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ORIGINAL ARTICLE

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

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Transcriptome analysis has been widely used to make biomarker panels to diagnose cancers. In breast cancer, the age of the patient has been known to be associated with clinical features. As clinical transcriptome data have accumulated significantly, we classified all human genes based on age-specific differential expression between normal and breast cancer cells using public data. We retrieved the values for gene expression levels in breast cancer and matched normal cells from The Cancer Genome Atlas. We divided genes into two classes by paired t test without considering age in the first classification. We carried out a secondary classification of genes for each class into eight groups, based on the patterns of the p-values, which were calculated for each of the three age groups we defined. Through this two-step classification, gene expression was eventually grouped into 16 classes. We showed that this classification method could be applied to establish a more accurate prediction model to diagnose breast cancer by comparing the performance of prediction models with different combinations of genes. We expect that our scheme of classification could be used for other types of cancer data.

Keywords: biomarkers, breast cancer, differentially expressed genes, gene classification

Introduction

Breast cancer is known to one of the leading causes of cancer death among females [1]. A massive number of research studies on the genomic characterization of breast cancer, particularly the discovery of differentially expressed genes (DEGs), have revealed clinically relevant molecular subtypes [2], which has increased the accuracy of the prognosis [3-5] and has resulted in successful targeted therapy [6, 7]. During recent decades, resources based on high-throughput sequencing technologies, such as The Cancer Genome Atlas (TCGA) [8] and International Cancer Genome Consortium (ICGC) [9], have facilitated more accurate detection of DEGs and cancer driver genes. The identification of DEGs is prominent, in that it leads to more accurate subtyping and more precise treatment for various types of cancers.

In transcriptome analysis based on microarray [10] or RNA sequencing [11] by next-generation sequencing, DEGs are usually identified by statistical tests, such as t test, nonparametric test, and Bayesian models [12]. Subsequent analysis of pathways and functional enrichment tests for DEGs are performed to increase the understanding of molecular mechanisms [13].

In the case of breast cancer, it is well known that molecular subtype and patient age are strongly associated with clinical features, such as survival rate. Fredholm *et al.* [14] reported that the 5-year survival rate was lowest in the of 25–34-year-old age group and decreased with increasing age. Likewise, Gnerlich *et al.* [15] reported that younger women were more likely to die from breast cancer than older ones, based on the statistics of 243,012 breast cancer patients. Recently, Azim *et al.* [16] studied genomic aberrations in young and elderly breast cancer patients based on TCGA data. They found that older patients had more somatic mutations and copy number variations (CNVs) and that 11 mutations and two CNVs were independently associated with age at diagnosis.

In this work, we aimed to classify human genes based on

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age-specific differential expression between normal and breast cancer cells. DEGs were identified based on their p-values for differential gene expression between tumor and matched normal cells. DEGs and non-DEGs were then classified based on age-specific differential expression by the three age groups we defined. To show an application of the classification, we compared the accuracy of prediction models that distinguish normal and tumor cells, constructed by support vector machine (SVM) using various combinations of genes by class. The performance of SVM was measured by the average area under the receiver operating characteristics curve value after 1,000 times bootstrap.

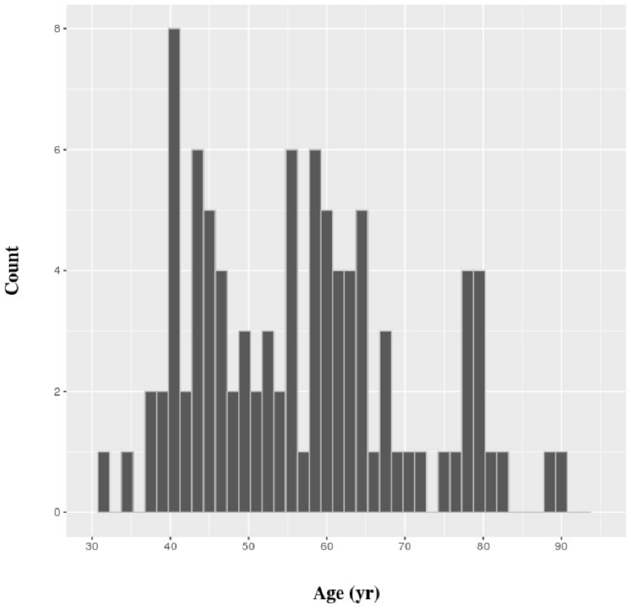

Fig. 1. Distribution of age of breast cancer patients analyzed in this work.

