



SOX11 promotes invasive growth and DCIS progression

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Title:

SOX11 promotes invasive growth and DCIS progression

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The following Authors declare that they have no conflict of interest:

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For Peer Review

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Abstract

Here, we show that SOX11, an embryonic mammary marker, normally silent in postnatal breast cells, is expressed in many ER- preinvasive DCIS lesions. Mature mammary epithelial cells engineered to express SOX11 display alterations in progenitor cell populations, including an expanded basal-like population with increased ALDH activity, and increased mammosphere-forming capacity. DCIS.com cells engineered to express SOX11 display increased ALDH activity, a feature of cancer stem cells. CD44+/CD24-/ALDH+ cell population is increased in DCIS.com cells that express SOX11. Upregulating SOX11 expression in DCIS.com cells leads to increased invasive growth both *in vitro* and when injected intraductally in a mouse model of DCIS that recapitulates human disease. Invasive lesions form sooner and tumour growth is augmented *in vivo*, suggesting SOX11 contributes to the progression of DCIS to invasive breast cancer. We identify potential downstream effectors of SOX11 during both microinvasive and invasive tumour growth stages, including several with established links to regulation of progenitor cell function and prenatal developmental growth. Our findings suggest SOX11 is a potential biomarker for DCIS lesions containing cells harbouring distinct biological features, which are likely to progress to invasive breast cancer.

Introduction

Embryonic breast epithelial cells are a unique cell population comprised of undifferentiated and highly plastic progenitor cells that ultimately give rise to all other postnatal breast epithelial cells [1]. There is increasing evidence that cancer stem or stem-like cells exist and perpetuate growth of cancer cells after therapy in many solid tumours [2, 3]. Cancer stem cells identified in skin, gut, and brain are very similar to healthy stem cells responsible for growing and renewing tissue in the body. Lineage tracing studies have indicated that embryonic mammary epithelial cells are multipotent *in vivo* [4] but their involvement in breast cancer is not yet clear. Tumours may develop from progenitor-like cells of diverse stages of cellular differentiation [5-7] and embryonic mammary progenitor cells have potential links to breast cancer that remain to be explored [8].

We analysed embryonic mouse mammary gene signatures and showed remarkable similarities exist between embryonic breast cells and breast cancer cells [9]. We found an embryonic mammary epithelial signature was activated in mouse *Brca1*^{-/-} tumours and human basal-like breast cancers. A small network comprised of embryonic genes with known roles in progenitor/stem cell regulation, was found activated in some breast cancers. One network component, *SOX11*, is not detected in the normal mature postnatal breast and is highly expressed in basal-like and HER2⁺ breast cancers [9]. *SOX11* is known to promote tissue remodelling, progenitor cell expansion and differentiation of a number of cell types [10], including neural progenitor cells [11]. Induced expression of *SOX11* in embryonic stem cells [12] and embryonic kidney cells [13] leads to induction of genes that regulate

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developmental processes, including organogenesis. *SOX11* expression within pre-invasive breast lesions or invasive breast cancers may therefore represent tissues containing cells that have distinct features more typically associated with prenatal mammary progenitor cells and patterns of growth which are unique compared to those characteristic of the mature postnatal breast [14-16].

DCIS presents a clinical problem and biomarkers are needed that can identify DCIS lesions that are likely to progress and require treatment with more aggressive therapies. *SOX11* has been found to be highly expressed in preinvasive lesions, including DCIS [17]. Higher levels of *SOX11* have been detected in atypical ductal hyperplasia (ADH) that are associated with breast cancer compared to ADH not associated with cancer [18]. Therefore, *SOX11* is an attractive candidate for mediating DCIS progression. Here, we analyse the effects of upregulating *SOX11* expression in both mature breast cells and DCIS cells from the MCF10A progression series.

Materials and methods

Cell Culture

Table S1A provides details of cell lines and media. DCIS.com-Luc cells were generated by transducing cells with Lentiviral Expression Particles for firefly luciferase (LVP325, Amsbio).

Expression Vectors

SOX11 coding sequence (GENEID: 6664) from clone HsCD00295480 [19] in pENTR223.1 plasmid (DNASU) [20] was subcloned into pLenti6.3/V5-DEST Gateway vector (ThermoFisher).

Flow Cytometry Analyses and Fluorescence-Activated Cell Sorting

After trypsinisation, 5×10^4 MCF10A or DCIS.com cells expressing SOX11 or control LacZ vector were resuspended in 100 μ l PBS plus 10% FCS and incubated with combinations of antibodies: CD49f-PE (1:100), EpCAM-PerCPCy5.5 (1:20), CD24-FITC (1:20), CD24-PE-Cy7 (1:100) and CD44-APC (1:20) (BD Biosciences) for 30 min at room temperature. Cells were resuspended in 0.5 ml PBS plus 10% FCS and DAPI and filtered through 50 μ m filters. Unstained and single-antibody stained cells were used for compensation. Using a BD fluorescence-activated cell sorting (FACS) LSRII flow cytometer, samples were analysed using BD FACS Diva (BD Biosciences). Aldehyde dehydrogenase (ALDH) activity was measured using Aldefluor assay (StemCell Technologies); cells were also co-stained with Aldefluor and CD49f-PE and EpCAM-PerCPCy5.5.

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Spheroid formation

5x10³ cells were plated in 96-well ultra low attachment plates (Corning 7007; spheroids formed after 4 days). (Table S1A). Spheroid images were obtained starting on day 4 using a Celigo cytometer (Nexcelom).

Clonogenic assays

250 MCF10A cells were plated per well in 6-well (Falcon F3046) plates. After 7 days, plates were stained with 0.2% crystal violet, 20% methanol in PBS. Clones were counted and percentage relative to number of cells plated was calculated.

For mammosphere assays, 5x10³ MCF10A cells/ml were plated in low attachment 6-well plates (Corning 3471) and incubated in medium (Table S1A) supplemented with 2% NeuroCult SM1 without Vitamin A (Stem Cell Technologies) and 0.65% of Methylcellulose (R&D Systems). After 14 days, wells were scanned using Celigo cytometer. Mammosphere-forming efficiency was calculated by dividing the number of mammospheres by the number of cells plated per well.

Immunofluorescence

Antibodies and staining protocol are in Table S1B. Images were captured with Leica Microsystems TCS-SP2 confocal microscope.

Western blotting

Western blotting was performed as described [9]. Antibodies details are in Table S1C.

Transmigration, spheroid and invasion assays

DCIS.com cells were grown in serum-free medium for 24h and used in 96 Collagen I Cell Invasion Assays (Cultrex). 5×10^4 cells were plated per well coated with 1% or 0.1% collagen, or left uncoated. Transmigration was measured after 48h.

5×10^3 cells were plated per well in spheroid formation ECM medium of 96-well 3D spheroid BME cell invasion assay (3500-096-K, Cultrex). 3 days later, matrix and 1 hour later media was added (Table S1A). Spheres were measured every 2 days using Celigo and images were acquired to assess spheroid morphology.

3D spheroid invasion assays were performed. Spheroids from 5×10^3 DCIS.com cells were embedded in serum-free medium 2.2 mg/ml of Collagen I (354249 Corning). Complete or serum-free media was added after 1h. Images were acquired after 48h using Celigo. Total area of matrix invaded by cells was calculated using Image J after marking the area manually.

Proliferation and viability assays

3×10^3 cells were plated in 96-well plates (655098, Greiner Bio-one) for 24 hours. Cell titer glo (Promega) was used following manufacturer's protocol. Fluorescence was measured with a Victor X5 plate reader (Perkin-Elmer).

Cleaved caspase 3 assays

5×10^3 cells were plated in ultralow attachment 96-well plates. 5 days after spheroid formation for MCF10A cells or day 8 days for DCIS.com cells,

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spheroids were incubated for one hour with NucView™-488 Caspase-3 substrate at a final concentration of 10 uM. Fluorescence was measured with Celigo.

Statistical Analysis

Experiments were analysed with a 2-tailed Student's test with confidence interval of 95% when number of groups were equal to 2 or with a parametric ANOVA and *post-hoc* test when the number of groups was >2 unless otherwise specified.

Animal experiments

SCID/beige mice, purchased from Charles River (Harlow, UK), were housed in IVC cages on 12h light/dark cycle and received food and water *ad libitum*. All work was carried out under UK Home Office project (70/7413, 70/7712) and personal licenses (090/02921, I5F252069, IFFDC436E) following local ethical approval from The Institute of Cancer Research Ethics Committee and in accordance with local and national guidelines. As biological replicates, n=4-5 animals were used. Intraductal injections of 5x10⁴ cells were performed as described by [21] with slight modifications, including chemical removal of fur and mice were not surgically opened. For mammary fat pad injections, 2.5x10⁶ cells were injected into mammary gland 4 of 10-12 week-old female mice. Engrafted mammary glands or tumours were harvested 6-12 weeks after intraductal injections and 6 weeks after mammary fat pad injections, fixed in formalin or snap-frozen.

RNA isolation

RNA was isolated from tumours or mammary gland 4 harbouring microinvasive lesions of each biological replicate (n=4-5 for each time point) using TRIzol (Fisher Scientific), followed by a second extraction with RNAeasyPlus Micro kit (74034, Qiagen) and DNase treatment. RNAClean and concentrator-5 (Zymo research) were used. RNA concentration and sample purity were determined with Qubit fluorometer (Invitrogen) and Nanodrop spectrophotometer. RNA Integrity Number (RIN) was measured with a Bioanalyzer and Agilent RNA Pico kit (Agilent technologies).

cDNA synthesis

1 µg of each RNA sample was retrotranscribed using QuantiTect Reverse Transcription kit in final volume of 20µl. cDNA was diluted eight-fold for subsequent qRT-PCR analysis as previously described [9].

Quantitative Real-time PCR (qRT-PCR)

Table S2 lists probes and methods.

Gene Expression Profiling

Sequence files were trimmed using trim_galore (http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/) using default settings. Trimmed data was separately mapped to the GRCh38 and GRCm38 genome assemblies using hisat2 (v2.0.5) with options --sp 1000,1000 --omixed--no-discordant, and was filtered to remove non-primary alignments.

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Species-specific read sets were generated by removing any read which produced a valid alignment in both human and mouse from both species results. The remaining data was imported into SeqMonk (<http://www.bioinformatics.babraham.ac.uk/projects/seqmonk/>) with a filter of MAPQ>=20. Reads were quantitated over the transcript set from Ensembl v78 with annotated mis-spliced, pseudogene and unannotated transcripts removed. Initial quantitation was raw read counts from the opposing strand to the transcript, collating all exons for each gene into a single measure. This allowed gene level differential expression to be assessed using DESeq2 (<https://bioconductor.org/packages/release/bioc/html/DESeq2.html>) with a cutoff of FDR < 0.05. Subsequent visualisation was done by requantitating expression as log2 FPM (fragments per million reads of library). RNA sequencing data have been deposited in European Nucleotide Archive with accession number PRJEB19633.

Immunohistochemistry

IHC was performed on formalin-fixed paraffin embedded DCIS samples from 22 ER+, 22 ER-, 17 HER2+, and 6 mixed cases collected through the ICICLE study (MREC 08/H0502/4). Samples were stained with two SOX11 antibodies as described previously [9] (Table S3).

Scoring guidelines

Expression status of SOX11 antibody (Abcam ab170916) was determined using a semi-quantitative scoring system based on staining intensity and proportion of positive cells expressed as percentage. Staining

intensity was divided into four grades (intensity scores): no staining (0), weak staining (1), moderate staining (2) and strong staining (3). The proportion of positive cells was divided into five grades (percentage scores): <10% (0), 10–25% (1), 26–50% (2), 51–75% (3) and 76–100% (4). SOX11 staining status was determined by the following formula: overall score = intensity score x percentage score. Overall score of ≤ 4 was defined as low expression; >4 was defined as high expression.

Survival analysis

mRNA expression and survival data were used to evaluate the prognostic importance of SOX11. Data obtained from GEO, EGA, and TCGA using Kaplan-Meier Plotter survival analysis tool (<http://kmplot.com>) and METABRIC [22] were used to generate Kaplan–Meier survival curves and determine statistical significance using the Wald-test and log-rank test.

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Results

Effect of SOX11 levels on postnatal mammary progenitor cell profiles

We confirmed SOX11 is not expressed in normal mature breast tissue, as expected for an embryonic mammary marker (Figure 1A). We detected SOX11 expression in triple negative (ER-, PR-, HER2-) and HER2+ breast cancer cells lines (Figure 1B). We did not detect significant expression of SOX11 in DCIS.com or MCF10A cells, ER- cell lines from a progression series that are often used as models to study DCIS and normal mammary epithelial cell (MEC) growth, respectively (Figure 1B). To study the effects of expressing SOX11 in a normal MEC line, we stably transduced SOX11 into MCF10A cells (Figure 1C) and were able to detect nuclear SOX11 expression in MCF10A-SOX11 cells (Figure 1D).

CD49f and EpCAM expression separates distinct subpopulations in cells isolated from human breast epithelium [23]. Flow cytometry analysis using EpCAM and CD49f also identifies cell subpopulations in non-tumourigenic basal cell lines [24]. MCF10A cells display heterogeneity and contain two separate subpopulations (Figure 1E): EpCAM+/CD49f⁺ and EpCAM⁻/CD49f⁺. An increase in the EpCAM⁻/CD49f⁺ basal-like population is observed in MCF10A population expressing SOX11 (27.44% ± 14.58%) compared to MCF10A-control cells (11.38% ± 7.69%) (Figure 1E). Aldehyde dehydrogenase (ALDH) activity is 1.76-fold greater in EpCAM⁻/CD49f⁺ basal-like MCF10A-SOX11 cells compared to MCF10A-control cells, suggesting an expanded population associated with stem cell properties (Figure 1F and S1). EpCAM⁻/CD49f⁺/ALDH⁺ cells are detected at 4.26-fold greater frequency in MCF10-SOX11 versus MCF10A-control populations.

Effect of SOX11 expression on postnatal MEC growth, morphogenesis and clonogenicity

We observed a slight but significant reduction in cell growth in MCF10A-SOX11 compared to MCF10A-LacZ cells (Figure 2A). Morphological differences were observed when MCF10A-SOX11 mammospheres are compared to MCF10A-LacZ-control mammospheres grown using a variety of culture conditions; MCF10A-SOX11 mammospheres appear more compact and solid than controls (Figure 2B and S2A-B). These observations are compatible with SOX11 altering the growth features of normal MECs that we hypothesised from clinical data. MCF10A-SOX11 cells are not more clonogenic, but form more clones with basal/myoepithelial morphology, compared to MCF10A-control cells (Figure 2C-D). MCF10A-SOX11 cells have greater mammosphere-forming capacity and produce mammospheres with distinguishable phenotypes compared to MCF10A-control cells (Figure 2C-D). Cleaved caspase 3 (CC3) levels were slightly reduced in MCF10A-SOX11 compared to MCF10A-control mammospheres (Figure 2E). No invasive growth was observed when MCF10A-SOX11 spheroids were used in 3D invasion assays (Figure S2C). No morphological differences are observed in MCF10A-SOX11 spheroids compared to MCF10A-LacZ-control spheroids grown without hydrogel (Figure S2D).

Effect of SOX11 levels on DCIS

We stably transduced SOX11 into DCIS.com cells to study the effects of expressing SOX11 in a cell line that is used to model DCIS formation and

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its progression to invasive disease (Figure S3). DCIS-SOX11 spheroids appear similar in morphology to DCIS-controls spheroids when they form (=day 0), but show a slight reduction in volume after 14 days (Figure 3A). Cell growth is slightly reduced in DCIS-SOX11 cells compared to controls (Figure 3B). We assessed CC3 levels as a possible mechanism underlying the more compact and less necrotic phenotype observed in DCIS-SOX11 spheroids. We detected lower levels of caspase 3 activity in DCIS-SOX11 spheroids compared to DCIS-control spheroids (Figure 3C-D). By FACs analysis, we detected over 2-fold higher ALDH activity in DCIS-SOX11 cell populations compared to controls (Figure 3E). CD44+/CD24- population is increased 1.5-fold in DCIS-SOX11 cells (Figure 3F). 7.7-fold increase of CD44+/CD24-/ALDH+ cells were detected in DCIS-SOX11 cells compared to control cell populations; no significant change was detected in the frequency of CD44+/CD24+/ALDH+ cells (Figure 3G and S4). EpCAM/CD49f+/ALDH+ cells are detected at higher frequency in DCIS-SOX11 cells compared to controls (Figure 3H).

SOX11 promotes invasive growth of DCIS cells in vitro

Cell migration through collagen was significantly increased with DCIS-SOX11 cells compared to control cells using transwell assays. (Figure S5A). Results from 3-D invasion assays show SOX11 significantly increases invasion of DCIS-spheroids through Collagen (Figure 4A-B and S5B). We measured levels of melanoma inhibitory activity (MIA), a gene in the PAM50 test, which is characteristically high in basal-like breast cancer, and decreased upon siRNA-mediated knockdown of SOX11 in breast cancer cells,

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3 in a recent study [25]. MIA is secreted by melanoma cells after their malignant
4 transformation, and plays a key role in melanoma progression and invasion.
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6 We found DCIS-SOX11 cells express over four-fold greater levels of MIA
7 compared to DCIS-LacZ control cells (Figure S6). Neither MCF10A-LacZ nor
8 MCF10A-SOX11 cells express detectable levels of MIA. These results show
9 that SOX11 expression can lead to profound phenotypic changes when
10 expressed in mature ER-, PR-, HER2- breast cells, but acquisition of invasive
11 phenotype is context-dependent.
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20 21 22 ***SOX11 promotes growth and progression of DCIS cells in vivo***

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24 Using the mouse mammary intraductal (MIND) model developed by
25 Behbod *et al.* [21], we injected DCIS-control and DCIS-SOX11 cells into the
26 mammary ducts of female mice. We collected mammary glands six-seven
27 weeks later and sectioned through a subset of them. Mammary glands from
28 mice injected intraductally with DCIS-controls cells contain *in situ* lesions and
29 some microinvasion (Figure 4C). Mammary glands from mice injected
30 intraductally with DCIS-SOX11 cells had extensive microinvasion and
31 invasion (Figure 4D and S7). We detected significantly more bioluminescence
32 in mice injected intraductally with DCIS-SOX11 cells six-seven weeks after
33 xenografting (Figure 4E). We also collected mammary glands from the same
34 cohort of mice twelve weeks after xenografting; invasive tumours formed from
35 both DCIS-control and DCIS-SOX11 cells. Significantly more bioluminescence
36 was observed in DCIS-SOX11 tumours and these were larger than control-
37 DCIS tumours (Figure S7). RNA sequencing of lesions collected at the
38 microinvasive stage (six-seven weeks post-injection) show deregulated RNA
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expression of ECM components and cell shape regulators and increased expression of secreted growth factors and peptides (Table 1). Invasive tumours collected twelve weeks after injection of DCIS cells into mammary ducts show increased expression of genes encoding signal peptides, ECM components, and regulators of embryonic organ morphogenesis (Table 2). Down-regulated genes in the lesions and tumours that form after intraductal DCIS injections include glycoproteins, endopeptidase inhibitors, and regulators of neuron projection, apoptosis and cell adhesion (Table S4).

We also injected DCIS-control and DCIS-SOX11 cells directly into the mammary fat pads of female mice. IVIS imaging showed that DCIS-SOX11 cells displayed more bioluminescence and greater tumour volume 6 weeks after injection of cells (Figure S7). Invasive tumours that formed after mammary fat pad injections of DCIS-SOX11 cells show elevated expression of genes associated with organogenesis and developmental processes (Table S5), with similar gene signatures to those injected intraductally. A number of candidate effectors of SOX11 signalling in DCIS were identified including *ALDH1A1* and *HORMAD1*, which have established links to breast cancer. *ALDH1* is a marker of normal and malignant human mammary stem cells and predictor of poor clinical outcome [26]. *ALDH1A1* isoform expression is a cancer stem cell marker and predictor of progression and poor survival [27, 28]. Elevated *HORMAD1* expression suppresses RAD51-dependent homologous recombination and drives the use of alternative forms of DNA repair [29].

Quantitative RT-PCR analysis detected higher levels of *SOX11*, *FHAD1*, *HORMAD1*, and *TFAP2B* in from DCIS-SOX11 versus DCIS-LacZ

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3 tumours (Figure 6A). We used IHC to stain ALDH1A1 and detected
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5 ALDH1A1+ cells in early lesions collected between six-seven weeks after
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7 injection of control DCIS cells and DCIS-SOX11 cells. (Figure 6B). In tumours
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9 formed after injection of DCIS-control cells into the mammary fat pad,
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11 dispersed ALDH1A1+ cells were detected predominantly in the tumour interior
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13 (Figure 6C). We detected large clusters of ALDH1A1+ cells in the interior
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15 portion of the tumour, as well as at the tumour periphery, in DCIS-SOX11
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17 tumours (Figure 6C). ALDH1A1+ cells are detected in DCIS lesions from ER-,
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19 SOX11+ DCIS cases (Figure S8).
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25 ***SOX11 is expressed in breast cancers that progress to form metastasis***
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27 ***and in pre-invasive breast lesions***
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31 Higher levels of SOX11 expression are associated with worse outcome
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33 in patients with lymph node-negative breast cancer, with an increased
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35 likelihood for the disease to progress to form distant metastasis and
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37 decreased overall survival (Figure 6A-B and S9) [30]. High levels of nuclear
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39 SOX11 was detected by IHC in ER- DCIS lesions compared to ER+ DCIS
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41 (P=0.0002, Fisher's Exact Test) in a small cohort of pure DCIS cases, (13/22
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43 ER-, 6/17 HER2+, 1/22 ER+, and in DCIS and invasive components of 4/6
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45 mixed cases) (Figure 6C-D and S10).
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Discussion

We investigated the consequences of expressing SOX11, an embryonic mammary factor, using normal breast and DCIS cell lines originating from the MCF10A progression series. MCF10A and DCIS.com cells do not express significant levels of SOX11 [31]. Our findings show engineering SOX11 expression in MCF10A cells significantly alters progenitor cell features and confers distinct traits to mature postnatal MECs. SOX11 expression results in an expanded basal-like population. ALDH activity, a marker of human luminal progenitor cells [32] is increased significantly within the basal-like population of MCF10A cells. These findings suggest that SOX11 expression in mature MECs increases a population of cells with features of both basal and luminal lineages. A large percentage of prenatal mammary cells express markers associated with both the basal and luminal lineages in both mouse and human mammary epithelium [14, 33]. Increased frequency of basal-like clones and mammosphere-forming capacity in MCF10-SOX11 cells is consistent with the finding that ALDH+ cells from normal breast epithelium have stem cell properties [26]. MCF10A-SOX11 cells have a slight growth disadvantage compared to controls and do not exhibit invasive properties. Expression of SOX11 in normal postnatal MECs alters progenitor cell features and morphogenesis without promoting invasion.

Expression profiling of the lesions and tumours that formed after intraductal injection of DCIS.com cells expressing SOX11 identified a large number of candidate downstream effectors, during both microinvasive and invasive growth stages. Many have significant links to stem cell biology and embryonic developmental processes. *ALDH1A1* plays a role in proliferation

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3 and differentiation of mammary progenitor cells in the normal breast;
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5 clonogenicity is decreased upon *ALDH1A1* knockdown [34]. *TFAP2B* is
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7 thought to stimulate cell proliferation and suppress terminal differentiation of
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9 specific cell types during embryonic development [35]. Mutations in *TFAP2B*
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11 cause Char syndrome, a disorder characterised by defective heart,
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13 craniofacial and limb development [36]. Cancer/testis (CT) genes are
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15 expressed by germ cells, quiescent in somatic cells, but activated in various
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17 cancers. *CT46/HORMAD1*, a meiotic gene, is a driver of homologous
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19 recombination deficiency in triple negative breast cancers [29].
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23 Many genes found upregulated in DCIS-SOX11 lesions encode ECM
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25 components or ECM modulators including signal peptides and secreted
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27 growth factors. The ECM is highly modified in cancer and can drive disease
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29 progression at the primary tumour site or its metastasis. SOX11 may
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31 contribute to propagation of invasive phenotypic changes in DCIS.com cells
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33 by generating ECM cleavage products including signal peptides with potential
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35 signalling functions and local release of growth factors. Together, our findings
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37 suggest that breast lesions expressing SOX11 have altered progenitor/stem
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39 cell populations and increased propensity for tissue remodelling and invasion.
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43 SOX11 is expressed in a variety of other cancers including glioma,
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45 lung, mantle cell lymphoma (MCL), ovarian, and prostate cancer [37, 38].
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47 SOX11 is aberrantly expressed in most aggressive MCL and is considered a
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49 reliable biomarker in MCL pathology [39]. *SOX11* is most highly expressed in
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51 basal-like and HER2+ breast cancers but further studies are needed to
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53 assess whether it will be a useful biomarker for clinical use [9, 25].
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Our results show the effect of SOX11 expression in mammary cells from the MCF10A series is context dependent. Invasive growth is dramatically increased in DCIS.com cells engineered to express SOX11, but not in MCF10A-SOX11 cells. DCIS.com cells are clonally derived from H-Ras-transformed MCF10A cells and it is plausible that without expression of a driver of malignant phenotype such as HRAS, SOX11 will not promote invasive growth. Three additional predicted cancer driver mutations (EPHA7, MAP3K12 and PCSK5), were identified that were acquired during transformation of non-malignant MCF10A cells to malignant DCIS.com cells that also could be implicated in the cell-context dependency of SOX11 to promote invasion [31].

A recent molecular study of DCIS and early stage invasive breast cancers detected high levels of SOX11 in samples of pure DCIS and invasive tumours [40]. High levels of SOX11 were detected predominantly in basal-like and HER2+ lesions. SOX11 is co-expressed amongst a cluster of genes that identify a distinct DCIS subgroup with gene expression characteristics more similar to advanced tumours [41]. Functional annotation of genes expressed within this DCIS subtype found enrichment of genes associated with developmental processes and organ morphogenesis. Using *in vitro* and *in vivo* studies of DCIS.com cells, we show that SOX11 promotes cell survival and invasion of DCIS cells and increases the ALDH+ population, including the CD44+/CD24-/ALDH+ subset. CD44+/CD24-/ALDH+ phenotype is thought to increase tumourigenicity of breast cancer cells [26]. Collectively, this supports the notion that DCIS lesions that express SOX11 possess properties that

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3 make them aggressive and cause them to progress to invasive breast
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5 cancer.

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7 59% ER- DCIS cases that we tested by IHC were SOX11+. High SOX11
8 expression is associated with poor overall survival in all breast cancer patients
9 [9] and poor outcome in patients with lymph node negative disease, a group
10 that normally has good predicted outcome. However, the datasets used for
11 the survival analyses do not represent DCIS. In order to establish whether
12 SOX11 overexpression in DCIS is associated with an increased risk of
13 developing invasive disease, analysis of a large number of pure DCIS
14 samples with long-term follow up is required. The Sloane Project, a UK wide
15 prospective audit of screen detected DCIS (<http://www.sloaneproject.co.uk>)
16 and LORIS, a UK phase III trial comparing surgery with active monitoring for
17 low risk DCIS will be useful for evaluating the clinical value of SOX11
18 expression and correlation with DCIS progressing to invasive breast cancer
19 [42].

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21 We have related SOX11 expression to increased invasive growth and
22 progression of DCIS cells. We identified potential downstream effectors of
23 SOX11 in DCIS, which adds new biological information that may contribute to
24 a better understanding of the pathology and identification of suitable treatment
25 options for patients with breast lesions that express SOX11. SOX11 is a
26 potential biomarker for ER- DCIS that may be at a higher risk of progression.
27 Further investigations are needed to determine if patients with DCIS lesions
28 expressing SOX11 are more likely to develop invasive disease.
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Statement of author contributions

EO, BAH designed the experiments.

EO, PB performed *in vitro* experiments.

NK, PB, BAH performed *in vivo* experiments.

DK, FD, PB, BAH performed tumour staining and tumour scoring.

SH performed bioinformatics and survival analysis.

VS, EJS provided DCIS case samples and associated clinical data.

BAH and EO wrote the manuscript with input and approval from all authors.

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Tables

Table 1 and 2. Potential downstream SOX11 targets identified using RNA-seq of tumours formed after intraductal and fat pad injections of DCIS-control and DCIS-SOX11 cells.

- 1. List of top upregulated genes in DCIS-SOX11 lesions from samples collected 6 weeks after intraductal mammary injection.
- 2. List of top upregulated genes in DCIS-SOX11 lesions from all intraductal samples (6 weeks and 12 weeks after mammary intraductal injections).

Table 1. List of top upregulated genes in lesions from DCIS-SOX11 samples collected 6 weeks after intraductal mammary injection of compared to DCIS-control lesions. Log2FC indicates ($\log_2(\text{DCIS-SOX11}) - \log_2(\text{DCIS-control})$).

Gene	log2FC
FHAD1	5.3392467
UGT2B28	4.79066443
LRRC31	4.1190376
PIP	3.9638702
AGMO	3.9168392
TFAP2B	3.7775288
DUOX1	3.6588801
GSTM1	3.6003848
OLFM4	3.2495492
HHIPL2	3.0788153
SLC14A1	3.0049578
COX6B2	2.9759872
SIDT1	2.4203497
ALDH1A1	2.1891004
VAV3	2.1827067
HORMAD1	2.0911084
F5	2.083366
ELN	2.029894
SCGB1D2	1.810388
HSD17B2	1.5279316
FZD4	1.5128815

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Table 2. List of top upregulated genes in DCIS-SOX11 lesions from all intraductal samples. Log2FC indicates (log2(DCIS-SOX11)-log2(DCIS-control)).

Gene	log2FC
FHAD1	5.2158456
DUOX1	3.8396916
GSTM1	3.4844713
FABP6	3.4173422
FILIP1	2.9833927
AGMO	2.9238105
QPR1	2.9094748
HLA-DPA1	2.8897848
S100A7	2.7633967
FMOD	2.6771894
S100A8	2.5575514
KCNJ5	2.5571022
COX6B2	2.5369272
TFAP2B	2.5153782
XG	2.385934
PIP	2.324072
ROR2	2.1787367
SLC35F3	2.0892406
SLC4A8	2.0528436
FHL1	2.0478764
OLFM4	2.0403762
SHISA2	2.028072
TNFAIP6	2.023
NDRG4	1.9837015
TRIM6	1.978967
GAL3ST2	1.8982594
RINL	1.8655803
CLCA2	1.8368406
SYT12	1.8143466
VAV3	1.7891986
FBLN5	1.7790818
RMRP	1.7490951
APOC1	1.7350571
COL17A1	1.7191944
FLRT3	1.6746507
ARHGAP24	1.639564
ZNF503-AS2	1.6393551
S100A9	1.6338024
HORMAD1	1.6259812
CFI	1.5933018
KCND1	1.5714868
TAF7L	1.5505905
RAD51AP2	1.543372
ELN	1.5045118

Figure legends

Figure 1. Expression of SOX11 in postnatal mammary epithelial cells alters progenitor cell populations.

A. SOX11 expression is not detected in normal mature breast tissue. Scale bar: 200 μ m

B. SOX11 is expressed in some basal-like breast cancer and HER2+ cell lines, but not in MCF10A or DCIS.com cells.

C. Western blot of MCF10A-LacZ control and MCF10A-SOX11 cells. SOX11 levels (indicated by numerical values) were measured by densitometry and normalised dividing by the tubulin values.

D. Immunofluorescence staining of MCF10A-LacZ control and MCF10A-SOX11 cells with DAPI (blue in inset) and SOX11 (white). Scale bar: 50 μ m

E. Representative FACS analysis of EpCAM/CD49f sorted MCF10A-control and MCF10A-SOX11 cell populations. Experiment was performed 5 times. The average percentage of Epcam⁺/CD49f⁺ cells in each population are shown (media $\pm$ SD). A t-student test was performed.

F. ALDH activity levels in MCF10A-control and MCF10A-SOX11 cells were detected using the Aldefluor assay. Cells were stained and sorted with CD49f and EpCAM antibodies and ALDH activity was measured using the Aldefluor kit. Representative ALDH activity after FACS analysis in EpCAM-/CD49f+ MCF10A-control and MCF10A-SOX11 cell populations are shown. +DEAB plots display the negative control; cells incubated with DEAB, the specific inhibitor of ALDH, were used to establish the baseline fluorescence of these cells. Experiment was performed 4 times and a t-student test was performed.

The frequency of EpCAM⁺/CD49f⁺ basal-like ALDH⁺ cells (left graph) and EpCAM⁺/CD49f⁺/ALDH⁺ cells (right graph) in MCF10A-SOX11 compared to MCF10A-LacZ control populations are shown. Error bars represent SD.

Figure 2. Effect of SOX11 expression on postnatal mammary epithelial cell growth, morphogenesis and clonogenicity.

A. Cell titer glo assay results of MCF10A-LacZ control and MCF10A-SOX11 cells. Experiment was performed 3 times (n=18 in each sample) and ANOVA and ulterior multiple comparisons were used for statistical analysis. The values obtained in each time point (counts per second (cps)) were normalised dividing by the value obtained at day 0 in each population. $p<0.05$ MCF10A-SOX11 vs MCF10A-LacZ; $p<0.0001$ MCF10A-SOX11 vs MCF10A-luc.

B. Representative images of MCF10A-LacZ control and MCF10A-SOX11 mammospheres that were grown from spheroids formed in low attachment plates, 10 and 14 days after addition of BME. Experiments were repeated 3 times. Scale bar: 200 μ m

C. Quantification of clonogenicity and mammosphere-initiating capacity. Percentage of MCF10A cell populations plated in 2D culture that form colonies (left). Percentage of colonies with basal or myoepithelial morphology of the total cell number plated in 2D culture (center). Percentage of mammospheres formed from cells in 3D culture (right). All experiments were repeated 3 times *** $p<0.001$, *** $p<0.0001$.

D. Typical morphologies observed for colonies from MCF10A-LacZ and MCF10A-SOX11 cells in Figure 2C (left) Scale bar: 1 mm and for mammospheres derived from single MCF10A-LacZ and MCF10A-SOX11

cells embedded in methylcellulose (right). Single cells proliferate and form cell clusters with a large central lumen in MCF10A-SOX11 mammospheres.

Scale bar: 200 μm

E. Quantification of cleaved caspase 3 levels (left) and representative images of MCF10A-luc, MCF10A-LacZ and MCF10A-SOX11 spheroids 5 days after sphere formation. Experiment repeated 3 times; $p < 0.05$. Scale bar: 200 μm

All error bars represent SD.

Figure 3. Effect of SOX11 expression on DCIS cells.

A. Spheroids from DCIS-LacZ and DCIS-SOX11 cells at day 14 grown in BME (top images). Relative growth curves showing area (μm^2), volume (μm^3) and perimeter (μm) of DCIS-SOX11 compared to DCIS-LacZ control spheroids. Scale bar: 200 μm

B. Cell titer glo assay results of DCIS-LacZ control and DCIS-SOX11 cells. Experiment was performed 3 times ($n=56$ in each sample) and Student's t test and ulterior multiple comparisons were used for statistical analysis. The values obtained in each time point (counts per second (cps)) were normalised dividing by the value obtained at day 0 in each population. $p < 0.0001$ for the three time-points.

C. Representative images of cleaved caspase 3 activity in spheroids from DCIS-LacZ control and DCIS-SOX11 cells 8 days after spheres had formed.

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D. Relative cleaved caspase3 activity intensity (counts fluorescence units (CFU)) detected in spheroids from DCIS-SOX11 cells compared to DCIS-LacZ at day 8.

E. ALDH activity in DCIS-control versus DCIS-SOX11 in populations.

F. Frequency of CD44+/CD24- cells in DCIS-SOX11 compared to DCIS-control populations.

G. Frequency of ALDH-CD44+/CD24-/ALDH+ cells in DCIS-SOX11 compared to DCIS-control populations.

H. Frequency of EpCAM-/CD49f+/ALDH+ cells in DCIS-SOX11 compared to DCIS-control populations.

All error bars represent SD.

Figure 4. SOX11 increases invasive activity of DCIS cells *in vitro* and promotes growth and progression of DCIS cells *in vivo*.

A. Representative images of DCIS-LacZ control and DCIS-SOX11 spheroid invasion in Collagen I at day 2. Scale bar: 500 µm. Error bars represent SD.

B. Area of spheroid invasion of DCIS-SOX11 compared to DCIS-LacZ control in Collagen I at day 2. p=0.0162; experiment repeated 3 times.

C. Representative images of *in situ* and microinvasive lesions formed from DCIS-LacZ controls cells that appear in mice injected intraductally six to seven weeks after xenografting. Lamin A/C stain detects human cells. Scale bar: 100 µm

D. Representative images of *in situ*, microinvasive lesions, and invasive lesions formed from DCIS-SOX11 cells that appear in mice injected intraductally six to seven weeks after xenografting. Lamin A/C stain detects human cells. Scale bar: 100 μ m

E. Results from intraductal injections of DCIS-LacZ control and DCIS-SOX11 cells. Representative images and quantification of *in vivo* bioluminescence six to seven weeks after injection of DCIS-LacZ control and DCIS-SOX11 cells. Results expressed in photons per second (p/s); $p < 0.0001$. Each dot represents total photon count from each injected mammary gland. Error bars represent SEM.

Figure 5. Downstream effectors of SOX11 signalling identified in a mouse model of DCIS that recapitulates human disease.

A. Quantitative RT-PCR analysis of *SOX11* and potential *SOX11* downstream effectors, *FHAD1*, *HORMAD1*, *TFAP2B*, in tumour samples; $p < 0.0001$. Results are expressed as fold-change. Error bars represent SD.

B. ALDH1A1 staining of DCIS lesions that form after mammary intraductal injections of DCIS-LacZ control and DCIS-SOX11 cells. Scale bar: 100 μ m

C. ALDH1A1 staining of tumours that form after mammary fat pad injections of DCIS-LacZ control and DCIS-SOX11 cells. Scale bar: 100 μ m

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Figure 6. SOX11, an embryonic mammary epithelial marker, predicts poor clinical outcome in breast cancer patients and is expressed in pre-invasive breast lesions.

A. Disease-free survival (DSS) curves for 1032 breast cancer patients with lymph node negative disease with low and high SOX11 expression from analysis of microarray data from the METABRIC dataset. Expression data were stratified into quartiles based on SOX11 expression, and the lowest expression quartile (Q1) was treated as baseline for the subsequent pair-wise comparisons with the remaining quartiles. Statistical significance of pair-wise comparisons was assessed using Wald-test.

B. Overall survival (OS) curves for 1032 breast cancer patients with lymph node negative disease with low and high SOX11 expression from analysis of microarray data from the METABRIC dataset. Expression data were stratified into quartiles based on SOX11 expression, was treated as baseline for the subsequent pair-wise comparisons with the remaining quartiles. Statistical significance of pair-wise comparisons was assessed using Wald-test.

C-D. H&E stain (C) and SOX11 expression (D) in DCIS lesions.

Scale bar: 200 µm

Supplementary Information

Table S1. Cell line details, media, antibodies, staining protocol.

Table S2. Probes and protocol for quantitative real-time PCR.

Table S3. Antibodies and conditions used for IHC.

Table S4. RNA-sequencing data and results from functional annotation clustering of lesions and tumours from intraductal injection of DCIS-LacZ and DCIS-SOX11 cells.

Table S5. RNA-sequencing data and functional annotation clustering of tumours from injection of DCIS-LacZ and DCIS-SOX11 cells into mammary fat pad.

Figure S1.

ALDH activity in bulk populations of MCF10A-LacZ and MCF10A-SOX11 cells.

Inset plots display the negative control; cells incubated with DEAB, the specific inhibitor of ALDH, were used to establish the baseline fluorescence of these cells.

Figure S2. Examples of mammospheres formed from MCF10A-LacZ and MCF10A-SOX11 cells.

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A) Mammospheres that form when spheroids are embedded in BME after spheroid formation. Day 1, 3 and 5 after BME mixed with SFM was added to spheroids with complete media on top.

B) Mammospheres that form when spheroids are embedded in BME after spheroid formation. Day 0 and 18 after BME mixed with SFM was added with SFM on top.

C) Spheroids embedded in 2.2mg/ml of Collagen I with complete media added on top at Day 0 and Day 3.

D) Spheroids formed in low attachment plates in normal media at days 4, 7, 10 and 14 (no hydrogel).

Day 0 = 4 days after plating cells to form spheroids on low attachment plates in A-D.

Figure S3. Western blot of DCIS-LacZ control and DCIS-SOX11 cells. The levels of SOX11 were measured by densitometry and normalised dividing by the tubulin values.

Figure S4. Frequency of CD44+/CD24+/ALDH+ cells in DCIS-SOX11 compared to DCIS-control populations.

Figure S5.

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3 A. Results from transwell invasion assays of DCIS-LacZ control and DCIS-
4 SOX11 cells through 0.1% Collagen. (units in Counts per second (cps)),
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7 $p=0.0014$. Experiment was performed three times.
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10 B. Representative images of invasion from spheroids (red areas circled in
11 yellow) grown in serum-free (SF) or serum-containing (+serum) media 48
12 hours after addition of Collagen I and invasion media. 'Area invaded' at the
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17 end point includes area at $T=0$.
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22 **Figure S6.** Western blot of DCIS-LacZ control and DCIS-SOX11 cells. The
23 levels of MIA were measured by densitometry and normalised dividing by the
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27 tubulin values.
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32 **Figure S7.**

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34 A. Mammary glands were collected six weeks after intraductal injection.
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36 Samples from each cohort (DCIS-LacZ and DCIS-SOX11) were fixed in
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38 formalin and embedded in paraffin. One mammary gland from the first three
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42 mice that had been embedded from each cohort were sectioned and scored
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44 for presence of *in situ*, microinvasive and invasive lesions.

45 B. Tumours volumes from four mammary glands from each cohort (DCIS-
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47 LacZ and DCIS-SOX11) collected twelve weeks after intraductal injections.
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50 $p=0.0286$. Mann-Whitney test was used.

51 C. Results from mammary fat pad injections of DCIS-LacZ control and DCIS-
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60 SOX11 cells. Representative images and quantification of *in vivo*

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bioluminescence six weeks after injection of DCIS-LacZ control and DCIS-SOX11 cells. Results expressed in photons per second (p/s); $p=0.0034$.

D. Tumours volumes from mammary glands from each cohort (DCIS-LacZ and DCIS-SOX11) collected six weeks after mammary fat pad injections. $p=0.1111$. Mann-Whitney test was used.

Figure S8. SOX11+ DCIS case stained with ALDH1A1. Scale bar: 200 μ m

Figure S9.

A. Distant metastasis-free survival (DMFS) curves for breast cancer patients with lymph node negative disease with low and high SOX11 expression from analysis of microarray data of 988 patients using Kaplan-Meier Plotter survival analysis tool (<http://kmplot.com>). Expression data was dichotomised compared to the highest quartile expression level.

B. Overall survival (OS) curves for breast cancer patients with lymph node negative disease with low and high SOX11 expression from analysis of microarray data of 594 patients using Kaplan-Meier Plotter survival analysis tool (<http://kmplot.com>). Expression data was dichotomised compared to the highest quartile expression level.

Figure S10.

