Table List

Extended Data Table. 1 | Primer sequence used in qRT-PCR

Gene	Forward Primer	Reverse Primer
IL1B	ATGATGGCTTATTACAGTGGCAA	GTCGGAGATTCGTAGCTGGA
SOD2	CCCGACCTGCCCTACGACTAC	AACGCCTCCTGGTACTTCTCCTC
CAT	GCGGTCAAGAACTTCACTGAGGTC	TCACAGATTTGCCTTCTCCCTTGC
ICAM1	GTCACCTATGGCAACGACTCCTTC	AGTGTCTCCTGGCTCTGGTTCC
DLL4	GCCCTTCAATTTCACCTGGC	CAATAACCAGTTCTGACCCACAG
NOTCH2	GATCACCCGAATGGCTATGAAT	GGGGTCACAGTTGTCAATGTT
ADAM17	GTGGATGGTAAAAACGAAAGCG	GGCTAGAACCCTAGAGTCAGG
RBPJ	AACAAATGGAACGCGATGGTT	GGCTGTGCAATAGTTCTTTCCTT
HES5	TCCTGGAGATGGCTGTCAGCTA	CGTGGAGCGTCAGGAACTGCA
ZNF281	TAGTGCAGAACCTGGGTCATC	ACACGGTAGGCATTTCTACTGA
DSP	GCAGGATGTACTATTCTCGGC	CCTGGATGGTGTTCTGGTTCT
CD274	GGACAAGCAGTGACCATCAAG	CCCAGAATTACCAAGTGAGTCCT
VEGFA	AGGGCAGAATCATCACGAAGT	AGGGTCTCGATTGGATGGCA
PDCD1	CCAGGATGGTTCTTAGACTCCC	TTTAGCACGAAGCTCTCCGAT

Extended Data Table. 2 | List of differentially expressed genes by transcriptome sequencing
(|log2(FoldChange)| >= 1 & padj<= 0.05)

Gene_id	High_1	High_2	High_3	Control_1	Control_2	Control_3	Average_high	Average_con	Log$_2$FC	Padj
ENSG00000058085	22285.7	23522.8	22147.8	3031.9	2745.1	2952.5	22652.1	2909.8	3.0	0.00E+00
ENSG00000170498	9505.6	10812.2	9616.4	27.5	16.4	19.6	9978.1	21.2	8.9	0.00E+00
ENSG00000163083	5322.5	5186.6	5510.3	118.2	109.7	85.8	5339.8	104.6	5.7	0.00E+00
ENSG00000162493	7656.8	7575.0	7294.1	29.8	22.1	31.7	7508.6	27.9	8.1	0.00E+00
ENSG00000125872	4248.2	4370.2	4678.1	218.0	229.0	232.1	4432.2	226.4	4.3	0.00E+00
ENSG00000183018	3048.5	3081.2	3175.3	65.4	66.4	56.9	3101.7	62.9	5.6	0.00E+00
ENSG00000135636	3939.0	4116.5	4037.4	70.0	57.7	56.9	4031.0	61.5	6.0	0.00E+00
ENSG00000130508	2746.9	2729.9	2730.8	205.4	229.0	219.1	2735.9	217.8	3.6	0.00E+00
ENSG00000171345	62.2	46.6	50.6	3700.9	3316.6	2905.9	53.2	3307.8	(6.0)	0.00E+00
ENSG00000096696	3786.7	3444.4	3698.5	181.3	207.8	282.5	3643.2	223.9	4.0	6.67E-290
ENSG00000117525	7975.6	7657.4	7132.3	1069.5	1280.6	1188.6	7588.4	1179.6	2.7	3.84E-263
ENSG00000105699	1543.4	1575.3	1542.5	51.6	42.3	53.1	1553.7	49.0	5.0	3.02E-253
ENSG00000218336	214.5	240.7	206.0	2051.8	1935.9	1985.7	220.4	1991.2	(3.2)	1.47E-238
ENSG00000105472	1598.9	1840.9	1909.4	42.5	25.0	32.6	1783.1	33.4	5.8	6.24E-238
ENSG00000074416	6901.3	7177.1	6685.0	1637.6	1684.7	1586.7	6921.1	1636.3	2.1	5.63E-226
ENSG00000167772	161.8	186.5	185.2	2386.9	1893.5	2147.0	177.8	2142.5	(3.6)	1.64E-223
ENSG00000151651	1312.7	1317.2	1380.7	70.0	77.0	62.5	1336.9	69.8	4.3	4.05E-222
ENSG00000235162	8032.1	8033.6	7753.1	2104.6	2117.7	2013.7	7939.6	2078.7	1.9	2.91E-219
ENSG00000115008	1713.8	1631.6	1541.6	165.2	154.9	132.4	1629.0	150.8	3.4	1.10E-210
ENSG00000169439	1598.0	1636.0	1523.5	179.0	157.8	161.3	1585.8	166.0	3.3	6.31E-210
ENSG00000115461	10517.6	10642.0	10031.1	2771.4	2874.0	2645.8	10396.9	2763.7	1.9	4.08E-206
ENSG00000135114	386.8	455.3	411.1	3123.7	2680.6	2810.8	417.8	2871.7	(2.8)	1.42E-203
ENSG00000090339	2083.4	2257.2	2171.4	306.4	255.0	311.4	2170.7	290.9	2.9	3.93E-203
ENSG00000135318	10227.5	9554.6	9939.9	2343.3	2395.8	2640.2	9907.3	2459.8	2.0	1.60E-197
ENSG00000075275	45.0	49.9	46.1	1193.5	1068.0	1232.5	47.0	1164.6	(4.6)	3.07E-195
ENSG00000170909	1217.9	1204.5	1313.9	101.0	89.5	76.4	1245.4	89.0	3.8	1.04E-191
ENSG00000156265	1213.1	1183.9	1107.8	32.1	56.8	51.3	1168.3	46.7	4.6	5.85E-190
ENSG00000134762	2117.9	1891.8	1935.6	281.2	282.9	317.9	1981.8	294.0	2.8	6.67E-183
ENSG00000148677	2878.1	2671.4	2511.2	303.0	317.5	211.6	2686.9	277.4	3.3	5.11E-182
ENSG00000138771	2295.0	2278.9	2376.5	403.9	459.9	444.7	2316.8	436.2	2.4	1.01E-179
ENSG00000125730	1222.7	1398.6	1192.8	112.5	87.6	100.7	1271.3	100.2	3.7	1.06E-176
ENSG00000111057	25415.6	25109.0	25268.1	8939.5	9062.6	9122.3	25264.2	9041.5	1.5	1.41E-175
ENSG00000153292	1386.4	1484.2	1534.4	176.7	193.4	197.6	1468.3	189.3	3.0	6.38E-174
ENSG00000112096	5569.5	6064.7	5267.2	1381.7	1380.7	1303.3	5633.8	1355.2	2.1	1.72E-171
ENSG00000072210	701.8	812.0	770.8	3598.8	3562.9	3275.1	761.5	3478.9	(2.2)	4.19E-165
ENSG00000138166	2799.6	2533.7	2595.2	529.0	560.0	582.7	2642.8	557.2	2.2	6.13E-164
ENSG00000214049	1142.2	1045.1	1106.9	17.2	21.2	19.6	1098.1	19.3	5.8	6.98E-163
ENSG00000050165	23100.5	23519.6	23253.0	7862.0	7006.5	7501.1	23291.0	7456.5	1.6	6.62E-162
ENSG00000155093	870.3	1014.8	1021.1	44.8	40.4	35.4	968.7	40.2	4.6	1.43E-160
ENSG00000178726	995.8	1103.7	1022.0	91.8	91.4	108.1	1040.5	97.1	3.4	1.16E-154
ENSG00000173482	1481.2	1486.4	1484.7	213.4	250.2	254.5	1484.1	239.4	2.6	2.47E-153
ENSG00000189337	1171.0	1185.0	1138.6	158.4	162.6	136.1	1164.8	152.4	2.9	6.47E-149
ENSG00000105339	3492.8	3569.0	3529.6	943.3	1028.6	936.9	3530.5	969.6	1.9	1.97E-148
ENSG00000108846	302.6	302.5	289.2	1566.4	1772.3	1835.6	298.1	1724.8	(2.5)	4.77E-147
ENSG00000182809	438.5	448.8	431.9	2583.2	2107.1	2358.6	439.8	2349.6	(2.4)	7.88E-147
ENSG00000154764	919.2	879.2	990.4	13.8	22.1	21.4	929.6	19.1	5.6	1.07E-144
ENSG00000181019	3245.8	3511.6	3273.8	11551.4	10563.6	10368.7	3343.7	10827.9	(1.7)	4.93E-142
ENSG00000166073	5524.5	5666.9	5426.3	1824.6	1660.7	1735.9	5539.2	1740.4	1.7	2.92E-141
ENSG00000261115	1601.8	1640.3	1650.0	276.6	333.9	279.7	1630.7	296.7	2.5	1.09E-140
ENSG00000214517	6685.9	6468.1	6132.9	2142.5	2046.5	2068.7	6429.0	2085.9	1.6	6.48E-138
ENSG00000171388	899.0	898.8	879.2	96.4	107.8	94.2	892.3	99.4	3.2	3.36E-134
ENSG00000123689	3141.4	3381.5	3183.5	789.5	744.7	619.0	3235.4	717.8	2.2	2.43E-132
ENSG00000134954	8811.5	8722.0	8388.3	2976.8	3146.3	2900.3	8640.6	3007.8	1.5	4.86E-132
ENSG00000128510	749.7	775.2	780.7	2990.6	3340.6	2847.2	768.5	3059.4	(2.0)	2.20E-129
ENSG00000186815	3889.2	4537.2	4463.0	1188.9	1144.0	1183.1	4296.5	1172.0	1.9	6.39E-128
ENSG00000118503	1671.7	1710.8	1692.5	286.9	224.2	319.8	1691.7	276.9	2.6	1.15E-127
ENSG00000139292	883.7	835.9	1041.0	73.4	75.0	91.4	920.2	80.0	3.5	2.23E-127

ENSG00000124107	976.6	910.7	909.0	9.2	12.5	14.0	932.1	11.9	6.3	3.22E-125
ENSG00000182985	2222.3	2255.0	2139.8	608.2	567.7	611.6	2205.7	595.8	1.9	5.79E-123
ENSG00000169174	152.2	157.2	188.9	1238.2	1244.1	1046.9	166.1	1176.4	(2.8)	1.15E-119
ENSG00000066056	839.7	910.7	929.8	128.5	100.1	103.5	893.4	110.7	3.0	2.82E-118
ENSG00000076706	3343.4	3298.0	3245.8	1113.1	1073.8	1040.4	3295.7	1075.8	1.6	3.49E-118
ENSG00000088766	3158.6	3124.5	3110.3	1063.8	1018.0	1025.5	3131.1	1035.8	1.6	1.19E-116
ENSG00000111348	3730.2	4078.6	3725.6	1235.9	1231.6	1268.8	3844.8	1245.4	1.6	3.99E-115
ENSG00000065534	654.9	711.2	691.3	31.0	15.4	13.1	685.8	19.8	5.2	4.80E-115
ENSG00000019582	1285.9	1422.4	1398.8	300.7	285.8	294.6	1369.0	293.7	2.2	1.02E-114
ENSG00000189410	939.3	824.0	933.4	107.9	112.6	77.4	898.9	99.3	3.2	1.76E-114
ENSG00000169429	2911.6	3214.5	2551.8	605.9	552.3	447.5	2892.7	535.2	2.4	1.57E-112
ENSG00000137809	2628.2	3025.9	2815.7	477.4	311.7	491.3	2823.3	426.8	2.7	1.03E-110
ENSG00000149596	1648.7	1740.1	1720.5	446.4	456.1	410.2	1703.1	437.6	2.0	2.37E-110
ENSG00000101210	35.4	32.5	25.3	786.1	590.8	639.5	31.1	672.1	(4.4)	4.48E-110
ENSG00000138675	2431.9	2172.6	2158.8	507.2	599.4	579.9	2254.4	562.2	2.0	8.14E-109
ENSG00000100342	910.5	977.9	899.1	3528.8	2994.3	3428.9	929.2	3317.3	(1.8)	1.79E-108
ENSG00000188064	2012.6	2121.7	2075.6	587.6	570.6	499.7	2070.0	552.6	1.9	3.08E-108
ENSG00000154734	3430.6	3502.9	3404.9	1171.7	1226.8	1116.9	3446.1	1171.8	1.6	7.77E-108
ENSG00000132334	1283.9	1367.1	1321.1	274.3	282.9	317.9	1324.1	291.7	2.2	1.38E-107
ENSG00000105993	6827.6	6936.4	6790.7	2782.8	2719.1	2603.8	6851.6	2701.9	1.3	3.13E-107
ENSG00000163362	1068.5	1178.5	1199.1	238.7	205.9	220.0	1148.7	221.5	2.4	1.35E-106
ENSG00000125968	737.2	801.2	679.5	2964.2	2591.1	3050.4	739.3	2868.6	(2.0)	3.34E-106
ENSG00000164761	586.0	642.9	564.8	43.6	31.8	40.1	597.9	38.5	4.0	1.27E-105
ENSG00000160932	12500.5	12370.2	13187.5	4337.8	3486.9	4030.2	12686.1	3951.6	1.7	4.90E-105
ENSG00000136167	8047.4	7986.9	7785.6	3129.4	2778.7	3017.8	7940.0	2975.3	1.4	1.92E-104
ENSG00000176658	2399.4	2400.3	2472.3	710.3	718.7	795.2	2424.0	741.4	1.7	2.24E-104
ENSG00000205336	587.9	668.9	722.0	2578.6	2352.5	2621.5	659.6	2517.5	(1.9)	4.37E-103
ENSG00000137642	523.7	595.2	628.0	35.6	35.6	34.5	582.3	35.2	4.0	8.83E-103
ENSG00000101938	573.5	570.3	540.4	41.3	33.7	41.0	561.4	38.7	3.9	4.31E-102
ENSG00000091490	1103.9	1043.0	1007.5	223.8	191.5	201.4	1051.5	205.5	2.4	5.29E-102
ENSG00000232810	552.5	573.5	525.0	27.5	35.6	25.2	550.3	29.4	4.2	3.57E-101
ENSG00000122641	1742.6	1589.4	1669.9	446.4	459.9	468.0	1667.3	458.1	1.9	8.98E-101
ENSG00000122862	9407.0	9290.1	9037.2	3992.4	3973.7	3925.8	9244.7	3964.0	1.2	1.10E-100
ENSG00000179776	58.4	44.5	24.4	674.8	713.0	613.4	42.4	667.1	(4.0)	5.26E-100
ENSG00000182240	672.1	710.1	685.9	76.9	80.8	100.7	689.4	86.1	3.0	6.15E-98
ENSG00000136044	2491.3	2607.4	2390.1	825.1	754.3	811.1	2496.3	796.8	1.6	1.61E-97
ENSG00000108691	556.3	732.9	573.8	21.8	15.4	10.3	621.0	15.8	5.3	2.62E-96
ENSG00000182934	7922.0	8062.8	7812.7	3450.7	3236.7	3358.0	7932.5	3348.5	1.2	1.30E-95
ENSG00000101255	3875.8	3964.7	4259.7	1447.1	1276.8	1411.5	4033.4	1378.4	1.5	3.01E-94
ENSG00000008513	2264.4	2327.7	2370.2	750.5	735.1	808.3	2320.8	764.6	1.6	8.41E-94
ENSG00000164283	1195.9	1079.8	1116.9	260.5	258.8	270.4	1130.9	263.2	2.1	9.35E-94
ENSG00000184564	46.0	35.8	45.2	641.5	598.5	949.1	42.3	729.7	(4.1)	2.18E-92
ENSG00000175592	6943.5	6802.0	6592.8	2817.3	2683.5	2517.1	6779.4	2672.6	1.3	5.18E-92
ENSG00000136244	697.0	832.6	600.9	63.1	49.1	73.6	710.2	61.9	3.5	7.70E-92
ENSG00000087245	55.5	40.1	44.3	721.8	510.9	691.7	46.6	641.5	(3.8)	6.00E-91
ENSG00000196139	36.4	34.7	26.2	550.8	455.1	531.4	32.4	512.4	(4.0)	7.87E-91
ENSG00000125538	4151.5	4460.2	3882.0	1412.7	1181.5	1179.3	4164.6	1257.8	1.7	1.26E-90
ENSG00000067141	973.7	984.4	947.9	196.2	209.8	227.5	968.7	211.2	2.2	3.50E-90
ENSG00000108551	1165.2	1337.8	1236.2	205.4	145.3	236.8	1246.4	195.8	2.7	3.50E-90
ENSG00000049759	4272.2	4240.1	4109.7	1618.1	1711.7	1707.0	4207.3	1678.9	1.3	6.13E-90
ENSG00000186642	651.1	647.2	651.5	90.7	87.6	104.4	649.9	94.2	2.8	1.03E-89
ENSG00000147689	34.5	28.2	24.4	573.8	453.2	498.8	29.0	508.6	(4.1)	1.54E-89
ENSG00000175591	680.7	833.7	738.3	119.3	108.7	110.9	750.9	113.0	2.7	4.28E-89
ENSG00000163735	656.8	684.1	600.0	50.5	74.1	84.8	647.0	69.8	3.2	4.75E-89
ENSG00000168209	517.0	542.1	474.4	2764.5	2141.8	2065.9	511.2	2324.1	(2.2)	1.67E-88
ENSG00000076641	545.7	511.7	556.6	45.9	61.6	41.0	538.0	49.5	3.4	9.75E-88
ENSG00000130340	3841.3	4054.7	3819.6	1513.6	1484.6	1582.1	3905.2	1526.8	1.4	1.74E-87
ENSG00000213401	498.8	519.3	476.2	48.2	42.3	35.4	498.1	42.0	3.6	4.48E-87

ENSG00000164649	2669.4	2753.7	2657.6	962.8	964.1	848.4	2693.6	925.1	1.5	4.88E-87
ENSG00000180353	14.4	18.4	11.7	492.3	486.9	448.4	14.8	475.9	(5.0)	4.88E-87
ENSG00000184292	3812.6	4125.2	3960.6	10556.4	10150.8	9318.0	3966.1	10008.4	(1.3)	6.49E-87
ENSG00000151503	6172.7	6025.7	5939.5	2599.2	2617.1	2442.5	6046.0	2553.0	1.2	9.67E-87
ENSG00000110031	1147.0	1243.5	1210.9	328.2	280.0	298.3	1200.5	302.2	2.0	1.13E-86
ENSG00000198624	1316.5	1470.1	1341.9	385.6	373.3	339.3	1376.2	366.1	1.9	5.11E-86
ENSG00000140545	4153.4	4605.5	4461.2	1711.0	1562.6	1687.4	4406.7	1653.7	1.4	8.61E-86
ENSG00000169129	749.7	801.2	815.1	142.3	99.1	136.1	788.6	125.8	2.7	9.77E-86
ENSG00000167601	15476.3	15541.3	15984.2	7464.9	7194.1	6957.5	15667.3	7205.5	1.1	9.34E-85
ENSG00000134602	549.6	521.5	566.6	55.1	60.6	71.8	545.9	62.5	3.1	1.18E-84
ENSG00000196878	13797.9	14052.8	14435.4	6372.4	5775.9	5667.3	14095.4	5938.5	1.2	1.21E-84
ENSG00000132470	284.4	279.7	368.7	1484.9	1745.4	1390.0	310.9	1540.1	(2.3)	1.09E-83
ENSG00000099204	767.9	749.1	672.3	119.3	87.6	122.1	729.8	109.7	2.7	1.59E-83
ENSG00000169242	797.6	970.3	856.6	140.0	99.1	151.0	874.8	130.0	2.8	3.02E-83
ENSG00000164099	923.9	1009.3	1103.3	2905.6	2909.6	2965.6	1012.2	2926.9	(1.5)	1.03E-82
ENSG00000147676	568.7	563.8	538.6	74.6	58.7	77.4	557.0	70.2	3.0	1.95E-82
ENSG00000089060	1988.6	2162.9	2167.8	737.9	714.9	730.9	2106.4	727.9	1.5	4.45E-82
ENSG00000117152	239.4	238.5	253.0	1012.2	938.1	1019.0	243.6	989.7	(2.0)	8.88E-82
ENSG00000115339	1126.0	975.7	1008.4	254.8	204.0	214.4	1036.7	224.4	2.2	9.03E-82
ENSG00000168077	1134.6	1177.4	1198.2	3044.5	2898.0	3003.8	1170.1	2982.1	(1.3)	1.19E-81
ENSG00000196352	5548.4	5540.0	5196.7	2187.3	2040.7	2291.5	5428.4	2173.2	1.3	5.34E-81
ENSG00000010278	4652.3	4937.2	4561.5	1769.5	1691.5	1450.6	4717.0	1637.2	1.5	1.62E-80
ENSG00000147394	3737.9	3827.1	3610.0	1535.4	1531.8	1585.8	3725.0	1551.0	1.3	3.50E-79
ENSG00000011028	2674.2	2977.1	2748.8	8145.4	6911.2	7406.9	2800.0	7487.8	(1.4)	1.19E-78
ENSG00000013619	745.9	778.4	821.4	141.2	154.9	174.3	781.9	156.8	2.3	4.22E-78
ENSG00000185442	9.6	11.9	13.6	465.9	401.2	456.8	11.7	441.3	(5.2)	5.08E-78
ENSG00000149428	10600.9	11044.3	10679.0	5049.3	4522.2	4688.4	10774.7	4753.3	1.2	7.44E-78
ENSG00000071242	819.6	879.2	827.7	198.5	156.8	144.5	842.2	166.6	2.3	1.83E-77
ENSG00000134202	18.2	17.3	21.7	472.8	389.7	388.8	19.1	417.1	(4.4)	2.60E-77
ENSG00000169299	2038.4	1947.1	1868.7	671.3	675.4	709.5	1951.4	685.4	1.5	6.17E-77
ENSG00000163739	3035.1	3502.9	2945.8	949.0	940.0	738.4	3161.3	875.8	1.9	6.80E-77
ENSG00000130726	12897.9	13491.2	13605.9	6496.4	6251.2	6411.2	13331.6	6386.3	1.1	8.73E-77
ENSG00000099860	1588.4	1722.7	1561.5	483.1	436.8	359.9	1624.2	426.6	1.9	1.08E-76
ENSG00000042062	1140.3	1159.0	1233.4	216.9	292.5	193.0	1177.6	234.1	2.3	1.11E-76
ENSG00000196405	25.9	26.0	28.9	416.6	375.2	408.3	26.9	400.0	(3.9)	3.63E-76
ENSG00000179046	654.9	642.9	632.5	89.5	99.1	125.9	643.4	104.8	2.6	5.88E-76
ENSG00000095752	969.9	1005.0	895.5	221.5	164.5	143.6	956.8	176.5	2.4	8.79E-76
ENSG00000176014	18454.0	19090.8	19108.0	8708.9	7446.2	7669.8	18884.3	7941.6	1.3	1.04E-74
ENSG00000197381	2493.2	2449.1	2472.3	935.3	1013.2	928.5	2471.5	959.0	1.4	1.52E-74
ENSG00000132182	7.7	3.3	9.9	490.0	506.1	510.9	7.0	502.3	(6.1)	7.52E-74
ENSG00000197971	2625.3	2765.7	2690.1	983.5	1020.9	850.2	2693.7	951.5	1.5	1.07E-73
ENSG00000159840	6682.1	6723.9	6703.1	2945.8	2745.1	3104.5	6703.0	2931.8	1.2	2.07E-73
ENSG00000185483	849.3	826.1	894.6	160.7	161.6	212.6	856.7	178.3	2.3	3.42E-73
ENSG00000161681	703.7	807.7	849.4	145.7	171.3	157.6	786.9	158.2	2.3	4.71E-73
ENSG00000196562	2440.6	2600.9	2532.9	789.5	605.2	811.1	2524.8	735.3	1.8	7.46E-73
ENSG00000135821	4073.0	4101.3	4114.2	1810.9	1836.8	1680.9	4096.2	1776.2	1.2	4.70E-72
ENSG00000112297	921.1	950.8	985.0	223.8	270.4	236.8	952.3	243.6	2.0	1.16E-71
ENSG00000128917	400.2	391.4	420.2	9.2	13.5	9.3	403.9	10.7	5.2	3.77E-71
ENSG00000170525	693.2	665.7	640.7	2230.9	1922.4	1898.1	666.5	2017.1	(1.6)	9.08E-71
ENSG00000184588	493.1	467.3	487.1	72.3	67.4	69.9	482.5	69.9	2.8	9.73E-71
ENSG00000173848	821.5	828.3	777.1	2508.6	2113.9	2444.4	809.0	2355.6	(1.5)	1.40E-70
ENSG00000123908	5909.4	5476.1	5963.0	2381.2	2623.8	2434.2	5782.8	2479.7	1.2	1.79E-70
ENSG00000184602	253.7	254.8	238.6	975.4	907.3	885.7	249.0	922.8	(1.9)	1.21E-69
ENSG00000178038	589.8	581.1	614.5	90.7	122.2	97.9	595.1	103.6	2.5	1.56E-69
ENSG00000186480	7863.6	8295.9	8029.6	3562.0	3864.0	3439.1	8063.0	3621.7	1.2	8.62E-69
ENSG00000133321	101.5	116.0	91.3	638.0	537.8	633.9	102.9	603.3	(2.6)	1.48E-68
ENSG00000096433	7419.3	7401.5	7932.0	3485.2	3541.7	3662.9	7584.3	3563.3	1.1	2.03E-68
ENSG00000138356	563.9	558.3	597.3	115.9	90.4	80.2	573.2	95.5	2.6	7.05E-68

ENSG00000088836	2539.2	2847.0	3016.3	897.4	1047.8	959.3	2800.8	968.2	1.5	9.60E-68
ENSG00000125798	658.7	623.4	641.6	149.2	123.2	126.8	641.2	133.0	2.3	1.23E-67
ENSG00000104341	6907.1	7108.8	6995.0	3493.2	3290.6	3424.2	7003.6	3402.7	1.0	5.36E-67
ENSG00000185507	2765.1	2832.9	2798.5	1120.0	914.1	1069.3	2798.8	1034.5	1.4	9.48E-67
ENSG00000184254	1354.8	1547.1	1494.6	4095.7	4208.5	3565.0	1465.5	3956.4	(1.4)	1.22E-66
ENSG00000163661	3432.5	3476.9	3561.2	1332.3	1267.2	1028.3	3490.2	1209.3	1.5	2.68E-66
ENSG00000087253	36.4	36.9	38.0	379.8	348.3	404.6	37.1	377.6	(3.3)	8.65E-66
ENSG00000126016	877.0	822.9	905.4	158.4	229.0	193.9	868.4	193.8	2.2	1.71E-65
ENSG00000076067	4353.5	4479.7	4223.5	1939.4	1988.8	2062.2	4352.3	1996.8	1.1	3.20E-65
ENSG00000106976	245.1	211.4	275.6	898.5	953.5	974.2	244.0	942.1	(1.9)	5.57E-65
ENSG00000144583	1375.9	1342.2	1344.6	462.5	475.3	399.9	1354.2	445.9	1.6	1.40E-64
ENSG00000168497	513.2	421.7	469.0	72.3	66.4	64.3	468.0	67.7	2.8	4.37E-64
ENSG00000186174	6920.5	7310.4	7325.7	3573.5	3494.6	3570.6	7185.5	3546.2	1.0	8.55E-64
ENSG00000113140	4661.8	5027.2	4830.8	13345.0	10824.3	13401.4	4839.9	12523.6	(1.4)	2.20E-63
ENSG00000060656	1128.8	1160.0	1266.9	385.6	300.2	312.3	1185.3	332.7	1.8	2.87E-63
ENSG00000134013	4655.1	4906.9	4731.4	11181.9	9698.6	10480.6	4764.5	10453.7	(1.1)	9.41E-63
ENSG00000028277	440.4	470.5	447.3	73.4	76.0	66.2	452.7	71.9	2.7	1.16E-62
ENSG00000165323	495.0	351.3	440.1	21.8	38.5	43.8	428.8	34.7	3.6	1.95E-62
ENSG00000179833	2538.2	2404.6	2436.2	960.5	1078.6	998.5	2459.7	1012.5	1.3	5.19E-62
ENSG00000107485	341.8	311.2	298.2	1095.9	982.4	1052.5	317.1	1043.6	(1.7)	8.96E-62
ENSG00000108854	4473.2	4009.2	4225.3	1909.5	1929.1	1924.2	4235.9	1921.0	1.1	9.21E-62
ENSG00000111331	11863.8	11722.9	11706.5	5024.0	4225.8	5270.1	11764.4	4840.0	1.3	4.58E-61
ENSG00000113070	811.0	872.7	712.1	177.9	199.2	202.3	798.6	193.1	2.0	4.85E-61
ENSG00000163814	13349.8	13748.1	13181.2	6253.1	5889.4	6784.1	13426.4	6308.9	1.1	5.75E-61
ENSG00000153208	590.7	594.1	625.3	126.2	128.9	147.3	603.4	134.2	2.2	7.71E-61
ENSG00000171316	654.9	556.2	652.4	115.9	138.6	131.5	621.2	128.6	2.3	7.72E-61
ENSG00000134247	2360.1	2391.6	2400.0	1073.0	1016.0	1042.3	2383.9	1043.8	1.2	9.14E-61
ENSG00000172375	971.8	892.3	848.5	270.8	230.9	255.4	904.2	252.4	1.8	2.35E-60
ENSG00000188486	3015.0	3127.8	3010.9	1371.3	1249.8	1158.8	3051.2	1260.0	1.3	2.42E-60
ENSG00000136542	217.3	227.7	240.4	775.8	811.1	820.4	228.5	802.4	(1.8)	3.45E-60
ENSG00000104419	3618.2	3884.5	3766.3	1596.3	1292.2	1519.6	3756.3	1469.3	1.4	4.55E-60
ENSG00000182621	115.9	108.4	126.5	554.3	535.0	565.0	116.9	551.4	(2.2)	4.68E-60
ENSG00000124191	356.2	435.8	381.3	1242.8	1158.4	1265.1	391.1	1222.1	(1.6)	8.96E-60
ENSG00000260401	414.6	436.9	462.7	74.6	73.1	61.5	438.0	69.7	2.7	2.71E-59
ENSG00000142871	25922.1	25326.9	23403.0	12295.0	12759.2	11815.6	24884.0	12289.9	1.0	4.57E-59
ENSG00000114850	7467.2	7142.4	6620.0	3355.5	3292.5	3070.9	7076.5	3239.6	1.1	4.60E-59
ENSG00000118523	26626.8	26491.3	24192.7	10069.9	9632.2	11924.7	25770.3	10542.3	1.3	6.48E-59
ENSG00000205795	1326.1	1586.1	1515.4	526.7	471.5	469.9	1475.9	489.4	1.6	9.65E-59
ENSG00000169499	438.5	462.9	419.3	1239.4	1231.6	1199.8	440.2	1223.6	(1.5)	2.36E-58
ENSG00000149557	1567.4	1621.9	1586.8	648.4	549.4	555.6	1592.0	584.5	1.4	2.75E-58
ENSG00000141458	4165.9	4178.3	4187.4	1907.3	2003.2	2083.6	4177.2	1998.0	1.1	3.22E-58
ENSG00000080031	309.3	319.8	324.4	25.2	26.9	31.7	317.8	28.0	3.5	3.74E-58
ENSG00000161249	345.6	331.8	288.3	20.7	28.9	25.2	321.9	24.9	3.7	5.09E-58
ENSG00000137801	8582.6	8938.8	8587.0	23673.1	20311.3	28017.5	8702.9	24000.6	(1.5)	5.42E-58
ENSG00000085063	10047.5	10747.2	9814.3	5125.0	4639.6	4961.5	10203.0	4908.7	1.1	7.61E-58
ENSG00000120451	4419.6	4561.0	4494.6	2248.1	2169.7	2266.4	4491.8	2228.0	1.0	1.50E-57
ENSG00000011422	2345.8	2356.9	2195.8	938.7	792.8	939.7	2299.5	890.4	1.4	3.21E-57
ENSG00000138772	2772.8	2525.0	2642.2	1177.4	1185.4	1123.4	2646.7	1162.1	1.2	3.48E-57
ENSG00000162494	4525.9	4546.9	4634.7	1.1	1.0	1.9	4569.2	1.3	11.7	4.52E-57
ENSG00000124839	340.9	358.9	325.3	37.9	43.3	35.4	341.7	38.9	3.1	7.01E-57
ENSG00000099284	24.9	29.3	28.0	337.4	308.9	287.1	27.4	311.1	(3.5)	1.17E-56
ENSG00000276231	286.3	287.3	315.4	10.3	14.4	10.3	296.3	11.7	4.7	1.73E-56
ENSG00000197457	1156.6	1277.1	1208.1	3399.1	2988.5	2824.8	1214.0	3070.8	(1.3)	2.43E-56
ENSG00000183287	870.3	861.9	866.6	267.4	275.2	224.7	866.3	255.7	1.8	2.44E-56
ENSG00000170421	33722.5	36441.6	34542.9	17716.1	15601.5	14933.1	34902.3	16083.6	1.1	1.41E-55
ENSG00000197329	1110.6	1039.7	1063.6	375.3	385.8	345.9	1071.3	369.0	1.5	1.87E-55
ENSG00000077150	2623.4	2973.8	2887.1	1247.4	1068.0	1101.0	2828.1	1138.8	1.3	3.12E-55
ENSG00000125148	40328.0	45268.8	40021.5	21095.7	19297.1	18851.5	41872.8	19748.1	1.1	4.05E-55

ENSG00000140105	1223.6	1379.0	1215.4	2938.9	2817.2	2932.9	1272.7	2896.3	(1.2)	5.92E-55
ENSG00000166578	336.1	415.2	351.5	47.1	44.3	26.1	367.6	39.1	3.2	1.33E-54
ENSG00000115380	7918.1	7817.8	8036.8	15741.1	15110.8	17378.5	7924.3	16076.8	(1.0)	3.92E-54
ENSG00000115415	6322.1	6101.6	5991.9	2763.3	2475.6	2984.2	6138.5	2741.1	1.2	7.36E-54
ENSG00000104884	2567.9	2617.1	2690.1	1215.3	1056.5	1019.9	2625.0	1097.2	1.3	9.73E-54
ENSG00000023445	730.5	560.5	709.3	141.2	156.8	150.1	666.8	149.4	2.2	1.04E-53
ENSG00000176170	2472.1	2816.6	2696.4	1059.2	818.8	1005.9	2661.7	961.3	1.5	2.28E-53
ENSG00000163545	552.5	653.7	585.5	154.9	130.9	123.1	597.2	136.3	2.1	2.32E-53
ENSG00000187498	3341.5	3768.5	3431.1	9002.6	7393.3	8605.8	3513.7	8333.9	(1.2)	2.38E-53
ENSG00000138623	1871.8	2025.2	1949.1	856.1	811.1	860.5	1948.7	842.6	1.2	1.14E-52
ENSG00000187134	26.8	39.0	65.1	1857.9	1575.1	1580.2	43.6	1671.1	(5.3)	1.32E-52
ENSG00000013016	1713.8	2117.3	2015.1	712.6	632.1	730.9	1948.8	691.9	1.5	1.52E-52
ENSG00000187957	41.2	31.4	32.5	313.3	292.5	368.2	35.0	324.7	(3.2)	2.04E-52
ENSG00000104856	808.1	851.1	858.4	284.6	250.2	227.5	839.2	254.1	1.7	2.65E-52
ENSG00000163975	951.7	1027.8	1005.7	2898.7	2432.3	2366.1	995.1	2565.7	(1.4)	4.04E-52
ENSG00000133401	1246.6	1086.3	1298.5	377.5	400.3	435.4	1210.5	404.4	1.6	5.09E-52
ENSG00000123384	1685.1	2020.9	2010.6	4397.5	4359.6	4818.9	1905.5	4525.3	(1.2)	6.78E-52
ENSG00000187244	1841.2	1759.6	1924.7	794.1	804.4	790.6	1841.8	796.3	1.2	9.52E-52
ENSG00000198053	4660.9	4846.2	4772.0	2326.1	2083.1	2382.9	4759.7	2264.0	1.1	1.02E-51
ENSG00000119326	3637.4	3448.7	3726.5	1730.5	1775.2	1791.8	3604.2	1765.8	1.0	1.06E-51
ENSG00000087074	1288.7	1426.7	1369.0	542.8	534.0	488.5	1361.5	521.8	1.4	1.71E-51
ENSG00000213654	316.0	319.8	321.7	41.3	28.9	14.9	319.2	28.4	3.5	2.07E-51
ENSG00000124920	674.0	732.9	692.2	189.3	193.4	219.1	699.7	200.6	1.8	3.34E-51
ENSG00000163629	361.9	342.6	391.3	1056.9	1110.3	1329.4	365.3	1165.6	(1.7)	4.71E-51
ENSG00000008394	610.9	572.4	586.5	1388.6	1437.5	1444.1	589.9	1423.4	(1.3)	1.47E-50
ENSG00000100906	2559.3	2861.1	2669.3	1213.0	981.4	1017.1	2696.6	1070.5	1.3	2.31E-50
ENSG00000174080	23.9	19.5	17.2	301.8	236.7	276.9	20.2	271.8	(3.7)	4.82E-50
ENSG00000198727	22862.1	22230.5	21173.7	43955.1	46229.0	53673.6	22088.8	47952.6	(1.1)	6.10E-50
ENSG00000137968	47.9	35.8	44.3	286.9	382.9	364.5	42.6	344.8	(3.0)	7.84E-50
ENSG00000077942	1776.1	1953.6	1866.0	4316.0	3751.5	4123.4	1865.2	4063.6	(1.1)	8.73E-50
ENSG00000133612	2273.0	2329.8	2515.7	1071.8	1060.3	1104.7	2372.8	1079.0	1.1	9.28E-50
ENSG00000108602	38.3	62.9	47.9	1248.5	1435.5	862.4	49.7	1182.1	(4.6)	1.45E-49
ENSG00000063601	2774.7	2623.6	2646.7	1318.6	1296.0	1245.5	2681.7	1286.7	1.1	1.80E-49
ENSG00000121895	705.6	581.1	705.7	140.0	184.7	138.9	664.2	154.5	2.1	2.31E-49
ENSG00000099250	2104.5	2050.1	2221.1	4217.3	4245.1	4628.7	2125.2	4363.7	(1.0)	3.46E-49
ENSG00000265190	637.7	719.9	701.2	1755.8	1824.3	1584.9	686.3	1721.6	(1.3)	4.19E-49
ENSG00000145990	542.9	556.2	528.6	123.9	150.1	138.9	542.6	137.6	2.0	7.51E-49
ENSG00000139318	2431.0	2530.4	2312.4	1129.2	1065.1	1152.3	2424.6	1115.5	1.1	1.51E-48
ENSG00000160957	2049.9	2185.7	2218.4	985.8	1013.2	960.2	2151.3	986.4	1.1	1.75E-48
ENSG00000112559	248.0	267.8	258.4	21.8	5.8	14.0	258.1	13.9	4.3	5.01E-48
ENSG00000145284	183.8	177.8	191.6	630.0	602.3	651.7	184.4	628.0	(1.8)	5.32E-48
ENSG00000062282	418.4	471.6	409.3	101.0	84.7	79.2	433.1	88.3	2.3	2.84E-47
ENSG00000155760	598.4	681.9	677.7	1686.9	1503.9	1665.0	652.7	1618.6	(1.3)	3.17E-47
ENSG00000157570	248.0	271.0	289.2	10.3	4.8	5.6	269.4	6.9	5.3	5.14E-47
ENSG00000128805	614.7	622.3	608.1	195.1	151.1	146.4	615.0	164.2	1.9	5.45E-47
ENSG00000169252	857.9	818.5	827.7	303.0	297.3	274.1	834.7	291.5	1.5	1.01E-46
ENSG00000167642	3766.6	4285.7	4094.3	1869.4	1477.9	1473.9	4048.9	1607.1	1.3	1.03E-46
ENSG00000088387	5403.9	4955.7	5628.7	2269.9	2545.9	2621.5	5329.4	2479.1	1.1	1.08E-46
ENSG00000177283	328.4	407.6	387.7	1591.7	1173.8	1182.1	374.6	1315.9	(1.8)	1.38E-46
ENSG00000114019	4506.7	4606.6	4645.5	2302.0	2382.3	2061.3	4586.3	2248.5	1.0	1.57E-46
ENSG00000147454	851.2	858.6	831.3	1763.8	1916.6	1939.1	847.1	1873.2	(1.1)	2.76E-46
ENSG00000148154	2423.3	2371.0	2282.6	1124.6	1146.9	1164.4	2359.0	1145.3	1.0	3.00E-46
ENSG00000165072	2938.4	2997.7	2794.9	1410.4	1485.6	1432.0	2910.3	1442.6	1.0	3.02E-46
ENSG00000178104	2526.7	2416.6	2584.4	1140.7	1235.4	1224.1	2509.2	1200.1	1.1	3.11E-46
ENSG00000128422	505.5	528.0	421.1	2061.0	1368.2	1983.9	484.9	1804.4	(1.9)	5.18E-46
ENSG00000170873	1318.4	1238.1	1288.6	530.2	445.5	520.2	1281.7	498.6	1.4	6.00E-46
ENSG00000181649	2794.8	2625.8	2825.6	1222.2	908.3	1088.0	2748.8	1072.8	1.4	9.24E-46
ENSG00000189068	261.4	272.1	215.1	23.0	16.4	14.9	249.5	18.1	3.8	1.26E-45

ENSG00000204381	944.0	882.5	881.9	323.6	335.8	337.5	902.8	332.3	1.4	1.39E-45
ENSG00000059378	2185.9	2222.5	2136.2	1044.3	889.0	1001.3	2181.5	978.2	1.2	1.82E-45
ENSG00000152377	1867.0	1830.0	1864.2	5228.3	4388.4	6601.4	1853.8	5406.0	(1.5)	1.93E-45
ENSG00000128284	329.4	415.2	400.3	1182.0	1069.9	1049.7	381.6	1100.6	(1.5)	2.71E-45
ENSG00000111907	401.2	431.5	400.3	95.2	91.4	76.4	411.0	87.7	2.2	2.73E-45
ENSG00000110848	260.4	237.4	270.2	32.1	19.2	19.6	256.0	23.7	3.5	4.17E-45
ENSG00000143162	1318.4	1289.1	1233.4	562.3	511.9	495.0	1280.3	523.1	1.3	4.85E-45
ENSG00000109220	712.3	717.7	772.6	229.5	228.0	259.2	734.2	238.9	1.6	6.16E-45
ENSG00000104522	1935.0	2001.3	2002.4	964.0	830.3	884.7	1979.6	893.0	1.2	8.61E-45
ENSG00000079308	402.1	422.8	426.5	73.4	95.3	97.9	417.2	88.9	2.2	1.01E-44
ENSG00000116852	349.5	336.1	349.7	59.7	67.4	66.2	345.1	64.4	2.4	1.12E-44
ENSG00000179542	0.0	3.3	8.1	288.0	313.7	366.4	3.8	322.7	(6.4)	4.85E-44
ENSG00000074410	70.9	104.1	121.1	554.3	445.5	557.5	98.7	519.1	(2.4)	5.42E-44
ENSG00000214022	2351.5	2698.5	2634.1	1229.0	1075.7	1101.9	2561.3	1135.6	1.2	5.75E-44
ENSG00000001617	3862.4	4163.1	4369.0	2141.4	1960.9	2021.2	4131.5	2041.1	1.0	6.80E-44
ENSG00000185567	2109.3	2487.0	2663.9	6002.9	6922.8	5455.6	2420.1	6127.1	(1.3)	8.47E-44
ENSG00000213853	156.1	190.8	164.5	586.4	578.3	578.9	170.4	581.2	(1.8)	9.22E-44
ENSG00000182272	163.7	182.1	169.9	565.7	575.4	565.9	171.9	569.0	(1.7)	1.80E-43
ENSG00000116604	1892.9	2031.7	1866.0	905.4	860.2	926.7	1930.2	897.4	1.1	3.48E-43
ENSG00000174306	2860.9	2845.9	3027.1	1363.3	1517.3	1438.5	2911.3	1439.7	1.0	3.68E-43
ENSG00000133805	745.9	788.2	775.3	274.3	248.2	283.4	769.8	268.6	1.5	4.82E-43
ENSG00000164442	2975.8	3031.3	2986.5	1510.2	1354.7	1549.4	2997.8	1471.5	1.0	4.99E-43
ENSG00000184584	2034.6	2161.8	2217.5	1059.2	1018.0	985.4	2138.0	1020.9	1.1	6.94E-43
ENSG00000134668	136.9	99.7	136.4	471.6	554.2	625.6	124.4	550.5	(2.1)	1.05E-42
ENSG00000235109	54.6	73.7	50.6	321.3	334.8	358.9	59.6	338.4	(2.5)	1.17E-42
ENSG00000128965	349.5	351.3	368.7	66.6	66.4	81.1	356.5	71.4	2.3	1.80E-42
ENSG00000137440	1044.6	1087.4	1058.1	305.3	394.5	254.5	1063.4	318.1	1.7	2.29E-42
ENSG00000180573	61.3	46.6	63.3	373.0	292.5	391.6	57.0	352.3	(2.6)	2.99E-42
ENSG00000169851	2081.5	2001.3	2143.4	967.4	945.8	1044.1	2075.4	985.8	1.1	3.25E-42
ENSG00000121691	1158.5	1232.7	1189.2	2613.0	2318.8	2501.3	1193.5	2477.7	(1.1)	3.25E-42
ENSG00000071051	1196.8	1237.0	1230.7	476.2	409.9	523.9	1221.5	470.0	1.4	5.99E-42
ENSG00000198930	291.1	357.8	240.4	41.3	18.3	17.7	296.4	25.8	3.6	1.37E-41
ENSG00000188641	539.0	573.5	547.6	1247.4	1277.8	1238.1	553.4	1254.4	(1.2)	1.48E-41
ENSG00000033100	2790.0	3109.3	2963.0	1510.2	1313.4	1411.5	2954.1	1411.7	1.1	1.67E-41
ENSG00000180263	844.5	648.3	855.7	215.7	244.4	229.3	782.8	229.8	1.8	2.28E-41
ENSG00000177675	393.5	367.5	403.9	93.0	69.3	89.5	388.3	83.9	2.2	2.31E-41
ENSG00000174938	387.8	458.6	464.5	1187.7	1061.3	1151.4	436.9	1133.4	(1.4)	4.33E-41
ENSG00000128335	566.8	612.5	594.6	1540.0	1296.0	1579.3	591.3	1471.8	(1.3)	4.89E-41
ENSG00000069424	2214.6	2272.4	2423.5	1082.2	1036.2	866.1	2303.5	994.8	1.2	9.41E-41
ENSG00000134955	1596.1	1720.5	1746.7	818.2	742.8	730.0	1687.8	763.7	1.1	9.66E-41
ENSG00000092068	219.3	268.9	234.9	20.7	30.8	24.2	241.0	25.2	3.2	1.15E-40
ENSG00000148400	2038.4	2039.3	2266.3	824.0	956.4	991.0	2114.7	923.8	1.2	1.27E-40
ENSG00000092964	1012.0	1015.9	1060.9	2128.7	2131.2	2477.0	1029.6	2245.7	(1.1)	2.84E-40
ENSG00000164684	317.9	229.8	300.0	2.3	4.8	4.7	282.6	3.9	6.1	3.95E-40
ENSG00000124225	660.6	850.0	803.3	6487.2	4235.4	6387.9	771.3	5703.5	(2.9)	3.98E-40
ENSG00000112414	4297.1	3543.0	4129.6	1650.2	1906.0	1848.7	3989.9	1801.6	1.1	5.33E-40
ENSG00000143819	534.3	611.5	615.4	1364.5	1314.3	1377.9	587.0	1352.2	(1.2)	5.68E-40
ENSG00000092929	1934.1	2167.2	2205.7	1000.7	1009.3	936.9	2102.3	982.3	1.1	7.44E-40
ENSG00000133597	1126.9	1134.0	1177.4	522.1	442.6	450.3	1146.1	471.7	1.3	7.72E-40
ENSG00000196754	2769.9	3127.8	2794.0	7086.2	6018.3	5775.4	2897.2	6293.3	(1.1)	7.93E-40
ENSG00000109929	2973.9	2623.6	2813.9	1075.3	1358.6	1240.9	2803.8	1224.9	1.2	9.33E-40
ENSG00000187688	581.2	538.8	584.6	1295.6	1258.5	1253.0	568.2	1269.0	(1.2)	1.53E-39
ENSG00000146909	1342.4	1357.4	1302.1	617.4	582.1	515.5	1333.9	571.7	1.2	1.61E-39
ENSG00000149571	381.1	449.9	451.8	97.5	108.7	108.1	427.6	104.8	2.0	1.64E-39
ENSG00000173334	730.5	716.6	730.1	278.9	249.2	268.5	725.8	265.5	1.5	1.81E-39
ENSG00000182704	560.1	607.1	593.7	1416.1	1299.9	1278.1	587.0	1331.4	(1.2)	2.80E-39
ENSG00000168398	183.8	223.3	204.2	13.8	8.7	14.9	203.8	12.4	4.0	3.01E-39
ENSG00000137752	203.9	203.8	188.0	640.3	572.5	596.7	198.6	603.2	(1.6)	5.69E-39

