Supporting Information

**Supplementary Table 1:** List of 287 genes obtained by Phenolyzer curated seed genes list, ordered according to Phenolyzer weighted score, from the most likely to the least likely associated to the inputted phenotype (for further details on weighted score calculation see *Yang, Robinson and Wang, 2015*)*.* Near to each gene the relative enriched GOID and terms are listed.

|  |  |  |
| --- | --- | --- |
| **­­Gene Name** | **GOID** | **GO Biological processes** |
| *RET* | GO:0035799 | ureter maturation |
| *HNF1B* | GO:0060681 | branch elongation involved in ureteric bud branching |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching |
| GO:1900200 | mesenchymal cell apoptotic process involved in metanephros development |
| GO:0061218 | negative regulation of mesonephros development |
| GO:1900211 | regulation of mesenchymal cell apoptotic process involved in metanephros development |
| GO:1901145 | mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:1900212 | negative regulation of mesenchymal cell apoptotic process involved in metanephros development |
| GO:0072039 | regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:0072040 | negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:0072179 | nephric duct formation |
| GO:0072181 | mesonephric duct formation |
| GO:0061017 | hepatoblast differentiation |
| GO:0061215 | mesonephric nephron development |
| GO:0061206 | mesonephros morphogenesis |
| GO:0061228 | mesonephric nephron morphogenesis |
| GO:0072114 | pronephros morphogenesis |
| GO:0035565 | regulation of pronephros size |
| GO:0039020 | pronephric nephron tubule development |
| GO:0061235 | mesenchymal stem cell maintenance involved in mesonephric nephron morphogenesis |
| GO:1901146 | mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis |
| GO:0061295 | regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis |
| GO:0061296 | negative regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis |
| *ATRX* | GO:1901581 | negative regulation of telomeric RNA transcription from RNA pol II promoter |
| GO:1901582 | positive regulation of telomeric RNA transcription from RNA pol II promoter |
| GO:0035127 | post-embryonic limb morphogenesis |
| GO:0035128 | post-embryonic forelimb morphogenesis |
| GO:0097393 | telomeric repeat-containing RNA transcription |
| GO:0097394 | telomeric repeat-containing RNA transcription by RNA polymerase II |
| GO:1901580 | regulation of telomeric RNA transcription from RNA pol II promoter |
| *PAX2* | GO:0002072 | optic cup morphogenesis involved in camera-type eye development |
| GO:0035799 | ureter maturation |
| GO:1900200 | mesenchymal cell apoptotic process involved in metanephros development |
| GO:1900211 | regulation of mesenchymal cell apoptotic process involved in metanephros development |
| GO:1901145 | mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:1900212 | negative regulation of mesenchymal cell apoptotic process involved in metanephros development |
| GO:0072039 | regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:0072040 | negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis |
| GO:0072179 | nephric duct formation |
| GO:2000594 | positive regulation of metanephric DCT cell differentiation |
| GO:0039017 | pattern specification involved in pronephros development |
| GO:0061360 | optic chiasma development |
| GO:0021633 | optic nerve structural organization |
| GO:0021634 | optic nerve formation |
| GO:0072004 | kidney field specification |
| GO:2000595 | regulation of optic nerve formation |
| GO:1900204 | apoptotic process involved in metanephric collecting duct development |
| GO:0035566 | regulation of metanephros size |
| GO:1900214 | regulation of apoptotic process involved in metanephric collecting duct development |
| GO:0039003 | pronephric field specification |
| GO:0072309 | mesenchymal stem cell maintenance involved in metanephric nephron morphogenesis |
| GO:1900215 | negative regulation of apoptotic process involved in metanephric collecting duct development |
| GO:1901147 | mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis |
| GO:2000597 | positive regulation of optic nerve formation |
| GO:1900205 | apoptotic process involved in metanephric nephron tubule development |
| GO:0072304 | regulation of mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis |
| GO:1900217 | regulation of apoptotic process involved in metanephric nephron tubule development |
| GO:0072305 | negative regulation of mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis |
| GO:1900218 | negative regulation of apoptotic process involved in metanephric nephron tubule development |
| GO:2000592 | regulation of metanephric DCT cell differentiation |
| *FREM2* | - | - |
| *GRIP1* | - | - |
| *FRAS1* | - | - |
| *LHX1* | GO:0097379 | dorsal spinal cord interneuron posterior axon guidance |
| GO:0035846 | oviduct epithelium development |
| GO:0035847 | uterine epithelium development |
| GO:0035849 | nephric duct elongation |
| GO:0035852 | horizontal cell localization |
| *ITGA8* | - | - |
| *BCOR* | GO:0000415 | negative regulation of histone H3-K36 methylation |
| GO:0070171 | negative regulation of tooth mineralization |
| *SALL4* | - | - |
| *EYA1* | GO:0072513 | positive regulation of secondary heart field cardioblast proliferation |
| GO:0071600 | otic vesicle morphogenesis |
| *NAA10* | - | - |
| *MUC1* | - | - |
| *SIX5* | - | - |
| *SIX1* | GO:0060681 | branch elongation involved in ureteric bud branching |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching |
| GO:0072106 | regulation of ureteric bud formation |
| GO:0072107 | positive regulation of ureteric bud formation |
| GO:0072198 | mesenchymal cell proliferation involved in ureter development |
| GO:1905278 | positive regulation of epithelial tube formation |
| GO:0072191 | ureter smooth muscle development |
| GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development |
| GO:0072193 | ureter smooth muscle cell differentiation |
| GO:0072513 | positive regulation of secondary heart field cardioblast proliferation |
| GO:0060681 | branch elongation involved in ureteric bud branching |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching |
| GO:0072106 | regulation of ureteric bud formation |
| GO:0072107 | positive regulation of ureteric bud formation |
| GO:1905278 | positive regulation of epithelial tube formation |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development |
| GO:0072513 | positive regulation of secondary heart field cardioblast proliferation |
| GO:0072198 | mesenchymal cell proliferation involved in ureter development |
| GO:0072191 | ureter smooth muscle development |
| GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development |
| GO:0072193 | ureter smooth muscle cell differentiation |
| *TP63* | GO:0035844 | cloaca development |
| GO:0048807 | female genitalia morphogenesis |
| GO:0060197 | cloacal septation |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development |
| GO:0035844 | cloaca development |
| GO:0048807 | female genitalia morphogenesis |
| GO:0060197 | cloacal septation |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development |
| *BMP4* | GO:0060235 | lens induction in camera-type eye |
| GO:0010159 | specification of animal organ position |
| GO:0060592 | mammary gland formation |
| GO:0060681 | branch elongation involved in ureteric bud branching |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching |
| GO:0061209 | cell proliferation involved in mesonephros development |
| GO:0061218 | negative regulation of mesonephros development |
| GO:0072179 | nephric duct formation |
| GO:0072198 | mesenchymal cell proliferation involved in ureter development |
| GO:0072191 | ureter smooth muscle development |
| GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development |
| GO:0072193 | ureter smooth muscle cell differentiation |
| GO:0090191 | negative regulation of branching involved in ureteric bud morphogenesis |
| GO:0072096 | negative regulation of branch elongation involved in ureteric bud branching |
| GO:0072097 | negative regulation of branch elongation involved in ureteric bud branching by BMP signaling pathway |
| GO:0061150 | renal system segmentation |
| GO:0072200 | negative regulation of mesenchymal cell proliferation involved in ureter development |
| GO:0048391 | intermediate mesoderm formation |
| GO:0072192 | ureter epithelial cell differentiation |
| GO:1901963 | regulation of cell proliferation involved in outflow tract morphogenesis |
| GO:0003134 | endodermal-mesodermal cell signaling involved in heart induction |
| GO:0048392 | intermediate mesodermal cell differentiation |
| GO:0060503 | bud dilation involved in lung branching |
| GO:1901964 | positive regulation of cell proliferation involved in outflow tract morphogenesis |
| GO:0055018 | regulation of cardiac muscle fiber development |
| GO:0003130 | BMP signaling pathway involved in heart induction |
| GO:0055020 | positive regulation of cardiac muscle fiber development |
| GO:0060994 | regulation of transcription from RNA polymerase II promoter involved in kidney development |
| GO:0072099 | anterior/posterior pattern specification involved in ureteric bud development |
| GO:0072100 | specification of ureteric bud anterior/posterior symmetry |
| GO:2000004 | regulation of metanephric S-shaped body morphogenesis |
| GO:2000005 | negative regulation of metanephric S-shaped body morphogenesis |
| GO:2000006 | regulation of metanephric comma-shaped body morphogenesis |
| GO:2000007 | negative regulation of metanephric comma-shaped body morphogenesis |
| GO:0061149 | BMP signaling pathway involved in ureter morphogenesis |
| GO:0061151 | BMP signaling pathway involved in renal system segmentation |
| GO:0061155 | pulmonary artery endothelial tube morphogenesis |
| GO:0061216 | regulation of transcription from RNA polymerase II promoter involved in mesonephros development |
| GO:0071893 | BMP signaling pathway involved in nephric duct formation |
| GO:0072101 | specification of ureteric bud anterior/posterior symmetry by BMP signaling pathway |
| *TBX1* | GO:0060017 | parathyroid gland development |
| GO:0060827 | regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
| GO:0060829 | negative regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
| GO:0060823 | canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
| GO:0021644 | vagus nerve morphogenesis |
| GO:0035981 | tongue muscle cell differentiation |
| GO:2001035 | regulation of tongue muscle cell differentiation |
| GO:2001037 | positive regulation of tongue muscle cell differentiation |
| *FANCD2* | GO:1902298 | cell cycle DNA replication maintenance of fidelity |
| GO:0033600 | negative regulation of mammary gland epithelial cell proliferation |
| GO:1990505 | mitotic DNA replication maintenance of fidelity |
| GO:1990426 | mitotic recombination-dependent replication fork processing |
| *REN* | - | - |
| *FANCA* | GO:1901999 | homogentisate metabolic process |
| GO:1902000 | homogentisate catabolic process |
| *FANCC* | - | - |
| *FANCE* | - | - |
| *FANCB* | GO:1990414 | replication-born double-strand break repair via sister chromatid exchange |
| *CHD7* | GO:0003226 | right ventricular compact myocardium morphogenesis |
| *BRCA2* | GO:1902298 | cell cycle DNA replication maintenance of fidelity |
| GO:0033600 | negative regulation of mammary gland epithelial cell proliferation |
| GO:1990505 | mitotic DNA replication maintenance of fidelity |
| GO:1990426 | mitotic recombination-dependent replication fork processing |
| *BRIP1* | - | - |
| *FANCG* | - | - |
| *FANCM* | GO:0071932 | replication fork reversal |
| *FANCF* | - | - |
| *FANCL* |  - |  - |
| *RAD51C* | GO:0007066 | female meiosis sister chromatid cohesion |
| *PALB2* | - | - |
| *FANCI* | - | - |
| *SIX3* | GO:0060235 | lens induction in camera-type eye |
| GO:0003404 | optic vesicle morphogenesis |
| GO:0009946 | proximal/distal axis specification |
| *DHCR7* | GO:0016132 | brassinosteroid biosynthetic process |
| *SLX4* | GO:0048257 | 3'-flap endonuclease activity |
| *ELN* | - | - |
| *WNT4* | GO:0060129 | thyroid-stimulating hormone-secreting cell differentiation |
| GO:0031945 | positive regulation of glucocorticoid metabolic process |
| GO:0032346 | positive regulation of aldosterone metabolic process |
| GO:2000225 | negative regulation of testosterone biosynthetic process |
| GO:2000019 | negative regulation of male gonad development |
| GO:2000180 | negative regulation of androgen biosynthetic process |
| GO:0031948 | positive regulation of glucocorticoid biosynthetic process |
| GO:0032349 | positive regulation of aldosterone biosynthetic process |
| GO:0061369 | negative regulation of testicular blood vessel morphogenesis |
