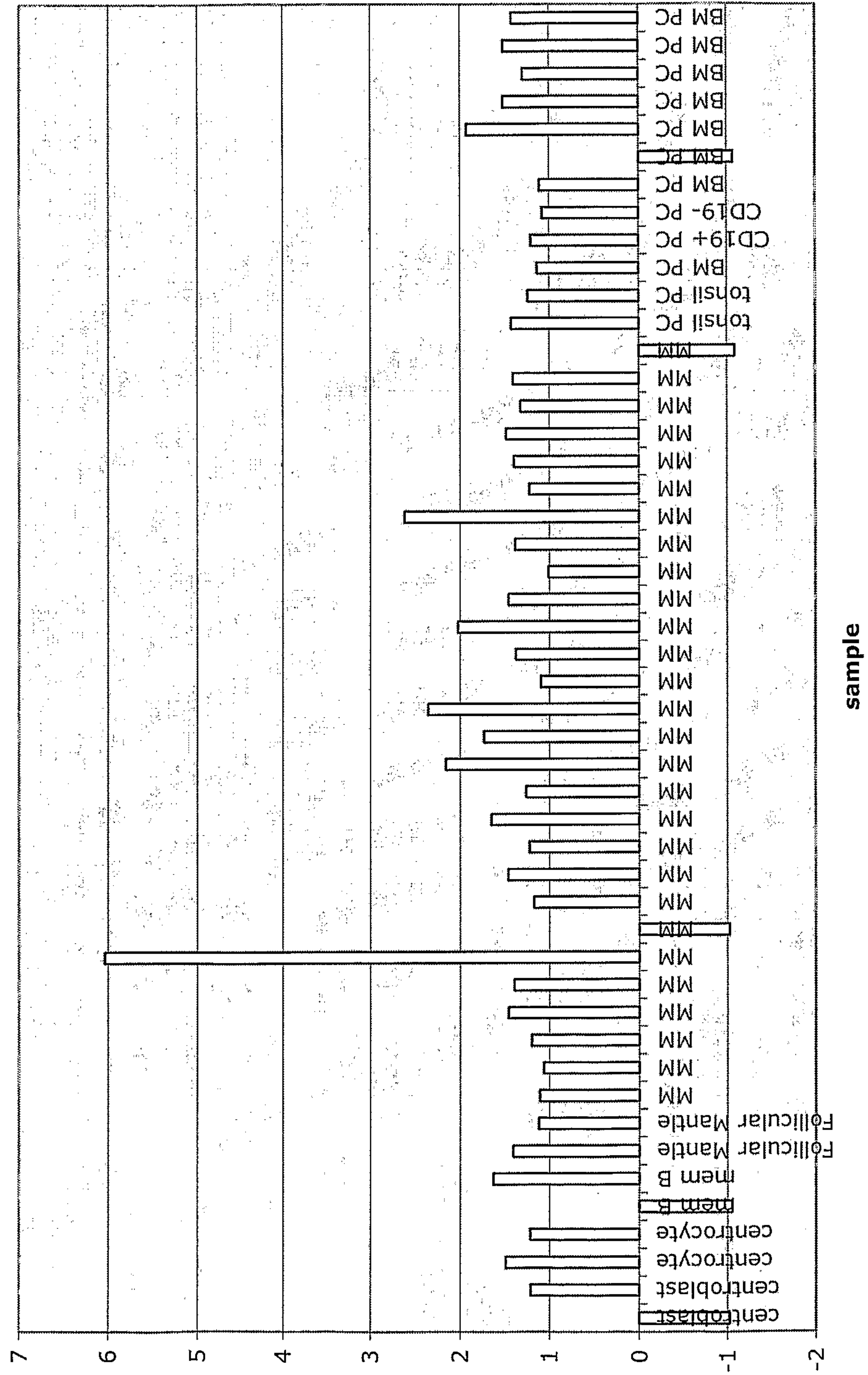


FIGURE 84A

TAHO13/DNA256363/GPR2

GPR2 UNQ12100

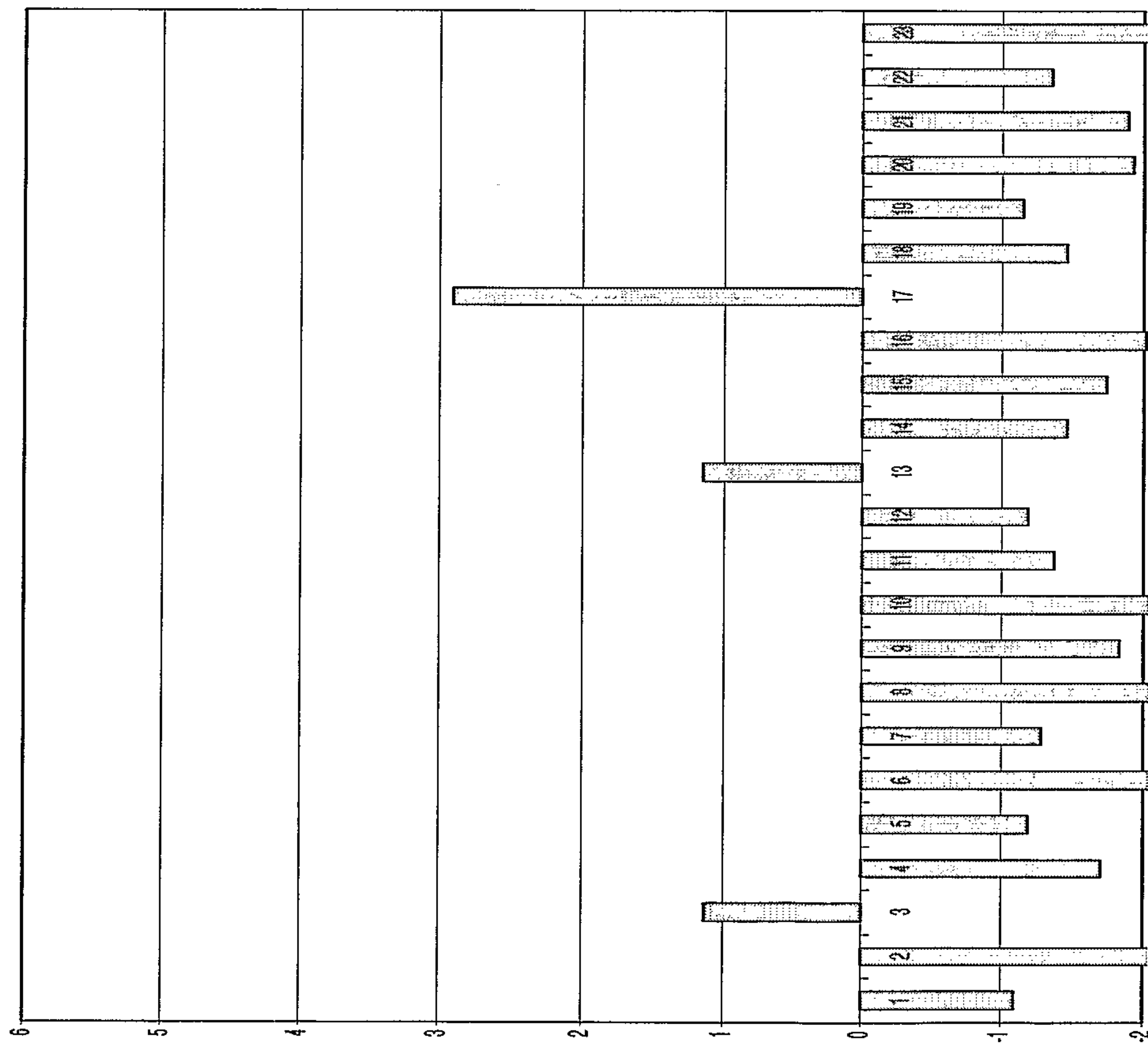
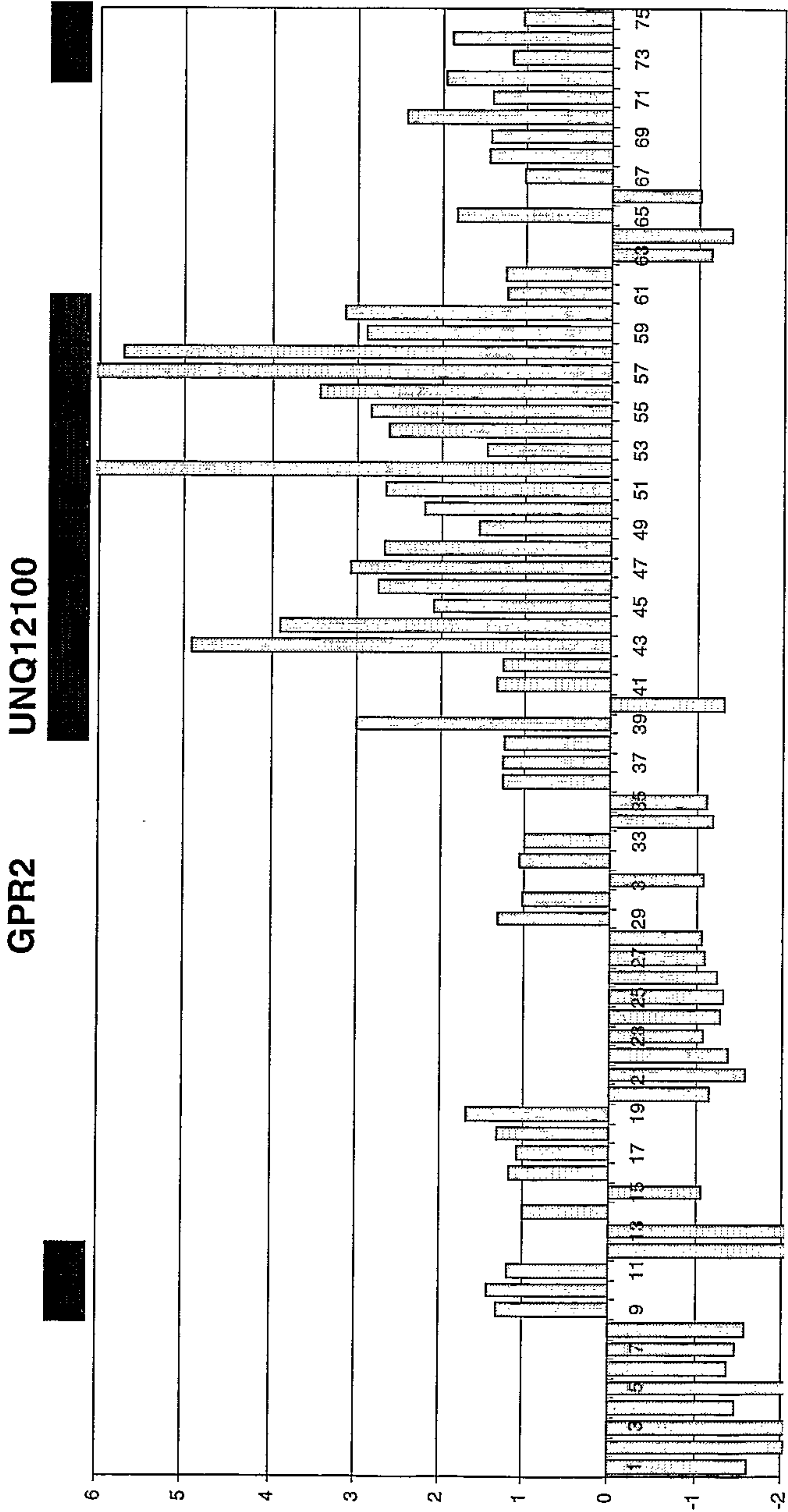


FIGURE 84B

TAHO13/DNA256363/GPR2



= multiple myeloma samples

TAHO15/DNA58721/NAG14 (LRRC4)

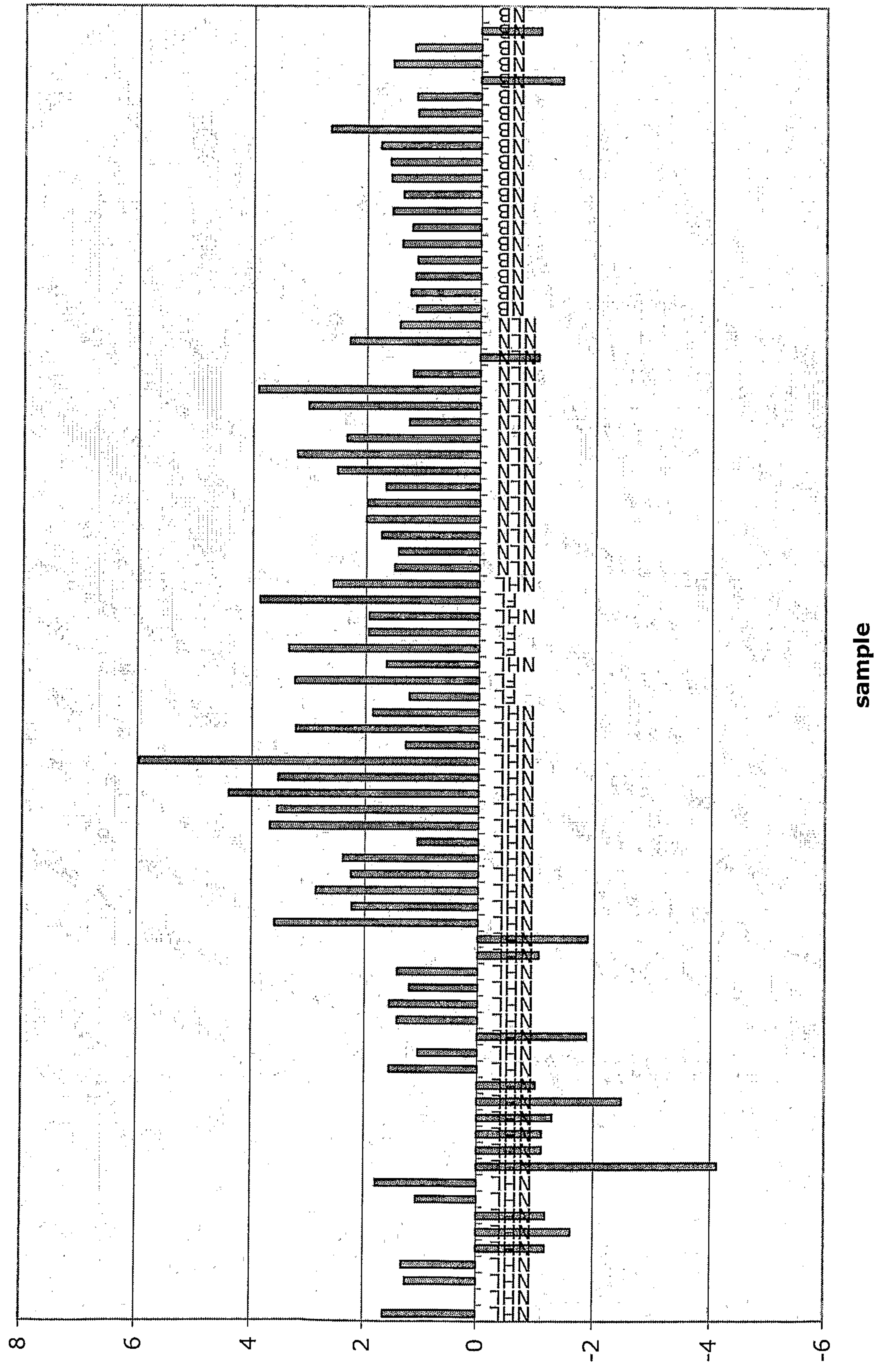
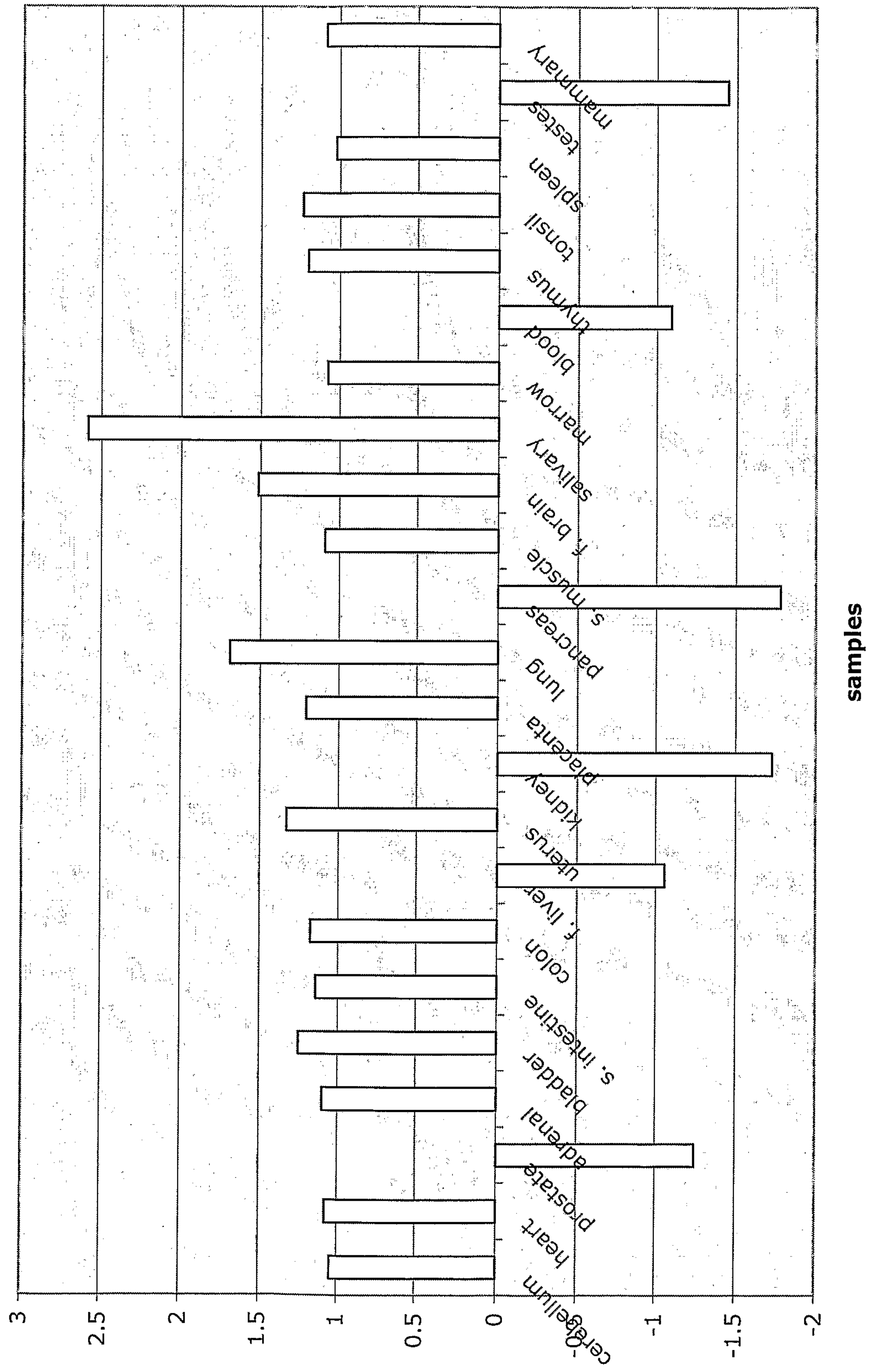


FIGURE 85B

TAHO15/DNA58721/NAG14 (LRRC4)

LRRC4

LPRC4

TAHO15/DNA58721/NAG14 (LRRC4)

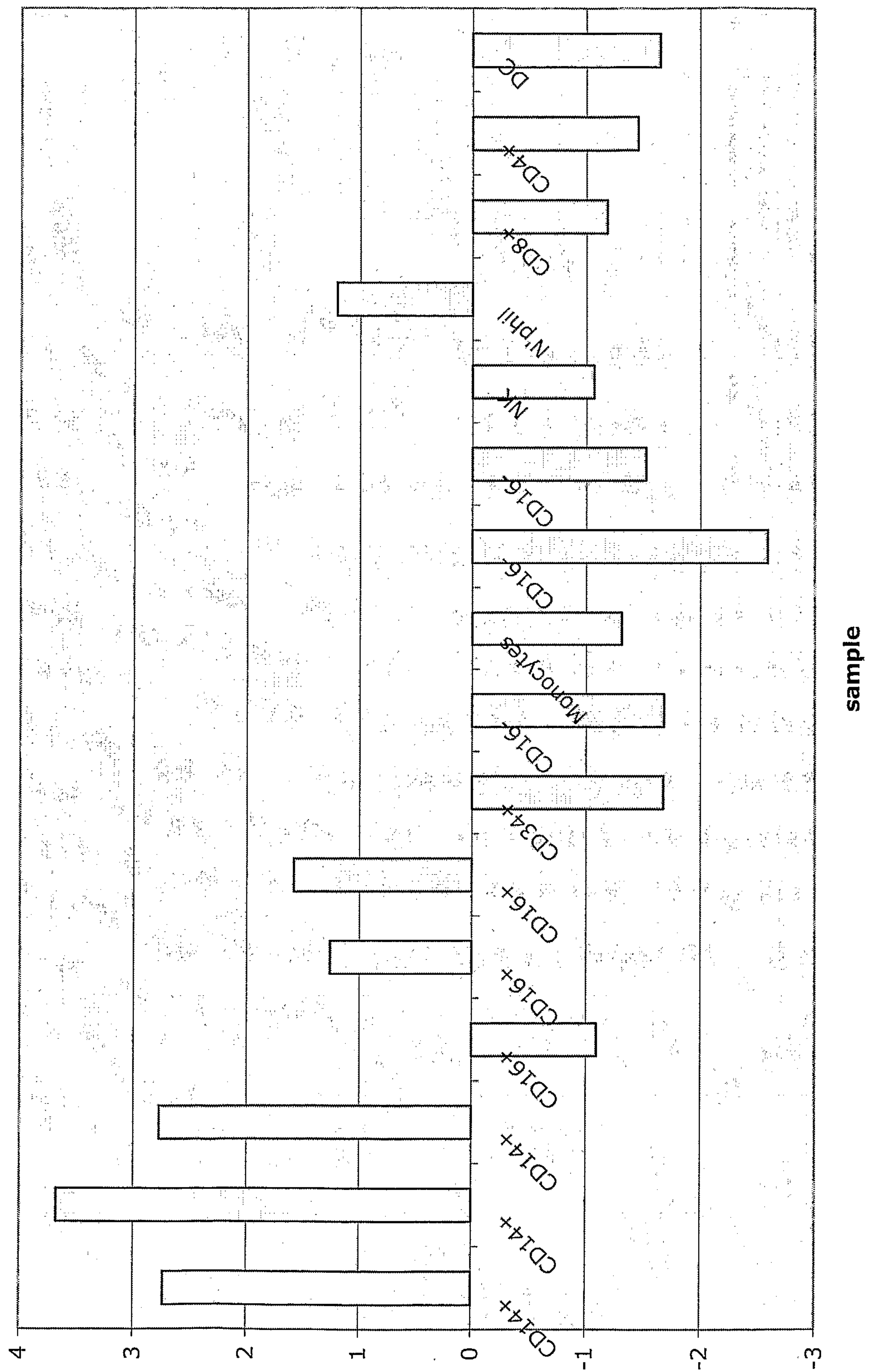
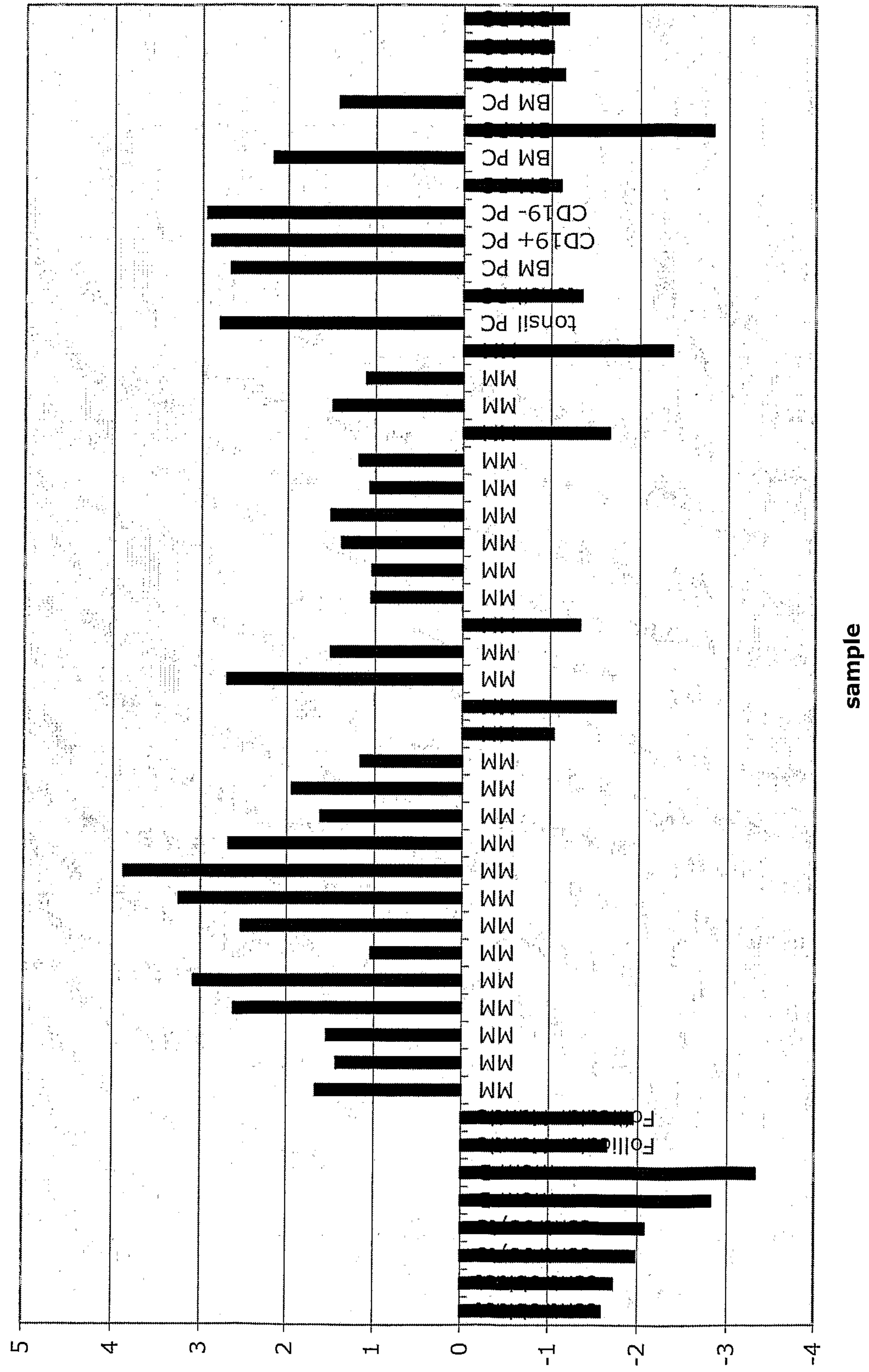