A. H&E stain, SOX11 and p63 expression in DCIS lesions from a mixed ER-, HER2+ case with high grade DCIS. scale bar: 100 μ m

B. H&E stain, SOX11 and p63 expression in invasive breast cancer from a mixed ER-, HER2+ case with high grade DCIS (DCIS shown in A). scale bar: 100 μ m

For Peer Review

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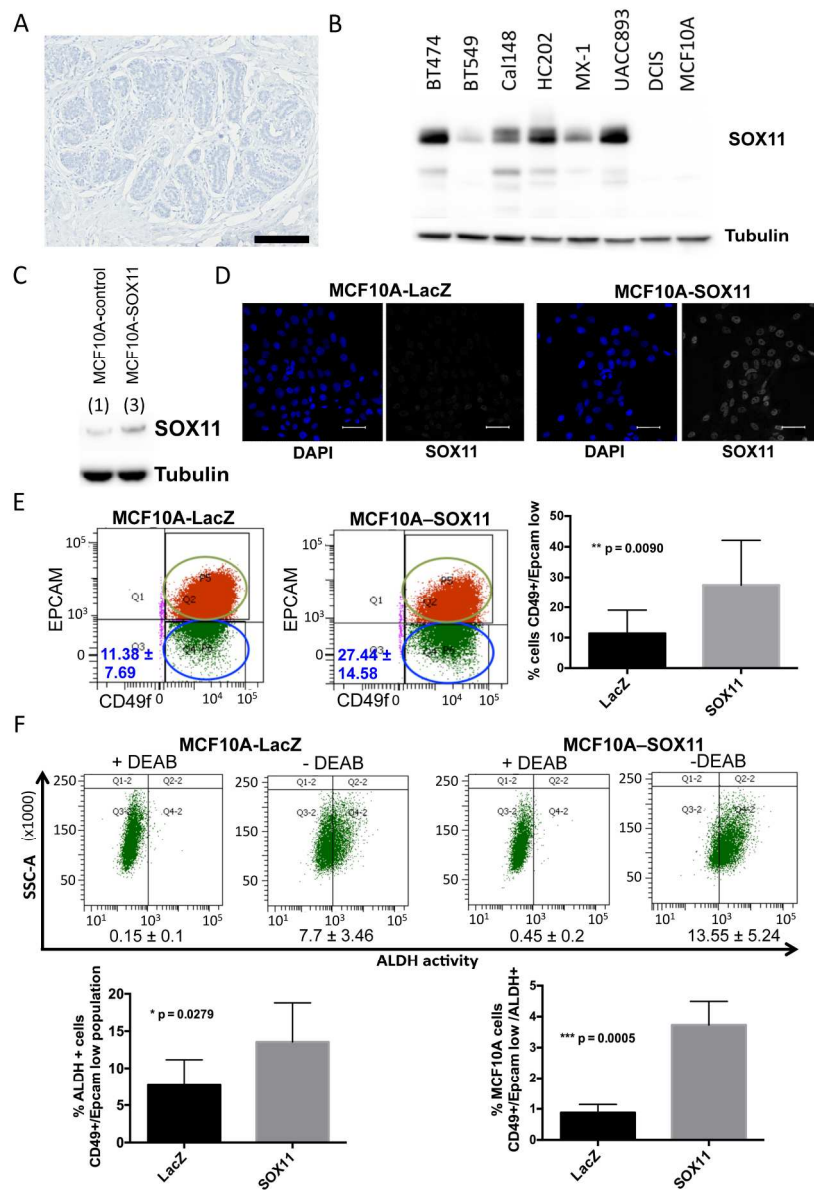
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170x244mm (300 x 300 DPI)

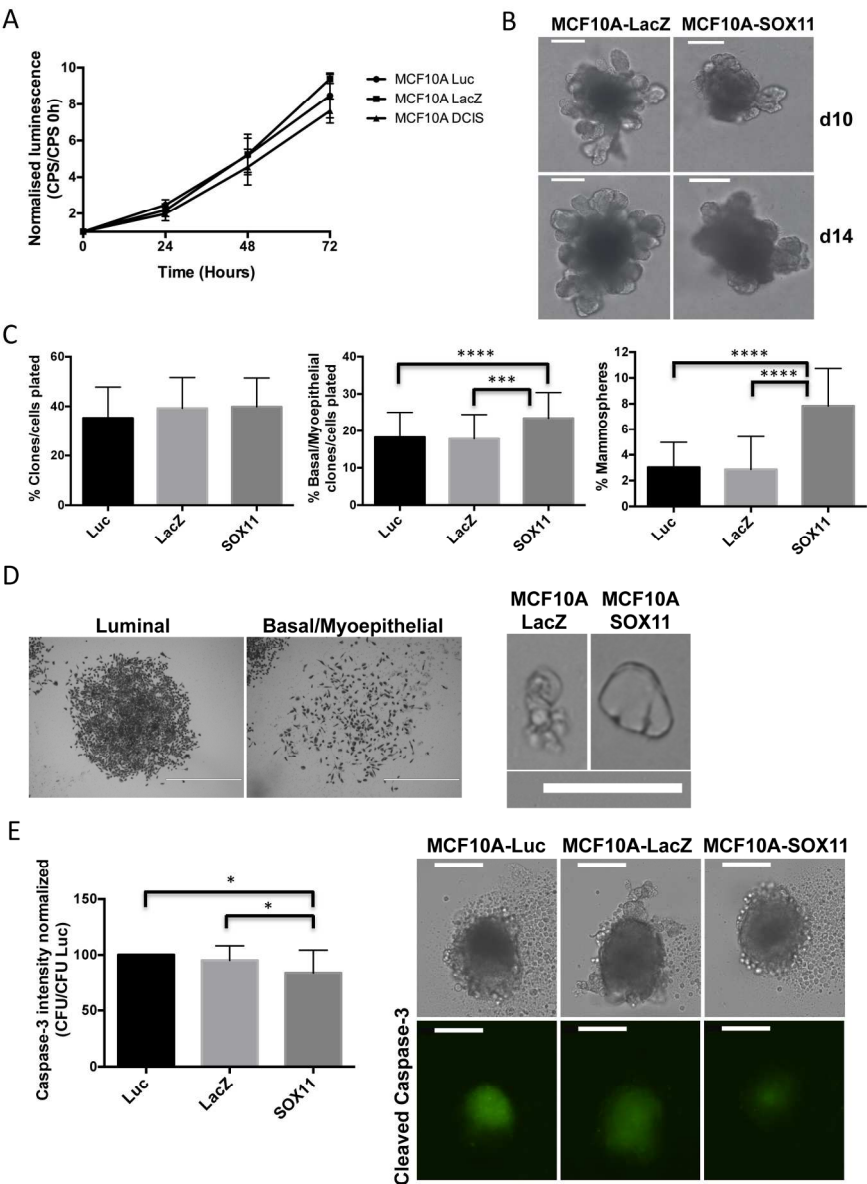


Figure 2

170x220mm (300 x 300 DPI)

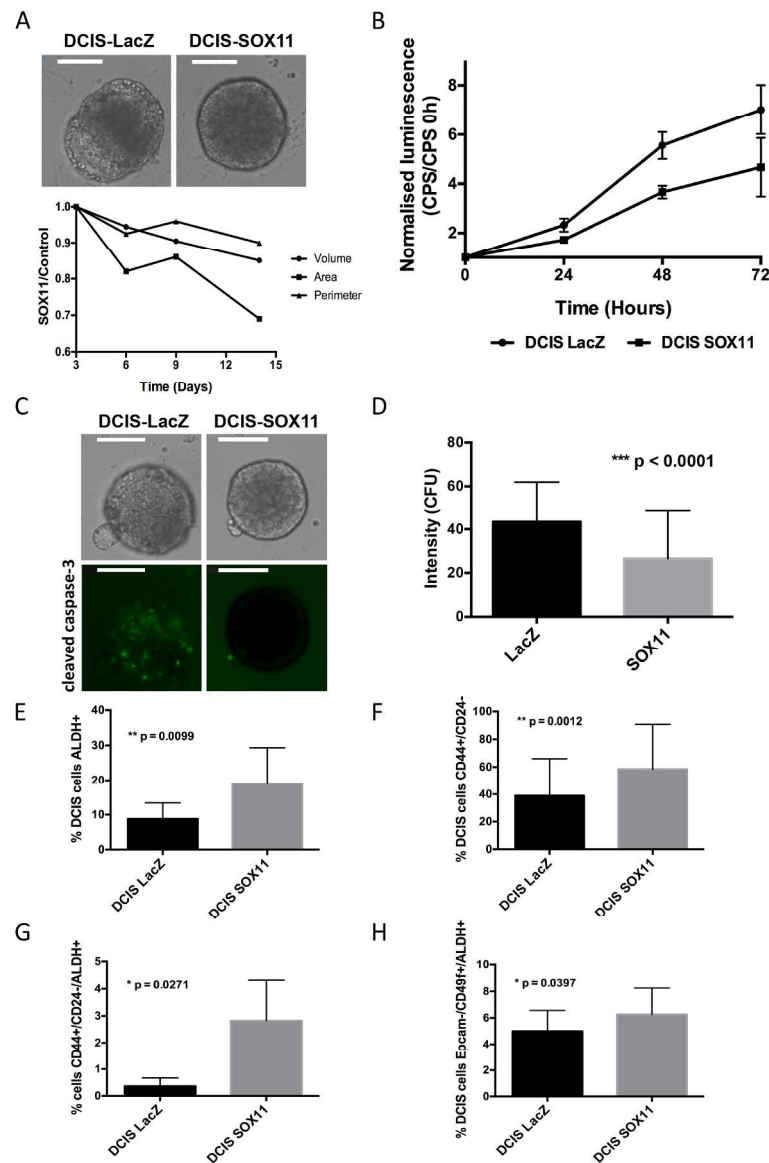


Figure 3

160x250mm (300 x 300 DPI)

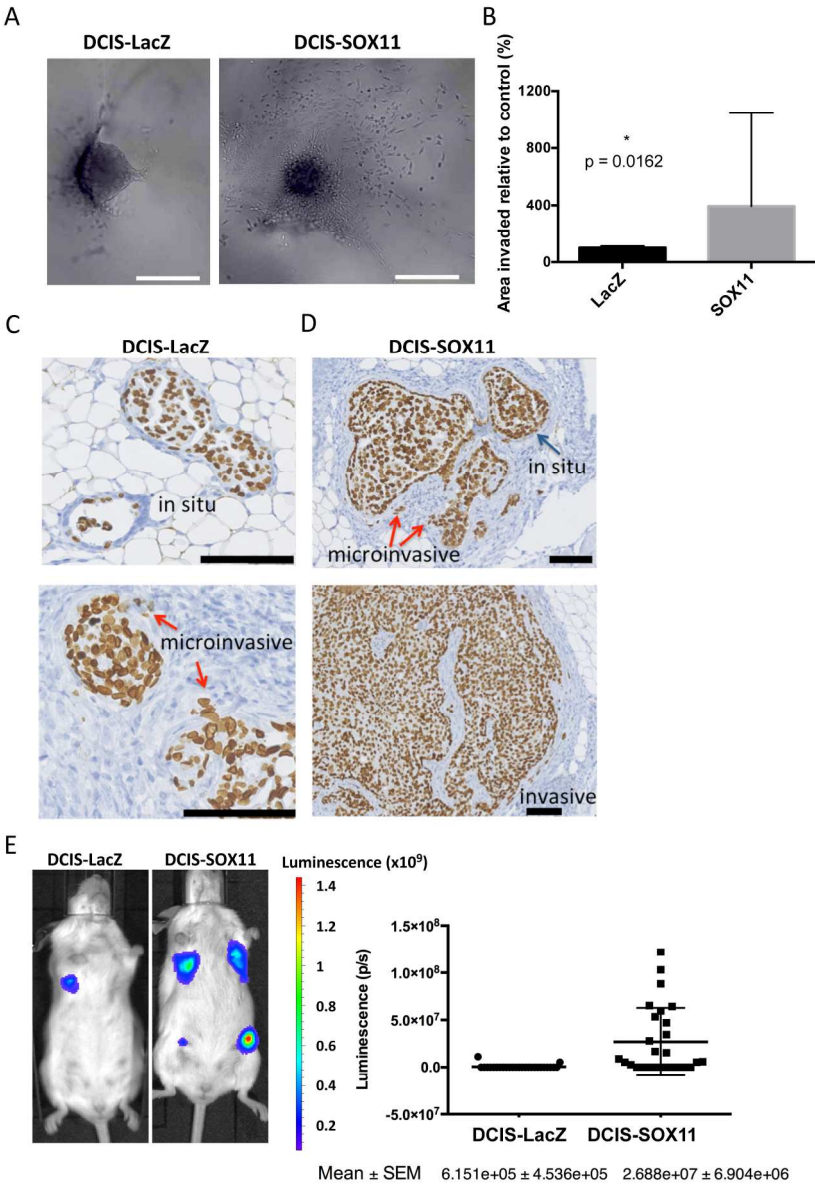


Figure 4

170x244mm (300 x 300 DPI)

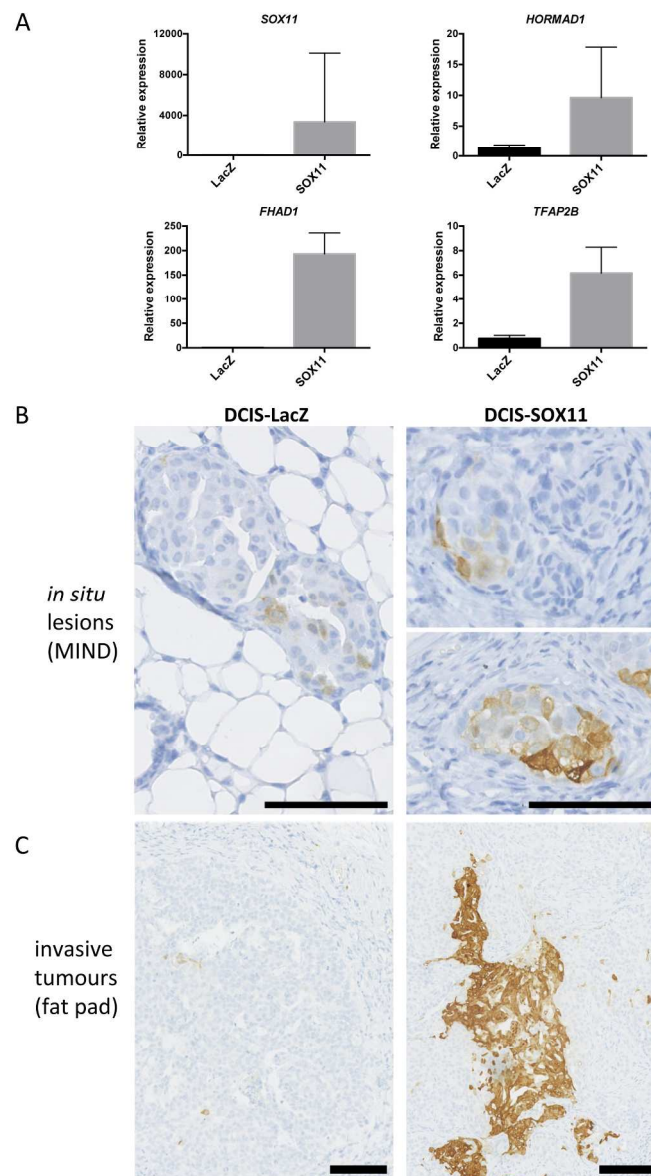


Figure 5

144x251mm (300 x 300 DPI)

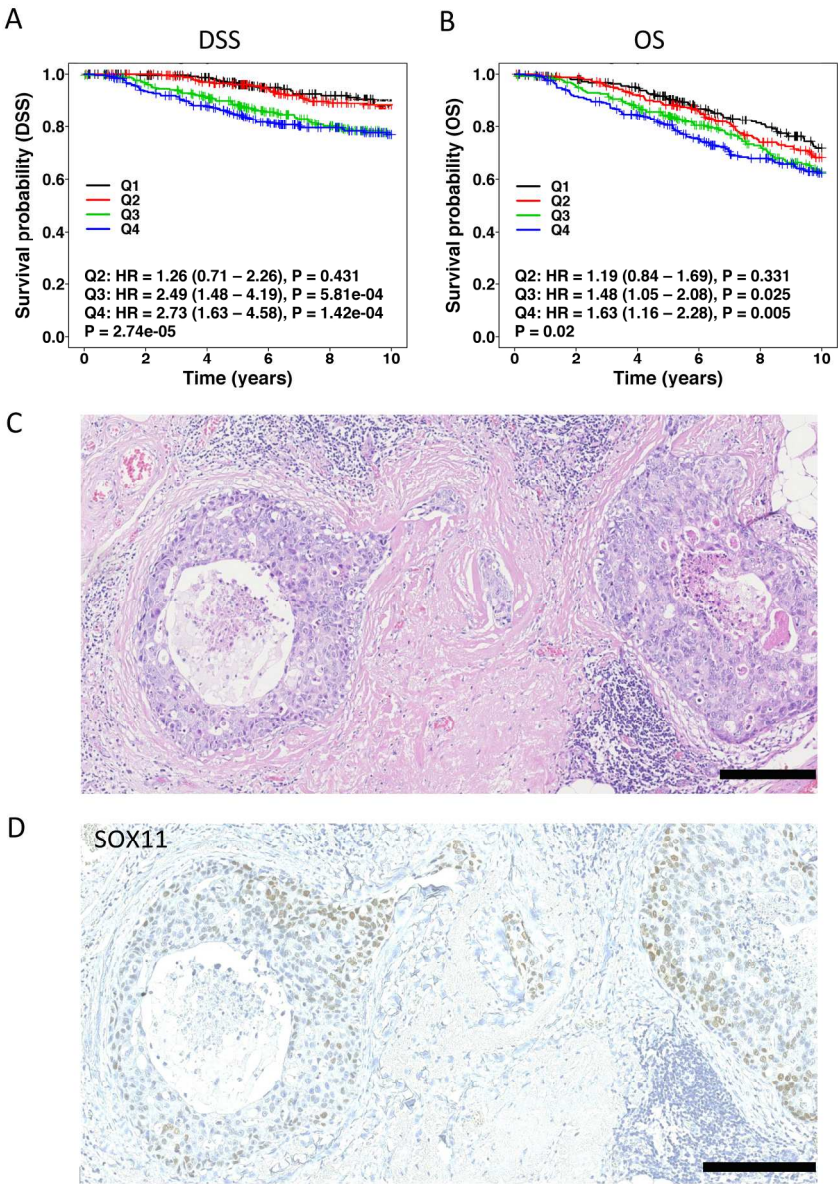


Figure 6

170x234mm (300 x 300 DPI)

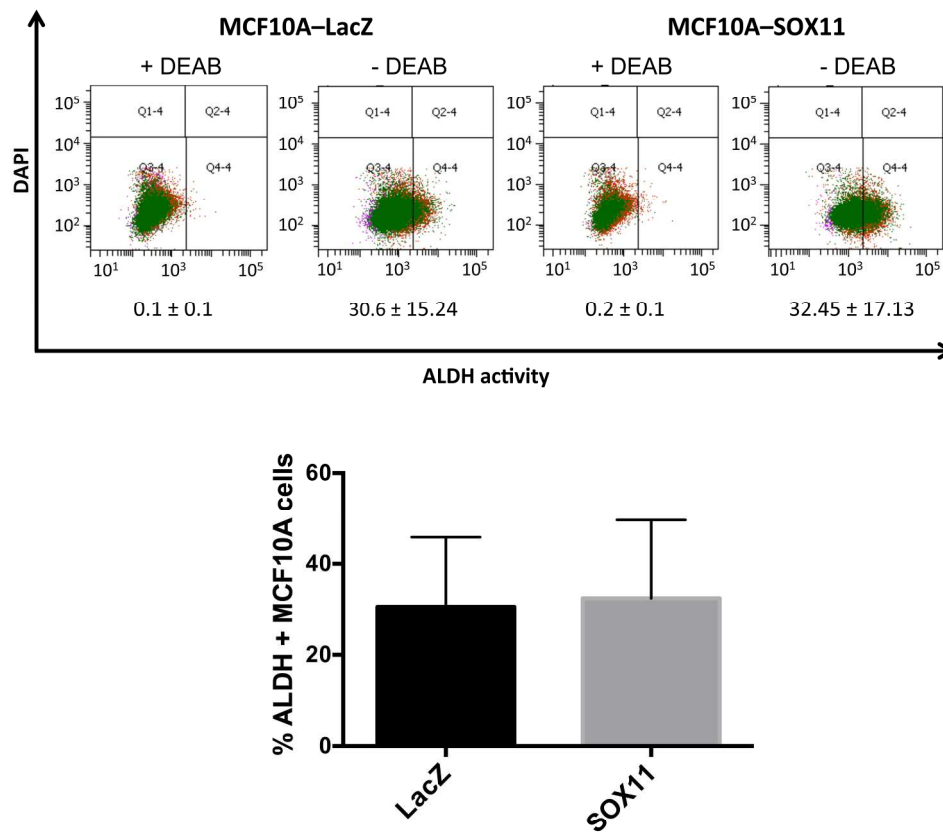


Figure S1

210x239mm (300 x 300 DPI)

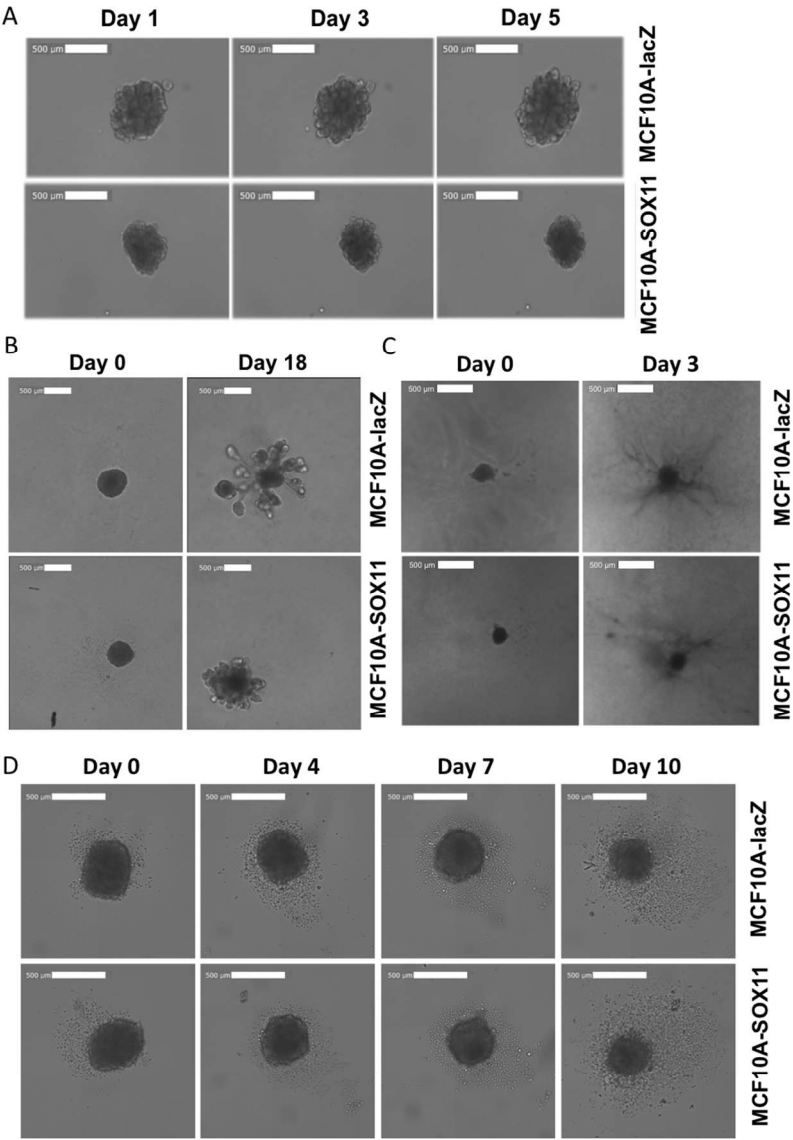


Figure S2

352x509mm (72 x 72 DPI)



Figure S3

67x85mm (300 x 300 DPI)

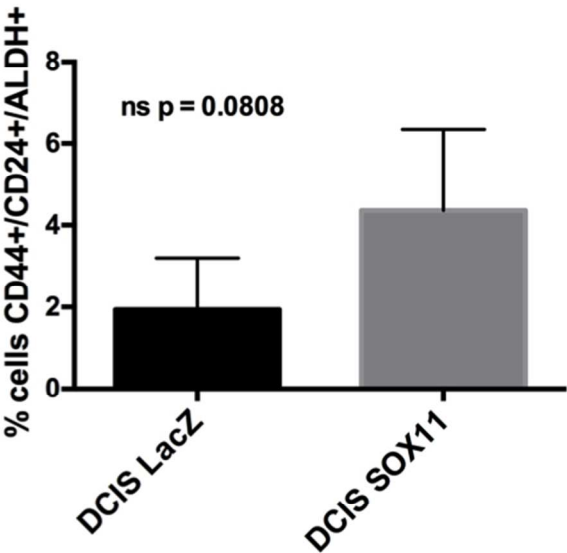
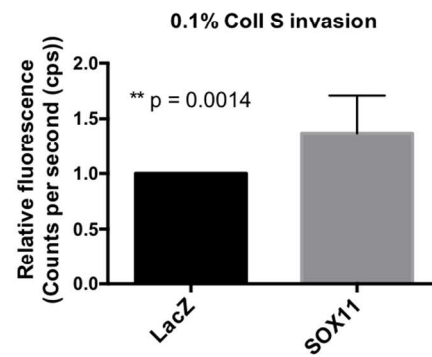


Figure S4

282x357mm (72 x 72 DPI)

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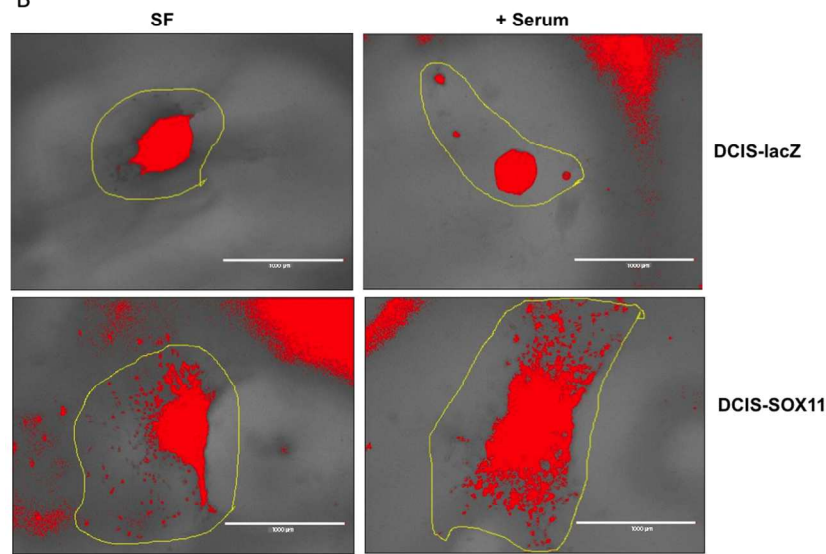


Figure S5

352x509mm (72 x 72 DPI)

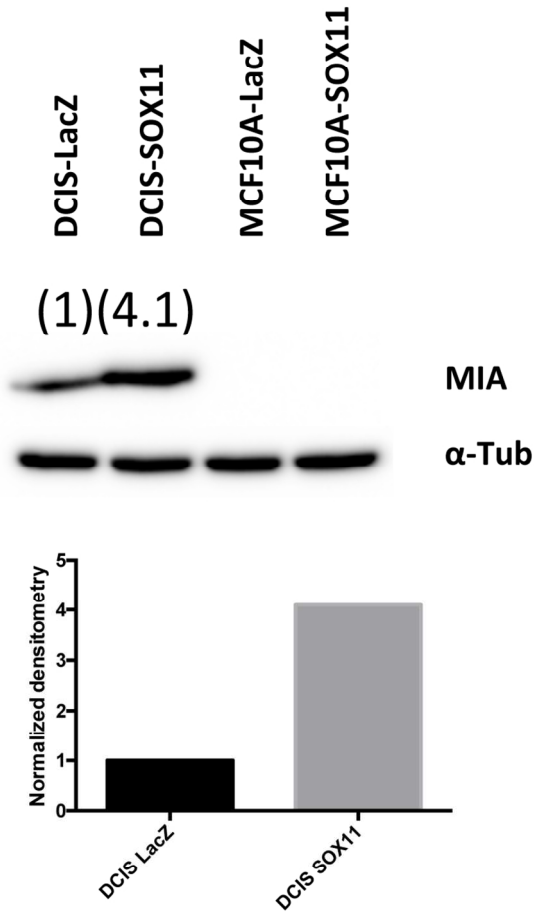


Figure S6

89x141mm (300 x 300 DPI)

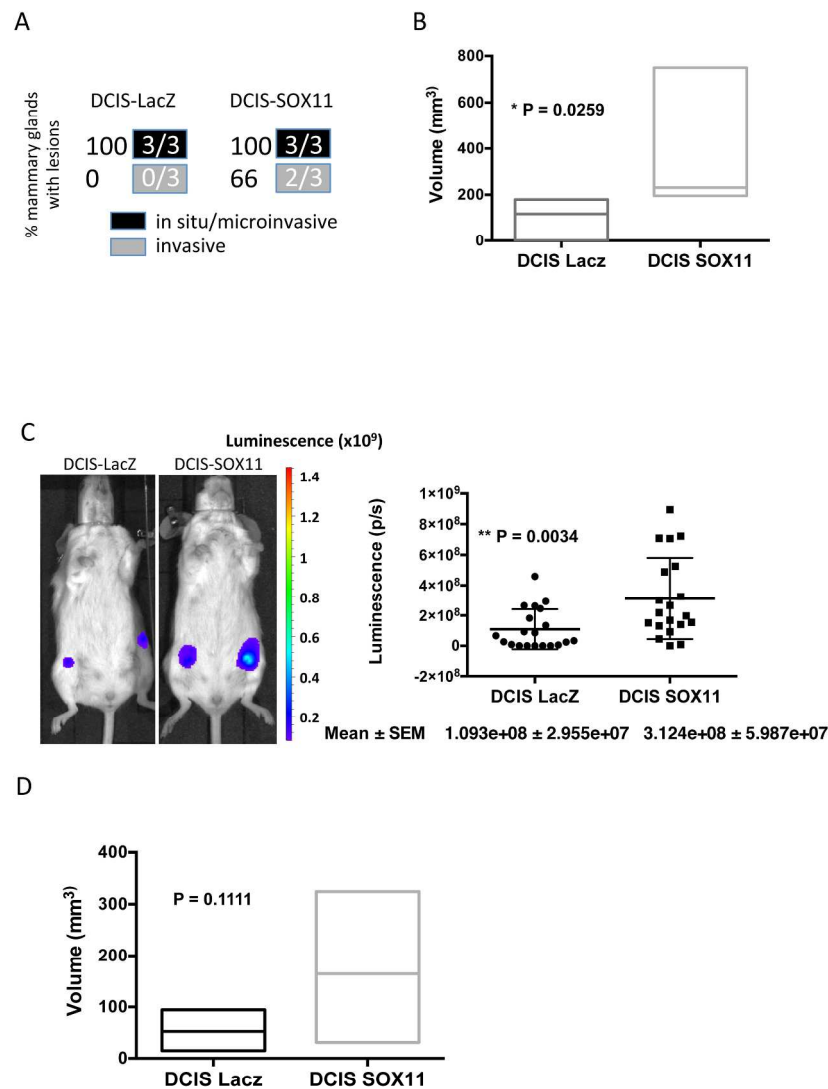


Figure S7

191x274mm (300 x 300 DPI)

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SOX11+ ER- DCIS case

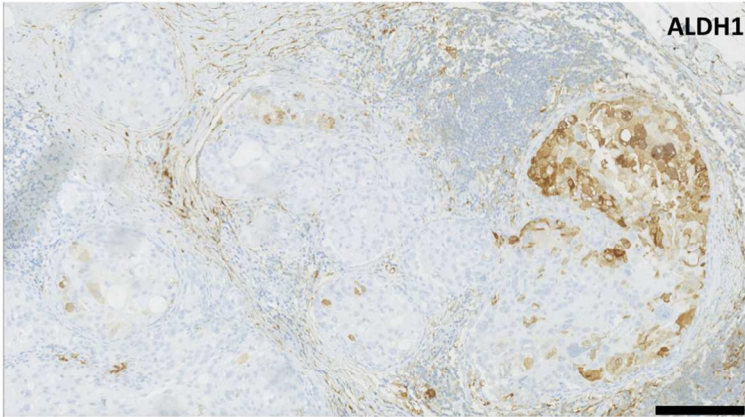


Figure S8

352x509mm (72 x 72 DPI)

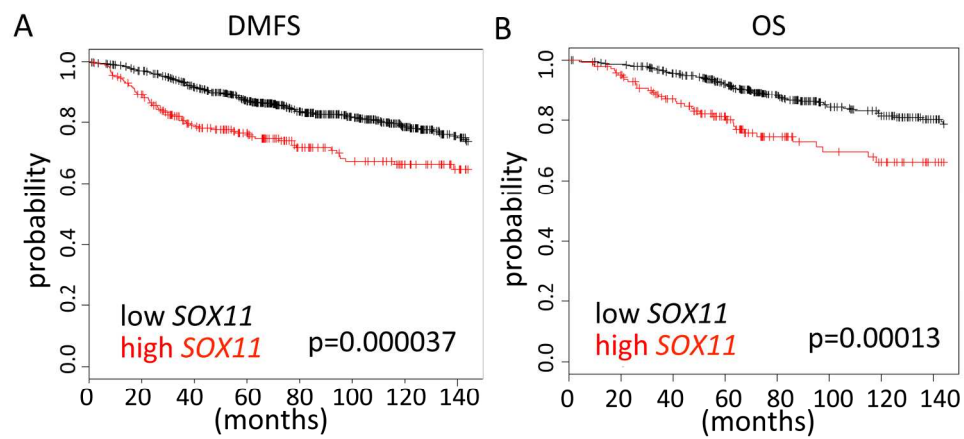


Figure S9

182x107mm (300 x 300 DPI)

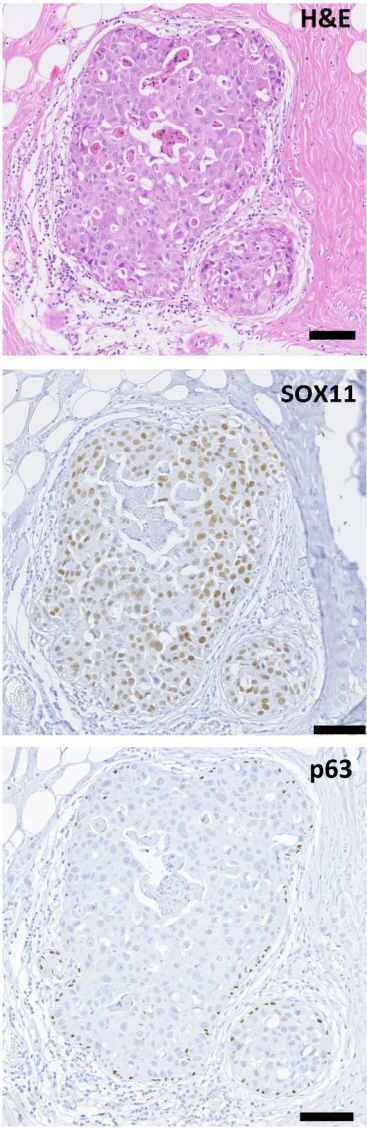


Figure S10A

167x271mm (300 x 300 DPI)

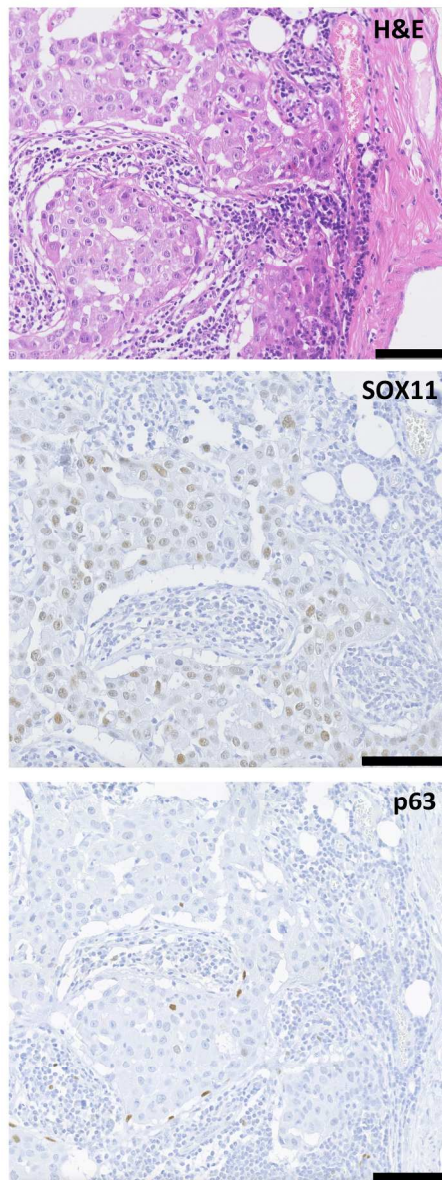


Figure S10B

169x270mm (300 x 300 DPI)

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Table S1A. Cell lines used in Figure 1

Cell line	Origin	Media
MCF10A	ATCC; LGC Standards (Middlesex, UK)	DMEM/F12 (ThermoFisher Scientific) 5% Horse serum(ThermoFisher Scientific) 20 ng/ml epidermal growth factor (EGF) (Peprotech, London, UK) 500 ng/ml hydrocortisone (Sigma, Poole, UK) 100 ng/ml cholera toxin (Sigma) 10 mg/ml insulin (Sigma)
MCF10DCIS.com	Dr. Gillian Farnie	Advanced DMEM/F12 (ThermoFisher Scientific) 5% Horse serum
BT474	CLS Cell lines service	DMEM:F12 2 mM L-glutamine (Sigma) 5µg/ml Insulin 5% FBS (ThermoFisher Scientific)
BT549	ATCC	RPMI-1640 (ThermoFisher Scientific) 10% FBS 0.023 IU/ml insulin
Cal148	CLS (Eppelheim, Germany)	DMEM (ThermoFisher Scientific) 20% FBS 10ng/ml EGF
HCC202	Dr. Paul Huang, ICR, London	RPMI-1640 10% FBS
MX-1	DSMZ (Braunschweig, Germany)	DMEM:F12 5% FBS
UACC893	ATCC	Leibovitz's L-15 Medium (ThermoFisher Scientific) 10% FBS

SF Media
DMEM/F12 (ThermoFisher Scientific)
0.5% Horse serum(ThermoFisher Scientific)
500 ng/ml hydrocortisone (Sigma, Poole, UK)
100 ng/ml cholera toxin (Sigma)
10 mg/ml insulin (Sigma)
Advanced DMEM/F12 (ThermoFisher Scientific)
0.5% Horse serum

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Table S1B. Antibodies and protocol used in Immunofluorescence

Protein	Antibody
SOX11	Mouse monoclonal clone SOX11-C1 50-9773-82 (Ebioscience)

Cells were fixed with 4% paraformaldehyde and permeabilised in 0.25% Triton X-100.

Cells were fixed with 4% paraformaldehyde and permeabilised in 0.25% Triton X-100. Primary antibody was diluted in PBS plus 1% BSA. After washing, cells were incubated with secondary antibody (dilution 1:200) and DAPI (1:5000).

