## SUPPLEMENTARY MATERIAL

**corresponding to:**

# Identification and functional analysis of novel genes expressed in the Anterior Visceral Endoderm

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**Supp. Table 1**: DAVID analysis of Ad upregulated population regarding Biological Processes (p ≤0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_BP_ALL | pattern specification process | RT | | 15 | 9,0 | 6,1E-8 | 7,3E-5 |
| ☐ | GOTERM_BP_ALL | embryonic development | RT | | 22 | 13,2 | 6,9E-8 | 4,2E-5 |
| ☐ | GOTERM_BP_ALL | regionalization | RT | | 12 | 7,2 | 1,2E-6 | 4,6E-4 |
| ☐ | GOTERM_BP_ALL | tube development | RT | | 13 | 7,8 | 1,3E-6 | 4,0E-4 |
| ☐ | GOTERM_BP_ALL | brain development | RT | | 13 | 7,8 | 3,3E-6 | 8,0E-4 |
| ☐ | GOTERM_BP_ALL | anterior/posterior pattern formation | RT | | 10 | 6,0 | 3,8E-6 | 7,6E-4 |
| ☐ | GOTERM_BP_ALL | embryonic morphogenesis | RT | | 14 | 8,4 | 5,9E-6 | 1,0E-3 |
| ☐ | GOTERM_BP_ALL | negative regulation of cellular process | RT | | 26 | 15,6 | 6,5E-6 | 9,7E-4 |
| ☐ | GOTERM_BP_ALL | nervous system development | RT | | 21 | 12,6 | 1,3E-5 | 1,8E-3 |
| ☐ | GOTERM_BP_ALL | negative regulation of biological process | RT | | 27 | 16,2 | 1,4E-5 | 1,6E-3 |
| ☐ | GOTERM_BP_ALL | multicellular organismal development | RT | | 40 | 24,0 | 1,7E-5 | 1,8E-3 |
| ☐ | GOTERM_BP_ALL | anatomical structure morphogenesis | RT | | 24 | 14,4 | 2,1E-5 | 2,1E-3 |
| ☐ | GOTERM_BP_ALL | central nervous system development | RT | | 13 | 7,8 | 4,0E-5 | 3,7E-3 |
| ☐ | GOTERM_BP_ALL | developmental process | RT | | 41 | 24,6 | 5,1E-5 | 4,3E-3 |
| ☐ | GOTERM_BP_ALL | anatomical structure development | RT | | 35 | 21,0 | 5,7E-5 | 4,6E-3 |
| ☐ | GOTERM_BP_ALL | respiratory system development | RT | | 8 | 4,8 | 6,2E-5 | 4,6E-3 |
| ☐ | GOTERM_BP_ALL | organ morphogenesis | RT | | 16 | 9,6 | 7,8E-5 | 5,5E-3 |
| ☐ | GOTERM_BP_ALL | Wnt receptor signaling pathway | RT | | 8 | 4,8 | 8,3E-5 | 5,5E-3 |
| ☐ | GOTERM_BP_ALL | organ development | RT | | 29 | 17,4 | 9,4E-5 | 5,9E-3 |
| ☐ | GOTERM_BP_ALL | regulation of transcription from RNA polymerase II promoter | RT | | 16 | 9,6 | 1,2E-4 | 7,0E-3 |
| ☐ | GOTERM_BP_ALL | positive regulation of gene expression | RT | | 14 | 8,4 | 1,4E-4 | 8,2E-3 |
| ☐ | GOTERM_BP_ALL | anatomical structure formation involved in morphogenesis | RT | | 12 | 7,2 | 1,7E-4 | 9,0E-3 |
| ☐ | GOTERM_BP_ALL | lung development | RT | | 7 | 4,2 | 2,7E-4 | 1,4E-2 |
| ☐ | GOTERM_BP_ALL | respiratory tube development | RT | | 7 | 4,2 | 2,9E-4 | 1,5E-2 |
| ☐ | GOTERM_BP_ALL | regulation of cell proliferation | RT | | 14 | 8,4 | 3,7E-4 | 1,8E-2 |
| ☐ | GOTERM_BP_ALL | forebrain development | RT | | 8 | 4,8 | 3,9E-4 | 1,8E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of transcription | RT | | 13 | 7,8 | 4,2E-4 | 1,9E-2 |
| ☐ | GOTERM_BP_ALL | system development | RT | | 31 | 18,6 | 5,0E-4 | 2,1E-2 |
| ☐ | GOTERM_BP_ALL | morphogenesis of a branching structure | RT | | 7 | 4,2 | 5,0E-4 | 2,1E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of transcription, DNA-dependent | RT | | 12 | 7,2 | 5,1E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of macromolecule metabolic process | RT | | 15 | 9,0 | 5,3E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of RNA metabolic process | RT | | 12 | 7,2 | 5,4E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | chordate embryonic development | RT | | 12 | 7,2 | 5,6E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | transforming growth factor beta receptor signaling pathway | RT | | 5 | 3,0 | 5,8E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of transcription from RNA polymerase II promoter | RT | | 11 | 6,6 | 6,0E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | embryonic development ending in birth or egg hatching | RT | | 12 | 7,2 | 6,1E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | regulation of RNA metabolic process | RT | | 25 | 15,0 | 6,3E-4 | 2,0E-2 |
| ☐ | GOTERM_BP_ALL | embryonic organ development | RT | | 9 | 5,4 | 7,1E-4 | 2,2E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 13 | 7,8 | 7,9E-4 | 2,4E-2 |
