

**ADVANCED
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Supporting Information

for *Adv. Healthcare Mater.*, DOI: 10.1002/adhm.201700903

**Biomaterial Scaffolds as Pre-metastatic Niche Mimics
Systemically Alter the Primary Tumor and Tumor
Microenvironment**

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Supporting Information

Biomaterial scaffolds as pre-metastatic niche mimics systemically alter the primary tumor and tumor microenvironment

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Table S1: Differentially regulated genes identified in Mock vs. Scaffold primary tumor cells.

List of 892 differentially regulated genes from Scaffold PT tdTomato+ cells compared to Mock PT tdTomato+ cells determined using cufflinks methodology ($p < 0.01$).

Gene Name	RefSeq ID	Location	Strand	Mock - Avg RPKM	PLG - Avg RPKM	Log2 Fold Change	Test Statistic	p-value
-	CUFF.12142.1	chr2:89156871-89157196	-	4.65322	32.7797	2.8165	3.66192	0.00005
-	CUFF.6661.1	chr14:106207810-106209401	-	1.52404	10.6096	2.7994	6.74468	0.00005
RMRP	NR_003051	chr9:35657748-35658015	-	8.20355	25.2483	1.62186	3.36781	0.00005
MIR3648	NR_037421	chr21:9825438-9826569	-	7.64999	17.8137	1.21946	4.52809	0.00005
SNORD60	NR_002736	chr16:2204819-2205350	-	35.9236	68.2684	0.926286	2.72564	0.00005
MTRNR2L9	NM_001190706	chr6:62284008-62284534	+	10.1269	19.1386	0.918289	2.98215	0.00005
-	CUFF.6626.1	chr14:105185950-105188873	-	1.67449	3.12944	0.902183	3.44124	0.00005
CTU1	NM_145232	chr19:51594108-51611657	-	9.88843	18.0019	0.864339	2.85693	0.00005
PDGFB	NM_002608	chr22:39619685-39640957	-	1.78409	3.22968	0.856204	2.76512	0.00005
NME3	NM_002513	chr16:1820321-1821710	-	39.9614	69.6245	0.800988	3.40697	0.00005
RPS29	NM_001032	chr14:50043390-50053134	-	2984.28	5176.48	0.794591	3.3379	0.00005
C4orf48	NM_001141936	chr4:2043720-2045697	+	44.2353	75.9297	0.779468	2.91308	0.00005
COMTD1	NM_144589	chr10:76993729-76995770	-	6.67553	11.3009	0.759478	2.38771	0.00005
BBC3	NM_014417	chr19:47724079-47736109	-	4.23183	7.1496	0.75658	2.6278	0.00005
SYT12	NM_001177880	chr11:66790190-66818334	+	1.16197	1.9419	0.740901	2.48019	0.00005
TCEB2	NM_207013	chr16:2821415-2827306	-	155.11	257.513	0.73136	2.23299	0.00005
CKB	NM_001823	chr14:103985995-103989196	-	53.7748	88.2093	0.714001	2.63505	0.00005
PPP1R35	NM_145030	chr7:100032912-100034152	-	28.3265	45.8475	0.694689	2.93437	0.00005
KISS1	NM_002256	chr1:204159469-204165845	-	10.5137	16.9374	0.687934	2.47536	0.00005
LINC00116	NR_027063	chr2:110969106-110980517	-	4.16922	6.66732	0.67733	2.44165	0.00005
WFDC3	NM_080614	chr20:44402847-44420547	-	19.462	31.1215	0.67725	2.30637	0.00005
C9orf142	NM_183241	chr9:139886788-139888428	+	23.277	36.8417	0.662433	2.69535	0.00005
UBL5	NM_024292	chr19:9938556-9940797	+	261.536	412.894	0.65876	2.91223	0.00005
APOC1	NM_001645	chr19:45417921-45422606	+	22.7565	35.8684	0.656436	2.36229	0.00005
C19orf24	NM_017914	chr19:1275520-1279243	+	20.7078	32.6141	0.655322	2.6307	0.00005
-	CUFF.16900.1	chr5:14509534-14510312	-	25.3798	39.9272	0.653694	2.65924	0.00005
JOSD2	NM_001270639	chr19:51009254-51014612	-	15.0503	23.6585	0.652559	2.48425	0.00005
CRIP2	NR_073085	chr14:105939275-105946507	+	15.3743	24.1595	0.652075	2.62504	0.00005
SCAND1	NM_016558	chr20:34541539-34543281	-	63.884	100.327	0.65119	2.85236	0.00005
TPGS1	NM_033513	chr19:507497-519654	+	12.0848	18.9686	0.650422	2.49855	0.00005
TMEM258	NR_030342	chr11:61556602-61560085	-	308.929	481.424	0.640034	2.63985	0.00005
C14orf80	NM_001134875	chr14:105956192-105967225	+	7.67849	11.8933	0.631259	2.41714	0.00005
TSPO	NM_001256530	chr22:43547520-43559248	+	89.8418	138.898	0.628565	2.73776	0.00005
PRKCDBP	NM_145040	chr11:6340176-6341740	-	60.2487	93.1365	0.628415	2.86029	0.00005
HAGHL	NM_032304	chr16:776936-779715	+	8.99639	13.9011	0.627784	2.42103	0.00005
RPS19	NM_001022	chr19:42363988-42375484	+	1164.24	1797.09	0.626268	2.45674	0.00005
ZNF579	NM_152600	chr19:56088728-56092937	-	8.59243	13.2536	0.625241	2.59102	0.00005
RPSAP58	NR_003662	chr19:23945816-24010919	+	31.9928	49.2339	0.621905	2.68532	0.00005
MST1	NM_020998	chr3:49721380-49726196	-	3.39213	5.21271	0.619845	2.27015	0.00005
RPS21	NM_001024	chr20:60962121-60963576	+	2830.58	4330.09	0.613299	2.54784	0.00005
COX7C	NM_001867	chr5:85913777-85916583	+	777.959	1189.87	0.613033	2.69051	0.00005

ALKBH7	NM_032306	chr19:6372444-6375261	+	18.7956	28.6687	0.609078	2.47182	0.00005
MRPL41	NM_032477	chr9:140446309-140447007	+	55.3858	84.4581	0.60872	2.5477	0.00005
NDUFB2	NM_004546	chr7:140396481-140406446	+	100.709	153.307	0.606241	2.5034	0.00005
PGF	NM_00120701_2	chr14:75408533-75422467	-	21.6818	32.949	0.603753	2.27498	0.00005
IL11	NM_000641	chr19:55875750-55881831	-	7.76951	11.7945	0.602219	2.47731	0.00005
MT1X	NM_005952	chr16:56716382-56718108	+	454.098	685.21	0.593543	2.59732	0.00005
IER5L	NM_203434	chr9:131937831-131940540	-	17.4985	26.3356	0.589785	2.61196	0.00005
MYEOV2	NM_00116342_4	chr2:241065980-241075764	-	85.8687	129.195	0.589347	2.39908	0.00005
VGf	NM_003378	chr7:100805790-100813235	-	8.16845	12.2565	0.585417	2.41575	0.00005
RABAC1	NM_006423	chr19:42460833-42463528	-	65.6099	98.1314	0.580801	2.46091	0.00005
RPS15	NM_001018	chr19:1438363-1440492	+	896.858	1338.3	0.577446	2.52793	0.00005
DDIT4	NM_019058	chr10:74033677-74035797	+	153.624	228.105	0.570294	2.50728	0.00005
RPL37A	NM_000998	chr2:217363520-217366188	+	2917.61	4330.88	0.569873	2.35512	0.00005
RPL34	NM_033625	chr4:109541722-109551639	+	536.63	787.339	0.553057	2.41334	0.00005
DUSP1	NM_004417	chr5:172195072-172198264	-	25.8878	37.9054	0.550131	2.38906	0.00005
PLEKHO1	NM_016274	chr1:150121870-150131825	+	8.96047	13.1062	0.548605	2.21169	0.00005
JUNB	NM_002229	chr19:12902310-12904125	+	63.0632	91.3801	0.535082	2.50362	0.00005
SPHK1	NM_182965	chr17:74380690-74383941	+	31.3116	45.2648	0.531693	2.30885	0.00005
CEBPB	NM_005194	chr20:48807120-48809227	+	51.6627	74.584	0.529745	2.50035	0.00005
IER2	NM_004907	chr19:13261277-13265720	+	130.388	187.903	0.527178	2.40185	0.00005
HEY1	NM_00104070_8	chr8:80676245-80680098	-	12.0674	17.3862	0.526821	2.15744	0.00005
BHLHE40	NM_003670	chr3:5021097-5026865	+	83.4528	119.427	0.517099	2.26443	0.00005
SNHG5	NR_003038	chr6:86386725-86388451	-	572.173	817.309	0.514431	2.29951	0.00005
LSM7	NM_016199	chr19:2321520-2328614	-	89.9091	128.302	0.513001	2.21521	0.00005
NAT14	NM_020378	chr19:55996068-55998937	+	30.1155	42.7373	0.504987	2.17891	0.00005
TLR4	NM_003266	chr9:120466453-120479769	+	8.05052	5.59384	-0.525243	-2.22998	0.00005
TMTC2	NM_152588	chr12:83080304-83528674	+	5.03072	3.45135	-0.543602	-2.18485	0.00005
ZC3H12C	NM_033390	chr11:109959290-110042841	+	5.83281	3.98851	-0.548341	-2.30888	0.00005
ITGA2	NM_002203	chr5:52285156-52390609	+	51.756	34.739	-0.575168	-2.55347	0.00005
ZNF367	NM_153695	chr9:99148225-99180669	-	6.7212	4.45518	-0.593234	-2.37517	0.00005
RGPD3	NM_00114401_3	chr2:107021136-107084801	-	6.87198	4.52622	-0.60242	-2.5259	0.00005
IFIT2	NM_001547	chr10:91061706-91069033	+	36.281	23.6424	-0.617835	-2.80101	0.00005
REL	NM_002908	chr2:61108630-61155497	+	1.37174	0.856965	-0.678699	-2.30947	0.00005
SAMD9	NM_00119330_7	chr7:92728826-92747336	-	8.97339	5.60151	-0.679838	-3.01954	0.00005
GCNT1	NM_00109763_6	chr9:79056582-79122332	+	3.21666	1.97025	-0.707181	-2.75397	0.00005
PPIAL4B	NM_00114388_3	chr1:149553003-149553787	+	14.6365	8.42766	-0.796371	-2.74045	0.00005
TBC1D8B	NM_017752	chrX:106045919-106119377	+	1.57993	0.861222	-0.875404	-2.8911	0.00005
LINC00506	NR_104153	chr3:87138430-87206219	+	1.43493	0.781068	-0.877456	-2.38672	0.00005
RGPD1, RGPD2	NM_00102445_7_1	chr2:87140935-87241556	+	2.94724	1.51449	-0.960527	-3.44689	0.00005
CDKL5	NM_00103734_3	chrX:18443725-18671749	+	0.641384	0.326452	-0.974316	-2.26738	0.00005
-	CUFF.13943.1	chr21:44258959-44261464	+	1.41943	0.655065	-1.1156	-2.82859	0.00005
-	CUFF.5694.1	chr13:56811582-56813858	+	1.79706	0.462321	-1.95867	-3.7191	0.00005
-	CUFF.12487.1	chr2:139009503-139011103	-	0.939486	0.10529	-3.15751	-2.80175	0.00005
-	CUFF.20955.1	chr8:122152137-122152605	+	1.61263	5.2531	1.70376	2.97619	0.0001
FAM27E3	NR_103833	chr9:67784944-67786625	-	0.472637	1.08148	1.1942	2.469	0.0001

FAM229A	NM_00116767 6	chr1:32826871- 32827844	-	3.82477	7.00342	0.872685	2.37476	0.0001
FOXSI	NM_004118	chr20:30432102- 30434459	-	6.47873	10.0724	0.636631	2.38841	0.0001
RPSAP9	NR_026890	chr9:79013515- 79014954	+	8.88254	13.2102	0.572609	2.21857	0.0001
MACROD1	NM_014067	chr11:63766030- 63933585	-	18.7417	27.5905	0.557921	2.28535	0.0001
ZNF292	NM_015021	chr6:87865269- 87975321	+	8.04138	5.69256	-0.498366	-2.19376	0.0001
RPPH1	NR_002312	chr14:20811230- 20811570	-	5.55218	12.3455	1.15286	2.44011	0.00015
NOG	NM_005450	chr17:54671060- 54672951	+	2.1359	3.70825	0.795898	2.47149	0.00015
PRR24	NM_178511	chr19:47777659- 47778980	+	8.41242	13.4656	0.678683	2.21556	0.00015
SDF2L1	NM_022044	chr22:21996542- 21998588	+	12.0467	18.5373	0.621798	2.2359	0.00015
GAMT	NM_138924	chr19:1397025- 1401569	-	18.0975	26.8598	0.569661	2.26386	0.00015
C16orf91	NM_00127205 1	chr16:1469745- 1470801	-	13.496	19.768	0.550634	2.11001	0.00015
TRAPPC5	NM_00104246 1	chr19:7745707- 7747748	+	43.5747	63.4662	0.542498	2.2236	0.00015
MINOS1,MINO S1-NBL1,NBL1	NM_00127816 6	chr1:19923471- 19984949	+	20.0239	29.0096	0.534805	2.23552	0.00015
LGALS1	NM_002305	chr22:38071613- 38075809	+	1284.5	1857.47	0.532126	2.18961	0.00015
ATAD3B	NM_031921	chr1:1407164- 1431582	+	7.95246	11.4547	0.526466	2.17348	0.00015
PPP1R37	NM_019121	chr19:45595065- 45650543	+	8.86064	12.5778	0.505395	2.23636	0.00015
H1FX	NM_006026	chr3:129033614- 129035120	-	86.4479	121.049	0.485692	2.22628	0.00015
ERC1	NR_027948	chr12:1100404- 1605099	+	8.38569	6.00945	-0.480695	-2.11829	0.00015
ZNF808	NM_00103988 6	chr19:53030909- 53064392	+	2.37249	1.48819	-0.672845	-2.22554	0.00015
-	CUFF.9285.1	chr17:45132070- 45134122	+	2.8474	1.66288	-0.775962	-2.28931	0.00015
KREMEN2	NM_00125372 5	chr16:3014217- 3018384	+	0.975085	1.809	0.891595	2.30741	0.0002
-	CUFF.6118.1	chr14:50053304- 50054517	+	13.1446	20.9103	0.669746	2.29041	0.0002
C16orf13	NM_032366	chr16:684427-686366	-	34.568	50.7993	0.555369	2.21371	0.0002
RPL31	NM_00109857 7	chr2:101618691- 101636155	+	1439.02	2106.15	0.549514	2.21185	0.0002
IFI27L2	NM_032036	chr14:94594118- 94595957	-	70.3751	101.747	0.531848	2.1611	0.0002
LAMTOR4	NM_00100839 5	chr7:99746530- 99751833	+	57.2308	81.3293	0.506982	2.09894	0.0002
CCDC85B	NM_006848	chr11:65657875- 65659106	+	121.411	168.798	0.475401	2.14276	0.0002
C5orf42	NM_023073	chr5:37079854- 37249530	-	2.055	1.41172	-0.541687	-2.15388	0.0002
KLHL4	NM_019117	chrX:86772684- 86925050	+	9.4595	6.43382	-0.556088	-2.03647	0.0002
IL7R	NM_002185	chr5:35856766- 35879705	+	4.10428	2.73483	-0.58568	-2.31605	0.0002
TMEM238	NM_00119076 4	chr19:55890612- 55895627	-	1.6521	4.46323	1.43378	2.48187	0.00025
TSEN54	NM_207346	chr17:73512609- 73520820	+	9.16672	13.6948	0.579145	2.13589	0.00025
SERTAD1	NM_013376	chr19:40928407- 40931932	-	12.8533	18.5801	0.531623	2.13434	0.00025
ID1	NM_002165	chr20:30193086- 30194317	+	33.6204	48.5177	0.529176	2.25274	0.00025
SNRPD2	NM_004597	chr19:46190712- 46195443	-	306.229	437.836	0.51578	2.10382	0.00025
RPS9	NM_001013	chr19:54704710- 54711515	+	977.866	1393.82	0.511332	2.13513	0.00025
NENF	NM_013349	chr1:212606229- 212619721	+	24.0258	33.8423	0.49424	2.03398	0.00025
CLCF1,POLD4	NM_00116621 2	chr11:67118236- 67141648	-	46.2786	64.9162	0.488236	2.09834	0.00025
GSTO1	NM_00119100 2	chr10:106013952- 106027222	+	121.806	169.122	0.473472	2.11309	0.00025
C19orf10	NM_019107	chr19:4657557- 4670415	-	69.3385	95.5304	0.462304	2.03633	0.00025
FAT4	NM_00129130 3	chr4:126237567- 126414087	+	0.967129	0.662547	-0.545687	-2.10938	0.00025
MAN1A2	NM_006699	chr1:117907681- 118071446	+	8.3911	5.55741	-0.594447	-2.16395	0.00025
FAM95C	NR_047651	chr9:38540564- 38545369	-	0.840808	1.349	0.682045	2.03445	0.0003
TFF3	NM_003226	chr21:43731777- 43735712	-	10.1882	15.7872	0.631858	2.11115	0.0003
ECH1	NM_00117802 9	chr16:2289873- 2301602	-	22.5858	33.8467	0.583599	2.28251	0.0003