FIGURE 85D

LRRC4

TAHO15/DNA58721/NAG14 (LRRC4)



FCRH1

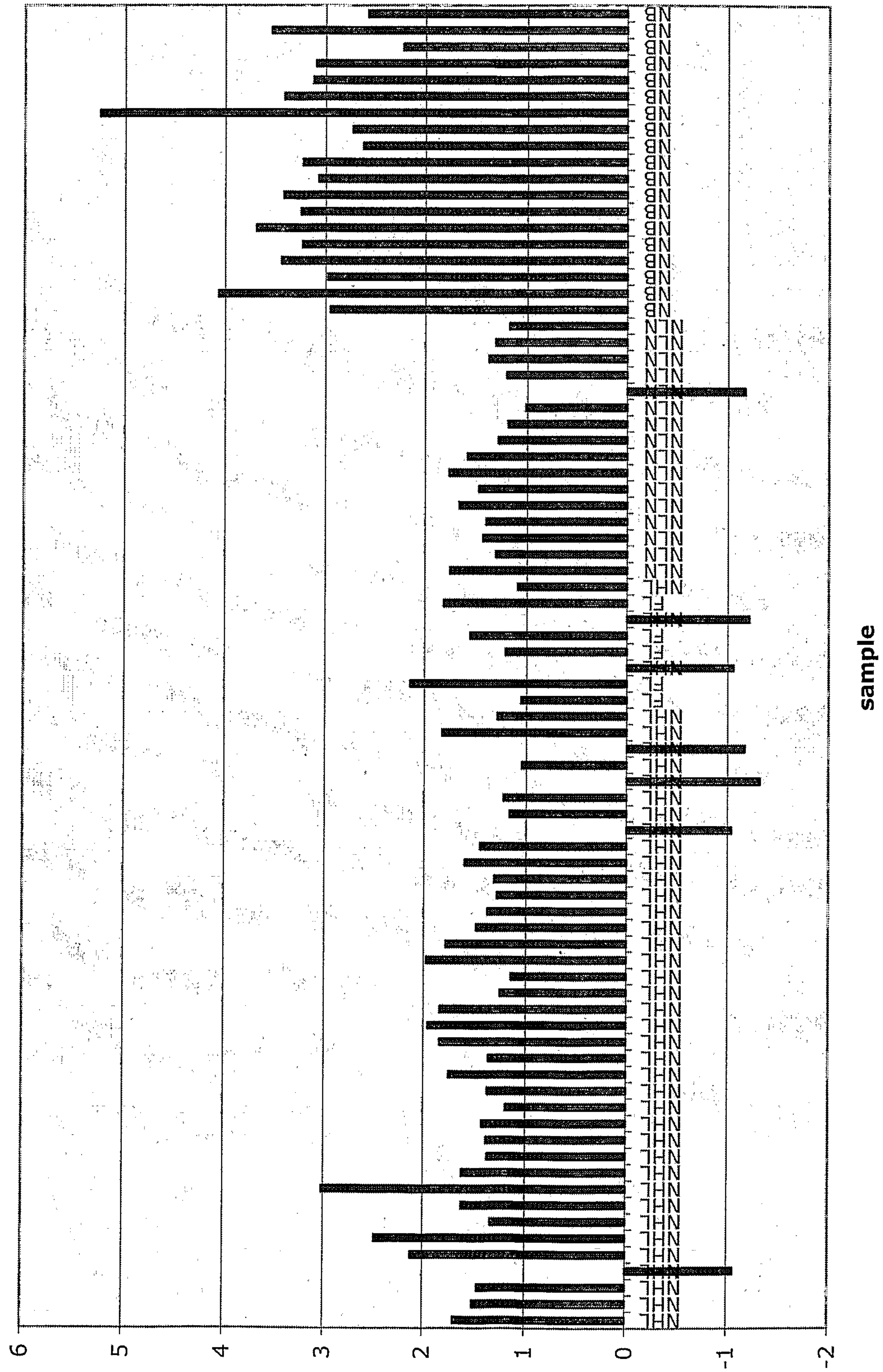
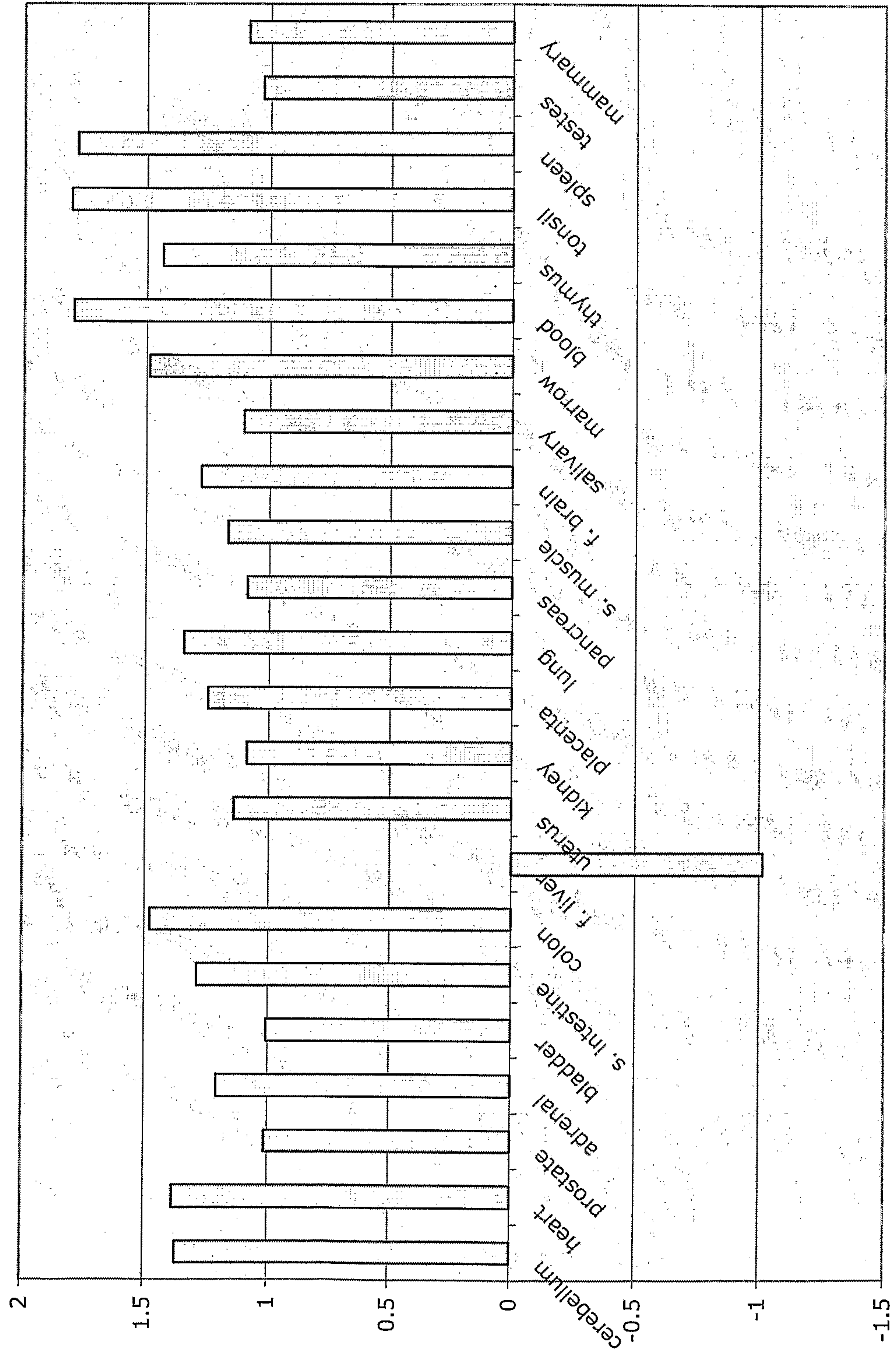


FIGURE 86B

TAHO17/DNA340394/FcRH1

FCRH1

samples

FCRH1

sample

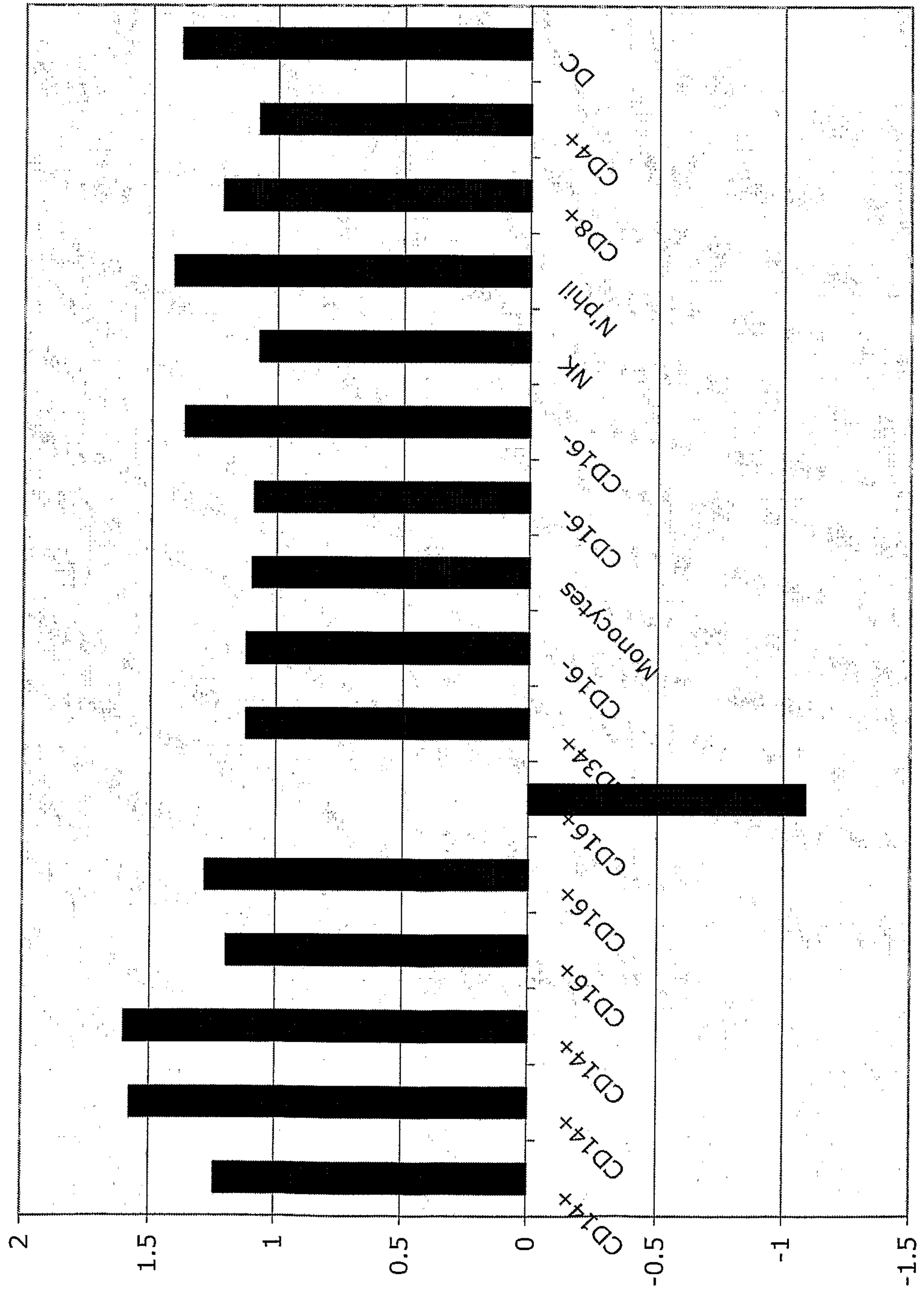
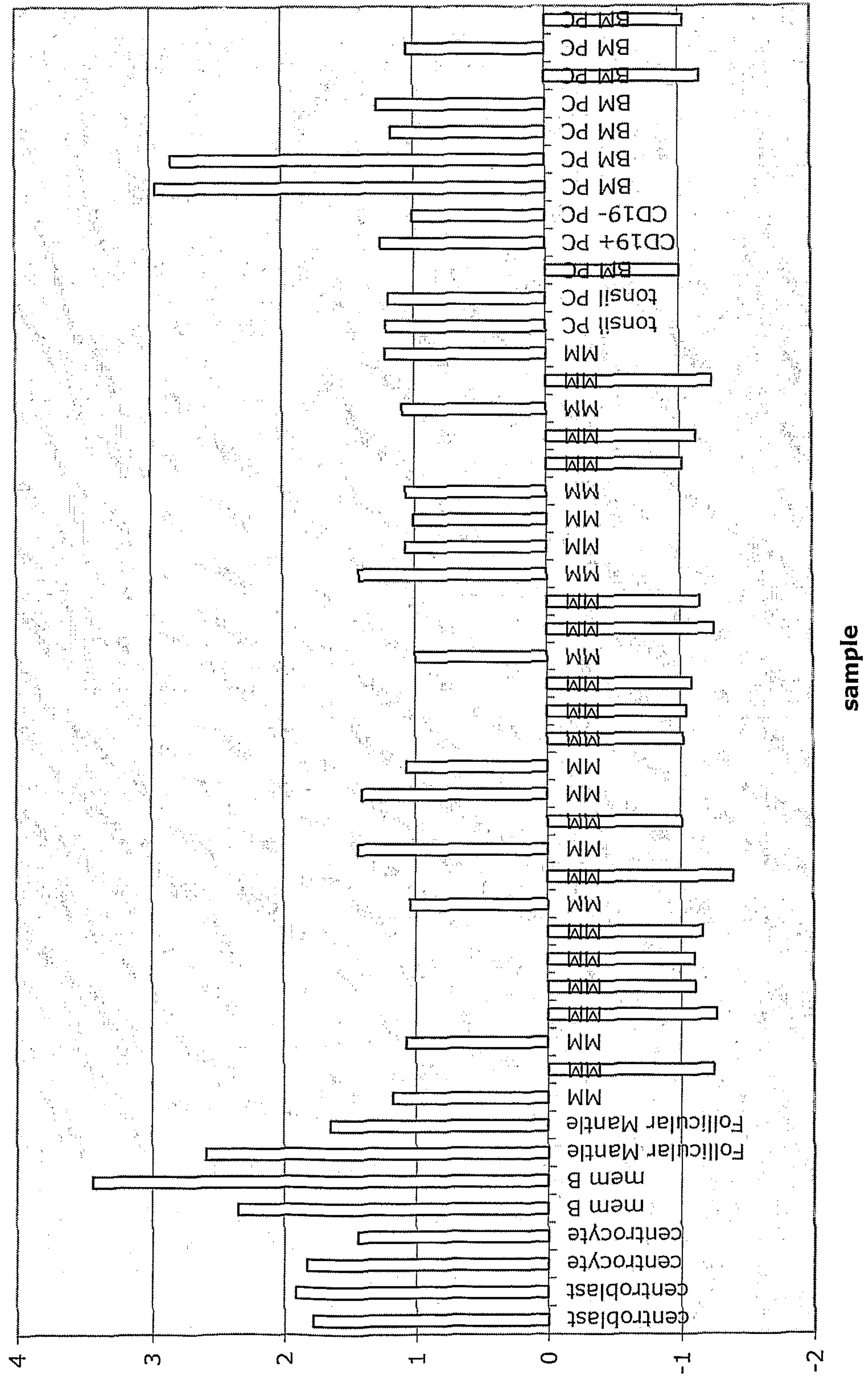


