SUPPLEMENTARY INFORMATION

Classification of Genes Based on Age-Related Differential Expression in Breast Cancer

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http://www.genominfo.org/src/sm/gni-15-156-s001.pdf

Supplementary Table 1. Table of 16 gene classes based on age-specific expression

Gene name | Entrez ID	Gene class
AASS|10157	A1
ABCA10|10349	A1
ABCA5|23461	A1
ABCB1|5243	A1
ACBD3|64746	A1
ACCS|84680	A1
ACVR2A|92	A1
ADAM33|80332	A1
ADAMTS5|11096	A1
ADAR|103	A1
ADIPOR1|51094	A1
ALDH1A2|8854	A1
AMOTL1|154810	A1
AMOTL2|51421	A1
AMT|275	A1
ANAPC4|29945	A1
ANKRD29|147463	A1
ANXA1|301	A1
AP1S1|1174	A1
APBB1|322	A1
APCDD1|147495	A1
APOO|79135	A1
ARF1|375	A1
ARHGAP19|84986	A1
ARHGEF10|9639	A1
ARID5B|84159	A1
ARRB1|408	A1
ASB1|51665	A1
ATP6AP1|537	A1
ATP6V0B|533	A1
AUH|549	A1
BAI3|577	A1
BBS2|583	A1
BCL2L2|599	A1
BCL6|604	A1
BOLA2|552900	A1
C16orf59|80178	A1
C16orf86|388284	A1
C17orf108|201229	A1
C17orf48|56985	A1
C1QTNF9B|387911	A1
C1orf190|541468	A1
C1orf31|388753	A1
C20orf194|25943	A1
C21orf34|388815	A1
C2orf40|84417	A1
C2orf67|151050	A1
C4orf49|84709	A1

C5orf4|10826	A1
C5orf53|492311	A1
C6orf129|154467	A1
C8orf79|57604	A1
CACHD1|57685	A1
CALCOCO1|57658	A1
CAPN11|11131	A1
CAPZA1|829	A1
CBX3|11335	A1
CBX7|23492	A1
CC2D2A|57545	A1
CCDC46|201134	A1
CCDC93|54520	A1
CD200|4345	A1
CD276|80381	A1
CDADC1|81602	A1
CDC14B|8555	A1
CEP68|23177	A1
CES2|8824	A1
CFL1|1072	A1
CHL1|10752	A1
CIT|11113	A1
CLCN6|1185	A1
CLDN11|5010	A1
CLDN19|149461	A1
CNTNAP3|79937	A1
COL17A1|1308	A1
CRIM1|51232	A1
CX3CL1|6376	A1
CYP2U1|113612	A1
DAB2IP|153090	A1
DCP1A|55802	A1
DDX26B|203522	A1
DFNB59|494513	A1
DLGAP2|9228	A1
DLK2|65989	A1
DMD|1756	A1
DNAH1|25981	A1
DNAJC18|202052	A1
DNAJC27|51277	A1
DOCK1|1793	A1
DPY19L2|283417	A1
DPY30|84661	A1
DPYSL2|1808	A1
DST|667	A1
DTYMK|1841	A1
DUSP6|1848	A1
EDN3|1908	A1
EDNRB|1910	A1
EEPD1|80820	A1
EFHA2|286097	A1

EIF2AK1|27102	A1
EIF3L|51386	A1
ERCC6L|54821	A1
ESD|2098	A1
EVC2|132884	A1
EZH1|2145	A1
F3|2152	A1
FAM122A|116224	A1
FAM126A|84668	A1
FAM13C|220965	A1
FAM189A2|9413	A1
FAM82A1|151393	A1
FBXO31|79791	A1
FGF1|2246	A1
FIGF|2277	A1
FLJ10038|55056	A1
FLJ13197|79667	A1
FOXO4|4303	A1
FXYD1|5348	A1
GEMIN6|79833	A1
GGPS1|9453	A1
GNAL|2774	A1
GNE|10020	A1
GPRASP1|9737	A1
GPRASP2|114928	A1
GRIA4|2893	A1
GSPT2|23708	A1
H2AFY|9555	A1
H2AFZ|3015	A1
H3F3A|3020	A1
HERC2P2|400322	A1
HLF|3131	A1
HNRNPAB|3182	A1
HNRNPF|3185	A1
HNRNPL|3191	A1
HNRNPU|3192	A1
HOXA2|3199	A1
HOXA3|3200	A1
HOXA4|3201	A1
HOXA5|3202	A1
HOXA6|3203	A1
HYMAI|57061	A1
IGSF10|285313	A1
IL11RA|3590	A1
IL17RD|54756	A1
IL33|90865	A1
ING3|54556	A1
INPP1|3628	A1
INTS7|25896	A1
ISM1|140862	A1
ITM2A|9452	A1

KCNE1|3753	A1
KCTD12|115207	A1
KIAA1614|57710	A1
KIRREL|55243	A1
KLF9|687	A1
KLHDC1|122773	A1
KLHL21|9903	A1
KLHL29|114818	A1
KLHL3|26249	A1
KL|9365	A1
LCA5|167691	A1
LCAT|3931	A1
LDB2|9079	A1
LETMD1|25875	A1
LGR4|55366	A1
LIFR|3977	A1
LIMS2|55679	A1
LMBRD1|55788	A1
LOC100132707|100132707	A1
LOC134466|134466	A1
LOC285830|285830	A1
LOC339290|339290	A1
LOC399959|399959	A1
LOC728264|728264	A1
LPCAT2|54947	A1
LRCH1|23143	A1
LRIG3|121227	A1
LRP4|4038	A1
LRRC3B|116135	A1
LRRTM2|26045	A1
LSM4|25804	A1
LUZP1|7798	A1
MAB21L1|4081	A1
MAGI1|9223	A1
MAMDC2|256691	A1
MAML2|84441	A1
MANF|7873	A1
MAPKBP1|23005	A1
MATN2|4147	A1
MAZ|4150	A1
MBOAT7|79143	A1
MEG3|55384	A1
MEIS2|4212	A1
METTL7A|25840	A1
MICAL3|57553	A1
MID1|4281	A1
MLF1IP|79682	A1
MME|4311	A1
MOBKL2B|79817	A1
MOBKL2C|148932	A1
MPDZ|8777	A1

MTMR10|54893	A1
MYLK|4638	A1
N4BP2L1|90634	A1
NAA20|51126	A1
NAB1|4664	A1
NAP1L5|266812	A1
NBLA00301|79804	A1
NCRNA00086|399668	A1
NCRNA00087|644596	A1
NDEL1|81565	A1
NDRG2|57447	A1
NEIL3|55247	A1
NFAT5|10725	A1
NGFR|4804	A1
NISCH|11188	A1
NPHP3|27031	A1
NR2C1|7181	A1
NR3C1|2908	A1
NR3C2|4306	A1
NRIP2|83714	A1
NTF4|4909	A1
OR2A1|346528	A1
OR2A9P|441295	A1
OXTR|5021	A1
PAFAH1B3|5050	A1
PAK3|5063	A1
PAK7|57144	A1
PAMR1|25891	A1
PAR-SN|347746	A1
PARK2|5071	A1
PARP1|142	A1
PCDHGB7|56099	A1
PCNX|22990	A1
PDE1C|5137	A1
PDGFD|80310	A1
PDLIM4|8572	A1
PELI2|57161	A1
PER1|5187	A1
PHF10|55274	A1
PHF17|79960	A1
PIGU|128869	A1
PIK3R1|5295	A1
PKD2|5311	A1
PKMYT1|9088	A1
PLAGL1|5325	A1
PLEKHH2|130271	A1
PLEKHM3|389072	A1
PLK1S1|55857	A1
PLSCR4|57088	A1
PMM2|5373	A1
PNMAL2|57469	A1

PNRC1|10957	A1
POU6F1|5463	A1
PPAP2B|8613	A1
PPIAL4C|653598	A1
PPL|5493	A1
PPM1F|9647	A1
PPP4C|5531	A1
PPP4R1L|55370	A1
PRCD|768206	A1
PRDX1|5052	A1
PRIMA1|145270	A1
PRNP|5621	A1
PROS1|5627	A1
PRX|57716	A1
PSENEN|55851	A1
PSKH1|5681	A1
PSMA5|5686	A1
PSMC4|5704	A1
PSMD14|10213	A1
PTBP1|5725	A1
PTCH1|5727	A1
PTPN21|11099	A1
PYCR1|5831	A1
PZP|5858	A1
RAB11FIP2|22841	A1
RAB8A|4218	A1
RABIF|5877	A1
RAPGEF2|9693	A1
RAPGEF3|10411	A1
RASSF9|9182	A1
RBM9|23543	A1
RBMS2|5939	A1
RCBTB2|1102	A1
REV1|51455	A1
RGNEF|64283	A1
RGN|9104	A1
RHOJ|57381	A1
RND3|390	A1
RNF180|285671	A1
RNF187|149603	A1
RNF214|257160	A1
RNF38|152006	A1
ROBO3|64221	A1
RPS6KA3|6197	A1
RRN3P1|730092	A1
RUNDC3B|154661	A1
RUSC1|23623	A1
SAE1|10055	A1
SAMD5|389432	A1
SASH1|23328	A1
SAV1|60485	A1

SCN2B|6327	A1
SCN3A|6328	A1
SCN4B|6330	A1
SEC14L1|6397	A1
SEMA3D|223117	A1
SH3BGRL2|83699	A1
SKA3|221150	A1
SLC20A1|6574	A1
SLC25A44|9673	A1
SLC27A1|376497	A1
SLC27A6|28965	A1
SLC35A2|7355	A1
SMC6|79677	A1
SMYD4|114826	A1
SNCA|6622	A1
SOBP|55084	A1
SPRY2|10253	A1
SRP9|6726	A1
SRPX|8406	A1
SSPN|8082	A1
SSTR1|6751	A1
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STAT5B|6777	A1
SYNE2|23224	A1
SYNM|23336	A1
TBC1D4|9882	A1
TBRG1|84897	A1
TCEAL7|56849	A1
TCP11L2|255394	A1
TDRD10|126668	A1
TDRD6|221400	A1
TEF|7008	A1
TGFBR3|7049	A1
THRB|7068	A1
THSD1|55901	A1
TIMM17A|10440	A1
TINAGL1|64129	A1
TLE4|7091	A1
TMEM220|388335	A1
TMEM63B|55362	A1
TMEM8A|58986	A1
TMTC1|83857	A1
TPO|7173	A1
TRIM11|81559	A1
TRIM59|286827	A1
TRPC1|7220	A1
TRPC6|7225	A1
TSC1|7248	A1
TSHZ2|128553	A1
TSLP|85480	A1
TSPYL2|64061	A1

TSTA3|7264	A1
TTC28|23331	A1
TUBA1C|84790	A1
TUBE1|51175	A1
TUBG2|27175	A1
USP44|84101	A1
UTRN|7402	A1
VAMP2|6844	A1
WASF2|10163	A1
WBP4|11193	A1
WDR86|349136	A1
WHAMML2|440253	A1
YAP1|10413	A1
ZBTB4|57659	A1
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ZFP36L2|678	A1
ZNF132|7691	A1
ZNF204P|7754	A1
ZNF280D|54816	A1
ZNF391|346157	A1
ZNF502|91392	A1
ZNF660|285349	A1
ZNF781|163115	A1
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?|653553	A2
A1BG|1	A2
AADAC|13	A2
ABCA1|19	A2
ABCA8|10351	A2
ABCB10|23456	A2
ABCB8|11194	A2
ABCB9|23457	A2
ABCC5|10057	A2
ABCC6|368	A2
ABCD2|225	A2
ABCD3|5825	A2
ABCD4|5826	A2
ABCF1|23	A2
ABCF3|55324	A2
ABCG1|9619	A2
ABHD12|26090	A2
ABHD14B|84836	A2
ABHD1|84696	A2
ABHD6|57406	A2
ABL1|25	A2
ABL2|27	A2
ABLIM1|3983	A2
ABLIM3|22885	A2
ABR|29	A2
ABTB1|80325	A2
ACACB|32	A2

ACAD11|84129	A2
ACADS|35	A2
ACADVL|37	A2
ACAT2|39	A2
ACBD4|79777	A2
ACOT7|11332	A2
ACOT8|10005	A2
ACP1|52	A2
ACP2|53	A2
ACSBG2|81616	A2
ACSL1|2180	A2
ACSL5|51703	A2
ACSM5|54988	A2
ACSS2|55902	A2
ACTA2|59	A2
ACTB|60	A2
ACTG1|71	A2
ACTL6A|86	A2
ACTR1B|10120	A2
ACTR2|10097	A2
ACTR3|10096	A2
ACVR1C|130399	A2
ADAD2|161931	A2
ADAM12|8038	A2
ADAM15|8751	A2
ADAM19|8728	A2
ADAM8|101	A2
ADAMTS12|81792	A2
ADAMTS14|140766	A2
ADAMTS18|170692	A2
ADAMTS1|9510	A2
ADAMTS3|9508	A2
ADAMTS6|11174	A2
ADAMTS7|11173	A2
ADAMTS9|56999	A2
ADAMTSL2|9719	A2
ADAP1|11033	A2
ADARB1|104	A2
ADAT2|134637	A2
ADCK2|90956	A2
ADCK5|203054	A2
ADCY4|196883	A2
ADCY5|111	A2
ADCY6|112	A2
ADCYAP1R1|117	A2
ADC|113451	A2
ADD1|118	A2
ADD3|120	A2
ADH1A|124	A2
ADH1B|125	A2
ADH4|127	A2

ADH5|128	A2
ADHFE1|137872	A2
ADIPOQ|9370	A2
ADORA2A|135	A2
ADORA3|140	A2
ADPRHL2|54936	A2
ADRA1A|148	A2
ADRA2A|150	A2
ADRB2|154	A2
ADRBK2|157	A2
ADRM1|11047	A2
ADSS|159	A2
AEBP1|165	A2
AFF1|4299	A2
AG2|387763	A2
AGAP11|119385	A2
AGER|177	A2
AGFG2|3268	A2
AGPAT2|10555	A2
AGR3|155465	A2
AGTRAP|57085	A2
AGXT2L2|85007	A2
AHCTF1|25909	A2
AHCY|191	A2
AHDC1|27245	A2
AHNAK|79026	A2
AHSA1|10598	A2
AIF1L|83543	A2
AIFM1|9131	A2
AIG1|51390	A2
AIMP2|7965	A2
AK3|50808	A2
AK5|26289	A2
AKAP11|11215	A2
AKAP13|11214	A2
AKAP1|8165	A2
AKAP2|11217	A2
AKAP3|10566	A2
AKAP5|9495	A2
AKAP7|9465	A2
AKR1C1|1645	A2
AKR1C2|1646	A2
AKR1C3|8644	A2
AKT1|207	A2
ALAD|210	A2
ALDH18A1|5832	A2
ALDH1A1|216	A2
ALDH1A3|220	A2
ALDH1B1|219	A2
ALDH1L1|10840	A2
ALDH2|217	A2

ALDH3A2|224	A2
ALDH7A1|501	A2
ALDOC|230	A2
ALG11|440138	A2
ALG1|56052	A2
ALG3|10195	A2
ALG6|29929	A2
ALKBH3|221120	A2
ALKBH6|84964	A2
ALS2CR4|65062	A2
ALS2CR8|79800	A2
ALX4|60529	A2
AMIGO1|57463	A2
AMIGO3|386724	A2
AMMECR1|9949	A2
AMZ2|51321	A2
ANAPC11|51529	A2
ANGEL2|90806	A2
ANGPTL1|9068	A2
ANGPTL6|83854	A2
ANGPTL7|10218	A2
ANG|283	A2
ANK2|287	A2
ANKDD1A|348094	A2
ANKFY1|51479	A2
ANKK1|255239	A2
ANKRD11|29123	A2
ANKRD22|118932	A2
ANKRD36|375248	A2
ANKRD40|91369	A2
ANKRD53|79998	A2
ANKRD58|347454	A2
ANKRD5|63926	A2
ANKRD6|22881	A2
ANKS1A|23294	A2
ANLN|54443	A2
ANO2|57101	A2
ANO9|338440	A2
ANP32E|81611	A2
ANXA11|311	A2
ANXA3|306	A2
ANXA6|309	A2
AP1G2|8906	A2
AP1M2|10053	A2
AP1S3|130340	A2
AP2A2|161	A2
AP2M1|1173	A2
AP2S1|1175	A2
AP3B1|8546	A2
AP3D1|8943	A2
AP4M1|9179	A2

APBA1|320	A2
APCDD1L|164284	A2
APEH|327	A2
APEX2|27301	A2
APH1A|51107	A2
APITD1|378708	A2
APLF|200558	A2
APOA1BP|128240	A2
APOB48R|55911	A2
APOBEC3C|27350	A2
APOB|338	A2
APOC2|344	A2
APPL2|55198	A2
APTX|54840	A2
AQP1|358	A2
AQP7P1|375719	A2
AQP7P3|441432	A2
AQPEP|206338	A2
ARAP1|116985	A2
ARAP3|64411	A2
ARC|23237	A2
ARF3|377	A2
ARF4|378	A2
ARF5|381	A2
ARFGAP1|55738	A2
ARFIP2|23647	A2
ARG2|384	A2
ARGLU1|55082	A2
ARHGAP11A|9824	A2
ARHGAP20|57569	A2
ARHGAP21|57584	A2
ARHGAP23|57636	A2
ARHGAP24|83478	A2
ARHGAP26|23092	A2
ARHGAP29|9411	A2
ARHGAP32|9743	A2
ARHGAP39|80728	A2
ARHGAP42|143872	A2
ARHGAP5|394	A2
ARHGAP6|395	A2
ARHGDIB|397	A2
ARHGEF11|9826	A2
ARHGEF17|9828	A2
ARHGEF37|389337	A2
ARHGEF6|9459	A2
ARHGEF7|8874	A2
ARID1B|57492	A2
ARID3A|1820	A2
ARID4A|5926	A2
ARID5A|10865	A2
ARL10|285598	A2

ARL11|115761	A2
ARL1|400	A2
ARL2|402	A2
ARL3|403	A2
ARL4A|10124	A2
ARL4C|10123	A2
ARL6IP1|23204	A2
ARL8A|127829	A2
ARL8B|55207	A2
ARMC10|83787	A2
ARMC1|55156	A2
ARMC6|93436	A2
ARMC7|79637	A2
ARMCX1|51309	A2
ARNT2|9915	A2
ARPC1B|10095	A2
ARPC2|10109	A2
ARPC3|10094	A2
ARPC4|10093	A2
ARPC5L|81873	A2
ARPC5|10092	A2
ARRDC2|27106	A2
ARRDC3|57561	A2
ARSB|411	A2
ARSI|340075	A2
ART4|420	A2
ARV1|64801	A2
ASB13|79754	A2
ASF1B|55723	A2
ASNA1|439	A2
ASPH|444	A2
ASPM|259266	A2
ASPN|54829	A2
ASPRV1|151516	A2
ASPSCR1|79058	A2
ASTN1|460	A2
ASXL1|171023	A2
ATAD2|29028	A2
ATF3|467	A2
ATF5|22809	A2
ATF6B|1388	A2
ATF7|11016	A2
ATG16L1|55054	A2
ATG2B|55102	A2
ATG4C|84938	A2
ATG4D|84971	A2
ATG9B|285973	A2
ATIC|471	A2
ATL1|51062	A2
ATM|472	A2
ATOH8|84913	A2

ATOX1|475	A2
ATP13A1|57130	A2
ATP13A2|23400	A2
ATP1B2|482	A2
ATP2B4|493	A2
ATP2C2|9914	A2
ATP5C1|509	A2
ATP6AP2|10159	A2
ATP6V1D|51382	A2
ATP6V1F|9296	A2
ATP7B|540	A2
ATP8B1|5205	A2
ATPIF1|93974	A2
ATRIP|84126	A2
ATXN1L|342371	A2
ATXN3|4287	A2
ATXN7L3|56970	A2
AUP1|550	A2
AURKAPS1|6791	A2
AURKA|6790	A2
AURKB|9212	A2
AVPI1|60370	A2
AVPR1A|552	A2
AXIN1|8312	A2
AXIN2|8313	A2
AZI2|64343	A2
B3GALNT1|8706	A2
B3GALNT2|148789	A2
B3GALT1|8708	A2
B3GALT2|8707	A2
B3GAT3|26229	A2
B3GNT1|11041	A2
B3GNT4|79369	A2
B4GALNT3|283358	A2
B4GALT1|2683	A2
B4GALT3|8703	A2
B4GALT4|8702	A2
B4GALT6|9331	A2
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GPR62|118442	B4
GRIN2D|2906	B4
KIAA0913|23053	B4
LOC284276|284276	B4
LOC401127|401127	B4
MARCH4|57574	B4
MLLT6|4302	B4
NEUROG2|63973	B4
NKPD1|284353	B4
NMNAT3|349565	B4
NPAS3|64067	B4
SEMA6C|10500	B4
SF1|7536	B4
STAU1|6780	B4
SYNPO2|171024	B4
TMEM79|84283	B4
TPTE2P3|220115	B4
WSCD2|9671	B4
ZFYVE28|57732	B4
ZNF487|642819	B4
ZNF589|51385	B4
AMIGO2|347902	B5
BRMS1L|84312	B5
C11orf31|280636	B5
C11orf93|120376	B5
CA11|770	B5
CDK6|1021	B5
CSDAP1|440359	B5
CSDA|8531	B5
CYP20A1|57404	B5
CYP39A1|51302	B5
DCHS2|54798	B5
DISC1|27185	B5
GNAQ|2776	B5
IGF2BP2|10644	B5
LPPR5|163404	B5
MAP2|4133	B5
OCA2|4948	B5
SMOC1|64093	B5
CAPN3|825	B6
CLCA4|22802	B6
GLT25D2|23127	B6
JPH2|57158	B6
LOC285419|285419	B6
MYH3|4621	B6

