

Supplementary Materials

S1. Results

S1.1. Differentially Expressed Pathways in HFD-Fed AKO Compared to HFD-fed WT Mice

Using Reactome molecular pathway analysis, we determined the differentially expressed pathways in HFD-fed AKO mice compared to HFD-fed WT mice ($FDR \leq 0.01$). There were 39 pathways in total. 9 of these pathways were unrelated to ribosomal protein subunits and were examined further for transcript function (Supplemental Table S1). These 9 differentially expressed pathways were related to metabolism. Transcripts associated with the electron transport chain [1–8] and citric acid cycle [9–12] were downregulated and upregulated, respectively. Transcripts associated with Golgi transport were upregulated [13–45]. Transcripts relating to mRNA polyadenylation were upregulated [46–51]. Transcripts relating to Wnt/ β -Catenin signaling were upregulated [52–57].

Supplemental Table S1. Differentially Expressed Pathways in HFD-fed AKO Compared to HFD-fed WT Mice. Pathways with $FDR \leq 0.01$ are displayed. Pathway name, stable identifier, log fold change (log2), and false discovery rate for each pathway are displayed. Within each pathway, gene ID, Ensembl ID, gene description, log fold change (log2), log10 adjusted p -value, and relevant known function are displayed.

Reactome Pathway	Gene Symbol	Ensembl ID	Gene Description	Log FC	padj	Known Function
Formation of ATP by chemiosmotic coupling (R-HSA-163210) LFC: -0.13 FDR: 2.40×10^{-4}	<i>Atp5j2</i> <i>Atp5h</i>	ENSMUST0000161741 ENSMUST0000043931	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2 ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit D	-0.27 - 0.26	1.82×10^{-2} 3.98×10^{-2}	Inhibition is neuroprotective in aging and AD [58]
Cristae formation (R-HSA-8949613) LFC: -0.09 FDR: 6.07×10^{-3}	<i>Atp5j2</i> <i>Atp5h</i>	ENSMUST0000161741 ENSMUST0000043931	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2 ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit D	-0.27 - 0.26	1.82×10^{-2} 3.98×10^{-2}	Inhibition is neuroprotective in aging and AD [58]
	<i>Hspa9</i>	ENSMUST0000025217	Heat shock protein 9	0.28	1.69×10^{-2}	Oxidative stress sensor [59], Downregulated in AD brain [60]
	<i>Samm50</i>	ENSMUST0000023071	SAMM50 sorting and assembly machinery component	0.37	1.12×10^{-2}	Negative regulator of mitochondrial fragmentation [61]
	<i>Ndufb2</i> <i>Ndufb4</i> <i>Ndufb11</i> <i>Ndufs8</i> <i>Ndufa4</i> <i>Ndufb9</i> <i>Ndufa2</i>	ENSMUST0000119379 ENSMUST0000023514 ENSMUST0000116621 ENSMUST0000237341 ENSMUST0000204978 ENSMUST0000022980 ENSMUST0000014438	NADH:ubiquinone oxidoreductase subunit B2 NADH:ubiquinone oxidoreductase subunit B4 NADH:ubiquinone oxidoreductase subunit B11 NADH:ubiquinone oxidoreductase core subunit S8 Ndufa4, mitochondrial complex associated NADH:ubiquinone oxidoreductase subunit B9 NADH:ubiquinone oxidoreductase subunit A2	-0.32 - 0.29 - 0.28 - 0.27 - 0.25 - 0.23 - 0.20	2.39×10^{-2} 2.89×10^{-2} 3.32×10^{-2} 4.63×10^{-2} 4.69×10^{-2} 4.16×10^{-2} 4.83×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]

Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins (R-HSA-163200) LFC: -0.04 FDR: 8.45×10^{-7}	<i>mt-Nd3</i>	ENSMUST0000082411	Mitochondrially encoded NADH dehydrogenase 3	-0.23	4.06×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]
	<i>Acad9</i>	ENSMUST0000011492	Acyl-Coenzyme A dehydrogenase family, member 9	0.29	2.59×10^{-2}	Role in fatty acid oxidation, downregulation associated with neurological disease [2]
	<i>Timmdc1</i>	ENSMUST0000002925	Translocase of inner mitochondrial membrane domain containing 1	0.36	9.17×10^{-3}	Loss is associated with axonal neuropathy and cognitive decline [3]
	<i>Ndufb2</i>	ENSMUST0000119379	NADH:ubiquinone oxidoreductase subunit B2	-0.32	2.39×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]
	<i>Ndufb4</i>	ENSMUST0000023514	NADH:ubiquinone oxidoreductase subunit B4	0.29	2.89×10^{-2}	
	<i>Ndufb11</i>	ENSMUST0000023514	NADH:ubiquinone oxidoreductase subunit B11	0.28	3.32×10^{-2}	
	<i>Ndufs8</i>	ENSMUST0000023514	NADH:ubiquinone oxidoreductase core subunit S8	0.27	4.63×10^{-2}	
	<i>Ndufa4</i>	ENSMUST0000116621	NADH:ubiquinone oxidoreductase subunit B11	0.25	4.69×10^{-2}	
	<i>Ndufb9</i>	ENSMUST00000237341	NADH:ubiquinone oxidoreductase subunit A2	0.23	4.16×10^{-2}	
	<i>Ndufa2</i>	ENSMUST00000237341	Ndufa4, mitochondrial complex associated	0.20	4.83×10^{-2}	
	<i>Cox7b</i>	ENSMUST0000033582	Cytochrome c oxidase subunit 7B	-0.31	1.13×10^{-2}	Loss leads to decrease in oxidative stress and amyloid formation in AD mice [4]
	<i>Uqcrh</i>	ENSMUST0000078676	Ubiquinol-cytochrome c reductase hinge protein	-0.29	3.04×10^{-2}	Positive regulator of apoptosis via cytochrome c release [5]
	<i>Atp5j2</i>	ENSMUST0000161741	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F2	-0.27	1.82×10^{-2}	Inhibition is neuroprotective in aging and AD [58]
	<i>Atp5h</i>	ENSMUST0000043931	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit D	0.26	3.98×10^{-2}	
	<i>mt-Nd3</i>	ENSMUST0000082411	Mitochondrially encoded NADH dehydrogenase 3	-0.23	4.06×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]
	<i>mt-Co3</i>	ENSMUST0000082409	Mitochondrially encoded cytochrome c oxidase III	-0.21	3.87×10^{-2}	Loss leads to decrease in oxidative stress and amyloid formation in AD mice [4]
	<i>mt-Cytb</i>	ENSMUST0000082421	Mitochondrially encoded cytochrome b	0.21	4.53×10^{-2}	Decreased in AD brain [6]
	<i>Acad9</i>	ENSMUST0000011492	Acyl-Coenzyme A dehydrogenase family, member 9	0.29	2.59×10^{-2}	Role in fatty acid oxidation, downregulation associated with neurological disease [2]
	<i>Sdhα</i>	ENSMUST0000022062	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0.29	1.02×10^{-2}	Downregulation is associated with oxidative stress and insulin resistance [7]
	<i>Timmdc1</i>	ENSMUST0000002925	Translocase of inner mitochondrial membrane domain containing 1	0.36	9.17×10^{-3}	Loss is associated with axonal neuropathy and cognitive decline [3]
	<i>Taco1</i>	ENSMUST0000002048	Translational activator of mitochondrially encoded cytochrome c oxidase I	0.40	3.68×10^{-2}	Loss associated with motor dysfunction and mitochondrial disease in mice [8]

