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(54) Titre : GENES ASSOCIES A L'OSTEOARTHRITE CANINE ET PROCEDES ET COMPOSITIONS CONNEXES
(54) Title: GENES ASSOCIATED WITH CANINE OSTEOARTHRITIS AND RELATED METHODS AND COMPOSITIONS

(57) **Abrégé/Abstract:**

Described herein is a combination containing polynucleotide molecules that are differentially expressed in osteoarthritis. Also described are methods that may be used for diagnosis and prognosis of osteoarthritis, as well as methods that may be used to screen test substances for effectiveness in treatment modalities for osteoarthritis. Also described are devices and kits that may be used with the described methods.



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(54) Title: GENES ASSOCIATED WITH CANINE OSTEOARTHRITIS AND RELATED METHODS AND COMPOSITIONS

(57) Abstract: Described herein is a combination containing polynucleotide molecules that are differentially expressed in osteoarthritis. Also described are methods that may be used for diagnosis and prognosis of osteoarthritis, as well as methods that may be used to screen test substances for effectiveness in treatment modalities for osteoarthritis. Also described are devices and kits that may be used with the described methods.

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GENES ASSOCIATED WITH CANINE OSTEOARTHRITIS AND RELATED METHODS AND COMPOSITIONS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims benefit of U.S. Application No. 60/541,346, filed February 2, 2004, the disclosure of which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] This invention relates to the field of degenerative joint diseases, such as osteoarthritis. More particularly, the invention relates to novel compositions, devices and methods based on unique profiles of gene expression associated with osteoarthritis.

BACKGROUND OF THE INVENTION

[0003] Osteoarthritis (OA), also commonly referred to as degenerative joint disease, is recognized in humans and all veterinary species (Richardson et al., (1997) *Vet. Clin. North Am.* 27:883-911). OA is a prevalent and debilitating disease in canines and is often associated with hip dysplasia (Martinez, S. (1997) Osteoarthritis, *Vet. Clinics of N. Am.: Small Animal Practice* 27 (4):735-758.). There is a high degree of similarity between canine and human osteoarthritis, thus making it an excellent animal model for the study of human osteoarthritis. While causative factors remain largely unknown, the disease is characterized by the imbalance of cartilage matrix degradation outweighing cartilage matrix synthesis. Chondrocyte apoptosis and inflammation may also be associated with the disease (Pelletier, J., et al. (2001) *Arthritis & Rheumatism* 44 (6):1237-1247; Lotz, M. (1999) *Osteoarthritis and Cartilage* 7: 389-391).

[0004] The disease is typically slow in progression and characterized by degeneration of articular cartilage with a loss of both proteoglycan and collagen and by proliferation of new bone. In addition, an inflammatory response can occur within the synovial membrane. Canine osteoarthritis can arise as a secondary condition resulting, in particular, from hip dysplasia or from osteochondritis dissecans (Martinez, *supra*). Acquired conditions involving traumatic events can also lead to osteoarthritis in the dog (Martinez et al., *Vet. Clin. North Am.* 27:759-775,

1997). Treatment modalities for osteoarthritis can include the administration of anti-inflammatory drugs as well as the manipulation of dietary fatty acids (Richardson et al., *supra*).

[0005] Diagnosis of canine osteoarthritis is typically based upon symptomatology. Dogs having osteoarthritis show a lameness which may have a gradual onset but can flare up acutely after exercise. The lameness is exacerbated by rest but decreases after a few minutes of activity. Cold damp conditions, obesity and prolonged exercise often worsen signs of lameness (Pederson et al, in *Textbook of Veterinary Internal Medicine, 5th Ed.*, Ettinger et al., ed., W.B. Saunders and Co., Philadelphia, 2000, pp. 1862-1886).

[0006] With the emergence of the genomic sciences, it has become apparent that not only is the regulation of gene expression intimately involved in normal homeostasis, alterations in the differential expression of genes is one aspect in the development of diseases. As a result, the evaluation of gene expression patterns in disease has become increasingly recognized as being crucial to the understanding of disease processes at the molecular level. (Going et al., *European J. Cancer* 35:1895-1904, 1999; Wang et al., *Cardiovasc. Res.* 35:414-421). A number of approaches have emerged for studying comparative gene expression and the current emphasis has been on high throughput analysis methods. (for review see Carulli et al, *J. Cell. Biochem. Suppl.* 30/32:286-296, 1998; Kozian et al., *Trends Biotechnol* 17:73-78, 1999). Recent methods developed for high throughput analysis of differential gene expression include, for example, EST sequencing (Adams et al., *Science* 252:1651-1656, 1991; Adams et al., *Nature* 377:3-16, 1995), microarray hybridization (Schena et al., *Science* 270:467-470, 1995), and differential display (Liang et al., *Science* 257:967-970, 1992; Welsh et al., *Nucleic Acids Res.* 20:4965-4970, 1992).

[0007] Gene expression in osteoarthritis, and particularly in canine osteoarthritis, has not been comprehensively studied. Accordingly, a need exists to identify nucleic acid sequences and their encoded proteins which are differentially expressed in osteoarthritis. This information would be useful to diagnose the osteoarthritic disease state, or pre-disposition to the disease, in a subject, as well as to identify substances useful in the treatment or prevention of osteoarthritis.

SUMMARY OF THE INVENTION

[0008] In accordance with an aspect of the present invention, a number of polynucleotides comprising at least a fragment of a gene have been identified as being differentially expressed in osteoarthritic or pre-osteoarthritic subjects, compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic.

[0009] In accordance with an aspect of the present invention, differentially expressed genes, gene fragments, and encoded gene products, as well as the expression patterns associated with the group of genes, are used to advantage in a number of methods for the detection of

changes in gene expression associated with osteoarthritis, particularly canine osteoarthritis. Additional aspects of the invention relate to methods for the identification of agents useful in treating and/or preventing osteoarthritis.

[0010] In accordance with additional aspects of the present invention, compositions, devices and test kits are provided to facilitate the practice of methods provided according to certain embodiments of the invention.

[0011] Other features and advantages of the present invention will be understood by reference to the detailed description and the examples that follow.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] **Figure 1** shows representative gels used in differential display analysis of canine osteoarthritis. **A.** Differential display of osteoarthritic vs. normal transcripts loaded in duplicate prior to band excision (D=osteoarthritic (Diseased), N=Normal). **B.** The same gel after band excision.

[0013] **Figure 2** shows quantitative PCR analysis (qPCR) for selected OA-associated transcripts in canine cartilage. RNA expression is shown in arbitrary units. (OA AVG = average expression for osteoarthritic cartilage; C AVG = average expression in normal control).

TABLE 1: Correlation of Gene ID Numbers with Sequence ID Numbers.

Gene ID	SEQ ID	Gene ID	SEQ ID	Gene ID	SEQ ID	Gene ID	SEQ ID
1028c	1	768a	2	141c	3	1548c	4
1357a	5	168c	6	383d	7	2127c	8
530b	9	1405c	10	1765a	11	166a	12
1797a	13	1729a	14	1857c	15	523a	16
2172c	17	58a	18	244a	19	70d	20
1472a	21	452a	22	1481c	23	1940e	24
1930a	25	739a	26	1612a	27	14a	28
1727a	29	1220b	30	33a	31	1146a	32
1738b	33	810a	34	1993b	35	2147a	36
1678a	37	56a	38	1814c	39	129b	40
1924a	41	557b	42	1254a	43	1292c	44
2221c	45	490c	46	907a	47	469d	48
713a	49	1372a	50	482a	51	1098a	52
1785a	53	1624b	54	1441d	55	553b	56
2179a	57	1257b	58	1506d	59	1939c	60
2007a	61	13a	62	1288a	63	1949a	64
142.2c	65	1054a	66	1404c	67	8a	68
46a	69	1985a	70	326e	71	85.1c	72
1675a	73	574a	74	2159b	75	2108b	76
45.1b	77	2173a	78	1676a	79	581a	80
1695a	81	1414b	82	151b	83	112d	84
461a	85	1615b	86	310h	87	297a	88
1801b	89	23a	90	1739a	91	170a	92
1955a	93	2088a	94	2243b	95	1440a	96
2351c	97	1415b	98	2074b	99	2250a	100

1740a	101		81a	102		1248b	103		82b	104
1147a	105		12a	106		2201a	107		2266b	108
795a	109		206a	110		327f	111		212a	112
2083e	113		555b	114		1296a	115		272d	116
1709a	117		1945a	118		1631d	119		24a	120
1284a	121		184a	122		936b	123		1a	124
1677b	125		747a	126		737a	127		2166a	128
479c	129		2040d	130		1502a	131		72a	132
1917f	133		1650a	134		1620a	135		1951a	136
2355c	137		1394b	138		2071a	139		340a	140
368b	141		736a	142		17a	143		1475a	144
143.2c	145		1540a	146		1521b	147		2156c	148
2035d	149		1919a	150		1648a	151		1241a	152
1713a	153		144.2a	154		2255a	155		690a	156
2163a	157		979a	158		1747a	159		507a	160
890a	161		395a	162		1309b	163		1462a	164
1086c	165		1313a	166		1439b	167		153b	168
1790a	169		961a	170		493a	171		1463a	172
172a	173		1454d	174		1143d	175		766b	176
1412b	177		1423b	178		850a	179		148a	180
1696a	181		1396b	182		2141a	183		1503c	184
639a	185		1682a	186		2153a	187		2241a	188
2263b	189		1438a	190		2059b	191		1646a	192
465b	193		990a	194		1488b	195		1452a	196
1270a	197		2142a	198		945a	199		1367a	200
2198b	201		1139a	202		1138a	203		1008a	204
552a	205		2374a	206		1532a	207		2118a	208
1366a	209		1262b	210		144.1c	211		21a	212
1246a	213		1253a	214		2224a	215		1015d	216
2252b	217		154a	218		718a	219		11b	220
363a	221		370a	222		1551a	223		376a	224
84.2c	225		380a	226		372a	227		2148a	228
1800a	229		1090d	230		60a	231		96e	232
2015e	233		128a	234		621b	235		1174d	236
947a	237		1964a	238		619b	239		2222b	240
1468c	241		1629a	242		174a	243		2085c	244
1461a	245		764b	246		731a	247		1051a	248
613a	249		531a	250		1471a	251		1381a	252
44c	253		1892a	254		76b	255		366a	256
994b	257		1954e	258		409a	259		2120a	260
638b	261		329d	262		1853a	263		2247a	264
1746a	265		1081a	266		2002c	267		785b	268
1092b	269		1784a	270		1511b	271		1812b	272
1885c	273		1619a	274		2344a	275		1477a	276
360a	277		568a	278		1109a	279		1282b	280
1276a	281		1728a	282		1923b	283		2020b	284
556b	285		1711a	286		49a	287		1271a	288
1497c	289		967b	290		1329a	291		464b	292
1490a	293		188b	294		178a	295		631b	296
1244b	297		758b	298		1807a	299		276a	300
204a	301		543a	302		1764a	303		711a	304
35c	305		1401c	306		3c	307		494a	308
1616a	309		1070b	310		1928a	311		597c	312
1505c	313		1941e	314		742a	315		1299c	316
1960a	317		1191a	318		562a	319		2223a	320
2099a	321		342a	322		1347b	323		738b	324
1744a	325		1918a	326		1060a	327		1224b	328
861c	329		2033a	330		1349b	331		715a	332
1621a	333		379a	334		570b	335		1504d	336

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441a	337	1943a	338	1033c	339	1758a	340
1772a	341	1707c	342	1474a	343	1920a	344
34a	345	2205a	346	1712a	347	1010a	348
1382d	349	269b	350	1972a	351	1298a	352
567b	353	949c	354	1545b	355	472a	356
1557a	357	489c	358	1495a	359	1302a	360
18a	361	182a	362	991b	363	1513b	364
992a	365	1032d	366	1373a	367	1400a	368
226a	369	1354a	370	1953a	371	794a	372
1604a	373	1245b	374	192a	375	1398a	376
1651a	377	64.2a	378	2161c	379	1618b	380
1516a	381	1803a	382	1593b	383	2109a	384
392a	385	1533a	386	1317a	387	1137b	388
51a	389	1708a	390	862c	391	1371a	392
2117b	393	1818a	394	851d	395	2113a	396
99b	397	92c	398	91f	399	90c	400
86.2d	401	86.1d	402	83d	403	80.1b	404
7a	405	78e	406	74c	407	73b	408
6b	409	68a	410	67a	411	66a	412
65.2a	413	63a	414	62c	415	59a	416
57a	417	55a	418	52a	419	50.1c	420
4a	421	43a	422	38a	423	37c	424
35b	425	2b	426	29a	427	27a	428
26a	429	25a	430	22b	431	20a	432
19c	433	16b	434	15b	435	10c	436
102a	437	103a	438	104a	439	106a	440
111a	441	120a	442	121b	443	122c	444
123c	445	124a	446	126a	447	130b	448
131a	449	132a	450	134b	451	135a	452
136b	453	142.1c	454	145b	455	146b	456
147b	457	150a	458	152b	459	157b	460
158a	461	159a	462	161b	463	162b	464
164c	465	165a	466	173a	467	175a	468
176a	469	177b	470	179b	471	180a	472
183a	473	185a	474	186a	475	187b	476
189a	477	190b	478	191a	479	195a	480
196a	481	197b	482	127b	483	105e	484
107.1a	485	107.2a	486	108a	487	109a	488
117.1d	489	117.2b	490	137b	491	140b	492
194a	493	181d	494	198e	495	199d	496
200a	497	201a	498	202a	499	203a	500
205a	501	208c	502	209a	503	210a	504
211b	505	214a	506	215a	507	216a	508
217b	509	218e	510	219g	511	220d	512
221b	513	222b	514	223a	515	224a	516
225a	517	227a	518	228a	519	229a	520
230a	521	231a	522	232a	523	233b	524
234a	525	235a	526	236a	527	237c	528
238a	529	239a	530	240a	531	241a	532
242a	533	243a	534	245a	535	246a	536
247a	537	248a	538	249a	539	250a	540
251a	541	252a	542	253b	543	254a	544
255a	545	257a	546	258a	547	260c	548
261c	549	262c	550	263b	551	266d	552
267d	553	268b	554	270b	555	273a	556
274b	557	275b	558	277a	559	278a	560
280c	561	282d	562	283a	563	284b	564
285b	565	286a	566	289a	567	291a	568
292b	569	294a	570	295a	571	296a	572

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299a	573		301b	574		302a	575		499a	576
498a	577		497a	578		496c	579		495a	580
491a	581		359a	582		351b	583		344a	584
343b	585		338a	586		337c	587		336a	588
335a	589		334a	590		328b	591		325b	592
324a	593		312a	594		311c	595		309a	596
308c	597		307b	598		306b	599		303a	600
300b	601		163a	602		573b	603		561b	604
560b	605		559c	606		554c	607		551b	608
549a	609		542a	610		540a	611		539a	612
538a	613		537c	614		536a	615		535a	616
534b	617		533b	618		527a	619		526a	620
521b	621		520a	622		519a	623		517c	624
516c	625		515a	626		514a	627		513a	628
512b	629		509b	630		508a	631		505b	632
504a	633		503a	634		502a	635		501b	636
500a	637		345b	638		362b	639		364a	640
367a	641		369a	642		371a	643		374a	644
377b	645		378a	646		381a	647		386b	648
389c	649		390a	650		391a	651		393b	652
397b	653		455c	654		456c	655		457c	656
458b	657		459a	658		462b	659		466b	660
474a	661		478a	662		480a	663		483a	664
484a	665		485f	666		486a	667		487a	668
488a	669		545a	670		548c	671		558a	672
571a	673		572b	674		578c	675		579a	676
582c	677		584b	678		587b	679		590a	680
595a	681		684a	682		685a	683		686b	684
687a	685		688a	686		691a	687		692a	688
695a	689		696a	690		697a	691		698a	692
699a	693		700a	694		701a	695		702a	696
704b	697		706b	698		708a	699		709a	700
710a	701		712a	702		714a	703		716b	704
717b	705		719a	706		720a	707		722b	708
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728b	713		730b	714		732a	715		733a	716
734a	717		740b	718		741b	719		743a	720
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759b	729		761a	730		762a	731		763d	732
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775a	737		780a	738		781a	739		783a	740
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789a	745		791b	746		792a	747		797a	748
798a	749		799a	750		969a	751		968a	752
966a	753		964a	754		963c	755		959a	756
957c	757		956d	758		953a	759		952a	760
946a	761		944d	762		943b	763		942b	764
939a	765		938b	766		935b	767		934b	768
931a	769		930a	770		928a	771		927a	772
926a	773		925a	774		923a	775		921c	776
919b	777		918a	778		916c	779		915a	780
914a	781		913a	782		912b	783		911a	784
910c	785		909a	786		906a	787		905a	788
904a	789		902a	790		900a	791		899a	792
896b	793		894b	794		893a	795		891a	796
885a	797		883c	798		843a	799		841b	800
839a	801		838b	802		837c	803		836a	804
834b	805		833a	806		832a	807		831a	808

828a	809		826b	810		824b	811		823a	812
821a	813		820a	814		817a	815		816a	816
815a	817		813a	818		811a	819		808b	820
1633a	821		1632a	822		1627a	823		1625b	824
1614b	825		1613b	826		1607a	827		1605b	828
1544b	829		1526a	830		1524a	831		1522b	832
1520a	833		1519a	834		1518a	835		1514a	836
1512a	837		1508b	838		1507a	839		1493a	840
1492a	841		1487b	842		1486d	843		1482a	844
1480a	845		1476a	846		1469a	847		1466b	848
1460a	849		1459c	850		1422a	851		1418a	852
1409b	853		1407a	854		1406a	855		1402b	856
1399a	857		1397b	858		1369c	859		1364d	860
1325b	861		1324a	862		1321a	863		1318a	864
1316b	865		1312a	866		1301a	867		1289a	868
1285a	869		1277a	870		1273b	871		1272a	872
1269b	873		1267a	874		1266a	875		1263b	876
1251a	877		1195a	878		1194a	879		1193b	880
1192b	881		1189a	882		1188b	883		1185a	884
1184a	885		1183a	886		1182a	887		1178a	888
1175a	889		1172a	890		1171a	891		1170a	892
1167b	893		1166b	894		1132a	895		1126b	896
1117a	897		1111b	898		1104b	899		1103a	900
1101a	901		1048c	902		1023c	903		1014d	904
1009c	905		1239b	906		1240a	907		1243a	908
1368a	909		1370a	910		1383a	911		408a	912
415b	913		421a	914		443b	915		863c	916
864c	917		867d	918		870e	919		874e	920
881c	921		940a	922		941a	923		958a	924
975a	925		980b	926		981a	927		987a	928
993b	929		996a	930		1012a	931		1013a	932
1018a	933		1019a	934		1020a	935		1022a	936
1026b	937		1029a	938		1031a	939		1034a	940
1036a	941		1057b	942		1177c	943		1252a	944
1255a	945		1264c	946		1274c	947		1275c	948
1279c	949		1281c	950		1286d	951		1287c	952
1290d	953		1310a	954		1424a	955		1426a	956
1427a	957		1428a	958		1430a	959		1431a	960
1432a	961		1435a	962		1436b	963		1437c	964
1444b	965		1445b	966		1446a	967		1447a	968
1448a	969		1451a	970		1455c	971		1542c	972
1549a	973		1611a	974		1639a	975		1641b	976
1152d	977		1158c	978		1159b	979		1163d	980
1420c	981		1771b	982		1859a	983		1861a	984
1886a	985		1889a	986		1900b	987		1905a	988
2110a	989		2129a	990		2137b	991		2143a	992
2225b	993		2234a	994		2237b	995		2238a	996
2239b	997		2248a	998		2267a	999		436c	1000
446f	1001		524a	1002		525f	1003		529b	1004
541b	1005		547c	1006		563a	1007		564a	1008
565a	1009		566a	1010		575b	1011		589a	1012
591a	1013		609a	1014		610a	1015		611a	1016
612b	1017		614a	1018		617a	1019		620a	1020
622a	1021		623a	1022		624b	1023		625a	1024
626a	1025		629a	1026		630a	1027		632a	1028
633a	1029		634a	1030		637c	1031		640b	1032
641a	1033		642a	1034		825d	1035		846a	1036
847a	1037		852a	1038		948a	1039		1242a	1040
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1731a	1069		1748b	1070		1749a	1071		1750a	1072
1751a	1073		1816a	1074		1880a	1075		1884a	1076
1887a	1077		1895b	1078		1903a	1079		1912a	1080
1914b	1081		1921a	1082		1967a	1083		1968a	1084
1977a	1085		1979a	1086		1981a	1087		1982a	1088
1986b	1089		1987a	1090		1988a	1091		1990a	1092
1992b	1093		1994a	1094		2073b	1095		2075a	1096
2076c	1097		2078a	1098		2086a	1099		2092c	1100
2093a	1101		2094a	1102		2097a	1103		2100b	1104
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2150a	1117		2154a	1118		2158c	1119		2160a	1120
2162b	1121		2167a	1122		2170a	1123		2171c	1124
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445e	1129		856c	1130		1216a	1131		1705a	1132
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1971b	1145		2095a	1146		2144a	1147		2146a	1148
384c	1149		600e	1150		878c	1151		1011a	1152
1021a	1153		1025a	1154		1037c	1155		1039c	1156
1040b	1157		1058a	1158		1059a	1159		1061a	1160
1062a	1161		1063b	1162		1064a	1163		1068a	1164
1069a	1165		1071b	1166		1072a	1167		1073a	1168
1121a	1169		1122b	1170		1130a	1171		1134a	1172
1135a	1173		1136b	1174		1176a	1175		1180a	1176
1190b	1177		1204a	1178		1208a	1179		1215b	1180
1217a	1181		1227b	1182		1236a	1183		1249a	1184
1297a	1185		1308c	1186		1314a	1187		1355a	1188
1361a	1189		1363b	1190		1386a	1191		1388a	1192
1390a	1193		1391a	1194		1417a	1195		1510a	1196
1536b	1197		1537c	1198		1546b	1199		1547c	1200
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1596b	1209		1597a	1210		1598a	1211		1599a	1212
1600a	1213		1601a	1214		1602a	1215		1603a	1216
1609c	1217		1617a	1218		1626c	1219		1628a	1220
1637c	1221		1642a	1222		1657a	1223		1661a	1224
1662a	1225		1663a	1226		1665a	1227		1671b	1228
1672a	1229		1688c	1230		1691b	1231		1715a	1232
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2204b	1241		2230a	1242		1035a	1243		1124a	1244
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1087c	1257		1093b	1258		1094b	1259		1102a	1260
1106a	1261		1108a	1262		1112a	1263		1116a	1264
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1341a	1269		1449a	1270		1457b	1271		1458a	1272
1479a	1273		1485b	1274		1489a	1275		1499a	1276
1501a	1277		1509a	1278		1525a	1279		1531c	1280

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1534b	1281	1535a	1282	1828b	1283	1834b	1284
1927a	1285	1929c	1286	1937c	1287	1942b	1288
1944a	1289	1946b	1290	1947a	1291	1948b	1292
1950a	1293	1952a	1294	1956a	1295	1958b	1296
2003a	1297	2021a	1298	2022a	1299	2023b	1300
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2056d	1305	2065a	1306	2070a	1307	1334a	1308
1453a	1309	2066b	1310	1737b	1311	1741a	1312
1779b	1313	1891a	1314	1911b	1315	1922a	1316
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1378b	1345	1376a	1346	995a	1347	989a	1348
2258a	1349	2084c	1350	1250a	1351	1002b	1352
583e	1353	2229a	1354	1001a	1355	1002b	1356
1003a	1357	1004a	1358	1005a	1359	1006b	1360
1007a	1361	1042a	1362	1044c	1363	1045a	1364
1099c	1365	1120a	1366	1125a	1367	1212b	1368
1225b	1369	1226d	1370	1304a	1371	1322c	1372
1515c	1373	1527a	1374	1528b	1375	1539c	1376
1541a	1377	1561a	1378	1690a	1379	1692a	1380
1736b	1381	1763b	1382	1766a	1383	1777a	1384
1883b	1385	1888c	1386	1898a	1387	2043b	1388
2045d	1389	2130b	1390	2139a	1391	213a	1392 /
2140b	1393	2165a	1394	2199a	1395	2210a	1396
2254a	1397	2264b	1398	2268a	1399	265a	1400
365b	1401	492a	1402	550a	1403	635a	1404
726b	1405	750b	1406	772b	1407	776a	1408
777a	1409	793a	1410	800b	1411	801b	1412
803b	1413	804a	1414	806b	1415	827b	1416
855c	1417	877e	1418	880e	1419	932b	1420
933b	1421	984a	1422	986a	1423	988b	1424
989a	1425	997a	1426	1016b	1427	1027a	1428
1030a	1429	1038b	1430	1052b	1431	1053a	1432
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1165d	1437	1260c	1438	1315c	1439	1348b	1440
1352b	1441	1360b	1442	1387b	1443	1403a	1444
1413b	1445	1416a	1446	1419a	1447	1442d-r	1448
1443a	1449	1450a	1450	1483a	1451	1562a	1452
1564a	1453	1565c	1454	1567a	1455	1568a	1456
1569b	1457	1570a	1458	1572a	1459	1573a	1460
1574b	1461	1575a	1462	1576a	1463	1577a	1464
1578a	1465	1579a	1466	1580b	1467	1581a	1468
1583a	1469	1584a	1470	1585b	1471	1586a	1472
1628d	1473	1630b	1474	1666d	1475	1669d	1476
1670d	1477	1755a	1478	1759b	1479	1760c	1480
1775a	1481	1778c	1482	1780a	1483	1809a	1484
1846d	1485	1849d	1486	1852a	1487	1863c	1488
1864b	1489	1865e	1490	1879a	1491	1894a	1492
1906a	1493	1961e	1494	1966a	1495	1989b	1496
1991d	1497	2008a	1498	2013a	1499	2014f	1500
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2043b	1505	2044a	1506	2045d	1507	2046a	1508
2048a	1509	2101c	1510	2107b	1511	2124a-r	1512
2235a	1513	2240a	1514	2251d	1515	2271a	1516

2341b	1517		2356a	1518		2358b	1519		2371a	1520
2373a	1521		322a	1522		805a	1523		924a	1524
965a	1525		898a	1526		879c	1527		865e	1528
627b	1529		406a-r	1530		321a	1531		320a	1532
319b	1533		317a	1534		315a	1535		314a	1536
313a	1537		2249a	1538		2189b	1539		2134b	1540
2125a	1541		1811b	1542		1553b	1543		1393b	1544
1389b	1545		1377b	1546		1356a	1547		1353a	1548
1041a	1549		1635a	1550		1385b	1551		1365a	1552
50.2b	1553		48b	1554		440a	1555		413a	1556
2123a	1557		1323br	1558						

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

Definitions:

[0014] The following definitions are provided to facilitate an understanding of the present invention:

[0015] "Nucleic acid" or a "nucleic acid molecule" as used herein refers to any DNA or RNA molecule, either single or double stranded and, if single stranded, the molecule of its complementary sequence in either linear or circular form. In discussing nucleic acid molecules, a sequence or structure of a particular nucleic acid molecule may be described herein according to the normal convention of providing the sequence in the 5' to 3' direction. With reference to nucleic acids according to aspects of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA molecule that is separated from sequences with which it is immediately contiguous in the naturally occurring genome of the organism in which it originated. For example, an "isolated nucleic acid" may comprise a DNA molecule inserted into a vector, such as a plasmid or virus vector, or integrated into the genomic DNA of a prokaryotic or eukaryotic cell or host organism.

[0016] When applied to RNA, the term "isolated nucleic acid" refers primarily to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively, the term may refer to an RNA molecule that has been sufficiently separated from other nucleic acids with which it would be associated in its natural state (i.e., in cells or tissues). An isolated nucleic acid (either DNA or RNA) may further represent a molecule produced directly by biological or synthetic means and separated from other components present during its production.

[0017] The terms "percent similarity", "percent identity" and "percent homology" when referring to a particular sequence are used as set forth in the University of Wisconsin GCG software program.

[0018] A "polynucleotide," "polynucleotide molecule" or "polynucleotide sequence" refers to a chain of nucleotides. It may refer to a DNA or RNA molecule, either single or double

stranded and, if single stranded, the molecule of its complementary sequence in either linear or circular form. Preferably, the chain has from about 50 to 10,000 nucleotides, more preferably from about 150 to 3,500 nucleotides. In some instances, the sequences will be fully complementary (no mismatches) when aligned. In other instances, there may be up to about a 30% mismatch in the sequences.

[0019] The term "oligonucleotide," as used herein refers to sequences, primers and probes of the present invention, and is defined as a nucleic acid molecule comprised of two or more ribo or deoxyribonucleotides, preferably more than three. The exact size of the oligonucleotide will depend on various factors and on the particular application and use of the oligonucleotide.

[0020] A "fragment" refers to a nucleic acid sequence that is preferably at least about 10 nucleic acids in length, more preferably about 40 nucleic acids, and most preferably about 100 nucleic acids in length and encompasses, for example, fragments consisting of nucleic acids 1-100, 300-400, 500-600, 800-900 of SEQ ID NOs:1-1558 or fragments of similar length at the 3' end of SEQ ID NOs:1-1558. A "fragment" can also mean a stretch of at least about 100 consecutive nucleotides that contains one or more deletions, insertions or substitutions. A "fragment" can also mean the whole coding sequence of a gene and may include 5' and 3' untranslated regions. A "fragment" can also refer to polypeptide sequences which are preferably at least about 5 to about 15 amino acids in length, most preferably at least about 10 amino acids long, and which retain some biological activity or immunological activity of a sequence.

[0021] The term "gene" or "genes" refers to the partial or complete coding sequence of a gene. The term also refers to 5' or 3' untranslated regions of a transcript. The phrase "gene differentially expressed in osteoarthritis" refers to a gene whose amount of mRNA expressed from that gene or the amount of gene product translated from the mRNA is detectably different, i.e. either greater or lesser, in cells from subjects having osteoarthritis or in pre-osteoarthritic subjects compared to the amount of mRNA or translated gene product in cells from normal subjects which are neither osteoarthritic nor pre-osteoarthritic. As used herein, "pre-osteoarthritis" or "pre-osteoarthritic" is intended to mean that a subject is predisposed to developing osteoarthritis at a later date, but may not have any overt signs or symptoms of osteoarthritis. Preferably, the abundance of transcription or translation products of a differentially expressed gene derived from an osteoarthritic or pre-osteoarthritic sample differs by least about 1.15 fold, more preferably at least about 1.2 fold, more preferably at least about 1.3 fold, more preferably at least about 1.4 fold, more preferably at least about 1.5 fold, , more preferably at least about 1.6 fold, more preferably at least about 1.75 fold, more preferably at

least about 2 fold, more preferably at least about 3 fold, more preferably at least about 10 fold, more preferably at least about 20 fold than that in a normal sample. The phrase "gene differentially expressed in osteoarthritis" also refers to genes that are not detectable in the normal transcript profile but are preferably at levels of at least about 2 copies per cell, more preferably at least about 3 copies per cell, in the osteoarthritic or pre-osteoarthritic tissue transcript profile.

[0022] The terms "osteoarthritis (OA)-related" and "osteoarthritis (OA)-associated genes" refer to genes that are differentially expressed in osteoarthritis as defined herein.

[0023] As used herein, the terms "reporter," "reporter system," "reporter gene," or "reporter gene product" refer to an operative genetic system in which a nucleic acid comprises a gene that encodes a product that when expressed produces a reporter signal that is a readily measurable, e.g., by biological assay, immunoassay, radioimmunoassay, or by colorimetric, fluorogenic, chemiluminescent or other methods. The nucleic acid may be either RNA or DNA, linear or circular, single or double stranded, antisense or sense polarity, and is operatively linked to the necessary control elements for the expression of the reporter gene product. The required control elements will vary according to the nature of the reporter system and whether the reporter gene is in the form of DNA or RNA, but may include, but not be limited to, such elements as promoters, enhancers, translational control sequences, poly A addition signals, transcriptional termination signals and the like.

[0024] The terms "transform," "transfect," "transduce," refer to any method or means by which a nucleic acid is introduced into a cell or host organism and may be used interchangeably to convey the same meaning. Such methods include, but are not limited to, transfection, electroporation, microinjection, PEG-fusion and the like.

[0025] The term "functional" as used herein implies that the nucleic or amino acid sequence is functional for the recited assay or purpose.

[0026] The phrase "consisting essentially of" when referring to a particular nucleotide or amino acid means a sequence having the properties of a given SEQ ID NO. For example, when used in reference to an amino acid sequence, the phrase includes the sequence *per se* and molecular modifications that would not affect the basic and novel characteristics of the sequence.

[0027] A "vector" is a replicon, such as a plasmid, cosmid, bacmid, phage, artificial chromosome (BAC, YAC) or virus, into which another genetic sequence or element (either DNA or RNA) may be inserted so as to bring about the replication of the attached sequence or element. A "replicon" is any genetic element, for example, a plasmid, cosmid, bacmid, phage, artificial chromosome (BAC, YAC) or virus, that is capable of replication largely under its own control. A replicon may be either RNA or DNA and may be single or double stranded.

[0028] The term "probe" as used herein refers to either a probe for a nucleic acid or a probe for a protein. When used in connection with nucleic acids, a "probe" refers to an oligonucleotide, polynucleotide or nucleic acid, either RNA or DNA, whether occurring naturally as in a purified restriction enzyme digest or produced synthetically, which is capable of annealing with or specifically hybridizing to a nucleic acid with sequences complementary to the probe. A probe may be either single stranded or double stranded. The exact length of the probe will depend upon many factors, including temperature, source of probe and method of use. For example, for diagnostic applications, depending on the complexity of the target sequence, an oligonucleotide probe typically contains about 10-100, preferably about 15-50, more preferably about 15-25 nucleotides. In certain diagnostic applications, a polynucleotide probe preferably contains about 90-1150 nucleotides, more preferably about 300-600 nucleotides, more preferably about 300 nucleotides. The probes herein are selected to be "substantially" complementary to different strands of a particular target nucleic acid sequence. This means that the probes must be sufficiently complementary so as to be able to "specifically hybridize" or anneal with their respective target strands under a set of pre-determined conditions. Therefore, the probe sequence need not reflect the exact complementary sequence of the target. For example, a non complementary nucleotide fragment may be attached to the 5' or 3' end of the probe, with the remainder of the probe sequence being complementary to the target strand. Alternatively, non complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the sequence of the target nucleic acid to anneal therewith specifically. When used in connection with a protein, a "probe" is a protein binding substance capable of specifically binding a particular protein or protein fragment to the substantial exclusion of other proteins or protein fragments. Such binding substances may be any molecule to which the protein or peptide specifically binds, including DNA (for DNA binding proteins), antibodies (as described in greater detail herein), cell membrane receptors, peptides, cofactors, lectins, sugars, polysaccharides, cells, cell membranes, organelles and organellar membranes.

[0029] "Array" refers to an ordered arrangement of at least two probes on a substrate. At least one of the probes represents a control or standard, and the other, a probe of diagnostic interest. The arrangement of from about two to about 40,000 probes on a substrate assures that the size and signal intensity of each labeled complex formed between a probe and a sample nucleic acid or protein binding substance is individually distinguishable.

[0030] A "hybridization complex" is formed between nucleic acid molecules of a sample when the purines of one molecule hydrogen bond with the pyrimidines of the

complementary molecule, e.g., 5'-A-G-T-C-3' base pairs with 3'-T-C-A-G-5'. The degree of complementarity and the use of nucleotide analogs affect the efficiency and stringency of hybridization reactions.

[0031] The term "specifically hybridize" refers to the association between two single stranded nucleic acid molecules of sufficiently complementary sequence to permit such hybridization under pre determined conditions generally used in the art (sometimes termed "substantially complementary"). For example, the term may refer to hybridization of a nucleic acid probe with a substantially complementary sequence contained within a single stranded DNA or RNA molecule according to an aspect of the invention, to the substantial exclusion of hybridization of the nucleic acid probe with single stranded nucleic acids of non-complementary sequence.

[0032] "Sample" is used in its broadest sense as containing nucleic acids, proteins, antibodies, and the like. A sample may comprise, for example, a bodily fluid; the soluble fraction of a cell preparation, or an aliquot of media in which cells were grown; a chromosome, an organelle, or membrane isolated or extracted from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; a cell; a tissue or a tissue biopsy; a tissue print; a fingerprint, buccal cells, skin, or hair; and the like.

[0033] A "standard" refers to a control sample that comprises material from a source in a normal (as opposed to OA-related) biological state. An OA-related biological state may include, for example, one in which the source has OA, is predisposed to develop OA, or exhibits certain biological characteristics of OA. For example, a standard sample may comprise nucleic acids or proteins from a normal subject that is not osteoarthritic or pre-osteoarthritic. Standard samples may also include samples from normal cells or tissue that have not been treated to elicit an immune response that may model certain aspects of OA.

[0034] "Specific binding" refers to a special and precise interaction between two molecules which is dependent upon their structure, particularly their molecular side groups. For example, the intercalation of a regulatory protein into the major groove of a DNA molecule, the hydrogen bonding along the backbone between two single stranded nucleic acids, or the binding between an epitope of a protein and an agonist, antagonist, or antibody.

[0035] The term "primer" as used herein refers to a nucleic acid molecule, either RNA or DNA, either single stranded or double stranded, either derived from a biological system, generated by restriction enzyme digestion, or produced synthetically which, when placed in the proper environment, is able to functionally act as an initiator of template-dependent nucleic acid synthesis. When presented with an appropriate nucleic acid template, suitable nucleoside

triphosphate precursors of nucleic acids, a polymerase enzyme, suitable cofactors and conditions such as appropriate temperature and pH, the primer may be extended at its 3' terminus by the addition of nucleotides by the action of a polymerase or similar activity to yield an primer extension product. The primer may vary in length depending on the particular conditions and requirement of the application. For example, in diagnostic applications according to particular embodiments of the invention, a primer may be an oligonucleotide primer, preferably about 15 - 25 or more nucleotides in length. The primer must be of sufficient complementarity to the desired template to prime the synthesis of the desired extension product, that is, to be able anneal with the desired template strand in a manner sufficient to provide the 3' hydroxyl moiety of the primer in appropriate juxtaposition for use in the initiation of synthesis by a polymerase or similar enzyme. It is not required that the primer sequence represent an exact complement of the desired template. For example, a non complementary nucleotide sequence may be attached to the 5' end of an otherwise complementary primer. Alternatively, non complementary bases may be interspersed within the oligonucleotide primer sequence, provided that the primer sequence has sufficient complementarity with the sequence of the desired template strand to functionally provide a template primer complex for the synthesis of the extension product.

[0036] Amino acid residues described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form may be substituted for any L amino acid residue, provided the desired properties of the polypeptide are retained. All amino acid residue sequences represented herein conform to the conventional left-to-right amino terminus to carboxy terminus orientation.

[0037] A "fragment" or "portion" of a polypeptide means a stretch of amino acid residues of at least about five to seven contiguous amino acids, often at least about seven to nine contiguous amino acids, typically at least about nine to thirteen contiguous amino acids and, most preferably, at least about twenty to thirty or more contiguous amino acids. Fragments of the polypeptide sequence, antigenic determinants, or epitopes are useful for eliciting immune responses to a portion of the protein amino acid sequence.

[0038] Different "variants" of the differentially expressed polypeptides exist in nature. These variants may be alleles characterized by differences in the nucleotide sequences of the gene coding for the protein, or may involve different RNA processing or post translational modifications. The skilled person can produce variants having single or multiple amino acid substitutions, deletions, additions or replacements. These variants may include, *inter alia*: (a) variants in which one or more amino acids residues are substituted with conservative or non conservative amino acids, (b) variants in which one or more amino acids are added to the

polypeptide, (c) variants in which one or more amino acids include a substituent group, and (d) variants in which the polypeptide is fused with another peptide or polypeptide such as a fusion partner, a protein tag or other chemical moiety, that may confer useful properties to the polypeptide, such as, for example, an epitope for an antibody, a polyhistidine sequence, a biotin moiety and the like. Other polypeptides of the invention may include variants in which amino acid residues from one species are substituted for the corresponding residue in another species, either at the conserved or non conserved positions. In another embodiment, amino acid residues at non conserved positions are substituted with conservative or non conservative residues. The techniques for obtaining these variants, including genetic (suppressions, deletions, mutations, etc.), chemical, and enzymatic techniques are known to the person having ordinary skill in the art. To the extent such allelic variations, analogues, fragments, derivatives, mutants, and modifications, including alternative nucleic acid processing forms and alternative post translational modification forms result in derivatives of the differentially expressed polypeptide that retain any of the biological properties of the differentially expressed polypeptide, they are included within the scope of this invention.

[0039] The term "isolated protein" or "isolated and purified protein" refers primarily to a protein produced by expression of an isolated nucleic acid molecule according to an aspect the invention. Alternatively, this term may refer to a protein that has been sufficiently separated from other proteins with which it would naturally be associated, so as to exist in "substantially pure" form. "Isolated" is not meant to exclude artificial or synthetic mixtures with other compounds or materials, or the presence of impurities that do not interfere with the fundamental activity, and that may be present, for example, due to incomplete purification, addition of stabilizers, or compounding into, for example, immunogenic preparations or pharmaceutically acceptable preparations.

[0040] The term "substantially pure" refers to a preparation comprising at least about 50-60% by weight of a given material (e.g., nucleic acid, protein, etc.). More preferably, the preparation comprises at least about 75% by weight, and most preferably about 90-95% by weight of the given compound. Purity is measured by methods appropriate for the given material (e.g. chromatographic methods, agarose or polyacrylamide gel electrophoresis, HPLC analysis, and the like).

[0041] The term "tag," "tag sequence" or "protein tag" refers to a chemical moiety, either a nucleotide, oligonucleotide, polynucleotide or an amino acid, peptide or protein or other chemical, that when added to another sequence, provides additional utility or confers useful properties, particularly in the detection or isolation, of that sequence. Thus, for example, a

homopolymer nucleic acid sequence or a nucleic acid sequence complementary to a capture oligonucleotide may be added to a primer or probe sequence to facilitate the subsequent isolation of an extension product or hybridized product. In the case of protein tags, histidine residues (e.g., 4 to 8 consecutive histidine residues) may be added to either the amino or carboxy terminus of a protein to facilitate protein isolation by chelating metal chromatography. Alternatively, amino acid sequences, peptides, proteins or fusion partners representing epitopes or binding determinants reactive with specific antibody molecules or other molecules (e.g., flag epitope, c myc epitope, transmembrane epitope of the influenza A virus hemagglutinin protein, protein A, cellulose binding domain, calmodulin binding protein, maltose binding protein, chitin binding domain, glutathione S transferase, and the like) may be added to proteins to facilitate protein isolation by procedures such as affinity or immunoaffinity chromatography. Chemical tag moieties include such molecules as biotin, which may be added to either nucleic acids or proteins and facilitates isolation or detection by interaction with avidin reagents, and the like. Numerous other tag moieties are known to, and can be envisioned by, the trained artisan, and are contemplated to be within the scope of this definition.

[0042] An "antibody" or "antibody molecule" is any immunoglobulin, including antibodies and fragments thereof, that binds to a specific antigen. The term includes polyclonal, monoclonal, chimeric, and bispecific antibodies. As used herein, antibody or antibody molecule contemplates both an intact immunoglobulin molecule and an immunologically active portion of an immunoglobulin molecule such as those portions known in the art as Fab, Fab', F(ab')₂ and F(v).

[0043] As used herein, the term "subject" or "patient" refers to both humans and animals, unless specified that the "subject" or "patient" is an animal or a human. Animal subjects are preferably vertebrates, and more preferably, mammals.

[0044] "Therapeutic modality" refers to any means of treating and/or preventing a disease, condition or disorder.

[0045] In one aspect of the present invention, a number of genes have been identified that are differentially expressed in osteoarthritic subjects as compared to non-osteoarthritic subjects. These genes and gene fragments, as well as their encoded proteins and fragments, may be used, for example, in a variety of diagnostic and prognostic assays, as well as assays useful in screening test substances for effectiveness in treatment modalities for osteoarthritis.

[0046] In certain embodiments of the invention, expression of at least one differentially expressed gene may be measured. In preferred embodiments, expression of two or more differentially expressed genes may be measured, providing a gene expression pattern or gene

expression profile. More preferably, measurement of a multiplicity of differentially expressed genes may be performed, providing additional information for a gene expression pattern or profile.

[0047] In various embodiments of the present invention, changes in gene expression may be measured in one or both of two ways: (1) measuring transcription through detection of mRNA produced by a particular gene; and (2) measuring translation through detection of protein produced by a particular transcript.

[0048] Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, PCR (including, without limitation, RT-PCR and qPCR), RNase protection, Northern blotting and other hybridization methods. The genes that are assayed or interrogated according to the present invention are typically in the form of mRNA or reverse transcribed mRNA. The genes may be cloned and/or amplified. The cloning itself does not appear to bias the representation of genes within a population. However, it may be preferable to use polyA+ RNA as a source, as it can be used with fewer processing steps.

[0049] In accordance with aspects of the present invention, 1558 genes have been identified whose functions are closely associated with osteoarthritis (OA). The association is determined by comparing expression of the genes in normal tissue and tissue from subjects diagnosed with OA. The genes so identified fall into two broad categories. The first category comprises known genes, many of whose association with OA had heretofore been unappreciated. These genes are listed in Table 6, along with their corresponding gene ID numbers and SEQ ID NOs.

