



**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 p-value  $\leq 0.05$  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  $\geq 0.05$  only in transcriptomics are in blue, only in proteomics in purple and in both in orange). (\*p-value  $\leq 0.05$ , \*\*p-value  $\leq 0.01$ , \*\*\*p-value  $\leq 0.001$ , \*\*\*\*p-value  $\leq 0.0001$ ; D: day; GLI3FL: GLI3 full length; GLI3R: GLI3 repressor).