Respiratory electron transport (R-HSA-611105) LFC: -0.03 FDR: 2.92×10^{-5}	<i>Ndufb2</i>	ENSMUST0000119379	NADH:ubiquinone oxidoreductase subunit B2	-0.32	2.39×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]
	<i>Ndufb4</i>	ENSMUST0000023514	NADH:ubiquinone oxidoreductase subunit B4	0.29	2.89×10^{-2}	
	<i>Ndufb11</i>	ENSMUST00000204978	NADH:ubiquinone oxidoreductase subunit B11	0.28	3.32×10^{-2}	
	<i>Ndufs8</i>	ENSMUST0000022980	NADH:ubiquinone oxidoreductase core subunit S8	0.27	4.63×10^{-2}	
	<i>Ndufa4</i>	ENSMUST0000014438	NADH:ubiquinone oxidoreductase subunit A2	0.25	4.69×10^{-2}	
	<i>Ndufb9</i>	ENSMUST00000237341	NADH:ubiquinone oxidoreductase subunit B1	0.23	4.16×10^{-2}	
	<i>Ndufa2</i>	ENSMUST0000082411	NADH:ubiquinone oxidoreductase hinge protein	0.20	4.83×10^{-2}	
	<i>Cox7b</i>	ENSMUST0000033582	Cytochrome c oxidase subunit 7B	-0.31	1.13×10^{-2}	
	<i>Uqcrh</i>	ENSMUST0000078676	Ubiquinol-cytochrome c reductase	-0.29	3.04×10^{-2}	
	<i>mt-Nd3</i>	ENSMUST0000082409	Mitochondrially encoded NADH dehydrogenase 3	-0.23	4.06×10^{-2}	
The citric acid (TCA) cycle and respiratory electron transport (R-HSA-1428517) LFC: 0.03 FDR: 2.71×10^{-3}	<i>mt-Co3</i>	ENSMUST0000082421	Mitochondrially encoded cytochrome c oxidase III	-0.21	3.87×10^{-2}	Loss leads to decrease in oxidative stress and amyloid formation in AD mice [4]
	<i>mt-Cytb</i>	ENSMUST0000082421	Mitochondrially encoded cytochrome b	0.21	4.53×10^{-2}	
	<i>Acad9</i>	ENSMUST0000011492	Acy-Coenzyme A dehydrogenase family, member 9	0.29	2.59×10^{-2}	
	<i>Sdha</i>	ENSMUST0000022062	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0.29	1.02×10^{-2}	
	<i>Timmdc1</i>	ENSMUST0000002925	Translocase of inner mitochondrial membrane domain containing 1	0.36	9.17×10^{-3}	
	<i>Taco1</i>	ENSMUST0000002048	Translational activator of mitochondrially encoded cytochrome c oxidase I	0.40	3.68×10^{-2}	
	<i>Ndufb2</i>	ENSMUST0000119379	NADH:ubiquinone oxidoreductase subunit B2	-0.32	2.39×10^{-2}	
	<i>Ndufb4</i>	ENSMUST0000023514	NADH:ubiquinone oxidoreductase subunit B4	0.29	2.89×10^{-2}	
	<i>Ndufb11</i>	ENSMUST00000204978	NADH:ubiquinone oxidoreductase subunit B11	0.28	3.32×10^{-2}	
	<i>Ndufs8</i>	ENSMUST0000022980	NADH:ubiquinone oxidoreductase core subunit S8	0.27	4.63×10^{-2}	
	<i>Ndufa4</i>	ENSMUST0000014438	NADH:ubiquinone oxidoreductase subunit A2	0.25	4.69×10^{-2}	
	<i>Ndufb9</i>	ENSMUST00000237341	NADH:ubiquinone oxidoreductase subunit B1	0.23	4.16×10^{-2}	
	<i>Ndufa2</i>	ENSMUST0000082411	NADH:ubiquinone oxidoreductase hinge protein	0.20	4.83×10^{-2}	
	<i>Cox7b</i>	ENSMUST0000033582	Cytochrome c oxidase subunit 7B	-0.31	1.13×10^{-2}	