FIGURE 86D

FCRH1

TAHO17/DNA340394/FcRH1



IRTA2

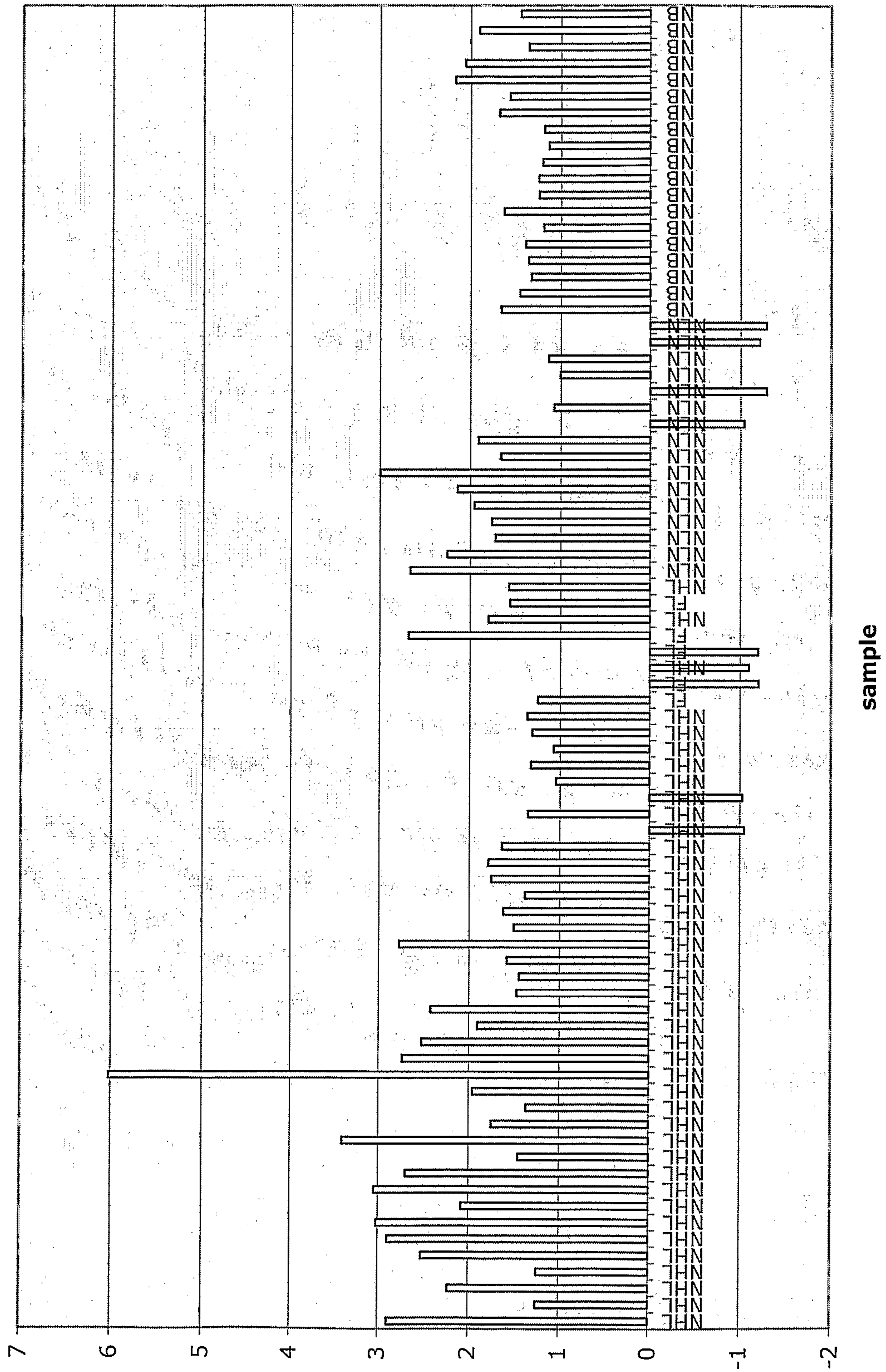


FIGURE 87B**IRTA2**

TAHO18/DNA56041/IRTA2

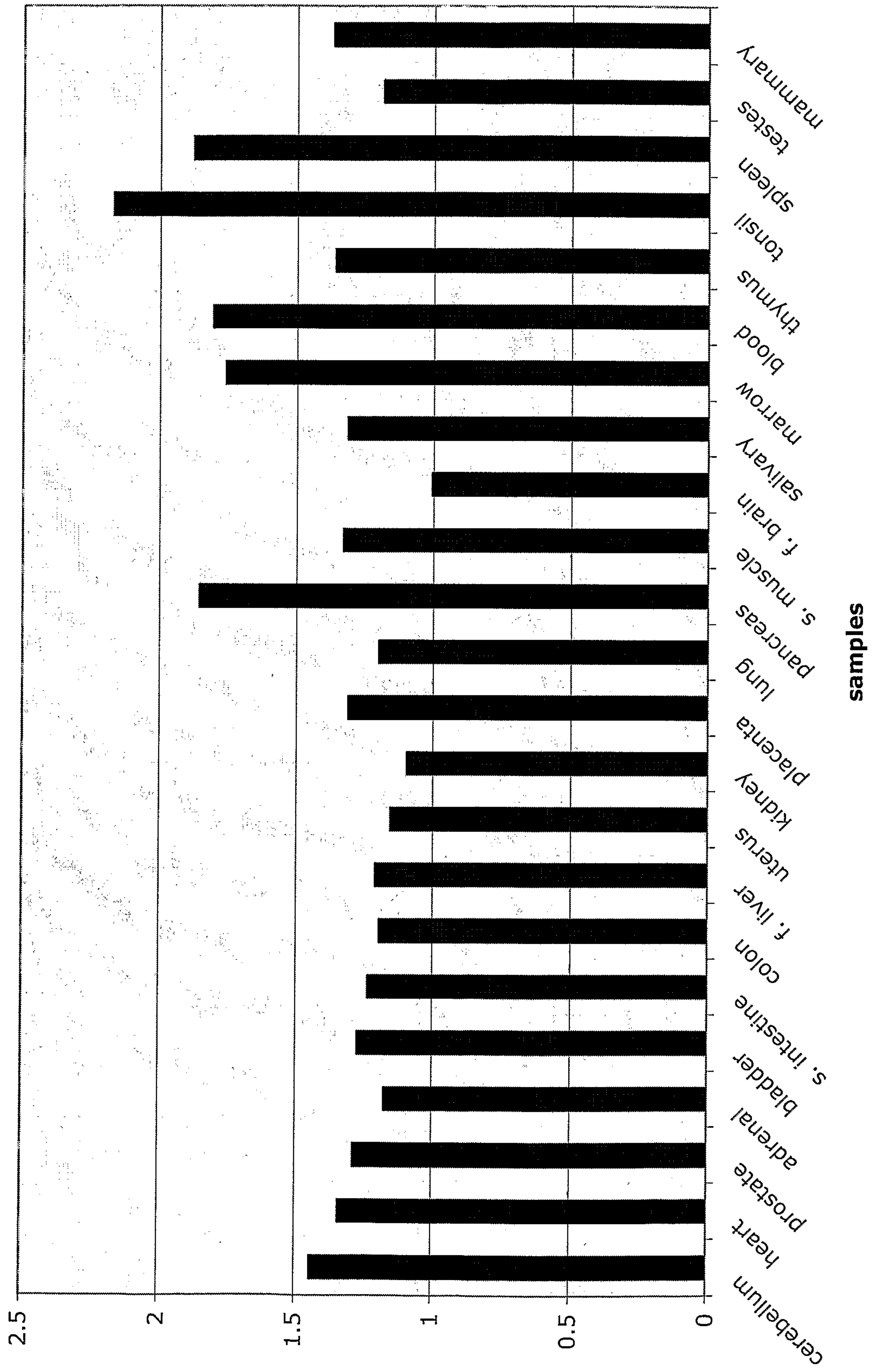


FIGURE 87C

TAHO18/DNA56041/IRTA2

IRTA2

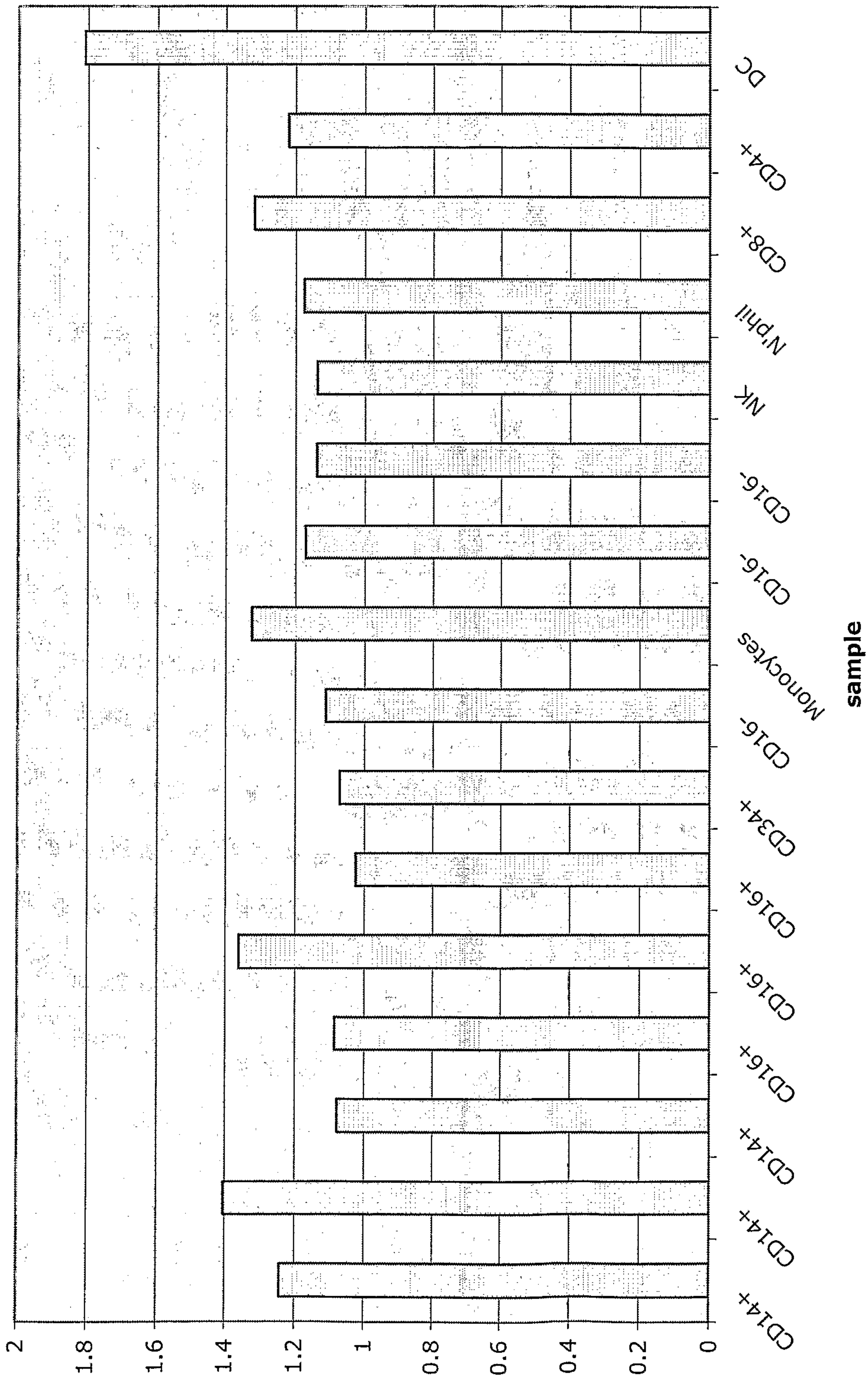
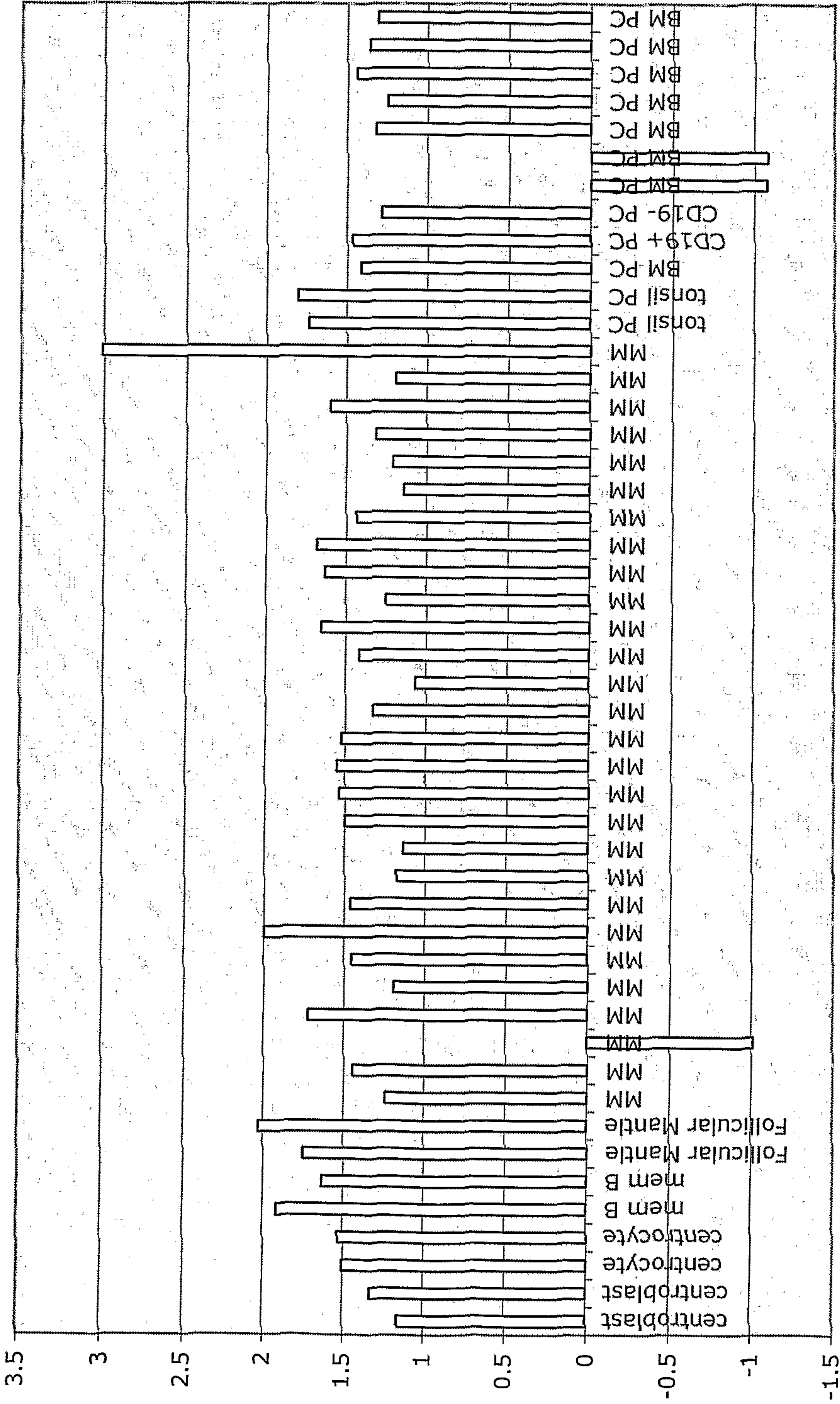


FIGURE 87D

TAHO18/DNA56041/IRTA2

IRTA2



sample

FIGURE 88A

TAHO20/DNA257955/FcRH3

FCRH3

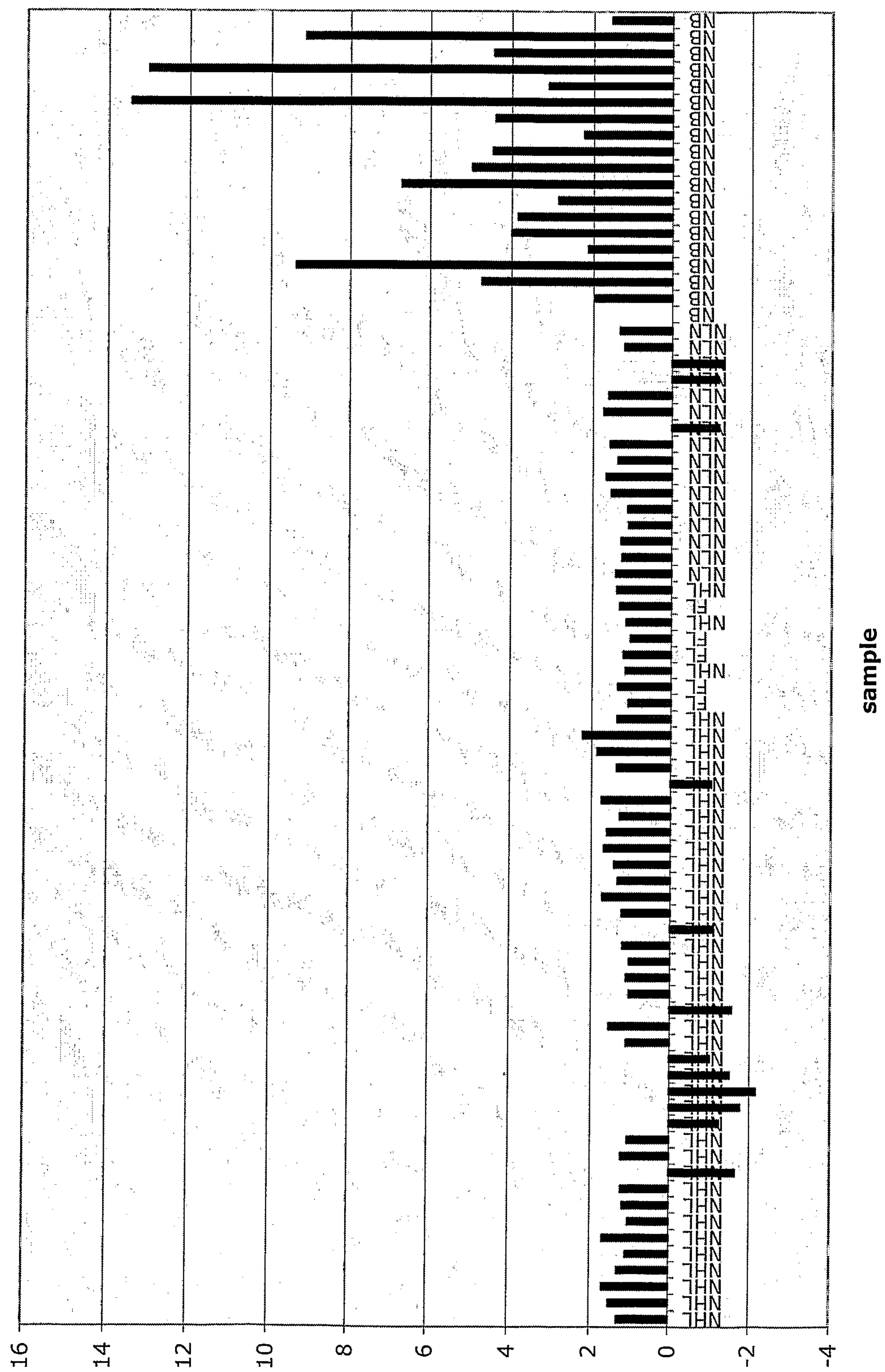


FIGURE 88B

TAHO20/DNA257955/FcRH3

FCRH3

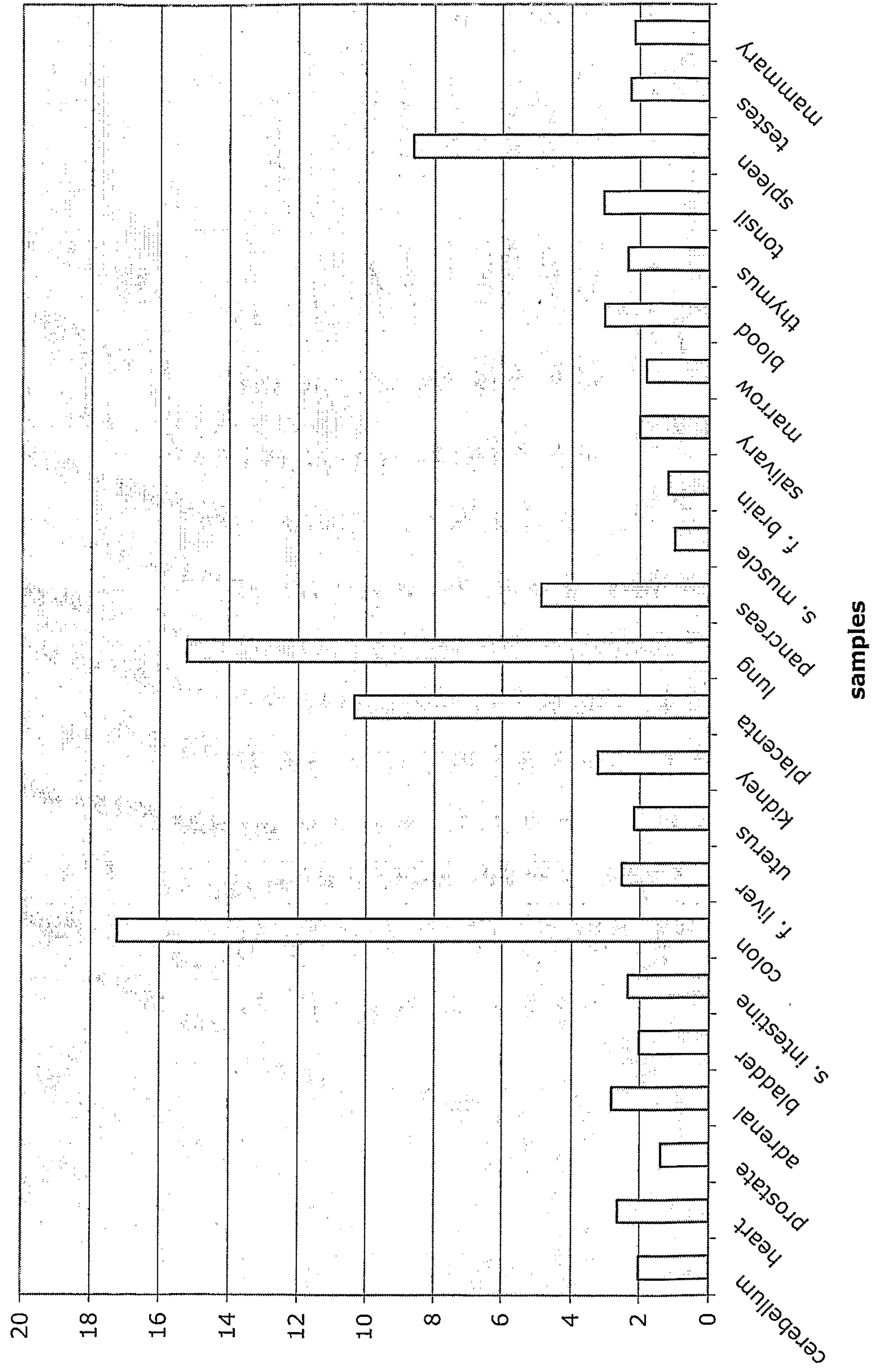


FIGURE 88C

FCRH3

TAHO20/DNA257955/FcRH3

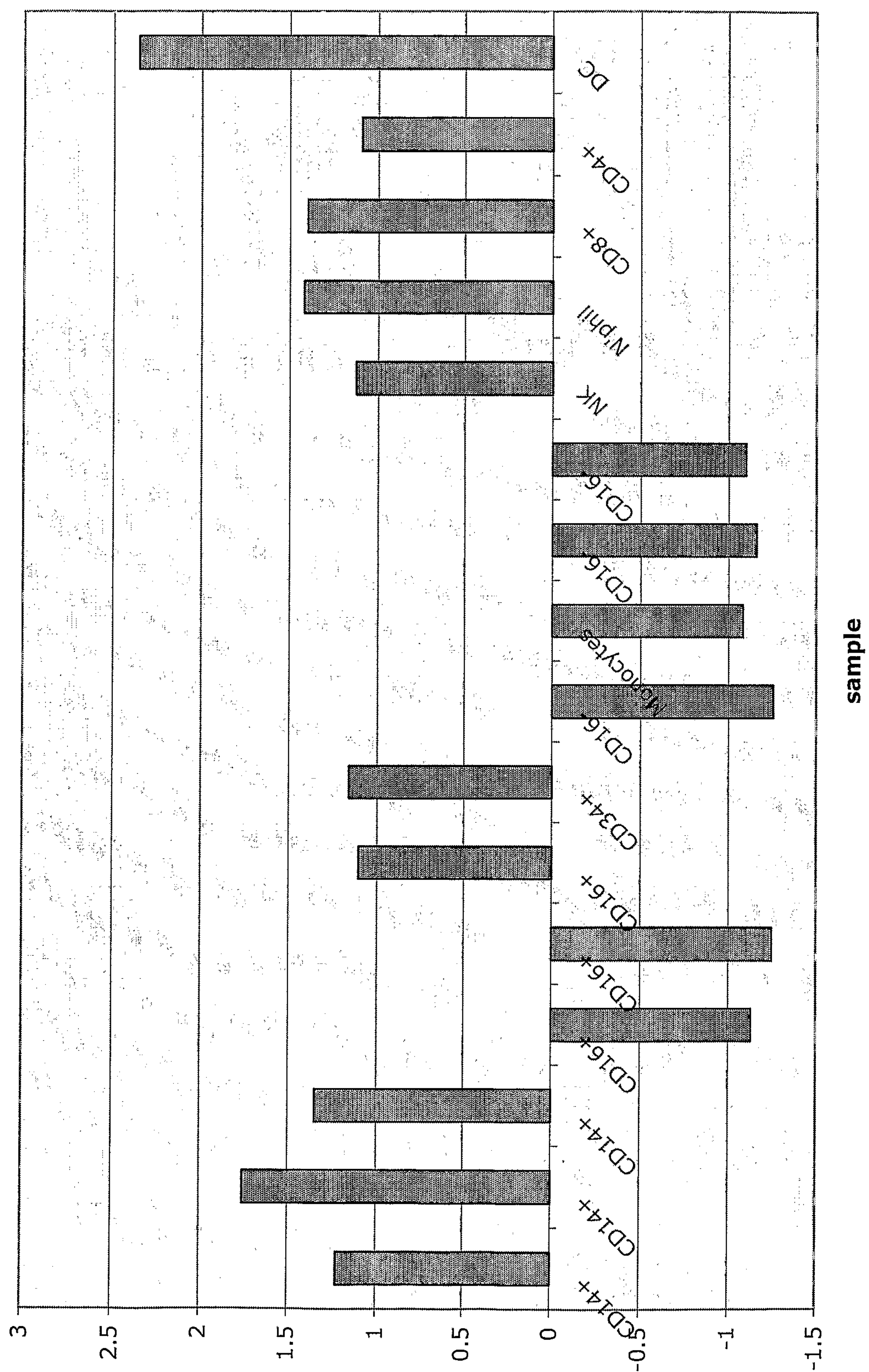
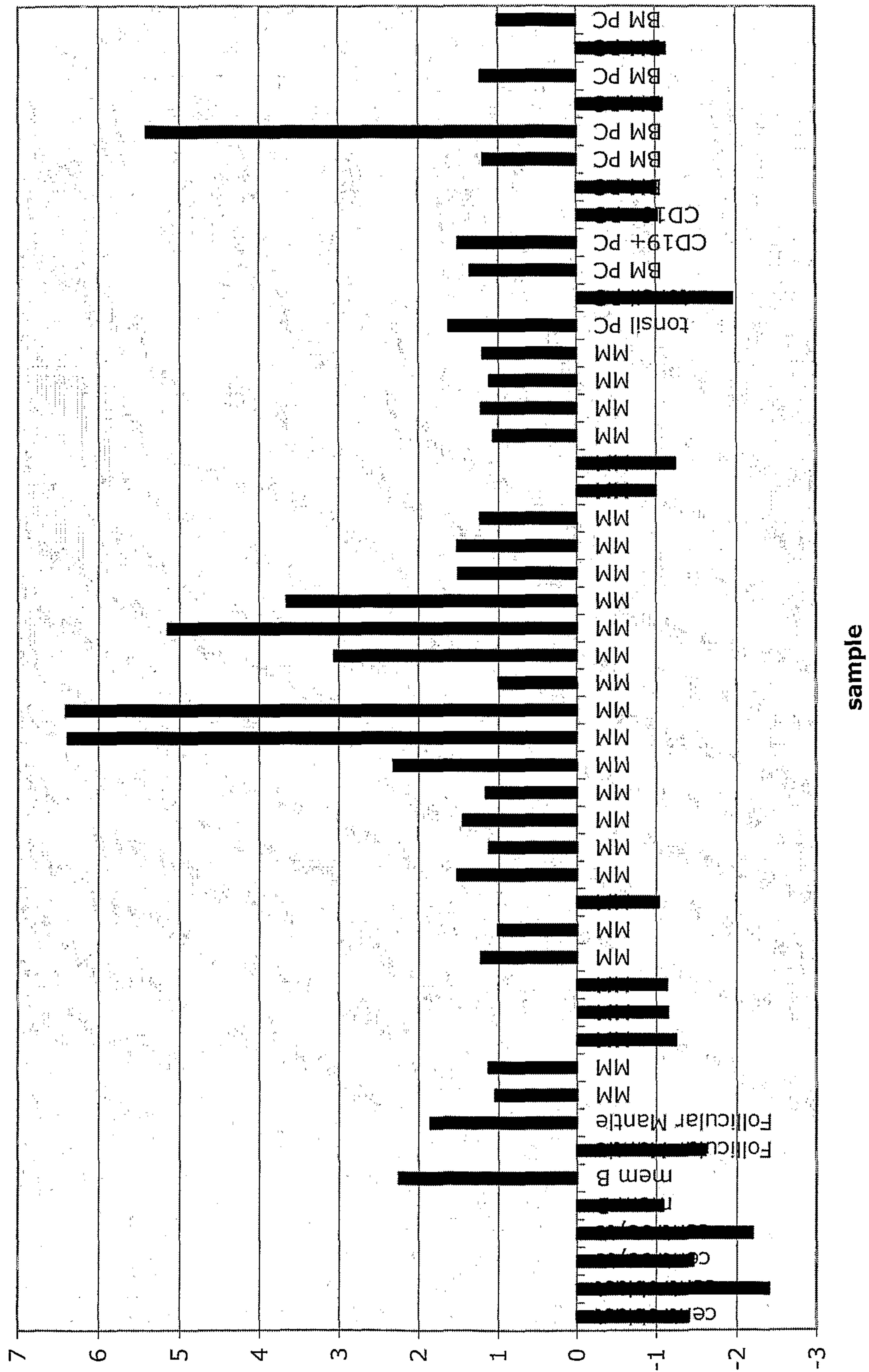