MYH7B|57644	B6
PLP1|5354	B6
TPM3|7170	B6
ALPL|249	B7
CHST2|9435	B7
KCTD14|65987	B7
KSR1|8844	B7
MRAP2|112609	B7
NAV3|89795	B7
PLA2G4A|5321	B7
TUBB2B|347733	B7
ANKRD35|148741	B8
ASXL3|80816	B8
SEC1|653677	B8

Supplementary Table 2. Functional enrichment analysis for each class by ToppGene

	Category	ID	Name	p.value	q.value.Bonferroni	q.value.FDR.B.H	q.value.FDR.B.Y	Hit.Count.in.Query.List	Hit.Count.in.Genome
A3	GO: Molecular Function	GO:0008201	Heparin binding	2.50E-06	3.64E-03	3.64E-03	2.87E-02	21	167
A3	GO: Biological Process	GO:0048514	Blood vessel morphogenesis	1.51E-08	9.00E-05	7.40E-05	6.86E-04	51	551
A3	GO: Biological Process	GO:0001944	Vasculature development	2.48E-08	1.48E-04	7.40E-05	6.86E-04	58	677
A3	GO: Biological Process	GO:0001568	Blood vessel development	3.80E-08	2.27E-04	7.56E-05	7.00E-04	56	651
A3	GO: Biological Process	GO:0001525	Angiogenesis	7.52E-08	4.49E-04	1.12E-04	1.04E-03	44	464
A3	GO: Biological Process	GO:0072359	Circulatory system development	2.85E-07	1.70E-03	2.83E-04	2.63E-03	76	1,058
A3	GO: Biological Process	GO:0072358	Cardiovascular system development	2.85E-07	1.70E-03	2.83E-04	2.63E-03	76	1,058
A3	GO: Biological Process	GO:0022610	Biological adhesion	4.66E-07	2.78E-03	3.97E-04	3.68E-03	100	1,542
A3	GO: Biological Process	GO:0007155	Cell adhesion	5.94E-07	3.54E-03	4.42E-04	4.10E-03	99	1,530
A3	GO: Biological Process	GO:0045765	Regulation of angiogenesis	9.39E-07	5.60E-03	6.22E-04	5.77E-03	27	239
A3	GO: Biological Process	GO:0072659	Protein localization to plasma membrane	3.19E-06	1.90E-02	1.77E-03	1.64E-02	25	225
A3	GO: Biological Process	GO:0022603	Regulation of anatomical structure morphogenesis	3.26E-06	1.94E-02	1.77E-03	1.64E-02	76	1,128
A3	GO: Biological Process	GO:1990778	Protein localization to cell periphery	3.74E-06	2.23E-02	1.86E-03	1.72E-02	25	227
A3	GO: Biological Process	GO:0031589	Cell-substrate adhesion	4.68E-06	2.79E-02	2.15E-03	1.99E-02	31	322
A3	GO: Biological Process	GO:0006261	DNA-dependent DNA replication	5.51E-06	3.29E-02	2.35E-03	2.18E-02	18	134
A3	GO: Biological Process	GO:1901342	Regulation of vasculature development	6.31E-06	3.76E-02	2.51E-03	2.32E-02	27	264
A3	GO: Biological Process	GO:2000351	Regulation of endothelial cell apoptotic process	7.86E-06	4.68E-02	2.93E-03	2.71E-02	10	45
A3	GO: Cellular Component	GO:0005811	Lipid droplet	3.43E-08	2.27E-05	2.27E-05	1.60E-04	15	67
A3	GO: Cellular Component	GO:0005912	Adherens junction	1.92E-07	1.27E-04	6.35E-05	4.49E-04	44	484
A3	GO: Cellular Component	GO:0070161	Anchoring junction	5.60E-07	3.69E-04	1.23E-04	8.70E-04	44	503
A3	GO: Cellular Component	GO:0005924	Cell-substrate adherens junction	1.06E-06	7.03E-04	1.76E-04	1.24E-03	37	398
A3	GO: Cellular Component	GO:0030055	Cell-substrate junction	1.44E-06	9.47E-04	1.89E-04	1.34E-03	37	403

A3	GO: Cellular Component	GO:0005925	Focal adhesion	2.10E-06	1.38E-03	2.31E-04	1.63E-03	36	393
A3	GO: Cellular Component	GO:0030054	Cell junction	3.68E-05	2.43E-02	3.47E-03	2.45E-02	75	1,200
A3	Mouse Phenotype	MP:0005666	Abnormal adipose tissue physiology	7.74E-07	3.71E-03	3.71E-03	3.35E-02	19	111
A3	Mouse Phenotype	MP:0001614	Abnormal blood vessel morphology	1.96E-06	9.39E-03	4.70E-03	4.25E-02	92	1,233
A3	Pubmed	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	2.77E-27	1.03E-22	1.03E-22	1.14E-21	94	1,743
A3	Pubmed	17081983	Global, in vivo, and site-specific phosphorylation dynamics in signaling networks.	1.53E-26	5.67E-22	2.83E-22	3.14E-21	87	1,546
A3	Pubmed	26638075	A dynamic protein interaction landscape of the human centrosome-cilium interface.	4.04E-24	1.49E-19	4.98E-20	5.52E-19	91	1,820
A3	Pubmed	19322201	Ubiquitin-mediated proteolysis of HuR by heat shock.	4.99E-23	1.85E-18	4.62E-19	5.12E-18	85	1,672
A3	Pubmed	25921289	Temporal proteomics of NGF-TrkA signaling identifies an inhibitory role for the E3 ligase Cbl-b in neuroblastoma cell differentiation.	1.67E-22	6.18E-18	1.24E-18	1.37E-17	91	1,922
A3	Pubmed	22863883	A high-throughput approach for measuring temporal changes in the interactome.	2.50E-21	9.26E-17	1.54E-17	1.71E-16	76	1,456
A3	Pubmed	16169070	A human protein-protein interaction network: a resource for annotating the proteome.	4.28E-21	1.59E-16	2.26E-17	2.51E-16	82	1,683
A3	Pubmed	21832049	Interactions of pathological hallmark proteins: tubulin polymerization promoting protein/p25, beta-amyloid, and alpha-synuclein.	3.42E-20	1.26E-15	1.58E-16	1.75E-15	86	1,891
A3	Pubmed	26673895	A deep proteomics perspective on CRM1-mediated nuclear export and nucleocytoplasmic partitioning.	4.34E-19	1.61E-14	1.79E-15	1.98E-14	60	1,039
A3	Pubmed	20467437	Direct interaction between hnRNP-M and CDC5L/PLRG1 proteins affects alternative splice site choice.	4.43E-17	1.64E-12	1.64E-13	1.82E-12	42	581
A3	Pubmed	12975309	The Secreted Protein Discovery Initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.	6.42E-17	2.38E-12	2.16E-13	2.40E-12	55	987
A3	Pubmed	24711643	Identifying biological pathways that underlie primordial short stature using network analysis.	7.53E-17	2.79E-12	2.32E-13	2.58E-12	56	1,024
A3	Pubmed	21900206	A directed protein interaction network for investigating intracellular signal transduction.	2.65E-16	9.81E-12	7.55E-13	8.38E-12	58	1,123
A3	Pubmed	16189514	Towards a proteome-scale map of the human protein-protein interaction network.	4.12E-16	1.52E-11	1.09E-12	1.21E-11	70	1,573
A3	Pubmed	23533145	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine.	1.82E-15	6.74E-11	4.49E-12	4.98E-11	55	1,068
A3	Pubmed	27880917	Phenotypic and Interaction Profiling of the Human Phosphatases Identifies Diverse Mitotic Regulators.	3.50E-15	1.30E-10	8.10E-12	8.98E-11	54	1,050
A3	Pubmed	19056867	Large-scale proteomics and phosphoproteomics of urinary exosomes.	3.73E-15	1.38E-10	8.12E-12	9.00E-11	53	1,017
A3	Pubmed	8125298	Oligo-capping: a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides.	3.19E-14	1.18E-09	6.56E-11	7.28E-10	74	1,881
A3	Pubmed	19946888	Defining the membrane proteome of NK cells.	6.69E-14	2.48E-09	1.30E-10	1.45E-09	55	1,166
A3	Pubmed	16335952	Human plasma N-glycoproteome analysis by	1.51E-13	5.58E-09	2.79E-10	3.10E-09	25	257

			immunoaffinity subtraction, hydrazide chemistry, and mass spectrometry.						
A3	Pubmed	27068509	Extracellular matrix remodelling in response to venous hypertension: proteomics of human varicose veins.	7.04E-13	2.60E-08	1.24E-09	1.38E-08	19	146
A3	Pubmed	17353931	Large-scale mapping of human protein-protein interactions by mass spectrometry.	9.26E-13	3.43E-08	1.56E-09	1.73E-08	56	1,284
A3	Pubmed	21423176	Analysis of the myosin-II-responsive focal adhesion proteome reveals a role for ?-Pix in negative regulation of focal adhesion maturation.	1.66E-12	6.15E-08	2.67E-09	2.97E-08	25	286
A3	Pubmed	15146197	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation.	2.22E-12	8.23E-08	3.43E-09	3.81E-08	50	1,085
A3	Pubmed	15342556	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions.	2.63E-12	9.73E-08	3.89E-09	4.32E-08	52	1165
A3	Pubmed	15302935	Large-scale characterization of HeLa cell nuclear phosphoproteins.	3.00E-12	1.11E-07	4.27E-09	4.74E-08	41	773
A3	Pubmed	27173435	An organelle-specific protein landscape identifies novel diseases and molecular mechanisms.	8.87E-12	3.28E-07	1.22E-08	1.35E-07	55	1,321
A3	Pubmed	21145461	Dynamics of cullin-RING ubiquitin ligase network revealed by systematic quantitative proteomics.	3.30E-11	1.22E-06	4.30E-08	4.77E-07	63	1,698
A3	Pubmed	25468996	E-cadherin interactome complexity and robustness resolved by quantitative proteomics.	3.37E-11	1.25E-06	4.30E-08	4.77E-07	33	565
A3	Pubmed	21516116	Next-generation sequencing to generate interactome datasets.	5.22E-11	1.93E-06	6.43E-08	7.14E-07	49	1,147
A3	Pubmed	19738201	Proteomic analysis of integrin-associated complexes identifies RCC2 as a dual regulator of Rac1 and Arf6.	2.04E-10	7.55E-06	2.44E-07	2.70E-06	36	708
A3	Pubmed	23251661	Novel genetic loci identified for the pathophysiology of childhood obesity in the Hispanic population.	2.24E-10	8.28E-06	2.59E-07	2.87E-06	39	817
A3	Pubmed	16710414	The DNA sequence and biological annotation of human chromosome 1.	5.77E-10	2.14E-05	6.47E-07	7.18E-06	44	1,034
A3	Pubmed	20360068	Systematic analysis of human protein complexes identifies chromosome segregation proteins.	1.16E-09	4.30E-05	1.27E-06	1.40E-05	51	1,341
A3	Pubmed	15231748	Functional proteomics mapping of a human signaling pathway.	1.78E-09	6.57E-05	1.88E-06	2.08E-05	31	591
A3	Pubmed	25852190	Integrative analysis of kinase networks in TRAIL-induced apoptosis provides a source of potential targets for combination therapy.	2.18E-09	8.08E-05	2.25E-06	2.49E-05	25	401
A3	Pubmed	27559042	Glycoproteomics Reveals Decorin Peptides With Anti-Myostatin Activity in Human Atrial Fibrillation.	2.68E-09	9.93E-05	2.68E-06	2.98E-05	13	99
A3	Pubmed	16964243	A probability-based approach for high-throughput protein phosphorylation analysis and site localization.	3.00E-09	1.11E-04	2.91E-06	3.23E-05	28	503
A3	Pubmed	20551380	Proteomics characterization of extracellular space components in the human aorta.	3.45E-09	1.28E-04	3.27E-06	3.63E-05	13	101
A3	Pubmed	16381901	The LIFEdb database in 2006.	4.21E-09	1.56E-04	3.84E-06	4.26E-05	34	720
A3	Pubmed	11076863	DNA cloning using in vitro site-specific recombination.	4.26E-09	1.58E-04	3.84E-06	4.26E-05	36	794
A3	Pubmed	15489336	From ORFeome to biology: a functional genomics pipeline.	4.51E-09	1.67E-04	3.97E-06	4.41E-05	34	722
A3	Pubmed	25609649	Proteomic analyses reveal distinct chromatin-associated and soluble transcription factor complexes.	8.06E-09	2.98E-04	6.94E-06	7.70E-05	37	852

A3	Pubmed	19615732	Defining the human deubiquitinating enzyme interaction landscape.	2.20E-08	8.14E-04	1.85E-05	2.05E-04	40	1,005
A3	Pubmed	15242332	Vectorial proteomics reveal targeting, phosphorylation and specific fragmentation of polymerase I and transcript release factor (PTRF) at the surface of caveolae in human adipocytes.	2.92E-08	1.08E-03	2.40E-05	2.66E-04	7	23
A3	Pubmed	20734064	A large-scale candidate gene association study of age at menarche and age at natural menopause.	3.63E-08	1.34E-03	2.92E-05	3.24E-04	19	275
A3	Pubmed	20589320	mRNA levels of CD31, CD144, CD146 and von Willebrand factor do not serve as surrogate markers for circulating endothelial cells.	4.74E-08	1.75E-03	3.68E-05	4.08E-04	4	4
A3	Pubmed	20628624	Evaluation of candidate stromal epithelial cross-talk genes identifies association between risk of serous ovarian cancer and TERT, a cancer susceptibility "hot-spot".	4.78E-08	1.77E-03	3.68E-05	4.08E-04	15	172
A3	Pubmed	24332808	PRP19 transforms into a sensor of RPA-ssDNA after DNA damage and drives ATR activation via a ubiquitin-mediated circuitry.	4.87E-08	1.80E-03	3.68E-05	4.08E-04	21	340
A3	Pubmed	22681889	The mRNA-bound proteome and its global occupancy profile on protein-coding transcripts.	6.29E-08	2.33E-03	4.58E-05	5.09E-04	34	805
A3	Pubmed	15815621	Generation and annotation of the DNA sequences of human chromosomes 2 and 4.	6.32E-08	2.34E-03	4.58E-05	5.09E-04	24	442
A3	Pubmed	24255178	Protein interaction network of the mammalian Hippo pathway reveals mechanisms of kinase-phosphatase interactions.	7.47E-08	2.76E-03	5.26E-05	5.84E-04	24	446
A3	Pubmed	23383273	VCP phosphorylation-dependent interaction partners prevent apoptosis in Helicobacter pylori-infected gastric epithelial cells.	7.54E-08	2.79E-03	5.26E-05	5.84E-04	19	288
A3	Pubmed	22446626	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation.	8.48E-08	3.14E-03	5.81E-05	6.45E-04	11	89
A3	Pubmed	17207965	hORFeome v3.1: a resource of human open reading frames representing over 10,000 human genes.	9.49E-08	3.51E-03	6.39E-05	7.09E-04	54	1,674
A3	Pubmed	28065597	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome.	9.75E-08	3.61E-03	6.44E-05	7.15E-04	23	419
A3	Pubmed	12107410	Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: over 6000 non-redundant transcripts, novel genes, and splice variants.	9.97E-08	3.69E-03	6.48E-05	7.19E-04	12	111
A3	Pubmed	26167880	SR protein kinases promote splicing of nonconsensus introns.	1.34E-07	4.94E-03	8.52E-05	9.46E-04	21	361
A3	Pubmed	17474147	Systematic identification of SH3 domain-mediated human protein-protein interactions by peptide array target screening.	1.37E-07	5.08E-03	8.61E-05	9.55E-04	20	330
A3	Pubmed	20634891	Maternal genes and facial clefts in offspring: a comprehensive search for genetic associations in two population-based cleft studies from Scandinavia.	1.44E-07	5.33E-03	8.88E-05	9.86E-04	20	331
A3	Pubmed	22113938	A bead-based approach for large-scale identification of in vitro kinase substrates.	1.61E-07	5.96E-03	9.69E-05	1.08E-03	14	163
A3	Pubmed	16713569	A protein-protein interaction network for human inherited ataxias and disorders of Purkinje cell degeneration.	1.62E-07	6.01E-03	9.69E-05	1.08E-03	28	608
A3	Pubmed	22268729	Proteomic identification of common SCF ubiquitin ligase	1.92E-07	7.09E-03	1.13E-04	1.25E-03	28	613

			FBXO6-interacting glycoproteins in three kinds of cells.						
A3	Pubmed	24550385	Characterizing WW domain interactions of tumor suppressor WWOX reveals its association with multiprotein networks.	2.15E-07	7.94E-03	1.24E-04	1.38E-03	16	220
A3	Pubmed	12621583	Refinement of a 400-kb critical region allows genotypic differentiation between isolated lissencephaly, Miller-Dieker syndrome, and other phenotypes secondary to deletions of 17p13.3.	2.31E-07	8.53E-03	1.27E-04	1.41E-03	6	19
A3	Pubmed	17724803	Expression of angiopoietin-1, 2 and 4 and Tie-1 and 2 in gastrointestinal stromal tumor, leiomyoma and schwannoma.	2.31E-07	8.53E-03	1.27E-04	1.41E-03	4	5
A3	Pubmed	9151733	Cloning and functional characterization of Roaz, a zinc finger protein that interacts with O/E-1 to regulate gene expression: implications for olfactory neuronal development.	2.31E-07	8.53E-03	1.27E-04	1.41E-03	4	5
A3	Pubmed	22412018	A promiscuous biotin ligase fusion protein identifies proximal and interacting proteins in mammalian cells.	2.59E-07	9.58E-03	1.41E-04	1.56E-03	12	121
A3	Pubmed	23667531	The SOX2-interactome in brain cancer cells identifies the requirement of MSI2 and USP9X for the growth of brain tumor cells.	2.69E-07	9.95E-03	1.44E-04	1.60E-03	18	282
A3	Pubmed	23455922	Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS.	3.06E-07	1.13E-02	1.62E-04	1.79E-03	23	447
A3	Pubmed	22990118	Charting the landscape of tandem BRCT domain-mediated protein interactions.	3.64E-07	1.35E-02	1.90E-04	2.11E-03	29	671
A3	Pubmed	25281560	Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes.	4.01E-07	1.48E-02	2.06E-04	2.28E-03	28	636
A3	Pubmed	22261194	Proteomics analysis of cardiac extracellular matrix remodeling in a porcine model of ischemia/reperfusion injury.	4.16E-07	1.54E-02	2.11E-04	2.34E-03	9	64
A3	Pubmed	19692168	Genetic susceptibility to distinct bladder cancer subphenotypes.	4.41E-07	1.63E-02	2.21E-04	2.45E-03	22	422
A3	Pubmed	16303743	Signal sequence and keyword trap in silico for selection of full-length human cDNAs encoding secretion or membrane proteins from oligo-capped cDNA libraries.	6.04E-07	2.24E-02	2.98E-04	3.31E-03	22	430
A3	Pubmed	22952844	Targeted ubiquitination and degradation of G-protein-coupled receptor kinase 5 by the DDB1-CUL4 ubiquitin ligase complex.	6.28E-07	2.32E-02	3.06E-04	3.39E-03	13	156
A3	Pubmed	22586326	Functional proteomics establishes the interaction of SIRT7 with chromatin remodeling complexes and expands its role in regulation of RNA polymerase I transcription.	6.74E-07	2.49E-02	3.24E-04	3.60E-03	28	653
A3	Pubmed	19625176	PTEN identified as important risk factor of chronic obstructive pulmonary disease.	1.07E-06	3.96E-02	5.08E-04	5.64E-03	20	376
A3	Pubmed	20800603	Investigation of genetic susceptibility factors for human longevity - a targeted nonsynonymous SNP study.	1.33E-06	4.94E-02	6.22E-04	6.90E-03	18	315
A3	Pubmed	20346360	Genetic risk factors for hepatopulmonary syndrome in patients with advanced liver disease.	1.35E-06	4.98E-02	6.22E-04	6.90E-03	10	94
A3	Coexpression	20421987-TableS1	Human Lung_Hou10_1067genes	5.43E-30	5.65E-26	5.65E-26	5.55E-25	94	724