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Concentration	Fixation
1:200	4% PFA

Triton X-100. Primary antibody was diluted in PBS plus 1% BSA. After washin

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g, cells were incubated with secondary antibody (dilution 1:200) and DAPI (1:50)

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Table S1C. Antibodies used in Western blots

Protein	Antibody	Concentration
SOX11	Rabbit monoclonal Clone EPR8191(2) ab170916 (Abcam)	1:1000
MIA	Rabbit monoclonal Clone EPR15597 ab186731 (Abcam)	1:500
B-Tubulin	Mouse monoclonal T4026 (Sigma)	1:5000

Table S2. TaqMan Gene Expression Assays and protocol used in qRT-PCR

Gene	Probe	Dye
SOX11	Hs00846583_s1	FAM
HORMAD1	Hs00933665_s1	FAM
FHAD1	Hs00948384_s1	FAM
TFAP2B	Hs01560931_m1	FAM
GAPDH	Hs02786624_g1	VIC

The expressions of the listed genes were analyzed with qRT-PCR by using specific TaqMan Gene Expression Assay (Applied Biosystems, Life Technologies Corporation, Carlsbad, CA, USA) combined with FAM and normalized against GAPDH combined with VIC and analyzed as described previously in [16]. Melting temperature (T_m) = 58C for SOX11 and 60C for the rest of the probes

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Table S3. Antibodies used in Immunohistochemistry

Protein	Antibody	Concentration	Antigen retrival	Fixation
SOX11	Rabbit monoclonal Clone EPR8191(2) ab170916 (Abcam)	1:500	Pressure cooker Buffer citrate pH=6	Formalin
SOX11	Mouse monoclonal Clone SOX11-c1 50-9773-82 (EBioscience)	1:50	Pressure cooker Buffer citrate pH=6	Formalin
Lamin A + C	Rabbit monoclonal Clone EPR4100 ab108595 (Abcam)	1 : 500	Pressure cooker Buffer citrate pH=6	Formalin
p63	Mouse monoclonal Clone DAK-p63 M7317 (Dako)	1 : 50	Module Buffer pH=9	Formalin
ALDH1	Mouse monoclonal Clone 44/ALDH 611195 (BD)	1:50	Pressure cooker Buffer citrate pH=6	Formalin

Table S4B. Functional annotation clustering of upregulated genes in lesions and tumours fi

Annotation C| Enrichment Score: 2.276104154631925

Category	Term	Count	%
GOTERM_CC	GO:0044459~plasma membrane part	28	24.3478261
GOTERM_CC	GO:0005886~plasma membrane	38	33.0434783
SP_PIR_KEYM	membrane	40	34.7826087

Annotation C| Enrichment Score: 2.200847173304515

Category	Term	Count	%
SP_PIR_KEYM	Secreted	21	18.2608696
GOTERM_CC	GO:0044421~extracellular region part	15	13.0434783
GOTERM_CC	GO:0005576~extracellular region	23	20
GOTERM_CC	GO:0005615~extracellular space	9	7.82608696

Annotation C| Enrichment Score: 2.150760645162709

Category	Term	Count	%
GOTERM_BP	GO:0007155~cell adhesion	12	10.4347826
GOTERM_BP	GO:0022610~biological adhesion	12	10.4347826
SP_PIR_KEYM	cell adhesion	8	6.95652174

Annotation C| Enrichment Score: 2.0539507427984467

Category	Term	Count	%
SP_PIR_KEYM	signal	32	27.826087
UP_SEQ_FEA	signal peptide	32	27.826087
SP_PIR_KEYM	glycoprotein	37	32.173913
SP_PIR_KEYM	disulfide bond	27	23.4782609
UP_SEQ_FEA	disulfide bond	26	22.6086957
UP_SEQ_FEA	glycosylation site:N-linked (GlcNAc...)	34	29.5652174

Annotation C| Enrichment Score: 1.891291598877015

Category	Term	Count	%
GOTERM_CC	GO:0044421~extracellular region part	15	13.0434783
GOTERM_CC	GO:0005578~proteinaceous extracellular matrix	8	6.95652174
GOTERM_CC	GO:0031012~extracellular matrix	8	6.95652174
SP_PIR_KEYM	extracellular matrix	3	2.60869565

Annotation C| Enrichment Score: 1.6194682294865985

Category	Term	Count	%
GOTERM_BP	GO:0006461~protein complex assembly	9	7.82608696
GOTERM_BP	GO:0070271~protein complex biogenesis	9	7.82608696
GOTERM_BP	GO:0065003~macromolecular complex assembly	10	8.69565217

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4	GOTERM_BP_	GO:0043933~macromolecular complex subunit c	10	8.69565217
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6	Annotation C	Enrichment Score: 1.4575535436794433		
7	Category	Term	Count	%
8				
9	GOTERM_CC_	GO:0044459~plasma membrane part	28	24.3478261
10	GOTERM_CC_	GO:0005887~integral to plasma membrane	13	11.3043478
11	GOTERM_CC_	GO:0031226~intrinsic to plasma membrane	13	11.3043478
12	GOTERM_CC_	GO:0016021~integral to membrane	31	26.9565217
13				
14				
15	Annotation C	Enrichment Score: 1.2785333109067836		
16	Category	Term	Count	%
17				
18	GOTERM_CC_	GO:0030055~cell-substrate junction	5	4.34782609
19	GOTERM_CC_	GO:0005925~focal adhesion	4	3.47826087
20	GOTERM_CC_	GO:0005924~cell-substrate adherens junction	4	3.47826087
21	GOTERM_CC_	GO:0016323~basolateral plasma membrane	5	4.34782609
22	GOTERM_CC_	GO:0005912~adherens junction	4	3.47826087
23	GOTERM_CC_	GO:0070161~anchoring junction	4	3.47826087
24	GOTERM_CC_	GO:0005856~cytoskeleton	7	6.08695652
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29	Annotation C	Enrichment Score: 1.2249876679157494		
30	Category	Term	Count	%
31				
32	UP_SEQ_FEA	calcium-binding region:2; high affinity	3	2.60869565
33	SP_PIR_KEYW	inflammation	3	2.60869565
34	PIR_SUPERFA	PIRSF002353:S-100 protein	3	2.60869565
35	INTERPRO	IPR013787:S100/CaBP-9k-type, calcium binding,	3	2.60869565
36	INTERPRO	IPR001751:S100/CaBP-9k-type, calcium binding	3	2.60869565
37	SP_PIR_KEYW	calcium binding	4	3.47826087
38	SP_PIR_KEYW	EF hand	3	2.60869565
39	UP_SEQ_FEA	domain:EF-hand 2	4	3.47826087
40	UP_SEQ_FEA	domain:EF-hand 1	4	3.47826087
41	INTERPRO	IPR018249:EF-HAND 2	4	3.47826087
42	INTERPRO	IPR018247:EF-HAND 1	4	3.47826087
43	SP_PIR_KEYW	calcium	8	6.95652174
44	INTERPRO	IPR011992:EF-Hand type	4	3.47826087
45	INTERPRO	IPR018248:EF hand	3	2.60869565
46	GOTERM_MF	GO:0005509~calcium ion binding	8	6.95652174
47	GOTERM_BP_	GO:0006952~defense response	5	4.34782609
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51	Annotation C	Enrichment Score: 1.170093458152275		
52	Category	Term	Count	%
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54	INTERPRO	IPR003598:Immunoglobulin subtype 2	6	5.2173913
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SMART	SM00408:IGc2	6	5.2173913
INTERPRO	IPR007110:Immunoglobulin-like	8	6.95652174
SP_PIR_KEYW	Immunoglobulin domain	7	6.08695652
INTERPRO	IPR013098:Immunoglobulin I-set	4	3.47826087
INTERPRO	IPR013783:Immunoglobulin-like fold	8	6.95652174
UP_SEQ_FEA	domain:Ig-like C2-type	3	2.60869565
INTERPRO	IPR013151:Immunoglobulin	4	3.47826087
INTERPRO	IPR003599:Immunoglobulin subtype	4	3.47826087
SMART	SM00409:IG	4	3.47826087

Annotation C Enrichment Score: 0.8454072787236593

Category	Term	Count	%
GOTERM_BP	GO:0030036~actin cytoskeleton organization	5	4.34782609
GOTERM_BP	GO:0030029~actin filament-based process	5	4.34782609
SP_PIR_KEYW	cytoskeleton	6	5.2173913
GOTERM_BP	GO:0007010~cytoskeleton organization	5	4.34782609

Annotation C Enrichment Score: 0.8121312997056731

Category	Term	Count	%
SP_PIR_KEYW	SH2 domain	3	2.60869565
INTERPRO	IPR000980:SH2 motif	3	2.60869565
SMART	SM00252:SH2	3	2.60869565

Annotation C Enrichment Score: 0.7444249869610265

Category	Term	Count	%
GOTERM_BP	GO:0009611~response to wounding	7	6.08695652
GOTERM_BP	GO:0050817~coagulation	3	2.60869565
GOTERM_BP	GO:0007596~blood coagulation	3	2.60869565
GOTERM_BP	GO:0007599~hemostasis	3	2.60869565
GOTERM_BP	GO:0050878~regulation of body fluid levels	3	2.60869565
GOTERM_BP	GO:0042060~wound healing	3	2.60869565

Annotation C Enrichment Score: 0.7397981801859044

Category	Term	Count	%
GOTERM_BP	GO:0001501~skeletal system development	6	5.2173913
GOTERM_BP	GO:0048705~skeletal system morphogenesis	3	2.60869565
GOTERM_BP	GO:0048562~embryonic organ morphogenesis	3	2.60869565
GOTERM_BP	GO:0048568~embryonic organ development	3	2.60869565
GOTERM_BP	GO:0048598~embryonic morphogenesis	4	3.47826087

Annotation C Enrichment Score: 0.7189980095131909

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4	Category	Term	Count	%
5	SP_PIR_KEYW	glycoprotein	37	32.173913
6	UP_SEQ_FEA	glycosylation site:N-linked (GlcNAc...)	34	29.5652174
7	UP_SEQ_FEA	topological domain:Cytoplasmic	26	22.6086957
8	UP_SEQ_FEA	topological domain:Extracellular	20	17.3913043
9	SP_PIR_KEYW	membrane	40	34.7826087
10	UP_SEQ_FEA	transmembrane region	30	26.0869565
11	SP_PIR_KEYW	transmembrane	30	26.0869565
12	GOTERM_CC	GO:0031224~intrinsic to membrane	33	28.6956522
13	GOTERM_CC	GO:0016021~integral to membrane	31	26.9565217
14				
15	Annotation C	Enrichment Score: 0.7102397180101913		
16	Category	Term	Count	%
17	INTERPRO	IPR018029:C2 membrane targeting protein	3	2.60869565
18	INTERPRO	IPR000008:C2 calcium-dependent membrane tar	3	2.60869565
19	SMART	SM00239:C2	3	2.60869565
20				
21	Annotation C	Enrichment Score: 0.707301400421292		
22	Category	Term	Count	%
23	INTERPRO	IPR011993:Pleckstrin homology-type	5	4.34782609
24	UP_SEQ_FEA	domain:PH	4	3.47826087
25	INTERPRO	IPR001849:Pleckstrin homology	4	3.47826087
26	SMART	SM00233:PH	4	3.47826087
27				
28	Annotation C	Enrichment Score: 0.688623308686788		
29	Category	Term	Count	%
30	GOTERM_BP	GO:0070201~regulation of establishment of prot	4	3.47826087
31	GOTERM_BP	GO:0032880~regulation of protein localization	4	3.47826087
32	GOTERM_BP	GO:0051222~positive regulation of protein trans	3	2.60869565
33	GOTERM_BP	GO:0051223~regulation of protein transport	3	2.60869565
34	GOTERM_BP	GO:0051050~positive regulation of transport	4	3.47826087
35	GOTERM_BP	GO:0060341~regulation of cellular localization	3	2.60869565
36	GOTERM_BP	GO:0042981~regulation of apoptosis	6	5.2173913
37	GOTERM_BP	GO:0043067~regulation of programmed cell dea	6	5.2173913
38	GOTERM_BP	GO:0010941~regulation of cell death	6	5.2173913
39				
40	Annotation C	Enrichment Score: 0.5957106316173822		
41	Category	Term	Count	%
42	GOTERM_BP	GO:0030031~cell projection assembly	3	2.60869565
43	GOTERM_BP	GO:0006928~cell motion	5	4.34782609
44	GOTERM_BP	GO:0030030~cell projection organization	4	3.47826087
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Annotation C Enrichment Score: 0.5798437829465366

Category	Term	Count	%
GOTERM_BP	GO:0001568~blood vessel development	4	3.47826087
GOTERM_BP	GO:0001944~vasculature development	4	3.47826087
GOTERM_BP	GO:0001525~angiogenesis	3	2.60869565
GOTERM_BP	GO:0048514~blood vessel morphogenesis	3	2.60869565

Annotation C Enrichment Score: 0.558487459547507

Category	Term	Count	%
UP_SEQ_FEA	short sequence motif:Selectivity filter	3	2.60869565
GOTERM_CC	GO:0008076~voltage-gated potassium channel c	3	2.60869565
GOTERM_CC	GO:0034705~potassium channel complex	3	2.60869565
GOTERM_MF	GO:0005249~voltage-gated potassium channel a	3	2.60869565
SP_PIR_KEYM	potassium transport	3	2.60869565
SP_PIR_KEYM	potassium	3	2.60869565
GOTERM_MF	GO:0031420~alkali metal ion binding	4	3.47826087
GOTERM_MF	GO:0030955~potassium ion binding	3	2.60869565
GOTERM_CC	GO:0034703~cation channel complex	3	2.60869565
GOTERM_MF	GO:0005267~potassium channel activity	3	2.60869565
SP_PIR_KEYM	voltage-gated channel	3	2.60869565
GOTERM_MF	GO:0022843~voltage-gated cation channel activi	3	2.60869565
GOTERM_MF	GO:0015267~channel activity	5	4.34782609
GOTERM_MF	GO:0022803~passive transmembrane transporte	5	4.34782609
GOTERM_BP	GO:0006813~potassium ion transport	3	2.60869565
GOTERM_MF	GO:0022836~gated channel activity	4	3.47826087
GOTERM_BP	GO:0015672~monovalent inorganic cation transp	4	3.47826087
GOTERM_MF	GO:0005244~voltage-gated ion channel activity	3	2.60869565
GOTERM_MF	GO:0022832~voltage-gated channel activity	3	2.60869565
GOTERM_CC	GO:0034702~ion channel complex	3	2.60869565
SP_PIR_KEYM	ion transport	5	4.34782609
GOTERM_MF	GO:0005216~ion channel activity	4	3.47826087
GOTERM_MF	GO:0022838~substrate specific channel activity	4	3.47826087
SP_PIR_KEYM	transport	11	9.56521739
GOTERM_MF	GO:0005261~cation channel activity	3	2.60869565
SP_PIR_KEYM	ionic channel	3	2.60869565
GOTERM_BP	GO:0006811~ion transport	6	5.2173913
GOTERM_BP	GO:0030001~metal ion transport	4	3.47826087
GOTERM_MF	GO:0046873~metal ion transmembrane transpor	3	2.60869565
GOTERM_BP	GO:0006812~cation transport	4	3.47826087

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4	Annotation C Enrichment Score: 0.528996997282999		
5	Category	Term	Count %
6	GOTERM_MF	GO:0008047~enzyme activator activity	5 4.34782609
7	GOTERM_MF	GO:0030695~GTPase regulator activity	5 4.34782609
8	GOTERM_MF	GO:0060589~nucleoside-triphosphatase regulat	5 4.34782609
9	GOTERM_MF	GO:0005096~GTPase activator activity	3 2.60869565
10	GOTERM_MF	GO:0005083~small GTPase regulator activity	3 2.60869565
11			
12			
13			
14	Annotation C Enrichment Score: 0.5254204526484613		
15	Category	Term	Count %
16	GOTERM_BP	GO:0009611~response to wounding	7 6.08695652
17	GOTERM_BP	GO:0006954~inflammatory response	4 3.47826087
18	GOTERM_BP	GO:0006952~defense response	5 4.34782609
19			
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22	Annotation C Enrichment Score: 0.5080990671511021		
23	Category	Term	Count %
24	SP_PIR_KEYM	lipoprotein	10 8.69565217
25	UP_SEQ_FEA	nucleotide phosphate-binding region:GTP	6 5.2173913
26	SP_PIR_KEYM	gtp-binding	6 5.2173913
27	GOTERM_MF	GO:0003924~GTPase activity	5 4.34782609
28	SP_PIR_KEYM	transferase	14 12.173913
29	GOTERM_MF	GO:0005525~GTP binding	6 5.2173913
30	UP_SEQ_FEA	lipid moiety-binding region:S-palmitoyl cysteine	4 3.47826087
31	GOTERM_MF	GO:0019001~guanyl nucleotide binding	6 5.2173913
32	GOTERM_MF	GO:0032561~guanyl ribonucleotide binding	6 5.2173913
33	SP_PIR_KEYM	palmitate	4 3.47826087
34	SP_PIR_KEYM	tyrosine-protein kinase	3 2.60869565
35	KEGG_PATHV	hsa04916:Melanogenesis	3 2.60869565
36	GOTERM_BP	GO:0007187~G-protein signaling, coupled to cyc	3 2.60869565
37	GOTERM_BP	GO:0019935~cyclic-nucleotide-mediated signalir	3 2.60869565
38	GOTERM_BP	GO:0007243~protein kinase cascade	5 4.34782609
39	SP_PIR_KEYM	nucleotide-binding	13 11.3043478
40	GOTERM_MF	GO:0004713~protein tyrosine kinase activity	3 2.60869565
41	UP_SEQ_FEA	domain:Protein kinase	5 4.34782609
42	INTERPRO	IPR017441:Protein kinase, ATP binding site	5 4.34782609
43	SP_PIR_KEYM	phosphotransferase	3 2.60869565
44	INTERPRO	IPR000719:Protein kinase, core	5 4.34782609
45	SP_PIR_KEYM	kinase	6 5.2173913
46	SP_PIR_KEYM	serine/threonine-protein kinase	4 3.47826087
47	UP_SEQ_FEA	binding site:ATP	5 4.34782609
48	INTERPRO	IPR008271:Serine/threonine protein kinase, activ	4 3.47826087
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INTERPRO	IPR017442:Serine/threonine protein kinase-relat	4	3.47826087
GOTERM_MF	GO:0017076~purine nucleotide binding	14	12.173913
GOTERM_BP	GO:0006793~phosphorus metabolic process	8	6.95652174
GOTERM_BP	GO:0006796~phosphate metabolic process	8	6.95652174
GOTERM_BP	GO:0019932~second-messenger-mediated signa	3	2.60869565
INTERPRO	IPR002290:Serine/threonine protein kinase	3	2.60869565
UP_SEQ_FEA	nucleotide phosphate-binding region:ATP	7	6.08695652
GOTERM_MF	GO:0032555~purine ribonucleotide binding	13	11.3043478
GOTERM_MF	GO:0032553~ribonucleotide binding	13	11.3043478
GOTERM_MF	GO:0004674~protein serine/threonine kinase ac	4	3.47826087
SMART	SM00220:S_TKc	3	2.60869565
UP_SEQ_FEA	active site:Proton acceptor	5	4.34782609
GOTERM_MF	GO:0004672~protein kinase activity	5	4.34782609
GOTERM_BP	GO:0016310~phosphorylation	6	5.2173913
GOTERM_BP	GO:0006468~protein amino acid phosphorylatio	5	4.34782609
GOTERM_MF	GO:0000166~nucleotide binding	14	12.173913
SP_PIR_KEYM	transducer	5	4.34782609
GOTERM_BP	GO:0007166~cell surface receptor linked signal t	11	9.56521739
SP_PIR_KEYM	atp-binding	7	6.08695652
GOTERM_MF	GO:0030554~adenyl nucleotide binding	8	6.95652174
GOTERM_MF	GO:0001883~purine nucleoside binding	8	6.95652174
GOTERM_MF	GO:0001882~nucleoside binding	8	6.95652174
GOTERM_MF	GO:0005524~ATP binding	7	6.08695652
GOTERM_MF	GO:0032559~adenyl ribonucleotide binding	7	6.08695652
GOTERM_BP	GO:0007186~G-protein coupled receptor proteir	5	4.34782609
SP_PIR_KEYM	g-protein coupled receptor	3	2.60869565
SP_PIR_KEYM	receptor	5	4.34782609

Annotation C Enrichment Score: 0.4959651442377764

Category	Term	Count	%
GOTERM_BP	GO:0016477~cell migration	4	3.47826087
GOTERM_BP	GO:0048870~cell motility	4	3.47826087
GOTERM_BP	GO:0051674~localization of cell	4	3.47826087
GOTERM_BP	GO:0006928~cell motion	5	4.34782609

Annotation C Enrichment Score: 0.4888290002273781

Category	Term	Count	%
INTERPRO	IPR000210:BTB/POZ-like	3	2.60869565
INTERPRO	IPR011333:BTB/POZ fold	3	2.60869565
SMART	SM00225:BTB	3	2.60869565

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4	Annotation C	Enrichment Score: 0.4019758865026175		
5	Category	Term	Count	%
6	SP_PIR_KEYM	actin-binding	4	3.47826087
7	SP_PIR_KEYM	cytoskeleton	6	5.2173913
8	GOTERM_MF	GO:0003779~actin binding	4	3.47826087
9	GOTERM_MF	GO:0008092~cytoskeletal protein binding	4	3.47826087
10	GOTERM_CC	GO:0005856~cytoskeleton	7	6.08695652
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14	Annotation C	Enrichment Score: 0.3543628688723408		
15	Category	Term	Count	%
16	SP_PIR_KEYM	Signal-anchor	6	5.2173913
17	SP_PIR_KEYM	golgi apparatus	4	3.47826087
18	UP_SEQ_FEA	topological domain:Lumenal	3	2.60869565
19	GOTERM_CC	GO:0005794~Golgi apparatus	5	4.34782609
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23	Annotation C	Enrichment Score: 0.3405179279307354		
24	Category	Term	Count	%
25	GOTERM_BP	GO:0007050~cell cycle arrest	3	2.60869565
26	GOTERM_BP	GO:0022402~cell cycle process	6	5.2173913
27	GOTERM_BP	GO:0007049~cell cycle	7	6.08695652
28	GOTERM_BP	GO:0000278~mitotic cell cycle	3	2.60869565
29	GOTERM_BP	GO:0022403~cell cycle phase	3	2.60869565
30	GOTERM_CC	GO:0044430~cytoskeletal part	3	2.60869565
31				
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35	Annotation C	Enrichment Score: 0.31924234326974626		
36	Category	Term	Count	%
37	UP_SEQ_FEA	zinc finger region:C2H2-type 15	3	2.60869565
38	UP_SEQ_FEA	zinc finger region:C2H2-type 5	6	5.2173913
39	UP_SEQ_FEA	zinc finger region:C2H2-type 14	3	2.60869565
40	UP_SEQ_FEA	zinc finger region:C2H2-type 4	6	5.2173913
41	UP_SEQ_FEA	zinc finger region:C2H2-type 7	5	4.34782609
42	UP_SEQ_FEA	zinc finger region:C2H2-type 2	6	5.2173913
43	UP_SEQ_FEA	zinc finger region:C2H2-type 3	6	5.2173913
44	UP_SEQ_FEA	domain:KRAB	4	3.47826087
45	UP_SEQ_FEA	zinc finger region:C2H2-type 6	5	4.34782609
46	UP_SEQ_FEA	zinc finger region:C2H2-type 13	3	2.60869565
47	INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DN/	6	5.2173913
48	INTERPRO	IPR007087:Zinc finger, C2H2-type	7	6.08695652
49	INTERPRO	IPR001909:Krueppel-associated box	4	3.47826087
50	INTERPRO	IPR015880:Zinc finger, C2H2-like	7	6.08695652
51	UP_SEQ_FEA	zinc finger region:C2H2-type 12	3	2.60869565
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UP_SEQ_FEA`zinc finger region:C2H2-type 8	4	3.47826087
SMART SM00349:KRAB	4	3.47826087
SMART SM00355:ZnF_C2H2	7	6.08695652
GOTERM_MF GO:0043169~cation binding	28	24.3478261
SP_PIR_KEYM zinc	14	12.173913
UP_SEQ_FEA`zinc finger region:C2H2-type 11	3	2.60869565
GOTERM_MF GO:0043167~ion binding	28	24.3478261
SP_PIR_KEYM zinc-finger	11	9.56521739
GOTERM_MF GO:0046872~metal ion binding	27	23.4782609
SP_PIR_KEYM metal-binding	18	15.6521739
UP_SEQ_FEA`zinc finger region:C2H2-type 10	3	2.60869565
GOTERM_MF GO:0046914~transition metal ion binding	18	15.6521739
UP_SEQ_FEA`zinc finger region:C2H2-type 1	4	3.47826087
GOTERM_MF GO:0008270~zinc ion binding	15	13.0434783
SP_PIR_KEYM transcription regulation	12	10.4347826
UP_SEQ_FEA`zinc finger region:C2H2-type 9	3	2.60869565
SP_PIR_KEYM Transcription	12	10.4347826
GOTERM_BP GO:0006350~transcription	12	10.4347826
GOTERM_MF GO:0030528~transcription regulator activity	8	6.95652174
SP_PIR_KEYM dna-binding	9	7.82608696
GOTERM_BP GO:0006355~regulation of transcription, DNA-de	9	7.82608696
GOTERM_BP GO:0051252~regulation of RNA metabolic proce	9	7.82608696
SP_PIR_KEYM nucleus	20	17.3913043
GOTERM_BP GO:0045449~regulation of transcription	13	11.3043478
GOTERM_MF GO:0003677~DNA binding	11	9.56521739

Annotation C|Enrichment Score: 0.3081489488282201

Category	Term	Count	%
GOTERM_BP GO:0043623~cellular protein complex assembly		3	2.60869565
GOTERM_BP GO:0034622~cellular macromolecular complex a		3	2.60869565
GOTERM_BP GO:0034621~cellular macromolecular complex s		3	2.60869565

Annotation C|Enrichment Score: 0.2492554046211798

Category	Term	Count	%
GOTERM_BP GO:0008283~cell proliferation		5	4.34782609
GOTERM_BP GO:0006917~induction of apoptosis		4	3.47826087
GOTERM_BP GO:0012502~induction of programmed cell deat		4	3.47826087
GOTERM_BP GO:0043065~positive regulation of apoptosis		4	3.47826087
GOTERM_BP GO:0043068~positive regulation of programmed		4	3.47826087
GOTERM_BP GO:0010942~positive regulation of cell death		4	3.47826087
GOTERM_BP GO:0042981~regulation of apoptosis		6	5.2173913

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4	GOTERM_BP_GO:0043067~regulation of programmed cell dea	6	5.2173913
5	GOTERM_BP_GO:0010941~regulation of cell death	6	5.2173913
6	GOTERM_BP_GO:0006915~apoptosis	4	3.47826087
7	GOTERM_BP_GO:0012501~programmed cell death	4	3.47826087
8	GOTERM_BP_GO:0008219~cell death	4	3.47826087
9	GOTERM_BP_GO:0016265~death	4	3.47826087
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12	Annotation C Enrichment Score: 0.16860366137863061		
13	Category	Term	Count %
14			
15	GOTERM_BP_GO:0006352~transcription initiation	3	2.60869565
16	GOTERM_BP_GO:0006366~transcription from RNA polymerase	3	2.60869565
17	GOTERM_CC_GO:0044451~nucleoplasm part	5	4.34782609
18	GOTERM_BP_GO:0006351~transcription, DNA-dependent	3	2.60869565
19	GOTERM_BP_GO:0032774~RNA biosynthetic process	3	2.60869565
20	GOTERM_CC_GO:0005654~nucleoplasm	6	5.2173913
21	GOTERM_CC_GO:0005730~nucleolus	4	3.47826087
22	GOTERM_BP_GO:0010629~negative regulation of gene expres	3	2.60869565
23	GOTERM_MF_GO:0030528~transcription regulator activity	8	6.95652174
24	GOTERM_CC_GO:0031981~nuclear lumen	7	6.08695652
25	GOTERM_CC_GO:0031974~membrane-enclosed lumen	9	7.82608696
26	GOTERM_CC_GO:0043233~organelle lumen	8	6.95652174
27	GOTERM_BP_GO:0010605~negative regulation of macromolec	3	2.60869565
28	GOTERM_CC_GO:0070013~intracellular organelle lumen	7	6.08695652
29	GOTERM_CC_GO:0043232~intracellular non-membrane-bound	11	9.56521739
30	GOTERM_CC_GO:0043228~non-membrane-bounded organelle	11	9.56521739
31			
32			

33	Annotation C Enrichment Score: 0.11514283530264263		
34	Category	Term	Count %
35			
36	GOTERM_BP_GO:0043549~regulation of kinase activity	3	2.60869565
37	GOTERM_BP_GO:0051338~regulation of transferase activity	3	2.60869565
38	GOTERM_BP_GO:0042325~regulation of phosphorylation	3	2.60869565
39	GOTERM_BP_GO:0019220~regulation of phosphate metabolic	3	2.60869565
40	GOTERM_BP_GO:0051174~regulation of phosphorus metaboli	3	2.60869565
41			
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43	Annotation C Enrichment Score: 0.10509732228181311		
44	Category	Term	Count %
45			
46	GOTERM_MF_GO:0003712~transcription cofactor activity	3	2.60869565
47	GOTERM_MF_GO:0008134~transcription factor binding	3	2.60869565
48	GOTERM_MF_GO:0030528~transcription regulator activity	8	6.95652174
49			
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51 Annotation C Enrichment Score: 0.07959233331371082

Category	Term	Count	%
GOTERM_CC	GO:0031410~cytoplasmic vesicle	4	3.47826087
GOTERM_CC	GO:0031982~vesicle	4	3.47826087
GOTERM_CC	GO:0016023~cytoplasmic membrane-bounded v	3	2.60869565
GOTERM_CC	GO:0031988~membrane-bounded vesicle	3	2.60869565

Annotation C Enrichment Score: 0.0705041097926874

Category	Term	Count	%
GOTERM_MF	GO:0004175~endopeptidase activity	3	2.60869565
SP_PIR_KEYM	Protease	3	2.60869565
GOTERM_MF	GO:0070011~peptidase activity, acting on L-amir	3	2.60869565
GOTERM_MF	GO:0008233~peptidase activity	3	2.60869565
SP_PIR_KEYM	hydrolase	6	5.2173913
GOTERM_BP	GO:0006508~proteolysis	4	3.47826087

Annotation C Enrichment Score: 0.06059054021672356

Category	Term	Count	%
SP_PIR_KEYM	activator	3	2.60869565
GOTERM_MF	GO:0030528~transcription regulator activity	8	6.95652174
GOTERM_BP	GO:0006357~regulation of transcription from RN	3	2.60869565

Annotation C Enrichment Score: 0.05699378354938989

Category	Term	Count	%
GOTERM_BP	GO:0010628~positive regulation of gene express	4	3.47826087
GOTERM_MF	GO:0043565~sequence-specific DNA binding	4	3.47826087
GOTERM_MF	GO:0030528~transcription regulator activity	8	6.95652174
GOTERM_MF	GO:0003700~transcription factor activity	5	4.34782609
GOTERM_BP	GO:0045941~positive regulation of transcription	3	2.60869565
GOTERM_BP	GO:0045935~positive regulation of nucleobase, i	3	2.60869565
GOTERM_BP	GO:0010604~positive regulation of macromolec	4	3.47826087
GOTERM_BP	GO:0051173~positive regulation of nitrogen cor	3	2.60869565
GOTERM_BP	GO:0010557~positive regulation of macromolec	3	2.60869565
GOTERM_BP	GO:0031328~positive regulation of cellular biosy	3	2.60869565
GOTERM_BP	GO:0009891~positive regulation of biosynthetic	3	2.60869565

Annotation C Enrichment Score: 0.05656889494505134

Category	Term	Count	%
GOTERM_BP	GO:0051172~negative regulation of nitrogen cor	3	2.60869565
GOTERM_BP	GO:0031327~negative regulation of cellular bios	3	2.60869565
GOTERM_BP	GO:0009890~negative regulation of biosynthetic	3	2.60869565

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Annotation C		Enrichment Score: 0.02102153864187085	
Category	Term	Count	%
GOTERM_BP	GO:0008104~protein localization	4	3.47826087
GOTERM_BP	GO:0015031~protein transport	3	2.60869565
GOTERM_BP	GO:0045184~establishment of protein localizatic	3	2.60869565

For Peer Review

from DCIS-SOX11 cells compared to DCIS-lacZ cells injected into mammary duct.

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
3.19E-04	S100A7, GNAI1	82	2203	12782	1.9812008	0.04247817
0.00150124	GNAI1, S100A7	82	3777	12782	1.56827266	0.18480025
0.3099475	GAL3ST2, HSP27	112	6256	19235	1.09808869	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00150382	FMOD, OLFM1	112	1689	19235	2.13532416	0.26877231
0.00263335	FLRT3, FMOD	82	960	12782	2.43559451	0.30135164
0.00584448	FLRT3, FMOD	82	2010	12782	1.78367917	0.54940287
0.06794546	GPC4, CDH13	82	685	12782	2.04803276	0.99993017

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00557551	FLRT3, CDH13	89	700	13528	2.60571429	0.99087317
0.00563447	FLRT3, CDH13	89	701	13528	2.60199715	0.99131657
0.01123518	FLRT3, CDH13	112	422	19235	3.25575491	0.90464465

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.0024418	FMOD, OLFM1	112	3250	19235	1.69098901	0.39861196
0.00270072	FMOD, OLFM1	112	3250	19113	1.68026374	0.68057879
0.00982826	GAL3ST2, FMOD	112	4318	19235	1.47161177	0.8718291
0.01447074	FMOD, OLFM1	112	2924	19235	1.58584437	0.95177623
0.01839777	FMOD, OLFM1	112	2819	19113	1.57394339	0.99960482
0.02750263	GAL3ST2, FMOD	112	4129	19113	1.40522178	0.99999226

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00263335	FLRT3, FMOD	82	960	12782	2.43559451	0.30135164
0.00411845	FLRT3, GPC4	82	320	12782	3.89695122	0.42951324
0.00617804	FLRT3, GPC4	82	345	12782	3.61456345	0.56950498
0.4062012	FMOD, COL17A1	112	241	19235	2.13785566	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.01685555	FMOD, MC1R	89	505	13528	2.70891089	0.99999937
0.01685555	FMOD, MC1R	89	505	13528	2.70891089	0.99999937
0.0286257	FMOD, MC1R	89	665	13528	2.28571429	1

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0.04091526 FMOD, MC1R 89 710 13528 2.14084507 1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
3.19E-04	S100A7, GNA	82	2203	12782	1.9812008	0.04247817
0.0702985	FLRT3, CLCA2	82	1188	12782	1.70573622	0.99995049
0.08026895	FLRT3, CLCA2	82	1215	12782	1.66783097	0.99998857
0.82099969	GAL3ST2, HSC	82	5297	12782	0.9122559	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00553827	COL17A1, TNF	82	112	12782	6.95884146	0.53012953
0.02688397	TNS1, S100A7	82	102	12782	6.11286466	0.97543091
0.02967166	TNS1, S100A7	82	106	12782	5.88219052	0.98336797
0.03988007	COL17A1, TNF	82	203	12782	3.83936081	0.99605301
0.07534808	TNS1, S100A7	82	155	12782	4.02265932	0.99997639
0.09574777	TNS1, S100A7	82	172	12782	3.6250709	0.99999886
0.88328451	MTSS1, TNS1,	82	1381	12782	0.79011321	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00653115	S100A8, S100	112	21	19113	24.3788265	0.93703552
0.00907918	S100A8, S100	112	25	19235	20.6089286	0.84999603
0.00917436	S100A8, S100	58	19	7396	20.1343013	0.47056891
0.01246419	S100A8, S100	106	27	16659	17.4622642	0.97334528
0.01336831	S100A8, S100	106	28	16659	16.8386119	0.97954436
0.02180335	CDH13, S100A	112	103	19235	6.66955617	0.98979897
0.04703095	S100A8, S100	112	60	19235	8.58705357	0.9999555
0.08965715	S100A8, S100	112	182	19113	3.7505887	1
0.08965715	S100A8, S100	112	182	19113	3.7505887	1
0.15427004	S100A8, S100	106	215	16659	2.923914	1
0.15727488	S100A8, S100	106	217	16659	2.89696548	1
0.18198179	CDH13, CLCA1	112	803	19235	1.71099448	1
0.18667608	S100A8, S100	106	236	16659	2.66373521	1
0.19771358	S100A8, S100	106	130	16659	3.62677794	1
0.36092046	CDH13, CLCA1	83	919	12983	1.36166866	1
0.57182467	TNFAIP6, S100	89	615	13528	1.23577236	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00961782	A1BG, PTPRS,	106	205	16659	4.59981592	0.93876287

0.01276575	A1BG, PTPRS,	63	205	9079	4.21788618	0.59316807
0.03906331	A1BG, SEMA4	106	501	16659	2.50954694	0.99999003
0.05489397	A1BG, SEMA4	112	470	19235	2.55784574	0.99999206
0.05666217	PTPRS, ROR2,	106	138	16659	4.55537326	0.99999995
0.06034396	A1BG, SEMA4	106	553	16659	2.27356785	0.99999998
0.1205512	SEMA4G, ROF	112	103	19113	4.97044036	1
0.13521315	A1BG, PTPRS,	106	202	16659	3.11208668	1
0.34521396	SEMA4G, PTP	106	330	16659	1.90497427	1
0.39304584	SEMA4G, PTP	63	330	9079	1.74680135	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.05977097	MTSS1, WASF	89	226	13528	3.36283186	1
0.07206856	MTSS1, WASF	89	241	13528	3.15352697	1
0.3057288	MTSS1, TNS1,	112	636	19235	1.62019879	1
0.31535403	MTSS1, WASF	89	436	13528	1.74311927	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.13471437	TNS1, VAV3, I	112	111	19235	4.64165058	1
0.1549821	TNS1, VAV3, I	106	111	16659	4.24757777	1
0.17535196	TNS1, VAV3, I	63	111	9079	3.89489489	0.99999862

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.13082886	TNFAIP6, S10	89	530	13528	2.00754717	1
0.14240119	F5, FBLN5, PA	89	102	13528	4.47058824	1
0.14240119	F5, FBLN5, PA	89	102	13528	4.47058824	1
0.15592129	F5, FBLN5, PA	89	108	13528	4.22222222	1
0.23354353	F5, FBLN5, PA	89	141	13528	3.23404255	1
0.3535461	F5, FBLN5, PA	89	191	13528	2.38743455	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.05684972	CTSK, ROR2, C	89	319	13528	2.85893417	1
0.16506786	ROR2, MYC, C	89	112	13528	4.07142857	1
0.21437921	ROR2, MYC, C	89	133	13528	3.42857143	1
0.30827277	ROR2, MYC, C	89	172	13528	2.65116279	1
0.32247823	ROR2, GJA5, I	89	307	13528	1.98045603	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00982826	GAL3ST2, FM	112	4318	19235	1.47161177	0.8718291
0.02750263	GAL3ST2, FM	112	4129	19113	1.40522178	0.99999226
0.1123747	GAL3ST2, DU	112	3374	19113	1.31504044	1
0.2256906	FLRT3, CLCA2	112	2719	19113	1.25525403	1
0.3099475	GAL3ST2, HSE	112	6256	19235	1.09808869	1
0.49482254	GAL3ST2, HSE	112	4911	19113	1.04246662	1
0.51021594	GAL3ST2, HSE	112	4973	19235	1.03604105	1
0.76762701	GAL3ST2, HSE	82	5485	12782	0.937826	1
0.82099969	GAL3ST2, HSE	82	5297	12782	0.9122559	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.144064	SYT12, SYTL2,	106	106	16659	4.44793521	1
0.21381471	SYT12, SYTL2,	106	137	16659	3.44146812	1
0.24026349	SYT12, SYTL2,	63	137	9079	3.15571776	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.12463921	TNS1, VAV3, I	106	303	16659	2.59340557	1
0.15944389	VAV3, DEF6, I	112	237	19113	2.88019892	1
0.2541339	VAV3, DEF6, I	106	277	16659	2.26946393	1
0.29340618	VAV3, DEF6, I	63	277	9079	2.08102688	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.04426005	TNFSF14, CAS	89	121	13528	5.02479339	1
0.06095405	TNFSF14, CAS	89	138	13528	4.4057971	1
0.07048955	TNFSF14, CAS	89	67	13528	6.80597015	1
0.16967684	TNFSF14, CAS	89	114	13528	4	1
0.17726681	TNFSF14, CAS	89	223	13528	2.7264574	1
0.48179136	TNFSF14, CAS	89	248	13528	1.83870968	1
0.60586994	CDH13, VAV3	89	804	13528	1.13432836	1
0.61477387	CDH13, VAV3	89	812	13528	1.12315271	1
0.61808358	CDH13, VAV3	89	815	13528	1.1190184	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.10161265	CDH13, MTSS	89	83	13528	5.4939759	1
0.37327738	CDH13, MTSS	89	475	13528	1.6	1
0.43041624	CDH13, MTSS	89	368	13528	1.65217391	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.21369052	CDH13, S100A	89	245	13528	2.48163265	1
0.22390086	CDH13, S100A	89	251	13528	2.42231076	1
0.25039967	CDH13, S100A	89	148	13528	3.08108108	1
0.40008301	CDH13, S100A	89	211	13528	2.16113744	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.04337246	KCNJ5, KCND3	112	57	19113	8.98167293	0.99999999
0.10318543	KCNJ5, KCND3	82	86	12782	5.43760635	0.99999963
0.10318543	KCNJ5, KCND3	82	86	12782	5.43760635	0.99999963
0.13152612	KCNJ5, KCND3	83	100	12983	4.6926506	1
0.14258006	KCNJ5, KCND3	112	115	19235	4.48020186	1
0.16467824	KCNJ5, KCND3	112	126	19235	4.08907313	1
0.17457351	KCNJ5, KCND3	83	228	12983	2.74424012	1
0.19366669	KCNJ5, KCND3	83	128	12983	3.66613328	1
0.2038647	KCNJ5, KCND3	82	132	12782	3.54268293	1
0.20515908	KCNJ5, KCND3	83	133	12983	3.52830872	1
0.21461499	KCNJ5, KCND3	112	150	19235	3.43482143	1
0.23768828	KCNJ5, KCND3	83	147	12983	3.19227932	1
0.26274074	KCNJ5, CLCA2	83	412	12983	1.89832144	1
0.26413756	KCNJ5, CLCA2	83	413	12983	1.89372502	1
0.2793672	KCNJ5, KCND3	89	160	13528	2.85	1
0.31173229	KCNJ5, CLCA2	83	310	12983	2.01834435	1
0.34213301	KCNJ5, KCND3	89	318	13528	1.91194969	1
0.3496411	KCNJ5, KCND3	83	195	12983	2.40648749	1
0.3496411	KCNJ5, KCND3	83	195	12983	2.40648749	1
0.37403054	KCNJ5, KCND3	82	205	12782	2.28114218	1
0.42880414	KCNJ5, CLCA2	112	578	19235	1.48564941	1
0.44222778	KCNJ5, CLCA2	83	386	12983	1.62095012	1
0.46214959	KCNJ5, CLCA2	83	398	12983	1.57207725	1
0.49987396	KCNJ5, CLCA2	112	1670	19235	1.13122861	1
0.52123695	KCNJ5, KCND3	83	275	12983	1.7064184	1
0.5502617	KCNJ5, KCND3	112	318	19235	1.62019879	1
0.56446036	KCNJ5, CLCA2	89	768	13528	1.1875	1
0.58706827	KCNJ5, KCND3	89	465	13528	1.30752688	1
0.61748923	KCNJ5, KCND3	83	328	12983	1.43068616	1
0.70358844	KCNJ5, KCND3	89	553	13528	1.0994575	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.16158499	VAV3, RINL, A	83	335	12983	2.33465204	1
0.25162267	VAV3, RINL, R	83	404	12983	1.93591196	1
0.26413756	VAV3, RINL, R	83	413	12983	1.89372502	1
0.40610304	VAV3, RINL, A	83	220	12983	2.133023	1
0.5192755	VAV3, RAPGE	83	274	12983	1.71264621	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.13082886	TNFAIP6, S10	89	530	13528	2.00754717	1
0.35462733	TNFAIP6, S10	89	325	13528	1.87076923	1
0.57182467	TNFAIP6, S10	89	615	13528	1.23577236	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.0120253	GPC4, GNAL,	112	642	19235	2.67509457	0.91925207
0.02889513	GNAL, RAB7B	112	295	19113	3.47088378	0.99999577
0.04201121	GNAL, RAB7B	112	329	19235	3.13205601	0.99986727
0.044458	GNAL, MC1R,	83	211	12983	3.70667504	0.99999037
0.05817865	GAL3ST2, GST	112	1394	19235	1.72480273	0.99999615
0.08608795	GNAL, RAB7B	83	372	12983	2.52293043	1
0.08853645	GNAL, MC1R,	112	181	19113	3.77131018	1
0.09380913	GNAL, RAB7B	83	382	12983	2.45688513	1
0.09380913	GNAL, RAB7B	83	382	12983	2.45688513	1
0.12544316	GNAL, MC1R,	112	213	19235	3.22518444	1
0.13471437	CLK4, ROR2, I	112	111	19235	4.64165058	1
0.14786354	MC1R, GNAI1	36	99	5085	4.28030303	0.99999935
0.17198966	GNAL, MC1R,	89	115	13528	3.96521739	1
0.20723256	GNAL, MC1R,	89	130	13528	3.50769231	1
0.22053324	WNK4, TNFSF	89	370	13528	2.05405405	1
0.26581538	GNAL, RAB7B	112	1686	19235	1.32421941	1
0.28220811	CLK4, ROR2, I	83	166	12983	2.82689795	1
0.29017783	WNK4, CLK4,	112	469	19113	1.81931541	1
0.32264179	WNK4, CLK4,	106	455	16659	1.72703711	1
0.32330047	ADRBK2, ROR	112	201	19235	2.56329957	1
0.35277221	WNK4, CLK4,	106	476	16659	1.6508443	1
0.36518676	WNK4, CLK4,	112	688	19235	1.4977419	1
0.37759091	WNK4, CLK4,	112	381	19235	1.80305587	1
0.38636138	WNK4, CLK4,	112	542	19113	1.57427847	1
0.386484	WNK4, CLK4,	106	354	16659	1.77582347	1

0.39501956	WNK4, CLK4,	106	359	16659	1.75109056	1
0.43789925	RAB7B, GNAL	83	1918	12983	1.14176414	1
0.44851217	WNK4, CLK4,	89	973	13528	1.24974306	1
0.44851217	WNK4, CLK4,	89	973	13528	1.24974306	1
0.45382091	GNAL, MC1R,	89	235	13528	1.94042553	1
0.48769628	CLK4, ADRBK	106	259	16659	1.82039047	1
0.48875527	WNK4, CLK4,	112	962	19113	1.24174896	1
0.49702886	GNAL, RAB7B	83	1836	12983	1.10756096	1
0.49702886	GNAL, RAB7B	83	1836	12983	1.10756096	1
0.51373173	WNK4, CLK4,	83	430	12983	1.45508546	1
0.53191842	CLK4, ADRBK	63	259	9079	1.66924067	1
0.53428765	WNK4, CLK4,	112	658	19113	1.29674609	1
0.53666238	WNK4, CLK4,	83	606	12983	1.29060798	1
0.60137598	WNK4, CLK4,	89	800	13528	1.14	1
0.63658011	WNK4, CLK4,	89	667	13528	1.13943028	1
0.67977462	RAB7B, GNAL	83	2245	12983	0.97545818	1
0.74839311	GNAL, MC1R,	112	874	19235	0.98250041	1
0.7842117	FMOD, GNAL,	89	1856	13528	0.90086207	1
0.78535543	WNK4, CLK4,	112	1326	19235	0.90662707	1
0.88407805	WNK4, CLK4,	83	1577	12983	0.79351521	1
0.893304	WNK4, CLK4,	83	1601	12983	0.78161992	1
0.89732668	WNK4, CLK4,	83	1612	12983	0.77628629	1
0.91667851	WNK4, CLK4,	83	1477	12983	0.74133501	1
0.92281875	WNK4, CLK4,	83	1497	12983	0.73143073	1
0.94122218	GNAL, MC1R,	89	1123	13528	0.67675868	1
0.95230521	MC1R, GPR87	112	816	19235	0.631401	1
0.98427847	MC1R, PTPRS	112	1583	19235	0.54245443	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.26736647	CDH13, TNS1,	89	276	13528	2.20289855	1
0.32247823	CDH13, TNS1,	89	307	13528	1.98045603	1
0.32247823	CDH13, TNS1,	89	307	13528	1.98045603	1
0.37327738	CDH13, MTSS	89	475	13528	1.6	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.31167488	ZBTB49, KCNI	106	179	16659	2.6339728	1
0.31631582	ZBTB49, KCNI	106	181	16659	2.60486813	1
0.34648966	ZBTB49, KCNI	63	179	9079	2.41527002	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.17133425	MTSS1, TNS1,	112	247	19235	2.78123193	1
0.3057288	MTSS1, TNS1,	112	636	19235	1.62019879	1
0.33950727	MTSS1, TNS1,	83	326	12983	1.9192845	1
0.62228641	MTSS1, TNS1,	83	504	12983	1.24144196	1
0.88328451	MTSS1, TNS1,	82	1381	12782	0.79011321	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.09678328	GAL3ST2, COI	112	421	19235	2.44761622	1
0.66390092	GAL3ST2, GYL	112	588	19235	1.16830661	1
0.73296257	GAL3ST2, GYL	112	444	19113	1.15305261	1
0.81201323	GAL3ST2, GYL	82	872	12782	0.89379615	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.14463652	SESN2, SESN1	89	103	13528	4.42718447	1
0.30640827	MC1R, HORM	89	565	13528	1.61415929	1
0.39263892	MC1R, HORM	89	776	13528	1.37113402	1
0.69825951	MC1R, HORM	89	370	13528	1.23243243	1
0.75585733	MC1R, HORM	89	414	13528	1.10144928	1
0.98597054	MC1R, RHOU	82	952	12782	0.49121234	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.18287725	ZNF229, ZNF4	112	134	19113	3.82056237	1
0.20339344	ZNF229, ZBTE	112	538	19113	1.90317977	1
0.23159328	ZNF229, ZNF4	112	157	19113	3.26086215	1
0.24235191	ZNF229, ZBTE	112	575	19113	1.78071429	1
0.26691414	ZNF229, ZBTE	112	451	19113	1.89192667	1
0.27867206	ZNF229, ZBTE	112	608	19113	1.68406367	1
0.29442018	ZNF229, ZBTE	112	622	19113	1.6461587	1
0.30362416	ZNF229, ZNF3	112	332	19113	2.05604561	1
0.31503482	ZNF229, ZBTE	112	488	19113	1.74848141	1
0.32601603	ZNF229, ZNF4	112	201	19113	2.54704158	1
0.35396266	ZNF229, ZBTE	106	621	16659	1.51845775	1
0.37342552	ZNF229, ZBTE	106	784	16659	1.40321765	1
0.38819331	ZNF229, ZNF3	106	355	16659	1.77082115	1
0.3881996	ZNF229, ZBTE	106	797	16659	1.38032954	1
0.4313755	ZNF229, ZNF4	112	252	19113	2.03156888	1

