

Results

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1: GO: Molecular Function [\[Display Chart\]](#) 212 input genes in category / 662 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:0030280	structural constituent of skin epidermis		7.446E-10	4.394E-7	3.108E-6	4.929E-7	9	44
2	GO:0005200	structural constituent of cytoskeleton		1.327E-9	4.394E-7	3.108E-6	8.787E-7	13	130
3	GO:0005509	calcium ion binding		6.326E-8	1.396E-5	9.874E-5	4.188E-5	27	777
4	GO:0005198	structural molecule activity		2.871E-7	4.751E-5	3.361E-4	1.901E-4	28	892
5	GO:0051015	actin filament binding		1.846E-6	2.444E-4	1.728E-3	1.222E-3	13	240

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2: GO: Biological Process [\[Display Chart\]](#) 212 input genes in category / 4337 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:0030855	epithelial cell differentiation		3.428E-25	1.487E-21	1.331E-20	1.487E-21	56	1051
2	GO:0008544	epidermis development		2.556E-22	5.543E-19	4.962E-18	1.109E-18	38	500
3	GO:0060429	epithelium development		5.394E-20	7.798E-17	6.981E-16	2.339E-16	68	1979
4	GO:0031424	keratinization		3.061E-17	3.319E-14	2.971E-13	1.328E-13	17	89
5	GO:0030216	keratinocyte differentiation		7.325E-17	5.751E-14	5.148E-13	3.177E-13	22	195

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3: GO: Cellular Component [\[Display Chart\]](#) 212 input genes in category / 441 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:0001533	cornified envelope		1.690E-27	7.452E-25	4.969E-24	7.452E-25	22	69
2	GO:0005902	microvillus		9.735E-8	1.593E-5	1.062E-4	4.293E-5	11	131
3	GO:0005903	brush border		1.084E-7	1.593E-5	1.062E-4	4.780E-5	12	163
4	GO:0005911	cell-cell junction		6.603E-7	7.280E-5	4.854E-4	2.912E-4	21	590
5	GO:0045177	apical part of cell		1.498E-6	1.321E-4	8.807E-4	6.605E-4	20	569

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4: Human Phenotype [\[Display Chart\]](#) 86 input genes in category / 3174 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:0000982	Palmoplantar keratoderma		2.621E-12	6.177E-9	5.337E-8	8.320E-9	19	149
2	HP:0000972	Palmoplantar hyperkeratosis		6.802E-12	6.177E-9	5.337E-8	2.159E-8	19	157
3	HP:0007556	Plantar hyperkeratosis		8.556E-12	6.177E-9	5.337E-8	2.716E-8	19	159
4	HP:0010765	Palmar hyperkeratosis		8.556E-12	6.177E-9	5.337E-8	2.716E-8	19	159
5	HP:0001035	Abnormality of keratinization		9.731E-12	6.177E-9	5.337E-8	3.089E-8	23	250

[Show 45 more annotations](#)**5: Mouse Phenotype** [\[Display Chart\]](#) 166 input genes in category / 3526 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:0005381	digestive/alimentary phenotype	2.003E-11	3.960E-8	3.463E-7	7.064E-8	49	1391
2	MP:0001216	abnormal epidermal layer morphology	2.246E-11	3.960E-8	3.463E-7	7.921E-8	21	264
3	MP:0000467	abnormal esophagus morphology	7.669E-9	7.281E-6	6.367E-5	2.704E-5	10	64
4	MP:0000462	abnormal digestive system morphology	9.001E-9	7.281E-6	6.367E-5	3.174E-5	38	1090
5	MP:0001240	abnormal epidermis stratum corneum morphology	1.032E-8	7.281E-6	6.367E-5	3.640E-5	13	129