A3	Coexpression	19036130-TableS1a	Mouse Viral_Mendoza-Villanueva08_1830genes	7.15E-23	7.44E-19	3.72E-19	3.66E-18	131	1,561
A3	Coexpression	18310505-TableS8	Human StemCell_Matushansky08_297genes	6.38E-20	6.65E-16	1.67E-16	1.64E-15	46	269
A3	Coexpression	15793299-TableC	Mouse Breast_Astolfi05_1104genes_TumorGenes	6.40E-20	6.67E-16	1.67E-16	1.64E-15	87	872
A3	Coexpression	19038878-SuppTable3	Human Leukemia_Lenz08_385genes	7.17E-19	7.46E-15	1.35E-15	1.33E-14	51	349
A3	Coexpression	M2573	Genes consistently up-regulated in mammary stem cells both in mouse and human species.	7.78E-19	8.10E-15	1.35E-15	1.33E-14	61	489
A3	Coexpression	M1451	Top 100 probe sets contributing to the negative side of the 2nd principal component; associated with adipocytic differentiation.	5.99E-18	6.23E-14	8.91E-15	8.75E-14	25	80
A3	Coexpression	16440291-SuppTable1	Human HeadandNeck_Martens06_209genes	7.95E-18	8.28E-14	1.04E-14	1.02E-13	38	206
A3	Coexpression	M7396	Genes down-regulated in the Kras2LA mouse lung cancer model with mutated KRAS [GeneID=3845].	1.05E-16	1.09E-12	1.21E-13	1.19E-12	54	435
A3	Coexpression	M1834	Genes up-regulated in freshly isolated CD31- [GeneID=5175] (stromal stem cells from adipose tissue) versus the CD31+ (non-stem) counterparts.	1.35E-16	1.40E-12	1.40E-13	1.38E-12	41	260
A3	Coexpression	16488994-SuppTable1a	Mouse Lung_Lu06_856genes_Array MG_U74Av2	4.16E-16	4.33E-12	3.94E-13	3.87E-12	54	449
A3	Coexpression	18310505-TableS1	Human StemCell_Matushansky08_886genes	7.37E-16	7.68E-12	6.40E-13	6.29E-12	69	695
A3	Coexpression	16488994-SuppTable1b	Mouse Lung_Lu06_856genes_Array MEO430Av2	9.83E-16	1.02E-11	7.87E-13	7.74E-12	53	443
A3	Coexpression	16288205-GeneTable3	Human Breast_Charafe-Jauffret06_1309genes	1.96E-15	2.04E-11	1.46E-12	1.43E-11	79	884
A3	Coexpression	M19391	Genes down-regulated in prostate cancer samples.	7.19E-15	7.49E-11	4.99E-12	4.91E-11	54	480
A3	Coexpression	M17471	Genes up-regulated in invasive ductal carcinoma (IDC) relative to ductal carcinoma in situ (DCIS, non-invasive).	5.45E-14	5.67E-10	3.55E-11	3.48E-10	44	351
A3	Coexpression	18338247-SuppTable4B	Human Breast_Harvell08_428genes	7.33E-14	7.64E-10	4.49E-11	4.41E-10	41	311
A3	Coexpression	20421987-TableS2	Human Lung_Hou10_187genes	1.83E-13	1.90E-09	1.03E-10	1.00E-09	27	141
A3	Coexpression	19843711-TableS1	Human Kidney_Sallustio10_2134genes_DiscriminatedARPCsFromRPTEC/MSC	1.87E-13	1.95E-09	1.03E-10	1.00E-09	115	1,688
A3	Coexpression	15220918-TableS1a	Human Viral_Wang04_1482genes	2.17E-13	2.26E-09	1.13E-10	1.11E-09	90	1,178
A3	Coexpression	19843711-TableS2	Human Kidney_Sallustio10_2134genes_CompleteListAnalysis	2.49E-13	2.60E-09	1.24E-10	1.22E-09	114	1,674
A3	Coexpression	16293578-SuppTable2	Human StemCell_Cai06_1370genes	3.85E-13	4.00E-09	1.82E-10	1.79E-09	90	1,190
A3	Coexpression	15785748-Table3	Human Uterine_Santin05_178genes	6.60E-12	6.87E-08	3.00E-09	2.94E-08	26	151
A3	Coexpression	18498629-GeneList	Human Breast_Loi08_239genes	9.87E-12	1.03E-07	4.28E-09	4.21E-08	28	178
A3	Coexpression	M9192	Genes down-regulated in luminal-like breast cancer cell lines compared to the mesenchymal-like ones.	1.32E-11	1.38E-07	5.51E-09	5.42E-08	47	460
A3	Coexpression	M2129	Genes up-regulated in confluent IMR90 cells (fibroblast) after knockdown of RB1 [GeneID=5925] by RNAi.	1.82E-11	1.89E-07	7.27E-09	7.15E-08	53	566
A3	Coexpression	18006812-TableS1	Human Lymphoma_Piccaluga07_260genes	5.38E-11	5.60E-07	2.08E-08	2.04E-07	29	204
A3	Coexpression	M12225	Up-regulated genes in angioimmunoblastic lymphoma (AILT) compared to normal T lymphocytes.	6.07E-11	6.32E-07	2.26E-08	2.22E-07	29	205
A3	Coexpression	18435859-ShorterGeneList	Mouse Breast_Piechocki08_558genes	1.35E-10	1.41E-06	4.85E-08	4.77E-07	40	376
A3	Coexpression	M3837	Down-regulated genes in pediatric adrenocortical tumors (ACT) compared to the normal tissue.	1.42E-10	1.48E-06	4.93E-08	4.84E-07	50	545
A3	Coexpression	17975224-TableS6	Mouse Viral_Cho08_252genes	1.96E-10	2.04E-06	6.58E-08	6.47E-07	27	188

A3	Coexpression	18310505-Table1	Human StemCell_Matushansky08_69genes	2.28E-10	2.38E-06	7.43E-08	7.30E-07	15	55
A3	Coexpression	17683608-TableS1	Mouse StemCell_Ulloa-Montoya07_546genes	2.68E-10	2.80E-06	8.47E-08	8.33E-07	44	451
A3	Coexpression	M4995	Genes specifically up-regulated in Cluster IIb of urothelial cell carcinoma (UCC) tumors.	4.05E-10	4.22E-06	1.24E-07	1.22E-06	40	390
A3	Coexpression	M97	Genes up-regulated in glomeruli of kidneys from patients with diabetic nephropathy (type 2 diabetes mellitus).	4.27E-10	4.44E-06	1.27E-07	1.25E-06	18	86
A3	Coexpression	19286929-SuppTable1	Mouse Lung_Rangasamy09_2003genes	4.92E-10	5.13E-06	1.42E-07	1.40E-06	102	1,621
A3	Coexpression	17234769-TableS2b	Human StemCell_West07_669genes	5.16E-10	5.37E-06	1.45E-07	1.43E-06	48	530
A3	Coexpression	M12921	Genes up-regulated in brain from patients with Alzheimer's disease.	5.36E-10	5.58E-06	1.47E-07	1.44E-06	105	1,690
A3	Coexpression	M1533	All significantly down-regulated genes in kidney glomeruli isolated from TCF21 [Gene ID=6943] knockout mice.	5.64E-10	5.87E-06	1.51E-07	1.48E-06	64	830
A3	Coexpression	18535662-TableS2c	Mouse Lymphoma_Wu08_1148genes	1.15E-09	1.20E-05	3.01E-07	2.95E-06	48	543
A3	Coexpression	17660535-TableS4b	Mouse InnerEar_Sajan08_2230genes	1.47E-09	1.53E-05	3.74E-07	3.67E-06	115	1,948
A3	Coexpression	18535662-TableS1a	Mouse Lymphoma_Wu08_1813genes	1.69E-09	1.76E-05	4.20E-07	4.13E-06	67	913
A3	Coexpression	M80	Genes up-regulated in TC71 and EWS502 cells (Ewing's sarcoma) by EWSR1-FLI1 [GeneID=2130;2314] as inferred from RNAi knockdown of this fusion protein.	2.52E-09	2.62E-05	6.09E-07	5.99E-06	84	1276
A3	Coexpression	M2324	Genes up-regulated in uterus upon knockout of BMP2 [GeneID=650].	2.65E-09	2.76E-05	6.26E-07	6.15E-06	58	745
A3	Coexpression	15361855-SuppTable1	Human Ovarian_Donninger04_1191genes	3.46E-09	3.61E-05	7.85E-07	7.71E-06	69	970
A3	Coexpression	19139136-TableS3	Human Prostate_John-Aryankalayil09_2212genes	3.47E-09	3.61E-05	7.85E-07	7.71E-06	96	1,547
A3	Coexpression	17161497-SuppTable1	Human Lung_Dracheva07_162genes	3.74E-09	3.90E-05	8.30E-07	8.15E-06	22	146
A3	Coexpression	17724462-TableS2	Human StemCell_Nuytten08_2072genes	4.00E-09	4.12E-05	8.57E-07	8.43E-06	105	1,753
A3	Coexpression	17284527-TableS2	Human Lypmhoma_Leval07_832genes	4.11E-09	4.28E-05	8.74E-07	8.59E-06	52	639
A3	Coexpression	19408105-SuppTable4	Mouse Breast_Stein09_1780genes	5.19E-09	5.40E-05	1.08E-06	1.06E-05	45	514
A3	Coexpression	19061838-TableS7	Human Viral_Cairo08_982genes	5.91E-09	6.15E-05	1.21E-06	1.19E-05	60	801
A3	Coexpression	18381423-SuppTable1a	Human StemCell_Riggi08_262genes	1.12E-08	1.16E-04	2.24E-06	2.20E-05	24	182
A3	Coexpression	M2456	Genes requiring MLL [GeneID=4297] for H3K4me3 and expression in MEF cells (embryonic fibroblast).	1.34E-08	1.40E-04	2.64E-06	2.59E-05	31	289
A3	Coexpression	15972966-TableS2b	Human Colon_Lacroix05_61genes	1.46E-08	1.52E-04	2.82E-06	2.78E-05	12	44
A3	Coexpression	M1941	Genes with high-CpG-density promoters (HCP) bearing histone H3 dimethylation at K4 (H3K4me2) and trimethylation at K27 (H3K27me3) in brain.	1.51E-08	1.57E-04	2.86E-06	2.81E-05	72	1,069
A3	Coexpression	M17923	Genes up-regulated in cultured stromal stem cells from adipose tissue, compared to the freshly isolated cells.	1.55E-08	1.61E-04	2.88E-06	2.83E-05	39	425
A3	Coexpression	M5930	Genes defining epithelial-mesenchymal transition, as in wound healing, fibrosis and metastasis.	1.66E-08	1.73E-04	3.00E-06	2.95E-05	25	200
A3	Coexpression	M7517	Genes up-regulated in the luminal A subtype of breast cancer.	1.67E-08	1.74E-04	3.00E-06	2.95E-05	16	84
A3	Coexpression	M17788	Down-regulated genes whose expression profile is specific to Custer I of urothelial cell carcinoma (UCC) tumors.	2.15E-08	2.24E-04	3.79E-06	3.73E-05	36	378
A3	Coexpression	19605494-TableS2	Mouse Skin_Driskell09_1477genes	2.29E-08	2.39E-04	3.98E-06	3.91E-05	62	872
A3	Coexpression	M13256	Genes down-regulated in mesenchymal stem cells (MSC) engineered to express EWS-FLI1 [GeneID=2130;2321]	2.61E-08	2.72E-04	4.46E-06	4.38E-05	24	190

			fusion protein.						
A3	Coexpression	M8901	Down-regulated genes from the 324 genes identified by two analytical methods as changed in the mammary tumors induced by transgenic expression of ERBB2 [GeneID=2064].	2.83E-08	2.95E-04	4.75E-06	4.67E-05	21	149
A3	Coexpression	M13867	Genes up-regulated in HMLE cells (immortalized nontransformed mammary epithelium) after E-cadhedrin (CDH1) [GeneID=999] knockdown by RNAi.	4.44E-08	4.62E-04	7.34E-06	7.21E-05	28	256
A3	Coexpression	19861896-SuppTable1	Human Brain_Castells09_424gebes	4.88E-08	5.09E-04	7.95E-06	7.81E-05	35	373
A3	Coexpression	M1504	Adipocyte abundant genes up-regulated in 3T3-L1 cells (fibroblasts induced to differentiate to adipocytes) in response to troglitazone [PubChem=5591].	6.47E-08	6.73E-04	1.04E-05	1.02E-04	9	25
A3	Coexpression	20559987-TableS1	Rat Heart_Lara-Pezzi09_1421genes	7.22E-08	7.52E-04	1.14E-05	1.12E-04	55	757
A3	Coexpression	M1578	Genes down-regulated in freshly isolated CD31- [GeneID=5175] (stromal stem cells from adipose tissue) versus the CD31+ (non-stem) counterparts.	7.74E-08	8.06E-04	1.20E-05	1.18E-04	25	216
A3	Coexpression	M1999	The 'adult tissue stem' module: genes coordinately up-regulated in a compendium of adult tissue stem cells.	8.64E-08	9.00E-04	1.32E-05	1.30E-04	53	721
A3	Coexpression	M10952	Genes up-regulated in the atria of healthy hearts, compared to ventricles.	9.21E-08	9.60E-04	1.39E-05	1.37E-04	27	249
A3	Coexpression	M8513	Genes up-regulated in the normal-like subtype of breast cancer.	1.12E-07	1.17E-03	1.67E-05	1.64E-04	40	476
A3	Coexpression	M12432	Genes down-regulated in unstable atherosclerotic plaques compared to the stable ones.	1.21E-07	1.27E-03	1.75E-05	1.72E-04	11	43
A3	Coexpression	19505326-SuppTable3	Human Ovarian_Li09_2322genes_cisplatinresistance	1.23E-07	1.28E-03	1.75E-05	1.72E-04	102	1,804
A3	Coexpression	M14098	Genes down-regulated in primary fibroblast cell culture after infection with HCMV (AD169 strain) at 24 h time point that were not down-regulated at the previous time point, 20 h.	1.23E-07	1.28E-03	1.75E-05	1.72E-04	20	148
A3	Coexpression	M6520	Genes up-regulated in patients at the incipient stage of Alzheimer's disease.	1.46E-07	1.52E-03	2.05E-05	2.02E-04	35	390
A3	Coexpression	17724462-TableS1	Human StemCell_Nuytten08_1622genes	1.67E-07	1.74E-03	2.32E-05	2.28E-04	84	1,402
A3	Coexpression	M1484	Genes up-regulated in pancreatic cells from mice with double knockout of E2F1 [GeneID=1869] and E2F2 [GeneID=1870] compared to wild type.	1.71E-07	1.79E-03	2.35E-05	2.31E-04	20	151
A3	Coexpression	15972966-TableS2a	Human Colon_Lacroix05_114genes	2.40E-07	2.50E-03	3.25E-05	3.19E-04	14	77
A3	Coexpression	17676974-TableS1	Mouse StemCell_Chambers07_1667genes	2.49E-07	2.59E-03	3.29E-05	3.23E-04	76	1,236
A3	Coexpression	16288205-GeneTable2	Human Breast_Charafe-Jauffret06_1233genes	2.49E-07	2.60E-03	3.29E-05	3.23E-04	56	807
A3	Coexpression	19331821-SuppTable3	Human StemCell_Pilgaard09_26genes	3.25E-07	3.39E-03	4.24E-05	4.16E-04	8	22
A3	Coexpression	16498405-TableS3	Mouse Kidney_Takemoto06_388genes_cat1	4.23E-07	4.41E-03	5.44E-05	5.35E-04	29	302
A3	Coexpression	M4196	Genes up-regulated in PC3 cells (prostate cancer) after knockdown of EZH2 [GeneID=2146] by RNAi.	4.86E-07	5.06E-03	6.17E-05	6.07E-04	66	1,037
A3	Coexpression	16166195-TableS1b	Mouse Testicular_Denolet06_342genes	4.92E-07	5.12E-03	6.17E-05	6.07E-04	26	254
A3	Coexpression	M9908	Genes down-regulated in preneoplastic mammary tissues and whose expression is maintained in tumors.	5.00E-07	5.21E-03	6.20E-05	6.09E-04	13	70
A3	Coexpression	14766275-Fig.2	Human Uterine_Ferguson04_101genes	5.39E-07	5.61E-03	6.58E-05	6.47E-04	14	82

A3	Coexpression	M14027	Down-regulated genes in lung tissue of smokers with chronic obstructive pulmonary disease (COPD) vs smokers without disease (GOLD-2 vs GOLD-0).	5.43E-07	5.66E-03	6.58E-05	6.47E-04	17	120
A3	Coexpression	M4913	Genes down-regulated in adipose tissue mesenchymal stem cells (ASC) vs bone marrow mesenchymal stem cells (rBMSCs)	6.30E-07	6.56E-03	7.53E-05	7.40E-04	16	108
A3	Coexpression	M2571	Genes down-regulated during prostate cancer progression in the JOCK1 model due to inducible activation of FGFR1 [GeneID=2260] gene in prostate.	6.37E-07	6.63E-03	7.53E-05	7.40E-04	29	308
A3	Coexpression	M13206	Genes down-regulated in TC71 and EWS502 cells (Ewing's sarcoma) by EWSR1-FLI1 [GeneID=2130;2314] as inferred from RNAi knockdown of this fusion protein.	6.65E-07	6.93E-03	7.78E-05	7.65E-04	30	326
A3	Coexpression	M12176	Genes down-regulated in robust Cluster 2 (rC2) of hepatoblastoma samples compared to those in the robust Cluster 1 (rC1).	6.84E-07	7.13E-03	7.92E-05	7.78E-04	23	210
A3	Coexpression	19489030-SuppTable7	Human Prostate_Chambers09_259genes	7.18E-07	7.48E-03	8.22E-05	8.08E-04	22	195
A3	Coexpression	M1555	Adipocyte abundant genes down-regulated in 3T3-L1 cells (fibroblasts induced to differentiate to adipocytes) in response to TNF [GeneID=7124].	7.31E-07	7.61E-03	8.27E-05	8.13E-04	14	84
A3	Coexpression	17273163-Supp1a	Human Skin_Micke07_42genes	7.42E-07	7.73E-03	8.31E-05	8.17E-04	10	41
A3	Coexpression	M14427	Genes down-regulated in nasopharyngeal carcinoma (NPC) compared to the normal tissue.	8.59E-07	8.95E-03	9.52E-05	9.36E-04	80	1,367
A3	Coexpression	M2580	Genes consistently down-regulated in mature mammary luminal cells both in mouse and human species.	1.05E-06	1.09E-02	1.15E-04	1.13E-03	15	99
A3	Coexpression	M5905	Genes up-regulated during adipocyte differentiation (adipogenesis).	1.11E-06	1.15E-02	1.17E-04	1.15E-03	22	200
A3	Coexpression	M8469	Genes up-regulated in activated CD4 [GeneID=920] T cells: wildtype versus MIR17 [GeneID=406952] knockout.	1.11E-06	1.15E-02	1.17E-04	1.15E-03	22	200
A3	Coexpression	M8734	Genes up-regulated in T cells: control versus IL2 [GeneID=3558] stimulation for 17h.	1.11E-06	1.15E-02	1.17E-04	1.15E-03	22	200
A3	Coexpression	M13273	Genes down-regulated in papillary thyroid carcinoma (PTC) compared to normal tissue.	1.11E-06	1.16E-02	1.17E-04	1.15E-03	24	232
A3	Coexpression	15489886-TableS1b	Human Sarcoma_Mason04_549genes	1.19E-06	1.24E-02	1.24E-04	1.22E-03	37	464
A3	Coexpression	17471573-Table2	Human Viral_Santegoets07_103genes	1.31E-06	1.36E-02	1.35E-04	1.33E-03	14	88
A3	Coexpression	17206280-TableS1C	Mouse Breast_Park07_173genes	1.71E-06	1.78E-02	1.74E-04	1.71E-03	17	130
A3	Coexpression	M2675	Genes down-regulated in HUVEC cells (endothelium) by treatment with VEGFA [Gene ID=7422].	2.30E-06	2.40E-02	2.30E-04	2.26E-03	21	193
A3	Coexpression	M14142	Genes down-regulated in the invasive ductal carcinoma (IDC) compared to the invasive lobular carcinoma (ILC), the two major pathological types of breast cancer.	2.32E-06	2.42E-02	2.30E-04	2.26E-03	10	46
A3	Coexpression	17699775-SuppTable1	Human Lung_Johnson07_1334genes	2.32E-06	2.42E-02	2.30E-04	2.26E-03	57	888
A3	Coexpression	M18090	Genes down-regulated in PC3 cells (prostate cancer) after knockdown of NIPP1 [GeneID=5511] by RNAi.	2.57E-06	2.68E-02	2.52E-04	2.47E-03	55	848
A3	Coexpression	M5688	Genes up-regulated in Paneth cell (part of intestinal epithelium) of mice with hypomorphic (reduced function) form of ATG16L1 [GeneID=55054].	2.59E-06	2.69E-02	2.52E-04	2.47E-03	14	93
A3	Coexpression	M13944	Genes up-regulated in TMX2-28 cells (breast cancer) which do not express ESR1 [GeneID=2099]) compared to the	2.72E-06	2.84E-02	2.63E-04	2.58E-03	18	149