0.43747929	ZNF229, ZNF3	112	417	19113	1.63694758	1
0.43916373	ZNF229, ZNF3	63	355	9079	1.62378717	1
0.46491811	ZNF229, ZBTE	63	797	9079	1.26571867	1
0.48444618	S100A8, S100	83	4179	12983	1.0480515	1
0.50041412	ZBTB49, ZNF2	112	2189	19235	1.09838968	1
0.50956419	ZNF229, ZNF4	112	293	19113	1.74728791	1
0.52151828	S100A8, S100	83	4241	12983	1.03272983	1
0.53701999	ZNF229, ZBTE	112	1718	19235	1.09962269	1
0.55564401	S100A8, S100	83	4140	12983	1.02014144	1
0.55635222	ZBTB49, KCNI	112	2972	19235	1.04015454	1
0.58049975	ZNF229, ZNF4	112	334	19113	1.53280047	1
0.60654562	ZBTB49, KCNI	83	2785	12983	1.01098397	1
0.61329259	ZBTB49, ZNF3	112	542	19113	1.25942277	1
0.61371352	ZBTB49, KCNI	83	2311	12983	1.01528572	1
0.63061299	ZNF229, ZBTE	112	2026	19235	1.01722254	1
0.64515708	ZNF229, ZNF4	112	376	19113	1.3615834	1
0.66008327	ZNF229, ZBTE	112	2071	19235	0.99511968	1
0.82429874	ZNF229, ZBTE	89	2101	13528	0.86815802	1
0.85581619	ZNF350, IRX6	83	1512	12983	0.82762797	1
0.85603588	ZNF229, ZBTE	112	1868	19235	0.82744628	1
0.9049631	ZNF229, ZNF3	89	1773	13528	0.7715736	1
0.91746697	ZNF229, ZNF3	89	1813	13528	0.75455047	1
0.92615441	ZBTB49, IRX6	112	4283	19235	0.80196625	1
0.93454233	ZBTB49, ZNF2	89	2601	13528	0.7597078	1
0.94020618	ZNF229, ZBTE	83	2331	12983	0.73815468	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.28419355	FMOD, MC1R	89	162	13528	2.81481481	1
0.61646679	FMOD, MC1R	89	318	13528	1.43396226	1
0.67924937	FMOD, MC1R	89	357	13528	1.27731092	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.31535403	GPC4, CDH13	89	436	13528	1.74311927	1
0.34570466	VAV3, TNFSF1	89	320	13528	1.9	1
0.34749001	VAV3, TNFSF1	89	321	13528	1.894081	1
0.53354922	VAV3, TNFSF1	89	430	13528	1.41395349	1
0.53828377	VAV3, TNFSF1	89	433	13528	1.40415704	1
0.54142535	VAV3, TNFSF1	89	435	13528	1.39770115	1
0.60586994	CDH13, VAV3	89	804	13528	1.13432836	1

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4	0.61477387	CDH13, VAV3	89	812	13528	1.12315271	1
5	0.61808358	CDH13, VAV3	89	815	13528	1.1190184	1
6	0.75691555	VAV3, CASP1,	89	602	13528	1.00996678	1
7	0.7658376	VAV3, CASP1,	89	611	13528	0.99509002	1
8							
9	0.85361158	VAV3, CASP1,	89	719	13528	0.84561892	1
10	0.85688592	VAV3, CASP1,	89	724	13528	0.83977901	1
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14	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
15	0.10161265	MED26, MYC,	89	83	13528	5.4939759	1
16	0.45163451	MED26, MYC,	89	234	13528	1.94871795	1
17	0.46983922	ZNF350, MED	82	555	12782	1.40430675	1
18							
19	0.5697134	MED26, MYC,	89	292	13528	1.56164384	1
20	0.57716223	MED26, MYC,	89	296	13528	1.54054054	1
21							
22	0.66563653	ZNF350, MED	82	882	12782	1.06039489	1
23							
24	0.8264028	ZNF350, S100	82	698	12782	0.89328395	1
25	0.84497177	ZNF350, MYC	89	504	13528	0.9047619	1
26	0.85581619	ZNF350, IRX6	83	1512	12983	0.82762797	1
27	0.90956612	ZNF350, MED	82	1450	12782	0.75251472	1
28							
29	0.91738222	ZNF350, F5, N	82	1856	12782	0.75587416	1
30	0.95393387	ZNF350, F5, N	82	1820	12782	0.68517824	1
31	0.95583775	ZNF350, MYC	89	734	13528	0.62125341	1
32							
33	0.97665882	ZNF350, MED	82	1779	12782	0.61334814	1
34	0.97838701	MTSS1, ZNF3	82	2596	12782	0.66050021	1
35	0.97838701	MTSS1, ZNF3	82	2596	12782	0.66050021	1
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40	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
41	0.67924937	SPRY1, VAV3,	89	357	13528	1.27731092	1
42	0.70110122	SPRY1, VAV3,	89	372	13528	1.22580645	1
43	0.81161709	SPRY1, VAV3,	89	466	13528	0.97854077	1
44							
45	0.8290149	SPRY1, VAV3,	89	485	13528	0.94020619	1
46	0.8290149	SPRY1, VAV3,	89	485	13528	0.94020619	1
47							
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50	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
51	0.67263504	MED26, TFAP	83	363	12983	1.29274121	1
52	0.84051999	MED26, TFAP	83	513	12983	0.91474671	1
53	0.85581619	ZNF350, IRX6	83	1512	12983	0.82762797	1
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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.78016991	MTSS1, F5, SY	82	642	12782	0.9712028	1
0.80440821	MTSS1, F5, SY	82	670	12782	0.93061522	1
0.86915089	MTSS1, F5, SY	82	550	12782	0.8502439	1
0.88078477	MTSS1, F5, SY	82	568	12782	0.82329955	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.69002582	CTSK, CFI, CA	83	375	12983	1.25137349	1
0.77250778	CTSK, CFI, CA	112	484	19235	1.06451077	1
0.86715966	CTSK, CFI, CA	83	549	12983	0.85476332	1
0.88322082	CTSK, CFI, CA	83	574	12983	0.81753495	1
0.95146883	CTSK, DQX1, I	112	1555	19235	0.66266651	1
0.97195064	CTSK, HECTD2	89	1054	13528	0.57685009	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.80589783	MED26, TFAP	112	520	19235	0.99081387	1
0.85581619	ZNF350, IRX6	83	1512	12983	0.82762797	1
0.95404288	MED26, TFAP	89	727	13528	0.62723521	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.7350557	CDH13, TFAP	89	581	13528	1.0464716	1
0.74438693	IRX6, TFAP2B	83	607	12983	1.03078542	1
0.85581619	ZNF350, IRX6	83	1512	12983	0.82762797	1
0.873125	IRX6, TFAP2B	83	975	12983	0.8021625	1
0.88695915	TFAP2B, MYC	89	564	13528	0.80851064	1
0.91830301	TFAP2B, MYC	89	624	13528	0.73076923	1
0.92351306	CDH13, TFAP	89	857	13528	0.70945158	1
0.92681542	TFAP2B, MYC	89	644	13528	0.70807453	1
0.93075491	TFAP2B, MYC	89	654	13528	0.69724771	1
0.94174505	TFAP2B, MYC	89	685	13528	0.66569343	1
0.94492615	TFAP2B, MYC	89	695	13528	0.65611511	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.85661392	ZNF350, APO	89	519	13528	0.87861272	1
0.88513443	ZNF350, APO	89	561	13528	0.81283422	1
0.89227548	ZNF350, APO	89	573	13528	0.79581152	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.93234407	RAB7B, WNK4	89	882	13528	0.6893424	1
0.96237596	RAB7B, SYTL2	89	762	13528	0.5984252	1
0.963861	RAB7B, SYTL2	89	769	13528	0.59297789	1

For Peer Review

Benjamini FDR
0.04247817 0.37396934
0.06583983 1.74816839
0.91702427 99.0719102

Benjamini FDR
0.14488148 1.88050707
0.08575065 3.04794723
0.10763772 6.64956277
0.54952742 56.2203873

Benjamini FDR
0.99087317 8.27487519
0.90681508 8.35884842
0.28518748 13.2836364

Benjamini FDR
0.15591743 3.03688574
0.43482639 3.7301054
0.28993478 11.7142251
0.28600416 16.7959122
0.85900648 22.9734842
0.90498682 32.4304011

Benjamini FDR
0.08575065 3.04794723
0.10618196 4.72914537
0.09999273 7.01657365
0.93794982 99.8604952

Benjamini FDR
0.99143251 23.0958948
0.99143251 23.0958948
0.99775515 36.1526098

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4	0.99910469	47.553185
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8	Benjamini	FDR
9	0.04247817	0.37396934
10	0.53352903	57.500394
11	0.50895963	62.5531826
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13	0.99897337	99.9999998
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17	Benjamini	FDR
18	0.11828203	6.3114702
19	0.3375481	27.3785997
20		
21	0.33611243	29.7835464
22	0.39538529	37.981827
23		
24	0.50848545	60.1324811
25	0.55299056	69.3179953
26	0.99944165	100
27		
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30	Benjamini	FDR
31	0.60216908	8.79929129
32	0.37766291	10.8679937
33	0.47056891	9.07216849
34	0.83673728	15.3504993
35	0.72651236	16.3744417
36	0.36778557	24.2763337
37	0.51115553	45.5383292
38	0.9877773	73.2972081
39	0.9877773	73.2972081
40	0.99211146	89.2071372
41	0.98377182	89.7056689
42	0.7995049	92.0648594
43	0.98988212	93.5778174
44	0.98940536	94.644045
45	0.99660728	99.7064617
46	0.99994962	99.9997962
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55	Benjamini	FDR
56	0.93876287	12.0506623
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0.59316807	12.4504355
0.94380501	41.1064677
0.54291524	50.9430072
0.96566263	53.9312063
0.95011126	56.2637832
0.99276041	83.5644385
0.99474176	85.4882902
0.99705437	99.639807
0.99321486	99.4300342

Benjamini	FDR
0.99845284	61.4075397
0.9966933	68.5100438
0.92033478	98.9977396
0.99957434	99.7127819

Benjamini	FDR
0.74539229	83.88231
0.98801693	89.3272519
0.99882672	86.4027257

Benjamini	FDR
0.99961105	88.537654
0.99949481	90.6814929
0.99949481	90.6814929
0.99944365	92.7099024
0.99907147	98.357463
0.99951649	99.881667

Benjamini	FDR
0.99910935	59.5130368
0.99948791	93.8392289
0.99928156	97.5944928
0.99964318	99.6632963
0.9995846	99.7556386

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4	Benjamini	FDR
5	0.28993478	11.7142251
6	0.90498682	32.4304011
7	0.9934643	81.2811154
8	0.9982523	97.2552373
9	0.91702427	99.0719102
10	0.99966603	99.9932173
11	0.96575735	99.9877091
12	0.99866122	99.9999964
13	0.99897337	99.9999998
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19	Benjamini	FDR
20	0.99322959	87.3422743
21	0.99029237	95.9087853
22	0.99835763	94.1794507
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27	Benjamini	FDR
28	0.99589652	82.9451879
29	0.99777534	91.2972438
30	0.99498886	97.9673599
31	0.99770664	97.2518737
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37	Benjamini	FDR
38	0.99823167	50.3087184
39	0.9971766	62.1509398
40	0.99784544	67.6719928
41	0.99941131	94.344166
42	0.9989184	95.0922058
43	0.99982099	99.9961136
44	0.99996606	99.9999433
45	0.99996976	99.9999602
46	0.9999641	99.9999652
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53	Benjamini	FDR
54	0.99944735	80.8976458
55	0.99961018	99.9266945
56	0.99966902	99.9832601
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Benjamini FDR
0.99943533 97.5617095
0.99917266 98.0075129
0.99919173 98.8350196
0.99964675 99.962687

Benjamini FDR
0.93096479 46.3822732
0.56082027 72.1531046
0.56082027 72.1531046
0.99922582 84.0630545
0.75120732 85.6360096
0.7897515 89.6669104
0.99905242 91.7800368
0.99892393 93.9395805
0.78781691 93.1184605
0.99846649 94.972989
0.84449387 95.2518227
0.9989857 97.0828001
0.99842253 98.1121564
0.99750304 98.1582107
0.99952138 99.3662653
0.99734296 99.229007
0.99959706 99.844932
0.99682202 99.6313462
0.99682202 99.6313462
0.93733718 99.5909855
0.94563965 99.9144969
0.9984151 99.9501107
0.99858908 99.9689331
0.96766098 99.9840022
0.99804256 99.9931753
0.97303657 99.9958093
0.99995341 99.9997348
0.99995638 99.9998836
0.99886415 99.9996331
0.99999396 99.9999993

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5	Benjamini	FDR
6	0.99942487	89.9265813
7	0.99876026	97.7058431
8	0.99750304	98.1582107
9	0.99816776	99.8870334
10	0.99836375	99.992802
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15	Benjamini	FDR
16	0.99961105	88.537654
17	0.99945095	99.8846878
18	0.99994962	99.9997962
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24	Benjamini	FDR
25	0.26988474	14.153703
26	0.87283001	33.7777661
27	0.49676961	41.806774
28	0.99689742	44.6923615
29	0.54123436	53.0508384
30	0.99951033	69.037031
31	0.99247947	72.8313893
32	0.99807934	72.2760553
33	0.99807934	72.2760553
34	0.76946747	81.5630408
35	0.74539229	83.88231
36	0.94204875	82.3942021
37	0.99925791	94.5827036
38	0.99944839	97.2332957
39	0.99926572	97.8696809
40	0.89927785	97.9713357
41	0.99755993	98.6676689
42	0.99860435	99.1915487
43	0.99732909	99.4349268
44	0.9210098	99.2746616
45	0.99670407	99.691298
46	0.93283342	99.6760399
47	0.93043788	99.747428
48	0.99936388	99.8955876
49	0.99647412	99.8483409
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0.99441197 99.8741006
0.99870732 99.9448264
0.99975929 99.9898342
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0.99972374 99.9912452
0.99872564 99.9861794
0.99969317 99.991978
0.99878576 99.9870259
0.99878576 99.9870259
0.99855617 99.9916428
0.99507676 99.9612644
0.99974363 99.9978381
0.99777125 99.995545
0.9999664 99.9999325
0.99997577 99.9999838
0.99927616 99.9999637
0.99458446 99.9999972
0.99999871 100
0.9963578 99.9999996
0.99998591 100
0.99998844 100
0.99998807 100
0.99999465 100
0.99999534 100
1 100
0.99993158 100
0.99999748 100

Benjamini FDR
0.99942815 99.1820714
0.9995846 99.7556386
0.9995846 99.7556386
0.99961018 99.9266945

Benjamini FDR
0.9982522 99.3005067
0.99776893 99.3606398
0.9974086 98.775325

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5	Benjamini	FDR
6	0.79062901	90.6588035
7	0.92033478	98.9977396
8	0.99712831	99.5491104
9	0.99874894	99.9996887
10	0.99944165	100
11		
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15	Benjamini	FDR
16	0.71219276	72.3088579
17	0.98828535	99.9998937
18	0.99999764	99.9999991
19	0.99898018	99.9999997
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25	Benjamini	FDR
26	0.99931813	91.0497318
27	0.9996927	99.6489997
28	0.99963031	99.9548561
29	0.99999458	99.9999991
30	0.99999777	100
31	0.99999565	100
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37	Benjamini	FDR
38	0.99772967	94.1514419
39	0.99833405	95.9091386
40	0.99792151	97.5351579
41	0.99789666	97.9783259
42	0.99857187	98.7278979
43	0.99859024	98.9865214
44	0.99833601	99.2568807
45	0.99827548	99.3821247
46	0.998317	99.5101747
47	0.9983448	99.6097183
48	0.99587099	99.6987576
49	0.99640902	99.7993676
50	0.99575248	99.85386
51	0.99480083	99.8538799
52	0.99954031	99.9642187
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4 0.99949307 99.9692552
5 0.99365669 99.7484246
6 0.9922783 99.8453387
7 0.99880683 99.9821009
8 0.9651571 99.9842188
9 0.99970422 99.9955269
10 0.99761789 99.9932273
11 0.97154528 99.9939569
12 0.99805645 99.9974162
13 0.97045395 99.9964715
14 0.99989533 99.9995024
15 0.99905893 99.9994702
16 0.99994337 99.9998415
17 0.99899505 99.999583
18 0.98541174 99.99965
19 0.99996987 99.9999527
20 0.98876664 99.9998774
21 0.99999966 100
22 0.99998605 100
23 0.9986517 100
24 0.99999998 100
25 0.99999999 100
26 0.99979008 100
27 1 100
28 0.99999824 100
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40 Benjamini FDR
41 0.99949479 99.4287548
42 0.99996705 99.9999628
43 0.99999127 99.9999976
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46
47 Benjamini FDR
48 0.99957434 99.7127819
49 0.99956762 99.8574399
50 0.99951444 99.8633323
51 0.99992958 99.9992352
52 0.99992854 99.9993467
53 0.99992448 99.9994121
54 0.99996606 99.9999433
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4	0.99996976	99.9999602
5	0.9999641	99.9999652
6	0.99999754	100
7	0.99999798	100
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9	0.99999989	100
10	0.99999987	100
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14	Benjamini	FDR
15	0.99944735	80.8976458
16	0.99974481	99.9906879
17	0.96832057	99.9418135
18	0.99995355	99.9997801
19	0.99995006	99.9998321
20	0.99511277	99.9997401
21	0.99865983	99.9999999
22	0.99999984	100
23	0.99998605	100
24	0.99971717	100
25	0.99974423	100
26	0.99994077	100
27		
28	1	100
29	0.9999883	100
30	0.99998807	100
31	0.99998807	100
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39	Benjamini	FDR
40	0.99999127	99.9999976
41	0.99999431	99.9999992
42	0.99999947	100
43	0.99999969	100
44	0.99999969	100
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50	Benjamini	FDR
51	0.99930579	99.9999517
52	0.99998048	100
53	0.99998605	100
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Benjamini	FDR
0.99870081	99.9999981
0.99902671	99.9999995
0.99943306	100
0.99950542	100

Benjamini	FDR
0.99929417	99.9999763
0.99591125	99.9999992
0.99998557	100
0.99998839	100
0.99993759	100
1	100

Benjamini	FDR
0.99720276	99.9999999
0.99998605	100
1	100

Benjamini	FDR
0.99999688	99.9999999
0.99973861	99.9999981
0.99998605	100
0.99998573	100
0.99999997	100
0.99999999	100
0.99999999	100
1	100
1	100
1	100
1	100

Benjamini	FDR
0.99999989	100
0.99999997	100
0.99999997	100

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5	Benjamini	FDR
6	1	100
7	1	100
8	1	100
9	1	100
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For Peer Review

Table S4C. Downregulated genes in lesions and tumours from DCIS-SOX11 cells compared to DCI:

Probe	Chromosome	Start	End	Strand	Difference	Feature
RGS11	16	268301	275929	-	5.2471495	RGS11
FAM221A	7	23680130	23702650	+	4.6832404	FAM221A
ZNF28	19	52797409	52857600	-	4.5307574	ZNF28
CST5	20	23875935	23879750	-	3.5712364	CST5
NCMAP	1	24556111	24609325	+	3.534476	NCMAP
CD14	5	140631728	140633701	-	3.289661	CD14
CCDC68	18	54901509	54959508	-	2.931799	CCDC68
CD4	12	6789472	6820808	+	2.6412685	CD4
MGAT3	22	39457344	39492194	+	2.3938758	MGAT3
MUC16	19	8848844	8981342	-	2.372875	MUC16
MT1F	16	56657694	56659305	+	2.2635772	MT1F
AQP1	7	30921300	30925516	+	2.0998867	AQP1
FUT2	19	48695971	48705950	+	2.0158913	FUT2
SYNGR3	16	1989660	1994275	+	1.9353098	SYNGR3
CST6	11	66011841	66013505	+	1.8666239	CST6
SLC44A4	6	31863192	31879046	-	1.8376783	SLC44A4
FES	15	90883695	90895776	+	1.814775	FES
KLK1	19	50819153	50823784	-	1.7772535	KLK1
HES7	17	8120590	8124092	-	1.6915362	HES7
COL4A4	2	227002711	227164113	-	1.6749573	COL4A4
GPR98	5	90529344	91164221	+	1.6188954	GPR98
NKD1	16	50548330	50640739	+	1.548845	NKD1
ENTPD8	9	137434364	137441449	-	1.5179209	ENTPD8
MYBPC1	12	101568353	101686018	+	1.4817233	MYBPC1
CP	3	149162417	149222055	-	1.4666603	CP
NR4A1	12	52022832	52059507	+	1.4537516	NR4A1
ITGA1	5	52787896	52959210	+	1.4054496	ITGA1
GNG4	1	235547687	235650754	-	1.3522539	GNG4
ARL10	5	176365468	176401865	+	1.3184352	ARL10
NEGR1	1	71395940	72282734	-	1.2916242	NEGR1
CPAMD8	19	16892947	17026815	-	1.2735071	CPAMD8
COL4A3	2	227164565	227314792	+	1.2487429	COL4A3
CXCR4	2	136114349	136118165	-	1.2383603	CXCR4
TAGAP	6	159034468	159045152	-	1.22001	TAGAP
A4GALT	22	42692121	42695633	-	1.1976436	A4GALT
A2ML1	12	8822472	8876785	+	1.1877284	A2ML1
PER1	17	8140472	8156405	-	1.1546345	PER1
SECTM1	17	82321024	82334074	-	1.0947387	SECTM1
GAB2	11	78215297	78418348	-	1.0759344	GAB2

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4	EDAR	2	108894471	108989372 -	1.0631233 EDAR
5	HS6ST3	13	96090839	96839562 +	1.0392286 HS6ST3
6	MYH14	19	50188186	50310545 +	1.0303569 MYH14
7	DNM3	1	171841498	172418466 +	1.0292313 DNM3
8					
9	GADD45B	19	2476127	2478259 +	1.0196736 GADD45B
10	ITGB2	21	44885953	44931989 -	1.0115612 ITGB2
11	FBN3	19	8065402	8149846 -	1.0114043 FBN3
12					
13	BIK	22	43110748	43129712 +	0.98659587 BIK
14	CTSF	11	66563463	66568841 -	0.9781616 CTSF
15					
16	RARRES3	11	63536816	63546462 +	0.97065115 RARRES3
17	EXOC4	7	133253073	134065759 +	0.9635906 EXOC4
18	DLL1	6	170282206	170290473 -	0.95565915 DLL1
19					
20	ITGB3	17	47253846	47344292 +	0.94015884 ITGB3
21	ZNF550	19	57535257	57559863 -	0.9383552 ZNF550
22					
23	TSPAN2	1	115048011	115089500 -	0.935122 TSPAN2
24	TGM2	20	38127387	38166578 -	0.91480494 TGM2
25	APOBEC3A	22	38952751	38992778 +	0.91220516 APOBEC3A
26	NOV	8	119416306	119424353 +	0.9016888 NOV
27	SEMA6B	19	4542593	4559808 -	0.8835869 SEMA6B
28					
29	ARRDC2	19	18001132	18014102 +	0.8668933 ARRDC2
30	ROS1	6	117288300	117425855 -	0.8656578 ROS1
31	ITPKA	15	41493393	41503551 +	0.8628229 ITPKA
32					
33	CAPN8	1	223538008	223665734 -	0.85892725 CAPN8
34	NPFFR1	10	70247329	70283676 -	0.85283965 NPFFR1
35					
36	SLC1A1	9	4490444	4587469 +	0.8428092 SLC1A1
37	ZNF750	17	82829435	82840578 -	0.8372483 ZNF750
38	RIMKLA	1	42380795	42422578 +	0.8351226 RIMKLA
39					
40	IL34	16	70579895	70660682 +	0.8292446 IL34
41	PLA2G16	11	63573195	63614469 -	0.8146448 PLA2G16
42	CTSS	1	150730196	150765957 -	0.8062358 CTSS
43					
44	SPATA6L	9	4600520	4666666 -	0.79708195 SPATA6L
45	ZNF430	19	21020620	21060050 +	0.7933053 ZNF430
46	STRA6	15	74179466	74212267 -	0.7911806 STRA6
47					
48	NET1	10	5412551	5458463 +	0.78216267 NET1
49	SLC16A5	17	75087727	75106162 +	0.77890325 SLC16A5
50	INHA	2	219572195	219575713 +	0.77731526 INHA
51					
52	GPRC5A	12	12890782	12917937 +	0.75966835 GPRC5A
53	RFTN1	3	16315845	16514026 -	0.75564575 RFTN1
54	ELF3	1	202007945	202017188 +	0.7524533 ELF3
55					
56	MAFF	22	38201882	38216511 +	0.74701166 MAFF
57	ARRB2	17	4710489	4721499 +	0.74384975 ARRB2
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ZNF296	19	45071500	45076588 -	0.71728456 ZNF296
MITF	3	69739435	69968337 +	0.7071382 MITF
NMU	4	55595229	55636298 -	0.70698 NMU
ABHD2	15	89087459	89202360 +	0.7069402 ABHD2
PTPRJ	11	47980558	48170841 +	0.7062063 PTPRJ
TMPRSS3	21	42371890	42396846 -	0.6992502 TMPRSS3
HCG11	6	26523450	26526579 +	0.691273 HCG11
SCEL	13	77535674	77645263 +	0.69029355 SCEL
UNC13D	17	75827225	75844717 -	0.68104553 UNC13D
TFCP2L1	2	121216587	121285207 -	0.67640686 TFCP2L1
PCDHB2	5	141094578	141098703 +	0.66970253 PCDHB2
MBOAT1	6	20102145	20212399 -	0.66487336 MBOAT1
ZBTB7C	18	48026673	48410752 -	0.64966154 ZBTB7C
ST3GAL4	11	126355660	126414641 +	0.6486144 ST3GAL4
PMP22	17	15229777	15265326 -	0.64566135 PMP22
TMC8	17	78130770	78142968 +	0.6407565 TMC8
GLIPR1	12	75480680	75503853 +	0.63705635 GLIPR1
EMP1	12	13196716	13219939 +	0.6369848 EMP1
GRB10	7	50590063	50793462 -	0.6334119 GRB10
GMDS	6	1623806	2245692 -	0.6163149 GMDS
B3GALT4	6	33277132	33278825 +	0.6147189 B3GALT4
PFKP	10	3066333	3137712 +	0.609252 PFKP
SERPINB1	6	2832332	2842006 -	0.60507154 SERPINB1
PMAIP1	18	59899948	59904306 +	0.59444976 PMAIP1
FRMD4B	3	69169990	69542583 -	0.59351444 FRMD4B
LRRC8A	9	128882112	128918039 +	0.5920062 LRRC8A
NCOA7	6	125781161	125932030 +	0.5900841 NCOA7
BHLHE40	3	4979116	4985323 +	0.58533907 BHLHE40
CYP27C1	2	127184120	127220078 -	0.584919 CYP27C1
SLC43A3	11	57406954	57427580 -	0.5829177 SLC43A3
WEE1	11	9573681	9593457 +	0.56292963 WEE1
KRT18	12	52948871	52952901 +	0.55398273 KRT18
H1FO	22	37805093	37807436 +	0.54533863 H1FO
GDPD3	16	30104810	30113856 -	0.54030275 GDPD3
SYNJ2	6	157981887	158099176 +	0.5373821 SYNJ2
PSIP1	9	15464066	15511019 -	0.5357022 PSIP1
KRT8	12	52897187	52949882 -	0.5325012 KRT8
TMEM133	11	100991989	100993941 +	0.53218365 TMEM133
PRRT3	3	9945542	9952394 -	0.52513134 PRRT3
ZFP36	19	39406813	39409412 +	0.52410173 ZFP36
ZNF431	19	21142024	21196053 +	0.52325344 ZNF431

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4	CTSD	11	1752752	1763992 -	0.5196371 CTSD
5	OBFC1	10	103882542	103918205 -	0.5140524 OBFC1
6	ERMP1	9	5784573	5833117 -	0.50618744 ERMP1
7	SBK1	16	28292519	28323849 +	0.505394 SBK1
8	CD97	19	14381156	14408725 +	0.50038385 CD97
9	MISP	19	751126	764319 +	0.49860573 MISP
10	ZNF714	19	21082159	21125270 +	0.49540377 ZNF714
11	USP13	3	179652755	179789401 +	0.48414326 USP13
12	FUT3	19	5842888	5851474 -	0.48062277 FUT3
13	SLC25A25	9	128068201	128109245 +	0.4803319 SLC25A25
14	PIM3	22	49960513	49964080 +	0.4782567 PIM3
15	SH3BP2	4	2793023	2841098 +	0.47501898 SH3BP2
16	TACC1	8	38728186	38853028 +	0.47488117 TACC1
17	DOK7	4	3463311	3494483 +	0.47095633 DOK7
18	INTS4	11	77878720	77994678 -	0.46882224 INTS4
19	GGH	8	63015085	63039171 -	0.46715307 GGH
20	LIMS1	2	108534355	108687246 +	0.46707916 LIMS1
21	TIAM2	6	154832697	155257723 +	0.46543217 TIAM2
22	SPSB1	1	9292880	9369532 +	0.45619202 SPSB1
23	FBXL16	16	692500	705829 -	0.45602655 FBXL16
24	LMO7	13	75620434	75859870 +	0.45330763 LMO7
25	PLOD1	1	11934694	11975537 +	0.45147085 PLOD1
26	VTCN1	1	117143587	117210960 -	0.44402456 VTCN1
27	PIGA	X	15319451	15335554 -	0.4402156 PIGA
28	ZNF827	4	145757627	145938635 -	0.4390993 ZNF827
29	ERRFI1	1	8004404	8026308 -	0.43716812 ERRFI1
30	SAMD9	7	93099513	93118023 -	0.43443012 SAMD9
31	PRKCH	14	61187559	61550976 +	0.4323299 PRKCH
32	KANK1	9	470291	746106 +	0.42522717 KANK1
33	KDM4C	9	6757654	7175648 +	0.4244523 KDM4C
34	AHR	7	17298622	17346150 +	0.41511917 AHR
35	ATAD2	8	123319850	123416350 -	0.3977747 ATAD2
36	FUT1	19	48748011	48755390 -	0.39238644 FUT1
37	ATP9A	20	51596514	51768634 -	0.39222193 ATP9A
38	CDC42EP4	17	73283624	73312175 -	0.38693237 CDC42EP4
39	LY6E	8	143017982	143023832 +	0.38275242 LY6E
40	OTUD6B	8	91070196	91087095 +	0.3793249 OTUD6B
41	TINAGL1	1	31576485	31587686 +	0.37793684 TINAGL1
42	MEF2A	15	99565417	99716466 +	0.37545776 MEF2A
43	H1FX	3	129314771	129316277 -	0.36826658 H1FX
44	DSG2	18	31498043	31549008 +	0.3631301 DSG2
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ZDHHC21	9	14611071	14693471 -	0.3625431 ZDHHC21
UBA3	3	69054730	69080408 -	0.36164522 UBA3
PTTG1IP	21	44849585	44873903 -	0.35513973 PTTG1IP
TMF1	3	69019827	69052303 -	0.34824467 TMF1
CFL2	14	34706769	34714690 -	0.3476591 CFL2
SMAD3	15	67063763	67195195 +	0.34600163 SMAD3
MANBA	4	102631893	102760994 -	0.34515762 MANBA
NDUFC2-KCTI	11	78016971	78079865 -	0.34351683 NDUFC2-KCTI
KCTD14	11	78015715	78080219 -	0.3410282 KCTD14
OAS3	12	112938352	112973249 +	0.3388753 OAS3
CTS2	20	58995185	59007247 -	0.31918097 CTS2
MYO10	5	16661914	16936276 -	0.3126316 MYO10
CHMP4A	14	24209583	24213869 -	0.3126092 CHMP4A
NDUFC2	11	78068304	78080219 -	0.3097601 NDUFC2
MKNK2	19	2037465	2051244 -	0.3071785 MKNK2
RBPJ	4	26163455	26435131 +	0.30571842 RBPJ
PLEKHA5	12	19129752	19376400 +	0.29521227 PLEKHA5
TCTN2	12	123671113	123708403 +	0.28172016 TCTN2
CHD3	17	7884806	7912760 +	0.27825117 CHD3
RAPGEF2	4	159104178	159360169 +	0.27361298 RAPGEF2
MBOAT2	2	8852690	9003813 -	0.27339888 MBOAT2
HNRNPDL	4	82422564	82430225 -	0.27105045 HNRNPDL
TSPAN6	X	100627109	100637104 -	0.27080727 TSPAN6
STK26	X	132023265	132075943 +	0.26720715 STK26
FURIN	15	90868592	90883458 +	0.26672792 FURIN
LSR	19	35248392	35267964 +	0.25969028 LSR
PTMA	2	231707684	231713541 +	0.25668335 PTMA
SNX14	6	85505496	85594156 -	0.25649118 SNX14
CHCHD3	7	132784868	133082082 -	0.24262047 CHCHD3
ACTN4	19	38647670	38731583 +	0.2288084 ACTN4
EPS15L1	19	16355239	16472085 -	0.22565603 EPS15L1
ATP2C1	3	130850595	131016712 +	0.20948601 ATP2C1
SRRM1	1	24641231	24673267 +	0.20936394 SRRM1
SYPL1	7	106090503	106112576 -	0.2014041 SYPL1
H3F3B	17	75776434	75785486 -	0.194026 H3F3B
EIF2AK1	7	6022244	6059230 -	0.163589 EIF2AK1
PTPRA	20	2864184	3039076 +	0.1506381 PTPRA

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S-lacZ cells injected into mammary duct.

ID	Description	Type	Orientation	Distance	Ductal_Contr	Ductal_SOX1
ENSG00000000000	regulator of G-protein signaling 12	gene	Name match	0	0.82128817	-4.4258614
ENSG00000000000	family with sequence similarity 100, member A	gene	Name match	0	1.3831934	-3.300047
ENSG00000000000	zinc finger protein 100	gene	Name match	0	1.6707588	-2.8599985
ENSG00000000000	cystatin D [Sox10]	gene	Name match	0	0.8879843	-2.683252
ENSG00000000000	noncompact 1	gene	Name match	0	3.6476705	0.11319441
ENSG00000000000	CD14 molecule	gene	Name match	0	2.9433548	-0.3463062
ENSG00000000000	coiled-coil domain containing 100	gene	Name match	0	1.8856297	-1.0461693
ENSG00000000000	CD4 molecule	gene	Name match	0	-0.111897	-2.7531655
ENSG00000000000	mannosyl (alpha-1-6) N-acetylglucosaminyl transferase 1	gene	Name match	0	-2.8283088	-5.2221847
ENSG00000000000	mucin 16, cell surface associated	gene	Name match	0	5.5005975	3.1277225
ENSG00000000000	metallothionein 1	gene	Name match	0	0.13398014	-2.1295972
ENSG00000000000	Uncharacterized protein	gene	Name match	0	5.0998473	2.9999607
ENSG00000000000	fucosyltransferase 1	gene	Name match	0	0.86471814	-1.1511732
ENSG00000000000	synaptogyrin 1	gene	Name match	0	-0.0191832	-1.9544929
ENSG00000000000	cystatin E/M	gene	Name match	0	2.279343	0.412719
ENSG00000000000	solute carrier 10	gene	Name match	0	1.5948286	-0.2428498
ENSG00000000000	FES proto-oncogene	gene	Name match	0	1.652677	-0.162098
ENSG00000000000	kallikrein 1 [Serpine1]	gene	Name match	0	2.268713	0.49145946
ENSG00000000000	hes family bHLH transcription factor 1	gene	Name match	0	-0.7347429	-2.426279
ENSG00000000000	collagen, type I, alpha 1	gene	Name match	0	2.3592036	0.68424624
ENSG00000000000	G protein-coupled receptor 100	gene	Name match	0	0.9882655	-0.6306299
ENSG00000000000	naked cuticle	gene	Name match	0	2.529914	0.9810688
ENSG00000000000	ectonucleoside diphosphate kinase 1	gene	Name match	0	0.7085956	-0.8093253
ENSG00000000000	myosin binding protein C	gene	Name match	0	8.400754	6.9190307
ENSG00000000000	ceruloplasmin	gene	Name match	0	4.1527476	2.6860874
ENSG00000000000	nuclear receptor 1	gene	Name match	0	6.2428565	4.789105
ENSG00000000000	integrin, alpha 1	gene	Name match	0	1.8304602	0.4250106
ENSG00000000000	guanine nucleotide-binding protein (Gq class) 1	gene	Name match	0	1.9304944	0.57824045
ENSG00000000000	ADP-ribosyltransferase 1	gene	Name match	0	3.371658	2.053223
ENSG00000000000	neuronal growth factor 1	gene	Name match	0	1.5115217	0.21989751
ENSG00000000000	C3 and PZP-like domain containing 1	gene	Name match	0	3.3557065	2.0821993
ENSG00000000000	collagen, type I, alpha 2	gene	Name match	0	2.473997	1.2252542
ENSG00000000000	chemokine (C-C motif) ligand 1	gene	Name match	0	1.7354239	0.49706364
ENSG00000000000	T-cell activation-induced gene 1	gene	Name match	0	2.2251904	1.0051804
ENSG00000000000	alpha 1,4-galactosyltransferase 1	gene	Name match	0	2.9699967	1.772353
ENSG00000000000	alpha-2-macroglobulin	gene	Name match	0	6.4762588	5.2885303
ENSG00000000000	period circadian 1	gene	Name match	0	4.6641006	3.5094662
ENSG00000000000	secreted and transmembrane protein 1	gene	Name match	0	2.024982	0.9302433
ENSG00000000000	GRB2-associated protein 1	gene	Name match	0	4.235173	3.1592388

