

# Results

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**1: GO: Molecular Function** [\[Display Chart\]](#) 193 input genes in category / 745 annotations before applied cutoff / 19963 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0005201	extracellular matrix structural constituent		6.886E-9	5.130E-6	3.689E-5	5.130E-6	14	195
2	GO:0005198	structural molecule activity		1.435E-7	5.344E-5	3.843E-4	1.069E-4	27	892
3	GO:0008201	heparin binding		5.053E-7	1.255E-4	9.023E-4	3.764E-4	12	197
4	GO:1901681	sulfur compound binding		4.113E-6	7.660E-4	5.508E-3	3.064E-3	14	329
5	GO:0005539	glycosaminoglycan binding		1.422E-5	2.118E-3	1.523E-2	1.060E-2	12	272

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**2: GO: Biological Process** [\[Display Chart\]](#) 192 input genes in category / 5095 annotations before applied cutoff / 20720 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0035295	tube development		3.274E-13	1.668E-9	1.520E-8	1.668E-9	52	1880
2	GO:0033993	response to lipid		5.580E-12	1.422E-8	1.296E-7	2.843E-8	45	1567
3	GO:0035239	tube morphogenesis		9.535E-12	1.619E-8	1.476E-7	4.858E-8	43	1467
4	GO:0060429	epithelium development		2.996E-11	3.816E-8	3.478E-7	1.527E-7	50	1979
5	GO:0048732	gland development		6.400E-11	6.522E-8	5.943E-7	3.261E-7	31	851

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**3: GO: Cellular Component** [\[Display Chart\]](#) 193 input genes in category / 457 annotations before applied cutoff / 20932 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0031012	extracellular matrix		9.791E-13	2.411E-10	1.616E-9	4.474E-10	30	678
2	GO:0030312	external encapsulating structure		1.055E-12	2.411E-10	1.616E-9	4.822E-10	30	680
3	GO:0062023	collagen-containing extracellular matrix		2.124E-10	3.236E-8	2.169E-7	9.709E-8	24	541
4	GO:0009986	cell surface		1.234E-7	1.410E-5	9.449E-5	5.639E-5	31	1178
5	GO:0016324	apical plasma membrane		6.771E-6	5.298E-4	3.551E-3	3.094E-3	16	464

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**4: Human Phenotype** [\[Display Chart\]](#) 73 input genes in category / 2908 annotations before applied cutoff / 5060 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	HP:0100811	Aplasia/Hypoplasia of the colon		4.759E-6	6.919E-3	5.917E-2	1.384E-2	4	9
2	HP:0004388	Microcolon		4.759E-6	6.919E-3	5.917E-2	1.384E-2	4	9
3	HP:0010956	Fetal megacystis		2.823E-5	2.736E-2	2.340E-1	8.208E-2	3	5
4	HP:0003270	Abdominal distention		7.615E-5	4.314E-2	3.689E-1	2.214E-1	8	99
5	HP:0005245	Intestinal hypoplasia		8.234E-5	4.314E-2	3.689E-1	2.395E-1	4	17

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**5: Mouse Phenotype** [\[Display Chart\]](#) 158 input genes in category / 3587 annotations before applied cutoff / 12941 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	MP:0001544	abnormal cardiovascular system physiology		1.255E-7	4.501E-4	3.944E-3	4.501E-4	48	1841
2	MP:0003745	abnormal oral mucosa morphology		4.665E-7	8.242E-4	7.222E-3	1.673E-3	5	14
3	MP:0001663	abnormal digestive system physiology		7.419E-7	8.242E-4	7.222E-3	2.661E-3	23	589
4	MP:0005620	abnormal muscle contractility		9.191E-7	8.242E-4	7.222E-3	3.297E-3	18	381
5	MP:0005381	digestive/alimentary phenotype		1.284E-6	9.213E-4	8.073E-3	4.607E-3	38	1391

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**6: Domain** [\[Display Chart\]](#) 192 input genes in category / 1425 annotations before applied cutoff / 18678 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	IPR009030	Growth fac rcpt	<a href="#">InterPro</a>	6.475E-7	9.227E-4	7.234E-3	9.227E-4	11	156
2	PS00022	EGF 1	<a href="#">PROSITE</a>	2.470E-6	1.343E-3	1.053E-2	3.520E-3	13	255
3	IPR013032	EGF-like CS	<a href="#">InterPro</a>	3.191E-6	1.343E-3	1.053E-2	4.547E-3	13	261
4	PS01186	EGF 2	<a href="#">PROSITE</a>	3.769E-6	1.343E-3	1.053E-2	5.371E-3	13	265
5	SM00181	EGF	<a href="#">SMART</a>	5.974E-6	1.574E-3	1.234E-2	8.513E-3	12	235

