Supplementary Table 1

Patient	Age	Diagnosis	Blast_percent	Archer_fusionplex1	Archer_fusionplex2	Archer_fusionplex3
Pt_1	68	B ALL	90	*NA*		
Pt_2	67	Ph+ ALL	60	*NA*		
Pt_3	44	Ph+ ALL	98	*NA*		
Pt_4	43	B ALL	95	*NA*		
Pt_5	35	Ph+ ALL	90	BCR-ABL1		
Pt_6	43	B ALL	57	ETV6-ABL1		
Pt_7	68	Ph+ ALL	98	BCR-ABL1	IKZF1	
Pt_8	40	Ph+ ALL	80	BCR-ABL1		
Pt_9	46	Ph+ ALL	95	*NA*		
Pt_10	37	B ALL	85	*NA*		
Pt_11	52	Ph+ ALL	80	BCR-ABL1	IKZF1	PAX-MLLT3
Pt_12	32	Ph+ ALL	90	BCR-ABL1	IKZF1	
Pt_13	26	B ALL	90	*NA*		
Pt_14	24	B ALL	90	*NA*		
Pt_15	52	B ALL	54	*NA*		
Pt_16	30	Ph+ ALL	85	BCR-ABL1		
Pt_17	60	B ALL	85	*NA*		
Pt_18	22	Ph+ ALL	89	*NA*		

**NA* = analysis not available

Supplementary Table 2

Compound	Class	C1(nM)	C2 (nM)	C3 (nM)	C4 (nM)	C5 (nM)
Alisertib	Aurora inhibitor	1	10	100	1000	10000
Axitinib	VEGFR inhibitor	1	10	100	1000	10000
Belinostat	HDAC inhibitor	1	10	100	1000	10000
BGB324	Axl inhibitor	1	10	100	1000	10000
BMS_754807	IGF1R inhibitor	1	10	100	1000	10000
Bosutinib	BCR-ABL inhibitor	1	10	100	1000	10000
CEP-32496	BRAF inhibitor	1	10	100	1000	10000
Cerdulatinib	JAK, SYK inhibitor	1	10	100	1000	10000
Cobimetinib	MEK1/2 inhibitor	0,1	1	10	100	1000
Danusertib	Aurora, Ret, TrkA, FGFR-1 inhibitor	1	10	100	1000	10000
Daporinad	NAMPT inhibitor	0,1	1	10	100	1000
Dasatinib	BCR-ABL inhibitor	0,1	1	10	100	1000
Dexamethasone	glucocorticoid	1	10	100	1000	10000
Duvelisib	PI3K delta, gamma inhibitor	0,05	0,5	5	50	500
FRAX486	PAK1, 2, 3 inhibitor	0,5	5	50	500	500
Gedatolisib	PI3K/mTOR inhibitor	0,1	1	10	100	1000
Glasdegib	SMO inhibitor	0,1	1	10	100	1000
GSK_2334470	PDK1 inhibitor	1	10	100	1000	10000
GSK525762	BET inhibitor	1	10	100	1000	10000
Idasanutlin	MDM2 antagonist	1	10	100	1000	10000
Idelalisib	PI3K inhibitor	1	10	100	1000	10000
Imatinib	BCR-ABL inhibitor	1	10	100	1000	10000
JQ1	BET inhibitor	1	10	100	1000	10000
Lenalidomide	immunomodulatory	10	100	1000	10000	100000
Lestaurtinib	FLT3, JAK2, TrkA,TrkB,TrkC inhibitor	0,1	1	10	100	1000
LLL12	STAT3 inhibitor	1	10	100	1000	10000
Losmapimod	p38MAPK inhibitor	1	10	100	1000	10000
Luminespib	HSP90 inhibitor	0,1	1	10	100	1000
LY3009120	pan-RAF inhibitor	1	10	100	1000	10000
Mepacrine	anti-malaria	5	50	500	5000	50000
Methylprednisolone	glucocorticoid	1	10	100	1000	10000
Milciclib	CDK2 inhibitor	1	10	100	1000	10000
MK_2206	Akt inhibitor	0,1	1	10	100	1000
MLN_0128	mTOR inhibitor	0,1	1	10	100	1000
Navitoclax	Bcl-2 and Bcl-xL inhibitor	1	10	100	1000	10000
Nilotinib	BCR-ABL inhibitor	1	10	100	1000	10000
Nintedanib	VEGFR inhibitor	1	10	100	1000	10000
NVP_ABL001	selective allosteric inhibitor of BCR-ABL1	0,1	1	10	100	1000
NVP_AEW541	IGF1R inhibitor	1	10	100	1000	10000
NVP_LCL161	IAPs, SMAC mimetic	1	10	100	1000	10000
Onalespib	HSP90 inhibitor	0,25	2,5	25	250	2500

Osimertinib	EGFR(L858R/T790M) inhibitor	0,25	2,5	25	250	2500
Pexidartinib	KIT, CSF1R, FLT3 inhibitor	1	10	100	1000	10000
Pimozide	STAT5 inhibitor	0.01	0.01	1	10	100
Plicamycin	RNA synthesis inhibitor	1	10	100	1000	10000
Pomalidomide	immunomodulatory	1	10	100	1000	10000
Ponatinib	BCR-ABL inhibitor	0,1	1	10	100	1000
PRI_724	CBP/beta-catenin antagonist	1	10	100	1000	10000
Radotinib	BCR-ABL inhibitor	0.02	2	20	200	2000
Ralimetinib	p38MAPK inhibitor	1	10	100	1000	10000
Raloxifene	Selective estrogen receptor modulator	1	10	100	1000	10000
Ruxolitinib	JAK1&2 inhibitor	1	10	100	1000	10000
SAR405838	MDM2 antagonist	1	10	100	1000	10000
Saracatinib	Abl, Src inhibitor	1	10	100	1000	10000
SCH772984	ERK1&2 inhibitor	1	10	100	1000	10000
STAT5i	STAT5 inhibitor	0.05	0.05	5	50	500
Sunitinib	Broad TK inhibitor	0,1	1	10	100	1000
Temsirolimus	mTOR inhibitor	0,01	0,1	1	10	100
Tipifarnib	Farnesyltransferase inhibitor	1	10	100	1000	10000
Tivozanib	VEGFR inhibitor	1	10	100	1000	10000
Trametinib	MEK inhibitor	0,025	0,25	2,5	25	250
Ulixertinib	ERK inhibitor	1	10	100	1000	10000
Venetoclax	Selective Bcl-2 inhibitor	0,1	1	10	100	1000
Vistusertib	mTOR inhibitor	1	10	100	1000	10000

Supplementary Table 3

Combinations
1 Dasatinib + Venetoclax
2 Dasatinib + Navitoclax
3 Dasatinib + Idasanutlin
4 Idasanutlin + Venetoclax
5 Idasanutlin + Navitoclax

Drug	**C1**	**C2**	**C3**	**C4**	**max conc (nM)**
Dasatinib	0,1	1	10	100	1000
Venetoclax	0,1	1	10	100	1000
Navitoclax	0,1	1	10	100	1000
Idasanutlin	0,1	1	10	100	1000

Supplementary Table 4

Average RNA Sequencing Quality Metrics

rRNA rate	<1.5%
Intergenic reads rate	4.96%
Mapped total reads	104M
Duplication rate of mapped	32 %

Sample	End 2 Mapping Rate	Chimeric Pairs	Intragenic Rate	Num. Gaps	Exonic Rate	Mapping Rate	5' Norm	Genes Detected	Unique Rate of Mapped
Pt_1	0.9703094	92	0.9555849	418	0.5649719	0.97091013	0.39550638	25681	0.6825259
Pt_3	0.9734691	67	0.94243485	451	0.52546763	0.9741104	0.39176112	26250	0.6348773
Pt_4	0.97487175	100	0.951503	430	0.58998275	0.975475	0.34794357	25049	0.6030638
Pt_5	0.97500455	3793	0.9645156	536	0.63145006	0.97576714	0.37334397	24644	0.54246277
Pt_7	0.970839	50	0.954095	504	0.57221186	0.9715203	0.35785663	25535	0.6492417
Pt_8	0.962071	67	0.95519966	507	0.42832255	0.96269435	0.38937375	25607	0.74423116
Pt_9	0.9683872	124	0.9374307	434	0.40818152	0.96895516	0.39714733	26363	0.7549426
Pt_10	0.9699443	91	0.9438644	479	0.47450688	0.97054577	0.39443582	25852	0.7069164
Pt_11	0.9749382	54	0.9579407	472	0.4811238	0.9756304	0.40482184	25655	0.66060746
Pt_12	0.9725238	79	0.9393635	411	0.49692604	0.97310144	0.42839283	26902	0.6818304
Pt_13	0.9735868	57	0.94226354	446	0.6048979	0.97420466	0.38270766	24065	0.63423
Pt_14	0.9753656	143	0.9608526	470	0.62667716	0.97597027	0.36961144	25206	0.63925457
Pt_15	0.9678213	93	0.94389236	437	0.5291038	0.96851665	0.3892242	26185	0.7211983
Pt_16	0.9648	50	0.9453052	600	0.40361378	0.9653414	0.37942418	24977	0.7911804
Pt_17	0.97698164	122	0.9613474	452	0.59492195	0.97764295	0.41069722	25328	0.5982365
Pt_18	0.96885425	58	0.9423119	535	0.32583874	0.9695432	0.4431309	26561	0.7873528

Sample	3' Norm	Read Length	Mean Per Base Cov.	End 1 Mismatch Rate	Fragment Length StdDev	Estimated Library Size	Mapped	Intergenic Rate
Pt_1	0.6862117	151	83,61752	0.0025229577	251	65925855	108027000	0,043806836
Pt_3	0.67680407	151	67,22482	0.002534251	232	54840640	108533323	0,057012435
Pt_4	0.69160074	151	82,827736	0.0024538275	248	49055291	109273544	0,04789277
Pt_5	0.6338489	151	70,42719	0.0024966015	261	34787331	95979678	0,03496831
Pt_7	0.659212	151	72,77624	0.0026226582	229	54409698	101888666	0,045314766
Pt_8	0.63978	151	57,86288	0.0025600856	190	78738156	98063542	0,044360522
Pt_9	0.6452332	151	61,836433	0.0025568812	199	96367346	113891338	0,06210294
Pt_10	0.7010748	151	61,938477	0.0025903764	199	67753437	100100497	0,055640772
Pt_11	0.6900064	151	71,60971	0.002562218	235	66005452	118200559	0,041602332
Pt_12	0.66824174	151	78,72105	0.002382458	254	76320301	125428290	0,060133643
Pt_13	0.70398194	151	88,10936	0.0024144838	262	53234869	105602884	0,0572138
Pt_14	0.66996205	151	89,619316	0.002359957	279	53433676	103989411	0,03861252
Pt_15	0.6359463	151	76,67594	0.0024662386	211	72090194	99949868	0,055545826
Pt_16	0.70524687	151	41,508247	0.0025773195	182	74851594	73047153	0,054209724
Pt_17	0.6457579	151	84,99374	0.0024147357	269	48027839	108875228	0,03810907
Pt_18	0.65883225	151	40,176754	0.002585336	192	93053358	92766882	0,057305206

Sample	Total Purity Filtered Reads Sequenced	rRNA	Failed Vendor QC Check	Mean CV	Transcripts Detected	Mapped Pairs	Cumul. Gap Length	Gap %
Pt_1	111263646	1335942	0	0.765735	133026	53918005	32105	0.017732171
Pt_3	111417878	859700	0	0.7684564	134873	54184007	33137	0.019015664
Pt_4	112020856	1202319	0	0.7548408	129699	54547193	35502	0.020376502
Pt_5	98363304	1465023	0	0.7732993	129562	47913664	39548	0.021984095
Pt_7	104875492	787300	0	0.7771083	132115	50861466	45671	0.024843866
Pt_8	101863636	696950	0	0.7799276	131699	48952513	37343	0.021024393
Pt_9	117540362	816905	0	0.7477298	133997	56858733	31867	0.017842595
Pt_10	103138358	921541	0	0.75257456	132162	49966429	38023	0.021919379
Pt_11	121153004	947537	0	0.76727647	132148	59011542	32981	0.019162243
Pt_12	128895392	1311510	0	0.76444083	136047	62620697	29272	0.016424377
Pt_13	108399072	2464019	0	0.768121	126256	52715240	32843	0.01824596
Pt_14	106549766	1461969	0	0.7633192	131236	51912528	38387	0.022343576
Pt_15	103198922	1227860	0	0.7781335	132805	49886506	34967	0.019259261
Pt_16	75669758	417924	0	0.77818346	130178	36465089	44610	0.02273472
Pt_17	111365028	1180803	0	0.7755451	131531	54345155	37988	0.020580744
Pt_18	95681018	380714	0	0.7597193	134777	46315657	39944	0.022498313

Sample	Unpaired Reads	Intronic Rate	Mapped Unique Rate of Total	Expression Profiling Efficiency	Mapped Unique	End 2 Mismatch Rate	End 2 Antisense	Alternative Aligments	End 2 Sense
Pt_1	0	0.39061293	0.66267127	0.54853696	73731222	0.0054415874	43149588	10462333	2504823
Pt_3	0	0.41696724	0.6184406	0.5118635	68905346	0.0059883944	44119201	6419991	1603549
Pt_4	0	0.36152026	0.58827364	0.5755134	65898920	0.005550844	43131330	9711883	2195288
Pt_5	0	0.33306554	0.5293174	0.61614823	52065404	0.006309482	39248400	7040502	1257857
Pt_7	0	0.38188314	0.6307515	0.5559154	66150370	0.006080397	41286378	6425832	1567460
Pt_8	0	0.52687705	0.71646714	0.4123437	72981943	0.005571866	40387772	7114732	1686969
Pt_9	0	0.5292492	0.7315055	0.3955096	85981422	0.0056685223	45743414	7939955	2258982
Pt_10	0	0.46935758	0.6860947	0.46053064	70762680	0.0055449335	39350176	8127914	2903736
Pt_11	0	0.47681692	0.6445087	0.46939903	78084168	0.0058204797	49081288	7278415	1561802
Pt_12	0	0.44243738	0.6634902	0.48355943	85520826	0.00566683	49658250	9993419	2787310
Pt_13	0	0.33736566	0.61786985	0.5892944	66976517	0.005460283	41480356	15148043	2314317
Pt_14	0	0.3341755	0.62389344	0.6116183	66475703	0.0054367674	41639055	8058333	2111966
Pt_15	0	0.41478848	0.6984926	0.5124458	72083679	0.0055430355	40360587	7853672	1748511
Pt_16	0	0.5416915	0.76375914	0.38962507	57793473	0.0058404915	29783068	4977404	1261137
Pt_17	0	0.36642545	0.5848617	0.5816212	65133138	0.0053868135	43826909	6745202	2313039
Pt_18	0	0.6164732	0.7633726	0.31591475	73040267	0.005919033	38607075	4353559	1446730

Sample	Fragment Length Mean	End 1 Antisense	Split Reads	Base Mismatch Rate	End 1 Sense	End 1 % Sense	rRNA rate	End 1 Mapping Rate	No. Covered 5'	Duplication Rate of Mapped	End 2 % Sense
Pt_1	216	2484286	19526583	0.003980765	43300574	94.574005	0,01200699	0.9715108	915	0,31747413	5.4864864
Pt_3	197	1593292	18236867	0.0042588436	44283294	96.52701	0,007716	0.97475183	929	0,36512268	3.507114
Pt_4	229	2174538	21225443	0.003999764	43307054	95.218864	0,01073299	0.9760782	907	0,39693618	4.8432646
Pt_5	206	1244174	21764944	0.004397553	39482829	96.94508	0,014894	0.9765296	916	0,45753717	3.10534
Pt_7	201	1555706	18221090	0.0043485765	41434624	96.38127	0,007507	0.9722015	907	0,3507583	3.6576886
Pt_8	145	1676154	13436928	0.0040637725	40505808	96.026375	0,00684199	0.9633177	907	0,25576887	4.009458
Pt_9	163	2245645	14546061	0.0041108006	45879692	95.333755	0,00695	0.96952313	921	0,24505742	4.705978
Pt_10	165	2884206	14975346	0.004065584	39491881	93.19379	0,008935	0.9711472	890	0,2930836	6.872112
Pt_11	194	1551926	19040300	0.0041890186	49268968	96.94627	0,007821	0.97632265	916	0,33939257	3.083939
Pt_12	220	2768597	20706847	0.004021682	49849164	94.73829	0,010175	0.973679	932	0,31816956	5.314673
Pt_13	227	2287827	21825731	0.0039355285	41664152	94.79471	0,022731	0.9748226	915	0,36577	5.2844715
Pt_14	228	2091772	23626565	0.0038962157	41882079	95.24315	0,013721	0.9765751	919	0,36074546	4.8272386
Pt_15	175	1732425	18684967	0.0040024337	40532005	95.90098	0,01189799	0.96921194	919	0,27880165	4.1523356
Pt_16	145	1252015	9060102	0.004207885	29854688	95.9751	0,005523	0.9658828	888	0,20881964	4.062391
Pt_17	223	2295304	23528954	0.0038985948	44043315	95.04667	0,010603	0.9783042	924	0,40176344	5.013094
Pt_18	147	1439666	9281517	0.004249577	38722238	96.41535	0,00397899	0.9702322	913	0,21264718	3.6119664

