Supplementary for

Downregulation of CDH11 Promotes Metastasis and Resistance to Paclitaxel in Gastric Cancer Cells

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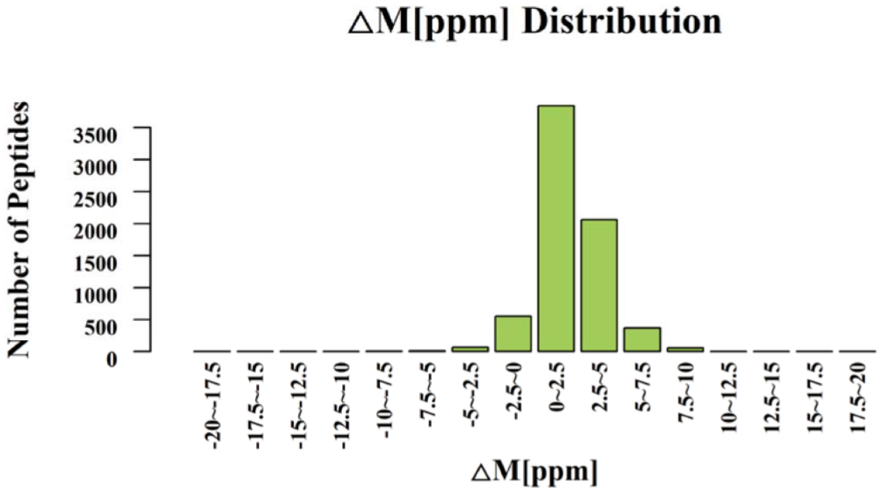
Supplementary Figure



Supplementary Figure S1. The mass deviation of all peptides. △M: Mass deviation.

Supplementary Tables

Table S1. Characteristics of patients

Symbol of patients before chemotherapy	**Sex**	**Age**	**PCI**	**Volume of ascites (ml)**	**Cycles before relapse**	**Sustain time before relapse (month)**	**Symbol of patients after chemotherapy**
a1	Male	40	10	700	6	5.5	b1
a2	Female	31	36	200	8	6	b2
a3	Female	46	39	15000	5	5	b3

PCI: peritoneal cancer index

Table S2. Proteins identified by TMT-based proteomics

Accession	Gene Name	Coverage	Peptides	PSMs	Unique Peptides	AAs	MW [kDa]	calc. pI	P value
Q13421	MSLN	14.9	9	30	9	630	68.9	6.38	0.021
P25940	COL5A3	1.1	1	2	1	1745	172.0	6.87	0.018
Q14767	LTBP2	4.2	6	7	6	1821	194.9	5.19	0.042
Q9UBX7	KLK11	9.9	3	4	3	282	31.0	8.94	0.046
Q9Y240	CLEC11A	13.9	4	4	4	323	35.7	5.16	0.023
P55287	CDH11	8.7	7	14	7	796	87.9	4.91	0.025
P22676	CALB2	4.1	1	1	1	271	31.5	5.15	0.037
Q14314	FGL2	12.5	4	8	4	439	50.2	7.39	0.042
P07437	TUBB	6.1	2	2	2	444	49.6	4.89	0.049
P25774	CTSS	10.3	3	3	3	331	37.5	8.34	0.046
Q13201	MMRN1	1.6	2	6	2	1228	138.0	7.93	0.035
Q6UXS9	CASP12	6.2	1	3	1	341	38.8	6.02	0.014
Q96CX2	KCTD12	3.7	1	1	1	325	35.7	5.64	0.022
P06727	APOA4	82.3	35	419	35	396	45.4	5.38	0.014
O15204	ADAMDEC1	3.6	1	1	1	470	52.7	7.34	0.019
P68363	TUBA1B	20.6	7	10	7	451	50.1	5.06	0.002
Q5HYA8	TMEM67	1.4	1	2	1	995	111.7	6.77	0.049
Q9Y5C1	ANGPTL3	2.4	1	1	1	460	53.6	6.7	0.044
Q01995	TAGLN	43.8	8	16	8	201	22.6	8.84	0.012
P68871	HBB	83.0	12	267	6	147	16.0	7.28	0.373
P69905	HBA1	71.8	10	132	10	142	15.2	8.68	0.374
P32119	PRDX2	54.5	10	65	9	198	21.9	5.97	0.379
P55327	TPD52	6.7	1	1	1	224	24.3	4.83	0.343
P00738	HP	50.5	21	136	21	406	45.2	6.58	0.133
P02042	HBD	83.0	11	155	5	147	16.0	8.05	0.371
Q5T619	ZNF648	2.1	1	17	1	568	62.3	8.62	0.374
P28330	ACADL	4.4	1	3	1	430	47.6	7.8	0.391
P00915	CA1	47.1	11	76	11	261	28.9	7.12	0.363
P00918	CA2	42.3	9	20	9	260	29.2	7.4	0.370
P07910	HNRNPC	11.1	4	7	4	306	33.7	5.08	0.384
P10451	SPP1	23.6	5	44	5	314	35.4	4.58	0.399
P29508	SERPINB3	15.6	6	10	6	390	44.5	6.81	0.344
P03956	MMP1	4.3	2	2	2	469	54.0	6.96	0.435
O95994	AGR2	9.7	1	1	1	175	20.0	9	0.308
Q06141	REG3A	31.4	4	13	4	175	19.4	7.64	0.444
P14174	MIF	7.8	1	2	1	115	12.5	7.88	0.381
P30041	PRDX6	51.3	9	18	9	224	25.0	6.38	0.372
P10599	TXN	40.0	5	11	5	105	11.7	4.92	0.363
P69891	HBG1	64.6	9	48	1	147	16.1	7.2	0.381

P02652	APOA2	68.0	7	104	7	100	11.2	6.62	0.416
P25815	S100P	10.5	1	3	1	95	10.4	4.88	0.330
P04040	CAT	50.7	22	62	22	527	59.7	7.39	0.379
P08779	KRT16	15.2	7	14	1	473	51.2	5.05	0.407
P05787	KRT8	22.8	13	25	8	483	53.7	5.59	0.388
Q13404	UBE2V1	6.8	1	1	1	147	16.5	7.93	0.432
P06744	GPI	16.5	9	20	9	558	63.1	8.32	0.378
Q13813	SPTAN1	10.1	25	34	25	2472	284.4	5.35	0.369
Q96C19	EFHD2	4.2	1	2	1	240	26.7	5.2	0.443
P15531	NME1	23.0	3	3	1	152	17.1	6.19	0.360
Q01518	CAP1	7.8	3	6	3	475	51.9	8.06	0.385
Q9H0N5	PCBD2	5.4	1	1	1	130	14.4	9.11	0.410
P09466	PAEP	3.9	1	1	1	180	20.6	5.57	0.278
Q06830	PRDX1	42.2	9	30	8	199	22.1	8.13	0.403
Q08174	PCDH1	1.4	1	1	1	1060	114.7	5.03	0.249
O14818	PSMA7	12.9	3	3	3	248	27.9	8.46	0.382
P26447	S100A4	15.8	2	5	2	101	11.7	6.11	0.450
Q9BZH6	WDR11	0.7	1	1	1	1224	136.6	6.92	0.434
P31949	S100A11	42.9	4	7	4	105	11.7	7.12	0.426
P69892	HBG2	64.6	9	45	1	147	16.1	7.2	0.415
P13667	PDIA4	27.0	15	25	15	645	72.9	5.07	0.368
P12107	COL11A1	1.2	1	1	1	1806	181.0	5.17	0.153
P07148	FABP1	50.4	5	10	5	127	14.2	7.18	0.460
Q6UX06	OLFM4	8.4	4	5	4	510	57.2	5.69	0.331
Q16851	UGP2	24.0	9	14	9	508	56.9	8.15	0.382
P04632	CAPNS1	2.6	1	1	1	268	28.3	5.2	0.370
P51858	HDGF	11.3	2	3	2	240	26.8	4.73	0.356
P02549	SPTA1	1.9	5	5	5	2419	279.8	5.05	0.370
P02730	SLC4A1	4.7	3	4	3	911	101.7	5.19	0.400
P15529	CD46	2.3	1	1	1	392	43.7	6.74	0.356
P02792	FTL	41.7	7	36	7	175	20.0	5.78	0.513
P27797	CALR	24.0	8	20	8	417	48.1	4.44	0.394
P40925	MDH1	29.3	9	16	9	334	36.4	7.36	0.391
Q86VD1	MORC1	0.7	1	3	1	984	112.8	7.85	0.479
Q8TAQ9	SUN3	2.0	1	3	1	357	40.5	7.83	0.344
P06703	S100A6	24.4	3	5	3	90	10.2	5.48	0.418
Q01082	SPTBN1	1.7	4	4	4	2364	274.4	5.57	0.405
Q15149	PLEC	0.2	1	1	1	4684	531.5	5.96	0.352
P30048	PRDX3	8.6	2	4	2	256	27.7	7.78	0.356
P00492	HPRT1	20.2	4	6	4	218	24.6	6.68	0.361
P07237	P4HB	36.2	17	26	17	508	57.1	4.87	0.374
P30046	DDT	28.8	4	10	4	118	12.7	7.3	0.428
P14314	PRKCSH	10.2	5	8	5	528	59.4	4.41	0.440