ENSG00000154529	123.5	70.5	105.7	443.0	447.4	469.9	99.9	453.4	(2.2)	1.10E-38
ENSG00000204219	17.2	17.3	19.9	207.7	201.1	196.7	18.2	201.8	(3.5)	1.40E-38
ENSG00000096060	972.8	979.0	936.2	382.1	419.5	359.9	962.6	387.2	1.3	1.49E-38
ENSG00000132932	368.6	344.8	346.1	86.1	79.9	80.2	353.2	82.0	2.1	3.09E-38
ENSG00000110057	1389.3	1462.5	1547.0	687.4	676.4	614.4	1466.3	659.4	1.2	4.68E-38
ENSG00000135074	1142.2	1244.6	1315.7	3019.2	2458.3	3000.0	1234.2	2825.9	(1.2)	6.97E-38
ENSG00000087842	66.1	75.9	81.3	373.0	375.2	309.5	74.4	352.6	(2.2)	6.97E-38
ENSG00000183486	1456.3	1440.8	1344.6	470.5	408.0	602.2	1413.9	493.6	1.5	7.50E-38
ENSG00000214530	1274.4	1324.8	1360.0	611.7	485.9	555.6	1319.7	551.1	1.3	8.72E-38
ENSG00000153246	395.4	387.0	435.5	1174.0	979.5	1341.5	406.0	1165.0	(1.5)	1.30E-37
ENSG00000143850	1189.2	1251.1	1136.8	516.4	543.6	530.5	1192.3	530.2	1.2	1.73E-37
ENSG00000148120	158.9	131.2	159.0	548.5	512.8	476.4	149.7	512.6	(1.8)	1.83E-37
ENSG00000154144	1009.2	1104.8	1078.9	463.6	459.9	461.5	1064.3	461.7	1.2	2.12E-37
ENSG00000099282	817.7	856.5	861.2	352.3	324.2	344.9	845.1	340.5	1.3	2.88E-37
ENSG00000167244	281.5	268.9	309.9	60.8	47.1	45.7	286.8	51.2	2.5	3.80E-37
ENSG00000122861	4889.7	5201.8	4812.7	2625.6	2160.1	2548.8	4968.1	2444.8	1.0	4.79E-37
ENSG00000168672	517.0	533.4	573.8	144.6	181.8	170.6	541.4	165.7	1.7	5.25E-37
ENSG00000078804	1441.9	1487.5	1454.8	694.3	665.8	730.9	1461.4	697.0	1.1	6.62E-37
ENSG00000120217	793.7	699.3	673.2	255.9	268.4	237.7	722.1	254.0	1.5	7.03E-37
ENSG00000174567	225.0	220.1	222.3	3.4	3.8	5.6	222.5	4.3	5.7	7.65E-37
ENSG00000025708	26.8	35.8	28.0	268.5	204.9	236.8	30.2	236.8	(3.0)	7.99E-37
ENSG00000170175	654.9	641.8	641.6	242.1	218.4	240.5	646.1	233.7	1.5	8.63E-37
ENSG00000133985	206.8	219.0	220.5	1.1	8.7	3.7	215.4	4.5	5.5	1.52E-36
ENSG00000275410	1027.3	1066.8	955.1	428.0	435.9	438.2	1016.4	434.0	1.2	1.56E-36
ENSG00000157224	1278.2	1198.0	1274.1	515.3	559.0	593.9	1250.1	556.0	1.2	1.65E-36
ENSG00000010818	1755.0	1604.5	1784.7	765.4	823.6	849.3	1714.7	812.8	1.1	1.75E-36
ENSG00000134030	2031.7	2156.4	2155.1	1113.1	971.8	931.3	2114.4	1005.4	1.1	2.29E-36
ENSG00000101333	3763.8	2734.2	3566.6	253.6	433.9	341.2	3354.9	342.9	3.3	3.03E-36
ENSG00000177706	1308.8	1516.7	1480.1	3134.0	2774.9	2884.4	1435.2	2931.1	(1.0)	3.16E-36
ENSG00000221867	402.1	452.1	394.0	121.6	103.9	110.0	416.1	111.9	1.9	5.16E-36
ENSG00000091986	421.3	372.9	376.8	989.2	910.2	929.5	390.3	943.0	(1.3)	7.09E-36
ENSG00000163874	833.0	934.5	828.6	335.1	337.7	361.7	865.4	344.8	1.3	9.76E-36
ENSG00000167552	1497.5	1773.7	1554.2	3804.2	3136.7	3894.1	1608.5	3611.6	(1.2)	1.18E-35
ENSG00000145335	63.2	87.8	75.0	409.7	342.5	317.0	75.3	356.4	(2.2)	1.30E-35
ENSG00000172379	231.7	260.2	251.2	28.7	40.4	43.8	247.7	37.6	2.7	1.30E-35
ENSG00000172889	844.5	907.4	928.9	392.5	347.3	355.2	893.6	365.0	1.3	1.67E-35
ENSG00000101871	459.6	416.3	459.0	974.3	1102.6	1061.9	445.0	1046.3	(1.2)	1.83E-35
ENSG00000203805	21.1	29.3	27.1	227.2	186.7	232.1	25.8	215.3	(3.1)	2.54E-35
ENSG00000154133	179.0	188.6	175.3	17.2	8.7	8.4	181.0	11.4	4.0	3.01E-35
ENSG00000088726	474.9	530.2	464.5	142.3	143.4	95.1	489.8	126.9	2.0	3.99E-35
ENSG00000158106	810.0	764.3	910.9	211.2	310.8	276.9	828.4	266.3	1.6	5.19E-35
ENSG00000162496	561.1	664.6	575.6	1435.6	1296.0	1330.4	600.4	1354.0	(1.2)	7.49E-35
ENSG00000166833	2202.1	2175.9	2176.8	978.9	1119.0	1159.7	2185.0	1085.9	1.0	1.21E-34
ENSG00000142675	239.4	229.8	256.6	32.1	46.2	36.4	241.9	38.2	2.7	1.52E-34
ENSG00000033867	2270.1	1837.6	2208.5	757.4	945.8	922.9	2105.4	875.4	1.3	2.20E-34
ENSG00000119900	6635.2	5565.0	6688.6	2489.1	3166.5	2919.9	6296.2	2858.5	1.1	3.09E-34
ENSG00000134802	1134.6	1229.4	1145.8	545.1	556.1	517.4	1169.9	539.5	1.1	3.81E-34
ENSG00000108448	96.7	100.8	97.6	374.1	345.4	374.8	98.4	364.8	(1.9)	5.11E-34
ENSG00000130762	165.6	169.1	179.8	8.0	14.4	10.3	171.5	10.9	4.0	8.01E-34
ENSG00000105835	3146.2	2763.5	2924.1	1331.2	1561.6	1501.9	2944.6	1464.9	1.0	8.91E-34
ENSG00000119938	236.5	253.7	266.6	672.5	631.2	686.2	252.3	663.3	(1.4)	1.56E-33
ENSG00000104951	181.0	241.8	193.4	14.9	22.1	27.0	205.4	21.4	3.2	2.30E-33
ENSG00000167680	843.5	921.5	947.9	383.3	283.8	259.2	904.3	308.8	1.6	3.73E-33
ENSG00000113083	505.5	449.9	540.4	1082.2	1235.4	1358.3	498.6	1225.3	(1.3)	6.98E-33
ENSG00000256235	147.4	148.5	159.0	483.1	436.8	549.1	151.7	489.7	(1.7)	1.66E-32
ENSG00000124098	624.3	654.8	628.9	1362.2	1243.1	1312.6	636.0	1306.0	(1.0)	2.04E-32
ENSG00000146232	846.4	938.9	896.4	403.9	328.1	371.0	893.9	367.7	1.3	3.26E-32
ENSG00000078596	196.3	169.1	202.4	4.6	3.8	3.7	189.3	4.1	5.6	4.21E-32

ENSG00000246705	243.2	270.0	247.6	848.0	708.2	633.9	253.6	730.0	(1.5)	4.86E-32
ENSG00000151150	399.3	337.2	399.4	101.0	96.2	111.9	378.6	103.0	1.9	5.80E-32
ENSG00000137266	234.6	221.2	209.6	44.8	26.0	21.4	221.8	30.7	2.9	1.18E-31
ENSG00000160094	232.7	272.1	301.8	741.3	673.5	737.4	268.9	717.4	(1.4)	1.93E-31
ENSG00000003989	598.4	563.8	591.9	237.5	212.6	192.0	584.7	214.1	1.5	2.86E-31
ENSG00000197461	1095.3	1114.5	1060.0	548.5	499.4	494.1	1089.9	514.0	1.1	3.52E-31
ENSG00000148848	473.9	417.4	495.2	1013.3	1051.6	1208.2	462.2	1091.1	(1.2)	3.56E-31
ENSG00000160190	652.0	721.0	640.7	211.2	225.1	279.7	671.2	238.7	1.5	4.02E-31
ENSG00000117461	281.5	261.3	249.4	773.5	647.5	663.8	264.1	694.9	(1.4)	4.86E-31
ENSG00000146966	1383.5	1374.7	1470.2	732.1	701.4	638.6	1409.5	690.7	1.0	4.97E-31
ENSG00000174939	22.0	23.9	30.7	208.9	210.7	168.7	25.5	196.1	(2.9)	6.13E-31
ENSG00000113361	0.0	0.0	2.7	996.1	879.4	1054.4	0.9	976.6	(10.0)	7.22E-31
ENSG00000118515	699.9	838.0	609.9	229.5	186.7	256.4	716.0	224.2	1.7	7.36E-31
ENSG00000113645	1238.9	1224.0	1316.6	648.4	608.1	568.7	1259.8	608.4	1.1	1.11E-30
ENSG00000160796	1142.2	1226.2	1347.3	532.5	568.6	598.5	1238.6	566.5	1.1	1.12E-30
ENSG00000163249	1263.8	1211.0	1256.0	632.3	633.1	596.7	1243.6	620.7	1.0	1.15E-30
ENSG00000113721	18.2	21.7	23.5	163.0	176.1	193.9	21.1	177.6	(3.1)	1.17E-30
ENSG00000167703	210.6	265.6	247.6	679.4	596.5	707.6	241.3	661.2	(1.5)	1.88E-30
ENSG00000225383	209.7	181.1	190.7	13.8	32.7	14.9	193.8	20.5	3.2	1.90E-30
ENSG00000050327	824.4	752.4	701.2	316.7	310.8	262.0	759.3	296.5	1.4	2.11E-30
ENSG00000223749	404.0	391.4	403.9	127.4	133.7	116.5	399.8	125.9	1.7	2.46E-30
ENSG00000266338	1051.3	1077.6	1092.5	495.7	541.7	510.9	1073.8	516.1	1.1	2.85E-30
ENSG00000273604	138.8	162.6	140.1	457.9	439.7	429.8	147.2	442.5	(1.6)	4.01E-30
ENSG00000212724	192.4	173.5	150.9	14.9	21.2	17.7	172.3	17.9	3.3	4.76E-30
ENSG00000198879	7.7	2.2	15.4	159.5	143.4	170.6	8.4	157.8	(4.2)	6.35E-30
ENSG00000164078	1243.7	1299.9	1394.3	643.8	592.7	668.4	1312.6	635.0	1.0	7.08E-30
ENSG00000174672	47.9	52.0	71.4	285.7	271.3	255.4	57.1	270.8	(2.2)	7.37E-30
ENSG00000166681	907.7	1020.2	968.7	2174.6	1836.8	1876.7	965.5	1962.7	(1.0)	7.50E-30
ENSG00000196639	659.7	612.5	631.6	250.2	208.8	264.8	634.6	241.2	1.4	1.21E-29
ENSG00000081041	205.9	256.9	172.6	25.2	26.0	34.5	211.8	28.6	2.9	1.23E-29
ENSG00000112769	654.9	729.6	739.2	1378.2	1413.4	1561.6	707.9	1451.1	(1.0)	1.31E-29
ENSG00000188112	413.6	468.4	422.0	152.6	143.4	128.7	434.7	141.5	1.6	1.70E-29
ENSG00000196104	26.8	36.9	39.8	230.7	181.8	246.1	34.5	219.5	(2.7)	1.93E-29
ENSG00000103485	395.4	432.6	423.8	954.8	874.6	902.4	417.3	910.6	(1.1)	1.99E-29
ENSG00000165474	177.1	181.1	165.4	16.1	9.6	26.1	174.5	17.3	3.3	2.09E-29
ENSG00000164096	455.7	444.5	436.5	1068.4	943.9	924.8	445.6	979.0	(1.1)	2.59E-29
ENSG00000083290	29.7	46.6	43.4	200.8	232.8	246.1	39.9	226.6	(2.5)	3.40E-29
ENSG00000057294	974.7	887.9	891.0	379.8	443.6	401.8	917.9	408.4	1.2	3.63E-29
ENSG00000182325	721.9	774.1	833.1	332.8	310.8	344.0	776.4	329.2	1.2	3.75E-29
ENSG00000116117	585.0	541.0	558.4	214.6	226.1	219.1	561.5	219.9	1.4	5.67E-29
ENSG00000068971	803.3	882.5	820.5	361.5	374.3	389.7	835.4	375.2	1.2	6.05E-29
ENSG00000197903	51.7	64.0	63.3	272.0	253.0	253.6	59.6	259.5	(2.1)	6.33E-29
ENSG00000026025	183.8	159.4	188.9	534.8	467.6	500.6	177.4	501.0	(1.5)	7.88E-29
ENSG00000147100	181.9	212.5	186.1	502.6	525.3	526.7	193.5	518.2	(1.4)	8.81E-29
ENSG00000131459	709.5	764.3	783.4	344.3	299.2	322.6	752.4	322.0	1.2	1.03E-28
ENSG00000161243	385.9	378.4	407.5	137.7	118.3	118.4	390.6	124.8	1.7	1.08E-28
ENSG00000104450	819.6	754.6	806.9	348.9	371.4	339.3	793.7	353.2	1.2	1.26E-28
ENSG00000170385	690.3	727.5	709.3	1351.8	1391.3	1602.6	709.0	1448.6	(1.0)	1.43E-28
ENSG00000271503	50.7	39.0	38.9	263.9	206.9	220.0	42.9	230.3	(2.4)	1.61E-28
ENSG00000156103	187.7	148.5	204.2	498.0	522.5	594.8	180.1	538.4	(1.6)	2.06E-28
ENSG00000147475	436.6	475.9	430.1	966.2	906.4	1018.0	447.6	963.5	(1.1)	2.16E-28
ENSG00000175198	247.0	243.9	237.7	624.3	569.6	596.7	242.9	596.8	(1.3)	2.40E-28
ENSG00000197872	370.5	356.7	371.4	105.6	118.3	120.3	366.2	114.7	1.7	2.74E-28
ENSG00000109321	202.0	246.1	224.1	44.8	45.2	42.0	224.1	44.0	2.3	3.32E-28
ENSG00000148484	625.2	651.6	619.0	1374.8	1171.9	1359.3	631.9	1302.0	(1.0)	3.58E-28
ENSG00000204959	357.1	382.7	374.1	82.6	122.2	67.1	371.3	90.6	2.0	5.01E-28
ENSG00000149564	203.0	226.6	193.4	31.0	44.3	31.7	207.6	35.6	2.5	5.66E-28
ENSG00000198771	264.3	248.3	218.7	3.4	1.0	1.9	243.7	2.1	6.9	6.90E-28

ENSG00000166145	1217.9	1327.0	1154.8	611.7	567.7	627.4	1233.2	602.2	1.0	9.08E-28
ENSG00000112218	136.0	150.7	132.8	4.6	8.7	11.2	139.8	8.1	4.1	9.85E-28
ENSG00000073756	445.2	510.6	394.0	115.9	110.6	159.4	449.9	128.7	1.8	1.49E-27
ENSG00000184939	174.3	185.4	189.8	463.6	519.6	486.6	183.1	489.9	(1.4)	1.54E-27
ENSG00000166900	782.2	750.2	651.5	284.6	319.4	297.4	728.0	300.5	1.3	1.68E-27
ENSG00000157110	372.4	371.9	419.3	846.9	823.6	951.8	387.9	874.1	(1.2)	2.08E-27
ENSG00000139044	140.7	152.9	152.7	5.7	2.9	3.7	148.8	4.1	5.2	2.32E-27
ENSG00000197496	397.3	490.0	429.2	938.7	942.0	991.9	438.9	957.5	(1.1)	2.73E-27
ENSG00000173273	521.8	500.9	541.3	1004.1	1055.5	1105.7	521.3	1055.1	(1.0)	4.44E-27
ENSG00000146038	175.2	136.6	164.5	21.8	17.3	16.8	158.8	18.6	3.1	5.73E-27
ENSG00000180730	690.3	735.1	688.6	1507.9	1274.9	1528.9	704.6	1437.2	(1.0)	5.76E-27
ENSG00000198743	2168.6	1870.2	2269.9	3727.3	4776.2	4440.4	2102.9	4314.6	(1.0)	5.95E-27
ENSG00000152223	1028.3	987.7	955.1	470.5	509.9	473.6	990.4	484.7	1.0	6.68E-27
ENSG00000156140	508.4	346.9	420.2	104.4	89.5	135.2	425.2	109.7	2.0	7.32E-27
ENSG00000228594	3.8	2.2	0.9	203.1	188.6	177.1	2.3	189.6	(6.4)	9.41E-27
ENSG00000090376	11.5	11.9	12.7	140.0	145.3	125.9	12.0	137.0	(3.5)	1.01E-26
ENSG00000112667	48.8	62.9	64.2	337.4	274.2	223.7	58.6	278.4	(2.2)	1.04E-26
ENSG00000128294	980.4	1065.7	1055.4	516.4	422.4	503.4	1033.9	480.7	1.1	1.42E-26
ENSG00000076826	190.5	168.0	168.1	24.1	21.2	32.6	175.6	26.0	2.8	1.72E-26
ENSG00000165572	251.8	238.5	269.3	636.9	663.9	565.9	253.2	622.2	(1.3)	1.93E-26
ENSG00000148426	595.5	600.6	585.5	222.6	267.5	202.3	593.9	230.8	1.4	1.97E-26
ENSG00000147889	567.8	679.8	666.0	1525.1	1344.1	1248.3	637.8	1372.5	(1.1)	2.06E-26
ENSG00000144749	494.0	537.7	449.1	174.4	195.3	174.3	493.6	181.4	1.4	2.59E-26
ENSG00000161544	127.3	169.1	179.8	13.8	21.2	16.8	158.8	17.2	3.2	2.82E-26
ENSG00000175920	135.0	133.4	158.1	3.4	6.7	1.9	142.2	4.0	5.1	3.76E-26
ENSG00000132661	1036.0	1003.9	1048.2	529.0	527.3	461.5	1029.4	505.9	1.0	3.79E-26
ENSG00000265763	138.8	153.9	169.9	492.3	456.1	400.9	154.2	449.7	(1.5)	5.26E-26
ENSG00000160255	195.3	221.2	249.4	40.2	51.0	45.7	222.0	45.6	2.3	7.01E-26
ENSG00000167191	857.9	884.7	895.5	429.2	428.2	440.0	879.3	432.5	1.0	7.17E-26
ENSG00000169515	125.4	147.4	168.1	3.4	6.7	0.9	147.0	3.7	5.3	7.36E-26
ENSG00000070182	219.3	232.0	229.5	47.1	40.4	59.7	226.9	49.0	2.2	7.64E-26
ENSG00000188707	316.9	390.3	374.1	122.8	97.2	109.1	360.4	109.7	1.7	8.04E-26
ENSG00000126709	2060.4	1955.8	1978.0	998.4	605.2	787.8	1998.1	797.1	1.3	8.40E-26
ENSG00000110080	1007.2	1124.3	970.5	524.4	495.5	485.7	1034.0	501.9	1.0	1.00E-25
ENSG00000182054	429.9	530.2	514.2	1216.4	996.8	1082.4	491.4	1098.5	(1.2)	1.16E-25
ENSG00000246082	85.2	77.0	78.6	296.1	288.6	266.6	80.3	283.8	(1.8)	1.18E-25
ENSG00000081913	944.0	1011.5	935.3	470.5	495.5	472.7	963.6	479.6	1.0	1.31E-25
ENSG00000102452	420.3	363.2	417.5	828.5	879.4	846.5	400.3	851.5	(1.1)	1.46E-25
ENSG00000168010	758.3	688.4	747.3	265.1	348.3	253.6	731.3	289.0	1.3	1.58E-25
ENSG00000119632	167.6	146.4	150.0	558.9	436.8	413.0	154.6	469.6	(1.6)	1.77E-25
ENSG00000154134	532.3	447.8	500.6	184.8	199.2	176.2	493.6	186.7	1.4	1.91E-25
ENSG00000182866	133.1	121.4	137.4	2.3	12.5	5.6	130.6	6.8	4.2	2.13E-25
ENSG00000140479	162.8	180.0	127.4	19.5	14.4	21.4	156.7	18.5	3.1	2.48E-25
ENSG00000137628	545.7	523.6	623.5	1099.4	1259.5	1439.4	564.3	1266.1	(1.2)	2.71E-25
ENSG00000165025	516.1	497.6	476.2	2.3	1.0	0.0	496.6	1.1	8.9	7.04E-25
ENSG00000117595	756.4	821.8	761.8	363.8	327.1	384.1	780.0	358.3	1.1	7.55E-25
ENSG00000134775	504.6	556.2	534.9	1115.4	982.4	1167.2	531.9	1088.3	(1.0)	1.13E-24
ENSG00000181026	1390.2	1502.6	1421.4	780.3	732.2	605.0	1438.1	705.9	1.0	1.15E-24
ENSG00000150551	29.7	34.7	47.9	241.0	175.1	203.2	37.4	206.4	(2.5)	1.67E-24
ENSG00000163132	313.1	341.5	350.6	120.5	96.2	104.4	335.1	107.0	1.7	1.78E-24
ENSG00000173705	67.0	66.1	68.7	291.5	218.4	289.0	67.3	266.3	(2.0)	2.50E-24
ENSG00000186166	757.3	781.7	694.9	368.4	319.4	335.6	744.6	341.1	1.1	3.41E-24
ENSG00000114948	698.0	655.9	628.9	303.0	300.2	300.2	660.9	301.1	1.1	3.41E-24
ENSG00000103647	805.2	890.1	847.6	426.9	419.5	383.2	847.6	409.9	1.0	3.53E-24
ENSG00000110723	263.3	188.6	250.3	49.3	57.7	46.6	234.1	51.2	2.2	3.78E-24
ENSG00000156273	1886.2	1304.2	1792.8	548.5	688.9	738.4	1661.1	658.6	1.3	3.81E-24
ENSG00000166965	215.4	245.0	204.2	662.1	552.3	514.6	221.6	576.3	(1.4)	5.05E-24
ENSG00000095587	174.3	184.3	184.3	32.1	18.3	39.2	181.0	29.9	2.6	5.75E-24

ENSG00000183876	205.9	248.3	181.6	45.9	33.7	47.5	211.9	42.4	2.3	6.32E-24
ENSG00000141447	367.7	426.1	410.2	888.2	786.1	869.8	401.3	848.0	(1.1)	6.48E-24
ENSG00000179104	429.9	449.9	410.2	153.8	165.5	173.4	430.0	164.2	1.4	7.40E-24
ENSG00000184731	271.9	268.9	285.5	2.3	1.9	0.0	275.4	1.4	7.7	7.40E-24
ENSG00000132535	104.4	81.3	99.4	272.0	354.1	370.1	95.0	332.1	(1.8)	7.71E-24
ENSG00000174365	297.8	285.1	282.8	84.9	75.0	97.0	288.6	85.6	1.8	8.13E-24
ENSG00000261713	35.4	40.1	41.6	228.4	280.0	158.5	39.0	222.3	(2.5)	8.84E-24
ENSG00000116525	325.5	341.5	348.8	679.4	724.5	770.1	338.6	724.6	(1.1)	8.98E-24
ENSG00000171476	115.9	117.1	124.7	6.9	10.6	9.3	119.2	8.9	3.7	9.74E-24
ENSG00000167895	111.1	142.0	143.7	17.2	9.6	12.1	132.3	13.0	3.4	9.83E-24
ENSG00000285904	132.1	142.0	104.8	12.6	3.8	10.3	126.3	8.9	3.8	1.07E-23
ENSG00000134326	462.5	487.9	415.7	157.2	143.4	190.2	455.3	163.6	1.5	1.08E-23
ENSG00000160145	329.4	337.2	374.1	128.5	114.5	107.2	346.9	116.7	1.6	1.39E-23
ENSG00000189056	198.2	164.8	201.5	33.3	29.8	43.8	188.2	35.6	2.4	1.45E-23
ENSG00000151617	603.2	598.5	537.7	205.4	228.0	268.5	579.8	234.0	1.3	1.61E-23
ENSG00000198355	948.8	1011.5	1035.6	542.8	464.7	427.9	998.6	478.5	1.1	1.85E-23
ENSG00000170153	1.9	1.1	3.6	135.4	146.2	172.5	2.2	151.4	(6.1)	1.86E-23
ENSG00000138685	359.0	290.6	343.4	757.4	885.2	701.1	331.0	781.2	(1.2)	1.95E-23
ENSG00000145882	164.7	195.1	158.1	443.0	448.4	441.0	172.7	444.1	(1.4)	2.73E-23
ENSG00000173530	366.7	395.7	406.6	786.1	809.2	779.4	389.7	791.5	(1.0)	2.99E-23
ENSG00000137941	93.8	73.7	107.5	286.9	326.2	310.4	91.7	307.8	(1.7)	3.77E-23
ENSG00000073060	362.9	348.0	372.3	753.9	729.3	733.7	361.1	739.0	(1.0)	4.13E-23
ENSG00000109472	6.7	11.9	3.6	120.5	104.9	120.3	7.4	115.2	(4.0)	4.96E-23
ENSG00000147419	368.6	358.9	361.4	786.1	773.6	701.1	363.0	753.6	(1.1)	5.32E-23
ENSG00000115129	227.9	252.6	209.6	593.3	535.0	521.1	230.0	549.8	(1.3)	5.81E-23
ENSG00000139209	4.8	0.0	2.7	113.6	161.6	137.0	2.5	137.4	(5.7)	7.15E-23
ENSG00000136114	198.2	162.6	197.0	451.0	469.5	471.7	185.9	464.1	(1.3)	1.38E-22
ENSG00000040731	15.3	17.3	19.9	103.3	161.6	185.5	17.5	150.1	(3.1)	1.55E-22
ENSG00000130038	889.5	878.2	843.1	417.7	469.5	380.4	870.2	422.5	1.0	1.96E-22
ENSG00000164400	113.9	153.9	103.0	9.2	1.0	2.8	123.6	4.3	4.9	2.00E-22
ENSG00000143878	475.9	492.2	447.3	951.3	868.8	1033.0	471.8	951.0	(1.0)	2.17E-22
ENSG00000110881	57.4	55.3	76.8	239.8	256.9	226.5	63.2	241.1	(1.9)	2.21E-22
ENSG00000163638	179.0	208.2	178.9	36.7	43.3	42.9	188.7	41.0	2.2	2.37E-22
ENSG00000111199	96.7	143.1	147.3	439.5	352.2	431.6	129.0	407.8	(1.7)	2.42E-22
ENSG00000164251	2062.4	2501.1	2134.4	1169.4	947.7	1215.7	2232.6	1110.9	1.0	2.84E-22
ENSG00000129757	134.0	140.9	134.6	25.2	11.5	16.8	136.5	17.9	3.0	3.27E-22
ENSG00000196611	188.6	161.5	189.8	3.4	1.0	0.9	180.0	1.8	6.7	4.04E-22
ENSG00000121858	97.7	114.9	98.5	348.9	302.1	524.9	103.7	391.9	(1.9)	4.99E-22
ENSG00000170743	110.1	152.9	116.6	13.8	3.8	14.9	126.5	10.8	3.6	7.57E-22
ENSG00000105851	130.2	122.5	108.4	4.6	17.3	7.5	120.4	9.8	3.6	1.03E-21
ENSG00000160712	153.2	132.3	146.4	16.1	25.0	4.7	143.9	15.2	3.2	1.21E-21
ENSG00000055163	754.5	799.0	684.0	379.8	346.4	342.1	745.8	356.1	1.1	1.23E-21
ENSG00000123213	397.3	380.5	352.4	736.7	815.9	748.6	376.8	767.1	(1.0)	1.31E-21
ENSG00000053747	223.1	200.6	237.7	486.6	545.5	513.7	220.4	515.3	(1.2)	1.43E-21
ENSG00000154721	23.0	11.9	17.2	154.9	110.6	144.5	17.4	136.7	(3.0)	1.77E-21
ENSG00000163728	490.2	399.0	468.1	845.8	993.9	1026.4	452.4	955.4	(1.1)	1.99E-21
ENSG00000135378	144.6	138.8	133.7	382.1	350.2	361.7	139.0	364.7	(1.4)	2.07E-21
ENSG00000149256	64.1	90.0	112.0	308.7	306.0	301.1	88.7	305.3	(1.8)	2.63E-21
ENSG00000106034	568.7	468.4	520.5	195.1	192.4	240.5	519.2	209.3	1.3	3.62E-21
ENSG00000180638	9.6	20.6	13.6	123.9	155.9	106.3	14.6	128.7	(3.2)	3.98E-21
ENSG00000134508	583.1	668.9	591.0	281.2	293.5	276.9	614.3	283.8	1.1	4.18E-21
ENSG00000198768	2.9	2.2	2.7	128.5	90.4	155.7	2.6	124.9	(5.6)	4.37E-21
ENSG00000121210	248.0	227.7	244.0	492.3	560.9	605.0	239.9	552.8	(1.2)	4.68E-21
ENSG00000163435	337.0	401.1	337.1	127.4	128.0	136.1	358.4	130.5	1.5	5.16E-21
ENSG00000185432	7.7	8.7	12.7	102.1	111.6	107.2	9.7	107.0	(3.5)	6.97E-21
ENSG00000153774	326.5	371.9	318.1	786.1	717.8	661.9	338.8	721.9	(1.1)	7.30E-21
ENSG00000173432	157.0	133.4	101.2	3.4	1.0	2.8	130.5	2.4	5.8	8.53E-21
ENSG00000079257	162.8	146.4	140.1	406.2	351.2	420.5	149.7	392.6	(1.4)	8.95E-21

ENSG00000234465	157.0	180.0	212.4	43.6	40.4	33.6	183.1	39.2	2.2	9.06E-21
ENSG00000221890	37.3	39.0	38.9	207.7	165.5	159.4	38.4	177.5	(2.2)	1.12E-20
ENSG00000108852	78.5	81.3	80.4	278.9	268.4	230.3	80.1	259.2	(1.7)	1.17E-20
ENSG00000071246	101.5	107.3	116.6	353.4	293.5	300.2	108.5	315.7	(1.5)	1.40E-20
ENSG00000170522	360.0	312.2	384.9	728.7	721.6	725.3	352.4	725.2	(1.0)	1.63E-20
ENSG00000143061	297.8	315.5	333.4	127.4	86.6	99.8	315.6	104.6	1.6	1.96E-20
ENSG00000108984	108.2	85.6	104.8	283.4	287.7	317.0	99.6	296.0	(1.6)	2.02E-20
ENSG00000116741	236.5	200.6	226.8	53.9	66.4	62.5	221.3	60.9	1.9	2.02E-20
ENSG00000063438	234.6	288.4	244.0	71.1	78.9	81.1	255.6	77.1	1.7	2.13E-20
ENSG00000112149	389.7	420.7	361.4	148.0	145.3	165.0	390.6	152.8	1.4	2.15E-20
ENSG00000153029	93.8	100.8	104.8	305.3	262.7	328.2	99.8	298.7	(1.6)	2.38E-20
ENSG00000172992	191.5	214.7	208.7	535.9	458.0	455.9	205.0	483.3	(1.2)	2.61E-20
ENSG00000253910	16.3	35.8	32.5	193.9	155.9	144.5	28.2	164.8	(2.6)	3.22E-20
ENSG00000178401	30.6	27.1	30.7	150.3	149.1	147.3	29.5	148.9	(2.3)	3.28E-20
ENSG00000166250	685.5	622.3	660.5	296.1	337.7	320.7	656.1	318.2	1.0	3.84E-20
ENSG00000170412	1004.4	1318.3	1228.0	616.2	500.3	576.1	1183.6	564.2	1.1	4.03E-20
ENSG00000130592	6.7	9.8	11.7	159.5	88.5	100.7	9.4	116.2	(3.6)	4.13E-20
ENSG00000165105	47.9	68.3	54.2	193.9	225.1	220.9	56.8	213.3	(1.9)	4.15E-20
ENSG00000141295	316.0	378.4	359.6	774.6	682.2	719.7	351.3	725.5	(1.0)	4.16E-20
ENSG00000124466	34.5	46.6	40.7	182.5	157.8	194.8	40.6	178.4	(2.1)	4.21E-20
ENSG00000158023	136.9	142.0	127.4	24.1	22.1	24.2	135.5	23.5	2.5	5.93E-20
ENSG00000133056	101.5	108.4	124.7	315.6	306.0	309.5	111.5	310.4	(1.5)	6.17E-20
ENSG00000165152	425.1	378.4	390.4	171.0	153.0	164.1	397.9	162.7	1.3	7.05E-20
ENSG00000211772	127.3	126.8	129.2	1.1	0.0	4.7	127.8	1.9	6.0	7.05E-20
ENSG00000158373	19.1	22.8	28.9	149.2	114.5	195.8	23.6	153.2	(2.7)	9.08E-20
ENSG00000143507	217.3	195.1	266.6	55.1	67.4	59.7	226.4	60.7	1.9	1.04E-19
ENSG00000120327	11.5	8.7	13.6	114.8	93.3	111.9	11.2	106.7	(3.2)	1.14E-19
ENSG00000160588	332.2	350.2	330.7	132.0	123.2	137.0	337.7	130.7	1.4	1.53E-19
ENSG00000175414	16.3	9.8	7.2	119.3	103.0	100.7	11.1	107.7	(3.3)	1.54E-19
ENSG00000123358	302.6	211.4	257.5	82.6	74.1	65.3	257.2	74.0	1.8	1.83E-19
ENSG00000104490	98.6	101.9	85.8	3.4	6.7	4.7	95.5	4.9	4.2	1.84E-19
ENSG00000170745	140.7	129.0	141.0	26.4	27.9	18.6	136.9	24.3	2.5	2.08E-19
ENSG00000146555	244.2	253.7	233.1	495.7	527.3	542.6	243.7	521.9	(1.1)	2.22E-19
ENSG00000104299	172.3	171.3	161.7	393.6	388.7	408.3	168.5	396.9	(1.2)	2.47E-19
ENSG00000158458	495.0	466.2	491.6	229.5	210.7	224.7	484.3	221.6	1.1	3.00E-19
ENSG00000111801	167.6	210.3	201.5	437.2	449.3	563.1	193.1	483.2	(1.3)	3.77E-19
ENSG00000178826	284.4	290.6	250.3	91.8	97.2	95.1	275.1	94.7	1.5	4.61E-19
ENSG00000232931	282.4	206.0	278.3	37.9	71.2	76.4	255.6	61.8	2.0	5.04E-19
ENSG00000166582	507.5	462.9	468.1	231.8	201.1	218.2	479.5	217.0	1.1	8.53E-19
ENSG00000110063	596.5	603.9	586.5	317.9	260.7	284.3	595.6	287.7	1.1	9.11E-19
ENSG00000189366	20.1	15.2	19.9	115.9	110.6	128.7	18.4	118.4	(2.7)	1.23E-18
ENSG00000117586	89.0	95.4	91.3	8.0	3.8	7.5	91.9	6.4	3.8	1.23E-18
ENSG00000119711	47.9	71.6	50.6	220.3	201.1	195.8	56.7	205.7	(1.9)	2.16E-18
ENSG00000100867	151.3	188.6	182.5	37.9	47.1	42.0	174.2	42.3	2.0	2.24E-18
ENSG00000131773	485.4	481.4	457.2	213.4	222.3	226.5	474.7	220.7	1.1	2.28E-18
ENSG00000104325	293.9	389.2	288.3	780.3	672.6	683.4	323.8	712.1	(1.1)	2.45E-18
ENSG00000196684	88.1	104.1	82.2	5.7	1.9	7.5	91.5	5.0	4.2	2.53E-18
ENSG00000064655	96.7	99.7	83.1	270.8	263.6	260.1	93.2	264.9	(1.5)	2.64E-18
ENSG00000165322	294.9	215.7	262.1	510.7	674.5	716.9	257.6	634.0	(1.3)	3.13E-18
ENSG00000158825	84.3	87.8	103.9	8.0	7.7	7.5	92.0	7.7	3.6	3.82E-18
ENSG00000078081	226.9	246.1	194.3	63.1	63.5	72.7	222.4	66.4	1.7	3.84E-18
ENSG00000250770	101.5	98.7	114.8	11.5	17.3	9.3	105.0	12.7	3.0	3.98E-18
ENSG00000178776	6.7	7.6	4.5	81.5	86.6	95.1	6.3	87.7	(3.8)	4.00E-18
ENSG00000213015	262.3	285.1	271.1	573.8	528.2	565.9	272.9	556.0	(1.0)	4.13E-18
ENSG00000196159	690.3	565.9	712.1	1155.6	1561.6	1315.4	656.1	1344.2	(1.0)	4.18E-18
ENSG00000101665	177.1	178.9	185.2	430.3	375.2	477.3	180.4	427.6	(1.2)	4.37E-18
ENSG00000144935	110.1	94.3	106.6	254.8	299.2	354.3	103.7	302.8	(1.5)	4.44E-18
ENSG00000262576	33.5	33.6	33.4	137.7	143.4	168.7	33.5	149.9	(2.2)	5.41E-18

ENSG00000165959	554.4	561.6	611.8	270.8	304.0	263.8	575.9	279.6	1.0	5.64E-18
ENSG00000162078	170.4	186.5	167.2	36.7	52.9	42.0	174.7	43.9	2.0	5.96E-18
ENSG00000088280	100.5	80.2	86.7	273.1	252.1	250.8	89.2	258.7	(1.5)	6.02E-18
ENSG00000171224	182.9	161.5	174.4	37.9	42.3	51.3	172.9	43.8	2.0	6.87E-18
ENSG00000111052	11.5	5.4	12.7	72.3	128.0	115.6	9.9	105.3	(3.4)	7.00E-18
ENSG00000143127	171.4	274.3	204.2	44.8	61.6	55.0	216.6	53.8	2.0	7.72E-18
ENSG00000164976	278.6	336.1	296.4	728.7	561.9	688.0	303.7	659.5	(1.1)	8.41E-18
ENSG00000158555	475.9	536.7	530.4	254.8	215.5	248.0	514.3	239.4	1.1	9.19E-18
ENSG00000177335	186.7	136.6	154.5	37.9	38.5	31.7	159.3	36.0	2.1	1.07E-17
ENSG00000163762	95.7	87.8	81.3	6.9	8.7	4.7	88.3	6.7	3.7	1.09E-17
ENSG00000099812	165.6	118.2	132.8	31.0	25.0	24.2	138.9	26.7	2.4	1.11E-17
ENSG00000149591	805.2	883.6	646.1	343.1	308.9	396.2	778.3	349.4	1.2	1.17E-17
ENSG00000144655	526.6	517.1	537.7	265.1	212.6	262.9	527.1	246.9	1.1	1.20E-17
ENSG00000118473	160.9	140.9	121.1	0.0	2.9	0.9	141.0	1.3	6.7	1.47E-17
ENSG00000168769	300.6	229.8	322.6	560.0	699.5	767.3	284.4	675.6	(1.2)	1.54E-17
ENSG00000101276	493.1	500.9	497.0	251.3	244.4	223.7	497.0	239.8	1.1	1.81E-17
ENSG00000280303	119.7	130.1	143.7	20.7	30.8	23.3	131.2	24.9	2.4	1.90E-17
ENSG00000137103	116.8	122.5	139.2	315.6	301.2	378.5	126.2	331.7	(1.4)	1.91E-17
ENSG00000143341	13.4	18.4	20.8	94.1	115.5	142.6	17.5	117.4	(2.7)	1.97E-17
ENSG00000154917	186.7	168.0	163.6	52.8	44.3	38.2	172.8	45.1	1.9	1.99E-17
ENSG00000146674	198.2	243.9	224.1	700.0	427.2	730.0	222.1	619.1	(1.5)	2.00E-17
ENSG00000099399	99.6	87.8	94.0	13.8	4.8	9.3	93.8	9.3	3.4	2.07E-17
ENSG00000184227	32.6	19.5	33.4	160.7	146.2	124.0	28.5	143.6	(2.3)	2.12E-17
ENSG00000114200	159.9	134.4	175.3	28.7	32.7	42.9	156.5	34.8	2.2	2.18E-17
ENSG00000156869	39.3	55.3	38.0	169.8	172.2	169.7	44.2	170.6	(2.0)	2.37E-17
ENSG00000173269	131.2	151.8	122.9	32.1	27.9	19.6	135.3	26.5	2.4	2.80E-17
ENSG00000154330	80.4	83.5	87.7	3.4	2.9	7.5	83.9	4.6	4.2	3.46E-17
ENSG00000101400	181.0	199.5	208.7	526.7	414.7	427.0	196.4	456.1	(1.2)	3.53E-17
ENSG00000163923	2.9	1.1	2.7	84.9	94.3	94.2	2.2	91.1	(5.3)	3.62E-17
ENSG00000153132	218.3	234.2	244.9	455.6	493.6	522.1	232.5	490.4	(1.1)	4.17E-17
ENSG00000137727	97.7	67.2	114.8	5.7	10.6	5.6	93.2	7.3	3.7	4.18E-17
ENSG00000154310	120.6	99.7	106.6	251.3	322.3	342.1	109.0	305.3	(1.5)	4.18E-17
ENSG00000185585	43.1	45.5	42.5	167.5	147.2	192.0	43.7	168.9	(2.0)	4.55E-17
ENSG00000250479	78.5	82.4	79.5	257.1	233.8	214.4	80.1	235.1	(1.6)	6.18E-17
ENSG00000171533	96.7	116.0	124.7	18.4	19.2	17.7	112.5	18.4	2.6	6.49E-17
ENSG00000025039	78.5	83.5	85.8	6.9	6.7	2.8	82.6	5.5	3.9	6.81E-17
ENSG00000110002	98.6	123.6	112.0	19.5	19.2	15.8	111.4	18.2	2.6	6.90E-17
ENSG00000103490	141.7	164.8	162.7	410.8	354.1	349.6	156.4	371.5	(1.2)	7.65E-17
ENSG00000144712	82.3	104.1	83.1	5.7	6.7	12.1	89.9	8.2	3.4	8.04E-17
ENSG00000138271	17.2	29.3	28.0	120.5	136.6	125.9	24.8	127.7	(2.4)	8.64E-17
ENSG00000112139	92.9	139.9	100.3	325.9	286.7	309.5	111.0	307.4	(1.5)	8.86E-17
ENSG00000164342	119.7	129.0	148.2	290.3	390.6	510.0	132.3	397.0	(1.6)	1.15E-16
ENSG00000171877	284.4	280.8	301.8	573.8	533.0	629.3	289.0	578.7	(1.0)	1.18E-16
ENSG00000162415	42.1	45.5	42.5	189.3	138.6	178.1	43.4	168.7	(2.0)	1.26E-16
ENSG00000167105	510.3	546.4	506.9	281.2	247.3	224.7	521.2	251.0	1.1	1.47E-16
ENSG00000185101	222.1	225.5	251.2	39.0	82.7	71.8	232.9	64.5	1.8	1.57E-16
ENSG00000196440	232.7	232.0	221.4	83.8	82.7	70.9	228.7	79.1	1.5	1.67E-16
ENSG00000189184	31.6	18.4	26.2	128.5	119.3	135.2	25.4	127.7	(2.3)	1.73E-16
ENSG00000136826	204.9	232.0	199.7	434.9	460.9	449.4	212.2	448.4	(1.1)	1.73E-16
ENSG00000105894	91.0	88.9	61.4	259.3	239.6	230.3	80.4	243.1	(1.6)	1.76E-16
ENSG00000125731	158.0	157.2	194.3	40.2	52.9	38.2	169.8	43.8	2.0	1.79E-16
ENSG00000159388	22.0	26.0	21.7	113.6	116.4	125.9	23.2	118.6	(2.4)	1.80E-16
ENSG00000165071	122.6	96.5	100.3	9.2	13.5	21.4	106.4	14.7	2.8	2.10E-16
ENSG00000115009	72.8	88.9	87.7	3.4	9.6	1.9	83.1	5.0	4.0	2.13E-16
ENSG00000181744	268.1	243.9	310.8	531.3	566.7	618.1	274.3	572.0	(1.1)	2.16E-16
ENSG00000187837	50.7	47.7	56.9	174.4	201.1	165.9	51.8	180.5	(1.8)	2.18E-16
ENSG00000131094	45.0	39.0	44.3	164.1	173.2	145.4	42.8	160.9	(1.9)	2.52E-16
ENSG00000105639	90.0	87.8	99.4	14.9	9.6	10.3	92.4	11.6	3.0	2.53E-16

ENSG00000156966	86.2	84.6	78.6	11.5	3.8	5.6	83.1	7.0	3.6	2.91E-16
ENSG00000069667	221.2	130.1	189.8	28.7	41.4	49.4	180.3	39.8	2.2	3.16E-16
ENSG00000147852	73.7	79.1	79.5	212.3	219.4	234.9	77.5	222.2	(1.5)	3.95E-16
ENSG00000160183	91.0	97.6	103.9	2.3	1.9	0.9	97.5	1.7	5.9	6.02E-16
ENSG00000133619	449.0	469.4	483.4	211.2	247.3	217.2	467.3	225.2	1.1	6.37E-16
ENSG00000106541	105.3	92.2	128.3	13.8	19.2	19.6	108.6	17.5	2.6	6.43E-16
ENSG00000164885	615.6	601.7	714.8	362.6	300.2	278.7	644.0	313.9	1.0	6.88E-16
ENSG00000056558	362.9	402.2	391.3	136.6	183.8	175.3	385.5	165.2	1.2	7.12E-16
ENSG00000231290	3.8	6.5	9.0	75.7	69.3	96.0	6.5	80.3	(3.6)	8.60E-16
ENSG00000178773	52.7	61.8	60.5	191.6	221.3	166.9	58.3	193.3	(1.7)	9.09E-16
ENSG00000121743	116.8	105.2	122.0	288.0	283.8	278.7	114.7	283.5	(1.3)	1.17E-15
ENSG00000149150	465.3	520.4	506.9	258.2	230.0	253.6	497.5	247.2	1.0	1.30E-15
ENSG00000079841	595.5	487.9	609.0	234.1	278.1	290.9	564.1	267.7	1.1	1.72E-15
ENSG00000112419	1660.2	1164.4	1621.1	584.1	807.3	725.3	1481.9	705.6	1.1	2.05E-15
ENSG00000177508	79.5	116.0	108.4	321.3	281.0	247.1	101.3	283.1	(1.5)	2.11E-15
ENSG00000131203	2.9	3.3	7.2	78.0	66.4	77.4	4.5	73.9	(4.0)	2.12E-15
ENSG00000146858	51.7	64.0	73.2	192.8	206.9	192.0	63.0	197.2	(1.6)	2.20E-15
ENSG00000047648	4.8	15.2	11.7	86.1	99.1	82.0	10.6	89.1	(3.1)	2.27E-15
ENSG00000144455	158.9	155.0	179.8	344.3	367.5	388.8	164.6	366.9	(1.2)	2.40E-15
ENSG00000124102	129.3	143.1	143.7	0.0	2.9	0.0	138.7	1.0	7.1	2.89E-15
ENSG00000228253	173.3	206.0	204.2	383.3	429.1	445.6	194.5	419.3	(1.1)	2.90E-15
ENSG00000100577	104.4	120.3	139.2	292.6	308.9	293.7	121.3	298.4	(1.3)	4.29E-15
ENSG00000146592	549.6	418.5	514.2	190.5	238.6	238.7	494.1	222.6	1.1	4.30E-15
ENSG00000214076	74.7	90.0	80.4	5.7	7.7	12.1	81.7	8.5	3.2	4.41E-15
ENSG00000065989	2.9	5.4	9.0	78.0	66.4	81.1	5.8	75.2	(3.7)	4.46E-15
ENSG00000167964	72.8	81.3	88.6	216.9	253.0	212.6	80.9	227.5	(1.5)	4.59E-15
ENSG00000156804	331.3	415.2	381.3	143.4	153.9	183.7	375.9	160.3	1.2	4.99E-15
ENSG00000087510	415.5	434.7	458.1	236.4	185.7	193.0	436.1	205.0	1.1	5.05E-15
ENSG00000141384	281.5	261.3	263.0	99.8	112.6	112.8	268.6	108.4	1.3	6.99E-15
ENSG00000275131	569.7	597.4	517.8	214.6	271.3	307.6	561.6	264.5	1.1	7.36E-15
ENSG00000169184	329.4	351.3	382.2	164.1	137.6	166.9	354.3	156.2	1.2	7.48E-15
ENSG00000105379	110.1	108.4	113.9	300.7	259.8	261.0	110.8	273.8	(1.3)	7.99E-15
ENSG00000183072	8.6	7.6	2.7	74.6	77.9	69.9	6.3	74.1	(3.6)	8.66E-15
ENSG00000162981	30.6	24.9	43.4	146.9	132.8	135.2	33.0	138.3	(2.1)	8.70E-15
ENSG00000257642	133.1	105.2	123.8	32.1	18.3	25.2	120.7	25.2	2.3	8.90E-15
ENSG00000064692	90.0	90.0	79.5	6.9	14.4	12.1	86.5	11.1	2.9	9.10E-15
ENSG00000272405	114.9	131.2	132.8	294.9	320.4	281.5	126.3	299.0	(1.2)	1.08E-14
ENSG00000146054	217.3	232.0	225.9	502.6	458.0	416.7	225.1	459.1	(1.0)	1.18E-14
ENSG00000171201	0.0	0.0	0.0	172.1	117.4	132.4	0.0	140.6	(9.6)	2.06E-14
ENSG00000185247	0.0	0.0	1.8	220.3	192.4	193.0	0.6	201.9	(8.3)	2.40E-14
ENSG00000120278	118.7	131.2	144.6	26.4	28.9	39.2	131.5	31.5	2.1	2.45E-14
ENSG00000187098	211.6	237.4	216.0	67.7	76.0	93.2	221.7	79.0	1.5	2.62E-14
ENSG00000127124	230.7	211.4	259.3	436.1	485.9	498.8	233.8	473.6	(1.0)	2.79E-14
ENSG00000132205	14.4	18.4	9.0	97.5	94.3	80.2	13.9	90.7	(2.7)	3.11E-14
ENSG00000165996	23.0	27.1	19.9	121.6	97.2	113.7	23.3	110.9	(2.3)	3.14E-14
ENSG00000197632	67.0	71.6	80.4	10.3	5.8	4.7	73.0	6.9	3.4	3.76E-14
ENSG00000138172	290.1	340.4	358.7	141.2	106.8	153.8	329.8	133.9	1.3	3.86E-14
ENSG00000184719	95.7	106.2	118.4	17.2	26.9	17.7	106.8	20.6	2.4	3.96E-14
ENSG00000268001	158.0	202.7	188.0	65.4	53.9	56.9	182.9	58.7	1.6	4.08E-14
ENSG00000149212	121.6	62.9	97.6	12.6	12.5	13.1	94.0	12.7	2.9	4.43E-14
ENSG00000107099	92.9	86.7	90.4	14.9	15.4	14.9	90.0	15.1	2.6	4.53E-14
ENSG00000145348	61.3	37.9	61.4	165.2	175.1	194.8	53.6	178.4	(1.7)	4.89E-14
ENSG00000256043	96.7	99.7	106.6	253.6	242.5	244.3	101.0	246.8	(1.3)	8.29E-14
ENSG00000113790	68.0	44.5	54.2	182.5	162.6	185.5	55.5	176.9	(1.7)	8.54E-14
ENSG00000118777	19.1	16.3	28.9	111.3	112.6	97.9	21.4	107.3	(2.3)	8.82E-14
ENSG00000159733	293.9	319.8	301.8	150.3	126.0	131.5	305.2	135.9	1.2	1.21E-13
ENSG00000108342	113.0	150.7	122.0	292.6	391.6	285.3	128.6	323.2	(1.3)	1.28E-13
ENSG00000164128	54.6	45.5	45.2	150.3	162.6	154.8	48.4	155.9	(1.7)	1.42E-13

