

Supplementary Material (Supplementary Table 15)

A quantitative transcriptome reference map of the normal human brain

Neurogenetics

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Supplementary table 15 Predicted housekeeping genes from three transcriptome maps (pool of tissues minus brain, adult and foetal brain) using two different SD as percentage of the mean value (≤ 30 and ≤ 40).

Gene name	Expression Value	Chr	Location	Data points	SD
Pool of tissues minus brain housekeeping genes having SD as % of the mean value ≤ 30 n= 3					
<i>POM121C</i>	349.05	chr7	7q11.2	416	27.84
Hs.714416	134.35	chr3	N/A	416	29.29
Hs.728191	122.59	chr7	N/A	384	28.67
Pool of tissues minus brain housekeeping genes having SD as % of the mean value ≤ 40 n= 29					
<i>RPS18</i>	5,071.80	chr6	6p21.3	460	38.72
<i>ACTG1</i>	3,472.62	chr17	17q25	3754	37.28
<i>RPS17L</i>	2,772.43	chr15	N/A	977	36.03
<i>RNASEK</i>	890.26	chr17	17p13.1	328	39.49
<i>EMC4</i>	431.26	chr15	15q14	672	34.33
Hs.706927	377.26	chr6	N/A	500	36.40
<i>POM121C</i>	349.05	chr7	7q11.2	416	27.84
Hs.3353	282.89	chr5	N/A	384	39.38
<i>TOMM5</i>	273.15	chr9	9p13.2	720	37.75
<i>SUMO4</i>	255.64	chr6	6q25	416	39.00
<i>DNAJB11</i>	234.79	chr3	3q27.3	336	34.18
<i>MRPL18</i>	227.83	chr6	6q25.3	526	39.21
<i>YTHDF1</i>	215.97	chr20	20q13.33	549	37.74
Hs.713747	198.08	chr1	N/A	421	36.71
<i>ACTR1B</i>	183.19	chr2	2q11.1-q11.2	491	37.49
<i>TMEM256</i>	179.85	chr17	17p13.1	328	35.69
<i>TMEM60</i>	155.15	chr7	7q11.23	336	37.33
<i>CNOT11</i>	152.02	chr2	2q11.2	327	39.38
<i>ATIC</i>	151.91	chr2	2q35	491	38.84

Hs.444517	150.98	chr4	N/A	384	39.65	
Hs.536748	143.73	chr10	N/A	328	36.98	
Hs.145500	140.32	chr20	N/A	384	33.21	
CXorf40A	135.77	chrX	Xq28	919	38.64	
Hs.714416	134.35	chr3	N/A	416	29.29	
Hs.46506	130.26	chr13	N/A	384	37.03	
Hs.728191	122.59	chr7	N/A	384	28.67	
WDR12	111.69	chr2	2q33.2	447	37.34	
AAR2	110.88	chr20	20pter-q12	526	35.04	
Hs.658719	103.56	chr19	N/A	384	31.87	
Adult brain housekeeping genes having SD as % of the mean value ≤ 30 n= 2						
Hs.705664	2042.48	chr7	N/A	36	28.34	
FUNDC1	117.87	chrX	Xp11.3	38	29.39	
Adult brain housekeeping genes having SD as % of the mean value ≤ 40 n= 15						
Hs.705664	2,042.48	chr7	N/A	36	28.34	
RPS17L	1,418.11	chr15	N/A	107	39.49	
TCEAL8	194.74	chrX	Xq22.1	38	38.34	
Hs.708183	187.11	chr2	N/A	36	34.19	
TSPYL5	180.63	chr8	8q22.1	54	37.60	
Hs.714416	177.19	chr3	N/A	36	37.11	
TTC1	176.85	chr5	5q33.3	58	38.60	
PTS	176.09	chr11	11q22.3	62	37.81	
Hs.718479	142.87	chr15	N/A	38	37.55	
Hs.648567	133.51	chr3	N/A	36	39.34	
Hs.613614	128.28	chr3	N/A	36	34.65	
FUNDC1	117.87	chrX	Xp11.3	38	29.39	
LOC100506365	116.55	chr8	N/A	66	37.82	
TIMM9	111.92	chr14	14q21	56	35.74	
PDRG1	106.18	chr20	20q11.21	35	37.60	
Foetal brain housekeeping genes having SD as % of the mean value ≤ 30 n= 40						
RPS18		chr6	6p21.3	3,796.16	32	27.78
MARCKSL1		chr1	1p35.1	2,873.92	31	29.93
CALM2		chr2	2p21	2,808.30	31	21.80
MRPS24		chr7	7p14	602.31	18	20.07
TCEAL3		chrX	Xq22.2	559.68	20	26.10
PPP1R18		chr6	6p21.3	411.78	17	29.22
SAT2		chr17	17p13.1	393.74	18	16.73
NARS		chr18	18q21.31	388.41	31	25.38
NUDT11		chrX	Xp11.22	341.69	28	23.72
RNF112		chr17	17p11.2	326.24	20	19.23
STRADB		chr2	2q33.1	309.21	23	23.40
HDGF		chr1	1q21-q23	302.90	28	28.76
C1orf122		chr1	1p34.3	298.82	20	25.79
SLC35B2		chr6	6p12.1-p11.2	277.77	17	29.68
MAP7D1		chr1	1p34.3	277.01	25	27.81
NSMCE1		chr16	16p12.1	248.19	17	28.14
GTDC2		chr3	3p22.1	219.18	18	19.37
PDRG1		chr20	20q11.21	207.19	18	17.79
LSM10		chr1	1p34.3	196.27	20	26.87
AGPAT4-IT1		chr6	6q26	189.23	20	29.72
CNEPIR1		chr16	16q12.1	189.17	18	14.39
ROGDI		chr16	16p13.3	178.05	28	27.31
MRPS35		chr12	12p11	161.03	28	28.60
SELO		chr22	22q13.33	153.47	22	29.43
LRP11		chr6	6q25.1	152.84	17	24.81