| ☐ | GOTERM_BP_ALL | branching morphogenesis of a tube | RT | | 6 | 3,6 | 9,0E-4 | 2,7E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of nitrogen compound metabolic process | RT | | 13 | 7,8 | 1,0E-3 | 3,0E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of macromolecule biosynthetic process | RT | | 13 | 7,8 | 1,1E-3 | 3,1E-2 |
| ☐ | GOTERM_BP_ALL | regulation of transcription | RT | | 32 | 19,2 | 1,1E-3 | 3,1E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of metabolic process | RT | | 15 | 9,0 | 1,1E-3 | 3,0E-2 |
| ☐ | GOTERM_BP_ALL | regulation of gene expression | RT | | 34 | 20,4 | 1,1E-3 | 2,9E-2 |
| ☐ | GOTERM_BP_ALL | regulation of transcription, DNA-dependent | RT | | 24 | 14,4 | 1,2E-3 | 3,1E-2 |
| ☐ | GOTERM_BP_ALL | regulation of nitrogen compound metabolic process | RT | | 33 | 19,8 | 1,5E-3 | 3,9E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of biological process | RT | | 24 | 14,4 | 1,5E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular biosynthetic process | RT | | 13 | 7,8 | 1,6E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | enzyme linked receptor protein signaling pathway | RT | | 9 | 5,4 | 1,6E-3 | 3,7E-2 |
| ☐ | GOTERM_BP_ALL | regulation of macromolecule metabolic process | RT | | 36 | 21,6 | 1,6E-3 | 3,7E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of biosynthetic process | RT | | 13 | 7,8 | 1,7E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | dorsal/ventral pattern formation | RT | | 5 | 3,0 | 1,7E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular process | RT | | 22 | 13,2 | 1,7E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | tissue development | RT | | 14 | 8,4 | 1,8E-3 | 3,8E-2 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular metabolic process | RT | | 14 | 8,4 | 1,9E-3 | 4,1E-2 |
| ☐ | GOTERM_BP_ALL | tube morphogenesis | RT | | 7 | 4,2 | 2,5E-3 | 5,2E-2 |
| ☐ | GOTERM_BP_ALL | regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 32 | 19,2 | 2,7E-3 | 5,5E-2 |
| ☐ | GOTERM_BP_ALL | regulation of primary metabolic process | RT | | 35 | 21,0 | 2,9E-3 | 5,7E-2 |
| ☐ | GOTERM_BP_ALL | regulation of cellular biosynthetic process | RT | | 33 | 19,8 | 2,9E-3 | 5,7E-2 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_BP_ALL | gastrulation | RT | | 5 | 3,0 | 2,9E-3 | 5,6E-2 |
| ☐ | GOTERM_BP_ALL | regulation of cellular metabolic process | RT | | 36 | 21,6 | 3,0E-3 | 5,7E-2 |
| ☐ | GOTERM_BP_ALL | tissue morphogenesis | RT | | 8 | 4,8 | 3,0E-3 | 5,6E-2 |
| ☐ | GOTERM_BP_ALL | regulation of biosynthetic process | RT | | 33 | 19,8 | 3,1E-3 | 5,7E-2 |
| ☐ | GOTERM_BP_ALL | regulation of macromolecule biosynthetic process | RT | | 32 | 19,2 | 3,3E-3 | 5,9E-2 |
| ☐ | GOTERM_BP_ALL | transmembrane receptor protein serine/threonine kinase signaling pathway | RT | | 5 | 3,0 | 3,5E-3 | 6,3E-2 |
| ☐ | GOTERM_BP_ALL | regulation of metabolic process | RT | | 37 | 22,2 | 4,1E-3 | 7,0E-2 |
| ☐ | GOTERM_BP_ALL | neural tube development | RT | | 5 | 3,0 | 4,4E-3 | 7,5E-2 |
| ☐ | GOTERM_BP_ALL | ureteric bud development | RT | | 4 | 2,4 | 4,6E-3 | 7,7E-2 |
| ☐ | GOTERM_BP_ALL | transcription | RT | | 25 | 15,0 | 6,5E-3 | 1,1E-1 |
| ☐ | GOTERM_BP_ALL | embryonic heart tube development | RT | | 3 | 1,8 | 7,1E-3 | 1,1E-1 |
| ☐ | GOTERM_BP_ALL | anterior/posterior axis specification | RT | | 3 | 1,8 | 8,0E-3 | 1,3E-1 |
| ☐ | GOTERM_BP_ALL | lung morphogenesis | RT | | 3 | 1,8 | 8,0E-3 | 1,3E-1 |
| ☐ | GOTERM_BP_ALL | heart development | RT | | 7 | 4,2 | 9,1E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cell proliferation | RT | | 7 | 4,2 | 9,3E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | embryonic organ morphogenesis | RT | | 6 | 3,6 | 9,5E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | ear development | RT | | 5 | 3,0 | 9,7E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of transcription from RNA polymerase II promoter | RT | | 7 | 4,2 | 1,1E-2 | 1,5E-1 |
| ☐ | GOTERM_BP_ALL | metanephros development | RT | | 4 | 2,4 | 1,1E-2 | 1,6E-1 |