| GO:2000066 | positive regulation of cortisol biosynthetic process |
| *PORCN* | - | - |
| *PTPN11* | GO:0061582 | intestinal epithelial cell migration |
| GO:0051463 | negative regulation of cortisol secretion |
| *RAI1* | - | - |
| *GLI3* | GO:0007442 | hindgut morphogenesis |
| GO:0061525 | hindgut development |
| GO:0060592 | mammary gland formation |
| GO:0060594 | mammary gland specification |
| GO:0007442 | hindgut morphogenesis |
| GO:0021776 | smoothened signaling pathway involved in spinal cord motor neuron cell fate specification |
| GO:0021775 | smoothened signaling pathway involved in ventral spinal cord interneuron specification |
| GO:0043585 | nose morphogenesis |
| GO:0060873 | anterior semicircular canal development |
| GO:0060875 | lateral semicircular canal development |
| GO:0022012 | subpallium cell proliferation in forebrain |
| GO:0060366 | lambdoid suture morphogenesis |
| GO:0060367 | sagittal suture morphogenesis |
| GO:0022018 | lateral ganglionic eminence cell proliferation |
| *NIPBL* | GO:0120187 | positive regulation of protein localization to chromatin |
| GO:0035261 | external genitalia morphogenesis |
| GO:1905309 | positive regulation of cohesin loading |
| GO:0061780 | mitotic cohesin loading |
| GO:0070550 | rDNA condensation |
| GO:1905405 | regulation of mitotic cohesin loading |
| GO:1905406 | positive regulation of mitotic cohesin loading |
| GO:1990414 | replication-born double-strand break repair via sister chromatid exchange |
| *MKKS* | GO:0051877 |  pigment granule aggregation in cell center |
| *SMARCB1* | GO:1900110 | negative regulation of histone H3-K9 dimethylation |
| GO:1902659 | regulation of glucose mediated signaling pathway |
| GO:1902661 | positive regulation of glucose mediated signaling pathway |
| *ARID1B* | - | - |
| *SMARCA4* | GO:1902659 | regulation of glucose mediated signaling pathway |
| GO:1902661 | positive regulation of glucose mediated signaling pathway |
| *SMARCE1* | - | - |
| *ARID1A* | GO:0002072 | optic cup morphogenesis involved in camera-type eye development |
| *PROKR2* | - | - |
| *NSDHL* | - | - |
| *FGF8* | GO:0090133 | mesendoderm migration |
| GO:0090134 | cell migration involved in mesendoderm migration |
| GO:0060128 | corticotropin hormone secreting cell differentiation |
| GO:0060129 | thyroid-stimulating hormone-secreting cell differentiation |
| GO:0033563 | dorsal/ventral axon guidance |
| GO:0030916 | otic vesicle formation |
| GO:0033563 | dorsal/ventral axon guidance |
| GO:0090133 | mesendoderm migration |
| GO:0090134 | cell migration involved in mesendoderm migration |
| GO:0060128 | corticotropin hormone secreting cell differentiation |
| GO:0060129 | thyroid-stimulating hormone-secreting cell differentiation |
| GO:0033563 | dorsal/ventral axon guidance |
| GO:0071600 | otic vesicle morphogenesis |
| GO:0030916 | otic vesicle formation |
| *COMT* | GO:0031337 | positive regulation of sulfur amino acid metabolic process |
| GO:0050666 | regulation of homocysteine metabolic process |
| GO:0050668 | positive regulation of homocysteine metabolic process |
| *SLC27A4* | GO:0062002 | regulation of all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity |
| GO:0052885 | all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity |
| GO:0001579 | medium-chain fatty acid transport |
| GO:0062003 | negative regulation of all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity |
| *WDR19* | - | - |
| *MCPH1* | - | - |
| *RAD21* | - | - |
| *JAG1* | GO:0061443 | endocardial cushion cell differentiation |
| GO:0061073 | ciliary body morphogenesis |
| GO:0061444 | endocardial cushion cell development |
| *DHCR24* | - | - |
| *STRA6* | GO:0043585 | nose morphogenesis |
| GO:0061143 | alveolar primary septum development |
| GO:0071938 | vitamin A transport |
| GO:0071939 | vitamin A import |
| *FGFR1* | GO:2000830 | positive regulation of parathyroid hormone secretion |
| GO:0021847 | ventricular zone neuroblast division |
| GO:0035607 | fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development |
| GO:1903465 | positive regulation of mitotic cell cycle DNA replication |
| GO:0005007 | fibroblast growth factor-activated receptor activity |
| GO:0035898 | parathyroid hormone secretion |
| *TFAP2A* | GO:0002072 | optic cup morphogenesis involved in camera-type eye development |
| GO:0021622 | oculomotor nerve morphogenesis |
| GO:0003404 | optic vesicle morphogenesis |
| GO:0021623 | oculomotor nerve formation |
| GO:0003409 | optic cup structural organization |
| GO:0003404 | optic vesicle morphogenesis |
| *MKS1* | GO:0003271  | smoothened signaling pathway involved in regulation of secondary heart field cardioblast proliferation |
| *MLXIPL* | - | - |
| *RIPK4* | - | - |
| *FREM1* | - | - |
| *TACR3* | - | - |
| *LIMK1* | - | - |
| *RARB* | - | - |
| *KISS1R* | - | - |
| *GDF6* | - | - |
| *TBX3* | GO:0010159 | specification of animal organ position |
| GO:0060592 | mammary gland formation |
| GO:0060592 | mammary gland formation |
| GO:0010159 | specification of animal organ position |
| GO:0060592 | mammary gland formation |
| GO:0060932 | His-Purkinje system cell differentiation |
| GO:0003167 | atrioventricular bundle cell differentiation |
| *PROK2* | - | - |
| *SEMA3E* | - | - |
| *EVC* | - | - |
| *EVC2* | - | - |
| *KMT2D* | - | - |
| *RFC2* | - | - |
| *ERCC4* | GO:1905768 | negative regulation of double-stranded telomeric DNA binding |
| GO:1901255 | nucleotide-excision repair involved in interstrand cross-link repair |
| *DUSP6* | - | - |
| *GP1BB* | - | - |
| *FGF17* | - | - |
| *SEMA3A* | GO:1903045  | neural crest cell migration involved in sympathetic nervous system development |
| *HS6ST1* | - | - |
| *LEMD3* | - | - |
| *HIRA* | - | - |
| *HMGA2* | GO:2000683 | regulation of cellular response to X-ray |
| GO:0031049 | programmed DNA elimination |
| GO:2000685 | positive regulation of cellular response to X-ray |
| GO:0031052 | chromosome breakage |
| GO:2000683 | regulation of cellular response to X-ray |
| *SALL1* | GO:0061034 | olfactory bulb mitral cell layer development |
| *GTF2I* | - | - |
| *GTF2IRD1* | GO:0014886  |  transition between slow and fast fiber |
| *BAZ1B* | - | - |
| *FLRT3* | GO:0003345 | proepicarduspdium cell migration involved in pericardium morphogenesis |
| *ARVCF* | - | - |
| *WDR11* | - | - |
| *PAX1* | GO:0060017  |  parathyroid gland development |
| *IL17RD* | - | - |
| *SOX10* | - | - |
| *NSMF* | - | - |
| *SPRY4* | - | - |
| *MEOX1* | - | - |
| *CLIP2* | - | - |
| *HESX1* | GO:0030916 | otic vesicle formation |
| GO:0071600 | otic vesicle morphogenesis |
| *TBL2* | - | - |
| *KDM6A* | - | - |
| *FLII* | - | - |
| *GDF3* | - | - |
| *PIK3CA* | - | - |
| *RPL26* | GO:1904803 | regulation of translation involved in cellular response to UV |
| GO:1902167 | positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator |
| GO:1902255 | positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator |
| *ROBO2* | GO:0050925 | negative regulation of negative chemotaxis |
| *TXNL4A* | - | - |
| *KCTD1* | - | - |
| *RAB40AL* | - | - |
| *NOTCH2* | GO:0035622 | intrahepatic bile duct development |
| GO:0061073 | ciliary body morphogenesis |
| *FAT4* | - | - |
| *PUF60* | - | - |
| *WNT3* | GO:1905474 | canonical Wnt signaling pathway involved in stem cell proliferation |
| *FGFR2* | GO:0035604 | fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow |
| GO:0035603 | fibroblast growth factor receptor signaling pathway involved in hemopoiesis |
| GO:0021847 | ventricular zone neuroblast division |
| GO:0035602 | fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptotic process in bone marrow cell |
| GO:0035607 | fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development |
| GO:0005007 | fibroblast growth factor-activated receptor activity |
| GO:0060592 | mammary gland formation |
| GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis |
| GO:0060915 | mesenchymal cell differentiation involved in lung development |
| GO:0060594 | mammary gland specification |
| GO:0060615 | mammary gland bud formation |
| GO:0060667 | branch elongation involved in salivary gland morphogenesis |
| GO:0030916 | otic vesicle formation |
| GO:0060595 | fibroblast growth factor receptor signaling pathway involved in mammary gland specification |
| GO:0060648 | mammary gland bud morphogenesis |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development |
| GO:0060737 | prostate gland morphogenetic growth |
| GO:0060523 | prostate epithelial cord elongation |
| GO:0071600 | otic vesicle morphogenesis |
| *FGFR3* | GO:1902178 | fibroblast growth factor receptor apoptotic signaling pathway |
| GO:0005007 | fibroblast growth factor-activated receptor activity |
| *FGF10* | GO:0060592 | mammary gland formation |
| GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis |
| GO:0060915 | mesenchymal cell differentiation involved in lung development |
| GO:0060594 | mammary gland specification |
| GO:0060615 | mammary gland bud formation |
| GO:0060667 | branch elongation involved in salivary gland morphogenesis |
| GO:0030916 | otic vesicle formation |
| GO:0060595 | fibroblast growth factor receptor signaling pathway involved in mammary gland specification |
| GO:0060648 | mammary gland bud morphogenesis |
| GO:0009946 | proximal/distal axis specification |
| GO:0050677 | positive regulation of urothelial cell proliferation |
| GO:0060432 | lung pattern specification process |
| GO:0060495 | cell-cell signaling involved in lung development |
| GO:0070352 | positive regulation of white fat cell proliferation |
| GO:0060436 | bronchiole morphogenesis |
| GO:0060496 | mesenchymal-epithelial cell signaling involved in lung development |
| GO:0061115 | lung proximal/distal axis specification |
| GO:0060876 | semicircular canal formation |
| GO:0060879 | semicircular canal fusion |
| GO:0060661 | submandibular salivary gland formation |
| GO:0048807 | female genitalia morphogenesis |
| GO:0060447 | bud outgrowth involved in lung branching |
| GO:0071600 | otic vesicle morphogenesis |
| *STS* | GO:0048807 | female genitalia morphogenesis |
| *SHH* | GO:0007442 | hindgut morphogenesis |
|  | GO:0061525 | hindgut development |
|  | GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis |
|  | GO:0072198 | mesenchymal cell proliferation involved in ureter development |
|  | GO:0072191 | ureter smooth muscle development |
|  | GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development |
|  | GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development |
|  | GO:0072193 | ureter smooth muscle cell differentiation |
|  | GO:0007418 | ventral midline development |
|  | GO:0007442 | hindgut morphogenesis |
|  | GO:0021938 | smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation |
|  | GO:0060459 | left lung development |
|  | GO:0060738 | epithelial-mesenchymal signaling involved in prostate gland development |
|  | GO:0060781 | mesenchymal cell proliferation involved in prostate gland development |
|  | GO:0060783 | mesenchymal smoothened signaling pathway involved in prostate gland development |
|  | GO:1905900 | negative regulation of smooth muscle tissue development |
|  | GO:1905901 | positive regulation of smooth muscle tissue development |
|  | GO:0009949 | polarity specification of anterior/posterior axis |
|  | GO:0060782 | regulation of mesenchymal cell proliferation involved in prostate gland development |
|  | GO:0030908 | protein splicing |
|  | GO:0060458 | right lung development |
|  | GO:0060737 | prostate gland morphogenetic growth |
|  | GO:0061189 | positive regulation of sclerotome development |
|  | GO:0061190 | regulation of sclerotome development |
|  | GO:0060516 | primary prostatic bud elongation |
|  | GO:0072195 | kidney smooth muscle cell differentiation |
|  | GO:2000062 | negative regulation of ureter smooth muscle cell differentiation |
|  | GO:2000063 | positive regulation of ureter smooth muscle cell differentiation |
|  | GO:0016539 | intein-mediated protein splicing |
|  | GO:0060447 | bud outgrowth involved in lung branching |
|  | GO:0060523 | prostate epithelial cord elongation |
|  | GO:2000061 | regulation of ureter smooth muscle cell differentiation |
|  | GO:2000356 | regulation of kidney smooth muscle cell differentiation |
|  | GO:2000357 | negative regulation of kidney smooth muscle cell differentiation |
|  | GO:2000358 | positive regulation of kidney smooth muscle cell differentiation |
| *CD96* | GO:0002728 | negative regulation of natural killer cell cytokine production |
| *ARX* | GO:0021831 | embryonic olfactory bulb interneuron precursor migration |
| *PQBP1* | - | - |
| *TBC1D24* | - | - |
| *DYNC2H1* | - | - |
| *KIF7* | - | - |
| *PIEZO2* | - | - |
| *JMJD1C* | - | - |
| *FEZF1* | - | - |