			parental MCF7 cells which do.						
A3	Coexpression	M14385	Genes down-regulated in fibroblasts with defective XPC [GeneID=7508] in response to cisplatin [PubChem=2767].	2.85E-06	2.97E-02	2.70E-04	2.65E-03	23	228
A3	Coexpression	20937356-TableS1	Rat Hypothalamic_Mansuy10_1270genes	2.85E-06	2.97E-02	2.70E-04	2.65E-03	57	894
A3	Coexpression	15845616-SuppTable3	Mouse Uterine_Jeong05_634genes	2.92E-06	3.04E-02	2.74E-04	2.69E-03	37	482
A3	Coexpression	M2270	Genes up-regulated during adipogenesis of 3T3-L1 cells (fibroblast).	3.58E-06	3.73E-02	3.33E-04	3.27E-03	7	21
A3	Coexpression	20220088-SuppTable1	Human Immune_Allen10_2900genes	3.68E-06	3.83E-02	3.39E-04	3.33E-03	96	1,798
A3	Coexpression	M7762	Genes down-regulated in macrophages: wildtype versus MYD88 [GeneID=4615] knockout.	4.07E-06	4.23E-02	3.68E-04	3.62E-03	21	200
A3	Coexpression	M4545	Genes up-regulated in comparison of thymic progenitors versus DN2 thymocytes.	4.07E-06	4.23E-02	3.68E-04	3.62E-03	21	200
A3	Coexpression	18631401-TableS3	Human Breast_Yau08_1518genes_OxidativeStress	4.44E-06	4.62E-02	3.98E-04	3.92E-03	67	1,129
A3	Coexpression	19658189-TableS4	Human EmbryonicStemCell_Xu09_1801genes	4.78E-06	4.98E-02	4.25E-04	4.18E-03	80	1,430
A3	Coexpression Atlas	GSM777059_500	Stromal Cells, LEC.MLN, gp38+ CD31+, Lymph Node, avg-4	2.33E-24	1.05E-20	6.46E-21	5.81E-20	68	439
A3	Coexpression Atlas	GSM777067_500	Stromal Cells, St.31-38-44-.SLN, CD45- gp38- CD31- CD44-, Lymph Node, avg-2	2.86E-24	1.29E-20	6.46E-21	5.81E-20	69	453
A3	Coexpression Atlas	GSM777063_500	Stromal Cells, LEC.SLN, gp38+ CD31+, Lymph Node, avg-4	9.97E-24	4.50E-20	1.21E-20	1.09E-19	68	450
A3	Coexpression Atlas	GSM777046_500	Stromal Cells, Fi.Sk, gp38+ CD140a+, Skin, avg-4	1.07E-23	4.83E-20	1.21E-20	1.09E-19	67	438
A3	Coexpression Atlas	PCBC_ratio_CardiacMyocyte_vs_SC_cfr-2X-p05	Cardiac Myocyte Cells_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	7.83E-23	3.54E-19	7.07E-20	6.36E-19	149	1,769
A3	Coexpression Atlas	GSM777050_500	Stromal Cells, FRC.MLN, gp38+ CD31- CD140a+, Lymph Node, avg-5	4.16E-22	1.88E-18	3.13E-19	2.82E-18	67	467
A3	Coexpression Atlas	GSM777032_500	Stromal Cells, BEC.MLN, gp38- CD31+, Lymph Node, avg-5	1.20E-20	5.43E-17	7.75E-18	6.97E-17	64	456
A3	Coexpression Atlas	GSM777055_500	Stromal Cells, FRC.SLN, gp38+ CD31- CD140a+, Lymph Node, avg-4	4.96E-20	2.24E-16	2.80E-17	2.52E-16	63	455
A3	Coexpression Atlas	PCBC_ctl_CardiacMyocyte_1000	Progenitor-Cell-Biology-Consortium_reference_CardiacMyocyte_top-relative-expression-ranked_1000	2.41E-19	1.09E-15	1.21E-16	1.09E-15	97	985
A3	Coexpression Atlas	gudmap_kidney_adult_RenCorpuscGlomer_1000	kidney_adult_RenCorpuscGlomer_top-relative-expression-ranked_1000	4.11E-19	1.85E-15	1.85E-16	1.67E-15	90	878
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_Podocytes_2500	gudmap_RNAseq_e15.5_Podocytes_2500	5.32E-19	2.40E-15	2.19E-16	1.97E-15	145	1,863
A3	Coexpression Atlas	GSM777043_500	Stromal Cells, Fi.MTS15+.Th, CD45- PDGFRa+ MTS15+, Thymus, avg-3	1.49E-18	6.72E-15	5.60E-16	5.04E-15	60	445
A3	Coexpression Atlas	gudmap_RNAseq_p2_CD2APMEISWT_2500	gudmap_RNAseq_p2_CD2APMEISWT_2500	3.03E-18	1.37E-14	1.05E-15	9.46E-15	141	1,822
A3	Coexpression Atlas	GSM777037_500	Stromal Cells, BEC.SLN, gp38- CD31+, Lymph Node, avg-4	6.76E-18	3.05E-14	2.18E-15	1.96E-14	60	459
A3	Coexpression Atlas	PCBC_ratio_BronchSmoothMuscl_vs_SC_cfr-2X-p05	Bronchial Smooth Muscle Cells_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	9.00E-18	4.07E-14	2.71E-15	2.44E-14	145	1,923
A3	Coexpression Atlas	JC_hmvEC_2500_K1	JC_hmvEC_top-relative-expression-ranked_2500_k-means-cluster#1	9.90E-18	4.47E-14	2.80E-15	2.51E-14	91	939

A3	Coexpression Atlas	PCBC_ratio_Lung Fibroblast_vs_SC_cfr-2X-p05	Lung Fibroblast_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	1.30E-17	5.86E-14	3.45E-15	3.10E-14	145	1,931
A3	Coexpression Atlas	gudmap_kidney_adult_Mesangium_Meis_1000	kidney_adult_Mesangium_Meis_top-relative-expression-ranked_1000	9.33E-17	4.22E-13	2.34E-14	2.11E-13	85	872
A3	Coexpression Atlas	gudmap_kidney_adult_RenalCapsule_1000	kidney_adult_RenalCapsule_top-relative-expression-ranked_1000	1.45E-16	6.57E-13	3.46E-14	3.11E-13	79	780
A3	Coexpression Atlas	gudmap_RNAseq_p2_Glomerlular Endothelial_2500	gudmap_RNAseq_p2_Glomerlular Endothelial_2500	2.76E-16	1.25E-12	6.24E-14	5.61E-13	129	1,686
A3	Coexpression Atlas	PCBC_ratio_PulmonMicrovasc_vs_SC_2X-p05	Pulmonary Microvascular_vs_Pluripotent Stem Cells-fold2.0_adjp0.05	4.07E-16	1.84E-12	8.49E-14	7.64E-13	136	1,831
A3	Coexpression Atlas	PCBC_ratio_PulmonMicrovasc_vs_SC_cfr-2X-p05	Pulmonary Microvascular_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	4.14E-16	1.87E-12	8.49E-14	7.64E-13	132	1,753
A3	Coexpression Atlas	Lungmap_Mouse_e16.5_Endothelial_Top_500_All	Lungmap_Mouse_e16.5_Endothelial_Top_500_All	2.20E-15	9.92E-12	4.31E-13	3.88E-12	55	446
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_ureter_1000	DevelopingLowerUrinaryTract_P1_ureter_emap-30363_top-relative-expression-ranked_1000	3.53E-15	1.60E-11	6.65E-13	5.98E-12	76	776
A3	Coexpression Atlas	PCBC_ratio_CardioEndothel_vs_SC_cfr-2X-p05	Cardiovascular Endothelial Cells_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	1.22E-14	5.52E-11	2.21E-12	1.99E-11	130	1,791
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_1000	kidney_adult_GlomCapSys_Tie2_top-relative-expression-ranked_1000	1.94E-14	8.75E-11	3.27E-12	2.94E-11	79	852
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_200	dev gonad_e11.5_F_ReproVasc_Flk_top-relative-expression-ranked_200	1.96E-14	8.84E-11	3.27E-12	2.94E-11	33	182
A3	Coexpression Atlas	GSM777067_100	Stromal Cells, St.31-38-44-.SLN, CD45- gp38- CD31- CD44-, Lymph Node, avg-2	2.38E-14	1.07E-10	3.84E-12	3.45E-11	23	85
A3	Coexpression Atlas	gudmap_RNAseq_p2_CD2APMEISWT_2500_K4	gudmap_RNAseq_p2_CD2APMEISWT_2500_K4	3.22E-14	1.45E-10	4.98E-12	4.48E-11	78	843
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_500	kidney_adult_RenMedVasc_Tie2_top-relative-expression-ranked_500	3.31E-14	1.49E-10	4.98E-12	4.48E-11	51	417
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_k2_500	dev gonad_e12.5_M_DevVasTestis_Flk_k-means-cluster#2_top-relative-expression-ranked_500	5.20E-14	2.35E-10	7.57E-12	6.81E-11	42	298
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_500	dev gonad_e11.5_F_ReproVasc_Flk_top-relative-expression-ranked_500	6.05E-14	2.73E-10	8.48E-12	7.63E-11	50	409
A3	Coexpression Atlas	BM Top 100 - adipose tissue subcutaneous	BM Top 100 - adipose tissue subcutaneous	6.20E-14	2.80E-10	8.48E-12	7.63E-11	21	72
A3	Coexpression Atlas	gudmap_kidney_P0_JuxtaGlom_Ren1_1000	kidney_P0_JuxtaGlom_Ren1_top-relative-expression-ranked_1000	6.45E-14	2.91E-10	8.57E-12	7.71E-11	81	906
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500	8.75E-14	3.95E-10	1.13E-11	1.02E-10	114	1,522
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_100	dev gonad_e11.5_M_ReproVasc_Flk_top-relative-expression-ranked_100	1.95E-13	8.80E-10	2.34E-11	2.10E-10	23	93
A3	Coexpression Atlas	endothelial_Top_500_All	endothelial_Top_500_All	1.96E-13	8.87E-10	2.34E-11	2.10E-10	55	496
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_adult_bladder_1000	DevelopingLowerUrinaryTract_adult_bladder_emap-29457_top-relative-expression-ranked_1000	1.97E-13	8.87E-10	2.34E-11	2.10E-10	70	736
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_gudmap_devVasOvary_Flk_200	dev gonad_e12.5_F_DevVasOvary_Flk_top-relative-expression-ranked_200	2.74E-13	1.24E-09	3.18E-11	2.86E-10	31	176
A3	Coexpression	gudmap_dev	dev gonad_e13.5_M_DevVasTestis_Flk_top-relative-	3.21E-13	1.45E-09	3.55E-11	3.19E-10	76	846

	Atlas	gonad_e13.5_M_gudmap_devVasTestis_Flk_1000	expression-ranked_1000						
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_500	kidney_adult_GlomCapSys_Tie2_top-relative-expression-ranked_500	3.22E-13	1.45E-09	3.55E-11	3.19E-10	50	427
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_500	dev gonad_e12.5_M_DevVasTestis_Flk_top-relative-expression-ranked_500	3.73E-13	1.69E-09	4.01E-11	3.61E-10	49	414
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_1000	kidney_adult_RenMedVasc_Tie2_top-relative-expression-ranked_1000	4.08E-13	1.84E-09	4.27E-11	3.84E-10	76	850
A3	Coexpression Atlas	JC_hmvEC_1000_K4	JC_hmvEC_top-relative-expression-ranked_1000_k-means-cluster#4	4.21E-13	1.90E-09	4.27E-11	3.84E-10	50	430
A3	Coexpression Atlas	geo_heart_2500_K2	geo_heart_top-relative-expression-ranked_2500_k-means-cluster#2	4.26E-13	1.92E-09	4.27E-11	3.84E-10	92	1,138
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_200	dev gonad_e13.5_F_DevVascOvary_Flk_top-relative-expression-ranked_200	4.39E-13	2.00E-09	4.31E-11	3.88E-10	31	179
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_200	dev gonad_e11.5_M_ReproVasc_Flk_top-relative-expression-ranked_200	6.96E-13	3.14E-09	6.68E-11	6.01E-10	31	182
A3	Coexpression Atlas	PCBC_ctl_CardioEndothel_1000	Progenitor-Cell-Biology-Consortium_reference_CardioEndothel_top-relative-expression-ranked_1000	8.09E-13	3.66E-09	7.61E-11	6.85E-10	83	986
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder detrusor (LCM)_1000	DevelopingLowerUrinaryTract_P2_bladder detrusor (LCM)_emap-30376_top-relative-expression-ranked_1000	9.73E-13	4.40E-09	8.94E-11	8.04E-10	70	761
A3	Coexpression Atlas	endothelial_Top_500_Cluster_4	endothelial_Top_500_Cluster_4	9.90E-13	4.47E-09	8.94E-11	8.04E-10	37	258
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_1000	DevelopingKidney_e15.5_Endothelial cells_emap-29977_top-relative-expression-ranked_1000	1.17E-12	5.30E-09	1.04E-10	9.34E-10	70	764
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_1000	dev gonad_e11.5_F_ReproVasc_Flk_top-relative-expression-ranked_1000	1.27E-12	5.74E-09	1.10E-10	1.00E-09	73	817
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_500	dev gonad_e11.5_M_ReproVasc_Flk_top-relative-expression-ranked_500	1.40E-12	6.31E-09	1.19E-10	1.07E-09	48	414
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder detrusor (LCM)_500	DevelopingLowerUrinaryTract_P2_bladder detrusor (LCM)_emap-30376_top-relative-expression-ranked_500	1.88E-12	8.51E-09	1.58E-10	1.42E-09	46	388
A3	Coexpression Atlas	lungmap/P1_Pericyte_Subclass_All subclasses	lungmap/P1_Pericyte_Subclass_All subclasses	1.96E-12	8.84E-09	1.61E-10	1.45E-09	31	189
A3	Coexpression Atlas	PCBC_ctl_PulmonMicrovasc_1000	Progenitor-Cell-Biology-Consortium_reference_PulmonMicrovasc_top-relative-expression-ranked_1000	2.01E-12	9.10E-09	1.62E-10	1.46E-09	82	985
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_InterstitTestis_Sma_1000	dev gonad_e13.5_M_InterstitTestis_Sma_top-relative-expression-ranked_1000	2.75E-12	1.24E-08	2.18E-10	2.00E-09	70	778
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500	2.99E-12	1.35E-08	2.33E-10	2.09E-09	118	1,686
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_100	dev gonad_e11.5_F_ReproVasc_Flk_top-relative-expression-ranked_100	3.43E-12	1.55E-08	2.58E-10	2.32E-09	22	96
A3	Coexpression Atlas	GSM777063_100	Stromal Cells, LEC.SLN, gp38+ CD31+, Lymph Node, avg-4	3.43E-12	1.55E-08	2.58E-10	2.32E-09	22	96
A3	Coexpression	gudmap_RNAseq_e15.5_Podocytes_2	gudmap_RNAseq_e15.5_Podocytes_2500_K0	3.58E-12	1.62E-08	2.65E-10	2.38E-09	90	1144

	Atlas	500_K0							
A3	Coexpression Atlas	PCBC_ctl_geo-heart_1000	geo_heart_top-relative-expression-ranked_1000	3.77E-12	1.71E-08	2.75E-10	2.47E-09	82	997
A3	Coexpression Atlas	BM Top 100 - adipose tissue	BM Top 100 - adipose tissue	4.06E-12	1.83E-08	2.87E-10	2.58E-09	19	70
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Endothelial-B(2)	lungmap/P1_Endothelial_Subclass_Endothelial-B(2)	4.07E-12	1.84E-08	2.87E-10	2.58E-09	35	244
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_k2_200	kidney_e15.5_SmlBldVes_Tie2_k-means-cluster#2_top-relative-expression-ranked_200	4.29E-12	1.94E-08	2.94E-10	2.64E-09	22	97
A3	Coexpression Atlas	GSM777046_100	Stromal Cells, Fi.Sk, gp38+ CD140a+, Skin, avg-4	4.29E-12	1.94E-08	2.94E-10	2.64E-09	22	97
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_200	kidney_adult_RenMedVasc_Tie2_top-relative-expression-ranked_200	5.01E-12	2.26E-08	3.38E-10	3.00E-09	29	172
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_Mesangium_2500_K3	gudmap_RNAseq_e15.5_Mesangium_2500_K3	5.81E-12	2.62E-08	3.86E-10	3.47E-09	35	247
A3	Coexpression Atlas	PCBC_ratio_Bronchial Smooth Muscle_vs_SC_cfr-2X-p05	Bronchial Smooth Muscle_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	6.00E-12	2.71E-08	3.93E-10	3.53E-09	123	1,806
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_1000_B	DevelopingLowerUrinaryTract_P1_bladder_B_emap-30374_top-relative-expression-ranked_1000	6.85E-12	3.09E-08	4.42E-10	4.00E-09	69	776
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_1000	dev gonad_e13.5_F_DevVascOvary_Flk_top-relative-expression-ranked_1000	7.88E-12	3.56E-08	5.01E-10	4.51E-09	72	831
A3	Coexpression Atlas	gudmap_developingKidney_e13.5_podocyte cells_1000_k5	DevelopingKidney_e13.5_podocyte cells_emap-27773_k-means-cluster#5_top-relative-expression-ranked_1000	8.55E-12	3.86E-08	5.36E-10	4.82E-09	28	164
A3	Coexpression Atlas	gudmap_kidney_adult_JuxtaGlom_Ren1_Captopr_1000	kidney_adult_JuxtaGlom_Ren1_Captopr_top-relative-expression-ranked_1000	8.66E-12	3.91E-08	5.36E-10	4.82E-09	69	780
A3	Coexpression Atlas	lungmap/P1_Pericyte_Subclass_Multiple	lungmap/P1_Pericyte_Subclass_Multiple	1.05E-11	4.76E-08	6.43E-10	5.78E-09	30	189
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_gudmap_devVasOvary_Flk_100	dev gonad_e12.5_F_DevVasOvary_Flk_top-relative-expression-ranked_100	1.16E-11	5.22E-08	6.87E-10	6.18E-09	21	92
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_100	dev gonad_e13.5_F_DevVascOvary_Flk_top-relative-expression-ranked_100	1.16E-11	5.22E-08	6.87E-10	6.18E-09	21	92
A3	Coexpression Atlas	BM Top 100 - adipose tissue omental	BM Top 100 - adipose tissue omental	1.19E-11	5.39E-08	7.01E-10	6.30E-09	19	74
A3	Coexpression Atlas	lungmap/P3_Endothelial_Subclass_Endothelial-B(1)	lungmap/P3_Endothelial_Subclass_Endothelial-B(1)	1.26E-11	5.68E-08	7.28E-10	6.55E-09	39	308
A3	Coexpression Atlas	gudmap_kidney_adult_RenalCapsule_500	kidney_adult_RenalCapsule_top-relative-expression-ranked_500	1.30E-11	5.89E-08	7.37E-10	6.63E-09	46	410
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Endothelial-B(1)	lungmap/P1_Endothelial_Subclass_Endothelial-B(1)	1.31E-11	5.90E-08	7.37E-10	6.63E-09	35	254
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_k2_200	dev gonad_e12.5_M_DevVasTestis_Flk_k-means-cluster#2_top-relative-expression-ranked_200	1.45E-11	6.55E-08	8.09E-10	7.27E-09	27	156
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_k4_500	dev gonad_e11.5_F_ReproVasc_Flk_k-means-cluster#4_top-relative-expression-ranked_500	1.48E-11	6.67E-08	8.14E-10	7.32E-09	33	229