ENSG00000078401	444.3	502.0	399.4	185.9	214.6	236.8	448.5	212.4	1.1	1.47E-13
ENSG00000124171	351.4	318.7	394.9	163.0	173.2	125.9	355.0	154.0	1.2	1.48E-13
ENSG00000188243	158.0	156.1	138.3	360.3	299.2	497.8	150.8	385.8	(1.4)	1.61E-13
ENSG00000184678	13.4	11.9	28.0	86.1	100.1	147.3	17.8	111.1	(2.6)	1.64E-13
ENSG00000157601	5019.0	4700.9	4700.7	1576.8	1094.9	1865.5	4806.8	1512.4	1.7	1.67E-13
ENSG00000171503	151.3	137.7	127.4	345.4	299.2	295.5	138.8	313.4	(1.2)	1.74E-13
ENSG00000179361	394.5	370.8	406.6	200.8	197.2	184.6	390.6	194.2	1.0	1.89E-13
ENSG00000189186	111.1	116.0	115.7	0.0	0.0	0.0	114.2	0.0	9.3	1.93E-13
ENSG00000174501	342.8	199.5	284.6	58.5	111.6	77.4	275.6	82.5	1.7	1.93E-13
ENSG00000213694	435.6	489.0	434.6	172.1	242.5	227.5	453.1	214.0	1.1	2.10E-13
ENSG00000166106	298.7	299.2	325.3	154.9	115.5	134.2	307.8	134.9	1.2	2.21E-13
ENSG00000229124	37.3	24.9	21.7	115.9	144.3	108.1	28.0	122.8	(2.1)	2.31E-13
ENSG00000128833	390.6	351.3	371.4	150.3	184.7	189.3	371.1	174.8	1.1	2.45E-13
ENSG00000171631	264.3	290.6	275.6	132.0	95.3	119.3	276.8	115.5	1.3	2.74E-13
ENSG00000159261	93.8	122.5	94.9	18.4	24.1	21.4	103.7	21.3	2.3	3.17E-13
ENSG00000163485	52.7	83.5	73.2	204.3	190.5	205.1	69.8	200.0	(1.5)	3.80E-13
ENSG00000107147	64.1	55.3	80.4	4.6	7.7	0.9	66.6	4.4	3.9	4.08E-13
ENSG00000108785	67.0	59.6	55.1	183.6	172.2	169.7	60.6	175.2	(1.5)	4.44E-13
ENSG00000153253	8.6	6.5	9.0	65.4	69.3	72.7	8.1	69.1	(3.1)	4.88E-13
ENSG00000119673	193.4	232.0	196.1	487.7	399.3	396.2	207.2	427.7	(1.0)	6.91E-13
ENSG00000163393	152.2	150.7	139.2	36.7	48.1	49.4	147.4	44.7	1.7	7.58E-13
ENSG00000135525	128.3	151.8	134.6	33.3	39.4	45.7	138.2	39.5	1.8	7.61E-13
ENSG00000239887	203.0	182.1	223.2	70.0	74.1	82.0	202.8	75.4	1.4	7.66E-13
ENSG00000164953	154.2	149.6	145.5	289.2	334.8	337.5	149.7	320.5	(1.1)	7.96E-13
ENSG00000162105	423.2	368.6	445.5	169.8	228.0	186.5	412.4	194.8	1.1	8.00E-13
ENSG00000147421	153.2	126.8	143.7	282.3	319.4	331.9	141.2	311.2	(1.1)	8.46E-13
ENSG00000163734	103.4	144.2	123.8	20.7	39.4	25.2	123.8	28.4	2.1	9.37E-13
ENSG00000115602	196.3	145.3	198.8	0.0	1.0	0.0	180.1	0.3	9.0	9.59E-13
ENSG00000125848	71.8	91.1	59.6	211.2	186.7	219.1	74.2	205.6	(1.5)	1.01E-12
ENSG00000141469	49.8	92.2	60.5	224.9	172.2	242.4	67.5	213.2	(1.7)	1.04E-12
ENSG00000167600	217.3	203.8	255.7	90.7	87.6	89.5	225.6	89.2	1.3	1.04E-12
ENSG00000146021	23.9	19.5	21.7	89.5	100.1	107.2	21.7	98.9	(2.2)	1.18E-12
ENSG00000178752	128.3	125.8	145.5	45.9	33.7	34.5	133.2	38.0	1.8	1.26E-12
ENSG00000176845	379.2	353.4	393.1	206.6	167.4	179.9	375.2	184.6	1.0	1.35E-12
ENSG00000102879	311.2	301.4	359.6	163.0	132.8	151.0	324.1	148.9	1.1	1.40E-12
ENSG00000206195	61.3	77.0	77.7	167.5	256.9	203.2	72.0	209.2	(1.5)	1.58E-12
ENSG00000177432	1.0	1.1	1.8	72.3	68.3	75.5	1.3	72.0	(5.8)	1.67E-12
ENSG00000244128	117.8	111.7	117.5	19.5	36.6	28.0	115.6	28.0	2.0	1.70E-12
ENSG00000173546	56.5	57.5	67.8	161.8	189.5	168.7	60.6	173.4	(1.5)	1.70E-12
ENSG00000106123	45.0	77.0	87.7	4.6	3.8	9.3	69.9	5.9	3.5	1.70E-12
ENSG00000175938	91.9	103.0	103.0	260.5	241.5	216.3	99.3	239.4	(1.3)	1.75E-12
ENSG00000186812	117.8	135.5	134.6	291.5	303.1	264.8	129.3	286.4	(1.1)	1.78E-12
ENSG00000137038	88.1	77.0	98.5	265.1	217.4	203.2	87.9	228.6	(1.4)	1.81E-12
ENSG00000134755	110.1	85.6	96.7	20.7	18.3	23.3	97.5	20.7	2.2	1.81E-12
ENSG00000204237	158.0	147.4	154.5	373.0	317.5	298.3	153.3	329.6	(1.1)	1.83E-12
ENSG00000185272	65.1	54.2	75.9	4.6	3.8	9.3	65.1	5.9	3.4	1.89E-12
ENSG00000125740	273.8	249.4	240.4	118.2	106.8	106.3	254.5	110.4	1.2	2.00E-12
ENSG00000254685	93.8	83.5	108.4	214.6	247.3	241.5	95.2	234.4	(1.3)	2.05E-12
ENSG00000179085	80.4	86.7	75.0	267.4	228.0	174.3	80.7	223.2	(1.5)	2.06E-12
ENSG00000109738	1.0	1.1	0.9	80.3	79.9	102.5	1.0	87.6	(6.5)	2.07E-12
ENSG00000185436	204.9	198.4	179.8	84.9	66.4	67.1	194.4	72.8	1.4	2.58E-12
ENSG00000154736	148.4	177.8	174.4	317.9	349.3	449.4	166.9	372.2	(1.2)	2.58E-12
ENSG00000101441	92.9	114.9	77.7	26.4	12.5	12.1	95.2	17.0	2.5	2.81E-12
ENSG00000064547	216.4	248.3	211.4	79.2	84.7	103.5	225.4	89.1	1.3	2.92E-12
ENSG00000120328	4.8	1.1	5.4	74.6	48.1	56.9	3.8	59.9	(3.9)	3.11E-12
ENSG00000133195	170.4	196.2	185.2	391.3	336.8	379.4	184.0	369.2	(1.0)	3.97E-12
ENSG00000180190	85.2	84.6	103.9	4.6	23.1	14.9	91.2	14.2	2.7	4.02E-12
ENSG00000107518	90.0	84.6	78.6	0.0	1.0	1.9	84.4	0.9	6.4	4.70E-12

ENSG00000164932	65.1	79.1	83.1	16.1	6.7	11.2	75.8	11.3	2.8	4.73E-12
ENSG00000006459	232.7	170.2	202.4	58.5	75.0	83.0	201.8	72.2	1.5	4.73E-12
ENSG00000164039	68.9	85.6	85.8	205.4	195.3	208.8	80.1	203.2	(1.3)	4.80E-12
ENSG00000149527	59.4	61.8	67.8	8.0	6.7	6.5	63.0	7.1	3.2	5.17E-12
ENSG00000162711	330.3	316.6	335.2	169.8	147.2	165.0	327.4	160.7	1.0	5.50E-12
ENSG00000277117	90.0	114.9	109.3	28.7	25.0	22.4	104.8	25.4	2.1	5.92E-12
ENSG00000236908	63.2	77.0	66.9	6.9	13.5	4.7	69.0	8.3	3.0	6.05E-12
ENSG00000249550	91.9	107.3	98.5	21.8	23.1	25.2	99.2	23.4	2.1	6.11E-12
ENSG00000205593	291.1	320.9	331.6	145.7	157.8	151.0	314.5	151.5	1.1	6.31E-12
ENSG00000141576	9.6	2.2	10.8	67.7	72.2	60.6	7.5	66.8	(3.1)	7.33E-12
ENSG00000176438	303.5	313.3	320.8	149.2	164.5	115.6	312.5	143.1	1.1	8.62E-12
ENSG00000238113	116.8	106.2	114.8	218.0	281.9	286.2	112.6	262.1	(1.2)	8.79E-12
ENSG00000087495	139.8	107.3	119.3	0.0	1.0	0.9	122.1	0.6	7.5	9.96E-12
ENSG00000166831	36.4	34.7	38.9	117.1	143.4	115.6	36.6	125.3	(1.8)	1.02E-11
ENSG00000167617	55.5	68.3	50.6	2.3	1.0	2.8	58.1	2.0	4.9	1.02E-11
ENSG00000116157	1.9	1.1	0.9	70.0	60.6	63.4	1.3	64.7	(5.6)	1.05E-11
ENSG00000168505	76.6	71.6	58.7	10.3	11.5	1.9	69.0	7.9	3.1	1.10E-11
ENSG00000205220	201.1	265.6	240.4	579.5	476.3	411.1	235.7	489.0	(1.1)	1.10E-11
ENSG00000140379	86.2	83.5	82.2	20.7	12.5	16.8	84.0	16.6	2.3	1.14E-11
ENSG00000251011	68.0	70.5	67.8	6.9	10.6	12.1	68.7	9.9	2.8	1.21E-11
ENSG00000249853	77.6	83.5	90.4	13.8	18.3	17.7	83.8	16.6	2.3	1.24E-11
ENSG00000140563	148.4	127.9	130.1	0.0	1.0	0.0	135.5	0.3	8.5	1.25E-11
ENSG00000104324	279.6	314.4	252.1	132.0	109.7	136.1	282.0	125.9	1.2	1.34E-11
ENSG00000276180	30.6	14.1	16.3	102.1	88.5	100.7	20.3	97.1	(2.2)	1.41E-11
ENSG00000175505	343.7	361.0	354.2	174.4	197.2	144.5	353.0	172.1	1.0	1.48E-11
ENSG00000120458	408.8	357.8	392.2	159.5	177.0	224.7	386.3	187.1	1.0	1.74E-11
ENSG00000101680	69.9	67.2	74.1	4.6	9.6	14.9	70.4	9.7	2.8	1.78E-11
ENSG00000253522	85.2	107.3	76.8	23.0	12.5	18.6	89.8	18.0	2.3	1.79E-11
ENSG00000162645	183.8	204.9	197.0	423.5	330.0	513.7	195.2	422.4	(1.1)	1.91E-11
ENSG00000135063	87.1	62.9	62.4	5.7	6.7	14.9	70.8	9.1	2.9	2.00E-11
ENSG00000147642	76.6	68.3	57.8	6.9	12.5	8.4	67.6	9.3	2.9	2.05E-11
ENSG00000281162	67.0	58.5	63.3	1.1	1.9	0.9	62.9	1.3	5.6	2.29E-11
ENSG00000056487	30.6	21.7	23.5	98.7	96.2	106.3	25.3	100.4	(2.0)	2.67E-11
ENSG00000113763	58.4	64.0	64.2	2.3	1.0	0.9	62.2	1.4	5.5	2.73E-11
ENSG00000154188	54.6	41.2	55.1	127.4	153.0	184.6	50.3	155.0	(1.6)	3.03E-11
ENSG00000234593	77.6	68.3	58.7	0.0	0.0	0.0	68.2	0.0	8.5	3.41E-11
ENSG00000231789	5.7	4.3	7.2	72.3	51.0	50.3	5.8	57.9	(3.3)	3.66E-11
ENSG00000198795	69.9	65.0	50.6	2.3	1.0	0.9	61.8	1.4	5.5	3.69E-11
ENSG00000169245	62.2	69.4	47.9	3.4	6.7	8.4	59.8	6.2	3.2	3.83E-11
ENSG00000166165	2.9	4.3	2.7	51.6	50.0	51.3	3.3	51.0	(4.0)	4.06E-11
ENSG00000151632	0.0	0.0	0.0	63.1	56.8	75.5	0.0	65.1	(8.5)	4.14E-11
ENSG00000134780	257.6	303.6	281.0	144.6	132.8	111.9	280.7	129.7	1.1	4.23E-11
ENSG00000258976	39.3	39.0	38.0	146.9	114.5	117.5	38.7	126.3	(1.7)	4.57E-11
ENSG00000113578	73.7	72.6	65.1	18.4	4.8	5.6	70.5	9.6	2.9	4.78E-11
ENSG00000164308	153.2	137.7	160.8	277.7	325.2	323.5	150.6	308.8	(1.0)	5.29E-11
ENSG00000183760	121.6	92.2	104.8	29.8	27.9	28.0	106.2	28.6	1.9	5.35E-11
ENSG00000215845	86.2	93.2	90.4	231.8	203.0	198.6	89.9	211.1	(1.2)	5.65E-11
ENSG00000134321	367.7	395.7	319.0	181.3	145.3	196.7	360.8	174.4	1.0	6.17E-11
ENSG00000171408	22.0	21.7	24.4	81.5	100.1	97.0	22.7	92.8	(2.0)	6.54E-11
ENSG00000141441	69.9	52.0	59.6	165.2	169.3	155.7	60.5	163.4	(1.4)	6.70E-11
ENSG00000187372	4.8	7.6	6.3	51.6	56.8	58.7	6.2	55.7	(3.2)	7.07E-11
ENSG00000172296	11.5	11.9	8.1	67.7	59.7	70.9	10.5	66.1	(2.7)	7.27E-11
ENSG00000135324	1.0	4.3	1.8	58.5	45.2	48.5	2.4	50.7	(4.5)	7.71E-11
ENSG00000151376	336.1	300.3	375.9	163.0	180.9	160.4	337.4	168.1	1.0	7.75E-11
ENSG00000257219	91.0	57.5	72.3	14.9	12.5	10.3	73.6	12.6	2.6	8.26E-11
ENSG00000151240	154.2	180.0	225.9	368.4	410.8	366.4	186.7	381.9	(1.0)	8.34E-11
ENSG00000170537	60.3	49.9	62.4	165.2	137.6	178.1	57.5	160.3	(1.5)	9.06E-11
ENSG00000135298	40.2	39.0	32.5	119.3	116.4	122.1	37.3	119.3	(1.7)	9.29E-11

ENSG00000170775	68.9	74.8	58.7	1.1	0.0	1.9	67.5	1.0	6.1	1.07E-10
ENSG00000038002	136.0	125.8	126.5	266.2	256.9	278.7	129.4	267.3	(1.0)	1.21E-10
ENSG00000104892	50.7	42.3	62.4	4.6	4.8	2.8	51.8	4.1	3.7	1.22E-10
ENSG00000121236	158.0	146.4	159.9	50.5	58.7	62.5	154.8	57.2	1.4	1.36E-10
ENSG00000126785	61.3	66.1	57.8	150.3	159.7	174.3	61.7	161.5	(1.4)	1.36E-10
ENSG00000120925	106.3	107.3	124.7	213.4	269.4	271.3	112.8	251.4	(1.2)	1.50E-10
ENSG00000001561	112.0	91.1	120.2	198.5	294.4	287.1	107.8	260.0	(1.3)	1.51E-10
ENSG00000183049	98.6	109.5	105.7	18.4	33.7	30.8	104.6	27.6	1.9	1.57E-10
ENSG00000101955	81.4	62.9	63.3	12.6	8.7	14.0	69.2	11.8	2.6	1.61E-10
ENSG00000181826	304.5	365.4	355.1	166.4	150.1	193.0	341.7	169.8	1.0	1.72E-10
ENSG00000120279	116.8	97.6	90.4	1.1	0.0	0.0	101.6	0.4	8.1	1.76E-10
ENSG00000146192	3.8	6.5	1.8	48.2	50.0	51.3	4.0	49.8	(3.7)	1.78E-10
ENSG00000110042	91.0	93.2	95.8	19.5	29.8	20.5	93.3	23.3	2.0	1.80E-10
ENSG00000112852	68.9	56.4	42.5	9.2	4.8	2.8	55.9	5.6	3.4	2.04E-10
ENSG00000109794	5.7	4.3	6.3	51.6	45.2	61.5	5.5	52.8	(3.3)	2.10E-10
ENSG00000082397	56.5	44.5	47.0	0.0	3.8	2.8	49.3	2.2	4.4	2.23E-10
ENSG00000170786	45.0	61.8	61.4	0.0	0.0	0.0	56.1	0.0	8.2	2.26E-10
ENSG00000006016	6.7	7.6	4.5	65.4	41.4	59.7	6.3	55.5	(3.2)	2.55E-10
ENSG00000119640	107.2	82.4	94.9	216.9	220.3	208.8	94.8	215.4	(1.2)	2.64E-10
ENSG00000145362	111.1	117.1	132.8	228.4	264.6	281.5	120.3	258.2	(1.1)	2.64E-10
ENSG00000262879	78.5	71.6	91.3	202.0	198.2	179.0	80.4	193.1	(1.3)	2.66E-10
ENSG00000176209	48.8	64.0	50.6	143.4	163.6	140.8	54.5	149.3	(1.5)	2.81E-10
ENSG00000278970	58.4	72.6	64.2	164.1	154.9	179.0	65.1	166.0	(1.4)	2.87E-10
ENSG00000196517	70.9	88.9	96.7	234.1	173.2	226.5	85.5	211.3	(1.3)	2.89E-10
ENSG00000172602	53.6	73.7	73.2	4.6	12.5	13.1	66.8	10.1	2.7	2.97E-10
ENSG00000244486	13.4	4.3	8.1	52.8	72.2	61.5	8.6	62.2	(2.8)	3.00E-10
ENSG00000134709	94.8	49.9	93.1	14.9	14.4	14.0	79.2	14.4	2.5	3.00E-10
ENSG00000166035	12.4	9.8	10.8	63.1	58.7	70.9	11.0	64.2	(2.5)	3.58E-10
ENSG00000152078	189.6	187.6	198.8	79.2	88.5	80.2	192.0	82.6	1.2	3.61E-10
ENSG00000153391	277.7	272.1	249.4	129.7	139.5	120.3	266.4	129.8	1.0	3.79E-10
ENSG00000157554	20.1	28.2	25.3	94.1	79.9	110.0	24.5	94.7	(2.0)	4.44E-10
ENSG00000197410	5.7	9.8	7.2	53.9	57.7	55.0	7.6	55.6	(2.9)	4.46E-10
ENSG00000180875	37.3	52.0	46.1	142.3	142.4	115.6	45.2	133.4	(1.6)	4.51E-10
ENSG00000160180	55.5	54.2	43.4	8.0	1.9	4.7	51.0	4.9	3.4	5.21E-10
ENSG00000183873	65.1	60.7	54.2	0.0	0.0	2.8	60.0	0.9	5.9	5.40E-10
ENSG00000163131	211.6	210.3	197.9	90.7	67.4	102.5	206.6	86.9	1.3	5.47E-10
ENSG00000224597	120.6	100.8	122.9	213.4	265.6	271.3	114.8	250.1	(1.1)	5.52E-10
ENSG00000137462	264.3	246.1	291.9	121.6	131.8	138.0	267.4	130.5	1.0	5.96E-10
ENSG00000102362	135.0	138.8	108.4	290.3	265.6	245.2	127.4	267.0	(1.1)	6.19E-10
ENSG00000178498	46.9	20.6	38.0	112.5	111.6	151.0	35.2	125.0	(1.8)	6.66E-10
ENSG00000179855	81.4	83.5	88.6	19.5	17.3	25.2	84.5	20.7	2.0	6.76E-10
ENSG00000184012	77.6	94.3	73.2	0.0	0.0	1.9	81.7	0.6	6.9	6.99E-10
ENSG00000118971	71.8	91.1	96.7	0.0	1.0	0.0	86.5	0.3	7.9	7.25E-10
ENSG00000137834	110.1	119.3	94.0	280.0	231.9	209.8	107.8	240.5	(1.2)	8.15E-10
ENSG00000261934	56.5	53.1	59.6	151.5	136.6	154.8	56.4	147.6	(1.4)	8.17E-10
ENSG00000198105	107.2	99.7	109.3	204.3	227.1	254.5	105.4	228.6	(1.1)	8.29E-10
ENSG00000217801	227.9	236.3	216.0	110.2	96.2	111.9	226.7	106.1	1.1	8.69E-10
ENSG00000183172	203.0	181.1	161.7	451.0	362.7	306.7	181.9	373.5	(1.0)	9.15E-10
ENSG00000101443	80.4	109.5	96.7	33.3	21.2	20.5	95.5	25.0	1.9	9.21E-10
ENSG00000145911	38.3	44.5	59.6	1.1	2.9	5.6	47.5	3.2	3.8	9.89E-10
ENSG00000197557	97.7	111.7	95.8	211.2	215.5	228.4	101.7	218.4	(1.1)	1.07E-09
ENSG00000241343	296.8	247.2	222.3	94.1	132.8	115.6	255.4	114.2	1.2	1.15E-09
ENSG00000130775	254.7	298.1	275.6	135.4	102.0	151.0	276.1	129.5	1.1	1.17E-09
ENSG00000128016	316.0	323.1	300.0	188.2	128.9	152.0	313.0	156.4	1.0	1.32E-09
ENSG00000130720	1.0	4.3	4.5	60.8	31.8	49.4	3.3	47.3	(3.9)	1.32E-09
ENSG00000254635	96.7	92.2	101.2	189.3	244.4	210.7	96.7	214.8	(1.2)	1.34E-09
ENSG00000137273	23.9	22.8	44.3	102.1	98.1	137.0	30.3	112.4	(1.9)	1.41E-09
ENSG00000231453	34.5	53.1	38.9	123.9	130.9	118.4	42.1	124.4	(1.6)	1.42E-09

ENSG00000184985	57.4	59.6	59.6	3.4	13.5	8.4	58.9	8.4	2.8	1.42E-09
ENSG00000065621	21.1	20.6	21.7	103.3	87.6	67.1	21.1	86.0	(2.0)	1.46E-09
ENSG00000149548	175.2	165.9	159.9	67.7	76.0	63.4	167.0	69.0	1.3	1.49E-09
ENSG00000155974	91.0	80.2	77.7	13.8	26.0	19.6	83.0	19.8	2.1	1.57E-09
ENSG00000171873	45.0	46.6	40.7	2.3	1.9	1.9	44.1	2.0	4.5	1.59E-09
ENSG00000168389	236.5	211.4	215.1	110.2	93.3	107.2	221.0	103.6	1.1	1.75E-09
ENSG00000221926	61.3	88.9	110.2	235.3	217.4	192.0	86.8	214.9	(1.3)	1.76E-09
ENSG00000120162	49.8	48.8	49.7	2.3	2.9	9.3	49.4	4.8	3.3	1.97E-09
ENSG00000114473	67.0	51.0	42.5	157.2	126.0	162.2	53.5	148.5	(1.5)	2.09E-09
ENSG00000099256	27.8	55.3	35.2	130.8	112.6	129.6	39.4	124.3	(1.7)	2.09E-09
ENSG00000178033	5.7	6.5	10.8	56.2	43.3	66.2	7.7	55.2	(2.8)	2.42E-09
ENSG00000222009	54.6	69.4	53.3	140.0	147.2	165.9	59.1	151.1	(1.4)	2.51E-09
ENSG00000244161	150.3	132.3	135.5	32.1	54.8	57.8	139.4	48.3	1.5	2.58E-09
ENSG00000243896	46.9	35.8	54.2	4.6	4.8	2.8	45.6	4.1	3.5	2.78E-09
ENSG00000169302	2.9	8.7	2.7	34.4	46.2	69.0	4.8	49.9	(3.4)	2.97E-09
ENSG00000154678	94.8	62.9	77.7	12.6	21.2	19.6	78.5	17.8	2.1	3.54E-09
ENSG00000275896	45.0	64.0	33.4	2.3	1.0	0.9	47.5	1.4	5.1	3.58E-09
ENSG00000057657	48.8	51.0	43.4	8.0	3.8	4.7	47.7	5.5	3.1	3.59E-09
ENSG00000117707	100.5	86.7	112.0	20.7	28.9	36.4	99.8	28.6	1.8	3.99E-09
ENSG00000285108	49.8	44.5	34.3	4.6	1.9	0.9	42.9	2.5	4.2	4.07E-09
ENSG00000116745	66.1	62.9	73.2	1.1	1.0	0.0	67.4	0.7	6.6	4.21E-09
ENSG00000140104	136.0	109.5	100.3	233.0	232.8	256.4	115.3	240.7	(1.1)	4.36E-09
ENSG00000083814	4.8	2.2	2.7	37.9	42.3	45.7	3.2	42.0	(3.7)	4.51E-09
ENSG00000137507	2.9	11.9	3.6	52.8	46.2	53.1	6.1	50.7	(3.1)	4.56E-09
ENSG00000153993	139.8	95.4	119.3	203.1	292.5	315.1	118.2	270.2	(1.2)	4.72E-09
ENSG00000184574	13.4	18.4	18.1	76.9	74.1	64.3	16.6	71.8	(2.1)	4.75E-09
ENSG00000104783	18.2	21.7	16.3	82.6	72.2	71.8	18.7	75.5	(2.0)	4.95E-09
ENSG00000278828	4.8	1.1	3.6	50.5	32.7	45.7	3.2	43.0	(3.7)	5.14E-09
ENSG00000038427	3916.0	3436.8	4227.2	1273.8	1243.1	1894.4	3860.0	1470.4	1.4	5.25E-09
ENSG00000064309	76.6	94.3	80.4	20.7	20.2	26.1	83.8	22.3	1.9	5.38E-09
ENSG00000136002	67.0	77.0	66.0	21.8	10.6	13.1	70.0	15.1	2.2	5.56E-09
ENSG00000113369	877.0	822.9	843.1	1668.6	2137.0	2854.6	847.7	2220.0	(1.4)	5.65E-09
ENSG00000131737	45.0	61.8	63.3	5.7	13.5	0.9	56.7	6.7	3.1	6.36E-09
ENSG00000151692	82.3	94.3	76.8	26.4	18.3	24.2	84.5	23.0	1.9	6.79E-09
ENSG00000178772	32.6	37.9	45.2	0.0	0.0	0.0	38.6	0.0	7.7	6.84E-09
ENSG00000077454	225.0	188.6	185.2	102.1	77.9	89.5	199.6	89.9	1.2	6.90E-09
ENSG00000119227	51.7	59.6	55.1	158.4	120.3	151.0	55.5	143.2	(1.4)	7.02E-09
ENSG00000262580	14.4	24.9	15.4	62.0	76.0	95.1	18.2	77.7	(2.1)	7.06E-09
ENSG00000134259	69.9	41.2	57.8	4.6	12.5	7.5	56.3	8.2	2.8	7.74E-09
ENSG00000130413	46.9	34.7	48.8	2.3	1.0	0.9	43.5	1.4	5.0	7.74E-09
ENSG00000152402	1.0	8.7	7.2	49.3	38.5	60.6	5.6	49.5	(3.2)	9.16E-09
ENSG00000165029	118.7	146.4	130.1	41.3	52.9	53.1	131.7	49.1	1.4	9.29E-09
ENSG00000076770	73.7	52.0	62.4	0.0	1.0	0.9	62.7	0.6	6.6	9.48E-09
ENSG00000171105	97.7	101.9	79.5	23.0	18.3	35.4	93.0	25.6	1.9	1.05E-08
ENSG00000117245	47.9	48.8	57.8	3.4	11.5	6.5	51.5	7.2	2.8	1.11E-08
ENSG00000253537	4.8	1.1	0.9	48.2	36.6	35.4	2.3	40.1	(4.1)	1.15E-08
ENSG00000243137	14.4	16.3	9.9	65.4	54.8	71.8	13.5	64.0	(2.3)	1.16E-08
ENSG00000182557	48.8	36.9	55.1	2.3	0.0	0.9	46.9	1.1	5.5	1.21E-08
ENSG00000081189	54.6	52.0	77.7	130.8	158.8	196.7	61.4	162.1	(1.4)	1.23E-08
ENSG00000126217	60.3	65.0	56.9	0.0	0.0	0.9	60.8	0.3	7.4	1.36E-08
ENSG00000153283	1.0	1.1	0.9	36.7	38.5	63.4	1.0	46.2	(5.6)	1.38E-08
ENSG00000114251	45.0	61.8	55.1	5.7	5.8	13.1	54.0	8.2	2.7	1.39E-08
ENSG00000162444	48.8	67.2	56.9	10.3	9.6	12.1	57.7	10.7	2.4	1.39E-08
ENSG00000119508	47.9	53.1	66.0	9.2	7.7	12.1	55.7	9.7	2.5	1.44E-08
ENSG00000111679	212.6	253.7	270.2	110.2	118.3	133.3	245.5	120.6	1.0	1.45E-08
ENSG00000161653	46.9	54.2	39.8	151.5	111.6	122.1	47.0	128.4	(1.5)	1.48E-08
ENSG00000177096	108.2	127.9	134.6	306.4	242.5	221.9	123.6	256.9	(1.1)	1.54E-08
ENSG00000110693	60.3	64.0	59.6	6.9	14.4	14.9	61.3	12.1	2.3	1.63E-08

ENSG00000185621	106.3	119.3	111.1	206.6	221.3	253.6	112.2	227.1	(1.0)	1.68E-08
ENSG00000154760	129.3	109.5	133.7	21.8	54.8	41.0	124.2	39.2	1.6	1.71E-08
ENSG00000163810	43.1	45.5	38.9	3.4	6.7	2.8	42.5	4.3	3.3	1.77E-08
ENSG00000163082	52.7	68.3	61.4	11.5	16.4	7.5	60.8	11.8	2.4	1.80E-08
ENSG00000147180	0.0	3.3	0.0	40.2	52.9	40.1	1.1	44.4	(5.5)	1.91E-08
ENSG00000104177	49.8	29.3	41.6	2.3	1.0	4.7	40.2	2.6	3.9	2.03E-08
ENSG00000184545	50.7	53.1	50.6	6.9	8.7	10.3	51.5	8.6	2.6	2.09E-08
ENSG00000121361	3.8	0.0	2.7	33.3	29.8	56.9	2.2	40.0	(4.2)	2.25E-08
ENSG00000276386	88.1	156.1	146.4	306.4	408.0	229.3	130.2	314.6	(1.3)	2.40E-08
ENSG00000130612	36.4	32.5	29.8	0.0	0.0	0.0	32.9	0.0	7.5	2.68E-08
ENSG00000115525	103.4	94.3	99.4	34.4	30.8	35.4	99.0	33.5	1.6	2.76E-08
ENSG00000100583	19.1	14.1	16.3	70.0	59.7	74.6	16.5	68.1	(2.0)	2.80E-08
ENSG00000179403	23.0	21.7	32.5	97.5	112.6	67.1	25.7	92.4	(1.8)	2.89E-08
ENSG00000168772	0.0	2.2	0.9	35.6	42.3	49.4	1.0	42.4	(5.4)	2.96E-08
ENSG00000142408	44.0	20.6	58.7	2.3	1.9	2.8	41.1	2.3	4.1	3.09E-08
ENSG00000231672	47.9	41.2	32.5	6.9	1.9	1.9	40.5	3.6	3.6	3.18E-08
ENSG00000270605	6.7	3.3	9.0	42.5	55.8	42.0	6.3	46.7	(2.9)	3.18E-08
ENSG00000008517	42.1	51.0	42.5	9.2	2.9	5.6	45.2	5.9	3.0	3.31E-08
ENSG00000225889	79.5	74.8	80.4	8.0	25.0	23.3	78.2	18.8	2.0	3.39E-08
ENSG00000115112	52.7	53.1	56.0	1.1	0.0	0.0	53.9	0.4	7.2	3.51E-08
ENSG00000223478	29.7	37.9	27.1	126.2	86.6	87.6	31.6	100.2	(1.7)	3.90E-08
ENSG00000103253	144.6	145.3	150.9	68.9	57.7	63.4	146.9	63.3	1.2	4.05E-08
ENSG00000103241	4.8	10.8	5.4	44.8	41.4	55.9	7.0	47.4	(2.8)	4.06E-08
ENSG00000189050	104.4	104.1	102.1	188.2	203.0	251.7	103.5	214.3	(1.1)	4.08E-08
ENSG00000131188	121.6	107.3	106.6	275.4	203.0	214.4	111.9	231.0	(1.0)	4.14E-08
ENSG00000108786	106.3	113.8	95.8	205.4	234.8	198.6	105.3	212.9	(1.0)	4.45E-08
ENSG00000104381	76.6	68.3	71.4	134.3	182.8	180.9	72.1	166.0	(1.2)	4.50E-08
ENSG00000054983	42.1	75.9	67.8	11.5	10.6	14.9	61.9	12.3	2.3	4.66E-08
ENSG00000084636	45.0	75.9	76.8	12.6	11.5	17.7	65.9	14.0	2.2	4.82E-08
ENSG00000279821	27.8	53.1	32.5	109.0	112.6	110.0	37.8	110.5	(1.6)	5.27E-08
ENSG00000237624	3.8	0.0	0.9	40.2	34.6	34.5	1.6	36.4	(4.5)	5.36E-08
ENSG00000180447	42.1	52.0	47.9	6.9	10.6	2.8	47.4	6.8	2.8	5.39E-08
ENSG00000169946	68.9	44.5	63.3	140.0	153.9	138.9	58.9	144.3	(1.3)	5.59E-08
ENSG00000162882	0.0	0.0	0.0	27.5	29.8	30.8	0.0	29.4	(7.4)	5.79E-08
ENSG00000173166	265.2	175.6	216.0	93.0	105.8	107.2	218.9	102.0	1.1	5.84E-08
ENSG00000130600	1.0	3.3	2.7	27.5	44.3	36.4	2.3	36.1	(4.0)	6.07E-08
ENSG00000198077	35.4	26.0	28.0	0.0	0.0	0.0	29.8	0.0	7.3	6.47E-08
ENSG00000182022	167.6	173.5	176.2	80.3	57.7	90.4	172.4	76.2	1.2	6.49E-08
ENSG00000172594	80.4	100.8	94.0	17.2	27.9	36.4	91.7	27.2	1.7	6.49E-08
ENSG00000134532	8.6	11.9	14.5	53.9	43.3	83.9	11.7	60.4	(2.4)	7.25E-08
ENSG00000110944	58.4	52.0	63.3	11.5	12.5	14.0	57.9	12.7	2.2	7.27E-08
ENSG00000160179	37.3	48.8	30.7	1.1	1.0	6.5	39.0	2.9	3.7	7.84E-08
ENSG00000142619	0.0	2.2	0.0	51.6	72.2	29.8	0.7	51.2	(6.3)	7.87E-08
ENSG00000134769	25.9	30.4	30.7	0.0	0.0	0.0	29.0	0.0	7.3	7.96E-08
ENSG00000236453	114.9	81.3	115.7	40.2	27.9	37.3	104.0	35.1	1.6	8.04E-08
ENSG00000129422	120.6	85.6	98.5	27.5	36.6	38.2	101.6	34.1	1.6	8.14E-08
ENSG00000176244	24.9	27.1	22.6	84.9	80.8	76.4	24.9	80.7	(1.7)	8.18E-08
ENSG00000230316	113.0	140.9	131.9	55.1	50.0	51.3	128.6	52.1	1.3	8.30E-08
ENSG00000110799	30.6	35.8	40.7	2.3	3.8	0.9	35.7	2.4	3.9	8.58E-08
ENSG00000182782	5.7	6.5	5.4	49.3	40.4	37.3	5.9	42.3	(2.8)	8.67E-08
ENSG00000163395	33.5	32.5	47.9	1.1	5.8	2.8	38.0	3.2	3.5	9.64E-08
ENSG00000108798	35.4	40.1	41.6	0.0	1.0	1.9	39.0	0.9	5.3	9.66E-08
ENSG00000198934	74.7	77.0	53.3	165.2	163.6	142.6	68.3	157.2	(1.2)	9.78E-08
ENSG00000138435	31.6	39.0	36.1	0.0	3.8	0.9	35.6	1.6	4.4	1.01E-07
ENSG00000115165	28.7	36.9	44.3	1.1	0.0	2.8	36.6	1.3	4.8	1.03E-07
ENSG00000105605	93.8	75.9	99.4	36.7	22.1	26.1	89.7	28.3	1.7	1.03E-07
ENSG00000112294	187.7	165.9	159.9	79.2	77.9	83.9	171.2	80.3	1.1	1.05E-07
ENSG00000103089	45.0	40.1	34.3	2.3	7.7	2.8	39.8	4.3	3.2	1.12E-07

ENSG00000011201	42.1	27.1	35.2	97.5	92.4	111.9	34.8	100.6	(1.5)	1.12E-07
ENSG00000186446	0.0	0.0	0.0	24.1	33.7	24.2	0.0	27.3	(7.2)	1.14E-07
ENSG00000271605	12.4	7.6	7.2	59.7	36.6	58.7	9.1	51.7	(2.5)	1.14E-07
ENSG00000174059	86.2	72.6	78.6	17.2	28.9	23.3	79.1	23.1	1.8	1.17E-07
ENSG00000232759	52.7	27.1	34.3	2.3	4.8	2.8	38.0	3.3	3.5	1.20E-07
ENSG00000062524	4.8	3.3	5.4	42.5	37.5	35.4	4.5	38.5	(3.1)	1.21E-07
ENSG00000187994	51.7	51.0	33.4	10.3	3.8	5.6	45.4	6.6	2.8	1.28E-07
ENSG00000187583	175.2	191.9	206.9	94.1	84.7	101.6	191.3	93.5	1.0	1.30E-07
ENSG00000234409	38.3	31.4	46.1	99.8	108.7	108.1	38.6	105.6	(1.4)	1.31E-07
ENSG00000132639	5.7	5.4	9.0	34.4	44.3	55.9	6.7	44.9	(2.7)	1.34E-07
ENSG00000237807	105.3	87.8	101.2	223.8	179.9	196.7	98.1	200.1	(1.0)	1.34E-07
ENSG00000164638	4.8	6.5	4.5	42.5	38.5	38.2	5.3	39.7	(2.9)	1.34E-07
ENSG00000142920	53.6	68.3	63.3	164.1	123.2	148.2	61.7	145.2	(1.2)	1.38E-07
ENSG00000169570	80.4	81.3	75.9	150.3	168.4	188.3	79.2	169.0	(1.1)	1.40E-07
ENSG00000071073	33.5	20.6	28.0	0.0	0.0	0.0	27.4	0.0	7.2	1.40E-07
ENSG00000138311	36.4	35.8	29.8	87.2	99.1	101.6	34.0	96.0	(1.5)	1.41E-07
ENSG00000168702	6.7	11.9	9.0	50.5	41.4	56.9	9.2	49.6	(2.4)	1.47E-07
ENSG00000104213	99.6	97.6	90.4	211.2	185.7	181.8	95.8	192.9	(1.0)	1.53E-07
ENSG00000155629	74.7	80.2	87.7	13.8	29.8	26.1	80.9	23.2	1.8	1.62E-07
ENSG00000130755	103.4	116.0	99.4	36.7	42.3	41.0	106.3	40.0	1.4	1.66E-07
ENSG00000105929	34.5	39.0	28.0	1.1	1.9	1.9	33.8	1.6	4.3	1.67E-07
ENSG00000136842	155.1	225.5	197.0	82.6	95.3	91.4	192.5	89.7	1.1	1.68E-07
ENSG00000038295	169.5	172.4	174.4	82.6	80.8	86.7	172.1	83.4	1.0	1.73E-07
ENSG00000180613	38.3	23.9	40.7	2.3	1.0	2.8	34.3	2.0	4.1	1.79E-07
ENSG00000147697	117.8	85.6	92.2	26.4	44.3	17.7	98.5	29.5	1.7	1.80E-07
ENSG00000179455	28.7	39.0	34.3	1.1	3.8	1.9	34.0	2.3	3.9	1.87E-07
ENSG00000115590	54.6	41.2	40.7	0.0	1.9	0.0	45.5	0.6	6.1	1.88E-07
ENSG00000177839	17.2	21.7	28.0	78.0	70.2	79.2	22.3	75.8	(1.8)	1.91E-07
ENSG00000154262	1.9	3.3	4.5	28.7	38.5	37.3	3.2	34.8	(3.4)	2.10E-07
ENSG00000154096	34.5	49.9	38.9	4.6	4.8	7.5	41.1	5.6	2.9	2.24E-07
ENSG00000172059	172.3	167.0	165.4	93.0	64.5	80.2	168.2	79.2	1.1	2.85E-07
ENSG00000134339	34.5	35.8	28.9	1.1	1.0	1.9	33.1	1.3	4.6	2.88E-07
ENSG00000102174	10.5	6.5	8.1	39.0	50.0	49.4	8.4	46.2	(2.5)	2.93E-07
ENSG00000170629	38.3	43.4	56.9	99.8	136.6	121.2	46.2	119.2	(1.4)	3.23E-07
ENSG00000166922	49.8	61.8	56.9	17.2	9.6	12.1	56.2	13.0	2.1	3.24E-07
ENSG00000259849	16.3	26.0	32.5	0.0	0.0	0.0	24.9	0.0	7.1	3.48E-07
ENSG00000134317	70.9	57.5	57.8	18.4	16.4	14.0	62.0	16.2	1.9	3.49E-07
ENSG00000079385	43.1	64.0	56.9	128.5	123.2	137.0	54.7	129.6	(1.2)	3.50E-07
ENSG00000010361	40.2	46.6	56.9	122.8	115.5	115.6	47.9	118.0	(1.3)	3.78E-07
ENSG00000183378	51.7	31.4	38.0	0.0	1.0	0.0	40.4	0.3	6.8	3.78E-07
ENSG00000185761	153.2	144.2	160.8	63.1	71.2	78.3	152.7	70.9	1.1	3.90E-07
ENSG00000102755	32.6	53.1	23.5	0.0	1.9	0.9	36.4	1.0	5.2	3.92E-07
ENSG00000165507	226.0	245.0	244.0	123.9	85.6	145.4	238.3	118.3	1.0	3.94E-07
ENSG00000111490	44.0	39.0	39.8	9.2	2.9	6.5	40.9	6.2	2.8	4.21E-07
ENSG00000261716	53.6	47.7	49.7	120.5	108.7	131.5	50.3	120.2	(1.3)	4.31E-07
ENSG00000154328	84.3	72.6	82.2	187.1	144.3	173.4	79.7	168.3	(1.1)	4.40E-07
ENSG00000107159	1.0	2.2	0.9	32.1	27.9	33.6	1.3	31.2	(4.6)	4.58E-07
ENSG00000275173	22.0	24.9	23.5	0.0	0.0	0.0	23.5	0.0	7.0	4.60E-07
ENSG00000086300	128.3	108.4	116.6	59.7	41.4	42.0	117.8	47.7	1.3	4.67E-07
ENSG00000212916	24.9	17.3	28.9	0.0	0.0	0.0	23.7	0.0	7.0	4.68E-07
ENSG00000127528	172.3	147.4	146.4	80.3	57.7	75.5	155.4	71.2	1.1	4.71E-07
ENSG00000228451	18.2	19.5	26.2	55.1	74.1	96.0	21.3	75.1	(1.8)	4.84E-07
ENSG00000107890	105.3	68.3	105.7	160.7	212.6	234.0	93.1	202.4	(1.1)	5.17E-07
ENSG00000176826	89.0	129.0	115.7	34.4	50.0	41.0	111.2	41.8	1.4	5.18E-07
ENSG00000170954	6.7	3.3	3.6	25.2	49.1	38.2	4.5	37.5	(3.1)	5.44E-07
ENSG00000179913	32.6	33.6	27.1	1.1	1.0	2.8	31.1	1.6	4.2	5.48E-07
ENSG00000233143	28.7	32.5	35.2	0.0	3.8	0.0	32.2	1.3	4.6	6.00E-07
ENSG00000145358	80.4	77.0	70.5	27.5	24.1	22.4	76.0	24.7	1.6	6.16E-07

ENSG00000233639	17.2	33.6	19.0	0.0	0.0	0.0	23.3	0.0	7.0	6.50E-07
ENSG00000171435	41.2	58.5	60.5	13.8	2.9	14.0	53.4	10.2	2.4	6.92E-07
ENSG00000261371	14.4	17.3	25.3	80.3	61.6	62.5	19.0	68.1	(1.8)	7.03E-07
ENSG00000149243	1.0	3.3	3.6	35.6	24.1	35.4	2.6	31.7	(3.6)	7.09E-07
ENSG00000164619	65.1	58.5	75.9	24.1	15.4	17.7	66.5	19.1	1.8	7.27E-07
ENSG00000105997	177.1	165.9	165.4	78.0	86.6	88.6	169.5	84.4	1.0	7.31E-07
ENSG00000073849	132.1	145.3	138.3	55.1	63.5	69.9	138.6	62.8	1.1	7.38E-07
ENSG00000172086	51.7	49.9	56.0	122.8	105.8	143.6	52.5	124.1	(1.2)	7.57E-07
ENSG00000187398	3.8	0.0	1.8	23.0	26.0	46.6	1.9	31.8	(4.0)	7.75E-07
ENSG00000138136	135.0	99.7	115.7	40.2	52.0	50.3	116.8	47.5	1.3	8.06E-07
ENSG00000074771	23.9	22.8	19.0	0.0	0.0	0.0	21.9	0.0	6.9	8.37E-07
ENSG00000116771	1.9	1.1	2.7	27.5	29.8	30.8	1.9	29.4	(3.9)	8.96E-07
ENSG00000272668	23.0	32.5	20.8	78.0	90.4	67.1	25.4	78.5	(1.6)	9.20E-07
ENSG00000171813	91.0	83.5	127.4	37.9	41.4	30.8	100.6	36.7	1.5	9.33E-07
ENSG00000100626	1.9	3.3	0.9	36.7	29.8	23.3	2.0	30.0	(3.9)	9.58E-07
ENSG00000048052	133.1	133.4	131.9	45.9	75.0	47.5	132.8	56.2	1.2	1.01E-06
ENSG00000125207	36.4	34.7	39.8	2.3	0.0	0.0	36.9	0.8	5.8	1.03E-06
ENSG00000176406	39.3	40.1	47.0	5.7	9.6	7.5	42.1	7.6	2.5	1.06E-06
ENSG00000095397	42.1	39.0	42.5	97.5	98.1	110.9	41.2	102.2	(1.3)	1.10E-06
ENSG00000123843	38.3	41.2	45.2	12.6	2.9	4.7	41.6	6.7	2.7	1.14E-06
ENSG00000142552	32.6	29.3	28.0	83.8	82.7	83.0	29.9	83.2	(1.5)	1.14E-06
ENSG00000175274	41.2	31.4	30.7	1.1	0.0	0.0	34.4	0.4	6.6	1.16E-06
ENSG00000204261	31.6	32.5	27.1	74.6	96.2	83.9	30.4	84.9	(1.5)	1.19E-06
ENSG00000163637	11.5	15.2	34.3	75.7	64.5	89.5	20.3	76.6	(1.9)	1.19E-06
ENSG00000074660	79.5	106.2	84.9	36.7	26.0	34.5	90.2	32.4	1.5	1.21E-06
ENSG00000204442	73.7	64.0	92.2	16.1	27.9	27.0	76.6	23.7	1.7	1.22E-06
ENSG00000064300	46.9	44.5	41.6	104.4	102.0	111.9	44.3	106.1	(1.3)	1.43E-06
ENSG00000197249	71.8	70.5	68.7	136.6	137.6	167.8	70.3	147.3	(1.1)	1.55E-06
ENSG00000134716	77.6	65.0	76.8	28.7	18.3	24.2	73.1	23.7	1.6	1.55E-06
ENSG00000186907	5.7	5.4	3.6	25.2	34.6	47.5	4.9	35.8	(2.9)	1.63E-06
ENSG00000171604	97.7	146.4	112.0	55.1	45.2	46.6	118.7	49.0	1.3	1.66E-06
ENSG00000254838	41.2	34.7	54.2	93.0	117.4	115.6	43.4	108.6	(1.3)	1.77E-06
ENSG00000186787	26.8	41.2	28.0	95.2	85.6	82.0	32.0	87.6	(1.5)	1.80E-06
ENSG00000141519	18.2	18.4	23.5	74.6	64.5	58.7	20.0	65.9	(1.7)	1.86E-06
ENSG00000119698	53.6	44.5	57.8	9.2	15.4	13.1	52.0	12.5	2.0	1.86E-06
ENSG00000145526	4.8	2.2	4.5	25.2	34.6	37.3	3.8	32.4	(3.1)	1.90E-06
ENSG00000126583	39.3	26.0	56.0	1.1	5.8	9.3	40.4	5.4	2.9	1.93E-06
ENSG00000188277	114.9	143.1	128.3	60.8	53.9	60.6	128.8	58.4	1.1	1.97E-06
ENSG00000142235	53.6	42.3	41.6	4.6	14.4	7.5	45.8	8.8	2.4	1.98E-06
ENSG00000121871	1.0	4.3	5.4	29.8	26.0	42.0	3.6	32.6	(3.2)	2.00E-06
ENSG00000073910	77.6	59.6	74.1	14.9	24.1	26.1	70.4	21.7	1.7	2.09E-06
ENSG00000100979	68.9	67.2	78.6	31.0	20.2	17.7	71.6	23.0	1.7	2.11E-06
ENSG00000179348	76.6	56.4	70.5	151.5	130.9	149.2	67.8	143.8	(1.1)	2.31E-06
ENSG00000171346	135.0	164.8	125.6	68.9	61.6	69.0	141.8	66.5	1.1	2.47E-06
ENSG00000196787	18.2	18.4	11.7	47.1	57.7	71.8	16.1	58.9	(1.9)	2.58E-06
ENSG00000111341	0.0	1.1	0.0	32.1	17.3	43.8	0.4	31.1	(6.5)	2.78E-06
ENSG00000159714	87.1	86.7	100.3	43.6	31.8	30.8	91.4	35.4	1.4	2.84E-06
ENSG00000108423	71.8	66.1	91.3	154.9	148.2	165.9	76.4	156.3	(1.0)	2.87E-06
ENSG00000167306	113.0	104.1	112.0	40.2	49.1	52.2	109.7	47.1	1.2	3.00E-06
ENSG00000019186	52.7	70.5	75.9	24.1	22.1	13.1	66.3	19.8	1.8	3.10E-06
ENSG00000154553	87.1	86.7	97.6	28.7	31.8	42.9	90.5	34.4	1.4	3.15E-06
ENSG00000123096	24.9	22.8	25.3	66.6	63.5	87.6	24.3	72.6	(1.6)	3.29E-06
ENSG00000228526	1.0	0.0	0.0	29.8	27.9	28.9	0.3	28.9	(6.4)	3.39E-06
ENSG00000213214	123.5	129.0	147.3	59.7	68.3	60.6	133.3	62.9	1.1	3.42E-06
ENSG00000171951	10.5	6.5	7.2	35.6	45.2	41.0	8.1	40.6	(2.3)	3.63E-06
ENSG00000262454	23.0	34.7	27.1	78.0	75.0	82.0	28.3	78.4	(1.5)	3.64E-06
ENSG00000128298	27.8	41.2	42.5	2.3	9.6	4.7	37.1	5.5	2.7	3.71E-06
ENSG00000204956	3.8	4.3	2.7	34.4	26.9	28.9	3.6	30.1	(3.1)	3.75E-06