RASSF7	NM_00114399 4	chr11:560971-564025	+	6.38124	9.3164	0.545934	2.07003	0.0003
SEC61B	NM_006808	chr9:101984570- 101992901	+	86.2935	124.593	0.5299	2.11652	0.0003
LIME1	NM_017806	chr20:62367978- 62370460	+	12.528	18.0296	0.525216	2.12241	0.0003
QTRT1	NM_031209	chr19:10812112- 10824043	+	37.915	53.3541	0.49283	2.14113	0.0003
RPS19BP1	NM_194326	chr22:39925098- 39928860	-	30.5757	42.9092	0.488904	2.09732	0.0003
SEC61G	NM_00101245 6	chr7:54819940- 54826939	-	246.523	332.775	0.432823	1.93976	0.0003
SLC22A15	NM_018420	chr1:116519118- 116612847	+	1.08015	0.65397	-0.723929	-2.09727	0.0003
NSFP1	NR_033799	chr17:44450179- 44500463	+	10.4496	6.26314	-0.738488	-2.22531	0.0003
-	CUFF.21274.1	chr9:31848676- 31973565	+	4.08231	1.52058	-1.42477	-2.54323	0.0003
UFSP1	NM_00101507 2	chr7:100486344- 100487339	-	2.07811	3.76369	0.856873	2.23223	0.00035
-	CUFF.12790.1	chr2:201689661- 201692056	-	0.822749	1.44385	0.811401	2.20832	0.00035
TPRA1	NM_00113605 3	chr3:127291907- 127309816	-	5.97784	8.82463	0.561912	2.10389	0.00035
GAS6	NM_000820	chr13:114523519- 114567046	-	43.516	63.0931	0.535937	2.17676	0.00035
ABL2	NM_00113600 1	chr1:179068381- 179198819	-	9.69077	7.12538	-0.443644	-1.95694	0.00035
ZNF737	NM_00115929 3	chr19:20720798- 20748626	-	0.86524	0.545004	-0.666834	-2.24827	0.00035
ASGR1	NM_00119721 6	chr17:7076751- 7082883	-	1.85067	3.17369	0.778116	2.05765	0.0004
PLEKHF1	NM_024310	chr19:30156327- 30166383	+	1.35996	2.25394	0.728886	2.16967	0.0004
CRELD2	NM_00113510 1	chr22:50312278- 50321188	+	7.40985	10.6696	0.525988	2.00896	0.0004
C1orf35	NM_024319	chr1:228288428- 228291022	-	10.9227	15.486	0.50364	1.9917	0.0004
DCXR	NM_016286	chr17:79993757- 79995573	-	24.5067	34.68	0.500925	2.01569	0.0004
ZNF581	NM_016535	chr19:56154986- 56156989	+	25.8192	35.9007	0.47557	2.02476	0.0004
GNB2	NM_005273	chr7:100271363- 100276792	+	61.2698	82.3969	0.427414	1.94279	0.0004
EREG	NM_001432	chr4:75230268- 75254477	+	38.9049	28.4024	-0.453938	-2.08619	0.0004
CPD	NM_001304	chr17:28705942- 28796675	+	24.1547	17.5281	-0.462637	-2.06438	0.0004
CHIC1	NM_00103984 0	chrX:72782984- 72906937	+	3.97126	2.81784	-0.495008	-2.04527	0.0004
-	CUFF.6289.1	chr14:66214816- 66217882	-	0.870963	0.418806	-1.05633	-2.10653	0.0004
OGFR	NM_007346	chr20:61436177- 61445352	+	47.8218	65.0109	0.443014	2.0189	0.00045
KLF7	NM_00127094 2	chr2:207938862- 208031970	-	8.42767	6.15594	-0.453155	-2.00622	0.00045
ZEB2	NR_033258	chr2:145141803- 145277958	-	5.59754	3.90685	-0.518788	-2.01418	0.00045
-	CUFF.5941.1	chr14:20947091- 20948651	-	0.837614	0.255436	-1.71332	-2.48656	0.00045
EXD3	NR_104599	chr9:140201346- 140317714	-	3.75585	5.93674	0.660533	2.09762	0.0005
METR1	NM_024042	chr16:765169-769731	+	15.9964	24.9052	0.638699	2.12175	0.0005
EFNA1	NM_004428	chr1:155100349- 155107386	+	3.27367	4.93478	0.592079	2.04817	0.0005
BRAT1	NM_152743	chr7:2577444- 2595392	-	16.7693	24.1228	0.524575	2.08984	0.0005
C19orf70	NM_205767	chr19:5678431- 5680911	-	68.0438	97.4309	0.517915	2.02053	0.0005
HSPBP1	NM_00113010 6	chr19:55773591- 55791761	-	30.8156	42.2982	0.456934	2.0048	0.0005
SNRPB	NM_003091	chr20:2442281- 2451499	-	290.83	398.328	0.453781	1.99077	0.0005
ADM	NM_001124	chr11:10326642- 10328923	+	48.4388	65.705	0.439838	1.90773	0.0005
BOP1	NM_015201	chr8:145486056- 145515120	-	36.929	49.7726	0.430598	1.95359	0.0005
EIF2AK2	NM_00113565 1	chr2:37326363- 37384295	-	13.1751	8.50605	-0.631255	-2.15165	0.0005
LAGE3	NM_006014	chrX:153704777- 153707596	-	19.0569	27.8388	0.546784	2.04265	0.00055
C9orf16	NM_024112	chr9:130922539- 130926207	+	34.4053	49.6675	0.529671	1.99565	0.00055
PLEKHH3	NM_024927	chr17:40819932- 40829048	-	4.76661	6.79689	0.511912	2.08779	0.00055
POLE4	NM_019896	chr2:75185775- 75196859	+	51.6011	72.1027	0.482653	2.02957	0.00055
PSMB10	NM_002801	chr16:67968407- 67970780	-	38.0041	52.9493	0.478457	2.03591	0.00055

FAM195B	NM_00128879 8	chr17:79780237- 79791170	-	36.5944	50.3915	0.461556	2.00341	0.00055
SEL1L	NM_00124498 4	chr14:81937891- 82000211	-	19.9689	14.7752	-0.434579	-1.9561	0.00055
B3GALT5	NM_006057	chr21:40984867- 41035125	+	0.692016	0.366493	-0.917022	-1.95107	0.00055
HEXIM2	NM_144608	chr17:43237928- 43248061	+	4.00846	6.05057	0.594022	1.92718	0.0006
SURF1	NM_003172	chr9:136218660- 136223361	-	24.5191	33.9729	0.470478	1.96419	0.0006
TMEM106B	NM_018374	chr7:12250848- 12276890	+	16.3941	12.016	-0.448214	-2.05793	0.0006
DDI2,RSC1A1	NM_006511	chr1:15943953- 15995516	+	5.91305	4.18264	-0.49949	-1.95952	0.0006
ADAM22	NM_021723	chr7:87563527- 87832369	+	2.29672	1.5953	-0.525747	-1.97241	0.0006
ANXA2P2	NR_003573	chr9:33624223- 33625532	+	9.31935	6.40482	-0.541071	-2.0062	0.0006
ELMO3	NM_024712	chr16:67233028- 67237927	+	1.34719	2.05928	0.612189	1.99011	0.00065
TSSC4	NM_005706	chr11:2421974- 2425106	+	9.69323	13.56	0.484307	1.93826	0.00065
BDP1	NM_018429	chr5:70751442- 70863674	+	5.87276	4.34437	-0.434893	-1.90767	0.00065
AIM2	NM_004833	chr1:159029679- 159046671	-	6.96846	4.76381	-0.548722	-2.02558	0.00065
HES4	NM_00114246 7	chr1:934342-935552	-	1.83503	3.49141	0.928011	2.1397	0.0007
MRPL55	NM_181462	chr1:228294380- 228297013	-	19.3152	30.7358	0.670184	2.06617	0.0007
RHBDL1	NM_00127872 0	chr16:725666-728268	+	5.45148	8.15317	0.580714	2.0797	0.0007
CTXN1	NM_206833	chr19:7989381- 7991051	-	10.924	15.4912	0.503949	1.92584	0.0007
HRAS	NM_176795	chr11:532242-535550	-	17.1538	24.0006	0.484541	1.96189	0.0007
RPLP2	NM_001004	chr11:809936-812876	+	1487.48	2033.04	0.450767	1.93281	0.0007
UBR1	NM_174916	chr15:43235098- 43398316	-	6.50271	4.75043	-0.452984	-1.96358	0.0007
ASCC3	NM_022091	chr6:100956071- 101329248	-	10.3277	7.46868	-0.467594	-1.91609	0.0007
PRELID2	NM_138492	chr5:145135907- 145214932	-	3.54271	2.48448	-0.511908	-2.01191	0.0007
ZNF354C	NM_014594	chr5:178487399- 178510736	+	3.39167	2.19085	-0.630507	-2.07504	0.0007
-	CUFF.12034.1	chr2:74345610- 74348957	+	1.24162	0.785055	-0.661363	-1.94211	0.0007
PDCD1LG2	NM_025239	chr9:5510528- 5511519	+	1.40573	0.846704	-0.731385	-2.05183	0.0007
-	CUFF.9290.1	chr17:45127749- 45130248	-	3.52833	1.93785	-0.864531	-2.04718	0.0007
-	CUFF.22569.1	chrX:55656068- 55660566	-	0.760905	0.395643	-0.943519	-2.10536	0.0007
ARL6IP4,OGF OD2	NM_00127838 0	chr12:123459354- 123467460	+	82.5813	114.543	0.472008	2.01753	0.00075
TMEM208	NM_014187	chr16:67261016- 67263182	+	44.1492	60.9322	0.464818	1.93888	0.00075
BAX	NR_027882	chr19:49458117- 49465055	+	73.1091	99.082	0.438572	1.88636	0.00075
TRIP11	NM_004239	chr14:92432373- 92507829	-	6.25918	4.59726	-0.445201	-1.90902	0.00075
SLC16A7	NM_004731	chr12:59989821- 60183635	+	2.62201	1.88492	-0.476173	-1.97108	0.00075
PCLO	NM_033026	chr7:82383321- 82792203	-	0.70674	0.494073	-0.516456	-1.9725	0.00075
TE T2	NM_00112720 8	chr4:106058460- 106200960	+	2.1784	1.51085	-0.527909	-1.90578	0.00075
-	CUFF.16718.1	chr4:177599903- 177602773	+	2.15746	1.37593	-0.648928	-1.99585	0.00075
TFF1	NM_003225	chr21:43782391- 43786644	-	7.64056	12.337	0.691243	2.01192	0.0008
LOC10028877 8	NR_028269	chr12:87984-91263	+	11.4196	16.7755	0.554847	1.93716	0.0008
RPL39	NM_001000	chrX:118920467- 118925622	-	2508.6	3441.7	0.45624	1.91817	0.0008
BBX	NM_00114256 8	chr3:107241783- 107530216	+	24.9061	18.396	-0.437107	-1.90481	0.0008
ZNF93	NM_031218	chr19:20011722- 20047085	+	2.76225	1.86826	-0.56415	-1.93877	0.0008
ATP5D	NM_00100197 5	chr19:1241749- 1244824	+	69.1483	97.1119	0.489955	1.99844	0.00085
WASH3P	NR_003659	chr15:102501016- 102516808	+	10.0265	13.9937	0.480958	1.94164	0.00085
RBX1	NM_014248	chr22:41347351- 41369019	+	45.5566	62.2766	0.45103	1.91929	0.00085
KIFC3	NM_00113010 0	chr16:57792052- 57837351	-	50.0491	67.0627	0.422166	1.92433	0.00085
LMBR1	NM_022458	chr7:156469226- 156685902	-	16.0256	11.6937	-0.454653	-1.94161	0.00085

CD14	NM_00104002 1	chr5:140011313- 140013286	-	2.54733	3.91743	0.620922	1.97126	0.0009
OSGIN1	NM_182981	chr16:83986827- 83999937	+	3.85679	5.56144	0.528059	1.95133	0.0009
GLTPD1	NM_00102988 5	chr1:1260143- 1264276	+	4.68524	6.6626	0.50796	1.96125	0.0009
APOL6	NM_030641	chr22:36044424- 36064456	+	2.61712	1.90972	-0.454619	-1.86086	0.0009
LIFR	NM_002310	chr5:38475065- 38595507	-	3.55798	2.57553	-0.466189	-1.92983	0.0009
SEMA3D	NM_152754	chr7:84624872- 84783000	-	0.564245	0.348915	-0.693446	-2.00736	0.0009
TSPAN4	NM_00102523 7	chr11:842824-867116	+	12.0717	16.9741	0.491709	1.94062	0.00095
FAM96B	NM_016062	chr16:66965958- 66968326	-	116.899	156.751	0.423206	1.8653	0.00095
LOC643387	NR_026923	chr2:239140327- 239142985	+	0.328545	0.689003	1.06842	2.11412	0.001
-	CUFF.9083.1	chr17:38439446- 38440453	-	1.08194	2.0174	0.898879	2.03742	0.001
YPEL4	NM_145008	chr11:57412560- 57417417	-	0.620297	1.07395	0.791891	1.86603	0.001
NEU4	NM_00116760 2	chr2:242750160- 242758739	+	0.954205	1.64209	0.783158	1.93046	0.001
-	CUFF.10452.1	chr19:13948019- 13953002	+	0.587309	0.932196	0.666512	1.98607	0.001
MFSD3	NM_138431	chr8:145734461- 145736589	+	13.1441	18.4273	0.487425	1.92128	0.001
CDC34	NM_004359	chr19:531733-542087	+	24.6463	33.5358	0.444334	1.9174	0.001
OAZ1	NM_004152	chr19:2269520- 2273487	+	366.683	498.624	0.443419	1.83619	0.001
GPX1	NM_000581	chr3:49394609- 49395791	-	348.311	472.45	0.439784	1.92954	0.001
C2orf27	NR_047675	chr20:3734146- 3749035	-	59.0884	78.82	0.415688	1.85216	0.001
HERC5	NM_016323	chr4:89378268- 89427319	+	16.2411	12.1527	-0.418377	-1.85179	0.001
PPFIBP1	NM_003622	chr12:27677045- 27848534	+	48.9332	36.5756	-0.419932	-1.85902	0.001
ZBTB26	NM_020924	chr9:125677898- 125693808	-	5.87894	4.10125	-0.519492	-1.94703	0.001
TMEM170B	NM_00110082 9	chr6:11538460- 11583757	+	1.36334	0.935437	-0.543432	-1.91549	0.001
RGPD1,RGPD 2	NM_00102445 7	chr2:88054818- 88285309	-	2.079	1.40476	-0.565563	-1.91812	0.001
-	CUFF.12143.1	chr2:89156872- 89157193	+	4.57763	24.6343	2.42799	2.45694	0.00105
KRT10	NM_000421	chr17:38974369- 38978863	-	49.8638	103.486	1.05336	2.16203	0.00105
NUBP2	NM_00128450 1	chr16:1832924- 1839192	+	21.6032	29.972	0.472371	1.96477	0.00105
PDRG1	NM_030815	chr20:30532758- 30539883	-	15.5587	21.2478	0.449591	1.8648	0.00105
CAPN15	NM_005632	chr16:577856-604636	+	12.1982	16.6064	0.445079	1.97861	0.00105
PAG1	NM_018440	chr8:81880046- 82024303	-	6.07853	4.52114	-0.427035	-1.86825	0.00105
SLFN5	NM_144975	chr17:33570068- 33600675	+	7.74541	5.24866	-0.561392	-1.90763	0.00105
NXT1	NM_013248	chr20:23331373- 23335408	+	22.4363	31.2747	0.479164	1.9062	0.0011
PTPRG	NM_002841	chr3:61547223- 62283246	+	19.4662	13.405	-0.538206	-1.92745	0.0011
PPP2R3B	NM_013239	chrY:244668-297690	-	1.93416	2.92325	0.595868	1.86292	0.00115
ZDHHC24	NM_207340	chr11:66306735- 66313671	-	4.69864	7.07033	0.589535	1.99668	0.00115
SCRN2	NM_00114502 3	chr17:45915047- 45918699	-	16.3279	22.4363	0.458495	1.89569	0.00115
PIM3	NM_00100185 2	chr22:50354143- 50357720	+	12.4827	17.0755	0.451992	1.89479	0.00115
RPS14	NM_00102507 0	chr5:149823792- 149829319	-	1444.03	1961.39	0.441781	1.83642	0.00115
RPS28	NM_001031	chr19:8386384- 8387280	+	988.518	1322.8	0.420261	1.86361	0.00115
HSPB1	NM_001540	chr7:75922755- 75933614	+	181.289	240.086	0.405263	1.8291	0.00115
GLTSCR2	NM_015710	chr19:48248793- 48260323	+	143.361	189.651	0.403687	1.81775	0.00115
NUP155	NM_00127831 2	chr5:37286571- 37371228	-	16.044	11.0594	-0.536763	-2.01286	0.00115
-	CUFF.15637.1	chr3:166797526- 166798937	+	0.983202	0.361236	-1.44455	-2.18405	0.00115
PMM1	NM_002676	chr22:41972890- 41985871	-	9.89537	13.8056	0.480429	1.87627	0.0012
MAP3K11	NM_002419	chr11:65365226- 65381720	-	16.9224	22.6634	0.421429	1.9234	0.0012
ZNF134	NM_003435	chr19:58125596- 58136099	+	10.2879	7.30494	-0.493997	-1.89402	0.0012

PTGS2	NM_000963	chr1:186640944-186649875	-	2.12212	1.45197	-0.547495	-1.91207	0.0012
PRKAR2A	NM_004157	chr3:48784017-48885451	-	13.4317	8.45415	-0.667908	-2.06629	0.0012
LDHD	NM_153486	chr16:75145575-75150670	-	0.729988	1.25583	0.782699	1.91585	0.00125
DOHH	NM_00114516 5	chr19:3490819-3500938	-	7.90001	11.0423	0.483115	1.91927	0.00125
RRP1	NM_003683	chr21:45209418-45223983	+	13.5347	18.4044	0.443386	1.89017	0.00125
ALDH16A1	NM_00114539 6	chr19:49956473-49974305	+	14.1915	19.1851	0.434962	1.9199	0.00125
ITGAV	NM_002210	chr2:187454790-187545629	+	35.0203	26.3017	-0.413039	-1.83793	0.00125
CREB1	NM_134442	chr2:208394386-208470497	+	13.026	9.72954	-0.420946	-1.89608	0.00125
KIAA1715	NM_030650	chr2:176788614-176867018	-	11.6457	8.69816	-0.421019	-1.83454	0.00125
HEATR5A	NM_015473	chr14:31760994-31889788	-	3.86498	2.84922	-0.439895	-1.84496	0.00125
-	CUFF.21432.1	chr9:42685754-42688999	+	3.46171	2.26825	-0.609905	-1.90168	0.00125
DTYMK	NM_00116503 1	chr2:242615157-242626383	-	30.0447	44.6634	0.571983	1.84636	0.0013
FRAT1	NM_005479	chr10:99079022-99081672	+	2.1563	3.15876	0.550802	1.86534	0.0013
KRT81,KRT83	NM_002282	chr12:52679695-52715182	-	84.6982	119.28	0.493952	1.91744	0.0013
DGCR6L	NM_033257	chr22:20301761-20307628	-	11.5372	15.8468	0.457901	1.82422	0.0013
FKBP8	NM_012181	chr19:18642568-18654413	-	109.007	146.155	0.423075	1.90118	0.0013
RASSF8	NM_00116474 6	chr12:26111109-26232825	+	12.4535	9.24067	-0.430487	-1.87329	0.0013
CSNK2A3	NM_00125668 6	chr11:11373489-11374904	-	1.71561	0.973218	-0.817888	-1.94705	0.0013
-	CUFF.16920.1	chr5:20831853-20835248	-	0.569623	0.307972	-0.887207	-2.05121	0.0013
KPTN	NR_111923	chr19:47978398-47987521	-	10.1527	13.9962	0.463163	1.86318	0.00135
RPS12	NM_001016	chr6:133135708-133138703	+	3092.97	4259.16	0.461576	1.82278	0.00135
MT2A	NM_005953	chr16:56642478-56643409	+	2245.04	3064.66	0.448987	1.86011	0.00135
IFIT3	NM_00103168 3	chr10:91087576-91100725	+	48.7126	36.3632	-0.421816	-1.90747	0.00135
ARID2	NM_152641	chr12:46123451-46301819	+	3.40964	2.49757	-0.449094	-1.84064	0.00135
ANKS3	NM_133450	chr16:4746511-4784378	-	5.82171	8.31376	0.514058	1.86029	0.0014
DNPH1	NM_006443	chr6:43193367-43197211	-	38.7833	53.1861	0.455613	1.82134	0.0014
TIMM13	NM_012458	chr19:2425622-2427914	-	26.2979	35.2788	0.423854	1.84312	0.0014
ARHGEF6	NM_004840	chrX:135747712-135863503	-	1.02817	0.690657	-0.574043	-1.81684	0.0014
CNTNAP3B	NM_00120138 0	chr9:43684862-43922473	+	1.21728	0.719226	-0.75915	-1.88489	0.0014
SLC39A4	NM_130849	chr8:145637798-145642279	-	20.2514	28.895	0.512803	1.88555	0.00145
D2HGDH	NM_152783	chr2:242673994-242708231	+	6.53515	9.02521	0.465739	1.8741	0.00145
RPL10	NM_006013	chrX:153625668-153630680	+	404.801	558.196	0.46356	1.83168	0.00145
TMUB1	NM_00113604 4	chr7:150778172-150780620	-	23.8529	32.2933	0.43707	1.86071	0.00145
WDR13	NM_00116642 6	chrX:48455880-48463582	+	26.2913	35.3238	0.426057	1.86352	0.00145
MRPS34	NM_023936	chr16:1821896-1823140	-	61.806	82.9225	0.424017	1.87022	0.00145
PAXIP1-AS1	NR_028090	chr7:154795143-154797413	+	2.36796	3.47366	0.552811	1.85274	0.0015
FAM73B	NM_032809	chr9:131798901-131834353	+	5.31482	7.63807	0.523187	1.87965	0.0015
-	CUFF.19562.2	chr7:55832169-55841603	+	28.477	39.9234	0.487435	1.9247	0.0015
MC1R	NM_002386	chr16:89984287-89987385	+	3.617	5.01977	0.47283	1.84244	0.0015
LINC00152	NR_024204	chr2:87754974-87821030	+	244.737	339.577	0.472505	1.82939	0.0015
RPUSD1	NM_058192	chr16:834951-838383	-	13.9555	18.9076	0.438129	1.87016	0.0015
MT1E	NM_175617	chr16:56659585-56661024	+	323.482	432.977	0.420608	1.84398	0.0015
PREPL	NM_00117160 6	chr2:44544748-44589011	-	10.7535	8.04421	-0.418788	-1.84877	0.0015
KIAA1377	NM_020802	chr11:101785507-101871796	+	1.73326	1.23501	-0.488967	-1.85856	0.0015
-	CUFF.6722.1	chr15:30763870-30766276	+	3.02731	1.88202	-0.685758	-1.90235	0.0015