A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_200	dev gonad_e12.5_M_DevVasTestis_Flk_top-relative-expression-ranked_200	1.60E-11	7.22E-08	8.70E-10	7.83E-09	29	180
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_1000	kidney_e15.5_SmlBldVes_Tie2_top-relative-expression-ranked_1000	2.09E-11	9.43E-08	1.12E-09	1.01E-08	70	813
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_k3_1000	kidney_adult_GlomCapSys_Tie2_k-means-cluster#3_top-relative-expression-ranked_1000	2.10E-11	9.50E-08	1.12E-09	1.01E-08	34	245
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_500	dev gonad_e13.5_F_DevVascOvary_Flk_top-relative-expression-ranked_500	2.15E-11	9.71E-08	1.13E-09	1.02E-08	46	416
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_1000	DevelopingKidney_e15.5_Endothelial cells_emap-29965_top-relative-expression-ranked_1000	2.18E-11	9.86E-08	1.13E-09	1.02E-08	67	761
A3	Coexpression Atlas	endothelial_SubClass_DCN-hi_Top_500_All	endothelial_SubClass_DCN-hi_Top_500_All	2.39E-11	1.08E-07	1.23E-09	1.10E-08	51	495
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_k4_500	kidney_adult_GlomCapSys_Tie2_k-means-cluster#4_top-relative-expression-ranked_500	2.50E-11	1.13E-07	1.27E-09	1.14E-08	25	137
A3	Coexpression Atlas	PCBC_ctl_PulmonMicrovasc_500	Progenitor-Cell-Biology-Consortium_reference_PulmonMicrovasc_top-relative-expression-ranked_500	2.58E-11	1.16E-07	1.29E-09	1.16E-08	51	496
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_k3_200	dev gonad_e11.5_F_ReproVasc_Flk_k-means-cluster#3_top-relative-expression-ranked_200	2.68E-11	1.21E-07	1.33E-09	1.20E-08	23	116
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_distal_ERK2_WT_2500	facebase_RNAseq_e14.5_palate_poster_distal_ERK2_WT_2500	2.81E-11	1.27E-07	1.38E-09	1.24E-08	107	1,522
A3	Coexpression Atlas	gudmap_RNAseq_e11.5_Ureteric_bud_2500	gudmap_RNAseq_e11.5_Ureteric_bud_2500	3.03E-11	1.37E-07	1.47E-09	1.33E-08	115	1,686
A3	Coexpression Atlas	gudmap_developingKidney_e13.5_podocyte cells_500_k2	DevelopingKidney_e13.5_podocyte cells_emap-27773_k-means-cluster#2_top-relative-expression-ranked_500	3.40E-11	1.53E-07	1.63E-09	1.46E-08	21	97
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_k2_100	dev gonad_e11.5_M_ReproVasc_Flk_k-means-cluster#2_top-relative-expression-ranked_100	3.42E-11	1.55E-07	1.63E-09	1.46E-08	16	53
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_gudmap_devVasOvary_Flk_k4_200	dev gonad_e12.5_F_DevVasOvary_Flk_k-means-cluster#4_top-relative-expression-ranked_200	3.89E-11	1.76E-07	1.83E-09	1.65E-08	20	88
A3	Coexpression Atlas	gudmap_kidney_adult_CortVasc_Tie2_k3_500	kidney_adult_CortVasc_Tie2_k-means-cluster#3_top-relative-expression-ranked_500	4.16E-11	1.88E-07	1.94E-09	1.74E-08	27	163
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_adult_bladder_500	DevelopingLowerUrinaryTract_adult_bladder_emap-29457_top-relative-expression-ranked_500	4.28E-11	1.93E-07	2.00E-09	1.77E-08	43	379
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_k3_500	dev gonad_e11.5_M_ReproVasc_Flk_k-means-cluster#3_top-relative-expression-ranked_500	4.82E-11	2.18E-07	2.20E-09	1.98E-08	32	226
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_k1_100	kidney_e15.5_SmlBldVes_Tie2_k-means-cluster#1_top-relative-expression-ranked_100	5.77E-11	2.61E-07	2.61E-09	2.34E-08	15	47
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_500	kidney_e15.5_SmlBldVes_Tie2_top-relative-expression-ranked_500	5.85E-11	2.64E-07	2.62E-09	2.35E-08	45	413
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_k2_200	dev gonad_e13.5_F_DevVascOvary_Flk_k-means-cluster#2_top-relative-expression-ranked_200	6.06E-11	2.74E-07	2.68E-09	2.41E-08	22	110
A3	Coexpression	gudmap_kidney_e15.5_SmlBldVes_Ti	kidney_e15.5_SmlBldVes_Tie2_k-means-cluster#4_top-	6.20E-11	2.80E-07	2.72E-09	2.45E-08	29	190

	Atlas	e2_k4_500	relative-expression-ranked_500						
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_gudmap_devVasOvary_Flk_500	dev gonad_e12.5_F_DevVasOvary_Flk_top-relative-expression-ranked_500	6.87E-11	3.10E-07	3.00E-09	2.67E-08	45	415
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_gudmap_devVasOvary_Flk_1000	dev gonad_e12.5_F_DevVasOvary_Flk_top-relative-expression-ranked_1000	6.91E-11	3.12E-07	3.00E-09	2.67E-08	69	817
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder stroma (LCM)_1000	DevelopingLowerUrinaryTract_P2_bladder stroma (LCM)_emap-30396_top-relative-expression-ranked_1000	8.45E-11	3.82E-07	3.60E-09	3.24E-08	67	785
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_k2_200	dev gonad_e13.5_M_DevVasTestis_Flk_k-means-cluster#2_top-relative-expression-ranked_200	9.36E-11	4.23E-07	4.00E-09	3.55E-08	23	123
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_k4_1000	kidney_e15.5_SmlBldVes_Tie2_k-means-cluster#4_top-relative-expression-ranked_1000	1.02E-10	4.61E-07	4.27E-09	3.84E-08	36	287
A3	Coexpression Atlas	JC_hmvEC_500_K1	JC_hmvEC_top-relative-expression-ranked_500_k-means-cluster#1	1.10E-10	4.95E-07	4.54E-09	4.08E-08	31	220
A3	Coexpression Atlas	lungmap/P3_Endothelial_Subclass_Endothelial-B(2)	lungmap/P3_Endothelial_Subclass_Endothelial-B(2)	1.22E-10	5.53E-07	5.00E-09	4.48E-08	37	303
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_1000_J	DevelopingLowerUrinaryTract_P1_bladder_J_emap-30374_top-relative-expression-ranked_1000	1.23E-10	5.54E-07	5.00E-09	4.48E-08	66	774
A3	Coexpression Atlas	gudmap_kidney_adult_RenCorpuscGlomer_500	kidney_adult_RenCorpuscGlomer_top-relative-expression-ranked_500	1.23E-10	5.57E-07	5.00E-09	4.48E-08	46	438
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_ureter_500	DevelopingLowerUrinaryTract_P1_ureter_emap-30363_top-relative-expression-ranked_500	1.27E-10	5.73E-07	5.07E-09	4.56E-08	43	392
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_1000	dev gonad_e11.5_M_ReproVasc_Flk_top-relative-expression-ranked_1000	1.45E-10	6.57E-07	5.76E-09	5.18E-08	67	795
A3	Coexpression Atlas	GSM791122_500	Fetal Liver, SC.STSL.FL, IgM- CD24- CD117+ IL7R- CD150- CD48- AA4.1+ CD43+, Fetal Liver, avg-2	1.57E-10	7.09E-07	6.17E-09	5.55E-08	44	410
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_500	DevelopingKidney_e15.5_Endothelial cells_emap-29977_top-relative-expression-ranked_500	2.29E-10	1.03E-06	8.92E-09	8.02E-08	42	384
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_nasal_Tgfbr2_WT_2500	facebase_RNAseq_e14.5_palate_poster_nasal_Tgfbr2_WT_2500	2.45E-10	1.11E-06	9.47E-09	8.52E-08	110	1,641
A3	Coexpression Atlas	gudmap_kidney_adult_RenalCapsule_k2_1000	kidney_adult_RenalCapsule_k-means-cluster#2_top-relative-expression-ranked_1000	2.74E-10	1.24E-06	1.05E-08	9.45E-08	41	371
A3	Coexpression Atlas	Lungmap_Mouse_e16.5_Matrix fibroblast_Top_500_All	Lungmap_Mouse_e16.5_Matrix fibroblast_Top_500_All	3.41E-10	1.54E-06	1.29E-08	1.16E-07	44	420
A3	Coexpression Atlas	PCBC_ctl_CardioEndothel_100	Progenitor-Cell-Biology-Consortium_reference_CardioEndothel_top-relative-expression-ranked_100	3.72E-10	1.68E-06	1.40E-08	1.26E-07	20	99
A3	Coexpression Atlas	gudmap_kidney_adult_CortVasc_Tie2_k2_1000	kidney_adult_CortVasc_Tie2_k-means-cluster#2_top-relative-expression-ranked_1000	4.29E-10	1.94E-06	1.60E-08	1.44E-07	36	302
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_100	dev gonad_e12.5_M_DevVasTestis_Flk_top-relative-expression-ranked_100	4.63E-10	2.09E-06	1.72E-08	1.54E-07	19	90
A3	Coexpression Atlas	GSM777059_100	Stromal Cells, LEC.MLN, gp38+ CD31+, Lymph Node, avg-4	5.66E-10	2.56E-06	2.06E-08	1.85E-07	19	91
A3	Coexpression	GSM791112_500	Stem Cells, SC.ST34F.BM, Lineage- cKit+ Sca-1+ flk2-	5.66E-10	2.56E-06	2.06E-08	1.85E-07	43	411

	Atlas		CD34+, Bone marrow, avg-2						
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_200	DevelopingKidney_e15.5_Endothelial cells_emap-29977_top-relative-expression-ranked_200	5.96E-10	2.69E-06	2.15E-08	1.94E-07	25	158
A3	Coexpression Atlas	lungmap/P1_MyoFB_Subclass_MyoFB-A	lungmap/P1_MyoFB_Subclass_MyoFB-A	6.05E-10	2.73E-06	2.17E-08	1.95E-07	32	249
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_k3_1000	dev gonad_e11.5_F_ReproVasc_Flk_k-means-cluster#3_top-relative-expression-ranked_1000	6.24E-10	2.82E-06	2.22E-08	2.00E-07	45	444
A3	Coexpression Atlas	gudmap_kidney_adult_Mesangium_Meis_500	kidney_adult_Mesangium_Meis_top-relative-expression-ranked_500	6.68E-10	3.02E-06	2.36E-08	2.12E-07	44	429
A3	Coexpression Atlas	geo_heart_2500_K3	geo_heart_top-relative-expression-ranked_2500_k-means-cluster#3	6.99E-10	3.16E-06	2.45E-08	2.20E-07	27	184
A3	Coexpression Atlas	facebase_RNAseq_e8.5_ParaxMesoderm_2500_K3	facebase_RNAseq_e8.5_ParaxMesoderm_2500_K3	7.54E-10	3.41E-06	2.61E-08	2.35E-07	23	136
A3	Coexpression Atlas	BM Top 100 - coronary artery	BM Top 100 - coronary artery	7.58E-10	3.42E-06	2.61E-08	2.35E-07	17	73
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_InterstitFLeydig_MafB_1000	dev gonad_e13.5_M_InterstitFLeydig_MafB_top-relative-expression-ranked_1000	7.89E-10	3.56E-06	2.70E-08	2.43E-07	64	773
A3	Coexpression Atlas	lungmap/P1_MyoFB_Subclass_MyoFB-D	lungmap/P1_MyoFB_Subclass_MyoFB-D	8.04E-10	3.63E-06	2.73E-08	2.46E-07	31	238
A3	Coexpression Atlas	JC_fibro_1000_K1	JC_fibro_top-relative-expression-ranked_1000_k-means-cluster#1	8.24E-10	3.72E-06	2.78E-08	2.50E-07	46	464
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_k4_500	dev gonad_e13.5_M_DevVasTestis_Flk_k-means-cluster#4_top-relative-expression-ranked_500	1.00E-09	4.40E-06	3.26E-08	2.93E-07	34	282
A3	Coexpression Atlas	gudmap_developingKidney_e13.5_podocyte cells_1000	DevelopingKidney_e13.5_podocyte cells_emap-27773_top-relative-expression-ranked_1000	1.23E-09	5.55E-06	4.07E-08	3.66E-07	68	855
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_k3_1000	dev gonad_e13.5_F_DevVascOvary_Flk_k-means-cluster#3_top-relative-expression-ranked_1000	1.24E-09	5.58E-06	4.07E-08	3.66E-07	52	570
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_e13.5_bladder mesenchyme_1000	DevelopingLowerUrinaryTract_e13.5_bladder mesenchyme_emap-3087_top-relative-expression-ranked_1000	1.32E-09	5.96E-06	4.32E-08	3.89E-07	67	838
A3	Coexpression Atlas	gudmap_kidney_P0_JuxtaGlom_Ren1_500	kidney_P0_JuxtaGlom_Ren1_top-relative-expression-ranked_500	1.46E-09	6.59E-06	4.74E-08	4.27E-07	45	456
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_500_k4	DevelopingKidney_e15.5_Endothelial cells_emap-29965_k-means-cluster#4_top-relative-expression-ranked_500	1.55E-09	6.99E-06	4.99E-08	4.49E-07	29	217
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_gudmap_devVasTestis_Flk_k4_1000	dev gonad_e12.5_M_DevVasTestis_Flk_k-means-cluster#4_top-relative-expression-ranked_1000	1.56E-09	7.03E-06	4.99E-08	4.49E-07	49	523
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_1000_k2	DevelopingKidney_e15.5_Endothelial cells_emap-29965_k-means-cluster#2_top-relative-expression-ranked_1000	1.75E-09	7.90E-06	5.56E-08	5.00E-07	35	303
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_B_1000_k1	DevelopingLowerUrinaryTract_P1_bladder_B_emap-30374_k-means-cluster#1_top-relative-expression-ranked_1000	1.83E-09	8.26E-06	5.78E-08	5.20E-07	27	192
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Ureteral Smooth Musc_1000	DevelopingKidney_e15.5_Ureteral Smooth Musc_emap-28812_top-relative-expression-ranked_1000	1.90E-09	8.60E-06	5.97E-08	5.37E-07	63	772
A3	Coexpression	gudmap_dev	dev gonad_e12.5_M_DevVasTestis_Flk_top-relative-	2.00E-09	9.22E-06	6.36E-08	5.72E-07	67	847

	Atlas	gonad_e12.5_M_gudmap_devVasTestis_Flk_1000	expression-ranked_1000						
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_500	dev gonad_e13.5_M_DevVasTestis_Flk_top-relative-expression-ranked_500	2.28E-09	1.03E-05	7.01E-08	6.30E-07	43	430
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_100	kidney_e15.5_SmlBldVes_Tie2_top-relative-expression-ranked_100	2.28E-09	1.03E-05	7.01E-08	6.30E-07	18	88
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-F	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-F	2.44E-09	1.10E-05	7.46E-08	6.71E-07	30	235
A3	Coexpression Atlas	PCBC_ctl_PulmonMicrovasc_100	Progenitor-Cell-Biology-Consortium_reference_PulmonMicrovasc_top-relative-expression-ranked_100	2.54E-09	1.15E-05	7.71E-08	6.93E-07	19	99
A3	Coexpression Atlas	PCBC_ctl_geo-heart_500	geo_heart_top-relative-expression-ranked_500	2.86E-09	1.29E-05	8.60E-08	7.73E-07	47	499
A3	Coexpression Atlas	PCBC_ctl_BronchSmoothMuscl_1000	Progenitor-Cell-Biology-Consortium_reference_BronchSmoothMuscl_top-relative-expression-ranked_1000	2.93E-09	1.32E-05	8.77E-08	7.89E-07	74	987
A3	Coexpression Atlas	gudmap_kidney_adult_CortVasc_Tie2_500	kidney_adult_CortVasc_Tie2_top-relative-expression-ranked_500	3.00E-09	1.37E-05	9.04E-08	8.13E-07	42	418
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_k2_100	dev gonad_e13.5_F_DevVascOvary_Flk_k-means-cluster#2_top-relative-expression-ranked_100	3.11E-09	1.41E-05	9.19E-08	8.27E-07	14	52
A3	Coexpression Atlas	JC_fibro_1000	JC_fibro_top-relative-expression-ranked_1000	4.00E-09	1.79E-05	1.16E-07	1.05E-06	74	994
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_k3_100	dev gonad_e13.5_M_DevVasTestis_Flk_k-means-cluster#3_top-relative-expression-ranked_100	4.09E-09	1.85E-05	1.19E-07	1.07E-06	14	53
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_200	kidney_adult_GlomCapSys_Tie2_top-relative-expression-ranked_200	4.12E-09	1.86E-05	1.19E-07	1.07E-06	25	173
A3	Coexpression Atlas	gudmap_kidney_adult_CortVasc_Tie2_1000	kidney_adult_CortVasc_Tie2_top-relative-expression-ranked_1000	4.94E-09	2.23E-05	1.42E-07	1.28E-06	66	847
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Ureteral Smooth Musc_500	DevelopingKidney_e15.5_Ureteral Smooth Musc_emap-28812_top-relative-expression-ranked_500	5.00E-09	2.27E-05	1.44E-07	1.29E-06	40	393
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder detrusor (LCM)_1000_k1	DevelopingLowerUrinaryTract_P2_bladder detrusor (LCM)_emap-30376_k-means-cluster#1_top-relative-expression-ranked_1000	5.41E-09	2.44E-05	1.54E-07	1.38E-06	30	243
A3	Coexpression Atlas	gudmap_kidney_e10.5_UretericTrunk_HoxB7_k3_1000	kidney_e10.5_UretericTrunk_HoxB7_k-means-cluster#3_top-relative-expression-ranked_1000	5.79E-09	2.61E-05	1.63E-07	1.47E-06	18	93
A3	Coexpression Atlas	gudmap_kidney_adult_Mesangium_Meis_k2_1000	kidney_adult_Mesangium_Meis_k-means-cluster#2_top-relative-expression-ranked_1000	5.91E-09	2.67E-05	1.66E-07	1.49E-06	37	348
A3	Coexpression Atlas	PCBC_ctl_CardiacMyocyte_500	Progenitor-Cell-Biology-Consortium_reference_CardiacMyocyte_top-relative-expression-ranked_500	6.43E-09	2.91E-05	1.79E-07	1.61E-06	46	495
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_Podocytes_2500_K2	gudmap_RNAseq_e15.5_Podocytes_2500_K2	6.62E-09	2.99E-05	1.84E-07	1.65E-06	36	334
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k5_1000	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k-means-cluster#5_top-relative-expression-ranked_1000	7.00E-09	3.17E-05	1.93E-07	1.74E-06	42	430
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_M_ReproVasc_Flk_k4_	dev gonad_e11.5_M_ReproVasc_Flk_k-means-cluster#4_top-relative-expression-ranked_1000	7.32E-09	3.31E-05	2.01E-07	1.80E-06	47	514

		1000							
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_Endothelial_2500	gudmap_RNAseq_e15.5_Endothelial_2500	7.56E-09	3.42E-05	2.06E-07	1.85E-06	114	1,829
A3	Coexpression Atlas	gudmap_kidney_adult_JuxtaGlom_Ren1_1000	kidney_adult_JuxtaGlom_Ren1_top-relative-expression-ranked_1000	7.90E-09	3.57E-05	2.14E-07	1.92E-06	63	801
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_200	dev gonad_e13.5_M_DevVasTestis_Flk_top-relative-expression-ranked_200	8.38E-09	3.79E-05	2.24E-07	2.02E-06	25	179
A3	Coexpression Atlas	gudmap_kidney_e15.5_SmlBldVes_Tie2_200	kidney_e15.5_SmlBldVes_Tie2_top-relative-expression-ranked_200	8.38E-09	3.79E-05	2.24E-07	2.02E-06	25	179
A3	Coexpression Atlas	geo_heart_1000_K2	geo_heart_top-relative-expression-ranked_1000_k-means-cluster#2	8.79E-09	3.97E-05	2.34E-07	2.10E-06	34	307
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k5_500	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k-means-cluster#5_top-relative-expression-ranked_500	9.14E-09	4.13E-05	2.41E-07	2.17E-06	26	193
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-H	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-H	9.84E-09	4.44E-05	2.58E-07	2.32E-06	28	221
A3	Coexpression Atlas	endothelial-mural Subclass Vend2	endothelial-mural Subclass Vend2	1.02E-08	4.59E-05	2.65E-07	2.39E-06	43	452
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder stroma (LCM)_500	DevelopingLowerUrinaryTract_P2_bladder stroma (LCM)_emap-30396_top-relative-expression-ranked_500	1.11E-08	5.01E-05	2.88E-07	2.59E-06	39	388
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_k2_500	kidney_adult_RenMedVasc_Tie2_k-means-cluster#2_top-relative-expression-ranked_500	1.19E-08	5.39E-05	3.08E-07	2.77E-06	24	169
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_k3_1000	dev gonad_e13.5_M_DevVasTestis_Flk_k-means-cluster#3_top-relative-expression-ranked_1000	1.26E-08	5.70E-05	3.24E-07	2.91E-06	47	523
A3	Coexpression Atlas	GSM791126_500	Fetal Liver, SC.LTSL.FL, IgM- CD24- CD117+ IL7R- CD150+ CD48- AA4.1+ CD43+, Fetal Liver, avg-3	1.32E-08	5.98E-05	3.38E-07	3.04E-06	41	423
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_gudmap_devVascOvary_Flk_k3_500	dev gonad_e13.5_F_DevVascOvary_Flk_k-means-cluster#3_top-relative-expression-ranked_500	1.34E-08	6.06E-05	3.41E-07	3.06E-06	24	170
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Ureteral Smooth Musc_1000_k2	DevelopingKidney_e15.5_Ureteral Smooth Musc_emap-28812_k-means-cluster#2_top-relative-expression-ranked_1000	1.71E-08	7.74E-05	4.33E-07	3.89E-06	31	270
A3	Coexpression Atlas	gudmap_kidney_adult_RenalCapsule_k1_500	kidney_adult_RenalCapsule_k-means-cluster#1_top-relative-expression-ranked_500	1.91E-08	8.61E-05	4.79E-07	4.30E-06	29	242
A3	Coexpression Atlas	BM Top 100 - saphenous vein	BM Top 100 - saphenous vein	2.06E-08	9.33E-05	5.15E-07	4.63E-06	15	69
A3	Coexpression Atlas	GSM777037_100	Stromal Cells, BEC.SLN, gp38- CD31+, Lymph Node, avg-4	2.25E-08	1.01E-04	5.52E-07	4.97E-06	17	90
A3	Coexpression Atlas	GSM777032_100	Stromal Cells, BEC.MLN, gp38- CD31+, Lymph Node, avg-5	2.25E-08	1.01E-04	5.52E-07	4.97E-06	17	90
A3	Coexpression Atlas	gudmap_developingKidney_e13.5_podocyte cells_500	DevelopingKidney_e13.5_podocyte cells_emap-27773_top-relative-expression-ranked_500	2.25E-08	1.02E-04	5.52E-07	4.97E-06	41	431
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_k1_200	kidney_adult_GlomCapSys_Tie2_k-means-cluster#1_top-relative-expression-ranked_200	2.33E-08	1.05E-04	5.69E-07	5.12E-06	14	60
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_500	DevelopingKidney_e15.5_Endothelial cells_emap-29965_top-relative-expression-ranked_500	2.60E-08	1.18E-04	6.32E-07	5.68E-06	38	384
A3	Coexpression Atlas	endothelial-mural Subclass Vsmc	endothelial-mural Subclass Vsmc	2.78E-08	1.26E-04	6.69E-07	6.01E-06	42	451