P02545	LMNA	26.1	17	26	17	664	74.1	7.02	0.435
P00441	SOD1	20.1	3	9	3	154	15.9	6.13	0.429
P06733	ENO1	45.9	15	33	15	434	47.1	7.39	0.370
Q5SRE5	NUP188	0.4	1	2	1	1749	195.9	6.73	0.423
P00491	PNP	23.2	5	8	5	289	32.1	6.95	0.409
Q14508	WFDC2	32.3	3	5	3	124	13.0	4.84	0.393
P04406	GAPDH	43.6	11	24	11	335	36.0	8.46	0.411
Q4ZHG4	FNDC1	1.6	2	3	2	1894	205.4	9.32	0.161
P62979	RPS27A	16.0	2	4	2	156	18.0	9.64	0.414
P0DP25	CALM3	42.3	5	14	5	149	16.8	4.22	0.488
Q15257	PTPA	2.2	1	1	1	358	40.6	5.94	0.350
Q99497	PARK7	41.8	6	8	6	189	19.9	6.79	0.417
P17174	GOT1	24.0	9	16	9	413	46.2	7.01	0.438
P28070	PSMB4	7.6	1	2	1	264	29.2	5.97	0.310
P28066	PSMA5	25.3	5	9	5	241	26.4	4.79	0.427
Q06481	APLP2	5.5	4	5	3	763	86.9	4.79	0.475
P40306	PSMB10	6.2	2	2	2	273	28.9	7.81	0.243
Q68BL8	OLFML2B	1.3	1	1	1	750	83.9	5.2	0.189
P02794	FTH1	39.9	5	11	5	183	21.2	5.55	0.445
P23528	CFL1	37.3	5	5	5	166	18.5	8.09	0.365
Q96C23	GALM	5.0	1	1	1	342	37.7	6.65	0.459
P00558	PGK1	28.1	10	14	10	417	44.6	8.1	0.419
Q03403	TFF2	21.7	2	3	2	129	14.3	5.81	0.532
P63208	SKP1	4.9	1	2	1	163	18.6	4.54	0.433
Q9BS40	LXN	4.1	1	1	1	222	25.7	5.78	0.444
O43278	SPINT1	11.9	6	8	6	529	58.4	6.29	0.327
Q9UGM3	DMBT1	22.0	5	13	5	2413	260.6	5.44	0.426
Q99436	PSMB7	10.8	3	3	3	277	29.9	7.68	0.456
Q13228	SELENBP1	18.2	8	13	8	472	52.4	6.37	0.424
Q9P2E9	RRBP1	0.9	1	1	1	1410	152.4	8.6	0.431
P12277	CKB	4.5	1	2	1	381	42.6	5.59	0.598
Q99715	COL12A1	11.5	27	38	27	3063	332.9	5.53	0.150
P25788	PSMA3	6.3	2	2	2	255	28.4	5.33	0.432
P01024	C3	60.7	87	491	87	1663	187.0	6.4	0.344
P49720	PSMB3	19.5	3	3	3	205	22.9	6.55	0.355
P07738	BPGM	18.5	4	7	4	259	30.0	6.54	0.477
P50395	GDI2	31.0	11	19	10	445	50.6	6.47	0.438
P22223	CDH3	3.0	2	3	1	829	91.4	4.75	0.280
Q15084	PDIA6	15.9	5	8	5	440	48.1	5.08	0.411
Q8N130	SLC34A3	1.3	1	3	1	599	63.5	8.27	0.273
P30740	SERPINB1	23.2	8	13	8	379	42.7	6.28	0.415
Q15063	POSTN	51.3	35	165	35	836	93.3	7.53	0.414
Q15582	TGFBI	44.2	24	86	24	683	74.6	7.71	0.260

O00592	PODXL	3.9	2	2	2	558	58.6	5.49	0.226
P02538	KRT6A	17.6	10	18	1	564	60.0	8	0.498
Q5JXB2	UBE2NL	6.5	1	1	1	153	17.4	5.92	0.409
Q9NUQ9	FAM49B	3.1	1	1	1	324	36.7	6.06	0.120
P60174	TPI1	56.6	12	27	12	286	30.8	5.92	0.425
P05783	KRT18	7.0	3	3	2	430	48.0	5.45	0.468
P35579	MYH9	2.9	5	8	5	1960	226.4	5.6	0.496
P05423	POLR3D	1.8	1	2	1	398	44.4	6.98	0.105
P13611	VCAN	4.2	13	26	13	3396	372.6	4.51	0.216
P60900	PSMA6	17.5	4	8	4	246	27.4	6.76	0.387
P05997	COL5A2	6.3	7	11	7	1499	144.8	6.46	0.126
P11142	HSPA8	20.1	12	20	7	646	70.9	5.52	0.460
P15311	EZR	35.3	20	34	15	586	69.4	6.27	0.429
P25786	PSMA1	19.8	5	7	5	263	29.5	6.61	0.449
P29966	MARCKS	3.3	1	2	1	332	31.5	4.45	0.550
P62258	YWHAE	42.4	9	18	6	255	29.2	4.74	0.478
P04424	ASL	8.6	3	5	3	464	51.6	6.48	0.347
P04080	CSTB	12.2	1	2	1	98	11.1	7.56	0.480
Q9NR99	MXRA5	7.0	16	25	16	2828	312.0	8.32	0.247
P02787	TF	37.7	24	52	24	698	77.0	7.12	0.274
P19652	ORM2	8.5	1	1	1	201	23.6	5.11	0.414
P09211	GSTP1	34.8	5	11	5	210	23.3	5.64	0.397
P28065	PSMB9	8.7	2	2	2	219	23.3	5.03	0.385
P22392	NME2	23.0	3	3	1	152	17.3	8.41	0.499
P00325	ADH1B	2.1	1	1	1	375	39.8	8.29	0.073
Q08380	LGALS3BP	32.8	15	65	15	585	65.3	5.27	0.301
O43707	ACTN4	25.9	19	26	11	911	104.8	5.44	0.416
P00338	LDHA	22.3	7	22	6	332	36.7	8.27	0.445
P0DOX5		27.6	10	51	5	449	49.3	8.72	0.452
P20700	LMNB1	3.8	2	2	2	586	66.4	5.16	0.345
P20142	PGC	2.1	1	1	1	388	42.4	4.46	0.497
Q9UL46	PSME2	3.8	1	1	1	239	27.4	5.73	0.438
Q06323	PSME1	8.0	2	2	2	249	28.7	6.02	0.543
P20618	PSMB1	17.8	3	4	3	241	26.5	8.13	0.298
P47972	NPTX2	2.8	1	1	1	431	47.0	5.63	0.406
P07384	CAPN1	1.1	1	1	1	714	81.8	5.67	0.336
P52209	PGD	2.3	1	1	1	483	53.1	7.23	0.452
P17936	IGFBP3	33.3	10	33	10	291	31.7	8.69	0.205
P20908	COL5A1	11.6	15	47	15	1838	183.4	5.06	0.189
P31946	YWHAB	29.3	7	12	2	246	28.1	4.83	0.503
O14950	MYL12B	16.3	2	2	2	172	19.8	4.84	0.496
P25789	PSMA4	30.7	6	11	6	261	29.5	7.72	0.468
P40121	CAPG	14.1	4	5	4	348	38.5	6.19	0.493

P46940	IQGAP1	2.2	2	2	2	1657	189.1	6.48	0.396
P18827	SDC1	5.5	1	4	1	310	32.4	4.63	0.479
P25787	PSMA2	20.9	3	4	3	234	25.9	7.43	0.096
P02768	ALB	71.1	44	209	44	609	69.3	6.28	0.140
P02775	PPBP	38.3	4	8	4	128	13.9	8.79	0.527
Q8WUT4	LRRN4	2.7	2	5	2	740	78.8	7.2	0.159
P14649	MYL6B	5.3	1	1	1	208	22.8	5.73	0.318
P20810	CAST	6.1	3	3	3	708	76.5	5.07	0.600
Q9NZP8	C1RL	31.6	13	47	11	487	53.5	7.2	0.285
P00995	SPINK1	10.1	1	1	1	79	8.5	7.61	0.197
P00352	ALDH1A1	7.0	3	3	3	501	54.8	6.73	0.507
P0DMV9	HSPA1B	15.1	9	14	5	641	70.0	5.66	0.381
P46926	GNPDA1	7.6	2	2	2	289	32.6	6.92	0.470
P30101	PDIA3	17.2	8	12	8	505	56.7	6.35	0.353
Q9H1E3	NUCKS1	3.7	1	1	1	243	27.3	5.08	0.434
P99999	CYCS	18.1	2	2	2	105	11.7	9.57	0.435
P07900	HSP90AA1	18.4	11	17	7	732	84.6	5.02	0.432
P08397	HMBS	4.7	1	1	1	361	39.3	7.18	0.617
P13716	ALAD	27.3	7	10	7	330	36.3	6.79	0.342
P61077	UBE2D3	7.5	1	1	1	147	16.7	7.8	0.430
P31431	SDC4	12.1	2	4	2	198	21.6	4.5	0.291
P67936	TPM4	35.5	10	18	5	248	28.5	4.69	0.550
Q9HC38	GLOD4	9.9	3	3	3	313	34.8	5.6	0.542
P01009	SERPINA1	33.7	13	26	13	418	46.7	5.59	0.474
P08833	IGFBP1	11.6	2	2	2	259	27.9	5.19	0.454
P00390	GSR	10.3	5	8	5	522	56.2	8.5	0.481
Q16568	CARTPT	12.9	1	1	1	116	12.8	8.25	0.198
P01718	IGLV3-27	8.8	1	1	1	113	12.2	5.01	0.470
Q12907	LMAN2	27.5	7	14	7	356	40.2	6.95	0.504
P39059	COL15A1	2.1	3	3	3	1388	141.6	5	0.330
O75347	TBCA	6.5	1	1	1	108	12.8	5.29	0.591
P35237	SERPINB6	9.6	3	5	3	376	42.6	5.27	0.599
A1L4H1	SSC5D	17.7	16	23	16	1573	165.6	6.13	0.467
P07339	CTSD	37.9	11	36	11	412	44.5	6.54	0.565
P37837	TALDO1	25.5	8	12	8	337	37.5	6.81	0.517
Q93045	STMN2	5.0	1	1	1	179	20.8	8.32	0.364
Q9NY33	DPP3	2.7	1	1	1	737	82.5	5.1	0.342
Q02985	CFHR3	6.1	2	28	1	330	37.3	7.55	0.501
Q04760	GLO1	4.9	1	1	1	184	20.8	5.31	0.601
O00468	AGRN	8.2	13	17	13	2067	217.1	6.39	0.340
P08758	ANXA5	10.6	3	4	3	320	35.9	5.05	0.603
P22626	HNRNPA2B1	6.5	2	2	2	353	37.4	8.95	0.402
P35858	IGFALS	40.0	20	126	20	605	66.0	6.79	0.337