| *GAS1* | - | - |
| *TMEM216* | - | - |
| *INSL3* | - | - |
| *SUFU* | GO:0021776 | smoothened signaling pathway involved in spinal cord motor neuron cell fate specification |
|  | GO:0021775 | smoothened signaling pathway involved in ventral spinal cord interneuron specification |
| *COPB2* | - | - |
| *GLI2* | GO:0007442 | hindgut morphogenesis |
|  | GO:0061525 | hindgut development |
|  | GO:0021965 | spinal cord ventral commissure morphogenesis |
|  | GO:0007418 | ventral midline development |
|  | GO:0060032 | notochord regression |
|  | GO:0021508 | floor plate formation |
|  | GO:0033505 | floor plate morphogenesis |
|  | GO:0021776 | smoothened signaling pathway involved in spinal cord motor neuron cell fate specification |
|  | GO:0021775 | smoothened signaling pathway involved in ventral spinal cord interneuron specification |
|  | GO:0021938 | smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation |
| *TGIF1* | - | - |
| *CENPJ* | - | - |
| *CDK6* | - | - |
| *PTEN* | GO:0051800 | phosphatidylinositol-3,4-bisphosphate 3-phosphatase activity |
|  | GO:2000808 | negative regulation of synaptic vesicle clustering |
| *RAP1A* | - | - |
| *RFWD3* | GO:0031049 | programmed DNA elimination |
|  | GO:0031052 | chromosome breakage |
| *MFSD2A* | GO:0051978 | lysophospholipid:sodium symporter activity |
|  | GO:0051977 | lysophospholipid transport |
|  | GO:0140348 | lysophosphatidylcholine flippase activity |
| *DZIP1L* | GO:1905349 | ciliary transition zone assembly |
| *DEAF1* | - | - |
| *NCAPD3* | - | - |
| *RAD51* | GO:0007066 | female meiosis sister chromatid cohesion |
|  | GO:1990414 | replication-born double-strand break repair via sister chromatid exchange |
|  | GO:1902298 | cell cycle DNA replication maintenance of fidelity |
|  | GO:1990505 | mitotic DNA replication maintenance of fidelity |
|  | GO:1990426 | mitotic recombination-dependent replication fork processing |
| *CIT* | - | - |
| *ASPM* | - | - |
| *SDCCAG8* | - | - |
| *CDK5RAP2* | - | - |
| *DYNC2LI1* | - | - |
| *GATA3* | GO:0060017 | parathyroid gland development |
|  | GO:0061209 | cell proliferation involved in mesonephros development |
|  | GO:0035799 | ureter maturation |
|  | GO:0061218 | negative regulation of mesonephros development |
|  | GO:0072179 | nephric duct formation |
|  | GO:0072106 | regulation of ureteric bud formation |
|  | GO:0072107 | positive regulation of ureteric bud formation |
|  | GO:1905278 | positive regulation of epithelial tube formation |
|  | GO:2000733 | regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:2000699 | fibroblast growth factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:2000702 | regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:2000703 | negative regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:2000734 | negative regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:2000701 | glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation |
|  | GO:0060995 | cell-cell signaling involved in kidney development |
|  | GO:2000683 | regulation of cellular response to X-ray |
|  | GO:1905277 | negative regulation of epithelial tube formation |
|  | GO:0061289 | Wnt signaling pathway involved in kidney development |
|  | GO:0072204 | cell-cell signaling involved in metanephros development |
|  | GO:0035898 | parathyroid hormone secretion |
|  | GO:0033600 | negative regulation of mammary gland epithelial cell proliferation |
|  | GO:2000606 | regulation of cell proliferation involved in mesonephros development |
|  | GO:0061290 | canonical Wnt signaling pathway involved in metanephric kidney development |
|  | GO:2000607 | negative regulation of cell proliferation involved in mesonephros development |
|  | GO:0002572 | pro-T cell differentiation |
| *PHC1* | - | - |
| *CEP135* | - | - |
| *NFIA* | - | - |
| *XRCC4* | - | - |
| *WDR34* | - | - |
| *VANGL1* | - | - |
| *BRCA1* | GO:0070512 | positive regulation of histone H4-K20 methylation |
|  | GO:0070510 | regulation of histone H4-K20 methylation |
| *SH2B1* | - | - |
| *DISP1* | GO:0007225 | patched ligand maturation |
| *KYNU* | GO:0034516  |  response to vitamin B6 |
| *PPP1R15B* | - | - |
| *GLI1* | GO:0007418 | ventral midline development |
|  | GO:0060032 | notochord regression |
|  | GO:0021938 | smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation |
| *CEP63* | - | - |
| *ZIC2* | - | - |
| *FOXH1* | - | - |
| *PHGDH* | GO:0051978 | lysophospholipid:sodium symporter activity |
|  | GO:0051977 | lysophospholipid transport |
|  | GO:0140348 | lysophosphatidylcholine flippase activity |
| *TAF13* | - | - |
| *RAP1B* | - | - |
| *INTU* | - | - |
| *CDON* | - | - |
| *LRP4* | GO:1901631 | positive regulation of presynaptic membrane organization |
| *SASS6* | - | - |
| *KIAA0753* | - | - |
| *RREB1* | GO:1903691 | positive regulation of wound healing, spreading of epidermal cells |
| *CCDC141* | - | - |
| *STIL* | - | - |
| *SOX11* | GO:0002072 | optic cup morphogenesis involved in camera-type eye development |
|  | GO:0035332 | positive regulation of hippo signaling |
|  | GO:0097166 | lens epithelial cell proliferation |
|  | GO:2001111 | positive regulation of lens epithelial cell proliferation |
|  | GO:2001109 | regulation of lens epithelial cell proliferation |
|  | GO:0061386 | closure of optic fissure |
| *NODAL* | GO:0033505 | floor plate morphogenesis |
|  | GO:0009946 | proximal/distal axis specification |
|  | GO:0060802 | epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification |
|  | GO:0010085 | polarity specification of proximal/distal axis |
|  | GO:0060459 | left lung development |
|  | GO:0090010 | transforming growth factor beta receptor signaling pathway involved in primitive streak formation |
|  | GO:0060460 | left lung morphogenesis |
|  | GO:0001831 | trophectodermal cellular morphogenesis |
|  | GO:0048321 | axial mesodermal cell differentiation |
|  | GO:0048322 | axial mesodermal cell fate commitment |
|  | GO:0048327 | axial mesodermal cell fate specification |
|  | GO:1900224 | positive regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry |
| *SEC24C* | - | - |
| *HSPA9* | - | - |
| *CEP152* | - | - |
| *CDC42* | GO:0060661 | submandibular salivary gland formation |
| *DCHS1* | - | - |
| *SF3B4* | - | - |
| *ALDH18A1* | GO:0019202 | amino acid kinase activity |
|  | GO:0006592 | ornithine biosynthetic process |
|  | GO:0004349 | glutamate 5-kinase activity |
| *WDR60* | - | - |
| *MCM5* | - | - |
| *DCC* | GO:0021965 | spinal cord ventral commissure morphogenesis |
|  | GO:0033563 | dorsal/ventral axon guidance |
| *WDR35* | - | - |
| *GEMIN4* | - | - |
| *CEP55* | - | - |
| *SON* | - | - |
| *PDE6D* | - | - |
| *RNU4ATAC* | - | - |
| *APC* | - | - |
| *PYCR2* | - | - |
| *PTCH1* | GO:0021997 | neural plate axis specification |
|  | GO:0035799 | ureter maturation |
| *ZIC3* | GO:0035545 | determination of left/right asymmetry in nervous system |
| *CEP120* | - | - |
| *FGF20* | - | - |
| *OFD1* | - | - |
| *ARID2* | - | - |
| *MBTPS2* | - | - |
| *TBX18* | GO:0060827 | regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
|  | GO:0060829 | negative regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
|  | GO:0060823 | canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation |
| *RMND1* | - | - |
| *WDR62* | - | - |
| *HNF4A* | - | - |
| *FUZ* | GO:0090299 | regulation of neural crest formation |
|  | GO:2000314 | negative regulation of fibroblast growth factor receptor signaling pathway involved in neural plate anterior/posterior pattern formation |
|  | GO:0090301 | negative regulation of neural crest formation |
| *PKHD1* | - | - |
| *IFT80* | - | - |
| *DLL1* | GO:0021687 | cerebellar molecular layer morphogenesis |
|  | GO:0021698 | cerebellar cortex structural organization |
|  | GO:0021688 | cerebellar molecular layer formation |
|  | GO:0021693 | cerebellar Purkinje cell layer structural organization |
|  | GO:0060844 | arterial endothelial cell fate commitment |
|  | GO:0060853 | Notch signaling pathway involved in arterial endothelial cell fate commitment |
| *MAD2L2* | - | - |
| *DPF2* | GO:1905453 | regulation of myeloid progenitor cell differentiation |
|  | GO:1905454 | negative regulation of myeloid progenitor cell differentiation |
| *HOXD13* | GO:0007442 | hindgut morphogenesis |
|  | GO:0061525 | hindgut development |
|  | GO:0048619 | embryonic hindgut morphogenesis |
| *ANKLE2* | - | - |
| *DLL4* | GO:0072554 | blood vessel lumenization |
| *UBE2T* | - | - |
| *CENPF* | - | - |
| *DACT1* | GO:0007442 | hindgut morphogenesis |
|  | GO:0061525 | hindgut development |
|  | GO:1904864 | negative regulation of beta-catenin-TCF complex assembly |
|  | GO:0048619 | embryonic hindgut morphogenesis |
| *KIF14* | GO:0021698 | cerebellar cortex structural organization |
|  | GO:0021685 | cerebellar granular layer structural organization |
|  | GO:0021693 | cerebellar Purkinje cell layer structural organization |
| *GREB1L* | - | - |
| *PBX1* | - | - |
| *TDGF1* | - | - |
| *TCTN3* | - | - |
| *ARL6* | - | - |
| *THOC6* | - | - |
| *IQSEC2* | - | - |
| *RXFP2* | - | - |
| *XRCC2* | - | - |
| *UPK3A* | - | - |
| *TBX6* | - | - |
| *FAM111A* | - | - |
| *FAM58A* | - | - |
| *SIX6* | - | - |
| *PITX2* | GO:0044867 | modulation by host of viral catalytic activity |
|  | GO:0044870 | modulation by host of viral glycoprotein metabolic process |
|  | GO:0044871 | negative regulation by host of viral glycoprotein metabolic process |
|  | GO:0044866 | modulation by host of viral exo-alpha-sialidase activity |
|  | GO:0052403 | negative regulation by host of symbiont catalytic activity |
|  | GO:0044869 | negative regulation by host of viral exo-alpha-sialidase activity |
| *VSX2* | - | - |
| *OTX2* | - | - |
| *VAX1* | - | - |
| *PITX3* | GO:0044867 | modulation by host of viral catalytic activity |
|  | GO:0044870 | modulation by host of viral glycoprotein metabolic process |
|  | GO:0044871 | negative regulation by host of viral glycoprotein metabolic process |
|  | GO:0044866 | modulation by host of viral exo-alpha-sialidase activity |
|  | GO:0052403 | negative regulation by host of symbiont catalytic activity |
|  | GO:1904935 | positive regulation of cell proliferation in midbrain |
|  | GO:0044869 | negative regulation by host of viral exo-alpha-sialidase activity |
| *RAX* | - | - |
| *SOX2* | - | - |
| *B3GALTL* | - | - |
| *RAF1* | - | - |
| *BRAF* | GO:0070413 | trehalose metabolism in response to stress |
| *SMC3* | - | - |
| *ANOS1* | - | - |
| *AXIN1* | - | - |
| *HDAC8* | - | - |
| *SMC1A* | - | - |
| *EIF4H* | - | - |
| *LAT2* | - | - |
| *FKBP6* | - | - |
| *TCF4* | - | - |
| *CTU2* | - | - |
| *BCL7B* | - | - |
| *UFD1L* | - | - |
| *WBSCR27* | - | - |
| *DNAJC30* | GO:1905706 | regulation of mitochondrial ATP synthesis coupled proton transport |
| *WBSCR22* | - | - |
| *RCC1L* | - | - |
| *A1CF* | - | - |
| *CRKL* | GO:0035685 | helper T cell diapedesis |
|  | GO:0060017 | parathyroid gland development |
| *RPS17* | - | - |
| *RPL35A* | - | - |
| *RPS7* | GO:1902255 | positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator |
| *RPS26* | - | - |
| *RPS10* | - | - |
| *RPL11* | GO:1902255 | positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator |
| *RPL5* | - | - |
| *RPL15* | - | - |
| *RPS24* | - | - |
| *RPS19* | - | - |
| *GATA1* | - | - |
| *DLG4* | - | - |
| *TNF* | GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis |
|  | GO:2000334 | positive regulation of blood microparticle formation |
|  | GO:0032724 | positive regulation of fractalkine production |
|  | GO:0050756 | fractalkine metabolic process |
|  | GO:1904997 | regulation of leukocyte adhesion to arterial endothelial cell |
|  | GO:0050751 | fractalkine biosynthetic process |
|  | GO:0002876 | positive regulation of chronic inflammatory response to antigenic stimulus |
|  | GO:1904999 | positive regulation of leukocyte adhesion to arterial endothelial cell |
|  | GO:0050752 | regulation of fractalkine biosynthetic process |
|  | GO:0061048 | negative regulation of branching involved in lung morphogenesis |
|  | GO:0045994 | positive regulation of translational initiation by iron |
|  | GO:0050754 | positive regulation of fractalkine biosynthetic process |
|  | GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis |
| *MX1* | - | - |
| *SMARCA2* | - | - |
| *PAX3* | - | - |
| *REEP3* | - | - |
| *TIMMDC1* | - | - |
| *FAM169B* | - | - |
| *DHFR* | - | - |