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4	ENSG000001:ectodysplasin gene	Name match	0	2.3984294	1.335306
5	ENSG000001:heparan sulfatase gene	Name match	0	1.4722476	0.433019
6	ENSG000001:myosin, heavy chain 10 gene	Name match	0	7.839458	6.809101
7	ENSG000001:dynamin 3 [S] gene	Name match	0	3.261281	2.2320497
8					
9	ENSG000000:growth arrest gene	Name match	0	4.229839	3.2101653
10	ENSG000001:integrin, beta gene	Name match	0	3.0725563	2.060995
11	ENSG000001:fibrillin 3 [S] gene	Name match	0	4.977926	3.9665215
12					
13	ENSG000001:BCL2-interacting protein 1 gene	Name match	0	2.9771278	1.9905319
14	ENSG000001:cathepsin F [S] gene	Name match	0	4.5509686	3.572807
15					
16	ENSG000001:retinoic acid receptor beta gene	Name match	0	2.2124865	1.2418354
17	ENSG000001:exocyst component 1 gene	Name match	0	5.586311	4.6227202
18	ENSG000001:delta-like 1 [C] gene	Name match	0	2.0741374	1.1184783
19					
20	ENSG000002:integrin, beta gene	Name match	0	6.5071635	5.5670047
21	ENSG000002:zinc finger protein 100 gene	Name match	0	2.4470775	1.5087223
22					
23	ENSG000001:tetraspanin 2 gene	Name match	0	6.1804447	5.2453227
24	ENSG000001:transglutaminase 2 gene	Name match	0	6.3394036	5.4245987
25	ENSG000001:apolipoprotein A-II gene	Name match	0	1.4640727	0.55186754
26	ENSG000001:nephroblastoma overexpressed gene	Name match	0	4.29801	3.396321
27	ENSG000001:sema domain gene	Name match	0	3.0648258	2.181239
28					
29	ENSG000001:arrestin domain 1 gene	Name match	0	4.837465	3.9705715
30	ENSG000000:ROS proto-oncogene c-abl gene	Name match	0	5.926892	5.061234
31					
32	ENSG000001:inositol-trisphosphate 3-kinase gamma gene	Name match	0	0.15343077	-0.7093921
33	ENSG000002:calpain 8 [S] gene	Name match	0	5.1123238	4.2533965
34	ENSG000001:neuropeptide Y gene	Name match	0	0.42285553	-0.4299841
35					
36	ENSG000001:solute carrier 12 gene	Name match	0	5.0162063	4.173397
37	ENSG000001:zinc finger protein 100 gene	Name match	0	4.9360466	4.0987983
38	ENSG000001:ribosomal mitoribosomal protein L31 gene	Name match	0	2.9222782	2.0871556
39					
40	ENSG000001:interleukin 34 gene	Name match	0	4.0482864	3.2190418
41	ENSG000001:phospholipase C gamma 1 gene	Name match	0	6.088303	5.2736583
42	ENSG000001:cathepsin S [S] gene	Name match	0	3.9030197	3.0967839
43					
44	ENSG000001:spermatogen gene	Name match	0	1.9478426	1.1507607
45	ENSG000001:zinc finger protein 100 gene	Name match	0	2.5671105	1.7738053
46	ENSG000001:stimulated by growth factor gene	Name match	0	7.252052	6.460871
47	ENSG000001:neuroepithelial cell adhesion molecule gene	Name match	0	7.4327006	6.650538
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49	ENSG000001:solute carrier 12 gene	Name match	0	3.6188042	2.839901
50	ENSG000001:inhibin, alpha gene	Name match	0	1.5370227	0.75970745
51					
52	ENSG000000:G protein-coupled receptor 127 gene	Name match	0	8.385033	7.6253643
53	ENSG000001:raftlin, lipid raft-associated protein gene	Name match	0	4.6811447	3.925499
54	ENSG000001:E74-like factor gene	Name match	0	8.083662	7.3312087
55					
56	ENSG000001:v-maf avian myeloblastosis virus oncogene gene	Name match	0	4.9960346	4.249023
57	ENSG000001:arrestin, beta gene	Name match	0	5.9389977	5.195148
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4	ENSG00000011	zinc finger pr	gene	Name match	0 2.5547335 1.837449
5	ENSG00000011	microphthal	n gene	Name match	0 1.9957508 1.2886126
6	ENSG00000011	neuromedin l	gene	Name match	0 1.962871 1.255891
7	ENSG00000011	abhydrolase c	gene	Name match	0 8.196801 7.489861
8	ENSG00000011	protein tyrosi	gene	Name match	0 4.7742505 4.068044
9	ENSG00000011	transmembra	gene	Name match	0 5.0859036 4.3866534
10	ENSG00000021	HLA complex	gene	Name match	0 3.0142155 2.3229425
11	ENSG00000011	sciellin [Sou	r gene	Name match	0 3.9314883 3.2411947
12	ENSG00000001	unc-13 homo	gene	Name match	0 7.45886 6.7778144
13	ENSG00000011	transcription	gene	Name match	0 9.567294 8.890887
14	ENSG00000011	protocadheri	n gene	Name match	0 4.8682017 4.198499
15	ENSG00000011	membrane b	gene	Name match	0 3.452777 2.7879035
16	ENSG00000011	zinc finger an	gene	Name match	0 4.408466 3.7588043
17	ENSG00000011	ST3 beta-gal	a gene	Name match	0 7.647583 6.9989686
18	ENSG00000011	peripheral m	y gene	Name match	0 5.516235 4.8705735
19	ENSG00000011	transmembra	gene	Name match	0 1.8409599 1.2002034
20	ENSG00000011	GLI pathogen	gene	Name match	0 6.509144 5.8720875
21	ENSG00000011	epithelial me	i gene	Name match	0 7.744554 7.107569
22	ENSG00000011	growth factor	gene	Name match	0 6.5528774 5.9194655
23	ENSG00000011	GDP-mannos	i gene	Name match	0 5.9035554 5.2872405
24	ENSG00000021	UDP-Gal:beta	gene	Name match	0 3.2162163 2.6014974
25	ENSG00000001	phosphofruct	gene	Name match	0 7.225446 6.6161942
26	ENSG00000001	serpin peptid	gene	Name match	0 7.0424614 6.43739
27	ENSG00000011	phorbol-12-r	gene	Name match	0 3.4135044 2.8190546
28	ENSG00000011	FERM domair	gene	Name match	0 6.091972 5.4984574
29	ENSG00000011	leucine rich r	e gene	Name match	0 7.246765 6.654759
30	ENSG00000011	nuclear recep	gene	Name match	0 5.7358975 5.1458135
31	ENSG00000011	basic helix-lo	gene	Name match	0 7.661354 7.076015
32	ENSG00000011	cytochrome F	gene	Name match	0 3.32938 2.744461
33	ENSG00000011	solute carrier	gene	Name match	0 5.4865737 4.903656
34	ENSG00000011	WEE1 G2 che	gene	Name match	0 5.4297123 4.8667827
35	ENSG00000011	keratin 18 [S	c gene	Name match	0 8.875158 8.321176
36	ENSG00000011	H1 histone fa	gene	Name match	0 8.109189 7.5638504
37	ENSG00000011	glycerophosp	gene	Name match	0 2.58813 2.0478272
38	ENSG00000001	synaptojanin	gene	Name match	0 5.792299 5.2549167
39	ENSG00000011	PC4 and SFRS	gene	Name match	0 5.614719 5.0790167
40	ENSG00000011	keratin 8 [So	l gene	Name match	0 10.203933 9.671432
41	ENSG00000011	transmembra	gene	Name match	0 2.7868817 2.254698
42	ENSG00000011	proline-rich t	i gene	Name match	0 2.497648 1.9725167
43	ENSG00000011	ZFP36 ring fin	gene	Name match	0 5.867951 5.343849
44	ENSG00000011	zinc finger pr	gene	Name match	0 5.0843453 4.561092
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4	ENSG000001: cathepsin D [gene	Name match	0	11.213397	10.69376
5	ENSG000001: oligonucleotide gene	Name match	0	4.753634	4.2395816
6	ENSG000000: endoplasmic gene	Name match	0	6.4808116	5.974624
7	ENSG000001: SH3 domain gene	Name match	0	3.0896175	2.5842235
8	ENSG000001: CD97 molecule gene	Name match	0	5.7063656	5.2059817
9	ENSG000000: mitotic spindle gene	Name match	0	4.8377795	4.339174
10	ENSG000001: zinc finger protein gene	Name match	0	3.069791	2.5743873
11	ENSG000000: ubiquitin specific gene	Name match	0	4.8541174	4.369974
12	ENSG000001: fucosyltransferase gene	Name match	0	4.4304786	3.9498558
13	ENSG000001: solute carrier gene	Name match	0	3.8348238	3.354492
14	ENSG000001: Pim-3 proto-oncogene	Name match	0	5.484165	5.0059085
15	ENSG000000: SH3-domain gene	Name match	0	6.8918133	6.4167943
16	ENSG000001: transforming, gene	Name match	0	4.5749097	4.1000285
17	ENSG000001: docking protein gene	Name match	0	6.080669	5.6097126
18	ENSG000001: integrator core gene	Name match	0	4.3000674	3.8312452
19	ENSG000001: gamma-glutamyl gene	Name match	0	4.488907	4.021754
20	ENSG000001: LIM and senes gene	Name match	0	6.236744	5.769665
21	ENSG000001: T-cell lymphoma gene	Name match	0	3.565966	3.1005337
22	ENSG000001: splanchnic/ryanodine gene	Name match	0	4.7291007	4.2729087
23	ENSG000001: F-box and leucine gene	Name match	0	4.7964234	4.340397
24	ENSG000001: LIM domain 7 gene	Name match	0	5.8819194	5.4286118
25	ENSG000000: procollagen-1 gene	Name match	0	7.8543243	7.4028535
26	ENSG000001: V-set domain gene	Name match	0	6.545685	6.1016603
27	ENSG000001: phosphatidylinositol gene	Name match	0	3.6084316	3.168216
28	ENSG000001: zinc finger protein gene	Name match	0	5.42158	4.9824805
29	ENSG000001: ERBB receptor gene	Name match	0	8.864993	8.427825
30	ENSG000002: sterile alpha repeat gene	Name match	0	3.7910101	3.35658
31	ENSG000000: protein kinase gene	Name match	0	4.165183	3.7328532
32	ENSG000001: (KN motif and gene	Name match	0	7.22385	6.7986226
33	ENSG000001: lysine (K)-specific gene	Name match	0	5.041189	4.616737
34	ENSG000001: aryl hydrocarbon gene	Name match	0	7.50553	7.0904107
35	ENSG000001: ATPase family gene	Name match	0	5.4040484	5.0062737
36	ENSG000001: fucosyltransferase gene	Name match	0	3.4120147	3.0196283
37	ENSG000000: ATPase, class gene	Name match	0	6.7042985	6.3120766
38	ENSG000001: CDC42 effect gene	Name match	0	7.052111	6.665179
39	ENSG000001: lymphocyte alpha gene	Name match	0	7.963493	7.5807405
40	ENSG000001: OTU domain gene	Name match	0	3.7122831	3.3329582
41	ENSG000001: tubulointerstitial gene	Name match	0	7.878536	7.5005994
42	ENSG000000: myocyte enhancer gene	Name match	0	6.4393897	6.063932
43	ENSG000001: H1 histone family gene	Name match	0	6.1117573	5.7434907
44	ENSG000000: desmoglein 2 gene	Name match	0	8.140893	7.777763
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4	ENSG00000011	zinc finger, D1 gene	Name match	0	5.8112216	5.4486785
5	ENSG00000011	ubiquitin-like gene	Name match	0	6.730593	6.368948
6	ENSG00000011	pituitary tum gene	Name match	0	8.391389	8.036249
7	ENSG00000011	TATA elemen gene	Name match	0	6.064853	5.7166085
8	ENSG00000011	cofilin 2 (mus gene	Name match	0	4.2269087	3.8792496
9	ENSG00000011	SMAD family gene	Name match	0	6.359635	6.0136333
10	ENSG00000011	mannosidase gene	Name match	0	4.181156	3.8359985
11	ENSG00000021	NDUFC2-KCTD gene	Name match	0	5.3894525	5.0459356
12	ENSG00000011	potassium ch gene	Name match	0	6.07658	5.735552
13	ENSG00000011	2'-5'-oligoadenylate gene	Name match	0	5.164364	4.8254886
14	ENSG00000011	cathepsin Z [S gene	Name match	0	6.9515395	6.6323586
15	ENSG00000011	myosin X [Sol gene	Name match	0	6.7950215	6.48239
16	ENSG00000021	charged mult gene	Name match	0	4.308039	3.99543
17	ENSG00000011	NADH dehydrogenase gene	Name match	0	5.8719172	5.562157
18	ENSG00000001	MAP kinase ir gene	Name match	0	7.7885613	7.481383
19	ENSG00000011	recombinase gene	Name match	0	5.8526797	5.5469613
20	ENSG00000001	pleckstrin homology gene	Name match	0	4.4910374	4.195825
21	ENSG00000011	tectonic family gene	Name match	0	3.7535684	3.4718482
22	ENSG00000011	chromodomain gene	Name match	0	7.197513	6.919262
23	ENSG00000011	Rap guanine binding gene	Name match	0	5.2258716	4.9522586
24	ENSG00000011	membrane bound gene	Name match	0	6.53055	6.257151
25	ENSG00000011	heterogeneous gene	Name match	0	7.6897902	7.41874
26	ENSG00000001	tetraspanin 6 gene	Name match	0	5.370811	5.1000037
27	ENSG00000011	serine/threonine gene	Name match	0	4.7328115	4.4656043
28	ENSG00000011	furin (paired like gene	Name match	0	7.602001	7.3352733
29	ENSG00000011	lipolysis stim gene	Name match	0	7.4764314	7.216741
30	ENSG00000011	prothymosin, gene	Name match	0	9.762162	9.505479
31	ENSG00000011	sorting nexin gene	Name match	0	5.4071484	5.150657
32	ENSG00000011	coiled-coil-helical gene	Name match	0	4.469776	4.2271557
33	ENSG00000011	actinin, alpha gene	Name match	0	10.006734	9.7779255
34	ENSG00000011	epidermal growth gene	Name match	0	4.3883586	4.1627026
35	ENSG00000001	ATPase, Ca++ gene	Name match	0	6.916214	6.706728
36	ENSG00000011	serine/arginine gene	Name match	0	6.4840546	6.2746906
37	ENSG00000001	synaptophysin gene	Name match	0	6.932178	6.730774
38	ENSG00000011	H3 histone, family gene	Name match	0	9.407147	9.213121
39	ENSG00000001	eukaryotic translation gene	Name match	0	6.4223366	6.2587476
40	ENSG00000011	protein tyrosine gene	Name match	0	5.8477383	5.6971
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Fat_Control	Fat_SOX11
0.54821527	-4.430589
1.3088119	-2.2373881
1.0892532	-2.4601002
0.10662353	-1.2926464
3.756108	0.66008484
3.0485876	-0.0292924
1.2413741	-3.0796113
0.06374265	-1.2456566
-4.436551	-4.9551744
4.0391054	2.7017448
0.50577056	-1.5539098
4.5906124	3.6142373
0.88082904	-1.47736
0.19708021	-2.0860271
1.748285	-0.6996162
2.118159	0.5386656
1.516717	-0.7087762
1.6961269	-0.0283154
-0.9523243	-1.2168844
1.5771586	0.0517175
0.25521618	-1.0245807
1.6325359	1.2186568
0.0076763	-0.5217952
7.784317	5.9516206
4.1988797	3.078171
5.4109535	5.0881543
0.35742998	-0.2889095
1.4970961	0.696905
2.79569	1.0464398
0.16154686	-0.3472847
3.787249	2.4598618
1.8634777	0.796669
1.5749593	0.07214447
1.1208985	0.49683008
1.8345903	1.2970695
5.1742334	4.460059
4.340376	4.760071
1.5578698	0.48204407
3.884739	2.9461787

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4	0.8269798	0.7182055
5	0.96528226	0.3148571
6	7.332385	6.271325
7	1.8538759	1.6367743
8	4.1171713	3.6777167
9	2.4814284	1.3450751
10	5.2222633	4.689569
11	2.6725354	1.8255723
12	4.7489634	4.075439
13	3.0403113	1.8407923
14	5.2853937	4.4000487
15	1.6703079	1.5549222
16	5.6722155	5.212739
17	2.6004052	1.6693962
18	5.2889414	4.326809
19	5.6641164	4.7441244
20	1.4907885	0.54009026
21	3.6126971	2.6010094
22	2.8496072	2.3534296
23	4.710332	3.8984764
24	4.2827716	4.0016017
25	0.40646666	-0.4713957
26	4.2068586	4.1283064
27	-0.2356192	-1.4298384
28	4.318524	3.7532966
29	4.0618324	4.2952127
30	2.7697906	2.030761
31	3.1173377	2.5955253
32	6.017398	5.361735
33	3.9943626	3.389357
34	1.6646395	1.1818501
35	1.904927	1.5410811
36	6.8141947	6.221092
37	7.1069307	7.0317583
38	3.9188118	2.967181
39	1.5548303	1.4865184
40	8.181597	7.587016
41	4.526002	4.313377
42	8.279421	7.812356
43	5.0659704	4.3217635
44	5.9644194	5.1956854
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2.4756157	2.49013
1.5216981	1.1360615
2.2147162	1.3715042
7.184809	7.2492623
4.701457	4.345549
5.016929	4.331923
2.683063	2.1613045
2.7104604	2.8841307
7.064429	6.4596086
9.491295	9.334271
4.721844	4.1567683
3.2098088	2.4834888
4.5864477	4.1753006
7.5648017	7.350038
4.9876547	4.72289
1.4521536	1.2260054
5.4294844	4.75859
7.1190743	6.857138
5.6521196	5.2049584
5.790019	5.3040533
3.0949986	2.9957066
7.053796	6.4840713
6.9625483	6.6031737
2.2458138	1.7323961
5.55009	5.4124846
6.801165	6.6518364
5.2422657	4.6909475
7.4071746	7.2890677
2.3683095	1.8690739
5.0775404	4.4147735
5.1570787	4.8459506
9.067083	8.643652
8.082582	7.65759
2.637838	2.0912678
5.6540513	4.9566207
5.3924117	4.9465914
10.204099	9.795908
2.5526721	1.9491379
2.5861163	2.344172
5.6248617	5.527783
4.79097	4.378592

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4	11.135318	11.081822
5	4.6648574	4.277667
6	6.1384034	6.1188498
7	3.0176888	2.3665526
8		
9	5.3368473	5.040082
10	4.2908335	3.782724
11	2.3378115	2.2140317
12		
13	4.4613104	4.193778
14	4.623178	4.3627357
15	3.6388545	3.530798
16		
17	5.5816298	5.4425974
18	6.6205583	6.140538
19	4.4106145	4.037855
20	6.095294	5.8190446
21	4.248146	3.8446288
22	4.310385	3.7119794
23	5.460598	4.9406004
24		
25	3.1278293	2.9860806
26	4.7051597	4.3918796
27	4.9027495	4.6342106
28		
29	5.4264193	5.176052
30	7.5400023	7.359989
31	6.35571	5.870552
32	3.2930996	3.0051513
33	5.223321	5.009927
34	8.7646	8.388733
35	3.1098492	2.763162
36	3.6867878	3.4724529
37	6.7815943	6.7772994
38	4.7361465	4.5693083
39	6.71175	6.3663416
40	5.0107737	4.6015377
41	3.1446526	2.9255831
42	6.3241916	6.060775
43	6.735668	6.365667
44	8.254158	8.012068
45	3.247582	3.1690183
46	7.7939863	7.578557
47	6.0074134	6.0273123
48	6.203909	5.8608437
49	7.590361	7.49409
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4 5.431926 5.2454123
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6 8.175048 7.895031
7 5.653487 5.6025987
8 3.9528623 3.6540196
9 6.207195 5.6945724
10 3.9335093 3.9732132
11 5.722665 5.3216476
12 6.4333243 6.0766973
13 4.6511397 4.3024263
14 6.76679 6.700499
15 6.0346327 5.9018416
16 4.5287056 4.159343
17 6.251916 5.854192
18 7.6294365 7.6971903
19 5.5871687 5.4148808
20 4.1657944 4.032117
21 3.6973088 3.5683773
22 7.1221185 6.834343
23 4.8295493 4.717621
24 6.3905807 6.0393744
25 7.572852 7.50309
26 5.368825 5.345067
27 4.232051 4.113078
28 7.2068496 7.1277914
29 7.3950872 7.176959
30 9.874621 9.481022
31 5.1047378 5.0862617
32 4.3220806 4.0814195
33 9.602462 9.588259
34 4.2564573 4.17547
35 6.53206 6.4099417
36 6.3656793 6.2148614
37 6.7055397 6.6444497
38 9.552568 9.358434
39 6.4492936 6.2478943
40 5.7474885 5.68084
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Table S4D. Functional annotation clustering of downregulated genes in lesions and tumours fr

Annotation C Enrichment Score: 3.2772809402522736			
Category	Term	Count	%
UP_SEQ_FEA	glycosylation site:N-linked (GlcNAc...)	46	4.38931298
SP_PIR_KEYM	glycoprotein	46	4.38931298
SP_PIR_KEYM	membrane	51	4.86641221
UP_SEQ_FEA	topological domain:Cytoplasmic	32	3.05343511
UP_SEQ_FEA	transmembrane region	40	3.81679389
SP_PIR_KEYM	transmembrane	40	3.81679389
GOTERM_CC	GO:0031224~intrinsic to membrane	45	4.29389313
UP_SEQ_FEA	topological domain:Extracellular	25	2.38549618
GOTERM_CC	GO:0016021~integral to membrane	42	4.00763359
Annotation C Enrichment Score: 3.2079466522282507			
Category	Term	Count	%
UP_SEQ_FEA	glycosylation site:N-linked (GlcNAc...)	46	4.38931298
SP_PIR_KEYM	glycoprotein	46	4.38931298
UP_SEQ_FEA	signal peptide	29	2.76717557
SP_PIR_KEYM	signal	29	2.76717557
UP_SEQ_FEA	disulfide bond	26	2.48091603
SP_PIR_KEYM	disulfide bond	26	2.48091603
GOTERM_CC	GO:0005576~extracellular region	19	1.8129771
Annotation C Enrichment Score: 1.974978106211693			
Category	Term	Count	%
GOTERM_MF	GO:0004866~endopeptidase inhibitor activity	6	0.57251908
GOTERM_MF	GO:0030414~peptidase inhibitor activity	6	0.57251908
SP_PIR_KEYM	protease inhibitor	4	0.38167939
GOTERM_MF	GO:0004857~enzyme inhibitor activity	6	0.57251908
GOTERM_MF	GO:0004867~serine-type endopeptidase inhibitor ac	3	0.28625954
Annotation C Enrichment Score: 1.7109375139936056			
Category	Term	Count	%
GOTERM_CC	GO:0043005~neuron projection	9	0.85877863
GOTERM_CC	GO:0043025~cell soma	6	0.57251908
GOTERM_CC	GO:0042995~cell projection	10	0.95419847
GOTERM_CC	GO:0030424~axon	4	0.38167939
GOTERM_CC	GO:0030425~dendrite	4	0.38167939
GOTERM_CC	GO:0044463~cell projection part	4	0.38167939
Annotation C Enrichment Score: 1.6440528659569473			

Category	Term	Count	%
SP_PIR_KEYM	transmembrane protein	11	1.04961832
GOTERM_CC	GO:0031226~intrinsic to plasma membrane	14	1.33587786
GOTERM_CC	GO:0005887~integral to plasma membrane	13	1.24045802
GOTERM_CC	GO:0044459~plasma membrane part	19	1.8129771

Annotation C Enrichment Score: 1.5403401656585556

Category	Term	Count	%
GOTERM_BP	GO:0006917~induction of apoptosis	8	0.76335878
GOTERM_BP	GO:0012502~induction of programmed cell death	8	0.76335878
GOTERM_BP	GO:0043065~positive regulation of apoptosis	9	0.85877863
GOTERM_BP	GO:0043068~positive regulation of programmed cell	9	0.85877863
GOTERM_BP	GO:0010942~positive regulation of cell death	9	0.85877863
GOTERM_BP	GO:0052548~regulation of endopeptidase activity	4	0.38167939
GOTERM_BP	GO:0052547~regulation of peptidase activity	4	0.38167939
GOTERM_BP	GO:0042981~regulation of apoptosis	10	0.95419847
GOTERM_BP	GO:0043067~regulation of programmed cell death	10	0.95419847
GOTERM_BP	GO:0010941~regulation of cell death	10	0.95419847
GOTERM_BP	GO:0043281~regulation of caspase activity	3	0.28625954
GOTERM_BP	GO:0051336~regulation of hydrolase activity	5	0.47709924
GOTERM_BP	GO:0051345~positive regulation of hydrolase activity	3	0.28625954
GOTERM_CC	GO:0005739~mitochondrion	3	0.28625954

Annotation C Enrichment Score: 1.5287267362879138

Category	Term	Count	%
GOTERM_BP	GO:0007155~cell adhesion	11	1.04961832
GOTERM_BP	GO:0022610~biological adhesion	11	1.04961832
GOTERM_BP	GO:0016337~cell-cell adhesion	4	0.38167939

Annotation C Enrichment Score: 1.4503270670653603

Category	Term	Count	%
GOTERM_CC	GO:0043235~receptor complex	5	0.47709924
GOTERM_BP	GO:0007229~integrin-mediated signaling pathway	4	0.38167939
GOTERM_CC	GO:0008305~integrin complex	3	0.28625954
SP_PIR_KEYM	integrin	3	0.28625954
SP_PIR_KEYM	cell adhesion	7	0.66793893
UP_SEQ_FEA	domain:VWFA	3	0.28625954
INTERPRO	IPR002035: von Willebrand factor, type A	3	0.28625954
KEGG_PATHV	hsa04810: Regulation of actin cytoskeleton	5	0.47709924
SMART	SM00327: VWA	3	0.28625954
GOTERM_BP	GO:0007160~cell-matrix adhesion	3	0.28625954

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4	GOTERM_BP_GO:0031589~cell-substrate adhesion	3	0.28625954	
5				
6	Annotation C Enrichment Score: 1.3746038097831221			
7	Category Term	Count	%	
8				
9	GOTERM_BP_GO:0012501~programmed cell death	10	0.95419847	
10	GOTERM_BP_GO:0006915~apoptosis	9	0.85877863	
11	GOTERM_BP_GO:0008219~cell death	10	0.95419847	
12	GOTERM_BP_GO:0016265~death	10	0.95419847	
13	SP_PIR_KEYM Apoptosis	4	0.38167939	
14				
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17	Annotation C Enrichment Score: 1.2951804904443684			
18	Category Term	Count	%	
19				
20	SP_PIR_KEYM cell adhesion	7	0.66793893	
21	GOTERM_MF GO:0005178~integrin binding	3	0.28625954	
22	GOTERM_MF GO:0032403~protein complex binding	4	0.38167939	
23				
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25	Annotation C Enrichment Score: 1.2794232879544034			
26	Category Term	Count	%	
27				
28	GOTERM_BP_GO:0008544~epidermis development	5	0.47709924	
29	GOTERM_BP_GO:0007398~ectoderm development	5	0.47709924	
30	GOTERM_BP_GO:0030855~epithelial cell differentiation	4	0.38167939	
31	GOTERM_BP_GO:0060429~epithelium development	4	0.38167939	
32				
33				
34	Annotation C Enrichment Score: 1.1764543414754383			
35	Category Term	Count	%	
36				
37	SP_PIR_KEYM Signal-anchor	8	0.76335878	
38	GOTERM_BP_GO:0006486~protein amino acid glycosylation	5	0.47709924	
39	GOTERM_BP_GO:0070085~glycosylation	5	0.47709924	
40	GOTERM_BP_GO:0043413~biopolymer glycosylation	5	0.47709924	
41	GOTERM_BP_GO:0009101~glycoprotein biosynthetic process	5	0.47709924	
42	GOTERM_CC_GO:0030173~integral to Golgi membrane	3	0.28625954	
43	SP_PIR_KEYM glycosyltransferase	5	0.47709924	
44	GOTERM_CC_GO:0031228~intrinsic to Golgi membrane	3	0.28625954	
45	UP_SEQ_FEA`topological domain:Lumenal	7	0.66793893	
46	GOTERM_BP_GO:0009100~glycoprotein metabolic process	5	0.47709924	
47	SP_PIR_KEYM transferase	12	1.14503817	
48	GOTERM_CC_GO:0031301~integral to organelle membrane	3	0.28625954	
49	GOTERM_CC_GO:0031300~intrinsic to organelle membrane	3	0.28625954	
50	GOTERM_CC_GO:0005794~Golgi apparatus	8	0.76335878	
51	GOTERM_CC_GO:0000139~Golgi membrane	3	0.28625954	
52	SP_PIR_KEYM golgi apparatus	5	0.47709924	
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GOTERM_CC_GO:0012505~endomembrane system	6	0.57251908
GOTERM_CC_GO:0044431~Golgi apparatus part	3	0.28625954
GOTERM_CC_GO:0031090~organelle membrane	6	0.57251908

Annotation C Enrichment Score: 1.1098623787480475

Category	Term	Count	%
GOTERM_CC_GO:0043235~receptor complex		5	0.47709924
KEGG_PATHV_hsa04640:Hematopoietic cell lineage		4	0.38167939
GOTERM_CC_GO:0045121~membrane raft		3	0.28625954
GOTERM_CC_GO:0009897~external side of plasma membrane		3	0.28625954
GOTERM_CC_GO:0009986~cell surface		4	0.38167939

Annotation C Enrichment Score: 1.0438596476559538

Category	Term	Count	%
GOTERM_CC_GO:0005576~extracellular region		19	1.8129771
GOTERM_CC_GO:0044421~extracellular region part		11	1.04961832
SP_PIR_KEYM_Secreted		14	1.33587786
GOTERM_CC_GO:0005615~extracellular space		7	0.66793893

Annotation C Enrichment Score: 0.8302092621074846

Category	Term	Count	%
GOTERM_BP_GO:0051050~positive regulation of transport		5	0.47709924
GOTERM_BP_GO:0051047~positive regulation of secretion		3	0.28625954
GOTERM_BP_GO:0060341~regulation of cellular localization		4	0.38167939
GOTERM_BP_GO:0051046~regulation of secretion		3	0.28625954

Annotation C Enrichment Score: 0.7883234667038367

Category	Term	Count	%
UP_SEQ_FEA`domain:Fibronectin type-III 3		3	0.28625954
INTERPRO_IPR008957:Fibronectin, type III-like fold		4	0.38167939
UP_SEQ_FEA`domain:Fibronectin type-III 2		3	0.28625954
UP_SEQ_FEA`domain:Fibronectin type-III 1		3	0.28625954
INTERPRO_IPR003961:Fibronectin, type III		3	0.28625954
SMART_SM00060:FN3		3	0.28625954

Annotation C Enrichment Score: 0.7752164745307089

Category	Term	Count	%
INTERPRO_IPR000169:Peptidase, cysteine peptidase active site		3	0.28625954
UP_SEQ_FEA`propeptide:Activation peptide		3	0.28625954
GOTERM_MF_GO:0004197~cysteine-type endopeptidase activity		3	0.28625954
SP_PIR_KEYM_zymogen		4	0.38167939

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4	SP_PIR_KEYW	thiol protease	3	0.28625954
5	GOTERM_MF	GO:0004175~endopeptidase activity	5	0.47709924
6	GOTERM_MF	GO:0008234~cysteine-type peptidase activity	3	0.28625954
7	SP_PIR_KEYW	Protease	5	0.47709924
8	SP_PIR_KEYW	hydrolase	11	1.04961832
9	GOTERM_MF	GO:0070011~peptidase activity, acting on L-amino a	5	0.47709924
10	GOTERM_MF	GO:0008233~peptidase activity	5	0.47709924
11	GOTERM_BP	GO:0006508~proteolysis	5	0.47709924
12				
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14				
15	Annotation C	Enrichment Score: 0.7621932548276306		
16	Category	Term	Count	%
17	INTERPRO	IPR011993:Pleckstrin homology-type	5	0.47709924
18	UP_SEQ_FEA	domain:PH	4	0.38167939
19	INTERPRO	IPR001849:Pleckstrin homology	4	0.38167939
20	SMART	SM00233:PH	4	0.38167939
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25	Annotation C	Enrichment Score: 0.7616460288066436		
26	Category	Term	Count	%
27	UP_SEQ_FEA	DNA-binding region:Basic motif	4	0.38167939
28	UP_SEQ_FEA	domain:Helix-loop-helix motif	3	0.28625954
29	INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region	3	0.28625954
30	SMART	SM00353:HLH	3	0.28625954
31	GOTERM_MF	GO:0030528~transcription regulator activity	7	0.66793893
32				
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36	Annotation C	Enrichment Score: 0.7011939125138277		
37	Category	Term	Count	%
38	GOTERM_MF	GO:0005201~extracellular matrix structural constitu	4	0.38167939
39	GOTERM_MF	GO:0005198~structural molecule activity	6	0.57251908
40	GOTERM_CC	GO:0031012~extracellular matrix	4	0.38167939
41	SP_PIR_KEYW	extracellular matrix	3	0.28625954
42	GOTERM_CC	GO:0005578~proteinaceous extracellular matrix	3	0.28625954
43				
44				
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46	Annotation C	Enrichment Score: 0.6808549034271686		
47	Category	Term	Count	%
48	GOTERM_BP	GO:0030097~hemopoiesis	4	0.38167939
49	GOTERM_BP	GO:0048534~hemopoietic or lymphoid organ develc	4	0.38167939
50	GOTERM_BP	GO:0002520~immune system development	4	0.38167939
51				
52				
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54	Annotation C	Enrichment Score: 0.6607578730858731		
55	Category	Term	Count	%
56	GOTERM_BP	GO:0010324~membrane invagination	4	0.38167939
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GOTERM_BP_GO:0006897~endocytosis	4	0.38167939
GOTERM_BP_GO:0016044~membrane organization	5	0.47709924
GOTERM_BP_GO:0016192~vesicle-mediated transport	5	0.47709924

Annotation C Enrichment Score: 0.6518647543713899

Category	Term	Count	%
GOTERM_BP_GO:0046649~lymphocyte activation		4	0.38167939
GOTERM_BP_GO:0045321~leukocyte activation		4	0.38167939
GOTERM_BP_GO:0001775~cell activation		4	0.38167939
GOTERM_BP_GO:0006955~immune response		6	0.57251908

Annotation C Enrichment Score: 0.6220299107496159

Category	Term	Count	%
GOTERM_BP_GO:0009611~response to wounding		7	0.66793893
GOTERM_BP_GO:0030334~regulation of cell migration		3	0.28625954
GOTERM_BP_GO:0040012~regulation of locomotion		3	0.28625954
GOTERM_BP_GO:0051270~regulation of cell motion		3	0.28625954

Annotation C Enrichment Score: 0.6219157589390967

Category	Term	Count	%
GOTERM_BP_GO:0009611~response to wounding		7	0.66793893
GOTERM_BP_GO:0006954~inflammatory response		5	0.47709924
GOTERM_BP_GO:0006955~immune response		6	0.57251908
GOTERM_BP_GO:0006952~defense response		5	0.47709924

Annotation C Enrichment Score: 0.6205520875567478

Category	Term	Count	%
GOTERM_BP_GO:0050804~regulation of synaptic transmission		3	0.28625954
GOTERM_BP_GO:0051969~regulation of transmission of nerve impulse		3	0.28625954
GOTERM_BP_GO:0031644~regulation of neurological system process		3	0.28625954
GOTERM_BP_GO:0044057~regulation of system process		4	0.38167939

Annotation C Enrichment Score: 0.5824244142074961

Category	Term	Count	%
GOTERM_BP_GO:0007267~cell-cell signaling		8	0.76335878
GOTERM_BP_GO:0007268~synaptic transmission		4	0.38167939
GOTERM_BP_GO:0019226~transmission of nerve impulse		4	0.38167939
GOTERM_BP_GO:0050877~neurological system process		8	0.76335878

Annotation C Enrichment Score: 0.5811996008997474

Category	Term	Count	%
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4	GOTERM_BP_GO:0042325~regulation of phosphorylation	7	0.66793893
5	GOTERM_BP_GO:0019220~regulation of phosphate metabolic pro	7	0.66793893
6	GOTERM_BP_GO:0051174~regulation of phosphorus metabolic pr	7	0.66793893
7	GOTERM_BP_GO:0016477~cell migration	4	0.38167939
8			
9	GOTERM_BP_GO:0042330~taxis	3	0.28625954
10	GOTERM_BP_GO:0006935~chemotaxis	3	0.28625954
11	GOTERM_BP_GO:0001932~regulation of protein amino acid phosp	3	0.28625954
12			
13	GOTERM_BP_GO:0048870~cell motility	4	0.38167939
14	GOTERM_BP_GO:0051674~localization of cell	4	0.38167939
15	GOTERM_BP_GO:0007626~locomotory behavior	3	0.28625954
16			
17	GOTERM_BP_GO:0031399~regulation of protein modification proc	3	0.28625954
18	GOTERM_BP_GO:0007610~behavior	4	0.38167939
19	GOTERM_BP_GO:0032268~regulation of cellular protein metabolic	4	0.38167939
20	GOTERM_BP_GO:0006928~cell motion	4	0.38167939
21			
22			

23	Annotation C Enrichment Score: 0.5476918047931075		
24	Category	Term	
25			Count %
26	UP_SEQ_FEA`repeat:LRR 11		3 0.28625954
27	UP_SEQ_FEA`repeat:LRR 10		3 0.28625954
28	UP_SEQ_FEA`repeat:LRR 9		3 0.28625954
29	UP_SEQ_FEA`repeat:LRR 8		3 0.28625954
30	UP_SEQ_FEA`repeat:LRR 7		3 0.28625954
31	UP_SEQ_FEA`repeat:LRR 6		3 0.28625954
32	UP_SEQ_FEA`repeat:LRR 5		3 0.28625954
33	UP_SEQ_FEA`repeat:LRR 4		3 0.28625954
34	UP_SEQ_FEA`repeat:LRR 3		3 0.28625954
35	UP_SEQ_FEA`repeat:LRR 1		3 0.28625954
36	UP_SEQ_FEA`repeat:LRR 2		3 0.28625954
37	SP_PIR_KEYM leucine-rich repeat		3 0.28625954
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43	Annotation C Enrichment Score: 0.5388418261151184		
44	Category	Term	
45			Count %
46	GOTERM_BP_GO:0042325~regulation of phosphorylation		7 0.66793893
47	GOTERM_BP_GO:0044093~positive regulation of molecular functi		8 0.76335878
48	GOTERM_BP_GO:0051174~regulation of phosphorus metabolic pr		7 0.66793893
49	GOTERM_BP_GO:0019220~regulation of phosphate metabolic pro		7 0.66793893
50	GOTERM_BP_GO:0043085~positive regulation of catalytic activity		7 0.66793893
51	GOTERM_BP_GO:0045860~positive regulation of protein kinase ac		4 0.38167939
52	GOTERM_BP_GO:0033674~positive regulation of kinase activity		4 0.38167939
53	GOTERM_BP_GO:0051347~positive regulation of transferase activ		4 0.38167939
54	GOTERM_BP_GO:0001932~regulation of protein amino acid phosp		3 0.28625954
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GOTERM_BP_GO:0000165~MAPKKK cascade	3	0.28625954
GOTERM_BP_GO:0045859~regulation of protein kinase activity	4	0.38167939
GOTERM_BP_GO:0043549~regulation of kinase activity	4	0.38167939
GOTERM_BP_GO:0051338~regulation of transferase activity	4	0.38167939
GOTERM_BP_GO:0031399~regulation of protein modification proc	3	0.28625954
GOTERM_BP_GO:0032268~regulation of cellular protein metabolic	4	0.38167939
GOTERM_BP_GO:0006468~protein amino acid phosphorylation	5	0.47709924
GOTERM_MF_GO:0046983~protein dimerization activity	4	0.38167939
GOTERM_BP_GO:0007243~protein kinase cascade	3	0.28625954
GOTERM_BP_GO:0006793~phosphorus metabolic process	6	0.57251908
GOTERM_BP_GO:0006796~phosphate metabolic process	6	0.57251908
GOTERM_BP_GO:0016310~phosphorylation	5	0.47709924
GOTERM_BP_GO:0007242~intracellular signaling cascade	7	0.66793893

Annotation C Enrichment Score: 0.5146295903729098

Category	Term	Count	%
GOTERM_BP_GO:0006873~cellular ion homeostasis		5	0.47709924
GOTERM_BP_GO:0030003~cellular cation homeostasis		4	0.38167939
GOTERM_BP_GO:0055082~cellular chemical homeostasis		5	0.47709924
GOTERM_BP_GO:0050801~ion homeostasis		5	0.47709924
GOTERM_BP_GO:0055080~cation homeostasis		4	0.38167939
GOTERM_BP_GO:0019725~cellular homeostasis		5	0.47709924
GOTERM_BP_GO:0006875~cellular metal ion homeostasis		3	0.28625954
GOTERM_BP_GO:0055065~metal ion homeostasis		3	0.28625954
GOTERM_BP_GO:0048878~chemical homeostasis		5	0.47709924
GOTERM_BP_GO:0030005~cellular di-, tri-valent inorganic cation h		3	0.28625954
GOTERM_BP_GO:0055066~di-, tri-valent inorganic cation homeost		3	0.28625954
GOTERM_BP_GO:0042592~homeostatic process		6	0.57251908

Annotation C Enrichment Score: 0.4916005355222842

Category	Term	Count	%
SP_PIR_KEYW	lysosome	3	0.28625954
GOTERM_CC_GO:0005764~lysosome		3	0.28625954
GOTERM_CC_GO:0000323~lytic vacuole		3	0.28625954
GOTERM_CC_GO:0005773~vacuole		3	0.28625954

Annotation C Enrichment Score: 0.4465843176032988

Category	Term	Count	%
GOTERM_CC_GO:0031410~cytoplasmic vesicle		7	0.66793893
GOTERM_CC_GO:0031982~vesicle		7	0.66793893
SP_PIR_KEYW	cytoplasmic vesicle	3	0.28625954

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4	GOTERM_CC_	GO:0016023~cytoplasmic membrane-bounded vesic	4	0.38167939
5	GOTERM_CC_	GO:0031988~membrane-bounded vesicle	4	0.38167939
6				
7	Annotation C	Enrichment Score: 0.40175074308212344		
8	Category	Term	Count	%
9	GOTERM_CC_	GO:0005624~membrane fraction	7	0.66793893
10	GOTERM_CC_	GO:0005626~insoluble fraction	7	0.66793893
11	GOTERM_CC_	GO:0000267~cell fraction	8	0.76335878
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15	Annotation C	Enrichment Score: 0.3732760349755133		
16	Category	Term	Count	%
17	GOTERM_BP_	GO:0048514~blood vessel morphogenesis	3	0.28625954
18	GOTERM_BP_	GO:0001568~blood vessel development	3	0.28625954
19	GOTERM_BP_	GO:0001944~vasculature development	3	0.28625954
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23	Annotation C	Enrichment Score: 0.3556467155157993		
24	Category	Term	Count	%
25	UP_SEQ_FEA`	domain:Ig-like C2-type 3	3	0.28625954
26	UP_SEQ_FEA`	domain:Ig-like C2-type 1	3	0.28625954
27	UP_SEQ_FEA`	domain:Ig-like C2-type 2	3	0.28625954
28	INTERPRO	IPR003599:Immunoglobulin subtype	3	0.28625954
29	INTERPRO	IPR013783:Immunoglobulin-like fold	4	0.38167939
30	SMART	SM00409:IG	3	0.28625954
31	SP_PIR_KEYW	Immunoglobulin domain	3	0.28625954
32	INTERPRO	IPR007110:Immunoglobulin-like	3	0.28625954
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34				
35	Annotation C	Enrichment Score: 0.29325798696051153		
36	Category	Term	Count	%
37	UP_SEQ_FEA`	DNA-binding region:Basic motif	4	0.38167939
38	GOTERM_BP_	GO:0048511~rhythmic process	3	0.28625954
39	GOTERM_BP_	GO:0010558~negative regulation of macromolecule	6	0.57251908
40	GOTERM_BP_	GO:0009890~negative regulation of biosynthetic prc	6	0.57251908
41	GOTERM_MF	GO:0016564~transcription repressor activity	4	0.38167939
42	SP_PIR_KEYW	transcription regulation	13	1.24045802
43	SP_PIR_KEYW	Transcription	13	1.24045802
44	GOTERM_BP_	GO:0031327~negative regulation of cellular biosynt	5	0.47709924
45	GOTERM_BP_	GO:0010605~negative regulation of macromolecule	6	0.57251908
46	GOTERM_BP_	GO:0016481~negative regulation of transcription	4	0.38167939
47	SP_PIR_KEYW	dna-binding	11	1.04961832
48	GOTERM_BP_	GO:0010629~negative regulation of gene expression	4	0.38167939
49	GOTERM_BP_	GO:0045934~negative regulation of nucleobase, nuc	4	0.38167939
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GOTERM_BP_GO:0051172~negative regulation of nitrogen compo	4	0.38167939
GOTERM_BP_GO:0045892~negative regulation of transcription, DI	3	0.28625954
GOTERM_BP_GO:0006350~transcription	13	1.24045802
GOTERM_BP_GO:0051253~negative regulation of RNA metabolic p	3	0.28625954
GOTERM_BP_GO:0006355~regulation of transcription, DNA-deper	11	1.04961832
GOTERM_MF_GO:0003700~transcription factor activity	6	0.57251908
GOTERM_BP_GO:0051252~regulation of RNA metabolic process	11	1.04961832
GOTERM_MF_GO:0043565~sequence-specific DNA binding	4	0.38167939
GOTERM_MF_GO:0016563~transcription activator activity	3	0.28625954
GOTERM_BP_GO:0006357~regulation of transcription from RNA p	4	0.38167939
GOTERM_MF_GO:0030528~transcription regulator activity	7	0.66793893
GOTERM_MF_GO:0003677~DNA binding	11	1.04961832
GOTERM_BP_GO:0045449~regulation of transcription	13	1.24045802
SP_PIR_KEYW nucleus	15	1.43129771

Annotation C Enrichment Score: 0.29182885710087814

Category	Term	Count	%
GOTERM_BP_GO:0010033~response to organic substance		7	0.66793893
GOTERM_BP_GO:0009725~response to hormone stimulus		3	0.28625954
GOTERM_BP_GO:0009719~response to endogenous stimulus		3	0.28625954

Annotation C Enrichment Score: 0.2853129147752369

Category	Term	Count	%
GOTERM_BP_GO:0051260~protein homooligomerization		3	0.28625954
GOTERM_BP_GO:0051259~protein oligomerization		3	0.28625954
GOTERM_BP_GO:0070271~protein complex biogenesis		3	0.28625954
GOTERM_BP_GO:0006461~protein complex assembly		3	0.28625954
GOTERM_BP_GO:0065003~macromolecular complex assembly		3	0.28625954
GOTERM_BP_GO:0043933~macromolecular complex subunit orga		3	0.28625954

Annotation C Enrichment Score: 0.24485207785098195

Category	Term	Count	%
GOTERM_BP_GO:0030030~cell projection organization		4	0.38167939
GOTERM_BP_GO:0048666~neuron development		3	0.28625954
GOTERM_BP_GO:0030182~neuron differentiation		3	0.28625954

Annotation C Enrichment Score: 0.21138567773786107

Category	Term	Count	%
GOTERM_BP_GO:0003006~reproductive developmental process		3	0.28625954
GOTERM_BP_GO:0048609~reproductive process in a multicellular		4	0.38167939
GOTERM_BP_GO:0032504~multicellular organism reproduction		4	0.38167939

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4	GOTERM_BP_GO:0007276~gamete generation	3	0.28625954	
5	GOTERM_BP_GO:0019953~sexual reproduction	3	0.28625954	
6				
7	Annotation C	Enrichment Score: 0.1998913144320727		
8	Category	Term	Count	%
9	SP_PIR_KEYM	phosphotransferase	4	0.38167939
10	SP_PIR_KEYM	ATP	4	0.38167939
11	UP_SEQ_FEA`	nucleotide phosphate-binding region:ATP	6	0.57251908
12	SP_PIR_KEYM	nucleotide-binding	9	0.85877863
13	SP_PIR_KEYM	kinase	4	0.38167939
14	SP_PIR_KEYM	atp-binding	7	0.66793893
15	GOTERM_MF_GO:0032555~	purine ribonucleotide binding	10	0.95419847
16	GOTERM_MF_GO:0032553~	ribonucleotide binding	10	0.95419847
17	GOTERM_MF_GO:0005524~	ATP binding	8	0.76335878
18	GOTERM_MF_GO:0032559~	adenyl ribonucleotide binding	8	0.76335878
19	UP_SEQ_FEA`	binding site:ATP	3	0.28625954
20	GOTERM_MF_GO:0017076~	purine nucleotide binding	10	0.95419847
21	GOTERM_MF_GO:0030554~	adenyl nucleotide binding	8	0.76335878
22	GOTERM_MF_GO:0001883~	purine nucleoside binding	8	0.76335878
23	GOTERM_MF_GO:0001882~	nucleoside binding	8	0.76335878
24	UP_SEQ_FEA`	active site:Proton acceptor	3	0.28625954
25	GOTERM_MF_GO:0004672~	protein kinase activity	3	0.28625954
26	GOTERM_MF_GO:0000166~	nucleotide binding	10	0.95419847
27				
28	Annotation C	Enrichment Score: 0.18403698162663604		
29	Category	Term	Count	%
30	GOTERM_MF_GO:0005525~	GTP binding	3	0.28625954
31	GOTERM_MF_GO:0019001~	guanyl nucleotide binding	3	0.28625954
32	GOTERM_MF_GO:0032561~	guanyl ribonucleotide binding	3	0.28625954
33				
34	Annotation C	Enrichment Score: 0.1748348622511788		
35	Category	Term	Count	%
36	UP_SEQ_FEA`	zinc finger region:C2H2-type 3	5	0.47709924
37	UP_SEQ_FEA`	zinc finger region:C2H2-type 6	4	0.38167939
38	INTERPRO	IPR015880:Zinc finger, C2H2-like	6	0.57251908
39	UP_SEQ_FEA`	domain:KRAB	3	0.28625954
40	UP_SEQ_FEA`	zinc finger region:C2H2-type 5	4	0.38167939
41	UP_SEQ_FEA`	zinc finger region:C2H2-type 1	4	0.38167939
42	SMART	SM00355:ZnF_C2H2	6	0.57251908
43	INTERPRO	IPR001909:Krueppel-associated box	3	0.28625954
44	UP_SEQ_FEA`	zinc finger region:C2H2-type 2	4	0.38167939
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UP_SEQ_FEA`zinc finger region:C2H2-type 8	3	0.28625954
GOTERM_MF GO:0046872~metal ion binding	24	2.29007634
GOTERM_MF GO:0043169~cation binding	24	2.29007634
SMART SM00349:KRAB	3	0.28625954
INTERPRO IPR007087:Zinc finger, C2H2-type	5	0.47709924
UP_SEQ_FEA`zinc finger region:C2H2-type 7	3	0.28625954
GOTERM_MF GO:0043167~ion binding	24	2.29007634
INTERPRO IPR013087:Zinc finger, C2H2-type/integrase, DNA-bi	4	0.38167939
UP_SEQ_FEA`zinc finger region:C2H2-type 4	3	0.28625954
SP_PIR_KEYM metal-binding	14	1.33587786
GOTERM_MF GO:0046914~transition metal ion binding	14	1.33587786
GOTERM_MF GO:0008270~zinc ion binding	11	1.04961832
SP_PIR_KEYM zinc	9	0.85877863
SP_PIR_KEYM zinc-finger	6	0.57251908

Annotation C| Enrichment Score: 0.17111548529034948

Category	Term	Count	%
GOTERM_BP_	GO:0007186~G-protein coupled receptor protein sig	8	0.76335878
SP_PIR_KEYM	transducer	5	0.47709924
SP_PIR_KEYM	g-protein coupled receptor	4	0.38167939

Annotation C| Enrichment Score: 0.09864436886263817

Category	Term	Count	%
GOTERM_BP_	GO:0050877~neurological system process	8	0.76335878
GOTERM_BP_	GO:0007600~sensory perception	4	0.38167939
GOTERM_BP_	GO:0050890~cognition	4	0.38167939

Annotation C| Enrichment Score: 0.036425109945670206

Category	Term	Count	%
GOTERM_BP_	GO:0010604~positive regulation of macromolecule r	4	0.38167939
GOTERM_BP_	GO:0010557~positive regulation of macromolecule l	3	0.28625954
GOTERM_BP_	GO:0031328~positive regulation of cellular biosynth	3	0.28625954
GOTERM_BP_	GO:0009891~positive regulation of biosynthetic pro	3	0.28625954

Annotation C| Enrichment Score: 0.026635032561101814

Category	Term	Count	%
GOTERM_CC_	GO:0005856~cytoskeleton	7	0.66793893
GOTERM_CC_	GO:0044430~cytoskeletal part	4	0.38167939
GOTERM_CC_	GO:0043228~non-membrane-bounded organelle	7	0.66793893
GOTERM_CC_	GO:0043232~intracellular non-membrane-bounded	7	0.66793893

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om DCIS-SOX11 cells compared to DCIS-lacZ cells injected into mammary duct.

