

**Transcriptional profiles reveal deregulation of lipid metabolism and inflammatory pathways in neurons
exposed to palmitic acid**

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Supplementary Table 1 List of differentially expressed genes (DEG) found with each pipeline. The merged rows between pipelines depict that the genes were found by different pipelines.

Salmon + DEseq2	Salmon + edgeR	STAR + fc + edgeR	STAR + fc + DEseq2
	Rnf113a1, Mogs, LOC103693189, LOC100911186, U1, Armcx1, AABR07003537.1, LOC103689968, AABR07034273.1, Fgd1, AABR07002775.1, Miip, Entpd7, LOC102552659, Faim, Mboat7, LOC108348074, LOC108348136, Syne4, LOC100359574, LOC691254, Cass4, Ccl9, Chd9, LOC100911951, Enpp6, Impad1, Klrb1b, Abhd1, AABR07003056.1, AABR07014125.1, Snip1	Serpine1, Slc16a5, Fndc3c1, Mir132, AABR07038886.1, Ucp2, Mir212, Acot1, AABR07003751.1, AABR07065531.19, 5S_rRNA, Rd3l, Maff, Pdk4, AABR07017825.7	Nfil3
Hells, LOC103692716, AABR07033249.1		Mki67	
	Lpcat1, Npas4		
	Ccl2, AABR07054460.4, Ier3, Gprc5a, Mobp, Cxcl1, Hmgcs2, Bhlha15, Trim66, Tns3, Cyp51, Fam49a, Tgm1, Cited2, Fgf5, Insig1		
	Angptl4, Ugt8, Cnp, Rnf145, Snn		

Supplementary Fig. 1 Gene Set Enrichment Analysis (GSEA) of Gene Ontology (GO) terms. The top biological processes analyzed by GO (y-axis) and the number of genes involved in each process that are altered (x-axis) are depicted in the graph. The affected lipid processes (yellow rectangles) and important biological and cellular processes for neurons (green rectangles) when they are exposed to PA are highlighted in rectangles

GSEA of GO terms