| ☐ | GOTERM_BP_ALL | cell fate specification | RT | | 4 | 2,4 | 1,2E-2 | 1,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of signal transduction | RT | | 6 | 3,6 | 1,2E-2 | 1,7E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of nitrogen compound metabolic process | RT | | 9 | 5,4 | 1,5E-2 | 2,0E-1 |
| ☐ | GOTERM_BP_ALL | neural tube patterning | RT | | 3 | 1,8 | 1,6E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | patterning of blood vessels | RT | | 3 | 1,8 | 1,6E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | regulation of developmental process | RT | | 11 | 6,6 | 1,6E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | hindbrain development | RT | | 4 | 2,4 | 1,7E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cellular metabolic process | RT | | 10 | 6,0 | 1,7E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cell communication | RT | | 6 | 3,6 | 1,7E-2 | 2,1E-1 |
| ☐ | GOTERM_BP_ALL | cellular developmental process | RT | | 22 | 13,2 | 1,9E-2 | 2,4E-1 |
| ☐ | GOTERM_BP_ALL | axis specification | RT | | 3 | 1,8 | 2,0E-2 | 2,4E-1 |
| ☐ | GOTERM_BP_ALL | nucleosome assembly | RT | | 4 | 2,4 | 2,1E-2 | 2,5E-1 |
| ☐ | GOTERM_BP_ALL | epithelium development | RT | | 7 | 4,2 | 2,2E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | ectoderm development | RT | | 5 | 3,0 | 2,2E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | angiogenesis | RT | | 5 | 3,0 | 2,2E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cellular biosynthetic process | RT | | 9 | 5,4 | 2,2E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | chromatin assembly | RT | | 4 | 2,4 | 2,2E-2 | 2,5E-1 |
| ☐ | GOTERM_BP_ALL | endoderm development | RT | | 3 | 1,8 | 2,2E-2 | 2,5E-1 |
| ☐ | GOTERM_BP_ALL | nucleosome organization | RT | | 4 | 2,4 | 2,3E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | protein-DNA complex assembly | RT | | 4 | 2,4 | 2,3E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of biosynthetic process | RT | | 9 | 5,4 | 2,3E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | ectoderm formation | RT | | 2 | 1,2 | 2,4E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | cell differentiation | RT | | 21 | 12,6 | 2,4E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of metabolic process | RT | | 10 | 6,0 | 2,8E-2 | 2,9E-1 |
| ☐ | GOTERM_BP_ALL | neurogenesis | RT | | 10 | 6,0 | 2,9E-2 | 2,9E-1 |
| ☐ | GOTERM_BP_ALL | urogenital system development | RT | | 5 | 3,0 | 3,0E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of transcription | RT | | 8 | 4,8 | 3,0E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | digestive system development | RT | | 3 | 1,8 | 3,0E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | cell fate commitment | RT | | 5 | 3,0 | 3,1E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | inner ear development | RT | | 4 | 2,4 | 3,4E-2 | 3,2E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of transcription, DNA-dependent | RT | | 7 | 4,2 | 3,8E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell migration | RT | | 4 | 2,4 | 3,8E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of RNA metabolic process | RT | | 7 | 4,2 | 3,9E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of Wnt receptor signaling pathway | RT | | 3 | 1,8 | 3,9E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 8 | 4,8 | 4,1E-2 | 3,6E-1 |
| ☐ | GOTERM_BP_ALL | cellular biosynthetic process | RT | | 33 | 19,8 | 4,3E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | cell migration | RT | | 6 | 3,6 | 4,4E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | regulation of biological process | RT | | 63 | 37,7 | 4,4E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | generation of neurons | RT | | 9 | 5,4 | 4,6E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | determination of left/right symmetry | RT | | 3 | 1,8 | 4,6E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | blood vessel development | RT | | 6 | 3,6 | 4,7E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of gene expression | RT | | 8 | 4,8 | 4,7E-2 | 3,9E-1 |

