# Results

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## Input Parameters [Show Detail]

## Training Results [Expand All] [Download All] [Sparse Matrix] Display pValues and Scores as  Scientific (4 significant digits) ▾  Table row limit  50 ▾

### 1: GO: Molecular Function [Display Chart] 201 input genes in category / 605 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 | | 4.699E-13 | 2.843E-10 | 1.985E-9 | 2.843E-10 | 11 | 44 |
| 2 | GO:0005200 | structural constituent of cytoskeleton | | 6.906E-10 | 2.089E-7 | 1.459E-6 | 4.178E-7 | 13 | 130 |
| 3 | GO:0005509 | calcium ion binding | | 4.934E-9 | 9.737E-7 | 6.800E-6 | 2.985E-6 | 28 | 777 |
| 4 | GO:0005198 | structural molecule activity | | 6.438E-9 | 9.737E-7 | 6.800E-6 | 3.895E-6 | 30 | 892 |
| 5 | GO:0004252 | serine-type endopeptidase activity | | 7.879E-8 | 8.225E-6 | 5.744E-5 | 4.767E-5 | 16 | 303 |

**Show 30 more annotations**

### 2: GO: Biological Process [Display Chart] 201 input genes in category / 4435 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:0008544 | epidermis development | | 1.012E-31 | 4.489E-28 | 4.029E-27 | 4.489E-28 | 46 | 500 |
| 2 | GO:0043588 | skin development | | 2.344E-28 | 5.197E-25 | 4.664E-24 | 1.039E-24 | 39 | 387 |
| 3 | GO:0030216 | keratinocyte differentiation | | 2.005E-27 | 2.964E-24 | 2.660E-23 | 8.892E-24 | 30 | 195 |
| 4 | GO:0009913 | epidermal cell differentiation | | 3.483E-26 | 3.861E-23 | 3.465E-22 | 1.545E-22 | 35 | 331 |
| 5 | GO:0031424 | keratinization | | 3.628E-25 | 3.218E-22 | 2.888E-21 | 1.609E-21 | 22 | 89 |

**Show 45 more annotations**

### 3: GO: Cellular Component [Display Chart] 202 input genes in category / 412 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 | | 8.421E-43 | 3.470E-40 | 2.290E-39 | 3.470E-40 | 30 | 69 |
| 2 | GO:0005911 | cell-cell junction | | 3.551E-12 | 7.316E-10 | 4.828E-9 | 1.463E-9 | 28 | 590 |
| 3 | GO:0070161 | anchoring junction | | 5.250E-11 | 7.210E-9 | 4.758E-8 | 2.163E-8 | 42 | 1419 |
| 4 | GO:0097209 | epidermal lamellar body | | 8.501E-9 | 8.756E-7 | 5.779E-6 | 3.502E-6 | 4 | 4 |
| 5 | GO:0005912 | adherens junction | | 9.818E-8 | 8.090E-6 | 5.339E-5 | 4.045E-5 | 13 | 204 |

**Show 41 more annotations**

### 4: Human Phenotype [Display Chart] 88 input genes in category / 3062 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 | | 3.050E-17 | 9.340E-14 | 8.037E-13 | 9.340E-14 | 29 | 250 |
| 2 | HP:0000962 | Hyperkeratosis | | 1.224E-15 | 1.874E-12 | 1.612E-11 | 3.747E-12 | 27 | 241 |
| 3 | HP:0000982 | Palmoplantar keratoderma | | 2.566E-15 | 2.619E-12 | 2.253E-11 | 7.856E-12 | 22 | 149 |
| 4 | HP:0000972 | Palmoplantar hyperkeratosis | | 7.980E-15 | 4.587E-12 | 3.947E-11 | 2.444E-11 | 22 | 157 |
| 5 | HP:0011368 | Epidermal thickening | | 8.514E-15 | 4.587E-12 | 3.947E-11 | 2.607E-11 | 31 | 358 |