[0050] According to another aspect of the invention, a second category comprises nucleic acid segments that do not demonstrate homology to previously identified sequences. Thus, this category is believed to include one or more novel genes. One preferred embodiment of the invention relates to an isolated nucleic acid molecule comprising a novel OA-associated gene, mRNA or cDNA produced from the OA-associated gene.

[0051] One aspect of the present invention relates to a combination of 1558 polynucleotide molecules that are differentially expressed in an osteoarthritic subject or in a pre-osteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic. In one embodiment of the invention described herein, segments of 1558 OA-related genes from canine cartilage were obtained by employing differential display. The nucleotide sequences of these polynucleotides are set forth herein as SEQ ID NOs:1-1558 (Table 1 shows the correlation between SEQ ID NO. and Gene ID Number). BLAST analysis of these

sequences identified homologies with of a number of nucleic acid sequences previously identified (Table 2) These include a number of previously identified nucleic acid sequences with no identified homologies to known genes. BLAST analysis also identified sequences showing homology to previously-identified genes; information including names of genes as well as database accession numbers for respective homologs of these is provided in Tables 2A and 2B.

Table 2A

CaMax Gene ID	Ensemble Gene ID	Ensemble Transcript ID	Description	Chrom No.	Chrom Loc.
CaMax: 1002b					
CaMax: 1002b					
CaMax: 1005a	ENSG00000138709	ENST00000264584 ENST00000326703 ENST00000326639		4	q28.2
CaMax: 1006b	ENSG00000152518	ENST00000282388	BUTYRATE RESPONSE FACTOR 2 (TIS11D PROTEIN) (EGF-RESPONSE FACTOR 2) (ERF-2). [Source:SWISSPROT;Acc:P47974]	2	p21
CaMax: 1007a	ENSG00000152518	ENST00000282388	BUTYRATE RESPONSE FACTOR 2 (TIS11D PROTEIN) (EGF-RESPONSE FACTOR 2) (ERF-2). [Source:SWISSPROT;Acc:P47974]	2	p21
CaMax: 1008a					
CaMax: 1008a					
CaMax: 1009c	ENSG00000122912	ENST00000265870	GRAVE'S DISEASE CARRIER PROTEIN (GDC) (GRAVE'S DISEASE AUTOANTIGEN) (GDA) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:P16260]	10	q21.3
CaMax: 1011a					
CaMax: 1011a					
CaMax: 1013a					
CaMax: 1015d	ENSG00000109775	ENST00000264689		4	q35.1
CaMax: 1016b					
CaMax: 1019a	ENSG00000160961	ENST00000292530	ZINC FINGER PROTEIN 333. [Source:SWISSPROT;Acc:Q96JL9]	19	p13.12
CaMax: 1020a	ENSG00000064989	ENST00000264152	CALCITONIN GENE-RELATED PEPTIDE TYPE 1 RECEPTOR PRECURSOR	2	q32.1

			(CGRP TYPE 1 RECEPTOR). [Source:SWISSPROT;Acc:Q16602]		
CaMax: 1026b					
CaMax: 1026b					
CaMax: 1028c					
CaMax: 1028c					
CaMax: 1029a	ENSG00000171567	ENST00000304782	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	2	q37.1
CaMax: 103a					
CaMax: 1044c	ENSG00000041880	ENST00000045065	POLY [ADP-RIBOSE] POLYMERASE-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP- RIBOSYLTRANSFERASE-3) (POLY[ADP-RIBOSE] SYNTHETASE-3) (PADPRT- 3) (HARP-3) (IRT1). [Source:SWISSPROT;Acc:Q9Y6F1]	3	p21.2
CaMax: 104a	ENSG00000169045	ENST00000326748 ENST00000329433	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H (HNRNP H). [Source:SWISSPROT;Acc:P31943]	5	q35.3
CaMax: 1050a					
CaMax: 1054a					
CaMax: 1057b					
CaMax: 1060a					
CaMax: 1061a	ENSG00000138336	ENST00000260906	LEUKEMIA-ASSOCIATED PROTEIN WITH A CXXC DOMAIN. [Source:SPTREMBL;Acc:Q8NFU7]	10	q21.3
CaMax: 1063b					
CaMax: 106a	ENSG00000167996	ENST00000301775	FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). [Source:SWISSPROT;Acc:P02794]	11	q12.3
CaMax: 1070b					
CaMax: 1072a					
CaMax: 1072a					
CaMax:					

1089d					
CaMax: 108a					
CaMax: 1090d					
CaMax: 1094b					
CaMax: 1094b					
CaMax: 1095a	ENSMUSG0000003 0693	ENSMUST0000003 2941 ENSMUST0000001 4058		7	B2
CaMax: 1096a	ENSMUSG0000003 0693	ENSMUST0000003 2941 ENSMUST0000001 4058		7	B2
CaMax: 1098a	ENSG00000135426	ENST00000316577 ENST00000257883		12	q13.2
CaMax: 109a	ENSG00000138688	ENST00000264501 ENST00000306802		4	q27
CaMax: 1105a	ENSG00000119396	ENST00000238339	RAS-RELATED PROTEIN RAB-14. [Source:SWISSPROT;Acc:P35 287]	9	q33.2
CaMax: 1106a	ENSG00000155755	ENST00000286196		2	q33.1
CaMax: 1108a	ENSG00000133121	ENST00000255486	STAR-RELATED LIPID TRANSFER PROTEIN 13 (STARD13) (START DOMAIN- CONTAINING PROTEIN 13) (46H23.2). [Source:SWISSPROT;Acc:Q9 Y3M8]	13	q13.1
CaMax: 1110b					
CaMax: 1110b					
CaMax: 1111b	ENSG00000080546	ENST00000302071 ENST00000237504	SESTRIN 1 (P53- REGULATED PROTEIN PA26). [Source:SWISSPROT;Acc:Q9 Y6P5]	6	q21
CaMax: 1112a	ENSG00000113391	ENST00000265139		5	q15
CaMax: 111a					
CaMax: 1120a	ENSG00000113384	ENST00000265070	GOLGI PHOSPHOPROTEIN 3; GOLGI PROTEIN; GOLGI PERIPHERAL MEMBRANE PROTEIN 1, 34 KDA; GOLGI- ASSOCIATED PROTEIN; COAT-PROTEIN. [Source:RefSeq;Acc:NM_0221 30]	5	p13.3
CaMax: 1121a	ENSG00000185511	ENST00000332847		2	p16.3
CaMax: 1131b					
CaMax: 1132a					

CaMax: 1134a	ENSG00000081189	ENST00000325423	MYOCYTE-SPECIFIC ENHANCER FACTOR 2C. [Source:SWISSPROT;Acc:Q06 413]	5	q14.3
CaMax: 1135a	ENSG00000128573	ENST00000324462 ENST00000265436 ENST00000324544	FORKHEAD BOX PROTEIN P2 (CAG REPEAT PROTEIN 44) (TRINUCLEOTIDE REPEAT- CONTAINING GENE 10 PROTEIN). [Source:SWISSPROT;Acc:O15 409]	7	q31.1
CaMax: 1137b					
CaMax: 1138a					
CaMax: 1139a					
CaMax: 1145a	ENSG00000106817	ENST00000311316	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:P39 059]	9	q22.33
CaMax: 1145a					
CaMax: 1146a					
CaMax: 1159b					
CaMax: 104a	ENSG00000169045	ENST00000326748 ENST00000329433	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H (HNRNP H). [Source:SWISSPROT;Acc:P31 943]	5	q35.3
CaMax: 1169b	ENSG00000140416	ENST00000267996 ENST00000334895 ENST00000288398 ENST00000317516	TROPOMYOSIN 1 ALPHA CHAIN (ALPHA- TROPOMYOSIN). [Source:SWISSPROT;Acc:P09 493]	15	q22.2
CaMax: 1177c	ENSG00000100839	ENST00000262237	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (CYTOPLASMIC DYNEIN HEAVY CHAIN 1) (DHC1) (FRAGMENT). [Source:SWISSPROT;Acc:Q14 204]	14	q32.32
CaMax: 1184a	ENSG00000156299	ENST00000286827	T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN). [Source:SWISSPROT;Acc:Q13 009]	21	q22.11
CaMax: 1184a					
CaMax: 1190b	ENSMUSG0000003 8954	ENSMUST0000004 3985 ENSMUST0000005 0630		17	C
CaMax: 1192b	ENSMUSG0000003 8954	ENSMUST0000004 3985 ENSMUST0000005 0630		17	C

CaMax: 11b					
CaMax: 120a					
CaMax: 120a					
CaMax: 1212b					
CaMax: 1213d	ENSG00000134215	ENST00000280840	VAV-3 PROTEIN. [Source:SWISSPROT;Acc:Q9 UKW4]	1	p13.3
CaMax: 1217a					
CaMax: 1220b					
CaMax: 1226d					
CaMax: 1226d					
CaMax: 123c					
CaMax: 123c					
CaMax: 1243a	ENSG00000065183	ENST00000183319 ENST00000309112	WD-REPEAT PROTEIN 3. [Source:SWISSPROT;Acc:Q9 UNX4]	1	p12
CaMax: 1245b					
CaMax: 1246a	ENSG00000109775	ENST00000264689		4	q35.1
CaMax: 1248b					
CaMax: 1253a	ENSG00000109775	ENST00000264689		4	q35.1
CaMax: 1257b					
CaMax: 1257b					
CaMax: 1260c					
CaMax: 1263b	ENSMUSG0000004 5004	ENSMUST0000005 1907		4	D3
CaMax: 1267a	ENSG00000175198	ENST00000310787	PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.4.1.3) (PCCASE ALPHA SUBUNIT) (PROPANOYL- COA:CARBON DIOXIDE LIGASE ALPHA SUBUNIT). [Source:SWISSPROT;Acc:P05 165]	13	q32.3
CaMax: 1267a	ENSG00000175198	ENST00000310787	PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.4.1.3) (PCCASE ALPHA SUBUNIT) (PROPANOYL- COA:CARBON DIOXIDE LIGASE ALPHA SUBUNIT). [Source:SWISSPROT;Acc:P05	13	q32.3

			165]		
CaMax: 1270a	ENSG00000144331	ENST00000272761		2	q31.2
CaMax: 1272a	ENSG00000113615	ENST00000265341 ENST00000322887	PROTEIN TRANSPORT PROTEIN SEC24A (SEC24- RELATED PROTEIN A) (FRAGMENT). [Source:SWISSPROT;Acc:O95 486]	5	q31.1
CaMax: 1273b					
CaMax: 1276a					
CaMax: 127b					
CaMax: 127b					
CaMax: 1282b					
CaMax: 1284b					
CaMax: 1287c	ENSG00000164190	ENST00000296607 ENST00000282516	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_1334 33]	5	p13.2
CaMax: 1288a	ENSG00000164190	ENST00000296607 ENST00000282516	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_1334 33]	5	p13.2
CaMax: 128a	ENSMUSG0000002 3944	ENSMUST0000002 4739	HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (TUMOR SPECIFIC TRANSPLANTATION 84 KDA ANTIGEN) (TSTA). [Source:SWISSPROT;Acc:P11 499]	17	C
CaMax: 1292c	ENSG00000079246	ENST00000328063	ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (KU86) (KU80) (86 KDA SUBUNIT OF KU ANTIGEN) (THYROID- LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 85 KDA SUBUNIT) (CTCBF) (CTC85) (NUCLEAR FACTOR IV) (DNA-REPAIR PROTEIN XRCC5). [Source:SWISSPROT;Acc:P13 010]	2	q35
CaMax: 1294b	ENSG00000136628	ENST00000259146 ENST00000335149	BIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)]. [Source:SWISSPROT;Acc:P07 814]	1	q41

CaMax: 1299c	ENSG00000163625	ENST00000295888 ENST00000322366	WD REPEAT AND FYVE DOMAIN CONTAINING 3 ISOFORM 1. [Source:RefSeq;Acc:NM_0149 91]	4	q21.23
CaMax: 129b					
CaMax: 129b					
CaMax: 12a					
CaMax: 1301a	ENSMUSG0000004 9076	ENSMUST0000005 8033		16	B2
CaMax: 1304a	ENSG00000168952	ENST00000323944	AMISYN; SYNTAXIN BINDING PROTEIN 6. [Source:RefSeq;Acc:NM_0141 78]	14	q12
CaMax: 1308c					
CaMax: 1308c					
CaMax: 130b					
CaMax: 1316b					
CaMax: 1318a					
CaMax: 1320					
CaMax: 1322c	ENSRNOG0000000 3359		UDP-N- ACETYLGLUCOSAMINE-- PEPTIDE N- ACETYLGLUCOSAMINYLT RANSFERASE 110 KDA SUBUNIT (EC 2.4.1.-) (O- GLCNAC TRANSFERASE P110 SUBUNIT). [Source:SWISSPROT;Acc:P56 558]	21	q31
CaMax: 1323br					
CaMax: 1323br					
CaMax: 1324a					
CaMax: 1324a					
CaMax: 1335b					
CaMax: 1335b					
CaMax: 1341a	ENSG00000166923	ENST00000300177 ENST00000322805	CYSTEINE KNOT SUPERFAMILY 1, BMP ANTAGONIST 1; GREMLIN. [Source:RefSeq;Acc:NM_0133 72]	15	q13.3
CaMax: 1352b					
CaMax: 1354a	ENSG00000171567	ENST00000304782	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE)	2	q37.1

			HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]		
CaMax: 1355a					
CaMax: 1355a					
CaMax: 1361a	ENSG00000033170	ENST00000315759 ENST00000261677	ALPHA-(1,6)- FUCOSYLTRANSFERASE (EC 2.4.1.68) (GLYCOPROTEIN 6-ALPHA- L- FUCOSYLTRANSFERASE) (GDP-FUCOSE-- GLYCOPROTEIN FUCOSYLTRANSFERASE) (GDP-L-FUC:N-ACETYL- BETA-D-GLUCOSAMINIDE ALPHA1,6- FUCOSYLTRANSFERASE) (ALPHA1-6FUCT) (FUCOSYLTRANSFERASE 8). [Source:SWISSPROT;Acc:Q9BYC5]	14	q23.3
CaMax: 1364d					
CaMax: 1364d					
CaMax: 1366a	ENSG00000064205	ENST00000190983	CONNECTIVE TISSUE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (CTGF-L) (WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 2) (WISP-2) (CONNECTIVE TISSUE GROWTH FACTOR- RELATED PROTEIN 58). [Source:SWISSPROT;Acc:O76076]	20	q13.12
CaMax: 1368a	ENSMUSG00000030871	ENSMUST00000033159		7	F3
CaMax: 1371a	ENSG00000119326	ENST00000325551 ENST00000325580	CATENIN (CADHERIN- ASSOCIATED PROTEIN), ALPHA-LIKE 1; ALPHA- CATULIN. [Source:RefSeq;Acc:NM_003798]	9	q31.3
CaMax: 137b	ENSG00000083771	ENST00000218546	M-PHASE PHOSPHOPROTEIN 8 (FRAGMENT). [Source:SWISSPROT;Acc:Q99549]	13	q12.11
CaMax: 1381a					
CaMax: 1381a					
CaMax: 1383a	ENSG00000067208	ENST00000263785	ECOTROPIC VIRAL INTEGRATION SITE 5; NEUROBLASTOMA STAGE 4S GENE.	1	p22.1

			[Source:RefSeq;Acc:NM_005665]		
CaMax: 1384a	ENSG00000099194	ENST00000266053	ACYL-COA DESATURASE (EC 1.14.19.1) (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE). [Source:SWISSPROT;Acc:O00767]	10	q24.31
CaMax: 1391a					
CaMax: 1394b					
CaMax: 1397b	ENSG00000111912	ENST00000229634 ENST00000318575	NUCLEAR RECEPTOR COACTIVATOR 7; ESTROGEN RECEPTOR ASSOCIATED PROTEIN 140 KDA. [Source:RefSeq;Acc:NM_181782]	6	q22.32
CaMax: 1399a					
CaMax: 13a					
CaMax: 1400a					
CaMax: 1401c	ENSG00000109756	ENST00000264431	PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 1; RA(RAS/RAP1A-ASSOCIATING)-GEF; PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR(GEF)1; RA(RAS/RAP1A-ASSOCIATING)-GEF; PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR(GEF)1. [Source:RefSeq;Acc:NM_014247]	4	q32.1
CaMax: 1403a					
CaMax: 1406a					
CaMax: 1409b	ENSG00000166170	ENST00000299204	BAG-FAMILY MOLECULAR CHAPERONE REGULATOR-5 (BAG-5). [Source:SWISSPROT;Acc:Q9UL15]	14	q32.32
CaMax: 1411a	ENSG00000058272	ENST00000261207 ENST00000312727	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 12A; MYOSIN PHOSPHATASE, TARGET SUBUNIT 1. [Source:RefSeq;Acc:NM_002480]	12	q21.2
CaMax:	ENSMUSG00000003	ENSMUST00000005		4	C7

1415b	4794	4209 ENSMUST0000004 6558			
CaMax: 1416a					
CaMax: 1419a					
CaMax: 141c					
CaMax: 141c					
CaMax: 142.1c					
CaMax: 142.1c					
CaMax: 1420c	ENSG00000128845	ENST00000267809 ENST00000310958	CELL CYCLE PROGRESSION 8 PROTEIN. [Source:RefSeq;Acc:NM_0207 39]	15	q21.3
CaMax: 1421a	ENSG00000172175	ENST00000313958 ENST00000303708	MUCOSA ASSOCIATED LYMPHOID TISSUE LYMPHOMA TRANSLOCATION PROTEIN 1 (EC 3.4.22.-) (MALT- LYMPHOMA ASSOCIATED TRANSLOCATION) (PARACASPASE). [Source:SWISSPROT;Acc:Q9 UDY8]	18	q21.31
CaMax: 1423b					
CaMax: 143.2c	ENSG00000152583	ENST00000282470	SPARC-LIKE PROTEIN 1 PRECURSOR (HIGH ENDOTHELIAL VENULE PROTEIN) (HEVIN) (MAST 9). [Source:SWISSPROT;Acc:Q14 515]	4	q22.1
CaMax: 143.2c	ENSG00000152583	ENST00000282470	SPARC-LIKE PROTEIN 1 PRECURSOR (HIGH ENDOTHELIAL VENULE PROTEIN) (HEVIN) (MAST 9). [Source:SWISSPROT;Acc:Q14 515]	4	q22.1
CaMax: 1431a					
CaMax: 144.2a					
CaMax: 144.2a					
CaMax: 1448a	ENSG00000154430	ENST00000284618	TESTICAN-3 PRECURSOR. [Source:SWISSPROT;Acc:Q9 BQ16]	4	q32.3
CaMax: 1449a	ENSG00000170631	ENST00000276816 ENST00000317284 ENST00000332620 ENST00000317099 ENST00000333589 ENST00000276823 ENST00000332158	ZINC FINGER PROTEIN CLONE 647. [Source:SWISSPROT;Acc:P15 622]	8	q24.3

		ENST00000292579 ENST00000331465			
CaMax: 1450a	ENSG00000170891	ENST00000307746	CYTOKINE-LIKE PROTEIN C17 PRECURSOR. [Source:SWISSPROT;Acc:Q9 NRR1]	4	p16.2
CaMax: 1452a					
CaMax: 1457b					
CaMax: 1459c	ENSG00000113387	ENST00000265073	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14). [Source:SWISSPROT;Acc:P53 999]	5	p13.3
CaMax: 1459c					
CaMax: 145b	ENSG00000147403	ENST00000276371	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN) (TUMOR SUPPRESSOR QM) (LAMININ RECEPTOR HOMOLOG). [Source:SWISSPROT;Acc:P27 635]	24	q28
CaMax: 1460a					
CaMax: 1460a					
CaMax: 1461a					
CaMax: 1461a					
CaMax: 1466b					
CaMax: 1466b					
CaMax: 1469a	ENSMUSG0000004 6599	ENSMUST0000006 0592	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5. [Source:RefSeq;Acc:NM_0232 11]	20	A2
CaMax: 146b	ENSG00000112365	ENST00000230122		6	q21
CaMax: 1469a	ENSMUSG0000004 6599	ENSMUST0000006 0592	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5. [Source:RefSeq;Acc:NM_0232 11]	20	A2
CaMax: 1472a					
CaMax: 1475a					
CaMax: 1476a	ENSG00000172201	ENST00000326913	DNA-BINDING PROTEIN INHIBITOR ID-4. [Source:SWISSPROT;Acc:P47 928]	6	p22.3
CaMax: 1477a	ENSG00000159388	ENST00000290551	BTG2 PROTEIN (NGF- INDUCIBLE ANTI- PROLIFERATIVE PROTEIN	1	q32.1

			PC3). [Source:SWISSPROT;Acc:P78 543]		
CaMax: 147b					
CaMax: 1481c	ENSG00000105997	ENST00000317201	HOMEBOX PROTEIN HOX-A3 (HOX-1E). [Source:SWISSPROT;Acc:O43 365]	7	p15.2
CaMax: 1482a	ENSG00000115998	ENST00000264434		2	p13.3
CaMax: 1484b					
CaMax: 1488b	ENSG00000122566	ENST00000265398 ENST00000312091	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2 / HNRNP B1). [Source:SWISSPROT;Acc:P22 626]	7	p15.2
CaMax: 148a					
CaMax: 1497c					
CaMax: 1497c					
CaMax: 1500b					
CaMax: 1504d					
CaMax: 1506d					
CaMax: 1506d					
CaMax: 150a	ENSG00000106853	ENST00000333580 ENST00000309195	NADP-DEPENDENT LEUKOTRIENE B4 12- HYDROXYDEHYDROGENA SE (EC 1.1.1.-). [Source:SWISSPROT;Acc:Q14 914]	9	q31.3
CaMax: 1516a	ENSG00000115998	ENST00000264434		2	p13.3
CaMax: 1519a					
CaMax: 1519a					
CaMax: 151b					
CaMax: 1520a					
CaMax: 1520a					
CaMax: 1521b	ENSG00000165421	ENST00000333218 ENST00000327431 ENST00000328257	PROTEIN PHOSPHATASE METHYLESTERASE-1. [Source:RefSeq;Acc:NM_0161 47]	11	q13.4
CaMax: 1522b					
CaMax: 1531c					

CaMax: 1532a					
CaMax: 1532a					
CaMax: 1534b	ENSG00000133637	ENST00000309041 ENST00000322687 ENST00000256013		12	q21.32
CaMax: 1534b					
CaMax: 1535a					
CaMax: 1541a					
CaMax: 1546b	ENSG00000151012	ENST00000280612	CYSTINE/GLUTAMATE TRANSPORTER (AMINO ACID TRANSPORT SYSTEM XC-) (XCT) (CALCIUM CHANNEL BLOCKER RESISTANCE PROTEIN CCBR1). [Source:SWISSPROT;Acc:Q9 UPY5]	4	q28.3
CaMax: 1548c					
CaMax: 1549a					
CaMax: 1551a	ENSG00000179454	ENST00000324772	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_0176 58]	14	q21.2
CaMax: 1554c					
CaMax: 1573a	ENSG00000178074	ENST00000319974		2	q33.1
CaMax: 1574b					
CaMax: 1574b					
CaMax: 1577a	ENSG00000144785	ENST00000273308	TRANSMEMBRANE PROTEIN 4. [Source:RefSeq;Acc:NM_0142 55]	12	q13.3
CaMax: 1578a					
CaMax: 157b					
CaMax: 157b					
CaMax: 1591a					
CaMax: 1591a					
CaMax: 1594a					
CaMax: 1596b					
CaMax: 1596b					
CaMax: 1598a					

CaMax: 159a					
CaMax: 159a					
CaMax: 15b	ENSG00000174132	ENST00000312637		5	q21.1
CaMax: 1602a	ENSG00000113838	ENST00000265025		3	q27.3
CaMax: 1604a					
CaMax: 1626c	ENSG00000183456	ENST00000330170		2	q33.1
CaMax: 1628d					
CaMax: 1629a					
CaMax: 1629a					
CaMax: 1630b					
CaMax: 1630b					
CaMax: 1631d	ENSG00000083290	ENST00000261504	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	17	p11.2
CaMax: 1635a	ENSG00000083290	ENST00000261504	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	17	p11.2
CaMax: 1635a	ENSG00000083290	ENST00000261504	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	17	p11.2
CaMax: 1639a					
CaMax: 1639a					
CaMax: 163a	ENSG00000006015	ENST00000326666 ENST00000326636		19	p13.11
CaMax: 1646a	ENSG00000120254	ENST00000265365		6	q25.1
CaMax: 1648a	ENSMUSG00000033207	ENSMUST00000036069		19	C1
CaMax: 164c	ENSG00000163734	ENST00000296026	MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (CXCL3) (GROWTH REGULATED PROTEIN GAMMA) (GRO-GAMMA). [Source:SWISSPROT;Acc:P19876]	4	q13.3
CaMax: 1659a					
CaMax: 1659a					
CaMax: 166a	ENSG00000162384	ENST00000294360		1	p32.3
CaMax: 1671b					
CaMax: 1671b					

CaMax: 1675a					
CaMax: 1676a					
CaMax: 1676a					
CaMax: 1678a					
CaMax: 1682a					
CaMax: 168c					
CaMax: 1690a	ENSRNOG0000001 7817		CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL PRECURSOR (EC 1.9.3.1) (COX IV-1) (CYTOCHROME C OXIDASE POLYPEPTIDE IV). [Source:SWISSPROT;Acc:P10 888]	19	q12
CaMax: 1691b	ENSG00000081177	ENST00000193422		14	q24.1
CaMax: 1692a	ENSRNOG0000001 7817		CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL PRECURSOR (EC 1.9.3.1) (COX IV-1) (CYTOCHROME C OXIDASE POLYPEPTIDE IV). [Source:SWISSPROT;Acc:P10 888]	19	q12
CaMax: 1693b	ENSG00000066468	ENST00000263455 ENST00000310977 ENST00000263451 ENST00000263454 ENST00000328075 ENST00000310973 ENST00000263453 ENST00000332961	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (FGFR-2) (KERATINOCYTE GROWTH FACTOR RECEPTOR 2). [Source:SWISSPROT;Acc:P21 802]	10	q26.13
CaMax: 1696a					
CaMax: 1696a					
CaMax: 16b					
CaMax: 1705a	ENSG00000132357	ENST00000254691	CASPASE RECRUITMENT DOMAIN PROTEIN 6. [Source:SWISSPROT;Acc:Q9 BX69]	5	p13.1
CaMax: 1709a					
CaMax: 1714a	ENSG00000033178	ENST00000322244		4	q13.2
CaMax: 1715a					
CaMax: 1717a	ENSG00000179010	ENST00000320912	T-CELL ACTIVATION PROTEIN. [Source:RefSeq;Acc:NM_0332 96]	4	p16.1
CaMax:	ENSG00000021355	ENST00000229479	LEUKOCYTE ELASTASE	6	p25.2

1721a			INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (M/NEI) (EI). [Source:SWISSPROT;Acc:P30 740]		
CaMax: 1722a	ENSG00000144674	ENST00000273176	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 4 (TRANS-GOLGI P230) (256 KDA GOLGIN) (GOLGIN-245) (72.1 PROTEIN). [Source:SWISSPROT;Acc:Q13 439]	3	p22.3
CaMax: 1724a	ENSG00000143147	ENST00000271357	G-PROTEIN COUPLED RECEPTOR. [Source:RefSeq;Acc:NM_1538 32]	1	q24.2
CaMax: 1725a					
CaMax: 1726a					
CaMax: 1726a					
CaMax: 1727a	ENSG00000131355	ENST00000253673	EGF-LIKE MODULE- CONTAINING MUCIN-LIKE RECEPTOR 3 ISOFORM A. [Source:RefSeq;Acc:NM_0325 71]	19	p13.12
CaMax: 1730a					
CaMax: 1738b					
CaMax: 1741a					
CaMax: 1744a	ENSG00000109883	ENST00000227288	LEUCINE-RICH REPEAT- CONTAINING G PROTEIN- COUPLED RECEPTOR 4 PRECURSOR (G PROTEIN- COUPLED RECEPTOR 48). [Source:SWISSPROT;Acc:Q9 BXB1]	11	p14.1
CaMax: 1744a					
CaMax: 174a	ENSG00000139688	ENST00000267164	TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF- BETA) (TRANSCRIPTION INITIATION FACTOR RAP30). [Source:SWISSPROT;Acc:P13 984]	13	q14.12
CaMax: 174a					
CaMax: 1750a					
CaMax: 1751a					
CaMax: 1755a					
CaMax:					

1755a					
CaMax: 1758a	ENSG00000104852	ENST00000221448	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (U1 SNRNP 70 KDA) (SNRNP70) (U1-70K). [Source:SWISSPROT;Acc:P08 621]	19	q13.33
CaMax: 1759b	ENSG00000179454	ENST00000324772	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_0176 58]	14	q21.2
CaMax: 1760c					
CaMax: 1760c					
CaMax: 1772a					
CaMax: 1775a	ENSG00000179562	ENST00000321407	GOLGI COILED COIL PROTEIN 1. [Source:SWISSPROT;Acc:Q96 CN9]	7	q32.1
CaMax: 1775a	ENSG00000179562	ENST00000321407	GOLGI COILED COIL PROTEIN 1. [Source:SWISSPROT;Acc:Q96 CN9]	7	q32.1
CaMax: 1778c					
CaMax: 1782b	ENSG00000184880	ENST00000332933	OK/SW-CL.87. [Source:SPTREMBL;Acc:Q8N I68]	11	q23.3
CaMax: 178a	ENSG00000135457	ENST00000257915 ENST00000307660	TRANSCRIPTION FACTOR CP2; TRANSCRIPTION FACTOR CP2, ALPHA GLOBIN. [Source:RefSeq;Acc:NM_0056 53]	12	q13.12
CaMax: 1794a					
CaMax: 1794a					
CaMax: 17a					
CaMax: 1800a					
CaMax: 1801b	ENSG00000166855	ENST00000300107	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX-LIKE, MITOCHONDRIAL PRECURSOR. [Source:SWISSPROT;Acc:O76 031]	15	q22.31
CaMax: 180a	ENSG00000171567	ENST00000304782	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_1457 02]	2	q37.1
CaMax: 1810a	ENSG00000102901	ENST00000219172		16	q22.1
CaMax: 1811b					

CaMax: 1812b	ENSG00000105492	ENST00000270604	SIALIC ACID BINDING IG-LIKE LECTIN 6 PRECURSOR (SIGLEC-6) (OBESITY- BINDING PROTEIN 1) (OB-BP1) (CD33 ANTIGEN-LIKE 1). [Source:SWISSPROT;Acc:O43 699]	19	q13.41
CaMax: 1814c	ENSG00000145730	ENST00000304400 ENST00000304406 ENST00000282992 ENST00000325306 ENST00000274392	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM). [Source:SWISSPROT;Acc:P19 021]	5	q21.1
CaMax: 1814c					
CaMax: 1818a					
CaMax: 1828b	ENSMUSG0000002 1613	ENSMUST0000005 3227 ENSMUST0000002 2108	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP). [Source:SWISSPROT;Acc:Q9 QUP5]	13	C3
CaMax: 1834b					
CaMax: 1849d					
CaMax: 1852a					
CaMax: 1853a	ENSRNOG0000001 3516		SPLICEOSOMAL PROTEIN SAP155 (FRAGMENT). [Source:SPTREMBL;Acc:Q9E T34]	9	q31
CaMax: 1857c	ENSRNOG0000001 5205		CYTOCHROME B5. [Source:SWISSPROT;Acc:P00 173]	18	q12.3
CaMax: 1859a	ENSG00000055609	ENST00000312661 ENST00000262189	MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA 3; ALR-LIKE PROTEIN. [Source:RefSeq;Acc:NM_0212 30]	7	q36.1
CaMax: 1863c					
CaMax: 1863c					
CaMax: 1864b	ENSMUSG0000003 3732	ENSMUST0000004 2012 ENSMUST0000005 4613		8	D3
CaMax: 186a	ENSG00000173210	ENST00000309868 ENST00000326685		5	q33.1
CaMax: 1874b					
CaMax: 1874b					
CaMax: 1879a					
CaMax:					

1879a					
CaMax: 1881b					
CaMax: 1894a	ENSG00000151806	ENST00000281543		4	p13
CaMax: 18a					
CaMax: 1912a					
CaMax: 1912a					
CaMax: 1913a					
CaMax: 1913a					
CaMax: 1917f	ENSG00000146414	ENST00000275233 ENST00000334592	SNF2 HISTONE LINKER PHD RING HELICASE. [Source:RefSeq;Acc:NM_1730 82]	6	q24.3
CaMax: 1919a	ENSG00000057019	ENST00000326857 ENST00000326840	ENDOTHELIAL AND SMOOTH MUSCLE CELL- DERIVED NEUROPILIN- LIKE PROTEIN; COAGULATION FACTOR V/VIII-HOMOLOGY DOMAINS PROTEIN 1. [Source:RefSeq;Acc:NM_0809 27]	3	q12.1
CaMax: 1920a	ENSMUSG0000002 2649	ENSMUST0000005 2314 ENSMUST0000002 3327		16	B5
CaMax: 1928a					
CaMax: 1929c	ENSG00000142207	ENST00000270201		21	q22.11
CaMax: 1930a	ENSG00000117868	ENST00000251527		7	q36.3
CaMax: 1940e	ENSG00000116957	ENST00000264180	BETA-TUBULIN COFACTOR E. [Source:RefSeq;Acc:NM_0031 93]	1	q42.3
CaMax: 1941e	ENSG00000070214	ENST00000185520	CDW92 ANTIGEN; CHOLINE TRANSPORTER- LIKE PROTEIN. [Source:RefSeq;Acc:NM_0805 46]	9	q31.1
CaMax: 1943a	ENSG00000154553	ENST00000284770 ENST00000284771 ENST00000284767	ALPHA-ACTININ-2- ASSOCIATED LIM PROTEIN; ENIGMA HOMOLOG. [Source:RefSeq;Acc:NM_0144 76]	4	q35.1
CaMax: 1944a					
CaMax: 1944a					
CaMax: 1945a					
CaMax: 1945a					

CaMax: 1948b					
CaMax: 1948b					
CaMax: 1949a					
CaMax: 1949a					
CaMax: 1950a	ENSG00000134215	ENST00000280840	VAV-3 PROTEIN. [Source:SWISSPROT;Acc:Q9UKW4]	1	p13.3
CaMax: 1953a	ENSG00000138386	ENST00000321041	NGFI-A BINDING PROTEIN 1 (EGR-1 BINDING PROTEIN 1) (TRANSCRIPTIONAL REGULATORY PROTEIN P54). [Source:SWISSPROT;Acc:Q13506]	2	q32.2
CaMax: 1954e					
CaMax: 1961e	ENSG00000157077	ENST00000287722 ENST00000287727	MOTHERS AGAINST DECAPENTAPLEGIC HOMOLOG INTERACTING PROTEIN (MADH-INTERACTING PROTEIN) (SMAD ANCHOR FOR RECEPTOR ACTIVATION) (RECEPTOR ACTIVATION ANCHOR) (HSARA) (NOVEL SERINE PROTEASE) (NSP). [Source:SWISSPROT;Acc:O95405]	1	p32.3
CaMax: 1967a	ENSG00000080469	ENST00000328494 ENST00000190846	ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (PEPTIDE TRANSPORTER TAP2) (PEPTIDE TRANSPORTER PSF2) (PEPTIDE SUPPLY FACTOR 2) (PSF-2) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 2). [Source:SWISSPROT;Acc:Q03519]	6	p21.32
CaMax: 1968a	ENSG00000138063	ENST00000260632	PELLINO PROTEIN. [Source:RefSeq;Acc:NM_020651]	2	p14
CaMax: 1982a	ENSG00000060718	ENST00000305302 ENST00000193186 ENST00000314022 ENST00000305262	COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:P12107]	1	p21.1
CaMax: 1989b					
CaMax: 1990a	ENSG00000166974	ENST00000300249	MICROTUBULE-ASSOCIATED PROTEIN, RP/EB FAMILY, MEMBER 2; T-CELL ACTIVATION PROTEIN, EB1 FAMILY; APC-BINDING PROTEIN EB1. [Source:RefSeq;Acc:NM_0142	18	q12.1

			68]		
CaMax: 1991d					
CaMax: 1a					
CaMax: 2002c					
CaMax: 2003a	ENSG00000081019	ENST00000261441		1	p13.2
CaMax: 2008a	ENSMUSG00000027883	ENSMUST00000029482	PINS. [Source:RefSeq;Acc:NM_029522]	3	F3
CaMax: 2013a	ENSG00000180530	ENST00000318948	NUCLEAR FACTOR RIP140 (NUCLEAR RECEPTOR INTERACTING PROTEIN 1). [Source:SWISSPROT;Acc:P48552]	21	q11.2
CaMax: 2014f					
CaMax: 2015e	ENSG00000174444	ENST00000307961	60S RIBOSOMAL PROTEIN L4 (L1). [Source:SWISSPROT;Acc:P36578]	15	q22.31
CaMax: 2020b	ENSG00000011566	ENST00000263881	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE KINASE 3 (EC 2.7.1.37) (MAPK/ERK KINASE KINASE KINASE 3) (MEK KINASE KINASE 3) (MEKKK 3) (GERMINAL CENTER KINASE RELATED PROTEIN KINASE) (GLK). [Source:SWISSPROT;Acc:Q8I VH8]	2	p22.1
CaMax: 2020b					
CaMax: 2022a	ENSG00000020577	ENST00000305831 ENST00000251091 ENST00000321411		14	q22.2
CaMax: 2023b					
CaMax: 2023b					
CaMax: 2024a					
CaMax: 2034a	ENSG00000172155	ENST00000326233	LATE ENVELOPE PROTEIN 4. [Source:RefSeq;Acc:NM_178352]	1	q21.3
CaMax: 2035d	ENSG00000161980	ENST00000293860	DNA-DIRECTED RNA POLYMERASES III 12.5 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III C11 SUBUNIT) (HSC11P) (HRPC11) (MY010 PROTEIN). [Source:SWISSPROT;Acc:Q9 Y2Y1]	16	p13.3
CaMax: 204a					
CaMax:	ENSG00000141331	ENST00000269073	POTENTIAL HELICASE	17	q24.2

2056d			WITH ZINC-FINGER DOMAIN. [Source:SWISSPROT;Acc:P42694]		
CaMax: 2059b					
CaMax: 205a					
CaMax: 2070a	ENSG00000129116	ENST00000261509 ENST00000335213 ENST00000333488	PALLADIN; CGI-151 PROTEIN. [Source:RefSeq;Acc:NM_016081]	4	q32.3
CaMax: 2073b					
CaMax: 2073b					
CaMax: 2074b	ENSG00000124406	ENST00000264449	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE 1A (EC 3.6.3.1) (CHROMAFFIN GRANULE ATPASE II) (ATPASE CLASS I TYPE 8A MEMBER 1). [Source:SWISSPROT;Acc:Q9Y2Q0]	4	p13
CaMax: 2075a	ENSG00000138709	ENST00000264584 ENST00000326703 ENST00000326639		4	q28.2
CaMax: 2076c					
CaMax: 2078a	ENSG00000122545	ENST00000322406	SEPTIN 7 (CDC10 PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:Q16181]	7	p14.2
CaMax: 2083e	ENSG00000085449	ENST00000233055 ENST00000272881	WD REPEAT AND FYVE DOMAIN CONTAINING 1 ISOFORM 1; PHOSPHOINOSITIDE-BINDING PROTEIN SR1; WD40 AND FYVE DOMAIN CONTAINING 1. [Source:RefSeq;Acc:NM_020830]	2	q36.1
CaMax: 2088a	ENSG00000152487	ENST00000302150		10	p12.31
CaMax: 2092c					
CaMax: 2095a					
CaMax: 2099a					
CaMax: 2099a					
CaMax: 20a					
CaMax: 20a					
CaMax: 2100b	ENSG00000166147	ENST00000316623	FIBRILLIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P35555]	15	q21.1
CaMax:					

2105a					
CaMax: 2108b					
CaMax: 2109a					
CaMax: 2110a	ENSG00000180837	ENST00000318177	ZINC FINGER PROTEIN 345 (ZINC FINGER PROTEIN HZF10). [Source:SWISSPROT;Acc:Q14 585]	19	q13.12
CaMax: 2113a					
CaMax: 211b	ENSG00000103222	ENST00000263013 ENST00000263018 ENST00000263015 ENST00000263019 ENST00000263017 ENST00000263014 ENST00000263016	MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 1. [Source:SWISSPROT;Acc:P33 527]	16	p13.11
CaMax: 2122a					
CaMax: 2123a	ENSG00000139370	ENST00000266771	PEPTIDE-HISTIDINE TRANSPORTER 4. [Source:RefSeq;Acc:NM_1456 48]	12	q24.32
CaMax: 2129a	ENSG00000143415	ENST00000271682	SMALL PROTEIN EFFECTOR 1 OF CDC42. [Source:RefSeq;Acc:NM_0202 39]	1	q21.3
CaMax: 2132a					
CaMax: 2135d	(				
CaMax: 2136b					
CaMax: 2141a					
CaMax: 2142a		l			
CaMax: 2160a					
CaMax: 2161c	ENSG00000138709	ENST00000264584 ENST00000326703 ENST00000326639		4	q28.2
CaMax: 2165a					
CaMax: 2167a					
CaMax: 2189b					
CaMax: 2198b					
CaMax: 2201a					
CaMax: 2201a					
CaMax: 2205a					
CaMax: 2210a					

CaMax: 2222b	ENSG00000117868	ENST00000251527		7	q36.3
CaMax: 2223a					
CaMax: 2224a	ENSG00000116690	ENST00000251819	PROTEOGLYCAN 4; MEGAKARYOCYTE STIMULATING FACTOR; PROTEOGLYCAN 4, (MEGAKARYOCYTE STIMULATING FACTOR, ARTICULAR SUPERFICIAL ZONE PROTEIN); JACOBS CAMPTODACTYLY- ARTHROPATHY- PERICARDITIS SYNDROME; CAMPTODACTYLY, ARTHROPATHY, COXA VARA, PERICARDITIS SYNDROME. [Source:RefSeq;Acc:NM_0058 07]	1	q31.1
CaMax: 2225b	ENSG00000151544	ENST00000281234		10	q25.3
CaMax: 2234a	ENSMUSG0000003 8760	ENSMUST0000003 8856	THYROTROPIN- RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBERIN RECEPTOR). [Source:SWISSPROT;Acc:P21 761]	15	D1
CaMax: 2235a					
CaMax: 2235a					
CaMax: 2238a	ENSG00000172572	ENST00000325802	CGMP-INHIBITED 3',5'- CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI-PDE A). [Source:SWISSPROT;Acc:Q14 432]	12	p12.2
CaMax: 2241a	ENSG00000172572	ENST00000325802	CGMP-INHIBITED 3',5'- CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI-PDE A). [Source:SWISSPROT;Acc:Q14 432]	12	p12.2
CaMax: 2238a	ENSG00000172572	ENST00000325802	CGMP-INHIBITED 3',5'- CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI-PDE A). [Source:SWISSPROT;Acc:Q14	12	p12.2

			432]		
CaMax: 224a					
CaMax: 2251d					
CaMax: 2252b	ENSG00000109775	ENST00000264689		4	q35.1
CaMax: 2258a					
CaMax: 2258a					
CaMax: 2258a					
CaMax: 225a					
CaMax: 2264b					
CaMax: 2264b					
CaMax: 2266b					
CaMax: 2267a	ENSG00000137801	ENST00000260356	THROMBOSPONDIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P07 996]	15	q14
CaMax: 231a					
CaMax: 2331c					
CaMax: 2341b	ENSG00000119397	ENST00000238341	/	9	q33.2
CaMax: 2351c					
CaMax: 2351c					
CaMax: 2241a	ENSG00000172572	ENST00000325802	CGMP-INHIBITED 3',5'- CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI-PDE A). [Source:SWISSPROT;Acc:Q14 432]	12	p12.2
CaMax: 235a					
CaMax: 2374a	ENSG00000137801	ENST00000260356	THROMBOSPONDIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P07 996]	15	q14
CaMax: 238a					
CaMax: 239a	ENSG00000119363	ENST00000238302	SPECTRIN ALPHA CHAIN, BRAIN (SPECTRIN, NON- ERYTHROID ALPHA CHAIN) (ALPHA-II SPECTRIN) (FODRIN ALPHA CHAIN). [Source:SWISSPROT;Acc:Q13 813]	9	q34.11

CaMax: 23a	ENSG00000162419	ENST00000294409	GLUCOCORTICOID MODULATORY ELEMENT BINDING PROTEIN 1 (GMEB-1) (PARVOVIRUS INITIATION FACTOR P96) (PIF P96) (DNA BINDING PROTEIN P96PIF). [Source:SWISSPROT;Acc:Q9 Y692]	1	p35.3
CaMax: 240a	ENSG00000154144	ENST00000284290		11	q24.2
CaMax: 243a					
CaMax: 245a	ENSG00000166800	ENST00000280706		11	p15.1
CaMax: 248a	ENSG00000162437	ENST00000294428		1	p31.3
CaMax: 24a					
CaMax: 258a					
CaMax: 261c					
CaMax: 261c					
CaMax: 267d	ENSG00000041982	ENST00000265131	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA- ASSOCIATED- EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C). [Source:SWISSPROT;Acc:P24 821]	9	q33.1
CaMax: 272d	ENSG00000141642	ENST00000269466	ELAC HOMOLOG 1. [Source:RefSeq;Acc:NM_0186 96]	18	q21.1
CaMax: 27a					
CaMax: 28s					
CaMax: 307b	ENSG00000141378	ENST00000311824	PROTEIN CGI-147. [Source:SWISSPROT;Acc:Q9 Y3E5]	17	q23.2
CaMax: 308c	ENSG00000116745	ENST00000262340	RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN 65KDA; RETINAL PIGMENT EPITHELIUM- SPECIFIC PROTEIN (65KD); RETINITIS PIGMENTOSA 20 (AUTOSOMAL RECESSIVE). [Source:RefSeq;Acc:NM_0003 29]	1	p31.2
CaMax: 310h					
CaMax: 311c					
CaMax:					