Supplementary Table 5
Significantly DE genes, Ph+ ALL vs Ph- ALL

baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	symbol	description
510.823126235093	6.17818192501723	0.510724249265082	11.4365596373187	2.7455829120501e-30	8.99672608620577e-26	RASSF8	Ras association domain family member 8 [Source:HGNC Symbol;Acc:HGNC:13232]
992.375377231769	6.02511003089792	0.549907948027653	10.620009173233	2.405374839793e-26	3.94096613751685e-22	VWA2	von Willebrand factor A domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24709]
3412.40549450382	5.92724408479871	0.550557634962839	10.5660147432035	4.28311063732102e-26	4.67829897879117e-22	SPATS2L	spermatogenesis associated serine rich 2 like [Source:HGNC Symbol;Acc:HGNC:24574]
12.0984486737449	5.41457439640544	0.728017005382373	4.38043581962695	1.18442175441198e-05	0.0021208268879001	KRT27	keratin 27 [Source:HGNC Symbol;Acc:HGNC:30841]
47.9956907482506	5.15626912062005	0.676238680180923	5.43963436899205	5.33900289572388e-08	2.3941318331954e-05	TDRD1	tudor domain containing 1 [Source:HGNC Symbol;Acc:HGNC:11712]
272.305712086428	4.99628960240642	0.575188922770756	8.42761695486863	3.52775627193521e-17	1.92662529197955e-13	WNT9A	Wnt family member 9A [Source:HGNC Symbol;Acc:HGNC:12778]
2785.6751780536	4.9297095924035	0.606953218594804	7.65478889914483	1.93630050303468e-14	6.34486948834404e-11	EPHA4	EPH receptor A4 [Source:HGNC Symbol;Acc:HGNC:3388]
583.97670139018	4.82760660634819	0.451950601784524	10.1287664774531	4.11811543604147e-24	3.37356016520517e-20	ELFN2	extracellular leucine rich repeat and fibronectin type III domain containing 2 [Source:HGNC Symbol;Acc:HGNC:29396]
18.3937735401898	4.66228756163586	0.706385464859642	3.75871935839942	0.000170785269175063	0.0171140418970289	C7orf72	chromosome 7 open reading frame 72 [Source:HGNC Symbol;Acc:HGNC:22564]
274.216400103606	4.50263010189722	0.563389609860655	7.55011039849341	4.34889445583871e-14	1.29549612299021e-10	TSPAN15	tetraspanin 15 [Source:HGNC Symbol;Acc:HGNC:23298]
62.3655561073093	4.43996992834729	0.726085977032482	5.59606787848946	2.19267882660479e-08	1.15886612564815e-05	FOLH1	folate hydrolase 1 [Source:HGNC Symbol;Acc:HGNC:3788]
62.3655561073093	4.43996992834729	0.726085977032482	5.59606787848946	2.19267882660479e-08	1.15886612564815e-05	FOLH1	folate hydrolase 1 [Source:HGNC Symbol;Acc:HGNC:3788]
167.687089090495	4.32223754847689	0.625597992685337	6.51443367326765	7.2964412934216e-11	1.039520818708e-07	RAB3B	RAB3B, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9778]
3023.08903143141	4.31167150963292	0.640521476241148	6.81903780851433	9.16522802332956e-12	1.76662465804978e-08	THBS1	thrombospondin 1 [Source:HGNC Symbol;Acc:HGNC:11785]
2609.63964244476	4.20915326960176	0.721501578313883	7.91330384737237	2.50646618864822e-15	9.12576489662498e-12	ADGRF1	adhesion G protein-coupled receptor F1 [Source:HGNC Symbol;Acc:HGNC:18990]
248.567476424885	4.12988544860158	0.638796251440734	6.13903570646704	8.30239060719448e-10	7.15928251096181e-07	FAM19A1	family with sequence similarity 19 member A1, C-C motif chemokine like [Source:HGNC Symbol;Acc:HGNC:21587]

1443.84169021088	4.06511978499697	0.581339198746792	6.77452305488507	1.24817330339031e-11	2.27223015586076e-08	NRXN3	neurexin 3 [Source:HGNC Symbol;Acc:HGNC:8010]
92.5650376338721	4.0240219428071	0.721920090798912	5.48799204717173	4.06528363364019e-08	1.95898844275179e-05	FAM26E	family with sequence similarity 26 member E [Source:HGNC Symbol;Acc:HGNC:21568]
31.850891426268	4.00598356013999	0.73121231717337	5.46236632506116	4.69829296803455e-08	2.23121252139936e-05	ECEL1	endothelin converting enzyme like 1 [Source:HGNC Symbol;Acc:HGNC:3147]
84.9155808703953	3.99019014899644	0.647041948107846	5.85971770378364	4.63654678533692e-09	3.30283402308522e-06	TMEM200A	transmembrane protein 200A [Source:HGNC Symbol;Acc:HGNC:21075]
99.67939668883	3.97248248904245	0.658049418699296	5.62423299748362	1.86334011844678e-08	1.0348801525638e-05	SCNN1A	sodium channel epithelial 1 alpha subunit [Source:HGNC Symbol;Acc:HGNC:10599]
319.601567725369	3.92370598277281	0.683263359613508	5.51562438211092	3.47543838401687e-08	1.7362934655859e-05	SLCO2B1	solute carrier organic anion transporter family member 2B1 [Source:HGNC Symbol;Acc:HGNC:10962]
185.393784185002	3.89690401068281	0.684984220882157	5.39017974390012	7.03872467762745e-08	3.03480171363811e-05	MIPOL1	mirror-image polydactyly 1 [Source:HGNC Symbol;Acc:HGNC:21460]
345.724779437813	3.87197963754537	0.543584596695772	6.6856074826033	2.29968660504799e-11	3.96611214074803e-08	SLC2A9	solute carrier family 2 member 9 [Source:HGNC Symbol;Acc:HGNC:13446]
71.5452845721131	3.86883606279076	0.706718997136342	5.08660936508859	3.6452155569047e-07	0.000119446423368653	PDE3A	phosphodiesterase 3A [Source:HGNC Symbol;Acc:HGNC:8778]
33.675329512224	3.84943915669472	0.670427580916489	5.3120459066684	1.08401285866132e-07	4.55396581443773e-05	OCA2	OCA2 melanosomal transmembrane protein [Source:HGNC Symbol;Acc:HGNC:8101]
58.4694201314098	3.81268067554541	0.643040808537259	5.39103890208434	7.0051506227293e-08	3.03480171363811e-05	MYL9	myosin light chain 9 [Source:HGNC Symbol;Acc:HGNC:15754]
55.5704958709243	3.80162279910268	0.733673569569015	3.62967212275803	0.000283781451777695	0.0255465676149767	NPNT	nephronectin [Source:HGNC Symbol;Acc:HGNC:27405]
64.9714947833498	3.79811561921893	0.459899526138947	7.45167004710992	9.21659970230747e-14	2.32315030034778e-10	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP) [Source:HGNC Symbol;Acc:HGNC:9602]
78.3693633018104	3.76195208759422	0.724096429486424	5.17118525862309	2.32613808915304e-07	8.56436998936705e-05	ADAMTSL1	ADAMTS like 1 [Source:HGNC Symbol;Acc:HGNC:14632]
125.318529860571	3.76097360422327	0.689991729924242	5.80299999517841	6.51387934152432e-09	4.44680829714727e-06	PRTFDC1	phosphoribosyl transferase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:23333]
132.207238414845	3.74422240681951	0.725715429874067	5.69557562454696	1.22956368728451e-08	7.74814286633438e-06	INHBB	inhibin beta B subunit [Source:HGNC Symbol;Acc:HGNC:6067]
39.1455254073129	3.7278797250275	0.760490959834886	4.28135093734089	1.85762137425138e-05	0.00292646813420525	PIK3C2G	phosphatidylinositol-4-phosphate 3-kinase catalytic subunit type 2 gamma [Source:HGNC Symbol;Acc:HGNC:8973]
1271.36265979161	3.71949812086204	0.543303613699744	6.20911299499079	5.3284500225972e-10	5.13537206883721e-07	COL6A3	collagen type VI alpha 3 chain [Source:HGNC Symbol;Acc:HGNC:2213]

224.27599644967	3.70541511980296	0.713862945638904	4.93947825512901	7.83318777999013e-07	0.00022515605015326	CALCRL	calcitonin receptor like receptor [Source:HGNC Symbol;Acc:HGNC:16709]
14.9922100514803	3.65364533260565	0.747419530532784	3.42193804002115	0.000621764808350365	0.0444846926638095	PRTG	protogenin [Source:HGNC Symbol;Acc:HGNC:26373]
712.458476047292	3.61800612119657	0.713476225079469	6.03691203952094	1.57091295194917e-09	1.28689189023676e-06	PEG10	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:14005]
27.3904469501444	3.61237918701457	0.737309803116808	4.50753511661495	6.55850785598893e-06	0.00127922134181574	CREB3L1	cAMP responsive element binding protein 3 like 1 [Source:HGNC Symbol;Acc:HGNC:18856]
601.939247339719	3.57798754292614	0.772914358835407	6.42536061153399	1.31557266961338e-10	1.65802635530351e-07	CHRDL1	chordin like 1 [Source:HGNC Symbol;Acc:HGNC:29861]
9.74616264015071	3.57400629998528	0.754429749368352	4.57335822613119	4.79968488792861e-06	0.000970839965479287	LY6H	lymphocyte antigen 6 family member H [Source:HGNC Symbol;Acc:HGNC:6728]
113.49916301203	3.56708251963466	0.721163885081507	4.68892093977547	2.7464946606755e-06	0.00061222542204772	SLC25A27	solute carrier family 25 member 27 [Source:HGNC Symbol;Acc:HGNC:21065]
7.70736966364097	3.558055981647	0.727391004660636	4.32744222636097	1.5085089583829e-05	0.00248878364991827	DRD5	dopamine receptor D5 [Source:HGNC Symbol;Acc:HGNC:3026]
360.403045461619	3.553675819541	0.734790676989201	5.1253535268495	2.96979968759987e-07	0.000104639135659433	GHR	growth hormone receptor [Source:HGNC Symbol;Acc:HGNC:4263]
9.1532143879798	3.53459649364628	0.635596842824641	4.39490878585734	1.10819276755151e-05	0.00199523409929274	MFSD6L	major facilitator superfamily domain containing 6 like [Source:HGNC Symbol;Acc:HGNC:26656]
3453.45729520424	3.52623957432316	0.616751252541937	5.63716911747861	1.7286832708813e-08	9.9378058631997e-06	MYO1B	myosin IB [Source:HGNC Symbol;Acc:HGNC:7596]
187.515329565255	3.51188937402791	0.728064762017026	5.19458716392404	2.05174627611136e-07	7.72777264087551e-05	NR5A2	nuclear receptor subfamily 5 group A member 2 [Source:HGNC Symbol;Acc:HGNC:7984]
383.408987907231	3.51184554718283	0.748028233199231	4.69814729953578	2.62532071206865e-06	0.000593078060968642	PLOD2	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 [Source:HGNC Symbol;Acc:HGNC:9082]
490.438660988447	3.50222326347875	0.657950492000953	5.14665140176464	2.65177451571142e-07	9.54871948690461e-05	KALRN	kalirin RhoGEF kinase [Source:HGNC Symbol;Acc:HGNC:4814]
25.5848642018504	3.5020462646211	0.730217370554286	4.29626912334481	1.73696692524261e-05	0.00274961025151449	MEI4	meiotic double-stranded break formation protein 4 [Source:HGNC Symbol;Acc:HGNC:43638]
213.920169827789	3.49773810418716	0.67830597551644	5.53774849010095	3.06384816269487e-08	1.56869025929977e-05	TMEM100	transmembrane protein 100 [Source:HGNC Symbol;Acc:HGNC:25607]
24.866291910307	3.49463615753624	0.762351581034244	4.74654856921004	2.06917055811663e-06	0.000502241339617525	PON3	paraoxonase 3 [Source:HGNC Symbol;Acc:HGNC:9206]
364.343434765837	3.48625807562883	0.731361830858266	5.50828178309951	3.62353055689353e-08	1.77217685504906e-05	FAM171B	family with sequence similarity 171 member B [Source:HGNC Symbol;Acc:HGNC:29412]

272.736216278611	3.48425799676668	0.661429649951524	5.11505145720577	3.13655438237867e-07	0.000107061056251859	MUC4	mucin 4, cell surface associated [Source:HGNC Symbol;Acc:HGNC:7514]
2281.97011586043	3.47948264904651	0.739300525028894	4.72748465029375	2.27318242044868e-06	0.000539765518501901	POU4F1	POU class 4 homeobox 1 [Source:HGNC Symbol;Acc:HGNC:9218]
26.0650109755384	3.46859982673017	0.764952898113386	4.73710891046907	2.16788674196852e-06	0.000518520531100909	SHISA6	shisa family member 6 [Source:HGNC Symbol;Acc:HGNC:34491]
84.1633461527277	3.3915295737625	0.606834468170825	5.11636566833813	3.1147893285896e-07	0.000107061056251859	GDPD4	glycerophosphodiester phosphodiesterase domain containing 4 [Source:HGNC Symbol;Acc:HGNC:24849]
68.4847456338976	3.38524976765537	0.752545326332251	4.34379281229773	1.40043600968369e-05	0.00236571648635856	ADAMTS9	ADAM metallopeptidase with thrombospondin type 1 motif 9 [Source:HGNC Symbol;Acc:HGNC:13202]
19.935674511609	3.3609223966975	0.72926646331553	4.2302752652835	2.33405523351187e-05	0.00359071933763929	SPAAR	small regulatory polypeptide of amino acid response [Source:HGNC Symbol;Acc:HGNC:27244]
195.642880208717	3.35376796395003	0.710374843676627	4.92779335909861	8.31635026833332e-07	0.000234922556545471	ANTXR1	anthrax toxin receptor 1 [Source:HGNC Symbol;Acc:HGNC:21014]
192.443758264741	3.3319582699559	0.644376059721302	4.65557048144315	3.23084855526562e-06	0.000710526479590226	TSPYL5	TSPY like 5 [Source:HGNC Symbol;Acc:HGNC:29367]
21.7955892920075	3.32706062913504	0.714090064144409	4.44283686232973	8.87804807172338e-06	0.00166237645265275	MAS1	MAS1 proto-oncogene, G protein-coupled receptor [Source:HGNC Symbol;Acc:HGNC:6899]
237.401405530933	3.3124848852074	0.664542887872809	4.60515555978478	4.12157647033987e-06	0.000860228138726731	STK33	serine/threonine kinase 33 [Source:HGNC Symbol;Acc:HGNC:14568]
24.237085913291	3.3034455496769	0.769826461660701	4.55924999193298	5.13366312644163e-06	0.0010320237627438	RHOJ	ras homolog family member J [Source:HGNC Symbol;Acc:HGNC:688]
1632.33974670822	3.2849827769351	0.724723318953692	7.37976036581833	1.58574685954528e-13	3.71155379239854e-10	CCL17	C-C motif chemokine ligand 17 [Source:HGNC Symbol;Acc:HGNC:10615]
222.124773793443	3.27528383915145	0.744701124316986	4.33168614378251	1.4797177183407e-05	0.00246128884236488	C18orf63	chromosome 18 open reading frame 63 [Source:HGNC Symbol;Acc:HGNC:40037]
93.3442988895622	3.2478503260849	0.688362833762431	4.77940747546935	1.75812556571779e-06	0.000429927302518212	DLGAP2	DLG associated protein 2 [Source:HGNC Symbol;Acc:HGNC:2906]
906.006220589364	3.23329917214399	0.531395891663915	5.72911076791704	1.00958457582909e-08	6.48667987858191e-06	PTP4A3	protein tyrosine phosphatase type IVA, member 3 [Source:HGNC Symbol;Acc:HGNC:9636]
100.24960964688	3.19808334307984	0.663058968977509	4.35743627215237	1.3159479699038e-05	0.00227694845087645	HSPA12B	heat shock protein family A (Hsp70) member 12B [Source:HGNC Symbol;Acc:HGNC:16193]
26.9443380253766	3.17178636181579	0.745907805842397	4.33536731590615	1.45516927596451e-05	0.00243280545075537	OPN4	opsin 4 [Source:HGNC Symbol;Acc:HGNC:14449]
1411.35560429843	3.16184271186978	0.621527751586893	5.20815901579572	1.90723447505206e-07	7.26700689284954e-05	CCR6	C-C motif chemokine receptor 6 [Source:HGNC Symbol;Acc:HGNC:1607]