LZTS2	NM_032429	chr10:102756864-102767593	+	24.9184	33.1832	0.413242	1.86479	0.00155
NSUN5	NM_148956	chr7:72716513-72722864	-	13.7806	18.3181	0.410624	1.74456	0.00155
-	CUFF.18009.1	chr6:9582920-9584869	+	0.719091	0.120337	-2.57909	-2.9985	0.00155
CBX8	NM_020649	chr17:77765962-77775222	-	3.54881	5.17507	0.544243	1.81593	0.0016
E4F1	NM_001288776	chr16:2273489-2285743	+	6.23356	9.01952	0.532995	1.93881	0.0016
SLC25A10	NM_001270888	chr17:79679266-79688046	+	9.28751	12.7437	0.45642	1.83104	0.0016
MRPL54	NM_172251	chr19:3762665-3767563	+	35.9028	48.939	0.446887	1.82068	0.0016
PPP1R16A	NM_032902	chr8:145703360-145727574	+	18.88	25.4178	0.428975	1.87552	0.0016
CCDC124	NM_138442	chr19:18043824-18054794	+	75.5504	100.46	0.411114	1.83871	0.0016
MAP9	NM_001039580	chr4:156263810-156298122	-	9.19784	6.88401	-0.418046	-1.81186	0.0016
PDP1	NM_001161781	chr8:94929083-94938296	+	9.76062	7.25763	-0.427474	-1.80989	0.0016
DYRK2	NM_006482	chr12:68042512-68059369	+	8.31403	6.11861	-0.442344	-1.86836	0.00165
MPHOSPH9	NM_022782	chr12:123636865-123717785	-	8.25852	6.01295	-0.457811	-1.83492	0.00165
SERTAD4	NM_019605	chr1:210406006-210419581	+	4.41918	2.81932	-0.64843	-1.89167	0.00165
WDR83OS	NM_016145	chr19:12778881-12780465	-	139.266	199.729	0.520201	1.82497	0.0017
WDR18	NM_024100	chr19:984328-994569	+	33.8816	45.2037	0.415938	1.82686	0.0017
MRPS26	NM_030811	chr20:3026675-3028896	+	84.7175	112.416	0.408117	1.8297	0.0017
TWF2	NM_007284	chr3:52262626-52273183	-	60.4466	79.609	0.397271	1.7817	0.0017
-	CUFF.16084.2	chr4:19731742-19939107	+	2.12659	1.00813	-1.07686	-2.0188	0.0017
NR4A1	NM_002135	chr12:52416616-52453291	+	2.03505	3.08119	0.598421	1.88593	0.00175
FIBCD1	NM_001145106	chr9:133777553-133814560	-	2.04567	2.92298	0.514868	1.81923	0.00175
NAGS	NM_153006	chr17:42082032-42086436	+	10.5415	14.2785	0.437768	1.7816	0.00175
-	CUFF.21148.1	chr8:146050701-146052057	+	0.778047	0.311904	-1.31875	-2.07589	0.00175
TMSB4X	NM_021109	chrX:12993226-12995346	+	3485.65	4854.63	0.477933	1.7866	0.0018
CPNE3	NM_003909	chr8:87526656-87573726	+	38.0002	28.8829	-0.395789	-1.80618	0.0018
YES1	NM_005433	chr18:721592-812733	-	21.9268	16.5859	-0.402732	-1.81054	0.0018
TBC1D5	NM_001134381	chr3:17198654-17784193	-	13.541	10.2381	-0.403385	-1.80529	0.0018
CDK6	NM_001145306	chr7:92234235-92465941	-	16.1769	12.1716	-0.410421	-1.85236	0.0018
CORO1A	NR_002454	chr16:30194140-30201202	+	1.39155	2.34419	0.752402	1.78516	0.00185
CCR1	NM_001295	chr3:46243200-46249832	-	1.03294	0.61888	-0.739025	-1.87088	0.00185
-	CUFF.12749.1	chr2:192106719-192108739	-	1.02672	0.438308	-1.22802	-2.10939	0.00185
TRABD	NM_025204	chr22:50624340-50638302	+	13.2383	17.8583	0.431875	1.85936	0.0019
CD320	NM_001165895	chr19:8367011-8373240	-	22.2221	29.9434	0.430243	1.82201	0.0019
MED1	NM_004774	chr17:37560506-37607527	-	16.2967	12.4078	-0.393328	-1.76676	0.0019
VGLL3	NM_016206	chr3:86987123-87040320	-	3.12893	2.32024	-0.431392	-1.76888	0.0019
PANK3	NM_024594	chr5:167975513-168006614	-	17.1032	12.277	-0.478306	-1.83496	0.0019
UBE2Q2P1	NR_003661	chr15:85070012-85114199	-	1.78478	1.09816	-0.700652	-1.80766	0.0019
SCARF2	NM_153334	chr22:20778874-20792146	-	1.07798	1.65593	0.619303	1.88732	0.00195
RAB27B	NM_004163	chr18:52495619-52562747	+	9.09787	6.88118	-0.402871	-1.75019	0.00195
DSEL	NM_032160	chr18:65173819-65183967	-	0.780477	0.536274	-0.541387	-1.78611	0.00195
FAM212A	NM_203370	chr3:49840592-49842463	+	0.871014	1.63033	0.904396	1.89679	0.002
C19orf60	NM_001100418	chr19:18699495-18703147	+	34.6434	48.3868	0.482034	1.82925	0.002
TRIB3	NM_021158	chr20:361308-378203	+	14.1983	19.2104	0.436169	1.81705	0.002
SHARPIN	NR_038270	chr8:145153536-145159140	-	26.6281	35.4548	0.413031	1.80007	0.002
SLK	NM_014720	chr10:105726988-105788968	+	23.2049	17.6779	-0.392479	-1.77162	0.002

PCYOX1	NM_016297	chr2:70485231-70508317	+	26.6496	20.2298	-0.39763	-1.79376	0.002
ITGA6	NM_000210	chr2:173292314-173371181	+	89.8967	67.8834	-0.40521	-1.7933	0.002
RAPH1	NM_203365	chr2:204298405-204400058	-	5.47634	4.12307	-0.409494	-1.76456	0.002
-	CUFF.16145.1	chr4:37867247-37872458	+	1.20926	0.822883	-0.555364	-1.80159	0.002
RPL29	NM_000992	chr3:52027644-52029958	-	1902.04	2594.09	0.447684	1.76646	0.00205
TSTA3	NM_003313	chr8:144694788-144699732	-	33.9832	45.2799	0.414049	1.8234	0.00205
UQCRCQ	NM_014402	chr5:132202319-132204536	+	41.6589	55.3562	0.410121	1.80463	0.00205
H2AFZ	NM_002106	chr4:100869244-100871512	-	201.395	264.932	0.395593	1.77082	0.00205
BCL9	NM_004326	chr1:147013271-147098020	+	2.17011	1.58156	-0.456415	-1.74737	0.00205
SNORD60	NR_002736	chr16:2204510-2205352	+	2.04618	4.58717	1.16467	1.86641	0.0021
TP53I13	NM_138349	chr17:27894477-27900175	+	14.446	19.7705	0.45268	1.81512	0.0021
DDX49	NM_019070	chr19:19030484-19039442	+	24.6219	32.4241	0.397126	1.77323	0.0021
AP2S1	NM_004069	chr19:47341419-47354203	-	187.96	247.467	0.396816	1.75693	0.0021
FAM110A	NM_031424	chr20:814340-826922	+	1.97432	2.98748	0.597575	1.74727	0.00215
DPM3	NM_153741	chr1:155112367-155113011	-	31.5096	45.0435	0.515527	1.76726	0.00215
JMJD6	NM_015167	chr17:74708914-74722881	-	10.0614	13.7744	0.453161	1.78618	0.00215
NARFL	NM_022493	chr16:779769-790997	-	6.70199	9.08545	0.438969	1.73825	0.00215
RPS5	NM_001009	chr19:58898636-58906171	+	1104.56	1485.63	0.427609	1.77617	0.00215
PHPT1	NM_00113586_1	chr9:139743268-139745495	+	33.9145	45.4584	0.422647	1.79326	0.00215
CYC1	NM_001916	chr8:145149938-145152430	+	108.969	142.814	0.390223	1.75831	0.00215
RIF1	NM_00117766_5	chr2:152266397-152333860	+	7.11065	5.38088	-0.402141	-1.77053	0.00215
MYSM1	NM_00108548_7	chr1:59120411-59165748	-	6.53279	4.91469	-0.410599	-1.76044	0.00215
ZNF148	NM_021964	chr3:124944513-125094198	-	6.90519	5.1846	-0.413446	-1.84428	0.0022
CDYL2	NM_152342	chr16:80631810-80838353	-	5.84021	4.29806	-0.442333	-1.79683	0.0022
BMS1P17	NR_073460_2	chr22:16162066-16172265	+	3.61109	2.03177	-0.8297	-1.89031	0.0022
-	CUFF.11222.1	chr19:52097817-52105035	+	1.32216	3.24818	1.29673	1.9931	0.00225
C19orf33	NM_033520	chr19:38794804-38795646	+	219.387	308.791	0.493148	1.75076	0.00225
TMEM186	NM_015421	chr16:8889037-8891505	-	9.40088	12.8074	0.446114	1.74285	0.00225
MRPL23	NM_021134	chr11:1968502-1977839	+	23.8785	32.4181	0.441087	1.77231	0.00225
IFT43	NR_045665	chr14:76452096-76550416	+	25.6473	34.4559	0.425948	1.74308	0.00225
TNFRSF12A	NM_016639	chr16:3070313-3072383	+	111.374	145.473	0.385343	1.74171	0.00225
PKD4	NM_002612	chr7:95212809-95225925	-	3.30257	2.36023	-0.484665	-1.78941	0.00225
-	CUFF.16941.1	chr5:25221159-25222623	+	0.921482	0.38195	-1.27057	-2.05413	0.00225
-	CUFF.17729.1	chr5:150548339-150549571	+	0.435144	1.00074	1.2015	1.9141	0.0023
ID3	NM_002167	chr1:23884421-23886285	-	3.72522	5.50981	0.564675	1.84584	0.0023
ZNRD1	NM_00127878_5	chr6:30029017-30032686	+	35.2262	48.0363	0.447479	1.75032	0.0023
ACAP3	NM_030649	chr1:1227764-1243464	-	4.09225	5.56532	0.443571	1.7889	0.0023
FAM193B	NM_00119094_6	chr5:176946784-176981548	-	10.7008	14.2539	0.413637	1.74037	0.0023
IGFN1	NM_00116458_6	chr1:201159952-201198080	+	0.836877	0.606039	-0.465606	-1.73477	0.0023
-	CUFF.7761.1	chr16:21884041-21885103	-	1.48615	0.708026	-1.0697	-1.95555	0.0023
SIVA1	NM_006427	chr14:105219470-105225996	+	47.2862	73.3103	0.632597	1.84988	0.00235
ZNF598	NM_178167	chr16:2047653-2059822	-	20.8464	27.4337	0.396152	1.80186	0.00235
TET1	NM_030625	chr10:70320117-70454402	+	1.11944	0.779306	-0.52252	-1.78892	0.00235
HES6	NM_018645	chr2:239146908-239148765	-	1.78394	2.80767	0.654307	1.81576	0.0024
NDUFA2	NM_00118501_2	chr5:140024948-140027370	-	45.458	70.322	0.629443	1.78239	0.0024

C16orf59	NM_025108	chr16:2510106-2514964	+	6.13181	8.46415	0.465052	1.76665	0.0024
ENO3	NM_001976	chr17:4853417-4860426	+	8.68456	11.7655	0.438037	1.74635	0.0024
PPP4C	NM_002720	chr16:30087308-30096695	+	60.8629	80.0537	0.395406	1.76626	0.0024
WNK4	NM_032387	chr17:40932649-40949475	+	0.842942	1.22213	0.535891	1.74165	0.00245
TBL3	NM_006453	chr16:2022064-2028751	+	17.3832	22.9174	0.39875	1.75172	0.00245
TNPO1	NM_153188	chr5:72112418-72210215	+	43.1299	32.7738	-0.396145	-1.76355	0.00245
KLF12	NM_007249	chr13:74260149-74708300	-	4.23965	3.20461	-0.4038	-1.70102	0.00245
-	CUFF.21660.1	chr9:70206955-70210197	-	3.33339	2.26264	-0.558983	-1.83417	0.00245
-	CUFF.18920.1	chr6:153305065-153308370	+	1.28986	0.856429	-0.590805	-1.74418	0.00245
DACH1	NM_004392	chr13:72012098-72441330	-	0.462909	0.72194	0.641152	1.74906	0.0025
ACYP1	NM_001107	chr14:75519928-75530736	-	15.8814	23.6235	0.572882	1.71963	0.0025
POLA1	NM_016937	chrX:24712017-25015102	+	6.35522	4.80865	-0.402311	-1.73779	0.0025
LRP6	NM_002336	chr12:12268961-12419941	-	6.63247	5.01406	-0.403566	-1.75387	0.0025
MFNG	NM_002405	chr22:37865101-37882478	-	0.574915	1.00421	0.804649	1.78254	0.00255
SPACA6P	NR_024330	chr19:52192647-52208443	+	2.55665	4.27317	0.741051	1.7839	0.00255
EFNA3	NM_004952	chr1:155051348-155060014	+	3.27224	4.79962	0.552642	1.77682	0.00255
FAM127A	NM_00107817_1	chrX:134166333-134167575	+	60.3637	79.3307	0.394198	1.75955	0.00255
NHLRC2	NM_198514	chr10:115614391-115676952	+	6.58298	4.82246	-0.448971	-1.77593	0.00255
NOXA1	NM_006647	chr9:140317847-140328858	+	4.40704	6.33587	0.523731	1.7329	0.0026
TRPM7	NM_017672	chr15:50849352-50979012	-	6.23519	4.69776	-0.408462	-1.77937	0.0026
DEXI	NM_014015	chr16:11022748-11036257	-	15.1762	21.5845	0.508186	1.7974	0.00265
MOB2	NM_00117222_3	chr11:1490678-1522453	-	8.08388	11.0383	0.449397	1.75409	0.00265
GUSBP3	NR_027386	chr5:68935290-69006354	-	4.19802	2.83981	-0.563914	-1.77603	0.00265
RAPGEF4	NM_00128290_1	chr2:173600067-173917620	+	0.620383	0.381901	-0.699961	-1.67498	0.00265
LPP	NM_005578	chr3:187871093-188608460	+	7.06223	5.39897	-0.387441	-1.72849	0.0027
FAM173A	NM_00127128_5	chr16:771142-772590	+	15.4799	22.7873	0.557837	1.79584	0.00275
FBXW9	NM_032301	chr19:12799730-12807455	-	7.18453	9.84655	0.454724	1.75436	0.00275
SLC2A4RG	NM_020062	chr20:62371211-62375403	+	27.0701	36.201	0.419329	1.74337	0.00275
TMOD3	NM_014547	chr15:52121825-52204331	+	36.6251	28.1653	-0.378915	-1.71985	0.00275
GAS7	NM_201433	chr17:9813926-10101868	-	2.38996	1.7707	-0.432669	-1.70931	0.00275
RPS17	NM_001021_1	chr15:82821158-82824952	-	1087.75	1472.86	0.437272	1.77782	0.0028
VPS28	NM_016208	chr8:145648984-145653946	-	56.8065	76.4957	0.429323	1.69455	0.0028
AHR	NM_001621	chr7:17338276-17385775	+	45.7624	35.129	-0.381503	-1.70145	0.0028
RPGRIP1L	NM_015272	chr16:53633290-53737795	-	4.54919	3.19839	-0.508263	-1.76154	0.0028
-	CUFF.21124.1	chr8:145672757-145674153	+	1.14428	1.8598	0.7007	1.76166	0.00285
SELO	NM_031454	chr22:50639408-50656045	+	10.8656	16.4058	0.594436	1.7396	0.00285
TMEM160	NM_017854	chr19:47542510-47551882	-	31.7933	46.3705	0.544483	1.77466	0.00285
JUND	NM_005354	chr19:18390504-18392466	-	46.3501	60.8832	0.393471	1.83053	0.00285
OAS2	NM_016817	chr12:113416238-113449528	+	5.56524	4.04523	-0.46022	-1.68898	0.00285
BIRC3	NM_001165	chr11:102188181-102210135	+	4.06061	2.94614	-0.462867	-1.82231	0.00285
RPL18A	NM_000980	chr19:17970687-17974133	+	1622.65	2174.73	0.422486	1.73486	0.0029
PPAP2C	NM_003712	chr19:281040-291435	-	18.62	24.839	0.415756	1.7235	0.0029
DPP7	NM_013379	chr9:140004992-140009195	-	31.5303	41.7209	0.404032	1.74975	0.0029
NOSIP	NM_015953	chr19:50058725-50083829	-	43.2999	56.9826	0.396157	1.72434	0.0029
CD96	NM_198196	chr3:111260777-111384458	+	42.3118	32.4513	-0.382782	-1.67651	0.0029