313a					
CaMax: 314a					
CaMax: 319b					
CaMax: 320a	ENSG00000090989	ENST00000317642 ENST00000333951	EXOCYST COMPLEX COMPONENT SEC3 (BM- 012). [Source:SWISSPROT;Acc:Q9 NV70]	4	q12
CaMax: 320a					
CaMax: 322a					
CaMax: 324a	ENSG00000135913	ENST00000258399		2	q35
CaMax: 326e	ENSMUSG0000002 5724	ENSMUST0000002 6818	MICROSOMAL SIGNAL PEPTIDASE 18 KDA SUBUNIT (EC 3.4.-.-) (SPASE 18 KDA SUBUNIT) (SPC18) (ENDOPEPTIDASE SP18). [Source:SWISSPROT;Acc:Q9 R0P6]	7	D2
CaMax: 327f					
CaMax: 327f					
CaMax: 328b	ENSG00000129116	ENST00000261509 ENST00000335213 ENST00000333488	PALLADIN; CGI-151 PROTEIN. [Source:RefSeq;Acc:NM_0160 81]	4	q32.3
CaMax: 336a	ENSG00000173320	ENST00000308497		4	q35.1
CaMax: 33a					
CaMax: 33a					
CaMax: 340a					
CaMax: 340a					
CaMax: 343b					
CaMax: 343b					
CaMax: 34a					
CaMax: 34a					
CaMax: 106a	ENSG00000167996	ENST00000301775	FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). [Source:SWISSPROT;Acc:P02 794]	11	q12.3
CaMax: 106a	ENSG00000167996	ENST00000301775	FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). [Source:SWISSPROT;Acc:P02 794]	11	q12.3
CaMax: 360a					
CaMax:					

360a					
CaMax: 364a	ENSG00000182944	ENST00000331029 ENST00000329871	RNA-BINDING PROTEIN EWS (EWS ONCOGENE) (EWING SARCOMA BREAKPOINT REGION 1 PROTEIN). [Source:SWISSPROT;Acc:Q01 844]	22	q12.2
CaMax: 370a					
CaMax: 374a	ENSG00000136938	ENST00000277182	ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER B (PHAPI2 PROTEIN) (SILVER-STAINABLE PROTEIN SSP29) (ACIDIC PROTEIN RICH IN LEUCINES). [Source:SWISSPROT;Acc:Q92 688]	9	q22.33
CaMax: 375d					
CaMax: 379a					
CaMax: 38a	ENSG00000145216	ENST00000306932 ENST00000273816	FIP1-LIKE 1; REARRANGED IN HYPEREOSINOPHILIA. [Source:RefSeq;Acc:NM_0309 17]	4	q12
CaMax: 391a					
CaMax: 392a					
CaMax: 392a					
CaMax: 395a					
CaMax: 395a					
CaMax: 397b					
CaMax: 3c	ENSRNOG00000000 6864			8	q24
CaMax: 406a-r					
CaMax: 406a-r					
CaMax: 408a					
CaMax: 409a					
CaMax: 415b	ENSG00000134001	ENST00000256383	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT) (EIF-2-ALPHA) (EIF- 2ALPHA) (EIF-2A). [Source:SWISSPROT;Acc:P05 198]	14	q23.3

CaMax: 421a					
CaMax: 43a	ENSG00000174132	ENST00000312637		5	q21.1
CaMax: 446f					
CaMax: 44c					
CaMax: 44c					
CaMax: 45.1b					
CaMax: 45.1b					
CaMax: 450a					
CaMax: 450a					
CaMax: 452a					
CaMax: 455c					
CaMax: 455c					
CaMax: 457c					
CaMax: 459a	ENSG00000102908	ENST00000317142	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (TONICITY-RESPONSIVE ENHANCER-BINDING PROTEIN) (TONE- BINDING PROTEIN) (TONEBP). [Source:SWISSPROT;Acc:O94 916]	16	q22.1
CaMax: 461a					
CaMax: 461a					
CaMax: 464b	ENSG00000035687	ENST00000263828	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) (ADSS) (AMPSASE). [Source:SWISSPROT;Acc:P30 520]	1	q44
CaMax: 465b	ENSG00000064309	ENST00000263577	SURFACE GLYCOPROTEIN, IG SUPERFAMILY MEMBER. [Source:RefSeq;Acc:NM_0169 52]	11	q24.2
CaMax: 46a					
CaMax: 472a					
CaMax: 472a					
CaMax: 478a	ENSG00000165169	ENST00000297871	T-COMPLEX ASSOCIATED- TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51	24	p11.4

			808]		
CaMax: 479c	ENSG00000165169	ENST00000297871	T-COMPLEX ASSOCIATED- TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51 808]	24	p11.4
CaMax: 482a					
CaMax: 487a	ENSG00000116584	ENST00000313695 ENST00000313667	RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 2 (GEF-H1 PROTEIN) (PROLIFERATING CELL NUCLEOLAR ANTIGEN P40). [Source:SWISSPROT;Acc:Q92 974]	1	q22
CaMax: 488a	ENSG00000159399	ENST00000290573	HEXOKINASE, TYPE II (EC 2.7.1.1) (HK II) (MUSCLE FORM HEXOKINASE). [Source:SWISSPROT;Acc:P52 789]	2	p12
CaMax: 48b					
CaMax: 48b					
CaMax: 490c					
CaMax: 490c					
CaMax: 494a					
CaMax: 494a					
CaMax: 498a					
CaMax: 50.1c					
CaMax: 50.1c					
CaMax: 501b					
CaMax: 504a					
CaMax: 505b					
CaMax: 507a					
CaMax: 516c					
CaMax: 517c					
CaMax: 51a					
CaMax: 51a					
CaMax: 520a	ENSG00000179454	ENST00000324772	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_0176 58]	14	q21.2

CaMax: 521b	ENSG00000081189	ENST00000325423	MYOCYTE-SPECIFIC ENHANCER FACTOR 2C. [Source:SWISSPROT;Acc:Q06 413]	5	q14.3
CaMax: 523a					
CaMax: 52a					
CaMax: 530b	ENSG00000100567	ENST00000216455	PROTEASOME SUBUNIT ALPHA TYPE 3 (EC 3.4.25.1) (PROTEASOME COMPONENT C8) (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8). [Source:SWISSPROT;Acc:P25 788]	14	q23.1
CaMax: 538a					
CaMax: 539a	ENSG00000133059	ENST00000255422 ENST00000335353	HDCMD38P. [Source:SPTREMBL;Acc:Q9P 1S5]	1	q32.1
CaMax: 540a					
CaMax: 543a					
CaMax: 545a	ENSG00000144785	ENST00000273308	TRANSMEMBRANE PROTEIN 4. [Source:RefSeq;Acc:NM_0142 55]	12	q13.3
CaMax: 547c	ENSG00000174560	ENST00000310012		6	q12
CaMax: 548c	ENSG00000174560	ENST00000310012		6	q12
CaMax: 550a	ENSG00000133226	ENST00000334537 ENST00000323848	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-L; SER/ARG- RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-LIKE). [Source:RefSeq;Acc:NM_0058 39]	1	p36.11
CaMax: 552a					
CaMax: 553b	ENSG00000180185	ENST00000326061		16	p13.3
CaMax: 555b	ENSG00000005812	ENST00000281993	F-BOX AND LEUCINE-RICH REPEAT PROTEIN 3A; F- BOX PROTEIN FBL3A. [Source:RefSeq;Acc:NM_0121 58]	13	q22.3
CaMax: 556b					
CaMax: 557b					
CaMax: 558a					
CaMax: 558a					

CaMax: 560b					
CaMax: 561b					
CaMax: 568a					
CaMax: 568a					
CaMax: 56a					
CaMax: 56a					
CaMax: 571a	ENSG00000143924	ENST00000318522	ECHINODERM MICROTUBULE- ASSOCIATED PROTEIN- LIKE 4 (EMAP-4) (RESTRICTEDLY OVEREXPRESSED PROLIFERATION- ASSOCIATED PROTEIN) (ROPP 120). [Source:SWISSPROT;Acc:Q9 HC35]	2	p21
CaMax: 574a					
CaMax: 579a	ENSG00000124193	ENST00000244020	SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55). [Source:SWISSPROT;Acc:Q13 247]	20	q13.11
CaMax: 57a	ENSG00000091409	ENST00000264107 ENST00000264106	INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F). [Source:SWISSPROT;Acc:P23 229]	2	q31.1
CaMax: 581a	ENSG00000115112	ENST00000263707	LBP-9. [Source:RefSeq;Acc:NM_0145 53]	2	q14.2
CaMax: 583e	ENSMUSG0000002 6193	ENSMUST0000005 5226 ENSMUST0000005 9577 ENSMUST0000002 7385		1	C3
CaMax: 58a					
CaMax: 597c	ENSG00000171634	ENST00000306378 ENST00000335221 ENST00000321866 ENST00000321892	FETAL ALZHEIMER ANTIGEN (FETAL ALZ-50- REACTIVE CLONE 1). [Source:SWISSPROT;Acc:Q12 830]	17	q24.2
CaMax: 59a					
CaMax: 59a					
CaMax: 609a					
CaMax: 611a					
CaMax:					

622a					
CaMax: 622a					
CaMax: 623a	ENSG00000140575	ENST00000268182	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195). [Source:SWISSPROT;Acc:P46940]	15	q26.1
CaMax: 624b					
CaMax: 626a					
CaMax: 626a					
CaMax: 628a	ENSG00000183762	ENST00000327813	KREMEN PROTEIN 1 PRECURSOR (KRINGLE-CONTAINING PROTEIN MARKING THE EYE AND THE NOSE) (DICKKOPF RECEPTOR). [Source:SWISSPROT;Acc:Q96MU8]	22	q12.1
CaMax: 635a	ENSG00000133226	ENST00000334537 ENST00000323848	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-L; SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-LIKE). [Source:RefSeq;Acc:NM_005839]	1	p36.11
CaMax: 638b	ENSG00000165169	ENST00000297871	T-COMPLEX ASSOCIATED-TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51808]	24	p11.4
CaMax: 639a					
CaMax: 63a					
CaMax: 63a					
CaMax: 64.2a	ENSG00000144560	ENST00000273038		3	p25.3
CaMax: 685a	ENSG00000125149	ENST00000219139	UPF0183 PROTEIN. [Source:SWISSPROT;Acc:Q9BSU1]	16	q22.1
CaMax: 690a					
CaMax: 690a					
CaMax: 692a	ENSG00000171567	ENST00000304782	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	2	q37.1
CaMax: 697a	ENSRNOG00000007325			8	q23
CaMax: 6b					

CaMax: 701a	ENSMUSG0000003 2077	ENSMUST0000003 6099		9	B
CaMax: 704b	ENSG00000119509	ENST00000262457 ENST00000262456	INVERSIN. [Source:RefSeq;Acc:NM_0144 25]	9	q22.33
CaMax: 704b	ENSG00000119509	ENST00000262457 ENST00000262456	INVERSIN. [Source:RefSeq;Acc:NM_0144 25]	9	q22.33
CaMax: 70d					
CaMax: 710a	ENSG00000123500	ENST00000243222	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:Q03 692]	6	q22.1
CaMax: 711a					
CaMax: 711a					
CaMax: 713a					
CaMax: 713a					
CaMax: 714a					
CaMax: 718a					
CaMax: 720a					
CaMax: 725a	ENSG00000133454	ENST00000335473 ENST00000335460 ENST00000335471 ENST00000335359		22	q12.1
CaMax: 726b	ENSG00000122912	ENST00000265870	GRAVE'S DISEASE CARRIER PROTEIN (GDC) (GRAVE'S DISEASE AUTOANTIGEN) (GDA) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:P16 260]	10	q21.3
CaMax: 72a					
CaMax: 72a					
CaMax: 731a					
CaMax: 731a					
CaMax: 736a	ENSG00000130066	ENST00000252349	DIAMINE ACETYLTRANSFERASE (EC 2.3.1.57) (SPERMIDINE/SPERMINE N(1)- ACETYLTRANSFERASE) (SSAT) (PUTRESCINE ACETYLTRANSFERASE). [Source:SWISSPROT;Acc:P21 673]	24	p22.11
CaMax: 739a	ENSG00000166938	ENST00000319194 ENST00000319212		15	q22.31

CaMax: 73b	ENSG00000112473	ENST00000230235 ENST00000325843	HISTIDINE-RICH MEMBRANE PROTEIN KE4. [Source:SWISSPROT;Acc:Q92 504]	6	p21.32
CaMax: 745a					
CaMax: 747a	ENSG00000164190	ENST00000296607 ENST00000282516	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_1334 33]	5	p13.2
CaMax: 749a					
CaMax: 74c					
CaMax: 753b	ENSMUSG0000003 9203	ENSMUST0000003 6300		4	C1
CaMax: 759b					
CaMax: 759b					
CaMax: 764b					
CaMax: 764b					
CaMax: 765a	ENSG00000102763	ENST00000251030 ENST00000281496		13	q14.11
CaMax: 768a					
CaMax: 76b					
CaMax: 785b	ENSG00000171867	ENST00000305832	MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27- 30) (PRP33-35C) (ASCR) (CD230 ANTIGEN). [Source:SWISSPROT;Acc:P04 156]	20	p13
CaMax: 788a					
CaMax: 789a	ENSG00000102471	ENST00000218652		13	q31.1
CaMax: 794a	ENSG00000123096	ENST00000242729	SARCOSPAN (K-RAS ONCOGENE-ASSOCIATED PROTEIN) (KIRSTEN-RAS- ASSOCIATED PROTEIN). [Source:SWISSPROT;Acc:Q14 714]	12	p12.1
CaMax: 795a	ENSG00000106554	ENST00000262570		7	q32.3
CaMax: 810a	ENSG00000131388	ENST00000253706		3	p25.1
CaMax: 813a					
CaMax: 815a					
CaMax: 81a					
CaMax: 820a					
CaMax: 820a					
CaMax:					

827b					
CaMax: 827b					
CaMax: 828a					
CaMax: 82b					
CaMax: 831a					
CaMax: 831a					
CaMax: 832a	ENSMUSG0000002 6193	ENSMUST0000005 5226 ENSMUST0000005 9577 ENSMUST0000002 7385		1	C3
CaMax: 833a	ENSG00000090581	ENST00000204679		16	p13.3
CaMax: 835c					
CaMax: 839a	ENSG00000068885	ENST00000326448		3	q25.33
CaMax: 841b					
CaMax: 841b					
CaMax: 847a					
CaMax: 85.1c	ENSG00000136003	ENST00000311893 ENST00000228459	NITROGEN FIXATION CLUSTER-LIKE. [Source:RefSeq;Acc:NM_0143 01]	12	q23.3
CaMax: 85.2b	ENSG00000149218	ENST00000278505		11	q21
CaMax: 850a					
CaMax: 851a					
CaMax: 856c	ENSG00000060982	ENST00000261192 ENST00000334327	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC (EC 2.6.1.42) (BCAT(C)) (ECA39 PROTEIN). [Source:SWISSPROT;Acc:P54 687]	12	p12.1
CaMax: 863c	ENSMUSG0000002 2676	ENSMUST0000002 3356	ZINC FINGER PROTEIN SLUG (NEURAL CREST TRANSCRIPTION FACTOR SLUG) (SNAIL HOMOLOG 2). [Source:SWISSPROT;Acc:P97 469]	16	B1
CaMax: 890a	ENSG00000175582	ENST00000310653 ENST00000334372	RAS-RELATED PROTEIN RAB-6A (RAB-6). [Source:SWISSPROT;Acc:P20 340]	11	q13.4
CaMax: 8a					
CaMax:					

905a					
CaMax: 906a					
CaMax: 907a					
CaMax: 909a	ENSG00000145730	ENST00000304400 ENST00000304406 ENST00000282992 ENST00000325306 ENST00000274392	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM). [Source:SWISSPROT;Acc:P19 021]	5	q21.1
CaMax: 90c	ENSMUSG0000002 3944	ENSMUST0000002 4739	HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (TUMOR SPECIFIC TRANSPLANTATION 84 KDA ANTIGEN) (TSTA). [Source:SWISSPROT;Acc:P11 499]	17	C
CaMax: 911a					
CaMax: 911a					
CaMax: 912b					
CaMax: 914a					
CaMax: 914a					
CaMax: 915a					
CaMax: 915a					
CaMax: 919b	ENSG00000104177	ENST00000267836 ENST00000324324	MYELIN GENE EXPRESSION FACTOR 2. [Source:RefSeq;Acc:NM_0161 32]	15	q21.1
CaMax: 91f					
CaMax: 91f					
CaMax: 919b	ENSG00000104177	ENST00000267836 ENST00000324324	MYELIN GENE EXPRESSION FACTOR 2. [Source:RefSeq;Acc:NM_0161 32]	15	q21.1
CaMax: 92c	ENSG00000084676	ENST00000288599 ENST00000326011	NUCLEAR RECEPTOR COACTIVATOR 1 ISOFORM 1. [Source:RefSeq;Acc:NM_0037 43]	2	p23.3
CaMax: 935b	ENSG00000125953	ENST00000246165	CHURCHILL PROTEIN (MY015 PROTEIN). [Source:SWISSPROT;Acc:Q8 WUH1]	14	q23.3
CaMax: 936b					
CaMax: 936b					
CaMax: 945a	ENSRNOG0000001 1175			4	q24
CaMax:					

947a					
CaMax: 947a					
CaMax: 949c	ENSG00000144592	ENST00000316654 ENST00000273079		3	p25.1
CaMax: 953a	ENSMUSG0000002 1290	ENSMUST0000002 1719	6.8 KDA MITOCHONDRIAL PROTEOLIPID. [Source:SWISSPROT;Acc:P56 379]	12	F2
CaMax: 963c	ENSG00000134644	ENST00000257075	PUMILIO HOMOLOG 1. [Source:RefSeq;Acc:NM_0146 76]	1	p35.2
CaMax: 96e					
CaMax: 981a					
CaMax: 984a					
CaMax: 984a					
CaMax: 986a	ENSG00000118971	ENST00000261254	G1/S-SPECIFIC CYCLIN D2. [Source:SWISSPROT;Acc:P30 279]	12	p13.32
CaMax: 990a	ENSG00000125398	ENST00000245479	TRANSCRIPTION FACTOR SOX-9. [Source:SWISSPROT;Acc:P48 436]	17	q24.3
CaMax: 992a					
CaMax: 994b	ENSG00000005700	ENST00000306270	INHIBITOR OF BRUTON'S TYRISOINE KINASE; BTK- BINDING PROTEIN. [Source:RefSeq;Acc:NM_0155 25]	6	q14.1
CaMax: 996a	ENSG00000008988	ENST00000009589	40S RIBOSOMAL PROTEIN S20. [Source:SWISSPROT;Acc:P17 075]	8	q12.1

Table 2B

CaMax Gene ID	Swissprot Ensemble	OMIM	RefSeq	Pfam	InterPro	Sig. Pep.	TMHMM	HUGO
CaMax: 1002b	ENST000 00244769							
CaMax: 1002b	ENST000 00244769							
CaMax: 1005a			NM_178043 NM_032239 NM_018078	PF05383	IPR001199			
CaMax: 1006b	TISD_HU MAN		NM_006887	PF04553 PF00642	IPR000571 IPR007635			ZFP36L2
CaMax: 1007a	TISD_HU MAN		NM_006887	PF04553 PF00642	IPR000571 IPR007635			ZFP36L2
CaMax: 1008a	ENST000 00245479							
CaMax: 1008a	ENST000 00245479							

CaMax: 1009c	GDC_HU MAN	139080	NM_152707	PF00153	IPR001993 IPR002167 IPR002067			SLC25A16
CaMax: 1011a	trembl AB 012223_1							
CaMax: 1011a	Transcript :ENSRNO T0000003 3408							
CaMax: 1013a	ENST000 00326567							
CaMax: 1015d			NM_018359					
CaMax: 1016b	Transcript :ENST000 00330345							
CaMax: 1019a	Z333_HU MAN		NM_032433	PF01352 PF00096	IPR007087 IPR007086 IPR001909			
CaMax: 1020a	CGRR_H UMAN	114190	NM_005795	PF02793 PF00002	IPR000832 IPR003287 IPR003289 IPR001688 IPR001879	Sigp	Tmhmm	CALCRL
CaMax: 1026b	trembl AB 012223_1							
CaMax: 1026b	Transcript :ENSRNO T0000003 5961							
CaMax: 1028c	trembl HS RBP1_1							
CaMax: 1028c	ENST000 00260780							
CaMax: 1029a			NM_145702	PF04218 PF03184	IPR004875 IPR006695			TIGD1
CaMax: 103a	ENST000 00287239							
CaMax: 1044c	PPO3_HU MAN	607726	NM_005485	PF05406 PF02877 PF00644	IPR001290 IPR004102			ADPRTL3
CaMax: 104a	ROH1_H UMAN	601035	NM_005520	PF00076	IPR000504			HNRPH1
CaMax: 1050a	ENST000 00322598							
CaMax: 1054a	ENST000 00261710							
CaMax: 1057b	trembl AB 012223_1							
CaMax: 1060a	pironly S7 2489							
CaMax: 1061a				PF02008	IPR002857			
CaMax: 1063b	ENST000 00277359							
CaMax: 106a	FRIH_HU MAN	134770	NM_002032	PF00210	IPR001519			FTH1
CaMax: 1070b	Transcript :ENST000 00322595							

CaMax: 1072a	trembl HS 09953_1							
CaMax: 1072a	ENST000 00295955							
CaMax: 1089d	gpnew 37 790758							
CaMax: 108a	ENST000 00297846							
CaMax: 1090d	swiss ATP 6_CANF A							
CaMax: 1094b	gpnew 37 790758							
CaMax: 1094b	ENSMUS T0000000 6525							
CaMax: 1095a			NM_019974 NM_133712	PF00089	IPR001254 IPR001314	Sigp		Prss20- pending 2300002A1 3Rik
CaMax: 1096a			NM_019974 NM_133712	PF00089	IPR001254 IPR001314	Sigp		Prss20- pending 2300002A1 3Rik
CaMax: 1098a			NM_014796					
CaMax: 109a			NM_032202		IPR001969			
CaMax: 1105a	RB14_HU MAN		NM_016322	PF00071	IPR001687 IPR001806			RAB14
CaMax: 1106a			NM_152388				Tmhmm	ALS2CR4
CaMax: 1108a	SR13_HU MAN		NM_052851	PF00620 PF01852	IPR001687 IPR000198 IPR002913			STARD13
CaMax: 1110b	gpnew 37 790758							
CaMax: 1110b	gpnew 37 790758							
CaMax: 1111b	SES1_HU MAN	606103	NM_014454	PF04636	IPR006730			SESN1
CaMax: 1112a			NM_032042		IPR000886 IPR001472	Sigp		
CaMax: 111a	Transcript :ENST000 00327492							
CaMax: 1120a			NM_022130	PF05719				GOLPH3
CaMax: 1121a					IPR000566			
CaMax: 1131b	gpnew 37 790758							
CaMax: 1132a	trembl PM 43360_1							
CaMax: 1134a	MEFC_H UMAN	600662	NM_002397	PF00319	IPR002100			MEF2C
CaMax: 1135a	FXP2_HU MAN	605317 602081	NM_148898 NM_148899 NM_148900 NM_014491	PF00904 PF00250	IPR007087 IPR001766 IPR000354			FOXP2

CaMax: 1137b	ENST000 00256429							
CaMax: 1138a	ENST000 00261765							
CaMax: 1139a	ENST000 00245479							
CaMax: 1145a	CA1E_H UMAN	120325	NM_001855	PF02210 PF01391	IPR008160 IPR003129 IPR001791	Sigp		COL15A1
CaMax: 1145a	CA1E_H UMAN							
CaMax: 1146a	ENST000 00308148							
CaMax: 1159b	ENST000 00296084							
CaMax: 104a	ROH1_H UMAN	601035	NM_005520	PF00076	IPR000504			HNRPH1
CaMax: 1169b	TPM1_H UMAN	191010	NM_000366	PF00261	IPR000533			TPM1
CaMax: 1177c	DYHC_H UMAN	600112	NM_001376	PF03028	IPR001687 IPR000169 IPR004273			DNCH1
CaMax: 1184a	TIAM_H UMAN	600687	NM_003253	PF00169 PF02196 PF00595 PF00621	IPR001331 IPR001849 IPR001478 IPR000219 IPR003116 IPR001472			TIAM1
CaMax: 1184a	TIAM_H UMAN							
CaMax: 1190b				PF02269	IPR003195			
CaMax: 1192b				PF02269	IPR003195			
CaMax: 11b	ENST000 00307407							
CaMax: 120a	swiss UB1 5_HUMA N							
CaMax: 120a	ENST000 00280377							
CaMax: 1212b	ENST000 00235420							
CaMax: 1213d	VAV3_H UMAN	605541	NM_006113	PF00307 PF00621 PF00169 PF00130 PF00017 PF00018	IPR002086 IPR002219 IPR001331 IPR000980 IPR001452 IPR003096 IPR001849 IPR001715 IPR000219			VAV3
CaMax: 1217a	ENST000 00305327							
CaMax: 1220b	Transcript :ENST000 00333521							
CaMax: 1226d	ENST000 00244769							
CaMax:	ENST000							

1226d	00244769							
CaMax: 123c	trembl AY 027883_1							
CaMax: 123c	ENST000 00313779							
CaMax: 1243a	WDR3_H UMAN	604737	NM_006784	PF00400 PF04003	IPR001680 IPR007148			WDR3
CaMax: 1245b	ENST000 00319046							
CaMax: 1246a			NM_018359					
CaMax: 1248b	ENST000 00263196							
CaMax: 1253a			NM_018359					
CaMax: 1257b	trembl BC 043468_1							
CaMax: 1257b	Genscan: AC07365 5.26.1.188 105.67776 .86719							
CaMax: 1260c	ENST000 00325918							
CaMax: 1263b				PF00036	IPR002048 IPR000694			
CaMax: 1267a	PCCA_H UMAN	232000 606054	NM_000282	PF00289 PF02786 PF02785 PF00364	IPR001882 IPR005479 IPR005481 IPR000089 IPR005482			PCCA
CaMax: 1267a	PCCA_H UMAN	232000 606054	NM_000282	PF00289 PF02786 PF02785 PF00364	IPR001882 IPR005479 IPR005481 IPR000089 IPR005482			PCCA
CaMax: 1270a			NM_152520	PF00096	IPR007087			
CaMax: 1272a	S24A_HU MAN	607183		PF04810 PF04811 PF04815 PF00626	IPR007123 IPR006895 IPR006896 IPR006900 IPR000694			SEC24A
CaMax: 1273b	trembl AB 012223_1							
CaMax: 1276a	trembl AB 012223_1							
CaMax: 127b	trembl AY 027883_1							
CaMax: 127b	ENST000 00313779							
CaMax: 1282b	Genscan: CAAA012 09745.1.1. 24557.315 9.16476							
CaMax: 1284b	ENSRNO T0000002 3862							
CaMax:			NM_133433					

1287c			NM_015384					
CaMax: 1288a			NM_133433 NM_015384					
CaMax: 128a	HS9B_M OUSE		NM_008302	PF02518 PF00183	IPR001404 IPR003594			Hspcb
CaMax: 1292c	KU86_H UMAN	194364	NM_021141	PF03731 PF02735 PF03730	IPR006164 IPR005160 IPR005161			XRCC5
CaMax: 1294b	SYEP_H UMAN	138295	NM_004446	PF00749 PF03950 PF00458 PF00587 PF03129 PF00043	IPR001589 IPR001412 IPR000738 IPR000924 IPR002316 IPR004046 IPR002314 IPR004154	)		EPRS
CaMax: 1299c			NM_014991 NM_178583	PF02138 PF00400 PF01363	IPR001680 IPR000306 IPR000409			WDFY3
CaMax: 129b	tremblnew AX40003 9_1							
CaMax: 129b	ENST000 00265677							
CaMax: 12a	ENST000 00288263							
CaMax: 1301a				PF00023	IPR002110			
CaMax: 1304a		607958	NM_014178					STXBP6
CaMax: 1308c	trembl AB 012223_1							
CaMax: 1308c	ENST000 00297641							
CaMax: 130b	ENSRNO T0000001 1463							
CaMax: 1316b	ENSRNO T0000002 4354							
CaMax: 1318a	LIN1_HU MAN							
CaMax: 1320	LIN1_HU MAN							
CaMax: 1322c	OGT1_R AT			PF00515	IPR001440			
CaMax: 1323br	trembl HS 09953_1							
CaMax: 1323br	ENST000 00295955							
CaMax: 1324a	trembl HS 09953_1							
CaMax: 1324a	ENST000 00295955							
CaMax: 1335b	pironly B3 4087							
CaMax: 1335b	ENST000 00321183							
CaMax: 1341a		603054	NM_013372	PF03045	IPR004133 IPR001472	Sigp		CKTSF1B 1

CaMax: 1352b	LIN1_NY CCO							
CaMax: 1354a			NM_145702	PF04218 PF03184	IPR004875 IPR006695			TIGD1
CaMax: 1355a	trembl AF 318340_1							
CaMax: 1355a	ENST000 00324229							
CaMax: 1361a	FUT8_HU MAN	602589	NM_178157 NM_178154 NM_178155 NM_178156 NM_004480	PF00018	IPR001452 IPR001472	Sigp	Tmhmm	FUT8
CaMax: 1364d	trembl AB 012223_1							
CaMax: 1364d	ENST000 00304487							
CaMax: 1366a	CTGL_H UMAN	603399	NM_003881	PF00219 PF00093 PF00090	IPR001525 IPR000867 IPR001007 IPR000884	Sigp		WISP2
CaMax: 1368a			NM_026140	PF00749	IPR001412 IPR000924			323040110 1Rik
CaMax: 1371a		604785	NM_003798	PF01044	IPR001033 IPR006077			CTNNAL1
CaMax: 137b	MPP8_H UMAN			PF00385 PF00023	IPR000953 IPR002110 IPR001472			
CaMax: 1381a	trembl S7 7350_1							
CaMax: 1381a	ENST000 00228938							
CaMax: 1383a		602942	NM_005665	PF00566	IPR001687 IPR000515 IPR000195			EVI5
CaMax: 1384a	ACOD_H UMAN	604031	NM_005063	PF00487	IPR001522 IPR005804		Tmhmm	SCD
CaMax: 1391a	ENST000 00222271							
CaMax: 1394b	ENST000 00256429							
CaMax: 1397b			NM_181782	PF01476	IPR002482			NCOA7
CaMax: 1399a	ENST000 00318060							
CaMax: 13a	ENST000 00295709							
CaMax: 1400a	trembl AB 012223_1							
CaMax: 1401c			NM_014247	PF00027 PF00595 PF00788 PF00617 PF00618	IPR000595 IPR001478 IPR001895 IPR000651 IPR000159			PDZGEF1
CaMax: 1403a	ENST000 00231061							
CaMax: 1406a	Transcript :ENST000 00298992							
CaMax:	BAG5_H	603885	NM_004873	PF02179	IPR003103			BAG5

1409b	UMAN							
CaMax: 1411a		602021	NM_002480	PF00023	IPR002110			PPP1R12A
CaMax: 1415b							Tmhmm	2900042B1 IRik
CaMax: 1416a	Transcript :ENST000 00336483							
CaMax: 1419a	ENST000 00325584							
CaMax: 141c	trembl BC 018999_1							
CaMax: 141c	Transcript :ENST000 00307901							
CaMax: 142.1c	tremblnew AK00130 1_1							
CaMax: 142.1c	ENST000 00311713							
CaMax: 1420c			NM_004748 NM_020739	PF02987	IPR001687 IPR004238		Tmhmm	
CaMax: 1421a	MLT1_H UMAN	604860	NM_006785 NM_173844	PF00531 PF00047 PF00656	IPR007110 IPR000488 IPR001309			MALT1
CaMax: 1423b	gpnew 37 790758							
CaMax: 143.2c	SPL1_HU MAN	606041	NM_004684	PF00050	IPR002048 IPR001999 IPR002350	Sigp		SPARCL1
CaMax: 143.2c	SPL1_HU MAN	606041	NM_004684	PF00050	IPR002048 IPR001999 IPR002350	Sigp		SPARCL1
CaMax: 1431a	Transcript :ENST000 00296858							
CaMax: 144.2a	trembl AY 157990_1							
CaMax: 144.2a	ENST000 00249297							
CaMax: 1448a	TIC3_HU MAN	607989	NM_016950	PF00050 PF00086	IPR000716 IPR002350	Sigp	Tmhmm	SPOCK3
CaMax: 1449a	Z271_HU MAN ZN16_HU MAN Z268_HU MAN ZF64_HU MAN	604754 601262 606024 604753	NM_006958 NM_003415	PF00096 PF01352	IPR001687 IPR007087 IPR007086 IPR000294 IPR001909			ZNF271 ZNF16 ZNF268
CaMax: 1450a	C17_HU MAN	607930	NM_018659			Sigp		
CaMax: 1452a	ENST000 00261976							
CaMax: 1457b	gp 345281 69							
CaMax: 1459c	P15_HU MAN	600503	NM_006713	PF02229	IPR003173 IPR001472			
CaMax: 1459c	TCP4_HU MAN							

CaMax: 145b	RL10_HU MAN	312173	NM_006013	PF00826	IPR001197			RPL10
CaMax: 1460a	trembl HS U93567_2							
CaMax: 1460a	ENST000 00322543							
CaMax: 1461a	trembl BC 049156_1							
CaMax: 1461a	ENSMUS T0000003 0311							
CaMax: 1466b	trembl AF 325902_1							
CaMax: 1466b	ENST000 00222271							
CaMax: 1469a			NM_023211				Tmhmm	Usmg5
CaMax: 146b	Y441_HU MAN		NM_014797	PF00651 PF02178 PF00096	IPR007087 IPR000345 IPR007086 IPR000210 IPR000637			ZNF450
CaMax: 1469a			NM_023211				Tmhmm	Usmg5
CaMax: 1472a	ENST000 00296084							
CaMax: 1475a	CN4B_R AT							
CaMax: 1476a	ID4_HU MAN	600581	NM_001546	PF00010	IPR001092 IPR000694			ID4
CaMax: 1477a	BTG2_H UMAN	601597	NM_006763	PF01211	IPR002087			BTG2
CaMax: 147b	ENST000 00317517							
CaMax: 1481c	HXA3_H UMAN	142954	NM_030661 NM_153631 NM_153632	PF00046	IPR001356 IPR001827 IPR002965 IPR000047 IPR000694			HOXA3
CaMax: 1482a			NM_017880		IPR000169			
CaMax: 1484b	UTRO_H UMAN							
CaMax: 1488b	ROA2_H UMAN	600124	NM_002137 NM_031243	PF00076	IPR000504			HNRPA2B 1
CaMax: 148a	ENST000 00271717							
CaMax: 1497c	swiss SEC 3_HUMA N							
CaMax: 1497c	ENST000 00317675							
CaMax: 1500b	ENST000 00322519							
CaMax: 1504d	ENST000 00278824							
CaMax: 1506d	trembl AY 061884_1							
CaMax: 1506d	ENST000 00229488							

CaMax: 150a	LB4D_H UMAN	601274	NM_012212	PF00107	IPR002085			LTB4DH
CaMax: 1516a			NM_017880		IPR000169			
CaMax: 1519a	gp 375890 39							
CaMax: 1519a	ENST000 00311733							
CaMax: 151b	ENST000 00281131							
CaMax: 1520a	trembl AY 267013_1							
CaMax: 1520a	ENST000 00261435							
CaMax: 1521b			NM_016147		IPR000734 IPR003089 IPR000639 IPR000379			
CaMax: 1522b	trembl AY 154463_1							
CaMax: 1531c	trembl AY 154463_1							
CaMax: 1532a	trembl BC 038422_1							
CaMax: 1532a	ENST000 00272761							
CaMax: 1534b	Y373_HU MAN		NM_014684 NM_025114	PF02524	IPR001687 IPR003900			
CaMax: 1534b	Y373_BO VIN							
CaMax: 1535a	ENST000 00277895							
CaMax: 1541a								
CaMax: 1546b	XCT_HU MAN	607933	NM_014331	PF00324	IPR004841 IPR002293		Tmhmm	SLC7A11
CaMax: 1548c	ENST000 00254926							
CaMax: 1549a	ENST000 00294618							
CaMax: 1551a			NM_017658	PF00651	IPR000210			BTBD5
CaMax: 1554c	trembl AB 012223_1							
CaMax: 1573a			NM_153689			Sigp		
CaMax: 1574b	trembl AB 012223_1							
CaMax: 1574b	ENST000 00310739							
CaMax: 1577a		605861	NM_014255		IPR000886 IPR008139	Sigp		TMEM4
CaMax: 1578a	gp 345350 28							
CaMax: 157b	trembl S7 7350_1							
CaMax: 157b	ENST000 00228938							
CaMax: 1591a	gp 348496 66							

CaMax: 1591a	Transcript :ENSRNO T0000001 0671							
CaMax: 1594a	ENSMUS T0000006 0486							
CaMax: 1596b	trembl AF 081111_2							
CaMax: 1596b	Transcript :ENST000 00319237							
CaMax: 1598a	LIN1_NY CCO							
CaMax: 159a	trembl CS AAE_1							
CaMax: 159a	Transcript :ENST000 00311190							
CaMax: 15b					IPR000694	Sigp	Tmhmm	
CaMax: 1602a			NM_018138					
CaMax: 1604a	ENSDAR T0000002 4018							
CaMax: 1626c				PF00076	IPR000504			
CaMax: 1628d	ENST000 00325761							
CaMax: 1629a	tremblnew BC02153 5_1							
CaMax: 1629a	ENST000 00229238							
CaMax: 1630b	tremblnew BC02153 5_1							
CaMax: 1630b	ENST000 00229238							
CaMax: 1631d			NM_014683	PF00069	IPR000719 IPR002290 IPR001245			ULK2
CaMax: 1635a			NM_014683	PF00069	IPR000719 IPR002290 IPR001245			ULK2
CaMax: 1635a			NM_014683	PF00069	IPR000719 IPR002290 IPR001245			ULK2
CaMax: 1639a	pironly B2 8096							
CaMax: 1639a	Transcript :ENST000 00329369							
CaMax: 163a			NM_017967					
CaMax: 1646a			NM_015440	PF00763 PF02882 PF01268	IPR000559 IPR000672			FTHFSDC 1
CaMax:				PF00629	IPR000998	Sigp		

1648a								
CaMax: 164c	MI2B_HU MAN	139111	NM_002090	PF00048	IPR001089 IPR002473 IPR001811			CXCL3
CaMax: 1659a	trembl S5 7162_1							
CaMax: 1659a	ENST000 00316200							
CaMax: 166a			NM_017887	PF05907				
CaMax: 1671b	trembl AB 012223_1							
CaMax: 1671b	Transcript :ENST000 00329369							
CaMax: 1675a	ENST000 00321491							
CaMax: 1676a	trembl AF 081104_2							
CaMax: 1676a	ENST000 00299933							
CaMax: 1678a	ENST000 00307746							
CaMax: 1682a	ENSRNO T0000001 5118							
CaMax: 168c	RL32_HU MAN							
CaMax: 1690a	CX41_RA T		NM_017202	PF02936	IPR004203			Tmhmm
CaMax: 1691b			NM_018199	PF01612	IPR000345 IPR002562			C14orf114
CaMax: 1692a	CX41_RA T		NM_017202	PF02936	IPR004203			Tmhmm
CaMax: 1693b	FGR2_H UMAN BFR2_HU MAN	176943 101200 101600 123150 123500	NM_022971 NM_022974 NM_022976 NM_022969 NM_022972 NM_022973 NM_000141 NM_023028 NM_023029 NM_022975 NM_022970 NM_023031 NM_023030	PF00047 PF00069	IPR000719 IPR001245 IPR007110	Sigp	Tmhmm	FGFR2
CaMax: 1696a	gp 375891 32							
CaMax: 1696a	ENST000 00259146							
CaMax: 16b	ENST000 00303924							
CaMax: 1705a	CAR6_H UMAN		NM_032587	PF00619	IPR001687 IPR001315 IPR001472			CARD6
CaMax: 1709a	Genscan: AC09196 6.3.1.9129 6.20868.4 6788							

CaMax: 1714a			NM_018227	PF00899 PF02134	IPR000594 IPR000127 IPR000205			
CaMax: 1715a	ENST000 00299230							
CaMax: 1717a			NM_033296					
CaMax: 1721a	ILEU_HU MAN	130135	NM_030666	PF00079	IPR000215 IPR001472			SERPINB1
CaMax: 1722a	GOA4_H UMAN	602509 270150	NM_002078	PF00904 PF01465	IPR006162 IPR001990 IPR000354 IPR000237 IPR001472			GOLGA4
CaMax: 1724a			NM_153832 NM_007369	PF00001	IPR000276		Tmhmm	
CaMax: 1725a	ENST000 00026952							
CaMax: 1726a	trembl AB 012223_1							
CaMax: 1726a	ENST000 00325761							
CaMax: 1727a		606101	NM_032571 NM_152939	PF01825 PF00002 PF00008	IPR000152 IPR001881 IPR001740 IPR000832 IPR003056 IPR006209 IPR000203	Sigp	Tmhmm	
CaMax: 1730a	ENST000 00222271							
CaMax: 1738b	ENST000 00318296							
CaMax: 1741a	ENST000 00221700							
CaMax: 1744a	LGR4_H UMAN	606666	NM_018490	PF01462 PF00560 PF00001	IPR007087 IPR002131 IPR000276 IPR001611 IPR000372	Sigp	Tmhmm	GPR48
CaMax: 1744a	LGR4_H UMAN							
CaMax: 174a	T2FB_HU MAN	189969	NM_004128	PF02270	IPR003196			GTF2F2
CaMax: 174a	T2FB_HU MAN							
CaMax: 1750a	ENST000 00282228							
CaMax: 1751a	ENST000 00319353							
CaMax: 1755a	trembl AK 051102_1							
CaMax: 1755a	Genscan: AL109926 .9.1.11429 8.7096.11 4020							
CaMax: 1758a	RU17_HU MAN	180740	NM_003089	PF00076	IPR000504			SNRP70
CaMax:			NM_017658	PF00651	IPR000210			BTBD5

1759b								
CaMax: 1760c	trembl AX 648027_1							
CaMax: 1760c	ENST000 00326555							
CaMax: 1772a	ENSMUS T0000005 3459							
CaMax: 1775a	GCC1_H UMAN	607418	NM_024523	PF01465	IPR000237			GCC1
CaMax: 1775a	GCC1_H UMAN	607418	NM_024523	PF01465	IPR000237			GCC1
CaMax: 1778c	Transcript :ENST000 00315390							
CaMax: 1782b						Sigp	Tmhmm	
CaMax: 178a		189889	NM_005653	PF04516	IPR007604 IPR001472			TFCP2
CaMax: 1794a	gp 345275 09							
CaMax: 1794a	ENST000 00310739							
CaMax: 17a	trembl AB 012223_1							
CaMax: 1800a	ENST000 00320480							
CaMax: 1801b	CLPX_H UMAN		NM_006660	PF00004	IPR001687 IPR000345 IPR003959	Sigp		CLPX
CaMax: 180a			NM_145702	PF04218 PF03184	IPR004875 IPR006695			TIGD1
CaMax: 1810a			NM_025082		IPR001472			
CaMax: 1811b	pironly B3 4087							
CaMax: 1812b	SIL6_HU MAN	604405	NM_001245	PF00047	IPR003006 IPR007110 IPR001472	Sigp	Tmhmm	SIGLEC6
CaMax: 1814c	AMD_HU MAN	170270	NM_000919 NM_138766 NM_138822 NM_138821	PF01082 PF03712 PF01436	IPR002086 IPR000323 IPR000720 IPR001258	Sigp	Tmhmm	PAM
CaMax: 1814c	AMD_BO VIN							
CaMax: 1818a	ENST000 00324450							
CaMax: 1828b	PLK_MO USE		NM_013500	PF00047 PF00193	IPR000538 IPR003006	Sigp		Crtl1
CaMax: 1834b	trembl AY 293286_1							
CaMax: 1849d	gpnew 37 790758							
CaMax: 1852a	Transcript :ENST000 00333606							
CaMax: 1853a						Sigp		
CaMax: 1857c	CYB5_R AT		NM_022245	PF00173	IPR001199			Tmhmm