| | Category | Term | | Count | % | P-Value | FDR |
|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_BP_ALL | DNA packaging | RT | 4 | 2,4 | 4,8E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | determination of bilateral symmetry | RT | 3 | 1,8 | 4,8E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | determination of symmetry | RT | 3 | 1,8 | 4,8E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | odontogenesis | RT | 3 | 1,8 | 5,0E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | ameboidal cell migration | RT | 3 | 1,8 | 5,0E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | morphogenesis of an epithelium | RT | 5 | 3,0 | 5,0E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of macromolecule metabolic process | RT | 9 | 5,4 | 5,1E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | vasculature development | RT | 6 | 3,6 | 5,1E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of macromolecule biosynthetic process | RT | 8 | 4,8 | 5,1E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cellular process | RT | 60 | 35,9 | 5,2E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | kidney development | RT | 4 | 2,4 | 5,5E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell motion | RT | 4 | 2,4 | 5,5E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | sensory organ development | RT | 6 | 3,6 | 5,6E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | cell development | RT | 10 | 6,0 | 5,7E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | chromatin assembly or disassembly | RT | 4 | 2,4 | 5,7E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | multicellular organismal process | RT | 44 | 26,3 | 5,8E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | regulation of locomotion | RT | 4 | 2,4 | 5,8E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | epithelial tube morphogenesis | RT | 4 | 2,4 | 6,0E-2 | 4,3E-1 |
| ☐ | GOTERM_BP_ALL | biosynthetic process | RT | 33 | 19,8 | 6,2E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | forebrain morphogenesis | RT | 2 | 1,2 | 6,2E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | biological regulation | RT | 65 | 38,9 | 6,2E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | in utero embryonic development | RT | 6 | 3,6 | 6,4E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | humoral immune response | RT | 3 | 1,8 | 7,0E-2 | 4,7E-1 |
| ☐ | GOTERM_BP_ALL | growth | RT | 5 | 3,0 | 7,0E-2 | 4,7E-1 |
| ☐ | GOTERM_BP_ALL | cell migration involved in gastrulation | RT | 2 | 1,2 | 7,0E-2 | 4,7E-1 |
| ☐ | GOTERM_BP_ALL | gland development | RT | 5 | 3,0 | 7,4E-2 | 4,8E-1 |
| ☐ | GOTERM_BP_ALL | blood vessel morphogenesis | RT | 5 | 3,0 | 7,5E-2 | 4,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of inflammatory response | RT | 3 | 1,8 | 7,6E-2 | 4,9E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of cell proliferation | RT | 6 | 3,6 | 7,8E-2 | 5,0E-1 |
| ☐ | GOTERM_BP_ALL | localization of cell | RT | 6 | 3,6 | 7,8E-2 | 5,0E-1 |
| ☐ | GOTERM_BP_ALL | cell motility | RT | 6 | 3,6 | 7,8E-2 | 5,0E-1 |
| ☐ | GOTERM_BP_ALL | gene expression | RT | 28 | 16,8 | 7,8E-2 | 4,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of signal transduction | RT | 10 | 6,0 | 8,4E-2 | 5,1E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell differentiation | RT | 7 | 4,2 | 9,0E-2 | 5,4E-1 |
| ☐ | GOTERM_BP_ALL | cellular macromolecule biosynthetic process | RT | 26 | 15,6 | 9,6E-2 | 5,6E-1 |
| ☐ | GOTERM_BP_ALL | protein maturation by peptide bond cleavage | RT | 3 | 1,8 | 9,6E-2 | 5,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of response to stimulus | RT | 3 | 1,8 | 9,6E-2 | 5,6E-1 |
| ☐ | GOTERM_BP_ALL | macromolecule biosynthetic process | RT | 26 | 15,6 | 9,8E-2 | 5,7E-1 |
| ☐ | GOTERM_BP_ALL | cell proliferation in forebrain | RT | 2 | 1,2 | 9,9E-2 | 5,7E-1 |
| ☐ | GOTERM_BP_ALL | forebrain regionalization | RT | 2 | 1,2 | 9,9E-2 | 5,7E-1 |