**Supplementary Table 2:** The gene enrichment analysis identified 343 enriched GO terms with a standard p <0.05. All GO terms and ClueGo generated groups are represented with associated p values corrected with Holm-Bonferroni method and are displayed ordered according to their corrected p value. All the groups with a corrected p value <0.05 are represented in Figure 1 in the manuscript and are here highlighted with the same color code. The term that was chosen by ClueGo for naming each group is in bold and the relative GOID is colored.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **GOID** | **GOTerm** | **Term P Value Corrected with Bonferroni step down** | **Group P Value Corrected with Bonferroni step down** | **GO****Groups** | **Associated Genes Found** |
| GO:0060592 | mammary gland formation | 0,0000 | 0,00000000000000000000002 | Group67 | *[BMP4, FGF10, FGFR2, GLI3, TBX3]* |
| GO:0007442 | hindgut morphogenesis | 0,0000 | 0,00000000000000000000002 | Group67 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0061525 | hindgut development | 0,0000 | 0,00000000000000000000002 | Group67 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0071600 | **otic vesicle morphogenesis** | 0,0000 | 0,00000000000000000000002 | Group67 | *[EYA1, FGF10, FGF8, FGFR2, HESX1]* |
| GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis | 0,0000 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2, SHH, TNF]* |
| GO:0030916 | otic vesicle formation | 0,0000 | 0,00000000000000000000002 | Group67 | *[FGF10, FGF8, FGFR2, HESX1]* |
| GO:0072198 | mesenchymal cell proliferation involved in ureter development | 0,0000 | 0,00000000000000000000002 | Group67 | *[BMP4, SHH, SIX1]* |
| GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development | 0,0000 | 0,00000000000000000000002 | Group67 | *[BMP4, SHH, SIX1]* |
| GO:0060594 | mammary gland specification | 0,0000 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2, GLI3]* |
| GO:0009946 | proximal/distal axis specification | 0,0001 | 0,00000000000000000000002 | Group67 | *[FGF10, NODAL, SIX3]* |
| GO:0072191 | ureter smooth muscle development | 0,0001 | 0,00000000000000000000002 | Group67 | *[BMP4, SHH, SIX1]* |
| GO:0072193 | ureter smooth muscle cell differentiation | 0,0001 | 0,00000000000000000000002 | Group67 | *[BMP4, SHH, SIX1]* |
| GO:0007418 | ventral midline development | 0,0004 | 0,00000000000000000000002 | Group67 | *[GLI1, GLI2, SHH]* |
| GO:0005007 | fibroblast growth factor-activated receptor activity | 0,0004 | 0,00000000000000000000002 | Group67 | *[FGFR1, FGFR2, FGFR3]* |
| GO:0021938 | smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation | 0,0004 | 0,00000000000000000000002 | Group67 | *[GLI1, GLI2, SHH]* |
| GO:0060661 | submandibular salivary gland formation | 0,0012 | 0,00000000000000000000002 | Group67 | *[CDC42, FGF10]* |
| GO:0060459 | left lung development | 0,0012 | 0,00000000000000000000002 | Group67 | *[NODAL, SHH]* |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development | 0,0012 | 0,00000000000000000000002 | Group67 | *[FGFR2, TP63]* |
| GO:0060915 | mesenchymal cell differentiation involved in lung development | 0,0012 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2]* |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development | 0,0012 | 0,00000000000000000000002 | Group67 | *[SHH, SIX1]* |
| GO:0060615 | mammary gland bud formation | 0,0012 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2]* |
| GO:0060667 | branch elongation involved in salivary gland morphogenesis | 0,0012 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2]* |
| GO:0060595 | fibroblast growth factor receptor signaling pathway involved in mammary gland specification | 0,0012 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2]* |
| GO:0060032 | notochord regression | 0,0029 | 0,00000000000000000000002 | Group67 | *[GLI1, GLI2]* |
| GO:0033505 | floor plate morphogenesis | 0,0029 | 0,00000000000000000000002 | Group67 | *[GLI2, NODAL]* |
| GO:0060197 | cloacal septation | 0,0029 | 0,00000000000000000000002 | Group67 | *[BMP4, TP63]* |
| GO:0060523 | prostate epithelial cord elongation | 0,0029 | 0,00000000000000000000002 | Group67 | *[FGFR2, SHH]* |
| GO:0072513 | positive regulation of secondary heart field cardioblast proliferation | 0,0029 | 0,00000000000000000000002 | Group67 | *[EYA1, SIX1]* |
| GO:0035607 | fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development | 0,0029 | 0,00000000000000000000002 | Group67 | *[FGFR1, FGFR2]* |
| GO:0060648 | mammary gland bud morphogenesis | 0,0029 | 0,00000000000000000000002 | Group67 | *[FGF10, FGFR2]* |
| GO:0072106 | regulation of ureteric bud formation | 0,0042 | 0,00000000000000000000002 | Group67 | *[GATA3, SIX1]* |
| GO:0072107 | positive regulation of ureteric bud formation | 0,0042 | 0,00000000000000000000002 | Group67 | *[GATA3, SIX1]* |
| GO:0035844 | cloaca development | 0,0042 | 0,00000000000000000000002 | Group67 | *[BMP4, TP63]* |
| GO:1905278 | positive regulation of epithelial tube formation | 0,0042 | 0,00000000000000000000002 | Group67 | *[GATA3, SIX1]* |
| GO:0048807 | female genitalia morphogenesis | 0,0042 | 0,00000000000000000000002 | Group67 | *[FGF10, TP63]* |
| GO:0060737 | prostate gland morphogenetic growth | 0,0042 | 0,00000000000000000000002 | Group67 | *[FGFR2, SHH]* |
| GO:0035898 | parathyroid hormone secretion | 0,0042 | 0,00000000000000000000002 | Group67 | *[FGFR1, GATA3]* |
| GO:0021847 | ventricular zone neuroblast division | 0,0042 | 0,00000000000000000000002 | Group67 | *[FGFR1, FGFR2]* |
| GO:0060447 | bud outgrowth involved in lung branching | 0,0042 | 0,00000000000000000000002 | Group67 | *[FGF10, SHH]* |
| GO:0060738 | epithelial-mesenchymal signaling involved in prostate gland development | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0070352 | positive regulation of white fat cell proliferation | 0,0308 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0009949 | polarity specification of anterior/posterior axis | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0010085 | polarity specification of proximal/distal axis | 0,0308 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0021508 | floor plate formation | 0,0308 | 0,00000000000000000000002 | Group67 | *[GLI2]* |
| GO:0030908 | protein splicing | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060458 | right lung development | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060516 | primary prostatic bud elongation | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000830 | positive regulation of parathyroid hormone secretion | 0,0308 | 0,00000000000000000000002 | Group67 | *[FGFR1]* |
| GO:0001831 | trophectodermal cellular morphogenesis | 0,0308 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0016539 | intein-mediated protein splicing | 0,0308 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060876 | semicircular canal formation | 0,0308 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:1903465 | positive regulation of mitotic cell cycle DNA replication | 0,0308 | 0,00000000000000000000002 | Group67 | *[FGFR1]* |
| GO:1900224 | positive regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry | 0,0308 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0060781 | mesenchymal cell proliferation involved in prostate gland development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0050677 | positive regulation of urothelial cell proliferation | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0060432 | lung pattern specification process | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0060495 | cell-cell signaling involved in lung development | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0060783 | mesenchymal smoothened signaling pathway involved in prostate gland development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060802 | epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:1905900 | negative regulation of smooth muscle tissue development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:1905901 | positive regulation of smooth muscle tissue development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060782 | regulation of mesenchymal cell proliferation involved in prostate gland development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0035604 | fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGFR2]* |
| GO:0060436 | bronchiole morphogenesis | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0060496 | mesenchymal-epithelial cell signaling involved in lung development | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0061115 | lung proximal/distal axis specification | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:0061189 | positive regulation of sclerotome development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0061190 | regulation of sclerotome development | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0090010 | transforming growth factor beta receptor signaling pathway involved in primitive streak formation | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine | 0,0311 | 0,00000000000000000000002 | Group67 | *[SIX1]* |
| GO:0035603 | fibroblast growth factor receptor signaling pathway involved in hemopoiesis | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGFR2]* |
| GO:0060460 | left lung morphogenesis | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0072195 | kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000062 | negative regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000063 | positive regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060873 | anterior semicircular canal development | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0060875 | lateral semicircular canal development | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0022012 | subpallium cell proliferation in forebrain | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0035602 | fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptotic process in bone marrow cell | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGFR2]* |
| GO:0048321 | axial mesodermal cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:2000061 | regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000356 | regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000357 | negative regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:2000358 | positive regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000000000002 | Group67 | *[SHH]* |
| GO:0060366 | lambdoid suture morphogenesis | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0060367 | sagittal suture morphogenesis | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0022018 | lateral ganglionic eminence cell proliferation | 0,0311 | 0,00000000000000000000002 | Group67 | *[GLI3]* |
| GO:0048322 | axial mesodermal cell fate commitment | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0048327 | axial mesodermal cell fate specification | 0,0311 | 0,00000000000000000000002 | Group67 | *[NODAL]* |
| GO:0060879 | semicircular canal fusion | 0,0311 | 0,00000000000000000000002 | Group67 | *[FGF10]* |
| GO:1902298 | **cell cycle DNA replication maintenance of fidelity** | 0,0000 | 0,00000000000000095436398 | Group65 | *[BRCA2, FANCD2, RAD51]* |
| GO:1990505 | mitotic DNA replication maintenance of fidelity | 0,0000 | 0,00000000000000095436398 | Group65 | *[BRCA2, FANCD2, RAD51]* |
| GO:1990426 | mitotic recombination-dependent replication fork processing | 0,0000 | 0,00000000000000095436398 | Group65 | *[BRCA2, FANCD2, RAD51]* |
| GO:0061218 | negative regulation of mesonephros development | 0,0001 | 0,00000000000000095436398 | Group65 | *[BMP4, GATA3, HNF1B]* |
| GO:0033600 | negative regulation of mammary gland epithelial cell proliferation | 0,0004 | 0,00000000000000095436398 | Group65 | *[BRCA2, FANCD2, GATA3]* |
| GO:2000683 | regulation of cellular response to X-ray | 0,0012 | 0,00000000000000095436398 | Group65 | *[GATA3, HMGA2]* |
| GO:0031049 | programmed DNA elimination | 0,0012 | 0,00000000000000095436398 | Group65 | *[HMGA2, RFWD3]* |
| GO:0031052 | chromosome breakage | 0,0012 | 0,00000000000000095436398 | Group65 | *[HMGA2, RFWD3]* |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development | 0,0012 | 0,00000000000000095436398 | Group65 | *[SHH, SIX1]* |
| GO:0072513 | positive regulation of secondary heart field cardioblast proliferation | 0,0029 | 0,00000000000000095436398 | Group65 | *[EYA1, SIX1]* |
| GO:0035607 | fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development | 0,0029 | 0,00000000000000095436398 | Group65 | *[FGFR1, FGFR2]* |
| GO:0072106 | regulation of ureteric bud formation | 0,0042 | 0,00000000000000095436398 | Group65 | *[GATA3, SIX1]* |
| GO:0072107 | positive regulation of ureteric bud formation | 0,0042 | 0,00000000000000095436398 | Group65 | *[GATA3, SIX1]* |
| GO:1905278 | positive regulation of epithelial tube formation | 0,0042 | 0,00000000000000095436398 | Group65 | *[GATA3, SIX1]* |
| GO:0061209 | cell proliferation involved in mesonephros development | 0,0042 | 0,00000000000000095436398 | Group65 | *[BMP4, GATA3]* |
| GO:0035898 | parathyroid hormone secretion | 0,0042 | 0,00000000000000095436398 | Group65 | *[FGFR1, GATA3]* |