FIGURE 88D

FCRH3

TAHO20/DNA257955/FcRH3



IRTA1

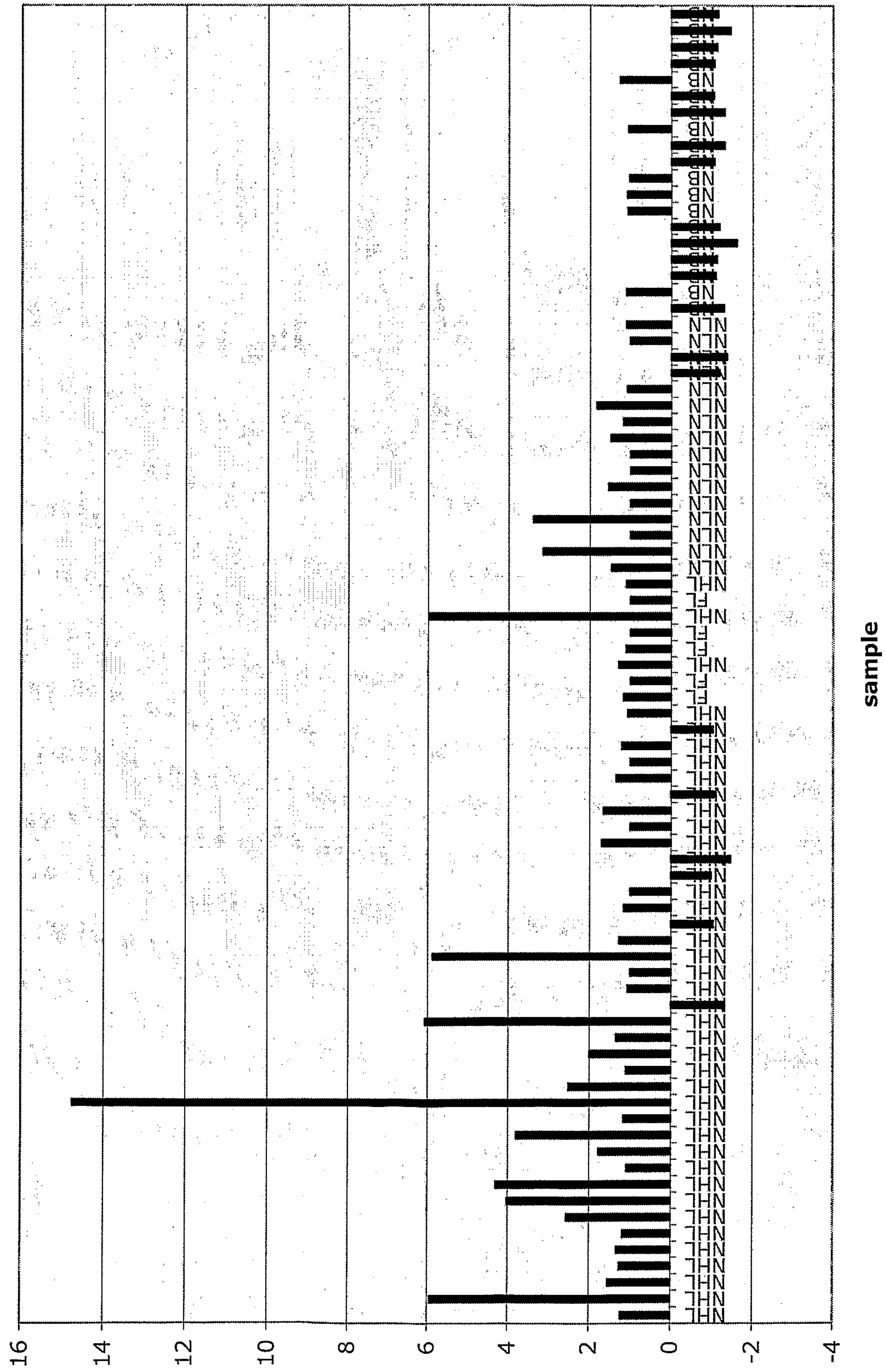
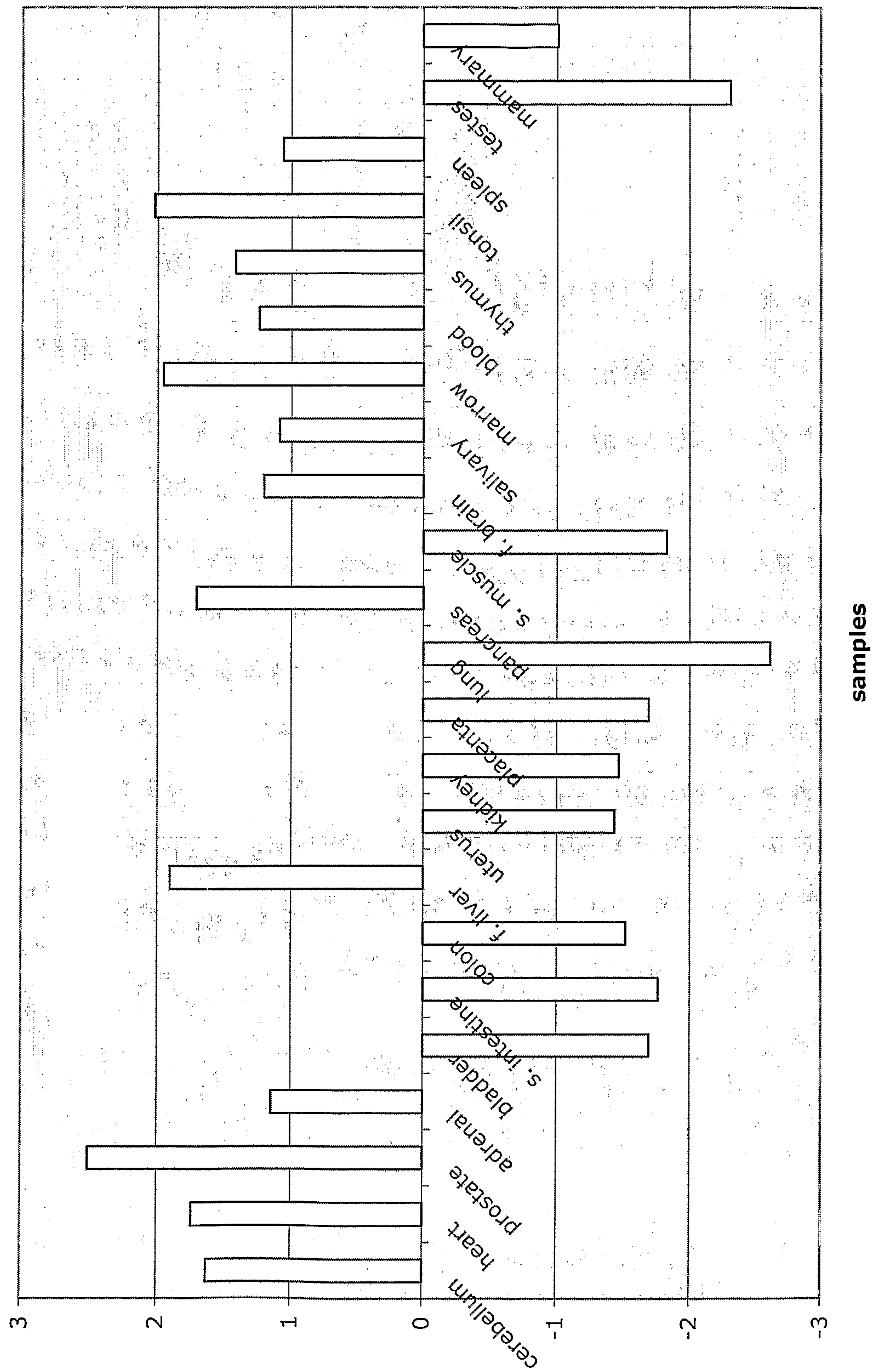
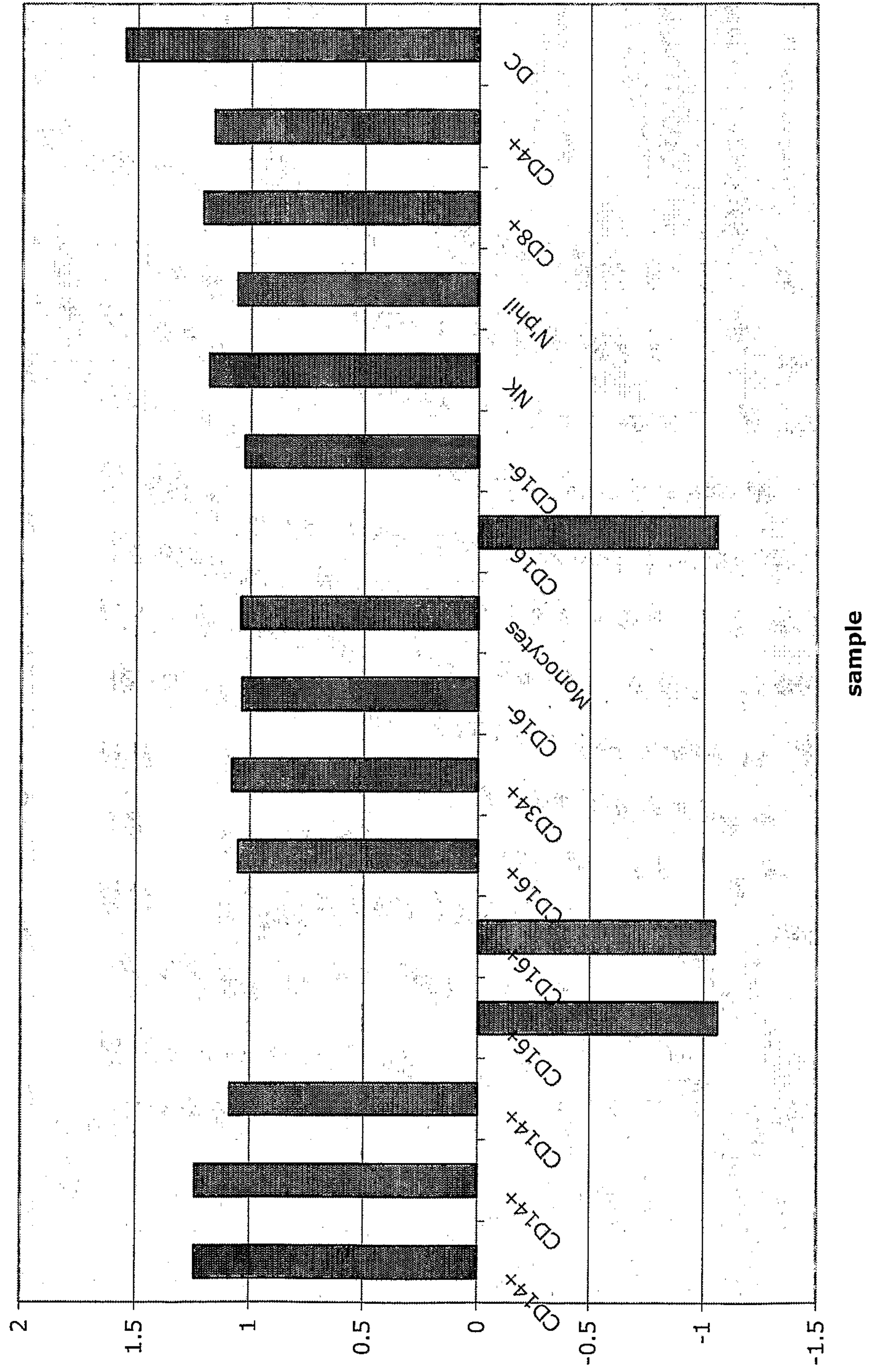


FIGURE 89B**IRTA1**

TAHO21/DNA329863/IRTA1



TAHO21/DNA329863/IRTA1



TAHO21/DNA329863/IRTA1

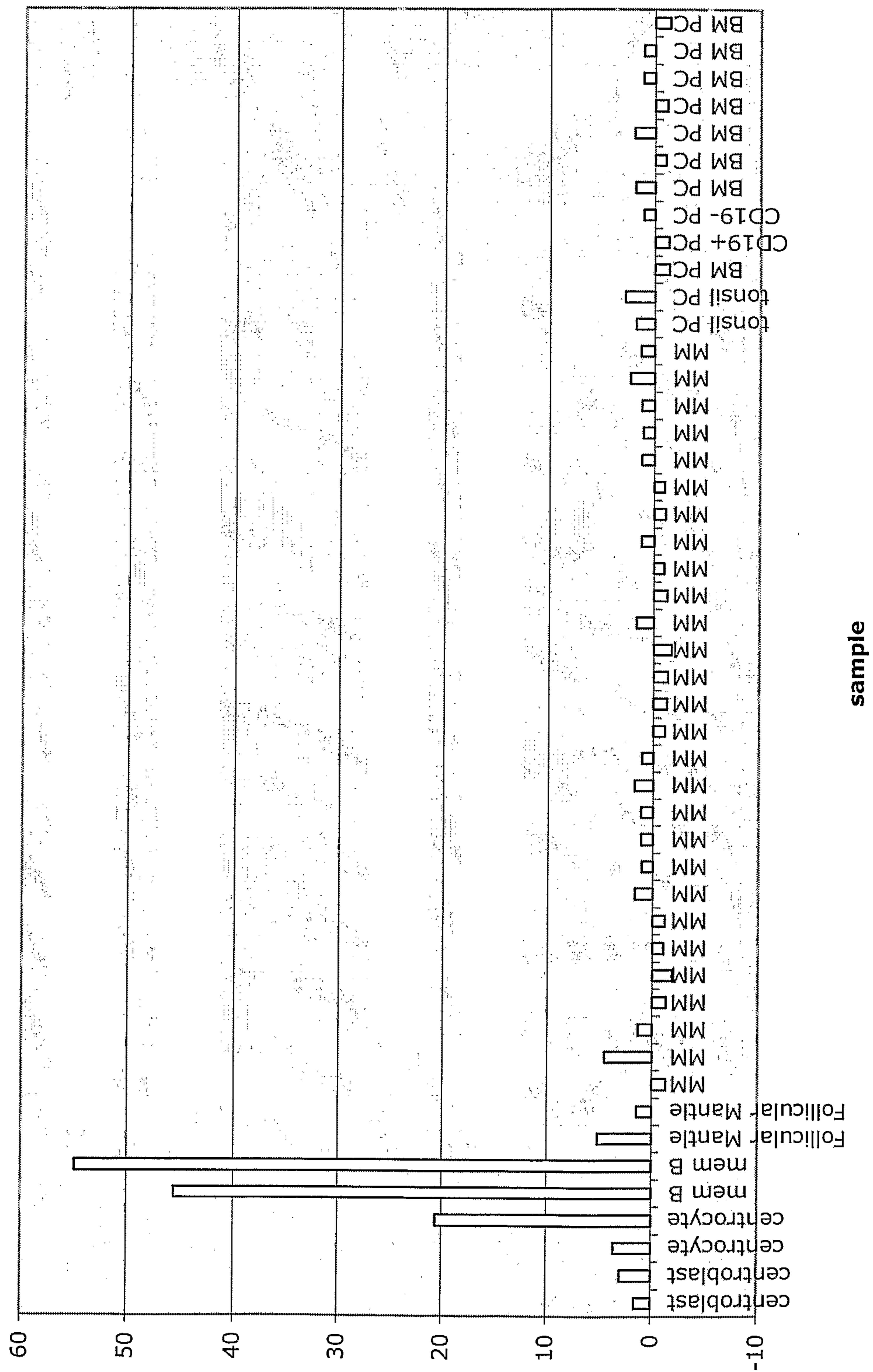


FIGURE 90A

CD19

TAHO25/DNA25820/CD19

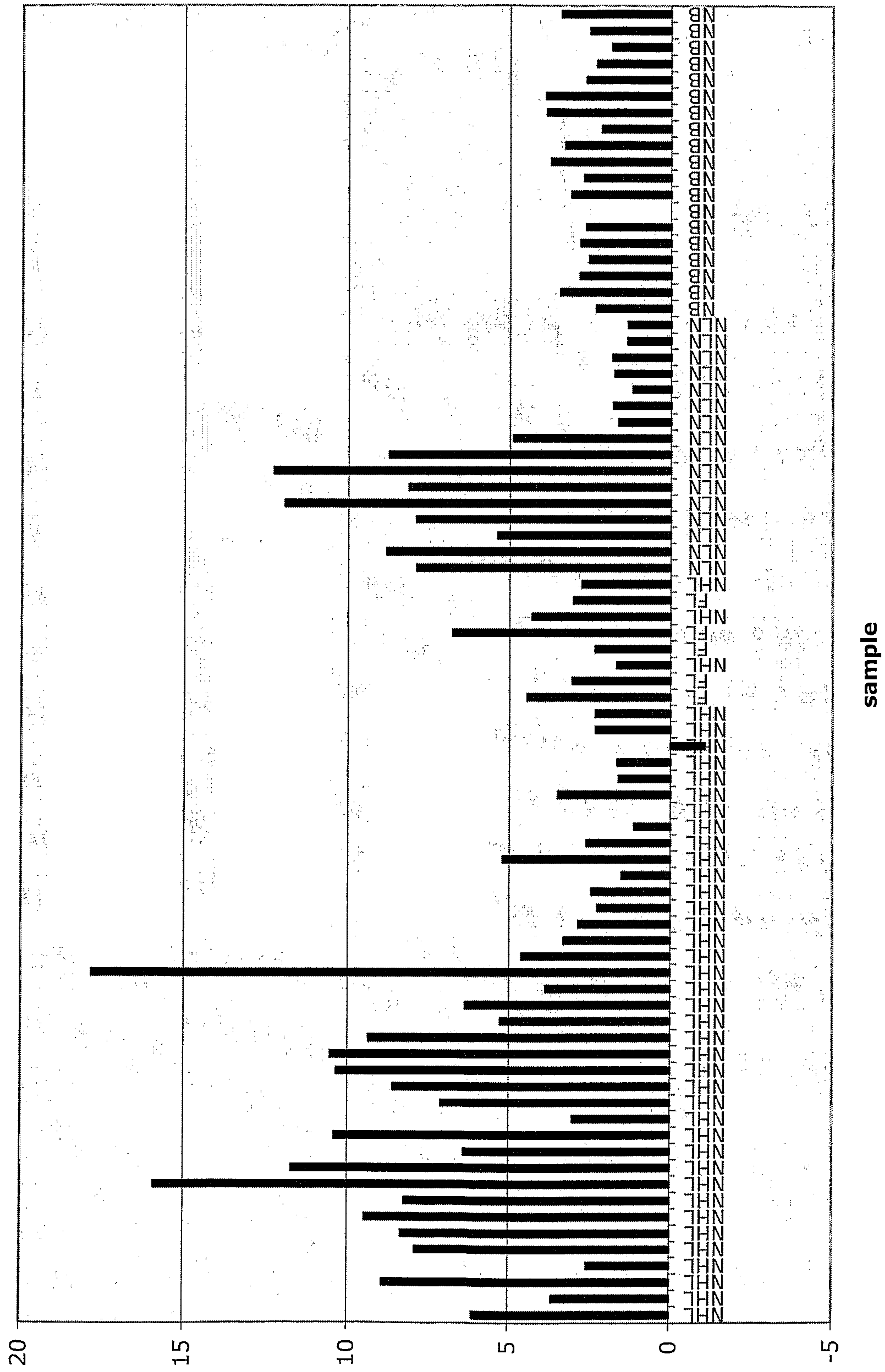


FIGURE 90B**CD19**

TAHO25/DNA225820/CD19

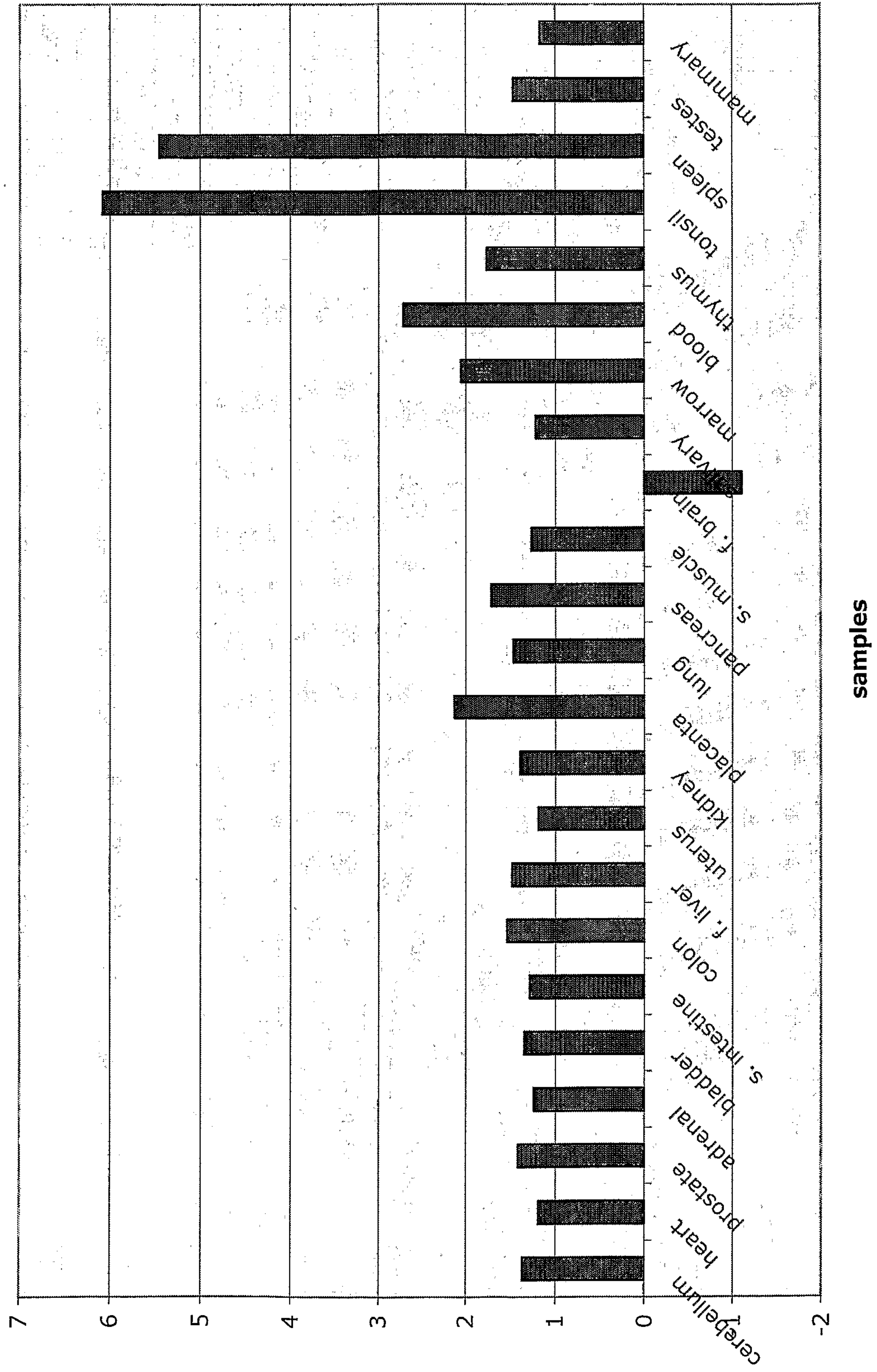
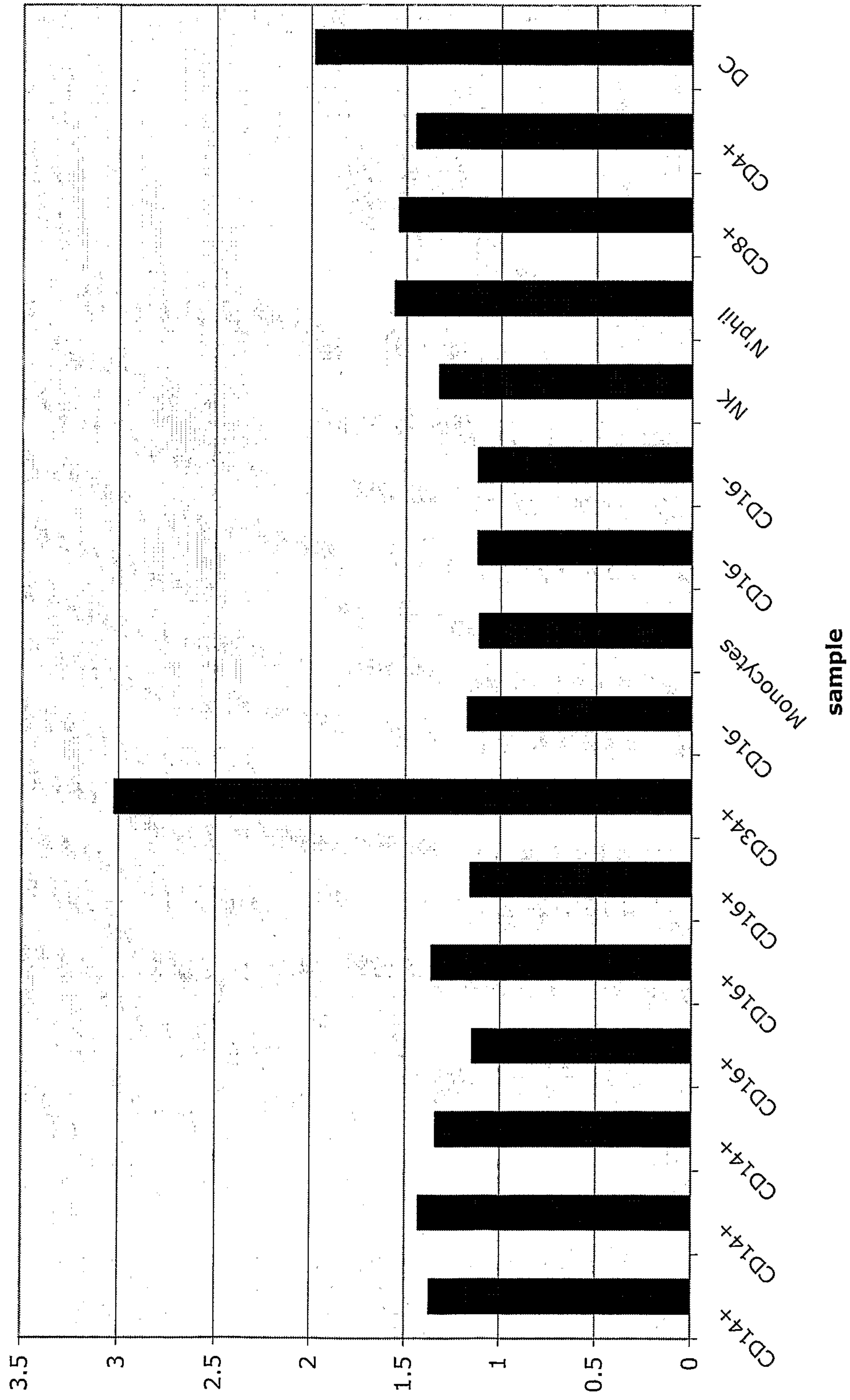