77 gene(s) from your list are not in the output.

**Supp. Table 2**: DAVID analysis of Ad upregulated population regarding Cellular Component (p ≤ 0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|----------|------|-----|-------|-------|---|---------|-----------|
| ☐ | GOTERM_CC_ALL | anchored to membrane | RT | | 7 | 4,2 | 6,9E-3 | 7,0E-1 |
| ☐ | GOTERM_CC_ALL | transcription factor complex | RT | | 7 | 4,2 | 1,2E-2 | 6,5E-1 |
| ☐ | GOTERM_CC_ALL | nucleus | RT | | 48 | 28,7 | 1,3E-2 | 5,4E-1 |
| ☐ | GOTERM_CC_ALL | nucleosome | RT | | 4 | 2,4 | 1,4E-2 | 4,6E-1 |
| ☐ | GOTERM_CC_ALL | protein-DNA complex | RT | | 4 | 2,4 | 2,3E-2 | 5,5E-1 |
| ☐ | GOTERM_CC_ALL | laminin-10 complex | RT | | 2 | 1,2 | 2,4E-2 | 5,0E-1 |
| ☐ | GOTERM_CC_ALL | intracellular organelle | RT | | 79 | 47,3 | 2,7E-2 | 4,8E-1 |
| ☐ | GOTERM_CC_ALL | organelle | RT | | 79 | 47,3 | 2,7E-2 | 4,4E-1 |
| ☐ | GOTERM_CC_ALL | laminin complex | RT | | 2 | 1,2 | 5,6E-2 | 6,6E-1 |
| ☐ | GOTERM_CC_ALL | nucleoplasm part | RT | | 9 | 5,4 | 5,8E-2 | 6,4E-1 |
| ☐ | GOTERM_CC_ALL | external side of plasma membrane | RT | | 5 | 3,0 | 8,8E-2 | 7,6E-1 |
| ☐ | GOTERM_CC_ALL | intracellular part | RT | | 87 | 52,1 | 8,9E-2 | 7,4E-1 |
| ☐ | GOTERM_CC_ALL | intracellular membrane-bounded organelle | RT | | 68 | 40,7 | 9,3E-2 | 7,2E-1 |
| ☐ | GOTERM_CC_ALL | membrane-bounded organelle | RT | | 68 | 40,7 | 9,4E-2 | 7,0E-1 |

72 gene(s) from your list are not in the output.

**Supp. Table 3**: DAVID analysis of Ad upregulated population regarding Molecular Function (p $\leq$ 0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_MF_ALL | DNA binding | RT | | 32 | 19,2 | 1,6E-5 | 4,4E-3 |
| ☐ | GOTERM_MF_ALL | binding | RT | | 108 | 64,7 | 2,1E-4 | 2,9E-2 |
| ☐ | GOTERM_MF_ALL | transcription factor activity | RT | | 16 | 9,6 | 1,2E-3 | 1,0E-1 |
| ☐ | GOTERM_MF_ALL | protein binding | RT | | 64 | 38,3 | 1,4E-3 | 9,3E-2 |
| ☐ | GOTERM_MF_ALL | sequence-specific DNA binding | RT | | 13 | 7,8 | 1,5E-3 | 8,1E-2 |
| ☐ | GOTERM_MF_ALL | transcription regulator activity | RT | | 20 | 12,0 | 2,9E-3 | 1,3E-1 |
| ☐ | GOTERM_MF_ALL | nucleic acid binding | RT | | 35 | 21,0 | 1,2E-2 | 3,8E-1 |
| ☐ | GOTERM_MF_ALL | transcription repressor activity | RT | | 6 | 3,6 | 2,6E-2 | 6,0E-1 |
| ☐ | GOTERM_MF_ALL | kinase activity | RT | | 12 | 7,2 | 6,1E-2 | 8,5E-1 |
| ☐ | GOTERM_MF_ALL | protein domain specific binding | RT | | 5 | 3,0 | 6,6E-2 | 8,5E-1 |
| ☐ | GOTERM_MF_ALL | protein kinase activity | RT | | 9 | 5,4 | 9,2E-2 | 9,1E-1 |

59 gene(s) from your list are not in the output.