1723.13619171894	3.15660802214742	0.613838326549394	4.88003666507101	1.06066119887849e-06	0.00028963121804042	PON2	paraoxonase 2 [Source:HGNC Symbol;Acc:HGNC:9205]
600.202532982416	3.15622440973415	0.74813974926276	5.4373900342723	5.40666978932066e-08	2.3941318331954e-05	LPL	lipoprotein lipase [Source:HGNC Symbol;Acc:HGNC:6677]
13.4311300847431	3.13809768244674	0.645878158110418	4.22322082690611	2.40835639146237e-05	0.00368771131941304	DAGLA	diacylglycerol lipase alpha [Source:HGNC Symbol;Acc:HGNC:1165]
292.911613183344	3.11490637284547	0.747702716946912	4.23364277267284	2.29936090061352e-05	0.00355403103732565	LYVE1	lymphatic vessel endothelial hyaluronan receptor 1 [Source:HGNC Symbol;Acc:HGNC:14687]
809.260314880112	3.11441455864768	0.443662168852789	6.29870942613548	3.00134017752313e-10	3.39130741162338e-07	PLXDC2	plexin domain containing 2 [Source:HGNC Symbol;Acc:HGNC:21013]
65.7712342735453	3.09220824206095	0.718546654445558	4.34653052516271	1.38307811229744e-05	0.0023604533116543	MATN3	matrilin 3 [Source:HGNC Symbol;Acc:HGNC:6909]
863.692167944551	3.08923236566523	0.768047245035247	6.2243113708858	4.8367566578685e-10	4.80275279287985e-07	LDB3	LIM domain binding 3 [Source:HGNC Symbol;Acc:HGNC:15710]
828.735091621745	3.07885345014972	0.764806383414398	5.43796415125602	5.38928141914519e-08	2.3941318331954e-05	ABCA9	ATP binding cassette subfamily A member 9 [Source:HGNC Symbol;Acc:HGNC:39]
203.643834455444	3.06856488045727	0.603451994130684	4.52129598409177	6.14621780809844e-06	0.00122060160688345	MCF2L	MCF.2 cell line derived transforming sequence like [Source:HGNC Symbol;Acc:HGNC:14576]
797.362883825421	3.0643529514408	0.553195178247405	4.86070133170368	1.16970614791655e-06	0.000306631448439436	KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3 [Source:HGNC Symbol;Acc:HGNC:6243]
266.418183561101	3.05967198997052	0.624161522224046	4.64201040886259	3.45035474802874e-06	0.000748174686453628	TNFRSF11A	TNF receptor superfamily member 11a [Source:HGNC Symbol;Acc:HGNC:11908]
598.756161469294	3.04315245668995	0.681041500987097	4.60045191253071	4.21575336914675e-06	0.000868816392454093	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2 [Source:HGNC Symbol;Acc:HGNC:3357]
24.3626664874286	3.0318156671069	0.689755477787321	3.99728486748709	6.40731770417982e-05	0.00820136666135017	JPH2	junctophilin 2 [Source:HGNC Symbol;Acc:HGNC:14202]
1063.78301388532	3.01544722791653	0.593615612711643	4.71341421557897	2.43600304006529e-06	0.000566120195864251	PRKCA	protein kinase C alpha [Source:HGNC Symbol;Acc:HGNC:9393]
328.360497325323	3.00785764806406	0.72944240322774	4.1326872139468	3.58546509179572e-05	0.00506416035034319	PCLO	piccolo presynaptic cytomatrix protein [Source:HGNC Symbol;Acc:HGNC:13406]
13.0852678091426	3.00676957560759	0.763039491886229	3.51979251639583	0.000431884506527388	0.0343494939560424	GRM8	glutamate metabotropic receptor 8 [Source:HGNC Symbol;Acc:HGNC:4600]
111.672465767101	3.00626937558365	0.77523018082249	4.31176699389279	1.61955054883093e-05	0.00263013690438415	PCDH15	protocadherin related 15 [Source:HGNC Symbol;Acc:HGNC:14674]
880.425732409331	3.00359488465445	0.653845172189505	4.35966270956605	1.30263067268553e-05	0.00227045754694466	TUNAR	TCL1 upstream neural differentiation-associated RNA [Source:HGNC Symbol;Acc:HGNC:44088]

44.6584780587781	3.00142336431526	0.752568869114286	3.77172444247412	0.000162123238643037	0.016601419637047	SYNDIG1	synapse differentiation inducing 1 [Source:HGNC Symbol;Acc:HGNC:15885]
1277.66624439953	2.98972811797501	0.426117343914396	6.32467722796171	2.5376245148865e-10	2.96974571799289e-07	RPS6KA2	ribosomal protein S6 kinase A2 [Source:HGNC Symbol;Acc:HGNC:10431]
100.815263773178	2.97993364251258	0.620696286576224	4.36964815400785	1.24446885656725e-05	0.00221623671152149	HHLA2	HERV-H LTR-associating 2 [Source:HGNC Symbol;Acc:HGNC:4905]
1167.544027203	2.97738160431894	0.524496102448232	5.27330129618335	1.33991315421796e-07	5.35442368748955e-05	JCAD	junctional cadherin 5 associated [Source:HGNC Symbol;Acc:HGNC:29283]
74.5600942675031	2.97544178751815	0.603823325017406	4.67607933922625	2.92411514244717e-06	0.000647414898565601	SYDE1	synapse defective Rho GTPase homolog 1 [Source:HGNC Symbol;Acc:HGNC:25824]
49.6893615229916	2.95608387477157	0.728203829262228	3.91627288134686	8.99284548165328e-05	0.0105999122569358	CCL2	C-C motif chemokine ligand 2 [Source:HGNC Symbol;Acc:HGNC:10618]
63.7744952145389	2.95464877463538	0.582619978018708	4.64080549163555	3.47053687563939e-06	0.000748174686453628	ARPIN	actin related protein 2/3 complex inhibitor [Source:HGNC Symbol;Acc:HGNC:28782]
1903.07907529798	2.93794556047654	0.638460157902334	4.40979098552638	1.03470438631576e-05	0.00187321510114888	KCNA5	potassium voltage-gated channel subfamily A member 5 [Source:HGNC Symbol;Acc:HGNC:6224]
23.0614285490348	2.92385605245512	0.673941629713164	4.23508278043142	2.28467526253384e-05	0.00355403103732565	LPIN3	lipin 3 [Source:HGNC Symbol;Acc:HGNC:14451]
8.35067667994578	2.90932594295448	0.761864330401319	3.41306726546359	0.000642360849211433	0.0456591763708465	ADGRF5	adhesion G protein-coupled receptor F5 [Source:HGNC Symbol;Acc:HGNC:19030]
58.1910462386733	2.9066529735807	0.670286746069097	4.02773855407664	5.63159161915846e-05	0.00735203164050137	ACVRL1	activin A receptor like type 1 [Source:HGNC Symbol;Acc:HGNC:175]
166.497516773713	2.90097136122262	0.660261542400267	4.42506428407865	9.64135685964691e-06	0.00176496079093246	VENTX	VENT homeobox [Source:HGNC Symbol;Acc:HGNC:13639]
49.4979208562718	2.89372480194295	0.624884721811723	4.16294773364704	3.14165300015984e-05	0.00455511882784237	P3H3	prolyl 3-hydroxylase 3 [Source:HGNC Symbol;Acc:HGNC:19318]
107.290082397613	2.88681560114985	0.777892588209925	4.97302532559831	6.59160459218411e-07	0.000191144866616539	CDH5	cadherin 5 [Source:HGNC Symbol;Acc:HGNC:1764]
52.8415246249686	2.88588409510632	0.690247663959396	4.04382074499112	5.25871310519827e-05	0.00706219307504659	KNDC1	kinase non-catalytic C-lobe domain containing 1 [Source:HGNC Symbol;Acc:HGNC:29374]
57.2687112785428	2.87507478560376	0.661049023648912	4.15011742370431	3.3230475602907e-05	0.00475500534740636	FRAS1	Fraser extracellular matrix complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:19185]
35.4369155832836	2.87481175217786	0.674069474961157	4.19528027896421	2.72534368369784e-05	0.00404090777499597	RNF150	ring finger protein 150 [Source:HGNC Symbol;Acc:HGNC:23138]
378.447036450222	2.85819479656639	0.668368496437307	4.09749272758844	4.17649284939815e-05	0.00582363053996079	CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]
837.84184419414	2.83926219106468	0.587993547048011	4.51823988275332	6.23558161102271e-06	0.00123088878451803	PCDH12	protocadherin 12 [Source:HGNC Symbol;Acc:HGNC:8657]

10.8526931876588	2.83660089248552	0.764576560540286	3.55424532031908	0.000379065447851711	0.0313679284567277	TMC1	transmembrane channel like 1 [Source:HGNC Symbol;Acc:HGNC:16513]
5.82732033942762	2.82476325799267	0.629153327822004	3.61581932653382	0.000299399148556941	0.0263021750667931	LRRC74A	leucine rich repeat containing 74A [Source:HGNC Symbol;Acc:HGNC:23346]
554.328259608272	2.81269842438792	0.488373308426907	5.23938026285809	1.61116742820521e-07	6.3595811130393e-05	NBEA	neurobeachin [Source:HGNC Symbol;Acc:HGNC:7648]
36.1115542151713	2.80469689205543	0.518680056725092	4.73756215232181	2.1630452834815e-06	0.000518520531100909	ANKRD29	ankyrin repeat domain 29 [Source:HGNC Symbol;Acc:HGNC:27110]
12.0401955814036	2.79907181346084	0.729515380019208	3.40436763854568	0.000663174316059822	0.0468635139087056	SNTG1	syntrophin gamma 1 [Source:HGNC Symbol;Acc:HGNC:13740]
38.5280297446675	2.79722673062451	0.725552736956086	4.87659280507227	1.07933919362084e-06	0.000292295757822874	AMBN	ameloblastin [Source:HGNC Symbol;Acc:HGNC:452]
194.847849416644	2.78784815299715	0.643118566433024	4.11499833737512	3.87182205556909e-05	0.00542612820100479	STON2	stonin 2 [Source:HGNC Symbol;Acc:HGNC:30652]
21.017417429435	2.776497140732	0.738161068344811	3.59418169341791	0.000325412701256915	0.0282093211502291	KCNC3	potassium voltage-gated channel subfamily C member 3 [Source:HGNC Symbol;Acc:HGNC:6235]
443.918053604896	2.75773799287186	0.678539963605728	3.87617617333116	0.000106110868339747	0.0122431018794254	IL2RA	interleukin 2 receptor subunit alpha [Source:HGNC Symbol;Acc:HGNC:6008]
41.7130899642758	2.7510031337018	0.758546181452857	3.56218740036146	0.000367777699163449	0.0309008708876613	PARD3B	par-3 family cell polarity regulator beta [Source:HGNC Symbol;Acc:HGNC:14446]
683.442381998116	2.74445840802029	0.703711257846614	3.76645307008853	0.000165583191394446	0.016902897244901	RFX8	RFX family member 8, lacking RFX DNA binding domain [Source:HGNC Symbol;Acc:HGNC:37253]
734.031955489596	2.72427814211943	0.781973928288475	4.47747401220434	7.55314186714542e-06	0.00145589031001542	SNX7	sorting nexin 7 [Source:HGNC Symbol;Acc:HGNC:14971]
399.37915061209	2.72117869743745	0.654911212976223	4.14287358392842	3.42981024346983e-05	0.00488643574165302	SGCE	sarcoglycan epsilon [Source:HGNC Symbol;Acc:HGNC:10808]
12.5436464187855	2.70787709576152	0.77559795284455	3.81239263398424	0.000137628019039699	0.0147019722380067	SLC10A2	solute carrier family 10 member 2 [Source:HGNC Symbol;Acc:HGNC:10906]
32.8810736762102	2.70433295444676	0.632751302736337	3.98357847910515	6.78852392300044e-05	0.00858866223586403	CA7	carbonic anhydrase 7 [Source:HGNC Symbol;Acc:HGNC:1381]
406.019882962994	2.70084060593274	0.590812170441738	4.35672128695952	1.32025209248818e-05	0.00227694845087645	C14orf132	chromosome 14 open reading frame 132 [Source:HGNC Symbol;Acc:HGNC:20346]
18.843504131539	2.70066905516759	0.762475836489073	3.95458184796104	7.66686227882474e-05	0.00923631408649004	FAM47A	family with sequence similarity 47 member A [Source:HGNC Symbol;Acc:HGNC:29962]
252.528201349816	2.69765394286676	0.628982356736262	3.96809864677921	7.24483458093936e-05	0.00889133855985846	DUSP26	dual specificity phosphatase 26 [Source:HGNC Symbol;Acc:HGNC:28161]
4.97634380568222	2.69634371358233	0.75802262930116	3.70166070501612	0.000214192923903905	0.0207040523023102	PRR16	proline rich 16 [Source:HGNC Symbol;Acc:HGNC:29654]
66.8170520616941	2.69074907097021	0.706378153556831	3.45970923551788	0.000540758967361242	0.0402717950965754	KIAA1217	KIAA1217 [Source:HGNC Symbol;Acc:HGNC:25428]

1532.03499372606	2.69060922892463	0.462398532997771	5.2112657541176	1.87556552684645e-07	7.23041543337698e-05	CRADD	CASP2 and RIPK1 domain containing adaptor with death domain [Source:HGNC Symbol;Acc:HGNC:2340]
4584.56696287787	2.68676174450211	0.67566053059238	4.16409931813552	3.12584035811168e-05	0.00455233497131572	ENAM	enamelin [Source:HGNC Symbol;Acc:HGNC:3344]
859.227489824327	2.68441730582714	0.779536723010419	5.98145512523522	2.21152988616094e-09	1.76749783682248e-06	GPC6	glypican 6 [Source:HGNC Symbol;Acc:HGNC:4454]
151.406217539905	2.6843664707022	0.773017332403026	5.5559916675342	2.76040039921301e-08	1.43575873462558e-05	CHRNA1	cholinergic receptor nicotinic alpha 1 subunit [Source:HGNC Symbol;Acc:HGNC:1955]
247.413654611569	2.68081843926683	0.533510139748009	4.5780464276998	4.69338538391662e-06	0.000955235107206086	ROBO3	roundabout guidance receptor 3 [Source:HGNC Symbol;Acc:HGNC:13433]
163.756088853536	2.68009657621128	0.632279491138271	4.08099698656162	4.484293653687e-05	0.00614817298928936	WWTR1	WW domain containing transcription regulator 1 [Source:HGNC Symbol;Acc:HGNC:24042]
111.201373054051	2.6735430274241	0.602510331068634	3.97952171147999	6.90540537864983e-05	0.00866473562616089	ROBO4	roundabout guidance receptor 4 [Source:HGNC Symbol;Acc:HGNC:17985]
8.38561744169742	2.66136029333765	0.773568811313063	3.54397350483578	0.000394144852433217	0.0321445165382294	ARHGEF15	Rho guanine nucleotide exchange factor 15 [Source:HGNC Symbol;Acc:HGNC:15590]
183.567756167135	2.65005777649225	0.650442264595859	3.72406315849818	0.000196041847159414	0.0191187477610705	TBC1D8B	TBC1 domain family member 8B [Source:HGNC Symbol;Acc:HGNC:24715]
18.3454785717325	2.64937097374683	0.750637103259968	3.4980231519214	0.000468720441941646	0.0364822599561612	TRAPPC3L	trafficking protein particle complex 3 like [Source:HGNC Symbol;Acc:HGNC:21090]
103.284373219429	2.64149912941644	0.677047975736993	3.7397677930434	0.000184190327854238	0.0181793634431556	PEAR1	platelet endothelial aggregation receptor 1 [Source:HGNC Symbol;Acc:HGNC:33631]
217.424763158659	2.62698133342708	0.710816205587112	3.42772534455085	0.000608660913751104	0.044082979556636	ARHGAP29	Rho GTPase activating protein 29 [Source:HGNC Symbol;Acc:HGNC:30207]
6.44641970627799	2.61184088068919	0.781689956331147	3.43917601666477	0.000583487724588816	0.0426779592842105	CLEC4M	C-type lectin domain family 4 member M [Source:HGNC Symbol;Acc:HGNC:13523]
258.673298012874	2.55365690249442	0.664085935156196	3.48139039303768	0.000498817886488852	0.0382793079729899	EPB41L3	erythrocyte membrane protein band 4.1 like 3 [Source:HGNC Symbol;Acc:HGNC:3380]
122.319988494765	2.54950305849414	0.670921397291216	3.73036580636397	0.000191201960965892	0.0187584007692526	CA6	carbonic anhydrase 6 [Source:HGNC Symbol;Acc:HGNC:1380]
6.09944956222507	2.54546195882413	0.74045486444531	3.52963019759805	0.000416140890534201	0.0333401092934589	LINGO4	leucine rich repeat and Ig domain containing 4 [Source:HGNC Symbol;Acc:HGNC:31814]
15.2687063817246	2.53974958471106	0.752413236228732	3.4706913277491	0.000519120368313957	0.0392853030690803	NES	nestin [Source:HGNC Symbol;Acc:HGNC:7756]

24.8672964767629	2.53193643788301	0.780835503697003	3.46052108017762	0.000539131020686432	0.0402420165964761	CACNG8	calcium voltage-gated channel auxiliary subunit gamma 8 [Source:HGNC Symbol;Acc:HGNC:13628]
175.280317168686	2.53052542577398	0.704329396973056	3.53867766997989	0.000402136561120617	0.0324587614075781	MTUS1	microtubule associated scaffold protein 1 [Source:HGNC Symbol;Acc:HGNC:29789]
474.902129416853	2.50908359662137	0.652177581490927	3.87177589870211	0.000108045267986183	0.0124225520749868	RNF157	ring finger protein 157 [Source:HGNC Symbol;Acc:HGNC:29402]
27.2956719892689	2.50080690187256	0.683461635861927	3.60251247561962	0.000315156269881624	0.0275387750706162	SERP2	stress associated endoplasmic reticulum protein family member 2 [Source:HGNC Symbol;Acc:HGNC:20607]
191.459484130885	2.49812819540256	0.669129367316266	3.58365978573355	0.000338813337959829	0.0291530650392323	FERMT1	fermitin family member 1 [Source:HGNC Symbol;Acc:HGNC:15889]
8.58124730695063	2.49689802868032	0.763151427964986	3.61762972938108	0.000297313318659022	0.0262597380749834	ARC	activity regulated cytoskeleton associated protein [Source:HGNC Symbol;Acc:HGNC:648]
16249.821024814	2.49116635406538	0.676964964417246	3.81759443439885	0.00013475921229717	0.0145735639226193	JCHAIN	joining chain of multimeric IgA and IgM [Source:HGNC Symbol;Acc:HGNC:5713]
7.92901201237655	2.49026169602798	0.61072611833277	3.54335849234815	0.00039506526528966	0.0321445165382294	CFAP69	cilia and flagella associated protein 69 [Source:HGNC Symbol;Acc:HGNC:26107]
13.6552651102544	2.48910627546746	0.507683773511552	4.21615333555979	2.4850482183314e-05	0.0037699101860316	VMO1	vitelline membrane outer layer 1 homolog [Source:HGNC Symbol;Acc:HGNC:30387]
67.9455085946231	2.46654532587567	0.661875461327264	3.49966465773939	0.000465843796449626	0.0363446893382413	CCDC149	coiled-coil domain containing 149 [Source:HGNC Symbol;Acc:HGNC:25405]
545.117478545158	2.44960999702342	0.669958379109	3.47973844446983	0.000501903518168843	0.0384254240277554	STARD13	StAR related lipid transfer domain containing 13 [Source:HGNC Symbol;Acc:HGNC:19164]
30.4256890538168	2.44341908236805	0.672908233767932	3.44877952706876	0.000563126284618699	0.0416535487457912	DGKI	diacylglycerol kinase iota [Source:HGNC Symbol;Acc:HGNC:2855]
1049.68282796595	2.442791850222	0.681484212173472	3.59446806048764	0.000325055016241101	0.0282093211502291	NINL	ninein like [Source:HGNC Symbol;Acc:HGNC:29163]
21.9648017184518	2.43258133924641	0.720874816956026	3.4972203676675	0.00047013330186485	0.0365055166718185	GRIN2A	glutamate ionotropic receptor NMDA type subunit 2A [Source:HGNC Symbol;Acc:HGNC:4585]
6.81920371390937	2.42351175105786	0.780049141658381	3.50287352754774	0.000460267945637417	0.0359953700301835	GPIHBP1	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1 [Source:HGNC Symbol;Acc:HGNC:24945]
39.1520417966574	2.40776873653611	0.782017651131973	4.48025485889967	7.4553963361866e-06	0.0014455528233824	RERG	RAS like estrogen regulated growth inhibitor [Source:HGNC Symbol;Acc:HGNC:15980]
29.6281881815683	2.39449261975371	0.680593272094304	3.50413912856792	0.00045808596392221	0.0359876862723344	BHLHA15	basic helix-loop-helix family member a15 [Source:HGNC Symbol;Acc:HGNC:22265]