ENSG00000115604	43.1	51.0	51.5	14.9	8.7	12.1	48.5	11.9	2.0	3.93E-06
ENSG00000242147	4.8	3.3	6.3	35.6	26.9	37.3	4.8	33.3	(2.8)	4.00E-06
ENSG00000282057	102.4	95.4	116.6	44.8	52.0	25.2	104.8	40.6	1.4	4.05E-06
ENSG00000271201	25.9	11.9	17.2	0.0	0.0	0.0	18.3	0.0	6.6	4.20E-06
ENSG00000204983	13.4	23.9	17.2	0.0	0.0	0.0	18.1	0.0	6.6	4.21E-06
ENSG00000171357	50.7	53.1	47.0	132.0	107.8	102.5	50.3	114.1	(1.2)	4.33E-06
ENSG00000279369	17.2	8.7	11.7	48.2	54.8	47.5	12.6	50.2	(2.0)	4.36E-06
ENSG00000140961	58.4	77.0	71.4	156.1	123.2	152.9	68.9	144.0	(1.1)	4.40E-06
ENSG00000043039	28.7	36.9	28.0	2.3	0.0	0.0	31.2	0.8	5.5	4.52E-06
ENSG00000171291	0.0	0.0	0.9	19.5	34.6	29.8	0.3	28.0	(6.3)	4.71E-06
ENSG00000070731	0.0	0.0	3.6	31.0	17.3	34.5	1.2	27.6	(4.4)	4.72E-06
ENSG00000111816	8.6	3.3	8.1	33.3	36.6	42.9	6.7	37.6	(2.5)	5.06E-06
ENSG00000237870	35.4	31.4	49.7	3.4	7.7	9.3	38.9	6.8	2.5	5.35E-06
ENSG00000010295	108.2	113.8	125.6	47.1	58.7	51.3	115.9	52.3	1.1	5.50E-06
ENSG00000149972	8.6	7.6	9.9	41.3	41.4	39.2	8.7	40.6	(2.2)	5.71E-06
ENSG00000185875	21.1	15.2	17.2	63.1	67.4	48.5	17.8	59.6	(1.7)	5.85E-06
ENSG00000132000	16.3	16.3	19.9	65.4	52.9	55.9	17.5	58.1	(1.7)	6.05E-06
ENSG00000103150	69.9	74.8	59.6	152.6	116.4	158.5	68.1	142.5	(1.1)	6.12E-06
ENSG00000168453	4.8	3.3	0.0	40.2	16.4	33.6	2.7	30.0	(3.5)	6.19E-06
ENSG00000196605	51.7	36.9	29.8	80.3	104.9	116.5	39.5	100.6	(1.4)	6.47E-06
ENSG00000137691	12.4	17.3	11.7	52.8	48.1	51.3	13.8	50.7	(1.9)	6.48E-06
ENSG00000152454	91.0	98.7	101.2	36.7	46.2	39.2	96.9	40.7	1.2	6.51E-06
ENSG00000279342	119.7	83.5	106.6	32.1	55.8	31.7	103.3	39.9	1.4	6.76E-06
ENSG00000141668	1.0	10.8	2.7	35.6	27.9	42.0	4.8	35.1	(2.9)	6.76E-06
ENSG00000180818	35.4	60.7	35.2	11.5	4.8	10.3	43.8	8.8	2.3	6.76E-06
ENSG00000174599	23.9	36.9	40.7	83.8	91.4	87.6	33.8	87.6	(1.4)	6.91E-06
ENSG00000105516	75.6	69.4	59.6	135.4	125.1	160.4	68.2	140.3	(1.0)	7.51E-06
ENSG00000169860	63.2	37.9	63.3	109.0	123.2	142.6	54.8	124.9	(1.2)	7.67E-06
ENSG00000127329	80.4	85.6	63.3	137.7	144.3	180.9	76.4	154.3	(1.0)	7.93E-06
ENSG00000182518	49.8	49.9	49.7	121.6	107.8	100.7	49.8	110.0	(1.1)	8.24E-06
ENSG00000092758	110.1	117.1	106.6	48.2	56.8	46.6	111.3	50.5	1.1	8.30E-06
ENSG00000132016	143.6	136.6	149.1	51.6	89.5	58.7	143.1	66.6	1.1	8.47E-06
ENSG00000182327	16.3	10.8	9.0	45.9	53.9	42.9	12.1	47.6	(2.0)	8.73E-06
ENSG00000122547	54.6	65.0	53.3	12.6	14.4	23.3	57.6	16.8	1.8	9.42E-06
ENSG00000230882	130.2	135.5	150.9	62.0	53.9	83.0	138.9	66.3	1.1	9.89E-06
ENSG00000065325	0.0	1.1	2.7	32.1	18.3	24.2	1.3	24.9	(4.3)	1.01E-05
ENSG00000102878	46.9	47.7	45.2	88.4	104.9	124.9	46.6	106.1	(1.2)	1.02E-05
ENSG00000250397	102.4	92.2	106.6	49.3	42.3	41.0	100.4	44.2	1.2	1.10E-05
ENSG00000248927	20.1	13.0	25.3	51.6	57.7	83.0	19.5	64.1	(1.7)	1.12E-05
ENSG00000100344	26.8	36.9	17.2	72.3	83.7	71.8	26.9	75.9	(1.5)	1.16E-05
ENSG00000227039	28.7	37.9	26.2	1.1	5.8	5.6	31.0	4.2	2.8	1.19E-05
ENSG00000171587	23.9	23.9	26.2	1.1	0.0	0.0	24.7	0.4	6.1	1.21E-05
ENSG00000273344	147.4	119.3	133.7	67.7	73.1	53.1	133.5	64.7	1.0	1.21E-05
ENSG00000169418	41.2	45.5	62.4	12.6	15.4	12.1	49.7	13.4	1.9	1.30E-05
ENSG00000020181	24.9	19.5	19.9	55.1	61.6	74.6	21.4	63.7	(1.6)	1.32E-05
ENSG00000263563	15.3	16.3	14.5	0.0	0.0	0.0	15.3	0.0	6.4	1.33E-05
ENSG00000166592	19.1	48.8	51.5	5.7	3.8	10.3	39.8	6.6	2.6	1.38E-05
ENSG00000091129	6.7	4.3	3.6	23.0	37.5	33.6	4.9	31.3	(2.7)	1.38E-05
ENSG00000101115	99.6	108.4	100.3	45.9	42.3	50.3	102.8	46.2	1.2	1.38E-05
ENSG00000267248	1.0	0.0	0.0	24.1	18.3	28.9	0.3	23.8	(6.1)	1.44E-05
ENSG00000125966	101.5	114.9	94.0	40.2	48.1	49.4	103.5	45.9	1.2	1.45E-05
ENSG00000251322	54.6	65.0	65.1	127.4	119.3	129.6	61.6	125.4	(1.0)	1.47E-05
ENSG00000197863	24.9	20.6	28.0	68.9	68.3	67.1	24.5	68.1	(1.5)	1.50E-05
ENSG00000254887	14.4	18.4	12.7	0.0	0.0	0.0	15.1	0.0	6.3	1.55E-05
ENSG00000196511	111.1	124.7	131.9	65.4	53.9	58.7	122.6	59.3	1.1	1.55E-05
ENSG00000280269	32.6	36.9	35.2	1.1	11.5	2.8	34.9	5.2	2.7	1.55E-05
ENSG00000259345	38.3	37.9	25.3	78.0	84.7	90.4	33.8	84.4	(1.3)	1.58E-05
ENSG00000266208	24.9	21.7	22.6	73.4	59.7	63.4	23.1	65.5	(1.5)	1.60E-05

ENSG00000198542	6.7	1.1	3.6	32.1	29.8	25.2	3.8	29.0	(2.9)	1.61E-05
ENSG00000277559	5.7	5.4	6.3	29.8	35.6	31.7	5.8	32.4	(2.5)	1.62E-05
ENSG00000164197	33.5	26.0	21.7	3.4	1.0	4.7	27.1	3.0	3.2	1.68E-05
ENSG00000205364	120.6	113.8	124.7	42.5	65.4	59.7	119.7	55.9	1.1	1.70E-05
ENSG00000163710	11.5	6.5	10.8	44.8	47.1	32.6	9.6	41.5	(2.1)	1.80E-05
ENSG00000136883	32.6	47.7	45.2	11.5	6.7	11.2	41.8	9.8	2.1	1.81E-05
ENSG00000165929	15.3	17.3	11.7	0.0	0.0	0.0	14.8	0.0	6.3	1.83E-05
ENSG00000271270	5.7	4.3	6.3	32.1	26.0	37.3	5.5	31.8	(2.5)	1.85E-05
ENSG00000183647	131.2	120.3	128.3	62.0	52.0	71.8	126.6	61.9	1.0	1.90E-05
ENSG00000271335	12.4	14.1	10.8	52.8	46.2	39.2	12.5	46.0	(1.9)	1.95E-05
ENSG00000177822	1.9	0.0	0.0	24.1	29.8	22.4	0.6	25.4	(5.3)	1.97E-05
ENSG00000137460	34.5	36.9	56.0	95.2	102.0	100.7	42.5	99.3	(1.2)	2.02E-05
ENSG00000106066	21.1	24.9	22.6	1.1	0.0	0.0	22.9	0.4	6.0	2.04E-05
ENSG00000130052	57.4	65.0	90.4	26.4	27.9	21.4	71.0	25.2	1.5	2.13E-05
ENSG00000187210	58.4	58.5	53.3	6.9	18.3	23.3	56.8	16.2	1.8	2.22E-05
ENSG00000136999	80.4	79.1	80.4	33.3	23.1	38.2	80.0	31.5	1.3	2.22E-05
ENSG00000171236	13.4	33.6	31.6	1.1	1.0	0.0	26.2	0.7	5.3	2.43E-05
ENSG00000203650	35.4	30.4	23.5	4.6	5.8	3.7	29.8	4.7	2.7	2.46E-05
ENSG00000078399	85.2	112.8	94.0	49.3	42.3	36.4	97.3	42.7	1.2	2.64E-05
ENSG00000146411	58.4	58.5	68.7	123.9	111.6	140.8	61.9	125.4	(1.0)	2.64E-05
ENSG00000166396	23.0	34.7	26.2	3.4	4.8	3.7	28.0	4.0	2.8	2.75E-05
ENSG00000278318	1.9	0.0	0.0	23.0	29.8	20.5	0.6	24.4	(5.2)	2.77E-05
ENSG00000179598	64.1	53.1	32.5	16.1	14.4	9.3	49.9	13.3	1.9	2.78E-05
ENSG00000247271	29.7	39.0	36.1	94.1	84.7	73.6	35.0	84.1	(1.3)	2.89E-05
ENSG00000275111	73.7	55.3	58.7	143.4	111.6	127.7	62.6	127.6	(1.0)	3.05E-05
ENSG00000273812	24.9	17.3	21.7	58.5	56.8	68.1	21.3	61.1	(1.5)	3.22E-05
ENSG00000100191	23.9	29.3	15.4	0.0	2.9	0.9	22.9	1.3	4.1	3.22E-05
ENSG00000139973	63.2	32.5	47.0	12.6	14.4	11.2	47.6	12.7	1.9	3.28E-05
ENSG00000185010	40.2	61.8	57.8	126.2	102.0	113.7	53.3	114.0	(1.1)	3.34E-05
ENSG00000135426	21.1	9.8	10.8	0.0	0.0	0.0	13.9	0.0	6.2	3.45E-05
ENSG00000185100	5.7	4.3	2.7	26.4	32.7	24.2	4.3	27.8	(2.7)	3.52E-05
ENSG00000148444	60.3	58.5	68.7	148.0	123.2	109.1	62.5	126.8	(1.0)	3.52E-05
ENSG00000105419	28.7	22.8	30.7	74.6	77.0	62.5	27.4	71.3	(1.4)	3.59E-05
ENSG00000163704	50.7	65.0	56.0	140.0	113.5	103.5	57.3	119.0	(1.1)	3.60E-05
ENSG00000138741	1.9	1.1	1.8	26.4	21.2	17.7	1.6	21.8	(3.7)	3.71E-05
ENSG00000087494	75.6	64.0	60.5	31.0	19.2	23.3	66.7	24.5	1.5	3.71E-05
ENSG00000083454	99.6	74.8	85.8	39.0	35.6	37.3	86.7	37.3	1.2	3.75E-05
ENSG00000258919	0.0	0.0	0.0	24.1	11.5	6.5	0.0	14.1	(6.3)	3.78E-05
ENSG00000244693	19.1	26.0	32.5	3.4	3.8	2.8	25.9	3.4	2.9	3.84E-05
ENSG00000259961	9.6	16.3	14.5	0.0	0.0	0.0	13.4	0.0	6.2	3.87E-05
ENSG00000275713	9.6	7.6	11.7	36.7	32.7	49.4	9.6	39.6	(2.0)	4.16E-05
ENSG00000231107	12.4	15.2	11.7	0.0	0.0	0.0	13.1	0.0	6.1	4.27E-05
ENSG00000204611	68.0	53.1	60.5	96.4	140.5	138.0	60.5	124.9	(1.0)	4.36E-05
ENSG00000006740	51.7	59.6	53.3	21.8	8.7	20.5	54.9	17.0	1.7	4.38E-05
ENSG00000127324	3.8	10.8	5.4	35.6	39.4	26.1	6.7	33.7	(2.4)	4.41E-05
ENSG00000198417	74.7	81.3	92.2	37.9	35.6	32.6	82.7	35.4	1.2	4.42E-05
ENSG00000229644	119.7	123.6	108.4	41.3	51.0	71.8	117.2	54.7	1.1	4.46E-05
ENSG00000272674	1.9	0.0	0.9	25.2	13.5	26.1	0.9	21.6	(4.5)	4.50E-05
ENSG00000186017	70.9	45.5	59.6	113.6	130.9	117.5	58.7	120.6	(1.0)	4.51E-05
ENSG00000231711	42.1	64.0	67.8	130.8	119.3	111.9	58.0	120.7	(1.1)	4.51E-05
ENSG00000146938	0.0	0.0	0.0	11.5	7.7	20.5	0.0	13.2	(6.2)	4.55E-05
ENSG00000158406	5.7	5.4	10.8	33.3	35.6	34.5	7.3	34.5	(2.2)	4.55E-05
ENSG00000169248	42.1	29.3	27.1	3.4	6.7	8.4	32.8	6.2	2.4	4.57E-05
ENSG00000149927	13.4	6.5	13.6	51.6	45.2	33.6	11.2	43.5	(1.9)	4.61E-05
ENSG00000257639	38.3	17.3	20.8	2.3	3.8	2.8	25.5	3.0	3.1	4.90E-05
ENSG00000148053	13.4	16.3	9.9	43.6	45.2	46.6	13.2	45.1	(1.8)	4.90E-05
ENSG00000221886	52.7	47.7	56.9	102.1	101.0	123.1	52.4	108.7	(1.1)	5.02E-05
ENSG00000268873	21.1	21.7	17.2	0.0	1.0	0.0	20.0	0.3	5.8	5.05E-05

ENSG00000243635	11.5	8.7	19.0	0.0	0.0	0.0	13.0	0.0	6.1	5.13E-05
ENSG00000154358	105.3	98.7	135.5	47.1	68.3	36.4	113.2	50.6	1.2	5.54E-05
ENSG00000198929	63.2	81.3	73.2	20.7	37.5	24.2	72.6	27.5	1.4	5.66E-05
ENSG00000165821	25.9	34.7	35.2	90.7	74.1	69.0	31.9	77.9	(1.3)	5.75E-05
ENSG00000180596	10.5	11.9	9.0	40.2	29.8	52.2	10.5	40.7	(2.0)	6.03E-05
ENSG00000182177	21.1	8.7	9.0	0.0	0.0	0.0	12.9	0.0	6.1	6.28E-05
ENSG00000170542	23.9	23.9	26.2	70.0	55.8	68.1	24.7	64.6	(1.4)	6.52E-05
ENSG00000274349	56.5	41.2	52.4	97.5	115.5	101.6	50.0	104.9	(1.1)	6.53E-05
ENSG00000082126	56.5	59.6	71.4	29.8	17.3	21.4	62.5	22.9	1.5	6.89E-05
ENSG00000197479	4.8	6.5	1.8	23.0	24.1	34.5	4.4	27.2	(2.7)	7.16E-05
ENSG00000237499	26.8	23.9	27.1	2.3	3.8	5.6	25.9	3.9	2.7	7.21E-05
ENSG00000082482	7.7	6.5	8.1	35.6	22.1	46.6	7.4	34.8	(2.2)	7.23E-05
ENSG00000107105	24.9	21.7	19.9	50.5	69.3	61.5	22.2	60.4	(1.5)	7.27E-05
ENSG00000204682	5.7	2.2	8.1	40.2	27.9	23.3	5.3	30.5	(2.5)	7.59E-05
ENSG00000105246	23.9	26.0	16.3	4.6	1.0	0.9	22.1	2.2	3.4	7.89E-05
ENSG00000235098	8.6	10.8	17.2	0.0	0.0	0.0	12.2	0.0	6.0	7.93E-05
ENSG00000277147	38.3	34.7	48.8	12.6	9.6	11.2	40.6	11.1	1.9	8.08E-05
ENSG00000196345	0.0	0.0	1.8	32.1	15.4	17.7	0.6	21.7	(5.1)	8.16E-05
ENSG00000158234	42.1	33.6	31.6	98.7	73.1	77.4	35.8	83.1	(1.2)	8.86E-05
ENSG00000226051	14.4	6.5	15.4	0.0	0.0	0.0	12.1	0.0	6.0	9.06E-05
ENSG00000229676	0.0	0.0	0.0	9.2	12.5	13.1	0.0	11.6	(6.0)	9.09E-05
ENSG00000184305	8.6	13.0	8.1	37.9	35.6	39.2	9.9	37.5	(1.9)	9.23E-05
ENSG00000152689	30.6	18.4	17.2	2.3	2.9	1.9	22.1	2.3	3.2	9.31E-05
ENSG00000147246	25.9	14.1	15.4	0.0	1.0	0.0	18.4	0.3	5.7	9.34E-05
ENSG00000274487	67.0	58.5	40.7	129.7	121.2	96.0	55.4	115.6	(1.1)	9.63E-05
ENSG00000135477	38.3	39.0	47.0	66.6	117.4	99.8	41.4	94.6	(1.2)	9.75E-05
ENSG00000213417	19.1	10.8	25.3	0.0	0.0	0.9	18.4	0.3	5.7	9.80E-05
ENSG00000185634	76.6	75.9	90.4	39.0	24.1	40.1	80.9	34.4	1.2	9.84E-05
ENSG00000260852	38.3	47.7	32.5	104.4	72.2	91.4	39.5	89.3	(1.2)	9.94E-05
ENSG00000279041	17.2	31.4	19.0	60.8	59.7	62.5	22.6	61.0	(1.4)	9.95E-05
ENSG00000268223	27.8	24.9	33.4	4.6	8.7	1.9	28.7	5.0	2.5	1.02E-04
ENSG00000049249	17.2	27.1	22.6	2.3	2.9	2.8	22.3	2.7	3.1	1.03E-04
ENSG00000172986	14.4	18.4	10.8	48.2	53.9	38.2	14.5	46.8	(1.7)	1.05E-04
ENSG00000168032	18.2	21.7	22.6	4.6	1.0	0.0	20.8	1.9	3.6	1.08E-04
ENSG00000198435	40.2	34.7	36.1	97.5	77.0	75.5	37.0	83.3	(1.2)	1.10E-04
ENSG00000165591	11.5	11.9	10.8	0.0	0.0	0.0	11.4	0.0	5.9	1.10E-04
ENSG00000244198	90.0	60.7	75.9	39.0	24.1	29.8	75.5	31.0	1.3	1.12E-04
ENSG00000139200	6.7	5.4	9.9	25.2	36.6	36.4	7.4	32.7	(2.1)	1.18E-04
ENSG00000223784	44.0	52.0	59.6	16.1	21.2	15.8	51.9	17.7	1.6	1.20E-04
ENSG00000103489	0.0	1.1	0.0	13.8	11.5	27.0	0.4	17.5	(5.6)	1.26E-04
ENSG00000138449	75.6	43.4	56.9	20.7	15.4	25.2	58.6	20.4	1.5	1.28E-04
ENSG00000227076	21.1	30.4	23.5	6.9	1.9	2.8	25.0	3.9	2.7	1.28E-04
ENSG00000170356	33.5	28.2	22.6	3.4	6.7	5.6	28.1	5.3	2.4	1.30E-04
ENSG00000166670	12.4	20.6	19.0	0.0	0.0	0.9	17.3	0.3	5.6	1.31E-04
ENSG00000160182	8.6	9.8	15.4	0.0	0.0	0.0	11.2	0.0	5.9	1.34E-04
ENSG00000239605	26.8	13.0	18.1	1.1	1.0	1.9	19.3	1.3	3.9	1.40E-04
ENSG00000261556	33.5	33.6	27.1	59.7	82.7	79.2	31.4	73.9	(1.2)	1.41E-04
ENSG00000117122	0.0	0.0	2.7	28.7	11.5	18.6	0.9	19.6	(4.3)	1.42E-04
ENSG00000278709	10.5	11.9	10.8	60.8	23.1	43.8	11.1	42.6	(1.9)	1.43E-04
ENSG00000100968	37.3	18.4	25.3	3.4	7.7	1.9	27.0	4.3	2.6	1.53E-04
ENSG00000151789	22.0	19.5	17.2	0.0	0.0	1.9	19.6	0.6	4.9	1.56E-04
ENSG00000179954	3.8	5.4	4.5	25.2	32.7	19.6	4.6	25.8	(2.5)	1.60E-04
ENSG00000177337	48.8	54.2	49.7	128.5	89.5	95.1	50.9	104.4	(1.0)	1.62E-04
ENSG00000187955	18.2	15.2	23.5	0.0	2.9	0.9	19.0	1.3	3.8	1.66E-04
ENSG00000283930	3.8	11.9	4.5	35.6	41.4	20.5	6.8	32.5	(2.3)	1.68E-04
ENSG00000221994	6.7	7.6	4.5	32.1	23.1	32.6	6.3	29.3	(2.2)	1.69E-04
ENSG00000188372	93.8	82.4	81.3	41.3	31.8	45.7	85.9	39.6	1.1	1.72E-04
ENSG00000129465	1.9	4.3	3.6	13.8	26.0	29.8	3.3	23.2	(2.8)	1.74E-04

ENSG00000153363	28.7	30.4	25.3	58.5	68.3	74.6	28.1	67.1	(1.3)	1.80E-04
ENSG00000183778	18.2	19.5	19.0	1.1	1.0	2.8	18.9	1.6	3.5	1.86E-04
ENSG00000118804	17.2	21.7	15.4	58.5	50.0	44.7	18.1	51.1	(1.5)	1.87E-04
ENSG00000253958	24.9	32.5	26.2	72.3	59.7	68.1	27.9	66.7	(1.3)	1.97E-04
ENSG00000047457	3.8	3.3	1.8	23.0	15.4	27.0	3.0	21.8	(2.9)	2.00E-04
ENSG00000205744	19.1	14.1	30.7	1.1	1.0	4.7	21.3	2.3	3.2	2.08E-04
ENSG00000276107	3.8	2.2	6.3	14.9	38.5	24.2	4.1	25.9	(2.6)	2.12E-04
ENSG00000116701	61.3	73.7	74.1	36.7	20.2	29.8	69.7	28.9	1.3	2.12E-04
ENSG00000230479	49.8	22.8	44.3	94.1	79.9	93.2	38.9	89.1	(1.2)	2.12E-04
ENSG00000273802	10.5	14.1	13.6	34.4	39.4	50.3	12.7	41.4	(1.7)	2.16E-04
ENSG00000156218	1.9	0.0	1.8	17.2	17.3	18.6	1.2	17.7	(3.8)	2.21E-04
ENSG00000162894	32.6	27.1	31.6	4.6	11.5	2.8	30.4	6.3	2.3	2.21E-04
ENSG00000249087	34.5	51.0	41.6	95.2	93.3	79.2	42.3	89.3	(1.1)	2.25E-04
ENSG00000204624	27.8	33.6	33.4	5.7	9.6	7.5	31.6	7.6	2.0	2.26E-04
ENSG00000146955	26.8	44.5	29.8	3.4	1.9	14.0	33.7	6.5	2.4	2.29E-04
ENSG00000143847	13.4	15.2	18.1	59.7	28.9	59.7	15.6	49.4	(1.7)	2.31E-04
ENSG00000143839	19.1	14.1	19.9	0.0	1.0	1.9	17.7	0.9	4.2	2.33E-04
ENSG00000169432	20.1	30.4	21.7	48.2	67.4	68.1	24.0	61.2	(1.4)	2.34E-04
ENSG00000125810	16.3	19.5	17.2	1.1	0.0	1.9	17.7	1.0	4.1	2.36E-04
ENSG00000153233	4.8	5.4	0.0	20.7	27.9	21.4	3.4	23.3	(2.8)	2.37E-04
ENSG00000180044	4.8	8.7	1.8	20.7	29.8	29.8	5.1	26.8	(2.4)	2.44E-04
ENSG00000198521	1.0	2.2	0.9	19.5	20.2	13.1	1.3	17.6	(3.7)	2.48E-04
ENSG00000270959	16.3	23.9	23.5	63.1	54.8	49.4	21.2	55.8	(1.4)	2.58E-04
ENSG00000234380	40.2	48.8	52.4	16.1	17.3	15.8	47.1	16.4	1.5	2.69E-04
ENSG00000272141	21.1	26.0	13.6	1.1	1.9	3.7	20.2	2.3	3.1	2.73E-04
ENSG00000100767	21.1	30.4	21.7	51.6	66.4	63.4	24.4	60.5	(1.3)	2.79E-04
ENSG00000136514	18.2	33.6	31.6	80.3	64.5	59.7	27.8	68.2	(1.3)	2.82E-04
ENSG00000168062	61.3	82.4	87.7	33.3	28.9	40.1	77.1	34.1	1.2	2.89E-04
ENSG00000154451	35.4	21.7	38.9	6.9	11.5	2.8	32.0	7.1	2.2	2.94E-04
ENSG00000254221	18.2	19.5	12.7	68.9	37.5	43.8	16.8	50.1	(1.6)	2.94E-04
ENSG00000038945	51.7	49.9	52.4	12.6	24.1	18.6	51.3	18.4	1.5	2.96E-04
ENSG00000168961	57.4	27.1	40.7	11.5	13.5	12.1	41.7	12.4	1.8	3.02E-04
ENSG00000135116	9.6	13.0	7.2	0.0	0.0	0.0	9.9	0.0	5.7	3.03E-04
ENSG00000277687	17.2	29.3	29.8	5.7	2.9	5.6	25.4	4.7	2.4	3.08E-04
ENSG00000176049	7.7	9.8	11.7	20.7	43.3	46.6	9.7	36.9	(1.9)	3.09E-04
ENSG00000146205	91.0	94.3	85.8	42.5	49.1	42.9	90.4	44.8	1.0	3.10E-04
ENSG00000115041	31.6	44.5	39.8	76.9	89.5	79.2	38.6	81.9	(1.1)	3.11E-04
ENSG00000162825	96.7	107.3	95.8	45.9	40.4	62.5	99.9	49.6	1.0	3.11E-04
ENSG00000077092	8.6	3.3	6.3	29.8	27.9	26.1	6.1	27.9	(2.2)	3.15E-04
ENSG00000263718	4.8	4.3	9.0	26.4	33.7	24.2	6.1	28.1	(2.2)	3.16E-04
ENSG00000249781	9.6	6.5	13.6	0.0	0.0	0.0	9.9	0.0	5.7	3.19E-04
ENSG00000160181	18.2	20.6	13.6	1.1	1.0	0.0	17.4	0.7	4.7	3.22E-04
ENSG00000109511	0.0	0.0	0.9	14.9	14.4	14.0	0.3	14.4	(5.4)	3.24E-04
ENSG00000119699	13.4	16.3	29.8	48.2	56.8	60.6	19.8	55.2	(1.5)	3.27E-04
ENSG00000152931	1.0	0.0	1.8	23.0	13.5	14.0	0.9	16.8	(4.1)	3.43E-04
ENSG00000242515	0.0	0.0	0.0	13.8	7.7	7.5	0.0	9.6	(5.7)	3.43E-04
ENSG00000077616	58.4	35.8	72.3	11.5	22.1	23.3	55.5	19.0	1.5	3.44E-04
ENSG00000135838	22.0	27.1	18.1	5.7	3.8	0.9	22.4	3.5	2.7	3.46E-04
ENSG00000122986	29.7	24.9	32.5	73.4	61.6	66.2	29.0	67.1	(1.2)	3.46E-04
ENSG00000163536	32.6	26.0	28.0	53.9	74.1	73.6	28.9	67.2	(1.2)	3.47E-04
ENSG00000237988	6.7	18.4	5.4	0.0	0.0	0.0	10.2	0.0	5.8	3.61E-04
ENSG00000259436	17.2	35.8	29.8	6.9	5.8	4.7	27.6	5.8	2.3	3.63E-04
ENSG00000128536	16.3	13.0	24.4	45.9	59.7	45.7	17.9	50.4	(1.5)	3.70E-04
ENSG00000186615	27.8	24.9	24.4	49.3	60.6	77.4	25.7	62.4	(1.3)	3.71E-04
ENSG00000270607	57.4	84.6	53.3	25.2	26.9	28.0	65.1	26.7	1.3	3.79E-04
ENSG00000119125	22.0	21.7	18.1	3.4	3.8	1.9	20.6	3.1	2.8	3.81E-04
ENSG00000236345	23.9	18.4	17.2	2.3	1.9	3.7	19.8	2.6	2.9	3.82E-04
ENSG00000100253	2.9	7.6	7.2	29.8	22.1	29.8	5.9	27.3	(2.2)	3.83E-04

ENSG00000162687	23.0	22.8	31.6	49.3	62.5	78.3	25.8	63.4	(1.3)	3.86E-04
ENSG00000132321	11.5	4.3	13.6	0.0	0.0	0.0	9.8	0.0	5.7	3.88E-04
ENSG00000166669	35.4	31.4	29.8	63.1	80.8	69.9	32.2	71.3	(1.1)	3.95E-04
ENSG00000198797	13.4	16.3	23.5	1.1	1.0	2.8	17.7	1.6	3.4	4.02E-04
ENSG00000251247	24.9	30.4	25.3	56.2	70.2	61.5	26.9	62.7	(1.2)	4.15E-04
ENSG00000184937	2.9	0.0	3.6	24.1	12.5	21.4	2.2	19.3	(3.1)	4.30E-04
ENSG00000166265	23.0	30.4	24.4	51.6	61.6	71.8	25.9	61.7	(1.3)	4.32E-04
ENSG00000163617	35.4	37.9	43.4	70.0	79.9	95.1	38.9	81.7	(1.1)	4.35E-04
ENSG00000160223	52.7	9.8	12.7	4.6	2.9	1.9	25.0	3.1	3.0	4.42E-04
ENSG00000173200	1.9	2.2	4.5	20.7	19.2	19.6	2.9	19.8	(2.8)	4.73E-04
ENSG00000105613	36.4	32.5	38.9	67.7	71.2	92.3	35.9	77.1	(1.1)	4.75E-04
ENSG00000126882	32.6	28.2	27.1	74.6	53.9	72.7	29.3	67.1	(1.2)	4.76E-04
ENSG00000120708	392.6	453.2	424.7	1082.2	632.1	1407.7	423.5	1040.7	(1.3)	4.77E-04
ENSG00000254951	22.0	17.3	14.5	1.1	2.9	1.9	17.9	2.0	3.2	4.78E-04
ENSG00000273297	17.2	21.7	12.7	42.5	54.8	44.7	17.2	47.4	(1.5)	4.80E-04
ENSG00000123201	2.9	0.0	0.9	12.6	13.5	24.2	1.3	16.8	(3.7)	4.87E-04
ENSG00000229953	23.9	13.0	15.4	49.3	62.5	37.3	17.4	49.7	(1.5)	4.92E-04
ENSG00000144857	21.1	24.9	15.4	56.2	47.1	54.1	20.5	52.5	(1.4)	5.00E-04
ENSG00000159208	22.0	14.1	24.4	2.3	2.9	3.7	20.2	3.0	2.8	5.15E-04
ENSG00000164125	0.0	1.1	0.0	17.2	7.7	15.8	0.4	13.6	(5.3)	5.36E-04
ENSG00000215866	0.0	0.0	0.0	8.0	13.5	5.6	0.0	9.0	(5.6)	5.37E-04
ENSG00000081138	0.0	0.0	0.0	6.9	13.5	6.5	0.0	9.0	(5.6)	5.50E-04
ENSG00000273443	37.3	32.5	46.1	10.3	8.7	16.8	38.7	11.9	1.7	5.56E-04
ENSG00000163219	4.8	7.6	15.4	0.0	0.0	0.0	9.2	0.0	5.6	5.75E-04
ENSG00000160233	12.4	19.5	9.0	0.0	1.0	0.0	13.7	0.3	5.2	5.79E-04
ENSG00000184489	37.3	49.9	42.5	21.8	13.5	6.5	43.2	13.9	1.7	5.90E-04
ENSG00000095739	21.1	14.1	18.1	66.6	34.6	48.5	17.7	49.9	(1.5)	6.07E-04
ENSG00000187624	3.8	4.3	2.7	28.7	17.3	17.7	3.6	21.2	(2.6)	6.17E-04
ENSG00000205707	34.5	37.9	30.7	60.8	86.6	73.6	34.4	73.7	(1.1)	6.17E-04
ENSG00000208005	20.1	8.7	11.7	0.0	0.0	0.9	13.5	0.3	5.2	6.19E-04
ENSG00000143443	42.1	32.5	37.0	86.1	74.1	72.7	37.2	77.6	(1.1)	6.23E-04
ENSG00000185477	8.6	6.5	17.2	24.1	42.3	48.5	10.8	38.3	(1.8)	6.25E-04
ENSG00000237862	47.9	45.5	64.2	20.7	20.2	21.4	52.5	20.8	1.3	6.28E-04
ENSG00000180914	59.4	55.3	58.7	23.0	31.8	14.9	57.8	23.2	1.3	6.31E-04
ENSG00000152208	0.0	0.0	0.0	6.9	8.7	10.3	0.0	8.6	(5.6)	6.35E-04
ENSG00000233184	10.5	14.1	9.9	43.6	31.8	34.5	11.5	36.6	(1.7)	6.40E-04
ENSG00000171462	29.7	40.1	36.1	76.9	77.9	68.1	35.3	74.3	(1.1)	6.56E-04
ENSG00000181885	23.0	17.3	19.0	1.1	4.8	2.8	19.8	2.9	2.7	6.57E-04
ENSG00000118946	21.1	26.0	28.0	3.4	3.8	8.4	25.0	5.2	2.2	6.73E-04
ENSG00000272808	15.3	18.4	11.7	35.6	58.7	37.3	15.2	43.9	(1.5)	7.07E-04
ENSG00000125864	18.2	10.8	10.8	39.0	44.3	36.4	13.3	39.9	(1.6)	7.11E-04
ENSG00000261780	13.4	15.2	20.8	2.3	1.0	1.9	16.5	1.7	3.3	7.11E-04
ENSG00000262823	7.7	6.5	11.7	0.0	0.0	0.0	8.6	0.0	5.5	7.16E-04
ENSG00000136531	13.4	17.3	9.9	39.0	36.6	43.8	13.6	39.8	(1.6)	7.31E-04
ENSG00000105538	10.5	8.7	7.2	29.8	35.6	28.0	8.8	31.1	(1.8)	7.31E-04
ENSG00000168952	17.2	20.6	9.0	0.0	1.0	0.9	15.6	0.6	4.5	7.47E-04
ENSG00000198754	1.0	1.1	0.9	17.2	10.6	16.8	1.0	14.9	(3.9)	7.51E-04
ENSG00000236423	22.0	27.1	30.7	9.2	2.9	6.5	26.6	6.2	2.1	7.51E-04
ENSG00000169067	42.1	47.7	46.1	14.9	18.3	17.7	45.3	17.0	1.4	7.64E-04
ENSG00000163888	23.9	23.9	18.1	67.7	47.1	48.5	22.0	54.4	(1.3)	7.65E-04
ENSG00000151575	44.0	24.9	40.7	74.6	70.2	90.4	36.5	78.4	(1.1)	7.68E-04
ENSG00000245060	40.2	35.8	23.5	70.0	72.2	72.7	33.2	71.6	(1.1)	7.68E-04
ENSG00000166704	0.0	0.0	0.0	4.6	9.6	11.2	0.0	8.5	(5.6)	7.76E-04
ENSG00000237440	21.1	23.9	31.6	52.8	55.8	71.8	25.5	60.1	(1.2)	7.78E-04
ENSG00000130881	1.0	2.2	0.0	18.4	13.5	13.1	1.0	15.0	(3.9)	7.79E-04
ENSG00000167083	10.5	13.0	14.5	0.0	0.0	0.9	12.7	0.3	5.1	7.84E-04
ENSG00000112936	0.0	1.1	0.0	12.6	9.6	14.9	0.4	12.4	(5.1)	8.04E-04
ENSG00000204706	74.7	79.1	67.8	23.0	42.3	36.4	73.9	33.9	1.1	8.20E-04

ENSG00000197568	30.6	31.4	32.5	75.7	60.6	67.1	31.5	67.8	(1.1)	8.23E-04
ENSG00000238266	18.2	32.5	23.5	2.3	8.7	3.7	24.7	4.9	2.3	8.26E-04
ENSG00000164778	1.9	1.1	0.0	17.2	8.7	19.6	1.0	15.2	(3.9)	8.26E-04
ENSG00000165194	0.0	1.1	1.8	17.2	18.3	9.3	1.0	14.9	(3.9)	8.59E-04
ENSG00000146426	38.3	43.4	30.7	78.0	91.4	64.3	37.5	77.9	(1.1)	8.70E-04
ENSG00000228960	44.0	44.5	40.7	20.7	11.5	14.9	43.1	15.7	1.5	8.95E-04
ENSG00000225151	28.7	30.4	49.7	13.8	8.7	11.2	36.3	11.2	1.7	8.96E-04
ENSG00000230910	6.7	2.2	2.7	23.0	22.1	18.6	3.9	21.2	(2.4)	9.00E-04
ENSG00000143869	46.0	44.5	47.0	13.8	22.1	15.8	45.8	17.2	1.4	9.06E-04
ENSG00000164647	50.7	64.0	49.7	29.8	18.3	19.6	54.8	22.6	1.3	9.15E-04
ENSG00000109265	56.5	46.6	69.6	28.7	24.1	20.5	57.6	24.4	1.2	9.22E-04
ENSG00000267106	5.7	5.4	6.3	20.7	30.8	23.3	5.8	24.9	(2.1)	9.23E-04
ENSG00000162881	0.0	0.0	0.0	8.0	7.7	8.4	0.0	8.0	(5.5)	9.36E-04
ENSG00000081853	1.0	4.3	5.4	23.0	13.5	27.0	3.6	21.2	(2.6)	9.42E-04
ENSG00000125895	45.0	51.0	40.7	19.5	16.4	16.8	45.5	17.5	1.4	1.00E-03
ENSG00000179743	17.2	30.4	15.4	63.1	61.6	38.2	21.0	54.3	(1.4)	1.00E-03
ENSG00000144834	9.6	8.7	12.7	36.7	34.6	28.9	10.3	33.4	(1.7)	1.00E-03
ENSG00000272068	35.4	16.3	28.9	72.3	57.7	59.7	26.9	63.2	(1.2)	1.02E-03
ENSG00000228223	20.1	20.6	19.9	50.5	51.0	46.6	20.2	49.4	(1.3)	1.02E-03
ENSG00000149403	5.7	4.3	15.4	0.0	0.0	0.0	8.5	0.0	5.5	1.03E-03
ENSG00000254837	24.9	31.4	16.3	59.7	48.1	65.3	24.2	57.7	(1.3)	1.03E-03
ENSG00000228623	1.0	1.1	0.0	9.2	22.1	12.1	0.7	14.5	(4.5)	1.05E-03
ENSG00000159899	17.2	9.8	15.4	34.4	34.6	55.0	14.1	41.4	(1.5)	1.06E-03
ENSG00000151917	3.8	3.3	6.3	18.4	25.0	22.4	4.5	21.9	(2.3)	1.09E-03
ENSG00000182118	55.5	73.7	56.0	32.1	27.9	22.4	61.8	27.5	1.2	1.10E-03
ENSG00000143494	19.1	23.9	25.3	56.2	52.9	51.3	22.8	53.5	(1.2)	1.12E-03
ENSG00000137878	76.6	84.6	73.2	33.3	38.5	44.7	78.1	38.8	1.0	1.12E-03
ENSG00000234546	0.0	0.0	1.8	19.5	14.4	9.3	0.6	14.4	(4.5)	1.13E-03
ENSG00000146374	6.7	5.4	7.2	27.5	25.0	24.2	6.5	25.6	(2.0)	1.13E-03
ENSG00000112812	54.6	60.7	66.9	35.6	23.1	22.4	60.7	27.0	1.2	1.16E-03
ENSG00000130940	46.9	60.7	57.8	23.0	27.9	19.6	55.2	23.5	1.2	1.18E-03
ENSG00000099251	25.9	17.3	21.7	39.0	62.5	57.8	21.6	53.1	(1.3)	1.18E-03
ENSG00000234155	37.3	20.6	36.1	8.0	10.6	8.4	31.4	9.0	1.8	1.18E-03
ENSG00000273055	35.4	33.6	41.6	17.2	12.5	6.5	36.9	12.1	1.6	1.18E-03
ENSG00000182261	23.0	9.8	13.6	0.0	2.9	0.9	15.4	1.3	3.5	1.18E-03
ENSG00000172349	14.4	15.2	12.7	1.1	0.0	0.9	14.1	0.7	4.4	1.19E-03
ENSG00000124216	11.5	11.9	9.9	49.3	19.2	42.0	11.1	36.8	(1.7)	1.19E-03
ENSG00000246763	84.3	55.3	60.5	26.4	28.9	35.4	66.7	30.2	1.1	1.21E-03
ENSG00000233922	9.6	5.4	3.6	21.8	29.8	25.2	6.2	25.6	(2.1)	1.21E-03
ENSG00000158683	14.4	14.1	19.9	1.1	2.9	1.9	16.1	2.0	3.0	1.25E-03
ENSG00000214274	13.4	11.9	14.5	34.4	38.5	40.1	13.3	37.7	(1.5)	1.25E-03
ENSG00000132692	25.9	23.9	25.3	51.6	66.4	52.2	25.0	56.7	(1.2)	1.26E-03
ENSG00000117594	11.5	10.8	20.8	1.1	1.9	0.0	14.4	1.0	3.8	1.28E-03
ENSG00000177465	27.8	22.8	20.8	49.3	57.7	56.9	23.8	54.6	(1.2)	1.29E-03
ENSG00000254531	46.0	32.5	31.6	96.4	66.4	68.1	36.7	76.9	(1.1)	1.29E-03
ENSG00000210174	25.9	23.9	22.6	40.2	64.5	64.3	24.1	56.3	(1.2)	1.31E-03
ENSG00000102854	18.2	19.5	10.8	2.3	1.9	1.9	16.2	2.0	3.0	1.31E-03
ENSG00000117010	37.3	31.4	41.6	56.2	86.6	85.8	36.8	76.2	(1.1)	1.32E-03
ENSG00000236830	34.5	28.2	30.7	8.0	12.5	7.5	31.1	9.3	1.7	1.32E-03
ENSG00000168913	0.0	0.0	0.9	14.9	10.6	8.4	0.3	11.3	(5.0)	1.39E-03
ENSG00000225932	22.0	31.4	21.7	0.0	8.7	6.5	25.0	5.1	2.3	1.41E-03
ENSG00000180616	5.7	6.5	9.0	25.2	21.2	34.5	7.1	27.0	(1.9)	1.41E-03
ENSG00000255693	13.4	11.9	23.5	2.3	2.9	0.9	16.3	2.0	3.0	1.42E-03
ENSG00000245552	4.8	2.2	2.7	14.9	26.0	15.8	3.2	18.9	(2.5)	1.43E-03
ENSG00000154263	13.4	15.2	9.0	28.7	38.5	42.9	12.5	36.7	(1.6)	1.43E-03
ENSG00000283787	1.0	2.2	0.9	19.5	14.4	9.3	1.3	14.4	(3.5)	1.43E-03
ENSG00000175984	61.3	54.2	56.0	24.1	31.8	19.6	57.2	25.1	1.2	1.44E-03
ENSG00000213888	40.2	26.0	32.5	82.6	71.2	56.9	32.9	70.2	(1.1)	1.46E-03

ENSG00000136574	20.1	10.8	20.8	1.1	1.0	4.7	17.2	2.3	2.9	1.49E-03
ENSG00000223745	39.3	49.9	34.3	56.2	103.9	93.2	41.2	84.5	(1.0)	1.50E-03
ENSG00000237036	22.0	15.2	18.1	70.0	40.4	36.4	18.4	48.9	(1.4)	1.50E-03
ENSG00000276805	11.5	14.1	17.2	31.0	49.1	39.2	14.3	39.7	(1.5)	1.53E-03
ENSG00000134853	12.4	7.6	13.6	0.0	1.0	0.0	11.2	0.3	5.0	1.57E-03
ENSG00000267221	24.9	32.5	38.9	63.1	60.6	80.2	32.1	68.0	(1.1)	1.60E-03
ENSG00000251320	0.0	1.1	3.6	14.9	13.5	16.8	1.6	15.1	(3.2)	1.61E-03
ENSG00000263004	1.9	3.3	5.4	29.8	10.6	20.5	3.5	20.3	(2.5)	1.65E-03
ENSG00000211445	50.7	37.9	51.5	14.9	25.0	14.9	46.7	18.3	1.4	1.66E-03
ENSG00000077274	7.7	13.0	12.7	0.0	1.0	0.0	11.1	0.3	4.9	1.66E-03
ENSG00000159556	0.0	1.1	0.0	8.0	9.6	14.9	0.4	10.9	(5.0)	1.68E-03
ENSG00000227507	25.9	21.7	12.7	3.4	1.9	5.6	20.1	3.7	2.4	1.70E-03
ENSG00000213468	7.7	11.9	13.6	0.0	0.0	0.9	11.0	0.3	4.9	1.71E-03
ENSG00000273712	0.0	0.0	0.0	2.3	13.5	7.5	0.0	7.7	(5.4)	1.71E-03
ENSG00000281406	22.0	27.1	27.1	50.5	52.9	66.2	25.4	56.5	(1.2)	1.72E-03
ENSG00000114646	8.6	9.8	7.2	40.2	26.0	22.4	8.5	29.5	(1.8)	1.72E-03
ENSG00000099869	14.4	23.9	20.8	4.6	1.9	4.7	19.7	3.7	2.4	1.72E-03
ENSG00000196460	18.2	19.5	21.7	4.6	3.8	3.7	19.8	4.1	2.3	1.77E-03
ENSG00000166086	75.6	83.5	47.9	11.5	41.4	29.8	69.0	27.6	1.3	1.77E-03
ENSG00000207607	8.6	2.2	12.7	0.0	0.0	0.0	7.8	0.0	5.4	1.78E-03
ENSG00000102230	5.7	0.0	2.7	23.0	15.4	16.8	2.8	18.4	(2.7)	1.80E-03
ENSG00000136895	6.7	6.5	14.5	29.8	24.1	41.0	9.2	31.6	(1.8)	1.80E-03
ENSG00000278175	23.0	23.9	15.4	59.7	52.0	39.2	20.7	50.3	(1.3)	1.80E-03
ENSG00000186897	3.8	1.1	9.0	16.1	33.7	20.5	4.7	23.4	(2.3)	1.82E-03
ENSG00000253716	27.8	30.4	28.9	66.6	47.1	74.6	29.0	62.8	(1.1)	1.84E-03
ENSG00000253837	22.0	22.8	19.9	39.0	51.0	62.5	21.6	50.8	(1.2)	1.86E-03
ENSG00000162975	12.4	13.0	7.2	0.0	1.0	0.0	10.9	0.3	4.9	1.87E-03
ENSG00000217236	8.6	11.9	9.0	28.7	32.7	30.8	9.9	30.7	(1.6)	1.87E-03
ENSG00000114771	68.9	64.0	94.0	35.6	35.6	42.0	75.6	37.7	1.0	1.87E-03
ENSG00000152760	25.9	18.4	16.3	1.1	1.9	7.5	20.2	3.5	2.5	1.89E-03
ENSG00000167676	4.8	9.8	4.5	25.2	24.1	24.2	6.4	24.5	(2.0)	1.89E-03
ENSG00000254428	65.1	52.0	63.3	29.8	27.9	27.0	60.1	28.3	1.1	1.89E-03
ENSG00000120051	13.4	16.3	19.9	0.0	3.8	2.8	16.5	2.2	2.8	1.89E-03
ENSG00000168490	1.9	5.4	4.5	21.8	14.4	23.3	4.0	19.8	(2.3)	1.95E-03
ENSG00000226476	32.6	20.6	30.7	64.3	65.4	53.1	28.0	60.9	(1.1)	1.95E-03
ENSG00000164116	2.9	2.2	4.5	16.1	16.4	21.4	3.2	18.0	(2.5)	1.96E-03
ENSG00000253661	16.3	5.4	5.4	29.8	37.5	27.0	9.0	31.5	(1.8)	1.97E-03
ENSG00000149043	9.6	3.3	1.8	14.9	24.1	30.8	4.9	23.2	(2.3)	1.99E-03
ENSG00000138944	0.0	0.0	0.9	12.6	7.7	11.2	0.3	10.5	(4.9)	1.99E-03
ENSG00000272482	8.6	5.4	12.7	48.2	30.8	17.7	8.9	32.2	(1.8)	2.00E-03
ENSG00000259065	17.2	13.0	17.2	48.2	30.8	46.6	15.8	41.9	(1.4)	2.00E-03
ENSG00000189431	13.4	18.4	9.0	49.3	35.6	30.8	13.6	38.6	(1.5)	2.01E-03
ENSG00000178127	35.4	27.1	45.2	4.6	15.4	14.0	35.9	11.3	1.6	2.03E-03
ENSG00000186827	12.4	15.2	11.7	0.0	1.0	1.9	13.1	0.9	3.7	2.05E-03
ENSG00000261327	3.8	0.0	2.7	16.1	9.6	24.2	2.2	16.6	(2.9)	2.09E-03
ENSG00000149294	13.4	11.9	12.7	1.1	1.0	0.0	12.7	0.7	4.2	2.15E-03
ENSG00000197134	0.0	0.0	0.0	5.7	6.7	8.4	0.0	7.0	(5.3)	2.19E-03
ENSG00000203499	31.6	27.1	26.2	48.2	73.1	60.6	28.3	60.6	(1.1)	2.22E-03
ENSG00000144227	21.1	6.5	12.7	2.3	0.0	0.0	13.4	0.8	4.3	2.22E-03
ENSG00000130649	52.7	30.4	47.9	12.6	12.5	23.3	43.6	16.1	1.4	2.23E-03
ENSG00000265799	1.0	5.4	3.6	18.4	18.3	17.7	3.3	18.1	(2.5)	2.24E-03
ENSG00000228439	11.5	27.1	7.2	31.0	59.7	42.9	15.3	44.5	(1.6)	2.28E-03
ENSG00000210176	21.1	24.9	31.6	56.2	74.1	44.7	25.9	58.4	(1.2)	2.29E-03
ENSG00000008323	10.5	14.1	17.2	25.2	56.8	37.3	13.9	39.8	(1.5)	2.30E-03
ENSG00000204257	47.9	36.9	44.3	26.4	12.5	9.3	43.0	16.1	1.4	2.34E-03
ENSG00000158164	11.5	9.8	16.3	36.7	46.2	26.1	12.5	36.3	(1.5)	2.40E-03
ENSG00000178568	8.6	5.4	6.3	24.1	20.2	30.8	6.8	25.0	(1.9)	2.43E-03
ENSG00000131196	10.5	5.4	9.0	24.1	29.8	29.8	8.3	27.9	(1.7)	2.44E-03

