|  |
| --- |
| **RSV *versus* Ctrl 6 days p.i.** |
| **Gene ID** | **Gene Symbol** | **Log2 Fold Change** | **P value** | **Padj** | **Alternative name & function** | **Biological pathway** | **Ref.** |
| ENSOARG00000020741 | TNFSF10 | 1.46 | 1.43E-09 | 1.10E-05 | TRAILpro-apoptotic | Apoptosis | [1, 2] |
| ENSOARG00000010042 | STC1 | 1.21 | 3.66E-06 | 1.00E-02 | Stanniocalcin-1pro-apoptotic | Apoptosis | [3] |
| ENSOARG00000014648 | RSAD2 | 1.55 | 3.89E-11 | 7.44E-07 | ViperinISG | IFN pathway | [4] |
| ENSOARG00000007233 | ISG15 | 1.61 | 1.73E-09 | 1.10E-05 | ISG | IFN pathway | [5] |
| ENSOARG00000025182 | BST-2A | 1.40 | 3.38E-09 | 1.62E-05 | ISGISG | IFN pathway | [6] |
| ENSOARG00000013440 | IFI44 | 1.37 | 4.11E-08 | 1.57E-04 | ISG | IFN pathway | [7] |
| ENSOARG00000002881 | OASL\* | 1.33 | 5.81E-07 | 1.85E-03 | ISG | IFN pathway | [8] |
| ENSOARG00000014800 | IFIT3 | 1.29 | 4.68E-06 | 1.12E-02 | RIG-GISG | IFN pathway | [9] |
| ENSOARG00000015177 | IFIT1 | 1.26 | 6.92E-06 | 1.32E-02 | ISG | IFN pathway | [10] |
| ENSOARG00000016787 | BST-2B | 1.03 | 6.53E-06 | 1.32E-02 | ISG | IFN pathway | [6] |
| ENSOARG00000001138 | HERC6\* | 1.25 | 1.35E-05 | 2.15E-02 | Linked to ISG15 activation | IFN pathway | [11] |
| ENSOARG00000001815 | IRF\* | 1.24 | 1.30E-05 | 2.15E-02 | IFN pathway | IFN pathway | [12] |
| ENSOARG00000013421 | IFI44L | 1.12 | 1.63E-05 | 2.40E-02 | ISG | IFN pathway | [7, 13] |
| ENSOARG00000014413 | IFI27L2\* | 1.10 | 3.18E-05 | 4.35E-02 | ISG12bISG | IFN pathway | [14] |
| ISG, interferon (IFN)-stimulated gene. |
| **RSV *versus* Ctrl 42 days p.i.** |
| **Gene ID** | **Gene Symbol** | **Log2 Fold Change** | **P value** | **Padj** | **Alternative name & function** | **Biological pathway** | **Ref.** |
| ENSOARG00000009964 | TRPC4 | 1.15 | 4.84E-05 | 2.74E-02 | Calcium channel Endothelial permeability Vasodilation | AngiogenesisEndotheliumCalcium | [15]  |
| ENSOARG00000001060 | KDR | 1.10 | 1.54E-04 | 4.82E-02 | VEGF Receptor 2 (VEGFR2) | AngiogenesisEndotheliumCalcium | [16] |
| ENSOARG00000003922 | MXRA8 | 0.99 | 7.96E-06 | 9.27E-03 | DICAMAngiogenesisCartilage formation | AngiogenesisEndotheliumCalcium | [17] |
| ENSOARG00000000498 | ITGA9 | 0.93 | 1.21E-04 | 4.49E-02 | Integrin 9Receptor of VCAM1 | AngiogenesisEndotheliumCalcium | [18] |
| ENSOARG00000012316 | PTTG1IP\* | 0.76 | 1.59E-04 | 4.85E-02 | Activator of FGF | AngiogenesisendotheliumCalcium | [19] |
| ENSOARG00000012715 | PTGIS | 0.73 | 1.25E-04 | 4.49E-02 | Prostaglandin I2Potent vasodilator Inhibition of blood clot formation | AngiogenesisEndotheliumCalcium | [20] |
| ENSOARG00000013623 | PPP3CA | -0.62 | 1.33E-04 | 4.49E-02 | CalcineurinCalcium signalingVEGF pathway | AngiogenesisEndotheliumCalcium | [21] |
| ENSOARG00000006037 | BMPER | -0.91 | 7.99E-05 | 3.79E-02 | Inhibition of BMP functionPro-angiogenic | AngiogenesisEndotheliumCalcium | [22] |
| ENSOARG00000011962 | TRPM2 | -1.23 | 1.41E-05 | 1.50E-02 | Endothelial barrier functionIncrease vascular permeability | AngiogenesisEndotheliumCalcium | [23]  |
| ENSOARG00000009518 | SOX4\* | 0.64 | 7.50E-05 | 3.70E-02 | Associated with Wnt signaling | DifferentiationDevelopment | [24] |
| ENSOARG00000011866 | PGAP6 | 0.62 | 1.33E-04 | 4.49E-02 | TMEM8AEmbryonic development | DifferentiationDevelopment | [25] |
| ENSOARG00000009005 | C2CD3 | -0.54 | 8.82E-05 | 4.00E-02 | Associated with SHH signaling | DifferentiationDevelopment | [26] |
| ENSOARG00000003978 | NOC3L | -0.55 | 7.41E-06 | 9.27E-03 | Adipogenesis | DifferentiationDevelopment | [27] |
