

Figure S6

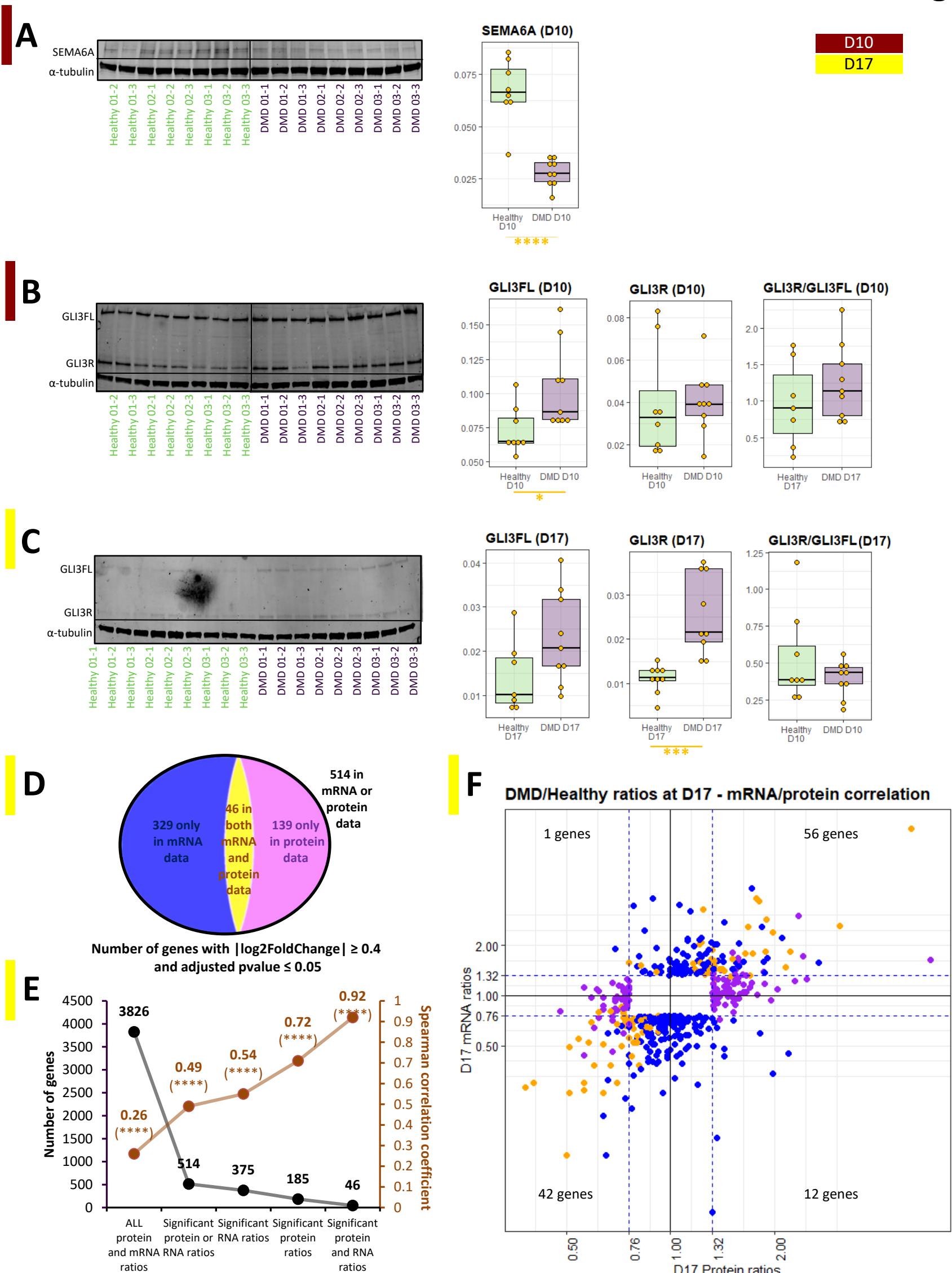


Figure S6 – Comparison of healthy and DMD cells at D10 and D17, protein analyses. Western blots and quantifications of **A)** SEMA6A at D10, **B)** GLI3 at D10 and **C)** GLI3 at D17. Omics comparison of mRNA and protein data at day 17: **D)** Venn diagram of the number of genes with $|\log_2\text{FoldChange}| \geq 0.4$ and adjusted pvalue ≤ 0.05 in either transcriptomic or proteomic data, **E)** their associated Spearman correlation coefficient in brown, as well as **D)** their correlation graph with the number of genes with $|\log_2\text{FoldChange}| \geq 0.4$ in both sets are indicated (genes with p-value ≥ 0.05 only in transcriptomics are in blue, only in proteomics in purple and in both in orange). (*p-value ≤ 0.05 , **p-value ≤ 0.01 , ***p-value ≤ 0.001 , ****p-value ≤ 0.0001 ; D: day; GLI3FL: GLI3 full length; GLI3R: GLI3 repressor).