**Show 45 more annotations**

### 5: Mouse Phenotype [Display Chart] 155 input genes in category / 3232 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:0001216 | abnormal epidermal layer morphology | | 7.653E-14 | 2.473E-10 | 2.142E-9 | 2.473E-10 | 23 | 264 |
| 2 | MP:0001240 | abnormal epidermis stratum corneum morphology | | 3.498E-11 | 5.652E-8 | 4.894E-7 | 1.130E-7 | 15 | 129 |
| 3 | MP:0005501 | abnormal skin physiology | | 5.281E-10 | 5.690E-7 | 4.926E-6 | 1.707E-6 | 19 | 270 |
| 4 | MP:0002796 | impaired skin barrier function | | 2.862E-9 | 2.312E-6 | 2.002E-5 | 9.248E-6 | 10 | 62 |
| 5 | MP:0005023 | abnormal wound healing | | 6.631E-9 | 4.286E-6 | 3.711E-5 | 2.143E-5 | 15 | 187 |

**Show 45 more annotations**

## 6: Domain [Display Chart] 201 input genes in category / 1135 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 | PF01023 | S 100 | Pfam | 6.411E-12 | 3.541E-9 | 2.696E-8 | 7.277E-9 | 9 | 27 |
| 2 | IPR013787 | S100 Ca-bd sub | InterPro | 9.361E-12 | 3.541E-9 | 2.696E-8 | 1.062E-8 | 9 | 28 |
| 3 | SM01394 | S 100 | SMART | 9.361E-12 | 3.541E-9 | 2.696E-8 | 1.062E-8 | 9 | 28 |
| 4 | PS00303 | S100 CABP | PROSITE | 2.914E-10 | 8.270E-8 | 6.295E-7 | 3.308E-7 | 8 | 27 |
| 5 | IPR001751 | S100/CaBP-9k CS | InterPro | 4.043E-10 | 9.177E-8 | 6.986E-7 | 4.589E-7 | 8 | 28 |

**Show 45 more annotations**

## 7: Pathway [Display Chart] 168 input genes in category / 1663 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 | 2.793E-22 | 2.756E-19 | 2.203E-18 | 4.645E-19 | 20 | 71 |
| 2 | 1457790 | Keratinization | BioSystems: REACTOME | 3.314E-22 | 2.756E-19 | 2.203E-18 | 5.512E-19 | 29 | 214 |
| 3 | 1270302 | Developmental Biology | BioSystems: REACTOME | 1.142E-11 | 6.332E-9 | 5.062E-8 | 1.900E-8 | 42 | 1078 |
| 4 | M5889 | Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins | MSigDB C2 BIOCARTA (v7.5.1) | 3.940E-11 | 1.638E-8 | 1.309E-7 | 6.552E-8 | 40 | 1026 |
| 5 | M5885 | Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors | MSigDB C2 BIOCARTA (v7.5.1) | 5.825E-10 | 1.937E-7 | 1.549E-6 | 9.687E-7 | 32 | 751 |

**Show 35 more annotations**

## 8: Pubmed [Display Chart] 205 input genes in category / 44618 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 | 4.556E-32 | 2.033E-27 | 2.294E-26 | 2.033E-27 | 23 | 107 |
| 2 | 26644517 | A keratin scaffold regulates epidermal barrier formation, mitochondrial lipid composition, and activity. | Pubmed | 5.382E-26 | 1.201E-21 | 1.355E-20 | 2.401E-21 | 17 | 62 |
| 3 | 31220272 | Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma. | Pubmed | 2.157E-22 | 3.208E-18 | 3.620E-17 | 9.624E-18 | 15 | 60 |
| 4 | 34905516 | Translational implications of Th17-skewed inflammation due to genetic deficiency of a cadherin stress sensor. | Pubmed | 4.945E-21 | 5.516E-17 | 6.224E-16 | 2.206E-16 | 12 | 30 |
| 5 | 19199708 | Proteomic analysis of human parotid gland exosomes by multidimensional protein identification technology (MudPIT). | Pubmed | 1.563E-20 | 1.266E-16 | 1.428E-15 | 6.972E-16 | 25 | 417 |