| GO:0021847 | ventricular zone neuroblast division | 0,0042 | 0,00000000000000095436398 | Group65 | *[FGFR1, FGFR2]* |
| GO:0060995 | cell-cell signaling involved in kidney development | 0,0308 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:0061289 | Wnt signaling pathway involved in kidney development | 0,0308 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:0072204 | cell-cell signaling involved in metanephros development | 0,0308 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000830 | positive regulation of parathyroid hormone secretion | 0,0308 | 0,00000000000000095436398 | Group65 | *[FGFR1]* |
| GO:0061290 | canonical Wnt signaling pathway involved in metanephric kidney development | 0,0308 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:0002572 | pro-T cell differentiation | 0,0308 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:1903465 | positive regulation of mitotic cell cycle DNA replication | 0,0308 | 0,00000000000000095436398 | Group65 | *[FGFR1]* |
| GO:2000733 | regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000699 | fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000702 | regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000703 | negative regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000734 | negative regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000701 | glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:1905277 | negative regulation of epithelial tube formation | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000685 | positive regulation of cellular response to X-ray | 0,0311 | 0,00000000000000095436398 | Group65 | *[HMGA2]* |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine | 0,0311 | 0,00000000000000095436398 | Group65 | *[SIX1]* |
| GO:2000606 | regulation of cell proliferation involved in mesonephros development | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:2000607 | negative regulation of cell proliferation involved in mesonephros development | 0,0311 | 0,00000000000000095436398 | Group65 | *[GATA3]* |
| GO:0060592 | mammary gland formation | 0,0000 | 0,00000000000000124657464 | Group68 | *[BMP4, FGF10, FGFR2, GLI3, TBX3]* |
| GO:0072179 | nephric duct formation | 0,0000 | 0,00000000000000124657464 | Group68 | *[BMP4, GATA3, HNF1B, PAX2]* |
| GO:0072198 | mesenchymal cell proliferation involved in ureter development | 0,0000 | 0,00000000000000124657464 | Group68 | *[BMP4, SHH, SIX1]* |
| GO:0072199 | **regulation of mesenchymal cell proliferation involved in ureter development** | 0,0000 | 0,00000000000000124657464 | Group68 | *[BMP4, SHH, SIX1]* |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching | 0,0001 | 0,00000000000000124657464 | Group68 | *[BMP4, HNF1B, SIX1]* |
| GO:0072191 | ureter smooth muscle development | 0,0001 | 0,00000000000000124657464 | Group68 | *[BMP4, SHH, SIX1]* |
| GO:0061218 | negative regulation of mesonephros development | 0,0001 | 0,00000000000000124657464 | Group68 | *[BMP4, GATA3, HNF1B]* |
| GO:0072193 | ureter smooth muscle cell differentiation | 0,0001 | 0,00000000000000124657464 | Group68 | *[BMP4, SHH, SIX1]* |
| GO:0060681 | branch elongation involved in ureteric bud branching | 0,0003 | 0,00000000000000124657464 | Group68 | *[BMP4, HNF1B, SIX1]* |
| GO:2000683 | regulation of cellular response to X-ray | 0,0012 | 0,00000000000000124657464 | Group68 | *[GATA3, HMGA2]* |
| GO:0060529 | squamous basal epithelial stem cell differentiation involved in prostate gland acinus development | 0,0012 | 0,00000000000000124657464 | Group68 | *[FGFR2, TP63]* |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development | 0,0012 | 0,00000000000000124657464 | Group68 | *[SHH, SIX1]* |
| GO:0003404 | optic vesicle morphogenesis | 0,0012 | 0,00000000000000124657464 | Group68 | *[SIX3, TFAP2A]* |
| GO:0010159 | specification of animal organ position | 0,0029 | 0,00000000000000124657464 | Group68 | *[BMP4, TBX3]* |
| GO:0060197 | cloacal septation | 0,0029 | 0,00000000000000124657464 | Group68 | *[BMP4, TP63]* |
| GO:0072106 | regulation of ureteric bud formation | 0,0042 | 0,00000000000000124657464 | Group68 | *[GATA3, SIX1]* |
| GO:0072107 | positive regulation of ureteric bud formation | 0,0042 | 0,00000000000000124657464 | Group68 | *[GATA3, SIX1]* |
| GO:0035844 | cloaca development | 0,0042 | 0,00000000000000124657464 | Group68 | *[BMP4, TP63]* |
| GO:1905278 | positive regulation of epithelial tube formation | 0,0042 | 0,00000000000000124657464 | Group68 | *[GATA3, SIX1]* |
| GO:0061209 | cell proliferation involved in mesonephros development | 0,0042 | 0,00000000000000124657464 | Group68 | *[BMP4, GATA3]* |
| GO:0048807 | female genitalia morphogenesis | 0,0042 | 0,00000000000000124657464 | Group68 | *[FGF10, TP63]* |
| GO:0035898 | parathyroid hormone secretion | 0,0042 | 0,00000000000000124657464 | Group68 | *[FGFR1, GATA3]* |
| GO:0060235 | lens induction in camera-type eye | 0,0042 | 0,00000000000000124657464 | Group68 | *[BMP4, SIX3]* |
| GO:0072181 | mesonephric duct formation | 0,0308 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0090191 | negative regulation of branching involved in ureteric bud morphogenesis | 0,0308 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0060738 | epithelial-mesenchymal signaling involved in prostate gland development | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0060995 | cell-cell signaling involved in kidney development | 0,0308 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0009949 | polarity specification of anterior/posterior axis | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0030908 | protein splicing | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0060458 | right lung development | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0061289 | Wnt signaling pathway involved in kidney development | 0,0308 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0072204 | cell-cell signaling involved in metanephros development | 0,0308 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0060516 | primary prostatic bud elongation | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0072114 | pronephros morphogenesis | 0,0308 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:1901963 | regulation of cell proliferation involved in outflow tract morphogenesis | 0,0308 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0003134 | endodermal-mesodermal cell signaling involved in heart induction | 0,0308 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0016539 | intein-mediated protein splicing | 0,0308 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0061290 | canonical Wnt signaling pathway involved in metanephric kidney development | 0,0308 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0039020 | pronephric nephron tubule development | 0,0308 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0060932 | His-Purkinje system cell differentiation | 0,0308 | 0,00000000000000124657464 | Group68 | *[TBX3]* |
| GO:0002572 | pro-T cell differentiation | 0,0308 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0003130 | BMP signaling pathway involved in heart induction | 0,0308 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0060994 | regulation of transcription from RNA polymerase II promoter involved in kidney development | 0,0308 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000733 | regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0072096 | negative regulation of branch elongation involved in ureteric bud branching | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000699 | fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:2000702 | regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:2000703 | negative regulation of fibroblast growth factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:2000734 | negative regulation of glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:2000701 | glial cell-derived neurotrophic factor receptor signaling pathway involved in ureteric bud formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0072097 | negative regulation of branch elongation involved in ureteric bud branching by BMP signaling pathway | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0060781 | mesenchymal cell proliferation involved in prostate gland development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0060783 | mesenchymal smoothened signaling pathway involved in prostate gland development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:1905900 | negative regulation of smooth muscle tissue development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:1905901 | positive regulation of smooth muscle tissue development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0060782 | regulation of mesenchymal cell proliferation involved in prostate gland development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0061150 | renal system segmentation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:1905277 | negative regulation of epithelial tube formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0061017 | hepatoblast differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0061189 | positive regulation of sclerotome development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0061190 | regulation of sclerotome development | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:0072200 | negative regulation of mesenchymal cell proliferation involved in ureter development | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine | 0,0311 | 0,00000000000000124657464 | Group68 | *[SIX1]* |
| GO:0061215 | mesonephric nephron development | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0048391 | intermediate mesoderm formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0061206 | mesonephros morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0061228 | mesonephric nephron morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0072192 | ureter epithelial cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0072195 | kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000062 | negative regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000063 | positive regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000606 | regulation of cell proliferation involved in mesonephros development | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0035565 | regulation of pronephros size | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0048392 | intermediate mesodermal cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0060503 | bud dilation involved in lung branching | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:1901964 | positive regulation of cell proliferation involved in outflow tract morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000061 | regulation of ureter smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000356 | regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000357 | negative regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000358 | positive regulation of kidney smooth muscle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[SHH]* |
| GO:2000607 | negative regulation of cell proliferation involved in mesonephros development | 0,0311 | 0,00000000000000124657464 | Group68 | *[GATA3]* |
| GO:0055018 | regulation of cardiac muscle fiber development | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0061235 | mesenchymal stem cell maintenance involved in mesonephric nephron morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:1901146 | mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0055020 | positive regulation of cardiac muscle fiber development | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0072099 | anterior/posterior pattern specification involved in ureteric bud development | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0072100 | specification of ureteric bud anterior/posterior symmetry | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000004 | regulation of metanephric S-shaped body morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000005 | negative regulation of metanephric S-shaped body morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000006 | regulation of metanephric comma-shaped body morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:2000007 | negative regulation of metanephric comma-shaped body morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0003167 | atrioventricular bundle cell differentiation | 0,0311 | 0,00000000000000124657464 | Group68 | *[TBX3]* |