**Supp. Table 4**: DAVID analysis of Pp upregulated population regarding Biological Processes (p ≤0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_BP_ALL | regulation of cell differentiation | RT | | 8 | 24,2 | 1,7E-6 | 9,5E-4 |
| ☐ | GOTERM_BP_ALL | regulation of multicellular organismal process | RT | | 9 | 27,3 | 1,8E-5 | 5,0E-3 |
| ☐ | GOTERM_BP_ALL | regulation of developmental process | RT | | 8 | 24,2 | 2,2E-5 | 4,0E-3 |
| ☐ | GOTERM_BP_ALL | anatomical structure development | RT | | 12 | 36,4 | 2,3E-4 | 3,1E-2 |
| ☐ | GOTERM_BP_ALL | system development | RT | | 11 | 33,3 | 6,6E-4 | 6,9E-2 |
| ☐ | GOTERM_BP_ALL | multicellular organismal development | RT | | 12 | 36,4 | 8,8E-4 | 7,8E-2 |
| ☐ | GOTERM_BP_ALL | anatomical structure morphogenesis | RT | | 8 | 24,2 | 1,4E-3 | 1,1E-1 |
| ☐ | GOTERM_BP_ALL | developmental process | RT | | 12 | 36,4 | 1,8E-3 | 1,2E-1 |
| ☐ | GOTERM_BP_ALL | embryonic morphogenesis | RT | | 5 | 15,2 | 2,4E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cell differentiation | RT | | 4 | 12,1 | 3,0E-3 | 1,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of anatomical structure morphogenesis | RT | | 4 | 12,1 | 3,3E-3 | 1,5E-1 |
| ☐ | GOTERM_BP_ALL | organ development | RT | | 9 | 27,3 | 3,3E-3 | 1,4E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell projection size | RT | | 2 | 6,1 | 4,8E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of axon diameter | RT | | 2 | 6,1 | 4,8E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | heart development | RT | | 4 | 12,1 | 5,3E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of developmental process | RT | | 4 | 12,1 | 5,5E-3 | 1,8E-1 |
| ☐ | GOTERM_BP_ALL | tissue morphogenesis | RT | | 4 | 12,1 | 6,4E-3 | 2,0E-1 |
| ☐ | GOTERM_BP_ALL | intermediate filament bundle assembly | RT | | 2 | 6,1 | 6,5E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of transcription, DNA-dependent | RT | | 8 | 24,2 | 6,8E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of RNA metabolic process | RT | | 8 | 24,2 | 7,4E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of biological process | RT | | 8 | 24,2 | 7,5E-3 | 1,9E-1 |
| ☐ | GOTERM_BP_ALL | pattern specification process | RT | | 4 | 12,1 | 1,0E-2 | 2,4E-1 |
| ☐ | GOTERM_BP_ALL | development of primary sexual characteristics | RT | | 3 | 9,1 | 1,2E-2 | 2,6E-1 |
| ☐ | GOTERM_BP_ALL | neurofilament cytoskeleton organization | RT | | 2 | 6,1 | 1,4E-2 | 2,9E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of muscle cell differentiation | RT | | 2 | 6,1 | 1,6E-2 | 3,1E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular process | RT | | 7 | 21,2 | 1,6E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | tissue development | RT | | 5 | 15,2 | 1,8E-2 | 3,2E-1 |
| ☐ | GOTERM_BP_ALL | cellular process | RT | | 21 | 63,6 | 1,8E-2 | 3,1E-1 |
| ☐ | GOTERM_BP_ALL | sex differentiation | RT | | 3 | 9,1 | 1,9E-2 | 3,1E-1 |
| ☐ | GOTERM_BP_ALL | transcription | RT | | 8 | 24,2 | 1,9E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | regulation of transcription | RT | | 9 | 27,3 | 1,9E-2 | 3,0E-1 |
| ☐ | GOTERM_BP_ALL | intermediate filament organization | RT | | 2 | 6,1 | 2,1E-2 | 3,1E-1 |
| ☐ | GOTERM_BP_ALL | embryonic development | RT | | 5 | 15,2 | 2,1E-2 | 3,1E-1 |
| ☐ | GOTERM_BP_ALL | multicellular organismal process | RT | | 13 | 39,4 | 2,4E-2 | 3,3E-1 |
| ☐ | GOTERM_BP_ALL | regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 9 | 27,3 | 2,6E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell development | RT | | 3 | 9,1 | 2,7E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of nitrogen compound metabolic process | RT | | 9 | 27,3 | 2,8E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of macromolecule biosynthetic process | RT | | 9 | 27,3 | 2,8E-2 | 3,5E-1 |
| ☐ | GOTERM_BP_ALL | regulation of gene expression | RT | | 9 | 27,3 | 3,1E-2 | 3,7E-1 |
| ☐ | GOTERM_BP_ALL | response to stimulus | RT | | 9 | 27,3 | 3,2E-2 | 3,7E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cellular biosynthetic process | RT | | 9 | 27,3 | 3,4E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | cell differentiation | RT | | 7 | 21,2 | 3,5E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | regulation of biosynthetic process | RT | | 9 | 27,3 | 3,5E-2 | 3,7E-1 |
| ☐ | GOTERM_BP_ALL | intermediate filament cytoskeleton organization | RT | | 2 | 6,1 | 3,5E-2 | 3,7E-1 |
| ☐ | GOTERM_BP_ALL | cellular biosynthetic process | RT | | 10 | 30,3 | 3,6E-2 | 3,7E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of cellular process | RT | | 6 | 18,2 | 3,9E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | intermediate filament-based process | RT | | 2 | 6,1 | 4,0E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of transcription | RT | | 4 | 12,1 | 4,0E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | cellular developmental process | RT | | 7 | 21,2 | 4,1E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of gene expression | RT | | 4 | 12,1 | 4,3E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | regulation of muscle cell differentiation | RT | | 2 | 6,1 | 4,3E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | biosynthetic process | RT | | 10 | 30,3 | 4,3E-2 | 3,8E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell cycle | RT | | 3 | 9,1 | 4,6E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of developmental process | RT | | 3 | 9,1 | 4,6E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | response to organic substance | RT | | 4 | 12,1 | 4,7E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 4 | 12,1 | 4,8E-2 | 3,9E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of nitrogen compound metabolic process | RT | | 4 | 12,1 | 5,1E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | response to chemical stimulus | RT | | 5 | 15,2 | 5,2E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | regulation of primary metabolic process | RT | | 9 | 27,3 | 5,2E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of macromolecule biosynthetic process | RT | | 4 | 12,1 | 5,2E-2 | 4,0E-1 |