	<i>Uqcrh</i>	ENSMUST0 0000078676	Ubiquinol-cytochrome c reductase hinge protein	-0.29	3.04×10^{-2}	Positive regulator of apoptosis via cytochrome c release [5]
	<i>Atp5j2</i> <i>Atp5h</i>	ENSMUST0 0000161741 ENSMUST0 0000043931	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit D	-0.27 - 0.26	1.82×10^{-2} 3.98×10^{-2}	Inhibition is neuroprotective in aging and AD [58]
	<i>mt-Nd3</i>	ENSMUST0 0000082411	Mitochondrially encoded NADH dehydrogenase 3	-0.23	4.06×10^{-2}	Partial inhibition of Complex I leads to reduced oxidative stress and increased long-term potentiation in AD mice [1]
	<i>mt-Co3</i>	ENSMUST0 0000082409	Mitochondrially encoded cytochrome c oxidase III	-0.21	3.87×10^{-2}	Loss leads to decrease in oxidative stress and amyloid formation in AD mice [4]
	<i>mt-Cytb</i>	ENSMUST0 0000082421	Mitochondrially encoded cytochrome b	0.21	4.53×10^{-2}	Decreased in AD brain [6]
	<i>Acad9</i>	ENSMUST0 0000011492	Acyl-Coenzyme A dehydrogenase family, member 9	0.29	2.59×10^{-2}	Role in fatty acid oxidation, downregulation associated with neurological disease [2]
	<i>Aco2</i>	ENSMUST0 0000023116	Aconitase 2, mitochondrial	0.29	1.42×10^{-2}	Suppressed by nitric oxide (Palmieri et al., 2020), Decreased in AD patient lymphocytes [9]
	<i>Sdhα</i>	ENSMUST0 0000022062	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	0.29	1.02×10^{-2}	Downregulation is associated with oxidative stress and insulin resistance [7]
	<i>Ogdh</i>	ENSMUST0 0000003461	Oxoglutarate (alpha- ketoglutarate) dehydrogenase (lipoamide)	0.30	3.73×10^{-2}	Inhibited by lipopolysaccharide and IFN- γ stimulation in macrophages [10]
	<i>Cs</i>	ENSMUST0 0000005826	Citrate synthase	0.32	1.53×10^{-2}	Downregulated in AD patient platelets [11]
	<i>Pdk2</i>	ENSMUST0 0000038431	Pyruvate dehydrogenase kinase, isoenzyme 2	0.35	4.52×10^{-2}	mRNA levels modulated during aging in brain [12]
	<i>Timmdc1</i>	ENSMUST0 0000002925	Translocase of inner mitochondrial membrane domain containing 1	0.36	9.17×10^{-3}	Loss is associated with axonal neuropathy and cognitive decline [3]
	<i>Taco1</i>	ENSMUST0 0000002048	Translational activator of mitochondrially encoded cytochrome c oxidase I	0.40	3.68×10^{-2}	Loss associated with motor disfunction and mitochondrial disease in mice [8]
Transport to the Golgi and subsequent modification (R-HSA-948021) LFC: 0.27 FDR: 5.71×10^{-3}	<i>Arcn1</i>	ENSMUST0 0000034607	Archain 1	0.24	2.71×10^{-2}	Loss is associated with increased ER stress [13]
	<i>Dctn4</i> <i>Dctn5</i> <i>Dctn1</i>	ENSMUST0 0000025505 ENSMUST0 0000033156 ENSMUST0 0000113919	Dynactin 4 Dynactin 5 Dynactin 1	0.25 0.30 0.56	4.42×10^{-2} 2.38×10^{-2} 2.10×10^{-2}	Positive regulators of retrograde axonal transport, decreased activity associated with neurodegeneration [14]
	<i>Ykt6</i>	ENSMUST0 0000002818	YKT6 v-SNARE homolog (S. cerevisiae)	0.26	1.97×10^{-2}	Negative regulator of α - synuclein, downregulated in PD brain [15]
	<i>Kdelr2</i>	ENSMUST0 0000110731	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	0.27	4.30×10^{-2}	Regulator of ER proteome homeostasis in response to ER stress [16]