A3	Coexpression Atlas	endothelial-mural	endothelial-mural	2.78E-08	1.26E-04	6.69E-07	6.01E-06	42	451
A3	Coexpression Atlas	endothelial_SubClass_DCN-hi_Top_500_Cluster_1	endothelial_SubClass_DCN-hi_Top_500_Cluster_1	2.87E-08	1.30E-04	6.85E-07	6.16E-06	28	232
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_adult_bladder_1000_k4	DevelopingLowerUrinaryTract_adult_bladder_emap-29457_k-means-cluster#4_top-relative-expression-ranked_1000	3.63E-08	1.64E-04	8.62E-07	7.75E-06	18	104
A3	Coexpression Atlas	gudmap_kidney_adult_RenCorpuscGlomer_k2_500	kidney_adult_RenCorpuscGlomer_k-means-cluster#2_top-relative-expression-ranked_500	3.85E-08	1.74E-04	9.10E-07	8.18E-06	19	116
A3	Coexpression Atlas	JC_hmvEC_1000	JC_hmvEC_top-relative-expression-ranked_1000	4.62E-08	2.09E-04	1.09E-06	9.78E-06	71	995
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_nasal_Tgfbr2_WT_2500_K0	facebase_RNAseq_e14.5_palate_poster_nasal_Tgfbr2_WT_2500_K0	5.14E-08	2.32E-04	1.20E-06	1.08E-05	24	182
A3	Coexpression Atlas	JC_hmvEC_500	JC_hmvEC_top-relative-expression-ranked_500	5.72E-08	2.58E-04	1.33E-06	1.20E-05	44	497
A3	Coexpression Atlas	gudmap_kidney_e10.5_UretericTrunk_HoxB7_k2_500	kidney_e10.5_UretericTrunk_HoxB7_k-means-cluster#2_top-relative-expression-ranked_500	6.27E-08	2.83E-04	1.45E-06	1.31E-05	13	55
A3	Coexpression Atlas	JC_iEC_1000_K3	JC_iEC_top-relative-expression-ranked_1000_k-means-cluster#3	6.91E-08	3.12E-04	1.59E-06	1.43E-05	22	158
A3	Coexpression Atlas	gudmap_RNAseq_p2_Glomerlular Endothelial_2500_K3	gudmap_RNAseq_p2_Glomerlular Endothelial_2500_K3	7.05E-08	3.18E-04	1.62E-06	1.45E-05	24	185
A3	Coexpression Atlas	gudmap_RNAseq_e11.5_Ureteric_bud_2500_K4	gudmap_RNAseq_e11.5_Ureteric_bud_2500_K4	7.19E-08	3.25E-04	1.64E-06	1.48E-05	53	662
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_CollectIng Duct_2500_K3	gudmap_RNAseq_e15.5_CollectIng Duct_2500_K3	7.24E-08	3.27E-04	1.64E-06	1.48E-05	29	257
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_200	DevelopingKidney_e15.5_Endothelial cells_emap-29965_top-relative-expression-ranked_200	7.75E-08	3.50E-04	1.75E-06	1.57E-05	22	159
A3	Coexpression Atlas	gudmap_kidney_adult_RenCorpuscGlomer_k3_200	kidney_adult_RenCorpuscGlomer_k-means-cluster#3_top-relative-expression-ranked_200	8.02E-08	3.62E-04	1.80E-06	1.62E-05	12	47
A3	Coexpression Atlas	gudmap_RNAseq_e15.5_Mesangium_2500	gudmap_RNAseq_e15.5_Mesangium_2500	8.09E-08	3.65E-04	1.81E-06	1.63E-05	112	1,867
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder stroma (LCM)_1000_k3	DevelopingLowerUrinaryTract_P2_bladder stroma (LCM)_emap-30396_k-means-cluster#3_top-relative-expression-ranked_1000	8.24E-08	3.72E-04	1.83E-06	1.64E-05	27	229
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_InterstitFLeydig_MafB_k3_1000	dev gonad_e13.5_M_InterstitFLeydig_MafB_k-means-cluster#3_top-relative-expression-ranked_1000	8.24E-08	3.72E-04	1.83E-06	1.64E-05	34	336
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Ureteral Smooth Musc_500_k5	DevelopingKidney_e15.5_Ureteral Smooth Musc_emap-28812_k-means-cluster#5_top-relative-expression-ranked_500	8.67E-08	3.92E-04	1.91E-06	1.71E-05	24	187
A3	Coexpression Atlas	PCBC_ratio_MESO-15_vs_MESO-5_cfr-2X-p05	Mesoderm Day 15_vs_Mesoderm Day 5-Confounder_removed-fold2.0_adjp0.05	8.69E-08	3.92E-04	1.91E-06	1.71E-05	74	1,071
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_500	dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_top-relative-expression-ranked_500	9.02E-08	4.08E-04	1.96E-06	1.77E-05	37	386
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_VascAssocMesenchStromOvary_Sma_1000	dev gonad_e13.5_F_VascAssocMesenchStromOvary_Sma_top-relative-expression-ranked_1000	9.04E-08	4.08E-04	1.96E-06	1.77E-05	60	798
A3	Coexpression	gudmap_developingLowerUrinaryTra	DevelopingLowerUrinaryTract_P2_bladder urothelium	9.46E-08	4.27E-04	2.04E-06	1.84E-05	59	780

	Atlas	ct_P2_bladder urothelium (LCM)_1000	(LCM)_emap-30380_top-relative-expression-ranked_1000						
A3	Coexpression Atlas	GSM605850_500	Myeloid Cells, MF.II-480hi.PC, F4/80hi CD115hi CD11b+ MHC II- CD11c-, Peritoneal Cavity, avg-3	1.01E-07	4.57E-04	2.18E-06	1.96E-05	40	438
A3	Coexpression Atlas	gudmap_kidney_e10.5_UretericTrunk_HoxB7_1000	kidney_e10.5_UretericTrunk_HoxB7_top-relative-expression-ranked_1000	1.08E-07	4.86E-04	2.30E-06	2.07E-05	60	802
A3	Coexpression Atlas	gudmap_kidney_adult_RenalCapsule_200	kidney_adult_RenalCapsule_top-relative-expression-ranked_200	1.15E-07	5.19E-04	2.45E-06	2.20E-05	23	176
A3	Coexpression Atlas	DevelopingLowerUrinaryTract_e14.5_ bladder_emap-6668_1000	DevelopingLowerUrinaryTract_e14.5_ bladder_emap-6668_top-relative-expression-ranked_1000	1.32E-07	5.97E-04	2.80E-06	2.52E-05	61	826
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_k2_1000	kidney_adult_RenMedVasc_Tie2_k-means-cluster#2_top-relative-expression-ranked_1000	1.45E-07	6.56E-04	3.07E-06	2.76E-05	32	312
A3	Coexpression Atlas	PCBC_ctl_CardioEndothel_500	Progenitor-Cell-Biology-Consortium_reference_CardioEndothel_top-relative-expression-ranked_500	1.54E-07	6.97E-04	3.23E-06	2.90E-05	43	497
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_J_1000_k2	DevelopingLowerUrinaryTract_P1_bladder_J_emap-30374_k-means-cluster#2_top-relative-expression-ranked_1000	1.54E-07	6.98E-04	3.23E-06	2.90E-05	28	251
A3	Coexpression Atlas	Facebase_RNAseq_ratio_e9.5_MandibularArch_vs_MaxillaryArch_1000	FacebaseRNAseq_ratio_e9.5_MandibularArch_vs_MaxillaryArch_top-relative-expression-ranked_1000	1.83E-07	8.25E-04	3.80E-06	3.42E-05	68	971
A3	Coexpression Atlas	GSM791102_500	Stem Cells, SC.LT34F.BM, Lineage- cKit+ Sca-1+ flk2- CD34-, Bone marrow, avg-3	1.99E-07	9.00E-04	4.13E-06	3.71E-05	35	365
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500_K3	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500_K3	2.48E-07	1.12E-03	5.10E-06	4.58E-05	19	130
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_500_B	DevelopingLowerUrinaryTract_P1_bladder_B_emap-30374_top-relative-expression-ranked_500	2.48E-07	1.12E-03	5.10E-06	4.58E-05	36	385
A3	Coexpression Atlas	gudmap_kidney_P0_JuxtaGlom_Ren1_k1_1000	kidney_P0_JuxtaGlom_Ren1_k-means-cluster#1_top-relative-expression-ranked_1000	2.63E-07	1.19E-03	5.37E-06	4.83E-05	16	94
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_ureter_200	DevelopingLowerUrinaryTract_P1_ureter_emap-30363_top-relative-expression-ranked_200	2.73E-07	1.23E-03	5.56E-06	5.00E-05	21	157
A3	Coexpression Atlas	GSM476663_100	Stem Cells, SC.LTSL.BM, CD117+ IL7R- CD150+ CD48- AA4.1+ CD43+, Bone marrow, avg-1	2.76E-07	1.25E-03	5.59E-06	5.03E-05	15	83
A3	Coexpression Atlas	lungmap/P1_MatrixFB_Subclass_MyoFB-F	lungmap/P1_MatrixFB_Subclass_MyoFB-F	2.97E-07	1.34E-03	5.99E-06	5.38E-05	28	259
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_distal_ERK2_WT_2500_K4	facebase_RNAseq_e14.5_palate_poster_distal_ERK2_WT_2500_K4	3.23E-07	1.46E-03	6.48E-06	5.83E-05	25	215
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_gudmap_devVasTestis_Flk_100	dev gonad_e13.5_M_DevVasTestis_Flk_top-relative-expression-ranked_100	3.25E-07	1.47E-03	6.49E-06	5.84E-05	15	84
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_F_VascAssocMesenchStromOvary_Sma_500	dev gonad_e13.5_F_VascAssocMesenchStromOvary_Sma_top-relative-expression-ranked_500	3.35E-07	1.51E-03	6.67E-06	6.00E-05	35	373
A3	Coexpression Atlas	gudmap_kidney_adult_JuxtaGlom_Ren1_Captopr_500	kidney_adult_JuxtaGlom_Ren1_Captopr_top-relative-expression-ranked_500	3.41E-07	1.54E-03	6.76E-06	6.08E-05	37	407
A3	Coexpression Atlas	gudmap_dev lower uro neuro_e15.5_PelvicGanglion_Sox10_k4_1000	dev lower uro neuro_e15.5_PelvicGanglion_Sox10_k-means-cluster#4_top-relative-expression-ranked_1000	3.48E-07	1.57E-03	6.86E-06	6.17E-05	28	261
A3	Coexpression Atlas	PCBC_ratio_MESO-30_vs_SC_cfr-2X-p05	Mesoderm Day 30_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	3.56E-07	1.61E-03	7.00E-06	6.29E-05	100	1,659

A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_GonadVasMes_Flk_1000	dev gonad_e11.5_F_GonadVasMes_Flk_top-relative-expression-ranked_1000	3.77E-07	1.70E-03	7.37E-06	6.63E-05	60	832
A3	Coexpression Atlas	PCBC_ratio_SC_vs_PulmonMicrovasc_cfr-2X-p05	Pluripotent Stem Cells_vs_Pulmonary Microvascular-Confounder_removed-fold2.0_adjp0.05	4.36E-07	1.97E-03	8.48E-06	7.63E-05	101	1,688
A3	Coexpression Atlas	GSM399442_100	Stem Cells, SC.LTSL.BM, IgM- CD24- CD117+ IL7R- CD150+ CD48- AA4.1+ CD43+, Bone marrow, avg-2	4.47E-07	2.02E-03	8.62E-06	7.75E-05	15	86
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_200_k4	DevelopingKidney_e15.5_Endothelial cells_emap-29965_k-means-cluster#4_top-relative-expression-ranked_200	4.47E-07	2.02E-03	8.62E-06	7.75E-05	15	86
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500_K1	facebase_RNAseq_e14.5_palate_poster_oral_Tgfbr2_WT_2500_K1	4.72E-07	2.13E-03	9.07E-06	8.15E-05	22	176
A3	Coexpression Atlas	endothelial_SubClass_MFSD2-hi_Top_500_Cluster_1	endothelial_SubClass_MFSD2-hi_Top_500_Cluster_1	4.75E-07	2.15E-03	9.09E-06	8.18E-05	28	265
A3	Coexpression Atlas	GSM791122_100	Fetal Liver, SC.STSL.FL, IgM- CD24- CD117+ IL7R- CD150- CD48- AA4.1+ CD43+, Fetal Liver, avg-2	5.22E-07	2.36E-03	9.94E-06	8.94E-05	15	87
A3	Coexpression Atlas	JC_fibro_2500_K5	JC_fibro_top-relative-expression-ranked_2500_k-means-cluster#5	6.48E-07	2.93E-03	1.23E-05	1.11E-04	59	826
A3	Coexpression Atlas	endothelial-mural Subclass Peric	endothelial-mural Subclass Peric	6.62E-07	2.99E-03	1.25E-05	1.13E-04	39	453
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P2_bladder stroma (LCM)_500_k2	DevelopingLowerUrinaryTract_P2_bladder stroma (LCM)_emap-30396_k-means-cluster#2_top-relative-expression-ranked_500	6.96E-07	3.14E-03	1.31E-05	1.18E-04	17	113
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500_K3	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500_K3	7.52E-07	3.40E-03	1.41E-05	1.27E-04	26	240
A3	Coexpression Atlas	ratio_EB_vs_SC_1000_K1	ratio_EmbryoidBody_vs_StemCell_top-relative-expression-ranked_1000_k-means-cluster#1	7.69E-07	3.47E-03	1.44E-05	1.29E-04	32	336
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_e14.5_ bladder_1000	DevelopingLowerUrinaryTract_e14.5_ bladder_emap-30872_top-relative-expression-ranked_1000	7.77E-07	3.51E-03	1.44E-05	1.30E-04	58	811
A3	Coexpression Atlas	GSM399442_500	Stem Cells, SC.LTSL.BM, IgM- CD24- CD117+ IL7R- CD150+ CD48- AA4.1+ CD43+, Bone marrow, avg-2	8.26E-07	3.73E-03	1.53E-05	1.38E-04	37	422
A3	Coexpression Atlas	Facebase_ST1_e8.5_ParaxMesoderm_500	e8.5_ParaxMesoderm_top-relative-expression-ranked_500	8.74E-07	3.95E-03	1.61E-05	1.45E-04	37	423
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k3_200	DevelopingKidney_e15.5_Endothelial cells_emap-29977_k-means-cluster#3_top-relative-expression-ranked_200	8.81E-07	3.98E-03	1.62E-05	1.46E-04	14	79
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_adult_bladder_500_k3	DevelopingLowerUrinaryTract_adult_bladder_emap-29457_k-means-cluster#3_top-relative-expression-ranked_500	9.48E-07	4.28E-03	1.73E-05	1.56E-04	16	103
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_ureter_1000_k2	DevelopingLowerUrinaryTract_P1_ureter_emap-30363_k-means-cluster#2_top-relative-expression-ranked_1000	1.02E-06	4.59E-03	1.85E-05	1.66E-04	22	184
A3	Coexpression Atlas	GSM791102_100	Stem Cells, SC.LT34F.BM, Lineage- cKit+ Sca-1+ flk2- CD34-, Bone marrow, avg-3	1.03E-06	4.67E-03	1.87E-05	1.69E-04	14	80
A3	Coexpression Atlas	GSM476663_500	Stem Cells, SC.LTSL.BM, CD117+ IL7R- CD150+ CD48- AA4.1+ CD43+, Bone marrow, avg-1	1.06E-06	4.79E-03	1.92E-05	1.72E-04	36	409
A3	Coexpression Atlas	gudmap_kidney_adult_Podocyte_MafB_1000	kidney_adult_Podocyte_MafB_top-relative-expression-ranked_1000	1.08E-06	4.86E-03	1.93E-05	1.73E-04	59	839
A3	Coexpression Atlas	gudmap_RNAseq_p2_Glomerlular Endothelial_2500_K4	gudmap_RNAseq_p2_Glomerlular Endothelial_2500_K4	1.08E-06	4.86E-03	1.93E-05	1.73E-04	35	392
A3	Coexpression Atlas	JC_iEC_500_K1	JC_iEC_top-relative-expression-ranked_500_k-means-cluster#1	1.24E-06	5.58E-03	2.21E-05	1.98E-04	16	105

A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_100	kidney_adult_GlomCapSys_Tie2_top-relative-expression-ranked_100	1.41E-06	6.36E-03	2.50E-05	2.25E-04	14	82
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_S-shaped body_1000_k2	DevelopingKidney_e15.5_S-shaped body_emap-27855_k-means-cluster#2_top-relative-expression-ranked_1000	1.46E-06	6.61E-03	2.59E-05	2.33E-04	22	188
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_k3_500	kidney_adult_RenMedVasc_Tie2_k-means-cluster#3_top-relative-expression-ranked_500	1.65E-06	7.44E-03	2.91E-05	2.61E-04	17	120
A3	Coexpression Atlas	gudmap_kidney_adult_CortVasc_Tie2_k3_200	kidney_adult_CortVasc_Tie2_k-means-cluster#3_top-relative-expression-ranked_200	1.74E-06	7.85E-03	3.06E-05	2.75E-04	11	51
A3	Coexpression Atlas	gudmap_kidney_adult_RenMedVasc_Tie2_k4_1000	kidney_adult_RenMedVasc_Tie2_k-means-cluster#4_top-relative-expression-ranked_1000	1.76E-06	7.94E-03	3.08E-05	2.77E-04	24	220
A3	Coexpression Atlas	lungmap/P1_MyoFB_Subclass_MyoFB-G	lungmap/P1_MyoFB_Subclass_MyoFB-G	1.90E-06	8.57E-03	3.30E-05	2.97E-04	26	252
A3	Coexpression Atlas	DevelopingKidney_e15.5_Endothelial cells_emap-29977_100	DevelopingKidney_e15.5_Endothelial cells_emap-29977_top-relative-expression-ranked_100	1.90E-06	8.58E-03	3.30E-05	2.97E-04	14	84
A3	Coexpression Atlas	PCBC_ratio_MESO-15_vs_SC_cfr-2X-p05	Mesoderm Day 15_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	1.98E-06	8.95E-03	3.43E-05	3.09E-04	98	1,679
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_e13.5_bladder mesenchyme_500	DevelopingLowerUrinaryTract_e13.5_bladder mesenchyme_emap-3087_top-relative-expression-ranked_500	2.08E-06	9.39E-03	3.58E-05	3.22E-04	36	421
A3	Coexpression Atlas	facebase_RNAseq_e8.5_FloorPlate_2500	facebase_RNAseq_e8.5_FloorPlate_2500	2.09E-06	9.44E-03	3.59E-05	3.23E-04	97	1,659
A3	Coexpression Atlas	lungmap/P3_Endothelial_Subclass_Endothelial-A	lungmap/P3_Endothelial_Subclass_Endothelial-A	2.13E-06	9.63E-03	3.64E-05	3.27E-04	29	302
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_k1_200	dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_k-means-cluster#1_top-relative-expression-ranked_200	2.13E-06	9.64E-03	3.64E-05	3.27E-04	11	52
A3	Coexpression Atlas	GSM791129_500	B cells, MLP.BM, CD19- IgM- CD43+ CD24intermediate AA4.1+ CD45R- CD, Bone marrow, avg-2	2.14E-06	9.68E-03	3.64E-05	3.27E-04	35	404
A3	Coexpression Atlas	GSM791124_500	B cells, MLP.BM, CD19- IgM- CD43+ CD24- AA4.1+ CD45R- CD117+ IL7R-, Bone marrow, avg-2	2.20E-06	9.92E-03	3.71E-05	3.34E-04	36	422
A3	Coexpression Atlas	80Dn_Top_500_All	80Dn_Top_500_All	2.23E-06	1.01E-02	3.76E-05	3.38E-04	40	494
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_1000_k1	DevelopingKidney_e15.5_Endothelial cells_emap-29965_k-means-cluster#1_top-relative-expression-ranked_1000	2.28E-06	1.03E-02	3.83E-05	3.44E-04	29	303
A3	Coexpression Atlas	GSM399454_500	Stem Cells, SC.STSL.BM, CD117+ IL7R- CD150- CD48- AA4.1+ CD43+, Bone marrow, avg-3	2.32E-06	1.05E-02	3.88E-05	3.49E-04	36	423
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-E	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-E	2.42E-06	1.09E-02	4.03E-05	3.62E-04	24	224
A3	Coexpression Atlas	lungmap/P3_Endothelial_Subclass_Endothelial-D	lungmap/P3_Endothelial_Subclass_Endothelial-D	2.43E-06	1.10E-02	4.04E-05	3.64E-04	29	304
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Endothelial cells_100_k1	DevelopingKidney_e15.5_Endothelial cells_emap-29965_k-means-cluster#1_top-relative-expression-ranked_100	2.47E-06	1.12E-02	4.09E-05	3.68E-04	9	34
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Pelvic Mesenchyme_1000_k2	DevelopingKidney_e15.5_Pelvic Mesenchyme_emap-8241_k-means-cluster#2_top-relative-expression-ranked_1000	2.60E-06	1.17E-02	4.28E-05	3.85E-04	29	305
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_InterstitFLeydig_MafB_500	dev gonad_e13.5_M_InterstitFLeydig_MafB_top-relative-expression-ranked_500	2.68E-06	1.21E-02	4.41E-05	3.96E-04	32	356
A3	Coexpression	gudmap_developingKidney_e15.5_Pel	DevelopingKidney_e15.5_Pelvic Mesenchyme_emap-	2.70E-06	1.22E-02	4.42E-05	3.97E-04	22	195

