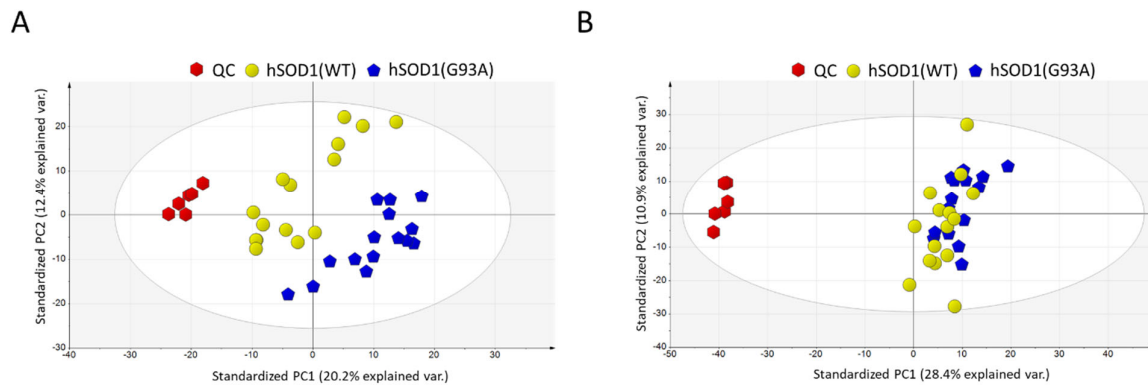


Altered proteome and secreted metabolome in primary astrocytes from the hSOD1(G93A) ALS mouse model

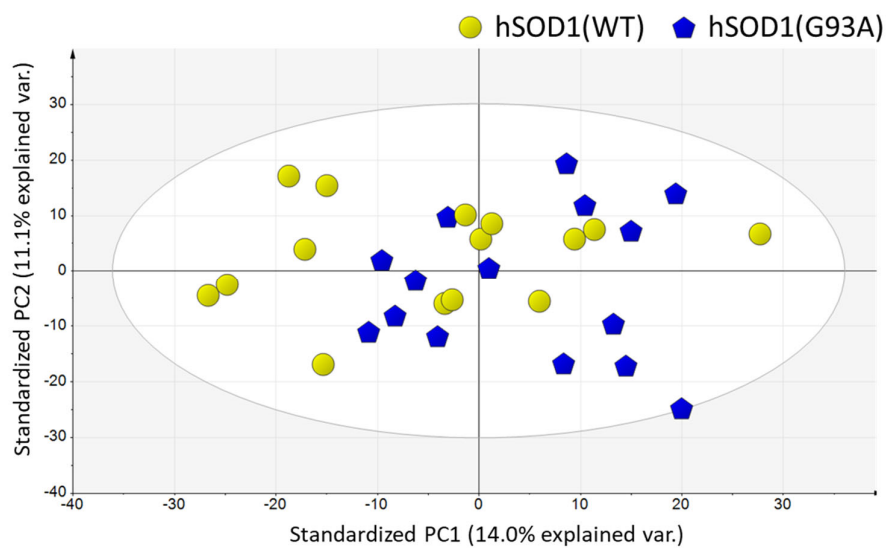
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Supplementary Materials

