

Results

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1: GO: Molecular Function [\[Display Chart\]](#) 218 input genes in category / 708 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		3.519E-11	2.492E-8	1.779E-7	2.492E-8	10	44
2	GO:0005200	structural constituent of cytoskeleton		1.616E-10	5.722E-8	4.086E-7	1.144E-7	14	130
3	GO:0005509	calcium ion binding		7.664E-9	1.809E-6	1.292E-5	5.426E-6	29	777
4	GO:0005198	structural molecule activity		1.172E-8	2.074E-6	1.481E-5	8.296E-6	31	892
5	GO:0005298	proline:sodium symporter activity		6.859E-8	9.713E-6	6.935E-5	4.856E-5	4	5

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2: GO: Biological Process [\[Display Chart\]](#) 217 input genes in category / 4577 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		9.160E-31	4.193E-27	3.776E-26	4.193E-27	63	1051
2	GO:0008544	epidermis development		5.118E-28	1.171E-24	1.055E-23	2.343E-24	44	500
3	GO:0060429	epithelium development		2.359E-26	3.599E-23	3.242E-22	1.080E-22	78	1979
4	GO:0009913	epidermal cell differentiation		6.770E-24	7.060E-21	6.358E-20	3.099E-20	34	331
5	GO:0030216	keratinocyte differentiation		7.712E-24	7.060E-21	6.358E-20	3.530E-20	28	195

[Show 45 more annotations](#)

3: GO: Cellular Component [\[Display Chart\]](#) 217 input genes in category / 449 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		9.921E-31	4.454E-28	2.978E-27	4.454E-28	24	69
2	GO:0005902	microvillus		1.221E-8	2.742E-6	1.833E-5	5.484E-6	12	131
3	GO:0045177	apical part of cell		2.922E-8	4.373E-6	2.923E-5	1.312E-5	23	569
4	GO:0016324	apical plasma membrane		8.754E-8	9.826E-6	6.569E-5	3.931E-5	20	464
5	GO:0098590	plasma membrane region		2.425E-7	2.178E-5	1.456E-4	1.089E-4	38	1498

[Show 41 more annotations](#)

4: Human Phenotype [\[Display Chart\]](#) 90 input genes in category / 2969 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:0001805	Onychogryposis		1.248E-10	1.909E-7	1.637E-6	3.705E-7	9	24
2	HP:0007446	Palmoplantar blistering		1.387E-10	1.909E-7	1.637E-6	4.117E-7	7	11
3	HP:0001035	Abnormality of keratinization		1.929E-10	1.909E-7	1.637E-6	5.728E-7	22	250
4	HP:0008404	Nail dystrophy		3.808E-10	2.826E-7	2.423E-6	1.131E-6	16	126
5	HP:0000982	Palmoplantar keratoderma		5.589E-10	3.226E-7	2.766E-6	1.659E-6	17	149

[Show 45 more annotations](#)**5: Mouse Phenotype** [\[Display Chart\]](#) 173 input genes in category / 3493 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:0001240	abnormal epidermis stratum corneum morphology	1.489E-11	5.202E-8	4.544E-7	5.202E-8	16	129
2	MP:0001216	abnormal epidermal layer morphology	4.978E-11	8.694E-8	7.595E-7	1.739E-7	21	264
3	MP:0005381	digestive/alimentary phenotype	1.018E-10	1.186E-7	1.036E-6	3.557E-7	49	1391
4	MP:0000764	abnormal tongue epithelium morphology	3.585E-10	3.130E-7	2.735E-6	1.252E-6	8	23
5	MP:0002796	impaired skin barrier function	4.990E-10	3.486E-7	3.045E-6	1.743E-6	11	62

[Show 45 more annotations](#)**6: Domain** [\[Display Chart\]](#) 218 input genes in category / 1235 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	1.539E-10	1.900E-7	1.462E-6	1.900E-7	11	63
2	SM01391	Filament	SMART	5.896E-10	2.479E-7	1.908E-6	7.282E-7	11	71
3	PS00226	IF	PROSITE	6.889E-10	2.479E-7	1.908E-6	8.508E-7	11	72
4	PF00038	Filament	Pfam	8.029E-10	2.479E-7	1.908E-6	9.916E-7	11	73
5	IPR001664	IF	InterPro	1.253E-9	3.096E-7	2.383E-6	1.548E-6	11	76

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 178 input genes in category / 1304 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	5.622E-16	7.331E-13	5.682E-12	7.331E-13	24	214
2	1457791	Formation of the cornified envelope	BioSystems: REACTOME	3.224E-13	2.102E-10	1.629E-9	4.205E-10	14	71
3	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	MSigDB C2 BIOCARTEA (v7.5.1)	2.641E-9	1.148E-6	8.899E-6	3.444E-6	32	751
4	M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	MSigDB C2 BIOCARTEA (v7.5.1)	3.865E-8	1.260E-5	9.765E-5	5.040E-5	36	1026
5	1270302	Developmental Biology	BioSystems: REACTOME	1.340E-7	3.494E-5	2.708E-4	1.747E-4	36	1078

