

**Supplementary Figure 1 –** Volcano plot showing RNA-Seq up- and downregulated genes between Alzheimer’s disease patients and controls, considering all brain regions. All 69 DEGs are shown, of which 22 are downregulated and 47 are upregulated**.**

**Supplementary Table 1 –** Sample information.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **ID** | **Group** | **Sex** | **Age (y)** | **Age of diagnosis (y)** | **Brain weight (g)** | **PMIc (h)** | **Cause of death** | ***APOE* genotype** |
| 533 | CTa | Female | 76 | - | 1260 | 10.42 | Myocardial infarction | E3/E4 |
| 537 | CTa | Male | 69 | - | 1165 | 32.5 | Cardiorespiratory arrest | E3/E3 |
| 586 | CTa | Male | 77 | - | 1255 | 9.5 | N/A | E3/E3 |
| 1419 | CTa | Male | 80 | - | 1305 | 13 | N/A | E3/E3 |
| 1495 | CTa | Female | 79 | - | 1150 | 17.3 | Pancreatic cancer | E3/E3 |
| 1547 | CTa | Female | 95 | - | 1160 | 23.75 | Liver metastases, but the origin of the primary cancer is uncertain | E3/E3 |
| 1062 | ADb | Female | 77 | 71 | 855 | 11.25 | Aspiration bronchopneumonia | E3/E3 |
| 1243 | ADb | Female | 89 | 78 | 845 | 10.75 | Confluent bronchopneumonia | E3/E4 |
| 1330 | ADb | Male | 79 | 73 | 910 | 19.25 | Cardiorespiratory arrest in the context of Alzheimer's disease, arterial hypertension and peripheral vascular disease | E4/E4 |
| 1427 | ADb | Female | 82 | 76 | 970 | 14 | Alzheimer’s dementia and cervical lymphoma | E3/E4 |
| 1518 | ADb | Male | 85 | 70 | 970 | 20.5 | Pneumonia in the context of Alzheimer's dementia | E3/E3 |
| 1560 | ADb | Female | 83 | 74 | 950 | 13.25 | Pneumonia, Alzheimer's dementia and nephrolithiasis with pyelonephritis | E3/E4 |

a Control

b Alzheimer’s disease

c Post-mortem interval

**Supplementary Table 2 –** Genes whose regulation of expression and H3K9 acetylation are found in the same direction.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Auditory cortex – upregulated** | | | | |
|  | **ChIP-Seq peak** | | **RNA-Seq** | |
| **Gene** | **Log2FCa** | **P-valueb** | **Log2FCa** | **Adj. P-valuec** |
| *PSTPIP1* | 6,00 | 8,31e-06 | 1,55 | 0,017 |
| *ARRDC2* | 89,68 | 1,30e-68 | 1,51 | 0,025 |
| *MYO15B* | 14,64 | 2,90e-34 | 1,61 | 0,011 |
| *PLXNB1* | 147,62 | 1,44e-128 | 1,33 | 0,017 |
| *FZD7* | 32,11 | 4,42e-19 | 1,43 | 0,011 |
| *PXN* | 7,57 | 3,87e-09 | 1,40 | 0,014 |
| *KLF2* | 23,62 | 1,48e-23 | 2,25 | 0,017 |
| *CDC42BPG* | 50,56 | 1,17e-33 | 2,61 | 0,020 |
| 20,30 | 1,63e-10 |
| *XRCC3* | 115,14 | 1,04e-94 | 1,49 | 0,011 |
| 38,20 | 7,22e-46 |
| 33,77 | 4,36e-38 |
| *VAC14-AS1* | 11,22 | 1,44e-38 | 1,43 | 0,016 |
| *CLDN5* | 51,30 | 1,17e-33 | 1,77 | 0,025 |
| *PKN3* | 6,37 | 1,57e-12 | 2,03 | 0,007 |
| *SLC16A3* | 12,55 | 1,32e-05 | 1,59 | 0,045 |
| *TRIOBP* | 46,87 | 2,80e-30 | 1,54 | 9,68E-05 |
| *PLXNB2* | 7,75 | 2,07e-13 | 1,07 | 0,026 |
| 35,06 | 1,30e-20 |
| 4,37 | 1,61e-05 |
| *ARHGEF1* | 47,24 | 2,80e-30 | 1,28 | 0,011 |
| *C22orf34* | 112,56 | 1,18e-92 | 2,36 | 0,015 |
| *SLC6A12* | 50,19 | 1,17e-33 | 1,70 | 0,035 |
| 43,55 | 5,66e-27 |
| *AJUBA* | 26,20 | 1,19e-14 | 1,65 | 0,049 |
| *COL8A2* | 28,42 | 4,25e-16 | 1,37 | 0,041 |
| *SLC4A11* | 24,91 | 6,18e-25 | 2,44 | 0,013 |
| *EPHB4* | 83,77 | 8,25e-63 | 1,89 | 0,017 |
| **Auditory cortex – downregulated** | | | | |
|  | **ChIP-Seq peak** | | **RNA-Seq** | |
| **Gene** | **Log2FCa** | **P-valueb** | **Log2FCa** | **Adj. P-valuec** |
| *SCAI* | 476,91 | 9,91e-101 | -1,10 | 0,044 |

a Log2 fold change

b P-value < 0.05, based on an FDR < 0.05

c Adjusted p-value < 0.05