| GO:0061149 | BMP signaling pathway involved in ureter morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0061151 | BMP signaling pathway involved in renal system segmentation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0061155 | pulmonary artery endothelial tube morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0061295 | regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0061296 | negative regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00000000000000124657464 | Group68 | *[HNF1B]* |
| GO:0061216 | regulation of transcription from RNA polymerase II promoter involved in mesonephros development | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0071893 | BMP signaling pathway involved in nephric duct formation | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0072101 | specification of ureteric bud anterior/posterior symmetry by BMP signaling pathway | 0,0311 | 0,00000000000000124657464 | Group68 | *[BMP4]* |
| GO:0007442 | hindgut morphogenesis | 0,0000 | 0,00000000000257262896695 | Group60 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0061525 | **hindgut development** | 0,0000 | 0,00000000000257262896695 | Group60 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0021776 | smoothened signaling pathway involved in spinal cord motor neuron cell fate specification | 0,0001 | 0,00000000000257262896695 | Group60 | *[GLI2, GLI3, SUFU]* |
| GO:0021775 | smoothened signaling pathway involved in ventral spinal cord interneuron specification | 0,0001 | 0,00000000000257262896695 | Group60 | *[GLI2, GLI3, SUFU]* |
| GO:0007418 | ventral midline development | 0,0004 | 0,00000000000257262896695 | Group60 | *[GLI1, GLI2, SHH]* |
| GO:0021938 | smoothened signaling pathway involved in regulation of cerebellar granule cell precursor cell proliferation | 0,0004 | 0,00000000000257262896695 | Group60 | *[GLI1, GLI2, SHH]* |
| GO:0060032 | notochord regression | 0,0029 | 0,00000000000257262896695 | Group60 | *[GLI1, GLI2]* |
| GO:0033505 | floor plate morphogenesis | 0,0029 | 0,00000000000257262896695 | Group60 | *[GLI2, NODAL]* |
| GO:0021965 | spinal cord ventral commissure morphogenesis | 0,0042 | 0,00000000000257262896695 | Group60 | *[DCC, GLI2]* |
| GO:0048619 | embryonic hindgut morphogenesis | 0,0042 | 0,00000000000257262896695 | Group60 | *[DACT1, HOXD13]* |
| GO:0033563 | dorsal/ventral axon guidance | 0,0042 | 0,00000000000257262896695 | Group60 | *[DCC, FGF8]* |
| GO:0021508 | floor plate formation | 0,0308 | 0,00000000000257262896695 | Group60 | *[GLI2]* |
| GO:0007442 | hindgut morphogenesis | 0,0000 | 0,00000000000468526484671 | Group62 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0061525 | hindgut development | 0,0000 | 0,00000000000468526484671 | Group62 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0060594 | **mammary gland specification** | 0,0000 | 0,00000000000468526484671 | Group62 | *[FGF10, FGFR2, GLI3]* |
| GO:0021776 | smoothened signaling pathway involved in spinal cord motor neuron cell fate specification | 0,0001 | 0,00000000000468526484671 | Group62 | *[GLI2, GLI3, SUFU]* |
| GO:0021775 | smoothened signaling pathway involved in ventral spinal cord interneuron specification | 0,0001 | 0,00000000000468526484671 | Group62 | *[GLI2, GLI3, SUFU]* |
| GO:0043585 | nose morphogenesis | 0,0029 | 0,00000000000468526484671 | Group62 | *[GLI3, STRA6]* |
| GO:0021508 | floor plate formation | 0,0308 | 0,00000000000468526484671 | Group62 | *[GLI2]* |
| GO:0061143 | alveolar primary septum development | 0,0311 | 0,00000000000468526484671 | Group62 | *[STRA6]* |
| GO:0071938 | vitamin A transport | 0,0311 | 0,00000000000468526484671 | Group62 | *[STRA6]* |
| GO:0060873 | anterior semicircular canal development | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0060875 | lateral semicircular canal development | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0022012 | subpallium cell proliferation in forebrain | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0060366 | lambdoid suture morphogenesis | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0060367 | sagittal suture morphogenesis | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0071939 | vitamin A import | 0,0311 | 0,00000000000468526484671 | Group62 | *[STRA6]* |
| GO:0022018 | lateral ganglionic eminence cell proliferation | 0,0311 | 0,00000000000468526484671 | Group62 | *[GLI3]* |
| GO:0060592 | **mammary gland formation** | 0,0000 | 0,00000000004170603723133 | Group56 | *[BMP4, FGF10, FGFR2, GLI3, TBX3]* |
| GO:0060664 | epithelial cell proliferation involved in salivary gland morphogenesis | 0,0000 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2, SHH, TNF]* |
| GO:0030916 | otic vesicle formation | 0,0000 | 0,00000000004170603723133 | Group56 | *[FGF10, FGF8, FGFR2, HESX1]* |
| GO:0060594 | mammary gland specification | 0,0000 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2, GLI3]* |
| GO:0060915 | mesenchymal cell differentiation involved in lung development | 0,0012 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2]* |
| GO:0060615 | mammary gland bud formation | 0,0012 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2]* |
| GO:0060667 | branch elongation involved in salivary gland morphogenesis | 0,0012 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2]* |
| GO:0060595 | fibroblast growth factor receptor signaling pathway involved in mammary gland specification | 0,0012 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2]* |
| GO:0010159 | specification of animal organ position | 0,0029 | 0,00000000004170603723133 | Group56 | *[BMP4, TBX3]* |
| GO:0060648 | mammary gland bud morphogenesis | 0,0029 | 0,00000000004170603723133 | Group56 | *[FGF10, FGFR2]* |
| GO:0009946 | **proximal/distal axis specification** | 0,0001 | 0,00000001262926387013220 | Group64 | *[FGF10, NODAL, SIX3]* |
| GO:0060459 | left lung development | 0,0012 | 0,00000001262926387013220 | Group64 | *[NODAL, SHH]* |
| GO:0060032 | notochord regression | 0,0029 | 0,00000001262926387013220 | Group64 | *[GLI1, GLI2]* |
| GO:0033505 | floor plate morphogenesis | 0,0029 | 0,00000001262926387013220 | Group64 | *[GLI2, NODAL]* |
| GO:0021965 | spinal cord ventral commissure morphogenesis | 0,0042 | 0,00000001262926387013220 | Group64 | *[DCC, GLI2]* |
| GO:0070352 | positive regulation of white fat cell proliferation | 0,0308 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0010085 | polarity specification of proximal/distal axis | 0,0308 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0021508 | floor plate formation | 0,0308 | 0,00000001262926387013220 | Group64 | *[GLI2]* |
| GO:0001831 | trophectodermal cellular morphogenesis | 0,0308 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0060876 | semicircular canal formation | 0,0308 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:1900224 | positive regulation of nodal signaling pathway involved in determination of lateral mesoderm left/right asymmetry | 0,0308 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0050677 | positive regulation of urothelial cell proliferation | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0060432 | lung pattern specification process | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0060495 | cell-cell signaling involved in lung development | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0060802 | epiblast cell-extraembryonic ectoderm cell signaling involved in anterior/posterior axis specification | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0060436 | bronchiole morphogenesis | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0060496 | mesenchymal-epithelial cell signaling involved in lung development | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0061115 | lung proximal/distal axis specification | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0090010 | transforming growth factor beta receptor signaling pathway involved in primitive streak formation | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0060460 | left lung morphogenesis | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0048321 | axial mesodermal cell differentiation | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0048322 | axial mesodermal cell fate commitment | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0048327 | axial mesodermal cell fate specification | 0,0311 | 0,00000001262926387013220 | Group64 | *[NODAL]* |
| GO:0060879 | semicircular canal fusion | 0,0311 | 0,00000001262926387013220 | Group64 | *[FGF10]* |
| GO:0072198 | **mesenchymal cell proliferation involved in ureter development** | 0,0000 | 0,00000010924600160682300 | Group59 | *[BMP4, SHH, SIX1]* |
| GO:0072199 | regulation of mesenchymal cell proliferation involved in ureter development | 0,0000 | 0,00000010924600160682300 | Group59 | *[BMP4, SHH, SIX1]* |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching | 0,0001 | 0,00000010924600160682300 | Group59 | *[BMP4, HNF1B, SIX1]* |
| GO:0072191 | ureter smooth muscle development | 0,0001 | 0,00000010924600160682300 | Group59 | *[BMP4, SHH, SIX1]* |
| GO:0072193 | ureter smooth muscle cell differentiation | 0,0001 | 0,00000010924600160682300 | Group59 | *[BMP4, SHH, SIX1]* |
| GO:0060681 | branch elongation involved in ureteric bud branching | 0,0003 | 0,00000010924600160682300 | Group59 | *[BMP4, HNF1B, SIX1]* |
| GO:2000729 | positive regulation of mesenchymal cell proliferation involved in ureter development | 0,0012 | 0,00000010924600160682300 | Group59 | *[SHH, SIX1]* |
| GO:0072513 | positive regulation of secondary heart field cardioblast proliferation | 0,0029 | 0,00000010924600160682300 | Group59 | *[EYA1, SIX1]* |
| GO:0072106 | regulation of ureteric bud formation | 0,0042 | 0,00000010924600160682300 | Group59 | *[GATA3, SIX1]* |
| GO:0072107 | positive regulation of ureteric bud formation | 0,0042 | 0,00000010924600160682300 | Group59 | *[GATA3, SIX1]* |
| GO:1905278 | positive regulation of epithelial tube formation | 0,0042 | 0,00000010924600160682300 | Group59 | *[GATA3, SIX1]* |
| GO:1905243 | cellular response to 3,3',5-triiodo-L-thyronine | 0,0311 | 0,00000010924600160682300 | Group59 | *[SIX1]* |
| GO:0072179 | **nephric duct formation** | 0,0000 | 0,00000015612510931621000 | Group58 | *[BMP4, GATA3, HNF1B, PAX2]* |
| GO:0035799 | ureter maturation | 0,0000 | 0,00000015612510931621000 | Group58 | *[GATA3, PAX2, PTCH1, RET]* |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching | 0,0001 | 0,00000015612510931621000 | Group58 | *[BMP4, HNF1B, SIX1]* |
| GO:0061218 | negative regulation of mesonephros development | 0,0001 | 0,00000015612510931621000 | Group58 | *[BMP4, GATA3, HNF1B]* |
| GO:0060681 | branch elongation involved in ureteric bud branching | 0,0003 | 0,00000015612510931621000 | Group58 | *[BMP4, HNF1B, SIX1]* |
| GO:1900200 | mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:1900211 | regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:1900212 | negative regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:0061209 | cell proliferation involved in mesonephros development | 0,0042 | 0,00000015612510931621000 | Group58 | *[BMP4, GATA3]* |
| GO:1901145 | mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:0072039 | regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:0072040 | negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00000015612510931621000 | Group58 | *[HNF1B, PAX2]* |
| GO:0007442 | **hindgut morphogenesis** | 0,0000 | 0,00000350065534133067000 | Group43 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0061525 | hindgut development | 0,0000 | 0,00000350065534133067000 | Group43 | *[DACT1, GLI2, GLI3, HOXD13, SHH]* |
| GO:0048619 | embryonic hindgut morphogenesis | 0,0042 | 0,00000350065534133067000 | Group43 | *[DACT1, HOXD13]* |
| GO:1904864 | negative regulation of beta-catenin-TCF complex assembly | 0,0311 | 0,00000350065534133067000 | Group43 | *[DACT1]* |
| GO:0072095 | regulation of branch elongation involved in ureteric bud branching | 0,0001 | 0,00001009374253541120000 | Group63 | *[BMP4, HNF1B, SIX1]* |
| GO:0061218 | **negative regulation of mesonephros development** | 0,0001 | 0,00001009374253541120000 | Group63 | *[BMP4, GATA3, HNF1B]* |
| GO:0060681 | branch elongation involved in ureteric bud branching | 0,0003 | 0,00001009374253541120000 | Group63 | *[BMP4, HNF1B, SIX1]* |
| GO:1900200 | mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:1900211 | regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:1900212 | negative regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:1901145 | mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:0072039 | regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:0072040 | negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00001009374253541120000 | Group63 | *[HNF1B, PAX2]* |