ENSG00000185345	1.0	2.2	1.8	16.1	15.4	10.3	1.6	13.9	(3.1)	2.47E-03
ENSG00000133107	6.7	8.7	5.4	0.0	0.0	0.0	6.9	0.0	5.2	2.50E-03
ENSG00000086696	6.7	8.7	5.4	0.0	0.0	0.0	6.9	0.0	5.2	2.50E-03
ENSG00000164604	25.9	26.0	25.3	5.7	6.7	9.3	25.7	7.3	1.8	2.52E-03
ENSG00000224424	1.9	9.8	5.4	25.2	27.9	17.7	5.7	23.6	(2.1)	2.53E-03
ENSG00000170989	34.5	34.7	28.0	59.7	56.8	82.0	32.4	66.2	(1.0)	2.70E-03
ENSG00000257557	2.9	2.2	5.4	19.5	24.1	12.1	3.5	18.6	(2.4)	2.74E-03
ENSG00000249867	20.1	16.3	26.2	1.1	2.9	8.4	20.9	4.1	2.3	2.74E-03
ENSG00000265458	12.4	7.6	6.3	36.7	25.0	25.2	8.8	29.0	(1.7)	2.75E-03
ENSG00000259146	4.8	6.5	6.3	19.5	23.1	25.2	5.9	22.6	(1.9)	2.75E-03
ENSG00000106804	23.9	14.1	30.7	57.4	48.1	54.1	22.9	53.2	(1.2)	2.78E-03
ENSG00000242599	12.4	7.6	9.9	0.0	0.0	0.9	10.0	0.3	4.8	2.78E-03
ENSG00000227706	1.0	0.0	0.0	14.9	5.8	9.3	0.3	10.0	(4.8)	2.82E-03
ENSG00000154556	8.6	11.9	14.5	20.7	31.8	55.0	11.7	35.8	(1.6)	2.88E-03
ENSG00000204949	0.0	1.1	0.0	5.7	13.5	10.3	0.4	9.8	(4.8)	2.88E-03
ENSG00000197837	16.3	13.0	11.7	32.1	44.3	33.6	13.7	36.7	(1.4)	2.92E-03
ENSG00000105499	16.3	27.1	26.2	3.4	3.8	9.3	23.2	5.5	2.0	2.92E-03
ENSG00000113248	1.0	0.0	1.8	14.9	6.7	15.8	0.9	12.5	(3.7)	2.98E-03
ENSG00000237484	12.4	10.8	13.6	33.3	40.4	28.9	12.3	34.2	(1.5)	3.01E-03
ENSG00000266865	31.6	16.3	31.6	4.6	10.6	6.5	26.5	7.2	1.9	3.02E-03
ENSG00000164418	38.3	44.5	23.5	70.0	68.3	73.6	35.4	70.7	(1.0)	3.07E-03
ENSG00000027869	19.1	10.8	17.2	4.6	1.9	0.9	15.7	2.5	2.7	3.09E-03
ENSG00000280219	34.5	22.8	22.6	6.9	10.6	5.6	26.6	7.7	1.8	3.09E-03
ENSG00000186212	45.0	60.7	68.7	26.4	19.2	33.6	58.1	26.4	1.1	3.13E-03
ENSG00000249863	40.2	21.7	38.0	10.3	13.5	10.3	33.3	11.4	1.6	3.20E-03
ENSG00000139971	58.4	42.3	44.3	23.0	19.2	21.4	48.3	21.2	1.2	3.25E-03
ENSG00000215105	2.9	11.9	5.4	25.2	23.1	26.1	6.7	24.8	(1.9)	3.27E-03
ENSG00000168993	17.2	22.8	19.0	3.4	6.7	2.8	19.7	4.3	2.2	3.31E-03
ENSG00000275894	28.7	20.6	26.2	5.7	7.7	8.4	25.2	7.3	1.8	3.36E-03
ENSG00000168243	1.0	1.1	0.9	8.0	13.5	14.0	1.0	11.8	(3.6)	3.39E-03
ENSG00000099260	0.0	0.0	0.0	6.9	5.8	6.5	0.0	6.4	(5.1)	3.42E-03
ENSG00000104894	36.4	22.8	25.3	63.1	52.9	61.5	28.2	59.2	(1.1)	3.46E-03
ENSG00000171658	1.0	0.0	0.0	8.0	9.6	10.3	0.3	9.3	(4.7)	3.48E-03
ENSG00000235421	18.2	3.3	28.9	0.0	3.8	1.9	16.8	1.9	3.1	3.50E-03
ENSG00000179299	7.7	5.4	6.3	0.0	0.0	0.0	6.5	0.0	5.1	3.52E-03
ENSG00000152270	6.7	5.4	7.2	0.0	0.0	0.0	6.5	0.0	5.1	3.55E-03
ENSG00000255031	38.3	22.8	45.2	64.3	88.5	64.3	35.4	72.4	(1.0)	3.56E-03
ENSG00000177494	38.3	70.5	58.7	21.8	28.9	24.2	55.8	25.0	1.2	3.57E-03
ENSG00000100628	12.4	11.9	11.7	1.1	1.9	0.0	12.0	1.0	3.6	3.58E-03
ENSG00000129048	2.9	1.1	0.9	8.0	17.3	14.9	1.6	13.4	(3.1)	3.64E-03
ENSG00000115657	4.8	6.5	11.7	25.2	32.7	21.4	7.7	26.5	(1.8)	3.68E-03
ENSG00000153404	19.1	15.2	24.4	6.9	2.9	3.7	19.6	4.5	2.2	3.76E-03
ENSG00000108176	34.5	47.7	36.1	10.3	14.4	20.5	39.4	15.1	1.4	3.77E-03
ENSG00000072818	19.1	42.3	29.8	57.4	73.1	60.6	30.4	63.7	(1.1)	3.80E-03
ENSG00000233845	7.7	4.3	7.2	0.0	0.0	0.0	6.4	0.0	5.1	3.80E-03
ENSG00000175894	8.6	13.0	12.7	1.1	1.0	0.0	11.4	0.7	4.1	3.91E-03
ENSG00000240086	1.0	1.1	0.0	16.1	8.7	9.3	0.7	11.3	(4.1)	3.91E-03
ENSG00000099864	0.0	0.0	0.9	5.7	11.5	10.3	0.3	9.2	(4.7)	3.92E-03
ENSG00000250360	0.0	0.0	0.0	4.6	5.8	8.4	0.0	6.3	(5.1)	3.99E-03
ENSG00000250102	0.0	0.0	0.0	2.3	8.7	8.4	0.0	6.4	(5.2)	3.99E-03
ENSG00000151025	0.0	1.1	0.9	5.7	17.3	11.2	0.7	11.4	(4.1)	4.04E-03
ENSG00000280187	11.5	11.9	11.7	28.7	39.4	28.9	11.7	32.3	(1.5)	4.08E-03
ENSG00000203635	47.9	41.2	58.7	24.1	26.9	13.1	49.3	21.4	1.2	4.08E-03
ENSG00000133424	0.0	1.1	1.8	10.3	9.6	14.9	1.0	11.6	(3.6)	4.12E-03
ENSG00000139874	8.6	9.8	9.0	1.1	0.0	0.0	9.1	0.4	4.7	4.14E-03
ENSG00000245213	9.6	8.7	8.1	32.1	21.2	28.9	8.8	27.4	(1.6)	4.17E-03
ENSG00000258393	8.6	9.8	9.0	0.0	1.0	0.0	9.1	0.3	4.7	4.18E-03
ENSG00000277734	16.3	13.0	12.7	1.1	1.0	3.7	14.0	1.9	2.8	4.32E-03

ENSG00000258376	4.8	9.8	9.0	23.0	25.0	28.9	7.9	25.6	(1.7)	4.35E-03
ENSG00000213889	22.0	26.0	23.5	51.6	52.0	48.5	23.8	50.7	(1.1)	4.35E-03
ENSG00000267519	529.5	634.2	448.2	367.2	239.6	193.0	537.3	266.6	1.0	4.44E-03
ENSG00000126947	11.5	17.3	12.7	1.1	2.9	1.9	13.8	2.0	2.8	4.45E-03
ENSG00000154162	0.0	0.0	0.0	11.5	3.8	3.7	0.0	6.4	(5.1)	4.55E-03
ENSG00000044524	3.8	5.4	4.5	18.4	10.6	31.7	4.6	20.2	(2.1)	4.62E-03
ENSG00000023171	15.3	11.9	24.4	6.9	1.0	1.9	17.2	3.2	2.5	4.68E-03
ENSG00000227640	0.0	0.0	0.0	11.5	2.9	4.7	0.0	6.3	(5.1)	4.69E-03
ENSG00000231890	8.6	6.5	15.4	24.1	35.6	31.7	10.2	30.5	(1.6)	4.69E-03
ENSG00000233223	8.6	10.8	9.0	32.1	26.9	25.2	9.5	28.1	(1.6)	4.74E-03
ENSG00000177679	0.0	0.0	0.0	9.2	2.9	6.5	0.0	6.2	(5.1)	4.76E-03
ENSG00000276966	5.7	7.6	11.7	23.0	21.2	37.3	8.4	27.1	(1.7)	4.89E-03
ENSG00000242574	14.4	5.4	7.2	0.0	1.0	0.0	9.0	0.3	4.6	5.08E-03
ENSG00000205559	12.4	16.3	13.6	50.5	30.8	28.9	14.1	36.7	(1.4)	5.14E-03
ENSG00000204876	9.6	39.0	17.2	8.0	1.0	4.7	21.9	4.6	2.3	5.15E-03
ENSG00000233589	28.7	27.1	39.8	2.3	18.3	8.4	31.9	9.7	1.7	5.19E-03
ENSG00000169777	7.7	15.2	4.5	0.0	0.0	0.9	9.1	0.3	4.6	5.21E-03
ENSG00000120337	14.4	14.1	14.5	2.3	1.0	3.7	14.3	2.3	2.6	5.21E-03
ENSG00000182612	5.7	7.6	11.7	33.3	33.7	15.8	8.4	27.6	(1.7)	5.21E-03
ENSG00000250988	8.6	8.7	17.2	35.6	26.9	34.5	11.5	32.3	(1.5)	5.34E-03
ENSG00000198719	36.4	51.0	43.4	20.7	19.2	17.7	43.6	19.2	1.2	5.56E-03
ENSG00000173762	7.7	7.6	6.3	24.1	22.1	24.2	7.2	23.5	(1.7)	5.57E-03
ENSG00000178852	22.0	21.7	23.5	39.0	64.5	43.8	22.4	49.1	(1.1)	5.65E-03
ENSG00000253730	0.0	0.0	0.0	9.2	4.8	3.7	0.0	5.9	(5.0)	5.84E-03
ENSG00000198203	14.4	13.0	10.8	39.0	25.0	36.4	12.7	33.5	(1.4)	5.94E-03
ENSG00000226887	21.1	19.5	19.9	9.2	0.0	4.7	20.2	4.6	2.2	6.06E-03
ENSG00000144596	2.9	4.3	4.5	23.0	13.5	15.8	3.9	17.4	(2.2)	6.12E-03
ENSG00000170345	67.0	79.1	54.2	18.4	23.1	50.3	66.8	30.6	1.1	6.15E-03
ENSG00000164100	1.9	3.3	2.7	14.9	11.5	16.8	2.6	14.4	(2.5)	6.15E-03
ENSG00000107731	17.2	27.1	19.9	5.7	2.9	8.4	21.4	5.7	1.9	6.16E-03
ENSG00000249207	13.4	20.6	17.2	2.3	5.8	2.8	17.1	3.6	2.2	6.16E-03
ENSG00000225886	41.2	29.3	32.5	4.6	5.8	22.4	34.3	10.9	1.6	6.23E-03
ENSG00000237476	3.8	2.2	3.6	13.8	17.3	15.8	3.2	15.6	(2.3)	6.38E-03
ENSG00000167771	50.7	51.0	57.8	31.0	16.4	28.9	53.2	25.4	1.1	6.41E-03
ENSG00000112299	8.6	6.5	9.9	0.0	0.0	0.9	8.4	0.3	4.5	6.44E-03
ENSG00000277224	1.9	0.0	0.0	9.2	13.5	8.4	0.6	10.3	(4.0)	6.53E-03
ENSG00000181218	6.7	6.5	11.7	27.5	21.2	28.9	8.3	25.9	(1.6)	6.53E-03
ENSG00000162849	16.3	44.5	23.5	12.6	6.7	6.5	28.1	8.6	1.7	6.54E-03
ENSG00000128610	26.8	36.9	28.0	13.8	11.5	8.4	30.6	11.2	1.5	6.60E-03
ENSG00000267858	14.4	14.1	10.8	37.9	27.9	34.5	13.1	33.4	(1.4)	6.60E-03
ENSG00000267288	5.7	3.3	2.7	14.9	23.1	14.0	3.9	17.3	(2.2)	6.64E-03
ENSG00000246596	60.3	34.7	55.1	19.5	27.9	21.4	50.0	23.0	1.1	6.76E-03
ENSG00000180425	23.9	24.9	10.8	52.8	38.5	45.7	19.9	45.7	(1.2)	6.79E-03
ENSG00000166387	46.9	59.6	31.6	25.2	15.4	19.6	46.1	20.1	1.2	6.80E-03
ENSG00000253731	23.0	19.5	17.2	37.9	43.3	50.3	19.9	43.8	(1.1)	6.83E-03
ENSG00000159905	15.3	14.1	20.8	35.6	46.2	36.4	16.7	39.4	(1.2)	6.89E-03
ENSG00000130433	18.2	11.9	22.6	3.4	5.8	2.8	17.6	4.0	2.1	6.94E-03
ENSG00000205426	13.4	10.8	14.5	1.1	2.9	1.9	12.9	2.0	2.7	6.96E-03
ENSG00000188897	3.8	4.3	3.6	17.2	17.3	15.8	3.9	16.8	(2.1)	7.01E-03
ENSG00000183145	2.9	0.0	1.8	16.1	20.2	3.7	1.6	13.3	(3.1)	7.03E-03
ENSG00000103021	38.3	55.3	31.6	10.3	19.2	21.4	41.7	17.0	1.3	7.09E-03
ENSG00000211448	1.0	0.0	1.8	10.3	15.4	6.5	0.9	10.7	(3.5)	7.12E-03
ENSG00000064989	7.7	11.9	9.0	23.0	24.1	35.4	9.5	27.5	(1.5)	7.21E-03
ENSG00000162009	7.7	3.3	7.2	20.7	25.0	18.6	6.0	21.4	(1.8)	7.25E-03
ENSG00000274750	16.3	31.4	13.6	48.2	35.6	56.9	20.4	46.9	(1.2)	7.25E-03
ENSG00000188681	6.7	3.3	6.3	18.4	20.2	21.4	5.4	20.0	(1.9)	7.28E-03
ENSG00000164690	15.3	9.8	9.0	1.1	1.0	1.9	11.4	1.3	3.1	7.35E-03
ENSG00000106772	5.7	8.7	9.9	1.1	0.0	0.0	8.1	0.4	4.5	7.41E-03

ENSG00000215009	8.6	11.9	13.6	2.3	1.0	0.9	11.4	1.4	3.1	7.45E-03
ENSG00000264920	14.4	16.3	12.7	33.3	35.6	35.4	14.4	34.8	(1.3)	7.58E-03
ENSG00000113494	15.3	10.8	12.7	3.4	1.9	0.9	12.9	2.1	2.7	7.59E-03
ENSG00000107954	21.1	9.8	29.8	1.1	8.7	3.7	20.2	4.5	2.1	7.73E-03
ENSG00000152578	3.8	2.2	2.7	12.6	14.4	16.8	2.9	14.6	(2.3)	7.75E-03
ENSG00000124134	46.9	43.4	40.7	20.7	17.3	22.4	43.6	20.1	1.1	7.79E-03
ENSG00000234690	1.0	0.0	0.9	9.2	9.6	10.3	0.6	9.7	(3.9)	7.83E-03
ENSG00000261008	15.3	7.6	6.3	27.5	26.9	29.8	9.7	28.1	(1.5)	7.85E-03
ENSG00000185736	10.5	10.8	9.0	2.3	0.0	0.0	10.1	0.8	3.9	7.87E-03
ENSG00000120322	1.9	0.0	0.9	9.2	10.6	11.2	0.9	10.3	(3.4)	7.88E-03
ENSG00000235890	11.5	11.9	9.9	1.1	1.9	0.9	11.1	1.3	3.1	7.96E-03
ENSG00000237594	0.0	3.3	2.7	14.9	12.5	11.2	2.0	12.9	(2.7)	8.06E-03
ENSG00000259683	6.7	5.4	4.5	16.1	19.2	24.2	5.5	19.8	(1.8)	8.12E-03
ENSG00000279673	1.9	1.1	2.7	17.2	16.4	5.6	1.9	13.1	(2.7)	8.13E-03
ENSG00000163121	5.7	4.3	6.3	0.0	0.0	0.0	5.5	0.0	4.9	8.19E-03
ENSG00000174004	44.0	46.6	41.6	24.1	6.7	24.2	44.1	18.4	1.3	8.19E-03
ENSG00000152785	7.7	4.3	9.0	18.4	24.1	26.1	7.0	22.8	(1.7)	8.33E-03
ENSG00000171450	0.0	0.0	0.0	5.7	6.7	3.7	0.0	5.4	(4.9)	8.33E-03
ENSG00000182324	11.5	15.2	19.9	32.1	30.8	50.3	15.5	37.8	(1.3)	8.35E-03
ENSG00000102359	7.7	6.5	3.6	23.0	18.3	20.5	5.9	20.6	(1.8)	8.36E-03
ENSG00000149781	47.9	41.2	56.0	26.4	26.0	16.8	48.4	23.1	1.1	8.40E-03
ENSG00000100739	5.7	10.8	7.2	0.0	1.0	0.0	7.9	0.3	4.5	8.43E-03
ENSG00000214975	38.3	37.9	19.9	16.1	6.7	12.1	32.0	11.6	1.5	8.48E-03
ENSG00000240241	1.0	2.2	0.0	4.6	16.4	11.2	1.0	10.7	(3.4)	8.48E-03
ENSG00000101825	1.9	1.1	0.9	12.6	9.6	10.3	1.3	10.8	(3.1)	8.49E-03
ENSG00000115935	9.6	13.0	14.5	1.1	3.8	0.0	12.3	1.7	2.9	8.52E-03
ENSG00000246174	12.4	18.4	9.9	45.9	31.8	26.1	13.6	34.6	(1.4)	8.61E-03
ENSG00000136928	23.0	54.2	22.6	63.1	71.2	66.2	33.3	66.8	(1.0)	8.61E-03
ENSG00000158813	46.0	58.5	49.7	19.5	27.9	28.0	51.4	25.1	1.0	8.81E-03
ENSG00000235016	43.1	44.5	34.3	12.6	26.0	13.1	40.6	17.2	1.2	9.00E-03
ENSG00000198832	31.6	24.9	28.0	11.5	11.5	8.4	28.2	10.5	1.4	9.02E-03
ENSG00000280143	21.1	15.2	18.1	8.0	3.8	1.9	18.1	4.6	2.0	9.05E-03
ENSG00000139835	36.4	41.2	42.5	19.5	16.4	18.6	40.0	18.2	1.1	9.43E-03
ENSG00000142233	10.5	7.6	7.2	23.0	23.1	28.0	8.5	24.7	(1.5)	9.53E-03
ENSG00000260823	26.8	24.9	20.8	4.6	9.6	9.3	24.2	7.8	1.6	9.53E-03
ENSG00000228709	35.4	40.1	27.1	13.8	12.5	15.8	34.2	14.0	1.3	9.58E-03
ENSG00000242110	23.9	16.3	14.5	53.9	38.5	32.6	18.2	41.7	(1.2)	9.65E-03
ENSG00000230896	13.4	19.5	14.5	31.0	42.3	36.4	15.8	36.6	(1.2)	9.66E-03
ENSG00000169507	1.0	0.0	0.0	4.6	10.6	7.5	0.3	7.5	(4.4)	9.74E-03
ENSG00000271366	12.4	5.4	5.4	0.0	1.0	0.0	7.8	0.3	4.4	9.78E-03
ENSG00000164855	54.6	41.2	67.8	21.8	35.6	22.4	54.5	26.6	1.0	9.91E-03
ENSG00000137392	3.8	7.6	4.5	0.0	0.0	0.0	5.3	0.0	4.8	9.91E-03
ENSG00000238133	8.6	13.0	15.4	2.3	1.9	1.9	12.3	2.0	2.6	1.00E-02
ENSG00000131242	11.5	21.7	13.6	1.1	3.8	4.7	15.6	3.2	2.2	1.01E-02
ENSG00000184515	26.8	29.3	27.1	9.2	12.5	9.3	27.7	10.3	1.4	1.02E-02
ENSG00000232259	8.6	8.7	10.8	1.1	1.0	0.0	9.4	0.7	3.8	1.02E-02
ENSG00000225091	17.2	13.0	10.8	2.3	2.9	2.8	13.7	2.7	2.4	1.03E-02
ENSG00000196967	30.6	23.9	35.2	36.7	70.2	73.6	29.9	60.2	(1.0)	1.03E-02
ENSG00000259366	10.5	17.3	16.3	28.7	47.1	30.8	14.7	35.5	(1.3)	1.03E-02
ENSG00000224050	13.4	7.6	2.7	0.0	1.0	0.0	7.9	0.3	4.4	1.04E-02
ENSG00000131781	37.3	24.9	17.2	55.1	52.0	54.1	26.5	53.7	(1.0)	1.06E-02
ENSG00000087076	24.9	31.4	19.9	65.4	41.4	48.5	25.4	51.8	(1.0)	1.07E-02
ENSG00000184949	9.6	18.4	15.4	26.4	48.1	31.7	14.5	35.4	(1.3)	1.07E-02
ENSG00000126878	39.3	52.0	34.3	24.1	16.4	16.8	41.9	19.1	1.1	1.08E-02
ENSG00000235054	2.9	6.5	6.3	0.0	0.0	0.0	5.2	0.0	4.8	1.08E-02
ENSG00000186868	27.8	13.0	17.2	43.6	37.5	47.5	19.3	42.9	(1.1)	1.08E-02
ENSG00000151778	43.1	27.1	43.4	19.5	18.3	11.2	37.9	16.3	1.2	1.10E-02
ENSG00000100557	8.6	18.4	8.1	2.3	1.0	1.9	11.7	1.7	2.8	1.11E-02

ENSG00000169071	14.4	7.6	9.9	1.1	1.9	0.9	10.6	1.3	3.0	1.11E-02
ENSG00000273983	1.9	3.3	0.0	9.2	10.6	14.9	1.7	11.6	(2.8)	1.12E-02
ENSG00000241288	13.4	4.3	9.9	20.7	26.9	32.6	9.2	26.7	(1.5)	1.13E-02
ENSG00000124159	18.2	21.7	9.0	2.3	5.8	2.8	16.3	3.6	2.1	1.13E-02
ENSG00000187566	12.4	20.6	18.1	4.6	1.0	6.5	17.0	4.0	2.1	1.14E-02
ENSG00000137745	46.0	49.9	50.6	20.7	15.4	33.6	48.8	23.2	1.1	1.14E-02
ENSG00000273669	14.4	19.5	18.1	5.7	5.8	1.9	17.3	4.5	2.0	1.14E-02
ENSG00000229692	5.7	4.3	8.1	28.7	13.5	20.5	6.1	20.9	(1.8)	1.15E-02
ENSG00000110328	6.7	18.4	9.9	2.3	1.0	1.9	11.7	1.7	2.8	1.16E-02
ENSG00000233215	0.0	0.0	0.0	4.6	6.7	3.7	0.0	5.0	(4.8)	1.17E-02
ENSG00000144837	6.7	5.4	0.0	14.9	18.3	18.6	4.0	17.3	(2.1)	1.18E-02
ENSG00000261324	23.9	14.1	21.7	33.3	43.3	53.1	19.9	43.2	(1.1)	1.18E-02
ENSG00000224081	22.0	10.8	12.7	2.3	4.8	2.8	15.2	3.3	2.2	1.18E-02
ENSG00000166707	15.3	21.7	23.5	48.2	37.5	42.9	20.2	42.9	(1.1)	1.19E-02
ENSG00000144792	0.0	0.0	0.0	6.9	6.7	1.9	0.0	5.2	(4.8)	1.19E-02
ENSG00000258404	1.0	0.0	0.0	2.3	11.5	8.4	0.3	7.4	(4.4)	1.21E-02
ENSG00000109927	31.6	30.4	28.0	9.2	14.4	12.1	30.0	11.9	1.3	1.22E-02
ENSG00000269899	18.2	23.9	22.6	9.2	1.9	8.4	21.5	6.5	1.7	1.22E-02
ENSG00000278763	1.0	7.6	1.8	18.4	13.5	14.9	3.5	15.6	(2.2)	1.23E-02
ENSG00000072163	8.6	23.9	9.9	1.1	2.9	3.7	14.1	2.6	2.4	1.23E-02
ENSG00000240970	39.3	28.2	19.0	8.0	10.6	13.1	28.8	10.6	1.4	1.25E-02
ENSG00000155367	28.7	29.3	27.1	11.5	8.7	13.1	28.4	11.1	1.4	1.25E-02
ENSG00000224269	25.9	24.9	29.8	11.5	11.5	7.5	26.9	10.2	1.4	1.25E-02
ENSG00000178965	2.9	3.3	3.6	10.3	14.4	18.6	3.2	14.5	(2.2)	1.26E-02
ENSG00000254245	1.0	1.1	1.8	11.5	7.7	11.2	1.3	10.1	(3.0)	1.27E-02
ENSG00000103196	22.0	39.0	41.6	11.5	12.5	17.7	34.2	13.9	1.3	1.28E-02
ENSG00000244300	13.4	14.1	18.1	28.7	29.8	48.5	15.2	35.7	(1.2)	1.28E-02
ENSG00000164129	0.0	0.0	0.0	3.4	7.7	3.7	0.0	5.0	(4.8)	1.28E-02
ENSG00000227128	26.8	31.4	27.1	8.0	17.3	5.6	28.5	10.3	1.5	1.29E-02
ENSG00000104833	11.5	6.5	10.8	0.0	1.0	1.9	9.6	0.9	3.3	1.31E-02
ENSG00000175611	8.6	10.8	5.4	20.7	26.0	24.2	8.3	23.6	(1.5)	1.33E-02
ENSG00000197140	6.7	1.1	9.9	17.2	22.1	23.3	5.9	20.9	(1.8)	1.33E-02
ENSG00000188511	13.4	7.6	1.8	0.0	0.0	0.9	7.6	0.3	4.4	1.34E-02
ENSG00000219395	5.7	5.4	3.6	0.0	0.0	0.0	4.9	0.0	4.7	1.34E-02
ENSG00000147231	33.5	41.2	44.3	21.8	22.1	8.4	39.7	17.4	1.2	1.37E-02
ENSG00000005961	1.9	1.1	3.6	12.6	6.7	18.6	2.2	12.7	(2.5)	1.37E-02
ENSG00000184060	0.0	0.0	0.0	8.0	1.0	6.5	0.0	5.2	(4.8)	1.37E-02
ENSG00000162892	9.6	7.6	9.0	1.1	0.0	0.9	8.7	0.7	3.7	1.40E-02
ENSG00000233403	15.3	3.3	13.6	1.1	1.9	0.9	10.7	1.3	3.0	1.40E-02
ENSG00000231513	0.0	0.0	0.0	2.3	5.8	6.5	0.0	4.9	(4.8)	1.41E-02
ENSG00000274428	6.7	4.3	3.6	0.0	0.0	0.0	4.9	0.0	4.7	1.41E-02
ENSG00000213145	4.8	5.4	3.6	12.6	21.2	16.8	4.6	16.9	(1.9)	1.43E-02
ENSG00000227992	46.0	30.4	42.5	14.9	24.1	14.9	39.6	18.0	1.1	1.43E-02
ENSG00000221230	6.7	6.5	1.8	0.0	0.0	0.0	5.0	0.0	4.7	1.45E-02
ENSG00000272153	23.0	23.9	31.6	14.9	6.7	7.5	26.2	9.7	1.5	1.46E-02
ENSG00000102271	0.0	0.0	0.0	9.2	2.9	2.8	0.0	5.0	(4.8)	1.46E-02
ENSG00000109743	20.1	14.1	8.1	3.4	2.9	2.8	14.1	3.0	2.2	1.46E-02
ENSG00000188910	11.5	10.8	13.6	2.3	0.0	3.7	12.0	2.0	2.6	1.46E-02
ENSG00000230400	10.5	8.7	7.2	0.0	0.0	1.9	8.8	0.6	3.7	1.48E-02
ENSG00000145703	31.6	24.9	23.5	8.0	15.4	5.6	26.7	9.7	1.5	1.49E-02
ENSG00000005108	0.0	1.1	0.0	4.6	4.8	11.2	0.4	6.9	(4.3)	1.49E-02
ENSG00000248995	20.1	10.8	9.0	5.7	1.0	0.9	13.3	2.5	2.5	1.50E-02
ENSG00000247796	23.9	13.0	6.3	62.0	26.0	27.0	14.4	38.3	(1.4)	1.51E-02
ENSG00000230863	3.8	3.3	1.8	10.3	18.3	12.1	3.0	13.6	(2.2)	1.51E-02
ENSG00000172062	250.9	229.8	186.1	874.4	857.3	244.3	222.3	658.7	(1.6)	1.52E-02
ENSG00000105982	49.8	53.1	40.7	17.2	34.6	16.8	47.9	22.9	1.1	1.53E-02
ENSG00000066248	12.4	15.2	8.1	24.1	37.5	27.0	11.9	29.6	(1.3)	1.55E-02
ENSG00000231908	1.0	2.2	3.6	17.2	12.5	7.5	2.2	12.4	(2.4)	1.55E-02

ENSG00000279347	11.5	17.3	15.4	3.4	1.0	5.6	14.7	3.3	2.1	1.57E-02
ENSG00000167554	0.0	1.1	0.0	3.4	5.8	11.2	0.4	6.8	(4.3)	1.58E-02
ENSG00000132329	4.8	14.1	17.2	4.6	0.0	0.9	12.0	1.8	2.8	1.58E-02
ENSG00000167207	9.6	10.8	5.4	1.1	1.0	0.0	8.6	0.7	3.7	1.61E-02
ENSG00000177694	13.4	10.8	10.8	21.8	27.9	37.3	11.7	29.0	(1.3)	1.61E-02
ENSG00000275882	23.0	27.1	19.9	43.6	98.1	22.4	23.3	54.7	(1.2)	1.61E-02
ENSG00000145428	1.0	2.2	1.8	10.3	11.5	9.3	1.6	10.4	(2.7)	1.64E-02
ENSG00000203814	3.8	3.3	4.5	14.9	21.2	10.3	3.9	15.4	(2.0)	1.64E-02
ENSG00000228705	8.6	4.3	7.2	1.1	0.0	0.0	6.7	0.4	4.2	1.64E-02
ENSG00000105696	1.9	3.3	1.8	11.5	8.7	15.8	2.3	12.0	(2.4)	1.65E-02
ENSG00000251257	0.0	0.0	1.8	13.8	7.7	4.7	0.6	8.7	(3.8)	1.65E-02
ENSG00000229915	18.2	21.7	12.7	4.6	7.7	1.9	17.5	4.7	1.9	1.65E-02
ENSG00000259877	13.4	17.3	11.7	28.7	34.6	33.6	14.2	32.3	(1.2)	1.65E-02
ENSG00000277369	1.9	3.3	0.0	16.1	4.8	13.1	1.7	11.3	(2.8)	1.67E-02
ENSG00000233822	5.7	4.3	4.5	18.4	12.5	20.5	4.9	17.1	(1.8)	1.67E-02
ENSG00000235381	6.7	6.5	6.3	21.8	21.2	16.8	6.5	19.9	(1.6)	1.68E-02
ENSG00000164841	20.1	26.0	11.7	3.4	4.8	8.4	19.3	5.5	1.8	1.70E-02
ENSG00000234694	7.7	0.0	0.0	19.5	10.6	14.0	2.6	14.7	(2.5)	1.73E-02
ENSG00000269906	46.9	34.7	47.9	17.2	24.1	22.4	43.2	21.2	1.0	1.75E-02
ENSG00000137441	15.3	18.4	17.2	5.7	1.9	6.5	17.0	4.7	1.8	1.75E-02
ENSG00000284837	6.7	6.5	1.8	23.0	13.5	16.8	5.0	17.7	(1.8)	1.76E-02
ENSG00000143502	11.5	11.9	9.0	2.3	2.9	0.0	10.8	1.7	2.7	1.76E-02
ENSG00000169122	5.7	8.7	5.4	0.0	1.0	0.0	6.6	0.3	4.2	1.77E-02
ENSG00000205978	6.7	5.4	18.1	25.2	32.7	25.2	10.1	27.7	(1.4)	1.77E-02
ENSG00000261220	21.1	31.4	19.0	11.5	5.8	8.4	23.8	8.5	1.5	1.78E-02
ENSG00000160161	4.8	0.0	8.1	12.6	19.2	20.5	4.3	17.5	(2.0)	1.79E-02
ENSG00000239704	0.0	0.0	0.0	4.6	1.9	7.5	0.0	4.7	(4.7)	1.79E-02
ENSG00000180096	16.3	23.9	17.2	29.8	39.4	51.3	19.1	40.2	(1.1)	1.81E-02
ENSG00000181029	5.7	8.7	6.3	19.5	18.3	23.3	6.9	20.4	(1.6)	1.84E-02
ENSG00000016402	9.6	4.3	13.6	0.0	1.9	0.9	9.2	1.0	3.2	1.87E-02
ENSG00000145075	10.5	13.0	10.8	23.0	26.9	33.6	11.5	27.8	(1.3)	1.90E-02
ENSG00000261305	4.8	6.5	1.8	14.9	13.5	19.6	4.4	16.0	(1.9)	1.91E-02
ENSG00000147174	7.7	15.2	9.0	27.5	15.4	42.0	10.6	28.3	(1.4)	1.92E-02
ENSG00000261428	25.9	22.8	19.0	10.3	7.7	6.5	22.5	8.2	1.5	1.92E-02
ENSG00000284430	8.6	10.8	10.8	0.0	0.0	3.7	10.1	1.2	2.9	1.94E-02
ENSG00000213185	12.4	21.7	18.1	3.4	7.7	3.7	17.4	5.0	1.8	1.96E-02
ENSG00000170011	3.8	2.2	4.5	18.4	11.5	13.1	3.5	14.3	(2.0)	1.97E-02
ENSG00000035664	25.9	41.2	29.8	12.6	16.4	13.1	32.3	14.0	1.2	1.97E-02
ENSG00000117600	0.0	0.0	0.0	5.7	3.8	3.7	0.0	4.4	(4.6)	1.97E-02
ENSG00000255568	11.5	8.7	15.4	3.4	1.9	1.9	11.8	2.4	2.3	1.97E-02
ENSG00000165816	6.7	3.3	3.6	0.0	0.0	0.0	4.5	0.0	4.6	1.98E-02
ENSG00000285669	1.9	3.3	2.7	9.2	15.4	12.1	2.6	12.2	(2.2)	1.98E-02
ENSG00000277758	2.9	5.4	4.5	13.8	21.2	12.1	4.3	15.7	(1.9)	1.99E-02
ENSG00000278330	28.7	13.0	18.1	6.9	4.8	7.5	19.9	6.4	1.6	1.99E-02
ENSG00000049089	5.7	6.5	8.1	17.2	17.3	26.1	6.8	20.2	(1.6)	2.00E-02
ENSG00000138400	10.5	13.0	8.1	28.7	22.1	28.0	10.6	26.3	(1.3)	2.03E-02
ENSG00000154548	5.7	1.1	7.2	0.0	0.0	0.0	4.7	0.0	4.7	2.03E-02
ENSG00000179057	30.6	27.1	42.5	18.4	11.5	14.9	33.4	14.9	1.2	2.03E-02
ENSG00000162998	0.0	0.0	4.5	5.7	14.4	13.1	1.5	11.1	(2.8)	2.04E-02
ENSG00000284681	30.6	28.2	28.0	12.6	12.5	12.1	28.9	12.4	1.2	2.05E-02
ENSG00000153294	2.9	2.2	0.0	8.0	7.7	15.8	1.7	10.5	(2.7)	2.06E-02
ENSG00000154274	30.6	22.8	19.0	10.3	9.6	7.5	24.1	9.1	1.4	2.07E-02
ENSG00000170965	19.1	14.1	20.8	1.1	6.7	7.5	18.0	5.1	1.8	2.07E-02
ENSG00000154153	11.5	10.8	19.0	35.6	25.0	35.4	13.8	32.0	(1.2)	2.08E-02
ENSG00000251350	20.1	27.1	17.2	2.3	13.5	3.7	21.5	6.5	1.7	2.11E-02
ENSG00000141314	4.8	3.3	5.4	14.9	12.5	20.5	4.5	16.0	(1.8)	2.11E-02
ENSG00000124602	17.2	20.6	15.4	6.9	2.9	6.5	17.7	5.4	1.7	2.12E-02
ENSG00000226312	16.3	19.5	17.2	6.9	2.9	6.5	17.7	5.4	1.7	2.14E-02

ENSG00000221821	23.9	13.0	13.6	28.7	37.5	43.8	16.8	36.7	(1.1)	2.14E-02
ENSG00000242732	7.7	17.3	9.0	1.1	3.8	0.9	11.3	2.0	2.5	2.14E-02
ENSG00000100276	0.0	1.1	0.9	9.2	8.7	5.6	0.7	7.8	(3.6)	2.15E-02
ENSG00000249459	15.3	15.2	13.6	25.2	36.6	35.4	14.7	32.4	(1.1)	2.16E-02
ENSG00000199266	17.2	8.7	11.7	1.1	1.9	4.7	12.6	2.6	2.3	2.17E-02
ENSG00000230257	5.7	2.2	2.7	20.7	11.5	11.2	3.5	14.5	(2.0)	2.17E-02
ENSG00000260442	16.3	17.3	18.1	41.3	31.8	35.4	17.2	36.2	(1.1)	2.19E-02
ENSG00000158315	16.3	22.8	17.2	48.2	35.6	32.6	18.7	38.8	(1.1)	2.21E-02
ENSG00000188833	3.8	1.1	8.1	9.2	14.4	28.0	4.3	17.2	(2.0)	2.22E-02
ENSG00000256802	3.8	7.6	7.2	20.7	19.2	16.8	6.2	18.9	(1.6)	2.22E-02
ENSG00000274565	6.7	6.5	9.0	21.8	22.1	18.6	7.4	20.9	(1.5)	2.25E-02
ENSG00000233381	30.6	21.7	13.6	67.7	39.4	32.6	22.0	46.6	(1.1)	2.25E-02
ENSG00000223802	4.8	0.0	0.9	14.9	10.6	8.4	1.9	11.3	(2.5)	2.25E-02
ENSG00000184599	6.7	7.6	9.0	0.0	1.0	0.9	7.8	0.6	3.6	2.26E-02
ENSG00000180764	21.1	31.4	18.1	10.3	8.7	7.5	23.5	8.8	1.4	2.27E-02
ENSG00000261122	0.0	0.0	0.0	3.4	6.7	2.8	0.0	4.3	(4.6)	2.27E-02
ENSG00000274276	102.4	79.1	76.8	323.6	146.2	126.8	86.1	198.9	(1.2)	2.31E-02
ENSG00000276934	11.5	7.6	6.3	1.1	1.0	0.9	8.5	1.0	3.1	2.31E-02
ENSG00000246089	15.3	9.8	16.3	41.3	26.9	27.0	13.8	31.8	(1.2)	2.34E-02
ENSG00000262468	14.4	17.3	23.5	29.8	39.4	45.7	18.4	38.3	(1.1)	2.35E-02
ENSG00000273796	20.1	16.3	22.6	47.1	32.7	40.1	19.7	40.0	(1.0)	2.37E-02
ENSG00000180155	41.2	29.3	21.7	10.3	17.3	11.2	30.7	12.9	1.2	2.37E-02
ENSG00000264932	1.0	1.1	0.9	2.3	14.4	9.3	1.0	8.7	(3.2)	2.38E-02
ENSG00000155719	6.7	10.8	8.1	1.1	1.9	0.0	8.6	1.0	3.1	2.41E-02
ENSG00000186496	12.4	9.8	8.1	26.4	29.8	19.6	10.1	25.3	(1.3)	2.45E-02
ENSG00000284644	9.6	7.6	6.3	0.0	1.9	0.0	7.8	0.6	3.6	2.46E-02
ENSG00000168918	9.6	11.9	4.5	1.1	0.0	1.9	8.7	1.0	3.1	2.47E-02
ENSG00000139344	1.9	2.2	3.6	12.6	6.7	16.8	2.6	12.0	(2.2)	2.49E-02
ENSG00000229167	4.8	3.3	5.4	17.2	13.5	15.8	4.5	15.5	(1.8)	2.50E-02
ENSG00000205177	23.9	23.9	31.6	11.5	11.5	10.3	26.5	11.1	1.3	2.50E-02
ENSG00000124635	3.8	5.4	5.4	21.8	7.7	21.4	4.9	17.0	(1.8)	2.50E-02
ENSG00000070831	10.5	8.7	9.9	13.8	38.5	24.2	9.7	25.5	(1.4)	2.51E-02
ENSG00000259807	0.0	2.2	0.0	12.6	3.8	7.5	0.7	8.0	(3.6)	2.53E-02
ENSG00000268916	7.7	16.3	12.7	3.4	1.9	2.8	12.2	2.7	2.2	2.53E-02
ENSG00000226695	10.5	11.9	9.0	2.3	1.9	1.9	10.5	2.0	2.4	2.54E-02
ENSG00000100055	11.5	29.3	18.1	11.5	3.8	2.8	19.6	6.0	1.7	2.54E-02
ENSG00000188404	15.3	15.2	10.8	3.4	5.8	0.9	13.8	3.4	2.0	2.54E-02
ENSG00000172733	4.8	3.3	5.4	16.1	17.3	13.1	4.5	15.5	(1.8)	2.55E-02
ENSG00000132911	1.0	4.3	8.1	0.0	0.0	0.0	4.5	0.0	4.6	2.56E-02
ENSG00000122254	7.7	1.1	4.5	0.0	0.0	0.0	4.4	0.0	4.6	2.56E-02
ENSG00000104237	27.8	30.4	38.0	16.1	7.7	18.6	32.0	14.1	1.2	2.57E-02
ENSG00000123572	26.8	19.5	24.4	3.4	6.7	14.9	23.6	8.4	1.5	2.61E-02
ENSG00000267414	5.7	4.3	0.9	14.9	7.7	21.4	3.7	14.7	(2.0)	2.62E-02
ENSG00000283689	1.9	4.3	2.7	13.8	9.6	14.0	3.0	12.5	(2.1)	2.62E-02
ENSG00000144406	0.0	0.0	0.0	2.3	2.9	7.5	0.0	4.2	(4.6)	2.64E-02
ENSG00000147003	21.1	5.4	9.9	1.1	4.8	0.9	12.1	2.3	2.4	2.66E-02
ENSG00000275405	6.7	15.2	11.7	0.0	4.8	0.9	11.2	1.9	2.5	2.67E-02
ENSG00000042980	4.8	6.5	6.3	1.1	0.0	0.0	5.9	0.4	4.0	2.68E-02
ENSG00000283982	1.9	1.1	0.9	11.5	9.6	5.6	1.3	8.9	(2.8)	2.69E-02
ENSG00000282988	0.0	0.0	2.7	5.7	6.7	13.1	0.9	8.5	(3.2)	2.69E-02
ENSG00000157404	13.4	17.3	20.8	3.4	3.8	8.4	17.2	5.2	1.7	2.69E-02
ENSG00000259424	0.0	0.0	0.9	8.0	4.8	4.7	0.3	5.8	(4.0)	2.69E-02
ENSG00000203724	10.5	10.8	9.0	26.4	32.7	16.8	10.1	25.3	(1.3)	2.69E-02
ENSG00000205078	14.4	19.5	16.3	34.4	33.7	35.4	16.7	34.5	(1.1)	2.70E-02
ENSG00000250305	10.5	15.2	18.1	2.3	1.0	7.5	14.6	3.6	2.0	2.70E-02
ENSG00000115598	1.0	1.1	0.0	6.9	9.6	5.6	0.7	7.4	(3.5)	2.74E-02
ENSG00000162814	1.9	1.1	4.5	14.9	7.7	13.1	2.5	11.9	(2.2)	2.74E-02
ENSG00000215262	7.7	7.6	11.7	0.0	1.9	1.9	9.0	1.3	2.8	2.75E-02

ENSG00000251867	20.1	20.6	9.9	2.3	7.7	4.7	16.9	4.9	1.8	2.79E-02
ENSG00000273108	2.9	3.3	6.3	0.0	0.0	0.0	4.2	0.0	4.5	2.80E-02
ENSG00000269388	0.0	2.2	0.9	9.2	7.7	7.5	1.0	8.1	(3.0)	2.81E-02
ENSG00000138061	16.3	14.1	22.6	2.3	6.7	7.5	17.7	5.5	1.7	2.83E-02
ENSG00000257596	27.8	28.2	14.5	13.8	7.7	4.7	23.5	8.7	1.5	2.84E-02
ENSG00000249855	1.9	1.1	1.8	14.9	9.6	4.7	1.6	9.7	(2.6)	2.87E-02
ENSG00000253309	4.8	15.2	7.2	29.8	23.1	18.6	9.1	23.9	(1.4)	2.87E-02
ENSG00000227533	0.0	0.0	0.0	1.1	6.7	4.7	0.0	4.2	(4.5)	2.87E-02
ENSG00000183798	9.6	15.2	14.5	3.4	2.9	3.7	13.1	3.4	2.0	2.88E-02
ENSG00000267244	23.0	37.9	47.0	8.0	19.2	20.5	36.0	15.9	1.2	2.89E-02
ENSG00000275557	8.6	8.7	13.6	2.3	1.9	1.9	10.3	2.0	2.4	2.90E-02
ENSG00000141294	16.3	18.4	17.2	37.9	26.9	42.0	17.3	35.6	(1.0)	2.92E-02
ENSG00000270547	9.6	7.6	7.2	1.1	0.0	1.9	8.1	1.0	3.0	2.93E-02
ENSG00000285094	1.9	11.9	4.5	1.1	0.0	0.0	6.1	0.4	4.1	2.93E-02
ENSG00000182795	14.4	18.4	18.1	8.0	4.8	3.7	17.0	5.5	1.6	2.96E-02
ENSG00000249835	7.7	2.2	2.7	0.0	0.0	0.0	4.2	0.0	4.5	2.96E-02
ENSG00000227764	1.9	1.1	0.0	9.2	10.6	4.7	1.0	8.1	(3.0)	2.96E-02
ENSG00000123342	16.3	14.1	14.5	29.8	36.6	28.9	14.9	31.8	(1.1)	2.96E-02
ENSG00000236617	0.0	0.0	0.0	8.0	3.8	0.9	0.0	4.3	(4.6)	2.96E-02
ENSG00000164082	4.8	4.3	8.1	0.0	0.0	0.9	5.8	0.3	4.0	2.99E-02
ENSG00000246898	13.4	4.3	7.2	17.2	24.1	26.1	8.3	22.5	(1.4)	3.01E-02
ENSG00000205832	0.0	0.0	0.0	6.9	4.8	0.9	0.0	4.2	(4.5)	3.03E-02
ENSG00000162755	9.6	9.8	21.7	37.9	22.1	35.4	13.7	31.8	(1.2)	3.03E-02
ENSG00000173208	4.8	1.1	0.0	6.9	7.7	18.6	2.0	11.1	(2.5)	3.04E-02
ENSG00000248103	0.0	0.0	0.0	3.4	2.9	5.6	0.0	4.0	(4.5)	3.07E-02
ENSG00000107742	21.1	19.5	14.5	39.0	29.8	42.0	18.3	36.9	(1.0)	3.08E-02
ENSG00000197093	20.1	7.6	13.6	2.3	1.0	6.5	13.7	3.3	2.1	3.09E-02
ENSG00000250073	12.4	15.2	6.3	2.3	3.8	0.9	11.3	2.4	2.3	3.10E-02
ENSG00000178301	6.7	22.8	22.6	42.5	37.5	32.6	17.4	37.5	(1.1)	3.11E-02
ENSG00000265817	0.0	2.2	0.0	3.4	8.7	10.3	0.7	7.5	(3.5)	3.13E-02
ENSG00000172748	15.3	19.5	17.2	39.0	30.8	35.4	17.3	35.1	(1.0)	3.15E-02
ENSG00000267904	23.0	23.9	28.0	11.5	12.5	7.5	24.9	10.5	1.3	3.17E-02
ENSG00000267370	1.9	5.4	0.9	9.2	17.3	9.3	2.7	11.9	(2.2)	3.19E-02
ENSG00000181804	6.7	9.8	5.4	17.2	16.4	26.1	7.3	19.9	(1.5)	3.22E-02
ENSG00000111700	1.0	0.0	3.6	6.9	13.5	8.4	1.5	9.6	(2.6)	3.23E-02
ENSG00000224746	13.4	6.5	6.3	1.1	1.9	0.9	8.7	1.3	2.7	3.23E-02
ENSG00000278456	6.7	7.6	6.3	8.0	28.9	23.3	6.9	20.1	(1.6)	3.24E-02
ENSG00000258315	13.4	10.8	14.5	4.6	3.8	1.9	12.9	3.4	1.9	3.24E-02
ENSG00000280445	22.0	10.8	13.6	4.6	4.8	4.7	15.5	4.7	1.7	3.28E-02
ENSG00000263874	28.7	33.6	29.8	9.2	20.2	12.1	30.7	13.8	1.1	3.29E-02
ENSG00000204428	12.4	5.4	10.8	19.5	26.9	25.2	9.6	23.9	(1.3)	3.30E-02
ENSG00000255100	1.9	0.0	0.9	8.0	7.7	7.5	0.9	7.7	(3.0)	3.30E-02
ENSG00000133863	5.7	5.4	5.4	1.1	0.0	0.0	5.5	0.4	3.9	3.30E-02
ENSG00000072201	43.1	31.4	28.9	18.4	15.4	16.8	34.5	16.8	1.0	3.31E-02
ENSG00000213123	13.4	11.9	14.5	34.4	25.0	28.0	13.3	29.1	(1.1)	3.33E-02
ENSG00000198729	8.6	5.4	7.2	1.1	1.0	0.0	7.1	0.7	3.4	3.37E-02
ENSG00000235772	14.4	7.6	17.2	3.4	4.8	1.9	13.0	3.4	2.0	3.38E-02
ENSG00000260219	9.6	10.8	17.2	28.7	28.9	27.0	12.5	28.2	(1.2)	3.38E-02
ENSG00000271609	6.7	9.8	9.0	1.1	1.0	1.9	8.5	1.3	2.7	3.41E-02
ENSG00000241170	38.3	14.1	21.7	3.4	11.5	12.1	24.7	9.0	1.4	3.43E-02
ENSG00000285106	33.5	43.4	30.7	17.2	21.2	14.9	35.9	17.8	1.0	3.45E-02
ENSG00000149633	9.6	10.8	18.1	3.4	1.9	4.7	12.8	3.3	1.9	3.56E-02
ENSG00000253485	7.7	13.0	8.1	24.1	21.2	24.2	9.6	23.2	(1.3)	3.57E-02
ENSG00000170899	9.6	10.8	17.2	24.1	35.6	25.2	12.5	28.3	(1.2)	3.60E-02
ENSG00000285331	8.6	6.5	6.3	25.2	16.4	16.8	7.1	19.5	(1.4)	3.61E-02
ENSG00000244668	0.0	0.0	0.0	3.4	7.7	0.9	0.0	4.0	(4.5)	3.61E-02
ENSG00000189132	4.8	6.5	0.9	0.0	0.0	0.0	4.1	0.0	4.4	3.62E-02
ENSG00000170688	2.9	8.7	0.9	0.0	0.0	0.0	4.1	0.0	4.5	3.63E-02