| | Category | Term | | | Count | % | P-Value | FDR |
|---|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_BP_ALL | positive regulation of cell cycle | RT | | 2 | 6,1 | 5,4E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | regulation of macromolecule metabolic process | RT | | 9 | 27,3 | 5,4E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | embryonic pattern specification | RT | | 2 | 6,1 | 5,5E-2 | 4,0E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of biological process | RT | | 6 | 18,2 | 5,7E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular biosynthetic process | RT | | 4 | 12,1 | 5,8E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of biosynthetic process | RT | | 4 | 12,1 | 5,9E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | mesoderm morphogenesis | RT | | 2 | 6,1 | 6,0E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | regulation of axonogenesis | RT | | 2 | 6,1 | 6,1E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | formation of primary germ layer | RT | | 2 | 6,1 | 6,3E-2 | 4,1E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cellular metabolic process | RT | | 9 | 27,3 | 6,4E-2 | 4,2E-1 |
| ☐ | GOTERM_BP_ALL | reproductive developmental process | RT | | 3 | 9,1 | 6,7E-2 | 4,3E-1 |
| ☐ | GOTERM_BP_ALL | organ morphogenesis | RT | | 4 | 12,1 | 6,9E-2 | 4,3E-1 |
| ☐ | GOTERM_BP_ALL | enzyme linked receptor protein signaling pathway | RT | | 3 | 9,1 | 7,1E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | regulation of neuron projection development | RT | | 2 | 6,1 | 7,3E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | regulation of transcription from RNA polymerase II promoter | RT | | 4 | 12,1 | 7,5E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | RT | | 9 | 27,3 | 7,6E-2 | 4,4E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell morphogenesis involved in differentiation | RT | | 2 | 6,1 | 7,8E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | cellular macromolecule biosynthetic process | RT | | 8 | 24,2 | 7,9E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | macromolecule biosynthetic process | RT | | 8 | 24,2 | 8,0E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of macromolecule metabolic process | RT | | 4 | 12,1 | 8,0E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of cellular metabolic process | RT | | 4 | 12,1 | 8,4E-2 | 4,6E-1 |
| ☐ | GOTERM_BP_ALL | regulation of metabolic process | RT | | 9 | 27,3 | 8,4E-2 | 4,5E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of transcription, DNA-dependent | RT | | 3 | 9,1 | 8,8E-2 | 4,6E-1 |
| ☐ | GOTERM_BP_ALL | development of primary female sexual characteristics | RT | | 2 | 6,1 | 8,8E-2 | 4,6E-1 |
| ☐ | GOTERM_BP_ALL | regulation of cell projection organization | RT | | 2 | 6,1 | 8,8E-2 | 4,6E-1 |
| ☐ | GOTERM_BP_ALL | negative regulation of RNA metabolic process | RT | | 3 | 9,1 | 8,9E-2 | 4,6E-1 |
| ☐ | GOTERM_BP_ALL | mesoderm development | RT | | 2 | 6,1 | 9,1E-2 | 4,7E-1 |
| ☐ | GOTERM_BP_ALL | positive regulation of metabolic process | RT | | 4 | 12,1 | 9,6E-2 | 4,8E-1 |
| ☐ | GOTERM_BP_ALL | cytoskeleton organization | RT | | 3 | 9,1 | 9,7E-2 | 4,8E-1 |
| ☐ | GOTERM_BP_ALL | female sex differentiation | RT | | 2 | 6,1 | 9,9E-2 | 4,8E-1 |