**Show 45 more annotations**

## 9: Interaction [Display Chart] 199 input genes in category / 7894 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 | | 7.640E-43 | 6.031E-39 | 5.760E-38 | 6.031E-39 | 50 | 360 |
| 2 | int:SSUH2 | SSUH2 interactions | | 2.236E-39 | 8.827E-36 | 8.431E-35 | 1.765E-35 | 39 | 199 |
| 3 | int:OR2A4 | OR2A4 interactions | | 8.705E-39 | 2.291E-35 | 2.188E-34 | 6.872E-35 | 35 | 145 |

| 4 | int:PPP2R2B | PPP2R2B interactions | | 5.058E-35 | 9.983E-32 | 9.535E-31 | 3.993E-31 | 38 | 235 |
| 5 | int:C18orf21 | C18orf21 interactions | | 1.639E-33 | 2.587E-30 | 2.471E-29 | 1.293E-29 | 32 | 151 |

**Show 45 more annotations**

## 10: Cytoband [Display Chart] 204 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 | 1q21 | | 2.685E-10 | 4.135E-8 | 2.323E-7 | 4.135E-8 | 10 | 91 |
| 2 | 1q21-q22 | 1q21-q22 | | 4.760E-9 | 3.665E-7 | 2.059E-6 | 7.330E-7 | 6 | 23 |
| 3 | 18q12.1 | 18q12.1 | | 1.896E-5 | 9.735E-4 | 5.469E-3 | 2.920E-3 | 4 | 26 |
| 4 | 18q21.3 | 18q21.3 | | 3.690E-5 | 1.136E-3 | 6.384E-3 | 5.682E-3 | 3 | 11 |
| 5 | 2q14 | 2q14 | | 3.690E-5 | 1.136E-3 | 6.384E-3 | 5.682E-3 | 3 | 11 |

**Show 4 more annotations**

## 11: Transcription Factor Binding Site [Display Chart] 192 input genes in category / 766 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 | 3.427E-12 | 2.625E-9 | 1.895E-8 | 2.625E-9 | 30 | 918 |
| 2 | TATAAA V$TATA 01 | TATAAA V$TATA 01 | TFBS | 3.057E-11 | 1.171E-8 | 8.452E-8 | 2.341E-8 | 31 | 1070 |
| 3 | M30042 | KMT2D TARGET GENES | MSigDB | 3.186E-7 | 8.134E-5 | 5.872E-4 | 2.440E-4 | 21 | 801 |
| 4 | GGGTGGRR V$PAX4 03 | GGGTGGRR V$PAX4 03 | TFBS | 2.510E-6 | 4.806E-4 | 3.470E-3 | 1.923E-3 | 23 | 1068 |
| 5 | TTANTCA UNKNOWN | TTANTCA UNKNOWN | TFBS | 9.056E-6 | 1.387E-3 | 1.002E-2 | 6.937E-3 | 18 | 758 |

**Show 13 more annotations**

## 12: Gene Family [Display Chart] 156 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 | 459 | S100 calcium binding proteins\|EF-hand domain containing | genenames.org | 4.736E-12 | 5.162E-10 | 2.722E-9 | 5.162E-10 | 8 | 21 |
| 2 | 1353 | Small proline rich proteins | genenames.org | 1.668E-10 | 9.091E-9 | 4.794E-8 | 1.818E-8 | 6 | 11 |
| 3 | 616 | Kallikreins | genenames.org | 2.790E-9 | 1.014E-7 | 5.346E-7 | 3.041E-7 | 6 | 16 |
| 4 | 1188 | Desmosomal cadherins | genenames.org | 1.828E-7 | 4.981E-6 | 2.626E-5 | 1.992E-5 | 4 | 7 |
| 5 | 609 | Keratins, type II | genenames.org | 3.102E-6 | 6.763E-5 | 3.566E-4 | 3.382E-4 | 5 | 27 |