<i>TCEAL8</i>	chrX	Xq22.1	151.05	24	21.72
<i>CCDC84</i>	chr11	11q23.3	148.59	18	11.80
<i>EID2</i>	chr19	19q13.2	145.16	18	13.13
<i>FAM210B</i>	chr20	20q13.2	143.47	24	29.85
<i>FAM160A2</i>	chr11	11p15.4	140.94	20	29.78
<i>WDR7</i>	chr18	18q21.31	131.13	31	22.73
<i>UBE2T</i>	chr1	1q32.1	130.78	20	28.15
<i>TBC1D10B</i>	chr16	16p11.2	129.15	28	29.52
<i>NAT8L</i>	chr4	4p16.3	129.13	20	27.47
<i>CELF6</i>	chr15	15q24	128.92	20	18.37
<i>APOA1BP</i>	chr1	1q21	127.46	18	25.97
<i>VPS25</i>	chr17	17q21.31	118.14	20	22.32
<i>KDELRL2</i>	chr7	7p22.1	116.80	31	28.96
<i>MRPL14</i>	chr6	6p21.3	103.72	20	28.23
<i>MAF1</i>	chr8	8q24.3	101.23	18	19.12
Foetal brain housekeeping genes having SD as % of the mean value ≤ 40 n= 229					
<i>TUBA1B</i>	chr12	12q13.12	6,954.45	58	30.78
<i>TUBA1A</i>	chr12	12q13.12	6,810.31	28	31.71
<i>ACTG1</i>	chr17	17q25	4,257.24	117	31.33
<i>RPS18</i>	chr6	6p21.3	3,796.16	32	27.78
<i>MLLT11</i>	chr1	1q21	3,609.52	31	33.50
<i>RPS13</i>	chr11	11p15	3,355.44	28	35.05
<i>EEF1G</i>	chr11	11q12.3	3,230.27	48	34.26
<i>RPS24</i>	chr10	10q22	3,046.43	33	39.99
<i>MARCKSL1</i>	chr1	1p35.1	2,873.92	31	29.93
<i>CALM2</i>	chr2	2p21	2,808.30	31	21.80
<i>RPS17L</i>	chr15	N/A	2,370.58	49	31.44
<i>RPL4</i>	chr15	15q22	2,309.89	58	30.92
<i>C12orf57</i>	chr12	12p13.31	2,191.88	18	38.16
<i>RPL24</i>	chr3	3q12	2,149.87	30	35.96
<i>HSPA8</i>	chr11	11q24.1	1,681.26	75	38.56
<i>INA</i>	chr10	10q24.33	1,623.45	31	38.18
<i>MRFAP1</i>	chr4	4p16.1	1,381.88	20	31.81
<i>NELL2</i>	chr12	12q12	1,372.50	33	34.53
<i>CNRIP1</i>	chr2	2p14	1,362.57	20	36.83
<i>PABPC1</i>	chr8	8q22.2-q23	1,310.07	48	39.47
<i>RPL23</i>	chr17	17q	1,247.43	31	34.40
<i>MIF</i>	chr22	22q11.23	1,188.78	29	36.91
<i>EPB41L4A-AS1</i>	chr5	5q22.2	1,162.46	20	37.06
<i>REEPI</i>	chr2	2p11.2	1,040.45	40	37.19
<i>NCAN</i>	chr19	19p12	963.64	31	39.02
<i>PCSK1N</i>	chrX	Xp11.23	888.44	28	34.47
<i>FAM127A</i>	chrX	Xq26	783.25	33	39.06
<i>MAGED4</i>	chrX	Xp11.22	713.13	17	38.44
<i>GSTA4</i>	chr6	6p12.1	665.91	33	35.75
<i>MRPS24</i>	chr7	7p14	602.31	18	20.07
<i>EIF3H</i>	chr8	8q24.11	583.68	33	38.45
<i>SCRNI</i>	chr7	7p14.3- p14.1	573.85	31	38.92
<i>AP2M1</i>	chr3	3q28	572.25	31	33.33
<i>TCEAL3</i>	chrX	Xq22.2	559.68	20	26.10
<i>TMEM181</i>	chr6	6q25.3	542.28	17	37.45
<i>STRAP</i>	chr12	12p12.3	524.18	33	31.80
<i>DDR1</i>	chr6	6p21.3	500.01	70	39.13
<i>KLHDC2</i>	chr14	14q21.3	483.61	28	31.82
<i>SEC11C</i>	chr18	18q21.32	481.76	20	36.32
<i>FBL</i>	chr19	19q13.1	478.39	34	35.91
<i>CUEDC2</i>	chr10	10q24.32	458.58	28	33.01

