## A - Top Diseases & Functions

| Diseases and Bio Functions | z-score Nx | z-score Hx |
|---|---|---|
| Accumulation of granulocytes | 2.26 | 0.00 |
| Activation of leukocytes | 2.10 | 0.91 |
| Activation of myeloid cells | 2.26 | 1.06 |
| Cancer | 2.03 | 2.03 |
| Cell death of cancer cells | 0.00 | 2.38 |
| Chemotaxis of antigen presenting cells | -0.37 | -2.05 |
| Digestive organ tumor | 1.40 | 3.55 |
| Efflux of lipid | 0.00 | -2.04 |
| Epithelial neoplasia | 1.14 | 2.16 |
| Epithelial-mesenchymal transition of tumor cell lines | 0.00 | 2.03 |
| Fibrosis | 2.00 | 0.49 |
| Flux of lipid | 0.00 | -2.22 |
| Neoplasia of carcinoma cell lines | 0.00 | 2.43 |
| Neuromuscular disease | -1.66 | -2.21 |
| Polarization of leukocytes | 2.01 | 0.00 |
| Quantity of bone marrow cells | 0.00 | -2.02 |
| Recruitment of leukocytes | -0.68 | -2.27 |
| Response of antigen presenting cells | -2.13 | 0.00 |
| Signaling of cells | -2.07 | 0.00 |
| Signaling of tumor cell lines | -2.22 | 0.00 |
| Transmigration of cells | 0.00 | -2.44 |

## B - Top Canonical pathways

| Canonical Pathway | p-val Nx | p-val Hx |
|---|---|---|
| Acute Phase Response Signaling | 1.05 | 2.22 |
| Agranulocyte Adhesion and Diapedesis | 3.41 | 1.80 |
| Atherosclerosis Signaling | 3.54 | 1.35 |
| Bladder Cancer Signaling | 2.71 | 1.63 |
| Dopamine Degradation | 2.40 | 0.58 |
| Ethanol Degradation IV | 2.58 | 1.24 |
| Fatty Acid alpha oxidation | 3.02 | 0.82 |
| Granulocyte Adhesion and Diapedesis | 4.86 | 3.27 |
| Guanine and Guanosine Salvage I | 1.18 | 2.61 |
| Guanosine Nucleotides Degradation III | 0.47 | 2.66 |
| HIF1 alpha Signaling | 1.77 | 2.03 |
| Histamine Degradation | 3.15 | 0.87 |
| Inhibition of Matrix Metalloproteases | 2.88 | 2.04 |
| Leukocyte Extravasation Signaling | 2.31 | 0.82 |
| LPS/IL-1 Mediated Inhibition of RXR Function | 3.85 | 1.13 |
| LXR/RXR Activation | 2.44 | 2.11 |
| Neuroprotective Role of THOP1 in Alzheimer's Disease | 2.18 | 0.99 |
| Oxidative Ethanol Degradation III | 2.78 | 1.38 |
| Purine Nucleotides Degradation II (Aerobic) | 0.36 | 2.07 |

| | | |
|---|---|---|
| Putrescine Degradation III | 2.78 | 0.73 |
| Retinoate Biosynthesis II | 1.01 | 2.15 |
| Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis | 2.48 | 1.85 |
| Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis | 3.09 | 2.35 |
| Tryptophan Degradation X | 2.78 | 0.73 |
| VDR/RXR Activation | 2.38 | 4.01 |

## C - Top Upstream regulators

| Upstream regulators | z-score Nx | z-score Hx |
|---|---|---|
| AGT | -2.41 | -0.99 |
| BMP4 | -1.31 | -2.05 |
| BMP6 | -2.65 | -1.71 |
| CCL5 | 0.00 | -2.43 |
| CD40LG | 2.10 | 0.00 |
| CDKN2A | 0.00 | -2.25 |
| CSF2 | -0.02 | 3.41 |
| HGF | -2.16 | 0.88 |
| HIF1A | 0.59 | 2.52 |
| HOXA9 | 2.00 | 0.00 |
| IFN Beta | -1.23 | -2.39 |
| IFNB1 | -1.02 | -2.24 |
| IFNG | 0.12 | -2.40 |
| IL17RA | 2.00 | 0.00 |
| IRF7 | -0.41 | -2.54 |
| MEF2C | 0.00 | 2.22 |
| MEOX2 | -2.41 | -0.52 |
| MLXIPL | 0.00 | -2.21 |
| NFIC | 0.00 | 2.00 |
| NFkB (complex) | 2.67 | 1.56 |
| NFKBIA | -1.56 | -2.18 |
| PDGF BB | -1.80 | -2.69 |
| POU4F1 | -2.14 | 0.00 |
| RELA | 2.06 | 1.08 |
| SATB1 | 1.20 | 2.24 |
| SOX2 | -2.00 | 0.00 |
| STAT1 | -0.36 | -2.11 |
| TAF4 | -0.92 | -2.16 |
| TCF3 | 0.00 | -2.89 |
| TGFB1 | -2.50 | -0.08 |
| Tnf (family) | 2.24 | 2.02 |
| TNFSF12 | 2.15 | 0.78 |
| WNT5A | -1.41 | -2.65 |

**Supplemental Table 1. Main biological functions associated with the alterations of *Vdac1*$^{-/-}$ MEF compared to Wt MEF (Wt) in normoxia (Nx) or hypoxia (Hx).** (**A**, **B**, **C**, and **D**): Significant

categories of (**A**) Diseases and functions (**B**) Canonical pathways and (**C**) Upstream regulators associated with the comparison of wild-type (Wt) and *Vdac1*$^{-/-}$ MEF in Nx or Hx using IPA™. Activation z-score (cut-off=2) or –log10 p-value (cut-off=2) are represented.