P36222	CHI3L1	40.7	12	29	12	383	42.6	8.46	0.189
Q8NBJ4	GOLM1	33.2	12	27	12	401	45.3	4.97	0.191
Q9Y5Y6	ST14	0.9	1	1	1	855	94.7	6.55	0.446
P12814	ACTN1	13.6	10	17	2	892	103.0	5.41	0.721
O00584	RNASET2	20.7	4	7	4	256	29.5	7.08	0.407
Q562R1	ACTBL2	14.9	4	28	1	376	42.0	5.59	0.255
O15389	SIGLEC5	1.3	1	1	1	551	60.7	7.27	0.800
P04075	ALDOA	35.7	12	19	10	364	39.4	8.09	0.467
O75326	SEMA7A	2.3	1	1	1	666	74.8	7.64	0.438
P09486	SPARC	39.9	11	35	11	303	34.6	4.84	0.460
Q92954	PRG4	12.4	16	46	16	1404	151.0	9.51	0.309
P06702	S100A9	44.7	5	9	5	114	13.2	6.13	0.571
P43652	AFM	61.8	35	376	35	599	69.0	5.9	0.348
P04216	THY1	18.0	2	4	2	161	17.9	8.73	0.555
P30044	PRDX5	5.1	1	1	1	214	22.1	8.7	0.381
P98172	EFNB1	5.8	2	3	2	346	38.0	8.94	0.335
P63104	YWHAZ	53.1	11	20	7	245	27.7	4.79	0.525
P07195	LDHB	37.7	12	40	11	334	36.6	6.05	0.585
P11597	CETP	3.0	1	1	1	493	54.7	6.09	0.373
Q9BRA2	TXNDC17	7.3	1	1	1	123	13.9	5.52	0.474
Q14956	GPNMB	4.7	2	7	2	572	63.9	6.64	0.397
P49746	THBS3	7.9	6	9	5	956	104.1	4.65	0.475
P02461	COL3A1	7.5	9	34	9	1466	138.5	6.61	0.590
P02452	COL1A1	15.8	18	55	18	1464	138.9	5.8	0.510
P49257	LMAN1	2.9	1	1	1	510	57.5	6.77	0.346
P08697	SERPINF2	47.3	22	182	22	491	54.5	6.29	0.635
Q01469	FABP5	10.4	1	1	1	135	15.2	7.01	0.254
P13727	PRG2	3.2	1	1	1	222	25.2	6.76	0.493
P42126	ECI1	5.0	1	1	1	302	32.8	8.54	0.458
P61981	YWHAG	34.4	8	13	4	247	28.3	4.89	0.572
Q02818	NUCB1	30.4	11	22	11	461	53.8	5.25	0.219
P22891	PROZ	18.8	8	22	8	400	44.7	5.97	0.545
O00299	CLIC1	16.2	3	3	3	241	26.9	5.17	0.183
P02679	FGG	71.7	28	259	28	453	51.5	5.62	0.708
O95336	PGLS	3.1	1	1	1	258	27.5	6.05	0.195
Q92692	NECTIN2	3.5	2	2	2	538	57.7	4.82	0.309
P26038	MSN	38.1	22	39	17	577	67.8	6.4	0.667
O75339	CILP	9.7	10	12	10	1184	132.5	8.41	0.351
Q9GZT8	NIF3L1	6.1	2	2	2	377	41.9	6.65	0.573
P12109	COL6A1	19.3	17	66	17	1028	108.5	5.43	0.246
Q13867	BLMH	9.5	4	5	4	455	52.5	6.27	0.565
P02763	ORM1	7.5	1	1	1	201	23.5	5.02	0.382
O94985	CLSTN1	16.0	15	29	15	981	109.7	4.91	0.307

Q13443	ADAM9	1.2	1	1	1	819	90.5	7.52	0.652
P06276	BCHE	35.0	17	68	17	602	68.4	7.42	0.293
P30086	PEBP1	30.5	4	8	4	187	21.0	7.53	0.567
Q9NP78	ABCB9	0.9	1	6	1	766	84.4	7.93	0.665
P29692	EEF1D	4.3	1	1	1	281	31.1	5.01	0.586
P19338	NCL	1.1	1	1	1	710	76.6	4.7	0.624
Q8IXL6	FAM20C	8.2	3	3	3	584	66.2	7.74	0.351
Q96GP6	SCARF2	1.4	1	1	1	870	92.4	8.44	0.534
P11021	HSPA5	35.9	19	34	16	654	72.3	5.16	0.210
P02743	APCS	33.2	8	47	8	223	25.4	6.54	0.440
P05154	SERPINA5	35.0	14	68	14	406	45.6	9.26	0.307
P28799	GRN	10.8	5	6	5	593	63.5	6.83	0.401
P01764	IGHV3-23	9.4	1	2	1	117	12.6	8.28	0.558
Q9BXR6	CFHR5	10.0	4	12	3	569	64.4	7.06	0.602
P16152	CBR1	10.1	2	2	2	277	30.4	8.32	0.534
Q15262	PTPRK	0.5	1	1	1	1439	162.0	5.9	0.553
P01019	AGT	31.3	12	165	12	485	53.1	6.32	0.390
P01860	IGHG3	48.0	13	108	6	377	41.3	7.9	0.790
Q92626	PXDN	1.2	1	1	1	1479	165.2	7.17	0.493
P02675	FGB	70.7	29	420	29	491	55.9	8.27	0.722
Q96A08	HIST1H2BA	7.1	1	1	1	127	14.2	10.3	0.619
Q9UI42	CPA4	10.7	3	3	3	421	47.3	6.7	0.454
P06454	PTMA	12.6	1	1	1	111	12.2	3.78	0.326
P16930	FAH	12.6	5	11	5	419	46.3	6.95	0.549
P04156	PRNP	3.6	1	2	1	253	27.6	9	0.771
Q96PD2	DCBLD2	5.2	3	3	3	775	85.0	7.17	0.211
P08123	COL1A2	11.1	13	32	13	1366	129.2	8.95	0.596
P07602	PSAP	24.8	12	25	12	524	58.1	5.17	0.751
P07996	THBS1	18.0	18	34	18	1170	129.3	4.94	0.496
Q96KN2	CNDP1	38.1	16	70	16	507	56.7	5.3	0.673
P22792	CPN2	30.3	14	111	14	545	60.5	5.99	0.208
P24593	IGFBP5	19.9	3	8	3	272	30.6	8.21	0.341
Q08345	DDR1	1.0	1	1	1	913	101.1	6.83	0.648
P27169	PON1	42.3	11	48	11	355	39.7	5.22	0.663
P04179	SOD2	22.5	5	8	5	222	24.7	8.25	0.741
P80188	LCN2	35.9	5	19	5	198	22.6	8.91	0.749
P08727	KRT19	12.8	5	10	2	400	44.1	5.14	0.590
P11717	IGF2R	3.3	7	8	7	2491	274.2	5.94	0.054
P63261	ACTG1	61.1	17	103	1	375	41.8	5.48	0.532
A6NMY6	ANXA2P2	10.0	3	3	3	339	38.6	6.95	0.748
P02790	HPX	58.9	25	1180	25	462	51.6	7.02	0.677
O95479	H6PD	7.3	6	7	6	791	88.8	7.3	0.162
P02751	FN1	50.5	86	809	86	2386	262.5	5.71	0.433