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
2.94E-07	LRRC8A, TSPA	103	4129	19113	2.06730514	1.55E-04
1.28E-06	LRRC8A, TSPA	104	4318	19235	1.97030766	2.58E-04
5.13E-04	NKD1, TSPAN	104	6256	19235	1.50776024	0.09808512
0.00113391	LRRC8A, TSPA	103	3374	19113	1.75993462	0.45066264
0.00351594	LRRC8A, TSPA	103	4911	19113	1.51140792	0.84427868
0.00479181	LRRC8A, TSPA	104	4973	19235	1.48764869	0.61919567
0.00592907	LRRC8A, TSPA	77	5485	12782	1.36189608	0.57779925
0.00794528	PTPRJ, SECTM	103	2719	19113	1.70617053	0.98518125
0.01837048	LRRC8A, TSPA	77	5297	12782	1.31621673	0.9320165

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
2.94E-07	LRRC8A, TSPA	103	4129	19113	2.06730514	1.55E-04
1.28E-06	LRRC8A, TSPA	104	4318	19235	1.97030766	2.58E-04
0.00546797	ITGB2, ITGB3,	103	3250	19113	1.65579388	0.94470143
0.00578235	ITGB2, ITGB3,	104	3250	19235	1.65034024	0.68827259
0.00627279	ITGB2, ITGB3,	103	2819	19113	1.71147243	0.96393621
0.0104143	ITGB2, ITGB3,	104	2924	19235	1.64457934	0.87806291
0.04505424	COL4A4, SECT	77	2010	12782	1.56915423	0.99874999

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00158558	COL4A3, CST6	77	145	12983	6.97698164	0.29468015
0.00200772	COL4A3, CST6	77	153	12983	6.61217214	0.35734121
0.01980978	CST6, CPAMD	104	107	19235	6.91409058	0.98207815
0.02090916	COL4A3, CST6	77	270	12983	3.74689755	0.9904268
0.10115877	CPAMD8, SER	77	92	12983	5.49816488	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
9.37E-04	NOV, DNM3,	77	342	12782	4.36842105	0.12704457
0.00321972	NOV, EXOC4,	77	168	12782	5.92857143	0.37350361
0.02202281	NOV, DNM3,	77	697	12782	2.38163558	0.96040272
0.06883546	NOV, MYH14,	77	159	12782	4.17610063	0.99996773
0.07298367	NOV, DNM3,	77	163	12782	4.07361963	0.99998311
0.16258929	DNM3, EXOC4	77	234	12782	2.83760684	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.0023248	PTPRJ, MGAT	104	642	19235	3.16895818	0.37363891
0.02601087	PTPRJ, SLC16	77	1215	12782	1.9127572	0.97810496
0.04696053	PTPRJ, SLC16	77	1188	12782	1.81649832	0.99906442
0.09343628	PTPRJ, ITGA1,	77	2203	12782	1.43168407	0.99999934

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00346575	COL4A3, UNC	84	320	13528	4.02619048	0.93401933
0.00352574	COL4A3, UNC	84	321	13528	4.01364783	0.93705726
0.00480181	COL4A3, UNC	84	430	13528	3.37076412	0.97692196
0.00500437	COL4A3, UNC	84	433	13528	3.3474101	0.98032208
0.00514302	COL4A3, UNC	84	435	13528	3.3320197	0.98235627
0.01392979	COL4A3, NR4	84	82	13528	7.85598142	0.99998302
0.01581927	COL4A3, NR4	84	86	13528	7.49058693	0.99999622
0.05737643	COL4A3, UNC	84	804	13528	2.00307984	1
0.06033871	COL4A3, UNC	84	812	13528	1.98334506	1
0.06147477	COL4A3, UNC	84	815	13528	1.97604441	1
0.08466652	COL4A3, NR4	84	79	13528	6.11573237	1
0.1525163	COL4A3, TGM	84	337	13528	2.38943055	1
0.30065754	COL4A3, TGM	84	179	13528	2.69912211	1
0.99074318	TGM2, BIK, PI	77	1087	12782	0.45814167	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.01034761	COL4A3, GMI	84	700	13528	2.5307483	0.99970964
0.01044546	COL4A3, GMI	84	701	13528	2.5271381	0.99973127
0.23991204	GMDS, PCDH	84	276	13528	2.33402346	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00500067	ITGA1, ITGB2,	77	116	12782	7.15517241	0.51660259
0.00907317	GAB2, ITGA1,	84	70	13528	9.20272109	0.99920464
0.01276848	ITGA1, ITGB2,	77	29	12782	17.1724138	0.84484815
0.02033042	ITGA1, ITGB2,	104	41	19235	13.5330675	0.98389339
0.02595151	COL4A3, MYB	104	422	19235	3.06792289	0.99493364
0.04335224	ITGA1, ITGB2,	103	62	19113	8.97886001	1
0.08025123	ITGA1, ITGB2,	100	79	16659	6.32620253	1
0.08685347	ITGA1, ITGB2,	41	215	5085	2.88428815	0.99383026
0.09582005	ITGA1, ITGB2,	61	79	9079	5.65200249	0.99947626
0.10355026	ITGA1, ITGB2,	84	89	13528	5.42857143	1

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0.12142517 ITGA1, ITGB2, 84 98 13528 4.93002915 1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.0123611	COL4A3, CXCI	84	611	13528	2.63580391	0.99994106
0.03106385	COL4A3, CXCI	84	602	13528	2.40768866	1
0.0316941	COL4A3, CXCI	84	719	13528	2.23988344	1
0.03292571	COL4A3, CXCI	84	724	13528	2.22441463	1
0.33431443	BIK, EDAR, PN	104	381	19235	1.94175247	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.02595151	COL4A3, MYB	104	422	19235	3.06792289	0.99493364
0.04669625	COL4A3, ITGA	77	59	12983	8.57340964	0.99997303
0.10740235	COL4A3, GRB	77	196	12983	3.44102836	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.02650172	ELF3, CST6, EI	84	184	13528	4.376294	1
0.03395387	ELF3, CST6, EI	84	199	13528	4.04642259	1
0.05198328	ELF3, TFPC2L	84	137	13528	4.70212026	1
0.16303465	ELF3, TFPC2L	84	227	13528	2.83784351	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00750328	MGAT3, A4G	104	421	19235	3.51452585	0.77993811
0.00790322	MGAT3, ST3C	84	128	13528	6.29092262	0.99799639
0.00790322	MGAT3, ST3C	84	128	13528	6.29092262	0.99799639
0.00790322	MGAT3, ST3C	84	128	13528	6.29092262	0.99799639
0.01613553	MGAT3, ST3C	84	158	13528	5.09644364	0.99999706
0.02692325	A4GALT, ST3C	77	43	12782	11.5813953	0.98088701
0.02805209	MGAT3, A4G	104	214	19235	4.32130661	0.99671722
0.03050939	A4GALT, ST3C	77	46	12782	10.826087	0.98881018
0.03167961	MGAT3, TMC	103	444	19113	2.92554448	0.99999996
0.03557691	MGAT3, ST3C	84	202	13528	3.9863272	1
0.12597837	MGAT3, A4G	104	1394	19235	1.59212559	1
0.1660126	A4GALT, ST3C	77	123	12782	4.04878049	1
0.21542719	A4GALT, ST3C	77	146	12782	3.4109589	1
0.26039934	SECTM1, MG	77	872	12782	1.52293578	1
0.30352042	A4GALT, ST3C	77	186	12782	2.67741935	1
0.38660225	MGAT3, A4G	104	588	19235	1.57272043	1

0.5002057	A4GALT, ST3C	77	782	12782	1.27365729	1
0.52485462	A4GALT, ST3C	77	294	12782	1.69387755	1
0.79145938	A4GALT, ST3C	77	1096	12782	0.90875912	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.00500067	ITGA1, ITGB2,	77	116	12782	7.15517241	0.51660259
0.02943172	ITGA1, CD4, I	41	86	5085	5.76857629	0.81230128
0.2088881	ITGA1, CD4, C	77	143	12782	3.48251748	1
0.26823024	ITGA1, CD4, I	77	170	12782	2.92941176	1
0.3423126	ITGA1, CD4, I	77	348	12782	1.90804598	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.04505424	COL4A4, SECT	77	2010	12782	1.56915423	0.99874999
0.05724048	NOV, COL4A4	77	960	12782	1.90208333	0.99980585
0.11675827	COL4A4, COL	104	1689	19235	1.53305324	1
0.22173529	SECTM1, CPA	77	685	12782	1.69635036	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.04818707	UNC13D, EDA	84	223	13528	3.61093316	1
0.14419889	UNC13D, INH	84	109	13528	4.43250328	1
0.1950675	UNC13D, EDA	84	248	13528	2.59754224	1
0.35244034	UNC13D, INH	84	202	13528	2.39179632	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.07264924	PTPRJ, MYBP	103	83	19113	6.70710025	1
0.09670977	PTPRJ, MYBP	100	184	16659	3.62152174	1
0.15298466	PTPRJ, MYBP	103	130	19113	4.28222554	1
0.15484383	PTPRJ, MYBP	103	131	19113	4.2495368	1
0.31201336	PTPRJ, MYBP	100	190	16659	2.63036842	1
0.35862682	PTPRJ, MYBP	61	190	9079	2.35004314	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.01931603	CAPN8, CTSS,	100	36	16659	13.8825	0.9953173
0.05803601	CTSS, KLK1, C	103	73	19113	7.6258811	1
0.06647899	CAPN8, CTSS,	77	72	12983	7.0254329	0.99999973
0.09873597	CTSS, KLK1, T	104	206	19235	3.59129948	1

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4	0.14638463	CAPN8, CTSS,	104	126	19235	4.40361722	1
5	0.17686788	CAPN8, CTSS,	77	375	12983	2.24813853	1
6	0.19981184	CAPN8, CTSS,	77	141	12983	3.5874551	1
7	0.26079359	CAPN8, CTSS,	104	484	19235	1.91066036	1
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9	0.32058589	PTPRJ, DNM3	104	1555	19235	1.30834158	1
10	0.40165755	CAPN8, CTSS,	77	549	12983	1.53561375	1
11	0.43487891	CAPN8, CTSS,	77	574	12983	1.46873162	1
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13	0.89618123	CAPN8, CTSS,	84	1054	13528	0.76398301	1
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17	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
18	0.10645059	DNM3, GRB1	100	303	16659	2.7490099	1
19	0.13336256	DNM3, GRB1	103	237	19113	3.13186678	1
20							
21	0.2275533	DNM3, GRB1	100	277	16659	2.40563177	1
22	0.27666988	DNM3, GRB1	61	277	9079	2.14925726	1
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26	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
27	0.05507504	MAFF, MITF, I	103	161	19113	4.61026352	1
28	0.12392495	MITF, HES7, E	103	114	19113	4.88323965	1
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30	0.14728911	MITF, HES7, E	100	114	16659	4.38394737	1
31	0.17369036	MITF, HES7, E	61	114	9079	3.91673857	0.99999939
32	0.89065594	MAFF, ELF3, I	77	1512	12983	0.78060366	1
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37	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
38	0.01393805	COL4A4, COL4	77	86	12983	7.8423437	0.95440426
39	0.31331177	COL4A4, COL4	77	634	12983	1.59568192	1
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41	0.33740592	NOV, COL4A4	77	345	12782	1.92463768	1
42	0.3707267	COL4A4, COL4	104	241	19235	2.3023061	1
43	0.57101191	COL4A4, COL4	77	320	12782	1.55625	1
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47	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
48	0.17656234	LRR8A, CD4,	84	236	13528	2.72962066	1
49	0.21403518	LRR8A, CD4,	84	260	13528	2.47765568	1
50	0.23991204	LRR8A, CD4,	84	276	13528	2.33402346	1
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55	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
56	0.1527456	DNM3, UNC1	84	220	13528	2.92813853	1
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0.1527456	DNM3, UNC1	84	220	13528	2.92813853	1
0.20592233	DNM3, UNC1	84	381	13528	2.11348581	1
0.47350837	DNM3, UNC1	84	576	13528	1.3979828	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.12327028	UNC13D, LRR	84	199	13528	3.23713807	1
0.1857522	UNC13D, LRR	84	242	13528	2.66194412	1
0.25800869	UNC13D, LRR	84	287	13528	2.24456612	1
0.41794034	SECTM1, UNC	84	690	13528	1.40041408	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.10662576	UNC13D, ELF3	84	530	13528	2.12704403	1
0.27791542	CXCR4, ABHD	84	169	13528	2.85883347	1
0.33004881	CXCR4, ABHD	84	192	13528	2.51636905	1
0.33229775	CXCR4, ABHD	84	193	13528	2.50333087	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.10662576	UNC13D, ELF3	84	530	13528	2.12704403	1
0.1390037	UNC13D, ELF3	84	325	13528	2.47765568	1
0.41794034	SECTM1, UNC	84	690	13528	1.40041408	1
0.52521145	UNC13D, ELF3	84	615	13528	1.30933024	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.2031236	COL4A4, BHLI	84	136	13528	3.55252101	1
0.22789011	COL4A4, BHLI	84	147	13528	3.2866861	1
0.24149557	COL4A4, BHLI	84	153	13528	3.15779645	1
0.29471119	COL4A4, BHLI	84	309	13528	2.08475882	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.07496105	COL4A4, PTPF	84	600	13528	2.14730159	1
0.2762923	COL4A4, PCD	84	298	13528	2.16171301	1
0.36376096	COL4A4, PCD	84	350	13528	1.84054422	1
0.62127208	COL4A4, COL4	84	1210	13528	1.06477765	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
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4	0.06635972	CXCR4, ITGA1	84	466	13528	2.41917024	1
5	0.07719187	CXCR4, ITGA1	84	485	13528	2.32439863	1
6	0.07719187	CXCR4, ITGA1	84	485	13528	2.32439863	1
7	0.23991204	GAB2, CXCR4	84	276	13528	2.33402346	1
8							
9	0.2574172	CXCR4, ITGA1	84	160	13528	3.01964286	1
10	0.2574172	CXCR4, ITGA1	84	160	13528	3.01964286	1
11	0.28702068	ITGB2, CD4, IL	84	173	13528	2.79273328	1
12							
13	0.29135448	GAB2, CXCR4	84	307	13528	2.09834031	1
14	0.29135448	GAB2, CXCR4	84	307	13528	2.09834031	1
15	0.50368877	CXCR4, ITGA1	84	274	13528	1.7632951	1
16							
17	0.54348949	ITGB2, CD4, IL	84	295	13528	1.6377724	1
18	0.55304155	CXCR4, ITGA1	84	469	13528	1.37354046	1
19	0.56030259	ITGB2, CD4, IL	84	474	13528	1.35905164	1
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21	0.56174651	GAB2, CXCR4	84	475	13528	1.35619048	1
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25	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
26	0.10315839	LRRC8A, CD14	103	102	19113	5.45773844	1
27	0.12926542	LRRC8A, CD14	103	117	19113	4.75802838	1
28	0.16232383	LRRC8A, CD14	103	135	19113	4.1236246	1
29	0.18897434	LRRC8A, CD14	103	149	19113	3.73616994	1
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31	0.2437061	LRRC8A, CD14	103	177	19113	3.1451374	1
32	0.30889204	LRRC8A, CD14	103	210	19113	2.65090153	1
33	0.34990397	LRRC8A, CD14	103	231	19113	2.40991048	1
34	0.39009312	LRRC8A, CD14	103	252	19113	2.2090846	1
35	0.47569433	LRRC8A, CD14	103	299	19113	1.86183719	1
36	0.50823217	LRRC8A, CD14	103	318	19113	1.75059535	1
37	0.50990862	LRRC8A, CD14	103	319	19113	1.74510759	1
38	0.51671794	LRRC8A, CD14	104	322	19235	1.72315456	1
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45	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
46	0.06635972	CXCR4, ITGA1	84	466	13528	2.41917024	1
47	0.06790187	COL4A3, CXCI	84	586	13528	2.19860231	1
48	0.07719187	CXCR4, ITGA1	84	485	13528	2.32439863	1
49	0.07719187	CXCR4, ITGA1	84	485	13528	2.32439863	1
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51	0.099633	COL4A3, CXCI	84	520	13528	2.16794872	1
52	0.15712906	CXCR4, ITGA1	84	223	13528	2.88874653	1
53	0.16900716	CXCR4, ITGA1	84	231	13528	2.78870336	1
54	0.18267448	CXCR4, ITGA1	84	240	13528	2.68412698	1
55	0.28702068	ITGB2, CD4, IL	84	173	13528	2.79273328	1
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0.31199208	CXCR4, ITGA1	84	184	13528	2.6257764	1
0.35535291	CXCR4, ITGA1	84	345	13528	1.86721877	1
0.37550615	CXCR4, ITGA1	84	357	13528	1.80445512	1
0.40053189	CXCR4, ITGA1	84	372	13528	1.73169483	1
0.54348949	ITGB2, CD4, IL	84	295	13528	1.6377724	1
0.56030259	ITGB2, CD4, IL	84	474	13528	1.35905164	1
0.59026345	CXCR4, ITGA1	84	667	13528	1.20725352	1
0.62037392	ITGA1, NR4A1	77	542	12983	1.24435712	1
0.66722747	CXCR4, ITGA1	84	370	13528	1.30579151	1
0.721626	PTPRJ, CXCR4	84	973	13528	0.9930994	1
0.721626	PTPRJ, CXCR4	84	973	13528	0.9930994	1
0.73116818	CXCR4, ITGA1	84	800	13528	1.00654762	1
0.79452613	RGS11, CXCR4	84	1256	13528	0.89755839	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.19706672	CXCR4, TGM2	84	374	13528	2.15304304	1
0.2044984	CXCR4, TGM2	84	254	13528	2.53618298	1
0.20464989	CXCR4, TGM2	84	380	13528	2.11904762	1
0.24243929	CXCR4, TGM2	84	409	13528	1.9687973	1
0.25635502	CXCR4, TGM2	84	286	13528	2.25241425	1
0.32053416	CXCR4, TGM2	84	466	13528	1.72797875	1
0.3390322	CXCR4, TGM2	84	196	13528	2.46501458	1
0.35911105	CXCR4, TGM2	84	205	13528	2.35679443	1
0.38505936	CXCR4, TGM2	84	512	13528	1.57273065	1
0.40721013	CXCR4, TGM2	84	227	13528	2.12838263	1
0.4327321	CXCR4, TGM2	84	239	13528	2.02151823	1
0.49178578	CXCR4, TGM2	84	751	13528	1.2866654	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.18995234	UNC13D, CTS	104	149	19235	3.72386422	1
0.35801278	UNC13D, CTS	77	211	12782	2.36018957	1
0.35801278	UNC13D, CTS	77	211	12782	2.36018957	1
0.44376816	UNC13D, CTS	77	252	12782	1.97619048	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.18183446	UNC13D, ARR	77	642	12782	1.80996885	1
0.2074749	UNC13D, ARR	77	670	12782	1.73432836	1
0.36495668	ARRB2, GPRC	104	238	19235	2.33132676	1

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0.64099593	UNC13D, ITGA	77	550	12782	1.20727273	1
0.66273523	UNC13D, ITGA	77	568	12782	1.16901408	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.34947233	SLC16A5, A4G	77	809	12782	1.43634116	1
0.38185611	SLC16A5, A4G	77	839	12782	1.38498212	1
0.46712729	SLC16A5, A4G	77	1083	12782	1.22622345	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.37237872	PTPRJ, CXCR4	84	211	13528	2.28977657	1
0.44527841	PTPRJ, CXCR4	84	245	13528	1.97201166	1
0.45767312	PTPRJ, CXCR4	84	251	13528	1.92487194	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.13828303	MYBPC1, CD4	103	122	19113	4.56302722	1
0.26940591	MYBPC1, CD4	103	190	19113	2.92994379	1
0.27138414	MYBPC1, CD4	103	191	19113	2.91460377	1
0.58679849	MYBPC1, CD4	100	330	16659	1.51445455	1
0.64297243	MYBPC1, TGM	100	553	16659	1.20499096	1
0.64706978	MYBPC1, CD4	61	330	9079	1.35305514	1
0.72075085	MYBPC1, CD4	104	470	19235	1.18054419	1
0.80287547	MYBPC1, CD4	100	501	16659	0.99754491	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.05507504	MAFF, MITF, I	103	161	19113	4.61026352	1
0.1853267	PER1, HES7, II	84	128	13528	3.77455357	1
0.24478922	TFCP2L1, PER	84	547	13528	1.76651867	1
0.27515178	TFCP2L1, PER	84	573	13528	1.6863625	1
0.28209296	ELF3, TFCEP2L	77	316	12983	2.13430873	1
0.40145435	MAFF, ZNF43	104	2026	19235	1.18675962	1
0.43195043	MAFF, ZNF43	104	2071	19235	1.16097296	1
0.45309639	TFCEP2L1, PER	84	561	13528	1.43536202	1
0.47146616	TFCEP2L1, PER	84	734	13528	1.31646555	1
0.53831587	TFCEP2L1, PER	84	459	13528	1.40346509	1
0.54919441	MAFF, ZNF43	104	1868	19235	1.08911732	1
0.60238054	TFCEP2L1, PER	84	504	13528	1.27815571	1
0.61315639	TFCEP2L1, PER	84	512	13528	1.25818452	1

0.62242755	TFCP2L1, PER	84	519	13528	1.24121479	1
0.64633108	TFCP2L1, HES	84	356	13528	1.35714286	1
0.65294596	MAFF, ZNF43	84	2101	13528	0.99648693	1
0.65540897	TFCP2L1, HES	84	362	13528	1.33464878	1
0.66154434	MAFF, ZNF43	84	1773	13528	0.99916741	1
0.6844158	MAFF, ELF3, I	77	975	12983	1.0376024	1
0.68979044	MAFF, ZNF43	84	1813	13528	0.9771229	1
0.69642102	MAFF, ELF3, I	77	607	12983	1.11110636	1
0.69733973	ELF3, MITF, N	77	410	12983	1.23373456	1
0.83051935	TFCP2L1, MIT	84	727	13528	0.88609419	1
0.89065594	MAFF, ELF3, I	77	1512	12983	0.78060366	1
0.89698651	MAFF, ZNF43	77	2331	12983	0.79567322	1
0.89709286	MAFF, ZNF43	84	2601	13528	0.80492851	1
0.99069297	MAFF, ZNF43	104	4283	19235	0.64774197	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.28099223	COL4A3, GRB	84	721	13528	1.56356912	1
0.6628336	GRB10, AQP1	84	367	13528	1.31646555	1
0.71517876	GRB10, AQP1	84	405	13528	1.19294533	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.11538355	PFKP, TGM2,	84	95	13528	5.08571429	1
0.28929556	PFKP, TGM2,	84	174	13528	2.77668309	1
0.82150325	PFKP, TGM2,	84	505	13528	0.95671853	1
0.82150325	PFKP, TGM2,	84	505	13528	0.95671853	1
0.91999094	PFKP, TGM2,	84	665	13528	0.72653061	1
0.93677378	PFKP, TGM2,	84	710	13528	0.6804829	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.39388079	DNM3, CXCR4	84	368	13528	1.7505176	1
0.61960522	CXCR4, ITGA1	84	339	13528	1.42520017	1
0.75502947	CXCR4, ITGA1	84	438	13528	1.10306588	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.47998492	CXCR4, BIK, ITGA1	84	262	13528	1.84405671	1
0.57885435	CXCR4, ZNF293	84	487	13528	1.32277305	1
0.57885435	CXCR4, ZNF293	84	487	13528	1.32277305	1

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4	0.70209178	CXCR4, ZNF29	84	395	13528	1.22314647	1
5	0.77680412	CXCR4, ZNF29	84	458	13528	1.05489707	1
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9	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
10	0.09340438	PFKP, FES, RC	104	201	19235	3.68063529	1
11	0.13313274	PFKP, MYH14	104	236	19235	3.13477836	1
12	0.58819326	PFKP, MYH14	103	962	19113	1.15735825	1
13	0.69090559	DNM3, ARL10	104	1686	19235	0.98728785	1
14	0.71785454	PFKP, FES, RC	104	688	19235	1.07530188	1
15	0.72194772	ENTPD8, PFKF	104	1326	19235	0.97636762	1
16	0.76547367	DNM3, ARL10	77	1836	12983	0.91835724	1
17	0.76547367	DNM3, ARL10	77	1836	12983	0.91835724	1
18	0.77608331	ENTPD8, PFKF	77	1477	12983	0.91325871	1
19	0.78813517	ENTPD8, PFKF	77	1497	12983	0.90105753	1
20	0.78935736	FES, ROS1, ITI	103	542	19113	1.02710207	1
21	0.809686	DNM3, ARL10	77	1918	12983	0.87909484	1
22	0.83164791	ENTPD8, PFKF	77	1577	12983	0.85534757	1
23	0.84327832	ENTPD8, PFKF	77	1601	12983	0.84252537	1
24	0.84839693	ENTPD8, PFKF	77	1612	12983	0.83677613	1
25	0.87058515	PFKP, FES, RC	103	658	19113	0.8460324	1
26	0.87591947	FES, ROS1, ITI	77	606	12983	0.8347049	1
27	0.92699728	DNM3, ARL10	77	2245	12983	0.75104851	1
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37	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
38	0.64500469	DNM3, ARL10	77	372	12983	1.35976121	1
39	0.65942148	DNM3, ARL10	77	382	12983	1.32416536	1
40	0.65942148	DNM3, ARL10	77	382	12983	1.32416536	1
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45	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
46	0.42527529	ZNF430, ZBTE	103	622	19113	1.49166485	1
47	0.48500256	ZNF430, ZNF2	103	488	19113	1.52100907	1
48	0.51580613	ZNF430, ZBTE	100	797	16659	1.25412798	1
49	0.53136491	ZNF430, ZNF2	103	332	19113	1.67677506	1
50	0.55076803	ZNF430, ZNF2	103	538	19113	1.37965135	1
51	0.5558189	ZNF430, ZBTE	103	542	19113	1.36946942	1
52	0.6154141	ZNF430, ZBTE	61	797	9079	1.12047226	1
53	0.62676097	ZNF430, ZNF2	100	355	16659	1.40780282	1
54	0.63415364	ZNF430, ZBTE	103	608	19113	1.22080991	1
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0.65560662	ZNF430, ZNF2	103	417	19113	1.33498638	1
0.66116878	ZNF430, NKD	77	4140	12983	0.97745153	1
0.68144875	ZNF430, NKD	77	4179	12983	0.96832959	1
0.68664012	ZNF430, ZNF2	61	355	9079	1.25776957	1
0.69100262	ZNF430, ZBTE	100	784	16659	1.06243622	1
0.69749346	ZNF430, ZNF2	103	451	19113	1.23434439	1
0.71245401	ZNF430, NKD	77	4241	12983	0.95417339	1
0.71924353	ZNF430, ZBTE	100	621	16659	1.07304348	1
0.8161273	ZNF430, ZNF2	103	575	19113	0.96815534	1
0.82385047	APOBEC3A, C	104	2972	19235	0.87124055	1
0.85789226	ZNF430, ZBTE	77	2785	12983	0.84759262	1
0.89079497	APOBEC3A, Z	77	2311	12983	0.80255919	1
0.91167826	APOBEC3A, Z	104	2189	19235	0.76042362	1
0.95875941	ZNF430, ZBTE	104	1718	19235	0.64593221	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.5400368	RGS11, CXCR4	84	1123	13528	1.1472671	1
0.69407716	CXCR4, NPFF	104	874	19235	1.05807736	1
0.81813022	CXCR4, NPFF	104	816	19235	0.90662707	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.62127208	COL4A4, COL4A3	84	1210	13528	1.06477765	1
0.88126653	COL4A3, ARR	84	810	13528	0.79529688	1
0.92401237	COL4A3, ARR	84	909	13528	0.70868039	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.90366997	MITF, NR4A1,	84	857	13528	0.75168084	1
0.91530159	MITF, NR4A1,	84	654	13528	0.73875055	1
0.9279054	MITF, NR4A1,	84	685	13528	0.70531804	1
0.9315835	MITF, NR4A1,	84	695	13528	0.69516958	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
0.84341182	DNM3, CST6,	77	1381	12782	0.84141926	1
0.92927511	DNM3, MYBP	77	952	12782	0.69747899	1
0.99916667	DNM3, CST6,	77	2596	12782	0.44761171	1
0.99916667	DNM3, CST6,	77	2596	12782	0.44761171	1

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Benjamini	FDR
1.55E-04	4.26E-04
2.58E-04	0.00160803
0.05030801	0.64220865
0.25882703	1.63283528
0.46199948	4.98245999
0.17559546	5.84746009
0.15840373	6.81626951
0.50439547	10.9303998
0.31891628	19.7573438

Benjamini	FDR
1.55E-04	4.26E-04
2.58E-04	0.00160803
0.51507064	7.64790465
0.1765653	7.01625703
0.48546578	8.72646971
0.23128213	12.3066445
0.37965031	42.1484122

Benjamini	FDR
0.29468015	1.99968166
0.19833998	2.52582242
0.36036615	22.1971605
0.68720174	23.584371
0.9649795	74.2716203

Benjamini	FDR
0.12704457	1.10625126
0.20848475	3.75612482
0.33210503	23.2308794
0.45573093	57.1160955
0.45691149	59.329941
0.70629673	87.8337349

Benjamini	FDR
0.11037661	2.87745691
0.34597558	26.8660528
0.37183762	43.5046192
0.52697726	68.7931239

Benjamini	FDR
0.74313297	5.17540322
0.60221486	5.26274008
0.61023779	7.10282869
0.54417742	7.39182475
0.4897711	7.58915714
0.59960696	19.3231332
0.61726918	21.6572467
0.85452549	59.523443
0.85761567	61.4273139
0.85202129	62.1349978
0.89295444	74.1829896
0.95087279	92.0580524
0.9657354	99.580519
0.99999873	100

Benjamini	FDR
0.59543077	14.7185435
0.56052791	14.847515
0.96513066	98.4988753

Benjamini	FDR
0.16617276	5.77784634
0.59020162	13.0219473
0.26696255	14.1491119
0.33824013	22.7139695
0.38150531	28.0960999
0.94634183	47.4347539
0.99953261	66.813838
0.92145233	59.2280162
0.97711464	65.2549415
0.92525707	81.2358855

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4	0.93539935	86.2140296
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8	Benjamini	FDR
9	0.58743801	17.3360798
10	0.78653861	38.3087064
11	0.77314109	38.9200733
12	0.76692106	40.0984737
13	0.90979954	99.3931902
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18	Benjamini	FDR
19	0.38150531	28.0960999
20	0.87805129	45.5964761
21	0.95604252	76.4561527
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26	Benjamini	FDR
27	0.75390833	33.7096884
28	0.75914586	41.0659118
29	0.83754393	55.8298309
30	0.94180347	93.4399778
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35	Benjamini	FDR
36	0.1944772	9.01518678
37	0.58833436	11.4367292
38	0.58833436	11.4367292
39	0.58833436	11.4367292
40	0.59739408	22.0417121
41	0.32681743	27.6752224
42	0.37910224	30.0172194
43	0.33530825	30.7768794
44	0.911806	37.3203018
45	0.75785439	42.5634114
46	0.74159679	81.5310382
47	0.69774788	88.4112275
48	0.74154927	94.387857
49	0.79030257	97.2152324
50	0.82593002	98.6351903
51	0.92461797	99.782532
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0.92412102 99.9734434
0.93262542 99.9854315
0.99285552 99.9999992

Benjamini FDR
0.16617276 5.77784634
0.81230128 25.5455274
0.74309065 93.8067042
0.79016773 97.5458078
0.85023823 99.3088034

Benjamini FDR
0.37965031 42.1484122
0.41385048 50.3295379
0.75002956 78.9325765
0.73979629 94.900731

Benjamini FDR
0.8275624 53.0435306
0.9488923 90.7774646
0.95446373 96.3901696
0.97622193 99.8707849

Benjamini FDR
0.97322598 66.5275396
0.9990814 73.8448718
0.98751669 91.0122462
0.98544586 91.2943043
0.99998911 99.2782351
0.99872161 99.0545912

Benjamini FDR
0.9953173 22.6775067
0.95743907 58.0029032
0.91973058 58.342057
0.72908768 72.8571828

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4	0.71987732	86.2678187
5	0.98618566	91.6058143
6	0.98841643	94.1427419
7	0.85904064	97.7417557
8	0.90503865	99.2160972
9	0.99870142	99.8552208
10	0.99906542	99.93003
11	0.99999004	100
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17	Benjamini	FDR
18	0.9979511	77.3290699
19	0.98498362	87.469245
20	0.99996066	96.6773867
21	0.99769559	96.6601177
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26	Benjamini	FDR
27	0.96397177	56.0460734
28	0.99050589	85.3366343
29	0.99932638	87.7656551
30	0.99151659	86.4976187
31	0.99999304	100
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37	Benjamini	FDR
38	0.64274794	16.3618973
39	0.99727859	99.1643033
40	0.85415222	99.245041
41	0.91923781	99.70036
42	0.94616547	99.9956695
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47	Benjamini	FDR
48	0.94933787	94.8880876
49	0.9522424	97.4940927
50	0.96513066	98.4988753
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55	Benjamini	FDR
56	0.94764316	92.0908801
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0.94764316 92.0908801
0.94816362 97.067547
0.98872211 99.9945623

Benjamini FDR
0.93351353 86.6505961
0.94918749 95.6949667
0.96449265 98.9619185
0.98299892 99.9747405

Benjamini FDR
0.92547043 82.197437
0.96660669 99.315383
0.9728113 99.7825838
0.97250929 99.7934909

Benjamini FDR
0.92547043 82.197437
0.95045203 89.8822691
0.98299892 99.9747405
0.99286511 99.9988824

Benjamini FDR
0.95335791 96.9052937
0.95981982 98.0913071
0.96419389 98.5460381
0.96434752 99.5224745

Benjamini FDR
0.87801103 69.659619
0.9673392 99.2914449
0.97593322 99.9013557
0.99670754 99.9999649

Benjamini FDR

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4	0.86347635	65.0419403
5	0.87714075	70.7604769
6	0.87714075	70.7604769
7	0.96513066	98.4988753
8	0.96586221	98.9491794
9	0.96586221	98.9491794
10	0.96649432	99.4362452
11	0.96563833	99.4864772
12	0.96563833	99.4864772
13	0.99079777	99.9977971
14	0.99374423	99.9993872
15	0.99430619	99.9995567
16	0.9946498	99.999655
17	0.99453401	99.9996719
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25	Benjamini	FDR
26	0.9879903	79.3997754
27	0.98641926	86.5816183
28	0.98574957	92.3479033
29	0.99183886	95.2133971
30	0.99785616	98.2633416
31	0.99905747	99.5304337
32	0.99948902	99.8067271
33	0.99977993	99.9234366
34	0.99995581	99.9914695
35	0.99996986	99.9966332
36	0.99996197	99.9967959
37	0.96919121	99.9890718
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45	Benjamini	FDR
46	0.86347635	65.0419403
47	0.86003598	65.9154242
48	0.87714075	70.7604769
49	0.87714075	70.7604769
50	0.92331617	79.940817
51	0.94892095	92.6945676
52	0.94493275	94.1210689
53	0.95204082	95.4390428
54	0.96649432	99.4362452
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0.96808837 99.6733454
0.9751907 99.8794003
0.97764011 99.9258335
0.98107059 99.9603422
0.99374423 99.9993872
0.9946498 99.999655
0.99609165 99.9998829
0.9999608 99.999558
0.99777979 99.999952
0.99899771 99.999997
0.99899771 99.999997
0.99912844 99.999998
0.99975537 100

Benjamini FDR
0.95352551 96.5249944
0.95198367 96.986017
0.94961672 96.9947901
0.96289329 98.5734829
0.96697725 98.9259352
0.97035546 99.7302028
0.97273732 99.8231721
0.97542227 99.8897246
0.9794496 99.9414227
0.98194159 99.9665915
0.98541308 99.9829664
0.99003305 99.9968338

Benjamini FDR
0.79159313 92.882324
0.84893751 99.4811626
0.84893751 99.4811626
0.89961281 99.9054241

Benjamini FDR
0.71782373 90.7682113
0.75460237 93.6740814
0.92075254 99.6640106

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4	0.96581385	99.9994772
5	0.96986872	99.999751
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9	Benjamini	FDR
10	0.84881764	99.3930303
11	0.86369431	99.6689449
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13	0.90945744	99.9431691
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17	Benjamini	FDR
18	0.97761425	99.91994
19	0.98605096	99.9879043
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21	0.98716422	99.9914412
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25	Benjamini	FDR
26	0.98401114	88.4629406
27	0.99867919	98.9484156
28		
29	0.99838689	98.9889856
30	1	99.9991313
31	1	99.9998735
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33	0.99998575	99.9982095
34	0.99466129	99.9999888
35	1	99.9999999
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39	Benjamini	FDR
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41	0.96397177	56.0460734
42	0.95159313	95.6604026
43	0.96241318	98.639733
44	0.96830387	99.2741589
45	0.99633367	98.528245
46	0.92901057	99.8400945
47	0.94168358	99.9170203
48	0.98689956	99.9902664
49	0.98886884	99.9942303
50	0.99381348	99.9992718
51	0.97586757	99.9954336
52	0.99645294	99.999926
53	0.99657502	99.9999514
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0.99662485	99.9999665
0.99759086	99.9999877
0.99774106	99.9999908
0.99763025	99.9999917
0.99776314	99.9999937
0.99994222	99.9999579
0.99842622	99.9999983
0.99991447	99.9999743
0.99988454	99.9999753
0.99989939	100
0.99999304	100
0.9999884	100
0.99998974	100
0.9999998	100

Benjamini	FDR
0.96507407	99.3586995
0.99771282	99.9999941
0.99891797	99.9999996

Benjamini	FDR
0.93051013	84.6893348
0.96611311	99.4631586
0.99987597	100
0.99987597	100
0.99999633	100
0.9999984	100

Benjamini	FDR
0.98093522	99.9530455
0.99676386	99.9999624
0.99944269	100

Benjamini	FDR
0.98922998	99.9955008
0.99555938	99.9998216
0.99555938	99.9998216

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4	0.99868075	99.9999991
5	0.99964174	100
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9	Benjamini	FDR
10	0.73125372	70.7727569
11	0.71308075	83.3403852
12	0.99998909	99.9997436
13	0.99408547	99.9999599
14	0.99500131	99.9999872
15	0.99417376	99.9999894
16	0.99995322	99.999999
17	0.99995322	99.999999
18	0.99995352	99.9999995
19	0.99995643	99.9999997
20	0.99999998	100
21	0.99997042	99.9999999
22	0.99998132	100
23	0.99998362	100
24	0.99998194	100
25	1	100
26	0.99998964	100
27	0.99999723	100
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37	Benjamini	FDR
38	0.99996821	99.9998118
39	0.99996646	99.999889
40	0.99996646	99.999889
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45	Benjamini	FDR
46	0.9998583	99.967671
47	0.99995509	99.9934221
48	1	99.9929726
49	0.99997331	99.9983267
50	0.99998028	99.9990941
51	0.99997773	99.9992311
52	0.99999351	99.9955895
53	1	99.9997728
54	0.99999676	99.999954
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0.99999793	99.9999808
0.99995085	99.999896
0.99995754	99.9999526
0.99998115	99.999486
1	99.9999812
0.99999941	99.9999971
0.99985593	99.9999871
1	99.9999947
0.99999999	100
0.99861948	100
0.99998341	100
0.99999083	100
0.99985928	100
0.9999841	100

Benjamini	FDR
0.99370105	99.9993123
0.99368796	99.9999647
0.99862377	99.9999999

Benjamini	FDR
0.99670754	99.9999649
0.99998163	100
0.99999692	100

Benjamini	FDR
0.99999207	100
0.9999955	100
0.99999742	100
0.99999784	100

Benjamini	FDR
0.99672097	100
0.99966523	100
1	100
1	100

Table S5D. Functional annotation clustering of downregulated genes in tumours from DCI

Annotation C Enrichment Score: 2.6457365991883015

Category	Term	Count	%
GOTERM_MF	GO:0004866~endopeptidase inhibitor activity	9	3.7037037
GOTERM_MF	GO:0030414~peptidase inhibitor activity	9	3.7037037
GOTERM_MF	GO:0004857~enzyme inhibitor activity	10	4.11522634

Annotation C Enrichment Score: 2.4050321071041934

Category	Term	Count	%
GOTERM_BP	GO:0006935~chemotaxis	9	3.7037037
GOTERM_BP	GO:0042330~taxis	9	3.7037037
GOTERM_BP	GO:0007626~locomotory behavior	10	4.11522634

Annotation C Enrichment Score: 2.2456253702859743

Category	Term	Count	%
INTERPRO	IPR001060:Fps/Fes/Fer/CIP4 homology	4	1.64609053
SMART	SM00055:FCH	4	1.64609053
UP_SEQ_FEA	domain:FCH	3	1.2345679

Annotation C Enrichment Score: 2.0267700476993076

Category	Term	Count	%
INTERPRO	IPR019565:Alpha-2-macroglobulin, thiol-ester b	3	1.2345679
INTERPRO	IPR011625:Alpha-2-macroglobulin, N-terminal 2	3	1.2345679
INTERPRO	IPR002890:Alpha-2-macroglobulin, N-terminal	3	1.2345679
INTERPRO	IPR011626:A-macroglobulin complement compc	3	1.2345679
INTERPRO	IPR001599:Alpha-2-macroglobulin	3	1.2345679
INTERPRO	IPR019742:Alpha-2-macroglobulin, conserved si	3	1.2345679
INTERPRO	IPR009048:Alpha-macroglobulin, receptor-bindin	3	1.2345679

Annotation C Enrichment Score: 1.9510993706080928

Category	Term	Count	%
INTERPRO	IPR002473:Small chemokine, C-X-C/Interleukin 8	4	1.64609053
INTERPRO	IPR001089:Small chemokine, C-X-C	3	1.2345679
INTERPRO	IPR001811:Small chemokine, interleukin-8-like	4	1.64609053
SMART	SM00199:SCY	4	1.64609053
GOTERM_MF	GO:0008009~chemokine activity	4	1.64609053
GOTERM_MF	GO:0042379~chemokine receptor binding	4	1.64609053

Annotation C Enrichment Score: 1.949689571254049

Category	Term	Count	%
GOTERM_BP	GO:0044243~multicellular organismal catabolic	4	1.64609053
GOTERM_BP	GO:0032963~collagen metabolic process	4	1.64609053
GOTERM_BP	GO:0044259~multicellular organismal macromo	4	1.64609053
GOTERM_BP	GO:0044236~multicellular organismal metabolic	4	1.64609053