ITPA	NM_181493	chr20:3189514-3204516	+	57.7265	78.8887	0.450583	1.72281	0.00295
NUDT16L1	NM_001193452	chr16:4743694-4745860	+	14.615	19.6615	0.427927	1.73931	0.00295
SLC25A1	NM_005984	chr22:19163088-19166376	-	39.1384	51.7272	0.402338	1.77315	0.00295
H2AFJ	NR_027716	chr12:14927270-14930936	+	10.1075	13.3228	0.398469	1.73022	0.00295
RPS17	NM_001021	chr15:83205501-83209295	-	1110.81	1461.03	0.395371	1.70252	0.00295
SCAF1	NM_021228	chr19:50145382-50161906	+	25.2085	32.9842	0.387861	1.79733	0.00295
SPEF1	NM_015417	chr20:3758151-3762102	-	0.693331	1.25936	0.861075	1.882	0.003
SPAG4	NM_003116	chr20:34203809-34208965	+	9.10438	13.2066	0.536628	1.71949	0.003
KIAA1430	NM_001292033	chr4:186080816-186125363	-	28.9362	22.2619	-0.378297	-1.73363	0.003
UBE2S	NM_014501	chr19:55912650-55919325	-	84.3382	110.436	0.388957	1.79619	0.00305
IFIT1	NM_001270930	chr10:91152303-91166244	+	21.3874	16.4375	-0.379775	-1.7223	0.00305
MTX3	NM_001167741	chr5:79272539-79287088	-	12.6582	9.69626	-0.384569	-1.71917	0.00305
PLCG2	NM_002661	chr16:81812863-81996298	+	4.65866	3.1181	-0.579247	-1.72907	0.00305
TUG1	NR_110492	chr22:31365197-31375380	+	28.825	22.2391	-0.374223	-1.69482	0.0031
CPED1	NM_001105533	chr7:120628751-120937693	+	2.87421	2.12636	-0.434778	-1.69211	0.0031
ZNF100	NM_173531	chr19:21906843-21950430	-	3.207	2.34691	-0.450463	-1.70329	0.0031
ARL5B	NM_178815	chr10:18948253-18970567	+	13.0135	9.49969	-0.454059	-1.79311	0.0031
ROMO1	NM_080748	chr20:34287193-34288902	+	181.62	267.024	0.556044	1.68278	0.00315
CHAMP1	NM_001164144	chr13:115079965-115092803	+	15.2886	11.7935	-0.374466	-1.63404	0.00315
NRIP1	NM_003489	chr21:16333556-16437168	-	2.32233	1.71472	-0.437599	-1.72627	0.00315
PPP2R4	NM_178001	chr9:131873228-131911225	+	37.3152	54.6428	0.55027	1.68498	0.0032
PBRM1	NM_018313	chr3:52579368-52719866	-	19.2949	14.8795	-0.374892	-1.68347	0.0032
PRKD3	NM_005813	chr2:37477646-37551985	-	19.9987	15.3064	-0.385769	-1.69355	0.0032
ATP11B	NM_014616	chr3:182511291-182639481	+	12.3371	9.4332	-0.387187	-1.74623	0.0032
XPR1	NM_004736	chr1:180601146-180859415	+	5.89885	4.50868	-0.387729	-1.6775	0.0032
CNTNAP3	NM_033655	chr9:39072764-39288405	-	1.56969	1.08615	-0.531257	-1.6907	0.0032
ARHGEF10L	NM_018125	chr1:17866326-18024370	+	1.20906	1.82013	0.590163	1.69314	0.00325
B4GALT7	NM_007255	chr5:177027119-177037346	+	12.9673	17.3831	0.422811	1.72898	0.00325
MEX3D	NM_001174118	chr19:1554668-1568057	-	10.2283	13.472	0.39739	1.73383	0.00325
EPB41L5	NM_001184938	chr2:120770604-120936697	+	1.19114	0.838154	-0.507054	-1.62955	0.00325
HAGH	NM_001040427	chr16:1859104-1877195	-	9.51666	12.8559	0.433905	1.68725	0.0033
PLA2G16	NM_001128203	chr11:63341944-63381941	-	50.033	65.7237	0.393534	1.68568	0.0033
CTDSPL2	NM_016396	chr15:44719550-44821497	+	13.262	10.0442	-0.400937	-1.66788	0.0033
CEP97	NM_024548	chr3:101443356-101489375	+	4.70447	3.45667	-0.44465	-1.74558	0.0033
PRTG	NM_173814	chr15:55903739-56035177	-	3.26688	2.21228	-0.562379	-1.66284	0.0033
ZNF699	NM_198535	chr19:9403668-9420433	-	1.57066	1.05678	-0.571692	-1.6924	0.0033
PTPRCAP	NM_005608	chr11:67202981-67205153	-	1.1284	2.09406	0.892018	1.81434	0.00335
MAFK	NM_002360	chr7:1570368-1582679	+	11.9996	16.489	0.458518	1.70933	0.00335
CHTF18	NM_022092	chr16:838605-848095	+	12.5122	16.7616	0.421821	1.74106	0.00335
COX8A	NM_004074	chr11:63742079-63744015	+	287.89	373.572	0.375867	1.66808	0.00335
RHOT2	NM_138769	chr16:718083-724174	+	41.0735	53.2915	0.375699	1.71276	0.00335
TRIM44	NM_017583	chr11:35684140-35832602	+	31.3276	23.0589	-0.442113	-1.73003	0.00335
PARP8	NM_001178055	chr5:49961413-50142356	+	7.27177	5.30577	-0.454743	-1.72246	0.00335
RAPGEF5	NM_012294	chr7:22157908-22396533	-	1.60021	1.1571	-0.467748	-1.72368	0.00335
UBXN7	NM_015562	chr3:196074556-196159345	-	9.78042	6.91662	-0.499829	-1.75236	0.00335

WDR31	NM_00101236 1	chr9:116076669- 116102620	-	0.80899	0.524184	-0.626049	-1.6621	0.00335
NIPAL1	NM_207330	chr4:48018791- 48042103	+	3.15384	1.96402	-0.683296	-1.86878	0.00335
PRADC1	NM_032319	chr2:73455134- 73460436	-	4.13612	5.916	0.516344	1.68673	0.0034
TRADD	NM_003789	chr16:67188089- 67193812	-	16.7301	22.2477	0.411213	1.69399	0.0034
SLC3A2	NR_037193	chr11:62623484- 62656355	+	53.3726	69.2206	0.375101	1.68091	0.0034
COPE	NM_007263	chr19:19010323- 19030199	-	100.746	130.146	0.369406	1.64141	0.0034
DSP	NM_00100884 4	chr6:7541870- 7586946	+	7.50603	5.7074	-0.395217	-1.69954	0.0034
HTR7P1	NR_002774	chr12:13153376- 13157764	+	1.61188	1.12189	-0.522818	-1.71994	0.0034
ZNF296	NM_145288	chr19:45574758- 45579688	-	1.99221	2.92459	0.553864	1.73985	0.00345
CERS6	NM_00125612 6	chr2:169312759- 169631644	+	3.34723	2.24541	-0.575992	-1.70073	0.00345
C19orf26	NM_152769	chr19:1229785- 1238194	-	1.60376	2.40929	0.587144	1.74412	0.0035
-	CUFF.10017.1	chr18:54267943- 54269280	+	0.773019	0.303318	-1.34967	-1.82592	0.0035
HINT2	NM_032593	chr9:35812957- 35815042	-	43.244	57.8045	0.418682	1.7045	0.00355
GHDC	NM_00114262 2	chr17:40341105- 40346550	-	15.4041	20.28	0.39674	1.73014	0.00355
TRMT1	NM_00113603 5	chr19:13215714- 13227600	-	35.3273	45.4685	0.364081	1.63535	0.00355
EXOC6B	NM_015189	chr2:72403065- 73053177	-	6.27179	4.74517	-0.402417	-1.65635	0.00355
PPIAL4G	NM_00112306 8	chr1:143767144- 143767881	-	11.4239	7.95018	-0.523001	-1.72503	0.00355
-	CUFF.18512.1	chr6:72092088- 72093715	-	1.00285	0.396026	-1.34044	-1.8594	0.00355
RIMKLB	NM_020734	chr12:8850476- 8935691	+	24.7541	18.9539	-0.385169	-1.69186	0.00365
FRMD4B	NM_015123	chr3:69217934- 69435455	-	3.55878	2.62074	-0.44141	-1.68932	0.00365
KITLG	NM_000899	chr12:88886570- 88974250	-	1.56993	1.11625	-0.492041	-1.70412	0.00365
-	CUFF.14176.1	chr22:25085463- 25085568	-	26409.5	12214.9	-1.11242	-1.94071	0.00365
AURKAIP1	NM_00112723 0	chr1:1309110- 1310818	-	31.9509	42.6049	0.415163	1.73182	0.0037
PLEKHJ1	NR_106847	chr19:2233155- 2236328	-	18.9744	25.1525	0.406652	1.64052	0.0037
BAZ2B	NM_00128997 5	chr2:160175286- 160527273	-	2.47241	1.8309	-0.433362	-1.70642	0.0037
LINC00630	NR_038988	chrX:102024095- 102161484	+	1.62211	1.074	-0.594872	-1.67001	0.0037
CEP112	NM_145036	chr17:63631658- 64188212	-	0.646002	0.413868	-0.642369	-1.60735	0.0037
ZNF593	NM_015871	chr1:26496388- 26497364	+	25.4808	34.7561	0.447856	1.72625	0.00375
RPL24	NM_000986	chr3:101399934- 101405563	-	1587.88	2091.64	0.397532	1.67504	0.00375
ARFGAP1	NR_104022	chr20:61904023- 61921142	+	49.347	64.3099	0.382078	1.6747	0.00375
BRWD3	NM_153252	chrX:79924987- 80065278	-	4.08536	3.09675	-0.399709	-1.69208	0.00375
GLTSCR1L	NM_015349	chr6:42749783- 42836296	+	3.66991	2.76215	-0.40995	-1.63174	0.00375
HERC6	NM_017912	chr4:89299891- 89364249	+	4.6406	3.41781	-0.44124	-1.70258	0.00375
TPM2	NM_003289	chr9:35681990- 35691141	-	39.5861	52.0324	0.394416	1.68521	0.0038
PANX1	NM_015368	chr11:93862027- 93918762	+	15.1629	11.3757	-0.414588	-1.6529	0.0038
EDEM2	NM_018217	chr20:33703160- 33735399	-	14.5868	19.7787	0.439287	1.66363	0.00385
ETHE1	NM_014297	chr19:44010870- 44045930	-	24.5888	32.8051	0.415918	1.66163	0.00385
MVD	NM_002461	chr16:88718348- 88729513	-	20.6998	27.1513	0.391403	1.68194	0.00385
NDUFS8	NM_002496	chr11:67798084- 67804114	+	107.295	138.705	0.370436	1.63299	0.00385
SLC36A4	NM_00128613 9	chr11:92877337- 92931141	-	8.18657	6.19876	-0.401278	-1.74248	0.00385
BTBD9	NM_00109927 2	chr6:38136227- 38607924	-	2.71605	2.04496	-0.409437	-1.67406	0.00385
NCOA1	NM_003743	chr2:24787166- 24993570	+	3.00319	2.25423	-0.413858	-1.67947	0.00385
RC3H2	NM_018835	chr9:125606843- 125667581	-	8.81602	5.90989	-0.576996	-1.80473	0.00385
FER1L4	NR_119376	chr20:34146507- 34196141	-	1.73471	2.3476	0.436491	1.67951	0.0039
PPP1R12C	NM_00127161 8	chr19:55602278- 55628977	-	29.3135	38.8883	0.407773	1.66993	0.0039

TOPBP1	NM_007027	chr3:133319449-133380801	-	15.3034	11.874	-0.366046	-1.64188	0.0039
USP33	NM_201626	chr1:78161674-78225564	-	20.6072	15.956	-0.369045	-1.64042	0.0039
PRICKLE2	NM_198859	chr3:64053837-64253819	-	14.7712	11.2732	-0.389888	-1.65039	0.0039
CENPC	NM_001812	chr4:68374826-68378214	+	2.12495	1.07626	-0.981404	-1.70728	0.0039
PRSS3	NM_002771	chr9:33750464-33799229	+	63.6879	83.85	0.396791	1.68115	0.00395
DVL1	NM_004421	chr1:1270658-1284492	-	23.4177	30.8303	0.396752	1.672	0.00395
CHCHD1	NM_203298	chr10:75541808-75543406	+	51.8846	67.9587	0.389353	1.66984	0.00395
GABPB2	NM_144618	chr1:151042998-151092229	+	1.39536	0.885677	-0.655784	-1.71031	0.00395
PHIP	NM_017934	chr6:79644136-79788154	-	7.0076	5.40176	-0.375492	-1.67379	0.004
MMGT1	NM_173470	chrX:135044231-135056158	-	14.9298	11.3559	-0.394757	-1.69303	0.004
ABHD16B	NM_080622	chr20:62492566-62494341	+	6.36226	8.76726	0.462586	1.7222	0.00405
ZNHIT2	NM_014205	chr11:64883875-64885170	-	11.7834	15.9994	0.441256	1.73483	0.00405
XAB2	NM_020196	chr19:7684410-7694439	-	27.3834	36.0294	0.395869	1.69913	0.00405
NFE2L3	NM_004289	chr7:26191822-26227023	+	37.125	28.8011	-0.366267	-1.65713	0.00405
ZEB1	NM_001128128	chr10:31608101-31818742	+	21.5475	16.6235	-0.374295	-1.68603	0.00405
COX14	NM_001257133	chr12:50505764-50514240	+	34.3548	49.0534	0.513842	1.70011	0.0041
FPGS	NM_001018078	chr9:130565137-130576360	+	21.0783	27.3673	0.376697	1.65102	0.0041
NCLN	NM_020170	chr19:3185875-3209573	+	25.1868	32.5553	0.370226	1.7026	0.0041
ZNF426	NM_024106	chr19:9636446-9649303	-	3.15878	2.32765	-0.440493	-1.62461	0.0041
APOA1	NM_000039	chr11:116706469-116708338	-	0.384963	1.01115	1.3932	1.84916	0.00415
CGB	NM_000737	chr19:49526126-49527632	-	0.628969	1.38467	1.13848	1.85676	0.00415
SDHAF1	NM_001042631	chr19:36486090-36487220	+	8.19114	11.263	0.459451	1.69644	0.00415
ASXL2	NM_018263	chr2:25956539-26101317	-	7.21546	5.27507	-0.451903	-1.65994	0.00415
TAF1C	NM_001243156	chr16:84211427-84220676	-	27.2831	35.2017	0.367638	1.68566	0.0042
CCNO	NM_021147	chr5:54526679-54529852	-	6.58578	9.43853	0.519208	1.71818	0.00425
FLYWCH2	NM_001142499	chr16:2933196-2949383	+	13.1503	17.6002	0.420492	1.65527	0.00425
S100A4	NM_002961	chr1:153516095-153518282	-	233.88	300.645	0.362291	1.6107	0.00425
EGFL7	NM_016215	chr9:139553308-139567130	+	9.83912	13.2563	0.430077	1.64904	0.0043
MSRB2	NM_012228	chr10:23384427-23410942	+	7.79607	10.3332	0.406469	1.62586	0.0043
TAOK1	NM_020791	chr17:27717854-27878921	+	13.5795	10.5375	-0.365901	-1.62879	0.0043
SMDT1	NM_033318	chr22:42475695-42480288	+	12.9613	17.1928	0.407587	1.65525	0.00435
PGP	NM_001042371	chr16:22611534-2264822	-	8.14718	10.7823	0.404296	1.66189	0.00435
MIF	NM_002415	chr22:24236565-24237409	+	705.504	909.787	0.366874	1.62826	0.00435
PTER	NM_001001484	chr10:16478942-16555744	+	18.9157	14.4046	-0.393052	-1.70395	0.00435
C1orf233	NM_001242659	chr1:1533388-1535476	-	1.32498	2.0217	0.609593	1.70756	0.0044
RPS27A	NR_039624	chr2:55459039-55462989	+	1141	1525.46	0.418946	1.65789	0.0044
SIX5	NM_175875	chr19:46268043-46272856	-	6.66109	8.78308	0.39897	1.6662	0.00445
ANKRD17	NM_032217	chr4:73940458-74124502	-	12.6635	9.76016	-0.375704	-1.67887	0.0045
MAL2	NM_052886	chr8:120220610-120257914	+	1.14608	0.733963	-0.642925	-1.66436	0.0045
-	CUFF.17220.1	chr5:69275089-69278915	+	2.12011	1.31782	-0.685984	-1.73891	0.0045
S100A6	NM_014624	chr1:153507076-153508717	-	2678.08	3620.13	0.434844	1.65397	0.00455
PPDPF	NM_024299	chr20:62152083-62153524	+	100.599	132.157	0.393635	1.65486	0.00455
NAT9	NM_015654	chr17:72766685-72772470	-	22.0385	28.5393	0.372927	1.61533	0.00455
ZNF431	NM_133473	chr19:21324833-21374919	+	3.1759	2.31236	-0.457798	-1.62712	0.00455
-	CUFF.15132.1	chr3:76622757-76625253	+	0.661704	0.344441	-0.941931	-1.77749	0.00455

TUBB3	NM_006086	chr16:89988417-90002505	+	60.6305	77.6491	0.356924	1.63547	0.0046
ZFYVE16	NM_001284236	chr5:79703832-79782031	+	7.65128	5.79562	-0.400738	-1.63066	0.00465
RNF208	NM_031297	chr9:140114699-140120775	-	5.18556	7.4584	0.524365	1.66818	0.0047
MAP2K2	NM_030662	chr19:4090320-4124126	-	72.46	94.1909	0.378403	1.65732	0.0047
TOR4A	NM_017723	chr9:140172280-140177093	+	13.0034	16.8734	0.375865	1.69062	0.0047
-	CUFF.3413.1	chr11:22835680-22836671	-	0.808222	0.269182	-1.58617	-1.68175	0.0047
RASL10A	NM_006477	chr22:29708922-29715355	-	0.715261	1.54053	1.10689	1.72649	0.00475
ZNF408	NM_001184751	chr11:46722317-46727466	+	5.10362	6.85575	0.425795	1.66767	0.00475
MRPL21	NM_181514	chr11:68658746-68671303	-	71.4427	92.5181	0.372949	1.62135	0.00475
NSMCE1	NM_145080	chr16:27236315-27280113	-	43.8352	56.5559	0.367587	1.58743	0.00475
CTTNBP2NL	NM_018704	chr1:112938800-113003786	+	8.47145	6.50051	-0.382056	-1.67086	0.0048
SHC2	NM_012435	chr19:416583-460996	-	0.650001	1.04174	0.680487	1.66963	0.00485
ZNF414	NM_032370	chr19:8575462-8579048	-	7.26228	9.93692	0.452377	1.66289	0.00485
POLR2L	NM_021128	chr11:839721-842529	-	48.5912	63.2906	0.381298	1.63085	0.00485
SLC52A2	NM_024531	chr8:145582217-145584948	+	34.7521	45.0907	0.37573	1.64074	0.00485
PSD3	NM_015310	chr8:18384638-18942463	-	13.7872	10.4679	-0.397357	-1.65181	0.00485
C6orf226	NM_001008739	chr6:42858003-42858554	-	11.6783	16.7407	0.519523	1.6837	0.0049
SELM	NM_080430	chr22:31500763-31503551	-	19.9616	26.7922	0.424588	1.59959	0.0049
CHCHD2	NM_016139	chr7:56169266-56174187	-	248.309	318.66	0.359883	1.61191	0.0049
NOTCH2	NM_001200001	chr1:120454176-120612317	-	16.6242	12.9367	-0.361813	-1.62692	0.0049
RRP8	NM_015324	chr11:6621144-6624880	-	5.91835	7.88555	0.414017	1.60223	0.00495
NPM3	NM_006993	chr10:103541080-103543170	-	51.7695	67.3858	0.380343	1.62841	0.00495
RNF126	NM_194460	chr19:647526-663233	-	31.0149	40.1834	0.373641	1.65733	0.00495
PRKCA	NM_002737	chr17:64298906-64806862	+	19.1619	14.9738	-0.355794	-1.60026	0.00495
CANX	NM_001746	chr5:179125564-179158639	+	249.802	190.024	-0.394601	-1.63328	0.00495
MANEA	NM_024641	chr6:96025373-96057328	+	9.45134	7.07563	-0.41766	-1.69254	0.00495
SAMHD1	NM_015474	chr20:35518950-35580246	-	13.8585	10.0271	-0.466869	-1.6759	0.00495
LOC100130238	NR_024563	chr12:132851977-132859828	+	1.51413	2.1416	0.500197	1.63511	0.005
SNRNP25	NM_024571	chr16:103829-107669	+	11.1823	14.7711	0.401561	1.57642	0.005
H2AFX	NM_002105	chr11:118964578-118966177	-	41.9827	54.2812	0.370657	1.67339	0.005
RABL6	NM_001173988	chr9:139702374-139735639	+	17.7079	22.8604	0.368457	1.61688	0.005
FRMD3	NM_174938	chr9:85857905-86153348	-	1.19358	0.813846	-0.552463	-1.49422	0.005
SLC27A5	NM_012254	chr19:59009700-59023432	-	1.3752	2.00067	0.54084	1.65838	0.00505
THOP1	NM_003249	chr19:2785506-2813599	+	21.8659	28.2069	0.36736	1.64783	0.00505
ATF7IP	NM_181352	chr12:14518566-14655869	+	15.2079	11.8083	-0.365015	-1.63149	0.00505
APOOL	NM_198450	chrX:84258898-84348323	+	3.83608	2.90068	-0.403242	-1.6274	0.00505
-	CUFF.19998.1	chr7:102272150-102273720	+	0.636244	1.21765	0.93645	1.74787	0.0051
JAG2	NM_002226	chr14:105607318-105635161	-	0.375965	0.579776	0.624897	1.62117	0.0051
AVP1	NM_021732	chr10:99437181-99447015	-	3.53872	4.9356	0.479998	1.62384	0.0051
NEO1	NM_002499	chr15:73344256-73597547	+	4.66537	3.55943	-0.390344	-1.62476	0.0051
GCSHP3	NR_033248	chr2:206981219-206985458	+	1.75484	1.00951	-0.797693	-1.6846	0.0051
HIF1A	NM_001530	chr14:62162119-62214977	+	80.0579	58.0201	-0.464491	-1.658	0.00515
-	CUFF.21919.1	chr9:115139857-115142076	-	0.948835	0.552298	-0.78071	-1.66622	0.00515
STK32C	NM_173575	chr10:134020996-134121477	-	4.4521	6.02547	0.436587	1.62172	0.0052
ERO1L	NM_014584	chr14:53106644-53162747	-	81.8293	62.8555	-0.380578	-1.63089	0.0052