[Show 26 more annotations](#)**8: Pubmed** [\[Display Chart\]](#) 223 input genes in category / 47210 annotations before applied cutoff / 44761 genes in category

	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	3.401E-31	1.606E-26	1.821E-25	1.606E-26	23	107
2	19199708	Proteomic analysis of human parotid gland exosomes by multidimensional protein identification technology (MudPIT).	Pubmed	1.122E-25	2.648E-21	3.002E-20	5.296E-21	30	417
3	31220272	Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma.	Pubmed	7.826E-22	1.232E-17	1.396E-16	3.695E-17	15	60
4	26644517	A keratin scaffold regulates epidermal barrier formation, mitochondrial lipid composition, and activity.	Pubmed	1.357E-21	1.602E-17	1.816E-16	6.407E-17	15	62
5	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	Pubmed	1.961E-21	1.851E-17	2.099E-16	9.256E-17	47	1744

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9: Interaction [\[Display Chart\]](#) 217 input genes in category / 9028 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:CCR1	CCR1 interactions	2.773E-24	2.504E-20	2.425E-19	2.504E-20	36	360
2	int:SSUH2	SSUH2 interactions	6.728E-22	3.037E-18	2.941E-17	6.074E-18	27	199
3	int:C18orf21	C18orf21 interactions	3.046E-21	9.166E-18	8.877E-17	2.750E-17	24	151
4	int:OR2A4	OR2A4 interactions	2.225E-20	5.022E-17	4.864E-16	2.009E-16	23	145
5	int:PPP2R2B	PPP2R2B interactions	5.751E-20	1.038E-16	1.006E-15	5.192E-16	27	235

[Show 45 more annotations](#)**10: Cytoband** [\[Display Chart\]](#) 221 input genes in category / 173 annotations before applied cutoff / 33040 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1q21-q22	1q21-q22	7.681E-9	1.329E-6	7.618E-6	1.329E-6	6	23
2	1q21	1q21	1.862E-7	1.611E-5	9.236E-5	3.222E-5	8	91
3	12q13.13	12q13.13	8.820E-5	5.086E-3	2.916E-2	1.526E-2	5	67
4	18q12.1	18q12.1	6.851E-4	2.963E-2	1.699E-1	1.185E-1	3	26

11: Transcription Factor Binding Site [\[Display Chart\]](#) 211 input genes in category / 850 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	8.478E-15	7.206E-12	5.277E-11	7.206E-12	35	918
2	TATAAA V\$TATA 01	TATAAA V\$TATA 01	TFBS	7.940E-11	3.374E-8	2.471E-7	6.749E-8	32	1070
3	CAGGTG V\$E12 Q6	CAGGTG V\$E12 Q6	TFBS	4.693E-7	1.145E-4	8.386E-4	3.989E-4	37	1950
4	M29981	GREB1 TARGET GENES	MSigDB	5.389E-7	1.145E-4	8.386E-4	4.580E-4	24	954
5	M29941	DLX2 TARGET GENES	MSigDB	3.435E-6	5.839E-4	4.276E-3	2.920E-3	12	290

[Show 10 more annotations](#)**12: Gene Family** [\[Display Chart\]](#) 157 input genes in category / 104 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	1.803E-8	9.425E-8	1.803E-8	6	11
2	648 Mucins	genenames.org	8.416E-7	2.917E-5	1.525E-4	8.752E-5	5	21
3	459 S100 calcium binding proteins EF-hand domain containing	genenames.org	8.416E-7	2.917E-5	1.525E-4	8.752E-5	5	21
4	609 Keratins, type II	genenames.org	3.201E-6	8.049E-5	4.207E-4	3.329E-4	5	27
5	608 Keratins, type I	genenames.org	3.870E-6	8.049E-5	4.207E-4	4.025E-4	5	28

[Show 11 more annotations](#)**13: Coexpression** [\[Display Chart\]](#) 222 input genes in category / 8464 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)	5.737E-47	4.856E-43	4.672E-42	4.856E-43	31	67
2	20421987-TableS4 Human Lung Hou10 518genes	GeneSigDB	1.736E-43	7.346E-40	7.068E-39	1.469E-39	49	380
3	20421987-TableS5 Human Lung Hou10 75genes	GeneSigDB	1.257E-41	3.546E-38	3.411E-37	1.064E-37	27	56
4	M10702 JAEGER METASTASIS DN	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	4.346E-40	7.571E-37	7.284E-36	3.678E-36	41	259

5	M40004	BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	4.472E-40	7.571E-37	7.284E-36	3.785E-36	34	140
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14: Coexpression Atlas [\[Display Chart\]](#) 222 input genes in category / 3320 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	2.388E-67	7.930E-64	6.887E-63	7.930E-64	61	247
2	PCBC ctl BronchioEpithel 500	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500	PCBC	4.662E-65	7.740E-62	6.722E-61	1.548E-61	74	496
3	PCBC ctl BronchioEpithel 1000	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000	PCBC	2.924E-56	3.236E-53	2.811E-52	9.709E-53	86	990
4	PCBC ctl BronchioEpithel 100	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100	PCBC	3.406E-52	2.827E-49	2.455E-48	1.131E-48	39	98
5	PCBC ctl SmallAirwayEpithel 500	Progenitor-Cell-Biology-Consortium reference SmallAirwayEpithel top-relative-expression-ranked 500	PCBC	5.124E-48	3.402E-45	2.955E-44	1.701E-44	61	493