P05067	APP	1.9	2	2	1	770	86.9	4.82	0.791
Q14766	LTBP1	2.7	4	5	4	1721	186.7	5.96	0.280
P13473	LAMP2	4.6	2	5	2	410	44.9	5.63	0.272
Q9NX02	NLRP2	1.3	1	1	1	1062	120.4	6.07	0.660
Q15485	FCN2	2.2	1	1	1	313	34.0	6.77	0.772
Q14126	DSG2	15.3	14	37	14	1118	122.2	5.24	0.101
P18669	PGAM1	22.8	5	12	5	254	28.8	7.18	0.723
P01859	IGHG2	25.8	8	44	3	326	35.9	7.59	0.655
P49788	RARRES1	3.1	1	2	1	294	33.3	8.51	0.530
P05546	SERPIND1	48.1	22	207	22	499	57.0	6.9	0.410
P08670	VIM	33.9	16	33	13	466	53.6	5.12	0.824
P20061	TCN1	11.1	3	4	3	433	48.2	5.03	0.811
P52565	ARHGDIA	10.8	2	2	2	204	23.2	5.11	0.595
P40199	CEACAM6	9.9	2	3	2	344	37.2	5.82	0.662
P35052	GPC1	2.3	1	1	1	558	61.6	7.3	0.350
P29622	SERPINA4	54.6	21	189	21	427	48.5	7.75	0.470
P98160	HSPG2	21.7	70	149	70	4391	468.5	6.51	0.319
P03952	KLKB1	54.4	33	197	33	638	71.3	8.22	0.445
O75874	IDH1	21.0	9	12	9	414	46.6	7.01	0.745
Q8NBS9	TXNDC5	16.0	6	11	6	432	47.6	5.97	0.707
Q15113	PCOLCE	13.4	4	7	4	449	47.9	7.43	0.540
P07858	CTSB	28.3	8	23	8	339	37.8	6.3	0.733
Q12866	MERTK	1.7	2	2	2	999	110.2	5.8	0.636
P55285	CDH6	3.4	2	5	2	790	88.3	4.93	0.175
P20062	TCN2	7.0	3	3	3	427	47.5	7.01	0.746
P62805	HIST1H4A	19.4	2	2	2	103	11.4	11.4	0.570
Q86WI1	PKHD1L1	1.6	4	5	4	4243	465.4	6.11	0.521
Q9H4A9	DPEP2	12.6	5	7	5	486	53.3	6.54	0.450
P62942	FKBP1A	12.0	1	2	1	108	11.9	8.16	0.668
Q9H299	SH3BGRL3	28.0	2	2	2	93	10.4	4.93	0.759
P00734	F2	59.0	35	579	35	622	70.0	5.9	0.644
P02533	KRT14	17.6	8	15	2	472	51.5	5.16	0.763
P12830	CDH1	14.1	10	31	9	882	97.4	4.73	0.598
P14618	PKM	32.6	14	16	14	531	57.9	7.84	0.723
P01705	IGLV2-23	7.1	1	1	1	113	11.9	5.91	0.657
P02749	APOH	58.8	16	312	16	345	38.3	7.97	0.625
Q9UK55	SERPINA10	35.6	13	54	13	444	50.7	8.27	0.532
Q8N2S1	LTBP4	2.5	3	4	3	1624	173.3	5.43	0.227
Q9HCB6	SPON1	11.9	8	10	8	807	90.9	6.11	0.538
P50502	ST13	4.6	1	1	1	369	41.3	5.27	0.699
P31150	GDI1	4.7	2	4	1	447	50.6	5.14	0.544
P00748	F12	33.0	17	77	17	615	67.7	7.74	0.603
Q14393	GAS6	2.5	2	3	2	721	79.6	6.21	0.530

P13647	KRT5	10.3	6	12	1	590	62.3	7.74	0.654
P36980	CFHR2	44.1	10	42	5	270	30.6	6.38	0.831
P11279	LAMP1	4.8	2	5	2	417	44.9	8.75	0.295
O95897	OLFM2	3.3	1	1	1	454	51.4	7.94	0.669
O75636	FCN3	51.5	12	58	12	299	32.9	6.67	0.847
Q6UVK1	CSPG4	2.0	3	4	3	2322	250.4	5.47	0.653
P05109	S100A8	31.2	3	6	3	93	10.8	7.03	0.862
P04275	VWF	25.3	51	109	51	2813	309.1	5.48	0.728
Q15828	CST6	14.1	2	4	2	149	16.5	8.09	0.706
O75368	SH3BGRL	10.5	1	1	1	114	12.8	5.25	0.790
O60279	SUSD5	4.1	2	2	2	629	68.0	4.91	0.847
P37802	TAGLN2	37.7	6	8	6	199	22.4	8.25	0.718
Q7Z7M0	MEGF8	2.2	4	4	4	2845	302.9	6.87	0.657
P13671	C6	51.3	42	254	42	934	104.7	6.76	0.699
P08294	SOD3	30.4	5	15	5	240	25.8	6.61	0.743
P06753	TPM3	24.6	9	16	4	285	32.9	4.72	0.862
P04066	FUCA1	8.6	4	5	4	466	53.7	6.84	0.466
Q12864	CDH17	6.6	4	4	4	832	92.2	5.14	0.841
Q14118	DAG1	12.6	6	14	6	895	97.4	8.56	0.268
Q14574	DSC3	1.9	2	2	2	896	99.9	6.1	0.575
Q86UN3	RTN4RL2	5.2	2	2	2	420	46.1	7.62	0.494
P07225	PROS1	37.4	20	102	20	676	75.1	5.67	0.456
P20933	AGA	3.2	1	2	1	346	37.2	6.28	0.663
P06732	CKM	4.5	1	1	1	381	43.1	7.25	0.215
Q8TDY8	IGDCC4	1.3	1	1	1	1250	134.1	6.2	0.669
Q9UBG0	MRC2	6.9	6	8	6	1479	166.6	5.83	0.616
Q9Y4L1	HYOU1	10.3	7	14	7	999	111.3	5.22	0.470
P54802	NAGLU	12.0	6	6	6	743	82.2	6.65	0.418
P02753	RBP4	73.1	12	412	12	201	23.0	6.07	0.753
P19827	ITIH1	36.2	27	545	27	911	101.3	6.79	0.717
Q04756	HGFAC	22.3	12	46	12	655	70.6	7.24	0.659
P08238	HSP90AB1	10.5	6	12	1	724	83.2	5.03	0.386
P05186	ALPL	2.1	1	1	1	524	57.3	6.67	0.848
Q96RD9	FCRL5	1.7	1	1	1	977	106.4	7.14	0.454
Q03591	CFHR1	49.7	13	87	1	330	37.6	7.39	0.780
Q9NR34	MAN1C1	1.3	1	1	1	630	70.9	7.46	0.750
O00462	MANBA	3.4	2	2	2	879	100.8	5.52	0.793
Q9NZD8	SPG21	3.2	1	3	1	308	34.9	6.28	0.633
P05155	SERPING1	29.2	16	174	16	500	55.1	6.55	0.806
P02671	FGA	41.0	33	387	33	866	94.9	6.01	0.880
P08581	MET	3.4	3	3	3	1390	155.4	7.33	0.400
Q99972	MYOC	6.5	3	3	3	504	56.9	5.54	0.779
P48740	MASP1	27.8	15	38	14	699	79.2	5.49	0.859

P27487	DPP4	8.9	7	14	7	766	88.2	6.04	0.313
P07108	DBI	9.2	1	1	1	87	10.0	6.57	0.886
Q6UX71	PLXDC2	14.4	6	9	6	529	59.5	6.46	0.374
P52799	EFNB2	4.8	1	2	1	333	36.9	8.85	0.779
P15144	ANPEP	26.7	22	40	22	967	109.5	5.48	0.602
P05156	CFI	42.2	23	249	23	583	65.7	7.5	0.696
P62937	PPIA	35.8	5	9	5	165	18.0	7.81	0.804
P12955	PEPD	26.4	10	18	10	493	54.5	6	0.737
P10153	RNASE2	19.9	2	7	2	161	18.3	8.73	0.669
A0A0J9YXX1	IGHV5-10-1	26.5	3	5	1	117	12.8	8.28	0.897
Q10588	BST1	20.1	6	17	6	318	35.7	7.8	0.790
Q13308	PTK7	1.8	2	3	2	1070	118.3	7.09	0.770
P07737	PFN1	65.0	6	11	6	140	15.0	8.27	0.889
Q9HCU0	CD248	9.5	5	7	5	757	80.8	5.35	0.869
P15169	CPN1	30.3	10	50	10	458	52.3	7.34	0.669
P07711	CTSL	3.6	1	3	1	333	37.5	5.45	0.657
P18428	LBP	10.0	4	10	4	481	53.4	6.7	0.860
P35590	TIE1	4.0	4	6	4	1138	125.0	7.03	0.583
A0A0C4DH25	IGKV3D-20	13.8	2	3	1	116	12.5	4.59	0.821
P68104	EEF1A1	8.7	3	3	3	462	50.1	9.01	0.924
P49747	COMP	26.8	15	41	13	757	82.8	4.6	0.889
Q96RW7	HMCN1	0.9	4	6	4	5635	613.0	6.49	0.727
P12111	COL6A3	28.7	71	212	71	3177	343.5	6.68	0.798
O00187	MASP2	10.3	5	13	5	686	75.7	5.63	0.822
P18206	VCL	41.4	42	55	42	1134	123.7	5.66	0.904
P0DOX3		24.6	8	29	8	512	56.2	8.02	0.832
P29279	CTGF	3.7	1	2	1	349	38.1	8	0.862
P01011	SERPINA3	54.1	21	1041	21	423	47.6	5.52	0.705
Q15904	ATP6AP1	3.8	1	1	1	470	52.0	6.14	0.776
P61204	ARF3	5.5	1	1	1	181	20.6	7.43	0.876
P02144	MB	14.3	2	2	2	154	17.2	7.68	0.715
P00747	PLG	60.4	44	512	44	810	90.5	7.24	0.932
P62328	TMSB4X	40.9	2	2	2	44	5.1	5.06	0.924
P04070	PROC	19.1	6	14	6	461	52.0	6.28	0.900
Q16394	EXT1	5.4	3	3	3	746	86.2	9.04	0.896
Q96B86	RGMA	4.0	1	1	1	450	49.3	7.42	0.794
P32942	ICAM3	3.3	2	2	2	547	59.5	5.43	0.755
Q49AG3	ZBED5	1.0	1	1	1	693	78.9	8.27	0.639
P43251	BTD	31.9	15	74	15	543	61.1	6.25	0.873
Q12905	ILF2	4.1	1	1	1	390	43.0	5.26	0.691
O43505	B4GAT1	7.2	2	3	2	415	47.1	7.2	0.796
P26927	MST1	43.6	23	66	23	711	80.3	7.68	0.891
P04180	LCAT	28.4	8	26	8	440	49.5	6.11	0.871