**Show 16 more annotations**

## 13: Coexpression [Display Chart] 204 input genes in category / 8142 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 | M40004 | BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS | MSigDB C8: Cell Type Signatures (v7.5.1) | 8.665E-71 | 7.055E-67 | 6.760E-66 | 7.055E-67 | 50 | 140 |
| 2 | M40122 | DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS | MSigDB C8: Cell Type Signatures (v7.5.1) | 3.990E-57 | 1.263E-53 | 1.210E-52 | 3.249E-53 | 42 | 130 |
| 3 | M4306 | ONDER CDH1 TARGETS 2 DN | MSigDB C2: CGP Curated Gene Sets (v7.5.1) | 4.653E-57 | 1.263E-53 | 1.210E-52 | 3.788E-53 | 61 | 472 |
| 4 | M10702 | JAEGER METASTASIS DN | MSigDB C2: CGP Curated Gene Sets (v7.5.1) | 1.401E-55 | 2.851E-52 | 2.732E-51 | 1.140E-51 | 50 | 259 |
| 5 | M40299 | DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS | MSigDB C8: Cell Type Signatures (v7.5.1) | 1.199E-54 | 1.952E-51 | 1.870E-50 | 9.759E-51 | 34 | 67 |

**Show 45 more annotations**

## 14: Coexpression Atlas [Display Chart] 204 input genes in category / 3315 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 | 1.171E-115 | 3.882E-112 | 3.371E-111 | 3.882E-112 | 86 | 247 |
| 2 | PCBC ctl BronchioEpithel 500 | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500 | PCBC | 4.020E-99 | 6.663E-96 | 5.786E-95 | 1.333E-95 | 94 | 496 |
| 3 | PCBC ctl BronchioEpithel 1000 | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000 | PCBC | 1.245E-91 | 1.375E-88 | 1.194E-87 | 4.126E-88 | 110 | 990 |
| 4 | PCBC ctl BronchioEpithel 100 | Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100 | PCBC | 2.468E-78 | 2.046E-75 | 1.776E-74 | 8.182E-75 | 51 | 98 |
| 5 | BM Top 100 - esophagus | BM Top 100 - esophagus | Body Map | 1.748E-73 | 1.159E-70 | 1.006E-69 | 5.795E-70 | 47 | 86 |

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## 15: ToppCell Atlas [Display Chart] 204 input genes in category / 22198 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 | 2.133E-143 | 4.734E-139 | 5.011E-138 | 4.734E-139 | 79 | 172 |
| 2 | 3188c7bd225cbcf46a21e2fb784336cdd9665995 | TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma\|TCGA-Skin / Sample Type by Project: Shred V9 | TCGA OncoMap | 6.040E-139 | 3.352E-135 | 3.548E-134 | 1.341E-134 | 79 | 190 |
| 3 | e2b26a03c6ab24d9b0f4150c47597be37767d86e | TCGA-Skin-Primary Tumor\|TCGA-Skin / Sample Type by Project: Shred V9 | TCGA OncoMap | 6.040E-139 | 3.352E-135 | 3.548E-134 | 1.341E-134 | 79 | 190 |
| 4 | 01fb45add4661bc86cd0a34fac35177907152dbb | TCGA-Skin-Primary Tumor-Melanoma\|TCGA-Skin / Sample Type by Project: Shred V9 | TCGA OncoMap | 6.040E-139 | 3.352E-135 | 3.548E-134 | 1.341E-134 | 79 | 190 |
| 5 | 03de28e1c963e99623e8b0e33bf2e8ef67dc3baa | Smart-seq2-tissue-resident (Smart-seq2)-myeloid-myeloid monocytic\|tissue-resident (Smart-seq2) / Per Platform+tissue group, by lineage subgroup, cell group, cell type | Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans. | 1.207E-116 | 5.358E-113 | 5.671E-112 | 2.679E-112 | 70 | 196 |