	Atlas	vic Mesenchyme_500_k4	8241_k-means-cluster#4_top-relative-expression-ranked_500						
A3	Coexpression Atlas	gudmap_kidney_adult_Mesangium_Meis_200	kidney_adult_Mesangium_Meis_top-relative-expression-ranked_200	3.04E-06	1.37E-02	4.96E-05	4.46E-04	20	167
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_InterstitLeydig_MafB_1000	dev gonad_e12.5_M_InterstitLeydig_MafB_top-relative-expression-ranked_1000	3.24E-06	1.46E-02	5.27E-05	4.74E-04	54	769
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Pelvic Mesenchyme_1000	DevelopingKidney_e15.5_Pelvic Mesenchyme_emap-8241_top-relative-expression-ranked_1000	3.28E-06	1.48E-02	5.31E-05	4.78E-04	56	809
A3	Coexpression Atlas	gudmap_developingGonad_e18.5_testes_1000_k4	DevelopingGonad_e18.5_testes_emap-11164_k-means-cluster#4_top-relative-expression-ranked_1000	3.50E-06	1.58E-02	5.64E-05	5.07E-04	28	293
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_InterstitLeydig_MafB_k1_1000	dev gonad_e12.5_M_InterstitLeydig_MafB_k-means-cluster#1_top-relative-expression-ranked_1000	3.82E-06	1.73E-02	6.15E-05	5.53E-04	29	311
A3	Coexpression Atlas	lungmap/P1_MyoFB_Subclass_MyoFB-F	lungmap/P1_MyoFB_Subclass_MyoFB-F	3.91E-06	1.77E-02	6.26E-05	5.63E-04	25	246
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_M_InterstitTestis_Sma_1000	dev gonad_e12.5_M_InterstitTestis_Sma_top-relative-expression-ranked_1000	3.94E-06	1.78E-02	6.28E-05	5.65E-04	55	794
A3	Coexpression Atlas	gudmap_developingGonad_e18.5_testes_1000	DevelopingGonad_e18.5_testes_emap-11164_top-relative-expression-ranked_1000	3.95E-06	1.78E-02	6.28E-05	5.65E-04	56	814
A3	Coexpression Atlas	gudmap_dev lower uro neuro_e15.5_PelvicGanglion_Sox10_1000	dev lower uro neuro_e15.5_PelvicGanglion_Sox10_top-relative-expression-ranked_1000	4.00E-06	1.81E-02	6.33E-05	5.70E-04	52	735
A3	Coexpression Atlas	gudmap_kidney_adult_GlomCapSys_Tie2_k4_100	kidney_adult_GlomCapSys_Tie2_k-means-cluster#4_top-relative-expression-ranked_100	4.16E-06	1.88E-02	6.57E-05	5.91E-04	9	36
A3	Coexpression Atlas	lungmap/P3_Epithelial_Subclass_AT1	lungmap/P3_Epithelial_Subclass_AT1	4.49E-06	2.03E-02	7.06E-05	6.35E-04	26	264
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_stage III -IV renal corpusc_1000_k3	DevelopingKidney_e15.5_stage III -IV renal corpusc_emap-27945_k-means-cluster#3_top-relative-expression-ranked_1000	4.72E-06	2.13E-02	7.40E-05	6.65E-04	15	103
A3	Coexpression Atlas	gudmap_kidney_adult_RenCorpuscGlomer_200	kidney_adult_RenCorpuscGlomer_top-relative-expression-ranked_200	4.79E-06	2.17E-02	7.49E-05	6.74E-04	20	172
A3	Coexpression Atlas	PCBC_ratio_MESO-15 blastocyst_vs_MESO-15 amniotic fluid MSC_cfr-2X-p05	MESO-15 blastocyst_vs_MESO-15 amniotic fluid MSC-Confounder_removed-fold2.0_adjp0.05	5.07E-06	2.29E-02	7.90E-05	7.11E-04	53	761
A3	Coexpression Atlas	Facebase_ST1_e8.5_NeuroEpith_FloorPlate_500_2	e8.5_NeuroEpith_FloorPlate_top-relative-expression-ranked_500_2	5.23E-06	2.36E-02	8.12E-05	7.30E-04	30	333
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_e13.5_bladder epithelial cells_1000	DevelopingLowerUrinaryTract_e13.5_bladder epithelial cells_emap-30875_top-relative-expression-ranked_1000	5.29E-06	2.39E-02	8.18E-05	7.35E-04	54	782
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_e13.5_bladder mesenchyme_1000_k2	DevelopingLowerUrinaryTract_e13.5_bladder mesenchyme_emap-3087_k-means-cluster#2_top-relative-expression-ranked_1000	5.76E-06	2.60E-02	8.89E-05	7.99E-04	14	92
A3	Coexpression Atlas	GSM791117_500	Stem Cells, SC.CMP.BM, Lineage- Kit+ Sca1- CD34+ FcgRlow, Bone marrow, avg-2	5.91E-06	2.67E-02	9.08E-05	8.17E-04	29	318
A3	Coexpression Atlas	GSM605862_500	Myeloid Cells, MF.Thio5.II-480hi.PC, CD115+ MHC II-F480hi Siglec F-, Peritoneal Cavity, avg-3	5.96E-06	2.69E-02	9.13E-05	8.21E-04	36	441
A3	Coexpression Atlas	lungmap/P3_MatrixFB_Subclass_MatrixFB-A	lungmap/P3_MatrixFB_Subclass_MatrixFB-A	6.00E-06	2.71E-02	9.13E-05	8.21E-04	25	252

A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Lymphatic Endothelial-B	lungmap/P1_Endothelial_Subclass_Lymphatic Endothelial-B	6.00E-06	2.71E-02	9.13E-05	8.21E-04	24	236
A3	Coexpression Atlas	Facebase_RNAseq_e9.5_Maxillary Arch_1000	FacebaseRNAseq_e9.5_Maxillary Arch_top-relative-expression-ranked_1000	6.13E-06	2.77E-02	9.29E-05	8.35E-04	63	969
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_bladder_500_J	DevelopingLowerUrinaryTract_P1_bladder_J_emap-30374_top-relative-expression-ranked_500	6.87E-06	3.10E-02	1.04E-04	9.33E-04	33	390
A3	Coexpression Atlas	brainmap/Mixed Age_intermediate_Subclass_intermediate1	brainmap/Mixed Age_intermediate_Subclass_intermediate1	7.03E-06	3.18E-02	1.06E-04	9.52E-04	30	338
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_S-shaped body_1000	DevelopingKidney_e15.5_S-shaped body_emap-27855_top-relative-expression-ranked_1000	7.32E-06	3.31E-02	1.10E-04	9.88E-04	55	811
A3	Coexpression Atlas	gudmap_kidney_P0_JuxtaGlom_Ren1_200	kidney_P0_JuxtaGlom_Ren1_top-relative-expression-ranked_200	7.42E-06	3.35E-02	1.11E-04	9.98E-04	20	177
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_adult_bladder_1000_k1	DevelopingLowerUrinaryTract_adult_bladder_emap-29457_k-means-cluster#1_top-relative-expression-ranked_1000	7.55E-06	3.41E-02	1.12E-04	1.01E-03	18	148
A3	Coexpression Atlas	gudmap_dev gonad_e13.5_M_InterstitTestis_Sma_200	dev gonad_e13.5_M_InterstitTestis_Sma_top-relative-expression-ranked_200	7.55E-06	3.41E-02	1.12E-04	1.01E-03	18	148
A3	Coexpression Atlas	PCBC_ratio_EB_vs_SC_cfr-2X-p05	Embryoid Body Cells_vs_Pluripotent Stem Cells-Confounder_removed-fold2.0_adjp0.05	7.62E-06	3.44E-02	1.13E-04	1.02E-03	102	1,823
A3	Coexpression Atlas	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500_K2	facebase_RNAseq_e14.5_palate_poster_proximal_ERK2_WT_2500_K2	8.00E-06	3.61E-02	1.18E-04	1.06E-03	74	1,209
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_VasAssMesen_MafB_k1_200	dev gonad_e12.5_F_VasAssMesen_MafB_k-means-cluster#1_top-relative-expression-ranked_200	8.49E-06	3.83E-02	1.25E-04	1.12E-03	9	39
A3	Coexpression Atlas	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-D	lungmap/P1_Endothelial_Subclass_Vascular Endothelial-D	8.56E-06	3.87E-02	1.26E-04	1.13E-03	23	225
A3	Coexpression Atlas	gudmap_developingKidney_e15.5_Podocyte cells_1000	DevelopingKidney_e15.5_Podocyte cells_emap-27915_top-relative-expression-ranked_1000	8.66E-06	3.91E-02	1.27E-04	1.14E-03	56	836
A3	Coexpression Atlas	gudmap_dev gonad_e11.5_F_ReproVasc_Flk_k3_100	dev gonad_e11.5_F_ReproVasc_Flk_k-means-cluster#3_top-relative-expression-ranked_100	8.70E-06	3.93E-02	1.27E-04	1.14E-03	7	22
A3	Coexpression Atlas	lungmap/P1_MatrixFB_Subclass_MatrixFB-E	lungmap/P1_MatrixFB_Subclass_MatrixFB-E	8.78E-06	3.97E-02	1.27E-04	1.14E-03	26	274
A3	Coexpression Atlas	gudmap_kidney_adult_JuxtaGlom_Ren1_Captopr_k4_1000	kidney_adult_JuxtaGlom_Ren1_Captopr_k-means-cluster#4_top-relative-expression-ranked_1000	8.79E-06	3.97E-02	1.27E-04	1.14E-03	20	179
A3	Coexpression Atlas	gudmap_dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_1000	dev gonad_e12.5_F_VasAssocMesStromOvary_Sma_top-relative-expression-ranked_1000	9.44E-06	4.26E-02	1.36E-04	1.22E-03	54	798
A3	Coexpression Atlas	gudmap_kidney_e10.5_UretericTrunk_HoxB7_500	kidney_e10.5_UretericTrunk_HoxB7_top-relative-expression-ranked_500	9.45E-06	4.27E-02	1.36E-04	1.22E-03	33	396
A3	Coexpression Atlas	endothelial-mural Subclass Vend1	endothelial-mural Subclass Vend1	9.79E-06	4.42E-02	1.40E-04	1.26E-03	36	451
A3	Coexpression Atlas	GSM854335_500	alpha beta T cells, preT.ETP.Th, Lin-/lo CD25- CD44+ cKit+, Thymus, avg-3	9.97E-06	4.50E-02	1.43E-04	1.28E-03	34	415
A3	Coexpression Atlas	gudmap_developingLowerUrinaryTract_P1_ureter_1000_k4	DevelopingLowerUrinaryTract_P1_ureter_emap-30363_k-means-cluster#4_top-relative-expression-ranked_1000	1.00E-05	4.52E-02	1.43E-04	1.28E-03	18	151
A3	Coexpression	gudmap_kidney_adult_RenMedVasc_	kidney_adult_RenMedVasc_Tie2_top-relative-expression-	1.02E-05	4.62E-02	1.45E-04	1.31E-03	13	84

	Atlas	Tie2_100	ranked_100						
A3	Computational	M16395 MODULE_47	ECM and collagens.	5.24E-09	3.84E-06	3.84E-06	2.75E-05	32	225
A3	Computational	M9982 MODULE_2	DRG (dorsal root ganglia) genes.	4.72E-07	3.46E-04	1.73E-04	1.24E-03	40	384
A3	Computational	M4051 MODULE_1	Ovary genes.	1.90E-05	1.39E-02	4.64E-03	3.33E-02	35	368
A3	Drug	D004237	Diuron	1.10E-27	3.51E-23	3.51E-23	3.84E-22	153	1,722
A3	Drug	C041786	palm oil	8.90E-22	2.83E-17	1.42E-17	1.55E-16	138	1,675
A3	Drug	C057693	troglitazone	7.58E-12	2.41E-07	7.15E-08	7.82E-07	95	1,306
A3	Drug	D015056	1-Methyl-3-isobutylxanthine	8.98E-12	2.86E-07	7.15E-08	7.82E-07	44	391
A3	Drug	C006703	benzo(b)fluoranthene	3.52E-11	1.12E-06	2.24E-07	2.45E-06	89	1,222
A3	Drug	C089730	rosiglitazone	1.78E-09	5.65E-05	9.42E-06	1.03E-04	100	1,552
A3	Drug	C023035	3,4,5,3',4'-pentachlorobiphenyl	3.63E-09	1.16E-04	1.65E-05	1.81E-04	81	1,174
A3	Drug	C548651	2-(1'H-indolo-3'-carbonyl)thiazole-4-carboxylic acid methyl ester	7.20E-09	2.29E-04	2.86E-05	3.13E-04	61	793
A3	Drug	C015559	trimellitic anhydride	8.20E-09	2.61E-04	2.90E-05	3.17E-04	112	1,862
A3	Drug	D004113	Succimer	1.63E-08	5.18E-04	5.18E-05	5.67E-04	82	1,235
A3	Drug	D007545	Isoproterenol	2.10E-08	6.68E-04	6.07E-05	6.65E-04	70	995
A3	Drug	C011559	tributyltin	7.85E-08	2.50E-03	2.08E-04	2.28E-03	32	316
A3	Drug	D058185	Magnetite Nanoparticles	1.56E-07	4.95E-03	3.81E-04	4.17E-03	81	1,280
A3	Drug	C023036	perfluorooctanoic acid	1.96E-07	6.25E-03	4.27E-04	4.67E-03	97	1,638
A3	Drug	D019324	beta-Naphthoflavone	2.01E-07	6.40E-03	4.27E-04	4.67E-03	58	810
A3	Drug	D003561	Cytarabine	2.16E-07	6.88E-03	4.30E-04	4.71E-03	47	598
A3	Drug	C009277	sodium arsenate	3.48E-07	1.11E-02	6.51E-04	7.12E-03	98	1,681
A3	Drug	CID000082145	2-bromopalmitate	3.86E-07	1.23E-02	6.83E-04	7.47E-03	13	66
A3	Drug	4282_UP	Hydralazine hydrochloride [304-20-1]; Up 200; 20.4uM; PC3; HT_HG-U133A	5.28E-07	1.68E-02	8.84E-04	9.67E-03	23	199
A3	Drug	C016030	pantogab	7.46E-07	2.37E-02	1.14E-03	1.25E-02	45	586
A3	Drug	C410127	PCB 180	7.53E-07	2.40E-02	1.14E-03	1.25E-02	93	1597
A3	Drug	C510784	ormosil	1.27E-06	4.03E-02	1.83E-03	2.00E-02	18	136
A3	Drug	C550453	dioxinodehydroeckol	1.38E-06	4.38E-02	1.90E-03	2.08E-02	6	12
A4	Pubmed	23020937	Range of genetic mutations associated with severe non-syndromic sporadic intellectual disability: an exome sequencing study.	1.11E-06	2.82E-03	2.61E-03	2.20E-02	2	2
A4	Pubmed	25162404	G protein beta 5 is targeted to D2-dopamine receptor-containing biochemical compartments and blocks dopamine-dependent receptor internalization.	3.32E-06	8.45E-03	2.61E-03	2.20E-02	2	3
A4	Pubmed	16204458	Non-EST based prediction of exon skipping and intron retention events using Pfam information.	3.32E-06	8.45E-03	2.61E-03	2.20E-02	2	3
A4	Pubmed	16710414	The DNA sequence and biological annotation of human chromosome 1.	1.31E-05	3.33E-02	2.61E-03	2.20E-02	8	1,034
A4	Pubmed	23020937	Range of genetic mutations associated with severe non-syndromic sporadic intellectual disability: an exome sequencing study.	1.11E-06	2.82E-03	2.61E-03	2.20E-02	2	2

A4	Pubmed	25162404	G protein beta 5 is targeted to D2-dopamine receptor-containing biochemical compartments and blocks dopamine-dependent receptor internalization.	3.32E-06	8.45E-03	2.61E-03	2.20E-02	2	3
A4	Pubmed	16204458	Non-EST based prediction of exon skipping and intron retention events using Pfam information.	3.32E-06	8.45E-03	2.61E-03	2.20E-02	2	3
A4	Pubmed	16710414	The DNA sequence and biological annotation of human chromosome 1.	1.31E-05	3.33E-02	2.61E-03	2.20E-02	8	1,034
A5	GO: Cellular Component	GO:0044420	extracellular matrix component	1.41E-05	2.25E-03	1.38E-03	7.79E-03	5	141
A5	GO: Cellular Component	GO:0005578	proteinaceous extracellular matrix	1.72E-05	2.75E-03	1.38E-03	7.79E-03	7	379
A5	GO: Cellular Component	GO:0031012	extracellular matrix	4.73E-05	7.57E-03	2.52E-03	1.43E-02	7	444
A5	Human Phenotype	HP:0005622	Broad long bones	3.10E-06	2.37E-03	2.37E-03	1.71E-02	3	10
A5	Pubmed	19578796	Association of genetic variants with chronic kidney disease in individuals with different lipid profiles.	1.84E-07	1.19E-03	8.21E-04	7.68E-03	5	152
A5	Pubmed	26915435	The anti-oxidative transcription factor Nuclear factor E2 related factor-2 (Nrf2) counteracts TGF-?1 mediated growth inhibition of pancreatic ductal epithelial cells - Nrf2 as determinant of pro-tumorigenic functions of TGF-?1.	6.80E-07	4.38E-03	8.21E-04	7.68E-03	2	2
A5	Pubmed	26226105	The Crosstalk between Nrf2 and TGF-?1 in the Epithelial-Mesenchymal Transition of Pancreatic Duct Epithelial Cells.	6.80E-07	4.38E-03	8.21E-04	7.68E-03	2	2
A5	Pubmed	19389097	Intense pulsed light effects on the expression of extracellular matrix proteins and transforming growth factor beta-1 in skin dermal fibroblasts cultured within contracted collagen lattices.	6.80E-07	4.38E-03	8.21E-04	7.68E-03	2	2
A5	Pubmed	17146610	Expression of decorin and collagens I and III in different layers of human skin in vivo: a laser capture microdissection study.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	27997896	Elevated THBS2, COL1A2, and SPP1 Expression Levels as Predictors of Gastric Cancer Prognosis.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	21858035	The role of serum biomarkers in predicting fibrosis progression in pediatric and adult hepatitis C virus chronic infection.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	25851604	The human 18S rRNA base methyltransferases DIMT1L and WBSCR22-TRMT112 but not rRNA modification are required for ribosome biogenesis.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	22379029	TGF-?-mediated downregulation of microRNA-196a contributes to the constitutive upregulated type I collagen expression in scleroderma dermal fibroblasts.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	24641356	In Crohn's disease fibrosis-reduced expression of the miR-29 family enhances collagen expression in intestinal fibroblasts.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	20704113	Effects of antisense transforming growth factor-beta1 gene transfer on the biological activities of tendon sheath fibroblasts.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3