CaMax: 1859a		606833	NM_170606 NM_021230	PF02178 PF00904 PF00628 PF00505 PF05964 PF05965 PF00856	IPR000194 IPR000345 IPR000637 IPR000910 IPR001965 IPR001214 IPR000354 IPR001472 IPR000694			MLL3
CaMax: 1863c	swiss PEN 2_HUMA N							
CaMax: 1863c	ENST000 00222266							
CaMax: 1864b			NM_133953		IPR003006			1810061H2 4Rik
CaMax: 186a			NM_014945	PF00412 PF02209	IPR001781 IPR003128			
CaMax: 1874b	trembl AX 648027_1							
CaMax: 1874b	ENST000 00326555							
CaMax: 1879a	trembl AX 648027_1							
CaMax: 1879a	ENST000 00326555							
CaMax: 1881b	ENST000 00253814							
CaMax: 1894a			NM_021927	PF00009 PF03144 PF00679	IPR001687 IPR000795 IPR001806 IPR000640 IPR004161			
CaMax: 18a	trembl AB 012223_1							
CaMax: 1912a	trembl BC 019022_1							
CaMax: 1912a	ENST000 00318072							
CaMax: 1913a	swiss CO G1_HUM AN							
CaMax: 1913a	ENST000 00299886							
CaMax: 1917f			NM_173082	PF00176 PF00538 PF00628 PF00271	IPR000345 IPR001841 IPR000330 IPR001650 IPR005818 IPR001965			SHPRH
CaMax: 1919a			NM_080927	PF00431 PF03815 PF00754	IPR000859 IPR000421 IPR004043		Tmhmm	
CaMax: 1920a								
CaMax: 1928a	ENSMUS T0000004 1864							
CaMax: 1929c	Y539_HU MAN							C21orf108
CaMax:				PF00168	IPR000008		Tmhmm	

1930a								
CaMax: 1940e		604934	NM_003193	PF01302 PF00560	IPR001611 IPR000938			TBCE
CaMax: 1941e		606105	NM_022109 NM_080546	PF04515	IPR007603	Sigp	Tmhmm	
CaMax: 1943a		605889	NM_014476	PF00595 PF00412	IPR001781 IPR001478			
CaMax: 1944a	trembl AK 025270_1							
CaMax: 1944a	ENST000 00319557							
CaMax: 1945a	gpnew 37 748505							
CaMax: 1945a	ENST000 00312037							
CaMax: 1948b	gpnew 37 748505							
CaMax: 1948b	ENST000 00312037							
CaMax: 1949a	gp 375906 86							
CaMax: 1949a	ENST000 00320480							
CaMax: 1950a	VAV3_H UMAN	605541	NM_006113	PF00307 PF00621 PF00169 PF00130 PF00017 PF00018	IPR002086 IPR002219 IPR001331 IPR000980 IPR001452 IPR003096 IPR001849 IPR001715 IPR000219			VAV3
CaMax: 1953a	NAB1_H UMAN	600800	NM_005966	PF04904 PF04905 PF04902	IPR006986 IPR006988 IPR006989			NAB1
CaMax: 1954e	ENST000 00321787							
CaMax: 1961e	MADI_H UMAN	603755	NM_007323 NM_004799 NM_007324	PF01363	IPR000345 IPR000306			MADHIP
CaMax: 1967a	TAP2_HU MAN	170261	NM_000544 NM_018833	PF00664 PF00005	IPR001687 IPR003439 IPR001140	Sigp	Tmhmm	TAP2
CaMax: 1968a			NM_020651	PF04710	IPR006800			PELI1
CaMax: 1982a	CA1B_H UMAN	120280 604841 154780	NM_080629 NM_080630 NM_001854	PF02210 PF01391 PF01410	IPR001687 IPR001230 IPR008160 IPR000885 IPR003129 IPR001791	Sigp		COL11A1
CaMax: 1989b	trembl AB 030650_1							
CaMax: 1990a		605789	NM_014268	PF00307 PF03271	IPR001715 IPR004953			MAPRE2
CaMax: 1991d	ENST000 00244096							
CaMax: 1a	ENST000 00322438							
CaMax:	ENSMUS							

2002c	T0000003 4996							
CaMax: 2003a			NM_018364		IPR001472 IPR000694			
CaMax: 2008a			NM_029522	PF00515 PF02188	IPR001440 IPR003109			Pins- pending
CaMax: 2013a	RI14_HU MAN	602490	NM_003489		IPR001687			NRIP1
CaMax: 2014f	ENSMUS T0000002 8222							
CaMax: 2015e	RL4_HU MAN	180479	NM_000968	PF00573	IPR002086 IPR002136 IPR001472			RPL4
CaMax: 2020b	M4K3_H UMAN	604921	NM_003618	PF00069 PF00780	IPR000719 IPR001180			MAP4K3
CaMax: 2020b	M4K3_M OUSE							
CaMax: 2022a			NM_015589	PF00536	IPR001660	Sigp		SAMD4
CaMax: 2023b	trembl BT 008100_1							
CaMax: 2023b	ENST000 00312547							
CaMax: 2024a	ENST000 00314543							
CaMax: 2034a			NM_178352		IPR003267			
CaMax: 2035d	RPCZ_H UMAN	606007	NM_016310	PF02150 PF01096	IPR001222 IPR001529			POLR3K
CaMax: 204a	ENST000 00276230							
CaMax: 2056d	HELZ_H UMAN	606699	NM_014877	PF00642	IPR001687 IPR000571			HELZ
CaMax: 2059b	ENST000 00282218							
CaMax: 205a	ENST000 00276230							
CaMax: 2070a			NM_016081	PF00047	IPR000634 IPR007110 IPR002965 IPR000694			
CaMax: 2073b	trembl AB 012223_1							
CaMax: 2073b	Transcript :ENST000 00320621							
CaMax: 2074b	A8A1_H UMAN		NM_006095	PF00702 PF00122	IPR001687 IPR001757 IPR008250 IPR005834		Tmhmm	ATP8A1
CaMax: 2075a			NM_178043 NM_032239 NM_018078	PF05383	IPR001199			
CaMax: 2076c	ENST000 00324643							
CaMax: 2078a	SEP7_HU MAN	603151	NM_001788	PF00735	IPR001687 IPR000038			CDC10
CaMax: 2083e			NM_020830 NM_178350	PF00400 PF01363	IPR001680 IPR000306			WDFY1

CaMax: 2088a			NM_182543	PF01189	IPR001678			
CaMax: 2092c	gpnew 37 790758							
CaMax: 2095a	ENST000 00258969							
CaMax: 2099a	swissnew SF30_HU MAN							
CaMax: 2099a	ENST000 00239010							
CaMax: 20a	trembl BC 001284_1							
CaMax: 20a	ENST000 00318446							
CaMax: 2100b	FBN1_H UMAN	134797 154700	NM_000138	PF00008 PF00683	IPR000152 IPR006209 IPR007087 IPR001881 IPR001438 IPR002212	Sigp		FBN1
CaMax: 2105a	ENST000 00319412							
CaMax: 2108b	Transcript :ENST000 00314393							
CaMax: 2109a	ENST000 00324450							
CaMax: 2110a	Z345_HU MAN		NM_003419	PF00096	IPR007087 IPR007086			ZNF345
CaMax: 2113a	ENST000 00324450							
CaMax: 211b	MRP1_H UMAN	158343	NM_004996 NM_019901 NM_019902 NM_019898 NM_019862 NM_019900 NM_019899	PF00664 PF00005	IPR001687 IPR000719 IPR003439 IPR001140		Tmhmm	ABCC1
CaMax: 2122a	ENST000 00321873							
CaMax: 2123a			NM_145648	PF00854	IPR001117 IPR000109		Tmhmm	SLC15A4
CaMax: 2129a			NM_020239	PF00786	IPR000095			
CaMax: 2132a	ENST000 00175091							
CaMax: 2135d	ENST000 00325604							
CaMax: 2136b	ENST000 00294665							
CaMax: 2141a	ENSMUS T0000000 0642							
CaMax: 2142a	Genscan: CAAA010 04319.1.1. 45274.201 6.41736							
CaMax:	ENST000							

2160a	00285599							
CaMax: 2161c			NM_178043 NM_032239 NM_018078	PF05383	IPR001199			
CaMax: 2165a	ENST000 00244769							
CaMax: 2167a	ENST000 00278483							
CaMax: 2189b	ENST000 00309655							
CaMax: 2198b	ENSMUS T0000000 0642							
CaMax: 2201a	ENST000 00244769							
CaMax: 2201a	ENST000 00244769							
CaMax: 2205a	ENST000 00274054							
CaMax: 2210a	ENST000 00244769							
CaMax: 2222b				PF00168	IPR000008		Tmhmm	
CaMax: 2223a	Transcript :ENST000 00228330							
CaMax: 2224a		604283	NM_005807	PF01033 PF05001 PF02818 PF00045	IPR000585 IPR001212 IPR002965 IPR004168 IPR000684 IPR001472	Sigp		PRG4
CaMax: 2225b				PF01436	IPR001258 IPR006663			
CaMax: 2234a	TRFR_M OUSE		NM_013696	PF00001	IPR000276 IPR002120		Tmhmm	Trhr
CaMax: 2235a	ENST000 00296412							
CaMax: 2235a	ENST000 00296412							
CaMax: 2238a	CN3A_H UMAN	123805	NM_000921	PF00233	IPR002073 IPR005829 IPR001917		Tmhmm	PDE3A
CaMax: 2241a	CN3A_H UMAN	123805	NM_000921	PF00233	IPR002073 IPR005829 IPR001917		Tmhmm	PDE3A
CaMax: 2238a	CN3A_H UMAN	123805	NM_000921	PF00233	IPR002073 IPR005829 IPR001917		Tmhmm	PDE3A
CaMax: 224a	trembl HS F8L1B_1							
CaMax: 2251d	swiss LIN 1_NYCC O							
CaMax: 2252b			NM_018359					
CaMax: 2258a	ENST000 00245479							
CaMax: 2258a	ENST000 00245479							

CaMax: 2258a	ENST000 00245479							
CaMax: 225a	gp 373618 16							
CaMax: 2264b	ENSMUS T0000000 0642							
CaMax: 2264b	ENSMUS T0000000 0642							
CaMax: 2266b	ENST000 00306715							
CaMax: 2267a	TSP1_HU MAN	188060	NM_003246	PF02210 PF00093 PF00090 PF00008 PF02412 PF05735	IPR006209 IPR001007 IPR000884 IPR003129 IPR003367 IPR001791	Sigp		THBS1
CaMax: 231a	ENST000 00317584							
CaMax: 2331c	ENST000 00296412							
CaMax: 2341b								
CaMax: 2351c	ENST000 00319965							
CaMax: 2351c	ENST000 00319965							
CaMax: 2241a	CN3A_H UMAN	123805	NM_000921	PF00233	IPR002073 IPR005829 IPR001917		Tmhmm	PDE3A
CaMax: 235a	Genscan: RNOR010 69968.119 47.48582							
CaMax: 2374a	TSP1_HU MAN	188060	NM_003246	PF02210 PF00093 PF00090 PF00008 PF02412 PF05735	IPR006209 IPR001007 IPR000884 IPR003129 IPR003367 IPR001791	Sigp		THBS1
CaMax: 238a	Genscan: AC01660 1.7.1.1452 64.1553.2 0016							
CaMax: 239a	SPCN_H UMAN	182810	NM_003127	PF00435 PF00018 PF00036	IPR002048 IPR000276 IPR001452 IPR002017			SPTAN1
CaMax: 23a	GME1_H UMAN	604409	NM_006582 NM_024482	PF01342	IPR000770			GMEB1
CaMax: 240a			NM_032811	PF05964 PF05965				
CaMax: 243a	trembl AB 012223_1							
CaMax: 245a			NM_144972	PF00056 PF02866	IPR001557 IPR001236 IPR000205 IPR000594			
CaMax:			NM_018211	PF00076	IPR000504			

248a					IPR001064			
CaMax: 24a	ENST000 00239392							
CaMax: 258a	gpnew 37 790758							
CaMax: 261c	gp 373618 50							
CaMax: 261c	ENST000 00322543							
CaMax: 267d	TENA_H UMAN	187380	NM_002160	PF00008 PF00041 PF00147	IPR006209 IPR002049 IPR003961 IPR002181	Sigp	Tmhmm	TNC
CaMax: 272d			NM_018696	PF00753	IPR001279			ELAC1
CaMax: 27a	ENSRNO T0000000 6484							
CaMax: 28s	Genscan: NA26110. 1.701.151 5							
CaMax: 307b	YCE7_H UMAN		NM_016077	PF01981	IPR002833	Sigp	Tmhmm	
CaMax: 308c		180069	NM_000329	PF03055	IPR004294			RPE65
CaMax: 310h	M172_M OUSE							
CaMax: 311c	ENST000 00315874							
CaMax: 313a	Genscan: AL136225 .8.1.42171 .4910.172 11							
CaMax: 314a	ENST000 00303575							
CaMax: 319b	ENSRNO T0000002 2117							
CaMax: 320a	SEC3_HU MAN	607879	NM_018261 NM_178237					
CaMax: 320a	SEC3_HU MAN							
CaMax: 322a	ENSRNO T0000002 2117							
CaMax: 324a			NM_020935	PF00443 PF02809	IPR001394 IPR003903			USP37
CaMax: 326e	SPC4_M OUSE		NM_019951	PF00461	IPR000508 IPR001733	Sigp	Tmhmm	Spc18- pending
CaMax: 327f	gp 373600 62							
CaMax: 327f	ENST000 00315821							
CaMax: 328b			NM_016081	PF00047	IPR000634 IPR007110 IPR002965 IPR000694			
CaMax:								

336a								
CaMax: 33a	trembl BC 024093_1							
CaMax: 33a	ENSRNO T0000000 6836							
CaMax: 340a	swiss PTN 3_HUMA N							
CaMax: 340a	ENST000 00262539							
CaMax: 343b	trembl AK 033094_1							
CaMax: 343b	ENST000 00269073							
CaMax: 34a	gp 345348 17							
CaMax: 34a	ENST000 00316410							
CaMax: 106a	FRIH_HU MAN	134770	NM_002032	PF00210	IPR001519			FTH1
CaMax: 106a	FRIH_HU MAN	134770	NM_002032	PF00210	IPR001519			FTH1
CaMax: 360a	tremblnew AK09446 1_1							
CaMax: 360a	ENST000 00291220							
CaMax: 364a	EWS_HU MAN	133450	NM_005243 NM_013986	PF00076 PF00641	IPR001064 IPR000504 IPR001876			EWSR1
CaMax: 370a	COX1_C ANFA							
CaMax: 374a	A32B_HU MAN		NM_006401	PF00560	IPR001611			ANP32B
CaMax: 375d	COX1_C ANFA							
CaMax: 379a	ENST000 00278407							
CaMax: 38a		607686	NM_030917	PF05182	IPR007854			FIP1L1
CaMax: 391a	ENST000 00293648							
CaMax: 392a	tremblnew BC03413 5_1							
CaMax: 392a	ENST000 00319311							
CaMax: 395a	trembl BC 051886_1							
CaMax: 395a	ENST000 00323751							
CaMax: 397b	ALU7_H UMAN							
CaMax: 3c								
CaMax: 406a-r	swiss CO X3_CAN FA							
CaMax:	Transcript							

406a-r	:ENST000 00332194							
CaMax: 408a	ALU1_H UMAN							
CaMax: 409a	ALU1_H UMAN							
CaMax: 415b	IF2A_HU MAN	603907	NM_004094	PF00575	IPR003029			EIF2S1
CaMax: 421a	gpnew 37 790758							
CaMax: 43a					IPR000694	Sigp	Tmhmm	
CaMax: 446f	ENST000 00239392							
CaMax: 44c	trembl AK 019226_1							
CaMax: 44c	ENST000 00264258							
CaMax: 45.1b	trembl AK 007837_1							
CaMax: 45.1b	ENST000 00314138							
CaMax: 450a	tremblnew HSM805 132_1							
CaMax: 450a	ENST000 00325086							
CaMax: 452a	ENST000 00218713							
CaMax: 455c	trembl BC 028178_1							
CaMax: 455c	ENST000 00317856							
CaMax: 457c	trembl HS U93569_1							
CaMax: 459a	NFT5_HU MAN	604708	NM_006599 NM_138713 NM_138714 NM_173214 NM_173215	PF00554 PF01833	IPR000451 IPR002909 IPR001472			NFAT5
CaMax: 461a	swissnew SF30_HU MAN							
CaMax: 461a	ENST000 00239010							
CaMax: 464b	PURA_H UMAN	103060	NM_001126	PF00709	IPR001114			ADSS
CaMax: 465b			NM_016952	PF00047 PF00041	IPR003961 IPR007110		Tmhmm	CDON
CaMax: 46a	ENST000 00282493							
CaMax: 472a	tremblnew BC01981 0_1							
CaMax: 472a	ENST000 00327301							
CaMax: 478a	TCTL_H UMAN	300302	NM_006520	PF03645	IPR005334			TCTE1L
CaMax: 479c	TCTL_H UMAN	300302	NM_006520	PF03645	IPR005334			TCTE1L

CaMax: 482a	Genscan: AP005117 .2.1.14879 0.13386.9 5160							
CaMax: 487a	ARH2_H UMAN	607560	NM_004723	PF00130 PF00621 PF00169	IPR002219 IPR001849 IPR000219			ARHGEF2
CaMax: 488a	HXK2_H UMAN	601125	NM_000189	PF00349 PF03727	IPR001312			HK2
CaMax: 48b	trembl AK 019226_1							
CaMax: 48b	ENST000 00264258							
CaMax: 490c	trembl AK 088660_1							
CaMax: 490c	ENSRNO T0000002 5796							
CaMax: 494a	trembl HS AB461_1							
CaMax: 494a	ENST000 00324722							
CaMax: 498a	ENSRNO T0000001 1463							
CaMax: 50.1c	swiss RL3 1_HUMA N							
CaMax: 50.1c	ENST000 00264258							
CaMax: 501b	ENSMUS T0000005 0981							
CaMax: 504a	ENST000 00267434							
CaMax: 505b	ENST000 00248673							
CaMax: 507a	ENSRNO T0000001 6310							
CaMax: 516c	Transcript :ENST000 00328854							
CaMax: 517c	Transcript :ENST000 00328854							
CaMax: 51a	trembl AY 072691_1							
CaMax: 51a	ENST000 00321758							
CaMax: 520a			NM_017658	PF00651	IPR000210			BTBD5
CaMax: 521b	MEFC_H UMAN	600662	NM_002397	PF00319	IPR002100			MEF2C
CaMax: 523a	ENST000 00300162							
CaMax: 52a	ENST000 00242208							
CaMax:	PSA3_HU	176843	NM_152132	PF00227	IPR000426			PSMA3

530b	MAN	176845	NM_002788		IPR001353			
CaMax: 538a	ENST000 00283629							
CaMax: 539a				PF00069	IPR000719 IPR002290 IPR001245			
CaMax: 540a	pironly JU 0033							
CaMax: 543a	gp 345338 74							
CaMax: 545a		605861	NM_014255		IPR000886 IPR008139	Sigp		TMEM4
CaMax: 547c			NM_014827	PF00642	IPR000571 IPR001472			
CaMax: 548c			NM_014827	PF00642	IPR000571 IPR001472			
CaMax: 550a		605975	NM_005839	PF01480	IPR002965 IPR002483 IPR001472			SRRM1
CaMax: 552a	ENST000 00318468							
CaMax: 553b			NM_031208	PF01557	IPR002529			
CaMax: 555b		605653	NM_012158	PF00646	IPR001810			FBXL3A FBXL3B
CaMax: 556b	tremblnew HSM805 356_1							
CaMax: 557b	NSF_HU MAN							
CaMax: 558a	trembl AF 352051_1							
CaMax: 558a	ENST000 00319272							
CaMax: 560b	RBB2_H UMAN							
CaMax: 561b	ENST000 00296499							
CaMax: 568a	trembl CF A388522_ 1							
CaMax: 568a	ENST000 00225430							
CaMax: 56a	gpnew 38 511552							
CaMax: 56a	ENST000 00202773							
CaMax: 571a	EML4_H UMAN	607442	NM_019063	PF03451 PF00400	IPR002048 IPR001254 IPR001680 IPR000560 IPR005108			EML4
CaMax: 574a	ENST000 00296412							
CaMax: 579a	SFR6_HU MAN	601944	NM_006275	PF00076	IPR000504 IPR001472			SFRS6
CaMax: 57a	ITA6_HU MAN	147556 226730	NM_000210	PF01839 PF00357	IPR000413	Sigp	Tmhmm	ITGA6
CaMax: 581a			NM_014553	PF04516	IPR007604			

CaMax: 583e				PF00039 PF00041	IPR006209 IPR000083 IPR002086 IPR003962 IPR003961			Fn1
CaMax: 58a	ENST000 00313783							
CaMax: 597c	FALZ_H UMAN	601819	NM_182641 NM_004459	PF02791 PF00628 PF00439	IPR001687 IPR000345 IPR001487 IPR006209 IPR001965 IPR004022 IPR000694			FALZ
CaMax: 59a	swissnew SMO2_M OUSE							
CaMax: 59a	ENST000 00230324							
CaMax: 609a	Genscan: RNOR010 94784.371 6.7206							
CaMax: 611a	Transcript :ENST000 00256653							
CaMax: 622a	gp 345323 52							
CaMax: 622a	Genscan: AC10793 9.5.1.1452 64.83212. 131724							
CaMax: 623a	IQG1_HU MAN	603379	NM_003870	PF00307 PF00397 PF00612 PF00616 PF03836	IPR001936 IPR001202 IPR001715 IPR000048 IPR000593			IQGAP1
CaMax: 624b	ENSMUS T0000005 8265							
CaMax: 626a	trembl BC 046507_1							
CaMax: 626a	ENST000 00261631							
CaMax: 628a	KRM1_H UMAN		NM_153379 NM_032045	PF00431	IPR000859		Tmhmm	KREMEN1 □
CaMax: 635a		605975	NM_005839	PF01480	IPR002965 IPR002483 IPR001472			SRRM1
CaMax: 638b	TCTL_H UMAN	300302	NM_006520	PF03645	IPR005334			TCTE1L
CaMax: 639a	ENST000 00309558							
CaMax: 63a	trembl AY 259036_1							
CaMax: 63a	Transcript :ENST000 00332194							
CaMax: 64.2a	Y121_HU MAN							

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CaMax: 685a	U183_HU MAN		NM_025187	PF03676	IPR005373			
CaMax: 690a	ENST000 00244411							
CaMax: 690a	ENST000 00244411							
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CaMax: 697a				PF00443	IPR005479 IPR001394			
CaMax: 6b	Z216_MO USE							
CaMax: 701a			NM_146000		IPR001472			D030060M 11Rik
CaMax: 704b		243305	NM_014425	PF00023 PF00612	IPR002110 IPR000048			INVS
CaMax: 704b		243305	NM_014425	PF00023 PF00612	IPR002110 IPR000048			INVS
CaMax: 70d	ENST000 00323467							
CaMax: 710a	CA1A_H UMAN	120110 156500 184250	NM_000493	PF01391 PF00386	IPR001073 IPR008160	Sigp		COL10A1
CaMax: 711a	trembl AK 019226_1							
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CaMax: 713a	trembl BC 008338_1							
CaMax: 713a	ENST000 00012559							
CaMax: 714a	Genscan: AL391495 .16.1.1429 52.28457. 34558							
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CaMax: 720a	NU4M_C ANFA							
CaMax: 725a				PF00063 PF00612	IPR001687 IPR001609 IPR000048			
CaMax: 726b	GDC_HU MAN	139080	NM_152707	PF00153	IPR001993 IPR002167 IPR002067			SLC25A16
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CaMax: 739a			NM_133375	PF00773	IPR001900			
CaMax: 73b	KE4_HU MAN	601416	NM_006979	PF02535	IPR002395 IPR003689	Sigp	Tmhmm	HKE4

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CaMax: 765a					IPR001687			
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CaMax:	ENST000							

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CaMax: 863c	SLUG_M OUSE		NM_011415	PF00096	IPR007087 IPR007086			Snai2
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CaMax: 909a	AMD_HU MAN	170270	NM_000919 NM_138766 NM_138822 NM_138821	PF01082 PF03712 PF01436	IPR002086 IPR000323 IPR000720 IPR001258	Sigp	Tmhmm	PAM
CaMax: 90c	HS9B_M OUSE		NM_008302	PF02518 PF00183	IPR001404 IPR003594			Hspcb
CaMax: 911a	trembl AB 012223_1							

CaMax: 911a	ENST000 00292530							
CaMax: 912b	gp 345354 83							
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CaMax: 914a	ENST000 00273342							
CaMax: 915a	swiss AL U6_HUM AN							
CaMax: 915a	ENST000 00262877							
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CaMax: 92c		602691	NM_147233 NM_003743 NM_147223	PF00010 PF00989	IPR001092 IPR000014 IPR001472			NCOA1
CaMax: 935b	CHUR_H UMAN		NM_145165		IPR000345			C14orf52
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994b				PF00415 PF00651	IPR000408 IPR002110 IPR000210			
CaMax: 996a	RS20_HU MAN	603682	NM_001023	PF00338	IPR001687 IPR001848			RPS20

[0052] One embodiment of the invention relates to a combination comprising two or more polynucleotide molecules selected from SEQ ID NOs:1-1558, or fragments thereof. Preferably, the combination comprises about 10 or more polynucleotide molecules, more preferably about 50 or more polynucleotide molecules, more preferably about 200 or more polynucleotide molecules, more preferably about 400 or more polynucleotide molecules, more preferably about 1000 or more polynucleotide molecules.

[0053] In a preferred embodiment, the invention relates to a combination of 396 differentially expressed polynucleotide molecules, whose sequences are represented by SEQ ID NOs:1-396. Table 3 identifies a list of gene sequences determined from clinical samples to be differentially expressed in OA versus normal subjects to a degree that is statistically significant ($p < 0.05$). Table 3 includes the gene IDs, expression values, standard deviations, and fold difference of expression (OA versus normal). Preferably, the combination comprises two or more of polynucleotide molecules selected from SEQ ID NOs:1-396 or fragments thereof.

[0054] In a particularly preferred embodiment, the invention relates to a combination of 217 differentially expressed polynucleotide molecules, whose sequences are represented by SEQ ID NOs:1-217. Table 4 identifies a list of gene sequences determined from clinical samples to be differentially expressed in OA versus normal subjects to a degree that is highly significant ($p < 0.01$). Table 4 includes the gene IDs, expression values, standard deviations, and fold difference of expression (OA versus normal). Preferably, the combination comprises two or more of polynucleotide molecules selected from SEQ ID NOs:1-217 or fragments thereof.

[0055] According to an aspect of the invention, one or more oligonucleotide or polynucleotide probes for interrogating a sample may be prepared using the sequence information set forth herein for any of the 1558 isolated gene fragments (SEQ ID NOs:1-1558). According to another aspect of the invention, probes may be prepared using the sequence information available for any of the genes or gene fragments identified in . The probes should be of sufficient length to specifically hybridize substantially exclusively with appropriate complementary genes or transcripts. Preferably, the oligonucleotide probes will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some embodiments, longer probes of at least about 30, 40, 50, 60, 70, 80, 90 or 100 nucleotides are desirable, and probes longer than about 100 nucleotides may be suitable in some embodiments. Preferably, a collection of two or

more nucleic acid probes for detecting expression of gene products differentially expressed in OA is provided, more preferably a collection of about 10 or more probes, more preferably a collection of about 50 or more probes, more preferably a collection of about 200 or more probes, more preferably a collection of about 400 or more probes, more preferably a collection of about 1000 or more probes.

[0056] In a preferred embodiment of the invention, one or more oligonucleotide or polynucleotide probes may be prepared using the sequence information set forth for any of SEQ ID NOs:1-396. Preferably, one or more oligonucleotide or polynucleotide probes may be prepared using the sequence information set forth for any of SEQ ID NOs:1-217.

[0057] In certain preferred embodiments of the present invention, immobilized nucleic acid probes may be used for the rapid and specific detection of nucleic acid molecules and their expression patterns. Typically, a nucleic acid probe is linked to a solid support and a target nucleic acid (e.g., a genomic nucleic acid, an amplicon, or, most commonly, an amplified mixture) is hybridized to the probe. Either the probe, or the target, or both, can be labeled, typically with a fluorophore or other tag, such as streptavidin. Where the target is labeled, hybridization may be detected by detecting bound fluorescence. Where the probe is labeled, hybridization is typically detected by quenching of the label. Where both the probe and the target are labeled, detection of hybridization is typically performed by monitoring a color shift resulting from proximity of the two bound labels. A variety of labeling strategies, labels, and the like, particularly for fluorescent based applications, are known in the art.

[0058] Another aspect of the invention relates to one or more probes comprising polypeptide binding agents that specifically bind to polypeptides produced by expression of one or more nucleic acid molecules comprising sequences selected from SEQ ID NOs:1-1558 or fragments thereof. According to another aspect of the invention, protein binding probes may be prepared using the sequence information available for any of the genes or gene fragments identified in Table 2. Preferably, a collection of two or more polypeptide probes for detecting expression of gene products differentially expressed in OA is provided, more preferably a collection of about 10 or more probes, more preferably a collection of about 50 or more probes, more preferably a collection of about 200 or more probes, more preferably a collection of about 400 or more probes, more preferably a collection of about 1000 or more probes.

[0059] In a preferred embodiment of the invention, probes comprising polypeptide binding agents specifically bind to polypeptides produced by nucleic acid molecules comprising sequences selected from SEQ ID NOs:1-396. In a particularly preferred embodiment, probes

comprising polypeptide binding agents specifically bind to polypeptides produced by nucleic acid molecules comprising sequences selected from SEQ ID NOs:1-217.

[0060] Assay techniques that can be used to determine levels of a protein in a sample are also well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assays. In the assay methods utilizing antibodies, both polyclonal and monoclonal antibodies are suitable for use in the present invention. Such antibodies may be immunologically specific for a particular protein, or an epitope of the protein, or a protein fragment, as would be well understood by those of skill in the art. Methods of making polyclonal and monoclonal antibodies immunologically specific for a protein or peptide are also well known in the art.

[0061] Preferred embodiments of the present invention may utilize antibodies for the detection and quantification of proteins produced by expression of the polynucleotides described herein. Though proteins may be detected by immunoprecipitation, affinity separation, Western blot analysis and the like, a preferred method utilizes ELISA-type methodology wherein the antibody is immobilized on a solid support and a target protein or peptide is exposed to the immobilized antibody. Either the probe, or the target, or both, can be labeled. A variety of labeling strategies, labels, and the like, are known in the art.

[0062] In particularly preferred embodiments of the invention, expression patterns or profiles of a plurality of genes differentially expressed in osteoarthritis are observed utilizing arrays of probes for detecting target nucleic acids or proteins. In one embodiment, arrays of oligonucleotide or polynucleotide probes may be utilized, whereas another embodiment may utilize arrays of antibodies or other proteins that bind specifically to the differentially expressed gene products. Such arrays are commercially available (e.g., through Affymetrix, Inc., Applied Biosystems, Inc., Agilent, Inc.), or they may be custom made according to known methods, such as, for example, *in-situ* synthesis on a solid support or attachment of pre-synthesized probes to a solid support via micro-printing techniques. In preferred embodiments, arrays of nucleic acid or protein-binding probes are custom made to specifically detect transcripts or proteins produced by two or more of the 1558 differentially expressed genes or gene fragments described herein. In one embodiment of the invention, arrays of nucleic acid or protein-binding probes are custom made to specifically detect transcripts or proteins produced by two or more of the genes or gene fragments identified in Table 2. In a preferred embodiment, arrays of nucleic acid or protein-binding probes are custom made to specifically detect transcripts or proteins produced by two or more of the 396 differentially expressed genes or gene fragments identified in Table 3. In a preferred embodiment, arrays of nucleic acid or protein-binding probes are custom made to

specifically detect transcripts or proteins produced by two or more of the 217 differentially expressed genes or gene fragments identified in Table 4.

[0063] Preferably, a collection of two or more nucleic acid or polypeptide probes for detecting expression of gene products differentially expressed in OA is immobilized on a support in discrete locations, more preferably a collection of about 10 or more probes, more preferably a collection of about 50 or more probes, more preferably a collection of about 200 or more probes, more preferably a collection of about 400 or more probes, more preferably a collection of about 1000 or more probes.

[0064] Since chondrocytes represent the cellular component of cartilage, a tissue affected by OA, the construction of a chondrocyte array may represent a powerful tool to study the gene expression profile of osteoarthritic chondrocytes. The use of differential display for transcript selection was used by the present inventors to enrich the clones represented on an array for transcripts associated with OA.

[0065] In one aspect of the invention, methods are provided for assaying OA-associated nucleic acids in a sample. Preferably, a combination comprising one or more polynucleotide molecules selected from SEQ ID NOs:1-1558, more preferably selected from SEQ ID NOs:1-396, more preferably selected from SEQ ID NOs:1-217, are used to prepare probes that are hybridized with nucleic acids of a test sample, forming hybridization complexes that are detected and compared with those of a standard, such that differences between the sample and standard hybridization complexes are indicative of differential expression of nucleic acids in the sample. In a preferred embodiment, nucleic acid probes are made to specifically detect transcripts or fragments thereof produced by one or more of the genes or gene fragments identified in Table 2. In certain preferred embodiments, the nucleic acids of the sample may be amplified prior to hybridization.

[0066] In another aspect of the invention, methods are provided for assaying OA-associated polypeptides in a sample. Preferably, polynucleotide sequences selected from SEQ ID NOs:1-1558, more preferably selected from SEQ ID NOs:1-396, more preferably selected from SEQ ID NOs:1-217 are used to prepare protein-binding probes that specifically bind to translation products of those polypeptides or fragments thereof. These probes are reacted with a test sample, forming binding complexes that are detected and compared with those of a standard, such that differences between the sample and standard binding complexes are indicative of differential expression of polypeptides in the sample. In a preferred embodiment, protein-binding probes are made to specifically detect polypeptides or fragments thereof produced by one or more of the genes or gene fragments identified in Table 2.

[0067] According to certain preferred embodiments of the invention, the assays described herein for the detection of OA-associated transcription and translation products may be used in methods useful for determining a diagnosis and/or prognosis for osteoarthritis in a patient. According to an embodiment of the invention, a typical diagnostic test will comprise obtaining a sample of cells or tissue from a patient in which OA-associated gene expression is expected to occur. Such cells or tissues include, but are not limited to, cartilage tissue and chondrocytes. The sample is then analyzed for either 1) increased or decreased expression of one or more selected genes, via detection of mRNA or protein, or 2) a particular gene expression profile, for example, via gene or protein array technology, as described herein. Such a diagnostic procedure should lead to a determination of whether indications of osteoarthritis are present in the patient.

[0068] In another embodiment of the invention, the diagnostic procedures described herein may also be extended to provide prognostic information regarding a patient's recovery from OA, or to monitor a patient's progress in response to a therapeutic regimen. In these situations, the diagnostic assay is performed at intervals during the patient's recovery or course of treatment, and a change in expression of a target gene, or a particular change in the pattern of gene expression, is indicative of the patient's level of recovery or improvement.

[0069] In one aspect of the invention, assays are provided for identifying substances effective in treatment modalities for osteoarthritis. In one embodiment of the invention, a method is provided for measuring the effect of a test substance on the expression profile of genes differentially expressed in osteoarthritis, comprising the steps of: a) obtaining a standard expression profile from a first sample by measuring transcription or translation products of two or more genes corresponding to two or more genes or gene fragments identified in Tables 1 and/or 2 in the absence of the test substance; b) obtaining a test expression profile from a second sample by measuring the transcription or translation products of two or genes or gene fragments identified in Tables 1 and/or 2 expressed in the presence of the test substance; c) comparing the standard expression profile the test expression profile, wherein a change in the test expression profile compared to the standard expression profile is indicative of an effect of the test substance on the expression profile of genes differentially expressed in osteoarthritis compared to a non-osteoarthritic condition. Preferably, the two or more genes or gene fragments correspond to two or more of the genes or gene fragments identified in Table 3 (SEQ ID NOs:1-396). More preferably, the two or more genes or gene fragments correspond to two or more of the genes or gene fragments identified in Table 4 (SEQ ID NOs:1-217). In certain preferred embodiments, the samples are obtained from cultured cells. In this case, the standard expression profile is

obtained from cells that have not been contacted with the test substance, while the test expression profile is obtained from cells that have been contacted with a test substance.

[0070] Test compounds may include proteins, polypeptides, nucleic acids, small molecule pharmaceuticals, vitamins, minerals, fatty acids, polysaccharides, extracts, nutraceuticals, and the like. In a preferred embodiment, the test compounds are nutrients that may be added to food or other dietary substances, or that may be taken as a dietary supplement. As exemplified herein, such nutrients include, but are not limited to, fatty acids such as omega-3 fatty acids (e.g., eicosapentaenoic acid) and omega-6 fatty acids (e.g., arachidonic acid), glucosamine, chondroitin sulfate and vitamin D derivatives such as 1 α ,25-dihydroxyvitamin D3 and 24R,25-dihydroxyvitamin D3.

[0071] One type of assay according to an embodiment of the invention involves measuring the activity of the protein encoded by one of the aforementioned OA-associated genes in the presence or absence of a candidate substance. Such activity assays are well known in the art. If a cell-free activity assay is available for the selected protein, such an assay is simply conducted on the purified protein in the presence or absence of the test substance. Candidate substances are selected based on their ability to positively or negatively regulate activity of the purified protein. It should be noted that assays of this type may be performed, for example, in a recombinant cellular system, as described below. They can also be performed, for example, in a cell-free system in some instances.

[0072] For such *in vitro* activity assays, it is desirable to have a source of the purified protein of interest. One or more of the protein products of the genes mentioned above may be commercially available, or purifiable in significant quantities from an appropriate biological source, e.g., cultured cells. Alternatively, the proteins may be recombinantly produced from an isolated gene or cDNA by expression in a suitable procaryotic or eucaryotic expression system, and thereafter purified, as is also well known in the art.

[0073] Another embodiment of the invention comprises *in vitro* cellular assays for expression of OA-associated genes or activity of their encoded proteins. For these embodiments, a nucleic acid construct comprising an OA-associated gene according to an aspect of the invention is introduced into host cells. In a preferred embodiment, mammalian cell lines are utilized. Host cells contemplated for use include, but are not limited, to NIH3T3, CHO, HELA, and COS, as well as non-mammalian cells such as yeast, bacteria and insect cells. The coding sequences are operably linked to appropriate regulatory expression elements suitable for the particular host cell to be utilized. Methods for introducing nucleic acids into host cells are well known in the art. Such methods include, but are not limited to, transfection, transformation,

calcium phosphate precipitation, electroporation and lipofection. The recombinant cells may be used to identify compounds which modulate expression of the OA-associated genes or activity of their encoded proteins.

[0074] For gene expression assays, it is preferred to prepare an artificial construct comprising the promoter of a selected OA-associated gene, operably linked to a reporter gene. The reporter construct may be introduced a cultured cell, including, without limitation, the standard host cell lines described above, or other suitable cells, for example, cartilage-related cells such as chondrocytes. The assay is performed by monitoring expression of the reporter gene in the presence or absence of a test compound. Candidate substances are selected based on their ability to positively or negatively affect expression of the gene.

[0075] In another embodiment of the invention, OA-associated genes and gene fragments described herein may be used to manipulate the genome of non-human animal subjects. Methods of manipulating the genomes of a variety of animals are known to those of skill in the art. Such methods may include, without limitation, the production of transgenic and gene-knockout animals. In a preferred embodiment of the invention, a gene or gene fragment identified in Table 2 is used to prepare a construct that is used to disrupt or "knock out" the corresponding endogenous gene in an animal, thus producing an animal having a null mutation for that gene locus. In some embodiments, the animals exhibit a reduction or complete elimination of the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs:1-1558. In some embodiments, the animals exhibit a reduction or complete elimination of the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NO: 1-396. In some embodiments, the animals exhibit a reduction or complete elimination of the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NO: 1-217. In other embodiments, the animals exhibit a reduction or complete elimination of the expression of one or more genes shown in Table 6. The transgenic animals are preferably mammals. In some embodiments, the transgenic animals are rodents (*e.g.*, mice and rats). In other embodiments, the animals are, for example, goats, cats, dogs, cows, pigs, sheep, horses, non-human primates, rabbits, and guinea pigs. In some embodiments, small interfering RNAs are used to functionally disrupt the genes. Briefly, gene expression is inhibited by a short interfering RNA (siRNA) through RNA interference (RNAi) or post-transcriptional gene silencing (PTGS) (see, for example, Ketting *et al.* (2001) *Genes Develop.* 15:2654-2659). siRNA molecules can target homologous mRNA molecules for destruction by cleaving the mRNA molecule within the region spanned by the siRNA molecule. Accordingly, siRNAs capable of targeting and cleaving mRNA of the gene products shown in Table 6 may be used to

decrease or eliminate expression of one or more of these genes. In other embodiments, siRNAs capable of targeting and cleaving mRNA of one or more of the genes shown in Table 1 (SEQ ID NOS:1-1558) may be used to decrease or eliminate expression of one or more of these genes.

[0076] In another embodiment of the invention, OA-associated genes and gene fragments described herein are used to design molecules that may be used to interfere with the expression of one or more OA-associated genes; such molecules may include, without limitation, RNA interference probes and antisense molecules.

[0077] Another aspect of the invention features compositions of matter to facilitate practice of the assays described above. These compositions may comprise collections of two or more probes or primers for use in detecting differentially expressed OA-related genes, gene fragments and encoded proteins according to certain aspects of the invention. In one embodiment, the compositions may comprise collections of two or more oligonucleotides or polynucleotides that specifically hybridize with nucleic acid molecules selected from SEQ ID NOS:1-1558. Preferably, the compositions may comprise collections of two or more oligonucleotides or polynucleotides that specifically hybridize with nucleic acid molecules selected from SEQ ID NOS:1-396. More preferably, the compositions may comprise collections of two or more oligonucleotides or polynucleotides that specifically hybridize with nucleic acid molecules selected from SEQ ID NOS:1-217. Preferably, the composition may comprise collections of two or more oligonucleotides or polynucleotides that specifically hybridize with genes and/or gene fragments selected from the genes and gene fragments identified in Table 2. The collection may comprise a primer pair for amplifying the sequence. In certain preferred embodiments, amplification may be performed using Polymerase Chain Reaction (PCR), more preferably quantitative PCR (qPCR). In a preferred embodiment, the collection comprises a larger plurality of probes, e.g., about 10, 50, 200, 400, 1000 or more probes, each of which hybridizes specifically with part or all of one of the sequences of SEQ ID NOS:1-1558. In a preferred embodiment, nucleic acid probes are immobilized on a solid support. In a particularly preferred embodiment, they are immobilized in an array format, most preferably in a miniature or micro-array. Such micro-arrays are known in the art, and are sometimes referred to as "DNA chips," "microchips," "biological chips" and other similar terms, and may contain the entire array of genes or gene fragments altered by OA, in addition to those represented in Tables 1 and 2.

[0078] In another embodiment, these compositions comprise two or more protein binding substances capable of specifically binding proteins or protein fragments encoded by the genes and gene fragments identified in Tables 1 and 2. In a preferred embodiment the binding

substances are antibodies and the collection comprises two or more antibodies for detecting two or more proteins or peptides encoded by SEQ ID NOS:1-1558, respectively. Preferably, these compositions comprise two or more protein binding substances capable of specifically binding proteins or protein fragments encoded by the genes and gene fragments of SEQ ID NOS:1-396. More preferably, these compositions comprise two or more protein binding substances capable of specifically binding proteins or protein fragments encoded by the genes and gene fragments of SEQ ID NOS:1-217. Such binding substances may be any molecule to which the protein or peptide specifically binds, including DNA (for DNA binding proteins), antibodies, cell membrane receptors, peptides, cofactors, lectins, sugars, polysaccharides, cells, cell membranes, organelles and organellar membranes. In a preferred embodiment, the collection comprises a larger plurality of antibodies, e.g., about 10, 50, 200, 400, 1000 or more, each of which binds immunospecifically with part or all of a protein or peptide encoded by genes or gene fragments identified in Tables 1 and/or 2. In a preferred embodiment, the antibodies are immobilized on a solid support. In a particularly preferred embodiment, they are immobilized in an array format, most preferably in a miniature or micro-array, as described above for oligonucleotide probes, and may contain the entire array of proteins altered by OA, in addition to genes or gene fragments identified in Tables 1 and 2.

[0079] Another embodiment of the present invention relates to substances or compounds identified in any of the methods described herein as having an effect on the expression profile of genes differentially expressed in OA. Preferably, such substances will be effective in the treatment and/or prevention of OA.

[0080] Still another aspect of the invention features test kits for use in one or more of the assays described herein. One type of kit comprises one or more pairs of primers for amplifying nucleic acids corresponding to the OA-associated genes and gene fragments described herein. The kit may further comprise samples of total mRNA derived from tissue of various physiological states, for use as controls. The kit may also comprise buffers, nucleotide bases, and other compositions to be used in hybridization and/or amplification reactions. Each solution or composition may be contained in a vial or bottle and all vials held in close confinement in a box for commercial sale.

[0081] Another type of kit comprises one or more nucleic acid or protein-binding probes, wherein the nucleic acid probe hybridizes specifically with a OA-associated gene or gene fragment according to certain aspects of the invention, or the protein-binding probe specifically binds to a protein encoded by the OA-associated gene or gene fragment. Preferably, the protein-binding probe is an antibody that is immunologically specific for the protein encoded by the OA-

associated gene or gene fragment. In preferred embodiments, the nucleic acid or protein-binding probes are immobilized on a solid support. In a particularly preferred embodiment, the kit comprises immobilized arrays of nucleic acid or protein-binding probes, the arrays comprising probes specific for a plurality of the OA-associated genes or gene fragments described herein, or proteins encoded thereby. These kits also may contain appropriate control samples of mRNA or protein from tissues of known physiological state, to be used as controls in the assays. They may further comprise buffers and reagents for performing the assays. Each solution, reagent or composition in the kit may be contained in a vial or bottle and all vials held in close confinement in a box for commercial sale. Preferably, kits may further comprise instructions for performing an assay of gene expression.