Q9UNN8	PROCR	16.4	3	8	3	238	26.7	7.18	0.916
P13797	PLS3	10.3	6	19	1	630	70.8	5.6	0.888
Q9Y6R7	FCGBP	14.4	35	78	35	5405	571.6	5.34	0.914
P12110	COL6A2	8.2	7	10	7	1019	108.5	6.21	0.789
Q9BUN1	MENT	2.3	1	1	1	341	36.7	8.59	0.893
P49641	MAN2A2	1.6	2	2	1	1150	130.5	6.84	0.834
P20851	C4BPB	30.2	6	21	6	252	28.3	5.14	0.940
P54289	CACNA2D1	14.3	12	14	12	1103	124.5	5.27	0.775
A0A0C4DH38	IGHV5-51	34.2	3	8	1	117	12.7	8.27	0.797
Q86SQ4	ADGRG6	0.9	1	1	1	1221	136.6	7.87	0.807
Q99983	OMD	9.7	3	4	3	421	49.5	5.59	0.934
P04003	C4BPA	39.4	21	152	21	597	67.0	7.3	0.951
P29401	TKT	10.8	5	8	5	623	67.8	7.66	0.957
A0A0C4DH34	IGHV4-28	7.7	1	3	1	117	13.1	9.29	0.961
Q92820	GGH	24.8	9	23	9	318	35.9	7.11	0.916
P05121	SERPINE1	8.7	4	4	4	402	45.0	7.2	0.958
P01344	IGF2	13.9	2	12	2	180	20.1	9.32	0.909
Q13740	ALCAM	19.7	9	25	9	583	65.1	6.25	0.877
P05556	ITGB1	13.0	8	10	8	798	88.4	5.39	0.929
P0DOY2	IGLC2	69.8	6	120	3	106	11.3	7.24	0.949
Q8NBP7	PCSK9	3.0	2	2	2	692	74.2	6.61	0.919
P24821	TNC	25.2	42	95	42	2201	240.7	4.89	0.969
P23142	FBLN1	27.9	15	49	15	703	77.2	5.22	0.966
Q6YHK3	CD109	10.5	12	20	12	1445	161.6	5.85	0.954
Q13332	PTPRS	2.9	3	3	3	1948	216.9	6.46	0.915
P05451	REG1A	31.9	6	27	5	166	18.7	5.94	0.986
P22570	FDXR	4.5	1	1	1	491	53.8	8.44	0.965
Q6FHJ7	SFRP4	26.0	7	16	7	346	39.8	8.82	0.957
P14625	HSP90B1	21.0	16	35	15	803	92.4	4.84	0.945
P07478	PRSS2	15.8	3	12	3	247	26.5	4.92	0.989
Q04917	YWHAH	22.4	6	11	2	246	28.2	4.84	0.983
P86452	ZBED6	1.0	1	1	1	979	109.9	6.55	0.903
P02774	GC	83.8	43	1424	43	474	52.9	5.54	0.981
P06396	GSN	66.8	39	418	39	782	85.6	6.28	0.985
Q12841	FSTL1	44.8	14	36	14	308	35.0	5.52	0.988
Q9BUD6	SPON2	12.4	3	5	3	331	35.8	5.52	0.997
A0A075B6K4	IGLV3-10	15.7	2	4	2	115	12.4	4.83	0.996
P56715	RP1	0.5	1	1	1	2156	240.5	5.8	0.997
P08195	SLC3A2	16.7	8	12	8	630	68.0	5.01	1.000
P55268	LAMB2	1.6	2	4	2	1798	195.9	6.52	1.000
P00751	CFB	58.5	42	619	42	764	85.5	7.06	0.993
Q16610	ECM1	51.9	22	130	22	540	60.6	6.71	0.990
P05019	IGF1	7.2	1	2	1	195	21.8	9.72	0.988

P21333	FLNA	4.6	7	10	7	2647	280.6	6.06	0.994
O00339	MATN2	1.2	1	1	1	956	106.8	6.27	0.988
Q14515	SPARCL1	35.4	20	54	20	664	75.2	4.81	0.975
P01593	IGKV1D-33	13.7	1	4	1	117	12.8	4.78	0.950
P04217	A1BG	53.3	15	328	15	495	54.2	5.86	0.951
Q14019	COTL1	12.0	2	4	2	142	15.9	5.67	0.982
Q13449	LSAMP	10.1	3	3	3	338	37.4	6.98	0.966
Q92859	NEO1	9.5	10	17	10	1461	159.9	6.54	0.901
P05062	ALDOB	20.6	6	7	5	364	39.4	7.87	0.979
P26572	MGAT1	2.5	1	1	1	445	50.8	9.16	0.959
P00533	EGFR	3.1	3	3	3	1210	134.2	6.68	0.883
Q9HCL0	PCDH18	1.7	2	2	2	1135	126.1	5.15	0.912
Q14964	RAB39A	3.7	1	1	1	217	25.0	7.65	0.878
Q9Y4D7	PLXND1	2.2	2	2	2	1925	211.9	7.15	0.947
P78417	GSTO1	27.0	7	10	7	241	27.5	6.6	0.942
P61916	NPC2	43.0	5	13	5	151	16.6	7.65	0.935
P01833	PIGR	13.0	8	12	8	764	83.2	5.74	0.956
P02766	TTR	40.8	4	15	4	147	15.9	5.76	0.797
P01033	TIMP1	45.4	7	47	7	207	23.2	8.1	0.895
P09668	CTSH	12.5	3	3	3	335	37.4	8.07	0.747
P01714	IGLV3-19	8.0	1	1	1	112	12.0	4.96	0.947
P61254	RPL26	7.6	1	5	1	145	17.2	10.6	0.954
P08185	SERPINA6	31.6	10	90	10	405	45.1	6.04	0.857
Q8IUX7	AEBP1	6.6	7	9	7	1158	130.8	5.11	0.885
Q9NTU7	CBLN4	3.5	1	2	1	201	21.8	8.73	0.926
Q07954	LRP1	4.9	21	31	21	4544	504.3	5.39	0.886
P10586	PTPRF	2.0	3	3	3	1907	212.7	6.3	0.833
P0DOX2		38.0	10	80	4	455	48.9	6.67	0.956
Q8N5G2	MACO1	1.1	1	1	1	664	76.1	9.07	0.887
P08603	CFH	57.4	62	1071	54	1231	139.0	6.61	0.797
Q9NPY3	CD93	12.1	7	14	7	652	68.5	5.44	0.893
A0A0C4DH31	IGHV1-18	9.4	1	4	1	117	12.8	8.84	0.936
P07911	UMOD	1.4	1	1	1	640	69.7	5.24	0.779
Q8NFD2	ANKK1	2.1	1	1	1	765	84.6	7.08	0.963
P35442	THBS2	9.8	9	16	9	1172	129.9	4.83	0.891
Q504Y2	PKDCC	2.0	1	1	1	493	54.1	8.41	0.919
O95445	APOM	48.4	8	23	8	188	21.2	6.01	0.965
P61158	ACTR3	1.9	1	2	1	418	47.3	5.88	0.892
P08709	F7	4.1	1	1	1	466	51.6	7.23	0.777
Q9H7P6	MVB12B	3.4	1	1	1	319	35.6	8.15	0.738
P0C0L5	C4B	62.2	87	1469	4	1744	192.6	7.27	0.892
Q9HBB8	CDHR5	7.1	4	5	4	845	88.2	4.93	0.776
Q96HD1	CRELD1	4.5	2	3	2	420	45.4	4.87	0.807