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## 16: Computational [Display Chart] 137 input genes in category / 365 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 | M2266 GNF2 SPRR1B | Neighborhood of SPRR1B | MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2) | 1.124E-29 | 4.101E-27 | 2.657E-26 | 4.101E-27 | 18 | 24 |
| 2 | M4992 MODULE 297 | Genes in the cancer module 297. | MSigDb: C4 - CM: Cancer Modules (v7.2) | 1.973E-26 | 2.400E-24 | 1.555E-23 | 7.200E-24 | 24 | 80 |
| 3 | M9185 MODULE 357 | Intermediate filaments and keratins. | MSigDb: C4 - CM: Cancer Modules (v7.2) | 1.973E-26 | 2.400E-24 | 1.555E-23 | 7.200E-24 | 24 | 80 |
| 4 | M18170 MODULE 154 | Intermediate filaments. | MSigDb: C4 - CM: Cancer Modules (v7.2) | 4.899E-24 | 4.470E-22 | 2.896E-21 | 1.788E-21 | 22 | 75 |

| 5 | M9365 GNF2 SERPINB5 | Neighborhood of SERPINB5 | MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2) | 6.675E-16 | 4.873E-14 | 3.157E-13 | 2.436E-13 | 12 | 28 |

**Show 19 more annotations**

### 17: MicroRNA [Display Chart] 205 input genes in category / 8181 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 lowEffct | hsa-miR-4289:mirSVR nonconserved lowEffect-0.1-0.5 | MicroRNA.org | 6.663E-14 | 3.033E-10 | 2.908E-9 | 5.451E-10 | 31 | 1715 |
| 2 | hsa-miR-325-3p:TargetScan | hsa-miR-325-3p | TargetScan | 7.415E-14 | 3.033E-10 | 2.908E-9 | 6.067E-10 | 31 | 1722 |
| 3 | hsa-miR-499-3p:mirSVR highEffct | hsa-miR-499-3p:mirSVR nonconserved highEffect-0.5 | MicroRNA.org | 3.580E-13 | 9.762E-10 | 9.358E-9 | 2.929E-9 | 26 | 1249 |
| 4 | hsa-miR-124-3p:Functional MTI (Weak) | Functional MTI (Weak) | miRTarbase | 1.514E-12 | 3.096E-9 | 2.968E-8 | 1.239E-8 | 27 | 1446 |
| 5 | hsa-miR-30a:mirSVR highEffct | hsa-miR-30a:mirSVR conserved highEffect-0.5 | MicroRNA.org | 2.652E-12 | 4.338E-9 | 4.159E-8 | 2.169E-8 | 30 | 1849 |

**Show 45 more annotations**

### 18: Drug [Display Chart] 204 input genes in category / 21031 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 | 3.455E-18 | 7.267E-14 | 7.653E-13 | 7.267E-14 | 42 | 937 |
| 2 | ctd:D004054 | Diethylstilbestrol | CTD | 2.525E-17 | 2.655E-13 | 2.796E-12 | 5.309E-13 | 48 | 1304 |
| 3 | CID000128831 | CK17 | Stitch | 2.828E-15 | 1.983E-11 | 2.088E-10 | 5.948E-11 | 13 | 57 |
| 4 | CID000005538 | 9cRA | Stitch | 1.967E-14 | 1.034E-10 | 1.089E-9 | 4.138E-10 | 51 | 1735 |
| 5 | ctd:C002202 | 4-oxoretinoic acid | CTD | 1.252E-13 | 5.268E-10 | 5.548E-9 | 2.634E-9 | 15 | 115 |

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### 19: Disease [Display Chart] 194 input genes in category / 5883 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 BeFree | 1.779E-21 | 1.047E-17 | 9.688E-17 | 1.047E-17 | 38 | 544 |
| 2 | C0870082 | Hyperkeratosis | DisGeNET BeFree | 1.469E-19 | 4.322E-16 | 4.001E-15 | 8.644E-16 | 19 | 97 |
| 3 | C0033860 | Psoriasis | DisGeNET BeFree | 3.643E-19 | 7.143E-16 | 6.613E-15 | 2.143E-15 | 49 | 1105 |
| 4 | C0013595 | Eczema | DisGeNET BeFree | 4.482E-14 | 6.592E-11 | 6.102E-10 | 2.637E-10 | 33 | 680 |
| 5 | C0011615 | Dermatitis, Atopic | DisGeNET BeFree | 1.497E-13 | 1.761E-10 | 1.631E-9 | 8.807E-10 | 32 | 666 |

**Show 45 more annotations**