

# Results

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### 1: GO: Molecular Function [\[Display Chart\]](#) 185 input genes in category / 542 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 |        | 6.910E-12 | 3.745E-9 | 2.574E-8 | 3.745E-9   | 10               | 44                  |
| 2 | GO:0005198 | structural molecule activity             |        | 8.589E-10 | 2.327E-7 | 1.600E-6 | 4.655E-7   | 30               | 892                 |
| 3 | GO:0005200 | structural constituent of cytoskeleton   |        | 3.122E-9  | 4.493E-7 | 3.088E-6 | 1.692E-6   | 12               | 130                 |
| 4 | GO:0005509 | calcium ion binding                      |        | 3.316E-9  | 4.493E-7 | 3.088E-6 | 1.797E-6   | 27               | 777                 |
| 5 | GO:0050786 | RAGE receptor binding                    |        | 1.803E-7  | 1.955E-5 | 1.344E-4 | 9.775E-5   | 5                | 15                  |

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### 2: GO: Biological Process [\[Display Chart\]](#) 185 input genes in category / 3901 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:0031424 | keratinization                 |        | 5.523E-26 | 2.155E-22 | 1.906E-21 | 2.155E-22  | 22               | 89                  |
| 2 | GO:0030216 | keratinocyte differentiation   |        | 1.760E-24 | 3.432E-21 | 3.036E-20 | 6.864E-21  | 27               | 195                 |
| 3 | GO:0009913 | epidermal cell differentiation |        | 1.548E-20 | 1.841E-17 | 1.629E-16 | 6.039E-17  | 29               | 331                 |
| 4 | GO:0008544 | epidermis development          |        | 1.888E-20 | 1.841E-17 | 1.629E-16 | 7.365E-17  | 34               | 500                 |
| 5 | GO:0043588 | skin development               |        | 1.054E-19 | 8.225E-17 | 7.276E-16 | 4.113E-16  | 30               | 387                 |

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### 3: GO: Cellular Component [\[Display Chart\]](#) 187 input genes in category / 368 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 |        | 6.393E-40 | 2.353E-37 | 1.526E-36 | 2.353E-37  | 28               | 69                  |
| 2 | GO:0005911 | cell-cell junction |        | 1.140E-10 | 2.097E-8  | 1.360E-7  | 4.194E-8   | 25               | 590                 |
| 3 | GO:0070161 | anchoring junction |        | 3.608E-8  | 4.426E-6  | 2.871E-5  | 1.328E-5   | 35               | 1419                |
| 4 | GO:0030057 | desmosome          |        | 2.869E-7  | 2.639E-5  | 1.712E-4  | 1.056E-4   | 6                | 31                  |
| 5 | GO:0005921 | gap junction       |        | 8.663E-7  | 6.376E-5  | 4.136E-4  | 3.188E-4   | 6                | 37                  |

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### 4: Human Phenotype [\[Display Chart\]](#) 69 input genes in category / 2842 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:0001035 | Abnormality of keratinization |        | 3.222E-17 | 9.157E-14 | 7.810E-13 | 9.157E-14  | 26               | 250                 |
| 2 | HP:0000982 | Palmoplantar keratoderma      |        | 1.391E-16 | 1.585E-13 | 1.352E-12 | 3.952E-13  | 21               | 149                 |
| 3 | HP:0000962 | Hyperkeratosis                |        | 1.673E-16 | 1.585E-13 | 1.352E-12 | 4.754E-13  | 25               | 241                 |
| 4 | HP:0000972 | Palmoplantar hyperkeratosis   |        | 4.188E-16 | 2.587E-13 | 2.207E-12 | 1.190E-12  | 21               | 157                 |
| 5 | HP:0007556 | Plantar hyperkeratosis        |        | 5.462E-16 | 2.587E-13 | 2.207E-12 | 1.552E-12  | 21               | 159                 |