GOTERM_BP_GO:0030574~collagen catabolic process 3 1.2345679

Annotation C Enrichment Score: 1.9061063075197975

Category	Term	Count	%
GOTERM_BP_GO:0030593~neutrophil chemotaxis		4	1.64609053
GOTERM_BP_GO:0030595~leukocyte chemotaxis		4	1.64609053
GOTERM_BP_GO:0060326~cell chemotaxis		4	1.64609053
GOTERM_BP_GO:0050900~leukocyte migration		4	1.64609053

Annotation C Enrichment Score: 1.811854496781343

Category	Term	Count	%
GOTERM_BP_GO:0048534~hemopoietic or lymphoid organ de		10	4.11522634
GOTERM_BP_GO:0002520~immune system development		10	4.11522634
GOTERM_BP_GO:0030097~hemopoiesis		9	3.7037037

Annotation C Enrichment Score: 1.7777918066228169

Category	Term	Count	%
GOTERM_BP_GO:0042098~T cell proliferation		4	1.64609053
GOTERM_BP_GO:0046651~lymphocyte proliferation		4	1.64609053
GOTERM_BP_GO:0070661~leukocyte proliferation		4	1.64609053
GOTERM_BP_GO:0032943~mononuclear cell proliferation		4	1.64609053

Annotation C Enrichment Score: 1.5373887640929902

Category	Term	Count	%
UP_SEQ_FEA`domain:Peptidase S1		6	2.4691358
INTERPRO IPR001314:Peptidase S1A, chymotrypsin		6	2.4691358
INTERPRO IPR018114:Peptidase S1/S6, chymotrypsin/Hap,		6	2.4691358
INTERPRO IPR001254:Peptidase S1 and S6, chymotrypsin/t		6	2.4691358
SMART SM00020:Tryp_SPc		6	2.4691358
SP_PIR_KEYM Serine protease		6	2.4691358
UP_SEQ_FEA`active site:Charge relay system		7	2.88065844
GOTERM_MF GO:0004252~serine-type endopeptidase activity		6	2.4691358
GOTERM_MF GO:0008236~serine-type peptidase activity		6	2.4691358
GOTERM_MF GO:0017171~serine hydrolase activity		6	2.4691358

Annotation C Enrichment Score: 1.5089639317393062

Category	Term	Count	%
GOTERM_BP_GO:0051223~regulation of protein transport		6	2.4691358
GOTERM_BP_GO:0070201~regulation of establishment of pro		6	2.4691358
GOTERM_BP_GO:0032880~regulation of protein localization		6	2.4691358

Annotation C Enrichment Score: 1.4605481494717263

Category	Term	Count	%
SP_PIR_KEYM zymogen		10	4.11522634

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GOTERM_MF	GO:0004175~endopeptidase activity	10	4.11522634
GOTERM_MF	GO:0070011~peptidase activity, acting on L-amino acids	13	5.34979424
SP_PIR_KEYW	Protease	11	4.52674897
GOTERM_MF	GO:0008233~peptidase activity	13	5.34979424
Annotation C Enrichment Score: 1.3464237468636655			
Category	Term	Count	%
BIOCARTA	h_thelperPathway:T Helper Cell Surface Molecules	3	1.2345679
BBID	55.Allergen_recognition_by_Th2_or_Th0_cell	3	1.2345679
KEGG_PATHV	hsa04514:Cell adhesion molecules (CAMs)	4	1.64609053
Annotation C Enrichment Score: 1.3233515015415784			
Category	Term	Count	%
GOTERM_BP	GO:0050716~positive regulation of interleukin-1 production	3	1.2345679
GOTERM_BP	GO:0050704~regulation of interleukin-1 secretion	3	1.2345679
GOTERM_BP	GO:0032732~positive regulation of interleukin-1 production	3	1.2345679
GOTERM_BP	GO:0032652~regulation of interleukin-1 production	3	1.2345679
GOTERM_BP	GO:0050715~positive regulation of cytokine secretion	3	1.2345679
GOTERM_BP	GO:0050707~regulation of cytokine secretion	3	1.2345679
GOTERM_BP	GO:0051222~positive regulation of protein transport	4	1.64609053
GOTERM_BP	GO:0050714~positive regulation of protein secretion	3	1.2345679
GOTERM_BP	GO:0050708~regulation of protein secretion	3	1.2345679
Annotation C Enrichment Score: 1.318074292534644			
Category	Term	Count	%
GOTERM_MF	GO:0030247~polysaccharide binding	7	2.88065844
GOTERM_MF	GO:0001871~pattern binding	7	2.88065844
GOTERM_MF	GO:0005539~glycosaminoglycan binding	6	2.4691358
GOTERM_MF	GO:0030246~carbohydrate binding	7	2.88065844
Annotation C Enrichment Score: 1.1917489217734492			
Category	Term	Count	%
GOTERM_BP	GO:0006468~protein amino acid phosphorylation	16	6.58436214
GOTERM_BP	GO:0006793~phosphorus metabolic process	21	8.64197531
GOTERM_BP	GO:0006796~phosphate metabolic process	21	8.64197531
GOTERM_BP	GO:0016310~phosphorylation	17	6.99588477
Annotation C Enrichment Score: 1.0895570756123978			
Category	Term	Count	%
SP_PIR_KEYW	kinase	15	6.17283951
GOTERM_MF	GO:0004672~protein kinase activity	14	5.76131687
UP_SEQ_FEA`	domain:Protein kinase	11	4.52674897
INTERPRO	IPR017441:Protein kinase, ATP binding site	11	4.52674897
UP_SEQ_FEA`	binding site:ATP	12	4.9382716

INTERPRO IPR000719:Protein kinase, core 11 4.52674897
 GOTERM_MF GO:0004674~protein serine/threonine kinase ac 10 4.11522634

Annotation C Enrichment Score: 0.9602119314059515

Category	Term	Count	%
GOTERM_BP	GO:0042981~regulation of apoptosis	17	6.99588477
GOTERM_BP	GO:0043067~regulation of programmed cell death	17	6.99588477
GOTERM_BP	GO:0010941~regulation of cell death	17	6.99588477

Annotation C Enrichment Score: 0.9017413268451007

Category	Term	Count	%
GOTERM_MF	GO:0001530~lipopolysaccharide binding	3	1.2345679
GOTERM_BP	GO:0002237~response to molecule of bacterial origin	3	1.2345679
GOTERM_BP	GO:0009617~response to bacterium	4	1.64609053

Annotation C Enrichment Score: 0.8912744262426376

Category	Term	Count	%
GOTERM_BP	GO:0016032~viral reproduction	4	1.64609053
GOTERM_BP	GO:0019058~viral infectious cycle	3	1.2345679
GOTERM_BP	GO:0022415~viral reproductive process	3	1.2345679

Annotation C Enrichment Score: 0.8354355127066374

Category	Term	Count	%
GOTERM_BP	GO:0008219~cell death	15	6.17283951
GOTERM_BP	GO:0016265~death	15	6.17283951
GOTERM_BP	GO:0006915~apoptosis	13	5.34979424
GOTERM_BP	GO:0012501~programmed cell death	13	5.34979424

Annotation C Enrichment Score: 0.7788571839789994

Category	Term	Count	%
GOTERM_BP	GO:0002253~activation of immune response	4	1.64609053
GOTERM_BP	GO:0002757~immune response-activating signal	3	1.2345679
GOTERM_BP	GO:0002764~immune response-regulating signal	3	1.2345679

Annotation C Enrichment Score: 0.7721699495733398

Category	Term	Count	%
SP_PIR_KEYW	transforming protein	3	1.2345679
SP_PIR_KEYW	autophosphorylation	3	1.2345679
SP_PIR_KEYW	ATP	4	1.64609053

Annotation C Enrichment Score: 0.7643406775581796

Category	Term	Count	%
GOTERM_MF	GO:0004674~protein serine/threonine kinase activity	10	4.11522634
INTERPRO	IPR008271:Serine/threonine protein kinase, acti	8	3.29218107

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SP_PIR_KEYW serine/threonine-protein kinase 8 3.29218107

Annotation C Enrichment Score: 0.7231614177986049

Category	Term	Count	%
INTERPRO	IPR001452:Src homology-3 domain	6	2.4691358
SMART	SM00326:SH3	6	2.4691358
UP_SEQ_FEA	domain:SH3	5	2.05761317
SP_PIR_KEYW	sh3 domain	5	2.05761317

Annotation C Enrichment Score: 0.7170446248563443

Category	Term	Count	%
GOTERM_BP_GO	GO:0032663~regulation of interleukin-2 product	3	1.2345679
GOTERM_BP_GO	GO:0050870~positive regulation of T cell activat	4	1.64609053
GOTERM_BP_GO	GO:0051251~positive regulation of lymphocyte	4	1.64609053
GOTERM_BP_GO	GO:0002696~positive regulation of leukocyte ac	4	1.64609053
GOTERM_BP_GO	GO:0002694~regulation of leukocyte activation	5	2.05761317
GOTERM_BP_GO	GO:0050867~positive regulation of cell activatio	4	1.64609053
GOTERM_BP_GO	GO:0050863~regulation of T cell activation	4	1.64609053
GOTERM_BP_GO	GO:0050865~regulation of cell activation	5	2.05761317
GOTERM_BP_GO	GO:0051249~regulation of lymphocyte activatio	4	1.64609053
UP_SEQ_FEA	domain:Ig-like V-type	3	1.2345679

Annotation C Enrichment Score: 0.6778583304009291

Category	Term	Count	%
UP_SEQ_FEA	repeat:LRR 9	5	2.05761317
UP_SEQ_FEA	repeat:LRR 8	5	2.05761317
UP_SEQ_FEA	repeat:LRR 6	6	2.4691358
UP_SEQ_FEA	repeat:LRR 11	4	1.64609053
UP_SEQ_FEA	repeat:LRR 5	6	2.4691358
UP_SEQ_FEA	repeat:LRR 10	4	1.64609053
UP_SEQ_FEA	repeat:LRR 7	5	2.05761317
UP_SEQ_FEA	repeat:LRR 4	6	2.4691358
UP_SEQ_FEA	repeat:LRR 13	3	1.2345679
UP_SEQ_FEA	repeat:LRR 12	3	1.2345679
UP_SEQ_FEA	repeat:LRR 3	6	2.4691358
UP_SEQ_FEA	repeat:LRR 2	6	2.4691358
UP_SEQ_FEA	repeat:LRR 1	6	2.4691358
SP_PIR_KEYW	leucine-rich repeat	6	2.4691358

Annotation C Enrichment Score: 0.6705317648098426

Category	Term	Count	%
GOTERM_BP_GO	GO:0051674~localization of cell	8	3.29218107
GOTERM_BP_GO	GO:0048870~cell motility	8	3.29218107
GOTERM_BP_GO	GO:0016477~cell migration	7	2.88065844

GOTERM_BP_GO:0006928~cell motion 8 3.29218107

Annotation C Enrichment Score: 0.6544587502225521

Category	Term	Count	%
GOTERM_CC_GO:0000779~condensed chromosome, centrom		4	1.64609053
GOTERM_CC_GO:0000777~condensed chromosome kinetoch		3	1.2345679
GOTERM_CC_GO:0000775~chromosome, centromeric region		4	1.64609053
GOTERM_CC_GO:0000793~condensed chromosome		4	1.64609053
GOTERM_CC_GO:0000776~kinetochore		3	1.2345679
GOTERM_BP_GO:0007059~chromosome segregation		3	1.2345679

Annotation C Enrichment Score: 0.6426153364178447

Category	Term	Count	%
GOTERM_BP_GO:0006897~endocytosis		6	2.4691358
GOTERM_BP_GO:0010324~membrane invagination		6	2.4691358
GOTERM_BP_GO:0016044~membrane organization		8	3.29218107

Annotation C Enrichment Score: 0.6338334775112134

Category	Term	Count	%
GOTERM_BP_GO:0055082~cellular chemical homeostasis		9	3.7037037
GOTERM_BP_GO:0048878~chemical homeostasis		11	4.52674897
GOTERM_BP_GO:0019725~cellular homeostasis		10	4.11522634
GOTERM_BP_GO:0006873~cellular ion homeostasis		8	3.29218107
GOTERM_BP_GO:0050801~ion homeostasis		8	3.29218107

Annotation C Enrichment Score: 0.5955748927592466

Category	Term	Count	%
SP_PIR_KEYW lysosome		5	2.05761317
GOTERM_CC_GO:0000323~lytic vacuole		5	2.05761317
GOTERM_CC_GO:0005764~lysosome		5	2.05761317

Annotation C Enrichment Score: 0.5919951300461574

Category	Term	Count	%
INTERPRO IPR017970:Homeobox, conserved site		6	2.4691358
SP_PIR_KEYW Homeobox		6	2.4691358
INTERPRO IPR012287:Homeodomain-related		6	2.4691358
INTERPRO IPR001356:Homeobox		5	2.05761317
SMART SM00389:HOX		5	2.05761317

Annotation C Enrichment Score: 0.5697573039988909

Category	Term	Count	%
GOTERM_BP_GO:0006749~glutathione metabolic process		3	1.2345679
GOTERM_BP_GO:0006518~peptide metabolic process		3	1.2345679
GOTERM_BP_GO:0006732~coenzyme metabolic process		4	1.64609053

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GOTERM_BP_GO:0006575~cellular amino acid derivative met	4	1.64609053
GOTERM_BP_GO:0006790~sulfur metabolic process	3	1.2345679
GOTERM_BP_GO:0051186~cofactor metabolic process	4	1.64609053
Annotation C Enrichment Score: 0.5641942754322211		
Category	Term	Count %
GOTERM_BP_GO:0001932~regulation of protein amino acid p		6 2.4691358
GOTERM_BP_GO:0031399~regulation of protein modification		6 2.4691358
GOTERM_BP_GO:0032268~regulation of cellular protein meta		8 3.29218107
Annotation C Enrichment Score: 0.5537778808931171		
Category	Term	Count %
GOTERM_MF_GO:0008528~peptide receptor activity, G-protei		4 1.64609053
GOTERM_MF_GO:0001653~peptide receptor activity		4 1.64609053
GOTERM_MF_GO:0042277~peptide binding		4 1.64609053
Annotation C Enrichment Score: 0.5516809803160089		
Category	Term	Count %
GOTERM_BP_GO:0043065~positive regulation of apoptosis		9 3.7037037
GOTERM_BP_GO:0043068~positive regulation of programme		9 3.7037037
GOTERM_BP_GO:0010942~positive regulation of cell death		9 3.7037037
GOTERM_BP_GO:0006917~induction of apoptosis		7 2.88065844
GOTERM_BP_GO:0012502~induction of programmed cell dea		7 2.88065844
Annotation C Enrichment Score: 0.5420725015881858		
Category	Term	Count %
GOTERM_BP_GO:0043583~ear development		4 1.64609053
GOTERM_BP_GO:0048704~embryonic skeletal system morph		3 1.2345679
GOTERM_BP_GO:0048705~skeletal system morphogenesis		4 1.64609053
GOTERM_BP_GO:0042471~ear morphogenesis		3 1.2345679
GOTERM_BP_GO:0048706~embryonic skeletal system develop		3 1.2345679
UP_SEQ_FEA`DNA-binding region:Homeobox		4 1.64609053
GOTERM_BP_GO:0048568~embryonic organ development		4 1.64609053
GOTERM_BP_GO:0048562~embryonic organ morphogenesis		3 1.2345679
Annotation C Enrichment Score: 0.5292189899634967		
Category	Term	Count %
GOTERM_BP_GO:0001568~blood vessel development		6 2.4691358
GOTERM_BP_GO:0001944~vasculature development		6 2.4691358
GOTERM_BP_GO:0048514~blood vessel morphogenesis		5 2.05761317
Annotation C Enrichment Score: 0.519590428426698		
Category	Term	Count %
UP_SEQ_FEA`repeat:TPR 3		4 1.64609053

UP_SEQ_FEA`repeat:TPR 1	4	1.64609053
UP_SEQ_FEA`repeat:TPR 2	4	1.64609053
SP_PIR_KEYW tpr repeat	4	1.64609053
UP_SEQ_FEA`repeat:TPR 4	3	1.2345679

Annotation C Enrichment Score: 0.4969390319364281

Category	Term	Count	%
GOTERM_BP	GO:0006916~anti-apoptosis	6	2.4691358
GOTERM_BP	GO:0043066~negative regulation of apoptosis	7	2.88065844
GOTERM_BP	GO:0043069~negative regulation of programme	7	2.88065844
GOTERM_BP	GO:0060548~negative regulation of cell death	7	2.88065844

Annotation C Enrichment Score: 0.4959778147816573

Category	Term	Count	%
GOTERM_BP	GO:0019320~hexose catabolic process	3	1.2345679
GOTERM_BP	GO:0046365~monosaccharide catabolic process	3	1.2345679
GOTERM_BP	GO:0046164~alcohol catabolic process	3	1.2345679
GOTERM_BP	GO:0044275~cellular carbohydrate catabolic prc	3	1.2345679
GOTERM_BP	GO:0016052~carbohydrate catabolic process	3	1.2345679

Annotation C Enrichment Score: 0.4660559909689328

Category	Term	Count	%
GOTERM_BP	GO:0000278~mitotic cell cycle	8	3.29218107
GOTERM_BP	GO:0022403~cell cycle phase	8	3.29218107
GOTERM_BP	GO:0022402~cell cycle process	10	4.11522634

Annotation C Enrichment Score: 0.4648658458872357

Category	Term	Count	%
GOTERM_BP	GO:0019318~hexose metabolic process	5	2.05761317
GOTERM_BP	GO:0006006~glucose metabolic process	4	1.64609053
GOTERM_BP	GO:0005996~monosaccharide metabolic proces	5	2.05761317

Annotation C Enrichment Score: 0.4564736094687051

Category	Term	Count	%
GOTERM_BP	GO:0006633~fatty acid biosynthetic process	3	1.2345679
GOTERM_BP	GO:0046394~carboxylic acid biosynthetic proces	4	1.64609053
GOTERM_BP	GO:0016053~organic acid biosynthetic process	4	1.64609053

Annotation C Enrichment Score: 0.4482366227207559

Category	Term	Count	%
GOTERM_BP	GO:0015711~organic anion transport	3	1.2345679
GOTERM_BP	GO:0006820~anion transport	4	1.64609053
GOTERM_BP	GO:0046942~carboxylic acid transport	3	1.2345679
GOTERM_BP	GO:0015849~organic acid transport	3	1.2345679

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Annotation C Enrichment Score: 0.44205824672831445

Category	Term	Count	%
UP_SEQ_FEA	transmembrane region	70	28.8065844
SP_PIR_KEYW	transmembrane	70	28.8065844
GOTERM_CC	GO:0031224~intrinsic to membrane	78	32.0987654
GOTERM_CC	GO:0016021~integral to membrane	73	30.0411523

Annotation C Enrichment Score: 0.44069976240797265

Category	Term	Count	%
SP_PIR_KEYW	mitosis	5	2.05761317
SP_PIR_KEYW	cell division	6	2.4691358
GOTERM_BP	GO:0007067~mitosis	5	2.05761317
GOTERM_BP	GO:0000280~nuclear division	5	2.05761317
GOTERM_BP	GO:0000087~M phase of mitotic cell cycle	5	2.05761317
GOTERM_BP	GO:0048285~organelle fission	5	2.05761317
GOTERM_BP	GO:0051301~cell division	6	2.4691358
GOTERM_BP	GO:0000279~M phase	5	2.05761317

Annotation C Enrichment Score: 0.4390372613971224

Category	Term	Count	%
GOTERM_BP	GO:0042325~regulation of phosphorylation	9	3.7037037
GOTERM_BP	GO:0051174~regulation of phosphorus metabol	9	3.7037037
GOTERM_BP	GO:0019220~regulation of phosphate metabolic	9	3.7037037

Annotation C Enrichment Score: 0.40914267151447903

Category	Term	Count	%
GOTERM_BP	GO:0001816~cytokine production	3	1.2345679
GOTERM_BP	GO:0051789~response to protein stimulus	4	1.64609053
GOTERM_BP	GO:0001934~positive regulation of protein amir	3	1.2345679
GOTERM_BP	GO:0042327~positive regulation of phosphoryla	3	1.2345679
GOTERM_BP	GO:0045937~positive regulation of phosphate r	3	1.2345679
GOTERM_BP	GO:0010562~positive regulation of phosphorus	3	1.2345679
GOTERM_BP	GO:0032270~positive regulation of cellular prot	4	1.64609053
GOTERM_BP	GO:0051247~positive regulation of protein met	4	1.64609053
GOTERM_BP	GO:0031401~positive regulation of protein mod	3	1.2345679

Annotation C Enrichment Score: 0.40843874118096335

Category	Term	Count	%
INTERPRO	IPR000483:Cysteine-rich flanking region, C-term	3	1.2345679
SMART	SM00082:LRRCT	3	1.2345679
INTERPRO	IPR001611:Leucine-rich repeat	4	1.64609053

Annotation C Enrichment Score: 0.39177656478496287

Category	Term	Count	%
UP_SEQ_FEA	domain:SH2	3	1.2345679
SP_PIR_KEYW	SH2 domain	3	1.2345679
INTERPRO	IPR000980:SH2 motif	3	1.2345679
SMART	SM00252:SH2	3	1.2345679

Annotation C Enrichment Score: 0.36444494472150707

Category	Term	Count	%
UP_SEQ_FEA	domain:PH	5	2.05761317
INTERPRO	IPR011993:Pleckstrin homology-type	6	2.4691358
INTERPRO	IPR001849:Pleckstrin homology	5	2.05761317
SMART	SM00233:PH	5	2.05761317

Annotation C Enrichment Score: 0.3631493772971953

Category	Term	Count	%
UP_SEQ_FEA	domain:EGF-like 3; calcium-binding	3	1.2345679
INTERPRO	IPR013091:EGF calcium-binding	3	1.2345679
INTERPRO	IPR001881:EGF-like calcium-binding	3	1.2345679
INTERPRO	IPR018097:EGF-like calcium-binding, conserved	3	1.2345679
SMART	SM00179:EGF_CA	3	1.2345679
INTERPRO	IPR000742:EGF-like, type 3	3	1.2345679
INTERPRO	IPR013032:EGF-like region, conserved site	4	1.64609053
INTERPRO	IPR006210:EGF-like	3	1.2345679
SMART	SM00181:EGF	3	1.2345679
SP_PIR_KEYW	egf-like domain	3	1.2345679

Annotation C Enrichment Score: 0.3614532952124279

Category	Term	Count	%
GOTERM_BP_GO	0048754~branching morphogenesis of a tub	3	1.2345679
GOTERM_BP_GO	0001763~morphogenesis of a branching stru	3	1.2345679
GOTERM_BP_GO	0035239~tube morphogenesis	3	1.2345679
GOTERM_BP_GO	0035295~tube development	4	1.64609053
GOTERM_BP_GO	0007389~pattern specification process	4	1.64609053

Annotation C Enrichment Score: 0.34061118556083336

Category	Term	Count	%
GOTERM_BP_GO	0052548~regulation of endopeptidase activi	3	1.2345679
GOTERM_BP_GO	0052547~regulation of peptidase activity	3	1.2345679
GOTERM_BP_GO	0051336~regulation of hydrolase activity	4	1.64609053

Annotation C Enrichment Score: 0.3162121165623899

Category	Term	Count	%
INTERPRO	IPR008266:Tyrosine protein kinase, active site	3	1.2345679
INTERPRO	IPR001245:Tyrosine protein kinase	3	1.2345679

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SMART	SM00219:TyrKc	3	1.2345679
GOTERM_MF	GO:0004713~protein tyrosine kinase activity	3	1.2345679
Annotation C Enrichment Score: 0.29286562049798204			
Category	Term	Count	%
GOTERM_BP	GO:0016311~dephosphorylation	4	1.64609053
GOTERM_MF	GO:0004725~protein tyrosine phosphatase activ	3	1.2345679
GOTERM_MF	GO:0004721~phosphoprotein phosphatase activ	3	1.2345679
GOTERM_MF	GO:0016791~phosphatase activity	4	1.64609053
Annotation C Enrichment Score: 0.29178516923503417			
Category	Term	Count	%
GOTERM_BP	GO:0051338~regulation of transferase activity	7	2.88065844
GOTERM_BP	GO:0045859~regulation of protein kinase activit	6	2.4691358
GOTERM_BP	GO:0043549~regulation of kinase activity	6	2.4691358
Annotation C Enrichment Score: 0.2853754913134388			
Category	Term	Count	%
GOTERM_CC	GO:0005740~mitochondrial envelope	8	3.29218107
GOTERM_CC	GO:0031966~mitochondrial membrane	7	2.88065844
GOTERM_CC	GO:0044429~mitochondrial part	9	3.7037037
Annotation C Enrichment Score: 0.28441721054035735			
Category	Term	Count	%
GOTERM_BP	GO:0051090~regulation of transcription factor a	3	1.2345679
GOTERM_BP	GO:0051101~regulation of DNA binding	3	1.2345679
GOTERM_BP	GO:0051098~regulation of binding	3	1.2345679
Annotation C Enrichment Score: 0.26822495811647357			
Category	Term	Count	%
GOTERM_BP	GO:0031328~positive regulation of cellular biosy	12	4.9382716
GOTERM_BP	GO:0009891~positive regulation of biosynthetic	12	4.9382716
GOTERM_BP	GO:0045944~positive regulation of transcrip	7	2.88065844
GOTERM_BP	GO:0045893~positive regulation of transcrip	8	3.29218107
GOTERM_BP	GO:0051254~positive regulation of RNA metabo	8	3.29218107
GOTERM_BP	GO:0051173~positive regulation of nitrogen con	10	4.11522634
GOTERM_BP	GO:0010557~positive regulation of macromolec	10	4.11522634
GOTERM_BP	GO:0045941~positive regulation of transcrip	8	3.29218107
GOTERM_BP	GO:0010628~positive regulation of gene expres	8	3.29218107
GOTERM_BP	GO:0045935~positive regulation of nucleobase,	8	3.29218107
Annotation C Enrichment Score: 0.2476948541618284			
Category	Term	Count	%
GOTERM_BP	GO:0006644~phospholipid metabolic process	4	1.64609053

GOTERM_BP_GO:0019637~organophosphate metabolic process 4 1.64609053
 GOTERM_BP_GO:0046486~glycerolipid metabolic process 3 1.2345679

Annotation C Enrichment Score: 0.2424207581176388

Category	Term	Count	%
UP_SEQ_FEA	nucleotide phosphate-binding region:ATP	17	6.99588477
SP_PIR_KEYM	atp-binding	18	7.40740741
GOTERM_MF_GO:0001882	~nucleoside binding	23	9.46502058
SP_PIR_KEYM	nucleotide-binding	22	9.05349794
GOTERM_MF_GO:0005524	~ATP binding	20	8.23045267
GOTERM_MF_GO:0032559	~adenyl ribonucleotide binding	20	8.23045267
GOTERM_MF_GO:0030554	~adenyl nucleotide binding	21	8.64197531
GOTERM_MF_GO:0001883	~purine nucleoside binding	21	8.64197531
GOTERM_MF_GO:0032553	~ribonucleotide binding	24	9.87654321
GOTERM_MF_GO:0032555	~purine ribonucleotide binding	24	9.87654321
GOTERM_MF_GO:0017076	~purine nucleotide binding	25	10.2880658
GOTERM_MF_GO:0000166	~nucleotide binding	28	11.5226337

Annotation C Enrichment Score: 0.2339195054313887

Category	Term	Count	%
GOTERM_BP_GO:0007204	~elevation of cytosolic calcium ion c	3	1.2345679
GOTERM_BP_GO:0051480	~cytosolic calcium ion homeostasis	3	1.2345679
GOTERM_BP_GO:0006875	~cellular metal ion homeostasis	4	1.64609053
GOTERM_BP_GO:0055065	~metal ion homeostasis	4	1.64609053
GOTERM_BP_GO:0030005	~cellular di-, tri-valent inorganic cat	4	1.64609053
GOTERM_BP_GO:0006874	~cellular calcium ion homeostasis	3	1.2345679
GOTERM_BP_GO:0055074	~calcium ion homeostasis	3	1.2345679

Annotation C Enrichment Score: 0.20527146276024807

Category	Term	Count	%
SP_PIR_KEYM	guanine-nucleotide releasing factor	3	1.2345679
GOTERM_MF_GO:0005085	~guanyl-nucleotide exchange factor	3	1.2345679
GOTERM_BP_GO:0051056	~regulation of small GTPase mediat	3	1.2345679

Annotation C Enrichment Score: 0.1958129398163255

Category	Term	Count	%
GOTERM_BP_GO:0045860	~positive regulation of protein kina	4	1.64609053
GOTERM_BP_GO:0033674	~positive regulation of kinase activi	4	1.64609053
GOTERM_BP_GO:0051347	~positive regulation of transferase a	4	1.64609053

Annotation C Enrichment Score: 0.19483616952981112

Category	Term	Count	%
GOTERM_MF_GO:0046872	~metal ion binding	56	23.0452675
GOTERM_MF_GO:0043167	~ion binding	57	23.4567901

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GOTERM_MF	GO:0043169~cation binding	56	23.0452675
Annotation C Enrichment Score: 0.1895471891965199			
Category	Term	Count	%
UP_SEQ_FEA`	repeat:1	4	1.64609053
UP_SEQ_FEA`	repeat:2	4	1.64609053
UP_SEQ_FEA`	repeat:3	3	1.2345679
Annotation C Enrichment Score: 0.18940660607174897			
Category	Term	Count	%
GOTERM_BP	GO:0051270~regulation of cell motion	4	1.64609053
GOTERM_BP	GO:0030334~regulation of cell migration	3	1.2345679
GOTERM_BP	GO:0040012~regulation of locomotion	3	1.2345679
Annotation C Enrichment Score: 0.16458960343084142			
Category	Term	Count	%
GOTERM_MF	GO:0022838~substrate specific channel activity	6	2.4691358
GOTERM_MF	GO:0015267~channel activity	6	2.4691358
GOTERM_MF	GO:0022803~passive transmembrane transport	6	2.4691358
GOTERM_MF	GO:0005216~ion channel activity	5	2.05761317
Annotation C Enrichment Score: 0.16268561660527697			
Category	Term	Count	%
UP_SEQ_FEA`	zinc finger region:C2H2-type 15	3	1.2345679
UP_SEQ_FEA`	zinc finger region:C2H2-type 14	3	1.2345679
UP_SEQ_FEA`	domain:KRAB	5	2.05761317
UP_SEQ_FEA`	zinc finger region:C2H2-type 12	4	1.64609053
UP_SEQ_FEA`	zinc finger region:C2H2-type 7	6	2.4691358
INTERPRO	IPR001909:Krueppel-associated box	5	2.05761317
UP_SEQ_FEA`	zinc finger region:C2H2-type 11	4	1.64609053
UP_SEQ_FEA`	zinc finger region:C2H2-type 13	3	1.2345679
SMART	SM00349:KRAB	5	2.05761317
UP_SEQ_FEA`	zinc finger region:C2H2-type 6	6	2.4691358
UP_SEQ_FEA`	zinc finger region:C2H2-type 8	5	2.05761317
UP_SEQ_FEA`	zinc finger region:C2H2-type 10	4	1.64609053
UP_SEQ_FEA`	zinc finger region:C2H2-type 9	4	1.64609053
Annotation C Enrichment Score: 0.14893413789505905			
Category	Term	Count	%
UP_SEQ_FEA`	zinc finger region:C2H2-type 3	9	3.7037037
INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DN	9	3.7037037
UP_SEQ_FEA`	zinc finger region:C2H2-type 5	7	2.88065844
UP_SEQ_FEA`	zinc finger region:C2H2-type 1	7	2.88065844
UP_SEQ_FEA`	zinc finger region:C2H2-type 2	7	2.88065844

INTERPRO	IPR007087:Zinc finger, C2H2-type	9	3.7037037
INTERPRO	IPR015880:Zinc finger, C2H2-like	9	3.7037037
SMART	SM00355:ZnF_C2H2	9	3.7037037

Annotation C Enrichment Score: 0.1442545392821464

Category	Term	Count	%
GOTERM_BP	GO:0051969~regulation of transmission of nerve	3	1.2345679
GOTERM_BP	GO:0031644~regulation of neurological system	3	1.2345679
GOTERM_BP	GO:0044057~regulation of system process	3	1.2345679

Annotation C Enrichment Score: 0.13700550472629017

Category	Term	Count	%
GOTERM_BP	GO:0006355~regulation of transcription, DNA-d	25	10.2880658
GOTERM_BP	GO:0051252~regulation of RNA metabolic proce	25	10.2880658
GOTERM_BP	GO:0045449~regulation of transcription	30	12.345679

Annotation C Enrichment Score: 0.1364390801679014

Category	Term	Count	%
INTERPRO	IPR005225:Small GTP-binding protein	4	1.64609053
UP_SEQ_FEA	nucleotide phosphate-binding region:GTP	4	1.64609053
SP_PIR_KEYW	gtp-binding	4	1.64609053
GOTERM_MF	GO:0005525~GTP binding	4	1.64609053
GOTERM_MF	GO:0019001~guanyl nucleotide binding	4	1.64609053
GOTERM_MF	GO:0032561~guanyl ribonucleotide binding	4	1.64609053

Annotation C Enrichment Score: 0.11615238469098707

Category	Term	Count	%
SP_PIR_KEYW	vision	3	1.2345679
GOTERM_BP	GO:0050953~sensory perception of light stimul	3	1.2345679
GOTERM_BP	GO:0007601~visual perception	3	1.2345679
SP_PIR_KEYW	sensory transduction	3	1.2345679

Annotation C Enrichment Score: 0.11260014161979574

Category	Term	Count	%
GOTERM_MF	GO:0003714~transcription corepressor activity	3	1.2345679
GOTERM_MF	GO:0016564~transcription repressor activity	4	1.64609053
GOTERM_MF	GO:0003712~transcription cofactor activity	3	1.2345679

Annotation C Enrichment Score: 0.09300881834073159

Category	Term	Count	%
SP_PIR_KEYW	G protein-coupled receptor	3	1.2345679
INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	4	1.64609053
INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	4	1.64609053
PIR_SUPERFA	PIRSF800006:rhodopsin-like G protein-coupled r	4	1.64609053

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Annotation C Enrichment Score: 0.09186957672865842

Category	Term	Count	%
GOTERM_CC	GO:0005789~endoplasmic reticulum membrane	4	1.64609053
GOTERM_CC	GO:0042175~nuclear envelope-endoplasmic ret	4	1.64609053
GOTERM_CC	GO:0044432~endoplasmic reticulum part	4	1.64609053

Annotation C Enrichment Score: 0.08375911213550115

Category	Term	Count	%
GOTERM_BP	GO:0031175~neuron projection development	4	1.64609053
GOTERM_BP	GO:0048812~neuron projection morphogenesis	3	1.2345679
GOTERM_BP	GO:0048858~cell projection morphogenesis	3	1.2345679
GOTERM_BP	GO:0032990~cell part morphogenesis	3	1.2345679
GOTERM_BP	GO:0000902~cell morphogenesis	4	1.64609053

Annotation C Enrichment Score: 0.08138944422340862

Category	Term	Count	%
GOTERM_BP	GO:0007276~gamete generation	5	2.05761317
GOTERM_BP	GO:0007283~spermatogenesis	4	1.64609053
GOTERM_BP	GO:0048232~male gamete generation	4	1.64609053
GOTERM_BP	GO:0048609~reproductive process in a multicell	6	2.4691358
GOTERM_BP	GO:0032504~multicellular organism reproductic	6	2.4691358
GOTERM_BP	GO:0019953~sexual reproduction	5	2.05761317

Annotation C Enrichment Score: 0.06021055288118063

Category	Term	Count	%
GOTERM_BP	GO:0006461~protein complex assembly	6	2.4691358
GOTERM_BP	GO:0070271~protein complex biogenesis	6	2.4691358
GOTERM_BP	GO:0043933~macromolecular complex subunit	8	3.29218107
GOTERM_BP	GO:0065003~macromolecular complex assembl	7	2.88065844

Annotation C Enrichment Score: 0.033939695930046

Category	Term	Count	%
GOTERM_BP	GO:0034613~cellular protein localization	5	2.05761317
GOTERM_BP	GO:0070727~cellular macromolecule localization	5	2.05761317
GOTERM_BP	GO:0006886~intracellular protein transport	4	1.64609053
GOTERM_BP	GO:0015031~protein transport	5	2.05761317
GOTERM_BP	GO:0045184~establishment of protein localizati	5	2.05761317
GOTERM_BP	GO:0008104~protein localization	6	2.4691358

Annotation C Enrichment Score: 0.031041417201957477

Category	Term	Count	%
GOTERM_CC	GO:0005667~transcription factor complex	3	1.2345679
GOTERM_CC	GO:0044451~nucleoplasm part	4	1.64609053

GOTERM_CC GO:0005654~nucleoplasm 4 1.64609053

Annotation C Enrichment Score: 0.02365039774338518

Category	Term	Count	%
INTERPRO	IPR003599:Immunoglobulin subtype	3	1.2345679
SMART	SM00409:IG	3	1.2345679
INTERPRO	IPR007110:Immunoglobulin-like	4	1.64609053

Annotation C Enrichment Score: 0.005339698815659179

Category	Term	Count	%
SP_PIR_KEYW	transcription regulation	18	7.40740741
SP_PIR_KEYW	Transcription	17	6.99588477
GOTERM_BP	GO:0006350~transcription	17	6.99588477

Annotation C Enrichment Score: 0.004702263581353127

Category	Term	Count	%
GOTERM_BP	GO:0045892~negative regulation of transcriptio	3	1.2345679
GOTERM_BP	GO:0051253~negative regulation of RNA metabo	3	1.2345679
GOTERM_BP	GO:0016481~negative regulation of transcriptio	3	1.2345679
GOTERM_BP	GO:0010629~negative regulation of gene expres	3	1.2345679
GOTERM_BP	GO:0045934~negative regulation of nucleobase,	3	1.2345679
GOTERM_BP	GO:0051172~negative regulation of nitrogen co	3	1.2345679
GOTERM_BP	GO:0010558~negative regulation of macromole	3	1.2345679
GOTERM_BP	GO:0031327~negative regulation of cellular bios	3	1.2345679
GOTERM_BP	GO:0009890~negative regulation of biosynthetic	3	1.2345679
GOTERM_BP	GO:0010605~negative regulation of macromole	4	1.64609053

Annotation C Enrichment Score: 0.0022307956893741743

Category	Term	Count	%
SP_PIR_KEYW	ubl conjugation pathway	3	1.2345679
GOTERM_BP	GO:0051603~proteolysis involved in cellular pro	4	1.64609053
GOTERM_BP	GO:0044257~cellular protein catabolic process	4	1.64609053
GOTERM_BP	GO:0030163~protein catabolic process	4	1.64609053
GOTERM_BP	GO:0019941~modification-dependent protein c	3	1.2345679
GOTERM_BP	GO:0043632~modification-dependent macromo	3	1.2345679
GOTERM_BP	GO:0044265~cellular macromolecule catabolic p	4	1.64609053
GOTERM_BP	GO:0009057~macromolecule catabolic process	4	1.64609053

Annotation C Enrichment Score: 1.9911816465780318E-4

Category	Term	Count	%
GOTERM_CC	GO:0031974~membrane-enclosed lumen	15	6.17283951
GOTERM_CC	GO:0043233~organelle lumen	13	5.34979424
GOTERM_CC	GO:0070013~intracellular organelle lumen	12	4.9382716

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S-SOX11 cells compared to DCIS-lacZ cells injected into mammary fat pad.