SSBP4	NM_032627	chr19:18528035-18545372	+	33.3507	43.8611	0.395229	1.64957	0.00525
CLTB	NM_001834	chr5:175819456-175843570	-	31.8636	41.775	0.390732	1.59111	0.00525
ACADS	NM_000017	chr12:121163571-121177811	+	5.57815	7.48074	0.423393	1.61781	0.0053
EXOSC4	NM_019037	chr8:145133522-145135551	+	38.428	50.054	0.38133	1.59797	0.0053
FAM156A,FAM156B	NM_001099684	chrX:52925015-52937585	+	10.0953	14.019	0.473709	1.58578	0.00535
IL6ST	NR_120480	chr5:55230925-55290838	-	23.0523	17.7948	-0.373457	-1.6239	0.00535
SLC44A1	NM_080546	chr9:108006894-108200745	+	11.8696	7.83238	-0.59975	-1.6397	0.00535
-	CUFF.19439.1	chr7:34966620-34967955	+	0.615596	1.15309	0.905455	1.74314	0.0054
-	CUFF.4583.1	chr12:16056556-16057367	-	2.53897	4.12969	0.701791	1.74814	0.0054
HMGCL	NM_000191	chr1:24128367-24151949	-	7.24754	9.67961	0.417458	1.59206	0.0054
ENDOD1	NM_015036	chr11:94822974-94865815	+	7.17405	5.51754	-0.378763	-1.60629	0.0054
C9orf116	NM_001048265	chr9:138387026-138391761	-	10.6107	14.5531	0.455806	1.58614	0.00545
SPSB3	NM_080861	chr16:1826713-1832581	-	24.0073	32.3676	0.43108	1.60066	0.00545
UBXN2B	NM_001077619	chr8:59323823-59364234	+	4.28808	3.23791	-0.405266	-1.63968	0.00545
AMOTL2	NM_016201	chr3:134074187-134094259	-	14.4927	11.1461	-0.378785	-1.62964	0.0055
AKR1C1	NM_001353	chr10:4951773-5020158	+	1.61244	2.40307	0.57563	1.6099	0.00555
ZNF517	NM_213605	chr8:146024261-146036714	+	1.62687	2.37492	0.54578	1.59876	0.00555
PDLIM4	NM_003687	chr5:131593351-131609147	+	14.5013	18.8108	0.375377	1.59143	0.00555
SFN	NM_006142	chr1:27189633-27190947	+	49.9654	64.4209	0.3666	1.60655	0.00555
AIP	NM_003977	chr11:67250505-67258579	+	46.0144	58.6908	0.35105	1.56249	0.00555
CLIC4	NM_013943	chr1:25071760-25170815	+	145.442	112.705	-0.367902	-1.62633	0.00555
CEMP1	NM_001048212	chr16:2578672-2581409	-	5.34885	8.17924	0.612736	1.6425	0.0056
PRRC2C	NM_015172	chr1:171454666-171562650	+	21.6702	16.9268	-0.356404	-1.57081	0.0056
PVRL3	NM_001243288	chr3:110790531-110920283	+	31.4672	23.8539	-0.399623	-1.6112	0.0056
DEAF1	NM_021008	chr11:644225-695740	-	10.6245	14.3821	0.436874	1.60157	0.00565
RNF215	NM_001017981	chr22:30774803-30783302	-	7.91	10.4382	0.400127	1.59132	0.00565
ATHL1	NM_025092	chr11:289138-295839	+	10.1043	13.061	0.370293	1.59337	0.00565
TTC21B	NM_024753	chr2:166729803-166810348	-	3.6717	2.7799	-0.401416	-1.61657	0.00565
-	CUFF.1596.1	chr1:178448949-178450196	-	0.431193	0.925492	1.10189	1.74274	0.0057
RPP25L	NM_148178	chr9:34610482-34612110	-	23.0718	30.374	0.396706	1.59001	0.0057
SSU72	NM_014188	chr1:1477053-1510852	-	46.1252	60.6351	0.3946	1.58378	0.0057
FSTL3	NM_005860	chr19:676387-683392	+	11.9251	15.5097	0.37917	1.58701	0.0057
GTPBP3	NM_001128855	chr19:17445791-17453540	+	18.9127	24.4068	0.367928	1.62841	0.0057
CLCN3	NM_173872	chr4:170541672-170644338	+	29.8184	23.2942	-0.356236	-1.60533	0.0057
CHRDL1	NM_001143981	chrX:109916952-110039427	-	9.28913	7.22007	-0.363531	-1.56842	0.0057
SEMA3B	NR_106932	chr3:50300426-50314743	+	6.08698	8.50993	0.483421	1.42695	0.00575
ZNF282	NM_003575	chr7:148892577-148923339	+	9.07573	12.2179	0.42891	1.60987	0.00575
ZNF417	NM_152475	chr19:58417142-58427978	-	3.59517	2.70113	-0.412496	-1.61998	0.00575
-	CUFF.8837.1	chr17:18965318-18965565	-	1.74947	19.1207	3.45015	2.99341	0.00585
TELO2	NM_016111	chr16:1543352-1560460	+	11.851	16.9706	0.518035	1.63396	0.00585
MIR210HG	NR_038262	chr11:565657-568457	-	3.74175	5.02019	0.424029	1.55047	0.00585
WBSR16	NM_001281441	chr7:74441224-74489717	-	22.318	29.5777	0.406306	1.6091	0.00585
VWTR1	NM_001168278	chr3:149235020-149421060	-	93.2146	71.9739	-0.373081	-1.6186	0.00585
ZNF844	NM_001136501	chr19:12175546-12188626	+	0.706876	0.449389	-0.653493	-1.59669	0.00585
HIST1H1E	NM_005321	chr6:26156559-26157343	+	1.10959	2.00937	0.856713	1.64311	0.0059

MPLKIP	NM_138701	chr7:40172342-40174480	-	42.6226	55.7874	0.388321	1.62228	0.0059
PYCR1	NM_001282279	chr17:79890259-79895204	-	19.9654	25.6967	0.364085	1.57791	0.0059
-	CUFF.11178.1	chr19:50094451-50094714	-	6.43315	1.81951	-1.82197	-2.53222	0.0059
PWWP2B	NM_001098637	chr10:134210702-134231358	+	1.74547	2.49916	0.517826	1.68597	0.00595
NIPAL2	NM_024759	chr8:99202055-99306621	-	2.89083	1.93102	-0.582123	-1.63864	0.00595
-	CUFF.18622.1	chr6:99874843-99876708	-	1.01622	0.57843	-0.812992	-1.68011	0.00595
GMFG	NM_004877	chr19:39818999-39826726	-	37.0738	48.3872	0.384224	1.5739	0.006
ZNF507	NM_001136156	chr19:32836514-32878573	+	10.2213	7.61292	-0.425061	-1.60771	0.006
HS6ST3	NM_153456	chr13:96743093-97491816	+	0.578285	0.399803	-0.532491	-1.60788	0.006
-	CUFF.9208.1	chr17:42111088-42112002	+	1.51464	0.801371	-0.918435	-1.61236	0.006
C10orf10	NM_007021	chr10:45471709-45474330	-	20.1772	28.9268	0.519678	1.57147	0.00605
EIF1	NM_005801	chr17:39845127-39847898	+	285.514	367.561	0.364419	1.605	0.00605
ETFB	NM_001985	chr19:51848409-51869672	-	62.0427	79.3382	0.354754	1.54425	0.00605
FRS2	NM_001278351	chr12:69864129-69973571	+	6.27444	4.81829	-0.380964	-1.6246	0.00605
-	CUFF.2427.1	chr10:47942208-47943709	+	2.48754	1.21509	-1.03365	-1.83863	0.00605
SLC4A7	NM_001258379	chr3:27414164-27525911	-	26.259	20.5592	-0.353032	-1.58312	0.0061
-	CUFF.8842.1	chr17:19290942-19294413	+	0.866501	0.569728	-0.604928	-1.61704	0.0061
ZNF771	NM_001142305	chr16:30418735-30429916	+	5.05691	7.03498	0.476292	1.65134	0.00615
MTFP1	NM_016498	chr22:30821611-30825041	+	14.9266	19.6291	0.395108	1.58602	0.00615
SIRT6	NM_001193285	chr19:4174106-4182596	-	11.6595	15.2264	0.385062	1.60011	0.00615
ADAM10	NM_001110	chr15:58887403-59042177	-	22.5488	17.6804	-0.350905	-1.59689	0.00615
CLSPN	NM_022111	chr1:36186384-36235582	-	5.47335	4.1596	-0.395978	-1.57724	0.00615
CEACAM19	NM_020219	chr19:45174690-45187627	+	1.40168	2.21119	0.657661	1.55907	0.0062
ALDH2	NM_000690	chr12:112204691-112247789	+	21.8131	29.5977	0.440289	1.61843	0.0062
MVB12A	NM_138401	chr19:17530862-17540480	+	47.5376	61.5734	0.373238	1.62031	0.0062
CKAP2L	NM_152515	chr2:113493926-113522254	-	3.95492	2.9553	-0.420345	-1.59655	0.0062
FBXL15	NM_024326	chr10:104179571-104182895	+	10.0045	14.6193	0.547215	1.63978	0.00625
ST6GAL1	NM_003032	chr3:186648315-186796341	+	7.21766	5.54471	-0.380418	-1.55957	0.0063
ZNF551	NM_001270938	chr19:58193337-58202176	+	2.54862	1.84372	-0.467098	-1.58608	0.0063
DDT	NM_001355	chr22:24313554-24322019	-	93.5258	126.242	0.432753	1.56469	0.00635
MYPOP	NM_001012643	chr19:46393281-46405862	-	5.36438	7.23922	0.432423	1.62049	0.00635
ZNF787	NM_001002836	chr19:56598729-56632742	-	23.2308	30.3484	0.385578	1.58943	0.00635
HOMER3	NM_004838	chr19:19040010-19052041	-	16.9219	21.9451	0.375008	1.57091	0.00635
XPO4	NM_022459	chr13:21351468-21477015	-	6.35212	4.95025	-0.359736	-1.56428	0.00635
ACER3	NM_018367	chr11:76571917-76737980	+	18.3306	14.0018	-0.388642	-1.59347	0.00635
RPL27	NM_000988	chr17:41150446-41154971	+	2307.63	3007.21	0.382015	1.569	0.0064
NHP2	NM_001034833	chr5:177576465-177580961	-	132.8	168.785	0.345927	1.54113	0.0064
FAM46A	NM_017633	chr6:82455447-82462428	-	7.34202	5.66771	-0.37341	-1.5931	0.0064
POLL	NM_001174084	chr10:103338639-103348027	-	8.92688	11.7727	0.399219	1.58222	0.00645
STRA13	NM_001271006	chr17:79976579-79980785	-	36.6006	47.4965	0.375954	1.56454	0.0065
ASAH2	NM_001143974	chr10:51945159-52008370	-	7.64818	5.32469	-0.522418	-1.59565	0.0065
-	CUFF.19397.1	chr7:30414363-30415506	-	0.439285	0.918488	1.0641	1.64034	0.00655
FKTN	NM_001198963	chr9:108320411-108403399	+	6.88346	5.29432	-0.378691	-1.57616	0.00655
ERN1	NM_001433	chr17:62116520-62207502	-	1.7784	1.07824	-0.721902	-1.71828	0.00655
C19orf48	NM_001290149	chr19:51300950-51308110	-	42.7296	54.7765	0.358323	1.56771	0.0066

WDR35	NM_001006657	chr2:20110029-20189884	-	21.7045	17.1743	-0.337741	-1.54583	0.0066
ABLIM1	NM_001003407	chr10:116190868-11644414	-	12.3671	9.68741	-0.352326	-1.54707	0.0066
TK1	NM_003258	chr17:76170160-76183285	-	22.0531	28.4624	0.368075	1.59253	0.00665
TRIP6	NM_003302	chr7:100464950-100471076	+	44.3943	56.3368	0.343702	1.55752	0.00665
MIB1	NM_020774	chr18:19321122-19450918	+	9.81379	7.67085	-0.355424	-1.57032	0.00665
ZNF107	NM_016220	chr7:64126461-64171960	+	2.3291	1.70226	-0.45232	-1.58335	0.00665
SCART1	NR_002934	chr10:135243258-135283058	+	0.628066	0.922389	0.55446	1.62704	0.0067
AXIN1	NM_003502	chr16:337440-402676	-	6.2649	8.25211	0.397471	1.57387	0.0067
RELT	NM_032871	chr11:73087405-73108519	+	5.5923	7.31545	0.387505	1.56915	0.0067
EGLN2,MIA,RAB4B	NM_053046	chr19:41281082-41314346	+	23.9027	30.9824	0.374277	1.53212	0.00675
CD151	NM_001039490	chr11:832952-838835	+	141.048	180.3	0.35422	1.56469	0.00675
SLC30A4	NM_013309	chr15:45774680-45815002	-	0.734446	0.486248	-0.594964	-1.56302	0.00675
EEF1A2	NM_001958	chr20:62119365-62130668	-	8.58231	11.3022	0.397169	1.57707	0.0068
OPLAH	NM_017570	chr8:145105949-145115655	-	5.08365	6.61429	0.379722	1.58415	0.0068
ZNF133	NM_003434	chr20:18268927-18297640	+	6.12104	7.95603	0.378271	1.53065	0.0068
POLD1	NM_001256849	chr19:50887580-50921275	+	21.5105	27.4188	0.350122	1.59804	0.0068
SIRPB1	NM_001135844	chr20:1542083-1600868	-	3.10607	2.15164	-0.529653	-1.55427	0.0068
ENKD1	NM_032140	chr16:67696850-67700628	-	11.8057	15.8949	0.429073	1.58073	0.00685
ATOX1	NM_004045	chr5:151122383-151138210	-	97.8331	125.671	0.361258	1.54712	0.00685
C9orf129	NM_001098808	chr9:96080481-96108696	-	3.21183	2.15758	-0.573984	-1.65047	0.00685
STK19	NM_032454_9	chr6:31981518-31981961	+	8.42588	12.4459	0.562767	1.59053	0.0069
EIF6	NM_002212	chr20:33866709-33872619	-	332.076	424.61	0.354621	1.53423	0.0069
TCAP	NM_003673	chr17:37821599-37822807	+	0.852909	1.54872	0.860609	1.70029	0.00695
OPRL1	NM_001200019	chr20:62711471-62731996	+	0.376146	0.609116	0.695426	1.50682	0.00695
RAB32	NM_006834	chr6:146864828-146876086	+	17.5883	22.9544	0.384158	1.55049	0.00695
EIF5	NM_183004	chr14:103800339-103811361	+	69.1931	54.2882	-0.349989	-1.58132	0.00695
ANTXR2	NM_001145794	chr4:80822771-80994626	-	54.7419	40.6709	-0.42865	-1.57413	0.00695
FER	NM_005246	chr5:108523288-108532535	-	4.37971	3.24958	-0.430581	-1.57146	0.00695
PIGQ	NM_004204	chr16:619698-634136	+	11.6712	15.3783	0.397948	1.57685	0.007
EMG1	NM_006331	chr12:7079944-7085165	+	68.9713	88.0315	0.352023	1.56607	0.007
PROSER1	NM_025138	chr13:39584002-39612237	-	11.1488	8.69561	-0.358533	-1.54754	0.007
DGKE	NM_003647	chr17:54911460-54946036	+	0.730998	0.520356	-0.490368	-1.54212	0.007
ADD3	NM_001121	chr10:111765726-111895323	+	12.8483	10.0202	-0.358665	-1.57473	0.00705
-	CUFF.22134.1	chr9:135468446-135469373	+	2.49754	3.75133	0.586894	1.59743	0.0071
-	CUFF.10188.1	chr19:1874926-1876285	+	3.7399	5.18828	0.472255	1.5675	0.0071
ERMP1	NM_024896	chr9:5784572-5833104	-	6.18517	4.77401	-0.373614	-1.55383	0.0071
ALMS1	NM_015120	chr2:73612886-73837046	+	2.88734	2.17606	-0.408025	-1.55349	0.0071
-	CUFF.12950.1	chr2:223426288-223429397	+	0.596316	0.348572	-0.774621	-1.7013	0.0071
NUDT3,RPS10,RPS10-NUDT3	NM_001014	chr6:34254973-34393902	-	1713.7	2245.5	0.389927	1.55914	0.00715
MIB2	NM_080875	chr1:1549156-1565990	+	5.34514	6.96839	0.382598	1.54753	0.00715
AFF4	NM_014423	chr5:132211011-132299354	-	19.64	15.4828	-0.34313	-1.53483	0.00715
LFNG	NM_001040168	chr7:2552163-2568810	+	20.2205	26.008	0.363139	1.56706	0.0072
PPARA	NM_005036	chr22:46546499-46639653	+	1.0542	0.787665	-0.420499	-1.54813	0.0072
PDGFA	NM_002607	chr7:536897-559734	-	14.3712	18.8599	0.392143	1.55648	0.00725