[Show 45 more annotations](#)**5: Mouse Phenotype** [\[Display Chart\]](#) 144 input genes in category / 2955 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:0005501 | abnormal skin physiology                      | 1.461E-10 | 4.317E-7 | 3.699E-6 | 4.317E-7   | 19               | 270                 |
| 2  | MP:0001216 | abnormal epidermal layer morphology           | 7.709E-10 | 1.139E-6 | 9.759E-6 | 2.278E-6   | 18               | 264                 |
| 3  | MP:0001240 | abnormal epidermis stratum corneum morphology | 1.813E-9  | 1.786E-6 | 1.530E-5 | 5.358E-6   | 13               | 129                 |
| 4  | MP:0003453 | abnormal keratinocyte physiology              | 1.370E-7  | 1.012E-4 | 8.671E-4 | 4.048E-4   | 9                | 75                  |
| 5  | MP:0002796 | impaired skin barrier function                | 3.938E-7  | 2.327E-4 | 1.994E-3 | 1.164E-3   | 8                | 62                  |

[Show 24 more annotations](#)**6: Domain** [\[Display Chart\]](#) 187 input genes in category / 1049 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 | PS00303   | S100 CABP       | <a href="#">PROSITE</a>  | 6.755E-9 | 1.874E-6 | 1.412E-5 | 7.086E-6   | 7                | 27                  |
| 2 | PF01023   | S 100           | <a href="#">Pfam</a>     | 6.755E-9 | 1.874E-6 | 1.412E-5 | 7.086E-6   | 7                | 27                  |
| 3 | IPR013787 | S100 Ca-bd sub  | <a href="#">InterPro</a> | 8.931E-9 | 1.874E-6 | 1.412E-5 | 9.369E-6   | 7                | 28                  |
| 4 | IPR001751 | S100/CaBP-9k CS | <a href="#">InterPro</a> | 8.931E-9 | 1.874E-6 | 1.412E-5 | 9.369E-6   | 7                | 28                  |
| 5 | SM01394   | S 100           | <a href="#">SMART</a>    | 8.931E-9 | 1.874E-6 | 1.412E-5 | 9.369E-6   | 7                | 28                  |

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 151 input genes in category / 1566 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 | 1457791 | Formation of the cornified envelope                                                          | BioSystems: REACTOME         | 4.338E-20 | 6.793E-17 | 5.389E-16 | 6.793E-17  | 18               | 71                  |
| 2 | 1457790 | Keratinization                                                                               | BioSystems: REACTOME         | 8.347E-19 | 6.536E-16 | 5.185E-15 | 1.307E-15  | 25               | 214                 |
| 3 | M5889   | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | MSigDB C2 BIOCARTEA (v7.5.1) | 2.064E-11 | 1.077E-8  | 8.547E-8  | 3.232E-8   | 38               | 1026                |
| 4 | 1270302 | Developmental Biology                                                                        | BioSystems: REACTOME         | 3.571E-10 | 1.398E-7  | 1.109E-6  | 5.592E-7   | 37               | 1078                |
| 5 | 1457778 | Metal sequestration by antimicrobial proteins                                                | BioSystems: REACTOME         | 9.360E-10 | 2.932E-7  | 2.326E-6  | 1.466E-6   | 5                | 6                   |

[Show 33 more annotations](#)**8: Pubmed** [\[Display Chart\]](#) 191 input genes in category / 40778 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 | 3.977E-29 | 1.622E-24 | 1.815E-23 | 1.622E-24  | 21               | 107                 |
| 2 | 34905516 | Translational implications of Th17-skewed inflammation due to genetic deficiency of a cadherin stress sensor.               | Pubmed | 1.154E-23 | 2.352E-19 | 2.633E-18 | 4.705E-19  | 13               | 30                  |
| 3 | 26644517 | A keratin scaffold regulates epidermal barrier formation, mitochondrial lipid composition, and activity.                    | Pubmed | 9.937E-21 | 1.351E-16 | 1.512E-15 | 4.052E-16  | 14               | 62                  |
| 4 | 31220272 | Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma.                 | Pubmed | 4.455E-19 | 4.541E-15 | 5.083E-14 | 1.817E-14  | 13               | 60                  |
| 5 | 28973166 | Activated Braf induces esophageal dilation and gastric epithelial hyperplasia in mice.                                      | Pubmed | 6.529E-19 | 5.325E-15 | 5.960E-14 | 2.662E-14  | 12               | 45                  |