| GO:0072181 | mesonephric duct formation | 0,0308 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0072114 | pronephros morphogenesis | 0,0308 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0039020 | pronephric nephron tubule development | 0,0308 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061017 | hepatoblast differentiation | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061215 | mesonephric nephron development | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061206 | mesonephros morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061228 | mesonephric nephron morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0035565 | regulation of pronephros size | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061235 | mesenchymal stem cell maintenance involved in mesonephric nephron morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:1901146 | mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061295 | regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0061296 | negative regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00001009374253541120000 | Group63 | *[HNF1B]* |
| GO:0060017 | **parathyroid gland development** | 0,0000 | 0,00002878871682428710000 | Group28 | *[CRKL, GATA3, PAX1, TBX1]* |
| GO:0002072 | **optic cup morphogenesis involved in camera-type eye development** | 0,0000 | 0,00005308171007430080000 | Group19 | *[ARID1A, PAX2, SOX11, TFAP2A]* |
| GO:0072179 | nephric duct formation | 0,0000 | 0,00014427823298999100000 | Group66 | *[BMP4, GATA3, HNF1B, PAX2]* |
| GO:1900200 | **mesenchymal cell apoptotic process involved in metanephros development** | 0,0029 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:1900211 | regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:1900212 | negative regulation of mesenchymal cell apoptotic process involved in metanephros development | 0,0029 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:1901145 | mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:0072039 | regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:0072040 | negative regulation of mesenchymal cell apoptotic process involved in nephron morphogenesis | 0,0042 | 0,00014427823298999100000 | Group66 | *[HNF1B, PAX2]* |
| GO:0072181 | mesonephric duct formation | 0,0308 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:2000594 | positive regulation of metanephric DCT cell differentiation | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0039017 | pattern specification involved in pronephros development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0021633 | optic nerve structural organization | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0072004 | kidney field specification | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0072114 | pronephros morphogenesis | 0,0308 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:1900204 | apoptotic process involved in metanephric collecting duct development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0035566 | regulation of metanephros size | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1900214 | regulation of apoptotic process involved in metanephric collecting duct development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0039003 | pronephric field specification | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0039020 | pronephric nephron tubule development | 0,0308 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0072309 | mesenchymal stem cell maintenance involved in metanephric nephron morphogenesis | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1900215 | negative regulation of apoptotic process involved in metanephric collecting duct development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1901147 | mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1900205 | apoptotic process involved in metanephric nephron tubule development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0072304 | regulation of mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1900217 | regulation of apoptotic process involved in metanephric nephron tubule development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0072305 | negative regulation of mesenchymal cell apoptotic process involved in metanephric nephron morphogenesis | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:1900218 | negative regulation of apoptotic process involved in metanephric nephron tubule development | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:2000592 | regulation of metanephric DCT cell differentiation | 0,0308 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0061017 | hepatoblast differentiation | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0061360 | optic chiasma development | 0,0311 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0061215 | mesonephric nephron development | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0021634 | optic nerve formation | 0,0311 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0061206 | mesonephros morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0061228 | mesonephric nephron morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:2000595 | regulation of optic nerve formation | 0,0311 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0035565 | regulation of pronephros size | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0061235 | mesenchymal stem cell maintenance involved in mesonephric nephron morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:1901146 | mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:2000597 | positive regulation of optic nerve formation | 0,0311 | 0,00014427823298999100000 | Group66 | *[PAX2]* |
| GO:0061295 | regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0061296 | negative regulation of mesenchymal cell apoptotic process involved in mesonephric nephron morphogenesis | 0,0311 | 0,00014427823298999100000 | Group66 | *[HNF1B]* |
| GO:0060129 | **thyroid-stimulating hormone-secreting cell differentiation** | 0,0029 | 0,00014427823298999100000 | Group50 | *[FGF8, WNT4]* |
| GO:0021965 | spinal cord ventral commissure morphogenesis | 0,0042 | 0,00014427823298999100000 | Group50 | *[DCC, GLI2]* |
| GO:0033563 | dorsal/ventral axon guidance | 0,0042 | 0,00014427823298999100000 | Group50 | *[DCC, FGF8]* |
| GO:0090133 | mesendoderm migration | 0,0308 | 0,00014427823298999100000 | Group50 | *[FGF8]* |
| GO:0090134 | cell migration involved in mesendoderm migration | 0,0308 | 0,00014427823298999100000 | Group50 | *[FGF8]* |
| GO:0060128 | corticotropin hormone secreting cell differentiation | 0,0308 | 0,00014427823298999100000 | Group50 | *[FGF8]* |
| GO:1902255 | **positive regulation of intrinsic apoptotic signaling pathway by p53 class mediator** | 0,0003 | 0,00043425108643800800000 | Group40 | *[RPL11, RPL26, RPS7]* |
| GO:1904803 | regulation of translation involved in cellular response to UV | 0,0311 | 0,00043425108643800800000 | Group40 | *[RPL26]* |
| GO:1902167 | positive regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator | 0,0311 | 0,00043425108643800800000 | Group40 | *[RPL26]* |
| GO:1990414 | **replication-born double-strand break repair via sister chromatid exchange** | 0,0003 | 0,00078696702973208800000 | Group54 | *[FANCB, NIPBL, RAD51]* |
| GO:0035261 | external genitalia morphogenesis | 0,0308 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:0120187 | positive regulation of protein localization to chromatin | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:1905309 | positive regulation of cohesin loading | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:0061780 | mitotic cohesin loading | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:0070550 | rDNA condensation | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:1905405 | regulation of mitotic cohesin loading | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:1905406 | positive regulation of mitotic cohesin loading | 0,0311 | 0,00078696702973208800000 | Group54 | *[NIPBL]* |
| GO:0003404 | **optic vesicle morphogenesis** | 0,0012 | 0,00078696702973208800000 | Group47 | *[SIX3, TFAP2A]* |
| GO:0060235 | lens induction in camera-type eye | 0,0042 | 0,00078696702973208800000 | Group47 | *[BMP4, SIX3]* |
| GO:0021622 | oculomotor nerve morphogenesis | 0,0308 | 0,00078696702973208800000 | Group47 | *[TFAP2A]* |
| GO:0021623 | oculomotor nerve formation | 0,0308 | 0,00078696702973208800000 | Group47 | *[TFAP2A]* |
| GO:0003409 | optic cup structural organization | 0,0311 | 0,00078696702973208800000 | Group47 | *[TFAP2A]* |
| GO:0005007 | **fibroblast growth factor-activated receptor activity** | 0,0004 | 0,00123759864346482000000 | Group55 | *[FGFR1, FGFR2, FGFR3]* |
| GO:0035607 | fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development | 0,0029 | 0,00123759864346482000000 | Group55 | *[FGFR1, FGFR2]* |
| GO:0021847 | ventricular zone neuroblast division | 0,0042 | 0,00123759864346482000000 | Group55 | *[FGFR1, FGFR2]* |
| GO:2000830 | positive regulation of parathyroid hormone secretion | 0,0308 | 0,00123759864346482000000 | Group55 | *[FGFR1]* |
| GO:1903465 | positive regulation of mitotic cell cycle DNA replication | 0,0308 | 0,00123759864346482000000 | Group55 | *[FGFR1]* |
| GO:0035604 | fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow | 0,0311 | 0,00123759864346482000000 | Group55 | *[FGFR2]* |
| GO:0035603 | fibroblast growth factor receptor signaling pathway involved in hemopoiesis | 0,0311 | 0,00123759864346482000000 | Group55 | *[FGFR2]* |
| GO:1902178 | fibroblast growth factor receptor apoptotic signaling pathway | 0,0311 | 0,00123759864346482000000 | Group55 | *[FGFR3]* |
| GO:0035602 | fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptotic process in bone marrow cell | 0,0311 | 0,00123759864346482000000 | Group55 | *[FGFR2]* |
| GO:0060129 | thyroid-stimulating hormone-secreting cell differentiation | 0,0029 | 0,00261216537232268000000 | Group61 | *[FGF8, WNT4]* |
| GO:0033563 | **dorsal/ventral axon guidance** | 0,0042 | 0,00261216537232268000000 | Group61 | *[DCC, FGF8]* |
| GO:0090133 | mesendoderm migration | 0,0308 | 0,00261216537232268000000 | Group61 | *[FGF8]* |
| GO:0032346 | positive regulation of aldosterone metabolic process | 0,0308 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:0090134 | cell migration involved in mesendoderm migration | 0,0308 | 0,00261216537232268000000 | Group61 | *[FGF8]* |
| GO:2000225 | negative regulation of testosterone biosynthetic process | 0,0308 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:0032349 | positive regulation of aldosterone biosynthetic process | 0,0308 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:0060128 | corticotropin hormone secreting cell differentiation | 0,0308 | 0,00261216537232268000000 | Group61 | *[FGF8]* |
| GO:0031945 | positive regulation of glucocorticoid metabolic process | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:2000019 | negative regulation of male gonad development | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:2000180 | negative regulation of androgen biosynthetic process | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:0031948 | positive regulation of glucocorticoid biosynthetic process | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:0061369 | negative regulation of testicular blood vessel morphogenesis | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:2000066 | positive regulation of cortisol biosynthetic process | 0,0311 | 0,00261216537232268000000 | Group61 | *[WNT4]* |
| GO:1902659 | **regulation of glucose mediated signaling pathway** | 0,0029 | 0,00570595639738426000000 | Group39 | *[SMARCA4, SMARCB1]* |
| GO:1902661 | positive regulation of glucose mediated signaling pathway | 0,0029 | 0,00570595639738426000000 | Group39 | *[SMARCA4, SMARCB1]* |
| GO:1900110 | negative regulation of histone H3-K9 dimethylation | 0,0308 | 0,00570595639738426000000 | Group39 | *[SMARCB1]* |
| GO:0051978 | **lysophospholipid:sodium symporter activity** | 0,0012 | 0,00570595639738426000000 | Group38 | *[MFSD2A, PHGDH]* |
| GO:0140348 | lysophosphatidylcholine flippase activity | 0,0012 | 0,00570595639738426000000 | Group38 | *[MFSD2A, PHGDH]* |
| GO:0051977 | lysophospholipid transport | 0,0029 | 0,00570595639738426000000 | Group38 | *[MFSD2A, PHGDH]* |
| GO:0021698 | cerebellar cortex structural organization | 0,0012 | 0,00988291818028353000000 | Group53 | *[DLL1, KIF14]* |
| GO:0021693 | **cerebellar Purkinje cell layer structural organization** | 0,0012 | 0,00988291818028353000000 | Group53 | *[DLL1, KIF14]* |
| GO:0021687 | cerebellar molecular layer morphogenesis | 0,0308 | 0,00988291818028353000000 | Group53 | *[DLL1]* |
| GO:0060844 | arterial endothelial cell fate commitment | 0,0308 | 0,00988291818028353000000 | Group53 | *[DLL1]* |
| GO:0021685 | cerebellar granular layer structural organization | 0,0311 | 0,00988291818028353000000 | Group53 | *[KIF14]* |
| GO:0021688 | cerebellar molecular layer formation | 0,0311 | 0,00988291818028353000000 | Group53 | *[DLL1]* |