Methods

All gene expression values in this work were gathered from TCGA. Eligible patients had complete clinical data and a gene expression dataset of breast cancer cells and matched normal cells. Eventually, we retrieved the gene expression values of tumor and matched normal cells of 96 patients. The distribution of their ages is shown in Fig. 1. The values for gene expression level that we used were generated by the Illumina Hi-Seq platform (Illumina, Inc., San Diego, CA, USA) and normalized by root square error methods [17]. All subsequent statistical analyses were carried out using R, version 3.2.3. SVM classifiers were constructed using the e1071 package of R, and a simple linear kernel was used. Functional enrichment analysis of gene classes was performed in ToppGene Suite [18].

Young patients were defined as ≤45 years of age, and

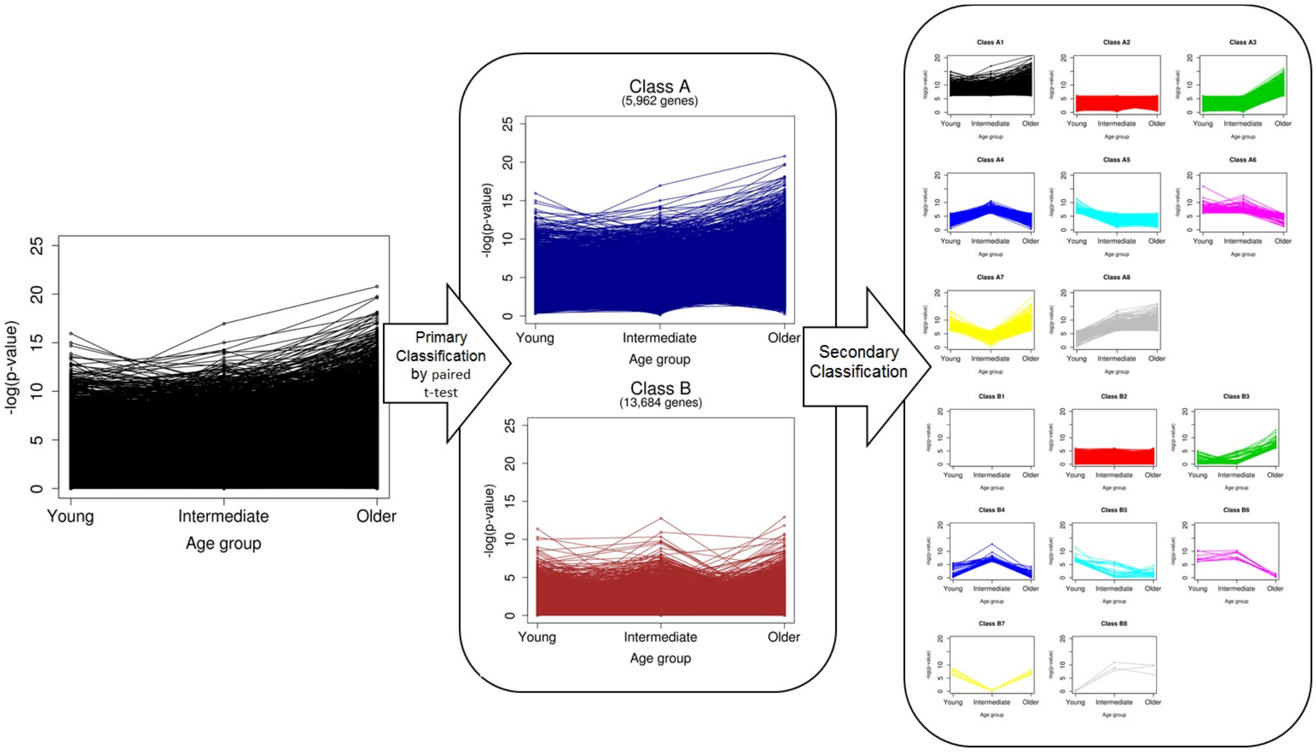

Fig. 2. Schematic view of overall procedures of the two-step classification.