[0082] In another aspect, the invention provides a method for altering biological profile of cells through inducing a change in the gene expression profile of the cells with respect to genes involved in OA. The method involves administering to cells an effective amount of a compound that alters the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs:1-1558. In some embodiments, the compound affects the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs:1-396. In some embodiments, the compound affects the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs:1-217. In other embodiments, the compound affects the expression of one or more genes having the gene products shown in Table 6. The invention also provides a method of affecting the expression of genes involved in OA comprising exposing cells to an effective amount of a compound that modulates expression of one or more genes having a sequence selected from SEQ ID NOs:1-1558. In some embodiments, the compound affects the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs: 1-396. In some embodiments, the compound affects the expression of one or more genes having a nucleic acid sequence selected from SEQ ID NOs: 1-217. In other embodiments, the compound affects the expression of one or more genes having the gene products shown in Table 6.

[0083] In some embodiments the cells are cells associated with symptoms of osteoarthritis. In some embodiments the cells are chondrocytes. In some embodiments the compounds are administered to cells *in vitro*. In other embodiments the compounds are administered to cells *in vivo*. The compounds may be administered to subjects *via* any route of administration. Preferably, the subjects are vertebrates. More preferably, the subjects are mammals including dogs, cats and humans.

[0084] The change in gene expression is preferably at least a 1.01 fold difference. More preferably, it is at least a 1.05, 1.10, 1.25, 1.50, 1.75, 2.0, 2.25, 2.50, 2.75, 3.0, 3.25, 3.50, 3.75, 4.0 fold difference or more.

[0085] Chondroitin sulfate was shown to have an effect on a wide variety of OA-associated genes as shown in detail in Tables 7-12. Glucosamine was also found to have an effect on a variety of OA-associated genes as shown in detail in Tables 13-18. $1\alpha,25$ -dihydroxyvitamin D3 and 24R,25-dihydroxyvitamin D3 also affected the expression of OA-related genes as shown in Tables 19-20. Eicosapentaenoic acid (EPA) and arachidonic acid (AA) were also shown to affect OA-related genes as shown in Tables 21-23.

[0086] The following examples are provided to describe the invention in greater detail. They are intended to illustrate, not to limit, the invention.

EXAMPLE 1

Extraction of RNA from chondrocytes

[0087] Normal and osteoarthritic canine cartilage chondrocytes (N_2 -flash frozen) were obtained and stored at -80°C . Osteoarthritic chondrocytes originated from canines clinically diagnosed with osteoarthritis undergoing total hip replacement. 300 to 500 mg were ground in N_2 (mortar and pestle) and transferred to a clean, pre-chilled, 50 ml tube. Trizol (2ml/100mg) was added and the mixture was homogenized using a Polytron for 2 x 30 seconds, and 1 minute (high speed). The homogenate was then centrifuged at $10,000 \times g$ for 10 minutes at 4°C . The supernatant was removed and 0.2 volumes chloroform added to the supernatant, vortexed, and centrifuged at $10,000 \times g$ for 15 minutes at 4°C . The upper aqueous phase was removed and 5 volumes of 4 M Guanidine thiocyanate, 25 mM sodium citrate, 0.5% sarkosyl, 0.1 M beta-mercaptoethanol and .475 volumes of 100 % ethanol were added to the upper aqueous phase. The solution was then applied to Qiagen RNAqueous mini-columns (cat # 74104), using a vacuum manifold (according to the manufacture's directions) for further purification of the RNA. The purified RNA was then ethanol precipitated to concentrate, resuspended in DEPC water and DNase I treated to remove residual DNA. The DNA-free™ DNase Treatment kit from Ambion (cat #1906) was used for DNase I treatment according to the manufacture's directions.

[0088] RNA was quantitated in a Beckman DU 640B spectrophotometer at 260 nm (Beckman Coulter, Inc., 4300 N. Harbor Boulevard, P.O. Box 3100, Fullerton, CA 92834-3100). Absorbance of 1 at 260nm is equivalent to 40 μg RNA/ml. Typical yields were 0.65 to 0.8

µg/µl. Quality of RNA was determined by the absorbance at 260 nm/280 nm with a typical ratio of 1.7 – 2.0. Quality was also assessed by electrophoresis in a 1% agarose gel/formaldehyde/Tris-borate-EDTA (TBE), pH 7.8 buffer (90mM Tris, 90mM boric acid, 2mM EDTA). Approximately 1 to 3.5 µg RNA was loaded (2 to 5 µl) after being mixed with 15 µl gel loading solution (10mM Tris pH 7.5, 1mM EDTA, 0.02% bromophenol blue, 10% glycerol). The gel was run at 50 Volts for 3-4 hours, stained with SYBR Green I (Molecular Probes, Inc., PO Box 22010, Eugene, OR 97402-0469, 4849 Pitchford Ave., Eugene, OR 97402-9165) at a dilution of 1:10,000 for 30 minutes in the dark and scanned using a Hitachi FMBIO II Fluorescent scanner at 505 nm (Hitachi Genetic Systems, 1201 Harbor Bay Parkway Ste. 150, Alameda, CA 94502).

Example 2

Differential Display

[0089] Fluorescent differential display was performed using one of three anchored primers in combination with one of 80 arbitrary primers (GenHunter). In all, 240 PCR reactions were carried out. Reactions were separated using PAGE and visualized using a fluorescent scanner (FMBIOII, Hitachi). Bands representing differentially expressed genes were excised, reamplified and run on an agarose gel to verify size. These were subsequently subcloned (PCR-TRAP, GenHunter) and sequenced.

[0090] Differential display was performed using GenHunter's RNAimage® kit or RNAspectra™ green fluorescent mRNA differential display systems (GenHunter Corporation, 624 Grassmere Park Drive, Suite 17, Nashville, TN 37211). Approximately 200 ng of RNA was reverse transcribed in the following reaction (final concentration): RT buffer (25 mM Tris-Cl, pH 8.3, 37.6 mM KCl, 1.5 mM MgCl₂, 5 mM DTT), 625 µM ea. dNTP, 50 pmol H-T₁₁G primer (GenHunter) (5' AAGCTTTTTTTTTTTTG 3') (SEQ ID NO:1559), or H-T₁₁C primer (GenHunter) (5' AAGCTTTTTTTTTTTTC 3') (SEQ ID NO:1560), or H-T₁₁A primer (GenHunter) (5' AAGCTTTTTTTTTTTTA 3') (SEQ ID NO:1561), in a total volume of 19 µl. 1µl (100 units/µl) of MMLV reverse transcriptase was added ten minutes into the 37°C step in a thermocycler (GeneAmp PCR System 9700, PE Applied Biosystems, 850 Lincoln Center Dr., Foster CA 94404) and the following reaction performed: 65°C 5 minutes, 37°C 60 minutes, 75°C 5 minutes followed by a hold at 4°C. Two µl of the reverse transcription reaction was used in the following polymerase chain reaction: PCR buffer (10mM Tris-Cl, pH 8.4, 50 mM KCl, 1.5 mM MgCl₂, 0.001% gelatin), 50 µM each dNTP, 5 pmol Fluorescein-labeled H-T₁₁G primer (GenHunter) (Fluorescein-labeled primer, 5' AAGCTTTTTTTTTTTTG 3') (SEQ ID NO:1562),

or Fluorescein-labeled H-T₁₁C primer (GenHunter) (Fluorescein-labeled primer, 5' AAGCTTTTTTTTTTTC 3') (SEQ ID NO:1563) or Fluorescein-labeled H-T₁₁A primer (GenHunter) (Fluorescein-labeled primer, 5' AAGCTTTTTTTTTTTTA 3') (SEQ ID NO:1564) one of the H-AP primers provided in the kit at 200 pM, 1 unit of Amplitaq DNA polymerase (PE Applied Biosystems, 850 Lincoln Center Dr., Foster CA 94404) in a total of 20 μ l.

[0091] The following thermocycler reaction was used: 40 cycles of 94°C 15 seconds, 40°C 2 minutes, 72°C 30 seconds, followed by 72°C 5 minutes and a 4°C hold.

[0092] 5 μ l of each PCR sample was mixed with 5 μ l blue dextran loading buffer and 10 μ l deionized formamide and electrophoresed on a 6% polyacrylamide gel at 55 watts for 3 hours in TBE buffer. The gel was scanned using a Hitachi FMBIO II at 505 nm. cDNA bands differentially expressed were excised with a razor, placed in a 1.5 ml tube, soaked in 100 μ l sterile water for 10 minutes and then boiled for 15 minutes. Tubes were centrifuged for 2 minutes at 10,000 x g and the supernatant transferred to a new tube. 10 μ l 3M sodium acetate, 5 μ l glycogen (10 mg/ml) and 450 μ l 100% ethanol was added to the supernatant and the tubes were placed at -80°C overnight. Samples were centrifuged at 10,000 x g for 10 minutes at 4 °C and the supernatant was removed. cDNA pellets were washed with cold (-20°C) 85% ethanol, spun as above for 1 minute and the supernatant was removed. cDNA pellets were resuspended in 10 μ l sterile water.

[0093] Four μ l samples of the cDNA extracts were amplified the same as in the above PCR reaction with the following exceptions: 40 μ l total reaction volume; 20 μ M ea. dNTP; 200 pM unlabeled primer H-T₁₁G , H-T₁₁C , or H-T₁₁A (GenHunter) and 2 units of Amplitaq DNA polymerase (PE Applied Biosystems). PCR conditions were the same as above. 15 μ l of the amplified cDNA extracts were mixed with 3 μ l 6X loading dye (0.25% bromophenol blue, 0.25% xylene cyanol FF, 30% glycerol) and electrophoresed in a 1.5% agarose gel. The gel was run at 100 volts for 2 to 3 hours in TBE buffer, stained/visualized the same as above. Bands were excised with a razor and cDNA extracted according to Qiagen's QIAEX® II Gel Extraction Kit (Qiagen, Inc., 28159 Avenue Stanford, Valencia, CA 91355). Three hundred μ l QX1 buffer and 10 μ l QIAEX® II suspension was added to each gel slice in a 1.5 ml tube and incubated at 50°C for 10 minutes. Tubes were vortexed every 2 minutes during incubation. Tubes were centrifuged 10,000 x g for 30 seconds and the supernatant was discarded. Pellets were washed once with 500 μ l Buffer QX1 and twice with buffer PE (vortexing and centrifuging as above for each wash). Pellet was air dried for 10 minutes and 20 μ l sterile water was added. Tubes were

incubated for 5 minutes at room temperature and cDNA was eluted by centrifugation as above for 30 seconds. Supernatant was then transferred to a new 1.5 ml tube and stored at -20°C.

[0094] Amplified gel purified cDNA was subcloned according to GenHunter's PCR-TRAP® Cloning System Kit (GenHunter Corporation, 624 Grassmere Park Drive, Suite 17, Nashville, TN 37211). 5 µl amplified gel purified cDNA was added to 300 ng PCR-TRAP® vector, ligase buffer (50 mM Tris-Cl, pH 7.8, 10 mM MgCl₂, 10 mM DTT, 10 mM ATP, 5 µg BSA) and 200 units T4 DNA ligase, mixed, and incubated overnight at 16°C. GH competent cells (*E. coli* del(*lac-pro*) *ara thi* (φ80dlacZdelM15)) were transformed with ligation reaction by mixing 10 µl ligation reaction to 100 µl GH competent cells on ice in 1.5 ml tubes. Tubes were incubated on ice for 45 minutes, heat shocked at 42°C for 2 minutes and then incubated on ice for 2 minutes. 400 µl LB broth (Luria-Bertani, Difco) was added to each tube and the tubes were incubated at 37°C for 1 hour with shaking (250 rpm). 200 µl of these transformations were plated onto LB-agar-tet plates (LB-agar, Difco, tetracycline 20 µg/ml) and incubated overnight at 37°C.

[0095] Colonies were checked for insert using GenHunter's colony lysate PCR protocol. Colonies were picked with a clean pipette tip and placed in 50 µl colony lysate buffer (GenHunter, TE with 0.1% Tween 20) in a microfuge tube. Tubes were boiled for 10 minutes, centrifuged at 10,000 x g for 2 minutes and the corresponding lysate (supernatant) was transferred to a new microfuge tube. 2.0 µl of lysate was added to PCR buffer, 20 µM ea. dNTP, 200 pmol ea. of Lgh (5' CGACAACACCGATAATC) (SEQ ID NO:1565) and Rgh (5' GACGCGAACGAAGCAAC) (SEQ ID NO:1566) primers and 1 unit of Amplitaq DNA polymerase (PE Applied Biosystems) in a total volume of 20 µl. The following thermocycler reaction was used: 30 cycles of 94°C for 30 seconds, 52°C for 40 seconds and 72°C for 1 minute followed by 72°C for 5 minutes and a 4°C hold. PCR products were analyzed in a 1.5% agarose gel the same as above.

[0096] 3-5 ml LB broth was inoculated with appropriate colonies and incubated overnight at 37°C at 250 rpm. Plasmids were isolated according to Qiagen's QIAprep Plasmid protocol. Bacteria were pelleted (10,000 x g, 30 seconds) using 2 x 1.5 ml inoculated broth and the supernatant was removed. Pelleted bacteria were resuspended in 250 µl buffer P1, 250 µl buffer P2 was then added and tubes were mixed by gentle inversion. 350 µl buffer N3 was added, tubes were mixed by gentle inversion and then centrifuged for 10 minutes. Supernatants were added to a QIAprep column and centrifuged for 30 seconds. Flow-throughs were discarded, 0.5 ml of buffer PB was added to column and tubes were centrifuged for 30 seconds. Columns

were washed with 0.75 ml buffer PE and centrifuged for 30 seconds. Flow-throughs were discarded and tubes were spun an additional minute. DNA was eluted from the column by adding 50 μ l sterile water to the column. The column was incubated at room temperature for 1 minute and then centrifuged for 1 minute. Resulting supernatant containing plasmid DNA was quantitated as above (absorbance of 1 at 260 nm equals 50 μ g/ml) with a typical yield of 350 μ g/ml and a 260nm/280nm ratio of 1.8.

[0097] Sequencing reactions used 200 to 500 ng plasmid DNA in the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit (PE Applied Biosystems, 850 Lincoln Center Dr., Foster CA 94404). 0.8 μ l of primer (0.16 μ M final concentration of either Lgh or Rgh, GenHunter) was added to plasmid DNA along with 4.0 μ l Terminator Reaction Mix (containing AmpliTaq DNA Polymerase, FS, deoxynucleoside triphosphates, $MgCl_2$, Tris-HCL buffer, pH 9.0, A-Dye Terminator labeled with dichloro(R6G), C-Dye Terminator labeled with dichloro(ROX), G-Dye Terminator labeled with dichloro(R110) and T-Dye Terminator labeled with dichloro(TAMRA)) and brought to a final volume of 10 μ l with sterile water. The following thermocycler reaction was used: 25 cycles of 96°C for 10 seconds, 50°C for 5 seconds, 60°C for 4 minutes followed by a 4°C hold.

[0098] Unincorporated dye-terminators were removed from the sequencing reactions according to Qiagen's DyeEx spin protocol. Prepared DyeEx spin columns were placed in 2.0 ml microfuge tubes and centrifuged at 750 x g for 3 minutes. Columns were placed in new tubes, sequencing reactions were added to columns and centrifuged, as above, for 3 minutes. The eluate was placed at 74°C until dry.

[0099] 5 μ l of formamide/blue dextran (5:1 ratio) was added to each dried sequencing pellets. 1.5 μ l to 2.0 μ l was then added to a 5% polyacrylamide gel (in TBE buffer) on a Perkin Elmer ABI Prism 377 automated DNA sequencer.

[0100] Each isolated plasmid clone was sequenced 2-6 times (2-6 different sequencing reactions, 1-3 times for each primer, Lgh or Rgh). Sequence files from the ABI 377 sequencer were transferred to Genetic Computer Group's Wisconsin Package and a corresponding consensus sequence was determined.

[0101] Approximately 1750 clones were isolated using differential display. All genes that appeared to be differentially expressed were selected. A representational polyacrylamide gel image is shown in Figure 1. Panel A represents the gel prior to band excision and panel B represents the same gel after band excision. Sizes of clones ranged from 90 b.p. to 1150 b.p., with an average size of 300 b.p. After filtering the sequences for redundant sequences, dimers, E. coli fragments, fragments <100 b.p. etc., 1558 remained. Sequences obtained (SEQ ID NOs:1-

1558) are shown in Table 1, which is appended herewith and which forms part of the present specification.

[0102] The sequences obtained were BLASTed against the human, mouse and dog public domain genomes to get a first hit. To be considered a hit at this stage, the match had to cover more than 50% of the sequence and an Expect value (E value) of less than 0.002. The first hits were used to extend the sequence using the respective genome. The sequences were either extended 2kb to the 5' or 3' side of the hit. The extended sequences were then used to BLAST against public domain protein databases (Ensembl, swissprot/trembl). The respective hits (those with an Expect value of less than 0.002, in this case) were consolidated and used for the annotations. In some cases, this strategy did not give hits, and in these situations the original sequences were BLASTed directly against swissprot/trembl or Ensembl proteins. In this case, hits were considered when the Expect value was less than 0.002.

[0103] Results of BLAST analysis (as of 1/28/04) of sequences isolated by differential display are shown in Table 2, which is appended herewith and which forms part of the present specification. The sequences are listed in the leftmost column by the gene ID designations (clone numbers) employed by the inventors herein. Many sequences matched with a Description of a previously-identified gene; the Description column also includes the source database and the corresponding database accession number. Table 2 includes additional information from a number of databases, including Ensemble Gene IDs, Ensemble Transcript IDs, Swissprot/Ensemble, OMIM (Online Mendelian Inheritance in Man), RefSeq, Pfam, InterPro and HUGO. Information is also shown regarding Chromosome Number (#) and Chromosome Location for many of the sequences. Additionally, the column labeled "Signal peptide" indicates the sequences for which a predicted signal peptide occurs in the amino acid sequence; the column labeled "TMHMM" (Transmembrane Hidden Markov Model) indicates sequences for which a predicted transmembrane region occurs in a protein sequence.

Table 6 lists clones demonstrating homology to previously-identified genes.

Table 6

CaMax Gene ID	Description	SEQ ID NO
CaMax: 1006b	BUTYRATE RESPONSE FACTOR 2 (TIS11D PROTEIN) (EGF-RESPONSE FACTOR 2) (ERF-2). [Source:SWISSPROT;Acc:P47974]	1360
CaMax: 1007a	BUTYRATE RESPONSE FACTOR 2 (TIS11D PROTEIN) (EGF-RESPONSE FACTOR 2) (ERF-2). [Source:SWISSPROT;Acc:P47974]	1361
CaMax: 1009c	GRAVE'S DISEASE CARRIER PROTEIN (GDC) (GRAVE'S DISEASE AUTOANTIGEN) (GDA) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:P16260]	905
CaMax: 1019a	ZINC FINGER PROTEIN 333. [Source:SWISSPROT;Acc:Q96JL9]	934
CaMax:	CALCITONIN GENE-RELATED PEPTIDE TYPE 1 RECEPTOR	

1020a	PRECURSOR (CGRP TYPE 1 RECEPTOR). [Source:SWISSPROT;Acc:Q16602]	935
CaMax: 1029a	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	938
CaMax: 1044c	POLY [ADP-RIBOSE] POLYMERASE-3 (EC 2.4.2.30) (PARP-3) (NAD(+) ADP- RIBOSYLTRANSFERASE-3) (POLY[ADP-RIBOSE] SYNTHETASE-3) (PADPRT-3) (HPARP-3) (IRT1). [Source:SWISSPROT;Acc:Q9Y6F1]	1363
CaMax: 104a	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H (HNRNP H). [Source:SWISSPROT;Acc:P31943]	439
CaMax: 1061a	LEUKEMIA-ASSOCIATED PROTEIN WITH A CXXC DOMAIN. [Source:SPTREMBL;Acc:Q8NFU7]	1160
CaMax: 106a	FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). [Source:SWISSPROT;Acc:P02794]	440
CaMax: 1105a	RAS-RELATED PROTEIN RAB-14. [Source:SWISSPROT;Acc:P35287]	1320
CaMax: 1108a	STAR-RELATED LIPID TRANSFER PROTEIN 13 (STARD13) (START DOMAIN- CONTAINING PROTEIN 13) (46H23.2). [Source:SWISSPROT;Acc:Q9Y3M8]	1262
CaMax: 1111b	SESTRIN 1 (P53-REGULATED PROTEIN PA26). [Source:SWISSPROT;Acc:Q9Y6P5]	898
CaMax: 1120a	GOLGI PHOSPHOPROTEIN 3; GOLGI PROTEIN; GOLGI PERIPHERAL MEMBRANE PROTEIN 1, 34 KDA; GOLGI- ASSOCIATED PROTEIN; COAT-PROTEIN. [Source:RefSeq;Acc:NM_022130]	1366
CaMax: 1134a	MYOCYTE-SPECIFIC ENHANCER FACTOR 2C. [Source:SWISSPROT;Acc:Q06413]	1172
CaMax: 1135a	FORKHEAD BOX PROTEIN P2 (CAG REPEAT PROTEIN 44) (TRINUCLEOTIDE REPEAT- CONTAINING GENE 10 PROTEIN). [Source:SWISSPROT;Acc:O15409]	1173
CaMax: 1145a	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:P39059]	1436
CaMax: 104a	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H (HNRNP H). [Source:SWISSPROT;Acc:P31943]	439
CaMax: 1169b	TROPOMYOSIN 1 ALPHA CHAIN (ALPHA-TROPOMYOSIN). [Source:SWISSPROT;Acc:P09493]	1322
CaMax: 1177c	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (CYTOPLASMIC DYNEIN HEAVY CHAIN 1) (DHC1) (FRAGMENT). [Source:SWISSPROT;Acc:Q14204]	943
CaMax: 1184a	T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN). [Source:SWISSPROT;Acc:Q13009]	885
CaMax: 1213d	VAV-3 PROTEIN. [Source:SWISSPROT;Acc:Q9UKW4]	1324
CaMax: 1243a	WD-REPEAT PROTEIN 3. [Source:SWISSPROT;Acc:Q9UNX4]	908
CaMax: 1267a	PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.4.1.3) (PCCASE ALPHA SUBUNIT) (PROPANOYL-COA:CARBON DIOXIDE LIGASE ALPHA SUBUNIT). [Source:SWISSPROT;Acc:P05165]	874
CaMax: 1267a	PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.4.1.3) (PCCASE ALPHA SUBUNIT) (PROPANOYL-COA:CARBON DIOXIDE LIGASE ALPHA SUBUNIT). [Source:SWISSPROT;Acc:P05165]	874
CaMax: 1272a	PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATED PROTEIN A) (FRAGMENT). [Source:SWISSPROT;Acc:O95486]	872
CaMax: 1287c	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_133433]	952
CaMax: 1288a	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_133433]	63
CaMax:	HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (TUMOR SPECIFIC	

128a	TRANSPLANTATION 84 KDA ANTIGEN) (TSTA). [Source:SWISSPROT;Acc:P11499]	234
CaMax: 1292c	ATP-DEPENDENT DNA HELICASE II, 80 KDA SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (KU86) (KU80) (86 KDA SUBUNIT OF KU ANTIGEN) (THYROID- LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 85 KDA SUBUNIT) (CTCBF) (CTC85) (NUCLEAR FACTOR IV) (DNA-REPAIR PROTEIN XRCC5). [Source:SWISSPROT;Acc:P13010]	44
CaMax: 1294b	BIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)]. [Source:SWISSPROT;Acc:P07814]	1245
CaMax: 1299c	WD REPEAT AND FYVE DOMAIN CONTAINING 3 ISOFORM 1. [Source:RefSeq;Acc:NM_014991]	316
CaMax: 1304a	AMISYN; SYNTAXIN BINDING PROTEIN 6. [Source:RefSeq;Acc:NM_014178]	1371
CaMax: 1322c	UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KDA SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT). [Source:SWISSPROT;Acc:P56558]	1372
CaMax: 1341a	CYSTEINE KNOT SUPERFAMILY 1, BMP ANTAGONIST 1; GREMLIN. [Source:RefSeq;Acc:NM_013372]	1269
CaMax: 1354a	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	370
CaMax: 1361a	ALPHA-(1,6)-FUCOSYLTRANSFERASE (EC 2.4.1.68) (GLYCOPROTEIN 6-ALPHA-L- FUCOSYLTRANSFERASE) (GDP-FUCOSE--GLYCOPROTEIN FUCOSYLTRANSFERASE) (GDP-L-FUC:N-ACETYL-BETA-D-GLUCOSAMINIDE ALPHA1,6-FUCOSYLTRANSFERASE) (ALPHA1-6FUCT) (FUCOSYLTRANSFERASE 8). [Source:SWISSPROT;Acc:Q9BYC5]	1189
CaMax: 1366a	CONNECTIVE TISSUE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (CTGF-L) (WNT1 INDUCIBLE SIGNALING PATHWAY PROTEIN 2) (WISP-2) (CONNECTIVE TISSUE GROWTH FACTOR-RELATED PROTEIN 58). [Source:SWISSPROT;Acc:O76076]	209
CaMax: 1371a	CATENIN (CADHERIN-ASSOCIATED PROTEIN), ALPHA-LIKE 1; ALPHA-CATULIN. [Source:RefSeq;Acc:NM_003798]	392
CaMax: 137b	M-PHASE PHOSPHOPROTEIN 8 (FRAGMENT). [Source:SWISSPROT;Acc:Q99549]	491
CaMax: 1383a	ECOTROPIC VIRAL INTEGRATION SITE 5; NEUROBLASTOMA STAGE 4S GENE. [Source:RefSeq;Acc:NM_005665]	911
CaMax: 1384a	ACYL-COA DESATURASE (EC 1.14.19.1) (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE). [Source:SWISSPROT;Acc:O00767]	1330
CaMax: 1397b	NUCLEAR RECEPTOR COACTIVATOR 7; ESTROGEN RECEPTOR ASSOCIATED PROTEIN 140 KDA. [Source:RefSeq;Acc:NM_181782]	858
CaMax: 1401c	PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) 1; RA(RAS/RAP1A-ASSOCIATING)-GEF; PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR(GEF)1; RA(RAS/RAP1A-ASSOCIATING)-GEF; PDZ DOMAIN CONTAINING GUANINE NUCLEOTIDE EXCHANGE FACTOR(GEF)1. [Source:RefSeq;Acc:NM_014247]	306
CaMax: 1409b	BAG-FAMILY MOLECULAR CHAPERONE REGULATOR-5 (BAG-5). [Source:SWISSPROT;Acc:Q9UL15]	853
CaMax: 1411a	PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 12A; MYOSIN PHOSPHATASE, TARGET SUBUNIT 1. [Source:RefSeq;Acc:NM_002480]	1247
CaMax: 1420c	CELL CYCLE PROGRESSION 8 PROTEIN. [Source:RefSeq;Acc:NM_020739]	981
CaMax: 1421a	MUCOSA ASSOCIATED LYMPHOID TISSUE LYMPHOMA TRANSLOCATION PROTEIN 1 (EC 3.4.22.-) (MALT-LYMPHOMA ASSOCIATED TRANSLOCATION) (PARACASPASE).	1248

	[Source:SWISSPROT;Acc:Q9UDY8]	
CaMax: 143.2c	SPARC-LIKE PROTEIN 1 PRECURSOR (HIGH ENDOTHELIAL VENABLE PROTEIN) (HEVIN) (MAST 9). [Source:SWISSPROT;Acc:Q14515]	145
CaMax: 143.2c	SPARC-LIKE PROTEIN 1 PRECURSOR (HIGH ENDOTHELIAL VENABLE PROTEIN) (HEVIN) (MAST 9). [Source:SWISSPROT;Acc:Q14515]	145
CaMax: 1448a	TESTICAN-3 PRECURSOR. [Source:SWISSPROT;Acc:Q9BQ16]	969
CaMax: 1449a	ZINC FINGER PROTEIN CLONE 647. [Source:SWISSPROT;Acc:P15622]	1270
CaMax: 1450a	CYTOKINE-LIKE PROTEIN C17 PRECURSOR. [Source:SWISSPROT;Acc:Q9NRR1]	1450
CaMax: 1459c	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14). [Source:SWISSPROT;Acc:P53999]	850
CaMax: 145b	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN) (TUMOR SUPPRESSOR QM) (LAMININ RECEPTOR HOMOLOG). [Source:SWISSPROT;Acc:P27635]	455
CaMax: 1469a	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5. [Source:RefSeq;Acc:NM_023211]	847
CaMax: 1469a	UPREGULATED DURING SKELETAL MUSCLE GROWTH 5. [Source:RefSeq;Acc:NM_023211]	847
CaMax: 1476a	DNA-BINDING PROTEIN INHIBITOR ID-4. [Source:SWISSPROT;Acc:P47928]	846
CaMax: 1477a	BTG2 PROTEIN (NGF-INDUCIBLE ANTI-PROLIFERATIVE PROTEIN PC3). [Source:SWISSPROT;Acc:P78543]	276
CaMax: 1481c	HOMEBOX PROTEIN HOX-A3 (HOX-1E). [Source:SWISSPROT;Acc:O43365]	23
CaMax: 1488b	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1 (HNRNP A2 / HNRNP B1). [Source:SWISSPROT;Acc:P22626]	195
CaMax: 150a	NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE (EC 1.1.1.-). [Source:SWISSPROT;Acc:Q14914]	458
CaMax: 1521b	PROTEIN PHOSPHATASE METHYLESTERASE-1. [Source:RefSeq;Acc:NM_016147]	147
CaMax: 1546b	CYSTINE/GLUTAMATE TRANSPORTER (AMINO ACID TRANSPORT SYSTEM XC-) (XCT) (CALCIUM CHANNEL BLOCKER RESISTANCE PROTEIN CCB1). [Source:SWISSPROT;Acc:Q9UPY5]	1199
CaMax: 1551a	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_017658]	223
CaMax: 1577a	TRANSMEMBRANE PROTEIN 4. [Source:RefSeq;Acc:NM_014255]	1464
CaMax: 1631d	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	119
CaMax: 1635a	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	1550
CaMax: 1635a	UNC-51-LIKE KINASE 2. [Source:RefSeq;Acc:NM_014683]	1550
CaMax: 164c	MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (CXCL3) (GROWTH REGULATED PROTEIN GAMMA) (GRO-GAMMA). [Source:SWISSPROT;Acc:P19876]	465
CaMax: 1690a	CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL PRECURSOR (EC 1.9.3.1) (COX IV-1) (CYTOCHROME C OXIDASE POLYPEPTIDE IV). [Source:SWISSPROT;Acc:P10888]	1379
CaMax: 1692a	CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL PRECURSOR (EC 1.9.3.1) (COX IV-1) (CYTOCHROME C OXIDASE POLYPEPTIDE IV). [Source:SWISSPROT;Acc:P10888]	1380
CaMax:	FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC	

1693b	2.7.1.112) (FGFR-2) (KERATINOCYTE GROWTH FACTOR RECEPTOR 2). [Source:SWISSPROT;Acc:P21802]	1333
CaMax: 1705a	CASPASE RECRUITMENT DOMAIN PROTEIN 6. [Source:SWISSPROT;Acc:Q9BX69]	1132
CaMax: 1717a	T-CELL ACTIVATION PROTEIN. [Source:RefSeq;Acc:NM_033296]	1060
CaMax: 1721a	LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (M/NEI) (EI). [Source:SWISSPROT;Acc:P30740]	1064
CaMax: 1722a	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 4 (TRANS-GOLGI P230) (256 KDA GOLGIN) (GOLGIN-245) (72.1 PROTEIN). [Source:SWISSPROT;Acc:Q13439]	1065
CaMax: 1724a	G-PROTEIN COUPLED RECEPTOR. [Source:RefSeq;Acc:NM_153832]	1066
CaMax: 1727a	EGF-LIKE MODULE-CONTAINING MUCIN-LIKE RECEPTOR 3 ISOFORM A. [Source:RefSeq;Acc:NM_032571]	29
CaMax: 1744a	LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-COUPLED RECEPTOR 4 PRECURSOR (G PROTEIN-COUPLED RECEPTOR 48). [Source:SWISSPROT;Acc:Q9BXB1]	325
CaMax: 174a	TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF-BETA) (TRANSCRIPTION INITIATION FACTOR RAP30). [Source:SWISSPROT;Acc:P13984]	243
CaMax: 1758a	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KDA (U1 SNRNP 70 KDA) (SNRNP70) (U1-70K). [Source:SWISSPROT;Acc:P08621]	340
CaMax: 1759b	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_017658]	1479
CaMax: 1775a	GOLGI COILED COIL PROTEIN 1. [Source:SWISSPROT;Acc:Q96CN9]	1481
CaMax: 1775a	GOLGI COILED COIL PROTEIN 1. [Source:SWISSPROT;Acc:Q96CN9]	1481
CaMax: 1782b	OK/SW-CL.87. [Source:SPTREMBL;Acc:Q8NI68]	1136
CaMax: 178a	TRANSCRIPTION FACTOR CP2; TRANSCRIPTION FACTOR CP2, ALPHA GLOBIN. [Source:RefSeq;Acc:NM_005653]	295
CaMax: 1801b	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX-LIKE, MITOCHONDRIAL PRECURSOR. [Source:SWISSPROT;Acc:O76031]	89
CaMax: 180a	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	472
CaMax: 1812b	SIALIC ACID BINDING IG-LIKE LECTIN 6 PRECURSOR (SIGLEC-6) (OBESITY- BINDING PROTEIN 1) (OB-BP1) (CD33 ANTIGEN-LIKE 1). [Source:SWISSPROT;Acc:O43699]	272
CaMax: 1814c	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM). [Source:SWISSPROT;Acc:P19021]	39
CaMax: 1828b	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP). [Source:SWISSPROT;Acc:Q9QUP5]	1283
CaMax: 1853a	SPLICEOSOMAL PROTEIN SAP155 (FRAGMENT). [Source:SPTREMBL;Acc:Q9ET34]	263
CaMax: 1857c	CYTOCHROME B5. [Source:SWISSPROT;Acc:P00173]	15
CaMax: 1859a	MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA 3; ALR-LIKE PROTEIN. [Source:RefSeq;Acc:NM_021230]	983
CaMax: 1917f	SNF2 HISTONE LINKER PHD RING HELICASE. [Source:RefSeq;Acc:NM_173082]	133
CaMax: 1919a	ENDOTHELIAL AND SMOOTH MUSCLE CELL-DERIVED NEUROPILIN-LIKE PROTEIN; COAGULATION FACTOR V/VIII-HOMOLOGY DOMAINS PROTEIN 1. [Source:RefSeq;Acc:NM_080927]	150
CaMax: 1940e	BETA-TUBULIN COFACTOR E. [Source:RefSeq;Acc:NM_003193]	24
CaMax:	CDW92 ANTIGEN; CHOLINE TRANSPORTER-LIKE PROTEIN.	314

1941e	[Source:RefSeq;Acc:NM_080546]	
CaMax: 1943a	ALPHA-ACTININ-2-ASSOCIATED LIM PROTEIN; ENIGMA HOMOLOG. [Source:RefSeq;Acc:NM_014476]	338
CaMax: 1950a	VAV-3 PROTEIN. [Source:SWISSPROT;Acc:Q9UKW4]	1293
CaMax: 1953a	NGFI-A BINDING PROTEIN 1 (EGR-1 BINDING PROTEIN 1) (TRANSCRIPTIONAL REGULATORY PROTEIN P54). [Source:SWISSPROT;Acc:Q13506]	371
CaMax: 1961e	MOTHERS AGAINST DECAPENTAPLEGIC HOMOLOG INTERACTING PROTEIN (MADH-INTERACTING PROTEIN) (SMAD ANCHOR FOR RECEPTOR ACTIVATION) (RECEPTOR ACTIVATION ANCHOR) (HSARA) (NOVEL SERINE PROTEASE) (NSP). [Source:SWISSPROT;Acc:O95405]	1494
CaMax: 1967a	ANTIGEN PEPTIDE TRANSPORTER 2 (APT2) (PEPTIDE TRANSPORTER TAP2) (PEPTIDE TRANSPORTER PSF2) (PEPTIDE SUPPLY FACTOR 2) (PSF-2) (PEPTIDE TRANSPORTER INVOLVED IN ANTIGEN PROCESSING 2). [Source:SWISSPROT;Acc:Q03519]	1083
CaMax: 1968a	PELLINO PROTEIN. [Source:RefSeq;Acc:NM_020651]	1084
CaMax: 1982a	COLLAGEN ALPHA 1(XI) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:P12107]	1088
CaMax: 1990a	MICROTUBULE-ASSOCIATED PROTEIN, RP/EB FAMILY, MEMBER 2; T-CELL ACTIVATION PROTEIN, EB1 FAMILY; APC-BINDING PROTEIN EB1. [Source:RefSeq;Acc:NM_014268]	1092
CaMax: 2008a	PINS. [Source:RefSeq;Acc:NM_029522]	1498
CaMax: 2013a	NUCLEAR FACTOR RIP140 (NUCLEAR RECEPTOR INTERACTING PROTEIN 1). [Source:SWISSPROT;Acc:P48552]	1499
CaMax: 2015e	60S RIBOSOMAL PROTEIN L4 (L1). [Source:SWISSPROT;Acc:P36578]	233
CaMax: 2020b	MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE KINASE 3 (EC 2.7.1.37) (MAPK/ERK KINASE KINASE KINASE 3) (MEK KINASE KINASE 3) (MEKKK 3) (GERMINAL CENTER KINASE RELATED PROTEIN KINASE) (GLK). [Source:SWISSPROT;Acc:Q8IVH8]	284
CaMax: 2034a	LATE ENVELOPE PROTEIN 4. [Source:RefSeq;Acc:NM_178352]	1501
CaMax: 2035d	DNA-DIRECTED RNA POLYMERASES III 12.5 KDA POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III C11 SUBUNIT) (HSC11P) (HRPC11) (MY010 PROTEIN). [Source:SWISSPROT;Acc:Q9Y2Y1]	149
CaMax: 2056d	POTENTIAL HELICASE WITH ZINC-FINGER DOMAIN. [Source:SWISSPROT;Acc:P42694]	1305
CaMax: 2070a	PALLADIN; CGI-151 PROTEIN. [Source:RefSeq;Acc:NM_016081]	1307
CaMax: 2074b	POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IA (EC 3.6.3.1) (CHROMAFFIN GRANULE ATPASE II) (ATPASE CLASS I TYPE 8A MEMBER 1). [Source:SWISSPROT;Acc:Q9Y2Q0]	99
CaMax: 2078a	SEPTIN 7 (CDC10 PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:Q16181]	1098
CaMax: 2083e	WD REPEAT AND FYVE DOMAIN CONTAINING 1 ISOFORM 1; PHOSPHOINOSITIDE-BINDING PROTEIN SR1; WD40 AND FYVE DOMAIN CONTAINING 1. [Source:RefSeq;Acc:NM_020830]	113
CaMax: 2100b	FIBRILLIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P35555]	1104
CaMax: 2110a	ZINC FINGER PROTEIN 345 (ZINC FINGER PROTEIN HZF10). [Source:SWISSPROT;Acc:Q14585]	989
CaMax: 211b	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1. [Source:SWISSPROT;Acc:P33527]	505
CaMax: 2123a	PEPTIDE-HISTIDINE TRANSPORTER 4. [Source:RefSeq;Acc:NM_145648]	1557

CaMax: 2129a	SMALL PROTEIN EFFECTOR 1 OF CDC42. [Source:RefSeq;Acc:NM_020239]	990
CaMax: 2224a	PROTEOGLYCAN 4; MEGAKARYOCYTE STIMULATING FACTOR; PROTEOGLYCAN 4, (MEGAKARYOCYTE STIMULATING FACTOR, ARTICULAR SUPERFICIAL ZONE PROTEIN); JACOBS CAMPTODACTYLY-ARTHROPATHY-PERICARDITIS SYNDROME; CAMPTODACTYLY, ARTHROPATHY, COXA VARA, PERICARDITIS SYNDROME. [Source:RefSeq;Acc:NM_005807]	215
CaMax: 2234a	THYROTROPIN-RELEASING HORMONE RECEPTOR (TRH-R) (THYROLIBERIN RECEPTOR). [Source:SWISSPROT;Acc:P21761]	994
CaMax: 2238a	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI- PDE A). [Source:SWISSPROT;Acc:Q14432]	996
CaMax: 2241a	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI- PDE A). [Source:SWISSPROT;Acc:Q14432]	188
CaMax: 2238a	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI- PDE A). [Source:SWISSPROT;Acc:Q14432]	996
CaMax: 2267a	THROMBOSPONDIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P07996]	999
CaMax: 2241a	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE A (EC 3.1.4.17) (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI- PDE A). [Source:SWISSPROT;Acc:Q14432]	188
CaMax: 2374a	THROMBOSPONDIN 1 PRECURSOR. [Source:SWISSPROT;Acc:P07996]	206
CaMax: 239a	SPECTRIN ALPHA CHAIN, BRAIN (SPECTRIN, NON-ERYTHROID ALPHA CHAIN) (ALPHA-II SPECTRIN) (FODRIN ALPHA CHAIN). [Source:SWISSPROT;Acc:Q13813]	530
CaMax: 23a	GLUCOCORTICOID MODULATORY ELEMENT BINDING PROTEIN 1 (GMEB-1) (PARVOVIRUS INITIATION FACTOR P96) (PIF P96) (DNA BINDING PROTEIN P96PIF). [Source:SWISSPROT;Acc:Q9Y692]	90
CaMax: 267d	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C). [Source:SWISSPROT;Acc:P24821]	553
CaMax: 272d	ELAC HOMOLOG 1. [Source:RefSeq;Acc:NM_018696]	116
CaMax: 307b	PROTEIN CGI-147. [Source:SWISSPROT;Acc:Q9Y3E5]	598
CaMax: 308c	RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN 65KDA; RETINAL PIGMENT EPITHELIUM-SPECIFIC PROTEIN (65KD); RETINITIS PIGMENTOSA 20 (AUTOSOMAL RECESSIVE). [Source:RefSeq;Acc:NM_000329]	597
CaMax: 320a	EXOCYST COMPLEX COMPONENT SEC3 (BM-012). [Source:SWISSPROT;Acc:Q9NV70]	1532
CaMax: 326e	MICROSOMAL SIGNAL PEPTIDASE 18 KDA SUBUNIT (EC 3.4.-.-) (SPASE 18 KDA SUBUNIT) (SPC18) (ENDOPEPTIDASE SP18). [Source:SWISSPROT;Acc:Q9R0P6]	71
CaMax: 328b	PALLADIN; CGI-151 PROTEIN. [Source:RefSeq;Acc:NM_016081]	591
CaMax: 106a	FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). [Source:SWISSPROT;Acc:P02794]	440
CaMax: 364a	RNA-BINDING PROTEIN EWS (EWS ONCOGENE) (EWING SARCOMA BREAKPOINT REGION 1 PROTEIN). [Source:SWISSPROT;Acc:Q01844]	640
CaMax: 374a	ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER B (PHAPI2 PROTEIN) (SILVER-STAINABLE PROTEIN SSP29) (ACIDIC PROTEIN RICH IN LEUCINES). [Source:SWISSPROT;Acc:Q92688]	644
CaMax:	FIP1-LIKE 1; REARRANGED IN HYPEREOSINOPHILIA.	423

38a	[Source:RefSeq;Acc:NM_030917]	
CaMax: 415b	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT) (EIF-2-ALPHA) (EIF- 2ALPHA) (EIF-2A). [Source:SWISSPROT;Acc:P05198]	913
CaMax: 459a	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (TONICITY-RESPONSIVE ENHANCER-BINDING PROTEIN) (TONE- BINDING PROTEIN) (TONEBP). [Source:SWISSPROT;Acc:O94916]	658
CaMax: 464b	ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP--ASPARTATE LIGASE) (ADSS) (AMPSASE). [Source:SWISSPROT;Acc:P30520]	292
CaMax: 465b	SURFACE GLYCOPROTEIN, IG SUPERFAMILY MEMBER. [Source:RefSeq;Acc:NM_016952]	193
CaMax: 478a	T-COMPLEX ASSOCIATED-TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51808]	662
CaMax: 479c	T-COMPLEX ASSOCIATED-TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51808]	129
CaMax: 487a	RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 2 (GEF-H1 PROTEIN) (PROLIFERATING CELL NUCLEOLAR ANTIGEN P40). [Source:SWISSPROT;Acc:Q92974]	668
CaMax: 488a	HEXOKINASE, TYPE II (EC 2.7.1.1) (HK II) (MUSCLE FORM HEXOKINASE). [Source:SWISSPROT;Acc:P52789]	669
CaMax: 520a	BTB (POZ) DOMAIN CONTAINING 5. [Source:RefSeq;Acc:NM_017658]	622
CaMax: 521b	MYOCYTE-SPECIFIC ENHANCER FACTOR 2C. [Source:SWISSPROT;Acc:Q06413]	621
CaMax: 530b	PROTEASOME SUBUNIT ALPHA TYPE 3 (EC 3.4.25.1) (PROTEASOME COMPONENT C8) (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8). [Source:SWISSPROT;Acc:P25788]	9
CaMax: 539a	HDCMD38P. [Source:SPTREMBL;Acc:Q9P1S5]	612
CaMax: 545a	TRANSMEMBRANE PROTEIN 4. [Source:RefSeq;Acc:NM_014255]	670
CaMax: 550a	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-L; SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-LIKE). [Source:RefSeq;Acc:NM_005839]	1403
CaMax: 555b	F-BOX AND LEUCINE-RICH REPEAT PROTEIN 3A; F-BOX PROTEIN FBL3A. [Source:RefSeq;Acc:NM_012158]	114
CaMax: 571a	ECHINODERM MICROTUBULE-ASSOCIATED PROTEIN-LIKE 4 (EMAP-4) (RESTRICTEDLY OVEREXPRESSED PROLIFERATION-ASSOCIATED PROTEIN) (ROPP 120). [Source:SWISSPROT;Acc:Q9HC35]	673
CaMax: 579a	SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55). [Source:SWISSPROT;Acc:Q13247]	676
CaMax: 57a	INTEGRIN ALPHA-6 PRECURSOR (VLA-6) (CD49F). [Source:SWISSPROT;Acc:P23229]	417
CaMax: 581a	LBP-9. [Source:RefSeq;Acc:NM_014553]	80
CaMax: 597c	FETAL ALZHEIMER ANTIGEN (FETAL ALZ-50-REACTIVE CLONE 1). [Source:SWISSPROT;Acc:Q12830]	312
CaMax: 623a	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195). [Source:SWISSPROT;Acc:P46940]	1022
CaMax: 628a	KREMEN PROTEIN 1 PRECURSOR (KRINGLE-CONTAINING PROTEIN MARKING THE EYE AND THE NOSE) (DICKKOPF RECEPTOR). [Source:SWISSPROT;Acc:Q96MU8]	1046
CaMax: 635a	SER/ARG-RELATED NUCLEAR MATRIX PROTEIN (PLENTY OF PROLINES 101-L; SER/ARG-RELATED NUCLEAR MATRIX	1404

	PROTEIN (PLENTY OF PROLINES 101-LIKE). [Source:RefSeq;Acc:NM_005839]	
CaMax: 638b	T-COMPLEX ASSOCIATED-TESTIS-EXPRESSED 1-LIKE (PROTEIN 91/23). [Source:SWISSPROT;Acc:P51808]	261
CaMax: 685a	UPF0183 PROTEIN. [Source:SWISSPROT;Acc:Q9BSU1]	683
CaMax: 692a	TIGGER TRANSPOSABLE ELEMENT DERIVED 1; JERKY (MOUSE) HOMOLOG-LIKE. [Source:RefSeq;Acc:NM_145702]	688
CaMax: 704b	INVERSIN. [Source:RefSeq;Acc:NM_014425]	697
CaMax: 704b	INVERSIN. [Source:RefSeq;Acc:NM_014425]	697
CaMax: 710a	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR. [Source:SWISSPROT;Acc:Q03692]	701
CaMax: 726b	GRAVE'S DISEASE CARRIER PROTEIN (GDC) (GRAVE'S DISEASE AUTOANTIGEN) (GDA) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG). [Source:SWISSPROT;Acc:P16260]	1405
CaMax: 736a	DIAMINE ACETYLTRANSFERASE (EC 2.3.1.57) (SPERMIDINE/SPERMINE N(1)- ACETYLTRANSFERASE) (SSAT) (PUTRESCINE ACETYLTRANSFERASE). [Source:SWISSPROT;Acc:P21673]	142
CaMax: 73b	HISTIDINE-RICH MEMBRANE PROTEIN KE4. [Source:SWISSPROT;Acc:Q92504]	408
CaMax: 747a	IDN3 PROTEIN ISOFORM A. [Source:RefSeq;Acc:NM_133433]	126
CaMax: 785b	MAJOR PRION PROTEIN PRECURSOR (PRP) (PRP27-30) (PRP33-35C) (ASCR) (CD230 ANTIGEN). [Source:SWISSPROT;Acc:P04156]	268
CaMax: 794a	SARCOSPAN (K-RAS ONCOGENE-ASSOCIATED PROTEIN) (KIRSTEN-RAS-ASSOCIATED PROTEIN). [Source:SWISSPROT;Acc:Q14714]	372
CaMax: 85.1c	NITROGEN FIXATION CLUSTER-LIKE. [Source:RefSeq;Acc:NM_014301]	72
CaMax: 856c	BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE, CYTOSOLIC (EC 2.6.1.42) (BCAT(C)) (ECA39 PROTEIN). [Source:SWISSPROT;Acc:P54687]	1130
CaMax: 863c	ZINC FINGER PROTEIN SLUG (NEURAL CREST TRANSCRIPTION FACTOR SLUG) (SNAIL HOMOLOG 2). [Source:SWISSPROT;Acc:P97469]	916
CaMax: 890a	RAS-RELATED PROTEIN RAB-6A (RAB-6). [Source:SWISSPROT;Acc:P20340]	161
CaMax: 909a	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM). [Source:SWISSPROT;Acc:P19021]	786
CaMax: 90c	HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (TUMOR SPECIFIC TRANSPLANTATION 84 KDA ANTIGEN) (TSTA). [Source:SWISSPROT;Acc:P11499]	400
CaMax: 919b	MYELIN GENE EXPRESSION FACTOR 2. [Source:RefSeq;Acc:NM_016132]	777
CaMax: 92c	NUCLEAR RECEPTOR COACTIVATOR 1 ISOFORM 1. [Source:RefSeq;Acc:NM_003743]	398
CaMax: 935b	CHURCHILL PROTEIN (MY015 PROTEIN). [Source:SWISSPROT;Acc:Q8WUH1]	767
CaMax: 953a	6.8 KDA MITOCHONDRIAL PROTEOLIPID. [Source:SWISSPROT;Acc:P56379]	759
CaMax: 963c	PUMILIO HOMOLOG 1. [Source:RefSeq;Acc:NM_014676]	755
CaMax: 986a	G1/S-SPECIFIC CYCLIN D2. [Source:SWISSPROT;Acc:P30279]	1423
CaMax: 990a	TRANSCRIPTION FACTOR SOX-9. [Source:SWISSPROT;Acc:P48436]	194
CaMax:	INHIBITOR OF BRUTON'S TYRISOINE KINASE; BTK-BINDING	257

994b	PROTEIN. [Source:RefSeq;Acc:NM_015525]	
CaMax: 996a	40S RIBOSOMAL PROTEIN S20. [Source:SWISSPROT;Acc:P17075]	930

EXAMPLE 3

Preparation of Microarray

[0104] Microarray probes were generated by PCR-amplifying clones isolated from differential display. Probes were spotted in duplicate onto poly-L-lysine coated slides using a GMS417 (Affymetrix) arrayer. Osteoarthritic cartilage samples were obtained from the femoral heads of clinically diagnosed canines undergoing total hip replacement. RNA was hybridized to the slides using the HC ExpressArray (Digene) kit and visualized using a GMS418 (Affymetrix) scanner. The Imogene (Biodiscovery) program was used for spot finding and subsequent data analysis was performed using GeneSight (Biodiscovery). Expression levels are represented after background subtraction, log (base 2) transformation and global slide signal normalization.