118.773586151417	2.36642903914062	0.430932806478197	4.78289165296349	1.72791273514593e-06	0.000425716124099713	GK3P	glycerol kinase 3 pseudogene [Source:HGNC Symbol;Acc:HGNC:4292]
105.005730685671	2.34383524577647	0.513264885253557	4.00465555436149	6.21079112794764e-05	0.00801240959372394	PIK3R6	phosphoinositide-3-kinase regulatory subunit 6 [Source:HGNC Symbol;Acc:HGNC:27101]
104.062426462053	2.33096902948192	0.552312085928729	3.68536748403197	0.000228372883962694	0.0216907903237379	SLC6A20	solute carrier family 6 member 20 [Source:HGNC Symbol;Acc:HGNC:30927]
30.0520545271972	2.31963448943348	0.517932280934164	3.84574506736388	0.000120186672471309	0.013486176796629	GPR162	G protein-coupled receptor 162 [Source:HGNC Symbol;Acc:HGNC:16693]
336.684952351462	2.31957173571422	0.54651898993967	3.84006144197405	0.000123003521930126	0.0136629810393436	EMILIN1	elastin microfibril interfacer 1 [Source:HGNC Symbol;Acc:HGNC:19880]
191.734703370437	2.30691004722653	0.504264261285566	4.04924481524365	5.13831717963201e-05	0.0069289044173773	SPTLC3	serine palmitoyltransferase long chain base subunit 3 [Source:HGNC Symbol;Acc:HGNC:16253]
1962.80348653293	2.29186860584798	0.583018940298888	3.43669379213438	0.000588860924655939	0.0429750440515052	GPRIN3	GPRIN family member 3 [Source:HGNC Symbol;Acc:HGNC:27733]
57.853297286766	2.26860235161099	0.781112352426949	4.41764461682192	9.97823065816696e-06	0.00181648145670453	HS3ST4	heparan sulfate-glucosamine 3-sulfotransferase 4 [Source:HGNC Symbol;Acc:HGNC:5200]
236.048083541565	2.266361835535	0.436598961986067	4.51078042604887	6.4589552220667e-06	0.00126734757315378	CARMIL1	capping protein regulator and myosin 1 linker 1 [Source:HGNC Symbol;Acc:HGNC:21581]
1858.28225606403	2.26408429830454	0.400689290248913	4.86469071516021	1.14635923862245e-06	0.00030493273137036	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2 [Source:HGNC Symbol;Acc:HGNC:9581]
249.474144077724	2.25154989709273	0.636408039757504	3.39970432625248	0.000674587567446982	0.047450851995674	MMP14	matrix metallopeptidase 14 [Source:HGNC Symbol;Acc:HGNC:7160]
819.964744650266	2.21159328495933	0.53018345373986	3.61903407317283	0.000295704705867108	0.0262592189752125	COLQ	collagen like tail subunit of asymmetric acetylcholinesterase [Source:HGNC Symbol;Acc:HGNC:2226]
496.995987171927	2.17286868418538	0.709970339142954	3.56047123799658	0.000370189859412833	0.0310239931284903	CR2	complement C3d receptor 2 [Source:HGNC Symbol;Acc:HGNC:2336]
302.730233082603	2.16429164028651	0.534346522375669	3.6254570767885	0.000288450806851407	0.025895769969608	SLC1A3	solute carrier family 1 member 3 [Source:HGNC Symbol;Acc:HGNC:10941]
1627.7385144071	2.15587128513375	0.367865644636724	5.06458276632318	4.09295786028616e-07	0.000131488277613585	S100A13	S100 calcium binding protein A13 [Source:HGNC Symbol;Acc:HGNC:10490]
64.9691674152933	2.15411604728458	0.57157766283795	3.41145668807171	0.000646167660554362	0.0458303504351631	RASIP1	Ras interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:24716]
76.6946599465213	2.09501497039021	0.500640388839619	3.54318048835475	0.000395332036282546	0.0321445165382294	MAFB	MAF bZIP transcription factor B [Source:HGNC Symbol;Acc:HGNC:6408]
165.226662338407	2.07463441347706	0.781478344261567	4.15358938278526	3.27300279361382e-05	0.00470393664654113	NTRK2	neurotrophic receptor tyrosine kinase 2 [Source:HGNC Symbol;Acc:HGNC:8032]

200.731895576469	2.06254274374442	0.475730746871866	3.66707939754807	0.000245336634710952	0.0228386103585468	KIAA1671	KIAA1671 [Source:HGNC Symbol;Acc:HGNC:29345]
305.156809345896	2.03990738430184	0.40431478492457	4.30740340112814	1.65182195283536e-05	0.00266634983992656	SCIMP	SLP adaptor and CSK interacting membrane protein [Source:HGNC Symbol;Acc:HGNC:33504]
16297.3015566173	2.02003731806019	0.22912462159179	7.46080012718239	8.59986238394521e-14	2.32315030034778e-10	GAB1	GRB2 associated binding protein 1 [Source:HGNC Symbol;Acc:HGNC:4066]
30.4430970486446	1.99623260686381	0.333340233349089	5.04204898438215	4.6057334370879e-07	0.000142559113632942	ENDOU	endonuclease, poly(U) specific [Source:HGNC Symbol;Acc:HGNC:14369]
219.255821104961	1.97428451030147	0.453350178438214	3.74199969225184	0.000182561738975399	0.0180730606125253	ARHGAP31	Rho GTPase activating protein 31 [Source:HGNC Symbol;Acc:HGNC:29216]
1023.44095384031	1.97426573721167	0.478846481509857	3.57461710928902	0.000350740798481165	0.0300249652293456	CNKSR3	CNKSR family member 3 [Source:HGNC Symbol;Acc:HGNC:23034]
58.7837142110803	1.97266274136577	0.488471789753487	3.45842608135967	0.000543341347165856	0.0403723566075528	NXPH3	neurexophilin 3 [Source:HGNC Symbol;Acc:HGNC:8077]
124.661819919339	1.96086424178048	0.337380790126652	4.91496009541126	8.88005450538383e-07	0.000246594598332557	ZDHHC15	zinc finger DHHC-type containing 15 [Source:HGNC Symbol;Acc:HGNC:20342]
446.379981979201	1.93444239422717	0.470878889336922	3.50682815189655	0.000453481908151943	0.0358929834935335	CD27	CD27 molecule [Source:HGNC Symbol;Acc:HGNC:11922]
257.138627137782	1.92996257663492	0.468021615752827	3.5368932553482	0.000404863263305981	0.0325959690712786	GAS6	growth arrest specific 6 [Source:HGNC Symbol;Acc:HGNC:4168]
219.66612461273	1.8998805831546	0.466770340011666	3.47635040078847	0.000508287713141673	0.0387338878702938	CUEDC1	CUE domain containing 1 [Source:HGNC Symbol;Acc:HGNC:31350]
1137.25662004218	1.8990920127238	0.449485117723996	3.54526837604305	0.000392213525754804	0.0321445165382294	MTSS1	MTSS1, I-BAR domain containing [Source:HGNC Symbol;Acc:HGNC:20443]
561.901457860764	1.89811960221293	0.432236128508589	3.76260336946712	0.000168153770189882	0.0169744778029598	IL21R	interleukin 21 receptor [Source:HGNC Symbol;Acc:HGNC:6006]
707.87432199718	1.89290559618954	0.320833272374709	4.9913147817203	5.99696719815814e-07	0.000178644201044769	CCDC152	coiled-coil domain containing 152 [Source:HGNC Symbol;Acc:HGNC:34438]
321.145530785277	1.88886450469293	0.779614778600122	4.31595715417709	1.58912803305061e-05	0.00260362736935012	RASEF	RAS and EF-hand domain containing [Source:HGNC Symbol;Acc:HGNC:26464]
27.0100556686905	1.82904822388202	0.411679223046543	3.71072096816622	0.000206669808059907	0.0200954192003176	SPACA6	sperm acrosome associated 6 [Source:HGNC Symbol;Acc:HGNC:27113]
1151.93147148435	1.82395449099761	0.35249944855603	4.30378614784206	1.67903742034009e-05	0.00268383893608313	CTDSPL	CTD small phosphatase like [Source:HGNC Symbol;Acc:HGNC:16890]
313.008274573079	1.81585847434022	0.398173117450576	3.79635266426506	0.000146840566799548	0.0153237952002789	C15orf52	chromosome 15 open reading frame 52 [Source:HGNC Symbol;Acc:HGNC:33488]
649.110451636333	1.79320190063088	0.304164039442251	4.91892318330901	8.70216094138013e-07	0.000243720008313798	C3orf52	chromosome 3 open reading frame 52 [Source:HGNC Symbol;Acc:HGNC:26255]
158.964377044911	1.78030314018725	0.364717516135608	4.04091113819894	5.32439322373113e-05	0.00712121294511109	DNAH7	dynein axonemal heavy chain 7 [Source:HGNC Symbol;Acc:HGNC:18661]

1843.02116284777	1.7690831435764	0.385962522477795	3.79729129887252	0.000146285847558917	0.0153146794019508	PHACTR1	phosphatase and actin regulator 1 [Source:HGNC Symbol;Acc:HGNC:20990]
1156.99550894749	1.73981748474248	0.277187685148976	5.15689947685824	2.51072501969559e-07	9.141270827265e-05	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5 [Source:HGNC Symbol;Acc:HGNC:10872]
7350.99987926577	1.71100752530055	0.316729811463711	4.43871129523426	9.04991126288331e-06	0.00167540956080317	NUDT4	nudix hydrolase 4 [Source:HGNC Symbol;Acc:HGNC:8051]
783.500525192629	1.66401877016772	0.383827325229159	3.56621439404172	0.000362175115112094	0.030586995288642	SNX8	sorting nexin 8 [Source:HGNC Symbol;Acc:HGNC:14972]
5853.38545456666	1.61815366388089	0.369148354413853	3.56329582880839	0.000366227561383415	0.0308497293866626	TMEM2	transmembrane protein 2 [Source:HGNC Symbol;Acc:HGNC:11869]
270.547595758921	1.43753744560609	0.309178875155729	3.64152013450975	0.000271032923336671	0.0247561312036364	AC072022.1	
147.965902517691	1.41264502411725	0.298778168229751	3.6705629266723	0.000242016877128835	0.0227220782001282	VASH1	vasohibin 1 [Source:HGNC Symbol;Acc:HGNC:19964]
8316.85827529801	1.31484478596752	0.280951765241993	3.57395052055272	0.000351635405930571	0.0300249652293456	EDEM1	ER degradation enhancing alpha-mannosidase like protein 1 [Source:HGNC Symbol;Acc:HGNC:18967]
313.482793234766	1.2673279752612	0.233057141517556	4.09125105862286	4.29052343540001e-05	0.00593214649498682	SELENON	selenoprotein N [Source:HGNC Symbol;Acc:HGNC:15999]
6401.94690132181	1.26665029125756	0.24034497579927	3.97289868001934	7.10032564997581e-05	0.00881133840516251	LPP	LIM domain containing preferred translocation partner in lipoma [Source:HGNC Symbol;Acc:HGNC:6679]
247.883929093682	1.25122001301303	0.269250494823412	3.49044595918951	0.000482215127651669	0.0371793536538585	ECT2L	epithelial cell transforming 2 like [Source:HGNC Symbol;Acc:HGNC:21118]
550.675697543634	0.846514647582926	0.140393865729315	3.76153393388242	0.000168874504509427	0.0169744778029598	RNF44	ring finger protein 44 [Source:HGNC Symbol;Acc:HGNC:19180]
149.752568255019	-4.34835873705086	0.706761127535214	-5.61545623039348	1.96044279434886e-08	1.05311130303645e-05	ROBO1	roundabout guidance receptor 1 [Source:HGNC Symbol;Acc:HGNC:10249]
304.689998778947	-3.98212954132138	0.747209524526148	-4.82028482742565	1.43353401456678e-06	0.00036401975768077	LAMP5	lysosomal associated membrane protein family member 5 [Source:HGNC Symbol;Acc:HGNC:16097]
547.553859957481	-3.83469378526549	0.663542671380716	-5.29976955554061	1.15948934064602e-07	4.74926833928609e-05	PTPRK	protein tyrosine phosphatase, receptor type K [Source:HGNC Symbol;Acc:HGNC:9674]
67.174097145466	-3.80217431645438	0.69442656814526	-5.04248685556512	4.59520330267986e-07	0.000142559113632942	ZNF99	zinc finger protein 99 [Source:HGNC Symbol;Acc:HGNC:13175]
151.648951798074	-3.62434027918731	0.782400268685035	-4.45997533724306	8.1969084839766e-06	0.00155257975261818	GOLGA8S	golgin A8 family member S [Source:HGNC Symbol;Acc:HGNC:44409]

59.3753489309547	-3.50027380409483	0.672227591407157	-4.7214501904814	2.34168981523995e-06	0.000548336535405152	KLHL13	kelch like family member 13 [Source:HGNC Symbol;Acc:HGNC:22931]
74.6564470522216	-3.324521196111	0.750867113900981	-4.0284959107056	5.61348370246452e-05	0.00735203164050137	RASAL1	RAS protein activator like 1 [Source:HGNC Symbol;Acc:HGNC:9873]
117.669695219274	-3.22288363901739	0.643242022603055	-4.54675794000904	5.44785929332256e-06	0.00108850886172923	MECOM	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:HGNC:3498]
69.2420297009199	-3.10333109502439	0.555942058639437	-5.04711551142401	4.48530195231204e-07	0.000142559113632942	ATP1A3	ATPase Na+/K+ transporting subunit alpha 3 [Source:HGNC Symbol;Acc:HGNC:801]
319.692031369761	-2.95348559645998	0.770302215546503	-3.39961512673365	0.000674807648620119	0.047450851995674	NELL1	neural EGFL like 1 [Source:HGNC Symbol;Acc:HGNC:7750]
1937.07995196128	-2.92556405689295	0.661926786434658	-3.98172397177738	6.84172081212356e-05	0.00862267336814096	IGLL1	immunoglobulin lambda like polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:5870]
56.3744523335769	-2.80362062922303	0.688270019801568	-3.66437282193973	0.000247945402476926	0.0230160763409742	PRR15	proline rich 15 [Source:HGNC Symbol;Acc:HGNC:22310]
18.6775183617935	-2.79798830700596	0.691463311181152	-3.62228147593015	0.000292016119035808	0.0260882253159006	TMEM132B	transmembrane protein 132B [Source:HGNC Symbol;Acc:HGNC:29397]
23.6595776433393	-2.77865628528677	0.723037816495288	-3.43091859955195	0.000601541077853092	0.0437057606188251	TFAP2A	transcription factor AP-2 alpha [Source:HGNC Symbol;Acc:HGNC:11742]
233.409333649414	-2.73245764967481	0.564345078243182	-4.34155542934452	1.41477576017956e-05	0.00237740369792635	TIFAB	TIFA inhibitor [Source:HGNC Symbol;Acc:HGNC:34024]
131.323937070538	-2.67366444346444	0.568375584399065	-4.21095187179311	2.54296923533296e-05	0.00384000073287514	DCANP1	dendritic cell associated nuclear protein [Source:HGNC Symbol;Acc:HGNC:24459]
548.4609942927	-2.66609738381045	0.610069602020319	-3.896310667135	9.76690930977053e-05	0.0113893980164612	PHLDB2	pleckstrin homology like domain family B member 2 [Source:HGNC Symbol;Acc:HGNC:29573]
16.8269369798557	-2.62822594985075	0.571284189608569	-4.08891795642043	4.33390093393699e-05	0.00596694394131291	SLC26A7	solute carrier family 26 member 7 [Source:HGNC Symbol;Acc:HGNC:14467]
11.5734690740221	-2.59201838093656	0.614725744804737	-3.74845927694618	0.000177924219371574	0.0177210359281694	SLC29A4	solute carrier family 29 member 4 [Source:HGNC Symbol;Acc:HGNC:23097]