| ENSOARG00000019294 | ABCA12 | -1.13 | 3.81E-05 | 2.56E-02 | Lung developmentABCA12 KO leads to alveolar collapse | DifferentiationDevelopment | [28] |
| ENSOARG00000020209 | CHPF | 0.86 | 5.82E-05 | 2.98E-02 | Chondroitin sulfate synthase-2Regulation of ECM | ECMRemodeling | [29]  |
| ENSOARG00000008205 | IGSF8 | 0.66 | 1.16E-04 | 4.49E-02 | Negative regulator of TGF-beta | ECMRemodeling | [30] |
| ENSOARG00000005315 | MMP1 | -1.06 | 1.43E-04 | 4.64E-02 | Breakdown of ECM | ECMRemodeling | [31, 32] |
| ENSOARG00000005084 | MMP3 | -1.41 | 1.19E-06 | 2.17E-03 | Breakdown of ECM | ECMRemodeling | [31, 32]  |
| ENSOARG00000024340 | Metazoa\_SRP | 1.85 | 2.47E-11 | 3.16E-07 | 7SL RNANon-coding RNA | Transcription regulation | [33]  |
| ENSOARG00000023771 | miRNA\* | 1.58 | 9.81E-09 | 4.19E-05 | Non-coding RNA | Transcription regulation |  |
| ENSOARG00000022840 | RNase\_MRP | 1.58 | 6.06E-10 | 3.88E-06 | Ribonuclease | Transcription regulation | [34] |
| ENSOARG00000022831 | 5\_8S\_rRNA | 1.53 | 7.01E-08 | 2.24E-04 | 5.8S ribosomal RNANon-coding RNA | Transcription regulation |  |
| ENSOARG00000021831 | miRNA\* | 1.43 | 3.88E-07 | 8.29E-04 | Non-coding RNA | Transcription regulation |  |
| ENSOARG00000023915 | RNaseP\_nuc | 1.34 | 2.66E-06 | 4.26E-03 | Ribonuclease | Transcription regulation |  |
| ENSOARG00000023715 | 7SK RNA | 1.18 | 2.09E-05 | 1.81E-02 | Non-coding RNA | Transcription regulation | [35] |
| ENSOARG00000012889 | CPSF2 | -0.47 | 5.13E-05 | 2.74E-02 | mRNA processingand polyadenylation | Transcription regulation | [36] |
| ENSOARG00000017276 | MAGE2\* | 1.18 | 1.76E-05 | 1.73E-02 | MAGE-like proteinProtein trafficking and recycling | Secretory pathway & cytoskeleton | [37] |
| ENSOARG00000005241 | MARCHF9 | 0.92 | 4.86E-05 | 2.74E-02 | Protein processing | Secretory pathway & cytoskeleton | [38] |
| ENSOARG00000018257 | TRIM3 | 0.59 | 3.92E-05 | 2.56E-02 | BERPInteract with myosins | Secretory pathway & cytoskeleton | [39, 40] |
| ENSOARG00000019076 | TBC1D20 | 0.41 | 1.67E-04 | 4.97E-02 | Inhibition of RAB1Autophagosome maturation | Secretory pathway & cytoskeleton | [41] |
| ENSOARG00000011359 | MAP7D3\* | -0.35 | 1.14E-04 | 4.49E-02 | Regulates microtubule assembly and stability | Secretory pathway & cytoskeleton | [42] |
| ENSOARG00000011149 | CRYBG1 | -0.89 | 1.27E-04 | 4.49E-02 | AIM1Suppresor of cell migration | Secretory pathway & cytoskeleton | [43] |
| ENSOARG00000006047 | PLS1 | -1.18 | 5.12E-05 | 2.74E-02 | Plastin-1/FimbrinCross-linking with actinFormation of filopodia | Secretory pathway & cytoskeleton | [44] |
| ENSOARG00000012318 | HMG20B | 0.77 | 2.12E-05 | 1.81E-02 | DNA repairMitosis | Other | [45] |
| ENSOARG00000013664 | SKA3 | -1.13 | 1.14E-04 | 4.49E-02 | Mitosis | Other | [46] |
| ENSOARG00000019275 | BARD1 | -1.22 | 2.85E-05 | 2.14E-02 | DNA repair | Other | [47] |
| ENSOARG00000009025 | ZNF503\* | 0.98 | 6.22E-06 | 8.85E-03 | Fanconi anemia | Other |   |
| ENSOARG00000009492 | COQ10A | 0.63 | 1.45E-04 | 4.64E-02 | Metabolism | Other |  |
| ENSOARG00000020345 | WDR53 | -0.35 | 1.21E-04 | 4.49E-02 | Unknown function | Other |  |
| ENSOARG00000000778 | MET | -0.78 | 9.06E-05 | 4.00E-02 | Receptor tyrosine kinase | Other |  |
| ENSOARG00000001759 | FANCL | -0.89 | 4.00E-05 | 2.56E-02 | Fanconi anemia | Other |  |
| ENSOARG00000004915 | TM4SF18 | -1.22 | 2.70E-05 | 2.14E-02 | Unknown function | Other |   |
| ENSOARG00000019309 | ATIC | -1.34 | 2.95E-07 | 7.56E-04 | Inosine monophosphate synthase | Other |   |

\* Genes annotated manually.

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