<i>LAMTOR4</i>	chr7	7q22.1	458.33	18	36.04
<i>FAM107B</i>	chr10	10p13	457.91	22	38.21
<i>BZW2</i>	chr7	7p21.1	450.92	28	38.72
<i>EMC4</i>	chr15	15q14	446.84	23	37.65
<i>TMEM35</i>	chrX	Xq22.1	440.51	28	34.94
<i>ACTR10</i>	chr14	14q23.1	416.27	28	37.10
<i>PPP1R18</i>	chr6	6p21.3	411.78	17	29.22
<i>YPEL5</i>	chr2	2p23.1	405.59	30	39.62
<i>ATP6V1F</i>	chr7	7q32	404.29	31	35.32
<i>C16orf45</i>	chr16	16p13.11	396.19	33	32.83
<i>SAT2</i>	chr17	17p13.1	393.74	18	16.73
<i>BRI3</i>	chr7	7q21.3	393.61	19	35.15
<i>BAG6</i>	chr6	6p21.3	392.51	57	39.41
<i>NARS</i>	chr18	18q21.31	388.41	31	25.38
<i>SV2A</i>	chr1	1q21.2	384.35	28	37.16
<i>LDOC1</i>	chrX	Xq27	370.21	31	37.11
<i>PSMD2</i>	chr3	3q27.1	365.93	28	35.94
<i>PFKM</i>	chr12	12q13.3	364.71	31	30.45
<i>MMADHC</i>	chr2	2q23.2	362.72	28	38.44
<i>ZCCHC17</i>	chr1	1p35.2	357.88	22	35.02
<i>C17orf49</i>	chr17	17p13.1	350.95	20	36.15
<i>CCT3</i>	chr1	1q23	347.32	31	39.52
<i>NUDT11</i>	chrX	Xp11.22	341.69	28	23.72
<i>C14orf166</i>	chr14	14q22.1	327.52	28	30.01
<i>RNF112</i>	chr17	17p11.2	326.24	20	19.23
<i>BOD1</i>	chr5	5q35.2	323.83	22	36.64
<i>ZNF706</i>	chr8	8q22.3	323.76	25	39.55
<i>SPARC</i>	chr5	5q31.3-q32	322.27	31	36.06
<i>HENMT1</i>	chr1	1p13.3	316.81	17	37.76
<i>IGFBP2</i>	chr2	2q33-q34	315.69	34	39.86
<i>MED19</i>	chr11	11q12.1	309.51	22	39.24
<i>STRADB</i>	chr2	2q33.1	309.21	23	23.40
<i>UFC1</i>	chr1	1q23.3	307.14	28	32.88
<i>MRPL51</i>	chr12	12p13.3-p13.1	305.92	20	36.83
<i>SDHAF2</i>	chr11	11q12.2	303.12	20	36.26
<i>HDGF</i>	chr1	1q21-q23	302.90	28	28.76
<i>TMEM9</i>	chr1		301.03	20	35.69
<i>C1orf122</i>	chr1	1p34.3	298.82	20	25.79
<i>YTHDF1</i>	chr20	20q13.33	288.50	28	31.76
<i>HERC1</i>	chr15	15q22	281.12	25	35.51
<i>TTC19</i>	chr17	17p12	278.20	28	35.63
<i>FAM96A</i>	chr15	15q22.31	278.08	20	39.65
<i>SLC35B2</i>	chr6	6p12.1-p11.2	277.77	17	29.68
<i>MAP7D1</i>	chr1	1p34.3	277.01	25	27.81
<i>VBPI</i>	chrX	Xq28	270.26	31	39.10
<i>GLO1</i>	chr6	6p21.3-p21.1	269.47	31	38.90
<i>NOA1</i>	chr4	4q12	265.73	20	37.09
<i>LYSMD2</i>	chr15	15q21.2	264.83	20	32.04
<i>RNF44</i>	chr5	5q35.2	264.60	28	31.26
<i>YTHDF2</i>	chr1	1p35	262.03	30	32.34
<i>OSTC</i>	chr4	4q25	258.25	18	34.45
<i>MRPL18</i>	chr6	6q25.3	257.55	28	38.55
<i>COQ5</i>	chr12	12q24.31	254.52	17	38.20
<i>NSMCE1</i>	chr16	16p12.1	248.19	17	28.14
<i>CHCHD10</i>	chr22	22q11.23	248.05	18	38.15
<i>MFF</i>	chr2	2q36.3	246.32	37	35.93