	<i>Man1a2</i> <i>Man2a2</i>	ENSMUST0 0000008907 ENSMUST0 0000098346	Mannosidase, alpha, class 1A, member 2 Mannosidase 2, alpha 2	0.28 0.65	3.16×10^{-2} 1.70×10^{-2}	Regulators of N-glycosylation [17]
	<i>Copz1</i> <i>Copg1</i>	ENSMUST0 0000100162 ENSMUST0 0000113607	Coatomer protein complex, subunit zeta 1 Coatomer protein complex, subunit gamma 1	0.30 0.46	1.59×10^{-2} 4.97×10^{-3}	Positive regulators of neurite outgrowth [18]
	<i>Tbc1d20</i>	ENSMUST0 0000028963	TBC1 domain family, member 20	0.32	4.24×10^{-2}	Downregulation leads to disrupted neuronal autophagic flux and motor dysfunction [19]
	<i>Cog4</i> <i>Cog1</i>	ENSMUST0 0000034203 ENSMUST0 0000018805	Component of oligomeric golgi complex 4 Component of oligomeric golgi complex 1	0.34 0.44	1.62×10^{-2} 8.60×10^{-3}	Regulator of Golgi vesicle trafficking, defects are associated with neurological disorders [20]
	<i>Gosr2</i> <i>Gosr1</i>	ENSMUST0 0000021329 ENSMUST0 0000010536	Golgi SNAP receptor complex member 2 Golgi SNAP receptor complex member 1	0.35 0.38	9.17×10^{-3} 6.24×10^{-3}	Regulator of ER to Golgi trafficking, dysregulation associated with neurological disorders [21]
	<i>Dynll2</i> <i>Dync1li1</i> <i>Dync1h1</i>	ENSMUST0 0000020775 ENSMUST0 0000047404 ENSMUST0 0000018851	Dynein light chain LC8-type 2 Dynein cytoplasmic 1 light intermediate chain 1 Dynein cytoplasmic 1 heavy chain 1	0.36 0.38 0.50	5.25×10^{-3} 7.11×10^{-3} 1.28×10^{-2}	Positive regulators of retrograde axonal transport [22], Downregulated in AD hippocampus [23]
	<i>Sec22b</i> <i>Sec24b</i> <i>Sec31a</i> <i>Sec24c</i> <i>Sec22c</i>	ENSMUST0 0000029476 ENSMUST0 0000001079 ENSMUST0 0000094578 ENSMUST0 0000048657 ENSMUST0 0000078547	SEC22 homolog B, vesicle trafficking protein Sec24 related gene family, member B (<i>S. cerevisiae</i>) Sec31 homolog A (<i>S. cerevisiae</i>) Sec24 related gene family, member C (<i>S. cerevisiae</i>) SEC22 homolog C, vesicle trafficking protein	0.36 0.40 0.46 0.49 0.82	3.74×10^{-2} 9.12×10^{-3} 7.12×10^{-3} 1.35×10^{-2} 3.28×10^{-3}	Regulators of vesicle trafficking, downregulated in aging and AD brains [24], Loss leads to neuronal apoptotic cell death [25]
	<i>Tmed9</i>	ENSMUST0 0000109905	Transmembrane p24 trafficking protein 9	0.38	1.50×10^{-2}	Positive regulator of autophagosome biogenesis [26]
	<i>Napa</i>	ENSMUST0 0000006181	N-ethylmaleimide sensitive fusion protein attachment protein alpha	0.41	2.59×10^{-2}	Loss leads to impairment of Golgi to ER trafficking and apoptosis [27]
	<i>Actr1a</i>	ENSMUST0 0000040270	ARP1 actin-related protein 1A, centracin alpha	0.41	4.56×10^{-3}	Positive regulator of retrograde axonal transport [28]
	<i>Trappc5</i> <i>Trappc9</i>	ENSMUST0 0000044857 ENSMUST0 0000089770	Trafficking protein particle complex 5 Trafficking protein particle complex 9	0.42 0.43	6.44×10^{-3} 3.92×10^{-2}	Loss leads to decreased social memory and obesity in mice [29]
	<i>Tubb6</i> <i>Tuba4a</i>	ENSMUST0 0000001513 ENSMUST0 0000186213	Tubulin, beta 6 class V Tubulin, alpha 4A	0.45 0.52	4.40×10^{-2} 8.60×10^{-3}	Downregulation leads to motor axon defects [30]
	<i>Tmem115</i>	ENSMUST0 0000010189	Transmembrane protein 115	0.45	7.28×10^{-3}	Regulator of Golgi to ER retrograde transport [31]
	<i>Arfgap1</i>	ENSMUST0 0000029092	ADP-ribosylation factor GTPase activating protein 1	0.46	1.28×10^{-2}	Regulator of targeting of GABA transporter 1 in axon terminals [32]