ENSG00000099958	4.8	6.5	3.6	13.8	22.1	11.2	5.0	15.7	(1.7)	3.66E-02
ENSG00000228696	20.1	7.6	23.5	39.0	41.4	28.9	17.1	36.4	(1.1)	3.69E-02
ENSG00000144362	18.2	13.0	19.0	42.5	28.9	31.7	16.7	34.3	(1.0)	3.69E-02
ENSG00000198963	18.2	17.3	21.7	8.0	4.8	8.4	19.1	7.1	1.4	3.72E-02
ENSG00000168852	2.9	1.1	0.0	11.5	7.7	6.5	1.3	8.6	(2.7)	3.72E-02
ENSG00000133958	5.7	0.0	3.6	11.5	18.3	9.3	3.1	13.0	(2.0)	3.72E-02
ENSG00000171724	0.0	0.0	1.8	3.4	13.5	4.7	0.6	7.2	(3.5)	3.73E-02
ENSG00000279970	4.8	8.7	7.2	0.0	1.0	0.9	6.9	0.6	3.4	3.73E-02
ENSG00000187066	13.4	9.8	10.8	1.1	4.8	1.9	11.3	2.6	2.1	3.77E-02
ENSG00000275632	23.9	21.7	22.6	6.9	12.5	8.4	22.7	9.3	1.3	3.77E-02
ENSG00000279198	42.1	26.0	34.3	16.1	20.2	14.0	34.2	16.8	1.0	3.77E-02
ENSG00000172345	29.7	23.9	21.7	3.4	13.5	13.1	25.1	10.0	1.3	3.80E-02
ENSG00000164796	7.7	7.6	7.2	1.1	1.0	0.9	7.5	1.0	2.9	3.81E-02
ENSG00000120664	4.8	2.2	4.5	19.5	9.6	12.1	3.8	13.7	(1.8)	3.83E-02
ENSG00000105383	24.9	13.0	25.3	10.3	6.7	7.5	21.1	8.2	1.4	3.84E-02
ENSG00000162999	7.7	16.3	12.7	23.0	27.9	30.8	12.2	27.2	(1.2)	3.86E-02
ENSG00000279170	1.0	3.3	2.7	9.2	10.6	11.2	2.3	10.3	(2.2)	3.87E-02
ENSG00000140057	0.0	1.1	2.7	13.8	8.7	3.7	1.3	8.7	(2.7)	3.88E-02
ENSG00000251580	3.8	6.5	6.3	27.5	19.2	6.5	5.6	17.8	(1.7)	3.88E-02
ENSG00000183153	1.9	1.1	0.9	13.8	5.8	5.6	1.3	8.4	(2.7)	3.91E-02
ENSG00000248019	7.7	1.1	1.8	18.4	9.6	13.1	3.5	13.7	(1.9)	3.94E-02
ENSG00000226386	1.0	1.1	0.0	5.7	7.7	6.5	0.7	6.7	(3.3)	3.96E-02
ENSG00000231584	16.3	26.0	20.8	11.5	7.7	5.6	21.0	8.3	1.4	4.00E-02
ENSG00000171189	20.1	13.0	9.0	5.7	2.9	3.7	14.1	4.1	1.8	4.00E-02
ENSG00000242082	4.8	7.6	3.6	0.0	0.0	0.9	5.3	0.3	3.9	4.00E-02
ENSG00000238142	16.3	13.0	12.7	29.8	40.4	20.5	14.0	30.3	(1.1)	4.02E-02
ENSG00000175697	2.9	5.4	2.7	11.5	21.2	7.5	3.7	13.4	(1.9)	4.02E-02
ENSG00000274628	2.9	0.0	0.9	8.0	5.8	11.2	1.3	8.3	(2.7)	4.04E-02
ENSG00000280326	7.7	7.6	7.2	0.0	1.9	0.9	7.5	1.0	2.9	4.04E-02
ENSG00000198400	3.8	9.8	2.7	1.1	0.0	0.0	5.4	0.4	3.9	4.05E-02
ENSG00000270060	28.7	31.4	24.4	6.9	18.3	12.1	28.2	12.4	1.2	4.06E-02
ENSG00000230612	2.9	1.1	0.0	6.9	9.6	8.4	1.3	8.3	(2.7)	4.08E-02
ENSG00000283050	7.7	23.9	9.0	28.7	23.1	40.1	13.5	30.6	(1.2)	4.10E-02
ENSG00000272196	1.0	2.2	0.9	4.6	8.7	11.2	1.3	8.1	(2.6)	4.13E-02
ENSG00000114805	6.7	19.5	7.2	20.7	20.2	40.1	11.1	27.0	(1.3)	4.13E-02
ENSG00000201512	15.3	18.4	17.2	5.7	6.7	5.6	17.0	6.0	1.5	4.15E-02
ENSG00000253438	7.7	3.3	12.7	2.3	1.0	0.0	7.9	1.1	2.9	4.15E-02
ENSG00000196366	29.7	21.7	19.0	14.9	5.8	8.4	23.4	9.7	1.3	4.17E-02
ENSG00000154118	1.0	0.0	0.0	6.9	4.8	3.7	0.3	5.1	(3.9)	4.19E-02
ENSG00000251364	7.7	7.6	9.0	1.1	1.9	0.9	8.1	1.3	2.6	4.20E-02
ENSG00000132026	1.0	2.2	5.4	10.3	14.4	10.3	2.8	11.7	(2.0)	4.25E-02
ENSG00000259456	12.4	13.0	13.6	27.5	32.7	23.3	13.0	27.9	(1.1)	4.28E-02
ENSG00000230937	0.0	2.2	1.8	11.5	7.7	5.6	1.3	8.3	(2.6)	4.28E-02
ENSG00000168874	2.9	5.4	4.5	18.4	11.5	12.1	4.3	14.0	(1.7)	4.29E-02
ENSG00000249684	1.9	8.7	5.4	1.1	0.0	0.0	5.3	0.4	3.9	4.30E-02
ENSG00000033122	20.1	10.8	20.8	0.0	4.8	10.3	17.2	5.0	1.7	4.34E-02
ENSG00000210100	1.9	1.1	7.2	13.8	24.1	4.7	3.4	14.2	(2.0)	4.35E-02
ENSG00000186007	1.9	5.4	9.0	13.8	16.4	19.6	5.5	16.6	(1.6)	4.36E-02
ENSG00000138028	1.0	1.1	0.9	4.6	6.7	10.3	1.0	7.2	(2.9)	4.36E-02
ENSG00000176383	10.5	14.1	13.6	28.7	26.9	26.1	12.7	27.2	(1.1)	4.39E-02
ENSG00000204936	16.3	18.4	9.0	6.9	3.8	2.8	14.6	4.5	1.7	4.39E-02
ENSG00000261189	9.6	14.1	7.2	2.3	1.9	2.8	10.3	2.3	2.1	4.41E-02
ENSG00000204584	14.4	14.1	9.0	5.7	1.9	2.8	12.5	3.5	1.9	4.44E-02
ENSG00000144821	8.6	3.3	7.2	11.5	24.1	18.6	6.4	18.1	(1.5)	4.46E-02
ENSG00000109705	27.8	34.7	29.8	17.2	19.2	6.5	30.8	14.3	1.1	4.46E-02
ENSG00000184619	4.8	4.3	11.7	21.8	14.4	21.4	7.0	19.2	(1.4)	4.48E-02
ENSG00000229932	35.4	17.3	28.0	8.0	14.4	13.1	26.9	11.8	1.2	4.50E-02
ENSG00000226007	2.9	1.1	1.8	18.4	6.7	4.7	1.9	9.9	(2.3)	4.50E-02

ENSG00000168309	7.7	9.8	4.5	1.1	1.0	0.9	7.3	1.0	2.9	4.52E-02
ENSG00000184408	9.6	9.8	2.7	23.0	15.4	20.5	7.3	19.6	(1.4)	4.52E-02
ENSG00000277182	1.9	4.3	5.4	10.3	13.5	15.8	3.9	13.2	(1.8)	4.54E-02
ENSG00000234648	24.9	32.5	5.4	63.1	48.1	26.1	20.9	45.8	(1.1)	4.56E-02
ENSG00000062582	24.9	21.7	27.1	10.3	6.7	14.9	24.6	10.7	1.2	4.56E-02
ENSG00000147160	5.7	15.2	6.3	2.3	1.9	0.9	9.1	1.7	2.4	4.57E-02
ENSG00000203279	0.0	2.2	1.8	8.0	10.6	5.6	1.3	8.1	(2.6)	4.59E-02
ENSG00000150722	28.7	10.8	17.2	57.4	32.7	28.0	18.9	39.4	(1.0)	4.59E-02
ENSG00000270441	12.4	10.8	16.3	25.2	32.7	26.1	13.2	28.0	(1.1)	4.67E-02
ENSG00000171860	5.7	9.8	10.8	1.1	1.0	2.8	8.8	1.6	2.4	4.67E-02
ENSG00000186517	1.9	4.3	0.9	9.2	15.4	6.5	2.4	10.4	(2.2)	4.68E-02
ENSG00000277406	15.3	10.8	6.3	3.4	3.8	0.0	10.8	2.4	2.2	4.72E-02
ENSG00000109667	18.2	17.3	15.4	3.4	9.6	4.7	17.0	5.9	1.5	4.72E-02
ENSG00000279766	22.0	9.8	8.1	1.1	3.8	5.6	13.3	3.5	1.9	4.73E-02
ENSG00000159374	9.6	8.7	20.8	0.0	6.7	2.8	13.0	3.2	2.0	4.74E-02
ENSG00000210077	7.7	2.2	6.3	6.9	23.1	20.5	5.4	16.8	(1.6)	4.74E-02
ENSG00000245156	26.8	17.3	33.4	8.0	16.4	9.3	25.9	11.2	1.2	4.76E-02
ENSG00000242338	23.0	24.9	28.0	6.9	10.6	15.8	25.3	11.1	1.2	4.79E-02
ENSG00000240668	3.8	9.8	8.1	1.1	1.0	0.9	7.2	1.0	2.8	4.79E-02
ENSG00000167994	18.2	21.7	22.6	13.8	6.7	4.7	20.8	8.4	1.3	4.80E-02
ENSG00000101230	7.7	15.2	6.3	1.1	1.0	3.7	9.7	1.9	2.3	4.80E-02
ENSG00000117407	20.1	14.1	19.0	5.7	6.7	7.5	17.7	6.6	1.4	4.81E-02
ENSG00000229373	12.4	11.9	15.4	2.3	7.7	0.9	13.2	3.6	1.9	4.84E-02
ENSG00000269688	21.1	29.3	18.1	10.3	9.6	9.3	22.8	9.8	1.2	4.86E-02
ENSG00000203780	11.5	16.3	9.0	20.7	27.9	30.8	12.3	26.4	(1.1)	4.92E-02
ENSG00000204131	4.8	5.4	4.5	1.1	0.0	0.0	4.9	0.4	3.8	4.96E-02
ENSG00000272505	10.5	4.3	13.6	2.3	1.9	1.9	9.5	2.0	2.2	4.97E-02
ENSG00000143036	26.8	32.5	28.0	19.5	12.5	10.3	29.1	14.1	1.1	4.97E-02
ENSG00000244479	20.1	22.8	18.1	3.4	12.5	7.5	20.3	7.8	1.4	4.98E-02
ENSG00000255135	7.7	20.6	11.7	32.1	31.8	22.4	13.3	28.8	(1.1)	4.99E-02

Extended Data Table. 3 | Candidate list of key proteins in proteomic sequencing
(|log2(FoldChange)| >= 1 & padj<= 0.05)

Protein IDs	Gene Name	FC	p-value	regulation	GOCC_num	GOMF_num	GOBP_num	KEGG_num	pathway_in_cancer	disease_with_cancer
P05362	ICAM1	14.28	0.00	UP	1.00	1.00	4.00	2.00	NO	YES
Q14435	GALNT3	9.51	0.00	UP	0.00	1.00	1.00	1.00	NO	YES
O95810	CAVIN2	9.31	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
P21589	NT5E	7.19	0.00	UP	1.00	0.00	0.00	2.00	NO	YES
Q9BY67	CADM1	6.39	0.00	UP	0.00	2.00	1.00	0.00	NO	YES
P13726	F3	5.93	0.00	UP	1.00	0.00	2.00	0.00	NO	YES
Q86WV6	STING1	5.85	0.02	UP	1.00	1.00	2.00	0.00	NO	YES
Q15147	PLCB4	5.44	0.00	UP	3.00	0.00	0.00	2.00	YES	YES
O14523	C2CD2L	5.05	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
Q7Z7K6	CENPV	4.95	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q03405	PLAUR	4.90	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
P04179	SOD2	4.53	0.00	UP	0.00	2.00	3.00	1.00	NO	YES
P24593	IGFBP5	4.32	0.01	UP	1.00	0.00	3.00	0.00	NO	YES
Q9P2B2	PTGFRN	4.11	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q99959	PKP2	3.99	0.00	UP	2.00	0.00	4.00	0.00	NO	YES
Q9UBP4	DKK3	3.95	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
O43520	ATP8B1	3.81	0.00	UP	0.00	2.00	2.00	0.00	NO	YES
Q9Y646	CPQ	3.81	0.01	UP	1.00	1.00	1.00	0.00	NO	YES
Q13753	LAMC2	3.79	0.00	UP	1.00	1.00	1.00	0.00	YES	YES
Q56VL3	OCIAD2	3.76	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
P16260	SLC25A16	3.58	0.01	UP	1.00	0.00	1.00	0.00	NO	YES
P50895	BCAM	3.57	0.00	UP	1.00	1.00	1.00	0.00	NO	YES
P08174	CD55	3.47	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
P21926	CD9	3.42	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
Q9HCG7	GBA2	3.33	0.01	UP	1.00	0.00	2.00	1.00	NO	YES
O75427	LRCH4	3.32	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
Q14393	GAS6	3.25	0.00	UP	2.00	2.00	10.00	1.00	NO	YES
P43121	MCAM	3.11	0.00	UP	3.00	0.00	1.00	0.00	NO	YES
O94832	MYO1D	3.05	0.00	UP	2.00	1.00	0.00	0.00	NO	YES
Q9Y446	PKP3	3.05	0.02	UP	1.00	0.00	4.00	0.00	NO	YES
Q6IAN0	DHRS7B	3.01	0.00	UP	0.00	1.00	0.00	0.00	NO	YES
P15954	COX7C	3.00	0.05	UP	1.00	0.00	0.00	2.00	NO	NO
Q07617	SPAG1	2.98	0.00	UP	3.00	0.00	2.00	0.00	NO	YES
P78563	ADARB1	2.97	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
Q8N442	GUF1	2.93	0.00	UP	2.00	0.00	0.00	0.00	NO	YES
O75190	DNAJB6	2.92	0.00	UP	2.00	4.00	4.00	0.00	NO	YES
O00584	RNASET2	2.92	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
O75110	ATP9A	2.89	0.05	UP	0.00	2.00	2.00	0.00	NO	YES
Q9NX76	CMTM6	2.89	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
P54132	BLM	2.88	0.03	UP	3.00	5.00	1.00	0.00	NO	YES
Q7L590	MCM10	2.87	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
Q9UMX3	BOK	2.87	0.00	UP	1.00	2.00	2.00	0.00	NO	YES
O14678	ABCD4	2.87	0.01	UP	1.00	3.00	1.00	1.00	NO	YES
Q9Y4L1	HYOU1	2.86	0.00	UP	1.00	1.00	1.00	0.00	NO	YES
Q96CU9	FOXRED1	2.85	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q53H12	AGK	2.84	0.00	UP	2.00	1.00	2.00	1.00	NO	YES
Q08431	MFGE8	2.83	0.00	UP	1.00	2.00	7.00	1.00	NO	YES
Q9Y6M7	SLC4A7	2.82	0.00	UP	2.00	1.00	1.00	0.00	NO	YES
Q06136	KDSR	2.77	0.00	UP	3.00	2.00	1.00	1.00	NO	YES
Q6ZNB6	NFXL1	2.77	0.00	UP	2.00	0.00	0.00	0.00	NO	YES
P08236	GUSB	2.75	0.00	UP	1.00	0.00	3.00	4.00	NO	YES
Q8IUW5	RELL1	2.73	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q9NPE2	NGRN	2.72	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
O43854	EDIL3	2.72	0.01	UP	2.00	1.00	5.00	0.00	NO	YES
O60245	PCDH7	2.70	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q8NCL4	GALNT6	2.69	0.00	UP	0.00	1.00	1.00	1.00	NO	YES
Q02539	H1-1	2.67	0.00	UP	0.00	2.00	0.00	0.00	NO	NO

Q9NZQ7	CD274	2.67	0.00	UP	1.00	0.00	2.00	0.00	NO	YES
O15118	NPC1	2.64	0.00	UP	2.00	1.00	4.00	0.00	NO	YES
P08240	SRPRA	2.63	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q8NEU8	APPL2	2.62	0.00	UP	1.00	2.00	4.00	0.00	NO	YES
P40261	NNMT	2.61	0.01	UP	1.00	0.00	3.00	1.00	NO	YES
O60437	PPL	2.55	0.03	UP	4.00	0.00	2.00	0.00	NO	YES
Q8NCG7	DAGLB	2.54	0.05	UP	1.00	0.00	0.00	0.00	NO	YES
P17275	JUNB	2.49	0.01	UP	0.00	3.00	4.00	0.00	NO	YES
P05026	ATP1B1	2.48	0.00	UP	1.00	2.00	2.00	1.00	NO	YES
O15533	TAPBP	2.47	0.00	UP	2.00	4.00	4.00	2.00	NO	YES
Q9NX40	OCIAD1	2.47	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
O43291	SPINT2	2.47	0.02	UP	2.00	0.00	3.00	0.00	NO	YES
Q96HD1	CRELD1	2.46	0.01	UP	0.00	1.00	0.00	0.00	NO	YES
Q13751	LAMB3	2.46	0.00	UP	1.00	1.00	1.00	0.00	YES	YES
P00749	PLAU	2.45	0.01	UP	1.00	0.00	2.00	0.00	NO	YES
Q4KMQ2	ANO6	2.44	0.00	UP	1.00	1.00	2.00	1.00	NO	YES
Q9Y5Q0	FADS3	2.42	0.01	UP	0.00	0.00	0.00	0.00	NO	YES
Q8TDR2	STK35	2.42	0.01	UP	0.00	1.00	1.00	0.00	NO	YES
Q9HAV7	GRPEL1	2.39	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
Q9H3K2	GHITM	2.39	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
A2RUS2	DENND3	2.39	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
Q96RQ1	ERGIC2	2.37	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q5UIP0	RIF1	2.37	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
Q8NF91	SYNE1	2.36	0.00	UP	2.00	1.00	1.00	0.00	NO	YES
Q96S97	MYADM	2.36	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
P60602	ROMO1	2.35	0.00	UP	0.00	0.00	1.00	0.00	NO	NO
P25445	FAS	2.34	0.00	UP	1.00	1.00	0.00	2.00	YES	YES
P23368	ME2	2.34	0.00	UP	1.00	3.00	3.00	1.00	NO	YES
Q8N556	AFAP1	2.34	0.00	UP	1.00	2.00	1.00	0.00	NO	YES
O75907	DGAT1	2.34	0.01	UP	0.00	0.00	1.00	2.00	NO	YES
Q96HP0	DOCK6	2.34	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
O75051	PLXNA2	2.33	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
O43278	SPINT1	2.31	0.02	UP	1.00	1.00	3.00	0.00	NO	YES
Q01995	TAGLN	2.31	0.01	UP	2.00	0.00	1.00	0.00	NO	YES
P15151	PVR	2.30	0.00	UP	1.00	1.00	2.00	0.00	NO	YES
Q9Y570	PPME1	2.30	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
P30530	AXL	2.29	0.00	UP	2.00	7.00	9.00	1.00	NO	YES
Q29983	MICA	2.29	0.02	UP	3.00	2.00	8.00	1.00	NO	YES
O75525	KHDRBS3	2.29	0.00	UP	0.00	1.00	1.00	0.00	NO	YES
Q96LW7	CARD19	2.29	0.03	UP	2.00	1.00	0.00	0.00	NO	YES
O95159	ZFPL1	2.28	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
P00367	GLUD1	2.27	0.00	UP	0.00	1.00	1.00	2.00	NO	YES
P13667	PDIA4	2.26	0.00	UP	2.00	0.00	1.00	0.00	NO	YES
P29597	TYK2	2.26	0.00	UP	1.00	3.00	1.00	1.00	NO	YES
O75414	NME6	2.24	0.00	UP	1.00	2.00	1.00	3.00	NO	NO
Q96K49	TMEM87B	2.21	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
Q6ZW49	PAXIP1	2.21	0.00	UP	0.00	0.00	2.00	0.00	NO	YES
P26022	PTX3	2.20	0.00	UP	1.00	0.00	2.00	0.00	NO	YES
Q9UM00	TMCO1	2.20	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q96I59	NARS2	2.20	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
Q96RD7	PANX1	2.19	0.00	UP	0.00	0.00	2.00	1.00	NO	YES
Q6PML9	SLC30A9	2.19	0.00	UP	2.00	0.00	1.00	0.00	NO	YES
Q969R5	L3MBTL2	2.19	0.04	UP	0.00	0.00	0.00	0.00	NO	YES
Q2PZI1	DPY19L1	2.18	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q9NSE4	IARS2	2.17	0.00	UP	1.00	2.00	2.00	0.00	NO	YES
Q9Y2H5	PLEKHA6	2.17	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
P78540	ARG2	2.16	0.00	UP	2.00	1.00	4.00	3.00	NO	YES
Q9HD45	TM9SF3	2.16	0.00	UP	0.00	0.00	2.00	0.00	NO	YES

Q8NB49	ATP11C	2.16	0.01	UP	0.00	2.00	2.00	1.00	NO	YES
Q03519	TAP2	2.15	0.00	UP	2.00	5.00	8.00	2.00	NO	YES
Q03518	TAP1	2.15	0.01	UP	2.00	8.00	8.00	2.00	NO	YES
O60291	MGRN1	2.15	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q9Y385	UBE2J1	2.14	0.00	UP	2.00	3.00	1.00	0.00	NO	YES
Q13641	TPBG	2.14	0.02	UP	0.00	0.00	3.00	0.00	NO	YES
O00635	TRIM38	2.14	0.01	UP	1.00	0.00	4.00	0.00	NO	YES
Q9NX58	LYAR	2.14	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
P11234	RALB	2.13	0.00	UP	3.00	1.00	2.00	0.00	YES	YES
O43826	SLC37A4	2.13	0.00	UP	0.00	0.00	1.00	1.00	NO	YES
Q06330	RBPJ	2.13	0.00	UP	1.00	1.00	3.00	1.00	NO	YES
P13196	ALAS1	2.12	0.04	UP	2.00	0.00	2.00	2.00	NO	YES
O75882	ATRN	2.12	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
Q96BI1	SLC22A18	2.12	0.01	UP	0.00	0.00	1.00	0.00	NO	YES
Q9Y3L5	RAP2C	2.11	0.00	UP	4.00	1.00	3.00	0.00	NO	YES
Q9HAT2	SIAE	2.10	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
P45954	ACADSB	2.10	0.00	UP	1.00	0.00	1.00	1.00	NO	YES
O95772	STARD3NL	2.10	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
P0CG08	GPR89B	2.10	0.00	UP	0.00	0.00	0.00	0.00	NO	NO
Q29980	MICB	2.09	0.02	UP	3.00	2.00	9.00	1.00	NO	YES
O15231	ZNF185	2.09	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
Q9BVT8	TMUB1	2.09	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q9NZM1	MYOF	2.09	0.00	UP	2.00	0.00	2.00	0.00	NO	YES
P26367	PAX6	2.09	0.00	UP	2.00	3.00	5.00	0.00	NO	YES
Q16270	IGFBP7	2.08	0.01	UP	0.00	2.00	1.00	0.00	NO	YES
O95208	EPN2	2.08	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
P30679	GNA15	2.08	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
P17544	ATF7	2.07	0.00	UP	0.00	4.00	4.00	0.00	NO	YES
Q9P246	STIM2	2.07	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q969S9	GFM2	2.07	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q8TAD7	OCC1	2.07	0.00	UP	0.00	0.00	0.00	0.00	NO	NO
Q9UHB6	LIMA1	2.06	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q9P2E5	CHPF2	2.06	0.00	UP	0.00	0.00	0.00	1.00	NO	YES
Q03164	KMT2A	2.06	0.00	UP	3.00	1.00	1.00	1.00	NO	YES
Q9BZM5	ULBP2	2.06	0.00	UP	3.00	1.00	2.00	1.00	NO	YES
P04439	HLA-A	2.05	0.03	UP	4.00	2.00	4.00	2.00	NO	YES
Q9P0U3	SENP1	2.05	0.01	UP	1.00	0.00	1.00	0.00	NO	YES
Q92597	NDRG1	2.05	0.04	UP	0.00	0.00	0.00	0.00	NO	YES
P29279	CCN2	2.05	0.00	UP	4.00	1.00	1.00	0.00	NO	YES
O15254	ACOX3	2.05	0.00	UP	1.00	0.00	1.00	3.00	NO	YES
Q14699	RFTN1	2.05	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
O76024	WFS1	2.05	0.00	UP	0.00	2.00	2.00	0.00	NO	YES
Q5ST30	VARS2	2.05	0.00	UP	1.00	2.00	2.00	0.00	NO	YES
P08473	MME	2.04	0.00	UP	1.00	2.00	1.00	0.00	NO	YES
Q9HC07	TMEM165	2.04	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q9H8M1	COQ10B	2.04	0.02	UP	1.00	0.00	0.00	0.00	NO	YES
Q9Y5X1	SNX9	2.04	0.00	UP	2.00	2.00	4.00	0.00	NO	YES
Q1KMD3	HNRNPUL2	2.04	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
Q969P0	IGSF8	2.04	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
P18859	ATP5PF	2.04	0.00	UP	1.00	0.00	1.00	2.00	NO	YES
O00754	MAN2B1	2.04	0.00	UP	1.00	0.00	0.00	0.00	NO	YES
P05783	KRT18	2.03	0.00	UP	2.00	0.00	0.00	0.00	NO	YES
P51572	BCAP31	2.03	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
Q8N7R7	CCNYL1	2.02	0.00	UP	1.00	1.00	0.00	0.00	NO	YES
P57088	TMEM33	2.02	0.00	UP	0.00	0.00	1.00	0.00	NO	YES
O14681	EI24	2.01	0.01	UP	1.00	0.00	0.00	0.00	NO	YES
Q13948	CUX1	2.01	0.00	UP	1.00	0.00	1.00	0.00	NO	YES
Q13444	ADAM15	2.01	0.00	UP	2.00	1.00	4.00	0.00	NO	YES

Q8NBN7	RDH13	2.01	0.01	UP	2.00	1.00	2.00	3.00	NO	YES
Q8IX01	SUGP2	2.00	0.00	UP	0.00	0.00	0.00	0.00	NO	YES
Q7Z2K6	ERMP1	2.00	0.02	UP	0.00	0.00	0.00	0.00	NO	YES
P42765	ACAA2	2.00	0.00	UP	2.00	0.00	2.00	1.00	NO	YES
P16333	NCK1	0.50	0.01	DOWN	1.00	1.00	2.00	1.00	NO	YES
Q99543	DNAJC2	0.50	0.01	DOWN	2.00	1.00	0.00	0.00	NO	YES
O15397	IPO8	0.50	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
P53396	ACLY	0.50	0.00	DOWN	1.00	2.00	3.00	1.00	NO	YES
Q9Y223	GNE	0.50	0.01	DOWN	1.00	1.00	1.00	2.00	NO	YES
P52788	SMS	0.50	0.00	DOWN	1.00	0.00	1.00	3.00	NO	YES
Q8N0X7	SPART	0.50	0.00	DOWN	1.00	1.00	2.00	0.00	NO	YES
Q13685	AAMP	0.50	0.01	DOWN	2.00	0.00	1.00	0.00	NO	YES
Q9Y287	ITM2B	0.50	0.03	DOWN	2.00	1.00	1.00	0.00	NO	YES
P36543	ATP6V1E1	0.50	0.00	DOWN	1.00	0.00	0.00	1.00	NO	YES
Q5T6F2	UBAP2	0.50	0.01	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q99598	TSNAX	0.49	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
P14174	MIF	0.49	0.00	DOWN	2.00	0.00	1.00	1.00	NO	YES
Q92530	PSMF1	0.49	0.01	DOWN	1.00	2.00	0.00	0.00	NO	YES
Q9UKK3	PARP4	0.49	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
P60520	GABARAPL2	0.49	0.00	DOWN	2.00	1.00	0.00	0.00	NO	YES
Q9UMY4	SNX12	0.49	0.01	DOWN	3.00	0.00	1.00	0.00	NO	YES
Q08752	PPID	0.49	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q9BXS5	AP1M1	0.49	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q99707	MTR	0.49	0.01	DOWN	1.00	0.00	1.00	4.00	NO	YES
Q9NRG0	CHRAC1	0.49	0.04	DOWN	0.00	0.00	0.00	0.00	NO	YES
O95786	RIGI	0.49	0.01	DOWN	1.00	2.00	2.00	1.00	NO	NO
O75794	CDC123	0.49	0.03	DOWN	0.00	0.00	0.00	0.00	NO	YES
P31939	ATIC	0.49	0.00	DOWN	1.00	1.00	3.00	3.00	NO	YES
O43252	PAPSS1	0.49	0.00	DOWN	1.00	2.00	0.00	2.00	NO	YES
P00441	SOD1	0.49	0.00	DOWN	2.00	1.00	3.00	1.00	NO	YES
P49770	EIF2B2	0.49	0.00	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q15121	PEA15	0.49	0.00	DOWN	3.00	0.00	1.00	0.00	NO	YES
P16949	STMN1	0.49	0.00	DOWN	1.00	1.00	1.00	0.00	NO	YES
P39687	ANP32A	0.49	0.00	DOWN	0.00	1.00	5.00	0.00	NO	YES
Q9NUI1	DECR2	0.49	0.01	DOWN	1.00	3.00	2.00	1.00	NO	YES
O14929	HAT1	0.48	0.01	DOWN	0.00	0.00	2.00	0.00	NO	YES
Q9Y266	NUDC	0.48	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q13085	ACACA	0.48	0.00	DOWN	1.00	1.00	2.00	1.00	NO	YES
O15067	PFAS	0.48	0.01	DOWN	1.00	1.00	1.00	2.00	NO	YES
P11413	G6PD	0.48	0.00	DOWN	2.00	2.00	3.00	4.00	NO	YES
Q6NXE6	ARMC6	0.48	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
P42694	HELZ	0.48	0.00	DOWN	1.00	1.00	1.00	0.00	NO	YES
Q7L5N1	COPS6	0.48	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q9Y371	SH3GLB1	0.48	0.00	DOWN	1.00	1.00	1.00	0.00	NO	YES
Q9H6S0	YTHDC2	0.48	0.00	DOWN	0.00	2.00	0.00	0.00	NO	YES
Q96GG9	DCUN1D1	0.48	0.00	DOWN	3.00	0.00	1.00	0.00	NO	YES
O14530	TXNDC9	0.48	0.00	DOWN	3.00	0.00	0.00	0.00	NO	YES
P48735	IDH2	0.48	0.00	DOWN	1.00	2.00	0.00	5.00	NO	YES
P61024	CKS1B	0.48	0.00	DOWN	0.00	0.00	1.00	0.00	YES	YES
Q9UJA5	TRMT6	0.48	0.04	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q15102	PAFAH1B3	0.48	0.00	DOWN	1.00	1.00	0.00	1.00	NO	YES
Q9BY42	RTF2	0.48	0.00	DOWN	1.00	0.00	2.00	0.00	NO	YES
O60925	PFDN1	0.48	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q9UNN5	FAF1	0.48	0.00	DOWN	2.00	1.00	1.00	0.00	NO	YES
P61289	PSME3	0.48	0.00	DOWN	1.00	0.00	0.00	1.00	NO	YES
Q7Z739	YTHDF3	0.48	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
O75815	BCAR3	0.48	0.00	DOWN	1.00	0.00	2.00	0.00	NO	YES
Q9Y3P9	RABGAP1	0.48	0.00	DOWN	4.00	1.00	1.00	0.00	NO	YES

Q01105	SET	0.48	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
P40123	CAP2	0.48	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
Q9NZD8	SPG21	0.47	0.02	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q8IXQ4	GPALPP1	0.47	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q8WVT3	TRAPPC12	0.47	0.01	DOWN	2.00	0.00	1.00	0.00	NO	YES
P49915	GMPS	0.47	0.00	DOWN	1.00	1.00	0.00	2.00	NO	YES
Q9NZL9	MAT2B	0.47	0.00	DOWN	2.00	0.00	1.00	4.00	NO	YES
P61758	VBP1	0.47	0.00	DOWN	3.00	1.00	0.00	0.00	NO	YES
Q14914	PTGR1	0.47	0.00	DOWN	0.00	1.00	0.00	0.00	NO	YES
P51784	USP11	0.47	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
P51965	UBE2E1	0.47	0.00	DOWN	1.00	3.00	1.00	0.00	NO	YES
P09884	POLA1	0.47	0.04	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9H3H3	C11orf68	0.47	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
O76054	SEC14L2	0.47	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q9Y237	PIN4	0.47	0.01	DOWN	1.00	3.00	4.00	0.00	NO	YES
P52735	VAV2	0.47	0.00	DOWN	1.00	0.00	1.00	2.00	NO	YES
Q07954	LRP1	0.47	0.01	DOWN	2.00	1.00	8.00	1.00	NO	YES
Q96EI5	TCEAL4	0.47	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9UKY7	CDV3	0.47	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q13404	UBE2V1	0.47	0.00	DOWN	2.00	1.00	0.00	0.00	NO	YES
Q00688	FKBP3	0.47	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
P08758	ANXA5	0.46	0.00	DOWN	3.00	1.00	5.00	0.00	NO	YES
Q05209	PTPN12	0.46	0.00	DOWN	1.00	3.00	4.00	0.00	NO	YES
P51812	RPS6KA3	0.46	0.00	DOWN	2.00	1.00	3.00	1.00	NO	YES
Q86Y56	DNAAF5	0.46	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
Q9Y4R8	TELO2	0.46	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9Y5S1	TRPV2	0.46	0.00	DOWN	0.00	2.00	2.00	0.00	NO	YES
Q9BQ70	TCF25	0.46	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
P35244	RPA3	0.46	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
Q13409	DYNC1I2	0.46	0.00	DOWN	3.00	0.00	0.00	0.00	NO	YES
Q9NRN7	AASDHPPT	0.46	0.00	DOWN	1.00	0.00	1.00	2.00	NO	YES
Q6PD74	AAGAB	0.46	0.03	DOWN	2.00	0.00	0.00	0.00	NO	YES
P84101	SERF2	0.46	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
O00329	PIK3CD	0.46	0.00	DOWN	1.00	1.00	4.00	5.00	YES	YES
Q15398	DLGAP5	0.46	0.04	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q92615	LARP4B	0.46	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
P37802	TAGLN2	0.46	0.00	DOWN	2.00	0.00	1.00	0.00	NO	YES
P20810	CAST	0.46	0.00	DOWN	1.00	0.00	2.00	0.00	NO	YES
Q9BVG4	PBDC1	0.46	0.02	DOWN	0.00	0.00	0.00	0.00	NO	YES
P52209	PGD	0.46	0.00	DOWN	1.00	1.00	2.00	4.00	NO	YES
Q9H2J4	PDCL3	0.46	0.00	DOWN	1.00	1.00	1.00	0.00	NO	YES
Q13526	PIN1	0.46	0.00	DOWN	3.00	3.00	5.00	0.00	NO	YES
Q9Y613	FHOD1	0.46	0.03	DOWN	3.00	0.00	0.00	0.00	NO	YES
Q0VDF9	HSPA14	0.46	0.00	DOWN	5.00	4.00	3.00	0.00	NO	YES
Q14166	TTLL12	0.45	0.01	DOWN	0.00	2.00	1.00	0.00	NO	YES
Q53FA7	TP53I3	0.45	0.00	DOWN	0.00	2.00	1.00	0.00	NO	YES
Q8NBI6	XXYLT1	0.45	0.00	DOWN	0.00	1.00	0.00	0.00	NO	YES
Q8WVY7	UBLCP1	0.45	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q15036	SNX17	0.45	0.04	DOWN	2.00	0.00	3.00	0.00	NO	YES
Q92734	TFG	0.45	0.00	DOWN	1.00	0.00	0.00	0.00	YES	YES
Q96RF0	SNX18	0.45	0.01	DOWN	1.00	2.00	5.00	0.00	NO	YES
Q969U7	PSMG2	0.45	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q9GZZ1	NAA50	0.45	0.00	DOWN	3.00	0.00	0.00	0.00	NO	YES
Q9P000	COMMD9	0.45	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
O14562	UBFD1	0.45	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
O95163	ELP1	0.45	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9H1I8	ASCC2	0.45	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
O75419	CDC45	0.45	0.01	DOWN	2.00	1.00	0.00	0.00	NO	YES

Q15056	EIF4H	0.44	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9Y6D6	ARFGEF1	0.44	0.00	DOWN	2.00	0.00	4.00	0.00	NO	YES
Q9BXB4	OSBPL11	0.44	0.01	DOWN	1.00	1.00	0.00	0.00	NO	YES
P41236	PPP1R2	0.44	0.02	DOWN	0.00	1.00	0.00	0.00	NO	YES
Q6FI81	CIAPIN1	0.44	0.00	DOWN	0.00	1.00	2.00	0.00	NO	YES
O43765	SGTA	0.44	0.00	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q99447	PCYT2	0.44	0.00	DOWN	0.00	2.00	0.00	2.00	NO	YES
P50395	GDI2	0.44	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
A5PLL7	PEDS1	0.44	0.00	DOWN	0.00	0.00	0.00	1.00	NO	NO
Q9UI26	IPO11	0.44	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q14738	PPP2R5D	0.44	0.00	DOWN	2.00	0.00	1.00	1.00	NO	YES
Q9Y4K0	LOXL2	0.44	0.00	DOWN	2.00	1.00	4.00	0.00	NO	YES
P31153	MAT2A	0.44	0.00	DOWN	2.00	1.00	3.00	4.00	NO	YES
P52701	MSH6	0.44	0.01	DOWN	1.00	3.00	0.00	0.00	YES	YES
Q9UKA4	AKAP11	0.44	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
P26639	TARS1	0.44	0.00	DOWN	2.00	3.00	0.00	0.00	NO	NO
P23193	TCEA1	0.44	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9NUQ3	TXLNG	0.44	0.01	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q9UNF0	PACSIN2	0.44	0.00	DOWN	4.00	1.00	2.00	0.00	NO	YES
P51570	GALK1	0.44	0.00	DOWN	1.00	1.00	0.00	3.00	NO	YES
P14550	AKR1A1	0.44	0.01	DOWN	1.00	6.00	8.00	4.00	NO	YES
P68036	UBE2L3	0.44	0.01	DOWN	3.00	3.00	1.00	0.00	NO	YES
P08582	MELTF	0.44	0.01	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q99471	PFDN5	0.44	0.00	DOWN	3.00	1.00	1.00	0.00	NO	NO
Q96GA3	LTV1	0.44	0.02	DOWN	1.00	0.00	1.00	0.00	NO	YES
A1X283	SH3PXD2B	0.44	0.01	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q96GY0	ZC2HC1A	0.43	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q15057	ACAP2	0.43	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
P12074	COX6A1	0.43	0.02	DOWN	0.00	0.00	0.00	2.00	NO	YES
P11532	DMD	0.43	0.00	DOWN	3.00	1.00	2.00	0.00	NO	YES
Q92688	ANP32B	0.43	0.00	DOWN	1.00	1.00	3.00	0.00	NO	YES
Q9NWK9	ZNHIT6	0.43	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
O14727	APAF1	0.43	0.00	DOWN	1.00	2.00	4.00	1.00	YES	YES
Q71RG4	TMUB2	0.43	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q15126	PMVK	0.43	0.00	DOWN	2.00	1.00	0.00	2.00	NO	YES
Q7Z2E3	APTX	0.43	0.01	DOWN	0.00	1.00	1.00	0.00	NO	YES
P11586	MTHFD1	0.43	0.00	DOWN	1.00	2.00	3.00	3.00	NO	YES
P33176	KIF5B	0.42	0.00	DOWN	2.00	1.00	2.00	0.00	NO	YES
Q9BXJ9	NAA15	0.42	0.00	DOWN	4.00	0.00	0.00	0.00	NO	YES
Q8NDV7	TNRC6A	0.42	0.02	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q8WXD5	GEMIN6	0.42	0.03	DOWN	1.00	0.00	0.00	0.00	NO	NO
P06132	UROD	0.42	0.00	DOWN	1.00	0.00	0.00	2.00	NO	YES
Q9C0B1	FTO	0.42	0.01	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q4V328	GRIPAP1	0.42	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
P20290	BTF3	0.42	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
P55060	CSE1L	0.42	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q5VZ89	DENND4C	0.42	0.02	DOWN	3.00	0.00	0.00	0.00	NO	YES
Q6PGP7	SKIC3	0.42	0.04	DOWN	2.00	0.00	0.00	0.00	NO	NO
Q9NUQ8	ABCF3	0.42	0.00	DOWN	2.00	3.00	1.00	0.00	NO	YES
P62841	RPS15	0.42	0.00	DOWN	0.00	1.00	2.00	1.00	NO	YES
Q7Z7L1	SLFN11	0.42	0.01	DOWN	1.00	1.00	0.00	0.00	NO	YES
P19474	TRIM21	0.42	0.02	DOWN	1.00	1.00	4.00	0.00	NO	YES
Q8N1G2	CMTR1	0.42	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9NRX4	PHPT1	0.41	0.01	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q9ULH7	MRTFB	0.41	0.01	DOWN	2.00	0.00	1.00	0.00	NO	YES
P35573	AGL	0.41	0.00	DOWN	3.00	0.00	3.00	1.00	NO	YES
Q9BV20	MRI1	0.41	0.00	DOWN	1.00	0.00	0.00	2.00	NO	YES
P06454	PTMA	0.41	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES

O95456	PSMG1	0.41	0.01	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q8N543	OGFOD1	0.41	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
P34932	HSPA4	0.41	0.00	DOWN	2.00	2.00	1.00	1.00	NO	YES
Q8NEY1	NAV1	0.41	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
P21399	ACO1	0.41	0.00	DOWN	1.00	0.00	2.00	3.00	NO	YES
P06737	PYGL	0.41	0.00	DOWN	1.00	3.00	2.00	1.00	NO	YES
Q96PZ0	PUS7	0.41	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q96IU4	ABHD14B	0.40	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9NP73	ALG13	0.40	0.03	DOWN	0.00	0.00	0.00	1.00	NO	YES
P11802	CDK4	0.40	0.01	DOWN	3.00	2.00	6.00	2.00	YES	YES
Q66K74	MAP1S	0.40	0.00	DOWN	2.00	1.00	1.00	0.00	NO	YES
P09913	IFIT2	0.40	0.00	DOWN	1.00	0.00	3.00	0.00	NO	YES
P36871	PGM1	0.40	0.00	DOWN	3.00	0.00	4.00	5.00	NO	YES
P29401	TKT	0.40	0.00	DOWN	3.00	2.00	1.00	4.00	NO	YES
P52306	RAP1GDS1	0.40	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q5TDH0	DDI2	0.40	0.00	DOWN	1.00	0.00	2.00	0.00	NO	YES
Q9Y2Z0	SUGT1	0.40	0.00	DOWN	3.00	0.00	0.00	0.00	NO	YES
O95817	BAG3	0.40	0.00	DOWN	2.00	1.00	4.00	0.00	NO	YES
Q9H993	ARMT1	0.40	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
O00418	EEF2K	0.40	0.04	DOWN	2.00	1.00	2.00	0.00	NO	YES
Q14558	PRPSAP1	0.40	0.00	DOWN	1.00	3.00	7.00	0.00	NO	YES
P56945	BCAR1	0.39	0.00	DOWN	2.00	2.00	4.00	1.00	NO	YES
Q9Y6D5	ARFGEF2	0.39	0.00	DOWN	2.00	0.00	4.00	0.00	NO	YES
Q7L5N7	LPCAT2	0.39	0.02	DOWN	0.00	1.00	0.00	1.00	NO	YES
Q9UHJ6	SHPK	0.39	0.02	DOWN	1.00	1.00	2.00	2.00	NO	YES
P13928	ANXA8	0.39	0.02	DOWN	2.00	0.00	4.00	0.00	NO	NO
Q9UDY4	DNAJB4	0.39	0.02	DOWN	3.00	5.00	4.00	0.00	NO	YES
Q9BTW9	TBCD	0.39	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
P49903	SEPHS1	0.39	0.01	DOWN	1.00	2.00	0.00	1.00	NO	YES
P00390	GSR	0.39	0.00	DOWN	2.00	2.00	2.00	2.00	NO	YES
P46934	NEDD4	0.39	0.00	DOWN	3.00	2.00	0.00	1.00	NO	YES
Q13153	PAK1	0.39	0.00	DOWN	4.00	4.00	4.00	2.00	NO	YES
Q9C0C9	UBE2O	0.39	0.00	DOWN	2.00	2.00	0.00	0.00	NO	YES
Q96S44	TP53RK	0.38	0.01	DOWN	0.00	1.00	1.00	0.00	NO	YES
Q15043	SLC39A14	0.38	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
O43847	NRDC	0.38	0.00	DOWN	5.00	3.00	4.00	0.00	NO	YES
P53999	SUB1	0.38	0.00	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q9H7D0	DOCK5	0.38	0.00	DOWN	2.00	1.00	3.00	0.00	NO	YES
Q9UKK9	NUDT5	0.38	0.00	DOWN	2.00	1.00	0.00	2.00	NO	YES
Q9NZT2	OGFR	0.38	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9UI12	ATP6V1H	0.38	0.00	DOWN	1.00	0.00	0.00	1.00	NO	YES
O15013	ARHGEF10	0.38	0.01	DOWN	4.00	0.00	0.00	0.00	NO	YES
Q9HAB8	PPCS	0.38	0.02	DOWN	1.00	1.00	2.00	3.00	NO	YES
Q2NKX8	ERCC6L	0.37	0.00	DOWN	2.00	1.00	2.00	0.00	NO	YES
Q9Y6K9	IKBKG	0.37	0.00	DOWN	2.00	2.00	4.00	2.00	YES	YES
P51808	DYNLT3	0.37	0.01	DOWN	1.00	0.00	1.00	0.00	NO	YES
Q9H910	JPT2	0.37	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q8IVF2	AHNAK2	0.37	0.02	DOWN	4.00	0.00	1.00	0.00	NO	YES
Q9BRX5	GINS3	0.37	0.02	DOWN	0.00	0.00	0.00	0.00	NO	YES
P23381	WARS1	0.37	0.00	DOWN	2.00	1.00	0.00	0.00	NO	NO
P57772	EEFSEC	0.36	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9UBB6	NCDN	0.36	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
P08670	VIM	0.36	0.01	DOWN	2.00	0.00	2.00	1.00	NO	YES
Q96FV2	SCRN2	0.36	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
P34949	MPI	0.36	0.00	DOWN	1.00	0.00	0.00	3.00	NO	YES
Q13617	CUL2	0.36	0.00	DOWN	1.00	1.00	1.00	0.00	YES	YES
P49773	HINT1	0.36	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
O60701	UGDH	0.36	0.00	DOWN	1.00	0.00	3.00	5.00	NO	YES

