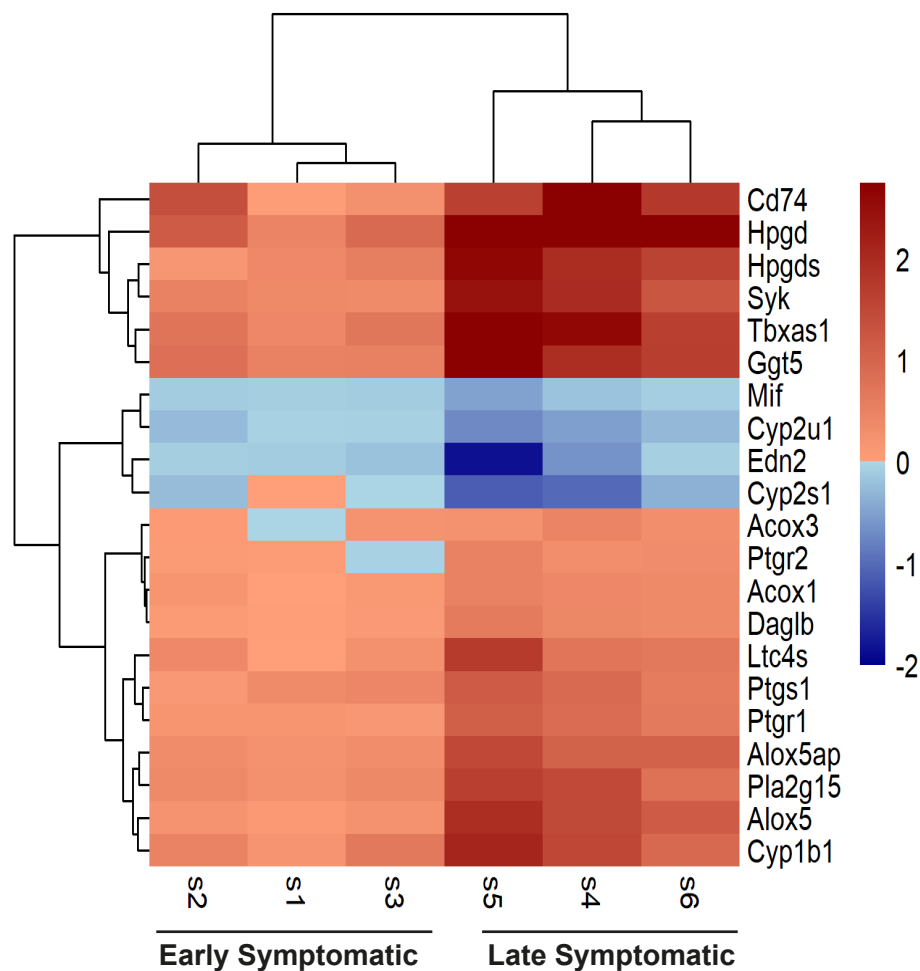


**Figure S1. Meta-analysis of late-symptomatic RNA-seq studies.** (A-C) Volcano-plots showing the dysregulated genes found on each of the three RNA-seq studies selected at late symptomatic . Blue, yellow and green dots indicates DEGs found in the study 4, 5 and 6 respectively. Grey dots indicate genes with no significant change. (D) A Venn diagram illustrating the overlapping DEGs across the three studies and the result of the meta-analysis (Late-MA). The meta-analysis (Late-MA) was performed using Fishers combined probability test where raw p-values were adjusted by the Benjamini-Hochberg false discovery rate (FDR) method and the adjusted p-values less than 0.01 were considered as statistically significant.

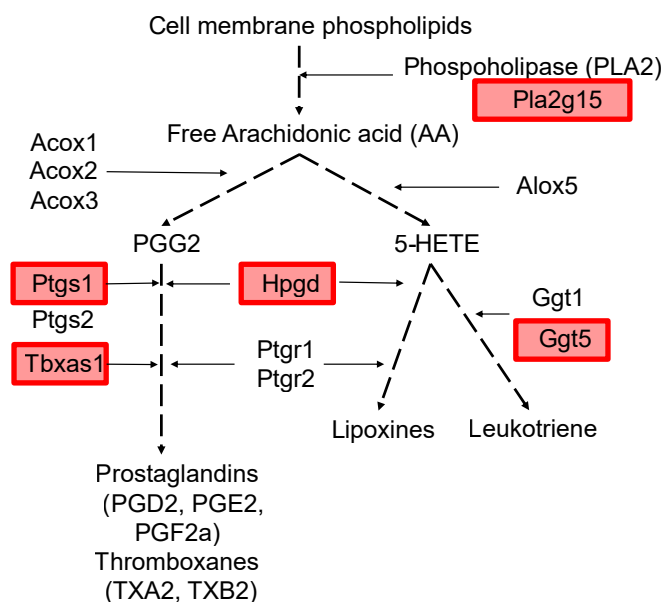


**A**

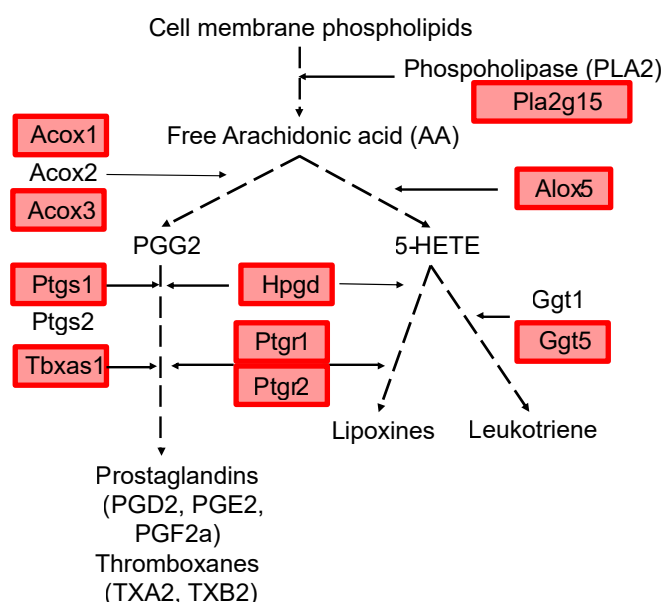


**B**

### Early Symptomatic



### Late Symptomatic



**Figure S3. Comparative transcriptional alterations in icosanoids metabolic pathways in the spinal cord of SOD1 mice at early- and late-symptomatic disease stages.** (A) The heatmap of the combination of the six transcriptomic studies (three early-symptomatic and three late-symptomatic) shows the expression level of the altered genes that participate in the icosanoids metabolic pathways. The heatmap colours indicate the expression levels by the log2-fold-change. Each column represents an individual RNA-seq study, and each row represents one gene. (B) The icosanoids biosynthesis pathways are represented, comparing the results from the Early-MA and the Late-MA. Coloured genes indicate that the gene was significantly altered in the meta-analysis. Blue indicates down-regulation and red indicates up-regulation.