	<i>Mgat4b</i> <i>Mgat5</i>	ENSMUST0000041725 ENSMUST0000038361	Mannoside acetylglucosaminyltransferase 4, isoenzyme B Mannoside acetylglucosaminyltransferase 5	0.47 0.70	1.50×10^{-2} 3.81×10^{-3}	Negative regulators of spontaneous inflammatory demyelination and neurodegeneration [33]
	<i>B4galt3</i> <i>B4galt6</i> <i>B4galt5</i>	ENSMUST0000064272 ENSMUST0000070080 ENSMUST0000109221	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	0.48 0.57 0.62	3.60×10^{-2} 4.56×10^{-3} 3.27×10^{-3}	Regulators of inflammatory cytokine response in LPS-treated microglia [34]
	<i>Uso1</i>	ENSMUST0000031355	USO1 vesicle docking factor	0.50	9.05×10^{-3}	Positive regulator of ER to Golgi transport [35]
	<i>St8sia3</i>	ENSMUST0000025477	ST8 alpha-N-acetyl-neuraminate alpha-2,8-sialyltransferase 3	0.52	5.84×10^{-3}	Regulator of dopamine D ₁ R and D ₂ R receptors, downregulated in neurodegenerative disease [36]
	<i>Cnih3</i>	ENSMUST0000027795	Cornichon family AMPA receptor auxiliary protein 3	0.54	2.00×10^{-2}	Positive regulator of hippocampal AMPAR synaptic transmission [37]
	<i>Arf3</i>	ENSMUST0000053183	ADP-ribosylation factor 3	0.56	7.12×10^{-2}	Paralog ARF6 mediates BACE1 and APP processing [38]
	<i>Ppp6r1</i>	ENSMUST0000064099	Protein phosphatase 6, regulatory subunit 1	0.56	4.91×10^{-3}	Negative regulator of NF-κB signaling [39]
	<i>Nsf</i>	ENSMUST0000103075	N-ethylmaleimide sensitive fusion protein	0.59	2.66×10^{-2}	Positive regulator of synaptic AMPA receptor function [40]
	<i>Sptbn2</i> <i>Sptbn1</i>	ENSMUST0000008991 ENSMUST0000011877	Spectrin beta, non-erythrocytic 2 Spectrin beta, non-erythrocytic 1	0.62 0.85	7.88×10^{-3} 4.89×10^{-3}	Loss leads to decrease in dendritic spine density and neurodegeneration [41]
	<i>Csnk1d</i>	ENSMUST0000070575	Casein kinase 1, delta	0.65	5.83×10^{-3}	Positive regulator of Wnt/β-catenin signaling [42]
	<i>Lman2</i> <i>Lman2l</i>	ENSMUST0000021940 ENSMUST0000125304	Lectin, mannose-binding 2 Lectin, mannose-binding 2-like	0.69 0.86	5.30×10^{-3} 5.07×10^{-3}	Regulator of glycoprotein transport and sorting, dysregulation associated with neurodegenerative disease [43]
	<i>Gbf1</i>	ENSMUST0000026254	Golgi-specific brefeldin A-resistance factor 1	0.69	7.23×10^{-3}	Dysregulation associated with Golgi fragmentation [44]
	<i>Fut8</i>	ENSMUST0000062804	Fucosyltransferase 8	0.84	3.62×10^{-3}	Loss leads to increased microgliosis under LPS stimulation [45]
Processing of Intronless Pre-mRNAs (R-HSA-77595) LFC: 0.29 FDR: 7.79×10^{-3}	<i>Cstf2</i> <i>Cstf1 Cstf2t</i>	ENSMUST0000113286 ENSMUST0000116375 ENSMUST0000066039	Cleavage stimulation factor, 3' pre-RNA subunit 2 Cleavage stimulation factor, 3' pre-RNA, subunit Cleavage stimulation factor, 3' pre-RNA subunit 2, tau	-0.70 0.33 0.34	3.86×10^{-2} 1.41×10^{-2} 1.29×10^{-2}	Positive regulators of 3' cleavage and polyadenylation [46]
	<i>Nudt21</i>	ENSMUST0000034204	Nudix (nucleoside diphosphate linked moiety X)-type motif 21	0.23	2.59×10^{-2}	Loss leads to dysregulated hippocampal alternative polyadenylation and learning deficits [47]