299.124686787908	-2.45889610372007	0.497708855426995	-4.34376691540477	1.40060119126453e-05	0.00236571648635856	BAHCC1	BAH domain and coiled-coil containing 1 [Source:HGNC Symbol;Acc:HGNC:29279]
62.7636675006276	-2.37301289293366	0.598617941275282	-3.49367092716265	0.000476427886392492	0.0368197853332764	SIT1	signaling threshold regulating transmembrane adaptor 1 [Source:HGNC Symbol;Acc:HGNC:17710]
136.023402103177	-2.29689023894542	0.501088757545523	-3.99262561946512	6.53456953099196e-05	0.00833170328371769	LTK	leukocyte receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:6721]
2115.35556049857	-2.27351507997327	0.559260672178648	-3.54323488198471	0.000395250499794322	0.0321445165382294	CD96	CD96 molecule [Source:HGNC Symbol;Acc:HGNC:16892]
42.7658843828793	-2.22496693832719	0.523206428076375	-3.68560520133124	0.000228159809581045	0.0216907903237379	FBXO39	F-box protein 39 [Source:HGNC Symbol;Acc:HGNC:28565]
250.226282169275	-2.09584815962747	0.414329384591123	-4.3270148394239	1.51143782450481e-05	0.00248878364991827	ZBTB46	zinc finger and BTB domain containing 46 [Source:HGNC Symbol;Acc:HGNC:16094]
2052.02893697977	-1.7981119287927	0.417755982942862	-3.58354029943246	0.000338968438108749	0.0291530650392323	GPM6B	glycoprotein M6B [Source:HGNC Symbol;Acc:HGNC:4461]
944.713614123541	-1.56163873573979	0.363922992068653	-3.47911788968745	0.000503067227414156	0.0384254240277554	PRDM15	PR/SET domain 15 [Source:HGNC Symbol;Acc:HGNC:13999]
28.6893933622846	-1.51423521360164	0.323197493742891	-3.75332967864688	0.000174501112536121	0.0174330867548281	SAMD10	sterile alpha motif domain containing 10 [Source:HGNC Symbol;Acc:HGNC:16129]
57.7626617805079	-1.17398222763552	0.20130776276224	-4.26951921025729	1.95894777760377e-05	0.00307133018069475	NR2F6	nuclear receptor subfamily 2 group F member 6 [Source:HGNC Symbol;Acc:HGNC:7977]
2343.94728769998	-1.04000567344706	0.189677916561471	-3.81088946325757	0.000138467676003623	0.0147019722380067	CCSAP	centriole, cilia and spindle associated protein [Source:HGNC Symbol;Acc:HGNC:29578]
3000.05230222647	-1.03724025981851	0.209501293756832	-3.46356865844934	0.000533060538102191	0.0399710016305094	MYC	MYC proto-oncogene, bHLH transcription factor [Source:HGNC Symbol;Acc:HGNC:7553]

Supplementary Table 6
Enrichr, Chea 2016 database, only P.adj<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
SUZ12 20075857 ChIP-Seq MESCs Mouse	100/4356	3.732591488321989E-12	2.4075215099676828E-9	1.9051320447020181	RAB3B;TMEM200A;RASEF;KNDC1;ANTXR1;SYDE1;PEG10;CREB3L1;MYC;FAM19A1;BAHCC1;PRKCA;VASH1;NPNT;SHISA6;GPRIN3;GPR162;SCNN1A;PRR16;PRR15;LY6H;PHLDB2;DGKI;TSPYL5;KCNE3;NXPH3;LPL;TNFRSF11A;GRIN2A;STK33;SNTG1;EPB41L3;ST3GAL5;SNX7;SNX8;GPM6B;DRD5;FBXO39;ARHGAP29;INHBB;HSPA12B;NR2F6;TDRD1;FERMT1;MAFB;NBEA;PDE3A;SPATS2L;NES;ACVRL1;ROBO3;DAGLA;KCNC3;PEAR1;ELFN2;CHRDL1;RERG;RNF157;SERP2;GHR;SGCE;PCLO;MECOM;PSTPIP2;GRM8;PHACTR1;RNF150;DLGAP2;NINL;PTGIR;ARHGEF15;GAB1;CTDSPL;WNT9A;DUSP26;PARD3B;MMP14;RHOJ;SLC29A4;VWA2;GAS6;CUEDC1;LTK;ZBTB46;PON2;ATP1A3;KCNA5;THBS1;RASIP1;PRTG;GPC6;NTRK2;LINGO4;ECEL1;PLXDC2;POU4F1;NELL1;MYO1B;FRAS1;FAM171B	50.131489078879966
ZNF217 24962896 ChIP-Seq MCF-7 Human	44/1522	4.617436286168348E-8	1.4891232022892922E-5	2.399114508644991	DAGLA;RASEF;PLOD2;PIK3C2G;STON2;PTPRK;KALRN;LPP;THBS1;RERG;ROBO1;MIPOL1;SERP2;MECOM;MYC;ENPP2;ST3GAL5;TMC1;TFAP2A;EPHA4;CD96;NTRK2;STARD13;MTUS1;CTDSPL;PRKCA;C14ORF132;VASH1;PLXDC2;MTSS1;PARD3B;KIAA1217;TSPAN15;TMEM2;MYO1B;NR5A2;MAFB;FRAS1;NBEA;CNKSR3;PRR15;SPATS2L;CUEDC1;TSPYL5	40.52306196852831
MTF2 20144788 ChIP-Seq MESCs Mouse	67/2981	1.6116454905470783E-7	3.4650378046762184E-5	1.8652016018462714	ACVRL1;RAB3B;DAGLA;RASEF;KNDC1;PEAR1;ELFN2;ANTXR1;RERG;NUDT4;GHR;GRM8;RNF150;DLGAP2;BAHCC1;EPHA4;ARHGEF15;MTUS1;GAB1;CTDSPL;PRKCA;WNT9A;VASH1;NPNT;DUSP26;PARD3B;MMP14;RHOJ;SCNN1A;PRR16;PRR15;VWA2;GAS6;LY6H;PHLDB2;CUEDC1;DGKI;CHRNA1;LTK;PON2;LPL;ATP1A3;TNFRSF11A;PRTG;GRIN2A;SNTG1;EPB41L3;ST3GAL5;SNX7;GPC6;GPM6B;DRD5;NTRK2;EDEM1;ECEL1;FBXO39;ARHGAP29;INHBB;POU4F1;TDRD1;FERMT1;NELL1;MAFB;FRAS1;NBEA;PDE3A;NES	29.173319729101188
AR 19668381 ChIP-Seq PC3 Human	74/3519	4.128684041157776E-7	6.657503016366913E-5	1.7451204427889382	CLEC4M;PLOD2;KNDC1;PIK3C2G;LDB3;PTPRK;CHRDL1;ROBO1;CREB3L1;RPS6KA2;MCF2L;GRM8;FAM19A1;PHACTR1;RNF150;TMC1;EPHA4;CD96;MTUS1;GAB1;PRKCA;NPNT;PARD3B;NR5A2;RHOJ;CNKSR3;SCNN1A;SLC29A4;COL6A3;DGKI;PRTFDC1;LTK;DNAH7;HHLA2;NXPH3;ZBTB46;PCDH15;PRDM15;SLC1A3;ATP1A3;TNFRSF11A;KLHL13;KALRN;LPP;THBS1;PRTG;GRIN2A;STK33;CALD1;SNTG1;GPC6;DRD5;TFAP2A;NTRK2;STARD13;OPN4;CRADD;EDEM1;TMEM132B;ECEL1;RASSF8;ARHGAP29;INHBB;PLXDC2;HSPA12B;HS3ST4;COLQ;SLC2A9;TSPAN15;NELL1;FRAS1;NBEA;SLC26A7;LPIN3	25.653509466354098
SUZ12 18974828 ChIP-Seq MESCs Mouse	48/1934	9.861725822227687E-7	1.2721626310673717E-4	2.0596703669216936	LTK;KCNE3;PON2;RASEF;LPL;KCNA5;PLOD2;TNFRSF11A;ANTXR1;CHRDL1;THBS1;RERG;GRIN2A;SNTG1;CREB3L1;GRM8;RNF150;DLGAP2;GPC6;GPM6B;DRD5;EPHA4;NTRK2;ECEL1;MTUS1;GAB1;CTDSPL;ARHGAP29;INHBB;VASH1;PLXDC2;NPNT;DUSP26;POU4F1;PARD3B;GPRIN3;TDRD1;NELL1;MAFB;FRAS1;PRR16;PDE3A;PRR15;VWA2;GAS6;LY6H;NES;DGKI	28.484076358804696
SUZ12 18692474 ChIP-Seq	45/1909	8.903354150592815E-6	9.571105711887276E-4	1.9562283048847022	ACVRL1;RAB3B;LTK;KCNE3;PON2;RASEF;LPL;TNFRSF11A;RERG;PRTG;GRIN2A;SNTG1;GRM8;RNF150;DLGAP2;GPC6;GPM6B;DRD5;EPHA4;NTRK2;ECEL1;GAB1;PRKCA;INHBB;WNT9A;VASH1;NPNT;DUSP26;POU4F1;MTSS1;PARD3B;NELL1;PTP4A3;MAFB;FRAS1;RHOJ;PRR16;PDE3A;VWA2;GAS6;LY6H;PHLDB2;NES;CUEDC1;DGKI	22.749140309896852

MESCs Mouse						
SMARCD1 25818293 ChIP-Seq ESCs Mouse	48/2119	1.2204212813162046E-5	0.001124531037784217	1.879850160276808	OCA2;PON2;MEI4;PCDH15;NRXN3;PLOD2;STON2;PTPRK;GDPD4;LPP;RASIP1;ROBO1;GHR;PRTG;GRIN2A;CACNG8;MECOM;SNTG1;GRM8;ST3GAL5;PHACTR1;RNF150;SNX7;SNX8;DLGAP2;GPC6;SAMD10;GPM6B;WWTR1;CRADD;ARHGEF15;TMEM132B;MTUS1;ABCA9;GAB1;HS3ST4;SHISA6;PARD3B;FERMT1;NELL1;MYO1B;FRAS1;NBEA;PRR16;SLC26A7;COL6A3;GAS6;DGKI	21.268115938087053
TP63 23658742 ChIP-Seq EP156T Human	70/3652	2.6634707132677645E-5	0.0021474232625721353	1.5906704903355404	RAB3B;TMEM200A;RASEF;KIAA1671;PLOD2;PIK3C2G;STON2;PTPRK;ANTXR1;NUDT4;ROBO1;ADAMTSL1;SERP2;MECOM;SPTLC3;PSTPIP2;PEG10;MYC;GRM8;ENPP2;CA6;TMC1;CD96;MTUS1;GAB1;CTDSPL;C15ORF52;WNT9A;MTSS1;RFX8;MMP14;TMEM2;NR5A2;CNKSR3;VWA2;LY6H;CUEDC1;DGKI;OCA2;CALCRL;HHLA2;NXPH3;SLC1A3;RASAL1;PCDH12;GDPD4;KLHL13;THBS1;STK33;CALD1;ST3GAL5;SNX7;GPC6;DRD5;TFAP2A;WWTR1;ANKRD29;NTRK2;CRADD;EDEM1;TMEM132B;PLXDC2;NR2F6;SLC2A9;FERMT1;MAS1;FRAS1;NBEA;SPATS2L;SLC26A7	16.75500217982376
ARNT 22903824 ChIP-Seq MCF-7 Human	28/1029	4.974791908923525E-5	0.0035652675347285262	2.258164676659045	RAB3B;PRDM15;SLC1A3;PIK3C2G;PTPRK;KLHL13;RERG;ROBO1;PCLO;SNTG1;PHACTR1;RNF150;NINL;GPC6;ADAMTS9;TFAP2A;EPHA4;ANKRD29;STARD13;RASSF8;INHBB;WNT9A;HS3ST4;RFX8;TMEM2;MYO1B;NBEA;SPATS2L	22.375119366780172
SMAD4 21799915 ChIP-Seq A2780 Human	51/2464	6.971437800660214E-5	0.004496577381425838	1.7176806595893732	KCNC3;RASEF;KIAA1671;ROBO1;ADAMTSL1;RNF157;PCLO;SPTLC3;RPS6KA2;SLCO2B1;GRM8;ENPP2;C3ORF52;FAM19A1;PHACTR1;ADAMTS9;CD96;GAB1;PRKCA;SHISA6;PARD3B;KIAA1217;GPRIN3;RFX8;TMEM2;COL6A3;ECT2L;DGKI;CALCRL;CCDC149;PCDH15;NRXN3;SLC1A3;KALRN;LPP;THBS1;GRIN2A;STK33;SNTG1;WWTR1;STARD13;OPN4;TMEM132B;PLXDC2;FERMT1;NELL1;MYO1B;FRAS1;NBEA;SPATS2L;NES	16.44010019273078
SUZ12 18555785 ChIP-Seq MESCs Mouse	28/1058	8.033714331791014E-5	0.00471067794909564	2.1962679133101677	ACVRL1;RASEF;ATP1A3;KCNA5;KNDC1;TNFRSF11A;ANTXR1;GHR;GRIN2A;PEG10;GRM8;RNF150;DLGAP2;DRD5;ECEL1;GAB1;NPNT;DUSP26;POU4F1;NELL1;MAFB;FRAS1;PRR16;PDE3A;LY6H;PHLDB2;NES;DGKI	20.70922178682309
AR 22383394 ChIP-Seq PROSTATE CANCER Human	41/1857	1.0478671711382985E-4	0.005632286044868355	1.832250741279492	RAB3B;DAGLA;TMEM200A;HHLA2;PCDH15;NRXN3;STON2;KALRN;CHRDL1;LPP;THBS1;MIPOL1;ADAMTSL1;SERP2;GHR;MECOM;CREB3L1;ST3GAL5;PHACTR1;EPHA4;WWTR1;ANKRD29;STARD13;SLC10A2;EDEM1;GAB1;PRKCA;C14ORF132;VASH1;NPNT;GPRIN3;NELL1;TMEM2;MYO1B;MAFB;NBEA;SPATS2L;SLC26A7;COL6A3;PHLDB2;DGKI	16.78998273248897
CEBPD 23245923 ChIP-Seq MEFs Mouse	17/504	1.3992462818086037E-4	0.006942414244358071	2.799183297108608	EPHA4;CALCRL;SLC10A2;MTUS1;SLC1A3;TNFRSF11A;PLXDC2;LPP;PARD3B;GHR;CDH5;MECOM;NBEA;MCF2L;ST3GAL5;RNF150;SNX7	24.841090867730948
CTBP2 25329375 ChIP-Seq	27/1053	1.816143670462131E-4	0.008367233338914818	2.127885945313331	RASEF;PCDH15;PLOD2;ELFN2;ROBO1;ADAMTSL1;TMEM100;GRIN2A;PCLO;SPTLC3;SNTG1;GRM8;ENPP2;GPC6;MUC4;EDEM1;TMEM132B;C14ORF132;DUSP26;HS3ST4;NELL1;FOLH1;MAFB;NBEA;PRR16;PDE3A;PHLDB2	18.32881153577147