P30566	ADSL	0.36	0.00	DOWN	1.00	0.00	3.00	3.00	NO	YES
P15291	B4GALT1	0.36	0.02	DOWN	1.00	1.00	1.00	2.00	NO	YES
P50151	GNG10	0.36	0.03	DOWN	0.00	0.00	0.00	0.00	YES	NO
Q96M27	PRRC1	0.36	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q86TU7	SETD3	0.35	0.04	DOWN	1.00	0.00	0.00	0.00	NO	YES
P63151	PPP2R2A	0.35	0.02	DOWN	1.00	0.00	0.00	1.00	NO	YES
O43592	XPOT	0.35	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9UK76	JPT1	0.35	0.03	DOWN	0.00	0.00	0.00	0.00	NO	YES
P51003	PAPOLA	0.35	0.00	DOWN	1.00	2.00	0.00	0.00	NO	YES
P54687	BCAT1	0.35	0.00	DOWN	1.00	0.00	2.00	5.00	NO	YES
Q8N806	UBR7	0.35	0.01	DOWN	0.00	0.00	1.00	0.00	NO	YES
Q9Y244	POMP	0.35	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
Q8IY21	DDX60	0.35	0.01	DOWN	2.00	1.00	0.00	0.00	NO	YES
P50583	NUDT2	0.35	0.00	DOWN	0.00	0.00	0.00	2.00	NO	YES
P29083	GTF2E1	0.34	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
O00762	UBE2C	0.34	0.01	DOWN	1.00	3.00	1.00	0.00	NO	YES
Q01813	PFKP	0.34	0.00	DOWN	1.00	1.00	3.00	5.00	NO	YES
Q9H814	PHAX	0.33	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
O75153	CLUH	0.33	0.00	DOWN	0.00	2.00	0.00	0.00	NO	YES
Q8NDH3	NPEPL1	0.33	0.01	DOWN	0.00	1.00	0.00	0.00	NO	YES
P15121	AKR1B1	0.33	0.04	DOWN	2.00	6.00	9.00	3.00	NO	YES
Q13885	TUBB2A	0.33	0.01	DOWN	2.00	2.00	2.00	0.00	NO	YES
Q6IA86	ELP2	0.33	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9NVS9	PNPO	0.33	0.00	DOWN	1.00	1.00	0.00	2.00	NO	YES
Q9NYT0	PLEK2	0.33	0.01	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9GZU8	PSME3IP1	0.32	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
P49354	FNTA	0.32	0.01	DOWN	2.00	0.00	0.00	0.00	NO	YES
P49585	PCYT1A	0.32	0.00	DOWN	1.00	3.00	0.00	2.00	NO	YES
Q8IWL3	HSCB	0.32	0.02	DOWN	2.00	1.00	0.00	0.00	NO	YES
P23921	RRM1	0.32	0.00	DOWN	0.00	1.00	0.00	3.00	NO	YES
P30043	BLVRB	0.31	0.01	DOWN	1.00	0.00	0.00	1.00	NO	YES
Q5TFE4	NT5DC1	0.31	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q07866	KLC1	0.31	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q9BV19	C1orf50	0.31	0.01	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q9UEE9	CFDP1	0.31	0.02	DOWN	0.00	0.00	2.00	0.00	NO	YES
O15347	HMGB3	0.31	0.01	DOWN	2.00	3.00	5.00	0.00	NO	YES
Q9NXG2	THUMPD1	0.31	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q9ULZ3	PYCARD	0.31	0.00	DOWN	4.00	3.00	6.00	0.00	NO	YES
Q96CV9	OPTN	0.31	0.01	DOWN	2.00	2.00	4.00	0.00	NO	YES
Q96DG6	CMBL	0.31	0.00	DOWN	1.00	0.00	0.00	1.00	NO	YES
Q9UIA9	XPO7	0.31	0.00	DOWN	0.00	0.00	1.00	0.00	NO	YES
Q96C90	PPP1R14B	0.31	0.02	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q9NVP2	ASF1B	0.31	0.00	DOWN	0.00	0.00	0.00	0.00	NO	YES
Q9HD15	SRA1	0.30	0.00	DOWN	2.00	0.00	0.00	0.00	NO	YES
P09104	ENO2	0.30	0.02	DOWN	0.00	0.00	0.00	3.00	NO	YES
P35520	CBS	0.29	0.00	DOWN	2.00	2.00	1.00	3.00	NO	NO
Q9H773	DCTPP1	0.29	0.00	DOWN	2.00	0.00	1.00	1.00	NO	YES
Q16566	CAMK4	0.28	0.00	DOWN	1.00	2.00	4.00	0.00	NO	YES
Q71U36	TUBA1A	0.28	0.03	DOWN	1.00	1.00	0.00	0.00	NO	YES
O95999	BCL10	0.28	0.01	DOWN	3.00	2.00	1.00	1.00	NO	YES
Q9NVM6	DNAJC17	0.28	0.04	DOWN	4.00	1.00	0.00	0.00	NO	YES
P29466	CASP1	0.27	0.00	DOWN	3.00	2.00	2.00	1.00	NO	YES
Q9BRT9	GINS4	0.27	0.01	DOWN	1.00	1.00	0.00	0.00	NO	YES
P51397	DAP	0.27	0.05	DOWN	0.00	0.00	1.00	0.00	NO	YES
P29034	S100A2	0.26	0.00	DOWN	1.00	1.00	0.00	0.00	NO	YES
Q93062	RBPMS	0.26	0.00	DOWN	1.00	2.00	0.00	0.00	NO	YES
P46821	MAP1B	0.26	0.00	DOWN	4.00	1.00	2.00	0.00	NO	YES
Q08426	EHHADH	0.25	0.00	DOWN	1.00	0.00	1.00	2.00	NO	YES

Q13509	TUBB3	0.25	0.01	DOWN	2.00	2.00	1.00	0.00	NO	YES
Q14195	DPYSL3	0.25	0.00	DOWN	4.00	2.00	8.00	0.00	NO	YES
P15559	NQO1	0.25	0.00	DOWN	1.00	3.00	6.00	2.00	YES	YES
Q96B97	SH3KBP1	0.24	0.01	DOWN	2.00	1.00	0.00	0.00	NO	YES
P51452	DUSP3	0.24	0.00	DOWN	1.00	1.00	1.00	0.00	NO	YES
Q96CP2	FLYWCH2	0.24	0.00	DOWN	1.00	0.00	0.00	0.00	NO	YES
Q16555	DPYSL2	0.23	0.00	DOWN	4.00	2.00	8.00	0.00	NO	YES
Q86X83	COMMD2	0.22	0.04	DOWN	0.00	0.00	0.00	0.00	NO	YES
P47895	ALDH1A3	0.19	0.00	DOWN	1.00	3.00	6.00	2.00	NO	YES
P48507	GCLM	0.18	0.00	DOWN	1.00	0.00	3.00	4.00	NO	YES
P11766	ADH5	0.18	0.00	DOWN	1.00	4.00	9.00	3.00	NO	YES
O60256	PRPSAP2	0.15	0.00	DOWN	2.00	3.00	7.00	0.00	NO	YES
Q15646	OASL	0.14	0.00	DOWN	1.00	1.00	4.00	0.00	NO	YES
Q9P0M6	MACROH2A2	0.10	0.00	DOWN	1.00	0.00	0.00	0.00	NO	NO
Q9Y547	IFT25	0.10	0.04	DOWN	1.00	0.00	0.00	0.00	NO	NO
P35080	PFN2	0.09	0.00	DOWN	2.00	0.00	1.00	0.00	NO	YES

Extended Data Table. 4 | List of key genes obtained from combined proteomic and transcriptomic analysis
(UP_Trans: log2(FC.trans) >= 1 & padj<= 0.05   DOWN_ Trans: log2(FC.trans) <= -1 & padj<= 0.05
UP_Prot: log2(FC.prot) >= 0.263 & padj<= 0.05   DOWN_Prot: log2(FC.prot) <= -0.263 & padj<= 0.05

Regulation	GeneName	GeneID	FC_trans	p_trans	ProteinID	FC_prot	p_prot	PPI_degree	Disease_with_cancer
UP-UP	LAMC2	ENSG00000058085	7.787	0.000	Q13753	3.791	0.000	18.000	YES
UP-UP	F3	ENSG00000117525	6.426	0.000	P13726	5.931	0.000	42.000	YES
UP-UP	MGLL	ENSG00000074416	4.229	0.000	Q99685	1.535	0.016	88.000	YES
UP-UP	IGFBP5	ENSG00000115461	3.762	0.000	P24593	4.324	0.010	10.000	YES
UP-UP	ICAM1	ENSG00000090339	7.468	0.000	P05362	14.284	0.001	88.000	YES
UP-UP	NT5E	ENSG00000135318	4.026	0.000	P21589	7.187	0.000	106.000	YES
UP-UP	KRT18	ENSG00000111057	2.794	0.000	P05783	2.029	0.001	8.000	YES
UP-UP	SOD2	ENSG00000112096	4.157	0.000	P04179	4.530	0.000	32.000	YES
UP-UP	DKK3	ENSG00000050165	3.124	0.000	Q9UBP4	3.954	0.003	6.000	YES
UP-UP	DENND3	ENSG00000105339	3.640	0.000	A2RUS2	2.389	0.005		YES
UP-UP	PPME1	ENSG00000214517	3.083	0.000	Q9Y570	2.296	0.000	14.000	YES
UP-UP	CADM1	ENSG00000182985	3.702	0.000	Q9BY67	6.386	0.000	18.000	YES
UP-UP	MCAM	ENSG00000076706	3.065	0.000	P43121	3.110	0.000	4.000	YES
UP-UP	ARHGDIB	ENSG00000111348	3.086	0.000	P52566	1.388	0.016	18.000	YES
UP-UP	DNAJB6	ENSG00000105993	2.536	0.000	O75190	2.924	0.001	16.000	YES
UP-UP	LCP1	ENSG00000136167	2.669	0.000	P13796	1.211	0.035	2.000	YES
UP-UP	MYO1D	ENSG00000176658	3.267	0.000	O94832	3.054	0.000		YES
UP-UP	APPL2	ENSG00000136044	3.133	0.000	Q8NEU8	2.616	0.000	6.000	YES
UP-UP	SRPRA	ENSG00000182934	2.369	0.000	P08240	2.630	0.000	46.000	YES
UP-UP	SNX9	ENSG00000130340	2.557	0.000	Q9Y5X1	2.042	0.001	18.000	YES
UP-UP	MFGE8	ENSG00000140545	2.665	0.000	Q08431	2.827	0.000	6.000	YES
UP-UP	AXL	ENSG00000167601	2.175	0.000	P30530	2.289	0.000	30.000	YES
UP-UP	LAMB3	ENSG00000196878	2.374	0.000	Q13751	2.456	0.000	12.000	YES
UP-UP	GALNT3	ENSG00000115339	4.637	0.000	Q14435	9.510	0.001	8.000	YES
UP-UP	CD55	ENSG00000196352	2.498	0.000	P08174	3.467	0.001	18.000	YES
UP-UP	CD9	ENSG00000010278	2.883	0.000	P21926	3.421	0.001	32.000	YES
UP-UP	ZNF185	ENSG00000147394	2.401	0.000	O15231	2.089	0.000	2.000	YES
UP-UP	HYOU1	ENSG00000149428	2.267	0.000	Q9Y4L1	2.857	0.000	30.000	YES
UP-UP	PGM2	ENSG00000169299	2.846	0.000	Q96G03	1.725	0.028	74.000	YES
UP-UP	TRIM28	ENSG00000130726	2.088	0.000	Q13263	1.499	0.002	66.000	YES
UP-UP	ADARB1	ENSG00000197381	2.577	0.000	P78563	2.970	0.000		YES
UP-UP	ZYX	ENSG00000159840	2.286	0.000	Q15942	1.231	0.024	28.000	YES
UP-UP	ITPR3	ENSG00000096433	2.128	0.000	Q14573	1.954	0.000	98.000	YES
UP-UP	PTX3	ENSG00000163661	2.889	0.000	P26022	2.202	0.001	20.000	YES
UP-UP	CAVIN2	ENSG00000168497	6.939	0.000	O95810	9.312	0.001	2.000	YES
UP-UP	OAS3	ENSG00000111331	2.431	0.000	Q9Y6K5	1.623	0.012	44.000	YES
UP-UP	CDCP1	ENSG00000163814	2.128	0.000	Q9H5V8	1.423	0.036	4.000	YES
UP-UP	PTGFRN	ENSG00000134247	2.285	0.000	Q9P2B2	4.108	0.000	8.000	YES
UP-UP	C2CD2L	ENSG00000172375	3.588	0.000	O14523	5.054	0.000		YES
UP-UP	NDRG1	ENSG00000104419	2.558	0.000	Q92597	2.053	0.036	2.000	YES
UP-UP	NPC1	ENSG00000141458	2.090	0.000	O15118	2.638	0.001	14.000	YES
UP-UP	CD59	ENSG00000085063	2.079	0.000	P13987	1.659	0.001	10.000	YES
UP-UP	PLAUR	ENSG00000011422	2.584	0.000	Q03405	4.896	0.000	10.000	YES
UP-UP	NFKB2	ENSG00000077150	2.486	0.000	Q00653	1.239	0.047	32.000	YES
UP-UP	ERCC2	ENSG00000104884	2.396	0.000	P18074	1.408	0.001	144.000	YES
UP-UP	BCAM	ENSG00000187244	2.314	0.000	P50895	3.569	0.000	2.000	YES
UP-UP	SIRPA	ENSG00000198053	2.103	0.000	P78324	1.469	0.020	24.000	YES
UP-UP	CTNNAL1	ENSG00000119326	2.041	0.000	Q9UBT7	1.530	0.002	6.000	YES
UP-UP	SPINT2	ENSG00000167642	2.522	0.000	O43291	2.471	0.020	2.000	YES
UP-UP	DOCK9	ENSG00000088387	2.149	0.000	Q9BZ29	1.785	0.000	4.000	YES
UP-UP	PCDH7	ENSG00000169851	2.105	0.000	O60245	2.700	0.000	2.000	YES
UP-UP	CHPF2	ENSG00000033100	2.094	0.000	Q9P2E5	2.064	0.000	4.000	YES
UP-UP	KCNAB2	ENSG00000069424	2.318	0.000	Q13303	1.210	0.034	12.000	YES
UP-UP	UNC13D	ENSG00000092929	2.141	0.000	Q70J99	1.684	0.002	8.000	YES
UP-UP	NOM1	ENSG00000146909	2.337	0.000	Q5C9Z4	1.845	0.000	36.000	YES
UP-UP	FKBP5	ENSG00000096060	2.486	0.000	Q13451	1.277	0.041	30.000	YES
UP-UP	UNC93B1	ENSG00000110057	2.226	0.000	Q9H1C4	1.588	0.016	8.000	YES

UP-UP	PLEKHA6	ENSG00000143850	2.247	0.000	Q9Y2H5	2.171	0.000		YES
UP-UP	PLAU	ENSG00000122861	2.033	0.000	P00749	2.451	0.006	12.000	YES
UP-UP	CD274	ENSG00000120217	2.844	0.000	Q9NZQ7	2.671	0.005	40.000	YES
UP-UP	PLCB4	ENSG00000101333	9.774	0.000	Q15147	5.437	0.001	66.000	YES
UP-UP	SLC4A7	ENSG00000033867	2.403	0.000	Q9Y6M7	2.823	0.000		YES
UP-UP	SLC43A3	ENSG00000134802	2.168	0.000	Q8NBI5	1.481	0.017		YES
UP-UP	CCNYL1	ENSG00000163249	2.005	0.000	Q8N7R7	2.024	0.004	2.000	YES
UP-UP	PKP2	ENSG00000057294	2.245	0.000	Q99959	3.986	0.000	20.000	YES
UP-UP	SPAG1	ENSG00000104450	2.248	0.000	Q07617	2.984	0.000	2.000	YES
UP-UP	SPINT1	ENSG00000166145	2.047	0.000	O43278	2.305	0.015	6.000	YES
UP-UP	CENPV	ENSG00000166582	2.213	0.000	Q7Z7K6	4.948	0.000		YES
UP-UP	KHDRBS3	ENSG00000131773	2.148	0.000	O75525	2.287	0.001		YES
UP-UP	TAGLN	ENSG00000149591	2.224	0.000	Q01995	2.305	0.010	6.000	YES
UP-UP	CDK5	ENSG00000164885	2.059	0.000	Q00535	1.404	0.012	38.000	YES
UP-UP	CPQ	ENSG00000104324	2.238	0.000	Q9Y646	3.811	0.006		YES
UP-UP	RELL1	ENSG00000181826	2.009	0.000	Q8IUW5	2.731	0.002		YES
UP-UP	LRCH4	ENSG00000077454	2.229	0.000	O75427	3.317	0.012		YES
UP-UP	NDUFV2	ENSG00000178127	3.127	0.001	P19404	1.417	0.020	178.000	YES
UP-UP	PIPSL	ENSG00000180764	2.671	0.008	A2A3N6	1.298	0.016		
DOWN-DOWN	OASL	ENSG00000135114	0.145	0.000	Q15646	0.140	0.001	34.000	YES
DOWN-DOWN	ALDH3A2	ENSG00000072210	0.219	0.000	P51648	0.630	0.024	76.000	YES
DOWN-DOWN	NQO1	ENSG00000181019	0.309	0.000	P15559	0.248	0.000	22.000	YES
DOWN-DOWN	MRC2	ENSG00000011028	0.374	0.000	Q9UBG0	0.554	0.025	4.000	YES
DOWN-DOWN	ALDH1A3	ENSG00000184254	0.370	0.000	P47895	0.192	0.000	64.000	YES
DOWN-DOWN	LPCAT2	ENSG00000087253	0.098	0.000	Q7L5N7	0.393	0.022	40.000	YES
DOWN-DOWN	LOXL2	ENSG00000134013	0.456	0.000	Q9Y4K0	0.442	0.001	6.000	YES
DOWN-DOWN	MELTF	ENSG00000163975	0.388	0.000	P08582	0.438	0.007		YES
DOWN-DOWN	LRP1	ENSG00000123384	0.421	0.000	Q07954	0.466	0.013	38.000	YES
DOWN-DOWN	MGST1	ENSG00000008394	0.414	0.000	P10620	0.714	0.002	36.000	YES
DOWN-DOWN	NRP1	ENSG00000099250	0.487	0.000	O14786	0.572	0.001	58.000	YES
DOWN-DOWN	ANXA8	ENSG00000265190	0.399	0.000	P13928	0.390	0.015		
DOWN-DOWN	FZD7	ENSG00000155760	0.403	0.000	O75084	0.666	0.035	56.000	YES
DOWN-DOWN	AHNAK2	ENSG00000185567	0.395	0.000	Q8IVF2	0.369	0.015	6.000	YES
DOWN-DOWN	CAT	ENSG00000121691	0.482	0.000	P04040	0.637	0.003	16.000	YES
DOWN-DOWN	DPYSL2	ENSG00000092964	0.458	0.000	Q16555	0.230	0.000	16.000	YES
DOWN-DOWN	EPHX1	ENSG00000143819	0.434	0.000	P07099	0.625	0.042	70.000	YES
DOWN-DOWN	S100A2	ENSG00000196754	0.460	0.000	P29034	0.263	0.002	2.000	YES
DOWN-DOWN	TRPV2	ENSG00000187688	0.448	0.000	Q9Y5S1	0.462	0.000	8.000	YES
DOWN-DOWN	CASP1	ENSG00000137752	0.329	0.000	P29466	0.273	0.000	82.000	YES
DOWN-DOWN	TUBA1A	ENSG00000167552	0.445	0.000	Q71U36	0.280	0.029	74.000	YES
DOWN-DOWN	VIM	ENSG00000026025	0.355	0.000	P08670	0.362	0.007	18.000	YES
DOWN-DOWN	ERLIN2	ENSG00000147475	0.464	0.000	O94905	0.779	0.039	12.000	YES
DOWN-DOWN	RSU1	ENSG00000148484	0.485	0.000	Q15404	0.638	0.004	12.000	YES
DOWN-DOWN	RBPMS	ENSG00000157110	0.444	0.000	Q93062	0.257	0.000	4.000	YES
DOWN-DOWN	SHISA2	ENSG00000180730	0.490	0.000	Q6UWI4	0.705	0.041		YES
DOWN-DOWN	IDH2	ENSG00000182054	0.447	0.000	P48735	0.478	0.003	36.000	YES
DOWN-DOWN	DDX60	ENSG00000137628	0.446	0.000	Q8IY21	0.347	0.013	24.000	YES
DOWN-DOWN	FGF2	ENSG00000138685	0.424	0.000	P09038	0.529	0.006	90.000	YES
DOWN-DOWN	TP53I3	ENSG00000115129	0.418	0.000	Q53FA7	0.453	0.001	4.000	YES
DOWN-DOWN	NLN	ENSG00000123213	0.491	0.000	Q9BYT8	0.542	0.001	2.000	YES
DOWN-DOWN	CFDP1	ENSG00000153774	0.469	0.000	Q9UEE9	0.311	0.017	14.000	YES
DOWN-DOWN	DCAKD	ENSG00000172992	0.424	0.000	Q8WVC6	0.781	0.002		YES
DOWN-DOWN	SCRN2	ENSG00000141295	0.484	0.000	Q96FV2	0.361	0.005		YES
DOWN-DOWN	INTS9	ENSG00000104299	0.424	0.000	Q9NV88	0.772	0.002	38.000	YES
DOWN-DOWN	ACOT1	ENSG00000184227	0.201	0.000	Q86TX2	0.550	0.029	24.000	YES
DOWN-DOWN	CLGN	ENSG00000153132	0.474	0.000	O14967	0.703	0.001	4.000	YES
DOWN-DOWN	PYCARD	ENSG00000103490	0.421	0.000	Q9ULZ3	0.308	0.004	48.000	YES
DOWN-DOWN	ETFB	ENSG00000105379	0.405	0.000	P38117	0.795	0.032	10.000	YES

DOWN-DOWN	EHHADH	ENSG00000113790	0.315	0.000	Q08426	0.255	0.003	90.000	YES
DOWN-DOWN	FLRT3	ENSG00000125848	0.359	0.000	Q9NZU0	0.526	0.044	6.000	YES
DOWN-DOWN	SYTL4	ENSG00000102362	0.477	0.000	Q96C24	0.652	0.011	12.000	YES
UP-DOWN	AGO2	ENSG00000123908	2.332	0.000	Q9UKV8	0.784	0.011	120.000	YES
DOWN-UP	EFEMP1	ENSG00000115380	0.493	0.000	Q12805	1.699	0.001	2.000	YES

Extended Data Table. 5 | Summary of differentially expressed genes and proteins across comparative groups

Compared group	Transcriptomics			Proteomics		
	UP	DOWN	ALL	UP	DOWN	ALL
High vs Control	1118	941	2059	1229	1327	2556
High vs Low	413	355	768	1260	1266	2526
High vs Middle	360	212	572	1094	1081	2175
Middle vs Low	359	484	843	723	820	1543
Middle vs Control	1089	1129	2218	894	1049	1943
Low vs Control	569	379	948	424	519	943

Extended Data Table. 6 | Significantly Differential SNV Mutations from Whole Genome Sequencing Based on Allele Frequency T-test Analysis (Minimum of 2 Mutated Samples per Group, Fold Change >= 1.2, p-value≤0.05)

Pos	Con_1_ Mutation	Con_2_ Mutation	Con_3_ Mutation	High_1_ Mutation	High_2_ Mutation	High_3_ Mutation	High_1	High_2	High_3	Con_1	Con_2	Con_3	Average_ high	Average_ con	High/Con	Regulation	P value
chrX_13356020_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.571	0.500	0.571	0.138	0.093	0.171	0.55	0.13	4.08	UP	0.000
chrX_13356017_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.550	0.500	0.572	0.159	0.125	0.171	0.54	0.15	3.56	UP	0.000
chr1_1177322_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.622	0.829	0.692	0.206	0.185	0.222	0.71	0.20	3.50	UP	0.001
chr15_30001243_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.423	0.609	0.418	0.111	0.115	0.214	0.48	0.15	3.30	UP	0.009
chr16_1993281_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.566	0.480	0.453	0.136	0.148	0.181	0.50	0.16	3.22	UP	0.001
chr3_58653313_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.514	0.440	0.559		0.160	0.158	0.50	0.16	3.17	UP	0.005
chr15_50995187_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.393	0.626	0.480	0.120		0.201	0.50	0.16	3.11	UP	0.035
chr9_135957299_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.529	0.637	0.333	0.111	0.154	0.221	0.50	0.16	3.08	UP	0.023
chr3_135864031_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.423	0.613	0.667	0.153		0.218	0.57	0.19	3.06	UP	0.030
chr6_41076129_snv		G -> T	G -> T	G -> T	G -> T	G -> T	0.533	0.348	0.550		0.176	0.143	0.48	0.16	2.99	UP	0.033
chr21_34537497_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.322	0.455	0.621	0.143	0.142	0.190	0.47	0.16	2.94	UP	0.025
chr19_55086449_snv		T -> A	T -> A	T -> A	T -> A	T -> A	0.531	0.516	0.643		0.157	0.227	0.56	0.19	2.93	UP	0.008
chr5_535299_snv	G -> A	G -> A		G -> A	G -> A	G -> A	0.483	0.566	0.407	0.133	0.199		0.49	0.17	2.92	UP	0.016
chrX_47485863_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.600	0.292	0.210	0.130	0.143	0.46	0.16	2.88	UP	0.032
chr12_93904421_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.462	0.391	0.192	0.130	0.148	0.45	0.16	2.88	UP	0.001
chr1_18808612_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.291	0.458	0.583	0.173	0.125	0.166	0.44	0.15	2.87	UP	0.028
chr19_45263618_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.481	0.579	0.221	0.157	0.166	0.52	0.18	2.87	UP	0.001
chr2_226516161_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.522	0.478	0.381	0.125	0.149	0.208	0.46	0.16	2.87	UP	0.003
chr14_58284075_snv	G -> A	G -> A		G -> A	G -> A	G -> A	0.577	0.375	0.522	0.153	0.190		0.49	0.17	2.86	UP	0.027
chr10_43278223_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.304	0.500	0.476	0.189	0.136	0.125	0.43	0.15	2.84	UP	0.013
chr19_13316425_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.704	0.607	0.619	0.333	0.238	0.111	0.64	0.23	2.83	UP	0.004
chr2_31806963_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.440	0.423	0.269	0.136		0.133	0.38	0.13	2.81	UP	0.041
chr19_48306167_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.552	0.714	0.375	0.142	0.262	0.185	0.55	0.20	2.79	UP	0.028
chr8_101734536_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.675	0.734	0.675	0.217	0.200	0.333	0.69	0.25	2.78	UP	0.001
chr14_77741889_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.296	0.483	0.500	0.141		0.167	0.43	0.15	2.77	UP	0.049
chr16_23641779_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.572	0.455	0.167	0.273	0.120	0.51	0.19	2.73	UP	0.005
chr14_93994913_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.417	0.458	0.526	0.130		0.214	0.47	0.17	2.72	UP	0.011
chr10_102309445_snv	G -> T	G -> T		G -> T	G -> T	G -> T	0.629	0.500	0.529	0.294	0.120		0.55	0.21	2.67	UP	0.025
chr3_33868453_snv	T -> G		T -> G	T -> G	T -> G	T -> G	0.435	0.545	0.648	0.148		0.263	0.54	0.21	2.64	UP	0.033
chr9_124990640_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.450	0.692	0.438	0.211	0.190	0.200	0.53	0.20	2.63	UP	0.017
chrX_108977451_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.500	0.667	0.318	0.142	0.199	0.231	0.50	0.19	2.60	UP	0.043
chr8_48890214_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.519	0.416	0.645		0.174	0.234	0.53	0.20	2.58	UP	0.035
chr6_29429726_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.485	0.348	0.435	0.143		0.185	0.42	0.16	2.58	UP	0.017
chr12_30955302_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.391	0.609	0.542	0.246	0.190	0.174	0.51	0.20	2.53	UP	0.010
chr13_46354258_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.500	0.469	0.333	0.153	0.208	0.159	0.43	0.17	2.50	UP	0.009
chr17_45810512_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.593	0.467	0.621	0.292	0.276	0.111	0.56	0.23	2.48	UP	0.011
chr20_30945968_snv		G -> A	G -> A	G -> A	G -> A	G -> A	0.160	0.226	0.211		0.071	0.091	0.20	0.08	2.46	UP	0.022
chr2_132122064_snv		T -> C	T -> C	T -> C	T -> C	T -> C	0.524	0.428	0.412		0.143	0.231	0.45	0.19	2.43	UP	0.017
chr12_89917550_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.616	0.478	0.471	0.111	0.250	0.285	0.52	0.22	2.42	UP	0.013
chr12_89917550_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.616	0.478	0.471	0.111	0.250	0.285	0.52	0.22	2.42	UP	0.013
chr10_104209390_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.533	0.500	0.409	0.165	0.300	0.138	0.48	0.20	2.39	UP	0.011
chr11_123526275_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.531	0.541	0.564	0.125	0.333	0.241	0.55	0.23	2.34	UP	0.007
chr11_7509484_snv	G -> A	G -> A		G -> A	G -> A	G -> A	0.263	0.285	0.378	0.153	0.111		0.31	0.13	2.34	UP	0.035
chr11_5759196_snv		G -> A	G -> A	G -> A	G -> A	G -> A	0.486	0.331	0.433		0.125	0.235	0.42	0.18	2.31	UP	0.046
chr9_140082047_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.428	0.542	0.632	0.160	0.267	0.266	0.53	0.23	2.31	UP	0.012

chr4_25792148_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.682	0.609	0.644	0.250	0.357	0.248	0.65	0.29	2.26	UP	0.001
chr16_70408919_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.350	0.435	0.214	0.148	0.208	0.43	0.19	2.25	UP	0.008
chr3_4687371_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.619	0.647	0.444	0.238	0.231	0.300	0.57	0.26	2.22	UP	0.010
chr1_46915339_snv		G -> T	G -> T	G -> T	G -> T	G -> T	0.543	0.520	0.357		0.250	0.176	0.47	0.21	2.22	UP	0.048
chr19_59061514_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.333	0.273	0.385	0.160	0.143	0.147	0.33	0.15	2.20	UP	0.005
chr19_14562679_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.394	0.471	0.357	0.217	0.152	0.186	0.41	0.19	2.20	UP	0.004
chr2_42669483_snv	T -> C		T -> C	T -> C	T -> C	T -> C	0.539	0.500	0.609	0.209		0.296	0.55	0.25	2.18	UP	0.011
chr5_41934379_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.533	0.611	0.385	0.318	0.166	0.219	0.51	0.23	2.17	UP	0.026
chr9_79325648_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.419	0.429	0.583	0.159	0.292	0.208	0.48	0.22	2.17	UP	0.017
chr17_7819020_snv	C -> A	C -> A		C -> A	C -> A	C -> A	0.522	0.459	0.444	0.227	0.211		0.48	0.22	2.17	UP	0.004
chr1_149983114_snv	T -> G		T -> G	T -> G	T -> G	T -> G	0.391	0.479	0.500	0.222		0.200	0.46	0.21	2.16	UP	0.011
chr2_171638798_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.478	0.332	0.496	0.248	0.229	0.129	0.44	0.20	2.16	UP	0.022
chr1_162494138_snv	C -> G	C -> G		C -> G	C -> G	C -> G	0.500	0.464	0.665	0.267	0.240		0.54	0.25	2.14	UP	0.037
chr5_236633_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.586	0.488	0.364	0.249	0.174	0.249	0.48	0.22	2.14	UP	0.021
chr11_46637745_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.437	0.231	0.333	0.154	0.178	0.143	0.33	0.16	2.11	UP	0.044
chr5_71737468_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.588	0.581	0.579	0.136	0.333	0.361	0.58	0.28	2.11	UP	0.012
chr8_47507825_snv	T -> C		T -> C	T -> C	T -> C	T -> C	0.400	0.500	0.333	0.210		0.199	0.41	0.20	2.01	UP	0.046
chr15_74273444_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.370	0.360	0.400	0.190	0.208	0.172	0.38	0.19	1.98	UP	0.000
chr10_101686972_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.522	0.524	0.316	0.273	0.230	0.52	0.27	1.89	UP	0.001
chr1_111827367_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.516	0.370	0.591	0.249	0.267	0.272	0.49	0.26	1.87	UP	0.024
chr5_122679692_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.444	0.560	0.615	0.239	0.375	0.250	0.54	0.29	1.87	UP	0.020
chr9_71509524_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.438	0.467	0.520	0.200	0.250	0.312	0.48	0.25	1.87	UP	0.005
chr7_141940492_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.682	0.593	0.693	0.267	0.389	0.400	0.66	0.35	1.86	UP	0.005
chr5_79783712_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.669	0.530	0.421	0.316	0.312	0.250	0.54	0.29	1.85	UP	0.030
chrX_100349606_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.429	0.406	0.320	0.235	0.248	0.148	0.39	0.21	1.83	UP	0.019
chr1_244998894_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.423	0.429	0.435	0.175	0.210	0.333	0.43	0.24	1.79	UP	0.017
chr19_59070391_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.293	0.325	0.393	0.238	0.179	0.156	0.34	0.19	1.76	UP	0.019
chr2_68753371_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.565	0.454	0.435	0.272	0.273	0.285	0.48	0.28	1.75	UP	0.007
chr5_32950281_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.524	0.584	0.609	0.370	0.421	0.200	0.57	0.33	1.73	UP	0.028
chr18_47340148_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.500	0.591	0.273	0.250	0.409	0.53	0.31	1.71	UP	0.019
chr5_140210561_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.470	0.546	0.500	0.250	0.405	0.291	0.51	0.32	1.60	UP	0.021
chr1_79111299_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.652	0.688	0.546	0.265	0.444	0.476	0.63	0.40	1.59	UP	0.041
chr1_175128081_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.556	0.556	0.563	0.409	0.249	0.402	0.56	0.35	1.58	UP	0.017
chr1_117250149_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.536	0.543	0.560	0.312	0.317	0.409	0.55	0.35	1.58	UP	0.003
chr7_104844110_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.503	0.458	0.542	0.333	0.312	0.345	0.50	0.33	1.52	UP	0.003
chr7_143755954_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.751	0.667	0.650	0.385	0.484	0.500	0.69	0.46	1.51	UP	0.008
chr1_36554312_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.559	0.500	0.584	0.389	0.409	0.300	0.55	0.37	1.50	UP	0.012
chr7_72951612_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.483	0.588	0.500	0.315	0.346	0.412	0.52	0.36	1.46	UP	0.019
chr19_35819584_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.606	0.522	0.565	0.440	0.416	0.333	0.56	0.40	1.42	UP	0.014
chr2_6111265_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.522	0.464	0.435	0.286	0.400	0.333	0.47	0.34	1.39	UP	0.033
chr20_21683959_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.628	0.623	0.649	0.500	0.474	0.395	0.63	0.46	1.39	UP	0.006
chr11_117332309_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.481	0.510		0.358	0.388	0.333	0.50	0.36	1.38	UP	0.010
chr19_4471336_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.552	0.600	0.500	0.429	0.379	0.411	0.55	0.41	1.36	UP	0.011
chr1_36030912_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.503	0.421	0.480	0.375	0.348	0.335	0.47	0.35	1.33	UP	0.013
chr19_37380558_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.500	0.500	0.516	0.444	0.364	0.347	0.51	0.39	1.31	UP	0.017
chr13_100196221_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.572	0.630	0.474	0.428	0.409	0.444	0.56	0.43	1.31	UP	0.048
chr3_151985199_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.545	0.524	0.616	0.440	0.416	0.440	0.56	0.43	1.30	UP	0.011

chr7_148454100_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.706	0.700	0.619	0.522	0.588	0.462	0.68	0.52	1.29	UP	0.030
chr5_170164543_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.500	0.519	0.474	0.420	0.417	0.368	0.50	0.40	1.24	UP	0.011
chr3_164906919_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.550	0.522	0.374	0.421	0.483	0.52	0.43	1.23	UP	0.048
chr2_99215518_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.533	0.500	0.500	0.616	0.615	0.644	0.51	0.63	0.82	DOWN	0.001
chr2_73928595_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.515	0.500	0.524	0.643	0.650	0.591	0.51	0.63	0.82	DOWN	0.004
chr1_223176032_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.542	0.600	0.519	0.727	0.644	0.667	0.55	0.68	0.82	DOWN	0.022
chr9_127708475_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.444	0.411	0.462	0.519	0.542	0.567	0.44	0.54	0.81	DOWN	0.007
chr21_47731427_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.480	0.519	0.500	0.625	0.650	0.600	0.50	0.63	0.80	DOWN	0.002
chr1_156374171_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.478	0.577	0.455	0.667	0.615	0.609	0.50	0.63	0.80	DOWN	0.038
chr9_140919523_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.400	0.500	0.393	0.545	0.538	0.542	0.43	0.54	0.80	DOWN	0.033
chr5_178510349_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.500	0.524	0.480	0.623	0.667	0.615	0.50	0.64	0.79	DOWN	0.003
chr9_98232055_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.464	0.389	0.542	0.607	0.611	0.572	0.47	0.60	0.78	DOWN	0.045
chr1_50646261_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.545	0.556	0.469	0.700	0.682	0.636	0.52	0.67	0.78	DOWN	0.011
chr3_40215921_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.536	0.520	0.500	0.682	0.625	0.730	0.52	0.68	0.76	DOWN	0.008
chr7_103185582_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.548	0.435	0.529	0.667	0.667	0.650	0.50	0.66	0.76	DOWN	0.011
chr5_177612414_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.484	0.417	0.600	0.650	0.650	0.677	0.50	0.66	0.76	DOWN	0.043
chr15_64447550_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.500	0.545	0.480	0.654	0.717	0.696	0.51	0.69	0.74	DOWN	0.002
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr3_9834677_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.424	0.515	0.403	0.700	0.545	0.607	0.45	0.62	0.72	DOWN	0.040
chr2_74273523_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.409	0.368	0.461	0.674	0.524	0.542	0.41	0.58	0.71	DOWN	0.037
chr5_131282300_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.530	0.500	0.613	0.857	0.715	0.51	0.73	0.70	DOWN	0.038
chr11_47266954_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.391	0.316	0.326	0.527	0.514	0.452	0.34	0.50	0.69	DOWN	0.010
chr1_205758042_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.476	0.412	0.500	0.636	0.626	0.750	0.46	0.67	0.69	DOWN	0.012
chr20_43753235_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.449	0.363	0.410	0.561	0.593	0.625	0.41	0.59	0.69	DOWN	0.004
chr19_32896540_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.443	0.500	0.304	0.588	0.577	0.655	0.42	0.61	0.69	DOWN	0.039
chr19_47570557_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.605	0.500	0.348	0.709	0.750	0.667	0.48	0.71	0.68	DOWN	0.046
chr19_47440541_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.467	0.400	0.476	0.680	0.632	0.679	0.45	0.66	0.67	DOWN	0.002
chr2_159824822_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.473	0.346	0.500	0.762	0.632	0.600	0.44	0.66	0.66	DOWN	0.031
chr9_37442305_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.437	0.414	0.389	0.637	0.625	0.630	0.41	0.63	0.66	DOWN	0.000
chr11_73825641_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.236	0.288	0.321	0.344	0.471	0.500	0.28	0.44	0.64	DOWN	0.044
chr7_64024135_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.280	0.400	0.550	0.682	0.620	0.637	0.41	0.65	0.63	DOWN	0.042
chr2_70527981_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.514	0.333	0.400	0.826	0.579	0.784	0.42	0.73	0.57	DOWN	0.028
chr21_31973400_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.552	0.428	0.333	0.750	0.766	0.824	0.44	0.78	0.56	DOWN	0.007
chr1_1182035_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.390	0.316	0.467	0.644	0.818	0.750	0.39	0.74	0.53	DOWN	0.007
chr1_11968125_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.261	0.367	0.343	0.710	0.571	0.600	0.32	0.63	0.52	DOWN	0.005
chr1_120140984_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.389	0.348	0.208	0.591	0.751	0.667	0.32	0.67	0.47	DOWN	0.008
chr1_1182532_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.219	0.303	0.336	0.453	0.721	0.667	0.29	0.61	0.47	DOWN	0.021
chr11_31086146_snv		C -> G	C -> G	C -> G	C -> G	C -> G	0.241	0.440	0.486		0.096	0.107	0.39	0.10	3.83	-	0.060
chr11_8291101_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.500	0.298	0.285	0.088		0.108	0.36	0.10	3.68	-	0.062
chr19_56936021_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.766	0.311	0.579		0.222	0.136	0.55	0.18	3.08	-	0.121
chr20_34561773_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.233	0.127	0.194	0.095		0.081	0.18	0.09	2.10	-	0.096
chr20_24523912_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.190	0.151	0.270		0.091	0.122	0.20	0.11	1.91	-	0.129
chr2_223918774_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.348	0.500	0.200	0.182	0.353	0.45	0.25	1.83	-	0.051

chr15_88402190_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.335	0.417	0.276	0.288	0.100	0.182	0.34	0.19	1.80	-	0.088
chr11_133777254_snv	C -> A	C -> A	C -> A	C -> A		C -> A	0.380		0.225	0.142	0.184	0.190	0.30	0.17	1.76	-	0.122
chr8_69148420_snv		C -> G	C -> G	C -> G	C -> G	C -> G	0.682	0.474	0.332		0.416	0.154	0.50	0.29	1.74	-	0.287
chr19_34992429_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.407	0.591	0.522	0.211	0.264	0.400	0.51	0.29	1.74	-	0.051
chr11_125482502_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.197	0.217	0.292	0.193	0.077	0.138	0.24	0.14	1.73	-	0.088
chr11_60185193_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.357	0.264	0.158	0.209	0.160	0.083	0.26	0.15	1.72	-	0.185
chr7_40127750_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.524	0.572	0.674	0.182	0.500	0.364	0.59	0.35	1.69	-	0.078
chr18_7231293_snv	T -> C	T -> C		T -> C	T -> C	T -> C	0.636	0.429	0.209	0.333	0.174		0.42	0.25	1.68	-	0.388
chr1_94635316_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.611	0.640	0.237	0.529	0.296	0.58	0.35	1.65	-	0.081
chr7_72951332_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.632	0.530	0.375	0.348	0.185	0.400	0.51	0.31	1.65	-	0.111
chrX_102930506_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.428	0.317	0.312	0.125		0.307	0.35	0.22	1.63	-	0.201
chr5_28927446_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.459	0.688	0.579	0.444	0.318	0.308	0.58	0.36	1.61	-	0.051
chr1_113261819_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.696	0.357	0.701	0.166	0.364	0.571	0.58	0.37	1.59	-	0.253
chr15_101084359_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.394	0.538	0.483	0.400	0.270	0.250	0.47	0.31	1.54	-	0.059
chr10_74896575_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.296	0.670	0.518	0.300	0.364	0.304	0.49	0.32	1.53	-	0.195
chr10_94051227_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.536	0.522	0.667	0.473	0.429	0.230	0.58	0.38	1.52	-	0.088
chr20_36719899_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.177	0.189	0.170	0.125	0.065	0.162	0.18	0.12	1.52	-	0.100
chr5_122951870_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.611	0.500	0.696	0.600	0.286	0.304	0.60	0.40	1.52	-	0.152
chr2_54481738_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.571	0.583	0.769	0.632	0.187	0.448	0.64	0.42	1.52	-	0.204
chr1_93803082_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.500	0.539	0.428	0.546	0.176	0.250	0.49	0.32	1.51	-	0.233
chr2_71205492_snv		T -> C	T -> C	T -> C	T -> C	T -> C	0.500	0.458	0.530		0.247	0.412	0.50	0.33	1.51	-	0.089
chr9_135458335_snv		C -> A	C -> A	C -> A	C -> A	C -> A	0.433	0.522	0.384		0.346	0.250	0.45	0.30	1.50	-	0.101
chr7_72949762_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.406	0.611		0.319	0.200	0.500	0.51	0.34	1.50	-	0.303
chr15_65426887_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.524	0.407	0.619	0.384	0.443	0.216	0.52	0.35	1.49	-	0.139
chr1_28976193_snv	A -> G		A -> G	A -> G	A -> G	A -> G	0.664	0.616	0.565	0.282		0.548	0.62	0.42	1.48	-	0.155
chr5_7348689_snv	A -> C	A -> C		A -> C	A -> C	A -> C	0.541	0.626	0.437	0.285	0.437		0.53	0.36	1.48	-	0.151
chr15_21938342_snv	C -> T	C -> T	C -> T		C -> T	C -> T		0.203	0.219	0.108	0.185	0.136	0.21	0.14	1.48	-	0.106
chr19_50017138_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.667	0.448	0.574	0.391	0.347	0.407	0.56	0.38	1.48	-	0.051
chr2_112969442_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.318	0.593	0.572	0.294	0.273	0.444	0.49	0.34	1.47	-	0.203
chr3_27872565_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.679	0.478	0.368	0.304	0.308	0.428	0.51	0.35	1.47	-	0.180
chr15_43644919_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.657	0.539	0.437	0.269	0.409	0.436	0.54	0.37	1.47	-	0.102
chr5_34192691_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.060	0.052	0.051		0.030	0.045	0.05	0.04	1.45	-	0.086
chr15_44038293_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.575	0.600	0.648	0.357	0.571	0.333	0.61	0.42	1.45	-	0.076
chr7_150693562_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.657	0.536	0.650	0.650	0.273	0.358	0.61	0.43	1.44	-	0.196
chr16_54967111_snv		C -> T	C -> T	C -> T		C -> T	0.521		0.333		0.333	0.263	0.43	0.30	1.43	-	0.327
chr5_140553956_snv	T -> A		T -> A	T -> A	T -> A		0.485	0.486		0.433		0.249	0.49	0.34	1.42	-	0.257
chr2_158142596_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.565	0.609	0.333	0.300	0.359	0.409	0.50	0.36	1.41	-	0.184
chr1_108115801_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.462	0.589	0.572	0.333	0.318	0.500	0.54	0.38	1.41	-	0.090
chr5_140534976_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.526	0.500	0.454	0.321	0.201	0.538	0.49	0.35	1.40	-	0.237
chr1_91176167_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.428	0.333	0.476	0.249	0.229	0.409	0.41	0.30	1.39	-	0.175
chr19_58280473_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.577	0.478	0.526	0.480	0.350	0.304	0.53	0.38	1.39	-	0.068
chr1_16971417_snv		G -> A	G -> A	G -> A	G -> A	G -> A	0.229	0.167	0.116		0.070	0.175	0.17	0.12	1.39	-	0.464
chr7_35758748_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.600	0.625	0.423	0.304	0.500	0.379	0.55	0.39	1.39	-	0.144
chr5_140256256_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.429	0.381	0.515	0.481	0.310	0.161	0.44	0.32	1.39	-	0.283
chr11_55605697_snv	C -> A	C -> A		C -> A	C -> A	C -> A	0.316	0.227	0.334	0.136	0.286		0.29	0.21	1.39	-	0.331
chr11_60860524_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.361	0.314	0.283	0.142	0.276	0.279	0.32	0.23	1.37	-	0.160
chr3_195373630_snv	A -> G		A -> G	A -> G		A -> G	0.212		0.184	0.178		0.111	0.20	0.14	1.37	-	0.279

chr7_32800838_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.584	0.723	0.611	0.461	0.588	0.352	0.64	0.47	1.37	-	0.099
chr11_115044495_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.320	0.518	0.535	0.303	0.391	0.318	0.46	0.34	1.36	-	0.180
chr18_21355789_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.583	0.423	0.661	0.516	0.363	0.350	0.56	0.41	1.36	-	0.173
chr5_79783438_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.412	0.393	0.524	0.375	0.184	0.421	0.44	0.33	1.36	-	0.235
chr19_54784838_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.653	0.409	0.524	0.333	0.400	0.437	0.53	0.39	1.36	-	0.145
chr1_16945516_snv	A -> C		A -> C	A -> C	A -> C	A -> C	0.064	0.063	0.169	0.093		0.053	0.10	0.07	1.35	-	0.628
chr4_7058730_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.629	0.732	0.400	0.500	0.481	0.62	0.46	1.35	-	0.096
chr15_90802331_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.517	0.391	0.652	0.438	0.259	0.461	0.52	0.39	1.35	-	0.246
chr2_163138039_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.333	0.333	0.707	0.267	0.449	0.308	0.46	0.34	1.34	-	0.441
chr20_34021682_snv		C -> A	C -> A	C -> A	C -> A	C -> A	0.189	0.174	0.153		0.190	0.067	0.17	0.13	1.34	-	0.430
chr19_46010778_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.611	0.429	0.467	0.500	0.352	0.281	0.50	0.38	1.33	-	0.217
chrX_46357130_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.591	0.437	0.381	0.437	0.333	0.51	0.38	1.33	-	0.080
chr15_41475419_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.454	0.531	0.545	0.535	0.214	0.406	0.51	0.39	1.32	-	0.269
chr5_35035385_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.484	0.552	0.461	0.360	0.481	0.292	0.50	0.38	1.32	-	0.120
chr22_32782811_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.462	0.652	0.683	0.577	0.357	0.429	0.60	0.45	1.32	-	0.201
chr7_12281918_snv		G -> A	G -> A		G -> A	G -> A		0.500	0.462		0.286	0.444	0.48	0.37	1.32	-	0.290
chr9_34048867_snv	G -> C	G -> C		G -> C	G -> C	G -> C	0.612	0.681	0.706	0.299	0.714		0.67	0.51	1.32	-	0.388
chr8_86786473_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.070	0.064	0.071	0.046		0.058	0.07	0.05	1.31	-	0.054
chr11_31848328_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.453	0.475	0.333	0.289	0.370	0.304	0.42	0.32	1.31	-	0.121
chr1_246887501_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.454	0.438	0.619	0.316	0.400	0.440	0.50	0.39	1.31	-	0.159
chr2_220342646_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.556	0.444	0.733	0.429	0.542	0.357	0.58	0.44	1.30	-	0.248
chr18_6576067_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.572	0.462	0.633	0.500	0.336	0.444	0.56	0.43	1.30	-	0.137
chr7_49976685_snv	C -> A	C -> A	C -> A		C -> A	C -> A		0.421	0.500	0.308	0.381	0.375	0.46	0.35	1.30	-	0.087
chr7_152133963_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.600	0.667	0.583	0.454	0.641	0.335	0.62	0.48	1.29	-	0.205
chr2_21934297_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.412	0.464	0.650	0.371	0.333	0.478	0.51	0.39	1.29	-	0.245
chr7_20874648_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.333	0.529	0.435	0.347	0.308	0.350	0.43	0.34	1.29	-	0.170
chr19_1596813_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.667	0.458	0.519	0.333	0.473	0.471	0.55	0.43	1.29	-	0.189
chr1_155922577_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.556	0.652	0.391	0.454	0.375	0.417	0.53	0.42	1.28	-	0.213
chr11_113281521_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.773	0.697	0.794	0.696	0.521	0.553	0.75	0.59	1.28	-	0.055
chr1_173860445_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.583	0.542	0.458	0.317	0.500	0.424	0.53	0.41	1.28	-	0.152
chr7_72949940_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.496	0.444		0.273	0.333	0.500	0.47	0.37	1.27	-	0.341
chr20_49521326_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.556	0.687	0.801	0.515	0.549	0.553	0.68	0.54	1.26	-	0.118
chr7_72951106_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.563	0.455	0.524	0.349	0.476	0.400	0.51	0.41	1.26	-	0.095
chr20_5482387_snv		A -> G	A -> G	A -> G	A -> G	A -> G	0.189	0.143	0.184		0.154	0.120	0.17	0.14	1.26	-	0.220
chr2_8822089_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.400	0.542	0.533	0.353	0.305	0.526	0.49	0.39	1.25	-	0.299
chr1_17198411_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.428	0.648	0.700	0.500	0.572	0.356	0.59	0.48	1.24	-	0.330
chr19_43710277_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.467	0.433	0.639	0.417	0.500	0.321	0.51	0.41	1.24	-	0.289
chrX_14024704_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.647	0.500	0.364	0.462	0.500	0.55	0.44	1.24	-	0.168
chr1_186158903_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.333	0.526	0.538	0.362	0.435	0.333	0.47	0.38	1.24	-	0.290
chr9_108153886_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.421	0.654	0.524	0.550	0.444	0.300	0.53	0.43	1.24	-	0.362
chrX_30670753_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.469	0.560	0.518	0.375	0.478	0.400	0.52	0.42	1.23	-	0.074
chr21_46419472_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.529	0.424	0.549	0.467	0.500	0.250	0.50	0.41	1.23	-	0.339
chr2_20871074_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.500	0.625	0.649	0.538	0.560	0.340	0.59	0.48	1.23	-	0.252
chr2_39828209_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.536	0.565	0.571	0.556	0.250	0.550	0.56	0.45	1.23	-	0.358
chr3_149683660_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.424	0.680	0.579	0.529	0.409	0.429	0.56	0.46	1.23	-	0.274
chr19_53868167_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.552	0.733	0.412	0.400	0.546	0.435	0.57	0.46	1.23	-	0.363
chr9_133559094_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.522	0.600	0.458	0.370	0.440	0.476	0.53	0.43	1.23	-	0.130