FIGURE 90C

CD19

TAHO25/DNA225820/CD19



TAHO25/DNA25820/CD19

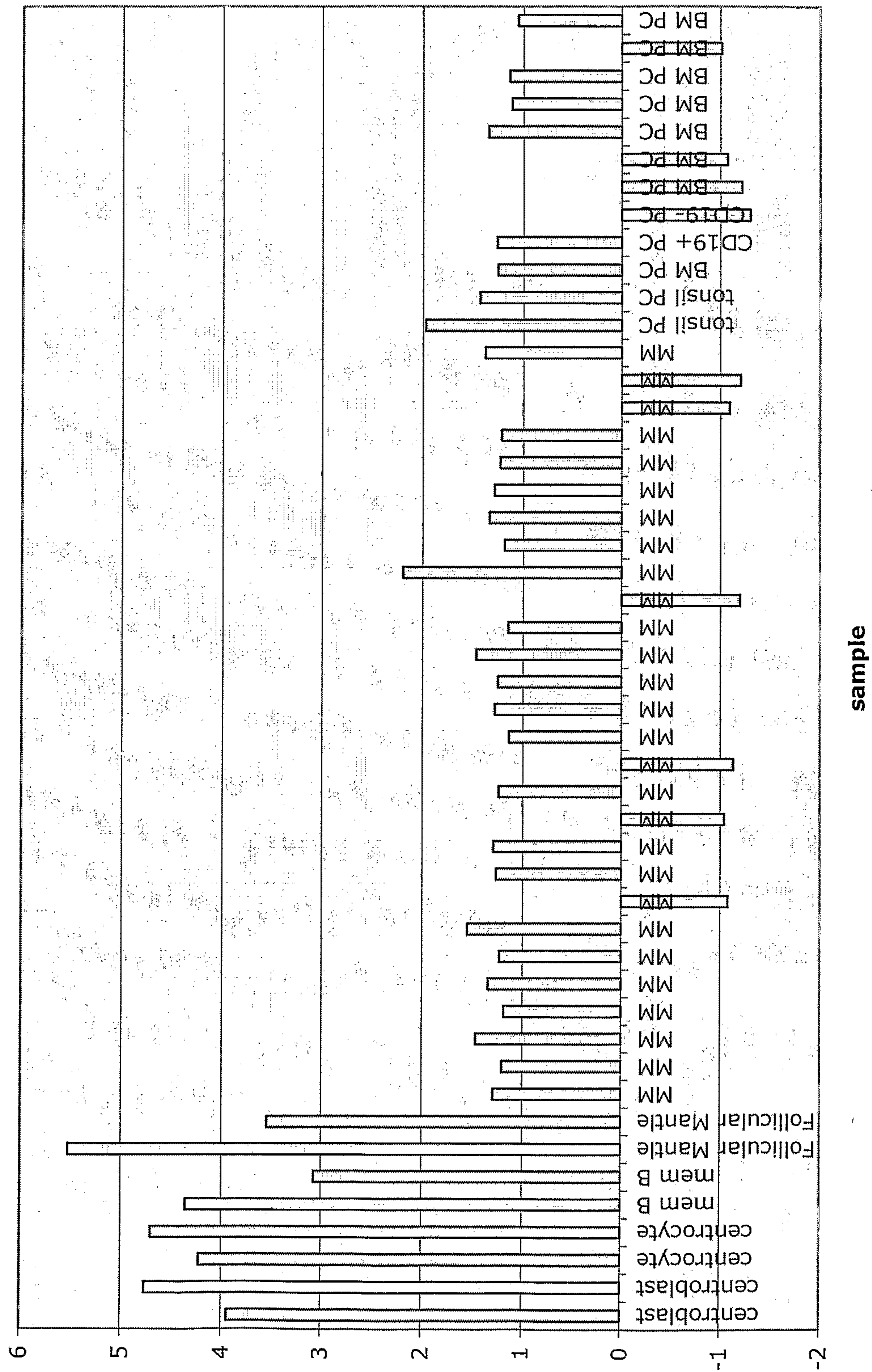


FIGURE 91A

TAHO26/DNA88116/CD22

CD22

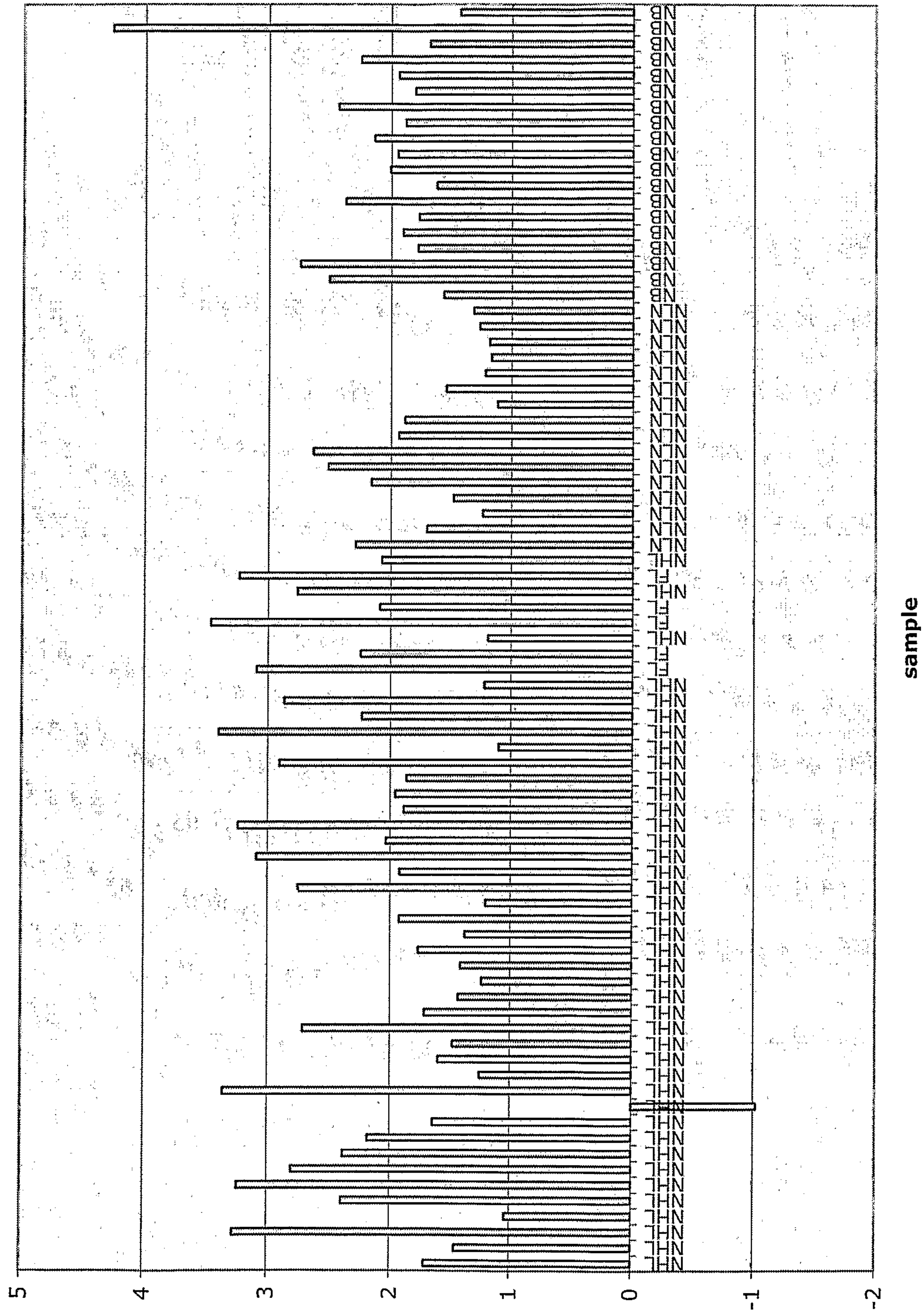


FIGURE 91B

CD22

TAHO26/DNA88116/CD22

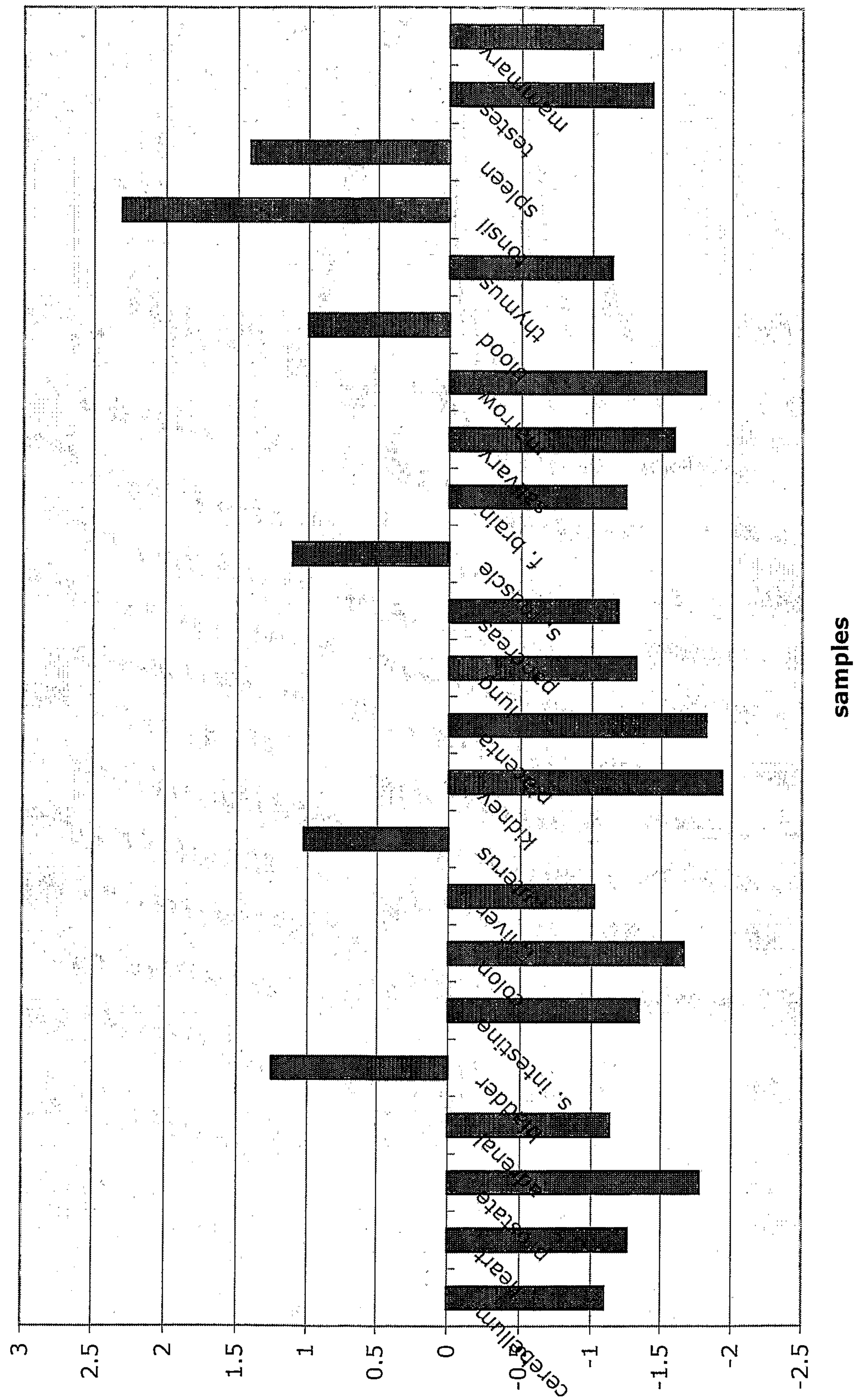
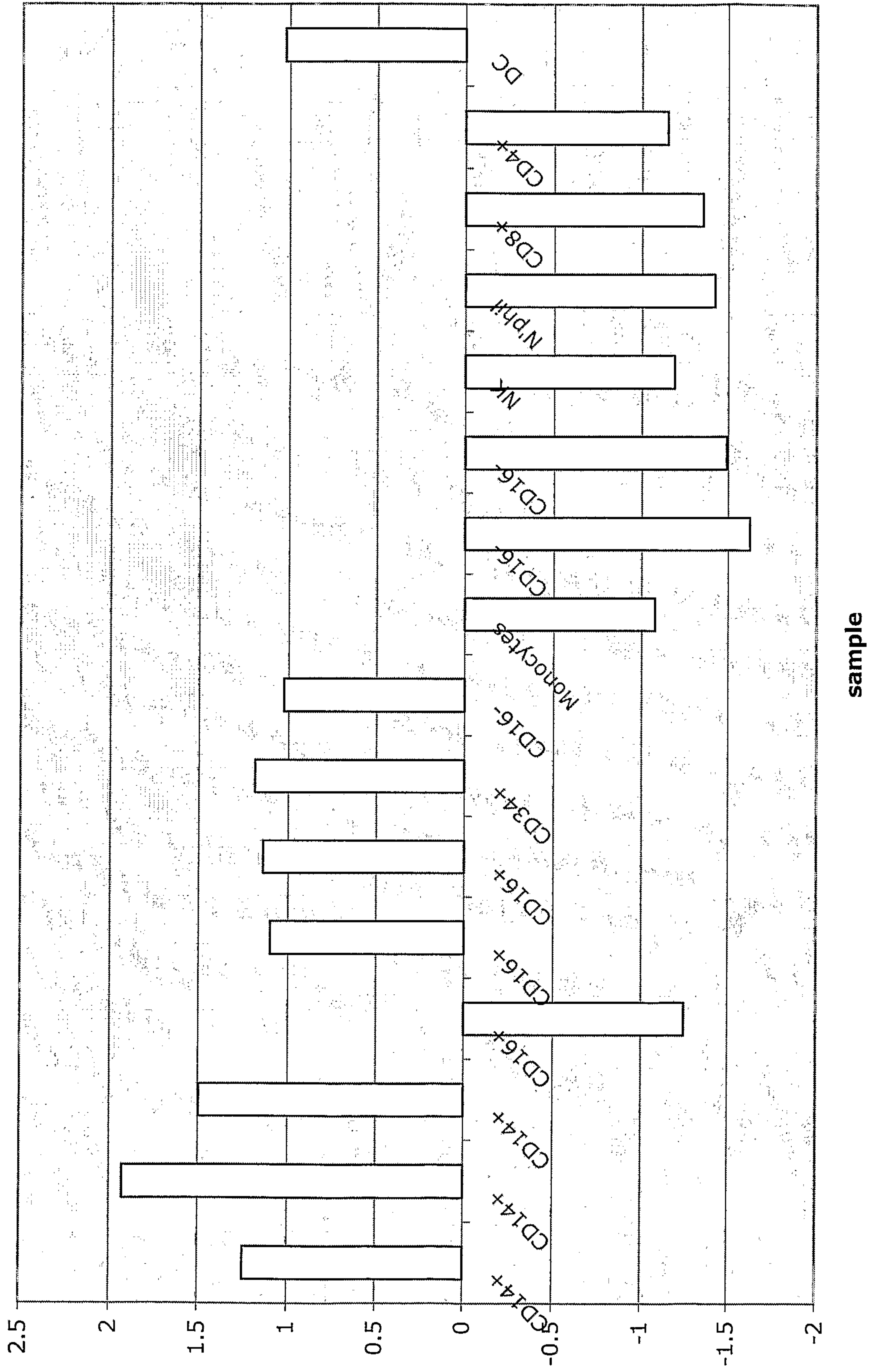