LNCAP Human						
GBX2 23144817 ChIP-Seq PC3 Human	12/286	1.9337087212627194E-4	0.008314947501429694	3.4819951832399965	GHR;NELL1;NR5A2;PCDH15;ABCA9;FAM19A1;SLC26A7;PHACTR1;RNF150;COLQ;ROBO1;PARD3B	29.77419468683292
P300 19829295 ChIP-Seq ESCs Human	42/2000	2.5400087692875893E-4	0.010239410351190595	1.7427385892116183	CCDC149;HHLA2;FAM47A;PRDM15;KIAA1671;PIK3C2G;PTPRK;TNFRSF11A;ANTXR1;MIPOL1;ADAMTSL1;CDH5;GRIN2A;PCLO;MECOM;SPTLC3;SNTG1;CREB3L1;C3ORF52;CCL2;DLGAP2;GPC6;MUC4;TFAP2A;EPHA4;CRADD;SLC10A2;PLXDC2;HS3ST4;SHISA6;PARD3B;KIAA1217;MAS1;NELL1;TMEM2;FRAS1;NBEA;CNKSR3;PRR16;PDE3A;COL6A3;DGKI	14.426691253776069
AHR 22903824 ChIP-Seq MCF-7 Human	20/690	2.7750800846911954E-4	0.01052898032132836	2.4054362860063745	TFAP2A;EPHA4;ANKRD29;STARD13;PRDM15;RASSF8;SLC1A3;INHBB;WNT9A;RERG;ROBO1;RFX8;TMEM2;PCLO;NBEA;SNTG1;SPATS2L;PHACTR1;GPC6;ADAMTS9	19.699707176248793
ZFP57 27257070 Chip-Seq ESCs Mouse	27/1088	3.0546525279714296E-4	0.010945838225230957	2.0594337319990235	PLOD2;PTPRK;GDPD4;CHRDL1;THBS1;RERG;ROBO1;CDH5;SPTLC3;SNTG1;PEG10;RNF150;GPC6;TMC1;EPHA4;CR2;SLC10A2;EDEM1;VASH1;PLXDC2;DUSP26;POU4F1;PARD3B;NBEA;PRR16;SPATS2L;FAM171B	16.668386331822752
WT1 25993318 ChIP-Seq PODOCYTE Human	63/3464	3.5825957477388944E-4	0.012161969775218879	1.509300163866875	RAB3B;ROBO3;DAGLA;LDB3;ELFN2;ANTXR1;NUDT4;ROBO1;RNF157;SERP2;TMEM100;EMILIN1;PHACTR1;RNF150;DLGAP2;BAHCC1;ADAMTS9;EPHA4;PTGIR;GAB1;CTDSPL;PRKCA;VASH1;DUSP26;MTSS1;SHISA6;PARD3B;RFX8;PTP4A3;CNKSR3;PRR15;COL6A3;VWA2;LTK;CCDC149;NXPH3;NRXN3;RASAL1;KALRN;LPP;THBS1;GRIN2A;CALD1;EPB41L3;ST3GAL5;GPC6;WWTR1;NTRK2;CRADD;SLC10A2;EDEM1;ARHGAP29;INHBB;PLXDC2;HSPA12B;NR2F6;TDRD1;TSPAN15;MAFB;FRAS1;PDE3A;SLC26A7;NES	11.975168998524289
AR 25329375 ChIP-Seq VCAP Human	40/1906	3.6905656826471495E-4	0.011902074326537056	1.7416065449573959	OCA2;PON3;CALCRL;KCNC3;PLOD2;STON2;KALRN;RERG;NUDT4;ROBO1;MIPOL1;RNF157;GHR;PRTG;PCLO;MECOM;SPTLC3;CALD1;MYC;ENPP2;ST3GAL5;CCL2;GPC6;DRD5;TMC1;EPHA4;CD96;NTRK2;STARD13;CRADD;EDEM1;RASSF8;MTSS1;KIAA1217;TMEM2;NR5A2;FRAS1;SPATS2L;SLC26A7;LY6H	13.766634518019675
RNF2 27304074 Chip-Seq ESCs Mouse	33/1467	3.855123532249063E-4	0.011840736563336408	1.8667956452748857	ROBO3;ZBTB46;FAM47A;RASEF;KCNA5;KALRN;RASIP1;RERG;RNF157;GRIN2A;JPH2;SNTG1;CREB3L1;DLGAP2;GPC6;BAHCC1;NTRK2;ARHGEF15;ECEL1;INHBB;WNT9A;POU4F1;SHISA6;PARD3B;TDRD1;ARHGAP31;NR5A2;MAFB;FRAS1;NBEA;PRR15;SPATS2L;VWA2	14.674763558233934
UBF1/2 26484160 Chip-Seq FIBROBLAST Human	41/2000	4.982779048706993E-4	0.014608602210981867	1.7012448132780085	DAGLA;CCDC149;RASEF;NRXN3;SLC1A3;PLOD2;PIK3C2G;PCDH12;PTPRK;ROBO1;MIPOL1;ADAMTSL1;SERP2;TMEM100;PRTG;GRIN2A;STK33;CREB3L1;MYC;PHACTR1;ADAMTS9;TMC1;PTGIR;CRADD;SLC10A2;EDEM1;RASSF8;ARHGAP29;ZNF99;PLXDC2;SHISA6;KIAA1217;TSPAN15;TMEM2;FOLH1;IL2RA;PDE3A;VWA2;DGKI;PRTFDC1;TSPYL5	12.936865410033231
STAT3 23295773 ChIP-Seq U87 Human	58/3165	5.47696833897327E-4	0.01535932425494678	1.520782941010665	RAB3B;DAGLA;KCNC3;PLOD2;PIK3C2G;PTPRK;ANTXR1;ROBO1;ADAMTSL1;SERP2;GHR;TIFAB;PSTPIP2;RPS6KA2;GRM8;CA6;RNF150;ADAMTS9;CR2;MTUS1;CTDSPL;PRKCA;PARD3B;KIAA1217;FOLH1;RHOJ;PRR16;DGKI;OCA2;DNAH7;NXPH3;PCDH15;NRXN3;LPL;SLC1A3;LPP;MIPOL1;STK33;CALD1;EPB41L3;IL21R;ST3GAL5;SNX8;GPC6;GPM6B;WWTR1;	11.420758464824747

					TMEM132B;ABCA9;RASSF8;PLXDC2;COLQ;MAS1;TSPAN15;NELL1;MYO1B;NBEA;PDE3A;SPATS2L	
SUZ12 18692474 ChIP-Seq MEFs Mouse	27/1135	5.870289179769193E-4	0.015776402170629703	1.974153216224615	ACVRL1;RAB3B;LTK;KCNE3;LPL;TNFRSF11A;GRIN2A;SNTG1;GRM8;GPC6;GPM6B;DRD5;EPHA4;NTRK2;ECEL1;GAB1;PRKCA;INHBB;DUSP26;POU4F1;PTP4A3;MAFB;PRR16;PDE3A;GAS6;LY6H;NES	14.688561597896372
IKZF1 21737484 ChIP-ChIP HCT116 Human	8/155	5.95489216060615E-4	0.015363621774363867	4.283228483469415	PTGIR;CACNG8;CALD1;KCNC3;CCR6;PLXDC2;ADAMTS9;MUC4	31.807799880639593
TP53 23651856 ChIP-Seq MEFs Mouse	58/3193	6.840988084616009E-4	0.016970912748374332	1.5074469177258865	ROBO3;ROBO4;DAGLA;PLOD2;LDB3;ANTXR1;ROBO1;ADAMTSL1;RNF157;GHR;JPH2;PCLO;MECOM;SIT1;RPS6KA2;FAM19A1;RNF150;DLGAP2;NINL;BAHCC1;TMC1;EPHA4;ARHGEF15;MTUS1;PRKCA;WNT9A;PARD3B;ARC;MMP14;PTP4A3;GAS6;PHLDB2;CUEDC1;MATN3;DGKI;OCA2;LTK;ZBTB46;PCDH15;SLC1A3;PCDH12;KALRN;LPP;THBS1;CALD1;EPB41L3;IL21R;GPC6;NTRK2;STARD13;OPN4;PLXDC2;COLQ;SLC2A9;NELL1;NBEA;PDE3A;NES	10.985381020194465
CEBPD 21427703 ChIP-Seq 3T3-L1 Mouse	36/1735	9.203196837480552E-4	0.021985414667314653	1.7219319119423153	CALCRL;LPL;SLC1A3;ANTXR1;LPP;THBS1;RERG;ROBO1;SERP2;GHR;SGCE;CDH5;MECOM;CALD1;PEG10;CREB3L1;MYC;ENPP2;CCL2;PHACTR1;GPC6;BAHCC1;TMC1;STARD13;SLC10A2;EDEM1;INHBB;PLXDC2;HSPA12B;GPRIN3;TMEM2;NBEA;CNKSR3;PRR16;GAS6;DGKI	12.037663471079751
SMC1 22415368 ChIP-Seq MEFs Mouse	40/2000	9.507964713948065E-4	0.02190227585891608	1.6597510373443984	ROBO3;TMEM200A;SLC1A3;PCDH12;STON2;PTPRK;PEAR1;ELFN2;ANTXR1;THBS1;RASIP1;SERP2;VMO1;GRIN2A;JPH2;MECOM;CREB3L1;MYC;FAM19A1;CCL2;EMILIN1;SNX7;GPC6;BAHCC1;EPHA4;CD96;NTRK2;CRADD;FAM26E;MFSD6L;ABCA9;PRKCA;INHBB;WNT9A;PLXDC2;MYO1B;CNKSR3;SPATS2L;NES;CUEDC1	11.548897151338025
CJUN 26792858 Chip-Seq BT549 Human	40/2000	9.507964713948065E-4	0.021147024967229318	1.6597510373443984	RAB3B;KIAA1671;SLC1A3;PLOD2;STON2;PTPRK;TNFRSF11A;SLC6A20;CHRDL1;RERG;ROBO1;ADAMTSL1;SERP2;GRIN2A;PCLO;SPTLC3;PEG10;CA6;GPC6;TFAP2A;ANKRD29;CRADD;MTUS1;ABCA9;GAB1;CTDSPL;ARHGAP29;PLXDC2;NPNT;HSPA12B;KIAA1217;TMEM2;MYO1B;CNKSR3;PRR16;PDE3A;GAS6;PHLDB2;PRTFDC1;TSPYL5	11.548897151338025
JARID2 20064375 ChIP-Seq MESCs Mouse	26/1117	0.0010193015325535456	0.02191498294990123	1.9316708581447788	LTK;RASEF;TNFRSF11A;ELFN2;PRTG;GRIN2A;JPH2;GRM8;RNF150;DLGAP2;DRD5;NTRK2;ECEL1;INHBB;NPNT;POU4F1;PARD3B;NELL1;MAFB;FRAS1;NBEA;PRR16;PDE3A;VWA2;NES;DGKI	13.306580616771273
JARID2 20075857 ChIP-Seq MESCs Mouse	28/1258	0.001281617025194806	0.026665902620988703	1.8470997235947197	LTK;NXPH3;RASEF;ATP1A3;ELFN2;GHR;PRTG;GRIN2A;MECOM;GRM8;DLGAP2;GPC6;GPM6B;DRD5;NTRK2;ECEL1;CTDSPL;WNT9A;DUSP26;SHISA6;FERMT1;NELL1;MAFB;FRAS1;PDE3A;VWA2;NES;DGKI	12.301005714629076
SOX2 21211035	60/3420	0.0012961239357923023	0.026124998080813592	1.4559219625828055	PLOD2;KNDC1;STON2;ANTXR1;ROBO1;ADAMTSL1;GHR;VMO1;CDH5;PSTPIP2;SLCO2B1;GRM8;FAM19A1;PHACTR1;DLGAP2;ADAMTS9;EPHA4;RNF44;GAB1;CTDSPL;PRKCA;DU	9.679518171587524

ChIP-Seq LN229 Gbm					SP26;ZDHHC15;PARD3B;GPRIN3;ARC;TMEM2;NR5A2;FOLH1;PRR16;PRR15;TSPYL5;CALCRL;KCNE3;DNAH7;PCDH15;PRDM15;NRXN3;SLC1A3;ATP1A3;KALRN;LPP;THBS1;GRIN2A;CALD1;ST3GAL5;SNX7;GPC6;NTRK2;STARD13;SLC10A2;TMEM132B;ECEL1;PLXDC2;TDRD1;SLC2A9;NELL1;MAFB;NBEA;CD27	
JUN 26020271 ChIP-Seq SMOOTH MUSCLE Human	39/2000	0.0017641228027997493	0.034480582054722375	1.6182572614107884	PON3;ROBO4;TMEM200A;RASEF;STON2;PTPRK;GDPD4;TNFRSF11A;ELFN2;ANTXR1;SERP2;TMEM100;STK33;MYC;SLCO2B1;C3ORF52;CA6;SNX7;GPIHBP1;TMC1;WWTR1;CD96;RNF44;MFSD6L;RASSF8;C14ORF132;WNT9A;KIAA1217;SLC2A9;TSPAN15;TMEM2;MYO1B;ENAM;SCNN1A;PRR16;FAM171B;GAS6;PHLDB2;PRTFDC1	10.259915626602439
TOP2B 26459242 ChIP-Seq MCF-7 Human	39/2000	0.0017641228027997493	0.03346644728840701	1.6182572614107884	OCA2;NRXN3;SLC1A3;PLOD2;KALRN;LPP;RERG;ROBO1;ADAMTSL1;GHR;JPH2;PCLO;MECOM;SPTLC3;SNTG1;PEG10;DLGAP2;DRD5;EPHA4;NTRK2;RNF44;EDEM1;TMEM132B;ABCA9;C14ORF132;NPNT;HS3ST4;PARD3B;FERMT1;MAS1;NELL1;NBEA;CNKSR3;PRR16;PRR15;SLC29A4;LY6H;ECT2L;DGKI	10.259915626602439
TBX3 20139965 ChIP-Seq MESCs Mouse	24/1068	0.0025228492464299487	0.04649250754135192	1.864888806004942	NTRK2;STARD13;DAGLA;RASEF;PCDH15;SLC1A3;PLXDC2;CHRDL1;POU4F1;MTSS1;RASIP1;NR2F6;GHR;TMEM100;MYO1B;NR5A2;SIT1;MYC;MCF2L;EPB41L3;PDE3A;RNF150;DLGAP2;GPC6	11.156448063444802
SMARCA4 23332759 ChIP-Seq OLIGODENDROCYTES Mouse	46/2522	0.0025502787109381838	0.045692493570975795	1.5136508270785554	CALCRL;PON2;MEI4;NRXN3;LPL;SLC1A3;PIK3C2G;STON2;PTPRK;NUDT4;ROBO1;SERP2;GHR;TMEM100;MECOM;SNTG1;MYC;EPB41L3;SNX7;ADAMTS9;GPM6B;TMC1;EPHA4;CD96;NTRK2;STARD13;CRADD;SLC10A2;TMEM132B;MTUS1;GAB1;PRKCA;PLXDC2;DUSP26;LYVE1;SHISA6;PARD3B;NR5A2;FOLH1;CNKSR3;PDE3A;SPATS2L;SLC26A7;NES;CUEDC1;DGKI	9.038845573372782

NCI Nature 2016 database, only P<0.10 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Combined Score	Genes
EPHA forward signaling Homo sapiens f25420e8-6191-11e5-8ac5-06603eb7f303	3/34	0.007850799846031632	1.0	7.32243104710764	35.49284740906143	EPHA4;ARHGEF15;PIK3R6
Thromboxane A2 receptor signaling Homo sapiens 27d5800d-6196-11e5-8ac5-06603eb7f303	3/56	0.030001822921021278	1.0	4.445761707172496	15.589050689679897	PTGIR;PRKCA;PIK3R6
SHP2 signaling Homo sapiens 85755aa4-6195-11e5-8ac5-06603eb7f303	3/57	0.031394823199539006	1.0	4.3677658877484165	15.117328088738082	NTRK2;IL2RA;GAB1
Neurotrophic factor-mediated Trk receptor signaling Homo sapiens 774988f5-6194-11e5-8ac5-06603eb7f303	3/61	0.037299882536403	1.0	4.081355009863275	13.422617923251844	NTRK2;MCF2L;GAB1
Validated nuclear estrogen receptor alpha network Homo sapiens 58949883-6196-11e5-8ac5-06603eb7f303	3/64	0.04207451045748936	1.0	3.8900414937759336	12.324869712021147	MYC;PRDM15;POU4F1
IL8- and CXCR1-mediated signaling events Homo sapiens f6a58ef3-6193-11e5-8ac5-06603eb7f303	2/28	0.04451070740410945	1.0	5.927682276229993	18.447098416897465	PRKCA;PIK3R6
Beta1 integrin cell surface interactions Homo sapiens 2fd0bc63-618d-11e5-8ac5-06603eb7f303	3/66	0.045419771393499536	1.0	3.7721614485099964	11.662798096890265	COL6A3;NPNT;THBS1
Signaling events mediated by VEGFR1 and VEGFR2 Homo sapiens d6f6ae1f-6195-11e5-8ac5-06603eb7f303	3/68	0.04889294413398138	1.0	3.66121552355382	11.049995794426364	CDH5;GAB1;PRKCA
IL2 signaling events mediated by STAT5 Homo sapiens 9938526b-6193-11e5-8ac5-06603eb7f303	2/30	0.050430896440373164	1.0	5.532503457814661	16.526424714340614	MYC;IL2RA
Syndecan-4-mediated signaling events Homo sapiens 076bc549-6196-11e5-8ac5-06603eb7f303	2/31	0.053491286061194694	1.0	5.354035604336769	15.677882563014219	PRKCA;THBS1
Regulation of Ras family activation Homo sapiens 397d91c7-6195-11e5-8ac5-06603eb7f303	2/31	0.053491286061194694	1.0	5.354035604336769	15.677882563014219	RASAL1;PRKCA
IL8- and CXCR2-mediated signaling events Homo sapiens fe78e284-6193-11e5-8ac5-06603eb7f303	2/34	0.06304957149588485	1.0	4.881620698071759	13.491989323178268	PRKCA;PIK3R6
IL2 signaling events mediated by PI3K Homo sapiens 8bbf39aa-6193-11e5-8ac5-06603eb7f303	2/35	0.06635491067396887	1.0	4.742145820983995	12.864196843047813	MYC;IL2RA
PDGFR-beta signaling pathway Homo sapiens c901a3e4-6194-11e5-8ac5-06603eb7f303	4/128	0.06930470200280744	1.0	2.5933609958506225	6.922309453111056	MYC;GAB1;PRKCA;PIK3R6
Class IB PI3K non-lipid kinase events Homo sapiens 263703f8-6191-11e5-8ac5-06603eb7f303	1/6	0.0701648752848036	0.97763059563493	13.831258644536652	36.748374069662006	PIK3R6
Signaling events regulated by Ret tyrosine kinase Homo sapiens e4431190-6195-11e5-8ac5-06603eb7f303	2/38	0.07660255718312824	1.0	4.3677658877484165	11.221335746674201	GAB1;PRKCA
BMP receptor signaling Homo sapiens 2a3c66e7-618e-11e5-8ac5-06603eb7f303	2/42	0.09097392706510637	1.0	3.951788184153329	9.473156804136863	CTDSPL;CHRDL1
EphrinA-EPHA pathway Homo sapiens 1fd12dbd-6192-11e5-8ac5-06603eb7f303	1/8	0.092446044133206	1.0	10.37344398340249	24.700519826984653	EPHA4
Ceramide signaling pathway Homo sapiens d3747df2-6190-11e5-8ac5-06603eb7f303	2/44	0.09843270201571447	1.0	3.7721614485099964	8.745311929753864	CRADD;MYC