[Show 45 more annotations](#)**6: Domain** [\[Display Chart\]](#) 211 input genes in category / 1258 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	IPR018039	Intermediate filament CS	InterPro	2.074E-9	2.609E-6	2.013E-5	2.609E-6	10	63
2	SM01391	Filament	SMART	6.928E-9	2.875E-6	2.218E-5	8.716E-6	10	71
3	PS00226	IF	PROSITE	7.967E-9	2.875E-6	2.218E-5	1.002E-5	10	72
4	PF00038	Filament	Pfam	9.141E-9	2.875E-6	2.218E-5	1.150E-5	10	73
5	IPR001664	IF	InterPro	1.364E-8	3.431E-6	2.647E-5	1.715E-5	10	76

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 174 input genes in category / 1541 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	1457790	Keratinization	BioSystems: REACTOME	3.847E-14	5.928E-11	4.693E-10	5.928E-11	22	214
2	1457791	Formation of the cornified envelope	BioSystems: REACTOME	4.742E-12	3.654E-9	2.893E-8	7.308E-9	13	71
3	1270302	Developmental Biology	BioSystems: REACTOME	7.334E-8	3.213E-5	2.544E-4	1.130E-4	36	1078
4	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	MSigDB C2 BIOCARTEA (v7.5.1)	8.341E-8	3.213E-5	2.544E-4	1.285E-4	29	751
5	1457778	Metal sequestration by antimicrobial proteins	BioSystems: REACTOME	3.796E-7	1.170E-4	9.264E-4	5.850E-4	4	6

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	32989256	Suppression of DDX39B sensitizes ovarian cancer cells to DNA-damaging chemotherapeutic agents via destabilizing BRCA1 mRNA.	Pubmed	6.369E-28	3.534E-23	4.064E-22	3.534E-23	21	107
2	19199708	Proteomic analysis of human parotid gland exosomes by multidimensional protein identification technology (MudPIT).	Pubmed	1.559E-23	4.326E-19	4.975E-18	8.652E-19	28	417
3	28973166	Activated Braf induces esophageal dilation and gastric epithelial hyperplasia in mice.	Pubmed	3.616E-20	5.120E-16	5.888E-15	2.007E-15	13	45
4	31220272	Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma.	Pubmed	3.691E-20	5.120E-16	5.888E-15	2.048E-15	14	60
5	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	Pubmed	1.816E-19	2.016E-15	2.318E-14	1.008E-14	44	1744

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9: Interaction [Display Chart] 210 input genes in category / 8296 annotations before applied cutoff / 19896 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	int:C18orf21	C18orf21 interactions		1.383E-21	1.147E-17	1.102E-16	1.147E-17	24	151
2	int:SSUH2	SSUH2 interactions		4.609E-21	1.912E-17	1.835E-16	3.824E-17	26	199
3	int:CCR1	CCR1 interactions		1.561E-20	4.317E-17	4.145E-16	1.295E-16	32	360
4	int:PPP2R2B	PPP2R2B interactions		2.403E-20	4.984E-17	4.785E-16	1.994E-16	27	235
5	int:PHF11	PHF11 interactions		1.119E-18	1.857E-15	1.783E-14	9.286E-15	21	137

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1q21-q22	1q21-q22		6.700E-9	1.166E-6	6.690E-6	1.166E-6	6	23
2	1q21	1q21		2.353E-6	2.047E-4	1.175E-3	4.095E-4	7	91
3	18q12.1	18q12.1		6.411E-4	3.719E-2	2.134E-1	1.116E-1	3	26
4	12q13.13	12q13.13		9.866E-4	4.292E-2	2.463E-1	1.717E-1	4	67

11: Transcription Factor Binding Site [Display Chart] 204 input genes in category / 801 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	TGANTCA V\$AP1 C	TGANTCA V\$AP1 C	TFBS	3.175E-12	2.543E-9	1.847E-8	2.543E-9	31	918
2	TATAAA V\$TATA 01	TATAAA V\$TATA 01	TFBS	2.826E-9	1.132E-6	8.220E-6	2.263E-6	29	1070
3	M29941	DLX2 TARGET GENES	MSigDB	5.239E-8	1.399E-5	1.016E-4	4.197E-5	14	290
4	M30042	KMT2D TARGET GENES	MSigDB	3.365E-6	6.739E-4	4.895E-3	2.696E-3	20	801
5	GGGTGGRR V\$PAX4 03	GGGTGGRR V\$PAX4 03	TFBS	7.012E-6	1.123E-3	8.159E-3	5.616E-3	23	1068