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**9: Interaction [Display Chart]** 186 input genes in category / 7329 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:SSUH2    | SSUH2 interactions    | 3.849E-36 | 2.821E-32 | 2.673E-31 | 2.821E-32  | 36               | 199                 |
| 2  | int:CCR1     | CCR1 interactions     | 1.011E-32 | 3.703E-29 | 3.509E-28 | 7.406E-29  | 41               | 360                 |
| 3  | int:C18orf21 | C18orf21 interactions | 1.820E-31 | 4.446E-28 | 4.213E-27 | 1.334E-27  | 30               | 151                 |
| 4  | int:OR2A4    | OR2A4 interactions    | 1.590E-30 | 2.913E-27 | 2.761E-26 | 1.165E-26  | 29               | 145                 |
| 5  | int:PPP2R2B  | PPP2R2B interactions  | 9.262E-27 | 1.358E-23 | 1.287E-22 | 6.788E-23  | 31               | 235                 |

[Show 45 more annotations](#)**10: Cytoband [Display Chart]** 190 input genes in category / 154 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 | 4.221E-11 | 6.500E-9 | 3.651E-8 | 6.500E-9   | 7                | 23                  |
| 2  | 1q21     | 1q21     | 5.832E-8  | 4.491E-6 | 2.523E-5 | 8.982E-6   | 8                | 91                  |
| 3  | 18q12.1  | 18q12.1  | 1.435E-5  | 7.364E-4 | 4.137E-3 | 2.209E-3   | 4                | 26                  |
| 4  | 2q14     | 2q14     | 2.985E-5  | 1.149E-3 | 6.457E-3 | 4.598E-3   | 3                | 11                  |
| 5  | 12q13.13 | 12q13.13 | 6.120E-4  | 1.885E-2 | 1.059E-1 | 9.425E-2   | 4                | 67                  |

[Show 1 more annotation](#)**11: Transcription Factor Binding Site [Display Chart]** 175 input genes in category / 798 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   | 2.880E-13 | 1.821E-10 | 1.322E-9 | 2.298E-10  | 30               | 918                 |
| 2 | TATAAA V\$TATA 01   | TATAAA V\$TATA 01   | TFBS   | 4.565E-13 | 1.821E-10 | 1.322E-9 | 3.643E-10  | 32               | 1070                |
| 3 | V\$AP1 Q2 01        | V\$AP1 Q2 01        | TFBS   | 3.201E-6  | 8.514E-4  | 6.181E-3 | 2.554E-3   | 10               | 233                 |
| 4 | GGGTGGRR V\$PAX4 03 | GGGTGGRR V\$PAX4 03 | TFBS   | 6.586E-6  | 1.314E-3  | 9.539E-3 | 5.255E-3   | 21               | 1068                |
| 5 | CAGGTG V\$E12 Q6    | CAGGTG V\$E12 Q6    | TFBS   | 8.766E-6  | 1.399E-3  | 1.016E-2 | 6.995E-3   | 30               | 1950                |

[Show 18 more annotations](#)**12: Gene Family [Display Chart]** 147 input genes in category / 102 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 | 1.163E-10 | 1.095E-8 | 5.702E-8 | 1.187E-8   | 6                | 11                  |
| 2  | 459 S100 calcium binding proteins EF-hand domain containing | genenames.org | 2.147E-10 | 1.095E-8 | 5.702E-8 | 2.190E-8   | 7                | 21                  |
| 3  | 1188 Desmosomal cadherins                                   | genenames.org | 1.439E-7  | 4.894E-6 | 2.548E-5 | 1.468E-5   | 4                | 7                   |
| 4  | 314 Gap junction proteins                                   | genenames.org | 7.809E-7  | 1.991E-5 | 1.037E-4 | 7.965E-5   | 5                | 22                  |
| 5  | 616 Kallikreins                                             | genenames.org | 7.070E-6  | 1.442E-4 | 7.510E-4 | 7.211E-4   | 4                | 16                  |

[Show 12 more annotations](#)**13: Coexpression [Display Chart]** 190 input genes in category / 8018 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  | M10702 JAEGER METASTASIS DN                              | MSigDB C2: CGP Curated Gene Sets (v7.5.1) | 4.846E-54 | 3.886E-50 | 3.717E-49 | 3.886E-50  | 48               | 259                 |
| 2  | M4306 ONDER CDH1 TARGETS 2 DN                            | MSigDB C2: CGP Curated Gene Sets (v7.5.1) | 5.360E-52 | 2.149E-48 | 2.056E-47 | 4.298E-48  | 56               | 472                 |
| 3  | M40004 BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS       | MSigDB C8: Cell Type Signatures (v7.5.1)  | 2.877E-44 | 7.690E-41 | 7.356E-40 | 2.307E-40  | 35               | 140                 |
| 4  | M40299 DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS | MSigDB C8: Cell Type Signatures (v7.5.1)  | 6.759E-43 | 1.355E-39 | 1.296E-38 | 5.419E-39  | 28               | 67                  |