KEA 2015 database, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Combined Score	Genes
PAK2	3/15	7.06347365139663E-4	0.30231667227977577	16.597510373443985	120.42163357445777	CALD1;MYC;MYL9
CSNK1A1	5/84	0.0034743197337771797	0.7435044230283164	4.939735230191661	27.970542280147225	DAGLA;PCLO;ENAM;EPB41L3;DLGAP2
CDK5	5/97	0.006397001006610164	0.9126388102763835	4.277708859135047	21.610668568069254	NTRK2;GRIN2A;MYC;KALRN;NES
CDK15	3/36	0.009203982425330309	0.984826119510343	6.915629322268326	32.42129333520625	GRIN2A;CALD1;NES
CDK18	3/37	0.009928410722557174	0.8498719578508942	6.72872042166648	31.035246350667034	GRIN2A;CALD1;NES
CDK11A	3/38	0.010685104910941845	0.7622041503138517	6.551648831622625	29.73730883424778	GRIN2A;CALD1;NES
MYLK4	1/1	0.012049887812373218	0.736764569099391	82.98755186721992	366.6970895655858	MYL9
MYLK3	1/1	0.012049887812373218	0.6446689979619672	82.98755186721992	366.6970895655858	MYL9
CIT	1/1	0.012049887812373218	0.5730391092995264	82.98755186721992	366.6970895655858	MYL9
LTK	1/1	0.012049887812373218	0.5157351983695737	82.98755186721992	366.6970895655858	LTK
MTOR	4/78	0.01463982634934086	0.569622334319808	4.255771890626662	17.976421457189655	MYC;ARHGAP29;PHLDB2;NES
CDK14	3/43	0.014960483367879994	0.5335905734543864	5.789829200038599	24.330848188385332	GRIN2A;CALD1;NES
EPHA4	1/2	0.023955228768517783	0.7886798394558162	41.49377593360996	154.83687380767483	EPHA4
PIK3CG	1/3	0.03571770591610492	1.0	27.662517289073303	92.17451588131405	PIK3C2G
PIM2	1/3	0.03571770591610492	1.0	27.662517289073303	92.17451588131405	MYC
PRKCA	10/442	0.042358813546768834	1.0	1.8775464223352922	5.93601090376095	GRIN2A;JPH2;PTGIR;KCNE3;IL2RA;PDE3A;PRKCA;KCNA5;MYL9;NR2F6
MYLK	1/4	0.0473390195675664	1.0	20.74688796680498	63.286729990769146	MYL9
INSR	4/113	0.04792561845926756	1.0	2.937612455476811	8.924775339924288	NTRK2;CALD1;GAB1;LPP

Bioplanet 2019 database, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
Rho GTPase cycle	7/123	7.344799646401101E-4	1.0	4.72286880545154	SYDE1;STARD13;ARHGAP31;MCF2L;RHOJ;ARHGAP29;KALRN	34.08186410410626
Thymic stromal lymphopoietin (TSLP) pathway	6/90	7.702250262285714E-4	0.5815198948025714	5.532503457814661	MYC;IL2RA;CCL2;CCR6;TNFRSF11A;CCL17	39.661564835162324
Low-density lipoprotein (LDL) pathway during atherogenesis	2/6	0.002100859666622271	1.0	27.662517289073303	CCL2;LPL	170.55072345675106
Phase I of biological oxidations: non-cytochrome P450 enzymes	2/7	0.0029178656964145657	1.0	23.710729104919974	PON3;PON2	138.39722242664922
Cytokine-cytokine receptor interaction	9/265	0.00499304218116831	1.0	2.8184451577546388	GHR;IL2RA;IL21R;CD27;CCL2;INHBB;CCR6;TNFRSF11A;CCL17	14.936941703576487
MAPK cascade role in angiogenesis	4/64	0.007425785012787047	1.0	5.186721991701245	ROBO4;MMP14;PRKCA;ROBO1	25.4294443685376
Ephrin receptor A forward pathway	3/34	0.007850799846031632	1.0	7.32243104710764	EPHA4;ARHGEF15;PIK3R6	35.49284740906143
Reversible hydration of carbon dioxide	2/12	0.008813339250145349	1.0	13.831258644536652	CA7;CA6	65.44244649127494
Vascular smooth muscle contraction	5/116	0.0132636919126241	1.0	3.5770496494491346	PTGIR;CALCRL;CALD1;PRKCA;MYL9	15.46260161752144
Aldosterone-regulated sodium reabsorption	3/42	0.014039181674892825	1.0	5.927682276229993	SCNN1A;ATP1A3;PRKCA	25.2869185971972
Cadmium-induced DNA biosynthesis and proliferation in macrophages	2/17	0.01745703716897542	1.0	9.763241396143519	MYC;PRKCA	39.521722582071035
Synaptic proteins at the synaptic junction	2/17	0.01745703716897542	1.0	9.763241396143519	PCLO;NRXN3	39.521722582071035
Neuroactive ligand-receptor interaction	8/272	0.01765571822809162	1.0	2.4408103490358797	CHRNA1;GHR;MAS1;GRIN2A;PTGIR;CALCRL;GRM8;DRD5	9.852808321073878
Pertussis toxin-insensitive CCR5	2/18	0.01948499755087271	1.0	9.220839096357768	CCL2;PRKCA	36.31268294960286

signaling in macrophage						
Telomeres, telomerase, cellular aging, and immortality	2/19	0.021606567524768253	1.0	8.735531775496833	MYC;PRKCA	33.4986499972385
Neuronal system	8/283	0.0217939514947282	1.0	2.345937861970881	CHRNA1;GRIN2A;CACNG8;RPS6KA2;KCNC3;SLC1A3;PRKCA;KCNA5	8.975846345890812
Binding of chemokines to chemokine receptors	3/54	0.027316490665269092	1.0	4.610419548178884	CCL2;CCR6;CCL17	16.598730776788134
Transmission across chemical synapses	6/190	0.027871381731980623	1.0	2.62065953264905	CHRNA1;GRIN2A;CACNG8;RPS6KA2;SLC1A3;PRKCA	9.382366964745284
CCR3 signaling in eosinophils	2/22	0.028507861611188002	1.0	7.544322897019993	PIK3C2G;PRKCA	26.839497425420223
Smooth muscle contraction	2/22	0.028507861611188002	1.0	7.544322897019993	CALD1;MYL9	26.839497425420223
Nitric oxide signaling pathway	2/22	0.028507861611188002	1.0	7.544322897019993	GRIN2A;PRKCA	26.839497425420223
TSH regulation of gene expression	4/97	0.029850426068272342	1.0	3.4221670873080376	MYC;ARHGAP29;CCL2;PHLDB2	12.017131935154822
Thromboxane A2 receptor signaling	3/56	0.030001822921021278	1.0	4.445761707172496	PTGIR;PRKCA;PIK3R6	15.589050689679897
Nitrogen metabolism	2/23	0.03097902832932554	1.0	7.216308858019123	CA7;CA6	25.07266685142142
SHP2 signaling	3/57	0.031394823199539006	1.0	4.3677658877484165	NTRK2;IL2RA;GAB1	15.117328088738082
Mechanism of gene regulation by peroxisome proliferators via PPAR-alpha	3/57	0.031394823199539006	1.0	4.3677658877484165	MYC;LPL;PRKCA	15.117328088738082
Jak-STAT signaling pathway	6/199	0.033835192559259375	1.0	2.502137242227736	GHR;PTP4A3;MYC;IL2RA;IL21R;PTPRK	8.472871790123595
Neurotrophic factor-mediated Trk receptor signaling	3/60	0.035773912027314135	1.0	4.149377593360996	NTRK2;MCF2L;GAB1	13.819652969035918
Maturity onset diabetes of the young	2/25	0.036163312120247336	1.0	6.639004149377594	NR5A2;BHLHA15	22.039569469922412

PIP2 hydrolysis	2/25	0.036163312120247336	1.0	6.639004149377594	DAGLA;DGKI	22.039569469922412
Platelet activation, signaling and aggregation	6/205	0.0382376706779388	1.0	2.428903957089364	DAGLA;PRKCA;GAS6;THBS1;PIK3R6;DGKI	7.927782465470397
Interleukin-9 regulation of target genes	2/26	0.0388718656281344 2	1.0	6.383657835939994	MYC;CCL2	20.730830122325457
Gastrin-CREB signaling pathway via PKC and MAPK	6/206	0.03900526603255446	1.0	2.4171131611811627	OPN4;DAGLA;RPS6KA2;PRKCA;KALRN;DGKI	7.841256775148828
Signal transduction	19/1020	0.04012706696884281	1.0	1.5458465543893907	NTRK2;OPN4;CALCRL;DAGLA;GAB1;ARHGAP29;KALRN;CHRDL1;GHR;ARHGAP31;MYC;MCF2L;GRM8;COL6A3;CCL2;CCR6;CCL17;DGKI;DRD5	4.970985235270855
eIF4E and p70 S6 kinase regulation	2/27	0.041655055949402366	1.0	6.147226064238512	GHR;PRKCA	19.537928547068844
Validated nuclear estrogen receptor alpha network	3/64	0.04207451045748936	1.0	3.8900414937759336	MYC;PRDM15;POU4F1	12.324869712021147
Epidermal growth factor receptor (EGFR) pathway	4/111	0.04539757315080996	1.0	2.9905424096295468	RPS6KA2;RHOJ;GAB1;PRKCA	9.247644215742422
Beta-1 integrin cell surface interactions	3/66	0.045419771393499536	1.0	3.7721614485099964	COL6A3;NPNT;THBS1	11.662798096890265

Encode and Chea consensus, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
SUZ12 CHEA	57/1684	5.096161565838674E-13	5.3000080284722215E-11	2.808961078641054	ACVRL1;TMEM200A;RASEF;PEAR1;ELFN2;ANTXR1;RERG;LAMP5;MECOM;PEG10;GRM8;CA7;RNF150;DLGAP2;GAB1;PRKCA;VASH1;NPNT;DUSP26;SHISA6;PARD3B;RHOJ;PRR16;PRR15;VWA2;GAS6;LY6H;PHLDB2;CUEDC1;DGKI;LTK;KCNE3;ZBTB46;PON2;LPL;KCNA5;TNFRSF11A;SLC6A20;GRIN2A;SNTG1;GPC6;GPM6B;DRD5;TFAP2A;NTRK2;ECEL1;INHBB;POU4F1;FERMT1;NELL1;ARHGAP31;FRAS1;MAFB;PDE3A;SPATS2L;FAM171B;NES	79.50797643639592
AR CHEA	30/1095	2.309800399508606E-5	0.001201096207744475	2.273631558006025	HHLA2;PCDH15;KALRN;CHRDL1;LPP;THBS1;GHR;MECOM;CREB3L1;PHACTR1;TMC1;EPHA4;STARD13;OPN4;EDEM1;GAB1;PRKCA;INHBB;NPNT;GPRIN3;NELL1;FRAS1;MAFB;NBEA;SPATS2L;COL6A3;SLC26A7;VWA2;PHLDB2;DGKI	24.272754734971794
REST CHEA	26/1280	0.006391217439532846	0.22156220457047202	1.6856846473029046	PCDH15;NRXN3;TNFRSF11A;ELFN2;LAMP5;GRIN2A;SNTG1;SPTLC3;SLCO2B1;DLGAP2;CCL17;GPIHBP1;DRD5;TMC1;EPHA4;NTRK2;CRADD;ECEL1;PRKCA;INHBB;POU4F1;SLC2A9;NELL1;ARC;SLC26A7;LY6H	8.517478809592312
EZH2 CHEA	8/237	0.008224575045234637	0.21383895117610055	2.8012675735770434	ACVRL1;ECEL1;GRM8;INHBB;RNF150;SLC6A20;ELFN2;DLGAP2	13.4478453697451
SMAD4 CHEA	14/584	0.011599847522382647	0.24127682846555903	1.989427613255272	STARD13;TMEM132B;NRXN3;KIAA1671;THBS1;ROBO1;ADAMTSL1;FERMT1;ARHGAP31;MYO1B;FRAS1;RPS6KA2;ECT2L;DGKI	8.866408025649054
TP63 CHEA	25/1399	0.03133190640739252	0.5430863777281371	1.48297984037205	OCA2;RASEF;SLC1A3;PCDH12;ANTXR1;STK33;PEG10;GRM8;ST3GAL5;TFAP2A;WWTR1;CRADD;MTUS1;CTDSPL;C15ORF52;PLXDC2;NR2F6;SLC2A9;FERMT1;MAS1;MMP14;TMEM2;FRAS1;SPATS2L;DGKI	5.135734663180917
TP53 CHEA	8/319	0.04005922635116332	0.595165648645855	2.08119252331586	EPHA4;NTRK2;NELL1;JPH2;CALD1;GAS6;GPC6;PARD3B	6.696021043319476
SOX2 CHEA	15/775	0.04890544683230316	0.6357708088199411	1.6062106813010308	TFAP2A;EPHA4;MTUS1;LPP;MTSS1;RERG;NUDT4;ADAMTSL1;ARC;NR5A2;CALD1;PEG10;SCNN1A;PHACTR1;GPC6	4.8473294095153046

MSigDB Oncogenic Signatures, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
VEGF A UP.V1 UP	9/196	6.409001000718936E-4	0.1211301189135879	3.8106528918621394	CHRNA1;ARC;KCNC3;ENPP2;CCL2;EMILIN1;MYL9;MTSS1;COLQ	28.018347307054846
CSR LATE UP.V1 DN	7/170	0.0046245750751206585	0.4370223445989022	3.4171344886502317	ACVRL1;ANKRD29;ROBO3;NBEA;CALD1;CCL2;GAS6	18.371782043064258
KRAS.KIDNEY UP.V1 UP	6/145	0.008340285489262123	0.5254379858235138	3.433967663471169	TMEM100;MAFB;EPB41L3;SLC1A3;KCNA5;DLGAP2	16.437228210745914
PIGF UP.V1 DN	7/194	0.009309058713831154	0.439853024228522	2.9943962013945327	ARC;LTK;KCNC3;MCF2L;ENPP2;ATP1A3;MYL9	14.004094230908049
WNT UP.V1 UP	6/180	0.022111868425911427	0.835828626499452	2.7662517289073305	CDH5;CD96;KRT27;KCNC3;CCL2;INHBB	10.543957902523628
PTEN DN.V1 UP	6/191	0.02849684882762119	0.8976507380700675	2.60693880211162	EPHA4;SIT1;PRR16;CD27;INHBB;KALRN	9.27538858231831
KRAS.PROSTATE UP.V1 UP	5/143	0.029680271601112102	0.8013673332300267	2.901662652699997	CR2;NBEA;NXPH3;SLC10A2;NES	10.20593886122497
KRAS.LUNG.BREAST UP.V1 DN	5/145	0.03124736810700751	0.7382190715280524	2.8616397195593075	FRAS1;AMBN;SYNDIG1;PDE3A;MYL9	9.917928536048757
ATM DN.V1 DN	5/149	0.03453496236240402	0.7252342096104845	2.7848171767523464	ACVRL1;NTRK2;HHLA2;SLC10A2;GRM8	9.373090496201431

Biocarta 2016, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Combined Score	Genes
Telomeres, Telomerase, Cellular Aging, and Immortality Homo sapiens h telPathway	2/15	0.013692307500393935	1.0	11.065006915629322	47.47907164777607	MYC;PRKCA
Cadmium induces DNA synthesis and proliferation in macrophages Homo sapiens h cdMacPathway	2/16	0.015525264834032	1.0	10.37344398340249	43.20836714476457	MYC;PRKCA
Nitric Oxide Signaling Pathway Homo sapiens h nos1Pathway	2/19	0.021606567524768253	1.0	8.735531775496833	33.4986499972385	GRIN2A;PRKCA
Mechanism of Gene Regulation by Peroxisome Proliferators via PPARa Homo sapiens h pparaPathway	3/52	0.02476589413991239	1.0	4.787743376954995	17.706452961747683	MYC;LPL;PRKCA
Growth Hormone Signaling Pathway Homo sapiens h ghPathway	2/22	0.028507861611188002	1.0	7.544322897019993	26.839497425420223	GHR;PRKCA
CCR3 signaling in Eosinophils Homo sapiens h CCR3Pathway	2/23	0.03097902832932554	1.0	7.216308858019123	25.07266685142142	PIK3C2G;PRKCA
Regulation of eIF4e and p70 S6 Kinase Homo sapiens h eif4Pathway	2/24	0.03353161297317188	1.0	6.915629322268326	23.480405354685843	GHR;PRKCA

Reactome 2016, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
Rho GTPase cycle Homo sapiens R-HSA-194840	7/122	6.99730714042046E-4	1.0	4.761580844840487	SYDE1;STARD13;ARHGAP31;MCF2L;RHOJ;ARHGAP29;KALRN	34.59200390321901
Diseases of glycosylation Homo sapiens R-HSA-3781865	5/88	0.004241527998131693	1.0	4.715201810637495	ADAMTSL1;ADAMTS9;THBS1;GPC6;MUC4	25.7583539123943
Diseases associated with O-glycosylation of proteins Homo sapiens R-HSA-3906995	4/62	0.006642222211633706	1.0	5.354035604336769	ADAMTSL1;ADAMTS9;THBS1;MUC4	26.846787316593158
Reversible hydration of carbon dioxide Homo sapiens R-HSA-1475029	2/12	0.008813339250145349	1.0	13.831258644536652	CA7;CA6	65.44244649127494
Defective B3GALTL causes Peters-plus syndrome (PpS) Homo sapiens R-HSA-5083635	3/37	0.009928410722557174	1.0	6.72872042166648	ADAMTSL1;THBS1;ADAMTS9	31.035246350667034
O-glycosylation of TSR domain-containing proteins Homo sapiens R-HSA-5173214	3/38	0.010685104910941845	1.0	6.551648831622625	ADAMTSL1;THBS1;ADAMTS9	29.73730883424778
Depolymerisation of the Nuclear Lamina Homo sapiens R-HSA-4419969	2/15	0.013692307500393935	1.0	11.065006915629322	PRKCA;LPIN3	47.47907164777607
Syndecan interactions Homo sapiens R-HSA-3000170	2/20	0.02381921634833939	1.0	8.298755186721992	PRKCA;THBS1	31.014627506144365
Neurotransmitter Receptor Binding And Downstream Transmission In The Postsynaptic Cell Homo sapiens R-HSA-112314	5/142	0.028915728725035107	1.0	2.922096896733096	CHRNA1;GRIN2A;CACNG8;RPS6KA2;PRKCA	10.354069269391557
Neuronal System Homo sapiens R-HSA-112316	8/301	0.029974854230399816	1.0	2.2056492190623236	CHRNA1;GRIN2A;CACNG8;RPS6KA2;KCNC3;SLC1A3;PRKCA;KCNA5	7.736086221297395
Chemokine receptors bind chemokines Homo sapiens R-HSA-380108	3/56	0.030001822921021278	1.0	4.445761707172496	CCL2;CCR6;CCL17	15.589050689679897
Muscle contraction Homo sapiens R-HSA-397014	6/196	0.031762972865536414	1.0	2.540435261241426	WWTR1;CACNG8;KCNE3;CALD1;ATP1A3;MYL9	8.763114682628133