[Show 13 more annotations](#)**12: Gene Family [Display Chart]** 157 input genes in category / 109 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	1353	Small proline rich proteins	genenames.org	1.734E-10	1.890E-8	9.967E-8	1.890E-8	6	11
2	648	Mucins	genenames.org	8.416E-7	3.058E-5	1.612E-4	9.173E-5	5	21
3	459	S100 calcium binding proteins EF-hand domain containing	genenames.org	8.416E-7	3.058E-5	1.612E-4	9.173E-5	5	21
4	608	Keratins, type I	genenames.org	3.870E-6	1.055E-4	5.561E-4	4.218E-4	5	28
5	24	Cadherin related Deafness associated genes	genenames.org	1.192E-5	2.598E-4	1.370E-3	1.299E-3	4	17

[Show 16 more annotations](#)**13: Coexpression [Display Chart]** 216 input genes in category / 8061 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	M40299	DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	2.320E-47	1.870E-43	1.790E-42	1.870E-43	31	67
2	20421987-TableS4	Human Lung Hou10 518genes	GeneSigDB	4.110E-44	1.657E-40	1.586E-39	3.313E-40	49	380
3	20421987-TableS5	Human Lung Hou10 75genes	GeneSigDB	5.754E-42	1.546E-38	1.480E-37	4.639E-38	27	56
4	M40122	DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	4.931E-40	9.938E-37	9.513E-36	3.975E-36	33	130

5	M40004	BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	7.520E-39	1.212E-35	1.161E-34	6.062E-35	33	140
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Show 45 more annotations

14: Coexpression Atlas [Display Chart] 215 input genes in category / 3388 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	esophagus	esophagus	Human Protein Atlas	2.003E-63	6.787E-60	5.908E-59	6.787E-60	58	247
2	PCBC ctl BronchioEpithel 500	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500	PCBC	1.084E-60	1.836E-57	1.598E-56	3.671E-57	70	496
3	PCBC ctl BronchioEpithel 1000	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000	PCBC	5.017E-53	5.666E-50	4.933E-49	1.700E-49	82	990
4	PCBC ctl BronchioEpithel 100	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100	PCBC	8.797E-53	7.451E-50	6.486E-49	2.980E-49	39	98
5	PCBC ctl SmallAirwayEpithel 500	Progenitor-Cell-Biology-Consortium reference SmallAirwayEpithel top-relative-expression-ranked 500	PCBC	1.076E-42	7.293E-40	6.349E-39	3.647E-39	56	493

Show 45 more annotations

15: ToppCell Atlas [Display Chart] 216 input genes in category / 21467 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	eb18aa179db1818f408c38e442ecfed8582d7dbc	TCGA-Head and Esophagus World / Sample Type by Project: Shred V9	TCGA OncoMap	2.580E-110	5.539E-106	5.844E-105	5.539E-106	66	172
2	3188c7bd225cbcf46a21e2fb784336cdd9665995	TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	1.324E-89	7.106E-86	7.498E-85	2.842E-85	58	190
3	e2b26a03c6ab24d9b0f4150c47597be37767d86e	TCGA-Skin-Primary Tumor TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	1.324E-89	7.106E-86	7.498E-85	2.842E-85	58	190
4	01fb45add4661bc86cd0a34fac35177907152dbb	TCGA-Skin-Primary Tumor-Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	1.324E-89	7.106E-86	7.498E-85	2.842E-85	58	190
5	a0c7d08469c513cecf87777c19876884f1511570	TCGA-Lung-Primary Tumor-Lung Carcinoma-Lung Squamous Cell Carcinoma-5 TCGA-Lung / Sample Type by Project: Shred V9	TCGA OncoMap	2.317E-85	9.948E-82	1.050E-80	4.974E-81	55	177