Microarray clone preparation

[0105] Culture blocks containing 1.5 mLs of Magnificent Broth (MB) plus tetracycline (50 mg/mL) were inoculated with appropriate clones from glycerol stocks and grown overnight with shaking at 37°C. These cultures were used to inoculate a second culture block that was grown for approximately 6 hours with shaking at 37°C. These 6-hour cultures were used to inoculate 2 replicate culture blocks which were grown overnight with shaking at 37°C. Cultures were centrifuged to pellet cells and plasmids isolated using the Qiagen 96-well culture system (Qiagen). Plasmid concentrations were determined using a spectrophotometer by measuring the absorbance at 260nm. All cDNA plasmid clones were amplified in duplicate using the following PCR reaction (final concentration): 10X PCR buffer (10mM Tris-HCl, pH 8.3, 50mM KCl, 2.5mM MgCl₂), 500uM ea. dNTP, 600 nM Rgh primer, 600 nM Lgh primer, 1μL (5units/μL) of Eppendorf Taq polymerase and 1μL (~100ng/μL) cDNA template in a total of 100μL. The reaction was performed in the following conditions: 94°C 30 seconds, 52°C 40 seconds, 72°C 1 minute for 40 cycles, followed by 72°C – 5min and 4°C - hold. Amplified products were verified on 1.5% agarose gel and purified using Minelute (Qiagen) protocol. The 200μL of PCR was added to the filter plate and vacuum was turned on to pull through all PCR reagents and liquid leaving only the cDNA bound to the filter. 30μL molecular grade water was added to the filter plate and incubated at room temperature on an orbital shaker at 900 rpm for 5 minutes. The supernatant containing the purified cDNA was aspirated from the filter plate. The cDNA's were dried for 2hrs or to completion in a speed vac at 45°C. 30μL Corning Universal Printing Buffer

was added to all cDNA's and resuspended over night at room temperature on an orbital shaker.

- 2 μ L's transferred for concentration analysis and the appropriate amount of Corning Universal Printing Buffer was added for a final concentration of 200 to 500 ng/uL. Plates were stored at – 20 °C until and after each array printing.

Clone arraying

[0106] Microscope slides (Goldseal cat# 3010) were submerged in a 10% NaOH (Fisher cat#S318-500) 57% EtOH solution and incubated at room temperature in an orbital shaker at 50rpm for 2 hours. Slides were rinsed in Milli-Q water 5X for 30 seconds each. While the slides remain in the last water rinse a 10% Poly-L-Lysine (Sigma cat#P8920), 10% 1X PBS (GibcoBRL cat#70013-032) was brought to 700mLs using Milli-Q water in plastic ware. Slides were submerged in coating solution and incubated at room temperature in orbital shaker at 50rpm for 1 hour. Slides were rinsed in Milli-Q water 5X for 30 seconds each and spun at 500rpm for 1 minute. Slides were incubated in 55°C oven for 10 min and kept in dessicator for at least 14 days and no longer than 3 months prior to arraying. cDNA clones were arrayed using the GMS 417 arrayer (Affymetrix). All slides were placed in a room temperature dessicator to dry overnight. The slides were rehydrated over boiling Milli-Q water (steam) and snap dried DNA side up on an 80°C heat block. To ensure efficient cross-linking the slides were baked for 2 hours at 80°C in an oven and then cross-linked with Stratalinker (120mJ, Stratagene). All slides were stored in a room temperature dessicator until used for cDNA hybridization.

cDNA microarray hybridization

[0107] All RNA samples were reverse transcribed using the following reaction: 5X Superscript II First Strand Buffer (Invitrogen), 1 μ L (1pmole/uL) of RT primer (Genisphere), 1 μ L Suprase-InTM Rnase inhibitor, 1 μ L 10mM ea. DNTP, 2 μ L 0.1 M DTT, 1 μ L Superscript II and 5 μ g total RNA. The reaction was performed at 42°C for 2hrs. The reaction was stopped by adding 3.5 μ L of 0.5 M NaOH/50 mM EDTA and incubating at 65°C for 10 minutes. The reaction was neutralized by adding 5 μ L of 1M Tris-HCL, pH 7.5. 101.5 μ L of 10mM Tris, pH 8, 1mM EDTA was added and the cDNA was purified and concentrated by following the Microcon YM-30 (Millipore) protocol. The concentrated cDNA was brought to a final volume of 10 μ L with Nuclease-free water and the following reagents added: 20 μ L of 2X hybridization buffer (Genisphere), 2 μ L dT LNA blocker and 8 μ L Nuclease-free water for a total of 40 μ L. The hybridization mixture was heated at 80°C for 10 minutes and loaded onto the microarray slide at the edge of the lifterSlip. The slide was then placed into a GeneMachines dual hybridization chamber and placed in a 60°C water bath overnight. The following day the slides were

processed according to the 3DNA Array 350 (Genisphere) protocol. Briefly, the slides were washed (2XSSC-.2%SDS, 2X SSC, .2X SSC), spun dry at 1000rpm for 1 min and the 3DNA capture hybridization performed. The slides were washed (2XSSC-.2%SDS, 2X SSC, .2X SSC) spun dry at 1000rpm for 1 min and scanned using a GMS 418 array scanner (Affymetrix).

Microarray analysis

[0108] Scanned images representing RNA transcripts bound to specific clones were quantified and checked for spot quality control using Imagene analysis software (BioDiscovery). Quantified images were analyzed using Genesight analysis software (BioDiscovery). The analysis represented subtraction of background surrounding the spots, averaging spot replicates, deletion of clone information representing clone hybridization signals not greater than 200 above background on all samples, log (base 2) transformation and global normalization of each slide (values expressed as percent of average spot intensity).

EXAMPLE 4

Expression Analysis Using Microarray

[0109] RNA was extracted from cartilage as described, *supra*. Microarray analysis (described *supra*) was performed on 8 osteoarthritic cartilage samples from clinically diagnosed canines undergoing total hip replacement and 8 normal cartilage samples. A standard T-test (two categories) was performed on the final hybridization signals for osteoarthritic characterization of cartilage samples ($p < 0.05$ and $p < 0.01$, results shown in Tables 3 and 4, respectively).

TABLE 3

Gene ID	OA AVG	STD	Normal AVG	STD	DIF(OA-N)	Fold
1028c	1.81	0.75	0.24	0.94	1.57	2.96
768a	1.99	0.54	0.88	0.55	1.11	2.16
141c	3.94	0.57	3.01	0.75	0.93	1.90
154a	0.80	0.85	0.06	0.56	0.74	1.67
1548c	5.49	0.41	4.79	0.46	0.69	1.62
718a	5.93	0.66	5.29	0.43	0.64	1.56
11b	-0.85	0.66	-1.46	0.30	0.60	1.52
363a	-0.24	0.52	-0.77	0.44	0.53	1.45
370a	6.06	0.46	5.54	0.61	0.51	1.43
1551a	0.71	0.51	0.23	0.49	0.48	1.40
376a	-0.66	0.42	-1.01	0.24	0.36	1.28
84.2c	0.39	0.35	0.04	0.28	0.36	1.28
380a	-1.61	0.22	-1.84	0.18	0.24	1.18
372a	0.11	0.25	-0.12	0.23	0.23	1.17
2148a	-1.81	0.23	-1.62	0.15	-0.20	1.15
1800a	-2.23	0.16	-1.98	0.24	-0.25	1.19
1357a	-2.01	0.12	-1.73	0.07	-0.28	1.21
168c	5.11	0.19	5.40	0.21	-0.29	1.22
1090d	6.26	0.22	6.55	0.23	-0.29	1.22

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60a	-0.18	0.34	0.11	0.25	-0.29	1.22
96e	5.50	0.16	5.80	0.35	-0.30	1.23
2015e	4.67	0.24	4.97	0.23	-0.30	1.23
383d	-1.78	0.18	-1.47	0.14	-0.30	1.24
128a	2.10	0.39	2.41	0.24	-0.31	1.24
621b	-2.03	0.27	-1.72	0.35	-0.32	1.25
1174d	-0.45	0.36	-0.12	0.18	-0.33	1.25
947a	0.71	0.29	1.04	0.27	-0.33	1.26
1964a	-2.34	0.18	-2.01	0.27	-0.33	1.26
619b	-2.11	0.21	-1.77	0.23	-0.34	1.26
2222b	-0.52	0.31	-0.18	0.33	-0.34	1.27
1468c	-1.26	0.28	-0.91	0.32	-0.34	1.27
1629a	-0.78	0.36	-0.44	0.17	-0.34	1.27
174a	-0.22	0.27	0.13	0.38	-0.35	1.27
2085c	3.62	0.47	3.97	0.16	-0.35	1.27
1461a	-1.73	0.26	-1.38	0.24	-0.35	1.27
764b	1.37	0.34	1.73	0.32	-0.36	1.28
731a	1.61	0.37	1.98	0.36	-0.36	1.28
1051a	2.30	0.34	2.67	0.36	-0.36	1.29
613a	-2.07	0.24	-1.70	0.30	-0.37	1.29
531a	-0.52	0.20	-0.15	0.36	-0.37	1.29
1471a	-1.75	0.35	-1.38	0.24	-0.37	1.30
1381a	6.20	0.33	6.57	0.26	-0.38	1.30
44c	4.99	0.36	5.37	0.31	-0.38	1.30
1892a	-0.02	0.25	0.36	0.38	-0.38	1.30
76b	-0.54	0.41	-0.16	0.19	-0.38	1.30
366a	-1.98	0.32	-1.60	0.20	-0.38	1.30
994b	-1.82	0.43	-1.44	0.24	-0.39	1.31
1954e	-1.85	0.20	-1.46	0.35	-0.39	1.31
2127c	0.08	0.23	0.48	0.31	-0.39	1.31
530b	1.39	0.21	1.78	0.23	-0.40	1.32
409a	-1.18	0.34	-0.78	0.38	-0.40	1.32
2120a	1.36	0.41	1.76	0.41	-0.40	1.32
1405c	3.41	0.34	3.81	0.16	-0.41	1.32
1765a	-1.60	0.28	-1.19	0.28	-0.41	1.33
638b	-1.51	0.31	-1.11	0.38	-0.41	1.33
329d	-2.04	0.47	-1.63	0.26	-0.41	1.33
1853a	1.27	0.40	1.68	0.44	-0.41	1.33
2247a	-0.56	0.44	-0.15	0.32	-0.41	1.33
166a	-0.97	0.34	-0.56	0.25	-0.41	1.33
1746a	1.41	0.43	1.83	0.31	-0.41	1.33
1797a	-1.79	0.25	-1.38	0.30	-0.42	1.33
1729a	3.95	0.37	4.37	0.23	-0.42	1.34
1857c	-0.91	0.16	-0.49	0.20	-0.42	1.34
1081a	-1.83	0.20	-1.41	0.38	-0.42	1.34
2002c	-0.35	0.35	0.08	0.37	-0.42	1.34
785b	0.98	0.41	1.40	0.42	-0.42	1.34
1092b	-1.84	0.32	-1.41	0.41	-0.42	1.34
1784a	-2.32	0.38	-1.89	0.35	-0.43	1.34

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523a	-1.36	0.28	-0.93	0.32	-0.43	1.34
2172c	-2.54	0.17	-2.11	0.11	-0.43	1.35
58a	-0.09	0.22	0.34	0.24	-0.43	1.35
411b	-1.73	0.44	-1.30	0.28	-0.43	1.35
1511b	-2.18	0.35	-1.75	0.41	-0.43	1.35
1812b	-2.11	0.23	-1.68	0.25	-0.43	1.35
1885c	-1.53	0.35	-1.09	0.45	-0.43	1.35
1619a	-1.58	0.41	-1.14	0.40	-0.43	1.35
2344a	-1.74	0.27	-1.30	0.51	-0.43	1.35
244a	-1.91	0.01	-1.47	0.12	-0.44	1.35
70d	-1.65	0.30	-1.21	0.34	-0.44	1.36
1477a	2.42	0.56	2.86	0.31	-0.44	1.36
1472a	0.07	0.40	0.51	0.23	-0.44	1.36
452a	-0.80	0.33	-0.36	0.21	-0.45	1.36
360a	-2.11	0.42	-1.66	0.22	-0.45	1.36
1481c	-1.53	0.19	-1.09	0.32	-0.45	1.36
568a	4.36	0.31	4.80	0.42	-0.45	1.36
1940e	-0.44	0.30	0.01	0.20	-0.45	1.36
1109a	-2.20	0.47	-1.75	0.18	-0.45	1.37
1930a	-2.00	0.27	-1.54	0.37	-0.45	1.37
1282b	-1.50	0.47	-1.04	0.35	-0.46	1.37
739a	-0.46	0.27	0.00	0.15	-0.46	1.37
1276a	-1.63	0.43	-1.17	0.51	-0.46	1.38
1728a	-0.95	0.47	-0.49	0.26	-0.46	1.38
1923b	-1.83	0.20	-1.37	0.36	-0.46	1.38
2020b	-2.44	0.43	-1.97	0.28	-0.46	1.38
556b	-0.33	0.54	0.13	0.43	-0.47	1.38
1711a	-1.92	0.24	-1.45	0.44	-0.47	1.38
49a	-1.19	0.37	-0.72	0.35	-0.47	1.38
1271a	-1.92	0.26	-1.45	0.36	-0.47	1.39
1612a	-0.56	0.41	-0.09	0.28	-0.47	1.39
1497c	-2.07	0.35	-1.59	0.35	-0.47	1.39
14a	-0.93	0.24	-0.45	0.30	-0.47	1.39
967b	-1.87	0.33	-1.39	0.42	-0.48	1.39
1727a	-1.68	0.31	-1.20	0.27	-0.48	1.39
1329a	-1.64	0.39	-1.16	0.51	-0.48	1.39
464b	-1.51	0.52	-1.04	0.21	-0.48	1.39
1490a	0.50	0.47	0.98	0.32	-0.48	1.40
188b	-1.65	0.31	-1.17	0.46	-0.48	1.40
178a	-1.99	0.31	-1.51	0.48	-0.48	1.40
631b	-2.23	0.00	-1.75	0.25	-0.48	1.40
1244b	-2.03	0.35	-1.55	0.42	-0.48	1.40
1220b	2.96	0.46	3.44	0.15	-0.48	1.40
758b	-0.39	0.43	0.09	0.31	-0.48	1.40
1807a	-2.60	0.18	-2.11	0.31	-0.49	1.40
33a	1.31	0.22	1.80	0.35	-0.49	1.40
276a	-1.80	0.40	-1.31	0.16	-0.49	1.40
204a	-1.25	0.50	-0.76	0.45	-0.49	1.40
543a	-2.07	0.39	-1.58	0.37	-0.49	1.40

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1764a	-0.26	0.37	0.23	0.41	-0.49	1.40
711a	4.68	0.49	5.17	0.48	-0.49	1.41
35c	-0.93	0.53	-0.44	0.29	-0.49	1.41
1401c	-1.65	0.43	-1.16	0.48	-0.49	1.41
3c	-1.75	0.40	-1.26	0.45	-0.49	1.41
494a	-1.49	0.40	-1.00	0.38	-0.50	1.41
1146a	0.55	0.33	1.04	0.34	-0.50	1.41
1616a	-1.25	0.43	-0.76	0.47	-0.50	1.41
1070b	-1.99	0.51	-1.49	0.10	-0.50	1.41
1738b	-1.57	0.25	-1.07	0.36	-0.50	1.41
1928a	4.38	0.63	4.88	0.35	-0.50	1.41
597c	-1.06	0.49	-0.56	0.28	-0.50	1.41
810a	-2.11	0.30	-1.61	0.28	-0.50	1.42
1505c	1.43	0.63	1.93	0.30	-0.50	1.42
1941e	-1.88	0.28	-1.38	0.54	-0.51	1.42
742a	-2.26	0.51	-1.75	0.26	-0.51	1.42
1993b	-1.33	0.38	-0.82	0.34	-0.51	1.42
1299c	-2.39	0.42	-1.88	0.40	-0.51	1.42
1960a	-1.43	0.54	-0.91	0.42	-0.51	1.43
1191a	0.47	0.53	0.99	0.35	-0.52	1.43
2147a	-1.63	0.41	-1.11	0.33	-0.52	1.43
562a	-2.16	0.44	-1.64	0.27	-0.52	1.43
1678a	6.05	0.47	6.57	0.26	-0.52	1.44
2223a	5.99	0.52	6.52	0.26	-0.52	1.44
2099a	-1.06	0.44	-0.53	0.43	-0.52	1.44
342a	-1.81	0.48	-1.28	0.41	-0.52	1.44
56a	3.79	0.23	4.32	0.38	-0.53	1.44
1347b	-2.05	0.45	-1.52	0.51	-0.53	1.45
738b	-1.75	0.52	-1.22	0.45	-0.54	1.45
1744a	0.72	0.61	1.26	0.23	-0.54	1.45
1814c	-1.03	0.40	-0.49	0.37	-0.54	1.45
1918a	-1.56	0.23	-1.02	0.65	-0.54	1.45
129b	0.47	0.26	1.01	0.26	-0.54	1.45
1924a	-0.46	0.34	0.08	0.41	-0.54	1.45
1060a	-1.90	0.48	-1.36	0.37	-0.54	1.45
557b	-1.56	0.24	-1.02	0.39	-0.54	1.45
1254a	-0.48	0.46	0.06	0.28	-0.54	1.46
1292c	-0.94	0.32	-0.40	0.47	-0.54	1.46
2221c	-0.01	0.25	0.53	0.33	-0.54	1.46
490c	4.71	0.34	5.26	0.42	-0.54	1.46
907a	-2.23	0.20	-1.68	0.29	-0.55	1.47
1224b	-1.32	0.59	-0.76	0.15	-0.56	1.47
469b	-0.61	0.31	-0.05	0.29	-0.56	1.47
713a	-1.30	0.34	-0.74	0.25	-0.56	1.47
861c	-2.49	0.52	-1.93	0.36	-0.56	1.47
1372a	1.49	0.32	2.05	0.30	-0.56	1.47
482a	-1.55	0.25	-0.99	0.39	-0.56	1.48
1098a	-2.29	0.30	-1.72	0.31	-0.56	1.48
1785a	-2.19	0.09	-1.63	0.27	-0.56	1.48

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1624b	-0.95	0.39	-0.38	0.36	-0.57	1.48
1441d	-1.09	0.29	-0.52	0.50	-0.57	1.48
553b	-0.76	0.16	-0.19	0.27	-0.57	1.48
2033a	-2.11	0.38	-1.54	0.43	-0.57	1.49
2179a	-2.12	0.29	-1.55	0.46	-0.57	1.49
1349b	-2.15	0.62	-1.58	0.13	-0.57	1.49
1257b	-0.76	0.22	-0.18	0.34	-0.58	1.49
1506d	-1.45	0.32	-0.88	0.36	-0.58	1.49
1939c	-2.37	0.07	-1.79	0.36	-0.58	1.49
2007a	-1.93	0.29	-1.35	0.20	-0.58	1.49
715a	-2.15	0.46	-1.57	0.38	-0.58	1.50
1621a	-1.42	0.26	-0.84	0.55	-0.58	1.50
13a	-0.25	0.52	0.33	0.24	-0.58	1.50
1288a	-1.12	0.25	-0.53	0.36	-0.58	1.50
379a	3.55	0.61	4.14	0.46	-0.59	1.50
1949a	-1.40	0.25	-0.82	0.50	-0.59	1.50
142.2c	1.04	0.28	1.63	0.26	-0.59	1.50
1054a	-0.73	0.26	-0.14	0.31	-0.59	1.50
570b	0.13	0.60	0.72	0.27	-0.59	1.50
1504d	0.69	0.55	1.28	0.39	-0.59	1.51
441a	-2.05	0.43	-1.46	0.38	-0.59	1.51
1943a	-1.74	0.31	-1.14	0.67	-0.59	1.51
1033c	-2.47	0.52	-1.88	0.29	-0.59	1.51
1404c	2.76	0.43	3.35	0.29	-0.59	1.51
8a	-0.51	0.51	0.08	0.30	-0.60	1.51
46a	-0.07	0.54	0.52	0.34	-0.60	1.51
1758a	1.42	0.63	2.02	0.23	-0.60	1.51
1985a	-1.92	0.23	-1.33	0.50	-0.60	1.51
326e	-0.12	0.25	0.48	0.24	-0.60	1.51
85.1c	-0.04	0.40	0.56	0.22	-0.60	1.51
1675a	-1.75	0.14	-1.15	0.40	-0.60	1.52
1772a	0.78	0.51	1.38	0.60	-0.60	1.52
1707c	-2.25	0.71	-1.64	0.30	-0.60	1.52
1474a	-2.38	0.36	-1.78	0.42	-0.60	1.52
574a	0.54	0.26	1.14	0.47	-0.61	1.52
1920a	-1.58	0.40	-0.97	0.74	-0.61	1.52
34a	-1.29	0.34	-0.68	0.70	-0.61	1.53
2205a	-1.01	0.49	-0.40	0.59	-0.61	1.53
1712a	2.61	0.63	3.22	0.60	-0.61	1.53
1010a	-2.60	0.42	-1.99	0.31	-0.61	1.53
1382d	-1.71	0.09	-1.10	0.71	-0.61	1.53
269b	-2.46	0.29	-1.85	0.41	-0.61	1.53
2159b	-2.29	0.29	-1.67	0.44	-0.62	1.53
1972a	-1.73	0.43	-1.11	0.61	-0.62	1.53
1298a	-1.70	0.39	-1.08	0.55	-0.62	1.53
2108b	0.49	0.54	1.10	0.29	-0.62	1.54
567b	-0.45	0.57	0.17	0.35	-0.62	1.54
45.1b	4.48	0.51	5.11	0.29	-0.62	1.54
949c	-1.76	0.39	-1.14	0.54	-0.62	1.54

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1545b	-1.84	0.48	-1.22	0.50	-0.63	1.54
2173a	2.84	0.40	3.47	0.49	-0.63	1.55
1676a	-1.90	0.07	-1.27	0.47	-0.63	1.55
581a	-1.77	0.16	-1.14	0.25	-0.63	1.55
472a	4.26	0.74	4.89	0.42	-0.63	1.55
1695a	0.22	0.30	0.85	0.59	-0.63	1.55
1414b	-0.28	0.42	0.35	0.39	-0.64	1.55
151b	0.13	0.48	0.77	0.28	-0.64	1.55
112d	0.04	0.49	0.68	0.40	-0.64	1.56
461a	-1.37	0.49	-0.73	0.24	-0.64	1.56
1557a	-1.79	0.28	-1.15	0.76	-0.64	1.56
1615b	-1.61	0.56	-0.97	0.34	-0.64	1.56
489c	1.81	0.65	2.46	0.29	-0.64	1.56
310h	-1.41	0.50	-0.76	0.25	-0.64	1.56
297a	-1.13	0.38	-0.48	0.25	-0.64	1.56
1495a	-1.30	0.64	-0.66	0.46	-0.64	1.56
1801b	-0.24	0.28	0.41	0.38	-0.65	1.56
23a	-1.60	0.45	-0.96	0.22	-0.65	1.56
1739a	-0.50	0.43	0.14	0.36	-0.65	1.57
170a	1.94	0.28	2.59	0.22	-0.65	1.57
1955a	-1.57	0.30	-0.93	0.52	-0.65	1.57
1302a	-2.16	0.80	-1.51	0.42	-0.65	1.57
2088a	-0.75	0.46	-0.10	0.29	-0.65	1.57
18a	0.01	0.67	0.66	0.39	-0.65	1.57
182a	-1.80	0.28	-1.15	0.55	-0.65	1.57
2243b	-2.44	0.24	-1.78	0.30	-0.65	1.57
1440a	1.14	0.42	1.79	0.36	-0.65	1.57
2351c	-1.39	0.37	-0.74	0.32	-0.65	1.57
1415b	-0.73	0.33	-0.07	0.32	-0.66	1.58
2074b	-1.62	0.48	-0.96	0.38	-0.66	1.58
2250a	-2.15	0.21	-1.49	0.39	-0.66	1.58
1740a	-1.62	0.49	-0.96	0.36	-0.66	1.58
81a	0.76	0.18	1.42	0.31	-0.66	1.58
1248b	0.18	0.52	0.85	0.18	-0.67	1.59
82b	0.44	0.58	1.10	0.26	-0.67	1.59
991b	-1.16	0.56	-0.50	0.70	-0.67	1.59
1513b	-2.06	0.40	-1.39	0.59	-0.67	1.59
992a	-1.22	0.54	-0.55	0.71	-0.67	1.59
1147a	-1.35	0.32	-0.68	0.29	-0.67	1.60
12a	-1.59	0.21	-0.92	0.39	-0.67	1.60
2201a	-1.89	0.24	-1.21	0.27	-0.68	1.60
1032d	-0.81	0.78	-0.12	0.27	-0.69	1.61
1373a	-2.37	0.22	-1.68	0.46	-0.69	1.61
2266b	-1.26	0.33	-0.57	0.27	-0.69	1.61
795a	-1.16	0.32	-0.47	0.19	-0.69	1.61
206a	-1.93	0.37	-1.25	0.52	-0.69	1.61
1400a	1.27	0.78	1.96	0.47	-0.69	1.61
327f	-0.25	0.63	0.44	0.23	-0.69	1.61
212a	-1.81	0.33	-1.12	0.27	-0.69	1.61

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2083e	-1.73	0.39	-1.04	0.28	-0.69	1.61
555b	0.58	0.33	1.28	0.16	-0.69	1.62
1296a	-2.22	0.41	-1.53	0.34	-0.69	1.62
226a	-2.32	0.72	-1.63	0.44	-0.69	1.62
272d	-2.17	0.22	-1.48	0.29	-0.69	1.62
1709a	-2.13	0.40	-1.43	0.34	-0.70	1.62
1945a	4.78	0.43	5.47	0.28	-0.70	1.62
1631d	2.12	0.58	2.82	0.28	-0.70	1.62
1354a	-2.29	0.66	-1.59	0.38	-0.70	1.62
24a	-1.08	0.39	-0.38	0.35	-0.70	1.63
1284a	-0.15	0.44	0.55	0.25	-0.71	1.63
184a	-1.80	0.27	-1.09	0.35	-0.71	1.63
936b	1.54	0.58	2.25	0.17	-0.71	1.63
1a	4.14	0.55	4.85	0.50	-0.71	1.63
1677b	5.86	0.55	6.57	0.26	-0.71	1.64
747a	-1.04	0.62	-0.33	0.21	-0.71	1.64
737a	0.67	0.46	1.38	0.48	-0.71	1.64
1953a	-1.46	0.35	-0.74	0.75	-0.72	1.64
794a	-0.98	0.85	-0.26	0.46	-0.72	1.65
2166a	-1.84	0.39	-1.12	0.33	-0.73	1.65
1604a	-2.12	0.49	-1.39	0.36	-0.73	1.66
479c	-1.62	0.45	-0.89	0.24	-0.73	1.66
1245b	-2.05	0.38	-1.32	0.56	-0.73	1.66
2040d	-2.46	0.37	-1.73	0.23	-0.73	1.66
1502a	-1.69	0.42	-0.95	0.38	-0.74	1.67
72a	-0.51	0.39	0.24	0.35	-0.74	1.68
1917f	-1.03	0.41	-0.28	0.44	-0.75	1.69
1650a	-1.85	0.41	-1.09	0.40	-0.76	1.69
192a	-1.83	0.41	-1.07	0.79	-0.76	1.69
1620a	-1.99	0.27	-1.23	0.43	-0.76	1.69
1951a	-1.81	0.32	-1.05	0.69	-0.76	1.70
1398a	-2.82	0.45	-2.05	0.43	-0.77	1.70
2355c	-1.79	0.48	-1.02	0.30	-0.77	1.70
1394b	1.65	0.77	2.42	0.24	-0.77	1.71
1651a	-2.01	0.24	-1.24	0.66	-0.77	1.71
2071a	-2.70	0.03	-1.93	0.28	-0.78	1.71
340a	-2.01	0.24	-1.23	0.38	-0.78	1.72
368b	-0.08	0.51	0.70	0.26	-0.78	1.72
736a	2.45	0.61	3.24	0.54	-0.79	1.73
64.2a	1.87	0.88	2.66	0.56	-0.79	1.73
17a	0.06	0.68	0.86	0.32	-0.80	1.74
1475a	-1.53	0.33	-0.73	0.39	-0.80	1.74
2161c	-1.79	0.44	-0.99	0.70	-0.80	1.74
143.2c	1.35	0.33	2.16	0.23	-0.81	1.75
1540a	-1.64	0.43	-0.83	0.57	-0.81	1.76
1521b	-1.05	0.59	-0.23	0.15	-0.82	1.76
2156c	-2.35	0.36	-1.53	0.39	-0.82	1.76
2035d	0.44	0.71	1.26	0.43	-0.82	1.77
1618b	0.76	0.88	1.59	0.38	-0.82	1.77

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1516a	-2.38	0.36	-1.55	0.45	-0.83	1.78
1803a	-1.30	0.55	-0.46	0.85	-0.83	1.78
1593b	-2.07	0.66	-1.23	0.31	-0.84	1.79
1919a	-1.03	0.43	-0.19	0.48	-0.84	1.79
1648a	-2.08	0.43	-1.24	0.56	-0.84	1.79
2109a	3.09	0.81	3.94	0.81	-0.84	1.79
1241a	-0.64	0.38	0.22	0.80	-0.86	1.82
392a	0.29	0.94	1.16	0.35	-0.86	1.82
1713a	-2.09	0.40	-1.23	0.42	-0.86	1.82
144.2a	0.63	0.27	1.50	0.27	-0.86	1.82
2255a	-1.13	0.35	-0.26	0.46	-0.87	1.83
1533a	-2.04	0.70	-1.17	0.37	-0.87	1.83
690a	-0.08	0.56	0.79	0.19	-0.87	1.83
1317a	-2.69	0.92	-1.82	0.61	-0.88	1.83
2163a	-1.44	0.74	-0.56	0.38	-0.88	1.84
979a	1.91	0.69	2.78	0.52	-0.88	1.84
1747a	-2.25	0.79	-1.37	0.41	-0.88	1.84
507a	-0.37	0.46	0.51	0.81	-0.88	1.84
890a	-0.61	0.58	0.28	0.39	-0.88	1.85
1137b	-0.71	1.21	0.18	0.36	-0.89	1.85
395a	-2.00	0.46	-1.11	0.29	-0.89	1.85
51a	-0.61	0.76	0.28	0.60	-0.89	1.85
1309b	-2.56	0.05	-1.66	0.23	-0.90	1.86
1462a	-0.23	0.28	0.68	0.39	-0.92	1.89
1708a	-1.09	0.57	-0.17	0.85	-0.92	1.89
1086c	-1.08	0.45	-0.16	0.74	-0.92	1.89
1313a	-2.71	0.38	-1.78	0.33	-0.93	1.91
1439b	-0.90	0.30	0.04	0.36	-0.94	1.91
153b	-0.48	0.31	0.46	0.95	-0.94	1.92
1790a	-2.28	0.33	-1.33	0.54	-0.95	1.93
961a	-0.73	0.63	0.22	0.43	-0.95	1.93
493a	0.99	0.89	1.94	0.28	-0.96	1.94
1463a	-0.08	0.21	0.88	0.17	-0.96	1.94
172a	2.00	0.43	2.97	0.35	-0.97	1.96
1454d	-1.78	0.39	-0.80	0.21	-0.97	1.96
1143d	-1.02	0.47	-0.05	0.52	-0.98	1.97
862c	-1.96	1.22	-0.98	0.56	-0.98	1.97
766b	-1.85	0.31	-0.86	0.50	-0.99	1.99
1412b	1.90	0.29	2.89	0.49	-0.99	1.99
1423b	3.55	0.77	4.54	0.20	-0.99	1.99
850a	-0.14	0.42	0.87	0.59	-1.01	2.02
148a	-0.73	0.40	0.32	0.27	-1.05	2.07
1696a	3.70	0.51	4.75	0.31	-1.05	2.07
1396b	-2.51	0.36	-1.45	0.49	-1.06	2.08
2141a	1.46	0.40	2.53	0.64	-1.07	2.10
1503c	-0.13	0.75	0.95	0.30	-1.08	2.11
639a	-1.04	0.62	0.04	0.50	-1.08	2.12
1682a	-0.59	0.32	0.50	0.38	-1.09	2.13
2153a	-0.83	0.49	0.26	0.41	-1.09	2.13

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2241a	-0.24	0.39	0.86	0.48	-1.10	2.15
2263b	-1.18	0.52	-0.08	0.42	-1.10	2.15
1438a	3.02	0.39	4.17	0.43	-1.15	2.22
2059b	-1.36	0.47	-0.13	0.49	-1.22	2.34
1646a	1.35	0.79	2.58	0.51	-1.23	2.35
851d	-1.81	0.47	-0.58	0.63	-1.23	2.35
465b	-1.16	0.37	0.08	0.68	-1.25	2.37
990a	2.62	0.67	3.87	0.96	-1.25	2.38
1488b	0.21	0.78	1.46	0.66	-1.25	2.38
1452a	2.09	0.61	3.35	0.28	-1.26	2.40
1270a	-1.47	0.36	-0.19	0.54	-1.28	2.43
2142a	0.23	0.57	1.52	1.18	-1.29	2.45
1371a	-3.40	1.22	-2.10	0.45	-1.30	2.46
945a	0.76	0.68	2.06	0.30	-1.30	2.47
2117b	2.31	1.27	3.62	1.12	-1.31	2.48
1367a	0.92	0.83	2.25	0.65	-1.33	2.51
1818a	2.82	0.88	4.16	1.23	-1.34	2.53
2198b	-0.03	0.54	1.32	1.21	-1.34	2.54
1139a	0.17	0.84	1.56	0.96	-1.39	2.61
851a	-1.51	0.60	-0.13	0.40	-1.39	2.62
1138a	2.33	0.75	3.73	0.88	-1.41	2.65
1008a	2.72	0.80	4.14	0.92	-1.42	2.67
2113a	2.70	1.23	4.13	1.11	-1.43	2.69
552a	0.19	0.55	1.65	0.46	-1.46	2.74
2374a	0.73	0.76	2.21	0.60	-1.48	2.79
1532a	-0.57	0.70	0.94	0.70	-1.51	2.85
2118a	-0.83	0.68	0.69	0.38	-1.52	2.86
1366a	1.60	0.90	3.14	0.82	-1.53	2.90
1262b	-0.27	0.47	1.28	1.13	-1.55	2.93
144.1c	2.31	0.40	4.24	0.49	-1.93	3.80
21a	0.69	0.77	2.95	0.77	-2.26	4.80
1246a	0.28	0.85	3.33	1.44	-3.05	8.29
1253a	-1.26	0.64	2.10	1.84	-3.36	10.26
2224a	0.08	0.44	3.48	0.64	-3.40	10.57
1015d	-1.04	0.52	3.01	1.83	-4.05	16.52
2252b	-0.50	0.58	3.90	1.80	-4.39	21.00

TABLE 4

Gene ID	OA AVG	STD	Normal AVG	STD	DIF(OA-N)	Fold
1028c	1.81	0.75	0.24	0.94	1.57	2.96
768a	1.99	0.54	0.88	0.55	1.11	2.16
141c	3.94	0.57	3.01	0.75	0.93	1.90
1548c	5.49	0.41	4.79	0.46	0.69	1.62
1357a	-2.01	0.12	-1.73	0.07	-0.28	1.21
168c	5.11	0.19	5.40	0.21	-0.29	1.22
383d	-1.78	0.18	-1.47	0.14	-0.30	1.24
2127c	0.08	0.23	0.48	0.31	-0.39	1.31

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530b	1.39	0.21	1.78	0.23	-0.40	1.32
1405c	3.41	0.34	3.81	0.16	-0.41	1.32
1765a	-1.60	0.28	-1.19	0.28	-0.41	1.33
166a	-0.97	0.34	-0.56	0.25	-0.41	1.33
1797a	-1.79	0.25	-1.38	0.30	-0.42	1.33
1729a	3.95	0.37	4.37	0.23	-0.42	1.34
1857c	-0.91	0.16	-0.49	0.20	-0.42	1.34
523a	-1.36	0.28	-0.93	0.32	-0.43	1.34
2172c	-2.54	0.17	-2.11	0.11	-0.43	1.35
58a	-0.09	0.22	0.34	0.24	-0.43	1.35
244a	-1.91	0.01	-1.47	0.12	-0.44	1.35
70d	-1.65	0.30	-1.21	0.34	-0.44	1.36
1472a	0.07	0.40	0.51	0.23	-0.44	1.36
452a	-0.80	0.33	-0.36	0.21	-0.45	1.36
1481c	-1.53	0.19	-1.09	0.32	-0.45	1.36
1940e	-0.44	0.30	0.01	0.20	-0.45	1.36
1930a	-2.00	0.27	-1.54	0.37	-0.45	1.37
739a	-0.46	0.27	0.00	0.15	-0.46	1.37
1612a	-0.56	0.41	-0.09	0.28	-0.47	1.39
14a	-0.93	0.24	-0.45	0.30	-0.47	1.39
1727a	-1.68	0.31	-1.20	0.27	-0.48	1.39
1220b	2.96	0.46	3.44	0.15	-0.48	1.40
33a	1.31	0.22	1.80	0.35	-0.49	1.40
1146a	0.55	0.33	1.04	0.34	-0.50	1.41
1738b	-1.57	0.25	-1.07	0.36	-0.50	1.41
810a	-2.11	0.30	-1.61	0.28	-0.50	1.42
1993b	-1.33	0.38	-0.82	0.34	-0.51	1.42
2147a	-1.63	0.41	-1.11	0.33	-0.52	1.43
1678a	6.05	0.47	6.57	0.26	-0.52	1.44
56a	3.79	0.23	4.32	0.38	-0.53	1.44
1814c	-1.03	0.40	-0.49	0.37	-0.54	1.45
129b	0.47	0.26	1.01	0.26	-0.54	1.45
1924a	-0.46	0.34	0.08	0.41	-0.54	1.45
557b	-1.56	0.24	-1.02	0.39	-0.54	1.45
1254a	-0.48	0.46	0.06	0.28	-0.54	1.46
1292c	-0.94	0.32	-0.40	0.47	-0.54	1.46
2221c	-0.01	0.25	0.53	0.33	-0.54	1.46
490c	4.71	0.34	5.26	0.42	-0.54	1.46
907a	-2.23	0.20	-1.68	0.29	-0.55	1.47
469d	-0.61	0.31	-0.05	0.29	-0.56	1.47
713a	-1.30	0.34	-0.74	0.25	-0.56	1.47
1372a	1.49	0.32	2.05	0.30	-0.56	1.47
482a	-1.55	0.25	-0.99	0.39	-0.56	1.48
1098a	-2.29	0.30	-1.72	0.31	-0.56	1.48
1785a	-2.19	0.09	-1.63	0.27	-0.56	1.48
1624b	-0.95	0.39	-0.38	0.36	-0.57	1.48
1441d	-1.09	0.29	-0.52	0.50	-0.57	1.48
553b	-0.76	0.16	-0.19	0.27	-0.57	1.48
2179a	-2.12	0.29	-1.55	0.46	-0.57	1.49

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1257b	-0.76	0.22	-0.18	0.34	-0.58	1.49
1506d	-1.45	0.32	-0.88	0.36	-0.58	1.49
1939c	-2.37	0.07	-1.79	0.36	-0.58	1.49
2007a	-1.93	0.29	-1.35	0.20	-0.58	1.49
13a	-0.25	0.52	0.33	0.24	-0.58	1.50
1288a	-1.12	0.25	-0.53	0.36	-0.58	1.50
1949a	-1.40	0.25	-0.82	0.50	-0.59	1.50
142.2c	1.04	0.28	1.63	0.26	-0.59	1.50
1054a	-0.73	0.26	-0.14	0.31	-0.59	1.50
1404c	2.76	0.43	3.35	0.29	-0.59	1.51
8a	-0.51	0.51	0.08	0.30	-0.60	1.51
46a	-0.07	0.54	0.52	0.34	-0.60	1.51
1985a	-1.92	0.23	-1.33	0.50	-0.60	1.51
326e	-0.12	0.25	0.48	0.24	-0.60	1.51
85.1c	-0.04	0.40	0.56	0.22	-0.60	1.51
1675a	-1.75	0.14	-1.15	0.40	-0.60	1.52
574a	0.54	0.26	1.14	0.47	-0.61	1.52
2159b	-2.29	0.29	-1.67	0.44	-0.62	1.53
2108b	0.49	0.54	1.10	0.29	-0.62	1.54
45.1b	4.48	0.51	5.11	0.29	-0.62	1.54
2173a	2.84	0.40	3.47	0.49	-0.63	1.55
1676a	-1.90	0.07	-1.27	0.47	-0.63	1.55
581a	-1.77	0.16	-1.14	0.25	-0.63	1.55
1695a	0.22	0.30	0.85	0.59	-0.63	1.55
1414b	-0.28	0.42	0.35	0.39	-0.64	1.55
151b	0.13	0.48	0.77	0.28	-0.64	1.55
112d	0.04	0.49	0.68	0.40	-0.64	1.56
461a	-1.37	0.49	-0.73	0.24	-0.64	1.56
1615b	-1.61	0.56	-0.97	0.34	-0.64	1.56
310h	-1.41	0.50	-0.76	0.25	-0.64	1.56
297a	-1.13	0.38	-0.48	0.25	-0.64	1.56
1801b	-0.24	0.28	0.41	0.38	-0.65	1.56
23a	-1.60	0.45	-0.96	0.22	-0.65	1.56
1739a	-0.50	0.43	0.14	0.36	-0.65	1.57
170a	1.94	0.28	2.59	0.22	-0.65	1.57
1955a	-1.57	0.30	-0.93	0.52	-0.65	1.57
2088a	-0.75	0.46	-0.10	0.29	-0.65	1.57
2243b	-2.44	0.24	-1.78	0.30	-0.65	1.57
1440a	1.14	0.42	1.79	0.36	-0.65	1.57
2351c	-1.39	0.37	-0.74	0.32	-0.65	1.57
1415b	-0.73	0.33	-0.07	0.32	-0.66	1.58
2074b	-1.62	0.48	-0.96	0.38	-0.66	1.58
2250a	-2.15	0.21	-1.49	0.39	-0.66	1.58
1740a	-1.62	0.49	-0.96	0.36	-0.66	1.58
81a	0.76	0.18	1.42	0.31	-0.66	1.58
1248b	0.18	0.52	0.85	0.18	-0.67	1.59
82b	0.44	0.58	1.10	0.26	-0.67	1.59
1147a	-1.35	0.32	-0.68	0.29	-0.67	1.60
12a	-1.59	0.21	-0.92	0.39	-0.67	1.60

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2201a	-1.89	0.24	-1.21	0.27	-0.68	1.60
2266b	-1.26	0.33	-0.57	0.27	-0.69	1.61
795a	-1.16	0.32	-0.47	0.19	-0.69	1.61
206a	-1.93	0.37	-1.25	0.52	-0.69	1.61
327f	-0.25	0.63	0.44	0.23	-0.69	1.61
212a	-1.81	0.33	-1.12	0.27	-0.69	1.61
2083e	-1.73	0.39	-1.04	0.28	-0.69	1.61
555b	0.58	0.33	1.28	0.16	-0.69	1.62
1296a	-2.22	0.41	-1.53	0.34	-0.69	1.62
272d	-2.17	0.22	-1.48	0.29	-0.69	1.62
1709a	-2.13	0.40	-1.43	0.34	-0.70	1.62
1945a	4.78	0.43	5.47	0.28	-0.70	1.62
1631d	2.12	0.58	2.82	0.28	-0.70	1.62
24a	-1.08	0.39	-0.38	0.35	-0.70	1.63
1284a	-0.15	0.44	0.55	0.25	-0.71	1.63
184a	-1.80	0.27	-1.09	0.35	-0.71	1.63
936b	1.54	0.58	2.25	0.17	-0.71	1.63
1a	4.14	0.55	4.85	0.50	-0.71	1.63
1677b	5.86	0.55	6.57	0.26	-0.71	1.64
747a	-1.04	0.62	-0.33	0.21	-0.71	1.64
737a	0.67	0.46	1.38	0.48	-0.71	1.64
2166a	-1.84	0.39	-1.12	0.33	-0.73	1.65
479c	-1.62	0.45	-0.89	0.24	-0.73	1.66
2040d	-2.46	0.37	-1.73	0.23	-0.73	1.66
1502a	-1.69	0.42	-0.95	0.38	-0.74	1.67
72a	-0.51	0.39	0.24	0.35	-0.74	1.68
1917f	-1.03	0.41	-0.28	0.44	-0.75	1.69
1650a	-1.85	0.41	-1.09	0.40	-0.76	1.69
1620a	-1.99	0.27	-1.23	0.43	-0.76	1.69
1951a	-1.81	0.32	-1.05	0.69	-0.76	1.70
2355c	-1.79	0.48	-1.02	0.30	-0.77	1.70
1394b	1.65	0.77	2.42	0.24	-0.77	1.71
2071a	-2.70	0.03	-1.93	0.28	-0.78	1.71
340a	-2.01	0.24	-1.23	0.38	-0.78	1.72
368b	-0.08	0.51	0.70	0.26	-0.78	1.72
736a	2.45	0.61	3.24	0.54	-0.79	1.73
17a	0.06	0.68	0.86	0.32	-0.80	1.74
1475a	-1.53	0.33	-0.73	0.39	-0.80	1.74
143.2c	1.35	0.33	2.16	0.23	-0.81	1.75
1540a	-1.64	0.43	-0.83	0.57	-0.81	1.76
1521b	-1.05	0.59	-0.23	0.15	-0.82	1.76
2156c	-2.35	0.36	-1.53	0.39	-0.82	1.76
2035d	0.44	0.71	1.26	0.43	-0.82	1.77
1919a	-1.03	0.43	-0.19	0.48	-0.84	1.79
1648a	-2.08	0.43	-1.24	0.56	-0.84	1.79
1241a	-0.64	0.38	0.22	0.80	-0.86	1.82
1713a	-2.09	0.40	-1.23	0.42	-0.86	1.82
144.2a	0.63	0.27	1.50	0.27	-0.86	1.82
2255a	-1.13	0.35	-0.26	0.46	-0.87	1.83

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690a	-0.08	0.56	0.79	0.19	-0.87	1.83
2163a	-1.44	0.74	-0.56	0.38	-0.88	1.84
979a	1.91	0.69	2.78	0.52	-0.88	1.84
1747a	-2.25	0.79	-1.37	0.41	-0.88	1.84
507a	-0.37	0.46	0.51	0.81	-0.88	1.84
890a	-0.61	0.58	0.28	0.39	-0.88	1.85
395a	-2.00	0.46	-1.11	0.29	-0.89	1.85
1309b	-2.56	0.05	-1.66	0.23	-0.90	1.86
1462a	-0.23	0.28	0.68	0.39	-0.92	1.89
1086c	-1.08	0.45	-0.16	0.74	-0.92	1.89
1313a	-2.71	0.38	-1.78	0.33	-0.93	1.91
1439b	-0.90	0.30	0.04	0.36	-0.94	1.91
153b	-0.48	0.31	0.46	0.95	-0.94	1.92
1790a	-2.28	0.33	-1.33	0.54	-0.95	1.93
961a	-0.73	0.63	0.22	0.43	-0.95	1.93
493a	0.99	0.89	1.94	0.28	-0.96	1.94
1463a	-0.08	0.21	0.88	0.17	-0.96	1.94
172a	2.00	0.43	2.97	0.35	-0.97	1.96
1454d	-1.78	0.39	-0.80	0.21	-0.97	1.96
1143d	-1.02	0.47	-0.05	0.52	-0.98	1.97
766b	-1.85	0.31	-0.86	0.50	-0.99	1.99
1412b	1.90	0.29	2.89	0.49	-0.99	1.99
1423b	3.55	0.77	4.54	0.20	-0.99	1.99
850a	-0.14	0.42	0.87	0.59	-1.01	2.02
148a	-0.73	0.40	0.32	0.27	-1.05	2.07
1696a	3.70	0.51	4.75	0.31	-1.05	2.07
1396b	-2.51	0.36	-1.45	0.49	-1.06	2.08
2141a	1.46	0.40	2.53	0.64	-1.07	2.10
1503c	-0.13	0.75	0.95	0.30	-1.08	2.11
639a	-1.04	0.62	0.04	0.50	-1.08	2.12
1682a	-0.59	0.32	0.50	0.38	-1.09	2.13
2153a	-0.83	0.49	0.26	0.41	-1.09	2.13
2241a	-0.24	0.39	0.86	0.48	-1.10	2.15
2263b	-1.18	0.52	-0.08	0.42	-1.10	2.15
1438a	3.02	0.39	4.17	0.43	-1.15	2.22
2059b	-1.36	0.47	-0.13	0.49	-1.22	2.34
1646a	1.35	0.79	2.58	0.51	-1.23	2.35
851d	-1.81	0.47	-0.58	0.63	-1.23	2.35
465b	-1.16	0.37	0.08	0.68	-1.25	2.37
990a	2.62	0.67	3.87	0.96	-1.25	2.38
1488b	0.21	0.78	1.46	0.66	-1.25	2.38
1452a	2.09	0.61	3.35	0.28	-1.26	2.40
1270a	-1.47	0.36	-0.19	0.54	-1.28	2.43
2142a	0.23	0.57	1.52	1.18	-1.29	2.45
945a	0.76	0.68	2.06	0.30	-1.30	2.47
1367a	0.92	0.83	2.25	0.65	-1.33	2.51
2198b	-0.03	0.54	1.32	1.21	-1.34	2.54
1139a	0.17	0.84	1.56	0.96	-1.39	2.61
1138a	2.33	0.75	3.73	0.88	-1.41	2.65

1008a	2.72	0.80	4.14	0.92	-1.42	2.67
552a	0.19	0.55	1.65	0.46	-1.46	2.74
2374a	0.73	0.76	2.21	0.60	-1.48	2.79
1532a	-0.57	0.70	0.94	0.70	-1.51	2.85
2118a	-0.83	0.68	0.69	0.38	-1.52	2.86
1366a	1.60	0.90	3.14	0.82	-1.53	2.90
1262b	-0.27	0.47	1.28	1.13	-1.55	2.93
144.1c	2.31	0.40	4.24	0.49	-1.93	3.80
21a	0.69	0.77	2.95	0.77	-2.26	4.80
1246a	0.28	0.85	3.33	1.44	-3.05	8.29
1253a	-1.26	0.64	2.10	1.84	-3.36	10.26
2224a	0.08	0.44	3.48	0.64	-3.40	10.57
1015d	-1.04	0.52	3.01	1.83	-4.05	16.52
2252b	-0.50	0.58	3.90	1.80	-4.39	21.00

[0110] The use of differential display to isolate gene transcripts has enabled the present inventors to develop a microarray chip enriched in transcripts involved in osteoarthritis. The use of this chip to analyze samples from canines with osteoarthritis (1) confirms the results from differential display and (2) enables further characterization of canine osteoarthritis at the molecular level. Transcripts analyzed by qPCR (discussed *infra*) have validated the differential expression analysis from the microarray.

EXAMPLE 5

Quantitative Polymerase Chain Reaction (qPCR)

[0111] Confirmation of changes in RNA transcripts was performed using quantitative PCR. Reverse transcriptase reactions were performed using Super ScriptTM II Reverse Transcriptase for RT-PCR (Invitrogen) according to the manufacture's directions. 1µg of RNA was added to 1.5µL 10 mM dNTP's, 1.5µL random hexamers and 0.6µL Oligo dT primers and brought to a final volume of 15 uL. Samples were incubated at 68°C for 10 minutes and then brought down to 4°C for at least 1 minute using a GeneAmp PCR System 9700 (Applied Biosystems). A portion (0.25X) of the above reaction was removed and used as a minus RT reaction (Negative Control containing No Super ScriptTM II Reverse Transcriptase). Using the same Super ScriptTM II Reverse Transcriptase kit, a master mix containing 3µL of 10X RT buffer, 6µL of 25mM MgCl₂, 3µL 0.1M DTT and 1.5µL RNase Inhibitor was made. A portion (0.25X) was removed and 0.375µL H₂O was added for the minus RT samples. To the remainder of the Master Mix, 1.125µL Super ScriptTM II Reverse Transcriptase was added for the positive RT reactions. All reactions were then incubated at 42°C for 1hour, boiled at 95°C for 5minutes, and the brought down to 4°C using a GeneAmp PCR System 9700. The samples were then diluted 1 part RT reaction to 29 Parts H₂O to create a stock of cDNA for experimentation.

[0112] Primers and 5' nuclease assay probes were designed based on selected sequences from the differential display using Primer Express™ v1.5 (Applied Biosystems Primer Express® Tutorial for Real Time Quantitative PCR Primer and Probe Design Tutorial). Minor groove Binding probes (ABI Custom Oligo Synthesis Factory) were ordered from ABI. All oligos were reconstituted with TE buffer pH=8.0 (Ambion) to 100µM stock concentration, and then diluted with TE buffer to a 5µM working stock concentration. TaqMan® Universal PCR Master Mix (Applied Biosystems) was used for quantitative PCR reactions according to the manufacture's directions. Primer concentration was 300µM each and Probe concentration was 200µM (determined optimal from earlier experiments). 4µl of RT and minus RT reactions were used for quantitative PCR reactions. All positive reactions were done in triplicate, and negative controls were performed singly. Standard qPCR conditions were used as described in the TaqMan® Universal Master Mix (Applied Biosystems, 50.0°C for 2 minutes, 95.0°C for 10 minutes, and 40-50 cycles of 95°C for 15 seconds then 60°C for 1 minute) at 0.5 volumes. Samples were run on an ABI Prism 7700 Sequence Detector using ABI Sequence Detector Program v1.7a.

[0113] All samples were run singularly against each primer/probe set to determine what standard curve should be used. Standard curves were generated using serial dilutions of liver RNA or RNA from experimental samples. Alternately, if the samples did not fall within either of the curve ranges, the sample with the lowest C_T (cycle threshold) would be re-reverse transcribed and a 1:10 serial dilution would be used as the standard curve for that primer/probe set. Values were normalized to G3PDH (glyceraldehyde-3-phosphate dehydrogenase) levels as determined by quantitative PCR. Inductions were calculated from each of the lowest sample's normalized value. Error bars represent standard error of the means.

[0114] Table 5 shows the primers and probes used for the qPCR analysis.

TABLE 5

I. Clone Target	SEQ ID NO:	Primers and Probes (5' – 3')
K9 G3PDH - Fwd	1567	GTC ATC ATC TCT GCT CCT TCT GC
- Rev	1568	TGA CAA TCT TGA GGG AGT TGT CA
- Probe	1569	6FAM - CTT CTC ATG GTT CAC GCC CAT CAC AAA - MGBNFQ
11B - Fwd	1570	TTG ATA CTC CTA GTC TTG TCT ATT CAC TGA
- Rev	1571	TCG AGT TTT TGC TCT TTG GAG AA
- Probe	1572	6FAM - TCA TTC AAC CCA GCA TTG AAC AAG GCT - MGBNFQ
59A - Fwd	1573	AGC AGG TGT TCA TCC CAG AAT G

- Rev	1574	GGG TGT GAC GCA CCA ACA G
- Probe	1575	6FAM - CCT ACA GCC AGG TGC AGT GTC ACA GC - MGBNFQ
127B - Fwd	1576	GCA TCC CCG AGC CTC AT
- Rev	1577	GGG TGC TAT ACA GTC CAG GTC AA
- Probe	1578	6FAM - TCT ATC TCC CCA GCT GCT TCC CCA C - MGBNFQ
141C - Fwd	1579	AAG GAA GTC CAA TAA ATT CTT TGT TTG
- Rev	1580	TGC CAG GAT TGT TGG TCT GTT
- Probe	1581	6FAM - CTC CTG CTG TTA CCC CAG TGA AGA GTG TTT T - MGBNFQ
159A - Fwd	1582	CAG GCT GCC AAC GAA TGG
- Rev	1583	AGA CCG GCT CTT GAG GAC AGA
- Probe	1584	6FAM - TGG CCT GCC TGA CAA GTA CTG AGC TTC - MGBNFQ
768A - Fwd	1585	CCA TCT TTT CTC CCT CCT CAA CT
- Rev	1586	GGT CTT CAG GTG ATG GTG GG
- Probe	1587	6FAM - TCT TCA GCG GGA CTC CCT CTT GGG - MGBNFQ
794A - Fwd	1588	AGT TTG GCT CCC TAA GTA GAT CAC TT
- Rev	1589	GAA TAC AGC TAC CAC CAA CTT TCA ATT
- Probe	1590	6FAM - CTA AAT GCT TTG GAT GAT TGT CCG CTT CTC A - MGBNFQ
851D - Fwd	1591	TGA ACA TGC TAA CCT GCG TCT C
- Rev	1592	GAC GTG TTT TCT CGG CTG GA
- Probe	1593	6FAM - CCC ACG TAG TCC GTG GGA GAC CC - MGBNFQ
2252B - Fwd	1594	CAT GTT GGT TCT GAA AAG GTC TGA
- Rev	1595	GGT GAG CCA AAA GCC ATA GCT
- Probe	1596	6FAM - CCT TTA CTC CGT GCA GAT CTA CTG CTC AGC - MGBNFQ
2258A - Fwd	1597	TGT GTT TTG TTT GTT TTG CTT GTT T
- Rev	1598	AGA AAG AAA AAA GGA AAG ATG AGT TCA
- Probe	1599	6FAM - CGC CCC CCA AAC CTT TTG TTC TCT C - MGBNFQ
1678A - Fwd	1600	ACT ATT TCA TAC CCT CTC CCA CTA CAA
- Rev	1601	CCC ACA AAT ACA ATT TAT ATT TAG CAG TGA
- Probe	1602	6FAM - TTT CCG TGC AGT TAC CTT TCA TTT TTA AAG CAA - MGBNFQ
1466B - Fwd	1603	ACA AGA CAT CCT ACC GCT GGT T
- Rev	1604	CAG CTC AGG ACC CTC GTA GAA
- Probe	1605	6FAM - CTG CAG CAT CGG CCC CAA GTG - MGBNFQ
2141A - Fwd	1606	TGA GAT TCA ACA CTT CCC AGT CAA
- Rev	1607	TGT CCC CAT GGT TAG GTG ACA
- Probe	1608	6FAM - TAT TTA CAT CAG GCA AAG CAG CAT CAG CAA - MGBNFQ
2267A - Fwd	1609	AAA TAA CAA AAG GTG AAA CTT CTA TAC AAA TAT T
- Rev	1610	AAG TTT GTA AGA CAC TTA AAC TCT TTC TGC

- Probe	1611	6FAM - CCA AAA ATT CTT TAC TCA GTC ACA CAA CAA ATG AGG - MGBNFQ
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EXAMPLE 6**qPCR analysis of Canine OA Cartilage**

[0115] qPCR was performed as described, *supra*, on 6 osteoarthritic cartilage samples from clinically diagnosed canines undergoing total hip replacement and 8 normal cartilage samples. Results are shown in Figure 2 (A-E).

EXAMPLE 7**Microarray Analysis of Treated OA Samples****A. *In Vitro* Chondrocyte Cell Culture**

[0116] Canine cartilage was digested in a 37°C shaking water bath using the following enzymes: trypsin (0.25%) for 25 minutes, hyaluronidase (150U/ml) for 1 hour, and collagenase (0.78%) overnight. Digested cartilage was filtered to obtain chondrocytes. Dulbecco's Modified Eagle Medium (DMEM) + 2.4% alginate (low melting) + cells were dropped from a 10cc syringe into calcium chloride (102 mM) to form "beads." Chondrocyte beads were cultured in DMEM/F12 + P/S (100 U/mL penicillin and 100 µg/mL streptomycin) + 10% Fetal Bovine Serum (FBS). Media was changed every other day. At the end of the treatment (see below), the chondrocyte beads were dissolved in sodium citrate (55mM) and EDTA (30mM). Suspensions were centrifuged at 1800 rpm for 10minutes. Cells were washed with phosphate buffer and centrifuged again at 1800 rpm for 5 minutes. One mL lysis binding solution (Ambion® RNAqueous™) was added to the isolated canine chondrocyte pellet, mixed thoroughly and stored at -20°C until RNA isolation could be performed.

B. RNA Isolation from Cell Culture

[0117] Samples were vortexed and homogenized using a Quiashredder (Qiagen) column according to manufacture's directions. The homogenized lysate was collected and 1 equal volume of 64% ethanol was added to it. This mixture was then applied to an RNAqueous™ filter cartridge, 700 uL at a time, and centrifuged for 1 minute at 10,000 rpm. The cartridge was washed using 700uL wash solution #1 and 500 uL wash solution #2/3 with centrifugation at 10,000 rpm for 1 minute for each wash. The filter cartridge was dried by centrifugation (10,000 rpm) for 1 minute. RNA was eluted 3 times by centrifugation (as above) using 30 uL aliquots of 95-100°C elution solution. The resulting RNA was DNase-treated and quantitated as stated

previously. Following RNA isolation, the RNA was prepared for microarray hybridization as stated previously.

C. Statistical Analysis of Cell Culture Microarray

[0118] Data were transformed to logarithm, base 2. Data were normalized using quantile normalization. After normalization, a concordance correlation was computed.

[0119] Differentially expressed genes were determined using a paired t test ($\alpha=0.05$) for the EPA vs. AA; EPAstim vs. AAstim; chondroitin sulfate and glucosamine 100 μ g vs. control, 100 μ g vs. 10 μ g and 10 μ g vs. control.

[0120] Differentially expressed genes were determined by first using ratios of AAstim vs. AA and EPAstim vs. EPA followed by a paired t test ($\alpha=0.05$) for the ratios of AAstim/AA and EPAstim/EPA.

[0121] Differentially expressed genes following a unidirectional trend for all glucosamine and chondroitin sulfate analyses were determined for each treatment pair where responses to the treatment resulted in increases or decreases, in the same direction, in all three samples.

[0122] Differentially expressed genes were determined using a Welch modified two-sample t test for both 1,25 D3 vs. control and 24,25 D3 vs. control ($\alpha=0.05$).

1. Chondroitin Sulfate Treatment

[0123] Chondrocytes were treated with chondroitin sulfate based on the recognition of chondroitin sulfate as a joint nutrient. Chondrocyte beads were treated with 100 μ g/mL, 10 μ g/mL or 0 μ g/mL (control) chondroitin sulfate (n=3) for 1 week in DMEM/F12 + P/S + 10% FBS. Media was changed every other day. After one week, the chondrocytes beads were dissolved in sodium citrate (55mM) and EDTA (30mM). Suspensions were centrifuged at 1800 rpm for 10minutes. Cells were washed with phosphate buffer and centrifuged again at 1800 rpm for 5 minutes. One mL lysis binding solution (Ambion® RNAqueous™) was added to the isolated canine chondrocyte pellet, mixed thoroughly and stored at -20°C until RNA isolation could be performed. One sample from the chondroitin sulfate treatment was removed due to poor correlation with the rest of the array data. This reduced this analysis to an n=3. The results are shown in Tables 7-12.

TABLE 7: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 100 μg/mL and 10 μg/mL Chondroitin Sulfate on
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Chondrocytes (p<0.5)		
Gene ID	DIF (100-10)	Fold
1071b	-0.21	1.15
1089d	0.23	1.17
1221a	-0.19	1.14
1228a	-0.44	1.36
1263b	-0.22	1.16
1304a	-0.14	1.10
143.2c	0.22	1.16
1477a	-0.22	1.17
1576a	-0.30	1.23
1577a	-0.12	1.09
158a	-0.23	1.17
1717a	-0.29	1.22
1732a	-0.10	1.07
1747a	-0.16	1.12
1749a	-0.49	1.40
1752a	-0.30	1.23
1917f	-0.43	1.35
2173a	-0.63	1.54
2267a	-0.55	1.47
2374a	-0.54	1.46
322a	-0.41	1.33
368b	-0.17	1.12
392a	-0.07	1.05
508	-0.17	1.12
639a	-0.26	1.20
711a	-0.24	1.18
720a	-0.17	1.12
73b	-0.24	1.18
753b	-0.26	1.20
831a	-0.38	1.30
91f	-0.27	1.21
936b	-0.21	1.16
997a	0.15	1.11

TABLE 8: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 100 µg/mL and 0 µg/mL Chondroitin Sulfate (Control) on Chondrocytes (p<0.5)

Gene ID	DIF (100-Control)	Fold
1044c	0.19	1.14
1136b	-0.32	1.25
1137b	-0.20	1.15
1212b	-0.31	1.24
1248b	-0.24	1.18
1254a	0.13	1.09

1304a	-0.35	1.28
143.2c	0.28	1.21
1450a	-0.12	1.09
1457b	0.10	1.07
1524a	0.24	1.18
159a	0.84	1.79
1741a	-0.42	1.34
1801b	0.26	1.20
1880a	-0.75	1.68
1911b	-0.24	1.18
1930a	-0.34	1.27
297a	-0.31	1.24
398b	-0.34	1.27
466b	-0.38	1.30
487a	-0.21	1.16
538a	-0.25	1.19
713a	-0.20	1.15
720a	-0.21	1.16
739a	-0.29	1.22
795a	-0.43	1.35
831a	-0.18	1.13
85.2b	-0.25	1.19
961a	-0.31	1.24
995a	-0.60	1.52
999a	-0.35	1.27

TABLE 9: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 10 µg/mL and 0 µg/mL Chondroitin Sulfate (Control) on Chondrocytes (p<0.5)

Gene ID	DIF (10-Control)	Fold
1050a	-0.27	1.21
1097c	-0.35	1.27
1163d	0.18	1.13
1366a	-0.12	1.09
1406a	0.13	1.10
145b	0.35	1.28
1554c	-0.73	1.66
170a	0.20	1.15
1764a	-0.11	1.08
1911b	-0.29	1.23
2088a	-0.13	1.10
2105a	0.23	1.17
2205a	-0.27	1.20
2266b	-0.16	1.12
33a	0.38	1.31
406a-r	-0.02	1.01
708a	0.13	1.10

768a	0.81	1.75
840d-r	-0.19	1.14
93e	0.14	1.10

TABLE 10: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 100 µg/mL and 10 µg/mL Chondroitin Sulfate on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (100-10)	Fold
491	1.21	2.32
498	0.18	1.13
508	-0.17	1.12
1016b	0.36	1.28
1044c	0.33	1.26
1089d	0.23	1.17
1091b	0.18	1.13
1106a	-0.25	1.19
111a	-0.11	1.08
1129a	-0.22	1.17
1133b	-0.12	1.09
1137b	0.20	1.15
11b	0.69	1.61
1212b	-0.24	1.18
1217a	-0.34	1.27
1221a	-0.19	1.14
1225b	-0.23	1.17
1228a	-0.44	1.36
1254a	0.15	1.11
1263b	-0.22	1.16
127b	0.31	1.24
128a	-0.43	1.35
129b	0.26	1.20
1304a	-0.14	1.10
132a	-0.35	1.27
1364d	0.29	1.22
1403a	-0.25	1.19
1406a	-0.14	1.11
1409b	-0.22	1.17
1416a	-0.33	1.25
142.1c	-0.11	1.08
142.2c	0.76	1.70
143.2c	0.22	1.16
144.1c	0.82	1.77
1453a	-0.13	1.09
1477a	-0.22	1.17
1489a	-0.18	1.14

1519a	0.42	1.34
1532a	0.22	1.16
154a	0.04	1.03
1577a	-0.12	1.09
158a	-0.23	1.17
159a	0.90	1.87
1612a	-0.13	1.10
1629a	-0.17	1.13
163a	-0.27	1.20
1646a	-0.06	1.04
1693b	-0.08	1.06
1705a	-0.34	1.26
1717a	-0.29	1.22
1732a	-0.10	1.07
1739a	-0.05	1.03
173a	-0.48	1.40
1741a	-0.21	1.16
1747a	-0.16	1.12
1749a	-0.49	1.40
1752a	-0.30	1.23
1760c	-0.09	1.07
1772a	-0.36	1.28
186a	0.27	1.21
1874b	-0.18	1.13
1880a	-0.40	1.32
1881b	-0.11	1.08
1892a	0.24	1.18
1945a	-0.07	1.05
1989b	-0.02	1.02
1990a	-0.37	1.29
2002c	-0.16	1.12
2008a	-0.05	1.03
2013a	0.05	1.04
2023b	-0.17	1.12
2047b	-0.17	1.13
2083e	-0.28	1.21
2095a	-0.48	1.40
2102a	-0.64	1.56
2108b	-0.13	1.09
2109a	-0.41	1.33
2117b	-0.37	1.29
211b	0.40	1.32
2148a	0.10	1.07
2173a	-0.63	1.54
2182b	0.26	1.20
2205a	0.34	1.27
2221c	0.21	1.16
2223a	-0.22	1.17
2267a	-0.55	1.47

2374a	-0.54	1.46
27a	-0.14	1.10
297a	-0.17	1.12
307b	0.15	1.11
309a	0.42	1.34
322a	-0.41	1.33
106a	0.15	1.11
106a	0.18	1.13
368b	-0.17	1.12
379a	-0.15	1.11
392a	-0.07	1.05
410c	-0.22	1.17
425c	-0.25	1.19
455c	-0.01	1.01
468f	-0.19	1.14
472a	-0.46	1.38
483a	0.15	1.11
545a	-0.12	1.08
553b	0.38	1.31
596e	-0.10	1.07
60a	-0.40	1.32
623a	0.64	1.56
639a	-0.26	1.20
63a	-0.25	1.19
67a	-0.56	1.47
704b	-0.39	1.31
711a	-0.24	1.18
713a	-0.26	1.20
718a	-0.18	1.14
720a	-0.17	1.12
736a	-1.16	2.23
737a	-0.22	1.16
73b	-0.24	1.18
753b	-0.26	1.20
759b	-0.28	1.21
795a	-0.19	1.14
812d-r	-0.19	1.14
831a	-0.38	1.30
833a	-0.28	1.22
84.2c	-0.33	1.26
840d-r	0.28	1.22
841b	-0.31	1.24
847a	-0.18	1.13
87.2b	-0.41	1.33
878c	-0.25	1.19
8a	-0.21	1.16
90c	-0.25	1.19
91f	-0.27	1.21
929a	-0.72	1.64

936b	-0.21	1.16
93e	-0.30	1.23
945a	-0.27	1.20
990a	-0.19	1.14
995a	-0.35	1.27
999a	-0.12	1.09

TABLE 11: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 100 µg/mL and 0 µg/mL (Control) Chondroitin Sulfate on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (100-Control)	Fold
1002b	-0.18	1.13
1026b	-0.11	1.08
1044c	0.19	1.14
106a	0.13	1.10
1133b	-0.20	1.15
1136b	-0.32	1.25
1137b	-0.20	1.15
1138a	-0.32	1.25
1159b	0.17	1.12
1183a	0.18	1.13
1189a	0.12	1.09
11b	1.14	2.20
1212b	-0.31	1.24
1217a	-0.45	1.37
1228a	-0.34	1.26
1240a	-0.03	1.02
1246a	-0.04	1.03
1248b	-0.24	1.18
1254a	0.13	1.09
1294b	0.40	1.32
1304a	-0.35	1.28
1366a	-0.26	1.19
136b	-0.41	1.33
1394b	-0.19	1.14
1403a	-0.28	1.21
1405c	-0.02	1.02
1409b	-0.15	1.11
141c	0.58	1.50
142.2c	1.01	2.02
1423b	-0.12	1.09
143.2c	0.28	1.21
1450a	-0.12	1.09
1456b	-0.09	1.06
146b	0.27	1.21

1472a	0.16	1.12
1477a	-0.45	1.37
1489a	-0.37	1.29
1519a	0.18	1.13
154a	-0.11	1.08
156b	0.35	1.27
158a	-0.27	1.21
159a	0.84	1.79
15b	-0.29	1.22
1612a	-0.34	1.27
1630b	-0.24	1.18
1631d	-0.26	1.20
1632a	-0.23	1.17
163a	-0.40	1.32
1695a	0.05	1.03
1705a	-0.46	1.37
1715a	-0.14	1.10
1717a	-0.24	1.18
1732a	-0.10	1.07
1734b	-0.27	1.21
1740a	-0.07	1.05
1741a	-0.42	1.34
1747a	-0.10	1.07
1749a	-0.36	1.28
1752a	-0.26	1.20
1758a	-0.21	1.16
1772a	-0.06	1.05
1811b	-0.19	1.14
1813b	-0.13	1.10
1874b	-0.36	1.29
1911b	-0.24	1.18
1917f	-0.41	1.33
1928a	-0.16	1.12
1930a	-0.34	1.27
1945a	-0.26	1.20
1948b	0.14	1.10
2013a	-0.17	1.12
2035d	-0.30	1.24
2047b	-0.22	1.17
205a	-0.29	1.22
2088a	-0.18	1.14
2129a	-0.17	1.12
2136b	0.23	1.17
2154a	-0.21	1.16
2266b	-0.18	1.14
2267a	-0.55	1.47
2374a	-0.54	1.45
297a	-0.31	1.24
319b	-0.39	1.31

322a	-0.36	1.28
32e	0.19	1.14
33a	0.20	1.15
106a	0.32	1.25
106a	0.15	1.11
392a	-0.15	1.11
398b	-0.34	1.27
401a	-0.20	1.15
406a-r	-0.03	1.02
421a	-0.19	1.14
425c	-0.36	1.28
44a	-0.18	1.13
472a	-0.29	1.22
487a	-0.21	1.16
50.2d	-0.25	1.19
538a	-0.25	1.19
553b	0.28	1.21
568a	-0.15	1.11
57a	-0.18	1.13
596e	-0.17	1.13
59a	0.39	1.31
60a	-0.30	1.23
616a	-0.19	1.14
61c	-0.14	1.10
639a	-0.26	1.20
63a	-0.18	1.13
6b	0.18	1.13
713a	-0.20	1.15
720a	-0.21	1.16
72a	-0.22	1.17
736a	-0.71	1.63
739a	-0.29	1.22
749a	-0.24	1.18
794a	-0.12	1.08
795a	-0.43	1.35
828a	-0.49	1.40
82b	0.21	1.16
831a	-0.18	1.13
833a	-0.26	1.20
84.1b	-0.10	1.07
84.2c	-0.35	1.28
844c-r	-0.09	1.06
85.2b	-0.25	1.19
890a	-0.08	1.06
91f	-0.15	1.11
936b	-0.15	1.11
953a	-0.04	1.03
961a	-0.31	1.24
995a	-0.60	1.52

996a	-0.08	1.06
999a	-0.35	1.27

TABLE 12: Differential Expression of OA-Associated Genes with Chondroitin Sulfate Treatment Comparing the Effect of 10 µg/mL and 0 µg/mL (Control) Chondroitin Sulfate on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (10-C)	Fold
491	-1.37	2.59
493	-0.05	1.04
498	-0.35	1.27
1016b	-0.50	1.42
1050a	-0.27	1.21
1072a	-0.48	1.40
1089d	-0.21	1.15
1105a	-0.40	1.32
1136b	-0.32	1.25
1137b	-0.39	1.31
1139a	-0.07	1.05
1145a	-0.11	1.08
1174d	-0.45	1.36
1217a	-0.11	1.08
1247a	-0.20	1.15
1304a	-0.21	1.15
131a	-0.21	1.16
1366a	-0.12	1.09
1406a	0.13	1.10
1409b	0.07	1.05
1411a	-0.18	1.13
145b	0.35	1.28
1500b	-0.24	1.18
1521b	-0.19	1.14
154a	-0.15	1.11
1632a	-0.20	1.15
1656a	0.16	1.12
1721a	-0.19	1.14
1739a	0.07	1.05
173a	0.37	1.29
1741a	-0.21	1.16
1747a	0.07	1.05
1758a	-0.19	1.14
1764a	-0.11	1.08
1772a	0.29	1.22
1811b	-0.16	1.12
1852a	0.38	1.30
1892a	-0.35	1.28

1895b	0.06	1.04
1908a	-0.12	1.09
1930a	-0.22	1.16
1945a	-0.19	1.14
1948b	0.19	1.14
2013a	-0.22	1.17
2088a	-0.13	1.10
2105a	0.23	1.17
2109a	0.68	1.61
2149d	-0.14	1.10
2205a	-0.27	1.20
2266b	-0.16	1.12
307b	-0.14	1.10
319b	-0.11	1.08
326e	0.22	1.17
32e	0.18	1.14
33a	0.38	1.31
348c	0.15	1.11
379a	0.21	1.16
406a-r	-0.02	1.01
413a	-0.17	1.12
421a	-0.13	1.10
472a	0.17	1.13
489c	0.04	1.03
530b	-0.24	1.18
538a	-0.48	1.39
56a	0.06	1.04
57a	-0.22	1.17
583e	-0.22	1.17
64.2a	-0.24	1.18
704b	0.23	1.17
708a	0.13	1.10
719a	-0.35	1.28
737a	0.11	1.08
749a	-0.29	1.23
753b	0.21	1.15
75c	0.24	1.19
795a	-0.25	1.19
828a	-0.65	1.57
831a	0.20	1.15
840d-r	-0.19	1.14
848a	0.09	1.07
87.2b	0.42	1.34
90c	0.27	1.20
91f	0.13	1.09
93e	0.14	1.10
945a	0.26	1.20
961a	-0.31	1.24
98d	0.15	1.11

995a	-0.25	1.19
999a	-0.23	1.17

2. Glucosamine Treatment

[0124] Glucosamine treatment was used to determine the effect of this joint health nutrient on the differential expression of OA-associated genes. Chondrocyte beads were treated with 100 µg/mL, 10 µg/mL or 0 µg/mL (control) glucosamine (n=3) for 1 week in DMEM/F12 + P/S + 10% FBS. Media was changed every other day. After one week, the chondrocytes beads were dissolved in sodium citrate (55mM) and EDTA (30mM). Suspensions were centrifuged at 1800 rpm for 10minutes. Cells were washed with phosphate buffer and centrifuged again at 1800 rpm for 5 minutes. One mL lysis binding solution (Ambion® RNAqueous™) was added to the isolated canine chondrocyte pellet, mixed thoroughly and stored at ~20°C until RNA isolation could be performed. The results are shown in Tables 13-18.

TABLE 13: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 100 µg/mL and 10 µg/mL Glucosamine on Chondrocytes (p<0.5)		
Gene ID	DIF (100-10)	Fold
1044c	-1.12	2.17
10c	-0.48	1.39
1131b	-0.80	1.74
1183a	-0.43	1.34
1257b	0.46	1.38
1479a	-0.49	1.41
1532a	0.34	1.27
1656a	-0.73	1.66
170a	-0.56	1.47
1896b	-0.59	1.51
2085c	-0.44	1.36
2137b	-0.67	1.59
322a	0.41	1.32
687a	-0.46	1.38
695a	-0.51	1.42
841b	0.79	1.73

TABLE 14: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 100 µg/mL and 0 µg/mL (Control) Glucosamine on Chondrocytes (p<0.5)		
Gene ID	DIF (100-C)	Fold

1413b	-1.73	3.31
1892a	0.94	1.92

TABLE 15: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 10 µg/mL and 0 µg/mL (Control) Glucosamine on Chondrocytes (p<0.5)

Gene ID	DIF (10-C)	Fold
1294b	-0.55	1.46
1364d	-0.67	1.59
1384a	1.61	3.04
150a	1.23	2.34
151b	1.18	2.27
1645a	0.43	1.34
2100b	-0.34	1.26
2198b	0.76	1.70
2210a	-0.51	1.43
38a	-0.57	1.48
457c	-1.57	2.96
464b	-0.34	1.27
623a	-0.56	1.47
63a	0.20	1.15
794a	-0.24	1.18

TABLE 16: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 100 µg/mL and 10 µg/mL Glucosamine on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (100-10)	Fold
508	-0.41	1.33
1004a	-0.68	1.60
1023c	-0.58	1.49
1026b	-0.52	1.43
1030a	-0.70	1.63
1044c	-1.12	2.17
1089d	-0.42	1.34
1094b	-0.35	1.28
1099c	-0.66	1.58
10c	-0.48	1.39
1104b	-0.79	1.73
1110b	-0.59	1.50
1131b	-0.80	1.74
1159b	-0.86	1.81
1183a	-0.43	1.34
1227b	-1.55	2.94

131a	-0.70	1.62
1405c	-0.40	1.32
1406a	-0.58	1.49
1423b	-0.73	1.66
1437a	-0.55	1.47
1479a	-0.49	1.41
1500b	-0.97	1.95
150a	-0.72	1.64
1584a	-0.80	1.74
1594a	-1.04	2.05
159a	0.56	1.48
1626c	-0.82	1.77
1639a	-0.58	1.50
1656a	-0.73	1.66
1669d	-0.69	1.61
1670d	-1.20	2.30
1849d	-0.54	1.45
1895b	-0.22	1.16
1896b	-0.59	1.51
2085c	-0.44	1.36
2092c	-0.52	1.43
2104a	-0.67	1.59
2117b	-1.00	1.99
2137b	-0.67	1.59
2167a	-0.83	1.77
2267a	-1.12	2.18
260c	-0.63	1.55
370a	0.24	1.18
413a	-0.40	1.32
421a	-0.58	1.49
48b	-0.89	1.85
687a	-0.46	1.38
695a	-0.51	1.42
706b	-0.39	1.31
720a	-0.42	1.34
847a	-0.50	1.41
863c-r	-0.45	1.36
87.2b	-0.87	1.83
906a	-0.36	1.28
981a	-0.70	1.62

TABLE 17: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 100 µg/mL and 0 µg/mL (Control) Glucosamine on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (100-C)	Fold
491	0.56	1.47

1026b	-0.30	1.23
1030a	-0.50	1.41
1040b	-0.63	1.55
106a	0.23	1.17
1094b	-0.14	1.10
111a	-0.85	1.81
1227b	-1.15	2.23
1413b	-1.73	3.31
146b	-0.57	1.49
1500b	-1.51	2.85
158a	-1.07	2.10
1630b	-1.23	2.34
1669d	-0.24	1.19
1670d	-0.26	1.20
2048a	-0.27	1.20
2331c	-0.74	1.67
283a	-0.69	1.62
370a	0.15	1.11
375d	-0.22	1.16
384c	-0.39	1.31

TABLE 18: Differential Expression of OA-Associated Genes with Glucosamine Treatment Comparing the Effect of 10 µg/mL and 0 µg/mL (Control) Glucosamine on Chondrocytes; Dataset shows a Unidirectional Trend in Fold Change Across All Samples

Gene ID	DIF (10-Control)	Fold
1006b	-0.79	1.73
104a	-0.53	1.44
106a	0.24	1.18
1072a	0.52	1.44
1089d	0.63	1.54
111a	-0.29	1.22
104a	-0.20	1.15
1190b	-0.52	1.43
130b	0.35	1.28
1364d	-0.67	1.59
1384a	1.61	3.04
1400a	-0.66	1.58
1405c	0.66	1.58
1437a	0.56	1.47
1466b	-0.75	1.68
146b	-0.27	1.20
1469a	0.57	1.48
150a	1.23	2.34
151b	1.18	2.27
1554c	-0.34	1.27
1631d	0.48	1.39

1645a	0.43	1.34
1670d	0.94	1.92
1683a	-1.36	2.57
1712a	0.18	1.14
1948b	0.25	1.19
1a	-1.05	2.07
2095a	-0.94	1.92
2117b	1.14	2.20
262c	-0.18	1.14
27a	0.10	1.07
283a	-0.32	1.25
421a	0.55	1.46
45.1b	0.15	1.11
457c	-1.57	2.96
459a	-0.40	1.32
468f	0.34	1.27
483a	-0.37	1.29
489c	0.22	1.16
490c	0.17	1.13
50.2d	0.30	1.23
52a	-1.14	2.20
530b	-0.24	1.18
553b	0.26	1.20
557b	-0.17	1.13
63a	0.20	1.15
795a	0.28	1.21
986a	-0.61	1.52
98d	0.17	1.13
996a	0.77	1.71

3. $1\alpha,25$ -dihydroxyvitamin D₃ (1,25 D3) and 24R,25-dihydroxyvitamin D₃ (24,25 D3) Treatment

[0125] 1,25 D3 and 24R,25D3 treatment was applied to chondrocytes based on their known effects on prostaglandin production and differential responses to the vitamin D3 metabolites in chondrocytes to determine the effect of these compounds on OA-associated gene expression. Chondrocyte beads were treated with 10^{-7} M 1,25 D3 or 10^{-7} M 24,25 D3 for 24 hours or without Vitamin D (equivalent ethanol was added to control), (n=3) in DMEM/F12 + P/S + 10% FBS. After 24 hours, the chondrocyte beads were dissolved in sodium citrate (55mM) and EDTA (30mM). Suspensions were centrifuged at 1800 rpm for 10 minutes. Cells were washed with phosphate buffer and centrifuged again at 1800 rpm for 5 minutes. One mL lysis binding solution (Ambion® RNAqueous™) was added to the isolated canine chondrocyte pellet, mixed thoroughly and stored at -20°C until RNA isolation could be performed. The results are shown in Tables 19 and 20.