elderly patients were defined as those ≥60 years of age (Fig. 1). The rest of the patients were defined as "intermediate." The statistical significance of differential expression between tumor and matched normal cells was determined by paired t test, based on a p-value threshold of 8.48×10^{-7}. The threshold value was set based on the Bonferroni correction, because a test was performed for each age group, and three age groups were defined for each of the 19,646 genes.

Results and Discussion

The overall scheme of our classification is depicted in Fig. 2. We first divided genes into two classes (A and B) by paired t test without considering age. A total of 5,962 genes in class A were defined as significant DEGs in breast cancer, and 13,684 in class B were nonsignificant. Ones who want to find biomarkers or driver genes are likely to investigate only genes in class A. However, we classified the genes of each class once again into eight groups, based on the pattern of p-values, which were calculated separately for every age group (secondary classification in Fig. 2). After a second round of classification, the genes were eventually divided into 16 classes (A1–B8) (Supplementary Table 1). The numbers of genes of the classes are shown in Table 1.

It was easily observed that there was no gene classified as class B1. Probably, this was because the significance of genes in class B was already tested in the primary classification step, and no genes showed significance over all age groups. The 377 genes in class A1 exhibited differential expression for every age group and all samples. These genes are the most powerful DEGs between normal and breast cancer cells. Genes of class 2, which did not have significantly different expression in any age group, accounted for the majority in both classes A and B. Indeed, classes 1 and 2 did not have any age-specific significance. Thus, we focused on the genes of classes 3–8, which showed age-specific differential expression (Fig. 3).

Functional enrichment analysis for each class was performed, but we could not find any relevant or intriguing biological implications or pathways related to breast cancer. Hence, we decided to provide the results of the analysis as raw data (Supplementary Table 2) rather than trying an unfeasible deduction.

To show an example of how the classification can be applied, we constructed prediction models that aimed to distinguish normal and breast cancer cells, using the expression values of various combinations of genes. We defined two types of combinations comprising gene lists. For type I combinations, genes were chosen evenly from each class. By contrast, genes were chosen randomly for type II combinations without considering gene class. For example, if we make a list composed of three genes from classes 3, 4, and 5, the type I combination should consist of a gene from class 3, another from class 4, and the other one from class 5, but a type II combination could be composed of any genes randomly chosen from the pool of the three classes.

We compared the accuracies of the SVM of type I and II combinations for three subsets each for classes A and B (Table 2). The performance of type I was significantly better than that of type II, except in two cases (classes 6-8 in both classes A and B), the genes of which were significantly differentially expressed in the two age groups.

These results highlight the value of gene classification based on our method. Based on the first classification, 13,684 genes in class B were probably considered genes that cannot distinguish normal and breast cancer cells. However, by adapting one more classification step based on age-specific differential expression, we identified 171 age-specific DEGs in classes B3–B8. Despite the underestimated value of the classes, we showed that a balanced selection of genes from these classes could be applied as biomarkers, identifying breast cancer from normal cells. For example, genes that are known to be high-penetrance breast cancer susceptibility genes, such as *TP53, STK11*, and *CDH11*, and mode-

Table 1. Definition of classification of genes based on age-specific significance and the corresponding number of genes

Secondary class	Young	Intermediate	Older	Primary class	
				A	B
1	Significant	Significant	Significant	377	0
2	Nonsignificant	Nonsignificant	Nonsignificant	4,495	13,548
3	Nonsignificant	Nonsignificant	Significant	781	69
4	Nonsignificant	Significant	Nonsignificant	56	29
5	Significant	Nonsignificant	Nonsignificant	44	18
6	Significant	Significant	Nonsignificant	28	9
7	Significant	Nonsignificant	Nonsignificant	71	8
8	Nonsignificant	Significant	Significant	110	3

Significances were defined based on the p-value of paired t test.