|   |        |                                                |                                          |           |           |           |           |    |     |
|---|--------|------------------------------------------------|------------------------------------------|-----------|-----------|-----------|-----------|----|-----|
| 5 | M40122 | DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS | MSigDB C8: Cell Type Signatures (v7.5.1) | 2.994E-40 | 4.800E-37 | 4.592E-36 | 2.400E-36 | 32 | 130 |
|---|--------|------------------------------------------------|------------------------------------------|-----------|-----------|-----------|-----------|----|-----|

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**14: Coexpression Atlas** [Display Chart] 188 input genes in category / 3236 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 | PCBC ctl BronchioEpithel 500     | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500     | PCBC                | 3.734E-82 | 1.208E-78 | 1.046E-77 | 1.208E-78  | 81               | 496                 |
| 2 | esophagus                        | esophagus                                                                                           | Human Protein Atlas | 2.949E-81 | 4.772E-78 | 4.132E-77 | 9.543E-78  | 66               | 247                 |
| 3 | PCBC ctl BronchioEpithel 1000    | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000    | PCBC                | 6.874E-77 | 7.415E-74 | 6.421E-73 | 2.224E-73  | 96               | 990                 |
| 4 | PCBC ctl BronchioEpithel 100     | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100     | PCBC                | 1.430E-69 | 1.157E-66 | 1.001E-65 | 4.626E-66  | 46               | 98                  |
| 5 | PCBC ctl SmallAirwayEpithel 1000 | Progenitor-Cell-Biology-Consortium reference SmallAirwayEpithel top-relative-expression-ranked 1000 | PCBC                | 9.043E-64 | 5.853E-61 | 5.068E-60 | 2.926E-60  | 86               | 987                 |

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**15: ToppCell Atlas** [Display Chart] 190 input genes in category / 21394 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 | 7.599E-122 | 1.626E-117 | 1.715E-116 | 1.626E-117 | 69               | 172                 |
| 2 | 3188c7bd225cbcf46a21e2fb784336cdd9665995 | TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma TCGA-Skin / Sample Type by Project: Shred V9              | TCGA OncoMap | 3.301E-111 | 1.766E-107 | 1.862E-106 | 7.063E-107 | 66               | 190                 |
| 3 | e2b26a03c6ab24d9b0f4150c47597be37767d86e | TCGA-Skin-Primary Tumor TCGA-Skin / Sample Type by Project: Shred V9                                               | TCGA OncoMap | 3.301E-111 | 1.766E-107 | 1.862E-106 | 7.063E-107 | 66               | 190                 |
| 4 | 01fb45add4661bc86cd0a34fac35177907152dbb | TCGA-Skin-Primary Tumor-Melanoma TCGA-Skin / Sample Type by Project: Shred V9                                      | TCGA OncoMap | 3.301E-111 | 1.766E-107 | 1.862E-106 | 7.063E-107 | 66               | 190                 |
| 5 | a0c7d08469c513cecf87777c19876884f1511570 | TCGA-Lung-Primary Tumor-Lung Carcinoma-Lung Squamous Cell Carcinoma-5 TCGA-Lung / Sample Type by Project: Shred V9 | TCGA OncoMap | 1.722E-95  | 7.369E-92  | 7.773E-91  | 3.684E-91  | 58               | 177                 |