	<i>Ncbp1</i> <i>Ncbp2</i>	ENSMUST0 0000030014 ENSMUST0 0000023460	Nuclear cap binding protein subunit 1 Nuclear cap binding protein subunit 2	0.25 0.28	3.87×10^{-2} 1.48×10^{-2}	Positive regulator of mRNA export from the nucleus [48]
	<i>Cpsf7</i> <i>Cpsf2</i>	ENSMUST0 0000038379 ENSMUST0 0000047357	Cleavage and polyadenylation specific factor 7 Cleavage and polyadenylation specific factor 2	0.28 0.34	2.41×10^{-2} 1.26×10^{-2}	Positive regulators of 3' cleavage and polyadenylation [46]
	<i>Wdr33</i>	ENSMUST0 0000025264	WD repeat domain 33	0.29	2.75×10^{-2}	Positive regulator of polyadenylation signal recognition [49]
	<i>Papola</i>	ENSMUST0 0000109901	Poly (A) polymerase alpha	0.39	3.72×10^{-2}	Positive regulator of polyadenylation [46]
	<i>Sympk</i>	ENSMUST0 0000023882	Symplekin	0.48	7.15×10^{-3}	Positive regulator of polyadenylation [50], Downregulated in AD brain [51]
Disassembly of the destruction complex and recruitment of AXIN to the membrane (R-HSA-4641262) LFC: 0.38 FDR: 7.21×10^{-3}	<i>Ppp2cb</i> <i>Ppp2r5a</i> <i>Ppp2r5e</i> <i>Ppp2r1a</i>	ENSMUST0 0000009774 ENSMUST0 0000067976 ENSMUST0 0000021447 ENSMUST0 0000007708	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform Protein phosphatase 2, regulatory subunit B', alpha Protein phosphatase 2, regulatory subunit B', epsilon Protein phosphatase 2, regulatory subunit A, alpha	0.25 0.26 0.31 0.37	1.94×10^{-2} 4.25×10^{-2} 2.85×10^{-2} 3.87×10^{-2}	Positive regulator of Wnt/ β -catenin signaling [52], Inhibition leads to spatial memory impairment [53]
	<i>Csnk1a1</i> <i>Csnk1g2</i>	ENSMUST0 0000165123 ENSMUST0 0000085435	Casein kinase 1, alpha 1 Casein kinase 1, gamma 2	0.26 0.33	3.90×10^{-2} 4.73×10^{-2}	Negative regulators of SMAD3 and TGF- β signaling [54]
	<i>Ctnnb1</i>	ENSMUST0 0000007130	Catenin (cadherin associated protein), beta 1	0.37	1.38×10^{-2}	Positive regulator of Wnt/ β -catenin signaling, neuronal survival and synaptic plasticity, negative regulator of A β production [55]
	<i>Gsk3b</i>	ENSMUST0 0000023507	Glycogen synthase kinase 3 beta	0.52	3.62×10^{-3}	Regulator of Wnt/ β -catenin signaling, loss leads to synaptic and social defects in mice [56]
	<i>Dvl3</i>	ENSMUST0 0000003318	Dishevelled segment polarity protein 3	0.72	2.23×10^{-2}	Positive regulator of Wnt/ β -catenin signaling, downregulated in AD brain [55]
	<i>Fzd1</i>	ENSMUST0 0000054294	Frizzled class receptor 1	0.73	3.81×10^{-3}	Positive regulator of Wnt/ β -catenin signaling, loss leads to impairment of neuronal differentiation [57]

References

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