YDJC	NM_00101796 4	chr22:21982378- 21984977	-	17.673	23.1156	0.38732	1.57841	0.00725
-	CUFF.18910.1	chr6:151712914- 151715629	+	1.74485	1.09186	-0.676322	-1.56286	0.00725
FBXL8,HSF4	NM_00104066 7	chr16:67193891- 67203848	+	22.096	28.8501	0.384788	1.59806	0.0073
ZNF358	NM_018083	chr19:7581004- 7585913	+	20.917	26.7949	0.357287	1.56353	0.0073
CDC42EP2,P OLA2	NM_006779	chr11:65029430- 65089900	+	26.7169	34.1542	0.354309	1.53689	0.0073
-	CUFF.20681.1	chr8:54424313- 54436578	-	1.81095	1.28234	-0.49797	-1.57477	0.0073
APLF	NM_173545	chr2:68694691- 68807396	+	1.4353	1.03316	-0.474284	-1.5578	0.00735
-	CUFF.13048.1	chr2:238007605- 238008904	-	2.03242	1.24327	-0.709055	-1.57376	0.00735
LTBP3	NM_00113014 4	chr11:65306030- 65325887	-	75.7832	101.829	0.426192	1.57073	0.0074
PGAP1	NM_024989	chr2:197697640- 197791693	-	2.9282	2.2572	-0.375477	-1.5556	0.0074
ZNF791	NM_153358	chr19:12721732- 12744724	+	7.8637	5.60486	-0.488529	-1.55829	0.0074
PCSK1N	NM_013271	chrX:48689502- 48694040	-	1.24749	2.22506	0.834818	1.75737	0.00745
FAM98C	NM_174905	chr19:38893765- 38899728	+	8.04238	10.7327	0.416314	1.56789	0.00745
N4BP2	NM_018177	chr4:40058455- 40159872	+	3.73266	2.89406	-0.367112	-1.5405	0.00745
PCMTD1	NM_052937	chr8:52730135- 52811746	-	8.88447	6.84793	-0.375619	-1.59302	0.00745
LOC646903	NR_036538	chr3:149689066- 149691029	+	1.25141	1.89877	0.601507	1.60742	0.0075
THAP7	NM_00100869 5	chr22:21354061- 21356404	-	9.00805	12.1537	0.432107	1.55927	0.0075
KIF22	NM_00125626 9	chr16:29802034- 29816706	+	24.4747	31.8046	0.377945	1.53479	0.0075
DENND4C	NM_017925	chr9:19230523- 19374666	+	2.82156	2.16784	-0.380232	-1.54315	0.0075
SLX1A,SLX1B, SULT1A3	NM_177552	chr16:29465822- 29476301	+	34.3146	47.0482	0.455316	1.54054	0.00755
LOC283352	NR_104172	chr12:129594235- 129597843	+	74.9975	99.6668	0.410271	1.52619	0.00755
PIDD1	NM_145886	chr11:799179-805250	-	6.46618	8.36485	0.371427	1.55992	0.00755
RB1	NM_000321	chr13:48877883- 49056026	+	15.8247	12.4454	-0.34656	-1.53156	0.00755
KLHL28	NM_017658	chr14:45393527- 45431179	-	9.37178	6.53236	-0.520719	-1.56562	0.00755
RHOC	NM_175744	chr1:113243749- 113250461	-	103.075	132.435	0.361593	1.55492	0.0076
ZNF275	NM_00108048 5	chrX:152599613- 152618384	+	1.75913	1.31704	-0.417562	-1.51751	0.00765
-	CUFF.1546.1	chr1:172901662- 172902837	+	0.611611	0.234681	-1.38191	-1.72934	0.00765
NRG4	NM_138573	chr15:76230237- 76304785	-	1.6523	1.20603	-0.454219	-1.55318	0.0077
-	CUFF.13644.1	chr20:54979950- 54981351	-	3.09296	4.31888	0.481666	1.57359	0.00775
P4HTM	NM_177938	chr3:49027341- 49044581	+	13.0485	16.7627	0.361375	1.53107	0.00775
ACTR1B	NM_005735	chr2:98272402- 98280561	-	22.453	28.6989	0.354088	1.51875	0.00775
PHF1	NM_002636	chr6:33378773- 33384230	+	20.678	26.332	0.348718	1.5369	0.00775
PSMG3	NM_00113434 0	chr7:1606970- 1609668	-	26.8227	35.1676	0.390793	1.54685	0.00785
WIBG	NM_032345	chr12:56295197- 56322333	-	12.8069	16.7347	0.385914	1.53163	0.00785
ARRDC4	NM_183376	chr15:98503933- 98517068	+	2.30371	1.71447	-0.426197	-1.52191	0.00785
KDM4B	NM_015015	chr19:4969124- 5153611	+	7.48603	9.62353	0.362365	1.5498	0.00795
RANGAP1	NM_00127865 1	chr22:41640781- 41682255	-	24.9918	31.6955	0.342822	1.53465	0.00795
C11orf96	NM_00114503 3	chr11:43964106- 43965433	+	0.820174	1.4872	0.858598	1.65427	0.008
PPP1R14B	NM_138689	chr11:64011951- 64014413	-	307.026	408.8	0.413034	1.52597	0.008
SPATC1L	NM_00114285 4	chr21:47581062- 47604373	-	9.68798	12.8824	0.411134	1.54877	0.008
ATP11C	NM_173694	chrX:138808505- 139015171	-	8.61085	6.70638	-0.360622	-1.56323	0.008
BMS1P5	NR_003611_1	chr10:48924581- 48952684	-	3.84369	2.86334	-0.42479	-1.51093	0.008
ZNF428	NM_182498	chr19:44111376- 44124014	-	23.4307	31.4588	0.425064	1.55324	0.00805
PARP14	NM_017554	chr3:122399672- 122449687	+	6.72281	5.26965	-0.351357	-1.52646	0.00805
SLC25A29	NM_00103935 5	chr14:100757448- 100772884	-	7.40794	9.68835	0.387178	1.57255	0.0081

PRR14L	NM_173566	chr22:32077334-32146120	-	2.8327	2.19203	-0.369912	-1.53949	0.0081
-	CUFF.21305.2	chr9:34664868-34666447	-	0.875443	1.68201	0.942105	1.66199	0.00815
ZNF467	NM_207336	chr7:149461325-149473407	-	2.03197	2.8972	0.511779	1.5774	0.00815
C6orf1	NM_001008703	chr6:34214157-34216885	-	37.117	47.6125	0.359259	1.4688	0.0082
MFSD10	NM_001146069	chr4:2932288-2936586	-	59.417	75.4731	0.345086	1.54836	0.0082
EGFR	NM_005228	chr7:55086510-55279381	+	33.2327	24.1341	-0.46153	-1.551	0.0082
GXYLT2	NM_001080393	chr3:72937323-73027223	+	11.4393	8.12598	-0.493385	-1.56155	0.0082
RRAD	NM_001128850	chr16:66955582-66959439	-	0.277699	0.614275	1.14536	1.54785	0.00825
CCDC28B	NM_024296	chr1:32666202-32670991	+	10.6355	14.2851	0.425622	1.52555	0.00825
HIGD2A	NM_138820	chr5:175815784-175816751	+	87.558	112.123	0.356775	1.52697	0.00825
SELK	NM_021237	chr3:53919226-53925989	-	47.2524	60.478	0.356023	1.5306	0.00825
ATRX	NM_000489	chrX:76760186-77041755	-	8.54482	6.75113	-0.339922	-1.50935	0.00825
NDOR1	NM_001144026	chr9:140100119-140113813	+	9.05067	11.5026	0.345862	1.53776	0.0083
MRPL12	NM_002949	chr17:79670400-79674556	+	63.8804	81.1002	0.344332	1.5245	0.0083
CCS	NM_005125	chr11:66360630-66373490	+	23.8141	30.7522	0.368874	1.51198	0.00835
MYOF	NM_013451	chr10:95066184-95242074	-	57.6544	45.3736	-0.345576	-1.50864	0.00835
WTIP	NM_001080436	chr19:34972880-34992085	+	1.70733	2.45411	0.52346	1.5966	0.00845
POLR2J2,UPK3BL	NM_001114403	chr7:102277195-102312176	-	22.7333	29.4377	0.372855	1.53478	0.00845
COMMD4	NM_001284379	chr15:75628337-75634268	+	37.9242	49.213	0.37592	1.53321	0.0085
SLC30A6	NM_001193513	chr2:32390910-32449439	+	15.4812	12.2555	-0.337081	-1.5188	0.0085
TRPV2	NM_016113	chr17:16318856-16340317	+	0.807305	1.16637	0.530841	1.50232	0.00855
ROGD1	NM_024589	chr16:4846963-4852951	-	3.5942	4.8635	0.436325	1.51468	0.00855
CCDC34	NM_080654	chr11:27360061-27384795	-	10.4348	13.5014	0.371701	1.5196	0.00855
ABHD8	NM_024527	chr19:17402940-17414282	-	11.9791	15.4446	0.36659	1.56654	0.0086
PTPN13	NM_080685	chr4:87515468-87736328	+	2.19193	1.69029	-0.374927	-1.49318	0.0086
SERINC3	NM_006811	chr20:43124864-43150726	-	131.68	100.837	-0.385015	-1.54523	0.0086
NR2F6	NM_005234	chr19:17342694-17357382	-	12.792	16.6892	0.383679	1.57577	0.00865
ALKBH2	NM_001145374	chr12:109525993-109531293	-	31.44	40.2183	0.355253	1.49802	0.00865
CDK2AP2	NM_005851	chr11:67273961-67276199	-	31.989	41.084	0.360998	1.54473	0.00875
LOC101929125	NR_109859	chr20:3790532-3792265	-	0.576433	1.09461	0.925187	1.60513	0.00885
POLR2E	NM_002695	chr19:1086578-1095391	-	39.4972	50.7934	0.36289	1.48747	0.00885
NSD1	NM_172349	chr5:176560080-176727214	+	4.91971	3.86938	-0.346473	-1.5146	0.00885
JMY	NM_152405	chr5:78531916-78623038	+	4.12572	3.22862	-0.353729	-1.50394	0.0089
ARL17A	CUFF.9289.4	chr17:45108952-45131949	-	3.44743	1.83625	-0.908759	-1.53735	0.0089
-	CUFF.13381.1	chr20:31442433-31446544	-	0.163854	0.525739	1.68194	1.80541	0.00895
STX17	NM_017919	chr9:102668915-102736818	+	5.51906	4.3098	-0.356801	-1.531	0.009
C9orf41	NM_152420	chr9:77595932-77643333	-	10.7438	8.25354	-0.380418	-1.55193	0.009
OXLD1	NM_001039842	chr17:79632066-79633669	-	14.8237	22.4382	0.59805	1.52247	0.00905
TAF13	NM_005645	chr1:109605117-109607094	+	12.196	17.4489	0.516731	1.55056	0.00905
XPOT	NM_007235	chr12:64798153-64842463	+	56.3977	44.8958	-0.329054	-1.49587	0.00905
ACSL4	NM_022977	chrX:108884564-108976635	-	33.9044	26.9769	-0.329752	-1.5061	0.00905
PIK3CA	NM_006218	chr3:178866159-178957599	+	6.54596	4.62587	-0.50088	-1.54246	0.00905
LOC101928796	NR_109931	chr21:47392884-47394867	+	0.909847	1.57173	0.78866	1.60873	0.0091
CACNB1	NM_199247	chr17:37329709-37353956	-	4.53322	5.94451	0.391019	1.51476	0.0091
PELI2	NM_021255	chr14:56585093-56768031	+	0.481119	0.313849	-0.616322	-1.5508	0.0091

NR1H2	NM_00125664 7	chr19:50879680- 50886285	+	36.9488	46.5149	0.332165	1.51028	0.00915
SCARB2	NM_00120425 5	chr4:77079892- 77135052	-	27.4613	21.9573	-0.322698	-1.47365	0.00915
-	CUFF.21188.1	chr9:3526348- 3532707	+	2.75969	1.99947	-0.464891	-1.52991	0.00915
-	CUFF.20559.1	chr8:27138812- 27139937	+	0.305752	0.72141	1.23846	1.64568	0.00925
BYSL	NM_004053	chr6:41888965- 41901141	+	16.5637	21.0791	0.347791	1.49534	0.00925
CASP8AP2	NM_012115	chr6:90539619- 90584155	+	5.4183	4.25808	-0.347636	-1.48563	0.00925
CSNK1G1	NM_022048	chr15:64457716- 64648442	-	5.27079	4.1337	-0.350587	-1.47982	0.00925
LOC728323	NR_024437	chr2:243030826- 243102469	+	1.66603	1.06538	-0.645045	-1.52232	0.00925
PTPN4	NM_002830	chr2:120517207- 120742689	+	1.51717	1.1444	-0.406782	-1.52821	0.0093
MRPS2	NM_016034	chr9:138392477- 138396519	+	56.5496	71.6034	0.340511	1.5106	0.00935
LRPPRC	NM_133259	chr2:44113363- 44223144	-	54.7285	42.8992	-0.351341	-1.4929	0.00935
MCTP1	NM_024717	chr5:94038449- 94620279	-	6.31231	4.83468	-0.384747	-1.50926	0.00935
BAD	NM_004322	chr11:64037300- 64052176	-	42.3527	58.0094	0.453834	1.51101	0.0094
SH2B1	NM_015503	chr16:28875029- 28885852	+	11.2308	14.707	0.389041	1.53048	0.0094
SLC25A6	NM_001636_1	chrX:1505045- 1511039	-	85.9051	108.136	0.332033	1.50641	0.0094
FBXL6, TMEM2 49	NM_012162	chr8:145576824- 145582194	-	11.9536	15.6455	0.388304	1.47414	0.00945
AGPAT2	NM_00101272 7	chr9:139567595- 139581911	-	15.3996	19.8286	0.364683	1.51467	0.00945
-	CUFF.22778.1	chrX:111007055- 111009517	+	0.678117	1.09819	0.695521	1.562	0.0095
QPCTL	NM_017659	chr19:46195741- 46207248	+	8.83183	11.4394	0.373229	1.51271	0.0095
LAMC1	NM_002293	chr1:182992595- 183114757	+	51.0289	40.3664	-0.338157	-1.49266	0.0095
ERCC4	NM_005236	chr16:14014014- 14046205	+	2.66862	1.99956	-0.416414	-1.50069	0.00955
ITGB3	NM_000212	chr17:45331201- 45396561	+	10.4305	7.55095	-0.466083	-1.49979	0.00955
RP9	NM_203288	chr7:33134410- 33149002	-	7.81443	10.2868	0.396587	1.51655	0.0096
CCDC9	NM_015603	chr19:47759731- 47777570	+	10.224	13.0484	0.351911	1.48643	0.0096
UBE2C	NM_181801	chr20:44441215- 44445596	+	142.35	179.613	0.335447	1.50243	0.0096
TMEM141	NM_032928	chr9:139685768- 139687769	+	17.4841	22.7252	0.378246	1.47216	0.00965
GPC2	NM_152742	chr7:99767229- 99774998	-	0.433838	0.719417	0.729672	1.497	0.0097
TMEM191A	NR_026815	chr22:21055402- 21059048	+	0.340391	0.918277	1.43174	1.52871	0.00975
ZNF608	NM_020747	chr5:123972610- 124082477	-	1.91741	1.44785	-0.405243	-1.49613	0.00975
RPL7L1	NM_198486	chr6:42847401- 42855504	+	79.5128	61.0476	-0.381252	-1.47302	0.0098
MEX3B	NM_032246	chr15:82334119- 82338484	-	1.12411	1.56753	0.479718	1.51065	0.00985
LEPREL2	NM_014262	chr12:6937538- 6949018	+	3.26394	4.37842	0.423797	1.48988	0.00985
USE1	NM_018467	chr19:17326155- 17330638	+	20.0128	25.9351	0.373983	1.49253	0.00985
TMEM219	NM_00108361 3	chr16:29973351- 29984373	+	39.1342	49.4932	0.338801	1.42996	0.00985
LIMCH1	NM_014988	chr4:41361624- 41702061	+	3.04708	2.35291	-0.372979	-1.50009	0.00985
-	CUFF.6288.1	chr14:66211412- 66214671	-	0.759757	0.49747	-0.610928	-1.5211	0.00985
-	CUFF.9982.1	chr18:46477086- 46478405	+	3.59312	2.49345	-0.527097	-1.52263	0.00995
-	CUFF.21566.1	chr9:68403710- 68404384	+	1.33029	0.544019	-1.29001	-1.40508	0.00995
NME1,NME1- NME2,NME2	NM_00101813 8	chr17:49230897- 49249105	+	984.506	1259.92	0.355866	1.48086	0.01
KLF16	NM_031918	chr19:1852398- 1863564	-	19.4556	24.8213	0.351394	1.50983	0.01
POLRMT	NM_005035	chr19:617223-633568	-	21.1866	26.566	0.326429	1.50076	0.01
CENPE	NM_001813	chr4:104026963- 104119566	-	3.40559	2.66731	-0.35252	-1.5141	0.01

Table S2: Gene expression validation in PT cells using RT-PCR. List of genes and

forward/reverse primer sequences used to characterize gene expression in PT populations (mock vs. scaffold), with corresponding RNAseq results gathered from Table S1.

Gene	Forward	Reverse
<i>CSNK2A3</i>	GAGCACAGAAAGCTACGACTAA	GGACCTTTGAAGTATCGGGAAG
<i>PDCD1LG2</i>	CCCTTCTGCATCATTGCTTTC	GCACTGTTCACTTCCCTCTT
<i>ITGAV</i>	GGAGTCTCGAGTCCTGATCATA	ACTGGCCCAACATCTTCTTC
<i>ZEB2</i>	CCAGGCACCTCCTCATTATTT	GCTGATGCTGTTGGCATAAAC
<i>REL</i>	TGGGCTTCTCACAACCATAG	CCTGCTCCATGTCTCTCTTAAC
<i>PDGFB</i>	GGTGGGTTAGAGATGGAGTTTG	GAACCAGAGGAAGAGGTGAATC
<i>DUSP1</i>	CCATCTGCCTTGCTTACCTTAT	GCTGAAGTTGGGAGAGATGATG
<i>ACTB</i>	TGTTACCAACTGGGACGACA	GGGGTGTGAAGGTCTCAA
<i>GAPDH</i>	AGGTCCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA

Gene	Log2 Fold Change	<i>p</i> -value	FDR-adjusted <i>p</i> -value
<i>CSNK2A3</i>	-0.817888	0.0013	0.0759382
<i>PDCD1LG2</i>	-0.731385	0.0007	0.0574069
<i>ITGAV</i>	-0.413039	0.00125	0.0751264
<i>ZEB2</i>	-0.518788	0.00045	0.0465317
<i>REL</i>	-0.678699	0.00005	0.00990952
<i>PDGFB</i>	0.856204	0.00005	0.00990952
<i>DUSP1</i>	0.550131	0.00005	0.00990952

Table S3: RT-PCR validation of gene expression in PT cells. List of genes identified using

RNAseq were used to validate gene expression in PT cells isolated from scaffold-bearing mice relative to mock surgery mice ($n = 3$ biological replicates, $n = 2$ technical replicates of each sample, $n = 6$ total).

Gene	Fold change	log2 FC	p -value	Pathway
<i>CSNK2A3</i>	0.914	-0.130	0.379	NF κ B
<i>PDCD1LG2</i>	0.940	-0.089	0.655	NF κ B
<i>ITGAV</i>	0.962	-0.056	0.718	Cell motility
<i>ZEB2</i>	1.043	0.060	0.829	Cell motility
<i>REL</i>	1.043	0.061	0.726	NF κ B
<i>PDGFB</i>	1.253	0.326	0.134	Cell motility
<i>DUSP1</i>	1.264	0.338	0.099	NF κ B

Table S4: RT-PCR validation of gene expression in MDA-MB-231 cells treated with CD45+ conditioned media. List of genes identified using RNAseq were used to validate gene

expression in MDA-MB-231 cells treated with Scaffold CD45+ media relative to Mock CD45+ media (* $p < 0.05$ according to the Student's t -test, $n = 3$ biological replicates, $n = 2$ technical replicates of each sample, $n = 6$ total).