Show 45 more annotations

16: Computational [Display Chart] 138 input genes in category / 359 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	M4992 MODULE 297	Genes in the cancer module 297.	MSigDb: C4 - CM: Cancer Modules (v7.2)	2.375E-26	4.263E-24	2.755E-23	8.525E-24	24	80

2	M9185 MODULE 357	Intermediate filaments and keratins.	MSigDb: C4 - CM: Cancer Modules (v7.2)	2.375E-26	4.263E-24	2.755E-23	8.525E-24	24	80
3	M18170 MODULE 154	Intermediate filaments.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.987E-22	2.378E-20	1.536E-19	7.133E-20	21	75
4	M2266 GNF2 SPRR1B	Neighborhood of SPRR1B	MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2)	7.956E-21	7.141E-19	4.614E-18	2.856E-18	14	24
5	M18849 MODULE 153	Genes in the cancer module 153.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.227E-14	8.807E-13	5.691E-12	4.403E-12	12	34

Show 15 more annotations

17: MicroRNA [Display Chart] 217 input genes in category / 8201 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-4289:mirSVR lowEffect	hsa-miR-4289:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	3.195E-13	2.620E-9	2.512E-8	2.620E-9	31	1715
2	hsa-miR-520f:mirSVR lowEffect	hsa-miR-520f:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	9.231E-13	3.785E-9	3.630E-8	7.570E-9	31	1787
3	hsa-miR-124-3p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	5.894E-12	1.611E-8	1.545E-7	4.834E-8	27	1446
4	hsa-miR-30a:mirSVR highEffect	hsa-miR-30a:mirSVR conserved highEffect-0.5	MicroRNA.org	1.159E-11	2.093E-8	2.007E-7	9.502E-8	30	1849
5	hsa-miR-30e:mirSVR highEffect	hsa-miR-30e:mirSVR conserved highEffect-0.5	MicroRNA.org	1.276E-11	2.093E-8	2.007E-7	1.047E-7	31	1982

Show 45 more annotations

18: Drug [Display Chart] 216 input genes in category / 20508 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:D004054	Diethylstilbestrol	CTD	7.256E-20	1.488E-15	1.563E-14	1.488E-15	53	1304
2	ctd:C103303	alitretinoin	CTD	1.354E-13	1.056E-9	1.110E-8	2.777E-9	22	300
3	ctd:D012906	Smoke	CTD	1.545E-13	1.056E-9	1.110E-8	3.169E-9	37	937
4	ctd:C002202	4-oxoretinoic acid	CTD	2.894E-13	1.484E-9	1.559E-8	5.935E-9	15	115
5	CID000005538	9cRA	Stitch	3.189E-12	1.308E-8	1.374E-7	6.540E-8	49	1735

Show 45 more annotations

19: Disease [Display Chart] 205 input genes in category / 6084 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	C0870082	Hyperkeratosis	DisGeNET BeFree	1.815E-12	1.104E-8	1.026E-7	1.104E-8	14	97
2	C0007124	Noninfiltrating Intraductal Carcinoma	DisGeNET BeFree	3.411E-11	1.038E-7	9.641E-7	2.075E-7	25	470
3	C0004763	Barrett Esophagus	DisGeNET BeFree	8.221E-11	1.321E-7	1.227E-6	5.002E-7	24	450
4	C0022579	Keratoderma	DisGeNET BeFree	8.685E-11	1.321E-7	1.227E-6	5.284E-7	8	24
5	C1335302	Pancreatic Ductal Adenocarcinoma	DisGeNET BeFree	1.236E-10	1.504E-7	1.397E-6	7.518E-7	35	959

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