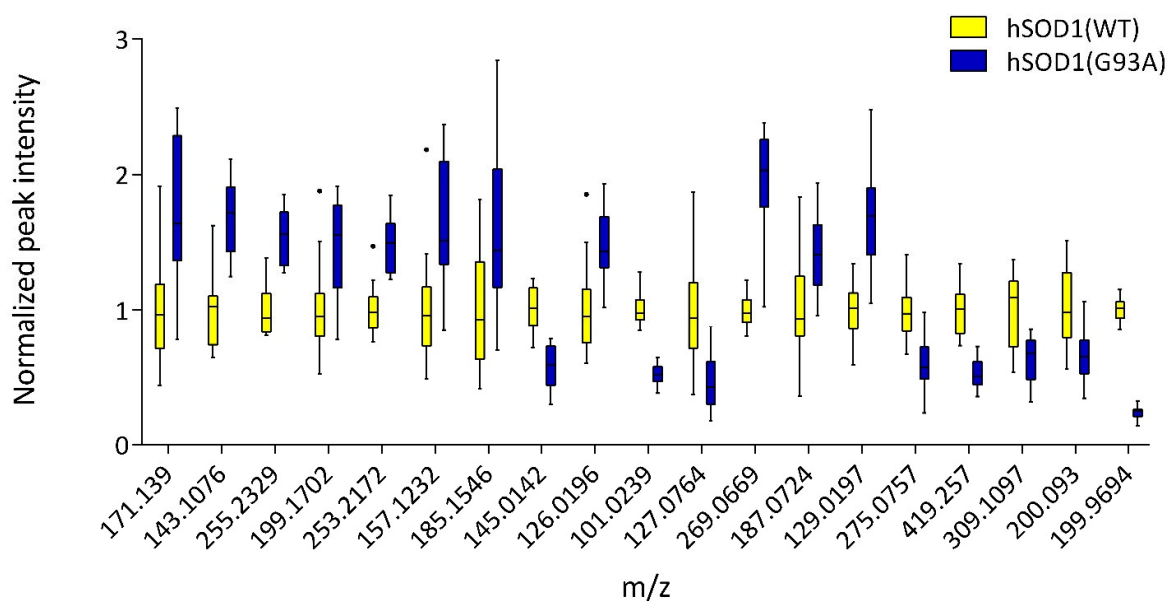
Supplementary Figures



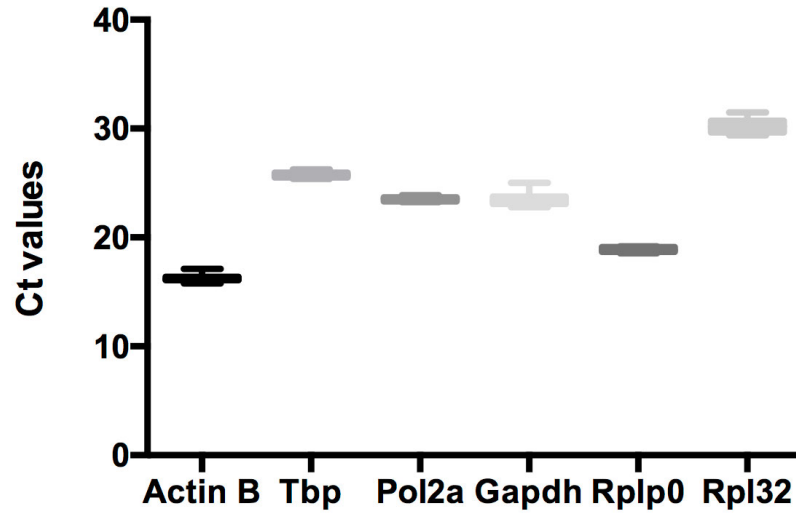
Supplementary Figure S1 – Score plots of metabolomics data. Principal component analysis (PCA) score plots of the metabolome data of CMs of hSOD1(WT) (*yellow circles*), hSOD1(G93A) (*blue pentagons*) primary astrocytes and of QC samples (*red hexagons*) acquired in the negative (panel A) and positive (panel B) ionization condition. Other details are as in Figure 1.



Supplementary Figure S2 - Score plot of metabolomics data acquired in the positive ionization mode. PCA score plot of metabolomics data of CMs of hSOD1(WT) (*yellow circles*), hSOD1(G93A) (*blue pentagons*) primary astrocytes acquired in the positive ionization condition. Other details are as in Figure 1



Supplementary Figure S3 – Altered amounts of 19 metabolites in the CM of hSOD1(G93A) astrocytes. Box-and-whisker plot showing the normalized abundance of the 19 significantly affected metabolites in the CM derived from hSOD1(WT) (yellow box) and hSOD(G93A) (blue box) astrocytes. For each metabolite, the corresponding measured m/z is reported in the graph (see Supplementary Table 1, in which for each m/z the corresponding systematic name is reported). The bottom and top of the boxes represent the 5th and 95th percentiles, the line in the middle indicates the median. n=15 for each hSOD1 genotype. Statistical significance was calculated with the Wilcoxon rank test and p-value of each metabolite is reported in Supplementary Table 1.



Supplementary Figure S4 – Identification and evaluation of reference genes for qRT-PCR analysis in primary spinal astrocytes. Analysis of cycle threshold (Ct) values of the 6-candidate reference genes across all samples. Expression data displayed as Ct values for each reference gene in all astrocyte samples. Data are reported as mean \pm standard deviation.