Gene	Fold change	log2 FC	p -value		Pathway
<i>CSNK2A3</i>	0.799	-0.323	0.036	*	NF κ B
<i>PDCD1LG2</i>	0.937	-0.093	0.571		NF κ B
<i>ITGAV</i>	0.933	-0.099	0.272		Cell motility
<i>ZEB2</i>	0.860	-0.218	0.144		Cell motility
<i>REL</i>	0.904	-0.145	0.176		NF κ B
<i>PDGFB</i>	0.866	-0.207	0.023	*	Cell motility
<i>DUSP1</i>	1.244	0.315	0.65		NF κ B

Table S5: Secreted factors identified in CD45+ conditioned media. List of 161 protein matched identified as secreted proteins in both Mock and Scaffold CD45+ conditioned media ($p < 0.05$). Matched proteins highlighted in green were more abundant in Scaffold CD45+ media.

Matched proteins highlighted in red were more abundant in Mock CD45+ media.

Accession	Description	MW [kDa]	Length	# PSM Mock 1	# PSM Mock 2	# PSM Mock 3	# PSM Scaffold 1	# PSM Scaffold 2	# PSM Scaffold 3	Log2FC
P28862	Stromelysin-1 OS=Mus musculus GN=Mmp3 PE=2 SV=2 - [MMP3_MOUSE]	53.8	477	1	1	2	10	9	4	2.523562
P28654	Decorin OS=Mus musculus GN=Dcn PE=2 SV=1 - [PGS2_MOUSE]	39.8	354	2	1	1	11	8	2	2.392317
P51569	Alpha-galactosidase A OS=Mus musculus GN=Gla PE=1 SV=1 - [AGAL_MOUSE]	47.6	419	1	1	1	5	6	1	2
P41245	Matrix metalloproteinase-9 OS=Mus musculus GN=Mmp9 PE=2 SV=2 - [MMP9_MOUSE]	80.5	730	3	2	2	6	10	5	1.807355
Q61830	Macrophage mannose receptor 1 OS=Mus musculus GN=Mrc1 PE=1 SV=2 - [MRC1_MOUSE]	164.9	1456	2	1	2	4	10	4	1.847997
O35657	Sialidase-1 OS=Mus musculus GN=Neu1 PE=1 SV=1 - [NEUR1_MOUSE]	44.6	409	1	1	1	5	4	2	1.874469
P56480	ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2 - [ATPB_MOUSE]	56.3	529	1	2	1	5	6	4	1.906891
Q8BG07	Phospholipase D4 OS=Mus musculus GN=Pld4 PE=2 SV=1 - [PLD4_MOUSE]	56.1	503	1	1	4	6	8	5	1.662965
Q8C845	EF-hand domain-containing protein D2 OS=Mus musculus GN=Efh2 PE=2 SV=1 - [Q8C845_MOUSE]	26.8	240	3	1	8	9	16	11	1.584963
E9PV48	Protein I830012O16Rik OS=Mus musculus GN=I830012O16Rik PE=4 SV=1 - [E9PV48_MOUSE]	47.2	403	2	2	1	4	7	5	1.678072
P28653	Biglycan OS=Mus musculus GN=Bgn PE=2 SV=1 - [PGS1_MOUSE]	41.6	369	6	2	9	20	18	11	1.527247
Q3TCN2	Putative phospholipase B-like 2 OS=Mus musculus GN=Plbd2 PE=1 SV=2 - [PLBL2_MOUSE]	66.2	594	1	1	1	2	3	4	1.584963
Q62095	ATP-dependent RNA helicase DDX3Y OS=Mus musculus GN=Ddx3y PE=1 SV=2 - [DDX3Y_MOUSE]	73.4	658	1	1	1	3	3	3	1.584963
Q9D964	Glycine amidinotransferase, mitochondrial OS=Mus musculus GN=Gatm PE=1 SV=1 - [GATM_MOUSE]	48.3	423	1	1	1	4	3	2	1.584963
O88668	Protein CREG1 OS=Mus musculus GN=Creg1 PE=2 SV=1 - [CREG1_MOUSE]	24.4	220	1	1	1	2	4	3	1.584963
S4R116	MCG2872, isoform CRA_b OS=Mus musculus GN=Ddx5 PE=3 SV=1 - [S4R116_MOUSE]	46.0	406	1	1	1	2	4	3	1.584963
P10852	4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1 - [4F2_MOUSE]	58.3	526	1	1	4	6	6	5	1.5025
Q8VDD5	Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4 - [MYH9_MOUSE]	226.2	1960	17	6	16	36	38	30	1.415037
Q8BH61	Coagulation factor XIII A chain OS=Mus musculus GN=F13a1 PE=2 SV=3 - [F13A_MOUSE]	83.2	732	4	1	2	8	5	4	1.280108
P29351	Tyrosine-protein phosphatase non-receptor type 6 OS=Mus musculus GN=Ptpn6 PE=1 SV=2 - [PTN6_MOUSE]	67.5	595	1	2	2	5	5	4	1.485427
D3Z7N2	Elongation factor 1-delta (Fragment) OS=Mus musculus GN=Eef1d PE=1 SV=1 - [D3Z7N2_MOUSE]	14.2	129	1	1	1	2	3	3	1.415037
A8DUK4	Beta-globin OS=Mus musculus GN=Hbbt1 PE=3 SV=1 - [A8DUK4_MOUSE]	15.7	147	4	2	4	7	10	8	1.321928
Q6WVG3	BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1 - [KCD12_MOUSE]	35.9	327	4	3	2	9	7	7	1.353637
P70158	Acid sphingomyelinase-like phosphodiesterase 3a OS=Mus musculus GN=Smpdl3a PE=2 SV=2 - [ASM3A_MOUSE]	49.8	445	1	1	1	2	4	2	1.415037
H7BX22	Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=1 - [H7BX22_MOUSE]	17.9	153	2	1	1	4	4	2	1.321928
Q99P91	Transmembrane glycoprotein NMB OS=Mus musculus GN=Gpnmb PE=1 SV=2 - [GPNMB_MOUSE]	63.6	574	7	1	4	9	11	7	1.169925
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1 - [LRP1_MOUSE]	504.4	4545	17	3	6	20	28	11	1.182203
P28063	Proteasome subunit beta type-8 OS=Mus musculus GN=Psb8 PE=1 SV=2 - [PSB8_MOUSE]	30.2	276	2	1	2	5	5	2	1.263034
Q04447	Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1 - [KCRB_MOUSE]	42.7	381	2	3	3	6	11	4	1.392317
P16858	Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2 - [G3P_MOUSE]	35.8	333	14	2	12	16	21	24	1.123382
O55131	Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1 - [SEPT7_MOUSE]	50.5	436	1	1	4	4	5	5	1.222392
P26039	Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2 - [TLN1_MOUSE]	269.7	2541	4	1	7	8	9	9	1.115477

E9Q4G8	CD166 antigen OS=Mus musculus GN=Alcam PE=4 SV=1 - [E9Q4G8_MOUSE]	61.9	555	3	2	1	5	6	3	1.222392
Q9Z0J0	Epididymal secretory protein E1 OS=Mus musculus GN=Npc2 PE=1 SV=1 - [NPC2_MOUSE]	16.4	149	3	1	3	5	5	5	1.099536
Q9JII6	Alcohol dehydrogenase [NADP(+)] OS=Mus musculus GN=Akr1a1 PE=1 SV=3 - [AK1A1_MOUSE]	36.6	325	5	2	5	9	10	7	1.115477
P61027	Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1 - [RAB10_MOUSE]	22.5	200	1	1	2	2	4	3	1.169925
P12265	Beta-glucuronidase OS=Mus musculus GN=Gusb PE=2 SV=2 - [BGLR_MOUSE]	74.1	648	18	3	11	22	31	13	1.044394
O08709	Peroxisome oxidoreductin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3 - [PRDX6_MOUSE]	24.9	224	1	1	3	3	5	3	1.137504
Q922R8	Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3 - [PDIA6_MOUSE]	48.1	440	7	5	8	12	19	11	1.070389
O09159	Lysosomal alpha-mannosidase OS=Mus musculus GN=Man2b1 PE=2 SV=4 - [MA2B1_MOUSE]	114.6	1013	28	9	14	31	44	26	0.985786
E9Q2Z4	Protein Gm16494 OS=Mus musculus GN=Gm16494 PE=4 SV=1 - [E9Q2Z4_MOUSE]	9.3	87	2	1	2	2	4	4	1
O88531	Palmitoyl-protein thioesterase 1 OS=Mus musculus GN=Ppt1 PE=2 SV=2 - [PPT1_MOUSE]	34.5	306	4	2	2	6	6	4	1
Q6IRU2	Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3 - [TPM4_MOUSE]	28.5	248	2	4	3	6	9	5	1.152003
P28656	Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap111 PE=1 SV=2 - [NP1L1_MOUSE]	45.3	391	2	1	2	3	5	2	1
P82198	Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfb1 PE=2 SV=1 - [BGH3_MOUSE]	74.5	683	2	1	1	2	4	2	1
P84096	Rho-related GTP-binding protein RhoG OS=Mus musculus GN=Rhog PE=2 SV=1 - [RHOG_MOUSE]	21.3	191	1	1	2	2	3	3	1
P09405	Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2 - [NUCL_MOUSE]	76.7	707	6	4	6	10	10	11	0.954196
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein OS=Mus musculus GN=Sh3bglr PE=3 SV=1 - [SH3L1_MOUSE]	12.8	114	4	2	3	6	5	6	0.917538
O70251	Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5 - [EF1B_MOUSE]	24.7	225	4	1	2	3	6	4	0.893085
Q9D8U8	Sorting nexin-5 OS=Mus musculus GN=Snx5 PE=1 SV=1 - [SNX5_MOUSE]	46.8	404	1	1	1	2	2	2	1
P81117	Nucleobindin-2 OS=Mus musculus GN=Nucb2 PE=1 SV=2 - [NUCB2_MOUSE]	50.3	420	1	1	1	2	2	2	1
Q61035	Histidine-tRNA ligase, cytoplasmic OS=Mus musculus GN=Hars PE=2 SV=2 - [SYHC_MOUSE]	57.4	509	1	1	1	2	2	2	1
Q60963	Platelet-activating factor acetylhydrolase OS=Mus musculus GN=Pla2g7 PE=2 SV=2 - [PAFA_MOUSE]	49.2	440	15	5	5	16	20	11	0.910733
P23492	Purine nucleoside phosphorylase OS=Mus musculus GN=Pnp PE=1 SV=2 - [PNPH_MOUSE]	32.3	289	6	2	6	9	10	7	0.893085
Q07797	Galectin-3-binding protein OS=Mus musculus GN=Lgals3bp PE=1 SV=1 - [LG3BP_MOUSE]	64.4	577	15	7	12	25	25	14	0.912537
P17897	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE=1 SV=1 - [LYZ1_MOUSE]	16.8	148	19	14	10	34	22	25	0.913585
P10605	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2 - [CATB_MOUSE]	37.3	339	100	64	59	125	175	112	0.885601
P37889	Fibulin-2 OS=Mus musculus GN=Fbln2 PE=1 SV=2 - [FBLN2_MOUSE]	131.7	1221	2	1	2	2	4	3	0.847997
P29416	Beta-hexosaminidase subunit alpha OS=Mus musculus GN=Hexa PE=2 SV=2 - [HEXA_MOUSE]	60.6	528	14	8	8	15	25	15	0.874469
O08807	Peroxisome oxidoreductin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1 - [PRDX4_MOUSE]	31.0	274	6	3	5	7	10	8	0.836501
P11152	Lipoprotein lipase OS=Mus musculus GN=Lpl PE=1 SV=3 - [LPL_MOUSE]	53.1	474	21	14	17	30	39	26	0.869416
Q03265	ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1 - [ATPA_MOUSE]	59.7	553	4	2	2	4	5	5	0.807355
P20060	Beta-hexosaminidase subunit beta OS=Mus musculus GN=Hexb PE=2 SV=2 - [HEXB_MOUSE]	61.1	536	14	7	10	17	24	13	0.800691
V9GX81	Protein Mroh6 OS=Mus musculus GN=Mroh6 PE=4 SV=1 - [V9GX81_MOUSE]	78.4	722	1	1	2	2	3	2	0.807355
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1 - [EIF3B_MOUSE]	91.3	803	1	1	2	2	3	2	0.807355
P06869	Urokinase-type plasminogen activator OS=Mus musculus GN=Plau PE=1 SV=1 - [UROK_MOUSE]	48.2	433	17	13	18	26	31	23	0.736966
P08905	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE=1 SV=2 - [LYZ2_MOUSE]	16.7	148	38	26	29	56	47	44	0.660514
P27773	Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2 - [PDIA3_MOUSE]	56.6	505	36	28	35	53	52	51	0.656046

P18242	Cathepsin D OS=Mus musculus GN=Ctsd PE=1 SV=1 - [CATD_MOUSE]	44.9	410	46	24	38	56	70	41	0.628817
O70370	Cathepsin S OS=Mus musculus GN=Ctss PE=1 SV=2 - [CATS_MOUSE]	38.4	340	24	14	20	33	30	25	0.601451
O89017	Legumain OS=Mus musculus GN=Lgmn PE=1 SV=1 - [LGMN_MOUSE]	49.3	435	23	16	20	26	39	25	0.60921
P06797	Cathepsin L1 OS=Mus musculus GN=Ctsl PE=1 SV=2 - [CATL1_MOUSE]	37.5	334	37	20	29	41	45	39	0.53952
Q61233	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4 - [PLSL_MOUSE]	70.1	627	43	32	36	54	58	46	0.509365
P62806	Histone H4 OS=Mus musculus GN=Hst1h4a PE=1 SV=2 - [H4_MOUSE]	11.4	103	23	16	23	26	34	27	0.488747
P24369	Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=1 SV=2 - [PPIB_MOUSE]	23.7	216	24	13	18	22	30	23	0.447459
P63101	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1 - [1433Z_MOUSE]	27.8	245	36	23	32	31	38	31	0.136062
P16627	Heat shock 70 kDa protein 1-like OS=Mus musculus GN=Hspa11 PE=2 SV=4 - [HS71L_MOUSE]	70.6	641	17	11	15	12	18	14	0.033167
P10107	Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2 - [ANXA1_MOUSE]	38.7	346	12	8	10	10	10	10	0
P07901	Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4 - [HS90A_MOUSE]	84.7	733	46	27	40	32	47	34	0
P11499	Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3 - [HS90B_MOUSE]	83.2	724	65	44	58	49	64	48	-0.05279
P63325	40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1 - [RS10_MOUSE]	18.9	165	7	4	6	6	6	4	-0.08746
Q9ERD7	Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1 - [TBB3_MOUSE]	50.4	450	26	21	25	20	31	18	-0.0614
P07356	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2 - [ANXA2_MOUSE]	38.7	339	38	18	32	21	29	26	-0.2115
Q9DBJ1	Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3 - [PGAM1_MOUSE]	28.8	254	28	16	18	15	20	19	-0.19931
P48678	Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2 - [LMNA_MOUSE]	74.2	665	36	18	25	21	27	20	-0.21632
P45591	Cofilin-2 OS=Mus musculus GN=Cfl2 PE=1 SV=1 - [COF2_MOUSE]	18.7	166	9	5	6	5	7	5	-0.23447
P17751	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4 - [TPIS_MOUSE]	32.2	299	39	23	23	24	25	21	-0.28011
A0A087WSP7	MCG121979, isoform CRA_a OS=Mus musculus GN=Matr3 PE=4 SV=1 - [A0A087WSP7_MOUSE]	56.7	508	2	1	2	1	2	1	-0.32193
P32921	Tryptophan--tRNA ligase, cytoplasmic OS=Mus musculus GN=Wars PE=1 SV=2 - [SYWC_MOUSE]	54.3	481	2	1	2	1	2	1	-0.32193
P62754	40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1 - [RS6_MOUSE]	28.7	249	2	1	2	1	2	1	-0.32193
Q8C4P0	Uncharacterized protein KIAA1958 homolog OS=Mus musculus PE=2 SV=1 - [K1958_MOUSE]	79.1	716	2	1	1	1	1	1	-0.41504
Q3THS6	S-adenosylmethionine synthase isoform type-2 OS=Mus musculus GN=Mat2a PE=2 SV=2 - [METK2_MOUSE]	43.7	395	2	1	1	1	1	1	-0.41504
F6RJC1	Teneurin-3 (Fragment) OS=Mus musculus GN=Tenn3 PE=4 SV=1 - [F6RJC1_MOUSE]	262.6	2354	2	1	1	1	1	1	-0.41504
P97351	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3 - [RS3A_MOUSE]	29.9	264	2	1	1	1	1	1	-0.41504
O55183	Stanniocalcin-1 OS=Mus musculus GN=Stc1 PE=2 SV=1 - [STC1_MOUSE]	27.5	247	2	1	1	1	1	1	-0.41504
A2AEX7	Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=1 SV=1 - [A2AEX7_MOUSE]	23.7	210	2	1	1	1	1	1	-0.41504
D3YZA1	Chromatin target of PRMT1 protein (Fragment) OS=Mus musculus GN=Chtop PE=4 SV=4 - [D3YZA1_MOUSE]	13.4	123	2	1	1	1	1	1	-0.41504
E9PYT5	Laminin subunit beta-1 OS=Mus musculus GN=Lamb1 PE=4 SV=1 - [E9PYT5_MOUSE]	63.1	564	2	1	1	1	1	1	-0.41504
F8VPK6	Xylosyltransferase 1 OS=Mus musculus GN=Xylt1 PE=4 SV=1 - [F8VPK6_MOUSE]	107.2	953	2	1	1	1	1	1	-0.41504
E9Q3P4	Protein Cenpf OS=Mus musculus GN=Cenpf PE=4 SV=1 - [E9Q3P4_MOUSE]	342.3	2997	2	1	1	1	1	1	-0.41504
Q8VCS3	Glycosaminoglycan xylosylkinase OS=Mus musculus GN=Fam20b PE=2 SV=1 - [XYLK_MOUSE]	46.6	409	2	1	1	1	1	1	-0.41504
B1AYJ9	Obg-like ATPase 1 OS=Mus musculus GN=Ola1 PE=4 SV=1 - [B1AYJ9_MOUSE]	31.7	281	2	1	1	1	1	1	-0.41504
Q3TJ56	Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=2 SV=1 - [Q3TJ56_MOUSE]	67.7	608	2	1	1	1	1	1	-0.41504
O35841	Apoptosis inhibitor 5 OS=Mus musculus GN=Api5 PE=1 SV=2 - [API5_MOUSE]	56.7	504	2	1	1	1	1	1	-0.41504
P70677	Caspase-3 OS=Mus musculus GN=Casp3 PE=1 SV=1 - [CASP3_MOUSE]	31.5	277	2	1	1	1	1	1	-0.41504
Q9Z121	C-C motif chemokine 8 OS=Mus musculus GN=Ccl8 PE=2 SV=1 - [CCL8_MOUSE]	11.0	97	2	1	1	1	1	1	-0.41504