TABLE 19: Differential Expression of OA-Associated Genes with 1 α ,25-dihydroxyvitamin D₃ Treatment on Chondrocytes (p<0.5)

Gene ID	median C	median 1,25 vD3	DIF (1,25-Control)	Fold
1023c	10.95	10.12	-0.83	1.77
1042a	11.30	10.86	-0.44	1.36
1068a	9.62	8.89	-0.73	1.66
1096a	9.68	9.36	-0.32	1.25
1101a	7.76	7.16	-0.60	1.51
1103a	7.92	7.29	-0.63	1.55
1120a	8.17	7.77	-0.40	1.32
1147a	8.04	7.43	-0.61	1.52
117.1d	8.60	8.16	-0.44	1.35
1174d	9.66	8.30	-1.36	2.57
1178a	8.12	7.55	-0.57	1.49
1275c	8.72	8.07	-0.64	1.56
1304a	8.92	8.07	-0.85	1.80
1447a	9.67	9.21	-0.46	1.37
1461a	7.89	6.96	-0.92	1.90
1503c	8.86	8.47	-0.40	1.32
1521b	9.79	8.50	-1.29	2.44
153b	8.49	8.03	-0.46	1.37
1554c	9.09	8.49	-0.61	1.52
1576a	8.27	7.66	-0.61	1.52
1582a	8.10	7.62	-0.47	1.39
1592a	8.03	7.35	-0.67	1.59
1601a	7.68	7.30	-0.38	1.30
1612a	10.11	8.71	-1.40	2.64
1779b	7.63	7.09	-0.54	1.45
1813b	11.20	10.19	-1.01	2.02
1849d	11.81	11.31	-0.49	1.41
185a	7.61	7.28	-0.34	1.26
1863c	10.52	9.95	-0.57	1.49
1889a	8.20	7.45	-0.75	1.68
1892a	9.71	8.90	-0.81	1.75
1920a	8.24	7.54	-0.70	1.62
192a	7.84	7.61	-0.23	1.17
1943a	7.71	7.35	-0.36	1.28
1991d	9.36	8.48	-0.88	1.84
2109a	10.56	11.72	1.16	2.23
2117b	9.27	11.06	1.79	3.46
2163a	8.69	7.49	-1.20	2.30
2179a	7.71	7.17	-0.54	1.45
2198b	9.71	8.36	-1.35	2.54
2201a	8.19	7.74	-0.45	1.37
2223a	15.42	14.58	-0.84	1.79
2263b	8.85	8.11	-0.74	1.67
2266b	8.69	7.92	-0.77	1.71
2337a	13.57	12.62	-0.95	1.93

234a	7.95	7.61	-0.33	1.26
2353a	8.43	7.96	-0.47	1.38
299a	7.62	7.90	0.29	1.22
106a	16.00	15.99	-0.01	1.00
367a	10.83	10.22	-0.61	1.52
388a	7.81	7.52	-0.29	1.22
415b	7.86	7.33	-0.53	1.44
478a	9.24	8.85	-0.38	1.30
5b	10.21	9.71	-0.51	1.42
61c	10.58	9.88	-0.70	1.62
719a	10.62	10.27	-0.35	1.27
721b	9.08	8.62	-0.46	1.38

TABLE 20: Differential Expression of OA-Associated Genes with 24R,25-dihydroxyvitamin D₃ Treatment on Chondrocytes (p<0.5)

Gene ID	median C	median 24,25 vD3	DIF (24,25-Control)	Fold
1023c	11.11	10.48	-0.64	1.56
1068a	9.68	9.21	-0.47	1.39
1098a	7.01	8.18	1.17	2.25
1285a	7.37	7.69	0.33	1.25
1335b	7.85	7.69	-0.16	1.12
1474a	6.94	7.70	0.76	1.69
1481c	7.70	7.39	-0.31	1.24
1592a	8.09	7.46	-0.63	1.55
16b	8.47	7.73	-0.74	1.67
1726a	7.88	7.37	-0.50	1.42
1779b	7.66	7.32	-0.35	1.27
2330b	8.01	7.74	-0.27	1.21
340a	7.71	8.41	0.69	1.62
371a	9.33	9.60	0.26	1.20
401a-r	7.17	7.55	0.39	1.31
449a	7.29	7.59	0.30	1.23
70d	7.88	8.23	0.35	1.28
725a	7.42	8.23	0.81	1.75
832a	8.37	9.04	0.67	1.59
996a	14.73	14.52	-0.22	1.16

4. Eicosapentaenoic acid (EPA) and Arachidonic Acid (AA) Treatment

[0126] Chondrocytes were treated with eicosapentaenoic acid (EPA) and arachidonic acid (AA) based on the recognition in the literature that EPA acts as an anti-inflammatory. AA was used as a control to represent a typical western diet. Chondrocytes were enriched with 50μM EPA or 50μM AA (using albumin as a carrier) for two weeks in DMEM/HAMS + P/S + 10% FBS. Media was changed every other day. Each set (n=3) was split and half were treated with stimulated monocyte neutrophil conditioned media (SMNCM) for one week with media changed

every other day. SMNCM was made by isolating monocytes and neutrophils from canine whole blood using NycoPrep™ according to the manufacture's directions. Monocytes and neutrophils were stimulated with lipopolysaccharide (20ng/mL) for 72 hours. The resulting supernatant was used as SMNCM in cell culture experimentation (SMNCM made up 10% of media used during experimentation). Chondrocyte beads were dissolved in sodium citrate (55mM) and EDTA (30mM). Suspensions were centrifuged at 1800 rpm for 10minutes. Cells were washed with phosphate buffer and centrifuged again at 1800 rpm for 5 minutes. One mL lysis binding solution (Ambion® RNAqueous™) was added to the isolated canine chondrocyte pellet, mixed thoroughly and stored at -20°C until RNA isolation could be performed. One sample from the EPA/AA stim treatment was removed due to poor correlation with the rest of the array data. This reduced these analyses to an n=3. The results are shown in Tables 21-23.

TABLE 21: Differential Expression of OA-Associated Genes Comparing AA Treatment with EPA Treatment of Chondrocytes (p<0.05)		
Gene ID	DIF (AA-EPA)	Fold
1190b	0.42	1.34
1381a	-0.12	1.08
1391a	0.26	1.20
1450a	-0.64	1.56
1451a	-0.85	1.80
1466b	0.33	1.26
1678a	-0.67	1.60
1730a	0.45	1.36
2095a	-0.35	1.28
493	-0.46	1.38
708a	0.51	1.43
99b	-0.17	1.13

TABLE 22: Differential Expression of OA-Associated Genes with Inflammatory Stimulation Comparing AA Treatment with EPA Treatment of Chondrocytes (p<0.05)		
Gene ID	DIF (AAs-EPAs)	Fold
1099c	1.12	2.17
1104b	0.73	1.66
1106a	0.46	1.38
1184a	0.54	1.45
1190b	0.56	1.47
128a	-0.68	1.60
1323b-r	-0.58	1.50
1339b	-1.58	2.98

1391a	0.88	1.84
1425a	0.68	1.61
1459c	-0.38	1.30
154a	-1.27	2.42
1576a	-0.33	1.26
1629a	-0.58	1.49
1639a	0.64	1.56
164c	-0.69	1.61
166a	-0.43	1.35
1752a	-0.27	1.20
2035d	-0.57	1.48
2113a	-0.90	1.86
2120a-r	0.28	1.22
35c	-0.19	1.14
65.2a	-0.86	1.82
90c	-0.61	1.53

TABLE 23: Differential Expression of OA-Associated Genes with Inflammatory Stimulation Comparing EPA Treatment and AA Treatment of Chondrocytes (p<0.05)

Gene ID	AAs-AA	EPAs-EPA	DIF ((AAs-AA)-(EPAs-EPA))	Fold
517	0.10	1.08	-0.98	1.97
1007a	-2.37	-2.00	-0.37	1.29
1030a	0.25	-0.23	0.48	1.39
1042a	0.89	0.51	0.38	1.30
104a	0.10	0.95	-0.85	1.80
1091b	1.20	0.90	0.30	1.23
1145a	-0.41	-0.55	0.14	1.10
1184a	1.48	0.94	0.55	1.46
1227b	1.47	1.13	0.35	1.27
1270a	0.19	-1.04	1.23	2.35
1339b	-1.91	0.09	-2.00	4.00
134b	0.83	0.16	0.66	1.58
1381a	-1.65	-2.22	0.56	1.47
1406a	0.46	0.09	0.37	1.29
1469a	0.77	1.36	-0.59	1.51
1549a	0.13	0.15	-0.02	1.01
154a	2.97	4.48	-1.51	2.85
1585b	0.28	-0.21	0.49	1.40
1598a	0.19	-0.09	0.27	1.21
1656a	1.28	0.36	0.92	1.89
1659a	0.19	0.03	0.16	1.12
1670d	1.52	0.68	0.84	1.79
1678a	-1.27	-1.76	0.49	1.40
1741a	0.02	-0.64	0.66	1.58
1895b	0.89	0.42	0.46	1.38
1929c	0.35	0.23	0.12	1.09
1930a	0.59	0.34	0.25	1.19

1981a	-0.04	-0.30	0.27	1.21
2008a	0.44	0.03	0.41	1.33
2255a	0.16	-0.08	0.25	1.19
253b	-0.18	0.19	-0.37	1.29
342a	0.02	0.13	-0.11	1.08
350b	-0.79	0.09	-0.87	1.83
364a	0.20	0.28	-0.08	1.06
384c	0.13	-0.19	0.31	1.24
465b	-0.13	-0.84	0.71	1.64
490c	-0.45	0.09	-0.54	1.45
516c	0.04	1.09	-1.05	2.07
687a	1.16	0.74	0.42	1.34
706b	0.70	-0.44	1.14	2.20
709a	0.53	0.09	0.44	1.36
758b	0.09	-0.18	0.27	1.21
89c	0.55	1.25	-0.70	1.62
981a	1.11	0.52	0.59	1.51

[0127] The experiments demonstrated that various treatments can affect the expression of OA-associated genes. In some cases, the effect on gene expression was statistically significant ($p < 0.05$). In other cases, although the change could not be demonstrated to be statistically significant due to the variability of expression, there was a definite trend for expression to be changed in one direction only (either increased expression or decreased expression). This unidirectional change is considered to be both biologically relevant and significant. In some cases, it is believed that down-regulation of expression of certain genes will have a beneficial biological effect on OA. For other genes, increased expression will have a beneficial biological effect. The invention allows the identification of genes that correlate with beneficial effects as demonstrated by regulation of compounds known to be involved in anti-inflammatory processes, for example. The invention also permits the identification of new compounds which should have beneficial effects based on their regulation of gene expression of the OA-associated genes described in this invention.

[0128] The results demonstrate that one can affect the biology of the cells with various treatments and have a direct impact on gene expression of OA-associated genes. The invention permits the rapid and powerful screening of compounds to identify candidate treatments and preventatives of OA in animals, particularly humans.

[0129] The disclosures of each patent, patent application, publication and accession number to database sequences cited or described in this document are hereby incorporated herein by reference, in their entirety.

[0130] Various modifications of the invention, in addition to those described herein, will be apparent to those skilled in the art from the foregoing description. Such modifications

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are also intended to fall within the scope of the appended claims.

What is Claimed:

1. A combination comprising a plurality of polynucleotide molecules wherein the polynucleotide molecules are differentially expressed in an osteoarthritic subject or in a pre-osteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic.
2. The combination of claim 1, wherein the plurality of polynucleotide molecules comprises two or more molecules selected from SEQ ID NOs:1-1558 or fragments thereof.
3. A method for the detection of differential expression of nucleic acids in a sample, comprising the steps of:
 - a) hybridizing a combination comprising a plurality of polynucleotide molecules wherein the polynucleotide molecules are differentially expressed in an osteoarthritic subject or in a pre-osteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic with nucleic acids of the sample, thereby forming one or more hybridization complexes;
 - b) detecting the hybridization complexes; and
 - c) comparing the hybridization complexes with those of a standard, wherein differences between the standard and sample hybridization complexes indicate differential expression of nucleic acids in the sample.
4. The method of claim 3, wherein the polynucleotide molecules hybridize with nucleic acid sequences selected from SEQ ID NOs:1-1558 or fragments thereof.
5. The method of claim 3, wherein the polynucleotide molecules hybridize with nucleic acid sequences selected from gene sequences identified in Table 2 or fragments thereof.
6. A method for the detection of differential expression of polypeptides in a sample, comprising the steps of:
 - a) reacting a combination comprising a plurality of protein binding molecules with polypeptides of the sample, thereby allowing specific binding to occur, wherein the proteins bound by the

protein-binding molecules are differentially expressed in an osteoarthritic subject or in a pre-osteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic;

b) detecting specific binding; and

c) comparing the specific binding in the sample with that of a standard, wherein differences between the standard and sample specific binding indicate differential expression of polypeptides in the sample.

7. The method of claim 3 or 6, further comprising the step of treating the sample with a test compound, wherein comparison to a standard is indicative of whether treatment with the test compound altered the differential expression of nucleic acids or polypeptides in the sample.

8. A composition of matter comprising a collection of two or more probes for detecting expression of genes differentially expressed in osteoarthritic or pre-osteoarthritic subjects compared to subjects that are not osteoarthritic or pre-osteoarthritic, wherein the probes comprise two or more of:

a) nucleic acid molecules that specifically hybridize to two or more of the genes or gene fragments identified in Tables 1 and 2, or fragments thereof; or

b) polypeptide binding agents that specifically bind to polypeptides produced by expression of two or more nucleic acid molecules comprising sequences selected from one or more of genes or gene fragments identified in Tables 1 and 2, or fragments thereof.

9. The composition of claim 8 wherein the genes or gene fragments comprise SEQ ID NOs:1-1558 or fragments thereof.

10. The composition of claim 8 wherein the gene or gene fragments comprise genes or gene fragments identified in Table 2.

11. A device for detecting expression of a plurality of genes differentially expressed in osteoarthritis, comprising a substrate to which is affixed, at known locations, a plurality of probes, wherein the probes comprise:

- a) a plurality of oligonucleotides or polynucleotides, each of which specifically hybridizes to a different sequence selected from any of SEQ ID NOS: 1-1558 or fragments thereof; or
- b) a plurality of polypeptide binding agents, each of which specifically binds to a different polypeptide or fragment thereof produced by expression of a nucleic acid molecule comprising a sequence selected from the genes or gene fragments comprising any of SEQ ID NOS: 1-1558 or fragments thereof.

12. A method for measuring the effect of a test compound on the expression of one or more genes differentially expressed in osteoarthritis, comprising the steps of:

- a) measuring standard expression by measuring transcription or translation products of one or more of the genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof, in a standard sample in the absence of the test compound;
- b) measuring test expression by measuring the transcription or translation products of one or more of the genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof, in a test sample in the presence of the test compound;
- c) comparing the standard expression to the test expression, wherein a change in the test expression compared to the standard expression is indicative of an effect of the test compound on the expression of genes differentially expressed in osteoarthritis compared to a non-osteoarthritic condition.

13. The method of claim 12, wherein said measuring utilizes a composition of matter comprising a plurality of probes, wherein the probes comprise two or more of two or more of the genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof.

14. The method of claim 12, wherein the standard and test samples are obtained from at least one mammalian subject.

15. A method for measuring the effect of a test compound on expression of an OA-associated gene, wherein the gene is selected from the group consisting of the genes identified in Table 6, the method comprising measuring production of transcription or translation products produced by expression of the gene in the presence or absence of the test compound, wherein a change in

the production of transcription or translation products in the presence of the test compound is indicative of an effect of the test compound on expression of the gene.

16. The method of claim 15, wherein the gene expression is measured by providing a DNA construct comprising a reporter gene coding sequence operably linked to transcription regulatory sequences of the OA-associated gene, and measuring formation of a reporter gene product in the presence or absence of the test compound.

17. A method to diagnose or develop a prognosis for a subject who exhibits signs of osteoarthritis, the method comprising:

- a) obtaining a sample from the subject;
- b) measuring in the sample the production of transcription or translation products produced by the expression of one or more OA-associated genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof;
- c) comparing the transcription or translation products of the sample with that of a standard, wherein a difference in the expression of any of the OA-associated genes or gene fragments is indicative of osteoarthritis.

18. A kit for detecting the presence of osteoarthritis or predisposition for osteoarthritis in a subject comprising one or more oligonucleotides of at least about 10 consecutive nucleotides of a sequence selected from sequences hybridizing to two or more genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof, wherein the oligonucleotides specifically bind to nucleic acids differentially expressed in an osteoarthritic subject or in a subject predisposed to osteoarthritis compared to expression in subjects which are not osteoarthritic or predisposed to osteoarthritis.

19. A kit for assaying the expression of genes differentially expressed in osteoarthritis, comprising a container containing a collection of two or more probes, wherein the probes comprise one or more of:

- a) oligonucleotides or polynucleotides that specifically hybridize to two or more genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof; or

b) polypeptide binding agents that specifically bind to polypeptides produced by expression of two or more genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof;

and instructions for performing an assay of gene expression.

20. A method of modulating osteoarthritis-associated gene expression in a cell by administering an effective amount of a compound under appropriate conditions to affect the expression of at least one gene associated with osteoarthritis having a sequence selected from SEQ ID NOS: 1-1588, or fragments thereof.

21. A method of modulating osteoarthritis-associated gene expression in a cell by administering an effective amount of a compound under appropriate conditions to affect the expression of at least one gene associated with osteoarthritis having a gene product identified in Table 6.

23. The method of claim 21 or 22, wherein the compound is a vitamin, mineral, nutraceutical, small molecule pharmaceutical, protein, polypeptide, nucleic acid, fatty acid or polysaccharide.

24. The method of claim 23, wherein the compound is eicosopentaenoic acid, arachidonic acid, glucosamine, chondroitin sulfate, 1 α ,25-dihydroxyvitamin D3, or 24R,25-dihydroxyvitamin D3.

25. A method for identifying compounds that modulate osteoarthritis-associated genes comprising:

a) measuring standard expression by measuring transcription or translation products of one or more of the genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof, in a standard sample in the absence of a test compound;

b) measuring test expression by measuring the transcription or translation products of one or more of the genes or gene fragments comprising any of SEQ ID NOS: 1-1558, or fragments thereof, in a test sample in the presence of the test compound; and

c) comparing the standard expression to the test expression, wherein a change in the test expression compared to the standard expression is indicative of an effect of the test compound on the expression of genes differentially expressed in osteoarthritis compared to a non-osteoarthritic condition.

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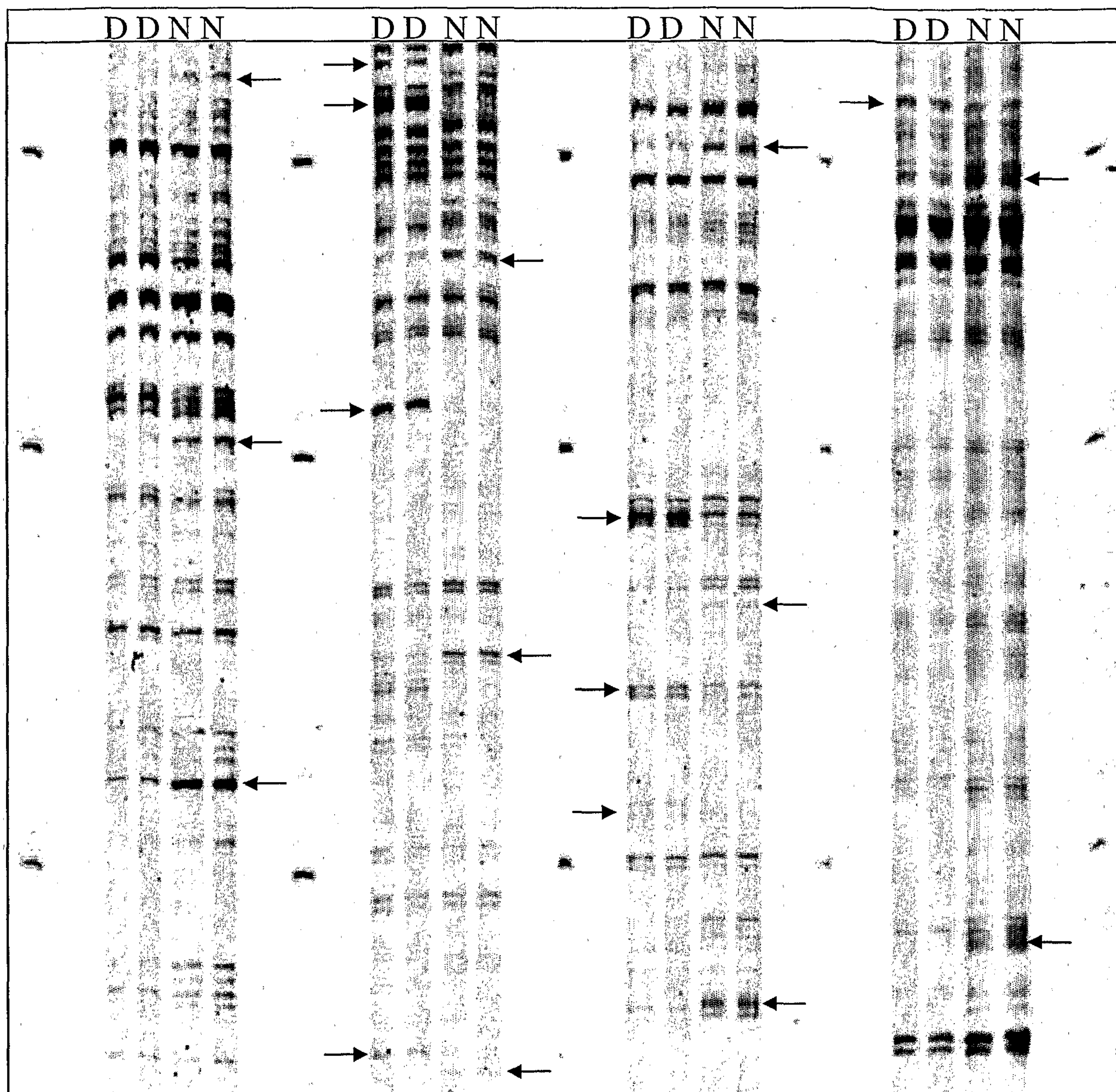


Figure 1a

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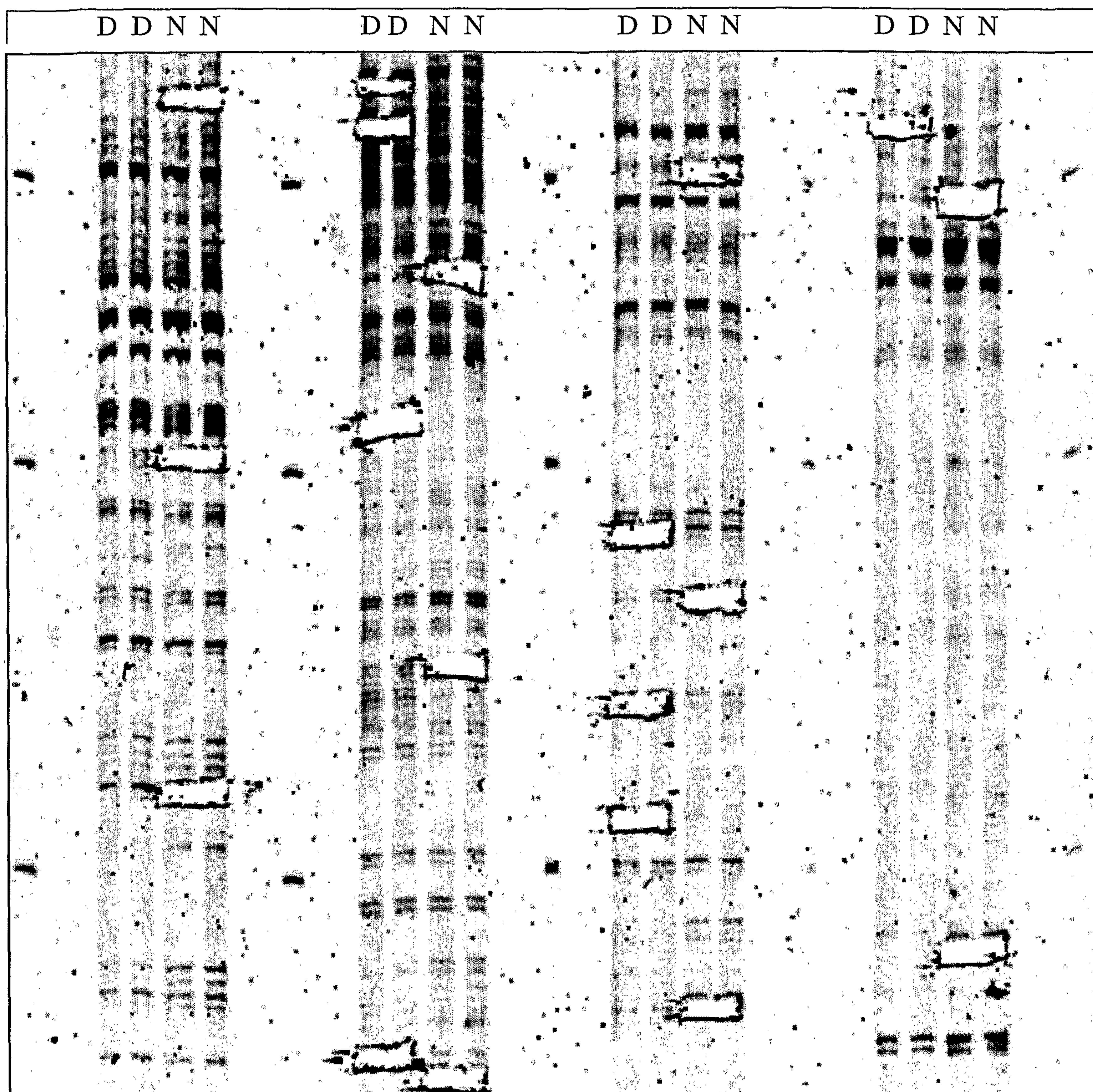


Figure 1b

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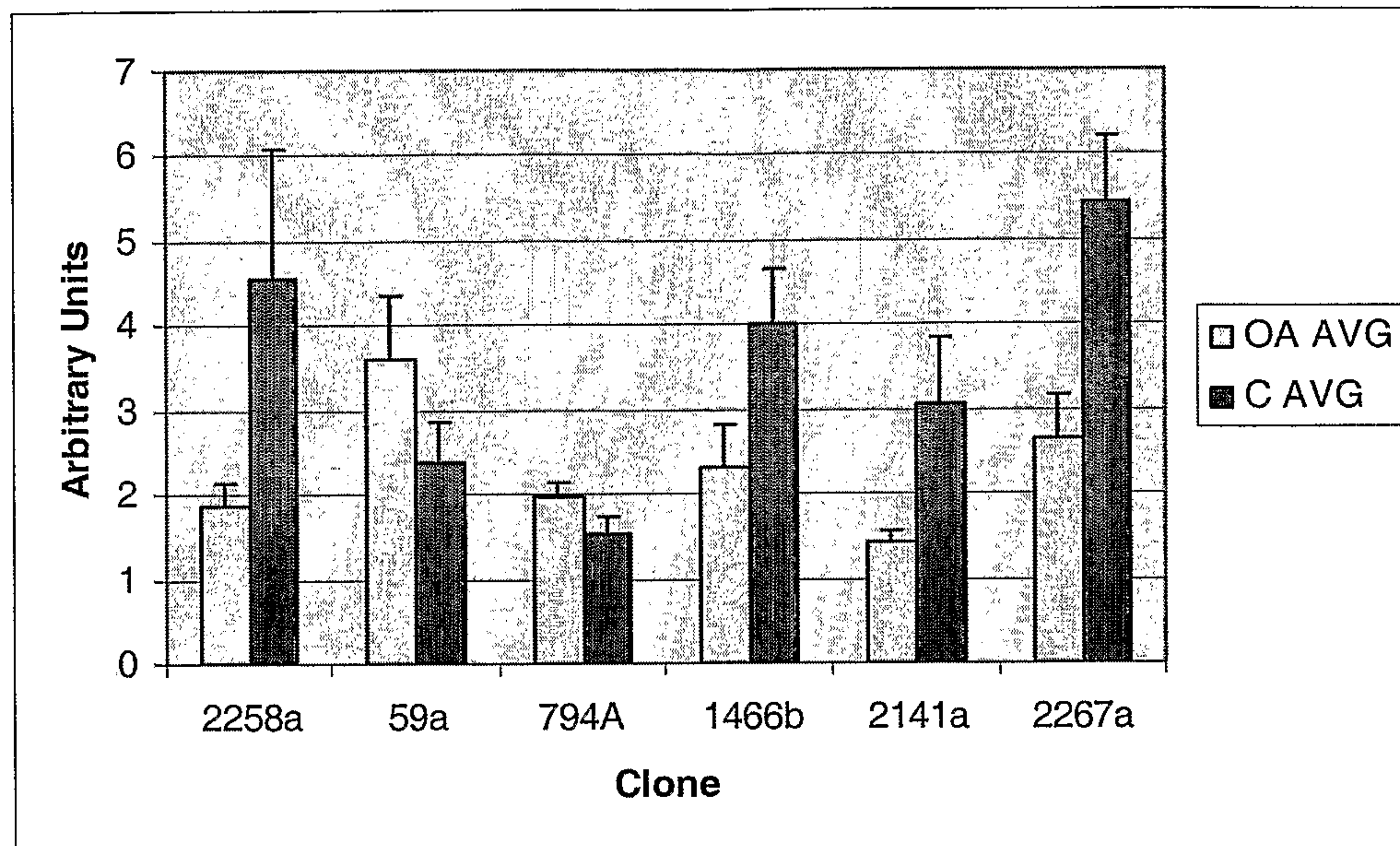


Figure 2a

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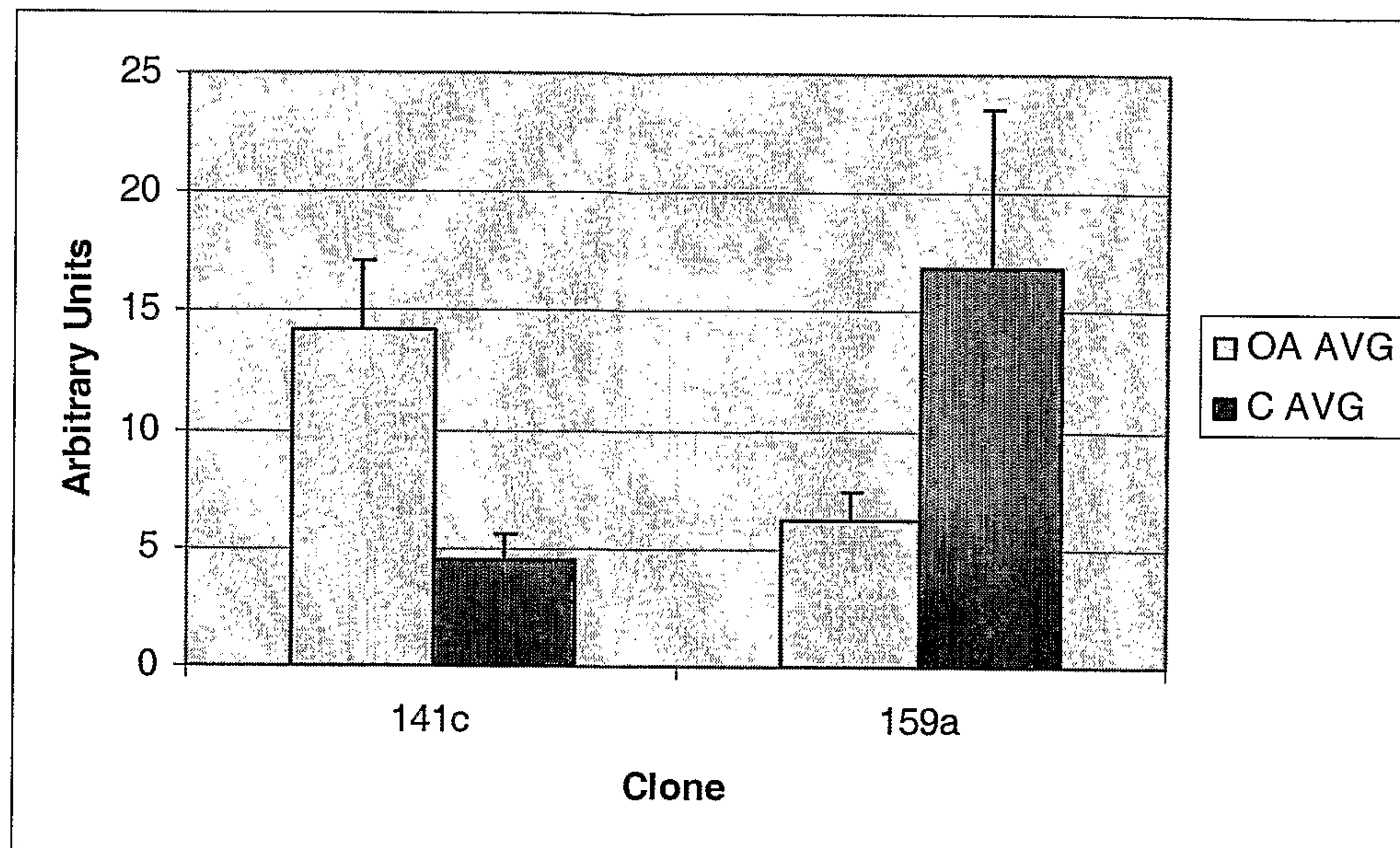


Figure 2b

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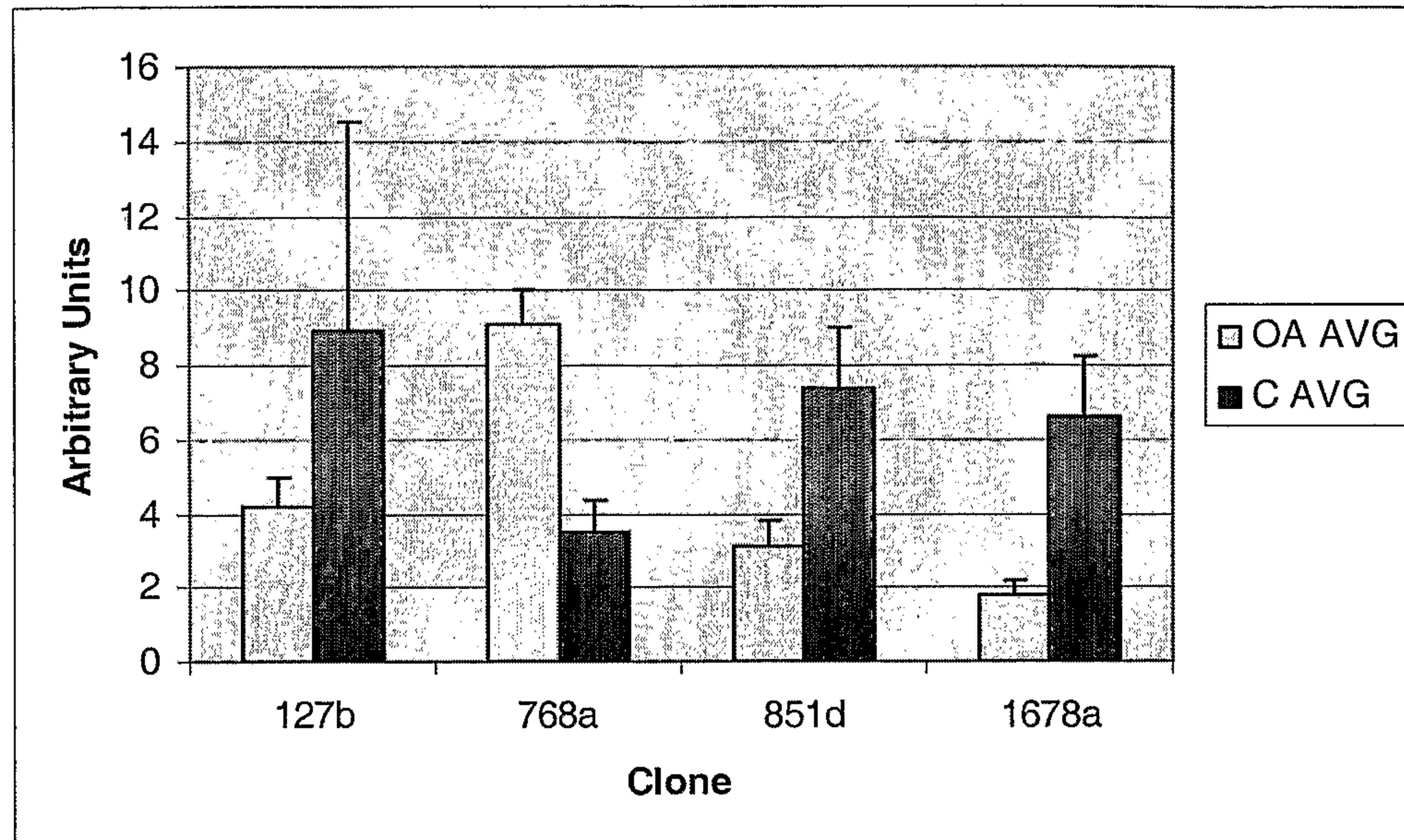


Figure 2c

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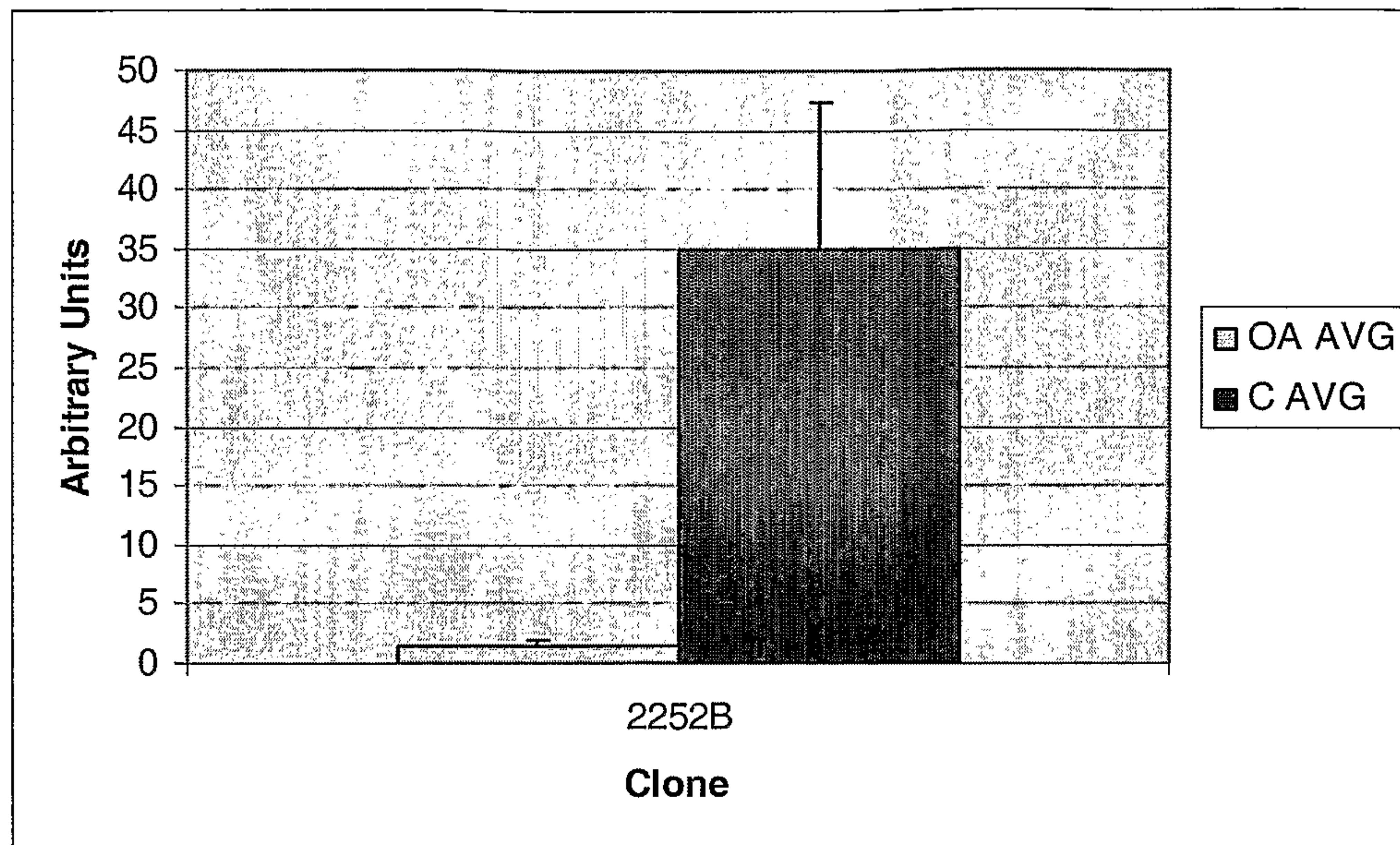


Figure 2d

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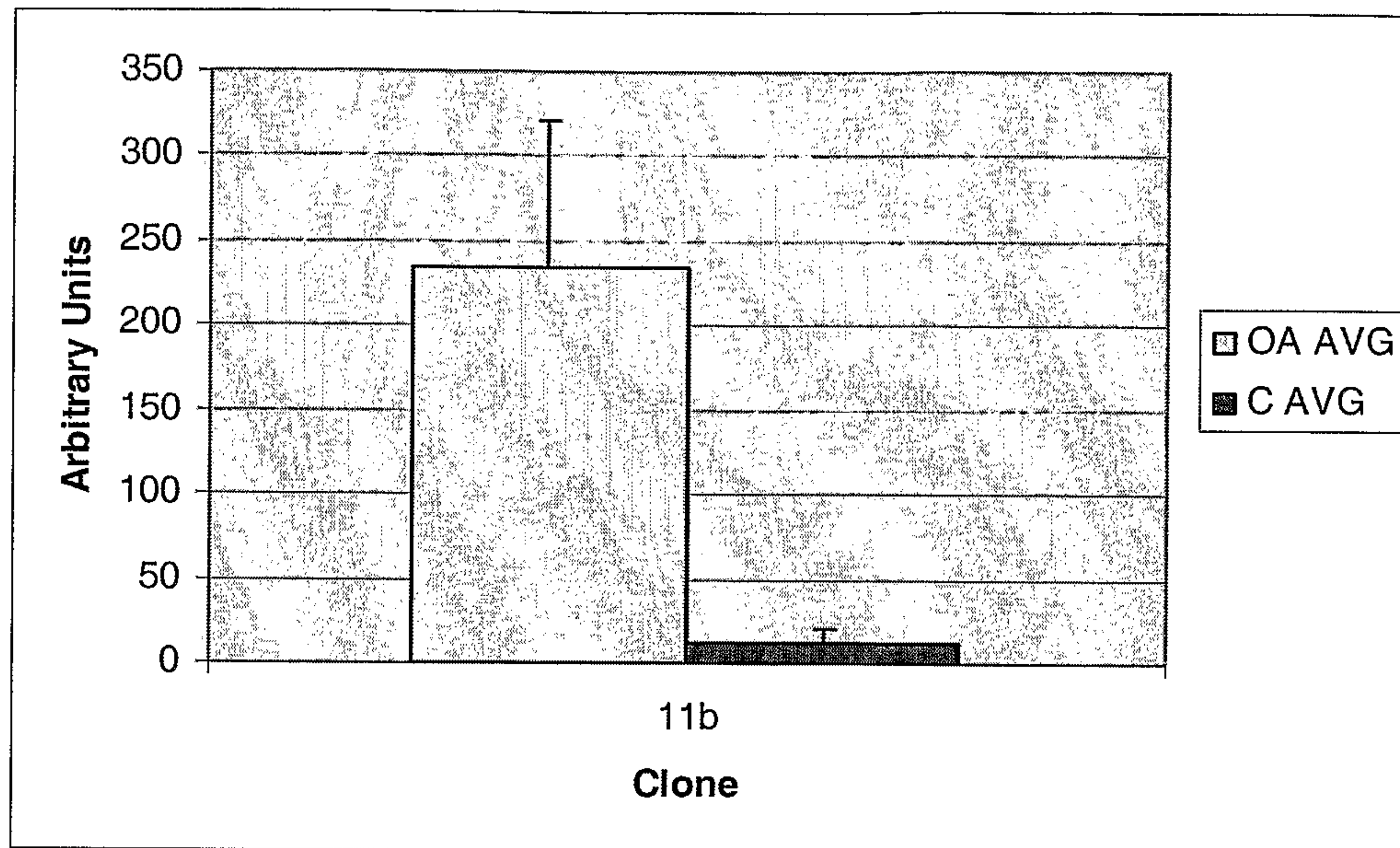


Figure 2e