FIGURE 91C

CD22

TAHO26/DNA88116/CD22



TAHO26/DNA88116/CD22

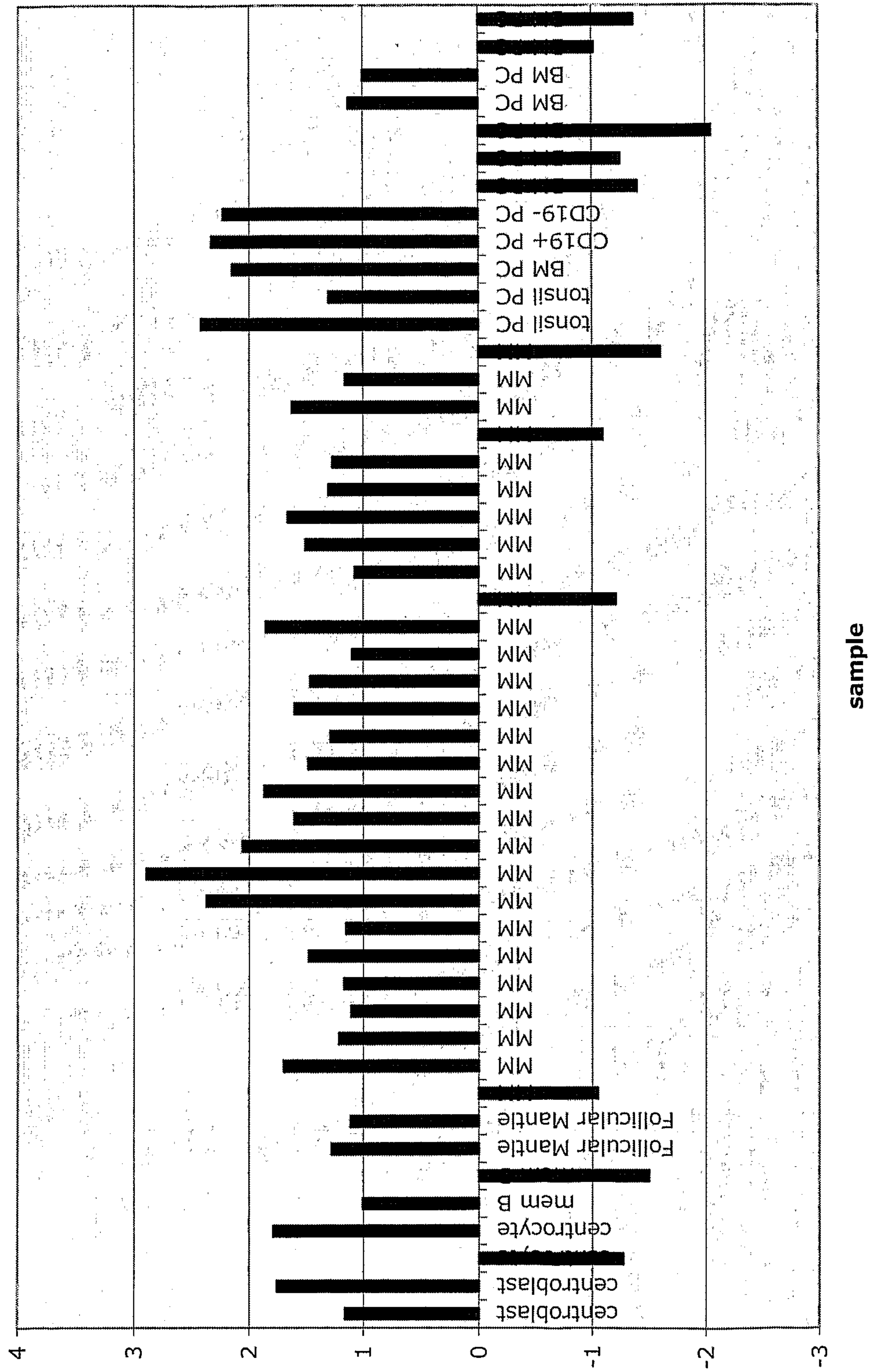


FIGURE 92A

TAHO27/DNA227752/CXCR3

CXCR3 UNQ8371

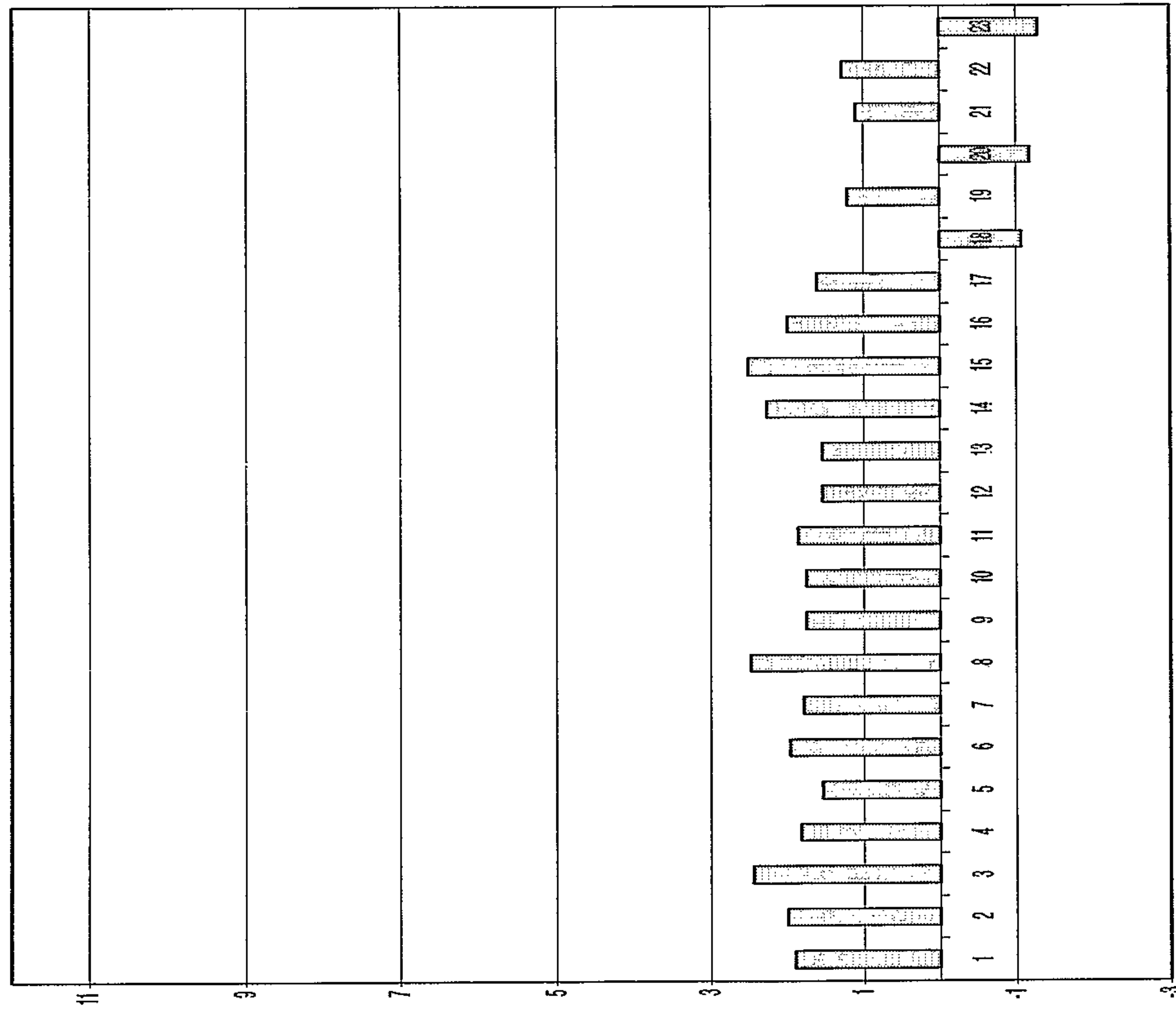
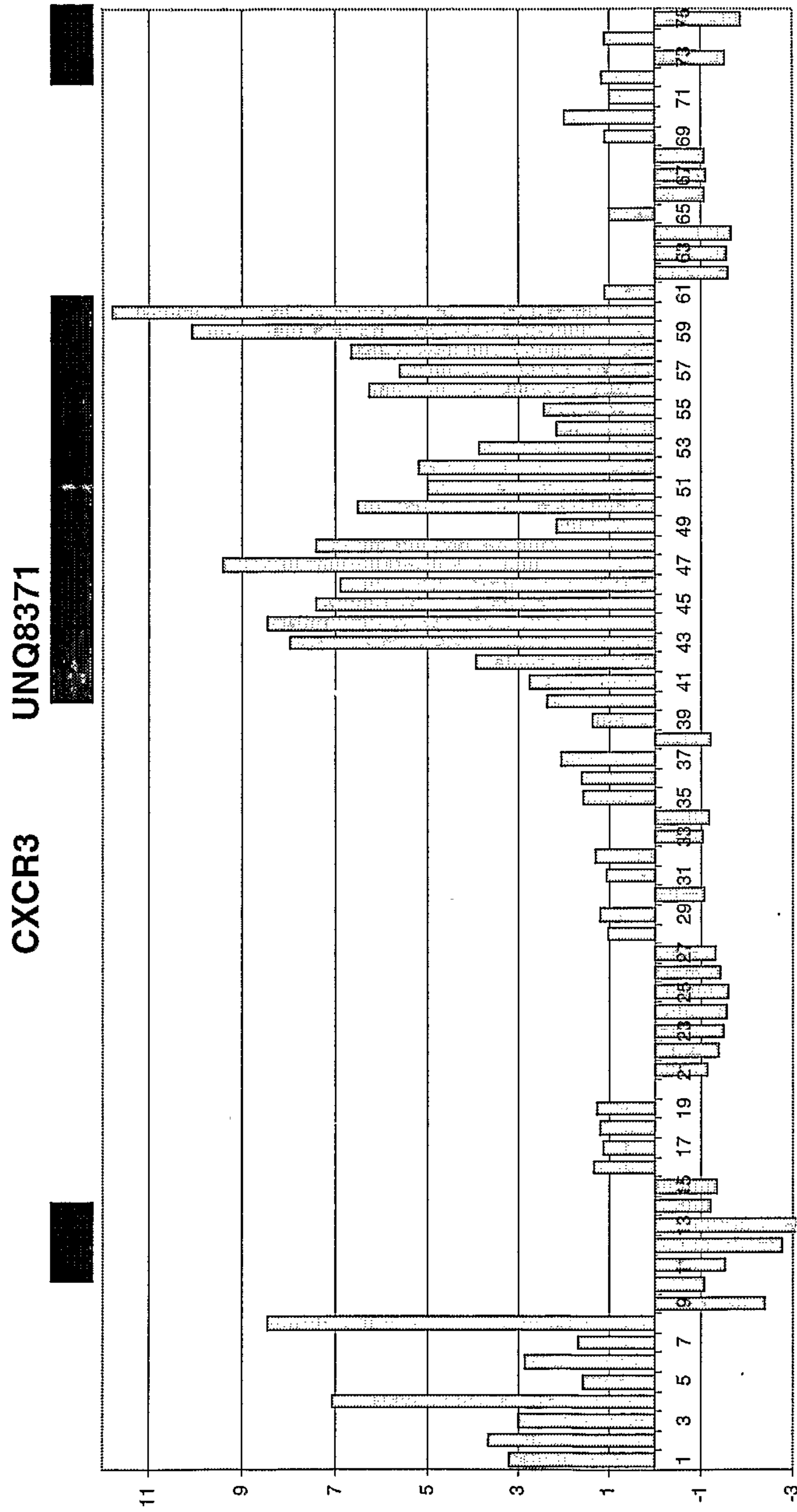


FIGURE 92B

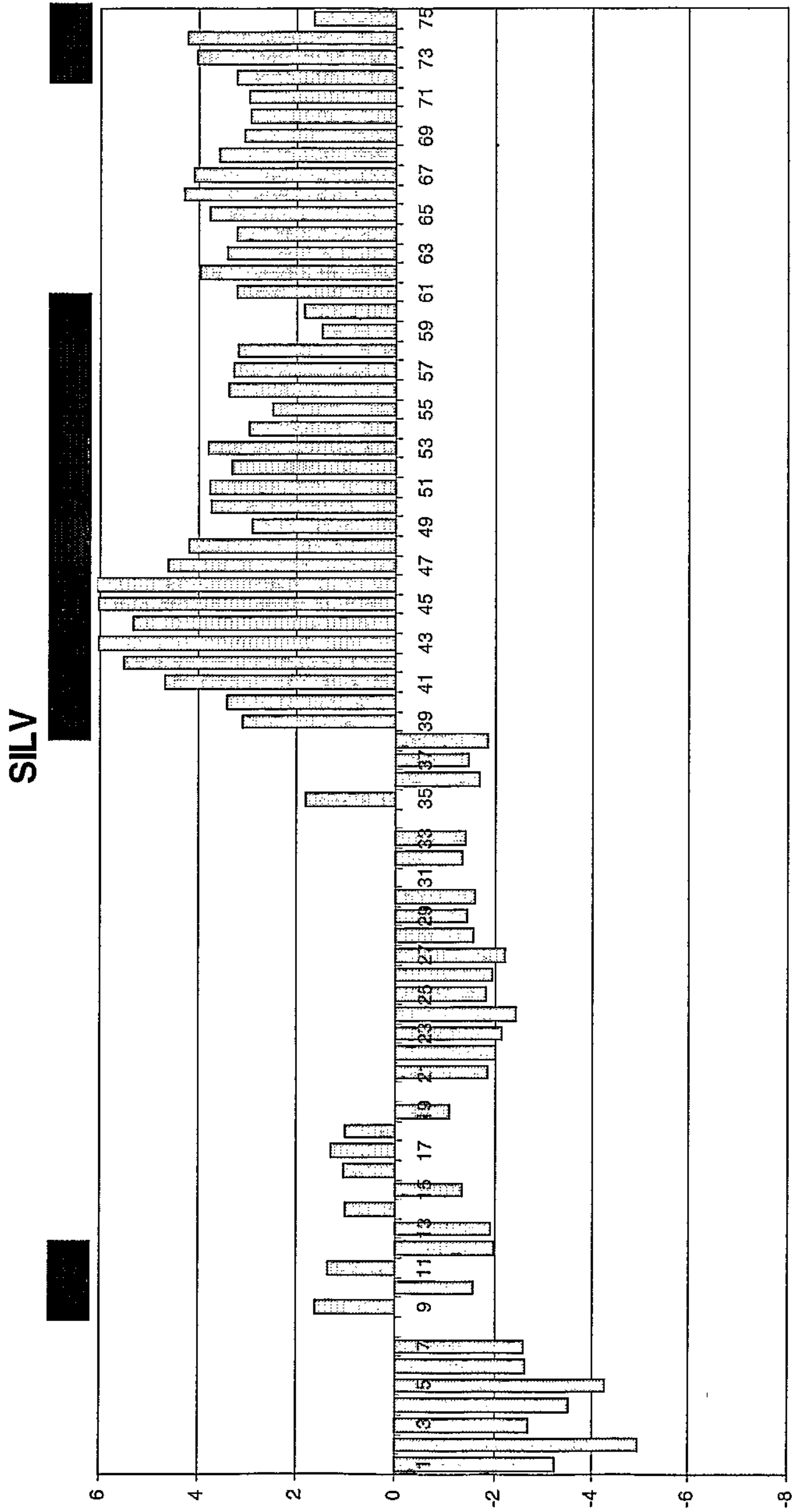
TAHO27/DNA227752/CXCR3



[redacted] = multiple myeloma samples

FIGURE 93B

TAHO28/DNA119476/SILV



[Redacted] = multiple myeloma samples

FIGURE 94A

TAHO29/DNA254890/KCNK4

KCNK4 UNQ1492

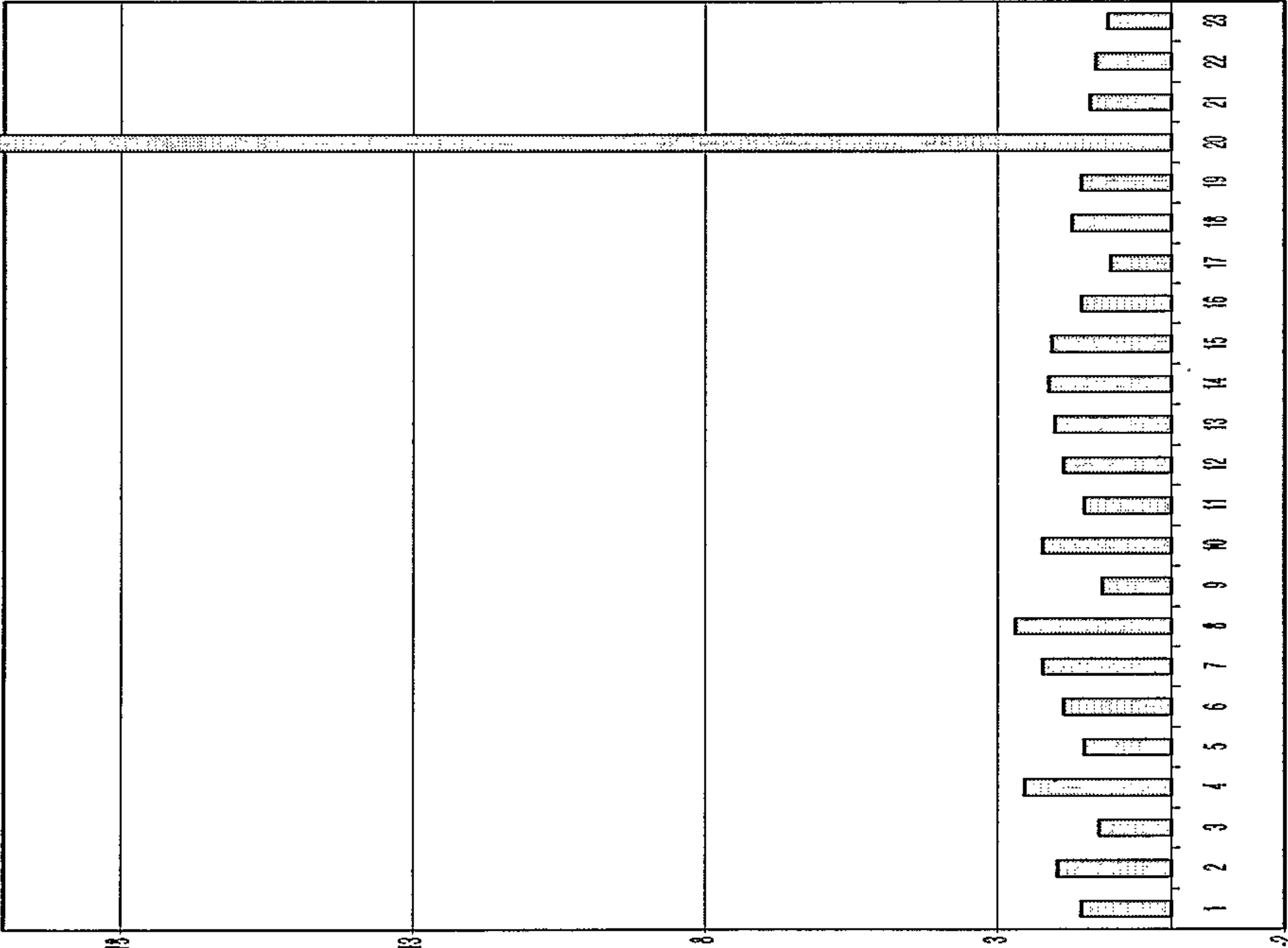
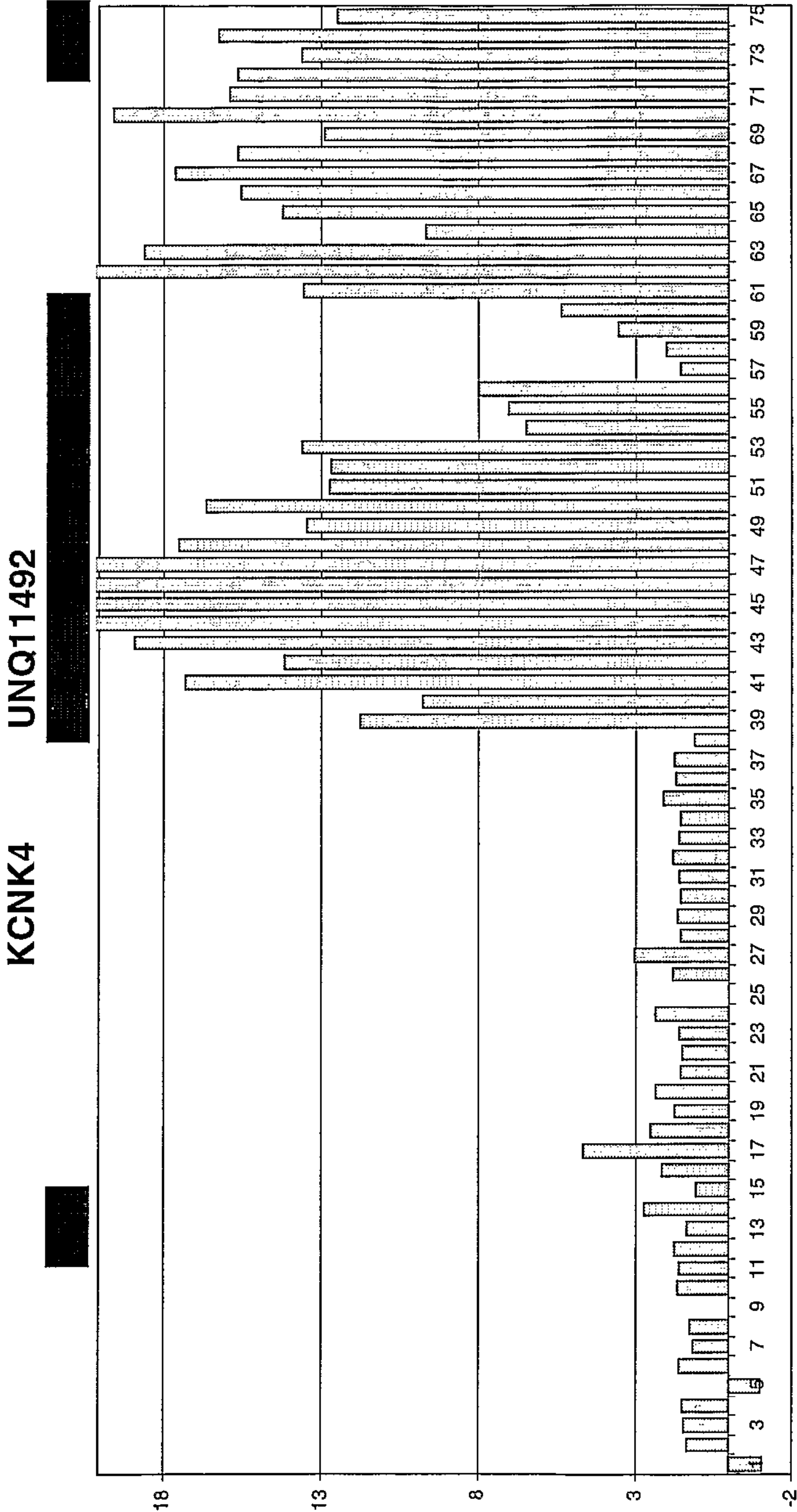


FIGURE 94B

TAHO29/DNA254890/KCNK4



multiple myeloma samples

FIGURE 95A

TAHO30/DNA219240/CXorf1

CXorf1 UNQ11757

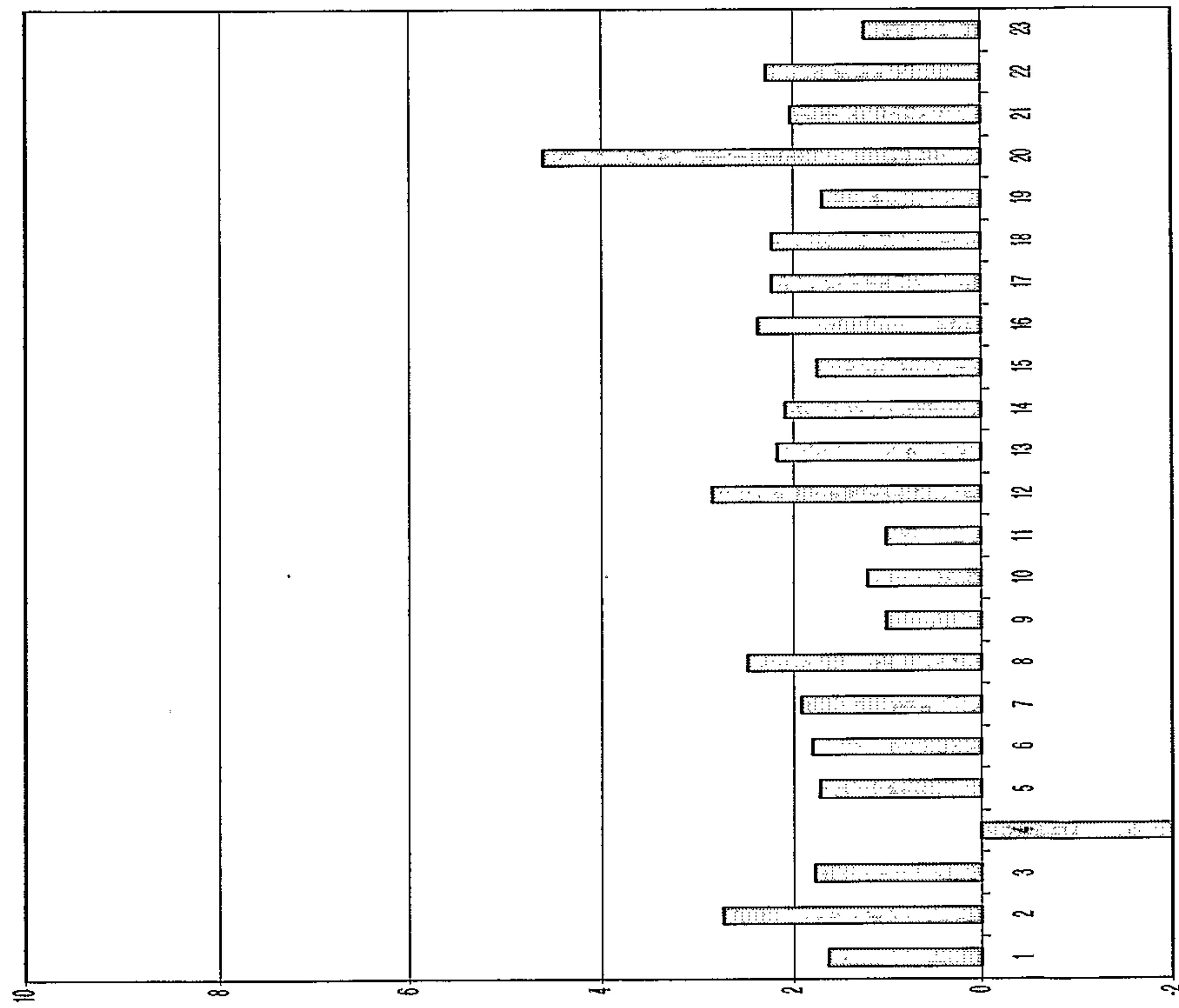
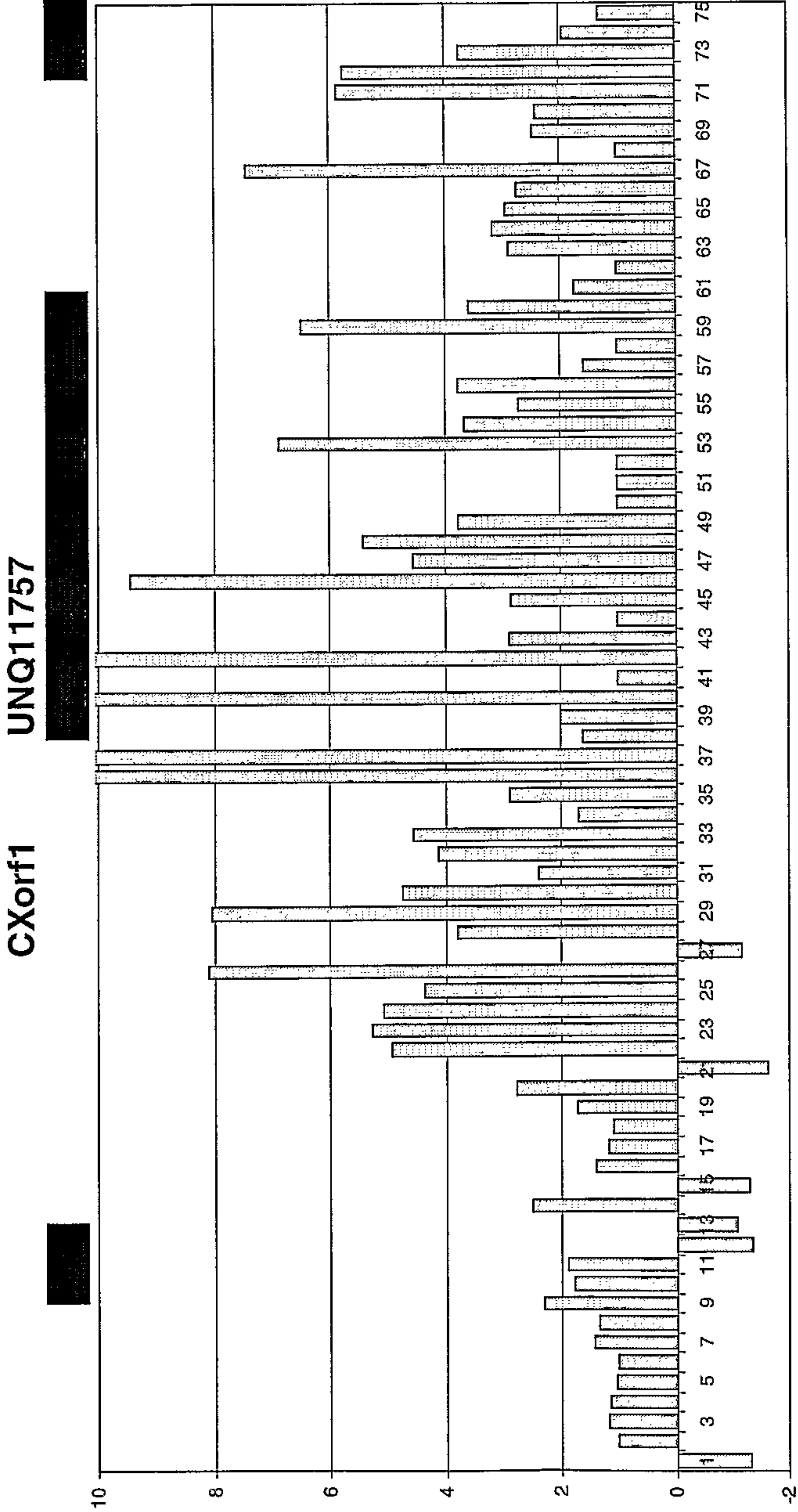