chr2_60586314_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.550	0.481	0.455	0.478	0.332	0.400	0.50	0.40	1.23	-	0.144
chr19_17004076_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.528	0.577	0.428	0.500	0.315	0.435	0.51	0.42	1.23	-	0.247
chr1_170632367_snv	G -> T	G -> T		G -> T	G -> T	G -> T	0.522	0.688	0.440	0.333	0.565		0.55	0.45	1.22	-	0.487
chr20_46286065_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.690	0.741	0.707	0.598	0.447	0.706	0.71	0.58	1.22	-	0.167
chr5_175307003_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.444	0.594	0.347	0.500	0.414	0.51	0.42	1.22	-	0.212
chr5_79783398_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.500	0.391	0.449	0.399	0.293	0.411	0.45	0.37	1.21	-	0.182
chr3_186330677_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.467	0.440	0.552	0.500	0.374	0.327	0.49	0.40	1.21	-	0.236
chr7_94023291_snv	A -> C	A -> C	A -> C	A -> C	A -> C		0.552	0.500		0.470	0.353	0.476	0.53	0.43	1.21	-	0.191
chr20_62197333_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.795	0.667	0.676	0.546	0.666	0.560	0.71	0.59	1.21	-	0.095
chr1_35888036_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.478	0.417	0.478	0.364	0.421	0.353	0.46	0.38	1.21	-	0.056
chr7_76681972_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.185	0.316		0.143	0.275	0.205	0.25	0.21	1.21	-	0.580
chr19_11275059_snv	A -> G		A -> G	A -> G	A -> G	A -> G	0.517	0.407	0.588	0.428		0.412	0.50	0.42	1.20	-	0.306
chrX_70525546_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.437	0.399	0.565	0.500	0.269	0.400	0.47	0.39	1.20	-	0.407
chr11_61404462_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.682	0.693	0.694	0.667	0.577	0.484	0.69	0.58	1.20	-	0.098
chr11_123496601_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.370	0.513	0.676	0.437	0.456	0.410	0.52	0.43	1.20	-	0.394
chr1_237804283_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.560	0.381	0.584	0.333	0.400	0.545	0.51	0.43	1.19	-	0.410
chr7_72949899_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.574	0.381		0.409	0.318	0.476	0.48	0.40	1.19	-	0.471
chr7_38726638_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.539	0.500	0.565	0.467	0.353	0.530	0.53	0.45	1.19	-	0.199
chr20_57227092_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.770	0.750	0.575	0.606	0.472	0.694	0.70	0.59	1.18	-	0.295
chr15_98980398_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.683	0.520	0.654	0.381	0.591	0.600	0.62	0.52	1.18	-	0.338
chr18_52605295_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.478	0.545	0.462	0.470	0.417	0.374	0.50	0.42	1.18	-	0.118
chr20_30061264_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.309	0.319	0.148	0.216	0.256	0.190	0.26	0.22	1.17	-	0.552
chr1_155869162_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.583	0.435	0.526	0.458	0.462	0.400	0.51	0.44	1.17	-	0.191
chr1_160511282_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.478	0.500	0.630	0.467	0.538	0.370	0.54	0.46	1.17	-	0.317
chr11_116618452_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.667	0.739	0.595	0.441	0.690	0.583	0.67	0.57	1.17	-	0.314
chr9_98643402_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.481	0.625	0.500	0.461	0.434	0.481	0.54	0.46	1.17	-	0.179
chr19_56910279_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.630	0.480	0.458	0.409	0.500	0.440	0.52	0.45	1.16	-	0.293
chr5_140571467_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.591	0.444	0.352	0.515	0.407	0.273	0.46	0.40	1.16	-	0.552
chr2_112187185_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.421	0.522	0.432	0.438	0.500	0.250	0.46	0.40	1.16	-	0.488
chr2_175436503_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.651	0.572	0.500	0.500	0.556	0.433	0.57	0.50	1.16	-	0.238
chr3_50332536_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.406	0.435	0.481	0.556	0.277	0.310	0.44	0.38	1.16	-	0.547
chr15_90328215_snv	G -> A	G -> A	G -> A		G -> A	G -> A		0.161	0.267	0.237	0.114	0.205	0.21	0.19	1.15	-	0.674
chr11_68524670_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.715	0.681	0.613	0.641	0.577	0.524	0.67	0.58	1.15	-	0.120
chr19_53497582_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.440	0.572	0.440	0.316	0.450	0.500	0.48	0.42	1.15	-	0.428
chr11_95709004_snv	G -> C		G -> C	G -> C	G -> C	G -> C	0.698	0.619	0.785	0.581		0.641	0.70	0.61	1.15	-	0.266
chr15_77904942_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.484	0.370	0.393	0.333	0.324	0.432	0.42	0.36	1.15	-	0.344
chr20_44803497_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.669	0.612	0.586	0.581	0.586	0.464	0.62	0.54	1.14	-	0.168
chr7_76103400_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.462	0.519	0.625	0.583	0.293	0.529	0.54	0.47	1.14	-	0.544
chr3_115520796_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.389	0.600	0.400	0.348	0.368	0.500	0.46	0.41	1.14	-	0.528
chr12_5342216_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.440	0.520	0.667	0.526	0.421	0.482	0.54	0.48	1.14	-	0.418
chr5_76788142_snv	G -> C	G -> C	G -> C		G -> C	G -> C		0.690	0.400	0.500	0.464	0.476	0.55	0.48	1.14	-	0.593
chr3_20228308_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.571	0.593	0.572	0.556	0.563	0.411	0.58	0.51	1.13	-	0.242
chr11_61569510_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.484	0.471	0.405	0.458	0.447	0.296	0.45	0.40	1.13	-	0.410
chr6_143074670_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.483	0.520	0.531	0.542	0.529	0.285	0.51	0.45	1.13	-	0.523
chr13_103528925_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.500	0.625	0.714	0.458	0.615	0.556	0.61	0.54	1.13	-	0.415
chr15_65619121_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.594	0.390	0.428	0.476	0.463	0.312	0.47	0.42	1.13	-	0.548
chr1_92480519_snv	A -> G	A -> G		A -> G	A -> G	A -> G	0.320	0.470	0.500	0.289	0.474		0.43	0.38	1.13	-	0.660

chr11_63178575_snv	G -> A	G -> A	G -> A		G -> A	G -> A		0.711	0.700	0.630	0.667	0.581	0.71	0.63	1.13	-	0.091
chr2_27458503_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.560	0.433	0.577	0.425	0.579	0.391	0.52	0.47	1.13	-	0.472
chr14_88470569_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.556	0.450	0.771	0.546	0.462	0.571	0.59	0.53	1.13	-	0.545
chrX_71822040_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.682	0.385	0.667	0.478	0.600	0.464	0.58	0.51	1.12	-	0.578
chr15_102265413_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.500	0.387	0.650	0.432	0.500	0.437	0.51	0.46	1.12	-	0.519
chr9_33044901_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.522	0.577	0.500	0.444	0.454	0.538	0.53	0.48	1.11	-	0.222
chr2_242174901_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.559	0.417	0.693	0.526	0.474	0.500	0.56	0.50	1.11	-	0.525
chr15_34502179_snv	A -> G	A -> G	A -> G	A -> G		A -> G	0.637		0.557	0.704	0.542	0.365	0.60	0.54	1.11	-	0.675
chr7_48273733_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.522	0.519	0.522	0.621	0.350	0.435	0.52	0.47	1.11	-	0.549
chr2_113535567_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.333	0.696	0.654	0.393	0.680	0.444	0.56	0.51	1.11	-	0.722
chr2_89064851_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.542	0.613	0.437	0.476	0.444	0.518	0.53	0.48	1.11	-	0.407
chr2_1639206_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.700	0.640	0.384	0.476	0.667	0.416	0.57	0.52	1.11	-	0.678
chrX_47047023_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.496	0.516	0.520	0.421	0.500	0.467	0.51	0.46	1.10	-	0.117
chr21_25800692_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.474	0.530	0.596	0.495	0.455	0.500	0.53	0.48	1.10	-	0.259
chr19_49793310_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.318	0.536	0.440	0.300	0.526	0.348	0.43	0.39	1.10	-	0.690
chr20_3850239_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.563	0.675	0.520	0.542	0.575	0.480	0.59	0.53	1.10	-	0.376
chr9_138418584_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.516	0.483	0.476	0.706	0.367	0.269	0.49	0.45	1.10	-	0.756
chr3_192992854_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.518	0.520	0.622	0.433	0.458	0.621	0.55	0.50	1.10	-	0.510
chr13_45378914_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.483	0.522	0.478	0.551	0.484	0.316	0.49	0.45	1.10	-	0.570
chr11_55587929_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.714	0.667	0.742	0.688	0.731	0.519	0.71	0.65	1.10	-	0.418
chr11_111600129_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.615	0.743	0.573	0.606	0.516	0.641	0.64	0.59	1.10	-	0.426
chr11_44748033_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.340	0.333	0.176	0.250	0.199	0.328	0.28	0.26	1.09	-	0.732
chr1_186159466_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.461	0.333	0.311	0.437	0.440	0.43	0.40	1.09	-	0.621
chr19_19038627_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.464	0.467	0.500	0.333	0.481	0.500	0.48	0.44	1.09	-	0.510
chr2_128457712_snv	A -> T		A -> T	A -> T	A -> T	A -> T	0.406	0.332	0.572	0.431		0.374	0.44	0.40	1.08	-	0.740
chr21_31853119_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.522	0.545	0.524	0.467	0.500	0.500	0.53	0.49	1.08	-	0.035
chr11_57799036_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.302	0.484	0.347	0.322	0.368	0.355	0.38	0.35	1.08	-	0.631
chr11_4700735_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.385	0.285	0.436	0.200	0.450	0.372	0.37	0.34	1.08	-	0.761
chr7_150418470_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.692	0.621	0.679	0.650	0.619	0.577	0.66	0.62	1.08	-	0.185
chr1_186650548_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.600	0.333	0.418	0.474	0.403	0.375	0.45	0.42	1.08	-	0.715
chr3_134079192_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.545	0.600	0.485	0.515	0.455	0.543	0.54	0.50	1.08	-	0.407
chr3_27872474_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.566	0.454	0.520	0.600	0.330	0.500	0.51	0.48	1.08	-	0.689
chr5_74895534_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.527	0.786	0.571	0.579	0.556	0.616	0.63	0.58	1.08	-	0.617
chr4_15691882_snv	G -> T	G -> T	G -> T	G -> T	G -> T		0.516	0.606	0.741	0.619	0.474	0.640	0.62	0.58	1.08	-	0.632
chr13_33110053_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.450	0.600	0.500	0.500	0.529	0.417	0.52	0.48	1.07	-	0.566
chr9_139740025_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.424	0.569	0.457	0.546	0.269	0.546	0.48	0.45	1.07	-	0.786
chr18_10677756_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.423	0.667	0.467	0.500	0.462	0.500	0.52	0.49	1.06	-	0.699
chr11_65487099_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.661	0.756	0.647	0.683	0.609	0.647	0.69	0.65	1.06	-	0.360
chr1_117556313_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.429	0.370	0.600	0.316	0.306	0.43	0.41	1.06	-	0.816
chr11_64598997_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.374	0.394	0.375	0.536	0.181	0.360	0.38	0.36	1.06	-	0.841
chrX_7890106_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.591	0.435	0.500	0.536	0.385	0.517	0.51	0.48	1.06	-	0.678
chr2_91806467_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.106	0.151	0.111	0.164	0.092	0.091	0.12	0.12	1.06	-	0.815
chr19_12636561_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.437	0.625	0.625	0.682	0.409	0.500	0.56	0.53	1.06	-	0.769
chr5_140793184_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.654	0.400	0.429	0.455	0.583	0.52	0.49	1.06	-	0.758
chr19_2051205_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.477	0.305	0.220	0.400	0.360	0.187	0.33	0.32	1.06	-	0.863
chr5_150039131_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.475	0.367	0.497	0.433	0.348	0.485	0.45	0.42	1.06	-	0.690
chr9_35755427_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.637	0.571	0.470	0.400	0.652	0.536	0.56	0.53	1.06	-	0.749

chr7_81330273_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.452	0.714	0.580	0.444	0.584	0.625	0.58	0.55	1.06	-	0.757
chr19_53075625_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.552	0.500	0.400	0.476	0.429	0.470	0.48	0.46	1.06	-	0.614
chr11_134136071_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.375	0.410	0.643	0.520	0.400	0.433	0.48	0.45	1.06	-	0.798
chr11_118985012_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.523	0.429	0.560	0.481	0.490	0.465	0.50	0.48	1.05	-	0.558
chr15_29385398_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.266	0.416	0.542	0.370	0.364	0.432	0.41	0.39	1.05	-	0.827
chr19_56888322_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.551	0.526	0.545	0.429	0.416	0.704	0.54	0.52	1.05	-	0.809
chrX_102883713_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.654	0.675	0.485	0.591	0.562	0.580	0.60	0.58	1.05	-	0.680
chr11_67757718_snv	G -> A	G -> A	G -> A	G -> A		G -> A	0.108		0.166	0.150	0.139	0.104	0.14	0.13	1.05	-	0.844
chr21_46875534_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.577	0.438	0.550	0.632	0.384	0.485	0.52	0.50	1.04	-	0.811
chr11_73744450_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.590	0.680	0.651	0.549	0.590	0.704	0.64	0.61	1.04	-	0.652
chr5_180242874_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.495	0.636	0.467	0.615	0.484	0.54	0.52	1.04	-	0.758
chr9_34834105_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.378	0.552	0.632	0.500	0.500	0.500	0.52	0.50	1.04	-	0.796
chr19_10460701_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.469	0.522	0.667	0.411	0.591	0.591	0.55	0.53	1.04	-	0.810
chr1_214523702_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.556	0.522	0.500	0.551	0.437	0.533	0.53	0.51	1.04	-	0.651
chr16_8588419_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.500	0.480	0.416	0.381	0.571	0.394	0.47	0.45	1.04	-	0.814
chrX_27765941_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.454	0.522	0.563	0.455	0.579	0.452	0.51	0.50	1.04	-	0.754
chr11_117871040_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.554	0.368	0.488	0.479	0.367	0.516	0.47	0.45	1.04	-	0.832
chr1_109244198_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.429	0.600	0.637	0.648	0.462	0.500	0.56	0.54	1.03	-	0.838
chr11_130754302_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.290	0.558	0.433	0.462	0.348	0.428	0.43	0.41	1.03	-	0.874
chr11_55928421_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.615	0.706	0.591	0.572	0.697	0.583	0.64	0.62	1.03	-	0.726
chr15_59425980_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.375	0.333	0.667	0.417	0.417	0.500	0.46	0.44	1.03	-	0.906
chr1_248636267_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.521	0.652	0.438	0.455	0.533	0.579	0.54	0.52	1.03	-	0.849
chr19_9674598_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.462	0.650	0.400	0.458	0.546	0.467	0.50	0.49	1.03	-	0.873
chr19_1597701_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.500	0.423	0.346	0.353	0.464	0.421	0.42	0.41	1.03	-	0.860
chr1_235610620_snv	G -> C	G -> C		G -> C	G -> C	G -> C	0.329	0.333	0.625	0.368	0.470		0.43	0.42	1.02	-	0.944
chr20_22400826_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.431	0.440	0.563	0.456	0.387	0.558	0.48	0.47	1.02	-	0.875
chr19_304665_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.394	0.600	0.474	0.435	0.500	0.500	0.49	0.48	1.02	-	0.871
chrX_153219793_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.515	0.362	0.467	0.454	0.379	0.482	0.45	0.44	1.02	-	0.868
chr1_154244504_snv	T -> A	T -> A		T -> A	T -> A	T -> A	0.579	0.528	0.675	0.539	0.625		0.59	0.58	1.02	-	0.864
chr2_186661368_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.419	0.421	0.476	0.461	0.293	0.538	0.44	0.43	1.02	-	0.920
chr7_107434838_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.632	0.375	0.480	0.437	0.375	0.650	0.50	0.49	1.02	-	0.944
chr11_118985024_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.467	0.410	0.556	0.482	0.490	0.442	0.48	0.47	1.01	-	0.895
chr11_105853193_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.568	0.714	0.643	0.500	0.750	0.651	0.64	0.63	1.01	-	0.929
chr9_140144521_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.535	0.420	0.500	0.400	0.466	0.577	0.49	0.48	1.01	-	0.952
chr11_57435062_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.323	0.429	0.454	0.429	0.364	0.405	0.40	0.40	1.01	-	0.955
chr2_191848422_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.450	0.464	0.238	0.421	0.333	0.391	0.38	0.38	1.01	-	0.977
chr9_35547210_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.626	0.500	0.500	0.577	0.500	0.540	0.54	0.54	1.01	-	0.953
chr12_90851_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.202	0.179	0.133	0.173	0.177	0.163	0.17	0.17	1.00	-	0.988
chr12_90851_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.202	0.179	0.133	0.173	0.177	0.163	0.17	0.17	1.00	-	0.988
chr11_102217162_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.226	0.368	0.428	0.393	0.285	0.343	0.34	0.34	1.00	-	0.996
chr7_22689435_snv	C -> T		C -> T	C -> T	C -> T	C -> T	0.592	0.461	0.637	0.313		0.814	0.56	0.56	1.00	-	0.999
chr15_51973633_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.577	0.366	0.593	0.531	0.461	0.548	0.51	0.51	1.00	-	0.987
chr11_123483491_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.509	0.449	0.450	0.486	0.454	0.475	0.47	0.47	1.00	-	0.920
chr22_25006249_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.912	0.905	0.889	0.914		0.901	0.90	0.91	0.99	-	0.622
chr11_27390143_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.625	0.590	0.560	0.581	0.713	0.496	0.59	0.60	0.99	-	0.943
chr5_34192536_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.067	0.067	0.043		0.067	0.052	0.06	0.06	0.99	-	0.969
chr1_204165951_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.656	0.344	0.421	0.455	0.333	0.649	0.47	0.48	0.99	-	0.970

chr19_41171785_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.546	0.500	0.637	0.708	0.444	0.550	0.56	0.57	0.99	-	0.945
chr2_20401632_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.547	0.483	0.526	0.682	0.417	0.478	0.52	0.53	0.99	-	0.936
chr3_89530929_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.526	0.506	0.400	0.428	0.524	0.500	0.48	0.48	0.99	-	0.897
chr12_65462636_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.611	0.500	0.474	0.474	0.526	0.613	0.53	0.54	0.98	-	0.881
chr5_34193207_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.044	0.048	0.043	0.036	0.055	0.047	0.05	0.05	0.98	-	0.870
chr12_114675876_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.454	0.550	0.565	0.665	0.579	0.360	0.52	0.53	0.98	-	0.910
chr20_5172187_snv		C -> T	C -> T	C -> T	C -> T	C -> T	0.375	0.364	0.447		0.300	0.509	0.40	0.40	0.98	-	0.921
chr9_136277927_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.591	0.543	0.368	0.679	0.625	0.54	0.56	0.98	-	0.905
chr20_31825957_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.565	0.449	0.497	0.553	0.475	0.519	0.50	0.52	0.98	-	0.782
chr11_57435401_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.675	0.667	0.565	0.714	0.533	0.708	0.64	0.65	0.98	-	0.828
chr9_89617682_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.437	0.480	0.533	0.471	0.444	0.572	0.48	0.50	0.98	-	0.809
chr12_104458068_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.556	0.437	0.476	0.471	0.562	0.476	0.49	0.50	0.97	-	0.786
chrX_41782544_snv	C -> T	C -> T	C -> T	C -> T	C -> T		0.731	0.720		0.784	0.755	0.700	0.73	0.75	0.97	-	0.562
chr18_12658375_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.485	0.435	0.400	0.546	0.500	0.316	0.44	0.45	0.97	-	0.860
chr9_123837291_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.530	0.458	0.279	0.352	0.359	0.600	0.42	0.44	0.97	-	0.901
chr11_72464226_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.604	0.676	0.513	0.659	0.528	0.672	0.60	0.62	0.96	-	0.755
chr19_44095991_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.734	0.600	0.529	0.786	0.588	0.61	0.63	0.96	-	0.834
chr2_170551184_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.556	0.444	0.560	0.611	0.333	0.684	0.52	0.54	0.96	-	0.851
chr19_49224095_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.538	0.400	0.368	0.346	0.539	0.478	0.44	0.45	0.96	-	0.818
chr15_32322743_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.644	0.500	0.454	0.625	0.524	0.526	0.53	0.56	0.95	-	0.718
chr15_64446188_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.448	0.679	0.609	0.515	0.621	0.688	0.58	0.61	0.95	-	0.747
chr2_42162786_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.394	0.632	0.409	0.500	0.546	0.462	0.48	0.50	0.95	-	0.778
chr19_46105398_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.466	0.522	0.701	0.524	0.500	0.751	0.56	0.59	0.95	-	0.802
chr9_77643428_snv	T -> C		T -> C	T -> C	T -> C	T -> C	0.500	0.471	0.538	0.450		0.609	0.50	0.53	0.95	-	0.708
chr2_33108083_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.556	0.494	0.425	0.500	0.533	0.524	0.49	0.52	0.95	-	0.523
chr20_26083894_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.513	0.467	0.459	0.462	0.560	0.500	0.48	0.51	0.95	-	0.451
chr3_130064402_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.647	0.384	0.385	0.531	0.476	0.500	0.47	0.50	0.94	-	0.750
chr11_60523825_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.667	0.690	0.613	0.651	0.714	0.737	0.66	0.70	0.94	-	0.270
chr4_1382709_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.353	0.360	0.368	0.398	0.238	0.520	0.36	0.39	0.94	-	0.775
chr19_1597583_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.347	0.482	0.374	0.400	0.333	0.556	0.40	0.43	0.93	-	0.731
chr20_1235272_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.509	0.456	0.510	0.580	0.581	0.420	0.49	0.53	0.93	-	0.565
chr2_174147040_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.567	0.556	0.412	0.385	0.607	0.655	0.51	0.55	0.93	-	0.720
chr3_37184288_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.428	0.591	0.478	0.437	0.625	0.545	0.50	0.54	0.93	-	0.641
chr5_34193569_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.042	0.058	0.033	0.056	0.041	0.046	0.04	0.05	0.93	-	0.716
chr19_2282686_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.667	0.478	0.637	0.632	0.500	0.55	0.59	0.93	-	0.609
chr20_3910860_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.439	0.490	0.485	0.524	0.359	0.638	0.47	0.51	0.93	-	0.688
chr15_90744661_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.486	0.581	0.481	0.529	0.547	0.590	0.52	0.56	0.93	-	0.350
chr9_116027481_snv	G -> C	G -> C	G -> C	G -> C	G -> C		0.480	0.542		0.583	0.632	0.435	0.51	0.55	0.93	-	0.659
chr6_10975300_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.546	0.461	0.473	0.500	0.516	0.579	0.49	0.53	0.93	-	0.345
chrX_37026878_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.609	0.486	0.333	0.572	0.520	0.454	0.48	0.52	0.92	-	0.674
chr15_64974583_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.333	0.324	0.455	0.351	0.500	0.354	0.37	0.40	0.92	-	0.657
chr19_13085170_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.474	0.360	0.476	0.476	0.505	0.440	0.44	0.47	0.92	-	0.435
chr20_42186833_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.474	0.500	0.400	0.539	0.500	0.452	0.46	0.50	0.92	-	0.375
chr2_207940054_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.421	0.450	0.265	0.440	0.364	0.429	0.38	0.41	0.92	-	0.630
chr2_175300114_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.500	0.572	0.683	0.539	0.766	0.600	0.59	0.64	0.92	-	0.593
chr13_28491541_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.600	0.600	0.263	0.667	0.455	0.469	0.49	0.53	0.92	-	0.762
chr19_36113872_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.574	0.533	0.520	0.667	0.565	0.538	0.54	0.59	0.92	-	0.325

chr11_19138664_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.583	0.631	0.500	0.642	0.700	0.525	0.57	0.62	0.92	-	0.471
chr9_138505493_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.514	0.454	0.500	0.478	0.600	0.522	0.49	0.53	0.92	-	0.333
chr2_105882555_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.238	0.461	0.342	0.556	0.409	0.40	0.44	0.92	-	0.745
chr12_101550476_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.583	0.425	0.350	0.421	0.652	0.412	0.45	0.50	0.91	-	0.706
chr2_38570540_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.588	0.572	0.458	0.637	0.545	0.588	0.54	0.59	0.91	-	0.358
chr1_214209146_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.619	0.474	0.476	0.434	0.583	0.700	0.52	0.57	0.91	-	0.615
chr17_61974486_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.273	0.522	0.292	0.480	0.296	0.414	0.36	0.40	0.91	-	0.740
chr13_114055407_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.586	0.379	0.473	0.625	0.412	0.542	0.48	0.53	0.91	-	0.614
chr15_72435139_snv		G -> C	G -> C	G -> C	G -> C	G -> C	0.524	0.457	0.435		0.552	0.486	0.47	0.52	0.91	-	0.349
chr3_132319269_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.600	0.440	0.440	0.552	0.609	0.467	0.49	0.54	0.91	-	0.505
chr2_152301851_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.556	0.444	0.625	0.636	0.722	0.444	0.54	0.60	0.90	-	0.578
chr15_90014120_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.514	0.476	0.496	0.514	0.577	0.559	0.50	0.55	0.90	-	0.066
chr11_67394957_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.422	0.294	0.372	0.319	0.454	0.436	0.36	0.40	0.90	-	0.514
chr21_19961901_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.652	0.449	0.362	0.423	0.600	0.609	0.49	0.54	0.90	-	0.620
chrX_44929583_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.461	0.588	0.500	0.568	0.600	0.564	0.52	0.58	0.89	-	0.195
chr7_63484712_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.333	0.364	0.545	0.454	0.462	0.474	0.41	0.46	0.89	-	0.499
chr11_125933212_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.588	0.570	0.541	0.630	0.665	0.609	0.57	0.63	0.89	-	0.033
chr2_25194953_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.575	0.526	0.429	0.496	0.720	0.500	0.51	0.57	0.89	-	0.509
chr13_95585200_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.533	0.368	0.381	0.500	0.520	0.423	0.43	0.48	0.89	-	0.426
chr11_113813887_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.341	0.379	0.310	0.320	0.393	0.447	0.34	0.39	0.89	-	0.359
chr15_91360099_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.516	0.344	0.519	0.372	0.602	0.581	0.46	0.52	0.89	-	0.564
chr1_205883975_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.452	0.678	0.576	0.731	0.582	0.612	0.57	0.64	0.89	-	0.411
chr15_56130342_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.350	0.263	0.474	0.316	0.505	0.406	0.36	0.41	0.89	-	0.600
chr11_72464421_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.686	0.581	0.529	0.653	0.675	0.700	0.60	0.68	0.89	-	0.183
chr19_10084867_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.370	0.548	0.527	0.752	0.402	0.478	0.48	0.54	0.89	-	0.631
chr2_86080797_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.654	0.577	0.517	0.632	0.714	0.630	0.58	0.66	0.88	-	0.191
chr4_57181218_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.278	0.437	0.266	0.293	0.437	0.384	0.33	0.37	0.88	-	0.557
chr19_38904091_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.452	0.565	0.429	0.550	0.474	0.621	0.48	0.55	0.88	-	0.329
chr15_25307191_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.423	0.621	0.461	0.552	0.682	0.481	0.50	0.57	0.88	-	0.454
chr5_172114851_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.484	0.387	0.819	0.645	0.654	0.630	0.56	0.64	0.88	-	0.576
chr3_50305159_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.486	0.405	0.524	0.623	0.234	0.760	0.47	0.54	0.88	-	0.698
chr3_122458037_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.583	0.389	0.385	0.552	0.500	0.500	0.45	0.52	0.87	-	0.391
chr2_102971808_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.579	0.626	0.370	0.588	0.583	0.632	0.53	0.60	0.87	-	0.397
chr9_212801_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.280	0.400	0.400	0.428	0.474	0.335	0.36	0.41	0.87	-	0.412
chr20_31331257_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.442	0.429	0.552	0.459	0.600	0.571	0.47	0.54	0.87	-	0.300
chr9_86450697_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.632	0.391	0.612	0.661	0.526	0.688	0.55	0.63	0.87	-	0.434
chr9_35071763_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.428	0.500	0.429	0.538	0.400	0.619	0.45	0.52	0.87	-	0.384
chr2_190635186_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.529	0.400	0.391	0.550	0.353	0.615	0.44	0.51	0.87	-	0.506
chr2_219513985_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.481	0.350	0.385	0.345	0.600	0.455	0.41	0.47	0.87	-	0.504
chr1_145117339_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.107	0.181	0.200	0.161	0.222	0.179	0.16	0.19	0.87	-	0.504
chr1_145117339_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.107	0.181	0.200	0.161	0.222	0.179	0.16	0.19	0.87	-	0.504
chr11_124949065_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.355	0.473	0.653	0.600	0.486	0.621	0.49	0.57	0.87	-	0.478
chr11_118965546_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.450	0.522	0.432	0.460	0.679	0.481	0.47	0.54	0.87	-	0.391
chr12_49993576_snv	A -> C	A -> C	A -> C	A -> C	A -> C	A -> C	0.382	0.556	0.556	0.688	0.600	0.444	0.50	0.58	0.86	-	0.437
chr11_63725125_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.250	0.429	0.340	0.394	0.375	0.413	0.34	0.39	0.86	-	0.362
chr19_58008025_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.545	0.316	0.545	0.429	0.737	0.465	0.47	0.54	0.86	-	0.577
chr2_241874406_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.441	0.333	0.477	0.584	0.620	0.250	0.42	0.48	0.86	-	0.618

chr7_4174444_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.576	0.444	0.632	0.683	0.593	0.651	0.55	0.64	0.86	-	0.211
chr20_22400865_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.397	0.401	0.558	0.500	0.454	0.628	0.45	0.53	0.86	-	0.368
chr18_55103081_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.626	0.461	0.600	0.674		0.643	0.56	0.66	0.85	-	0.247
chr1_23745623_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.563	0.529	0.385	0.630	0.600	0.500	0.49	0.58	0.85	-	0.278
chr1_244873164_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.500	0.696	0.500	0.500	0.723	0.766	0.57	0.66	0.85	-	0.406
chr2_102961876_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.451	0.421	0.556	0.444	0.691	0.542	0.48	0.56	0.85	-	0.372
chr7_479481_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.647	0.412	0.315	0.667	0.448	0.500	0.46	0.54	0.85	-	0.536
chr11_89818635_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.328	0.300	0.266	0.368	0.440	0.243	0.30	0.35	0.85	-	0.434
chr1_201438048_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.500	0.500	0.593	0.584	0.572	0.717	0.53	0.62	0.85	-	0.170
chr13_67798490_snv	A -> G		A -> G	A -> G		A -> G	0.179		0.305	0.350		0.224	0.24	0.29	0.84	-	0.664
chr20_42345047_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.531	0.491	0.344	0.478	0.578	0.568	0.46	0.54	0.84	-	0.257
chr2_86080503_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.563	0.457	0.458	0.692	0.450	0.616	0.49	0.59	0.84	-	0.306
chr1_145283237_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.129	0.188	0.176	0.190	0.167	0.232	0.16	0.20	0.84	-	0.289
chr1_145283237_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.129	0.188	0.176	0.190	0.167	0.232	0.16	0.20	0.84	-	0.289
chr13_27757804_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.600	0.375	0.360	0.556	0.524	0.515	0.45	0.53	0.84	-	0.332
chr19_8935096_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.416	0.616	0.458	0.656	0.588	0.539	0.50	0.59	0.84	-	0.234
chr15_54685278_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.524	0.478	0.611	0.526	0.684	0.724	0.54	0.64	0.83	-	0.211
chr13_106114659_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.400	0.546	0.300	0.532	0.500	0.464	0.42	0.50	0.83	-	0.324
chr19_50796536_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.676	0.519	0.449	0.631	0.714	0.632	0.55	0.66	0.83	-	0.201
chr1_11126126_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.600	0.471	0.391	0.500	0.688	0.583	0.49	0.59	0.83	-	0.276
chr1_211606700_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.533	0.455	0.500	0.522	0.706	0.577	0.50	0.60	0.82	-	0.148
chr12_1995490_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.291	0.429	0.425	0.381	0.437	0.572	0.38	0.46	0.82	-	0.324
chr11_121062228_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.540	0.537	0.370	0.441	0.728	0.595	0.48	0.59	0.82	-	0.351
chr2_133061609_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.500	0.474	0.484	0.563	0.750	0.467	0.49	0.59	0.82	-	0.268
chr2_89065300_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.497	0.464	0.556	0.667	0.450	0.737	0.51	0.62	0.82	-	0.282
chr5_177612333_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.474	0.471	0.683	0.713	0.714	0.567	0.54	0.66	0.82	-	0.227
chr20_22401007_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.431	0.467	0.512	0.536	0.551	0.649	0.47	0.58	0.81	-	0.063
chr2_174147137_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.630	0.572	0.500	0.664	0.637	0.800	0.57	0.70	0.81	-	0.102
chr19_50869176_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.529	0.409	0.567	0.551	0.611	0.696	0.50	0.62	0.81	-	0.138
chr18_70991405_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.641	0.350	0.471	0.357	0.818	0.632	0.49	0.60	0.81	-	0.508
chr1_143768905_snv	A -> G		A -> G	A -> G	A -> G	A -> G	0.146	0.178	0.114	0.259		0.102	0.15	0.18	0.81	-	0.623
chr20_3806584_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.437	0.553	0.449	0.565	0.682	0.533	0.48	0.59	0.81	-	0.123
chr3_8610214_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.348	0.565	0.571	0.648	0.688	0.500	0.49	0.61	0.81	-	0.276
chr11_113645305_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.414	0.333	0.310	0.307	0.500	0.503	0.35	0.44	0.81	-	0.307
chr18_72923005_snv	G -> T		G -> T	G -> T	G -> T	G -> T	0.522	0.572	0.364	0.566		0.639	0.49	0.60	0.81	-	0.266
chr3_38294872_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.628	0.480	0.435	0.752	0.611	0.550	0.51	0.64	0.81	-	0.214
chr18_45340982_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.522	0.384	0.441	0.412	0.668	0.593	0.45	0.56	0.81	-	0.274
chr20_61542547_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.405	0.308	0.327	0.366	0.497	0.429	0.35	0.43	0.80	-	0.156
chr2_89065238_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.529	0.500	0.411	0.625	0.530	0.637	0.48	0.60	0.80	-	0.075
chr1_4484898_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.412	0.447	0.462	0.462	0.526	0.656	0.44	0.55	0.80	-	0.142
chr5_72385836_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.370	0.643	0.609	0.668	0.773	0.580	0.54	0.67	0.80	-	0.264
chr5_178508823_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.579	0.546	0.563	0.664	0.591	0.852	0.56	0.70	0.80	-	0.149
chr2_36778777_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.393	0.421	0.530	0.450	0.563	0.667	0.45	0.56	0.80	-	0.211
chr1_27680864_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.405	0.447	0.583	0.429	0.688	0.680	0.48	0.60	0.80	-	0.296
chr20_49640487_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.449	0.304	0.310	0.529	0.317	0.488	0.35	0.44	0.80	-	0.324
chr11_55580000_snv	A -> T	A -> T	A -> T	A -> T	A -> T	A -> T	0.450	0.205	0.181	0.333	0.321	0.400	0.28	0.35	0.79	-	0.462
chr5_140811171_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.484	0.550	0.414	0.679	0.496	0.652	0.48	0.61	0.79	-	0.142

chr20_46609171_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.303	0.320	0.235	0.435	0.310	0.340	0.29	0.36	0.79	-	0.174
chr20_58524077_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.233	0.481	0.357	0.469	0.479	0.412	0.36	0.45	0.79	-	0.266
chr4_37021239_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.235	0.344	0.387	0.286	0.389	0.556	0.32	0.41	0.78	-	0.385
chr7_100469252_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.500	0.516	0.500	0.781	0.601	0.552	0.51	0.64	0.78	-	0.117
chr2_21227299_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.565	0.522	0.368	0.765	0.548	0.552	0.49	0.62	0.78	-	0.217
chr20_3869713_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.192	0.163	0.206	0.301	0.223	0.196	0.19	0.24	0.78	-	0.193
chr11_64217549_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.214	0.294	0.433	0.296	0.414	0.500	0.31	0.40	0.78	-	0.362
chr5_179224925_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.471	0.661	0.440	0.652	0.667	0.703	0.52	0.67	0.78	-	0.101
chr2_135956232_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.556	0.350	0.588	0.632	0.667	0.625	0.50	0.64	0.78	-	0.131
chr3_52579492_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.579	0.391	0.278	0.526	0.571	0.520	0.42	0.54	0.77	-	0.240
chr5_1318222_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.520	0.346	0.565	0.667	0.500	0.697	0.48	0.62	0.77	-	0.186
chr6_3010399_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.250	0.550	0.333	0.467	0.409	0.600	0.38	0.49	0.77	-	0.341
chr1_66840616_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.444	0.364	0.645	0.667	0.560	0.680	0.48	0.64	0.76	-	0.175
chr1_205052974_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.359	0.555	0.682	0.766	0.714	0.625	0.53	0.70	0.76	-	0.173
chr5_86563481_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.391	0.586	0.696	0.688	0.728	0.792	0.56	0.74	0.76	-	0.131
chrX_139175876_snv	G -> T	G -> T	G -> T	G -> T	G -> T		0.375	0.412		0.583	0.353	0.625	0.39	0.52	0.76	-	0.332
chr5_35876146_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.469	0.370	0.680	0.852	0.657	0.500	0.51	0.67	0.76	-	0.299
chr1_55252661_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.292	0.375	0.653	0.652	0.478	0.616	0.44	0.58	0.76	-	0.307
chr5_140531497_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.391	0.563	0.598	0.762	0.636	0.657	0.52	0.69	0.76	-	0.089
chr5_34194272_snv	A -> G	A -> G	A -> G	A -> G	A -> G	A -> G	0.044	0.062	0.055	0.083	0.084	0.047	0.05	0.07	0.75	-	0.253
chr11_46696402_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.368	0.206	0.370	0.450	0.483	0.322	0.31	0.42	0.75	-	0.230
chr19_47996296_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.452	0.519	0.389	0.667	0.647	0.496	0.45	0.60	0.75	-	0.085
chr1_81792426_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.385	0.560	0.500	0.632	0.600	0.692	0.48	0.64	0.75	-	0.051
chrX_48114181_snv	G -> T	G -> T	G -> T	G -> T		G -> T	0.609		0.420	0.715	0.735	0.609	0.51	0.69	0.75	-	0.142
chr5_81568164_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.381	0.647	0.381	0.652	0.613	0.630	0.47	0.63	0.74	-	0.144
chr15_64447694_snv	G -> A		G -> A	G -> A	G -> A	G -> A	0.601	0.625	0.384	0.797		0.657	0.54	0.73	0.74	-	0.187
chr1_41847381_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.402	0.400	0.484	0.667	0.480	0.598	0.43	0.58	0.74	-	0.067
chr1_20465470_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.593	0.571	0.384	0.560	0.750	0.793	0.52	0.70	0.74	-	0.131
chr19_38397303_snv	G -> A	G -> A	G -> A	G -> A	G -> A		0.481	0.429		0.702	0.667	0.500	0.46	0.62	0.73	-	0.135
chr7_101256759_snv	T -> A	T -> A	T -> A	T -> A	T -> A	T -> A	0.480	0.465	0.324	0.716	0.444	0.579	0.42	0.58	0.73	-	0.167
chr15_43029303_snv	C -> T	C -> T	C -> T	C -> T	C -> T		0.437	0.333		0.632	0.384	0.572	0.39	0.53	0.73	-	0.259
chr21_47394582_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.303	0.346	0.402	0.478	0.611	0.357	0.35	0.48	0.73	-	0.170
chr5_78076356_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.400	0.650	0.444	0.786	0.607	0.682	0.50	0.69	0.72	-	0.105
chr5_150280903_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.381	0.235	0.507	0.474	0.471	0.625	0.37	0.52	0.72	-	0.187
chr1_196620793_snv	C -> A	C -> A	C -> A	C -> A	C -> A	C -> A	0.411	0.476	0.423	0.640	0.722	0.481	0.44	0.61	0.71	-	0.073
chr1_158800451_snv	G -> T	G -> T	G -> T	G -> T	G -> T	G -> T	0.304	0.484	0.526	0.652	0.565	0.632	0.44	0.62	0.71	-	0.071
chr20_2126536_snv		T -> C	T -> C		T -> C	T -> C		0.388	0.447		0.657	0.528	0.42	0.59	0.70	-	0.132
chr20_24647196_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.302	0.204	0.135	0.349	0.322	0.242	0.21	0.30	0.70	-	0.194
chr3_3194152_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.579	0.293	0.400	0.714	0.546	0.556	0.42	0.61	0.70	-	0.143
chr11_93822120_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.414	0.309	0.224	0.481	0.415	0.464	0.32	0.45	0.70	-	0.078
chr5_172773676_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.414	0.366	0.538	0.566	0.571	0.762	0.44	0.63	0.69	-	0.078
chr20_46282782_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.407	0.174	0.266	0.351	0.325	0.549	0.28	0.41	0.69	-	0.268
chr5_175801739_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.600	0.357	0.480	0.731	0.600	0.763	0.48	0.70	0.69	-	0.064
chr1_158970002_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.530	0.589	0.421	0.882	0.733	0.630	0.51	0.75	0.69	-	0.056
chr4_52384_snv	G -> A	G -> A	G -> A	G -> A	G -> A	G -> A	0.056	0.110	0.102	0.138	0.078	0.175	0.09	0.13	0.69	-	0.281
chr5_147547179_snv	T -> C	T -> C	T -> C	T -> C	T -> C	T -> C	0.510	0.491	0.376	0.521	0.648	0.849	0.46	0.67	0.68	-	0.110
chr2_208628154_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.426	0.368	0.765	0.543	0.600	0.43	0.64	0.68	-	0.056

chr2_238600903_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.596	0.261	0.500	0.723	0.778	0.500	0.45	0.67	0.68	-	0.176
chr15_51297904_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.500	0.333	0.579	0.713	0.759	0.621	0.47	0.70	0.67	-	0.052
chr1_243665435_snv	T -> G	T -> G	T -> G	T -> G	T -> G	T -> G	0.500	0.464	0.385	0.505	0.846	0.679	0.45	0.68	0.66	-	0.095
chr1_1182162_snv	G -> C	G -> C	G -> C	G -> C	G -> C	G -> C	0.522	0.482	0.316	0.545	0.760	0.700	0.44	0.67	0.66	-	0.064
chr1_109648405_snv	G -> A	G -> A	G -> A	G -> A		G -> A	0.293		0.294	0.467	0.375	0.534	0.29	0.46	0.64	-	0.069
chr20_44575753_snv	C -> G	C -> G	C -> G	C -> G	C -> G	C -> G	0.342	0.250	0.219	0.400	0.591	0.307	0.27	0.43	0.62	-	0.150
chr18_5393188_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.461	0.235	0.412	0.617	0.747	0.467	0.37	0.61	0.61	-	0.086
chr1_12202693_snv	C -> T	C -> T	C -> T	C -> T	C -> T	C -> T	0.430	0.266	0.290	0.455	0.632	0.778	0.33	0.62	0.53	-	0.051

Extended Data Table. 7 | Significantly Differential INDEL Mutations from Whole Genome Sequencing Based on Allele Frequency T-test Analysis
(Minimum of 2 Mutated Samples per Group, Fold Change >= 1.2, p value≤0.05)

Pos	Con_1_Mutatio	Con_2_Mutation	Con_3_Mutatio	High_1_Mutatio	High_2_Mutation	High_3_Mutation	High_1	High_2	High_3	Con_1	Con_2	Con_3	Average_high	Average_con	High/Con	P value
chr7_141174737_indel	GA -> G	GA -> G	GA -> G	GA -> G	GA -> G		0.282	0.351		0.166	0.155	0.166	0.317	0.162	1.950	0.010
chr7_56564692_indel	AC -> TT	AC -> TT	AC -> TT	AC -> TT	AC -> TT	AC -> TT	0.462	0.464	0.600	0.249	0.200	0.352	0.509	0.267	1.905	0.019
chr1_7842352_indel		TC -> T	TC -> T		TC -> T	TC -> T		0.350	0.288		0.765	0.679	0.319	0.722	0.442	0.017
chr19_22498942_indel	GT -> CC	GT -> CC	GT -> CC	GT -> CC	GT -> CC	GT -> CC	0.500	0.688	0.265	0.249	0.470	0.200	0.484	0.306	1.581	0.295
chr5_536783_indel	CG -> TA	CG -> TA	CG -> TA	CG -> TA	CG -> TA		0.522	0.471		0.464	0.308	0.429	0.497	0.400	1.240	0.229
chr19_43359765_indel	GC -> TT	GC -> TT	GC -> TT	GC -> TT	GC -> TT		0.500	0.572		0.520	0.517	0.319	0.536	0.452	1.186	0.419
chr16_84230790_indel	C -> CTG		C -> CTG	C -> CTG	C -> CTG		0.829	0.922		0.837		0.837	0.876	0.837	1.046	0.495
chr9_141069897_indel		T -> TCAACGTGTACCACCACGAGGCCAGCGGTGAGACCCCCGTCCTTCCCCCACC	T -> TCAACGTGTACCACCACGAGGCCAGCGGTGAGACCCCCGTCCTTCCCCCACC	T -> TCAACGTGTACCACCACGAGGCCAGCGGTGAGACCCCCGTCCTTCCCCCACC	T -> TCAACGTGTACCACCACGAGGCCAGCGGTGAGACCCCCGTCCTTCCCCCACC	T -> TCAACGTGTACCACCACGAGGCCAGCGGTGAGACCCCCGTCCTTCCCCCACC	0.923	0.896	0.842		0.896	0.823	0.887	0.860	1.032	0.551
chr10_90691789_indel	G -> GATGATGATGATGATGATGATGATGATGATGATT	G -> GATGATGATGATGATGATGATGATGATGATGATT	G -> GATGATGATGATGATGATGATGATGATGATGATT	G -> GATGATGATGATGATGATGATGATGATGATGATT		G -> GATGATGATGATGATGATGATGATGATGATGATT	0.858		0.963	0.872	0.826	0.955	0.911	0.884	1.030	0.704
chr11_369395_indel	G -> GCCCCGCCCCGCCTTCCCGCGCCCCGCACCCCGCGCCCCGCCCCGCCTCC		G -> GCCCCGCCCCGCCTTCCCGCGCCCCGCACCCCGCGCCCCGCCCCGCCTCC	G -> GCCCCGCCCCGCCTTCCCGCGCCCCGCACCCCGCGCCCCGCCCCGCCTCC	G -> GCCCCGCCCCGCCTTCCCGCGCCCCGCACCCCGCGCCCCGCCCCGCCTCC	G -> GCCCCGCCCCGCCTTCCCGCGCCCCGCACCCCGCGCCCCGCCCCGCCTCC	0.961	0.961	0.929	0.924		0.942	0.950	0.933	1.019	0.340
chr9_132276934_indel	G -> GCTGCAGAGAGGAGCTACCCACTCCAGGGCCTCCTCTCTGCTGAGAGCTGCAGAGATGACGAGAGGACCAGC	G -> GCTGCAGAGAGGAGCTACCCACTCCAGGGCCTCCTCTCTGCTGAGAGCTGCAGAGATGACGAGAGGACCAGC		G -> GCTGCAGAGAGGAGCTACCCACTCCAGGGCCTCCTCTCTGCTGAGAGCTGCAGAGATGACGAGAGGACCAGC	G -> GCTGCAGAGAGGAGCTACCCACTCCAGGGCCTCCTCTCTGCTGAGAGCTGCAGAGATGACGAGAGGACCAGC		0.961	0.966		0.951	0.956		0.964	0.954	1.010	0.106
chr12_53207583_indel	C -> CCACCAAAGCCACCAGTGCCGAAACCAGCTCCGAAGCCGCCGG		C -> CCACCAAAGCCACCAGTGCCGAAACCAGCTCCGAAGCCGCCGG	C -> CCACCAAAGCCACCAGTGCCGAAACCAGCTCCGAAGCCGCCGG		C -> CCACCAAAGCCACCAGTGCCGAAACCAGCTCCGAAGCCGCCGG	0.969		0.965	0.959		0.967	0.967	0.963	1.004	0.465

chr6_142543799_indel	T -> TATCTGCACTGCTTCCTCTCTTCACCCATTTCTATTTTTTTTTCTTTAACTTGACTCATTTTGGAGCATTTGGATCAGATGTTCTAGTTTGGCCCATAAACAAAGCTCCATCAGTAGAAAAGTTAAGACATCC	T -> TATCTGCACTGCTTCCTCTCTTCACCCATTTCTATTTTTTTTTCTTTAACTTGACTCATTTTGGAGCATTTGGATCAGATGTTCTAGTTTGGCCCATAAACAAAGCTCCATCAGTAGAAAAGTTAAGACATCC	T -> TATCTGCACTGCTTCCTCTCTTCACCCATTTCTATTTTTTTTTCTTTAACTTGACTCATTTTGGAGCATTTGGATCAGATGTTCTAGTTTGGCCCATAAACAAAGCTCCATCAGTAGAAAAGTTAAGACATCC		T -> TATCTGCACTGCTTCCTCTCTTCACCCATTTCTATTTTTTTTTTCTTTAACTTGACTCATTTTGGAGCATTTGGATCAGATGTTCTAGTTTGGCCCATAAACAAAGCTCCATCAGTAGAAAAGTTAAGACATCC	T -> TATCTGCACTGCTTCCTCTCTTCACCCATTTCTATTTTTTTTTTCTTTAACTTGACTCATTTTGGAGCATTTGGATCAGATGTTCTAGTTTGGCCCATAAACAAAGCTCCATCAGTAGAAAAGTTAAGACATCC	0.949	0.969	0.971	0.969		0.968	0.963	0.969	0.994	0.587
chr10_5681687_indel	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCCTGGGTGCGGGCAGCCTC	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCTGGGTGCGGGCAGCCTC	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCCTGGGTGCGGGCAGCCTC	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCCTGGGTGCGGGCAGCCTC	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCCTGGGTGCGGGCAGCCTC	G -> GTCCATGAGTATCCGCAAAACTAAATAATAAGTGGGCGATGGTGCCCCCTGGGTGCGGGCAGCCTC	0.941	0.940	0.950	0.963	0.962	0.956	0.944	0.960	0.983	0.012
chr11_66512290_indel		G -> GGGC	G -> GGGC	G -> GGGC	G -> GGGC		0.896	0.851			0.848	0.931	0.874	0.890	0.982	0.767
chr1_228461971_indel	GC -> CT	GC -> CT	GC -> CT	GC -> CT	GC -> CT	GC -> CT	0.719	0.407	0.571	0.476	0.600	0.741	0.566	0.606	0.934	0.752
chr9_66491021_indel	CA -> C	CA -> C		CA -> C	CA -> C	CA -> C	0.287	0.225	0.300	0.296	0.286		0.271	0.291	0.930	0.548
chr7_76131644_indel	CA -> TG		CA -> TG	CA -> TG	CA -> TG		0.121	0.153		0.130		0.166	0.137	0.148	0.926	0.693
chrX_47966798_indel	TG -> CA	TG -> CA	TG -> CA	TG -> CA	TG -> CA	TG -> CA	0.435	0.333	0.600	0.526	0.435	0.556	0.456	0.506	0.902	0.594