Q14112	NID2	6.5	8	14	8	1375	151.2	5.29	0.925
Q6PCE3	PGM2L1	3.9	1	1	1	622	70.4	7.15	0.871
Q6PCB0	VWA1	1.6	1	3	1	445	46.8	7.68	0.756
P12318	FCGR2A	9.8	2	4	2	317	35.0	6.68	0.812
P19021	PAM	6.9	6	9	6	973	108.3	6.42	0.563
P35908	KRT2	23.2	14	26	11	639	65.4	8	0.891
P49908	SELENOP	12.6	6	23	6	381	43.2	7.87	0.872
Q9UIB8	CD84	4.6	1	1	1	345	38.8	7.06	0.729
Q93070	ART4	2.9	1	1	1	314	35.9	9.22	0.810
P08571	CD14	37.3	13	76	13	375	40.1	6.23	0.664
O75144	ICOSLG	17.9	4	6	4	302	33.3	5.31	0.802
P08572	COL4A2	1.5	2	3	2	1712	167.4	8.66	0.867
P0C0L4	C4A	61.4	86	1448	3	1744	192.7	7.08	0.921
P22105	TNXB	16.7	41	98	41	4242	457.9	5.17	0.662
Q96IY4	CPB2	26.2	11	51	11	423	48.4	7.71	0.906
Q13508	ART3	8.7	3	4	3	389	43.9	6.06	0.782
P01701	IGLV1-51	6.8	1	2	1	117	12.2	7.03	0.833
P05160	F13B	45.7	22	107	22	661	75.5	6.39	0.735
Q9P232	CNTN3	1.3	1	1	1	1028	112.8	6.3	0.848
O43493	TGOLN2	11.5	5	6	5	479	51.0	5.73	0.834
Q16706	MAN2A1	5.4	6	7	5	1144	131.1	7.58	0.637
P09601	HMOX1	5.6	1	1	1	288	32.8	8.25	0.904
O60462	NRP2	4.1	3	4	3	931	104.8	5.17	0.682
O95980	RECK	2.1	2	3	2	971	106.4	6.74	0.807
Q9BS26	ERP44	5.9	2	2	2	406	46.9	5.26	0.533
P06312	IGKV4-1	22.3	2	6	2	121	13.4	5.25	0.844
O00391	QSOX1	30.7	26	75	26	747	82.5	8.92	0.631
P13497	BMP1	1.6	1	1	1	986	111.2	6.9	0.787
P22352	GPX3	35.4	7	67	7	226	25.5	8.13	0.844
Q05707	COL14A1	2.1	3	3	3	1796	193.4	5.3	0.530
Q93063	EXT2	1.3	1	3	1	718	82.2	6.55	0.795
P35555	FBN1	4.9	11	11	11	2871	312.0	4.93	0.667
P07359	GP1BA	13.3	8	24	8	652	71.5	6.29	0.647
O75882	ATRN	24.3	30	117	30	1429	158.4	7.31	0.584
Q8NHW5	RPLP0P6	2.5	1	2	1	317	34.3	5.55	0.796
P17813	ENG	9.9	6	11	6	658	70.5	6.61	0.710
P15509	CSF2RA	3.5	1	1	1	400	46.2	7.75	0.834
P28838	LAP3	7.1	2	2	2	519	56.1	7.93	0.781
P36955	SERPINF1	54.5	21	191	21	418	46.3	6.38	0.814
Q9Y279	VSIG4	20.1	6	12	6	399	44.0	6.35	0.760
P01023	A2M	54.3	62	848	54	1474	163.2	6.46	0.776
P04264	KRT1	27.3	19	62	18	644	66.0	8.12	0.899
Q5SYB0	FRMPD1	0.4	1	2	1	1578	173.3	5.25	0.871

P02647	APOA1	50.6	14	52	14	267	30.8	5.76	0.691
Q9BY67	CADM1	9.3	3	5	3	442	48.5	5.07	0.075
P23470	PTPRG	4.3	5	8	5	1445	161.9	6.42	0.698
Q7Z7M8	B3GNT8	2.8	1	1	1	397	43.4	8.32	0.300
Q9H8J5	MANSC1	3.5	1	1	1	431	46.8	6.54	0.803
P02760	AMBP	47.7	14	270	14	352	39.0	6.25	0.542
P30043	BLVRB	7.3	1	1	1	206	22.1	7.65	0.886
Q9H8L6	MMRN2	4.7	3	8	3	949	104.3	5.86	0.673
Q9H4G4	GLIPR2	11.0	1	1	1	154	17.2	9.41	0.703
P06681	C2	45.1	30	251	30	752	83.2	7.42	0.696
P35443	THBS4	31.6	20	56	17	961	105.8	4.68	0.798
P52566	ARHGDIB	6.5	1	1	1	201	23.0	5.21	0.781
O15031	PLXNB2	1.1	2	2	2	1838	205.0	6.24	0.610
P07357	C8A	52.6	22	244	22	584	65.1	6.47	0.421
P31146	CORO1A	1.7	1	1	1	461	51.0	6.68	0.632
Q14520	HABP2	28.9	13	99	13	560	62.6	6.54	0.491
P07360	C8G	58.4	11	82	11	202	22.3	8.31	0.294
Q7Z7G0	ABI3BP	13.9	11	26	11	1075	118.6	9.44	0.742
P07998	RNASE1	14.7	1	3	1	156	17.6	8.79	0.823
Q16853	AOC3	10.5	7	11	7	763	84.6	6.52	0.397
Q99969	RARRES2	6.7	1	1	1	163	18.6	9.09	0.547
A0A075B6I0	IGLV8-61	7.4	1	4	1	122	12.8	4.55	0.866
P28062	PSMB8	4.3	1	1	1	276	30.3	7.43	0.581
Q8TDQ0	HAVCR2	8.3	2	2	2	301	33.4	5.72	0.720
P35527	KRT9	31.6	16	30	15	623	62.0	5.24	0.883
P19823	ITIH2	53.2	38	578	38	946	106.4	6.86	0.810
Q15848	ADIPOQ	27.0	5	16	5	244	26.4	5.74	0.722
Q86UD1	OAF	32.2	6	20	6	273	30.7	6.84	0.676
Q9UNW1	MINPP1	26.7	11	18	11	487	55.0	7.81	0.305
P10721	KIT	2.8	3	5	3	976	109.8	6.98	0.569
P00488	F13A1	26.9	18	61	18	732	83.2	6.09	0.668
P25311	AZGP1	58.1	20	336	20	298	34.2	6.05	0.635
Q9UBP4	DKK3	26.3	6	18	6	350	38.4	4.65	0.412
P07686	HEXB	4.7	3	4	3	556	63.1	6.76	0.585
Q9GZX9	TWSG1	4.0	1	1	1	223	25.0	5.34	0.569
Q01459	CTBS	18.7	6	13	6	385	43.7	6.64	0.658
P30530	AXL	2.0	1	1	1	894	98.3	5.39	0.655
P01031	C5	58.8	81	618	81	1676	188.2	6.52	0.402
Q92484	SMPDL3A	2.0	1	1	1	453	51.2	6.33	0.378
Q16787	LAMA3	0.5	1	1	1	3333	366.4	7.24	0.727
Q8TER0	SNED1	1.0	1	2	1	1413	152.1	6.98	0.636
P33151	CDH5	15.3	11	34	11	784	87.5	5.43	0.702
P40189	IL6ST	10.5	7	7	7	918	103.5	5.95	0.570

Q8TAT6	NPLOC4	1.2	1	1	1	608	68.1	6.38	0.497
P09382	LGALS1	44.4	5	7	5	135	14.7	5.5	0.725
Q96AP7	ESAM	4.6	2	3	2	390	41.2	9.32	0.629
A6QL64	ANKRD36	0.9	1	1	1	1941	217.3	8.66	0.584
P04792	HSPB1	9.3	2	2	2	205	22.8	6.4	0.858
P07358	C8B	50.4	28	188	28	591	67.0	8.13	0.113
P13489	RNH1	7.4	2	2	2	461	49.9	4.82	0.447
Q9HBR0	SLC38A10	2.9	2	3	2	1119	119.7	5.73	0.268
P01619	IGKV3-20	13.8	2	3	1	116	12.5	4.96	0.652
P53634	CTSC	10.6	3	5	3	463	51.8	6.99	0.512
P22692	IGFBP4	34.9	7	19	7	258	27.9	7.15	0.608
Q6UY14	ADAMTSL4	3.3	3	5	3	1074	116.5	8.34	0.275
A0A0C4DH55	IGKV3D-7	5.9	1	2	1	119	13.1	5.94	0.779
Q9BXX0	EMILIN2	1.2	1	1	1	1053	115.6	6.46	0.691
Q9UBR2	CTSZ	15.8	5	6	5	303	33.8	7.11	0.311
Q9BWV1	BOC	2.0	1	2	1	1114	121.0	7.01	0.766
Q9NZL9	MAT2B	5.4	1	3	1	334	37.5	7.36	0.818
P13598	ICAM2	20.0	5	18	5	275	30.6	7.43	0.610
A0A0B4J1V0	IGHV3-15	5.9	1	3	1	119	12.9	8.62	0.518
Q76M96	CCDC80	1.8	1	1	1	950	108.1	9.72	0.593
Q9UJJ9	GNPTG	23.9	5	12	5	305	34.0	6.95	0.456
P09619	PDGFRB	2.9	2	2	2	1106	123.9	4.98	0.579
Q00532	CDKL1	2.0	1	8	1	358	41.8	8.85	0.644
P13645	KRT10	38.4	18	43	16	584	58.8	5.21	0.719
P27930	IL1R2	2.0	1	2	1	398	45.4	7.9	0.709
P55290	CDH13	17.1	10	16	10	713	78.2	4.98	0.433
P15291	B4GALT1	12.8	3	7	3	398	43.9	8.65	0.220
O14498	ISLR	14.3	5	11	5	428	46.0	5.15	0.408
Q9NS71	GKN1	7.0	1	3	1	199	22.0	6.32	0.748
Q15223	NECTIN1	9.9	3	3	3	517	57.1	6.1	0.465
Q96FE7	PIK3IP1	4.2	1	1	1	263	28.2	5.01	0.685
P16070	CD44	5.3	4	16	4	742	81.5	5.33	0.601
Q9BTY2	FUCA2	24.2	11	17	11	467	54.0	6.25	0.547
Q9NPH3	IL1RAP	13.3	9	24	9	570	65.4	8.12	0.479
Q12884	FAP	2.0	2	9	1	760	87.7	6.65	0.609
P11362	FGFR1	5.7	4	5	4	822	91.8	6.21	0.635
P13796	LCP1	58.1	31	101	26	627	70.2	5.43	0.588
P12821	ACE	2.8	3	3	3	1306	149.6	6.39	0.103
Q9NY97	B3GNT2	17.1	5	6	5	397	46.0	8.54	0.096
P00450	CP	67.7	60	1192	60	1065	122.1	5.72	0.093
P0DOX8		41.7	8	110	4	216	22.8	6.76	0.746
P01782	IGHV3-9	9.3	1	1	1	118	12.9	7.08	0.508
Q4KWH8	PLCH1	0.5	1	2	1	1693	189.1	7.74	0.500