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15: ToppCell Atlas [\[Display Chart\]](#) 222 input genes in category / 22098 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	3.836E-107	8.477E-103	8.969E-102	8.477E-103	65	172
2	3188c7bd225cbcf46a21e2fb784336cdd9665995	TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	8.204E-89	4.532E-85	4.795E-84	1.813E-84	58	190
3	e2b26a03c6ab24d9b0f4150c47597be37767d86e	TCGA-Skin-Primary Tumor TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	8.204E-89	4.532E-85	4.795E-84	1.813E-84	58	190
4	01fb45add4661bc86cd0a34fac35177907152dbb	TCGA-Skin-Primary Tumor-Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	8.204E-89	4.532E-85	4.795E-84	1.813E-84	58	190
5	6a12b802cb181f979ebc72674f3626fb855024e3	TCGA-Stomach-Primary Tumor-Stomach Adenocarcinoma-Stomach Adenocarcinoma - NOS-4 TCGA-Stomach / Sample Type by Project: Shred V9	TCGA OncoMap	7.789E-85	3.443E-81	3.642E-80	1.721E-80	54	163

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16: Computational [\[Display Chart\]](#) 143 input genes in category / 346 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
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1	M4992 MODULE 297	Genes in the cancer module 297.	MSigDb: C4 - CM: Cancer Modules (v7.2)	6.531E-23	1.130E-20	7.260E-20	2.260E-20	22	80
2	M9185 MODULE 357	Intermediate filaments and keratins.	MSigDb: C4 - CM: Cancer Modules (v7.2)	6.531E-23	1.130E-20	7.260E-20	2.260E-20	22	80
3	M2266 GNF2 SPRR1B	Neighborhood of SPRR1B	MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2)	1.336E-20	1.541E-18	9.899E-18	4.622E-18	14	24
4	M18170 MODULE 154	Intermediate filaments.	MSigDb: C4 - CM: Cancer Modules (v7.2)	3.753E-19	3.246E-17	2.086E-16	1.298E-16	19	75
5	M18849 MODULE 153	Genes in the cancer module 153.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.894E-14	1.088E-12	6.992E-12	6.554E-12	12	34

[Show 15 more annotations](#)
17: MicroRNA [\[Display Chart\]](#) 223 input genes in category / 8136 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-3120:mirSVR highEffect	hsa-miR-3120:mirSVR nonconserved highEffect-0.5	MicroRNA.org	9.690E-11	5.927E-7	5.678E-6	7.884E-7	30	1962
2	hsa-miR-26b-5p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	1.535E-10	5.927E-7	5.678E-6	1.249E-6	29	1873
3	hsa-miR-1251:mirSVR lowEffect	hsa-miR-1251:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	2.545E-10	5.927E-7	5.678E-6	2.071E-6	22	1093
4	hsa-miR-30c:mirSVR highEffect	hsa-miR-30c:mirSVR conserved highEffect-0.5	MicroRNA.org	3.529E-10	5.927E-7	5.678E-6	2.871E-6	29	1942
5	hsa-miR-558:mirSVR lowEffect	hsa-miR-558:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	4.786E-10	5.927E-7	5.678E-6	3.894E-6	26	1591

[Show 45 more annotations](#)
18: Drug [\[Display Chart\]](#) 222 input genes in category / 21168 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:C002202	4-oxoretinoic acid	CTD	1.308E-19	2.769E-15	2.918E-14	2.769E-15	20	115
2	ctd:D004054	Diethylstilbestrol	CTD	1.454E-18	1.539E-14	1.622E-13	3.078E-14	52	1304
3	ctd:C103303	alitretinoin	CTD	2.570E-16	1.814E-12	1.911E-11	5.441E-12	25	300
4	ctd:D012906	Smoke	CTD	4.966E-16	2.628E-12	2.770E-11	1.051E-11	41	937
5	ctd:D019324	beta-Naphthoflavone	CTD	1.316E-12	5.571E-9	5.870E-8	2.785E-8	34	829

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19: Disease [\[Display Chart\]](#) 210 input genes in category / 5763 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	C0004763	Barrett Esophagus	DisGeNET BeFree	3.654E-12	2.106E-8	1.945E-7	2.106E-8	26	450
2	C0334037	Intestinal metaplasia	DisGeNET BeFree	1.207E-11	3.477E-8	3.212E-7	6.954E-8	20	266
3	C1832097	EPIDERMAL DIFFERENTIATION COMPLEX	DisGeNET BeFree	2.151E-10	4.132E-7	3.817E-6	1.240E-6	9	38
4	C1608408	Malignant transformation	DisGeNET BeFree	3.939E-10	5.675E-7	5.241E-6	2.270E-6	36	1027
5	C0870082	Hyperkeratosis	DisGeNET BeFree	6.070E-10	6.997E-7	6.463E-6	3.498E-6	12	97

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