Platelet activation, signaling and aggregation Homo sapiens R-HSA-76002	7/253	0.03410112062815847	1.0	2.2960982730060846	DAGLA;IL2RA;PRKCA;GAS6;THBS1;PIK3R6;DGKI	7.757195881999426
Phase 2 - plateau phase Homo sapiens R-HSA-5576893	2/26	0.03887186562813442	1.0	6.383657835939994	CACNG8;KCNE3	20.730830122325457
CREB phosphorylation through the activation of Ras Homo sapiens R-HSA-442742	2/27	0.041655055949402366	1.0	6.147226064238512	GRIN2A;RPS6KA2	19.537928547068844
Effects of PIP2 hydrolysis Homo sapiens R-HSA-114508	2/27	0.041655055949402366	1.0	6.147226064238512	DAGLA;DGKI	19.537928547068844
Transmission across Chemical Synapses Homo sapiens R-HSA-112315	6/211	0.0429901240771239	1.0	2.3598355981199974	CHRNA1;GRIN2A;CACNG8;RPS6KA2;SLC1A3;PRKCA	7.425894937662731
O-linked glycosylation Homo sapiens R-HSA-5173105	4/110	0.044162317711530785	1.0	3.0177291588079966	ADAMTSL1;ADAMTS9;THBS1;MUC4	9.414963090096993
Signal Transduction Homo sapiens R-HSA-162582	39/2465	0.04527087512489801	1.0	1.312987636033094	CALCRL;DAGLA;LPL;RASAL1;PTPRK;KALRN;CHRDL1;THBS1;PIK3R6;GHR;SYDE1;CDH5;GRIN2A;RPS6KA2;MYC;MCF2L;GRM8;CCL2;CCR6;CCL17;GPC6;DRD5;WWTR1;NTRK2;STARD13;OPN4;PTGIR;GAB1;ARHGAP29;PRKCA;INHBB;WNT9A;ARHGAP31;IL2RA;RHOJ;PDE3A;COL6A3;MYL9;DGKI	4.063816722852

KEGG 2019 Human, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
Cytokine-cytokine receptor interaction	10/294	0.003115232795512783	0.9594917010179372	2.822705845823807	ACVRL1;GHR;IL2RA;IL21R;CD27;CCL2;INHBB;TNFRSF11A;CCR6;CCL17	16.29110959387805
Amphetamine addiction	4/68	0.00917033734519437	1.0	4.881620698071759	ARC;GRIN2A;CREB3L1;PRKCA	22.903496243465533
Aldosterone-regulated sodium reabsorption	3/37	0.009928410722557174	1.0	6.72872042166648	SCNN1A;ATP1A3;PRKCA	31.035246350667034
Nitrogen metabolism	2/17	0.01745703716897542	1.0	9.763241396143519	CA7;CA6	39.521722582071035
Insulin secretion	4/86	0.020242436301075837	1.0	3.859886133359066	PCLO;CREB3L1;ATP1A3;PRKCA	15.053455837886013
Vascular smooth muscle contraction	5/132	0.021953529734756186	1.0	3.1434678737583304	PTGIR;CALCRL;CALD1;PRKCA;MYL9	12.004361072638043
PI3K-Akt signaling pathway	9/354	0.028265851587686543	1.0	2.109853013573388	GHR;NTRK2;CREB3L1;MYC;IL2RA;COL6A3;PRKCA;THBS1;PIK3R6	7.523948647463423
Aldosterone synthesis and secretion	4/98	0.03083656150476786	1.0	3.3872470149885676	DAGLA;CREB3L1;ATP1A3;PRKCA	11.784416059481181
Adrenergic signaling in cardiomyocytes	5/145	0.03124736810700751	1.0	2.8616397195593075	CACNG8;CREB3L1;ATP1A3;PRKCA;PIK3R6	9.917928536048757
Phospholipase D signaling pathway	5/148	0.03369377508966388	1.0	2.8036335090277	GRM8;GAB1;PRKCA;DGKI;PIK3R6	9.50555728980055
Glycerolipid metabolism	3/61	0.037299882536403	1.0	4.081355009863275	LPL;DGKI;LPIN3	13.422617923251844
Maturity onset diabetes of the young	2/26	0.03887186562813442	0.9977112177887834	6.383657835939994	NR5A2;BHLHA15	20.730830122325457
Parathyroid hormone synthesis, secretion and action	4/106	0.03941336600420486	0.9337935945611613	3.1316057308384875	MMP14;MAFB;CREB3L1;PRKCA	10.126517753139526
cAMP signaling pathway	6/212	0.04381665900641768	0.963966498141189	2.3487042981288657	GRIN2A;CREB3L1;PDE3A;ATP1A3;MYL9;DRD5	7.346139179439546
Long-term potentiation	3/67	0.04714047402966499	0.9679510667424545	3.715860531368056	GRIN2A;RPS6KA2;PRKCA	11.350554254315568
Glutamatergic synapse	4/114	0.04921836679100779	0.9474535607268999	2.911843925165611	GRIN2A;GRM8;SLC1A3;PRKCA	8.768984250959983

Panther 2016, only P<0.05 included

Term	Overlap	P-value	Adjusted P-value	Odds Ratio	Genes	Combined Score
Metabotropic glutamate receptor group III pathway Homo sapiens P00039	3/54	0.027316490665269092	1.0	4.610419548178884	GRIN2A;GRM8;SLC1A3	16.598730776788134
PDGF signaling pathway Homo sapiens P00047	4/112	0.046652012963392504	1.0	2.9638411381149967	MYC;RPS6KA2;PRKCA;RERG	9.084289277649845
Huntington disease Homo sapiens P00029	4/124	0.06319083975598899	1.0	2.6770178021683844	GRIN2A;DNAH7;RHOJ;KALRN	7.392841464071796
2-arachidonoylglycerol biosynthesis Homo sapiens P05726	1/6	0.0701648752848036	1.0	13.831258644536652	DAGLA	36.748374069662006
Interleukin signaling pathway Homo sapiens P00036	3/86	0.08557986624164342	1.0	2.8949146000192996	MYC;RPS6KA2;IL2RA	7.116583704402653
Muscarinic acetylcholine receptor 1 and 3 signaling pathway Homo sapiens P00042	2/42	0.09097392706510637	1.0	3.951788184153329	GRIN2A;PRKCA	9.473156804136863

Supplementary Table 7

Kasumi-2

Drug combination	Synergy score	Most synergistic area	Method
Navitoclax - dasatinib	2.017	7.17	ZIP
Venetoclax - idasanutlin	13.094	30.54	ZIP
Venetoclax - dasatinib	-0.389	5.63	ZP
Idasanutlin - dasatinib	2.013	8.61	ZIP
Navitoclax - idasanutlin	8.259	22.91	ZIP

NALM-21

Drug combination	Synergy score	Most synergistic area	Method
Navitoclax - dasatinib	18.118	24.26	ZIP
Venetoclax - idasanutlin	7.362	17.63	ZIP
Venetoclax - dasatinib	13.536	21.71	ZP
Idasanutlin - dasatinib	17.786	23.52	ZIP
Navitoclax - idasanutlin	4.995	16.41	ZIP

MHH-CALL-4

Drug combination	Synergy score	Most synergistic area	Method
Navitoclax - dasatinib	-0.6	2.72	ZIP
Venetoclax - idasanutlin	7.172	15.26	ZIP
Venetoclax - dasatinib	-0.294	3.52	ZP
Idasanutlin - dasatinib	-2.415	2.92	ZIP
Navitoclax - idasanutlin	4.303	12.89	ZIP

Single compound drug sensitivity scores

Drug	Kasumi-2	NALM-21	MHH-CALL-4
Dasatinib	4.7	23.8	0.9
Idasanutlin	4	10.8	9.1
Navitoclax	13.7	11.4	17.6
Venetoclax	22.7	21.8	18

Supplementary Table 8
Cibersort results

Input Sample	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	T cells CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)	T cells gamma delta
Pt_1	0,48940621	0	0,11752584	0,05757826	0,02398139	0,11769721	0,01095103	0	0	0
Pt_3	0,42752042	0	0,111297	0,01368172	0,08008593	0,16934629	0,01411626	0	0	0
Pt_4	0,62212572	0	0,02990109	0	0,08845354	0,13948822	0,01053765	0	0	0
Pt_5	0,43014894	0	0,07445067	0,00272206	0,07233965	0,15225626	0,00248034	0	0	0
Pt_7	0,57143616	0	0,04977108	0,05850536	0,021681	0,13348515	0,00475866	0	0	0
Pt_8	0,28104703	0	0,16797193	0,01343299	0,00471881	0,16113759	0,01577013	0	0	0
Pt_9	0,27440284	0	0,1197426	0,04698032	0,0413483	0,22820692	0,03025476	0	0	0
Pt_10	0,08718133	0	0,15938684	0,00185698	0,14409175	0,21492366	0	0	0	0
Pt_11	0,27644711	0	0,021639	0,01446325	0,02871856	0,22815901	0	0	0	0
Pt_12	0,44791642	0	0,16366861	0,01388177	0,07989307	0,09559835	0	0	0	0
Pt_13	0,50747881	0	0,16340155	0,01434802	0,02511304	0,08789635	0,00576268	0	0	0
Pt_14	0,40818746	0	0,05925323	0,0460171	0,0048934	0,26820023	0,0006	0	0	0
Pt_15	0,26968486	0	0,13326949	0	0,04170505	0,17816441	0,0129203	0	0	0,00248284
Pt_16	0,30704634	0	0,06802666	0	0,04279187	0,10003106	0,005647	0	0	0
Pt_17	0,25612716	0	0,04990274	0,12870866	0,01805766	0,27536369	0,02545662	0	0	0
Pt_18	0,30696733	0	0,07527251	0	0,04673226	0,22643246	0	0	0	0

Input Sample	NK cells resting	NK cells activated	Monocytes	Macrophages M0	Macrophages M1	Macrophages M2	Dendritic cells resting	Dendritic cells activated	Mast cells resting	Mast cells activated
Pt_1	0,08972951	0	0,03788398	0	0	0,01995297	0	0,00345396	0,00104523	0
Pt_3	0,05339082	0,00331935	0,0192846	0,00630801	0	0,02547949	0	0,00682087	0,0458004	0
Pt_4	0,01939523	0	0,02798657	0	0	0,00495727	0	0,00646234	0,0003	0
Pt_5	0,06946206	0	0,11091774	0,02339767	0	0	0	0,00496152	0,00319604	0
Pt_7	0,0310833	0,01820622	0,05806295	0,00691297	0	0,00942291	0	0	0,02153875	0
Pt_8	0,06020868	0	0,1714927	0,01882838	0	0	0	0,00191971	0,0218815	0
Pt_9	0,11469959	0	0,07529039	0,00280195	0	0,00507316	0	0,00321723	0	0
Pt_10	0,09132017	0	0,20174869	0,04093953	0	0	0	0,00728156	0	0,01279035
Pt_11	0,02352858	0,03146945	0,23862987	0,07001044	0	0	0	0,0089916	0,02145011	0
Pt_12	0,05674543	0	0,07545976	0,00926098	0	0	0	0,00394888	0,00205219	0
Pt_13	0,07560423	0	0,05960106	0	0	0,02827605	0	0,00412451	0	0
Pt_14	0,08573911	0	0,07187934	0,01489054	0	0,0004	0	0,00280459	0	0
Pt_15	0,04358987	0	0,23977542	0,02826303	0	0	0	0,00653271	0,02016911	0
Pt_16	0,06437322	0	0,23098338	0,03748237	0	0	0	0,00186095	0,01368523	0
Pt_17	0,10952485	0	0,0528709	0,0035614	0	0	0	0,00519901	0,01508254	0
Pt_18	0,09786735	0	0,12676245	0,03306316	0	0	0	0,00278954	0	0

Input Sample	Eosinophils	Neutrophils	P-value	Pearson Correlation	RMSE
Pt_1	0,03079442	0	0,04	0,18387534	1,03629911
Pt_3	0,02354885	0	0,02	0,21664567	1,01057504
Pt_4	0,05042941	0	0	0,47271536	0,88965418
Pt_5	0,04605083	0,00761623	0	0,28843343	0,97615803
Pt_7	0,0151355	0	0	0,31034979	0,98271536
Pt_8	0,07784525	0,0037453	0	0,25434415	0,97804991
Pt_9	0,05337769	0,00460424	0,04	0,17841716	1,0193098
Pt_10	0,03847915	0	0,02	0,20348728	0,99922343
Pt_11	0,03649302	0	0,02	0,20113291	1,00835584
Pt_12	0,05157455	0	0,02	0,20372252	1,01709099
Pt_13	0,02839371	0	0,06	0,16754489	1,04243164
Pt_14	0,03721237	0	0	0,35421172	0,94579409
Pt_15	0,02344291	0	0,06	0,16704462	1,01638294
Pt_16	0,04786867	0,08020325	0,08	0,14717542	1,03524593
Pt_17	0,06014477	0	0	0,23577572	1,00341775
Pt_18	0,08411293	0	0,24	0,0832868	1,05815279

Cibersort comparison, DSRT vs Hemap cohorts

Cell_type	p value	p. adjusted	Median_DSRT_cohort	IQR_DSRT_cohort	Median_Hemap_cohort	IQR_Hemap_cohort
CIBERSORT_B_cells_naive	3.448683e-02	4.741939e-02	0.357616900	0.1823528274	0.297376793	0.20911625
CIBERSORT_B_cells_memory	1.144429e-05	4.015428e-05	0.000000000	0.0000000000	0.046916479	0.18267441
CIBERSORT_Plasma_cells	4.016605e-01	4.650806e-01	0.093284754	0.0828832144	0.112156866	0.16747598
CIBERSORT_T_cells_CD8	4.110224e-06	1.808499e-05	0.013781748	0.0448651735	0.071285580	0.06326444
CIBERSORT_T_cells_CD4_naive	1.071453e-04	2.946494e-04	0.041526673	0.0508217136	0.000000000	0.03930808
CIBERSORT_T_cells_CD4_memory_resting	9.868604e-08	1.085546e-06	0.165241939	0.0973259349	0.043213376	0.09919984
CIBERSORT_T_cells_CD4_memory_activated	6.695438e-08	1.085546e-06	0.005704841	0.0127692934	0.000000000	0.00000000
CIBERSORT_T_cells_follicular_helper	3.153903e-06	1.734647e-05	0.000000000	0.0000000000	0.012308108	0.03610491
CIBERSORT_T_cells_regulatory__Tregs_	3.354227e-02	4.741939e-02	0.000000000	0.0000000000	0.000000000	0.00000000
CIBERSORT_T_cells_gamma_delta	7.168613e-01	7.168613e-01	0.000000000	0.0000000000	0.000000000	0.00000000
CIBERSORT_NK_cells_resting	1.277636e-05	4.015428e-05	0.066917638	0.0391865904	0.019905322	0.05210144
CIBERSORT_NK_cells_activated	3.962508e-04	8.829061e-04	0.000000000	0.0000000000	0.014404072	0.04993236
CIBERSORT_Monocytes	1.479929e-03	2.959859e-03	0.075375076	0.1222917588	0.039589995	0.05605885
CIBERSORT_Macrophages_M0	2.714431e-02	4.593653e-02	0.012075757	0.0260915205	0.000000000	0.01866645
CIBERSORT_Macrophages_M1	2.652702e-01	3.242191e-01	0.000000000	0.0000000000	0.000000000	0.00000000
CIBERSORT_Macrophages_M2	4.013210e-04	8.829061e-04	0.000000000	0.0061605983	0.016323807	0.02848970
CIBERSORT_Dendritic_cells_resting	4.827911e-01	5.057812e-01	0.000000000	0.0000000000	0.000000000	0.00000000
CIBERSORT_Dendritic_cells_activated	4.432138e-01	4.875352e-01	0.004036697	0.0036791092	0.005403422	0.01243414
CIBERSORT_Mast_cells_resting	3.359959e-02	4.741939e-02	0.002624115	0.0204893579	0.000000000	0.01204979
CIBERSORT_Mast_cells_activated	3.934120e-07	2.885021e-06	0.000000000	0.0000000000	0.024111167	0.05327747
CIBERSORT_Eosinophils	1.929110e-03	3.536701e-03	0.042264990	0.0205214492	0.017790855	0.03677692
CIBERSORT_Neutrophils	4.285680e-02	5.546175e-02	0.000000000	0.0009363248	0.000492018	0.01143310