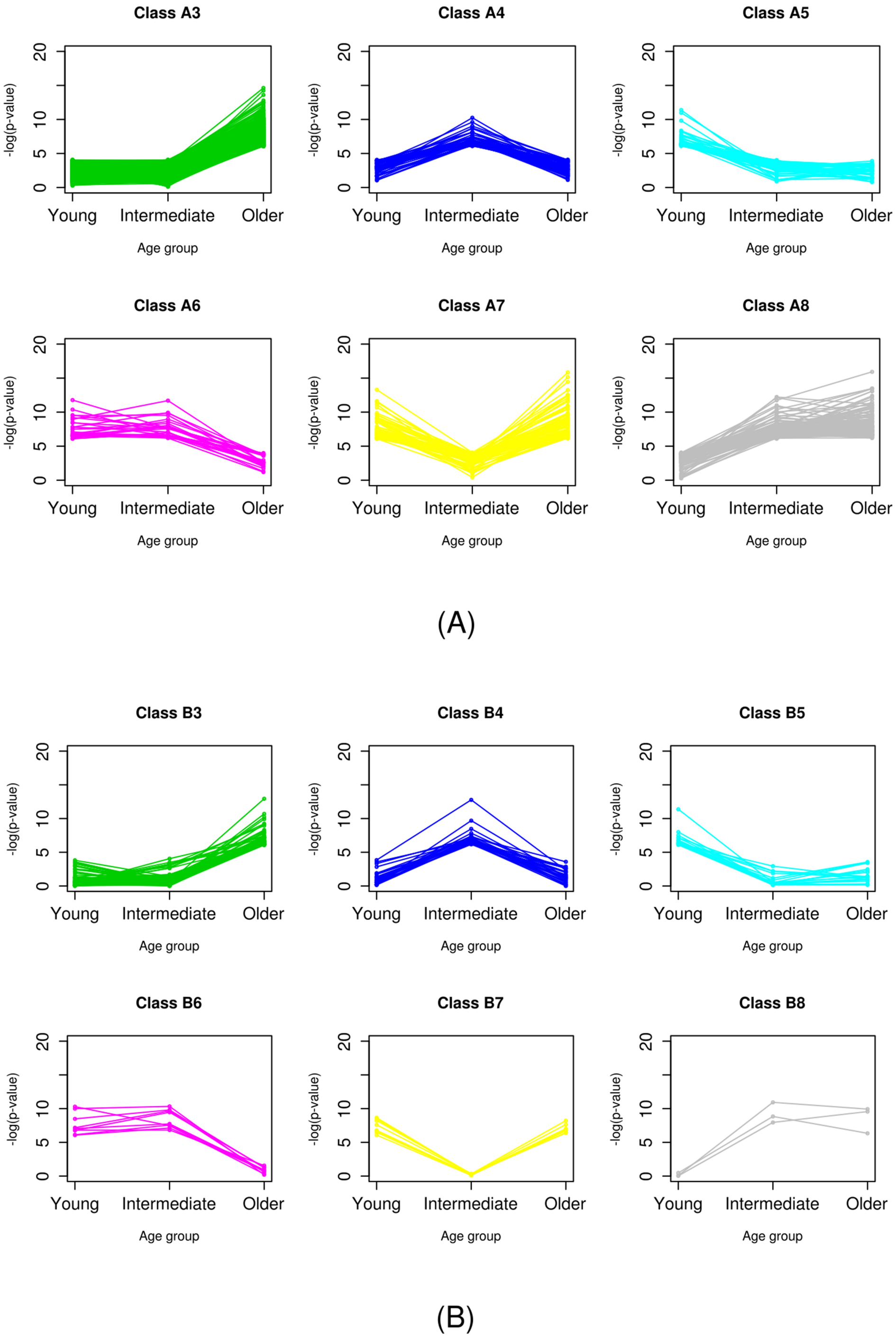

Fig. 3. Patterns of significance of age-specific differential expression of class A (A) and class B (B).

rate-penetrance genes, such as *RAD50, RAD51C, RAD51D, NBS1*, and *FANCM*, were classified in class B2 [19]. In addition to proposing the possibility of genes in class B as biomarkers, even for class A, we exhibited that our method of selecting biomarker genes based on secondary classification could be useful in making a combination of biomarker genes for a more accurate prediction by using different classes complementarily.