FIGURE 95B

TAHO30/DNA219240/CXorf1



[Black bar] = multiple myeloma samples

FIGURE 96A

TAHO31/DNA37151/LRRN5

LRRN5 UNQ256

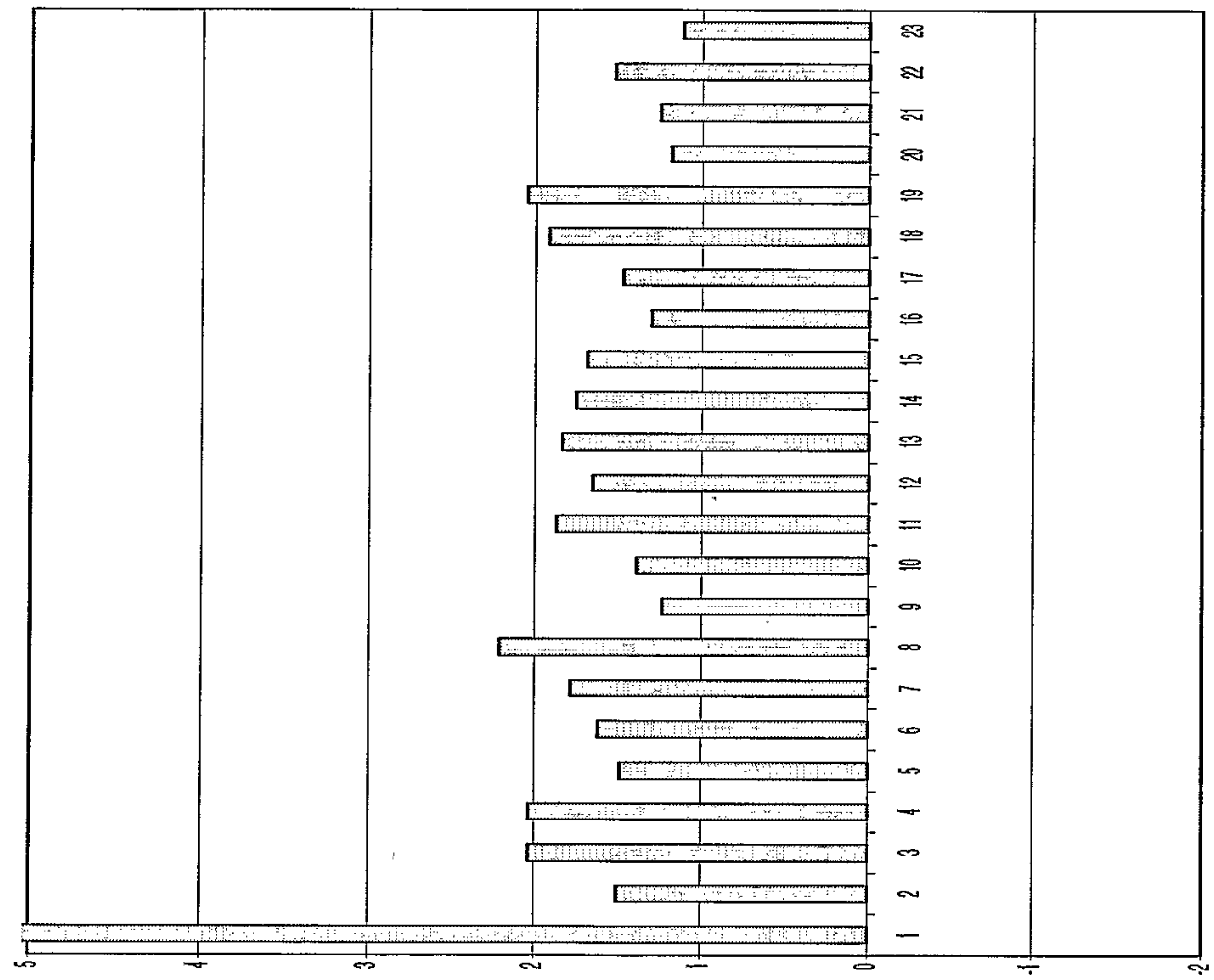
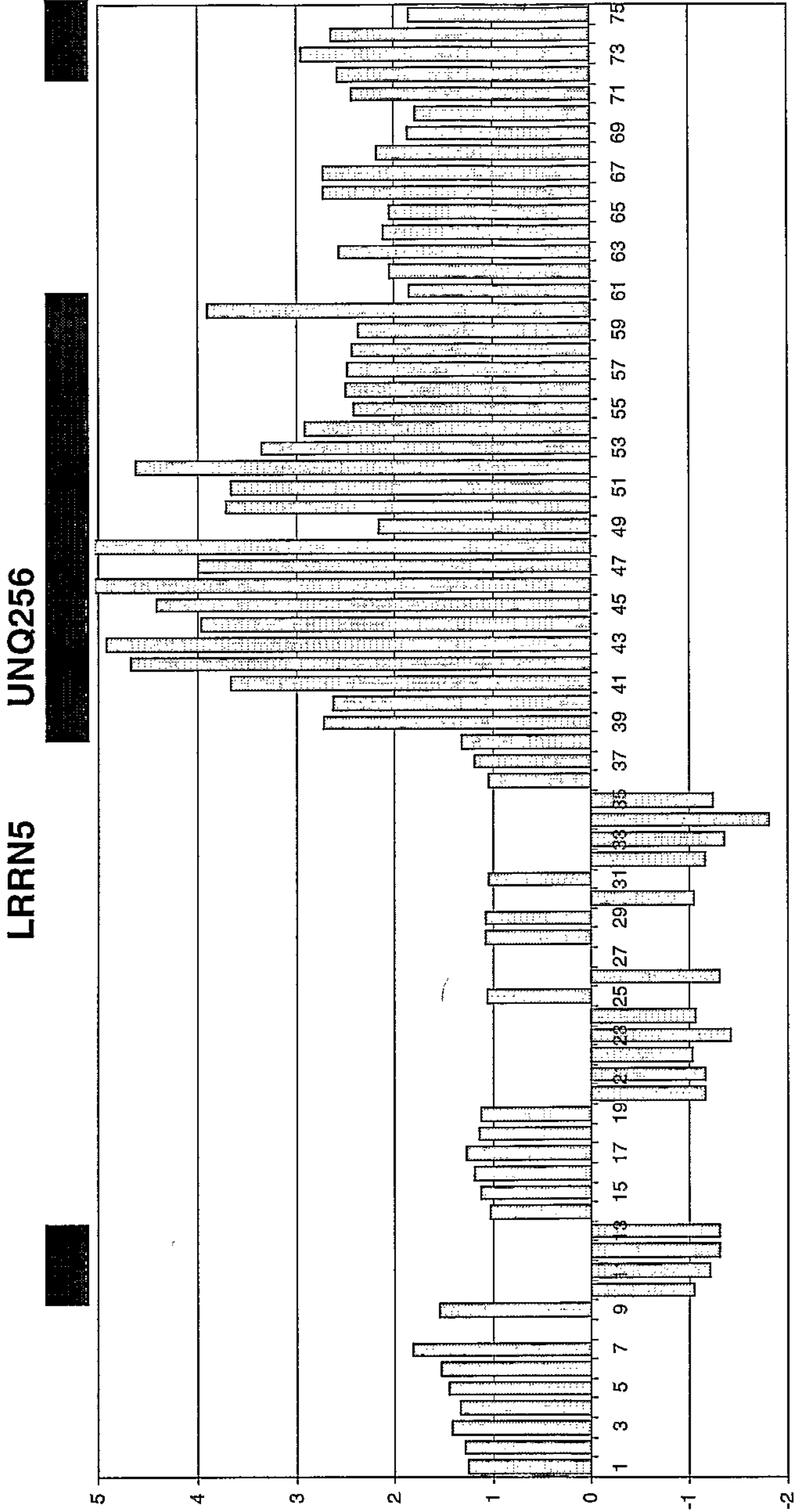


FIGURE 96B

TAHO31/DNA37151/LRRN5



= multiple myeloma samples

FIGURE 97A

TAHO32/DNA210233/UNQ9308

UNQ9308 UNQ9308

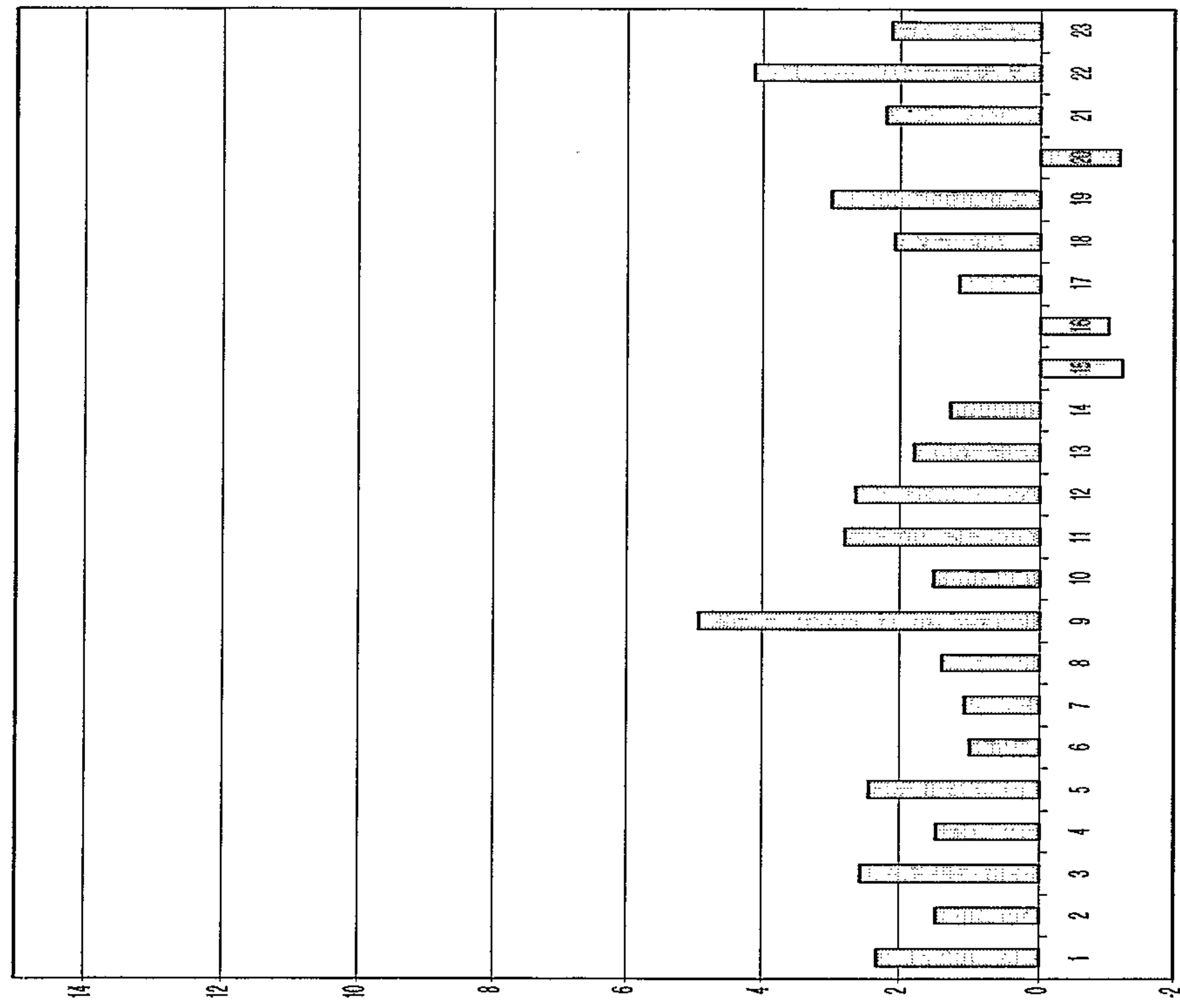
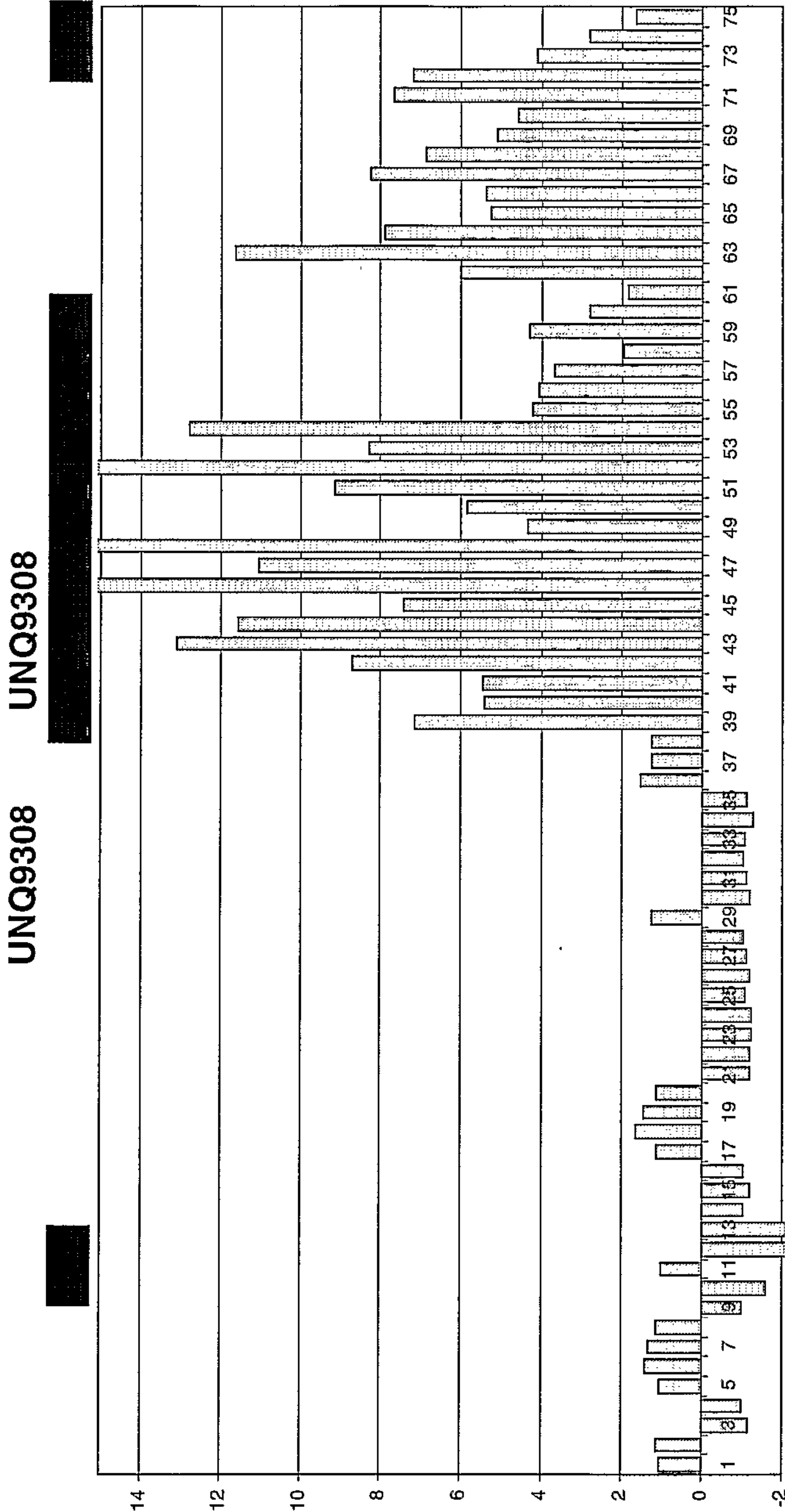


FIGURE 97B

TAHO32/DNA210233/UNQ9308
TAHO34/DNA260038/UNQ13267



[Redacted] = multiple myeloma samples

FIGURE 98A

TAHO33/DNA35918/IGSF4B

IGSF4B UN225

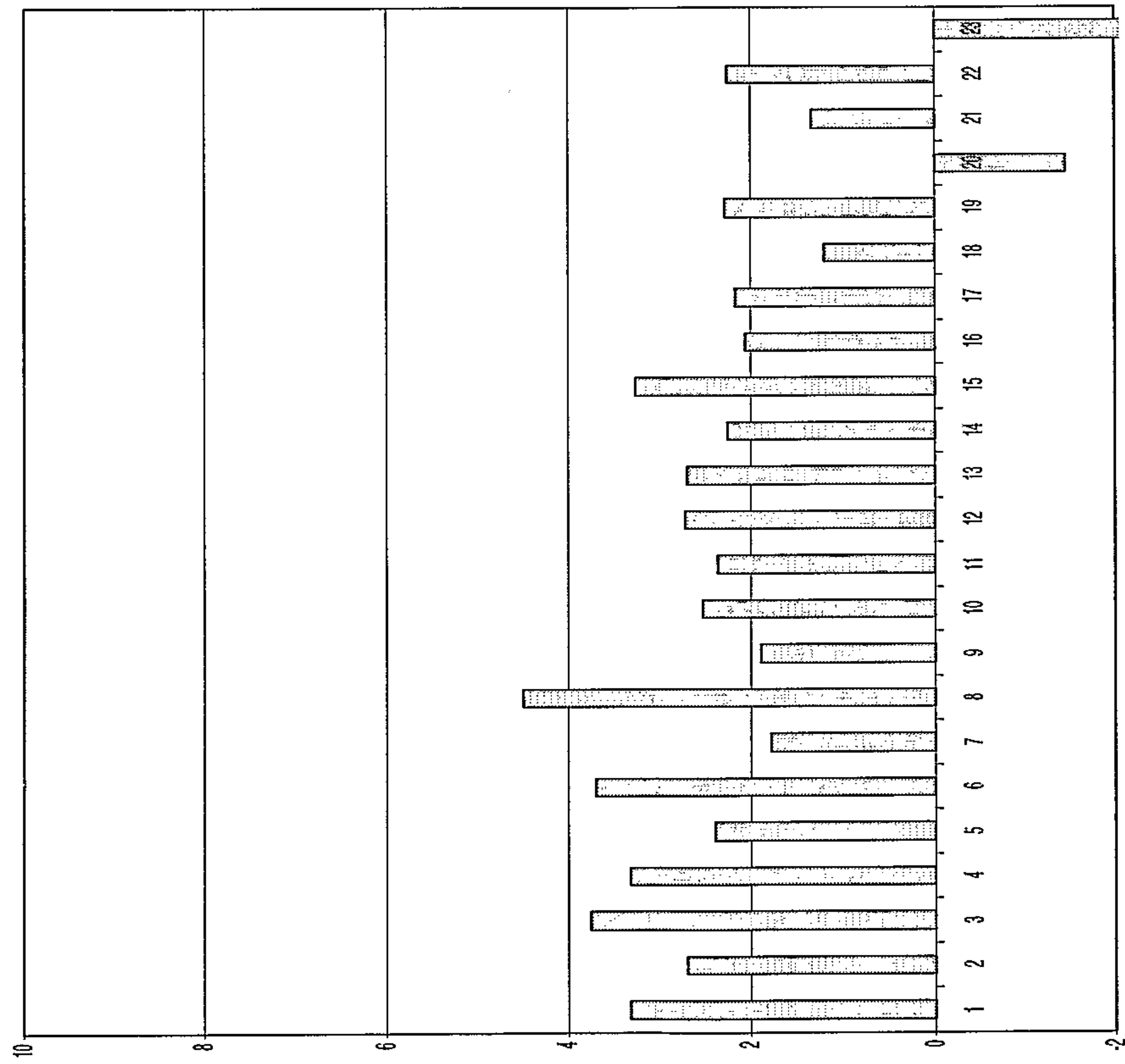
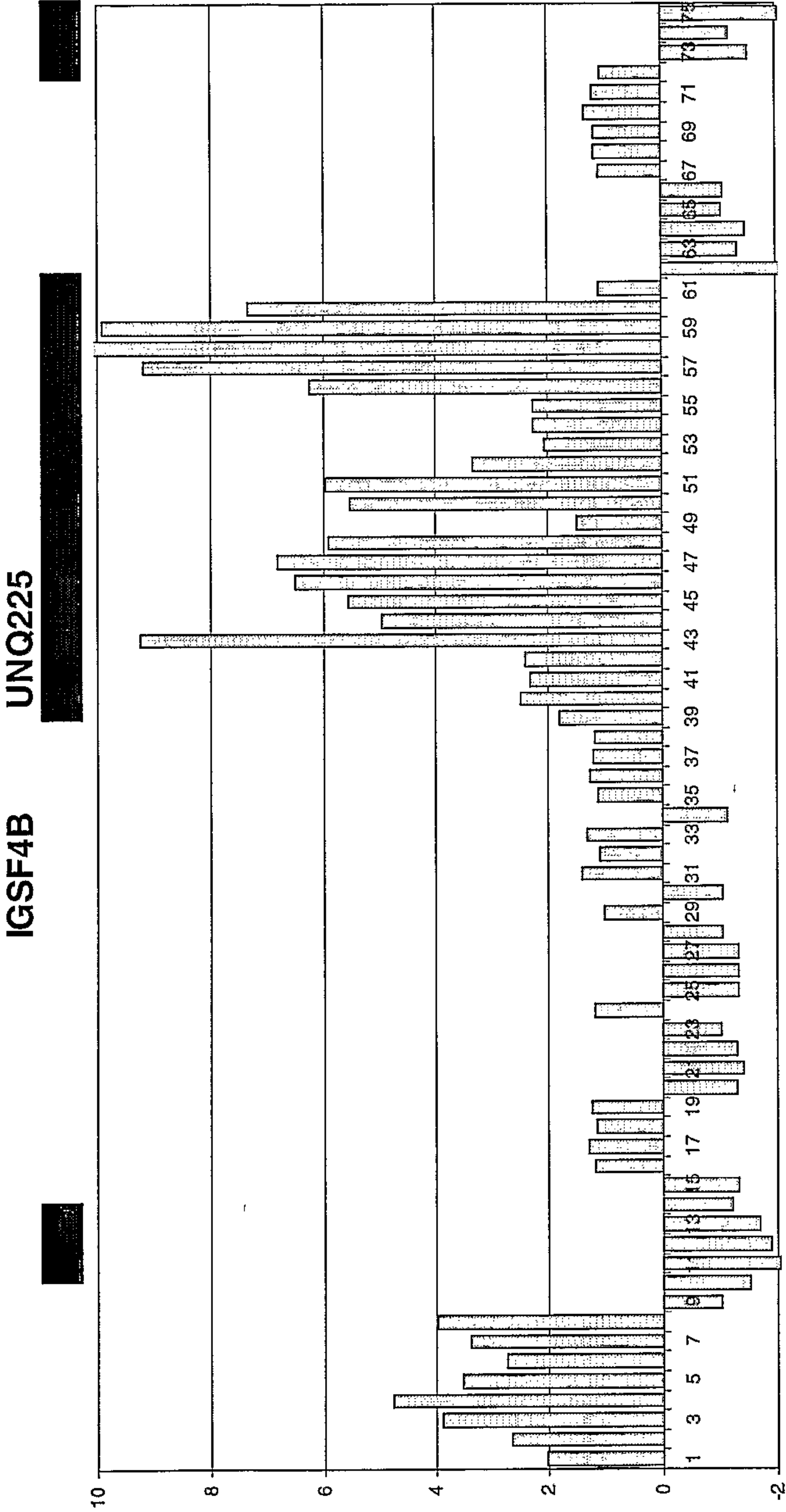