Q61189	Methylosome subunit pICln OS=Mus musculus GN=Clns1a PE=2 SV=1 - [IcLn_MOUSE]	26.0	236	2	1	1	1	1	1	-0.41504
O08848	60 kDa SS-A/Ro ribonucleoprotein OS=Mus musculus GN=Trove2 PE=1 SV=1 - [RO60_MOUSE]	60.1	538	2	1	1	1	1	1	-0.41504
P08207	Protein S100-A10 OS=Mus musculus GN=S100a10 PE=1 SV=2 - [S10AA_MOUSE]	11.2	97	2	1	1	1	1	1	-0.41504
A2CES4	U2 small nuclear ribonucleoprotein B' (Fragment) OS=Mus musculus GN=Snrbp2 PE=1 SV=1 - [A2CES4_MOUSE]	16.0	143	2	1	1	1	1	1	-0.41504
F7D1R5	Phospholipase A-2-activating protein (Fragment) OS=Mus musculus GN=Plaa PE=1 SV=1 - [F7D1R5_MOUSE]	23.5	214	2	1	1	1	1	1	-0.41504
F7C521	Polypyrimidine tract-binding protein 3 OS=Mus musculus GN=Ptbp3 PE=4 SV=1 - [F7C521_MOUSE]	11.0	104	2	1	1	1	1	1	-0.41504
F6R587	Copine-1 (Fragment) OS=Mus musculus GN=Cpne1 PE=4 SV=1 - [F6R587_MOUSE]	22.5	211	2	1	1	1	1	1	-0.41504
A0A0A0MQG2	Spectrin beta chain, non-erythrocytic 1 (Fragment) OS=Mus musculus GN=Sptbn1 PE=4 SV=1 - [A0A0A0MQG2_MOUSE]	244.1	2092	2	1	1	1	1	1	-0.41504
Q9DAT2	MRG/MORF4L-binding protein OS=Mus musculus GN=Mrgbp PE=2 SV=2 - [MRGBP_MOUSE]	22.4	204	2	1	1	1	1	1	-0.41504
P46061	Ran GTPase-activating protein 1 OS=Mus musculus GN=Rangap1 PE=1 SV=2 - [RAGP1_MOUSE]	63.5	589	2	1	1	1	1	1	-0.41504
Q8JZR2	Adapter molecule crk OS=Mus musculus GN=Crk PE=2 SV=1 - [Q8JZR2_MOUSE]	22.9	204	2	1	1	1	1	1	-0.41504
E9PYI8	Ubiquitin carboxyl-terminal hydrolase OS=Mus musculus GN=Usp14 PE=1 SV=1 - [E9PYI8_MOUSE]	52.3	458	2	1	1	1	1	1	-0.41504
P23198	Chromobox protein homolog 3 OS=Mus musculus GN=Cbx3 PE=1 SV=2 - [CBX3_MOUSE]	20.8	183	2	1	1	1	1	1	-0.41504
P02463	Collagen alpha-1(IV) chain OS=Mus musculus GN=Col4a1 PE=2 SV=4 - [CO4A1_MOUSE]	160.6	1669	2	1	1	1	1	1	-0.41504
A2BFF8	Cytoplasmic dynein 1 intermediate chain 2 OS=Mus musculus GN=Dync1i2 PE=1 SV=1 - [A2BFF8_MOUSE]	68.2	611	2	1	1	1	1	1	-0.41504
E9Q6R3	Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=1 - [E9Q6R3_MOUSE]	18.9	166	2	1	1	1	1	1	-0.41504
P01803	Ig heavy chain V region AMPC1 OS=Mus musculus PE=1 SV=1 - [HVM34_MOUSE]	12.7	113	2	1	1	1	1	1	-0.41504
O35988	Syndecan-4 OS=Mus musculus GN=Sdc4 PE=1 SV=1 - [SDC4_MOUSE]	21.5	198	4	2	2	2	2	2	-0.41504
Q99K51	Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3 - [PLST_MOUSE]	70.7	630	12	4	10	6	8	5	-0.45251
Q9WUM4	Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2 - [COR1C_MOUSE]	53.1	474	8	4	7	4	6	4	-0.44057
Q61508	Extracellular matrix protein 1 OS=Mus musculus GN=Ecm1 PE=1 SV=2 - [ECM1_MOUSE]	62.8	559	7	5	7	6	4	4	-0.44057
P50543	Protein S100-A11 OS=Mus musculus GN=S100a11 PE=1 SV=1 - [S10AB_MOUSE]	11.1	98	6	4	4	4	2	4	-0.48543
P16125	L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2 - [LDHB_MOUSE]	36.5	334	16	8	11	5	11	9	-0.48543
Q9CQI3	Glia maturation factor beta OS=Mus musculus GN=Gmfb PE=1 SV=3 - [GMFB_MOUSE]	16.7	142	3	1	2	1	2	1	-0.58496
Q6ZWZ4	60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=2 SV=1 - [Q6ZWZ4_MOUSE]	12.2	105	2	2	2	1	1	2	-0.58496
A0A0A6YXL3	60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=4 SV=1 - [A0A0A6YXL3_MOUSE]	9.9	87	2	2	2	2	1	1	-0.58496
Q9R1P3	Proteasome subunit beta type-2 OS=Mus musculus GN=Psb2 PE=1 SV=1 - [PSB2_MOUSE]	22.9	201	2	2	2	1	2	1	-0.58496
O08692	Myeloid bacterenecin (F1) OS=Mus musculus GN=Ngp PE=2 SV=1 - [O08692_MOUSE]	19.3	167	2	1	2	1	1	1	-0.73697
O08749	Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2 - [DLDH_MOUSE]	54.2	509	2	1	2	1	1	1	-0.73697
Q99N69	Leupaxin OS=Mus musculus GN=Lpxn PE=1 SV=2 - [LPXN_MOUSE]	43.4	386	2	1	2	1	1	1	-0.73697
Q6ZU9	40S ribosomal protein S27 OS=Mus musculus GN=Rps27 PE=1 SV=3 - [RS27_MOUSE]	9.5	84	2	1	2	1	1	1	-0.73697
Q5SUT0	RNA-binding protein EWS OS=Mus musculus GN=Ewsr1 PE=1 SV=1 - [Q5SUT0_MOUSE]	64.9	618	2	1	2	1	1	1	-0.73697
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrpc PE=1 SV=1 - [HNRPC_MOUSE]	34.4	313	13	10	7	5	8	6	-0.65896
F8WIX8	Histone H2A OS=Mus musculus GN=Hist1h2a PE=3 SV=1 - [F8WIX8_MOUSE]	13.6	125	18	17	12	10	10	8	-0.74723
A2BE92	Protein SET (Fragment) OS=Mus musculus GN=Set PE=1 SV=1 - [A2BE92_MOUSE]	17.6	151	4	4	4	2	3	2	-0.77761
P0C0S6	Histone H2A.Z OS=Mus musculus GN=H2afz PE=1 SV=2 - [H2AZ_MOUSE]	13.5	128	19	15	10	8	8	8	-0.87447

Q3UHX2	28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1 - [HAP28_MOUSE]	20.6	181	2	1	3	1	1	1	-1
G3UYV7	40S ribosomal protein S28 (Fragment) OS=Mus musculus GN=Rps28 PE=4 SV=1 - [G3UYV7_MOUSE]	6.3	56	5	3	4	2	2	2	-1
Q9Z1N5	Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1 - [DX39B_MOUSE]	49.0	428	11	7	8	3	10	1	-0.89308
G3UZ48	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=4 SV=1 - [G3UZ48_MOUSE]	52.0	464	7	3	2	2	3	1	-1
E9PZB3	Protein Gm5093 OS=Mus musculus GN=Gm5093 PE=3 SV=1 - [E9PZB3_MOUSE]	19.9	174	1	2	3	1	1	1	-1
S4R1N6	40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=3 SV=1 - [S4R1N6_MOUSE]	12.5	107	6	3	4	2	2	2	-1.11548
F8WHM5	Golgi apparatus protein 1 (Fragment) OS=Mus musculus GN=Glg1 PE=4 SV=1 - [F8WHM5_MOUSE]	132.3	1163	4	2	1	1	1	1	-1.22239
A0A023T672	RNA-binding protein 8A OS=Mus musculus GN=RBM8 PE=2 SV=1 - [A0A023T672_MOUSE]	19.9	174	3	2	2	1	1	1	-1.22239
P58321	Ubiquitin carboxyl-terminal hydrolase isozyme L4 OS=Mus musculus GN=Uchl4 PE=2 SV=1 - [UCHL4_MOUSE]	26.4	233	4	2	4	2	1	1	-1.32193
P63038	60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1 - [CH60_MOUSE]	60.9	573	5	2	6	1	2	2	-1.37851
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=2 - [DYHC1_MOUSE]	531.7	4644	3	1	4	1	1	1	-1.41504
P10148	C-C motif chemokine 2 OS=Mus musculus GN=Ccl2 PE=1 SV=1 - [CCL2_MOUSE]	16.3	148	4	4	5	2	2	1	-1.37851
P54728	UV excision repair protein RAD23 homolog B OS=Mus musculus GN=Rad23b PE=1 SV=2 - [RD23B_MOUSE]	43.5	416	6	1	3	1	1	1	-1.73697
E9Q070	Uncharacterized protein OS=Mus musculus GN=Gm8730 PE=3 SV=1 - [E9Q070_MOUSE]	34.2	317	9	6	2	1	2	2	-1.76553
Q9Z1R9	MCG124046 OS=Mus musculus GN=Prss1 PE=2 SV=1 - [Q9Z1R9_MOUSE]	26.1	246	46	52	27	11	7	8	-2.26534
Q45VK5	Interleukin enhancer-binding factor 3 OS=Mus musculus GN=Ilf3 PE=2 SV=1 - [Q45VK5_MOUSE]	76.3	703	11	1	8	1	1	1	-2.73697
Q9QUK9	MCG15083 OS=Mus musculus GN=Try5 PE=2 SV=1 - [Q9QUK9_MOUSE]	26.3	246	19	19	11	3	1	1	-3.29278

Figure S1: TRACER activity plots of MDA-MB-231 cells cultured in CD45+ media. TRACER line-plot data showing 15 TF reporter activity profiles for MDA-MB-231 cells cultured in Mock CD45+ or Scaffold CD45+ media over an 8 hour period normalized to control TA-FLuc activity. Red line plots = Mock CD45+, blue line plots = Scaffold CD45+ ($n = 3$ arrays, $n = 12$ total measurements per time point).

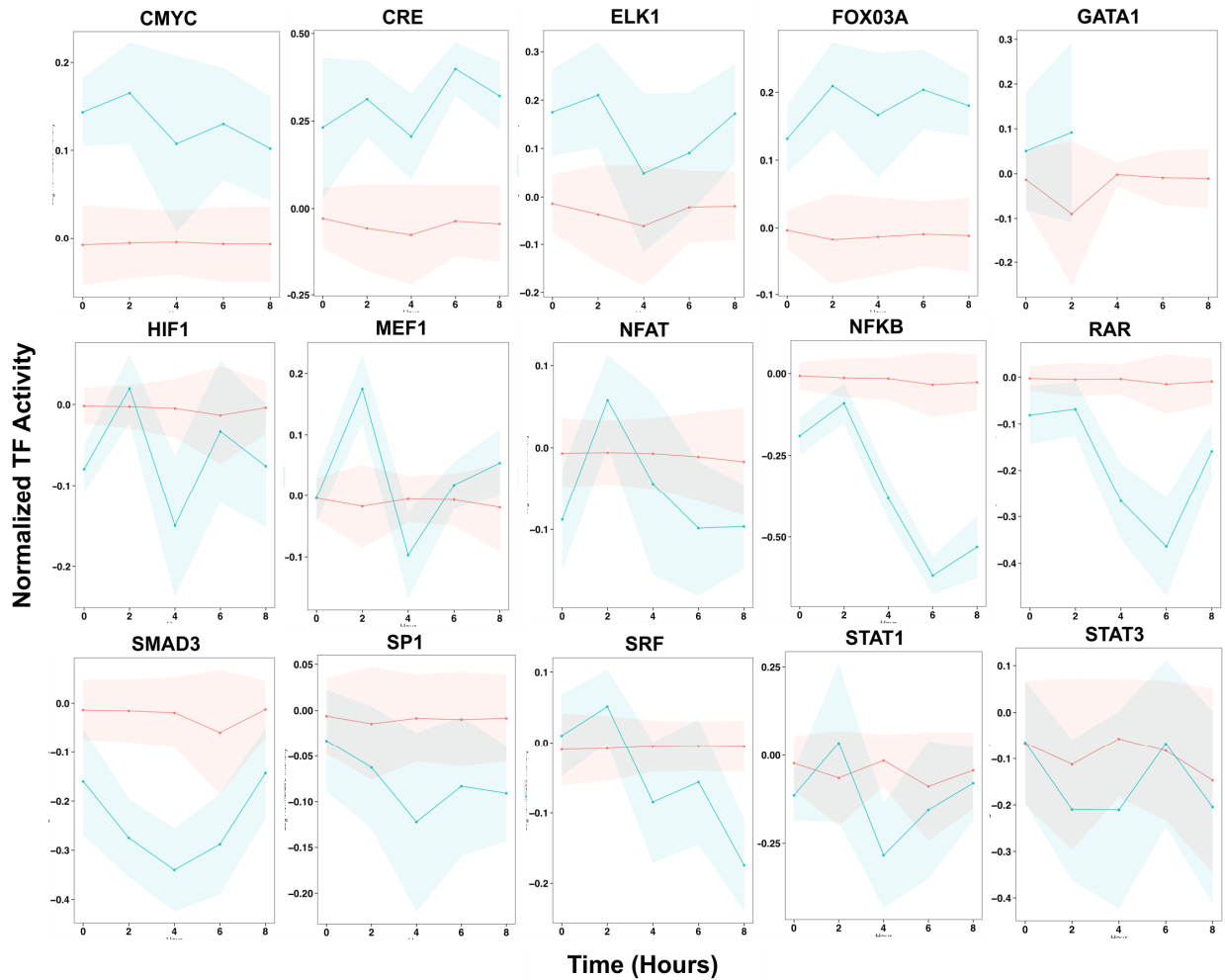


Table S6: Differentially regulated genes via NF B and SRF activity. List of 13 target genes of SRF and 23 target genes of NFκB among the differentially regulated genes identified by RNAseq ($p < 0.01$, FDR < 0.1). Shades of blue indicate down-regulation, and shades of red indicate up-regulation.

SRF Targets	Log2 Fold Change
PRKAR2A	-0.667908

NFκB Targets	Log2 Fold Change
ZC3H12C	-0.548341

TBC1D5	-0.403385
YES1	-0.402732
TBL3	0.39875
RRP1	0.443386
SNRPB	0.453781
C1orf35	0.50364
JUNB	0.535082
GAMT	0.569661
NR4A1	0.598421
FOXS1	0.636631
MRPL55	0.670184
PDGFB	0.856204

PTPRG	-0.538206
IGFN1	-0.465606
LMBR1	-0.454653
UBR1	-0.452984
HERC5	-0.418377
YES1	-0.402732
MRPS26	0.340511
TSTA3	0.414049
RPLP2	0.450767
SCRN2	0.458495
TMEM208	0.464818
D2HGDH	0.465739
TMSB4X	0.477933
IER2	0.527178
E4F1	0.532995
CBX8	0.544243
LAGE3	0.546784
MACROD1	0.557921
RABAC1	0.580801
FOXS1	0.636631
C19orf24	0.655322
TFF1	0.691243

Figure S2: Characterization of adaptive immune populations at the primary tumor. Flow cytometric characterization of innate and adaptive immune cell populations in Mock and Scaffold PTs from the immunocompetent Balb/C-4T1 tumor model ($n = 5$).

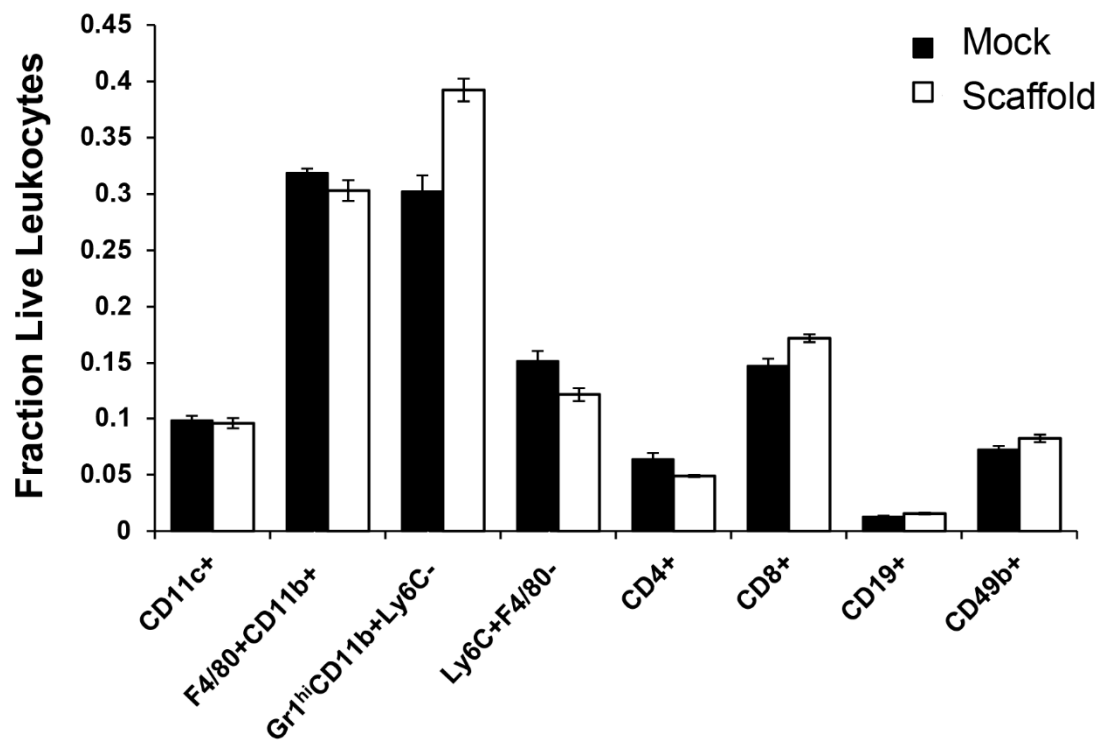


Table S7: Primers used in macrophage RT-PCR analysis. List of forward and reverse primer sequences used to characterize gene expression in macrophage subpopulations.

Gene	Forward	Reverse
<i>MHCII</i>	AGCCCCATCACTGTGGAGT	GATGCCGCTCAACATCTTGC
<i>Lyve1</i>	CTGGCTGTTTGCTACGTGAA	CATGAAACTTGCCTCGTGTG
<i>CCR2</i>	CTCAGTTCATCCACGGCATA	CAAGGCTCACCATCATCGTA
<i>Mafb</i>	GGGGCCAAATTGACATACAC	CTTAGGACGCAAAGCCTGTC
<i>CD163</i>	ATGGGTGGACACAGAATGGTT	CAGGAGCGTTAGTGACAGCAG
<i>Marco</i>	ACAGAGCCGATTTTGACCAAG	CAGCAGTGCAGTACCTGCC
<i>Ccl7</i>	GACAAAGAAGGGCATGGAAG	CATTCCTTAGGCGTGACCAT
<i>Arg</i>	CAGAAGAATGGAAGAGTCAG	CAGATATGCAGGGAGTCACC
<i>Ym1</i>	CCAGCATATGGGCATACCT	CAGACCTCAGTGGCTCCTTC
<i>Vcam1</i>	AGTTGGGGATTTCGGTTGTTCT	CCCCTCATTCTTACCACCC
<i>Itgb5</i>	GAAGTGCCACCTCGTGTGAA	GGACCGTGGATTGCCAAAGT
<i>Itgax</i>	CTGGATAGCCTTTCTTCTGCTG	GCACACTGTGTCCGA ACTCA
<i>MMP9</i>	CTGGACAGCCAGACACTAAAG	CTCGCGGCAAGTCTTCAGAG
<i>Actb</i>	TGTTACCAACTGGGACGACA	GGGGTGTTGAAGGTCTCAA
<i>Rplp0</i>	AGATTCGGGATATGCTGTTGGC	TCGGGTCCTAGACCAGTGTT
<i>GAPDH</i>	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA