

Table S1. The expression for the compiled 177 hMSCs biomarkers identified in the literature

Gene ID	Gene Name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coef- ficient of variation
1495	CTNNA1	117.4	120.1	124.3	117.8	127.6	119.3	121.8	120.1	4.0	0.03
10085	EDIL3	176.2	160.4	159.7	173.2	166.4	172.0	166.3	166.4	6.3	0.04
3490	IGFBP7	1375.9	1304.5	1208.1	1211.9	1166.4	1273.2	1232.8	1211.9	55.3	0.04
25923	ATL3	27.4	23.0	24.0	23.7	22.0	21.6	22.9	23.0	1.0	0.05
3916	LAMP1	195.8	187.7	193.8	203.4	194.5	177.4	191.4	193.8	9.6	0.05
5796	PTPRK	29.7	25.7	26.3	25.6	23.2	26.7	25.5	25.7	1.3	0.05
6717	SRI	26.0	28.9	25.2	25.8	28.0	26.8	26.9	26.8	1.5	0.06
1500	CTNND1	24.4	33.4	32.6	30.1	35.1	31.4	32.5	32.6	1.9	0.06
10082	GPC6	14.7	9.2	9.1	8.8	8.2	8.0	8.7	8.8	0.5	0.06
7045	TGFBI	1635.7	1003.3	939.6	930.3	857.7	992.1	944.6	939.6	58.0	0.06
23114	NFASC	21.7	24.3	25.2	27.0	27.1	28.3	26.4	27.0	1.6	0.06
51566	ARMCX3	24.5	32.5	31.2	32.1	30.5	27.6	30.8	31.2	1.9	0.06
4179	CD46	20.9	16.8	14.8	15.6	15.9	14.3	15.5	15.6	1.0	0.06
64778	FNDC3B	61.6	47.6	51.1	48.6	46.4	54.8	49.7	48.6	3.3	0.07
11171	STRAP	72.3	70.4	65.5	62.4	58.3	61.9	63.7	62.4	4.5	0.07
8910	SGCE	10.9	10.9	10.9	9.3	11.2	10.5	10.5	10.9	0.8	0.07
781	CACNA2D1	13.1	12.3	11.8	13.2	11.6	13.6	12.5	12.3	0.9	0.07
6443	SGCB	30.1	31.0	32.3	28.1	27.6	27.8	29.4	28.1	2.1	0.07
3688	ITGB1	810.3	787.9	801.8	942.6	834.5	819.7	837.3	819.7	61.5	0.07
3105	HLA-A	260.6	238.8	204.9	219.7	199.1	204.9	213.5	204.9	16.1	0.08
9217	VAPB	8.9	9.0	9.8	7.9	8.7	9.0	8.9	9.0	0.7	0.08
7416	VDAC1	102.3	111.1	118.7	120.0	107.3	98.7	111.1	111.1	8.7	0.08
23180	RFTN1	19.4	23.8	23.7	23.1	20.1	20.6	22.3	23.1	1.8	0.08
118429	ANTXR2	15.9	12.8	14.4	15.3	13.8	12.5	13.8	13.8	1.1	0.08
55161	TMEM33	5.3	4.5	4.5	4.1	3.7	3.9	4.1	4.1	0.3	0.08
27020	NPTN	99.9	97.8	109.1	96.8	112.7	92.1	101.7	97.8	8.7	0.09
9218	VAPA	17.2	15.8	16.7	18.9	15.5	15.7	16.5	15.8	1.4	0.09
79188	TMEM43	45.1	33.9	33.1	27.0	31.2	32.7	31.6	32.7	2.7	0.09
481	ATP1B1	9.2	9.8	11.3	10.9	12.5	10.7	11.1	10.9	1.0	0.09
3728	JUP	3.0	5.4	4.9	4.2	4.6	4.6	4.8	4.6	0.4	0.09
950	SCARB2	58.7	54.3	54.0	50.1	48.6	43.3	50.1	50.1	4.5	0.09
80856	KIAA1715	12.6	11.6	11.4	12.7	11.5	9.7	11.4	11.5	1.1	0.09
3068	HDGF	84.2	112.2	124.2	111.6	129.6	102.8	116.1	112.2	10.8	0.09
10134	BCAP31	59.7	70.3	63.9	59.8	68.5	55.5	63.6	63.9	6.1	0.10
6645	SNTB2	5.2	5.3	5.3	5.5	4.9	4.3	5.0	5.3	0.5	0.10
8826	IQGAP1	80.3	73.6	81.0	92.1	89.4	76.5	82.5	81.0	8.0	0.10

Table S1. Continued

Gene ID	Gene Name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coefficient of variation
3106	HLA-B	54.5	44.9	42.4	45.3	51.3	38.7	44.5	44.9	4.6	0.10
4267	CD99	403.0	572.5	708.4	644.0	646.5	544.8	623.2	644.0	65.1	0.10
10491	CRTAP	31.5	33.0	31.8	30.3	27.7	25.4	29.6	30.3	3.1	0.10
10857	PGRMC1	28.2	35.8	34.5	38.9	37.6	29.4	35.2	35.8	3.7	0.10
257194	NEGR1	9.1	10.6	10.6	10.6	8.2	9.5	9.9	10.6	1.1	0.11
9902	MRC2	99.8	108.8	84.3	94.3	95.4	83.7	93.3	94.3	10.2	0.11
4882	NPR2	7.5	8.1	7.6	6.4	6.3	7.6	7.2	7.6	0.8	0.11
3107	HLA-C	120.9	104.1	84.5	106.6	108.3	87.7	98.2	104.1	11.2	0.11
7094	TLN1	125.8	178.4	199.4	169.8	190.6	228.1	193.2	190.6	22.5	0.12
9843	HEPH	4.0	5.4	4.3	4.9	5.1	4.1	4.8	4.9	0.6	0.12
54867	TMEM214	34.3	39.5	33.7	32.0	34.9	28.5	33.7	33.7	4.0	0.12
3685	ITGAV	78.0	47.9	51.9	53.9	55.3	65.7	54.9	53.9	6.6	0.12
25932	CLIC4	209.0	210.3	200.7	162.4	177.7	219.0	194.0	200.7	23.4	0.12
5269	SERPINB6	40.5	39.5	39.1	43.7	41.3	31.2	38.9	39.5	4.7	0.12
7905	REEP5	45.1	34.0	36.0	41.3	36.2	29.4	35.4	36.0	4.3	0.12
8615	USO1	37.8	36.3	39.9	34.0	29.7	40.9	36.2	36.3	4.5	0.13
4240	MFGE8	400.9	328.5	323.3	370.4	418.4	310.0	350.1	328.5	44.4	0.13
221294	NT5DC1	5.0	5.1	5.5	3.8	5.1	5.1	4.9	5.1	0.6	0.13
1889	ECE1	38.0	37.6	33.3	30.1	26.5	31.5	31.8	31.5	4.1	0.13
8829	NRP1	71.3	50.8	50.8	50.2	43.1	37.4	46.5	50.2	6.0	0.13
476	ATP1A1	64.4	57.3	51.3	48.8	46.8	39.8	48.8	48.8	6.4	0.13
3956	LGALS1	1092.8	1156.2	966.1	1051.1	870.7	845.0	977.8	966.1	128.9	0.13
5802	PTPRS	12.7	16.2	13.5	16.4	13.7	11.9	14.3	13.7	1.9	0.13
81502	HM13	104.4	99.9	91.9	109.6	111.7	79.8	98.6	99.9	13.2	0.13
977	CD151	164.0	153.3	120.5	163.5	161.8	129.3	145.7	153.3	19.6	0.13
55379	LRRCS9	96.3	116.7	111.2	102.6	86.6	87.3	100.9	102.6	13.6	0.14
1499	CTNNB1	69.5	85.4	80.0	66.3	64.9	64.5	72.2	66.3	9.8	0.14
91663	MYADM	43.9	57.3	50.7	73.2	59.2	64.0	60.9	59.2	8.4	0.14
483	ATP1B3	46.7	32.1	32.3	32.0	35.0	23.7	31.0	32.1	4.3	0.14
682	BSG	248.2	250.6	216.3	273.9	238.5	189.6	233.8	238.5	32.3	0.14
3655	ITGA6	6.2	9.8	8.2	8.0	7.2	7.0	8.0	8.0	1.1	0.14
51604	PIGT	67.3	65.0	66.3	78.9	70.2	53.1	66.7	66.3	9.3	0.14
1605	DAG1	38.5	42.5	42.8	57.1	50.3	41.4	46.8	42.8	6.8	0.14
7417	VDAC2	78.1	75.0	68.1	77.6	88.1	58.6	73.5	75.0	11.0	0.15
4363	ABCC1	19.2	22.1	23.0	25.5	28.3	18.8	23.5	23.0	3.6	0.15
953	ENTPD1	1.5	1.1	0.8	1.2	0.9	1.0	1.0	1.0	0.1	0.15

Table S1. Continued

Gene ID	Gene Name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coefficient of variation
1956	EGFR	17.0	12.1	12.7	10.1	8.7	12.3	11.2	12.1	1.7	0.15
490	ATP2B1	31.3	25.2	24.4	22.8	19.7	30.1	24.5	24.4	3.8	0.16
7037	TFRC	37.2	32.2	32.9	25.1	23.0	31.5	28.9	31.5	4.6	0.16
966	CD59	139.9	95.0	85.0	83.3	75.5	61.1	80.0	83.3	12.6	0.16
6383	SDC2	88.6	53.8	52.2	36.3	41.6	50.5	46.9	50.5	7.6	0.16
975	CD81	98.7	75.0	62.5	59.1	58.7	47.6	60.6	59.1	9.8	0.16
162394	SILFN5	23.9	18.9	20.2	17.3	16.3	24.4	19.4	18.9	3.2	0.16
1192	CLIC1	295.7	279.7	280.6	339.4	301.7	212.4	282.8	280.6	46.2	0.16
51303	FKBP11	14.3	13.2	15.5	11.1	10.3	13.7	12.8	13.2	2.1	0.16
2817	GPC1	90.9	91.7	89.9	73.6	62.0	70.9	77.6	73.6	12.8	0.16
23385	NCSTN	52.0	48.8	53.0	39.1	54.9	62.3	51.6	53.0	8.5	0.17
7419	VDAC3	27.4	31.8	32.4	23.3	35.6	26.2	29.9	31.8	5.0	0.17
55243	KIRREL	19.1	19.6	17.0	16.1	12.7	19.5	17.0	17.0	2.8	0.17
3693	ITGB5	148.1	144.0	126.3	127.4	128.0	88.0	122.8	127.4	20.7	0.17
3675	ITGA3	67.2	67.7	57.3	81.4	73.6	54.1	66.8	67.7	11.3	0.17
9341	VAMP3	50.4	49.1	40.9	50.1	38.1	33.3	42.3	40.9	7.2	0.17
1012	CDH13	82.5	47.5	47.0	65.5	68.0	56.5	56.9	56.5	9.8	0.17
4756	NEO1	13.9	20.0	20.7	14.0	15.8	20.8	18.3	20.0	3.1	0.17
214	ALCAM	118.6	131.0	138.7	94.5	96.6	122.5	116.7	122.5	20.1	0.17
83604	TMEM47	44.1	31.5	35.0	31.0	30.0	44.5	34.4	31.5	5.9	0.17
967	CD63	694.8	911.0	791.9	888.2	693.7	588.8	774.7	791.9	135.0	0.17
6520	SLC3A2	69.8	61.0	55.8	46.9	38.4	57.0	51.8	55.8	9.1	0.18
4921	DDR2	32.6	22.6	20.3	17.1	20.9	27.5	21.7	20.9	3.8	0.18
3678	ITGA5	238.7	165.0	135.9	192.5	158.7	121.4	154.7	158.7	27.4	0.18
6810	STX4	26.6	37.6	32.5	40.7	42.7	26.8	36.0	37.6	6.5	0.18
4311	MME	9.9	11.0	11.2	7.8	8.8	7.7	9.3	8.8	1.7	0.18
54587	MXRA8	160.1	210.8	153.7	187.9	181.9	129.7	172.8	181.9	31.5	0.18
2022	ENG	169.3	220.3	208.6	148.5	148.2	198.2	184.8	198.2	34.1	0.18
83700	JAM3	20.9	21.9	20.3	13.9	15.4	18.3	18.0	18.3	3.3	0.19
355	FAS	8.9	14.2	12.9	9.6	9.1	11.5	11.5	11.5	2.1	0.19
3136	HLA-H	2.8	2.7	2.4	2.0	3.1	2.1	2.5	2.4	0.5	0.19
5355	PLP2	173.4	220.0	207.1	266.6	240.3	153.6	217.5	220.0	42.2	0.19
1277	COL1A1	7846.3	6205.6	6507.3	6103.8	8942.6	8808.9	7313.6	6507.3	1434.5	0.20
1292	COL6A2	1228.7	1349.4	1239.6	1517.2	1392.6	860.4	1271.8	1349.4	250.6	0.20
1291	COL6A1	1191.9	1215.0	1171.8	1482.5	1429.7	868.2	1233.4	1215.0	244.0	0.20
57136	APMAP	35.2	38.4	35.7	24.7	25.8	28.1	30.5	28.1	6.2	0.20

Table S1. Continued

Gene ID	Gene Name	Cluster	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coef- ficient of variation
7162	TPBG	Cluster3	20.8	16.5	15.7	16.7	13.6	9.7	14.4	15.7	2.9	0.20
960	CD44	Cluster4	286.1	185.9	192.6	230.8	226.5	131.7	193.5	192.6	39.9	0.21
976	CD97	-	18.5	21.7	17.0	15.2	13.6	13.7	16.2	15.2	3.4	0.21
102	ADAM10	Cluster2	42.5	44.2	42.9	28.4	31.5	46.6	38.7	42.9	8.2	0.21
4035	LRP1	-	134.8	122.4	121.1	190.2	186.2	157.7	155.5	157.7	33.3	0.21
961	CD47	Cluster4	12.1	9.1	8.6	12.3	10.7	7.0	9.5	9.1	2.0	0.21
871	SERPINH1	Cluster2	352.4	247.9	218.4	165.3	157.7	252.9	208.5	218.4	44.9	0.22
10938	EHD1	Cluster1	32.5	39.5	30.7	28.2	21.5	29.8	29.9	29.8	6.4	0.22
79827	CLMP	Cluster4	130.3	103.5	98.1	137.7	128.3	78.8	109.3	103.5	23.7	0.22
9761	MLEC	Cluster1	19.5	24.8	24.6	16.4	15.6	18.9	20.1	18.9	4.4	0.22
6510	SLC1A5	Cluster2	132.7	91.8	87.6	69.0	72.6	117.8	87.7	87.6	19.4	0.22
2050	EPHB4	Cluster1	6.1	7.5	6.9	5.1	4.5	5.2	5.8	5.2	1.3	0.22
93185	IGSF8	-	10.4	13.6	10.6	10.3	7.8	8.2	10.1	10.3	2.3	0.23
80381	CD276	Cluster4	100.5	87.5	73.5	91.3	87.3	47.5	77.4	87.3	18.0	0.23
6444	SGCD	-	16.0	15.5	16.5	14.6	16.1	8.2	14.2	15.5	3.4	0.24
4907	NT5E	Cluster4	98.2	105.4	97.6	113.5	100.5	54.8	94.4	100.5	22.9	0.24
1000	CDH2	Cluster2	73.9	69.6	75.1	44.9	52.5	83.7	65.1	69.6	16.1	0.25
54749	EPDR1	Cluster2	30.2	29.4	26.0	17.8	18.0	31.2	24.5	26.0	6.3	0.26
5817	PVR	Cluster2	44.9	28.3	26.2	19.7	17.4	33.2	25.0	26.2	6.4	0.26
6664	SOX11	Cluster1	0.4	1.2	1.0	0.8	0.6	0.8	0.9	0.8	0.2	0.26
286410	ATP11C	Cluster1	9.8	8.4	9.8	5.5	5.4	8.4	7.5	8.4	2.0	0.26
140885	SIRPA	Cluster2	26.5	35.3	39.6	24.9	25.8	46.2	34.3	35.3	9.1	0.26
5754	PTK7	Cluster1	19.3	20.6	16.5	11.3	11.4	18.5	15.7	16.5	4.2	0.27
10544	PROCR	Cluster4	11.4	10.0	8.6	13.6	10.5	6.3	9.8	10.0	2.7	0.27
3958	LGALS3	Cluster4	149.6	140.4	130.9	180.4	173.8	83.0	141.7	140.4	39.0	0.28
1009	CDH11	Cluster2	206.0	173.1	183.6	105.1	116.1	203.6	156.3	173.1	43.3	0.28
23446	SLC44A1	Cluster3	15.5	17.2	16.0	14.5	12.7	7.5	13.6	14.5	3.8	0.28
1464	CSPG4	Cluster4	15.0	14.2	11.0	20.2	15.7	10.1	14.2	14.2	4.1	0.28
1947	EFNB1	-	6.1	8.6	6.4	5.4	4.8	4.4	5.9	5.4	1.7	0.29
3383	ICAM1	Cluster1	1.2	1.9	1.6	1.0	1.0	1.4	1.4	1.4	0.4	0.30
5420	PODXL	Cluster4	8.6	33.5	31.9	35.5	31.6	13.9	29.3	31.9	8.7	0.30
221091	LRRN4CL	-	2.6	1.8	2.4	2.7	3.0	4.0	2.8	2.7	0.8	0.30
3679	ITGA7	Cluster2	5.0	6.2	5.0	3.5	3.7	6.9	5.1	5.0	1.5	0.30
4323	MMP14	Cluster4	358.5	578.3	497.1	570.6	523.1	229.7	479.8	523.1	143.8	0.30
79143	MBOAT7	Cluster1	15.0	15.5	12.5	8.6	7.2	10.0	10.8	10.0	3.3	0.30
10424	PGRMC2	Cluster2	39.2	34.5	32.7	18.4	22.4	40.8	29.8	32.7	9.2	0.31

Table S1. Continued

Gene ID	Gene Name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coefficient of variation
57124	CD248	245.9	373.8	370.3	226.7	332.9	544.2	369.6	370.3	114.3	0.31
6641	SNIB1	7.8	6.6	6.4	3.8	4.8	8.8	6.1	6.4	1.9	0.31
57153	SLC44A2	29.9	39.2	35.2	19.3	20.4	36.5	30.1	35.2	9.5	0.32
4071	TM4SF1	106.9	103.4	91.7	62.2	54.0	52.5	72.8	62.2	23.3	0.32
493	ATP2B4	68.6	41.6	43.3	82.0	74.2	48.6	57.9	48.6	18.8	0.32
3671	ISLR	133.9	101.9	76.5	127.9	116.8	50.7	94.8	101.9	31.3	0.33
8140	SLC7A5	84.2	43.8	38.1	23.1	22.3	50.9	35.6	38.1	12.7	0.36
1462	VCAN	113.4	109.1	138.3	96.4	104.8	213.6	132.4	109.1	48.1	0.36
7046	TGFBR1	17.4	13.1	13.4	8.1	9.6	21.0	13.0	13.1	5.0	0.38
5819	PVRL2	17.7	22.6	17.7	9.4	9.1	16.9	15.1	16.9	5.8	0.39
1295	COL8A1	113.8	205.7	196.0	85.1	89.0	171.8	149.5	171.8	58.4	0.39
1293	COL6A3	789.2	733.9	713.9	1388.3	1183.0	539.0	911.6	733.9	357.2	0.39
84168	ANTXR1	73.6	121.5	135.6	54.5	60.2	129.1	100.2	121.5	39.5	0.39
2335	FN1	7292.7	7148.9	7036.7	15578.7	14296.8	8124.2	10437.1	8124.2	4155.0	0.40
290	ANPEP	141.1	126.4	130.1	225.1	216.4	80.2	155.6	130.1	62.7	0.40
135228	CD109	21.1	20.4	20.5	36.6	33.9	12.9	24.9	20.5	10.0	0.40
5159	PDGFRB	64.4	116.7	98.8	59.7	63.0	41.8	76.0	63.0	30.7	0.40
7070	THY1	156.2	184.9	175.1	73.2	77.0	150.3	132.1	150.3	53.6	0.41
4059	BCAM	2.2	4.5	4.2	1.8	2.5	5.5	3.7	4.2	1.5	0.41
4008	LMO7	92.4	114.1	129.1	54.0	71.3	160.7	105.8	114.1	43.3	0.41
23670	TMEM2	5.5	9.1	8.8	3.3	4.1	7.5	6.6	7.5	2.7	0.41
2239	GPC4	8.0	13.1	13.1	5.3	5.7	13.5	10.1	13.1	4.2	0.42
4883	NPR3	42.6	51.5	54.2	25.5	24.3	67.7	44.6	51.5	19.0	0.43
22801	ITGA11	299.8	243.7	257.3	161.2	211.8	464.0	267.6	243.7	115.8	0.43
3672	ITGA1	4.6	2.6	3.2	1.2	1.7	4.3	2.6	2.6	1.2	0.47
3673	ITGA2	5.8	2.9	3.3	6.9	4.0	1.7	3.8	3.3	1.9	0.52
7412	VCAM1	16.0	10.1	13.2	7.0	10.0	24.2	12.9	10.1	6.7	0.52
4162	MCAM	6.5	34.3	36.1	9.8	9.4	26.9	23.3	26.9	13.0	0.56

Table S1. Continued

Gene ID	Gene Name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Average	Median	Stdev	normalized stdev/coefficient of variation
928	CD9	61.6	26.7	29.9	59.7	83.1	25.3	44.9	29.9	25.6	0.57
1969	EPHA2	6.2	8.9	6.5	1.8	1.9	6.3	5.1	6.3	3.1	0.61
3690	ITGB3	10.7	5.6	5.4	17.8	13.9	3.3	9.2	5.6	6.3	0.68
4045	LSAMP	0.8	1.6	1.5	0.3	0.2	2.1	1.1	1.5	0.8	0.72
8516	ITGA8	0.4	1.2	1.2	0.5	0.7	3.0	1.3	1.2	1.0	0.73

References:

- Niehage, Christian, et al. "The cell surface proteome of human mesenchymal stromal cells." *PLoS one* (2011): e20399.
- Cho, Kyung-Ah, et al. "RNA sequencing reveals a transcriptomic portrait of human mesenchymal stem cells from bone marrow, adipose tissue, and palatine tonsils." *Scientific reports* (2017): 17114.
- Lu, Feng-luan, et al. "Concise review: the surface markers and identity of human mesenchymal stem cells." *Stem cells* (2014): 1408-1419.

Table S2. The 20 genes with high correlation with CD90 and/or CD105

gene_id	gene_name	D0	Fl-Pr	Fl-Am	Fs-Pr	Fs-Am	TCP	Pearson coefficient	
								with THY1	with ENG
8826	IQGAP1	80.3	73.6	81.0	92.1	89.4	76.5	-0.92	-0.89
4882	NPR2	7.5	8.1	7.6	6.4	6.3	7.6	0.98	0.93
214	ALCAM	118.6	131.0	138.7	94.5	96.6	122.5	0.97	0.94
2022	ENG	169.3	220.3	208.6	148.5	148.2	198.2	0.92	1.00
83700	JAM3	20.9	21.9	20.3	13.9	15.4	18.3	0.96	0.81
57136	APMAP	35.2	38.4	35.7	24.7	25.8	28.1	0.91	0.77
102	ADAM10	42.5	44.2	42.9	28.4	31.5	46.6	0.93	0.85
4035	LRP1	134.8	122.4	121.1	190.2	186.2	157.7	-0.97	-0.85
9761	MLEC	19.5	24.8	24.6	16.4	15.6	18.9	0.90	0.91
286410	ATP11C	9.8	8.4	9.8	5.5	5.4	8.4	0.91	0.70
5754	PTK7	19.3	20.6	16.5	11.3	11.4	18.5	0.93	0.80
3383	ICAM1	1.2	1.9	1.6	1.0	1.0	1.4	0.90	0.98
57153	SLC44A2	29.9	39.2	35.2	19.3	20.4	36.5	0.96	0.97
493	ATP2B4	68.6	41.6	43.3	82.0	74.2	48.6	-0.89	-0.98
5819	PVRL2	17.7	22.6	17.7	9.4	9.1	16.9	0.97	0.90
2335	FN1	7292.7	7148.9	7036.7	15578.7	14296.8	8124.2	-0.98	-0.84
23670	TMEM2	5.5	9.1	8.8	3.3	4.1	7.5	0.92	0.99
928	CD9	61.6	26.7	29.9	59.7	83.1	25.3	-0.79	-0.92
1969	EPHA2	6.2	8.9	6.5	1.8	1.9	6.3	0.98	0.92
3690	ITGB3	10.7	5.6	5.4	17.8	13.9	3.3	-0.86	-0.91
7070	THY1	156.2	184.9	175.1	73.2	77.0	150.3		
2022	ENG	169.3	220.3	208.6	148.5	148.2	198.2		