<i>CECR7</i>	chr22	22q11.1	244.03	18	37.84
<i>TMEM126A</i>	chr11	11q14.1	235.86	20	38.60
<i>GOLPH3</i>	chr5	5p13.3	234.06	28	36.09
<i>LRWD1</i>	chr7	7q22.1	228.81	18	32.76
<i>HSPA5</i>	chr9	9q33.3	228.16	33	39.73
<i>ADPRHL2</i>	chr1	1p34.3	225.00	20	32.61
<i>MICU1</i>	chr10	10q22.1	222.90	31	36.04
<i>NFIL3</i>	chr9	9q22	222.78	31	39.47
<i>IGBP1</i>	chrX	Xq13.1- q13.3	221.90	31	36.42
<i>CASC3</i>	chr17	17q21.1	221.60	28	33.14
<i>GTDC2</i>	chr3	3p22.1	219.18	18	19.37
<i>SLITRK5</i>	chr13	13q31.2	219.05	31	34.34
<i>MRPL32</i>	chr7	7p14	218.05	20	37.87
<i>SHOC2</i>	chr10	10q25	217.60	18	36.19
<i>SMIM19</i>	chr8	8p11.21	213.12	18	35.33
<i>MEAI</i>	chr6	6p21.3- p21.1	210.66	31	38.07
<i>ITFG3</i>	chr16	16p13.3	208.96	20	38.25
<i>PDRG1</i>	chr20	20q11.21	207.19	18	17.79
<i>C9orf123</i>	chr9	9p24.1	202.44	19	32.63
<i>PAPD7</i>	chr5	5p15	198.13	31	35.92
<i>LSM10</i>	chr1	1p34.3	196.27	20	26.87
<i>TMEM63B</i>	chr6	6p21.1	195.46	17	30.49
<i>MRPL53</i>	chr2	2p13.1	193.66	20	30.64
<i>TRAP1</i>	chr16	16p13.3	192.60	33	39.27
<i>RPS19BP1</i>	chr22	22q13.1	192.24	20	38.13
<i>AGPAT4-IT1</i>	chr6	6q26	189.23	20	29.72
<i>CNEPIR1</i>	chr16	16q12.1	189.17	18	14.39
<i>KCTD10</i>	chr12	12q24.11	183.02	22	39.30
<i>TAF7</i>	chr5	5q31	182.49	31	30.82
<i>RBBP7</i>	chrX	Xp22.2	180.40	31	38.18
<i>ABRACL</i>	chr6	6q24.1	179.53	17	37.24
<i>ROGDI</i>	chr16	16p13.3	178.05	28	27.31
<i>SH3BP5L</i>	chr1	1q44	174.11	20	37.76
<i>SPAG7</i>	chr17	17p13.2	173.10	31	33.78
<i>TMEM130</i>	chr7	7q22.1	172.84	20	39.32
<i>ABHD10</i>	chr3	3q13.2	171.76	30	32.62
<i>RRAGC</i>	chr1	1p34	171.63	30	32.77
<i>MSANTD3</i>	chr9	9q31.1	167.92	22	35.93
<i>SUN2</i>	chr22	22q13.1	167.32	31	32.15
<i>SNRPA</i>	chr19	19q13.1	166.80	31	39.65
<i>TSHZ1</i>	chr18	18q22.3	166.14	22	36.18
<i>ARL16</i>	chr17	17q25.3	164.98	17	34.82
<i>ACBD6</i>	chr1	1q25.1	164.33	20	35.55
<i>HSDL1</i>	chr16	16q23.3	164.19	18	39.26
<i>SI00A16</i>	chr1	1q21	164.05	20	31.50
<i>C11orf87</i>	chr11	11q22.3	162.60	19	39.09
<i>MRPS35</i>	chr12	12p11	161.03	28	28.60
<i>ZBTB5</i>	chr9	9p13.2	158.75	31	32.71
<i>HINT2</i>	chr9	9p13.3	158.67	20	38.04
<i>DUSP28</i>	chr2	2q37.3	158.49	17	38.80
<i>SLC25A29</i>	chr14	14q32.2	157.28	22	30.69
<i>GSTM2</i>	chr1	1p13.3	156.81	31	30.48
<i>SELO</i>	chr22	22q13.33	153.47	22	29.43
<i>PDCD2L</i>	chr19	19q13.11	153.35	20	33.98
<i>LRP11</i>	chr6	6q25.1	152.84	17	24.81
<i>VAT1L</i>	chr16	16q23.1	151.34	20	33.63
<i>TCEAL8</i>	chrX	Xq22.1	151.05	24	21.72

<i>KIAA1279</i>	chr10	10q22.1	149.59	31	39.28
<i>SELT</i>	chr3	3q25.1	149.04	30	39.83
<i>CCDC84</i>	chr11	11q23.3	148.59	18	11.80
<i>MPLKIP</i>	chr7	7p14.1	148.33	18	31.53
<i>BAP1</i>	chr3	3p21.31- p21.2	147.73	33	38.50
<i>PSMA4</i>	chr15	15q25.1	146.51	34	30.97
<i>LRRC8D</i>	chr1	1p22.2	146.34	28	37.63
<i>TIMM9</i>	chr14	14q21	145.98	28	38.66
<i>EID2</i>	chr19	19q13.2	145.16	18	13.13
<i>HSD11B1L</i>	chr19	19p13.3	144.97	17	37.39
<i>PRAF2</i>	chrX	Xp11.23	143.48	31	32.94
<i>FAM210B</i>	chr20	20q13.2	143.47	24	29.85
<i>UBE2Q1</i>	chr1	1q21.3	142.94	30	37.07
<i>VPS4A</i>	chr16	16q22.1	142.91	25	31.55
<i>CPSF3L</i>	chr1	1p36.33	141.83	42	39.09
<i>FAM160A2</i>	chr11	11p15.4	140.94	20	29.78
<i>DOK6</i>	chr18	18q22.2	139.51	35	36.61
<i>MYO18A</i>	chr17	17q11.2	139.11	19	31.71
<i>PHC1</i>	chr12	12p13	135.83	33	39.56
<i>PSMD3</i>	chr17	17q21.1	135.00	31	38.11
<i>TMEM199</i>	chr17	17q11.2	134.73	20	35.22
<i>SBDS</i>	chr7	7q11.21	134.56	24	30.69
<i>COMTD1</i>	chr10	10q22.2	132.62	20	39.95
<i>DHCR24</i>	chr1	1p32.3	132.17	31	36.32
<i>PBX4</i>	chr19	19p12	131.50	20	30.99
<i>WDR7</i>	chr18	18q21.31	131.13	31	22.73
<i>RNF4</i>	chr4	4p16.3	130.83	34	39.87
<i>UBE2T</i>	chr1	1q32.1	130.78	20	28.15
<i>TBC1D10B</i>	chr16	16p11.2	129.15	28	29.52
<i>NAT8L</i>	chr4	4p16.3	129.13	20	27.47
<i>CELF6</i>	chr15	15q24	128.92	20	18.37
<i>APOA1BP</i>	chr1	1q21	127.46	18	25.97
<i>ZNF629</i>	chr16	16p11.2	127.22	28	35.64
<i>IFT52</i>	chr20	N/A	125.11	30	32.07
<i>TM2D2</i>	chr8	8p11.22	123.78	20	36.61
<i>TMEM246</i>	chr9	9q31.1	123.17	20	34.66
<i>BIRC6</i>	chr2	2p22.3	122.55	22	36.99
<i>TEX10</i>	chr9	9q31.1	121.78	28	31.01
<i>EXTL2</i>	chr1	1p21	119.93	31	38.83
<i>HILPDA</i>	chr7	7q32.1	119.91	30	37.16
<i>BCDIN3D</i>	chr12	12q13.12	119.56	17	39.32
<i>GGCT</i>	chr7	7p15-p14	119.03	31	35.62
<i>EIF2B3</i>	chr1	1p34.1	118.58	28	32.00
<i>VPS25</i>	chr17	17q21.31	118.14	20	22.32
Hs.734648	chr9	N/A	117.62	26	38.68
<i>GRHPR</i>	chr9	9q12	117.60	55	35.80
<i>KLHDC9</i>	chr1	1q23.3	117.34	18	30.53
<i>STRN4</i>	chr19	19q13.2	117.04	28	36.66
<i>KDELR2</i>	chr7	7p22.1	116.80	31	28.96
<i>PIH1D1</i>	chr19	19q13.33	116.22	25	32.74
<i>IER5L</i>	chr9	9q34.11	116.02	30	38.65
<i>NUTF2</i>	chr16	16q22.1	115.06	33	36.29
<i>TMEM222</i>	chr1	1p36.11	114.81	40	39.52
<i>COX14</i>	chr12	12q13.12	114.32	20	31.30
<i>ZKSCAN2</i>	chr16	16p12.1	113.74	17	37.61
<i>MEIS3</i>	chr19	19q13.32	113.73	20	31.85
<i>INO80C</i>	chr18	18q12.2	113.53	20	30.15
<i>MUS81</i>	chr11	11q13	111.77	30	39.90