Show 45 more annotations

**16: Computational** [Display Chart] 132 input genes in category / 377 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 | Genes in the cancer | MSigDb: C4 - CM: Cancer Modules | 7.616E- | 1.436E- | 9.347E- | 2.871E-24  | 24               | 80                  |

|   |                       |                                         |                                                      |               |               |               |           |    |    |
|---|-----------------------|-----------------------------------------|------------------------------------------------------|---------------|---------------|---------------|-----------|----|----|
|   | MODULE 297            | module 297.                             | (v7.2)                                               | 27            | 24            | 24            |           |    |    |
| 2 | M9185<br>MODULE 357   | Intermediate filaments<br>and keratins. | MSigDb: C4 - CM: Cancer Modules<br>(v7.2)            | 7.616E-<br>27 | 1.436E-<br>24 | 9.347E-<br>24 | 2.871E-24 | 24 | 80 |
| 3 | M18170<br>MODULE 154  | Intermediate filaments.                 | MSigDb: C4 - CM: Cancer Modules<br>(v7.2)            | 2.065E-<br>24 | 2.595E-<br>22 | 1.690E-<br>21 | 7.785E-22 | 22 | 75 |
| 4 | M9365 GN2<br>SERPINB5 | Neighborhood of<br>SERPINB5             | MSigDb: C4 - CGN: Cancer Gene<br>Neighborhood (v7.2) | 9.069E-<br>22 | 8.547E-<br>20 | 5.565E-<br>19 | 3.419E-19 | 15 | 28 |
| 5 | M2266 GN2<br>SPRR1B   | Neighborhood of<br>SPRR1B               | MSigDb: C4 - CGN: Cancer Gene<br>Neighborhood (v7.2) | 4.159E-<br>21 | 3.136E-<br>19 | 2.042E-<br>18 | 1.568E-18 | 14 | 24 |

Show 32 more annotations

**17: MicroRNA** [Display Chart] 191 input genes in category / 7996 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-325-3p:TargetScan     | TargetScan   | 2.549E-12 | 2.038E-8 | 1.949E-7 | 2.038E-8   | 28               | 1722                |
| 2  | hsa-miR-1293:mirSVR lowEffect | MicroRNA.org | 5.132E-12 | 2.052E-8 | 1.962E-7 | 4.103E-8   | 25               | 1392                |
| 3  | mmu-miR-30b-5p                | MirDB        | 3.412E-11 | 3.595E-8 | 3.439E-7 | 2.728E-7   | 21               | 1039                |
| 4  | mmu-miR-30c-5p                | MirDB        | 3.412E-11 | 3.595E-8 | 3.439E-7 | 2.728E-7   | 21               | 1039                |
| 5  | mmu-miR-384-5p                | MirDB        | 3.534E-11 | 3.595E-8 | 3.439E-7 | 2.826E-7   | 21               | 1041                |

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**18: Drug** [Display Chart] 189 input genes in category / 19790 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:D012906  | Smoke                     | CTD    | 1.705E-19 | 3.374E-15 | 3.533E-14 | 3.374E-15  | 42               | 937                 |
| 2 | ctd:D004054  | Diethylstilbestrol        | CTD    | 2.850E-17 | 2.820E-13 | 2.953E-12 | 5.640E-13  | 46               | 1304                |
| 3 | ctd:D015073  | 2-Acetylaminofluorene     | CTD    | 7.470E-15 | 4.928E-11 | 5.159E-10 | 1.478E-10  | 25               | 409                 |
| 4 | CID000005538 | 9cRA                      | Stitch | 6.040E-14 | 2.988E-10 | 3.129E-9  | 1.195E-9   | 48               | 1735                |
| 5 | CID000004792 | phorbol acetate myristate | Stitch | 2.230E-13 | 8.827E-10 | 9.242E-9  | 4.414E-9   | 42               | 1399                |

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**19: Disease** [Display Chart] 176 input genes in category / 5619 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 | C0037274 | Dermatologic disorders    | DisGeNET<br>BeFree | 3.857E-19 | 2.167E-15 | 1.996E-14 | 2.167E-15  | 34               | 544                 |
| 2 | C0037277 | Skin Diseases, Genetic    | DisGeNET<br>BeFree | 2.453E-15 | 6.891E-12 | 6.348E-11 | 1.378E-11  | 13               | 56                  |
| 3 | C0870082 | Hyperkeratosis            | DisGeNET<br>BeFree | 1.042E-14 | 1.585E-11 | 1.460E-10 | 5.857E-11  | 15               | 97                  |
| 4 | C4551675 | Keratoderma, Palmoplantar | DisGeNET<br>BeFree | 1.128E-14 | 1.585E-11 | 1.460E-10 | 6.340E-11  | 12               | 48                  |
| 5 | C0033860 | Psoriasis                 | DisGeNET<br>BeFree | 1.593E-13 | 1.565E-10 | 1.442E-9  | 8.952E-10  | 39               | 1105                |

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