P01742	IGHV1-69	15.4	2	3	2	117	12.7	9.17	0.786
P48637	GSS	5.5	3	3	3	474	52.4	5.92	0.227
P19022	CDH2	9.1	5	8	5	906	99.7	4.81	0.323
P03951	F11	39.2	21	66	21	625	70.1	8.1	0.579
P07333	CSF1R	6.7	4	13	4	972	107.9	6.37	0.445
P02745	C1QA	29.0	6	21	6	245	26.0	9.11	0.712
P39060	COL18A1	1.7	2	2	2	1754	178.1	6.01	0.497
P21810	BGN	3.0	1	1	1	368	41.6	7.52	0.691
P07307	ASGR2	16.4	5	6	5	311	35.1	6.25	0.374
P02765	AHSG	51.0	13	624	13	367	39.3	5.72	0.446
P04222	HLA-C	6.0	2	5	1	366	40.8	6.39	0.804
O15394	NCAM2	7.8	5	6	5	837	93.0	5.6	0.256
Q9NPR2	SEMA4B	5.0	5	5	5	832	92.1	6.95	0.569
O75083	WDR1	1.3	1	1	1	606	66.2	6.65	0.462
P05362	ICAM1	18.0	7	17	7	532	57.8	7.99	0.449
Q8IWV2	CNTN4	4.2	3	5	3	1026	113.4	7.47	0.625
P55103	INHBC	2.3	1	1	1	352	38.2	7.11	0.704
Q5KU26	COLEC12	0.9	1	2	1	742	81.5	5.69	0.391
Q8WZ75	ROBO4	7.1	6	7	6	1007	107.4	6.64	0.630
P05413	FABP3	6.8	1	2	1	133	14.8	6.8	0.531
Q9GZM5	YIPF3	2.9	1	1	1	350	38.2	5.76	0.387
P05452	CLEC3B	70.8	11	88	11	202	22.5	5.67	0.503
P08637	FCGR3A	12.2	4	18	1	254	29.1	8.07	0.366
O00533	CHL1	18.0	18	39	18	1208	135.0	5.76	0.319
Q9UQP3	TNN	1.8	1	8	1	1299	143.9	5.63	0.300
P20742	PZP	26.1	34	256	26	1482	163.8	6.38	0.764
P13591	NCAM1	17.1	12	31	12	858	94.5	4.87	0.167
P17900	GM2A	45.1	7	13	7	193	20.8	5.31	0.390
P01042	KNG1	59.2	43	742	43	644	71.9	6.81	0.360
P33908	MAN1A1	17.2	10	22	10	653	72.9	6.47	0.600
P12259	F5	6.2	11	15	11	2224	251.5	6.05	0.533
Q9NZ08	ERAP1	5.2	4	5	4	941	107.2	6.46	0.225
P98095	FBLN2	3.5	2	2	2	1184	126.5	4.82	0.474
P02746	C1QB	39.1	8	71	8	253	26.7	8.63	0.662
P16284	PECAM1	1.9	1	1	1	738	82.5	6.99	0.001
P09172	DBH	28.2	13	32	13	617	69.0	6.42	0.858
Q96S96	PEBP4	20.7	4	9	4	227	25.7	6.54	0.635
Q13103	SPP2	10.9	2	3	2	211	24.3	8.32	0.562
O14786	NRP1	20.3	14	28	14	923	103.1	5.88	0.320
P43121	MCAM	19.5	9	26	9	646	71.6	5.76	0.390
Q12860	CNTN1	16.7	14	20	14	1018	113.2	5.9	0.190
P54108	CRISP3	17.6	4	12	4	245	27.6	7.8	0.659
Q99784	OLFM1	11.5	5	19	5	485	55.3	6.95	0.073

Q6EMK4	VASN	11.0	6	21	6	673	71.7	7.39	0.369
Q14624	ITIH4	56.8	41	609	41	930	103.3	6.98	0.247
P09960	LTA4H	20.5	10	16	10	611	69.2	6.18	0.096
O00241	SIRPB1	5.3	2	2	1	398	43.2	6.52	0.627
P20774	OGN	40.9	13	37	13	298	33.9	5.63	0.705
P78324	SIRPA	9.3	4	4	3	504	54.9	6.98	0.324
Q08554	DSC1	1.5	1	1	1	894	99.9	5.43	0.505
P04196	HRG	43.2	21	379	21	525	59.5	7.5	0.471
P80108	GPLD1	20.0	17	52	17	840	92.3	6.37	0.594
P26992	CNTFR	2.4	1	2	1	372	40.6	6.76	0.448
P61769	B2M	55.5	5	17	5	119	13.7	6.52	0.532
Q12913	PTPRJ	5.0	5	9	5	1337	145.9	5.58	0.317
P09467	FBP1	4.7	1	2	1	338	36.8	6.99	0.538
P18065	IGFBP2	34.8	9	37	9	325	34.8	7.5	0.489
Q9H6X2	ANTXR1	1.8	1	1	1	564	62.7	7.61	0.354
Q02809	PLOD1	2.1	1	1	1	727	83.5	6.95	0.546
P07942	LAMB1	22.8	32	68	32	1786	197.9	4.94	0.314
P27918	CFP	33.0	12	49	12	469	51.2	7.9	0.525
O95497	VNN1	16.2	6	11	6	513	57.0	5.55	0.712
Q99941	ATF6B	1.4	1	1	1	703	76.7	6.27	0.231
P01876	IGHA1	56.4	14	213	9	353	37.6	6.51	0.662
P01706	IGLV2-11	13.4	2	2	1	119	12.6	7.24	0.826
A0A0C4DH68	IGKV2-24	10.8	1	2	1	120	13.1	8.53	0.727
P05534	HLA-A	18.9	6	11	5	365	40.7	6.34	0.821
P10643	C7	64.4	42	472	41	843	93.5	6.48	0.489
A0A0B4J1X5	IGHV3-74	15.4	2	4	1	117	12.8	8.66	0.437
P24043	LAMA2	14.0	37	55	37	3122	343.7	6.4	0.102
P23381	WARS	6.8	2	2	2	471	53.1	6.23	0.137
Q96EE4	CCDC126	8.6	1	2	1	140	15.7	9.88	0.442
Q9ULI3	HEG1	2.6	3	8	3	1381	147.4	6.18	0.590
P68032	ACTC1	41.6	12	63	3	377	42.0	5.39	0.155
P61160	ACTR2	3.0	1	1	1	394	44.7	6.74	0.478
P08174	CD55	8.9	4	8	4	381	41.4	7.59	0.104
O60888	CUTA	7.8	1	1	1	179	19.1	5.5	0.589
Q9H8M5	CNNM2	0.8	1	1	1	875	96.6	6.38	0.687
P02750	LRG1	51.6	13	205	13	347	38.2	6.95	0.419
P0DOX6		37.8	17	145	1	576	63.4	7.87	0.761
Q9NPG4	PCDH12	1.0	1	1	1	1184	128.9	5.29	0.523
P15151	PVR	9.8	4	13	4	417	45.3	6.52	0.122
P27348	YWHAQ	22.0	6	10	1	245	27.7	4.78	0.770
P0DOX7		53.7	7	96	3	214	23.4	7.17	0.473
Q9NZK5	ADA2	17.6	8	10	8	511	58.9	7.91	0.169
Q99650	OSMR	1.0	1	1	1	979	110.4	5.82	0.350