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
8.31E-04	COL4A3, HM9	178	145	12983	4.52719876	0.27992109
0.00117323	COL4A3, HM9	178	153	12983	4.29048249	0.37104616
0.01185194	COL4A3, HM9	178	270	12983	2.7014149	0.99099052
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00195561	CXCL1, CXCL1	192	160	13528	3.96328125	0.95713322
0.00195561	CXCL1, CXCL1	192	160	13528	3.96328125	0.95713322
0.01593452	CXCL1, CXCL1	192	274	13528	2.57147202	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.0025023	HMHA1, PAC	220	21	16659	14.4233766	0.71283802
0.00282692	HMHA1, PAC	126	21	9079	13.7248677	0.2839816
0.02591014	PACSIN1, FES	242	20	19113	11.8469008	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00722183	C3, CPAMD8,	220	10	16659	22.7168182	0.97293512
0.00875066	C3, CPAMD8,	220	11	16659	20.6516529	0.98743713
0.00875066	C3, CPAMD8,	220	11	16659	20.6516529	0.98743713
0.01041047	C3, CPAMD8,	220	12	16659	18.9306818	0.99454699
0.01041047	C3, CPAMD8,	220	12	16659	18.9306818	0.99454699
0.01041047	C3, CPAMD8,	220	12	16659	18.9306818	0.99454699
0.01041047	C3, CPAMD8,	220	12	16659	18.9306818	0.99454699
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
7.33E-04	CXCL1, CCL20	220	14	16659	21.6350649	0.30588526
0.01219756	CXCL1, CXCL3	220	13	16659	17.4744755	0.99778329
0.01655107	CXCL1, CCL20	220	41	16659	7.38758315	0.9997543
0.01856553	CXCL1, CCL20	126	41	9079	7.0298103	0.89044453
0.02463842	CXCL1, CCL20	178	46	12983	6.34245237	0.99994747
0.0290362	CXCL1, CCL20	178	49	12983	5.95413896	0.99999119
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00567148	KLK6, P2RX7,	192	26	13528	10.8397436	0.99989393
0.00700014	KLK6, P2RX7,	192	28	13528	10.0654762	0.99998766
0.00931272	KLK6, P2RX7,	192	31	13528	9.09139785	0.99999971
0.01513635	KLK6, P2RX7,	192	37	13528	7.61711712	1

0.03188974 KLK6, ADAMT 192 20 13528 10.56875 1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00193365	SAA1, CXCL3,	192	18	13528	15.6574074	0.95558819
0.01513635	SAA1, CXCL3,	192	37	13528	7.61711712	1
0.01744251	SAA1, CXCL3,	192	39	13528	7.22649573	1
0.04651224	SAA1, CXCL3,	192	57	13528	4.94444444	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.01162857	IL17C, LYN, RI	192	260	13528	2.7099359	0.99999999
0.01658822	IL17C, LYN, RI	192	276	13528	2.55283816	1
0.01901561	IL17C, LYN, RI	192	236	13528	2.68697034	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00631491	P2RX7, CXCR4	192	27	13528	10.4382716	0.99996257
0.02124916	P2RX7, CXCR4	192	42	13528	6.71031746	1
0.02401938	P2RX7, CXCR4	192	44	13528	6.40530303	1
0.02401938	P2RX7, CXCR4	192	44	13528	6.40530303	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.01106142	KLK6, KLK8, T	242	106	19113	4.47052861	0.99994199
0.01206303	KLK6, KLK8, T	220	104	16659	4.36861888	0.99762775
0.01253454	KLK6, KLK8, T	220	105	16659	4.32701299	0.99812969
0.01856429	KLK6, KLK8, T	220	116	16659	3.91669279	0.99991145
0.02178837	KLK6, KLK8, T	126	116	9079	3.72701149	0.92568558
0.02843495	KLK6, KLK8, T	242	136	19235	3.50662372	0.99989918
0.03826365	KLK6, LPL, KLI	242	196	19113	2.82069067	1
0.05937937	KLK6, KLK8, T	178	154	12983	2.84174814	1
0.09677229	KLK6, KLK8, T	178	178	12983	2.45859109	1
0.09995583	KLK6, KLK8, T	178	180	12983	2.43127341	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.02271603	P2RX7, SAA1,	192	114	13528	3.70833333	1
0.02845866	P2RX7, SAA1,	192	121	13528	3.49380165	1
0.04597918	P2RX7, SAA1,	192	138	13528	3.0634058	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.00119778	KLK6, GGT5, I	242	206	19235	3.85842093	0.31772298

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0.07136674	KLK6, KLK8, A	178	375	12983	1.94501873	1
0.07256366	KLK6, KLK8, A	178	549	12983	1.72713412	1
0.08594042	KLK6, KLK8, A	242	484	19235	1.80644252	1
0.09342675	KLK6, KLK8, A	178	574	12983	1.6519105	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.01467724	ITGB2, CD4, C	24	12	1437	14.96875	0.62313838
0.02280771	ITGB2, CD4, C	10	10	358	10.74	0.47586779
0.27289939	ITGB2, CD4, I	71	132	5085	2.17029449	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.0161407	P2RX7, SAA1,	192	14	13528	15.0982143	1
0.01845276	P2RX7, SAA1,	192	15	13528	14.0916667	1
0.02346426	P2RX7, SAA1,	192	17	13528	12.4338235	1
0.04131331	P2RX7, SAA1,	192	23	13528	9.19021739	1
0.04131331	P2RX7, SAA1,	192	23	13528	9.19021739	1
0.06664912	P2RX7, SAA1,	192	30	13528	7.04583333	1
0.0688691	P2RX7, SAA1,	192	67	13528	4.20646766	1
0.11379585	P2RX7, SAA1,	192	41	13528	5.1554878	1
0.19738794	P2RX7, SAA1,	192	58	13528	3.64439655	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.01883047	LPL, COMP, V	178	154	12983	3.31537283	0.99945185
0.01883047	LPL, COMP, V	178	154	12983	3.31537283	0.99945185
0.04269224	LPL, COMP, V	178	140	12983	3.12592295	0.99999997
0.35288382	LPL, COMP, V	178	354	12983	1.44228084	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.05072542	IRAK2, PDK1,	192	667	13528	1.69015492	1
0.05778513	IRAK2, PDK1,	192	973	13528	1.52068345	1
0.05778513	IRAK2, PDK1,	192	973	13528	1.52068345	1
0.10095932	IRAK2, PDK1,	192	800	13528	1.49723958	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.05219267	PDK1, STK31,	242	688	19235	1.73292451	0.99999996
0.07099999	PDK1, IRAK2,	178	606	12983	1.68504098	1
0.07418012	IRAK2, STK31	242	469	19113	1.85239387	1
0.07843682	IRAK2, STK31	220	455	16659	1.83065934	1
0.08326329	PDK1, STK31,	242	542	19113	1.74862005	1

0.09826037	IRAK2, STK31	220	476	16659	1.74989496	1
0.13384223	IRAK2, STK31	178	430	12983	1.69623726	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.10426012	COL4A3, AIFM	192	804	13528	1.48979063	1
0.11106111	COL4A3, AIFM	192	812	13528	1.47511289	1
0.11367997	COL4A3, AIFM	192	815	13528	1.46968303	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.01115055	P2RX7, TLR2,	178	12	12983	18.2345506	0.98807607
0.34328414	P2RX7, TLR2,	192	86	13528	2.45784884	1
0.51502214	P2RX7, CCL2C	192	193	13528	1.46027634	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.07894687	PAR6A, CXCR4	192	71	13528	3.96948357	1
0.12309695	CXCR4, OPRK	192	43	13528	4.91569767	1
0.2180693	CXCR4, OPRK	192	62	13528	3.40927419	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.13928569	COL4A3, KLK8	192	719	13528	1.4699235	1
0.1447088	COL4A3, KLK8	192	724	13528	1.4597721	1
0.1448635	COL4A3, AIFM	192	602	13528	1.52152547	1
0.15591847	COL4A3, AIFM	192	611	13528	1.49911348	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.14750157	IRAK2, LYN, C	192	94	13528	2.99822695	1
0.16690159	IRAK2, LYN, T	192	52	13528	4.06490385	1
0.18714203	IRAK2, LYN, T	192	56	13528	3.77455357	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.06749337	LYN, PIM1, FE	242	34	19235	7.01324745	1
0.12552251	LYN, PIM1, FE	242	49	19235	4.86633496	1
0.56951799	LYN, PIM1, M	242	236	19235	1.34717748	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.13384223	IRAK2, STK31	178	430	12983	1.69623726	1
0.18571069	IRAK2, STK31	220	354	16659	1.71124807	1

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0.2049028	STK31, SBK1,	242	381	19235	1.66894427	1
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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.1511761	PACSIN1, NO	220	213	16659	2.13303457	1
0.17019004	PACSIN1, NO	126	213	9079	2.02973396	1
0.18506945	PACSIN1, LYN	242	177	19113	2.23105477	1
0.26890714	PACSIN1, NO	242	210	19235	1.8924636	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.06664912	CD83, CD4, C	192	30	13528	7.04583333	1
0.0923871	CD83, TNFSF	192	76	13528	3.70833333	1
0.1575537	CD83, TNFSF	192	97	13528	2.90549828	1
0.18887927	CD83, TNFSF	192	106	13528	2.65880503	1
0.20582353	CD83, UNC13	192	166	13528	2.12223896	1
0.2069263	CD83, TNFSF	192	111	13528	2.53903904	1
0.22906725	CD83, TNFSF	192	117	13528	2.40883191	1
0.23359167	CD83, UNC13	192	175	13528	2.01309524	1
0.34783668	CD83, TNFSF	192	148	13528	1.90427928	1
0.46497398	CD83, CD4, C	242	124	19113	1.91079046	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.09159329	LRRC4, FSIP2,	242	135	19113	2.9251607	1
0.11973406	LRRC4, FSIP2,	242	149	19113	2.65031338	1
0.12733847	LRRC4, FSIP2,	242	210	19113	2.25655254	1
0.13821964	FSIP2, TLR2, C	242	102	19113	3.09722897	1
0.16476354	LRRC4, FSIP2,	242	231	19113	2.0514114	1
0.18372465	FSIP2, TLR2, C	242	117	19113	2.70014834	1
0.18506945	LRRC4, FSIP2,	242	177	19113	2.23105477	1
0.21481998	LRRC4, FSIP2,	242	252	19113	1.88046045	1
0.24876207	FSIP2, TLR2, F	242	76	19113	3.11760548	1
0.31875328	FSIP2, TLR2, F	242	91	19113	2.60371447	1
0.32465991	LRRC4, FSIP2,	242	299	19113	1.58486968	1
0.37761326	LRRC4, FSIP2,	242	319	19113	1.48550481	1
0.37847201	LRRC4, FSIP2,	242	318	19113	1.4901762	1
0.37860487	LRRC4, FSIP2,	242	322	19235	1.48105847	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.14444826	DNAH11, GAI	192	307	13528	1.83604777	1
0.14444826	DNAH11, GAI	192	307	13528	1.83604777	1
0.19599193	GAB2, CXCR4	192	276	13528	1.78698671	1

0.50840537 DNAH11, GAI 192 475 13528 1.18666667 1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.0722403	SPC25, HJURF	188	66	12782	4.12056738	0.99999999
0.20819738	SPC25, HJURF	188	58	12782	3.51669112	1
0.27252035	SPC25, HJURF	188	124	12782	2.19320522	1
0.29243387	SPC25, HJURF	188	129	12782	2.10819726	1
0.3111229	SPC25, HJURF	188	77	12782	2.64893617	1
0.31741988	SPC25, HJURF	192	81	13528	2.6095679	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.20070155	PACSIN1, P2R	192	220	13528	1.92159091	1
0.20070155	PACSIN1, P2R	192	220	13528	1.92159091	1
0.29312478	PACSIN1, P2R	192	381	13528	1.47944007	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.16993124	KLK6, P2RX7,	192	380	13528	1.66875	1
0.18832853	KLK6, LPL, P2	192	512	13528	1.51375326	1
0.21363129	KLK6, SLC12A	192	466	13528	1.5119814	1
0.27778072	KLK6, P2RX7,	192	374	13528	1.50713012	1
0.35667799	KLK6, P2RX7,	192	409	13528	1.37815811	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.1177353	UNC13D, HPS	242	149	19235	2.66723057	1
0.37254978	UNC13D, HPS	188	211	12782	1.61112232	1
0.37254978	UNC13D, HPS	188	211	12782	1.61112232	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.18730959	MEIS3, SIX1, I	220	232	16659	1.95834639	1
0.18928899	MEIS3, SIX1, I	242	242	19235	1.97066457	1
0.20408907	MEIS3, SIX1, I	220	238	16659	1.90897632	1
0.37290016	MEIS3, SIX1, I	220	235	16659	1.61112186	1
0.40637471	MEIS3, SIX1, I	126	235	9079	1.53309693	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.05897623	GSTA1, GGT5	192	28	13528	7.54910714	1
0.17192619	GSTA1, GGT5	192	53	13528	3.98820755	1
0.36537445	GSTA1, GGT5	192	153	13528	1.84204793	1

0.41201257	GSTA1, GGT5	192	166	13528	1.69779116	1
0.48494019	GSTA1, GGT5	192	115	13528	1.83804348	1
0.51534766	GSTA1, GGT5	192	195	13528	1.44529915	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.09814037	P2RX7, LYN, I	192	173	13528	2.44364162	1
0.40857901	P2RX7, LYN, I	192	295	13528	1.43305085	1
0.50616652	P2RX7, LYN, I	192	474	13528	1.18917018	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.2035615	CXCR4, OPRK	178	114	12983	2.55923517	1
0.2035615	CXCR4, OPRK	178	114	12983	2.55923517	1
0.52635054	CXCR4, OPRK	178	203	12983	1.43720596	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.26278138	COL4A3, P2R	192	430	13528	1.4747093	1
0.26880284	COL4A3, P2R	192	433	13528	1.46449192	1
0.27283967	COL4A3, P2R	192	435	13528	1.45775862	1
0.29629607	COL4A3, UNC	192	320	13528	1.54127604	1
0.30544516	COL4A3, UNC	192	321	13528	1.53647456	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.15082849	SIX1, SIX2, PR	192	95	13528	2.96666667	1
0.19225584	SIX1, SIX2, PR	192	57	13528	3.70833333	1
0.21058248	P2RX7, SIX1, I	192	112	13528	2.51636905	1
0.23892811	SIX1, SIX2, PR	192	66	13528	3.20265152	1
0.29656233	SIX1, SIX2, PR	192	77	13528	2.74512987	1
0.42696068	SIX1, LHX5, SI	242	190	19113	1.66272292	1
0.44299895	VEGFA, SIX1,	192	172	13528	1.63856589	1
0.56293859	SIX1, SIX2, PR	192	133	13528	1.58928571	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.26376986	CXCL17, CXCF	192	245	13528	1.7255102	1
0.28118253	CXCL17, CXCF	192	251	13528	1.68426295	1
0.34844122	CXCL17, CXCF	192	211	13528	1.66962875	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.25268129	LEPREL2, TTC	242	138	19113	2.2892562	1

0.29706997	LEPREL2, TTC	242	151	19113	2.09216792	1
0.29706997	LEPREL2, TTC	242	151	19113	2.09216792	1
0.32671898	LEPREL2, TTC	242	160	19235	1.98708678	1
0.346404	LEPREL2, TTC	242	97	19113	2.44265996	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.16995129	COMP, VEGF,	192	206	13528	2.05218447	1
0.38306365	COMP, VEGF,	192	354	13528	1.39324388	1
0.39335473	COMP, VEGF,	192	359	13528	1.37383937	1
0.4016651	COMP, VEGF,	192	360	13528	1.37002315	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.2546388	ALDOC, ENO2	192	69	13528	3.0634058	1
0.26512651	ALDOC, ENO2	192	71	13528	2.97711268	1
0.31741988	ALDOC, ENO2	192	81	13528	2.6095679	1
0.33813382	ALDOC, ENO2	192	85	13528	2.48676471	1
0.4570992	ALDOC, ENO2	192	109	13528	1.93922018	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.26866775	SPC25, PIM1,	192	370	13528	1.52342342	1
0.36823133	SPC25, PIM1,	192	414	13528	1.36151369	1
0.40410642	SPC25, PIM1,	192	565	13528	1.24705015	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.28787508	PDK1, ATF3, /	192	192	13528	1.83485243	1
0.36537445	PDK1, ATF3, /	192	153	13528	1.84204793	1
0.38323063	PDK1, ATF3, /	192	222	13528	1.5868994	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.30700584	LPL, GGT5, DI	192	79	13528	2.67563291	1
0.37300639	LPL, GGT5, KY	192	155	13528	1.81827957	1
0.37300639	LPL, GGT5, KY	192	155	13528	1.81827957	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.12781492	SLC16A3, SLC	192	44	13528	4.80397727	1
0.32850231	SLC16A3, SLC	192	143	13528	1.97086247	1
0.61754907	SLC16A3, SLC	192	147	13528	1.43792517	1
0.62124376	SLC16A3, SLC	192	148	13528	1.42820946	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.16443996	RARRES1, TSF	242	4911	19113	1.12574908	1
0.17912165	RARRES1, TSF	242	4973	19235	1.11881017	1
0.71052227	RARRES1, TSF	188	5485	12782	0.96684963	1
0.81476781	RARRES1, TSF	188	5297	12782	0.93698762	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.19752695	SPC25, SKA1,	242	183	19235	2.17167954	1
0.23782262	PARD6A, SPC	242	264	19235	1.80644252	1
0.37739233	SPC25, SKA1,	192	220	13528	1.60132576	1
0.37739233	SPC25, SKA1,	192	220	13528	1.60132576	1
0.38941182	SPC25, SKA1,	192	224	13528	1.57273065	1
0.40782859	SPC25, SKA1,	192	229	13528	1.53839156	1
0.40857901	PARD6A, SPC	192	295	13528	1.43305085	1
0.68671005	SPC25, SKA1,	192	329	13528	1.07079534	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.33728818	P2RX7, LYN, C	192	466	13528	1.36078326	1
0.377958	P2RX7, LYN, C	192	485	13528	1.30747423	1
0.377958	P2RX7, LYN, C	192	485	13528	1.30747423	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.13737493	LYN, CD4, CD	192	46	13528	4.5951087	1
0.19245565	P2RX7, LYN, C	192	107	13528	2.63395639	1
0.35865642	P2RX7, LYN, C	192	89	13528	2.375	1
0.39896446	P2RX7, LYN, C	192	97	13528	2.17912371	1
0.41378173	P2RX7, LYN, C	192	100	13528	2.11375	1
0.41378173	P2RX7, LYN, C	192	100	13528	2.11375	1
0.64259814	P2RX7, LYN, C	192	233	13528	1.20958512	1
0.67057664	P2RX7, LYN, C	192	243	13528	1.15980796	1
0.74461964	P2RX7, LYN, C	192	187	13528	1.13034759	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.32223798	LRRC4, TLR2,	220	88	16659	2.58145661	1
0.3424313	LRRC4, TLR2,	126	88	9079	2.45643939	1
0.53942815	LRRC4, TLR2,	220	213	16659	1.42202305	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.34181885	DAPP1, LYN, I	242	96	19113	2.46810434	1
0.4062012	DAPP1, LYN, I	242	111	19235	2.14820192	1
0.42997035	DAPP1, LYN, I	220	111	16659	2.0465602	1
0.45385594	DAPP1, LYN, I	126	111	9079	1.94744745	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.34916234	DAPP1, GAB2	242	237	19113	1.66623078	1
0.37472988	DAPP1, GAB2	220	303	16659	1.49945995	1
0.49972174	DAPP1, GAB2	220	277	16659	1.36683623	1
0.53302337	DAPP1, GAB2	126	277	9079	1.3006418	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.0790771	FBLN2, COMF	242	37	19113	6.40373018	1
0.24438478	FBLN2, COMF	220	72	16659	3.15511364	1
0.36053938	FBLN2, COMF	220	96	16659	2.36633523	1
0.36053938	FBLN2, COMF	220	96	16659	2.36633523	1
0.38222107	FBLN2, COMF	126	96	9079	2.25173611	1
0.72671476	FBLN2, COMF	220	194	16659	1.17097001	1
0.74387325	FBLN2, COMF	220	293	16659	1.03375737	1
0.74459547	FBLN2, COMF	220	201	16659	1.13018996	1
0.76885049	FBLN2, COMF	126	201	9079	1.07545605	1
0.78620546	FBLN2, COMF	242	230	19235	1.03674093	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.23370143	CXCR4, VEGF,	192	65	13528	3.25192308	1
0.28085711	CXCR4, VEGF,	192	74	13528	2.85641892	1
0.53789385	CXCR4, VEGF,	192	127	13528	1.66437008	1
0.60381368	CXCR4, VEGF,	192	220	13528	1.28106061	1
0.73111753	DNAH11, CXCR	192	267	13528	1.05555556	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.32261379	COL4A3, AIFM	192	82	13528	2.5777439	1
0.34328414	COL4A3, AIFM	192	86	13528	2.45784884	1
0.85867687	COL4A3, AIFM	192	337	13528	0.83630069	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.36527455	LYN, LMTK3, I	220	97	16659	2.34194002	1
0.46100606	LYN, LMTK3, I	220	118	16659	1.92515408	1

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0.48566227	LYN, LMTK3,	126	118	9079	1.8319209	1
0.6644941	LYN, LMTK3,	178	166	12983	1.31816028	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.36920254	DAPP1, PTPR	192	154	13528	1.83008658	1
0.41586153	DAPP1, PTPR	178	104	12983	2.1039866	1
0.66124796	DAPP1, PTPR	178	165	12983	1.32614913	1
0.66368154	DAPP1, PTPR	178	249	12983	1.17169803	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.43292622	P2RX7, CXCR	192	372	13528	1.32582885	1
0.53969722	P2RX7, CXCR	192	345	13528	1.22536232	1
0.57026987	P2RX7, CXCR	192	357	13528	1.18417367	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.4150105	EFHD1, CYP2	188	419	12782	1.29812624	1
0.51864904	EFHD1, CYP2	188	394	12782	1.20793282	1
0.6470545	PDK1, EFHD1	188	595	12782	1.02841051	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.42841684	IRAK2, PIM1,	192	103	13528	2.05218447	1
0.51188514	IRAK2, PIM1,	192	121	13528	1.74690083	1
0.63930678	IRAK2, PIM1,	192	153	13528	1.38153595	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.37447483	GLIS3, BMP3,	192	685	13528	1.23430657	1
0.39265466	GLIS3, BMP3,	192	695	13528	1.21654676	1
0.41884197	GLIS3, BMP3,	192	371	13528	1.32940252	1
0.51287303	GLIS3, BMP3,	192	477	13528	1.18169113	1
0.52176669	GLIS3, BMP3,	192	481	13528	1.17186417	1
0.56095604	GLIS3, BMP3,	192	644	13528	1.0940735	1
0.5797566	GLIS3, BMP3,	192	654	13528	1.07734455	1
0.68896484	GLIS3, BMP3,	192	564	13528	0.99940898	1
0.71820819	GLIS3, BMP3,	192	581	13528	0.97016638	1
0.78371594	GLIS3, BMP3,	192	624	13528	0.90331197	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.50159618	LPL, AGPAT9,	192	190	13528	1.48333333	1

0.53754359	LPL, AGPAT9,	192	200	13528	1.40916667	1
0.67011221	LPL, AGPAT9,	192	162	13528	1.30478395	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.15464418	DNAH11, PDK1,	242	962	19113	1.39568478	1
0.49719803	DNAH11, PDK1,	242	1326	19235	1.07896115	1
0.53246528	PDK1, DNAH11,	178	1612	12983	1.04068155	1
0.54484315	PDK1, DNAH11,	242	1686	19235	1.03715087	1
0.64210261	PDK1, DNAH11,	178	1477	12983	0.98765338	1
0.66575706	PDK1, DNAH11,	178	1497	12983	0.97445828	1
0.67016322	PDK1, DNAH11,	178	1577	12983	0.971276	1
0.69672664	PDK1, DNAH11,	178	1601	12983	0.95671596	1
0.70248952	PDK1, DNAH11,	178	1836	12983	0.95344055	1
0.70248952	PDK1, DNAH11,	178	1836	12983	0.95344055	1
0.70812105	DNAH11, STK11,	178	1918	12983	0.95070649	1
0.79245521	RBPMS2, DNAAF1,	178	2245	12983	0.90969695	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.46179946	P2RX7, CXCR4,	192	110	13528	1.92159091	1
0.4985275	P2RX7, CXCR4,	192	118	13528	1.79131356	1
0.52527653	P2RX7, CXCR4,	192	196	13528	1.43792517	1
0.55603325	P2RX7, CXCR4,	192	205	13528	1.37479675	1
0.62503374	P2RX7, CXCR4,	192	227	13528	1.24155653	1
0.73374734	P2RX7, CXCR4,	192	183	13528	1.15505464	1
0.74727794	P2RX7, CXCR4,	192	188	13528	1.12433511	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.44914331	RASGEF1B, RASGEF1B,	242	121	19235	1.97066457	1
0.61675345	RASGEF1B, RASGEF1B,	178	152	12983	1.43956978	1
0.87435761	RASGEF1B, RASGEF1B,	192	252	13528	0.83878968	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.61300329	P2RX7, CXCR4,	192	223	13528	1.26382661	1
0.63680783	P2RX7, CXCR4,	192	231	13528	1.22005772	1
0.66235373	P2RX7, CXCR4,	192	240	13528	1.17430556	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.62039336	CYP24A1, MMR1,	178	4140	12983	0.9866037	1
0.64286803	CYP24A1, MMR1,	178	4241	12983	0.98030595	1

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0.65268333	CYP24A1, MN	178	4179	12983	0.97739635	1
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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.59396809	SPRR3, NDRG	242	243	19113	1.30007142	1
0.60228987	SPRR3, NDRG	242	246	19113	1.28421689	1
0.75472677	SPRR3, NDRG	242	214	19113	1.10718699	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.51502214	LYN, CXCR4, \	192	193	13528	1.46027634	1
0.69258131	CXCR4, VEGF,	192	169	13528	1.25073964	1
0.75767597	CXCR4, VEGF,	192	192	13528	1.10091146	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.63591667	P2RX7, GPM€	178	398	12983	1.09957089	1
0.66600138	P2RX7, GPM€	178	412	12983	1.06220683	1
0.66808792	P2RX7, GPM€	178	413	12983	1.0596349	1
0.77612672	P2RX7, GPM€	178	386	12983	0.94479537	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.50564161	ZNF28, ZNF70	242	134	19113	1.76819415	1
0.59125428	ZNF28, ZNF70	242	157	19113	1.50915934	1
0.60537191	ZNF28, ZNF30	242	332	19113	1.18944787	1
0.61859542	ZNF28, ZNF30	242	252	19113	1.2536403	1
0.67538479	SALL4, ZNF28	242	451	19113	1.05072291	1
0.68967556	ZNF28, ZNF30	220	355	16659	1.06651729	1
0.71767076	ZNF28, ZNF30	242	293	19113	1.07821623	1
0.72327737	ZNF28, ZNF70	242	201	19113	1.1787961	1
0.72627071	ZNF28, ZNF30	126	355	9079	1.01486698	1
0.74020197	SALL4, ZNF28	242	488	19113	0.97105744	1
0.77427943	ZNF28, ZNF30	242	417	19113	0.94699447	1
0.79566606	ZNF28, ZNF30	242	334	19113	0.94586035	1
0.85612536	ZNF28, ZNF30	242	376	19113	0.84020573	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.53043741	GLIS3, SALL4,	242	622	19113	1.14278786	1
0.57371089	GLIS3, SALL4,	220	621	16659	1.09743083	1
0.67580947	GLIS3, SALL4,	242	538	19113	1.02761222	1
0.68269844	GLIS3, SALL4,	242	542	19113	1.02002836	1
0.78244586	SALL4, KLF8, i	242	608	19113	0.9093016	1

0.81440678	GLIS3, SALL4,	220	784	16659	0.869266	1
0.82807725	GLIS3, SALL4,	220	797	16659	0.85508726	1
0.86852024	GLIS3, SALL4,	126	797	9079	0.81367629	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.61754907	COL4A4, KLK8	192	147	13528	1.43792517	1
0.63930678	COL4A4, KLK8	192	153	13528	1.38153595	1
0.93509471	COL4A4, KLK8	192	309	13528	0.68406149	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.62078973	GLIS3, FOXA3	192	1773	13528	0.99349032	1
0.66566107	GLIS3, FOXA3	192	1813	13528	0.97157106	1
0.93925996	GLIS3, FOXA3	192	2601	13528	0.8126682	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.3763375	RND2, RND3,	220	167	16659	1.81371802	1
0.72195247	RND2, RND3,	242	295	19113	1.07090629	1
0.7835982	RND2, RND3,	242	329	19235	0.96636439	1
0.88648968	RND2, RND3,	178	372	12983	0.78428174	1
0.89692504	RND2, RND3,	178	382	12983	0.76375081	1
0.89692504	RND2, RND3,	178	382	12983	0.76375081	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.52179137	PROM1, RIM2	242	139	19235	1.7154706	1
0.81261434	PROM1, RIM2	192	216	13528	0.97858796	1
0.81261434	PROM1, RIM2	192	216	13528	0.97858796	1
0.99569105	PROM1, RIM2	242	595	19235	0.400757	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.59100962	ATF3, RELB, A	178	145	12983	1.50906625	1
0.8091592	ATF3, RELB, A	178	316	12983	0.92326838	1
0.96066297	ATF3, RELB, A	178	363	12983	0.60279506	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.42788257	GPR19, CXCR4	242	116	19235	2.05560701	1
0.99664446	GPR19, CXCR4	220	726	16659	0.41720511	1
0.99668196	GPR19, CXCR4	220	727	16659	0.41663124	1
0.99894891	GPR19, CXCR4	116	686	7396	0.37177038	1

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PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.75753939	AGPAT9, CD4	188	269	12782	1.01099423	1
0.78913096	AGPAT9, CD4	188	284	12782	0.95759664	1
0.88682303	AGPAT9, CD4	188	347	12782	0.78373904	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.70452031	EFHD1, KLK8,	192	256	13528	1.10091146	1
0.8064082	KLK8, CXCR4,	192	213	13528	0.99237089	1
0.86404166	KLK8, CXCR4,	192	245	13528	0.8627551	1
0.87992559	KLK8, CXCR4,	192	256	13528	0.82568359	1
0.88262324	P2RX7, KLK8,	192	356	13528	0.79166667	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.81301719	CXCR4, BIK, B	192	395	13528	0.89187764	1
0.81398097	BIK, BIRC3, C	192	308	13528	0.91504329	1
0.81398097	BIK, BIRC3, C	192	308	13528	0.91504329	1
0.82237359	CXCR4, VEGF,	192	487	13528	0.86806982	1
0.82237359	CXCR4, VEGF,	192	487	13528	0.86806982	1
0.8916549	CXCR4, BIK, B	192	458	13528	0.76919578	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.84553851	P2RX7, ALDO	192	505	13528	0.83712871	1
0.84553851	P2RX7, ALDO	192	505	13528	0.83712871	1
0.87983059	LPL, P2RX7, H	192	710	13528	0.79389671	1
0.9130445	P2RX7, HJURI	192	665	13528	0.74166667	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.8364847	EXOC4, SIX2,	192	411	13528	0.85715734	1
0.84060176	EXOC4, SIX2,	192	414	13528	0.85094605	1
0.90192392	EXOC4, SIX2,	192	374	13528	0.75356506	1
0.99524318	LYN, EXOC4, :	192	762	13528	0.46232502	1
0.99560498	LYN, EXOC4, :	192	769	13528	0.4581166	1
0.99569735	LYN, EXOC4, :	192	882	13528	0.47930839	1
PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.81598163	SIX1, ANKRD1	188	210	12782	0.9712766	1
0.98915621	SIX1, TRIM16	188	555	12782	0.49001342	1

0.99983995 SIX1, TRIM16 188 882 12782 0.30834178 1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.93338341	CD83, MYBPC	220	330	16659	0.68838843	1
0.94529096	CD83, MYBPC	126	330	9079	0.65505051	1
0.96254985	LRRC4, CD83,	220	501	16659	0.60457267	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.97498952	MAFF, GLIS3,	242	2026	19235	0.70617102	1
0.98960222	MAFF, GLIS3,	242	2071	19235	0.65244761	1
0.99889605	MAFF, GLIS3,	192	2101	13528	0.57010551	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.96310286	GLIS3, SALL4,	192	356	13528	0.59375	1
0.96570774	GLIS3, SALL4,	192	362	13528	0.58390884	1
0.98980214	GLIS3, SALL4,	192	459	13528	0.46051198	1
0.99428184	GLIS3, SALL4,	192	504	13528	0.41939484	1
0.99484543	GLIS3, SALL4,	192	512	13528	0.4128418	1
0.99529382	GLIS3, SALL4,	192	519	13528	0.4072736	1
0.99673614	GLIS3, SALL4,	192	547	13528	0.38642596	1
0.99728496	GLIS3, SALL4,	192	561	13528	0.37678253	1
0.99768264	GLIS3, SALL4,	192	573	13528	0.3688918	1
0.9983947	GLIS3, SALL4,	192	734	13528	0.38396912	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.98857161	UBA7, TNFAIF	242	509	19235	0.4684684	1
0.99186897	P2RX7, UBA7	192	600	13528	0.46972222	1
0.99215135	P2RX7, UBA7	192	603	13528	0.4673853	1
0.99373256	P2RX7, UBA7	192	622	13528	0.45310825	1
0.99771307	UBA7, TNFAIF	192	574	13528	0.36824913	1
0.99771307	UBA7, TNFAIF	192	574	13528	0.36824913	1
0.99820527	P2RX7, UBA7	192	725	13528	0.38873563	1
0.99910829	P2RX7, UBA7	192	781	13528	0.36086214	1

PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichm	Bonferroni
0.99898249	KLK6, PDK1, C	188	1856	12782	0.54948299	1
0.99976976	PDK1, KLK6, C	188	1820	12782	0.4856383	1
0.99987284	PDK1, KLK6, /	188	1779	12782	0.4586129	1

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6	Benjamini	FDR
7	0.15142537	1.15081555
8	0.14321289	1.62110583
9	0.54384063	15.2949106
10		
11		
12		
13	Benjamini	FDR
14	0.27018618	3.2268808
15	0.27018618	3.2268808
16	0.62992237	23.5974467
17		
18		
19		
20	Benjamini	FDR
21	0.3402557	3.54166534
22	0.2839816	3.18790156
23	0.9627076	33.4906988
24		
25		
26		
27		
28	Benjamini	FDR
29	0.59439666	9.90592693
30	0.58330549	11.8822727
31	0.58330549	11.8822727
32	0.58046059	13.9821977
33	0.58046059	13.9821977
34	0.58046059	13.9821977
35	0.58046059	13.9821977
36	0.58046059	13.9821977
37		
38		
39		
40	Benjamini	FDR
41	0.30588526	1.04965065
42	0.53418497	16.1910446
43	0.56444784	21.35305
44	0.66900836	19.302949
45	0.66542606	29.3424787
46	0.68773733	33.6510572
47		
48		
49		
50		
51	Benjamini	FDR
52	0.50537367	9.09031456
53	0.48566109	11.1045424
54	0.54721393	14.5106256
55	0.62529782	22.5524098
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0.711074 41.9032583

Benjamini FDR

0.29250715 3.1911894

0.62529782 22.5524098

0.62329705 25.5357774

0.79069663 54.9808224

Benjamini FDR

0.60976278 17.798273

0.61757592 24.4434529

0.61914489 27.5084474

Benjamini FDR

0.51715767 10.0710458

0.64908943 30.2250596

0.66265054 33.4614639

0.66265054 33.4614639

Benjamini FDR

0.8578659 15.8694168

0.57828123 16.0266242

0.5024012 16.6015912

0.57188153 23.6386899

0.57957257 22.2841569

0.56680375 32.2327994

0.98611591 45.4530654

0.80051274 57.3555302

0.85257628 75.7570115

0.84905187 76.9199394

Benjamini FDR

0.66290849 31.9567769

0.69612316 38.3550877

0.79357507 54.557233

Benjamini FDR

0.07361365 1.6035445

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3	0.80304836	64.3293874
4	0.79114068	64.9641857
5	0.76146979	70.2408682
6	0.85588562	74.4764627
7		
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10		
11	Benjamini	FDR
12	0.62313838	14.0305414
13	0.47586779	17.5526733
14	0.94670708	96.9243019
15		
16		

17		
18	Benjamini	FDR
19	0.62080828	23.8652396
20	0.63172597	26.8083415
21	0.6643017	32.824458
22	0.7713966	50.6861608
23	0.7713966	50.6861608
24	0.85242753	68.5179224
25	0.85243911	69.7494044
26	0.91725989	86.7913287
27	0.95387781	97.4888858
28		
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31		
32		
33	Benjamini	FDR
34	0.60883257	23.2538859
35	0.60883257	23.2538859
36	0.70799932	45.525889
37	0.99156558	99.7664414
38		
39		

40		
41	Benjamini	FDR
42	0.8064759	58.2005497
43	0.83585352	63.115129
44	0.83585352	63.115129
45	0.90114172	83.1921636
46		
47		

48		
49		
50	Benjamini	FDR
51	0.70518472	51.4713876
52	0.81935088	64.1327505
53	0.99884022	69.8019325
54	0.9662874	69.1372365
55	0.99825935	74.0905088
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0.98097771 77.430885
0.91521942 86.4732719

Benjamini FDR
0.90578012 84.1968136
0.91728878 86.0914712
0.9196757 86.7623598

Benjamini FDR
0.58763305 14.4539924
0.98131334 99.91292
0.99218323 99.9994582

Benjamini FDR
0.87349881 74.7917527
0.92164161 88.9317656
0.9589066 98.3785895

Benjamini FDR
0.93758825 91.9001526
0.93694986 92.7141471
0.93523222 92.7361979
0.93814824 94.1591872

Benjamini FDR
0.9367698 93.1026948
0.94389222 95.3101201
0.95304472 96.8941761

Benjamini FDR
0.71015571 61.0361205
0.81940214 83.6205318
0.96382443 99.9988446

Benjamini FDR
0.91521942 86.4732719
0.99890893 94.8012279

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3	0.83936089	95.4620674
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7	Benjamini	FDR
8	0.99706275	90.5480473
9	0.99592742	88.1761047
10	0.99870263	95.8386727
11	0.8698532	98.5369872
12		
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14		
15	Benjamini	FDR
16	0.85242753	68.5179224
17	0.89227498	80.2952979
18	0.9383585	94.3459244
19	0.95189953	97.0035477
20	0.95681736	97.8963315
21	0.95648714	97.9447467
22	0.96296784	98.7211724
23	0.96471186	98.841281
24	0.9816613	99.9225011
25	0.99999337	99.9939713
26		
27		
28		
29		
30		
31	Benjamini	FDR
32	0.99846705	77.5160556
33	0.99907923	86.2101259
34	0.99911215	87.9490225
35	0.9985306	90.0833119
36	0.99861073	93.9006121
37	0.99893786	95.7307022
38	0.99870263	95.8386727
39	0.9994868	97.6648455
40	0.99976635	98.8246524
41	0.99996285	99.7427625
42	0.99995994	99.7753112
43	0.99997661	99.9368075
44	0.99997038	99.9381486
45	0.92365414	99.836723
46		
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52	Benjamini	FDR
53	0.93852281	92.6768689
54	0.93852281	92.6768689
55	0.95399107	97.4146883
56		
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0.99226442 99.9993201

Benjamini FDR

0.76759533 62.3155483

0.86952715 95.2085671

0.9062903 98.4094328

0.91795912 98.8916736

0.9217941 99.2177229

0.97799272 99.8336492

Benjamini FDR

0.95407592 97.6570654

0.95407592 97.6570654

0.97457776 99.7010912

Benjamini FDR

0.94394668 95.5878595

0.95274142 96.9692729

0.95688234 98.2172955

0.97297821 99.5716355

0.98267648 99.9383455

Benjamini FDR

0.81080105 81.5399636

0.95509402 99.7680328

0.95509402 99.7680328

Benjamini FDR

0.99842812 94.9462297

0.85230039 94.1010258

0.99875287 96.2570699

0.99993766 99.8788819

0.99984792 99.7441478

Benjamini FDR

0.83107367 63.8887079

0.94138984 95.7622178

0.98359819 99.9509182

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3	0.98514112	99.9863398
4	0.99054952	99.9985148
5	0.99205995	99.9994642
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10	Benjamini	FDR
11	0.89738444	82.2869347
12	0.98475672	99.9849399
13	0.99218302	99.9992663
14		
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17	Benjamini	FDR
18	0.95005356	95.7947705
19	0.95005356	95.7947705
20	0.99836633	99.9969693
21		
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23		
24	Benjamini	FDR
25	0.97213999	99.3954936
26	0.97120104	99.4731121
27	0.97226057	99.5197906
28	0.97455968	99.7227846
29	0.97613595	99.7773699
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34	Benjamini	FDR
35	0.93544445	93.5401221
36	0.95345327	97.2058456
37	0.95690424	98.0978752
38	0.96592666	98.9693043
39	0.97405203	99.724537
40	0.9999883	99.9824885
41	0.98721023	99.9944858
42	0.99438249	99.9999052
43		
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47	Benjamini	FDR
48	0.97111911	99.4089328
49	0.97170735	99.6042185
50	0.98139366	99.9236961
51		
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53		
54	Benjamini	FDR
55	0.9997361	98.9163838
56		
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0.99993626 99.5814633
0.99993626 99.5814633
0.89918179 99.51839
0.99996832 99.8648625

Benjamini FDR
0.94240846 95.5896453
0.98362171 99.9694367
0.98416195 99.9769439
0.98492733 99.9817018

Benjamini FDR
0.97066076 99.2733309
0.97099984 99.4269204
0.97799272 99.8336492
0.98033903 99.9007415
0.98828827 99.9964117

Benjamini FDR
0.97185729 99.4714786
0.98388423 99.9544921
0.98478952 99.9829134

Benjamini FDR
0.97315315 99.6616362
0.98359819 99.9509182
0.98330173 99.969575

Benjamini FDR
0.97555087 99.7856056
0.98350067 99.9599248
0.98350067 99.9599248

Benjamini FDR
0.92715951 89.8884107
0.97942111 99.8735548
0.99667616 99.9999899
0.99672698 99.9999914

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6	Benjamini	FDR
7	0.99894081	93.8637989
8	0.860213	93.0211495
9	0.99508716	99.9999902
10		
11	0.997328	100
12		
13		

14	Benjamini	FDR
15	0.84234097	94.8601731
16	0.86039325	97.4345691
17	0.98377361	99.964372
18	0.98377361	99.964372
19	0.983985	99.9743001
20	0.9849184	99.9846165
21	0.98475672	99.9849399
22	0.99843795	99.9999996
23		
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28	Benjamini	FDR
29	0.9805572	99.898595
30	0.98354001	99.9649105
31	0.98354001	99.9649105
32		
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34		

35	Benjamini	FDR
36	0.9390253	91.593523
37	0.95234068	97.217405
38	0.98276486	99.9414468
39	0.98469086	99.9802676
40	0.98518762	99.9870124
41	0.98518762	99.9870124
42	0.99740717	99.9999967
43	0.99810579	99.9999992
44	0.99933847	100
45		
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47		
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49	Benjamini	FDR
50	0.9999378	99.629479
51	0.99994949	99.1750101
52	0.99999743	99.9985741
53		
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Benjamini	FDR
0.99997193	99.8493594
0.93155562	99.9115242
0.99996855	99.9693237
0.99986656	99.9014531

Benjamini	FDR
0.99996209	99.8734558
0.99991337	99.8838699
0.99999317	99.9953123
0.99987478	99.9835833

Benjamini	FDR
0.99859519	72.1902054
0.99957048	98.2279861
0.99995979	99.8395964
0.99995979	99.8395964
0.99992302	99.5961559
0.99999999	99.9999992
0.99999999	99.9999997
0.99999999	99.9999997
0.99999832	99.9999948
0.99306414	99.9999999

Benjamini	FDR
0.96384972	98.8440584
0.97224451	99.6012055
0.99304531	99.9997588
0.99622554	99.9999817
0.99918782	100

Benjamini	FDR
0.97861262	99.8536343
0.98131334	99.91292
0.99994154	100

Benjamini	FDR
0.99994684	99.855869
0.99998317	99.9862951

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2		
3	0.99983626	99.9504075
4	0.99840135	99.9999751
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8	Benjamini	FDR
9	0.98336124	99.9556502
10	0.99505298	99.9438551
11	0.99860964	99.9999715
12	0.99852879	99.9999742
13		
14		
15		
16		
17	Benjamini	FDR
18	0.98677622	99.9925543
19	0.99308187	99.9997741
20	0.99484237	99.9999286
21		
22		
23		
24	Benjamini	FDR
25	0.96633245	99.9068133
26	0.98207166	99.9926356
27	0.99306664	99.9998702
28		
29		
30		
31	Benjamini	FDR
32	0.98651471	99.9914975
33	0.9923199	99.9993964
34	0.99732352	99.9999962
35		
36		
37		
38		
39	Benjamini	FDR
40	0.9834709	99.9614688
41	0.98434873	99.976494
42	0.98528122	99.9887685
43	0.99226779	99.9994165
44	0.99228278	99.9995715
45	0.99433621	99.9998977
46	0.99532211	99.9999509
47	0.9984655	99.9999997
48	0.99900051	99.9999999
49	0.99965534	100
50		
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54	Benjamini	FDR
55	0.99184124	99.9991438
56		
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0.99314924 99.9997558
0.9981323 99.9999991

Benjamini FDR
0.9991025 92.645765
0.95246399 99.9906155
0.99808202 99.9974708
0.95665717 99.9975496
0.99871055 99.9999387
0.99828066 99.9999764
0.99791015 99.9999803
0.99856357 99.9999939
0.99858374 99.9999953
0.99858374 99.9999953
0.99860254 99.9999964
0.99965184 100

Benjamini FDR
0.98878108 99.9968982
0.99166107 99.999051
0.99249978 99.9996213
0.99404543 99.9998767
0.99684957 99.9999927
0.99921119 100
0.99935906 100

Benjamini FDR
0.93902294 99.9678558
0.99854339 99.9998412
0.99996421 100

Benjamini FDR
0.99650827 99.9999877
0.99727276 99.9999957
0.99796034 99.9999987

Benjamini FDR
0.99847358 99.9998609
0.99858392 99.9999405

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4	0.99868046	99.9999597
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6		
7	Benjamini	FDR
8	0.99999986	99.999917
9	0.99999987	99.9999399
10		
11	0.99999999	100
12		
13		
14	Benjamini	FDR
15	0.99218323	99.9994582
16		
17	0.99849598	99.9999997
18	0.99943449	100
19		
20		
21		
22	Benjamini	FDR
23	0.99870807	99.9999222
24	0.99812237	99.9999766
25	0.99801755	99.9999785
26		
27	0.99953698	99.9999999
28		
29		
30	Benjamini	FDR
31	0.99999805	99.9982346
32	0.99999989	99.999908
33		
34	0.99999985	99.9999467
35	0.99999988	99.9999686
36	0.99999998	99.9999974
37	0.99999998	99.9999951
38	0.99999999	99.9999997
39	0.99999999	99.9999998
40	0.99999999	99.9999998
41	0.99999707	99.9999637
42	0.99999999	99.9999999
43		
44	1	100
45	1	100
46	1	100
47		
48		
49	Benjamini	FDR
50		
51	0.999999	99.9992063
52	0.99999887	99.9995316
53	0.99999998	99.9999975
54	0.99999997	99.9999982
55		
56	1	100
57		
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1		
2		
3	1	100
4	1	100
5		
6	0.99999988	100
7		
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9		

Benjamini	FDR
0.99667616	99.9999899
0.99732352	99.9999962
0.99999778	100

Benjamini	FDR
0.99677232	99.9999912
0.99802867	99.9999989
0.99999832	100

Benjamini	FDR
0.99988183	99.8880939
0.99999999	99.9999998
0.99314186	99.9999999
0.99996817	100
0.99996693	100
0.99996693	100

Benjamini	FDR
0.95661835	99.9952286
0.99981742	100
0.99981742	100
0.99999942	100

Benjamini	FDR
0.99855538	99.9996073
0.99974686	100
0.99999907	100

Benjamini	FDR
0.93546254	99.9464282
1	100
1	100
1	100

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6	Benjamini	FDR
7	0.99597437	99.999999
8	0.99667815	99.999998
9	0.99869481	100
10		
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13	Benjamini	FDR
14	0.99876286	99.999999
15	0.99979554	100
16	0.99995029	100
17	0.99996852	100
18	0.99997093	100
19		
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23	Benjamini	FDR
24	0.99981441	100
25	0.99981424	100
26	0.99981424	100
27	0.99983609	100
28	0.99983609	100
29	0.999979	100
30		
31		
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33		
34	Benjamini	FDR
35	0.99991157	100
36	0.99991157	100
37	0.99996938	100
38	0.99999167	100
39		
40		
41		
42	Benjamini	FDR
43	0.99988891	100
44	0.99989943	100
45	0.99998566	100
46	1	100
47	1	100
48	1	100
49		
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53	Benjamini	FDR
54	0.99693366	100
55	0.99999807	100
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	1	100
Benjamini	FDR	
	1	100
	1	100
	1	100

Benjamini	FDR	
0.99996995		100
0.99999465		100
1		100

Benjamini	FDR	
0.9999998		100
0.99999985		100
1		100
1		100
1		100
1		100
1		100
1		100
1		100
1		100

Benjamini	FDR	
0.99999378		100
1		100
1		100
1		100
1		100
1		100
1		100
1		100

Benjamini	FDR	
1		100
1		100
1		100