In summary, we retrieved a gene expression dataset of breast cancer and matched normal cells from TCGA and then classified the genes into 16 classes by two-step classification. This classification could be applied to generate a more accurate prediction model for identifying cancer. Furthermore, we expect that our scheme of classification could be used for other types of cancer data.

Table 2. Comparison of performance of SVM models of different combinations of genes to distinguish breast cancer and normal cells

Input genes (N)	Sampling pool	Type I (one gene per class)	Type II (n random genes from the pool)	p-value
3	Classes A3–A5	0.9351	0.9215	4.732e-16
3	Classes A6–A8	0.9660	0.9662	0.8391
6	Classes A3–A8	0.9842	0.9743	2.2e-16
3	Classes B3–B5	0.8701	0.8522	1.441e-15
3	Classes B6–B8	0.9269	0.9392	0.4868
6	Classes B3–B8	0.9386	0.9227	6.984e-09

N input genes were sampled from each sampling pool by adopting two types of combinations (types I and II).
SVM, support vector machine.

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Authors' contribution

Conceptualization: ML
Data curation: GL
Formal analysis: GL, ML
Funding acquisition: ML
Methodology: GL
Writing – original draft: GL, ML
Writing – review & editing: ML

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Supplementary materials

Supplementary data including two tables can be found with this article online at http://www.genominfo.org/src/sm/gni-15-156-s001.pdf.

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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
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PHF17|79960	A1
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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
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ZP4|57829	B2

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ZXDC|79364	B2
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ACOT9|23597	B3
ACR|49	B3
ADH6|130	B3
AXL|558	B3
BCHE|590	B3
BRWD3|254065	B3
C10orf108|414235	B3
C11orf53|341032	B3
C1QTNF2|114898	B3
C1S|716	B3
C21orf62|56245	B3
CCDC92|80212	B3
CLEC2L|154790	B3
CLEC4F|165530	B3
COL15A1|1306	B3
CPS1|1373	B3
CRTAC1|55118	B3
DPP4|1803	B3
DZIP1|22873	B3
EIF1|10209	B3

ELMO1|9844	B3
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FGD5|152273	B3
FGF10|2255	B3
FKBP1B|2281	B3
FXYD2|486	B3
GABRA2|2555	B3
GLI1|2735	B3
GPER|2852	B3
HIBADH|11112	B3
HMGCR|3156	B3
HSPB11|51668	B3
IGF2|3481	B3
ILK|3611	B3
ITGB1|3688	B3
JDP2|122953	B3
LOC158696|158696	B3
LOC348926|348926	B3
LOC400804|400804	B3
MAGEE2|139599	B3
MAP1A|4130	B3
METTL6|131965	B3
MFAP5|8076	B3
MPZ|4359	B3
NAA35|60560	B3
NNMT|4837	B3
NTRK3|4916	B3
PKIG|11142	B3
PLS1|5357	B3
PPP1R1B|84152	B3
PRMT2|3275	B3
RAB3IL1|5866	B3
RFFL|117584	B3
RGS5|8490	B3
RPP30|10556	B3
S100B|6285	B3
SAMD10|140700	B3
SEPT4|5414	B3
SGTB|54557	B3
SHOX2|6474	B3
SNHG5|387066	B3
STX2|2054	B3
SULT1C4|27233	B3
THOC2|57187	B3
TSPAN18|90139	B3
UVRAG|7405	B3
XKR6|286046	B3
ZNF208|7757	B3
psiTPTE22|387590	B3
AJAP1|55966	B4
AKAP6|9472	B4

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CASP1|834	B4
CCDC68|80323	B4
CEP164|22897	B4
DIRC2|84925	B4
FLJ39582|439931	B4
GPR62|118442	B4
GRIN2D|2906	B4
KIAA0913|23053	B4
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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잽 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