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 165 input genes in category / 1713 annotations before applied cutoff / 13609 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	<a href="#">MSigDB C2 BIOCARTE (v7.5.1)</a>	4.903E-16	8.398E-13	6.738E-12	8.398E-13	47	1026
2	M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	<a href="#">MSigDB C2 BIOCARTE (v7.5.1)</a>	6.201E-9	5.311E-6	4.261E-5	1.062E-5	18	275
3	M3008	Genes encoding structural ECM glycoproteins	<a href="#">MSigDB C2 BIOCARTE (v7.5.1)</a>	1.524E-8	8.700E-6	6.980E-5	2.610E-5	15	196
4	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	<a href="#">MSigDB C2 BIOCARTE (v7.5.1)</a>	2.488E-8	1.066E-5	8.550E-5	4.263E-5	29	751
5	137939	Direct p53 effectors	<a href="#">BioSystems: Pathway Interaction Database</a>	5.824E-7	1.995E-4	1.601E-3	9.976E-4	11	132

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	24952961	A high-resolution spatiotemporal atlas of gene expression of the developing mouse brain.	<a href="#">Pubmed</a>	1.796E-19	1.193E-14	1.393E-13	1.193E-14	44	1937
2	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	<a href="#">Pubmed</a>	1.785E-15	5.685E-11	6.640E-10	1.185E-10	37	1744
3	26930384	Transcriptome of the inner circular smooth muscle of the developing mouse intestine: Evidence for regulation of visceral smooth muscle genes by the hedgehog target gene, cJun.	<a href="#">Pubmed</a>	2.569E-15	5.685E-11	6.640E-10	1.705E-10	14	140
4	23533145	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine.	<a href="#">Pubmed</a>	4.613E-14	7.657E-10	8.944E-9	3.063E-9	28	1070
5	28611215	Genome-wide CRISPR screen identifies HNRNPL as a prostate cancer dependency regulating RNA splicing.	<a href="#">Pubmed</a>	4.101E-12	5.446E-8	6.361E-7	2.723E-7	30	1489

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	int:APC	APC interactions		2.032E-9	1.823E-5	1.764E-4	1.823E-5	19	356
2	int:PPP2R2B	PPP2R2B interactions		5.242E-7	2.351E-3	2.276E-2	4.703E-3	13	235
3	int:GOT1	GOT1 interactions		2.480E-6	7.417E-3	7.179E-2	2.225E-2	13	270
4	int:SSUH2	SSUH2 interactions		4.047E-6	9.076E-3	8.785E-2	3.630E-2	11	199
5	int:ST6GALNAC6	ST6GALNAC6 interactions		7.887E-6	1.415E-2	1.370E-1	7.075E-2	8	104

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2q14	2q14		3.226E-5	5.355E-3	3.048E-2	5.355E-3	3	11

**11: Transcription Factor Binding Site** [\[Display Chart\]](#) 189 input genes in category / 866 annotations before applied cutoff / 26918 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	CAGGTG V\$E12 Q6	CAGGTG V\$E12 Q6	<a href="#">TFBS</a>	4.774E-11	4.134E-8	3.035E-7	4.134E-8	42	1950
2	TGGAAG V\$NFAT Q4 01	TGGAAG V\$NFAT Q4 01	<a href="#">TFBS</a>	1.102E-9	4.773E-7	3.505E-6	9.547E-7	34	1491
3	TATAAA V\$TATA 01	TATAAA V\$TATA 01	<a href="#">TFBS</a>	5.468E-7	1.421E-4	1.043E-3	4.735E-4	24	1070
4	V\$SRF C	V\$SRF C	<a href="#">TFBS</a>	6.563E-7	1.421E-4	1.043E-3	5.684E-4	10	181

5	CAGCTG V\$AP4 Q5	CAGCTG V\$AP4 Q5	TFBS	9.385E-7	1.625E-4	1.193E-3	8.127E-4	25	1184
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## 12: Gene Family [\[Display Chart\]](#) 138 input genes in category / 124 annotations before applied cutoff / 18084 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	733	Secreted frizzled-related proteins	<a href="#">genenames.org</a>	4.300E-6	5.332E-4	2.880E-3	5.332E-4	3	5
2	542	Endogenous ligands	<a href="#">genenames.org</a>	8.672E-5	3.760E-3	2.031E-2	1.075E-2	9	237
3	573	Small leucine rich repeat proteoglycans	<a href="#">genenames.org</a>	9.096E-5	3.760E-3	2.031E-2	1.128E-2	3	12
4	483	Chemokine ligands Endogenous ligands	<a href="#">genenames.org</a>	3.795E-4	1.176E-2	6.354E-2	4.705E-2	4	45
5	648	Mucins	<a href="#">genenames.org</a>	5.229E-4	1.297E-2	7.004E-2	6.484E-2	3	21

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## 13: Coexpression [\[Display Chart\]](#) 196 input genes in category / 8960 annotations before applied cutoff / 26258 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	15785748-Table3	Human Uterine Santin05 178genes	<a href="#">GeneSigDB</a>	1.213E-23	1.087E-19	1.052E-18	1.087E-19	23	151
2	M17572	SMID BREAST CANCER LUMINAL B DN	<a href="#">MSigDB C2: CGP Curated Gene Sets (v7.5.1)</a>	1.420E-20	6.363E-17	6.158E-16	1.273E-16	34	587
3	M14791	SABATES COLORECTAL ADENOMA DN	<a href="#">MSigDB C2: CGP Curated Gene Sets (v7.5.1)</a>	5.938E-18	1.773E-14	1.716E-13	5.320E-14	24	299
4	M41675	TRAVAGLINI LUNG ADVENTITIAL FIBROBLAST CELL	<a href="#">MSigDB C8: Cell Type Signatures (v7.5.1)</a>	6.190E-17	1.387E-13	1.342E-12	5.547E-13	23	296
5	M14134	TURASHVILI BREAST DUCTAL CARCINOMA VS DUCTAL NORMAL DN	<a href="#">MSigDB C2: CGP Curated Gene Sets (v7.5.1)</a>	9.683E-17	1.735E-13	1.679E-12	8.676E-13	20	206

Show 45 more annotations

## 14: Coexpression Atlas [\[Display Chart\]](#) 194 input genes in category / 3427 annotations before applied cutoff / 21235 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	gudmap developingLowerUrinaryTract P1 bladder B	DevelopingLowerUrinaryTract P1 bladder B emap-30374 top-relative-expression-ranked 500	<a href="#">Gudmap Mouse MOE430.2</a>	1.136E-22	3.893E-19	3.394E-18	3.893E-19	33	384
2	gudmap developingLowerUrinaryTract P2 bladder detrusor (LCM) 500	DevelopingLowerUrinaryTract P2 bladder detrusor (LCM) emap-30376 top-relative-expression-ranked 500	<a href="#">Gudmap Mouse MOE430.2</a>	1.871E-21	3.207E-18	2.795E-17	6.413E-18	32	388
3	gudmap developingLowerUrinaryTract P1 bladder 1000 B	DevelopingLowerUrinaryTract P1 bladder B emap-30374 top-relative-expression-ranked 1000	<a href="#">Gudmap Mouse MOE430.2</a>	3.872E-20	4.003E-17	3.490E-16	1.327E-16	41	774
4	gudmap kidney adult RenalCapsule 1000	kidney adult RenalCapsule top-relative-expression-ranked 1000	<a href="#">Gudmap Mouse MOE430.2</a>	4.673E-20	4.003E-17	3.490E-16	1.601E-16	41	778
5	gudmap developingLowerUrinaryTract adult bladder 500 k4	DevelopingLowerUrinaryTract adult bladder emap-29457 k-means-cluster#4 top-relative-expression-ranked 500	<a href="#">Gudmap Mouse MOE430.2</a>	1.979E-19	1.338E-16	1.166E-15	6.782E-16	19	107

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## 15: ToppCell Atlas [\[Display Chart\]](#) 196 input genes in category / 22379 annotations before applied cutoff / 45195 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	60c93ff2591f3896a34e58762be960b27ff4f83c	SmallIntestine GW trimst-2-Mesenchymal-myocytic-SMC (PART1/CAPN3+) SmallIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	<a href="#">Cells of the human intestinal tract mapped across space and time</a>	6.154E-36	1.377E-31	1.459E-30	1.377E-31	29	195
2	87d0e3b08154e5f704287a337ea7ae1ac40b4ac3	SmallIntestine GW trimst-1-Mesenchymal-myocytic-SMC (PART1/CAPN3+) SmallIntestine GW trimst-1 / Per Region, Age group, Lineage, cell class, cell type	<a href="#">Cells of the human intestinal tract mapped across space and time</a>	3.854E-34	4.313E-30	4.569E-29	8.626E-30	28	197

3	8debc80e0b8de623ad10fe410a569a157a9faa	SmallIntestine GW trimst-1.5-Mesenchymal-myocytic[SmallIntestine GW trimst-1.5 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	7.027E-31	5.242E-27	5.553E-26	1.573E-26	26	197
4	e1f3f0e974eb3fe1c05018beb9e124c7fb0cbe50	TCGA-Bladder-Primary Tumor-Urothelial Carcinoma-Non-Papillary Muscle Invasive Urothelial Carcinoma-4 TCGA-Bladder / Sample Type by Project: Shred V9	TCGA OncoMap	5.433E-30	3.040E-26	3.220E-25	1.216E-25	25	185
5	0d0682c2951a085b1b5a7615c29990fc7a4f4f1a	LargeIntestine GW trimst-2-Mesenchymal-myocytic-SMC (PART1/CAPN3+) LargeIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	2.443E-29	9.233E-26	9.780E-25	5.468E-25	25	196

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#### 16: Computational [Display Chart] 142 input genes in category / 416 annotations before applied cutoff / 10012 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M15336 MODULE 6	Trachea genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	6.024E-10	2.506E-7	1.656E-6	2.506E-7	25	413
2	M4515 MODULE 324	Metal / Ca ion binding.	MSigDb: C4 - CM: Cancer Modules (v7.2)	3.676E-7	6.120E-5	4.045E-4	1.529E-4	12	133
3	M9982 MODULE 2	DRG (dorsal root ganglia) genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	4.413E-7	6.120E-5	4.045E-4	1.836E-4	20	384
4	M4051 MODULE 1	Ovary genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	4.268E-6	3.806E-4	2.515E-3	1.776E-3	18	368
5	M14358 MODULE 88	Heart, liver, kidney and pancreas metabolic and xenobiotic response genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	4.574E-6	3.806E-4	2.515E-3	1.903E-3	29	834

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#### 17: MicroRNA [Display Chart] 197 input genes in category / 8544 annotations before applied cutoff / 59110 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-1468-3p		MirDB	4.241E-20	3.623E-16	3.489E-15	3.623E-16	34	1343
2	hsa-miR-148a:mirSVR lowEffect	hsa-miR-148a:mirSVR conserved lowEffect-0.1-0.5	MicroRNA.org	3.467E-15	1.264E-11	1.218E-10	2.962E-11	33	1838
3	hsa-miR-6867-5p		MirDB	4.439E-15	1.264E-11	1.218E-10	3.793E-11	28	1281
4	hsa-miR-520f:mirSVR lowEffect	hsa-miR-520f:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	1.025E-14	2.190E-11	2.109E-10	8.762E-11	32	1787
5	hsa-miR-4753-3p		MirDB	2.863E-14	4.891E-11	4.711E-10	2.446E-10	27	1272

Show 45 more annotations

#### 18: Drug [Display Chart] 196 input genes in category / 25790 annotations before applied cutoff / 22767 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ctd:D004237	Diuron	CTD	3.532E-17	9.110E-13	9.780E-12	9.110E-13	54	1735
2	CID000003285	ethynylestradiol	Stitch	3.913E-15	5.046E-11	5.417E-10	1.009E-10	43	1251
3	ctd:D015735	Mifepristone	CTD	4.674E-14	4.018E-10	4.314E-9	1.205E-9	28	553
4	ctd:D012906	Smoke	CTD	1.978E-13	1.275E-9	1.369E-8	5.100E-9	35	937
5	ctd:C015001	arsenite	CTD	8.272E-13	4.267E-9	4.580E-8	2.133E-8	47	1723

Show 45 more annotations

#### 19: Disease [Display Chart] 190 input genes in category / 7202 annotations before applied cutoff / 19383 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	C1800706	Idiopathic Pulmonary Fibrosis	DisGeNET BeFree	2.525E-13	1.818E-9	1.720E-8	1.818E-9	34	786

2	C0024117	Chronic Obstructive Airway Disease	<a href="#">DisGeNET BeFree</a>	2.033E-12	7.319E-9	6.924E-8	1.464E-8	41	1213
3	C0006142	Malignant neoplasm of breast	<a href="#">DisGeNET Curated</a>	1.724E-11	4.138E-8	3.914E-7	1.241E-7	37	1074
4	C0027051	Myocardial Infarction	<a href="#">DisGeNET BeFree</a>	4.815E-11	8.228E-8	7.783E-7	3.468E-7	45	1582
5	C0020538	Hypertensive disease	<a href="#">DisGeNET BeFree</a>	5.712E-11	8.228E-8	7.783E-7	4.114E-7	51	1973

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