A5	Pubmed	19858036	Hepatocyte growth factor suppresses transforming growth factor-beta-1 and type III collagen in human primary renal fibroblasts.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	16463783	[The influence of adrenaline on the expression of TGF-beta1, bFGF and I procollagen for hypertrophic scar].	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	21667357	The identification of novel mutations in COL1A1, COL1A2, and LEPRE1 genes in Chinese patients with osteogenesis imperfecta.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	25451260	Role of Flightless-I (Drosophila) homolog in the transcription activation of type I collagen gene mediated by transforming growth factor beta.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	26904167	TGF-? and Hypoxia/Reoxygenation Promote Radioresistance of A549 Lung Cancer Cells through Activation of Nrf2 and EGFR.	2.04E-06	1.31E-02	8.21E-04	7.68E-03	2	3
A5	Pubmed	18996919	Mutation and polymorphism spectrum in osteogenesis imperfecta type II: implications for genotype-phenotype relationships.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	26258650	Dysregulation of the Transforming Growth Factor ? Pathway in Induced Pluripotent Stem Cells Generated from Patients with Diamond Blackfan Anemia.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	26238954	A Preliminary Study on Racial Differences in 絶잼 MOX1, NFE2L2, and TGF?1 Gene Polymorphisms and Radiation-Induced Late Normal Tissue Toxicity.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	17884818	Transforming growth factor-beta regulates DNA binding activity of transcription factor Fli1 by p300/CREB-binding protein-associated factor-dependent acetylation.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	16849317	RACK1 binds to Smad3 to modulate transforming growth factor-beta1-stimulated alpha2(I) collagen transcription in renal tubular epithelial cells.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	24434151	Inhibitory role of Id1 on TGF-?-induced collagen expression in human dermal fibroblasts.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	1409674	Activation of expression of genes coding for extracellular matrix proteins in Tat-producing glioblastoma cells.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	18089612	Thrombospondin-1 and thrombospondin-2 mRNA and TSP-1 and TSP-2 protein expression in uterine fibroids and correlation to the genes COL1A1 and COL3A1 and to the collagen cross-link hydroxyproline.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	24361166	Relationship between the expressions of mitofusin-2 and procollagen in uterosacral ligament fibroblasts of postmenopausal patients with pelvic organ prolapse.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	19932771	MMP-12 catalytic domain recognizes and cleaves at multiple sites in human skin collagen type I and type III.	4.07E-06	2.63E-02	1.01E-03	9.44E-03	2	4
A5	Pubmed	18298657	Chondroitin sulphate decreases collagen synthesis in normal and scleroderma fibroblasts through a Smad-independent TGF-beta pathway--implication of C-Krox and Sp1.	6.79E-06	4.37E-02	1.46E-03	1.36E-02	2	5
A5	Pubmed	19790048	Hypoxia-inducible factor 1alpha inhibits the fibroblast-like markers type I and type III collagen during hypoxia-induced chondrocyte redifferentiation: hypoxia not only induces type II collagen and aggrecan, but it also inhibits	6.79E-06	4.37E-02	1.46E-03	1.36E-02	2	5

			type I and type III collagen in the hypoxia-inducible factor 1alpha-dependent redifferentiation of chondrocytes.						
A5	Pubmed	15365990	Stability related bias in residues replacing glycines within the collagen triple helix (Gly-Xaa-Yaa) in inherited connective tissue disorders.	6.79E-06	4.37E-02	1.46E-03	1.36E-02	2	5
A5	Pubmed	9675033	Decorin core protein fragment Leu155-Val260 interacts with TGF-beta but does not compete for decorin binding to type I collagen.	6.79E-06	4.37E-02	1.46E-03	1.36E-02	2	5
A5	Cytoband	2q31	2q31	1.22E-04	4.87E-03	4.87E-03	2.08E-02	2	13
A5	Cytoband	12q14.1	12q14.1	5.83E-04	2.33E-02	1.17E-02	4.99E-02	2	28
A5	Computational	M12987 GNF2_CDH11	Neighborhood of CDH11	2.04E-05	3.24E-03	3.24E-03	1.83E-02	3	25
A5	Computational	M11282 GNF2_PTX3	Neighborhood of PTX3	6.23E-05	9.90E-03	4.95E-03	2.80E-02	3	36
A5	Drug	C502971	2-phenyl-4-(3-pyridin-2-yl-1H-pyrazol-4-yl)pyridine	1.47E-07	1.14E-03	1.14E-03	1.08E-02	3	6
A6	Pubmed	18303054	IKAP localizes to membrane ruffles with filamin A and regulates actin cytoskeleton organization and cell migration.	3.68E-05	4.58E-02	1.78E-03	1.37E-02	2	17
A7	GO: Cellular Component	GO:0060203	Clathrin-sculpted glutamate transport vesicle membrane	6.84E-05	1.59E-02	7.93E-03	4.78E-02	2	4
A7	GO: Cellular Component	GO:0060199	Clathrin-sculpted glutamate transport vesicle	6.84E-05	1.59E-02	7.93E-03	4.78E-02	2	4
A7	Pubmed	24728074	Enhanced prediction of Src homology 2 (SH2) domain binding potentials using a fluorescence polarization-derived c-Met, c-Kit, ErbB, and androgen receptor interactome.	1.59E-06	7.91E-03	4.21E-03	3.82E-02	4	63
A7	Pubmed	23799130	Expression of ST3GAL4 leads to SLe(x) expression and induces c-Met activation and an invasive phenotype in gastric carcinoma cells.	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3
A7	Pubmed	25612003	Pathologic Regulation of Collagen I by an Aberrant Protein Phosphatase 2A/Histone Deacetylase C4/MicroRNA-29 Signal Axis in Idiopathic Pulmonary Fibrosis Fibroblasts.	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3
A7	Pubmed	19543515	Differential methylation pattern of ID4, SFRP1, and SHP1 between acute myeloid leukemia and chronic myeloid leukemia.	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3
A8	GO: Cellular Component	GO:0060203	Clathrin-sculpted glutamate transport vesicle membrane	6.84E-05	1.59E-02	7.93E-03	4.78E-02	2	4
A8	GO: Cellular Component	GO:0060199	Clathrin-sculpted glutamate transport vesicle	6.84E-05	1.59E-02	7.93E-03	4.78E-02	2	4
A8	Pubmed	24728074	Enhanced prediction of Src homology 2 (SH2) domain binding potentials using a fluorescence polarization-derived c-Met, c-Kit, ErbB, and androgen receptor interactome.	1.59E-06	7.91E-03	4.21E-03	3.82E-02	4	63
A8	Pubmed	23799130	Expression of ST3GAL4 leads to SLe(x) expression and induces c-Met activation and an invasive phenotype in gastric carcinoma cells.	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3
A8	Pubmed	25612003	Pathologic Regulation of Collagen I by an Aberrant Protein Phosphatase 2A/Histone Deacetylase C4/MicroRNA-29 Signal Axis in Idiopathic Pulmonary Fibrosis Fibroblasts.	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3
A8	Pubmed	19543515	Differential methylation pattern of ID4, SFRP1, and SHP1	5.20E-06	2.58E-02	4.21E-03	3.82E-02	2	3

			between acute myeloid leukemia and chronic myeloid leukemia.						
B3	Pubmed	20333644	Beta1 integrins mediate cell proliferation in three-dimensional cultures by regulating expression of the sonic hedgehog effector protein, GLI1.	1.69E-06	8.85E-03	2.21E-03	2.02E-02	2	2
B3	Pubmed	18727519	[Expression and significance of integrin beta1 and integrin-linked kinase in laryngeal carcinoma].	1.69E-06	8.85E-03	2.21E-03	2.02E-02	2	2
B3	Pubmed	21639857	Effect of dexamethasone on human osteoblasts in culture: involvement of ?1 integrin and integrin-linked kinase.	1.69E-06	8.85E-03	2.21E-03	2.02E-02	2	2
B3	Pubmed	12020426	Ionizing radiation induces up-regulation of functional beta1-integrin in human lung tumor cell lines in vitro.	1.69E-06	8.85E-03	2.21E-03	2.02E-02	2	2
B3	Pubmed	15304053	The regulation of integrin-linked kinase in human platelets: evidence for involvement in the regulation of integrin alpha 2 beta 1.	5.05E-06	2.65E-02	2.94E-03	2.69E-02	2	3
B3	Pubmed	22345562	Insulin-like growth factor-binding protein 2-driven glioma progression is prevented by blocking a clinically significant integrin, integrin-linked kinase, and NF-?B network.	5.05E-06	2.65E-02	2.94E-03	2.69E-02	2	3
B3	Pubmed	26693891	Twist induces epithelial-mesenchymal transition and cell motility in breast cancer via ITGB1-FAK/ILK signaling axis and its associated downstream network.	5.05E-06	2.65E-02	2.94E-03	2.69E-02	2	3
B3	Pubmed	15905178	Role of integrin-linked kinase in regulating phosphorylation of Akt and fibroblast survival in type I collagen matrices through a beta1 integrin viability signaling pathway.	5.05E-06	2.65E-02	2.94E-03	2.69E-02	2	3
B3	Pubmed	28188308	Tetraspanin 8 is a novel regulator of ILK-driven ?1 integrin adhesion and signaling in invasive melanoma cells.	5.05E-06	2.65E-02	2.94E-03	2.69E-02	2	3
B3	Computational	M9347 MODULE_176	Signaling.	1.82E-06	4.17E-04	4.17E-04	2.51E-03	8	230
B3	Computational	M16447 MODULE_112	Genes in the cancer module 112.	4.54E-06	1.04E-03	5.20E-04	3.12E-03	8	260
B3	Computational	M9982 MODULE_2	DRG (dorsal root ganglia) genes.	7.61E-05	1.74E-02	5.81E-03	3.49E-02	8	384
B4	Pubmed	15749123	Ethanol potentiates HIV-1 gp120-induced apoptosis in human neurons via both the death receptor and NMDA receptor pathways.	2.46E-05	1.78E-02	2.51E-03	1.79E-02	2	14
B5	Pubmed	10343102	Assignment of a human cold shock domain protein A intronless pseudogene (CSDAP1) to human chromosome 16 band p11.2 by in situ hybridization.	1.10E-07	1.36E-04	1.36E-04	1.05E-03	2	2
B5	Gene Family	1010	Cytochrome P450 family 20	6.60E-04	7.92E-03	3.96E-03	1.23E-02	1	1
B5	Gene Family	1015	Cytochrome P450 family 39	6.60E-04	7.92E-03	3.96E-03	1.23E-02	1	1
B5	Gene Family	106	Y box binding proteins	1.98E-03	2.37E-02	7.91E-03	2.46E-02	1	3
B5	Gene Family	1127	Phospholipid phosphatase related	3.29E-03	3.95E-02	9.88E-03	3.07E-02	1	5
B5	Coexpression	M9814	Genes down-regulated in poorly differentiated thyroid carcinoma (PDTC) compared to anaplastic thyroid carcinoma (ATC).	2.61E-07	4.02E-04	4.02E-04	3.19E-03	4	77
B6	GO: Cellular Component	GO:0030016	Myofibril	1.07E-08	6.18E-07	4.21E-07	1.96E-06	5	220
B6	GO: Cellular Component	GO:0043292	Contractile fiber	1.45E-08	8.42E-07	4.21E-07	1.96E-06	5	234
B6	GO: Cellular	GO:0030017	Sarcomere	7.65E-07	4.44E-05	1.48E-05	6.88E-05	4	198

	Component								
B6	GO: Cellular Component	GO:0044449	Contractile fiber part	1.06E-06	6.17E-05	1.54E-05	7.17E-05	4	215
B6	GO: Cellular Component	GO:0032982	Myosin filament	3.88E-05	2.25E-03	4.50E-04	2.09E-03	2	23
B6	GO: Cellular Component	GO:0016459	Myosin complex	3.46E-04	2.01E-02	3.35E-03	1.56E-02	2	68
B6	GO: Cellular Component	GO:0015629	Actin cytoskeleton	7.89E-04	4.58E-02	6.54E-03	3.04E-02	3	476
B6	Domain	PF02736	Myosin_N	1.67E-05	1.09E-03	2.95E-04	1.40E-03	2	15
B6	Domain	IPR004009	Myosin_N	1.67E-05	1.09E-03	2.95E-04	1.40E-03	2	15
B6	Domain	PF01576	Myosin_tail_1	2.43E-05	1.58E-03	2.95E-04	1.40E-03	2	18
B6	Domain	IPR002928	Myosin_tail	2.43E-05	1.58E-03	2.95E-04	1.40E-03	2	18
B6	Domain	IPR027401	Myosin-like_IQ_dom	2.72E-05	1.77E-03	2.95E-04	1.40E-03	2	19
B6	Domain	4.10.270.10	-	2.72E-05	1.77E-03	2.95E-04	1.40E-03	2	19
B6	Domain	IPR001609	Myosin_head_motor_dom	1.11E-04	7.24E-03	7.24E-04	3.44E-03	2	38
B6	Domain	SM00242	MYSc	1.11E-04	7.24E-03	7.24E-04	3.44E-03	2	38
B6	Domain	PS51456	MYOSIN_MOTOR	1.11E-04	7.24E-03	7.24E-04	3.44E-03	2	38
B6	Domain	PF00063	Myosin_head	1.11E-04	7.24E-03	7.24E-04	3.44E-03	2	38
B6	Domain	IPR029531	CAPN3	4.27E-04	2.78E-02	2.52E-03	1.20E-02	1	1
B6	Domain	SM00015	IQ	5.08E-04	3.30E-02	2.75E-03	1.31E-02	2	81
B6	Domain	IPR000048	IQ_motif_EF-hand-BS	6.27E-04	4.08E-02	3.11E-03	1.48E-02	2	90
B6	Domain	PS50096	IQ	6.69E-04	4.35E-02	3.11E-03	1.48E-02	2	93
B6	Pathway	1269869	Striated Muscle Contraction	1.08E-04	5.50E-03	5.50E-03	2.49E-02	2	34
B6	Pathway	1269896	Translocation of GLUT4 to the plasma membrane	3.61E-04	1.84E-02	7.61E-03	3.44E-02	2	62
B6	Pathway	P00016	Cytoskeletal regulation by Rho GTPase	4.48E-04	2.28E-02	7.61E-03	3.44E-02	2	69
B6	Pathway	P00044	Nicotinic acetylcholine receptor signaling pathway	7.78E-04	3.97E-02	9.92E-03	4.48E-02	2	91
B6	Pubmed	26871637	Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing.	2.88E-05	1.34E-02	3.10E-04	2.08E-03	3	374
B6	Pubmed	22266860	Sp1 phosphorylation by cyclin-dependent kinase 1/cyclin B1 represses its DNA-binding activity during mitosis in cancer cells.	3.68E-05	1.71E-02	3.10E-04	2.08E-03	2	54
B6	Cytoband	1p31-p22	1p31-p22	7.79E-04	7.01E-03	7.01E-03	1.98E-02	1	3
B6	Cytoband	4q28.1	4q28.1	4.15E-03	3.73E-02	1.57E-02	4.45E-02	1	16
B6	Gene Family	1098	Myosin heavy chains	9.50E-06	5.70E-05	5.70E-05	1.40E-04	2	15
B6	Gene Family	439	Collagen beta(1-O)galactosyltransferases	6.60E-04	3.96E-03	1.98E-03	4.85E-03	1	2
B6	Gene Family	867	Chloride channel accessory	1.32E-03	7.91E-03	1.98E-03	4.85E-03	1	4
B6	Gene Family	777	Tropomyosins	1.32E-03	7.91E-03	1.98E-03	4.85E-03	1	4
B6	Gene Family	975	EF-hand domain-containing|Calpains	4.94E-03	2.96E-02	5.93E-03	1.45E-02	1	15
B6	Drug	CID006419303	purealin	1.43E-06	2.47E-03	2.47E-03	1.99E-02	3	58
B6	Disease	C1850530	Flexion contractures of joints	1.00E-05	4.14E-03	1.57E-03	1.03E-02	3	93
B6	Disease	C0333068	Flexion contracture	1.04E-05	4.27E-03	1.57E-03	1.03E-02	3	94

B6	Disease	C0009918	Contracture of joint	1.14E-05	4.69E-03	1.57E-03	1.03E-02	3	97
B6	Disease	C0546264	Congenital Fiber Type Disproportion	1.66E-05	6.84E-03	1.71E-03	1.13E-02	2	13
B6	Disease	C0009917	Contracture	2.32E-05	9.58E-03	1.92E-03	1.26E-02	3	123
B7	Cytoband	6q14.2	6q14.2	1.15E-03	9.23E-03	9.23E-03	2.51E-02	1	5
B7	Cytoband	6p25	6p25	3.69E-03	2.95E-02	1.13E-02	3.07E-02	1	16
B7	Cytoband	12q14.3	12q14.3	4.61E-03	3.69E-02	1.13E-02	3.07E-02	1	20
B7	Cytoband	1q25	1q25	6.22E-03	4.97E-02	1.13E-02	3.07E-02	1	27
B7	Gene Family	1072	Alkaline phosphatases	1.10E-03	6.59E-03	4.12E-03	1.01E-02	1	4
B7	Gene Family	1157	Mitogen-activated protein kinase kinase kinases|RAF family	1.37E-03	8.24E-03	4.12E-03	1.01E-02	1	5
B7	Gene Family	832	Phospholipases|C2 domain containing phospholipases	5.21E-03	3.13E-02	1.04E-02	2.55E-02	1	19
B7	Gene Family	778	Tubulins	7.13E-03	4.28E-02	1.07E-02	2.62E-02	1	26
B8	Domain	IPR024818	ASXL3	1.07E-04	1.92E-03	7.21E-04	2.52E-03	1	1
B8	Domain	IPR026905	ASX-like_PHD	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	PF05066	HARE-HTH	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	IPR007759	HB1/Asxl_HTH	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	PF13922	PHD_3	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	IPR024811	ASX/ASX-like	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	PF13919	ASXH	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Domain	IPR028020	ASXH	3.20E-04	5.76E-03	7.21E-04	2.52E-03	1	3
B8	Pubmed	28100473	Delineating the phenotypic spectrum of Bainbridge-Ropers syndrome: 12 new patients with de novo, heterozygous, loss-of-function mutations in ASXL3 and review of published literature.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	15138607	Identification and characterization of ASXL3 gene in silico.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	27901041	Bainbridge-Ropers syndrome caused by loss-of-function variants in ASXL3: a recognizable condition.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	24044690	De novo frameshift mutation in ASXL3 in a patient with global developmental delay, microcephaly, and craniofacial anomalies.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	28431838	Global developmental delay and postnatal microcephaly: Bainbridge-Ropers syndrome with a new mutation in ASXL3.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	25856206	Unlike ASXL1 and ASXL2 mutations, ASXL3 mutations are rare events in acute myeloid leukemia with t(8;21).	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	23736028	Functional and cancer genomics of ASXL family members.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	10723735	Evolution of alpha 2-fucosyltransferase genes in primates: relation between an intronic Alu-Y element and red cell expression of ABH antigens.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	27075689	Novel splicing mutation in the ASXL3 gene causing Bainbridge-Ropers syndrome.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	23383720	De novo truncating mutations in ASXL3 are associated with a novel clinical phenotype with similarities to Bohring-Opitz syndrome.	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1
B8	Pubmed	28097878	Focusing on frequent ASXL1 mutations in myeloid	5.69E-05	1.71E-03	1.55E-04	6.20E-04	1	1

			neoplasms, and considering rarer ASXL2 and ASXL3 mutations.						
B8	Pubmed	7876235	Sequence and expression of a candidate for the human Secretor blood group alpha(1,2)fucosyltransferase gene (FUT2). Homozygosity for an enzyme-inactivating nonsense mutation commonly correlates with the non-secretor phenotype.	1.14E-04	3.41E-03	2.27E-04	9.09E-04	1	2
B8	Pubmed	9219535	Structure and expression of the gene encoding secretor-type galactoside 2-alpha-L-fucosyltransferase (FUT2).	1.14E-04	3.41E-03	2.27E-04	9.09E-04	1	2
B8	Pubmed	25450400	Repression of LXR? by a novel member of additional sex comb-like family, ASXL3.	1.14E-04	3.41E-03	2.27E-04	9.09E-04	1	2
B8	Pubmed	18067503	Sec1-FUT2-Sec1 hybrid allele generated by interlocus gene conversion.	1.14E-04	3.41E-03	2.27E-04	9.09E-04	1	2
B8	Pubmed	26167880	SR protein kinases promote splicing of nonconsensus introns.	1.39E-04	4.18E-03	2.61E-04	1.04E-03	2	361
B8	Pubmed	26647312	De novo dominant ASXL3 mutations alter H2A deubiquitination and transcription in Bainbridge-Ropers syndrome.	1.71E-04	5.12E-03	2.84E-04	1.14E-03	1	3
B8	Pubmed	25835095	Functional proteomics of the epigenetic regulators ASXL1, ASXL2 and ASXL3: a convergence of proteomics and epigenetics for translational medicine.	1.71E-04	5.12E-03	2.84E-04	1.14E-03	1	3
B8	Pubmed	16412590	Characterization of Asxl1, a murine homolog of Additional sex combs, and analysis of the Asx-like gene family.	2.27E-04	6.82E-03	3.59E-04	1.44E-03	1	4
B8	Pubmed	23932459	Genome-wide association study of lung function phenotypes in a founder population.	6.82E-04	2.05E-02	1.02E-03	4.09E-03	1	12
B8	Pubmed	24941225	Genetic variations affecting serum carcinoembryonic antigen levels and status of regional lymph nodes in patients with sporadic colorectal cancer from Southern China.	7.39E-04	2.22E-02	1.06E-03	4.22E-03	1	13
B8	Interaction	int:ASXL3	ASXL3 interactions	3.51E-04	2.46E-03	1.64E-03	4.25E-03	1	3
B8	Interaction	int:ANKRD35	ANKRD35 interactions	4.68E-04	3.28E-03	1.64E-03	4.25E-03	1	4
B8	Cytoband	18q11	18q11	1.73E-04	5.19E-04	5.19E-04	9.52E-04	1	2
B8	Cytoband	1q21.1	1q21.1	7.17E-03	2.15E-02	9.32E-03	1.71E-02	1	83
B8	Cytoband	19q13.33	19q13.33	9.32E-03	2.80E-02	9.32E-03	1.71E-02	1	108
B8	Gene Family	403	Ankyrin repeat domain containing|BRCA1 B complex	1.33E-02	1.33E-02	1.33E-02	1.33E-02	1	242
B8	Disease	C3809650	BAINBRIDGE-ROPERS SYNDROME	1.23E-04	2.35E-03	1.17E-03	4.16E-03	1	1
B8	Disease	cv:CN180235	Bainbridge-Ropers syndrome	1.23E-04	2.35E-03	1.17E-03	4.16E-03	1	1