P14543	NID1	3.8	5	7	5	1247	136.3	5.29	0.274
P11047	LAMC1	22.1	28	49	28	1609	177.5	5.12	0.303
P35916	FLT4	1.8	1	1	1	1363	152.7	6.3	0.738
Q6UXB8	PI16	22.2	8	29	8	463	49.4	5.39	0.549
P10909	CLU	31.0	15	153	15	449	52.5	6.27	0.457
P13987	CD59	23.4	3	5	3	128	14.2	6.48	0.255
Q13822	ENPP2	25.4	16	42	16	863	98.9	7.37	0.398
Q86VB7	CD163	26.5	25	89	25	1156	125.4	5.95	0.491
Q9NQ79	CRTAC1	14.1	8	18	8	661	71.4	5.12	0.236
Q9HDC9	APMAP	7.2	3	5	3	416	46.5	6.16	0.682
Q6KB66	KRT80	1.5	1	1	1	452	50.5	5.67	0.681
P02748	C9	52.1	27	269	27	559	63.1	5.59	0.082
P14207	FOLR2	23.5	5	10	5	255	29.3	7.53	0.398
P04004	VTN	43.1	14	249	14	478	54.3	5.8	0.536
Q16363	LAMA4	7.1	10	18	10	1823	202.4	6.28	0.280
Q9UGM5	FETUB	35.1	13	66	13	382	42.0	6.83	0.176
Q9BWP8	COLEC11	19.9	6	15	6	271	28.6	5.41	0.524
Q6ZN30	BNC2	1.0	1	8	1	1099	122.3	6.52	0.527
P02747	C1QC	25.3	5	36	5	245	25.8	8.41	0.544
O95998	IL18BP	8.8	2	3	2	194	21.1	7.39	0.380
P51884	LUM	43.2	14	253	14	338	38.4	6.61	0.365
P01700	IGLV1-47	11.1	1	1	1	117	12.3	5.91	0.358
A0A0B4J1U7	IGHV6-1	13.2	2	6	2	121	13.5	9.2	0.562
P01008	SERPINC1	58.6	31	1018	31	464	52.6	6.71	0.131
P14151	SELL	19.4	8	39	8	372	42.2	6.6	0.279
P01034	CST3	47.9	6	47	6	146	15.8	8.75	0.090
P21583	KITLG	3.3	1	1	1	273	30.9	6.14	0.295
P15090	FABP4	28.8	4	6	4	132	14.7	7.14	0.405
P00742	F10	23.4	11	20	11	488	54.7	5.94	0.441
P55058	PLTP	30.6	14	57	14	493	54.7	7.01	0.336
Q16270	IGFBP7	30.1	8	21	8	282	29.1	7.9	0.265
P01834	IGKC	80.4	6	144	2	107	11.8	6.52	0.598
Q8WUJ3	CEMIP	0.7	1	1	1	1361	152.9	7.85	0.099
Q12805	EFEMP1	43.6	17	62	17	493	54.6	5.07	0.373
Q9Y6Z7	COLEC10	14.8	4	6	4	277	30.7	7.33	0.194
P0DJD7	PGA4	2.1	1	1	1	388	42.0	4.34	0.402
P09871	C1S	41.3	23	171	22	688	76.6	4.96	0.455
Q16663	CCL15	16.8	1	1	1	113	12.2	8.18	0.092
Q96NZ9	PRAP1	41.1	4	6	4	151	17.2	5.36	0.469
P00746	CFD	62.8	14	67	14	253	27.0	7.71	0.273
Q9GZP0	PDGFD	3.2	1	1	1	370	42.8	7.97	0.674
O94769	ECM2	5.7	3	3	3	699	79.7	5.41	0.232
P01780	IGHV3-7	23.1	3	11	2	117	12.9	6.57	0.486

P05090	APOD	30.2	6	57	6	189	21.3	5.15	0.391
O43866	CD5L	47.8	12	41	12	347	38.1	5.47	0.440
Q92520	FAM3C	37.4	7	14	7	227	24.7	8.29	0.085
Q03167	TGFBR3	5.4	3	4	3	851	93.4	5.71	0.104
O75382	TRIM3	1.9	1	1	1	744	80.8	7.83	0.100
Q02487	DSC2	6.8	4	6	4	901	99.9	5.34	0.213
P19971	TYMP	9.3	3	3	3	482	49.9	5.53	0.276
P09603	CSF1	4.3	2	3	2	554	60.1	5.29	0.165
Q9Y646	CPQ	7.2	3	3	3	472	51.9	6.18	0.173
P01591	JCHAIN	41.5	6	24	6	159	18.1	5.24	0.323
P28482	MAPK1	1.9	1	7	1	360	41.4	6.98	0.226
P00740	F9	35.4	12	36	12	461	51.7	5.47	0.460
P41271	NBL1	7.7	2	3	2	181	19.4	5.29	0.132
P01824	IGHV4-39	20.0	2	9	2	125	13.9	9.26	0.286
Q9UM47	NOTCH3	0.5	1	1	1	2321	243.5	5.39	0.362
Q8N3T6	TMEM132C	1.6	1	1	1	1108	121.7	6.35	0.525
P22897	MRC1	10.0	13	23	13	1456	165.9	6.54	0.275
Q7Z3B1	NEGR1	6.5	2	6	2	354	38.7	6.21	0.128
P11684	SCGB1A1	27.5	3	3	3	91	10.0	5.06	0.084
Q4LDE5	SVEP1	21.4	60	130	60	3571	389.9	5.5	0.379
P00736	C1R	48.8	26	166	24	705	80.1	6.21	0.446
P19320	VCAM1	34.8	22	59	22	739	81.2	5.22	0.235
Q8IZF2	ADGRF5	4.4	4	5	4	1346	149.4	6.65	0.058
O76061	STC2	7.0	2	2	2	302	33.2	7.3	0.285
Q9UBX1	CTSF	4.5	2	2	2	484	53.3	8.22	0.219
P24592	IGFBP6	27.9	4	11	4	240	25.3	7.81	0.183
Q76LX8	ADAMTS13	8.1	10	11	10	1427	153.5	7.17	0.062
O75093	SLIT1	0.6	1	1	1	1534	167.8	6.57	0.210
P01871	IGHM	62.9	21	186	5	453	49.4	6.77	0.548
Q96PD5	PGLYRP2	35.1	13	176	13	576	62.2	7.55	0.386
P08887	IL6R	1.7	1	1	1	468	51.5	8.22	0.159
P08519	LPA	19.4	5	9	5	4548	501.0	5.88	0.403
P41222	PTGDS	25.3	5	45	5	190	21.0	7.8	0.375
P04746	AMY2A	14.5	6	12	6	511	57.7	7.05	0.486
Q06033	ITIH3	30.2	22	123	22	890	99.8	5.74	0.215
P23471	PTPRZ1	0.4	1	1	1	2315	254.4	4.88	0.220
P05543	SERPINA7	56.9	22	213	22	415	46.3	6.3	0.062
Q9UHG3	PCYOX1	10.5	5	6	5	505	56.6	6.18	0.293
P16035	TIMP2	35.5	9	18	9	220	24.4	7.49	0.135
Q6UWP8	SBSN	15.3	2	3	2	590	60.5	7.01	0.236
Q9Y275	TNFSF13B	4.6	1	2	1	285	31.2	6.25	0.470
Q13790	APOF	7.7	2	8	2	326	35.4	5.64	0.250
P32004	L1CAM	1.0	1	1	1	1257	139.9	6.24	0.078

P08254	MMP3	2.5	1	1	1	477	53.9	6.16	0.241
P08253	MMP2	55.0	30	98	30	660	73.8	5.47	0.181
Q9Y5Y7	LYVE1	15.2	5	14	5	322	35.2	8.28	0.138
P60709	ACTB	61.1	17	104	1	375	41.7	5.48	0.146
P46939	UTRN	0.4	1	1	1	3433	394.2	5.33	0.388
P11226	MBL2	31.5	6	20	6	248	26.1	5.49	0.052
A0A087WW87	IGKV2-40	10.7	1	5	1	121	13.3	4.61	0.322
P45877	PPIC	6.1	1	2	1	212	22.7	8.4	0.115
P98066	TNFAIP6	7.2	1	1	1	277	31.2	6.79	0.230
P02649	APOE	74.4	25	158	25	317	36.1	5.73	0.142
P07585	DCN	10.6	4	10	4	359	39.7	8.54	0.186
Q86TH1	ADAMTSL2	4.7	2	2	2	951	104.6	6.42	0.083
P04114	APOB	59.9	259	2604	259	4563	515.3	7.05	0.202
O14791	APOL1	19.1	8	15	8	398	43.9	5.81	0.239
A0A075B6I9	IGLV7-46	7.7	1	1	1	117	12.5	7.2	0.396
Q7LFX5	CHST15	2.3	1	1	1	561	64.9	8.29	0.171
P04278	SHBG	46.8	14	74	14	402	43.8	6.71	0.119
Q9UEW3	MARCO	8.1	4	5	4	520	52.6	8.78	0.254
Q13093	PLA2G7	16.1	6	6	6	441	50.0	7.56	0.226
Q8N9V7	TOPAZ1	1.2	1	1	1	1692	190.8	7.87	0.163
P35542	SAA4	27.7	4	15	4	130	14.7	9.07	0.186
P02741	CRP	23.2	5	18	5	224	25.0	5.63	0.159
P16233	PNLIP	9.0	3	3	3	465	51.1	6.73	0.376
Q6WN34	CHRDL2	1.6	1	1	1	429	47.5	7.88	0.053
P02654	APOC1	34.9	5	18	5	83	9.3	8.47	0.318
P02656	APOC3	34.3	3	21	3	99	10.8	5.41	0.331
P10645	CHGA	7.4	2	3	2	457	50.7	4.6	0.177
P02655	APOC2	49.5	4	15	4	101	11.3	4.72	0.248
P48304	REG1B	21.1	3	11	2	166	18.7	5.95	0.104