FIGURE 98B

TAHO33/DNA35918/IGSF4B



■ = multiple myeloma samples

FIGURE 99A

TAHO34/DNA260038/UNQ13267

BC021178 UNQ13267

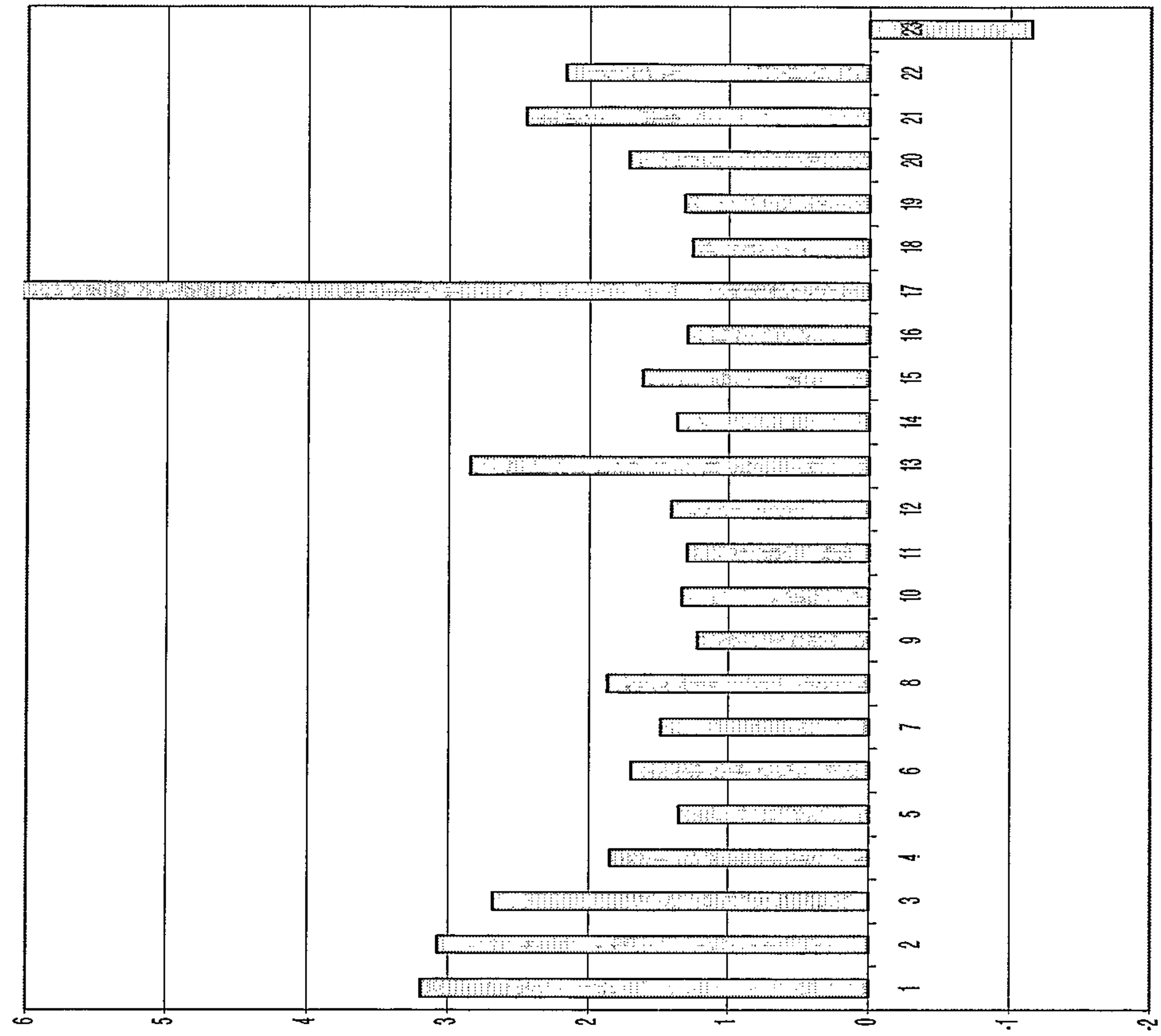
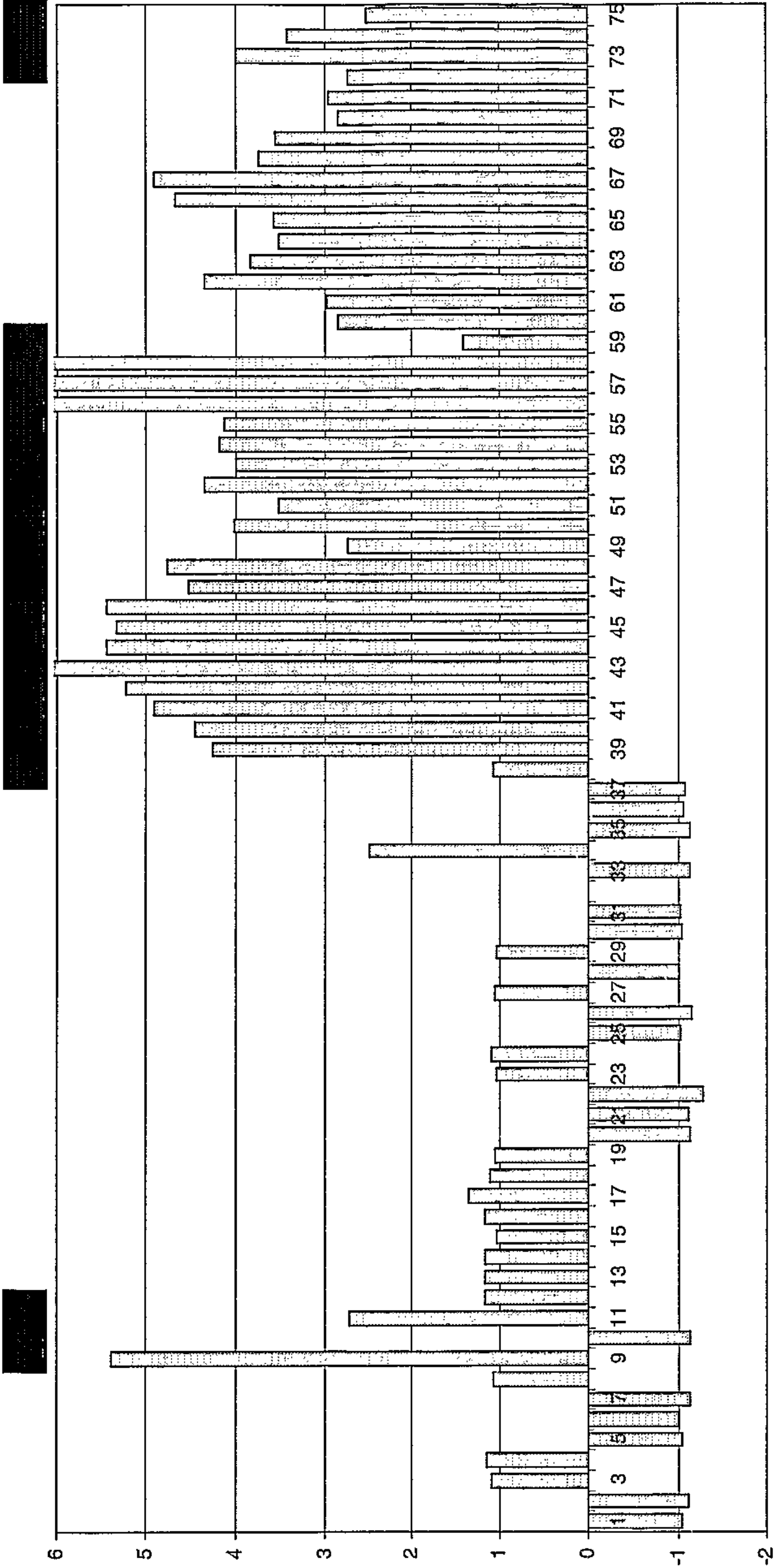


FIGURE 99B

TAHO34/DNA260038/UNQ13267

BC021178 UNQ13267



= multiple myeloma samples

FIGURE 100A

TAHO35/DNA334818/FLJ12681

FLJ12681 UNQ6034

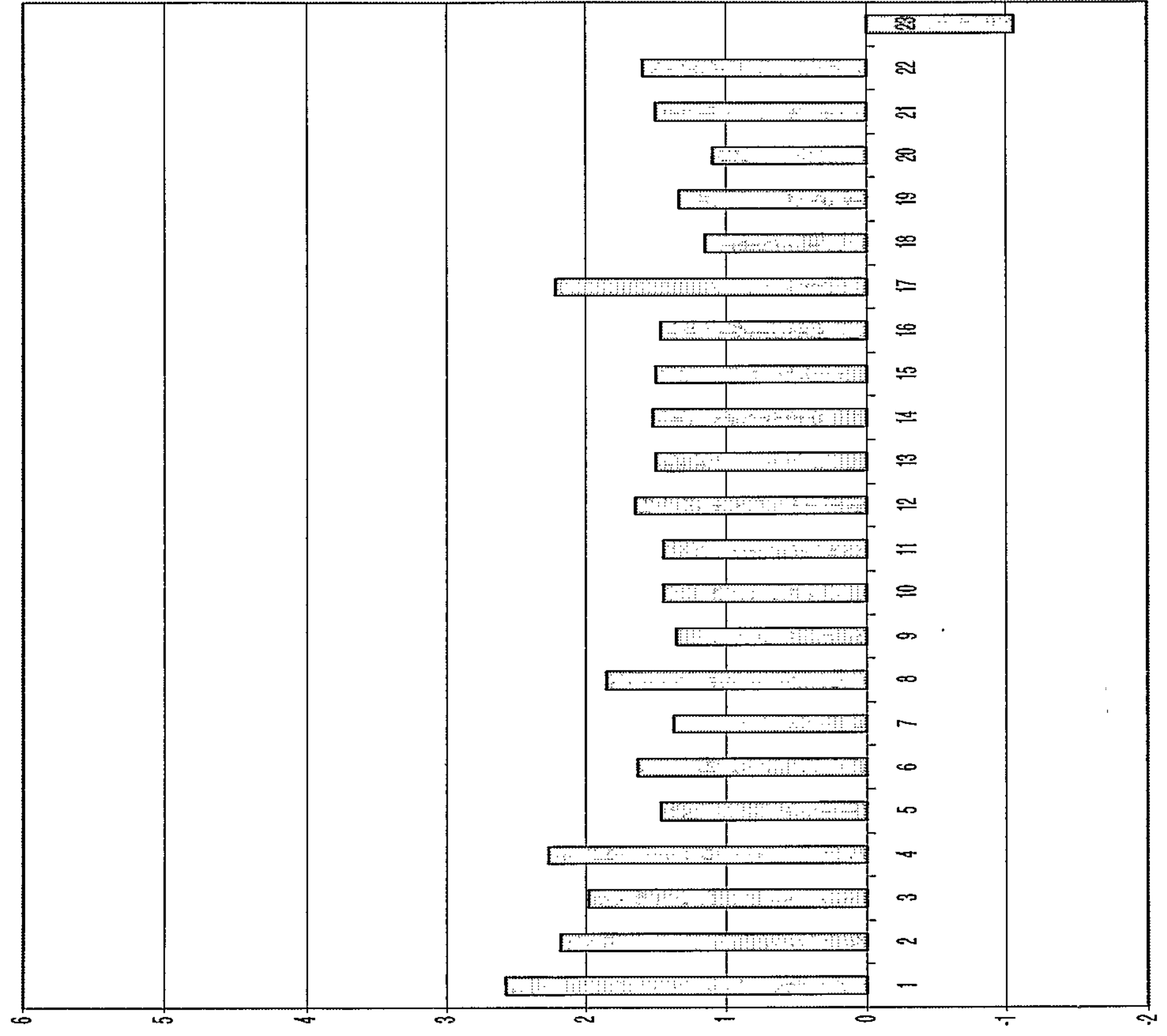
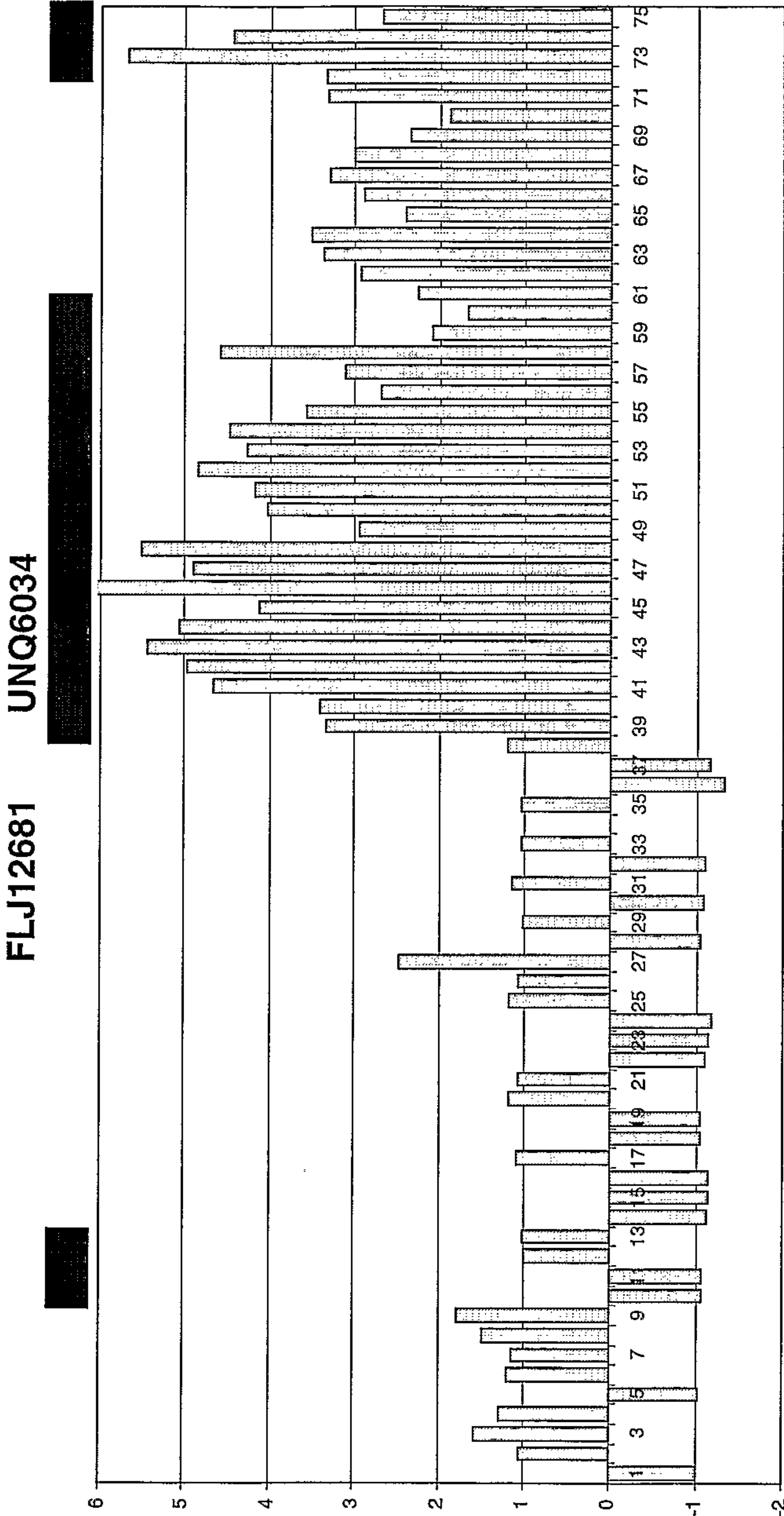


FIGURE 100B

TAHO35/DNA334818/FLJ12681



= multiple myeloma samples

FIGURE 101A

TAHO36/DNA257501/UNQ12376 (I_928646)

I_928646

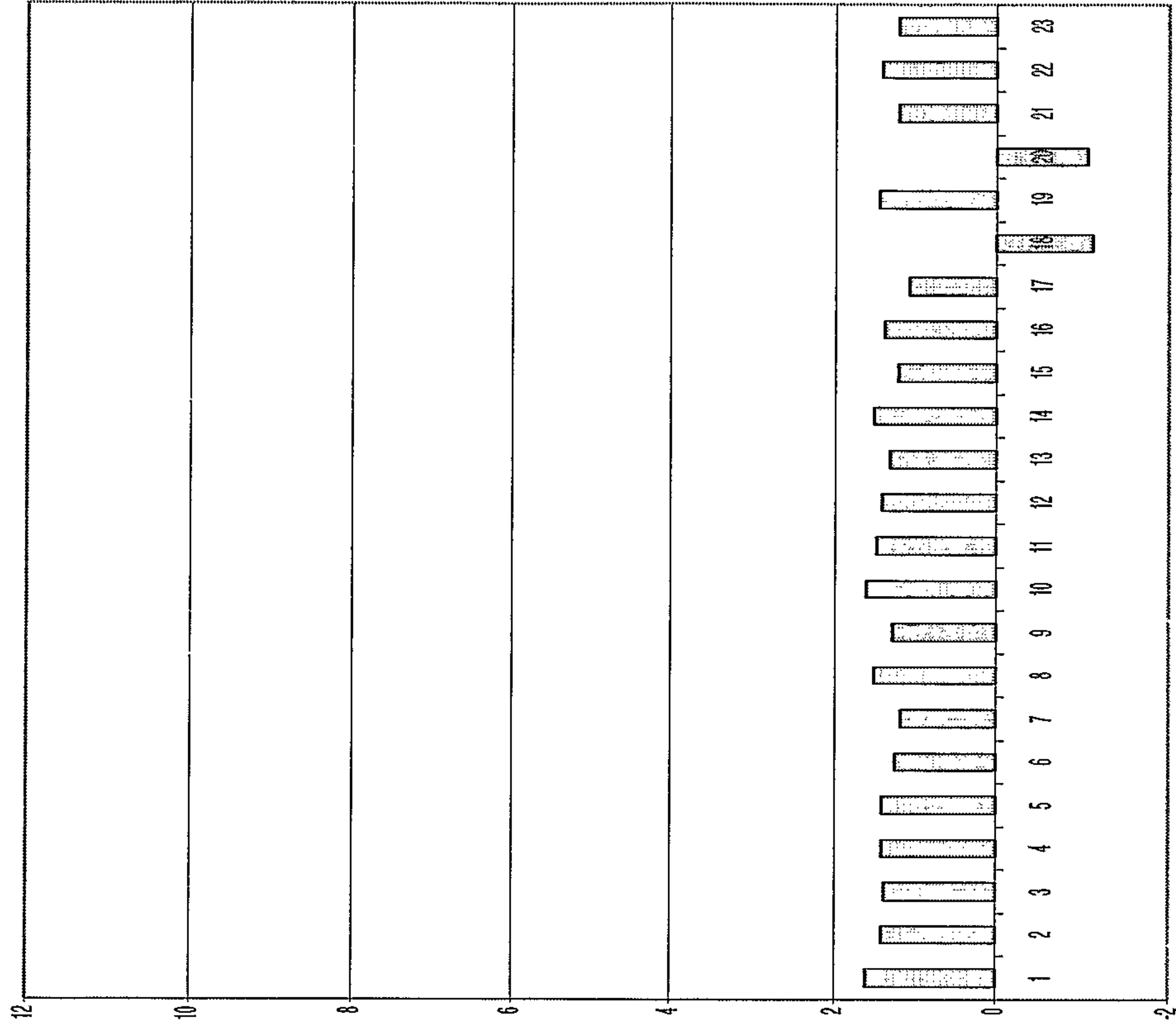
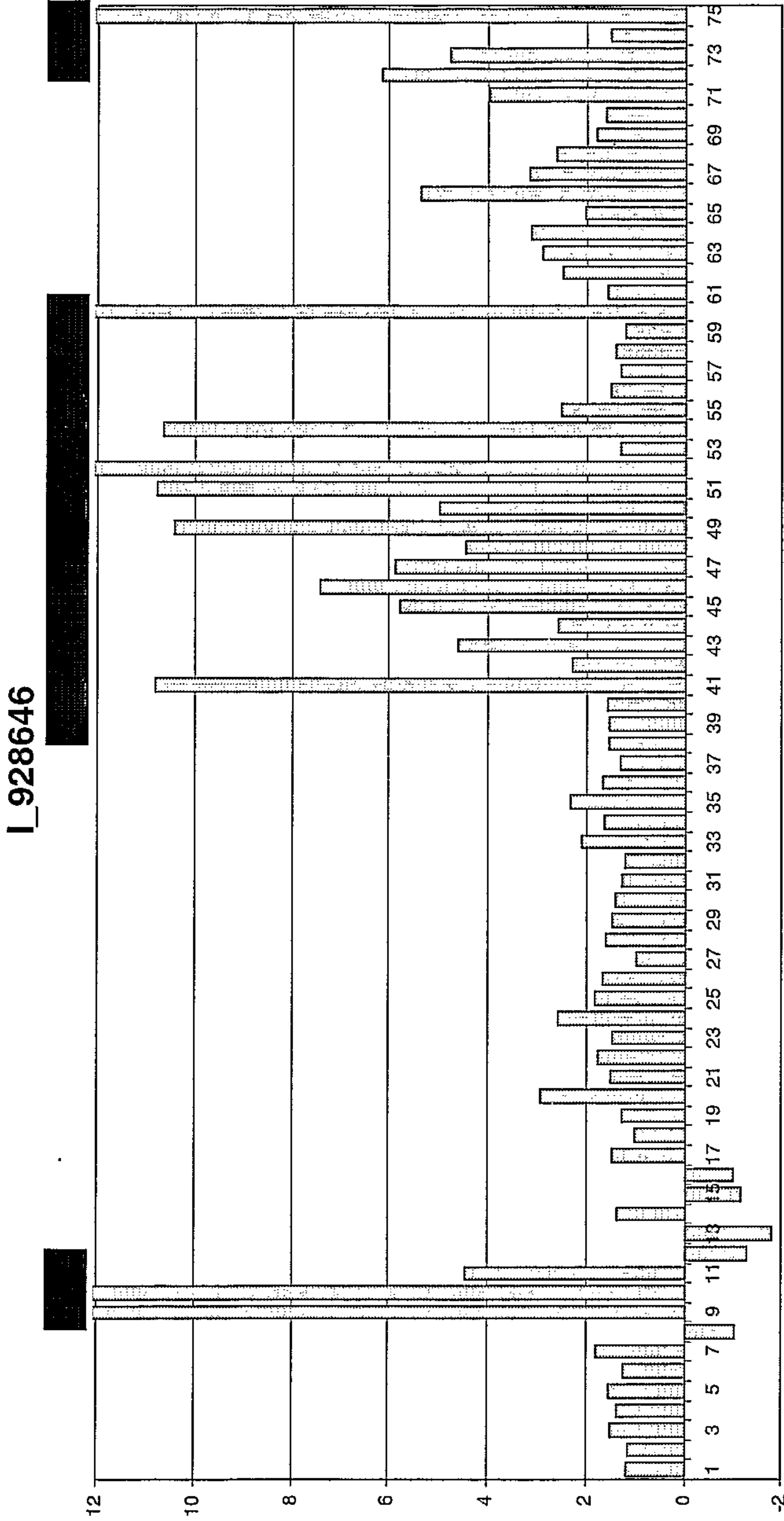


FIGURE 101B

TAHO36/DNA257501/UNQ12376/I_928646



= multiple myeloma samples