**10 gene(s)** from your list are not in the output.

**Supp. Table 5**: DAVID analysis of Pp upregulated population regarding Cellular Component (p ≤ 0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---|---|---|---|---|---|---|---|---|
| ☐ | GOTERM_CC_ALL | neurofilament | RT | | 2 | 6,1 | 7,5E-3 | 4,5E-1 |
| ☐ | GOTERM_CC_ALL | neurofilament cytoskeleton | RT | | 2 | 6,1 | 1,2E-2 | 3,8E-1 |
| ☐ | GOTERM_CC_ALL | intracellular organelle | RT | | 19 | 57,6 | 1,7E-2 | 3,6E-1 |
| ☐ | GOTERM_CC_ALL | organelle | RT | | 19 | 57,6 | 1,7E-2 | 2,9E-1 |
| ☐ | GOTERM_CC_ALL | intracellular | RT | | 21 | 63,6 | 2,9E-2 | 3,7E-1 |
| ☐ | GOTERM_CC_ALL | intracellular part | RT | | 20 | 60,6 | 4,5E-2 | 4,5E-1 |
| ☐ | GOTERM_CC_ALL | intracellular membrane-bounded organelle | RT | | 16 | 48,5 | 7,5E-2 | 5,8E-1 |
| ☐ | GOTERM_CC_ALL | membrane-bounded organelle | RT | | 16 | 48,5 | 7,5E-2 | 5,4E-1 |
| ☐ | GOTERM_CC_ALL | nucleus | RT | | 11 | 33,3 | 9,0E-2 | 5,6E-1 |

12 gene(s) from your list are not in the output.

**Supp. Table 6**: DAVID analysis of Pp upregulated population regarding Molecular Function (p ≤ 0.1)

| Sublist | Category | Term | RT | Genes | Count | % | P-Value | Benjamini |
|---------|----------|------|-----|-------|-------|-----|---------|-----------|
| ☐ | GOTERM_MF_ALL | transcription regulator activity | RT | | 9 | 27,3 | 4,5E-4 | 5,0E-2 |
| ☐ | GOTERM_MF_ALL | transcription factor activity | RT | | 7 | 21,2 | 1,2E-3 | 6,9E-2 |
| ☐ | GOTERM_MF_ALL | DNA binding | RT | | 9 | 27,3 | 5,6E-3 | 1,9E-1 |
| ☐ | GOTERM_MF_ALL | sequence-specific DNA binding | RT | | 5 | 15,2 | 1,2E-2 | 2,8E-1 |
| ☐ | GOTERM_MF_ALL | nucleic acid binding | RT | | 9 | 27,3 | 8,9E-2 | 8,8E-1 |

23 gene(s) from your list are not in the output.