| GO:0060853 | Notch signaling pathway involved in arterial endothelial cell fate commitment | 0,0311 | 0,00988291818028353000000 | Group53 | *[DLL1]* |
| GO:0044867 | modulation by host of viral catalytic activity | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:0044870 | modulation by host of viral glycoprotein metabolic process | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:0044871 | negative regulation by host of viral glycoprotein metabolic process | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:0044866 | **modulation by host of viral exo-alpha-sialidase activity** | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:0052403 | negative regulation by host of symbiont catalytic activity | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:0044869 | negative regulation by host of viral exo-alpha-sialidase activity | 0,0042 | 0,00988291818028353000000 | Group52 | *[PITX2, PITX3]* |
| GO:1904935 | positive regulation of cell proliferation in midbrain | 0,0308 | 0,00988291818028353000000 | Group52 | *[PITX3]* |
| GO:0061073 | **ciliary body morphogenesis** | 0,0042 | 0,02074592889975570000000 | Group44 | *[JAG1, NOTCH2]* |
| GO:0035622 | intrahepatic bile duct development | 0,0308 | 0,02074592889975570000000 | Group44 | *[NOTCH2]* |
| GO:0061443 | endocardial cushion cell differentiation | 0,0308 | 0,02074592889975570000000 | Group44 | *[JAG1]* |
| GO:0061444 | endocardial cushion cell development | 0,0311 | 0,02074592889975570000000 | Group44 | *[JAG1]* |
| GO:0060827 | regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation | 0,0311 | 0,07763034740949140000000 | Group36 | *[TBX18]* |
| GO:0060829 | negative regulation of canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation | 0,0311 | 0,07763034740949140000000 | Group36 | *[TBX18]* |
| GO:0060823 | canonical Wnt signaling pathway involved in neural plate anterior/posterior pattern formation | 0,0311 | 0,07763034740949140000000 | Group36 | *[TBX18]* |
| GO:1905453 | regulation of myeloid progenitor cell differentiation | 0,0311 | 0,07763034740949140000000 | Group33 | *[DPF2]* |
| GO:1905454 | negative regulation of myeloid progenitor cell differentiation | 0,0311 | 0,07763034740949140000000 | Group33 | *[DPF2]* |
| GO:0070512 | positive regulation of histone H4-K20 methylation | 0,0311 | 0,07763034740949140000000 | Group31 | *[BRCA1]* |
| GO:0070510 | regulation of histone H4-K20 methylation | 0,0311 | 0,07763034740949140000000 | Group31 | *[BRCA1]* |
| GO:0034516 | response to vitamin B6 | 0,0311 | 0,07763034740949140000000 | Group24 | *[KYNU]* |
| GO:0003345 | proepicardium cell migration involved in pericardium morphogenesis | 0,0311 | 0,07763034740949140000000 | Group21 | *[FLRT3]* |
| GO:1905349 | ciliary transition zone assembly | 0,0311 | 0,07763034740949140000000 | Group15 | *[DZIP1L]* |
| GO:1903045 | neural crest cell migration involved in sympathetic nervous system development | 0,0311 | 0,07763034740949140000000 | Group13 | *[SEMA3A]* |
| GO:0016132 | brassinosteroid biosynthetic process | 0,0311 | 0,07763034740949140000000 | Group10 | *[DHCR7]* |
| GO:0014886 | transition between slow and fast fiber | 0,0311 | 0,07763034740949140000000 | Group09 | *[GTF2IRD1]* |
| GO:0003271 | smoothened signaling pathway involved in regulation of secondary heart field cardioblast proliferation | 0,0311 | 0,07763034740949140000000 | Group08 | *[MKS1]* |
| GO:0070413 | trehalose metabolism in response to stress | 0,0311 | 0,07763034740949140000000 | Group04 | *[BRAF]* |
| GO:0007225 | patched ligand maturation | 0,0311 | 0,07763034740949140000000 | Group03 | *[DISP1]* |
| GO:0007066 | female meiosis sister chromatid cohesion | 0,0311 | 0,07763034740949140000000 | Group02 | *[RAD51C]* |
| GO:0003226 | right ventricular compact myocardium morphogenesis | 0,0311 | 0,07763034740949140000000 | Group00 | *[CHD7]* |
| GO:2000334 | positive regulation of blood microparticle formation | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0032724 | positive regulation of fractalkine production | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0050756 | fractalkine metabolic process | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:1904997 | regulation of leukocyte adhesion to arterial endothelial cell | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0050751 | fractalkine biosynthetic process | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0002876 | positive regulation of chronic inflammatory response to antigenic stimulus | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0050752 | regulation of fractalkine biosynthetic process | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0045994 | positive regulation of translational initiation by iron | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0050754 | positive regulation of fractalkine biosynthetic process | 0,0308 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:1904999 | positive regulation of leukocyte adhesion to arterial endothelial cell | 0,0311 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0061048 | negative regulation of branching involved in lung morphogenesis | 0,0311 | 0,08962638171853740000000 | Group57 | *[TNF]* |
| GO:0035332 | positive regulation of hippo signaling | 0,0308 | 0,12135546385556200000000 | Group49 | *[SOX11]* |
| GO:0097166 | lens epithelial cell proliferation | 0,0308 | 0,12135546385556200000000 | Group49 | *[SOX11]* |
| GO:2001111 | positive regulation of lens epithelial cell proliferation | 0,0308 | 0,12135546385556200000000 | Group49 | *[SOX11]* |
| GO:2001109 | regulation of lens epithelial cell proliferation | 0,0308 | 0,12135546385556200000000 | Group49 | *[SOX11]* |
| GO:0061386 | closure of optic fissure | 0,0308 | 0,12135546385556200000000 | Group49 | *[SOX11]* |
| GO:1901581 | negative regulation of telomeric RNA transcription from RNA pol II promoter | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:1901582 | positive regulation of telomeric RNA transcription from RNA pol II promoter | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:0035127 | post-embryonic limb morphogenesis | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:0035128 | post-embryonic forelimb morphogenesis | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:0097393 | telomeric repeat-containing RNA transcription | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:0097394 | telomeric repeat-containing RNA transcription by RNA polymerase II | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:1901580 | regulation of telomeric RNA transcription from RNA pol II promoter | 0,0308 | 0,12324768689260000000000 | Group51 | *[ATRX]* |
| GO:0097379 | dorsal spinal cord interneuron posterior axon guidance | 0,0308 | 0,12324768689260000000000 | Group48 | *[LHX1]* |
| GO:0035846 | oviduct epithelium development | 0,0308 | 0,12324768689260000000000 | Group48 | *[LHX1]* |
| GO:0035847 | uterine epithelium development | 0,0308 | 0,12324768689260000000000 | Group48 | *[LHX1]* |
| GO:0035849 | nephric duct elongation | 0,0308 | 0,12324768689260000000000 | Group48 | *[LHX1]* |
| GO:0035852 | horizontal cell localization | 0,0308 | 0,12324768689260000000000 | Group48 | *[LHX1]* |
| GO:0090299 | regulation of neural crest formation | 0,0308 | 0,12324768689260000000000 | Group42 | *[FUZ]* |
| GO:2000314 | negative regulation of fibroblast growth factor receptor signaling pathway involved in neural plate anterior/posterior pattern formation | 0,0308 | 0,12324768689260000000000 | Group42 | *[FUZ]* |
| GO:0090301 | negative regulation of neural crest formation | 0,0308 | 0,12324768689260000000000 | Group42 | *[FUZ]* |
| GO:0019202 | amino acid kinase activity | 0,0308 | 0,12324768689260000000000 | Group41 | *[ALDH18A1]* |
| GO:0006592 | ornithine biosynthetic process | 0,0311 | 0,12324768689260000000000 | Group41 | *[ALDH18A1]* |
| GO:0004349 | glutamate 5-kinase activity | 0,0311 | 0,12324768689260000000000 | Group41 | *[ALDH18A1]* |
| GO:0050666 | regulation of homocysteine metabolic process | 0,0308 | 0,12324768689260000000000 | Group37 | *[COMT]* |
| GO:0031337 | positive regulation of sulfur amino acid metabolic process | 0,0311 | 0,12324768689260000000000 | Group37 | *[COMT]* |
| GO:0050668 | positive regulation of homocysteine metabolic process | 0,0311 | 0,12324768689260000000000 | Group37 | *[COMT]* |
| GO:0051800 | phosphatidylinositol-3,4-bisphosphate 3-phosphatase activity | 0,0308 | 0,12324768689260000000000 | Group35 | *[PTEN]* |
| GO:2000808 | negative regulation of synaptic vesicle clustering | 0,0308 | 0,12324768689260000000000 | Group35 | *[PTEN]* |
| GO:1901255 | nucleotide-excision repair involved in interstrand cross-link repair | 0,0308 | 0,12324768689260000000000 | Group34 | *[ERCC4]* |
| GO:1905768 | negative regulation of double-stranded telomeric DNA binding | 0,0311 | 0,12324768689260000000000 | Group34 | *[ERCC4]* |
| GO:1901999 | homogentisate metabolic process | 0,0308 | 0,12324768689260000000000 | Group32 | *[FANCA]* |
| GO:1902000 | homogentisate catabolic process | 0,0308 | 0,12324768689260000000000 | Group32 | *[FANCA]* |
| GO:0070171 | negative regulation of tooth mineralization | 0,0308 | 0,12324768689260000000000 | Group30 | *[BCOR]* |
| GO:0000415 | negative regulation of histone H3-K36 methylation | 0,0311 | 0,12324768689260000000000 | Group30 | *[BCOR]* |
| GO:0061582 | intestinal epithelial cell migration | 0,0308 | 0,12324768689260000000000 | Group29 | *[PTPN11]* |
| GO:0051463 | negative regulation of cortisol secretion | 0,0311 | 0,12324768689260000000000 | Group29 | *[PTPN11]* |
| GO:0048257 | 3'-flap endonuclease activity | 0,0308 | 0,12324768689260000000000 | Group27 | *[SLX4]* |
| GO:0035685 | helper T cell diapedesis | 0,0308 | 0,12324768689260000000000 | Group26 | *[CRKL]* |
| GO:0035545 | determination of left/right asymmetry in nervous system | 0,0308 | 0,12324768689260000000000 | Group25 | *[ZIC3]* |
| GO:0002728 | negative regulation of natural killer cell cytokine production | 0,0308 | 0,12324768689260000000000 | Group23 | *[CD96]* |
| GO:0021997 | neural plate axis specification | 0,0308 | 0,12324768689260000000000 | Group22 | *[PTCH1]* |
| GO:0021831 | embryonic olfactory bulb interneuron precursor migration | 0,0308 | 0,12324768689260000000000 | Group20 | *[ARX]* |
| GO:0051877 | pigment granule aggregation in cell center | 0,0308 | 0,12324768689260000000000 | Group18 | *[MKKS]* |
| GO:1905706 | regulation of mitochondrial ATP synthesis coupled proton transport | 0,0308 | 0,12324768689260000000000 | Group17 | *[DNAJC30]* |
| GO:1905474 | canonical Wnt signaling pathway involved in stem cell proliferation | 0,0308 | 0,12324768689260000000000 | Group16 | *[WNT3]* |
| GO:1903691 | positive regulation of wound healing, spreading of epidermal cells | 0,0308 | 0,12324768689260000000000 | Group14 | *[RREB1]* |
| GO:0050925 | negative regulation of negative chemotaxis | 0,0308 | 0,12324768689260000000000 | Group12 | *[ROBO2]* |
| GO:1901631 | positive regulation of presynaptic membrane organization | 0,0308 | 0,12324768689260000000000 | Group11 | *[LRP4]* |
| GO:0072554 | blood vessel lumenization | 0,0308 | 0,12324768689260000000000 | Group07 | *[DLL4]* |
| GO:0071932 | replication fork reversal | 0,0308 | 0,12324768689260000000000 | Group06 | *[FANCM]* |
| GO:0070476 | rRNA (guanine-N7)-methylation | 0,0308 | 0,12324768689260000000000 | Group05 | *[BUD23]* |
| GO:0061034 | olfactory bulb mitral cell layer development | 0,0308 | 0,12324768689260000000000 | Group01 | *[SALL1]* |
| GO:0021644 | vagus nerve morphogenesis | 0,0308 | 0,13758378092810300000000 | Group46 | *[TBX1]* |
| GO:0035981 | tongue muscle cell differentiation | 0,0308 | 0,13758378092810300000000 | Group46 | *[TBX1]* |
| GO:2001035 | regulation of tongue muscle cell differentiation | 0,0308 | 0,13758378092810300000000 | Group46 | *[TBX1]* |
| GO:2001037 | positive regulation of tongue muscle cell differentiation | 0,0308 | 0,13758378092810300000000 | Group46 | *[TBX1]* |
| GO:0052885 | all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity | 0,0308 | 0,13758378092810300000000 | Group45 | *[SLC27A4]* |
| GO:0001579 | medium-chain fatty acid transport | 0,0308 | 0,13758378092810300000000 | Group45 | *[SLC27A4]* |
| GO:0062002 | regulation of all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity | 0,0311 | 0,13758378092810300000000 | Group45 | *[SLC27A4]* |
| GO:0062003 | negative regulation of all-trans-retinyl-ester hydrolase, 11-cis retinol forming activity | 0,0311 | 0,13758378092810300000000 | Group45 | *[SLC27A4]* |

**Supporting Information Figure 1**: We used the standard corrected p value < 0.05 and kept the default ClueGO features, that allow to extract from selected GO terms with at least three genes from the initial list and genes that represent at least 4% from the total number of genes associated to a specific term.