<i>ZNF513</i>	chr2	2p23.3	110.67	18	36.15
<i>SCNMI</i>	chr1	1q21.3	110.56	28	34.28
<i>C14orf169</i>	chr14	14q24.3	109.78	25	33.03
<i>YPEL4</i>	chr11	11q12.1	108.51	18	36.35
<i>ZRANB1</i>	chr10	10q26.13	108.49	22	36.92
<i>MORN2</i>	chr2	2p22.1	106.36	18	33.26
<i>C17orf97</i>	chr17	17p13.3	105.04	21	37.45
<i>SYNDIG1</i>	chr20	20p11.21	104.33	28	31.74
<i>KBTBD7</i>	chr13	13q14.11	104.09	18	36.11
<i>MRPL14</i>	chr6	6p21.3	103.72	20	28.23
<i>Hs.7572</i>	chr1	N/A	102.48	17	31.09
<i>TMEM55A</i>	chr8	8q21.3	101.95	18	34.02
<i>RNF123</i>	chr3	3p24.3	101.93	30	39.71
<i>NOL9</i>	chr1	1p36.31	101.62	32	31.19
<i>MAF1</i>	chr8	8q24.3	101.23	18	19.12
<i>VIPAS39</i>	chr14	14q24.3-q31	101.16	30	37.35
<i>SLC25A1</i>	chr22	22q11.21	100.11	37	39.88

Genes are sorted in descending order of expression value. n: number of genes. N/A: not available.