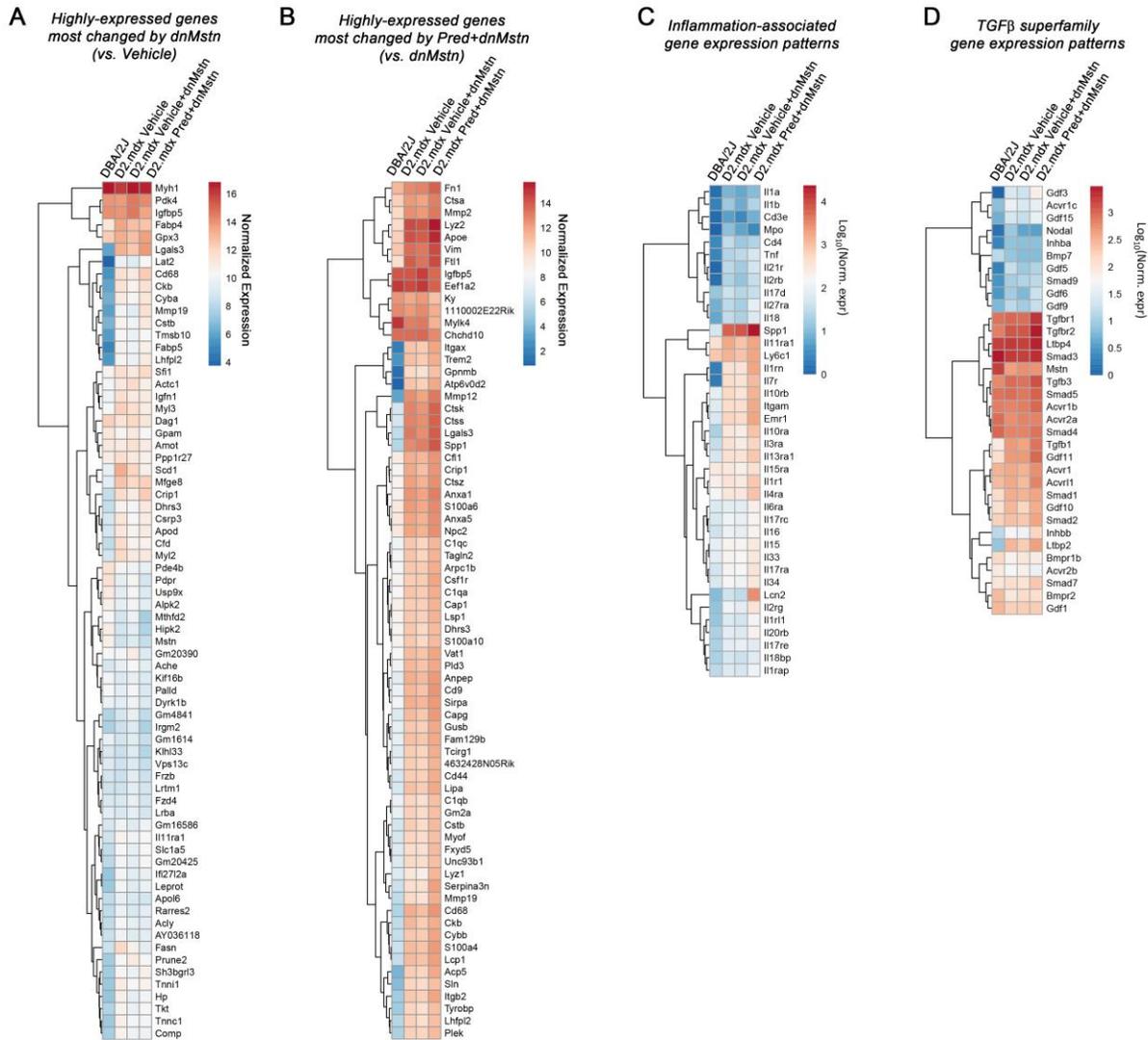


SUPPLEMENTAL MATERIAL



**Figure S1. Additional clustered heatmaps from transcriptomic analyses.** Clustered heatmaps depicting most affected highly-expressed genes associated with (A) myostatin inhibition (D2.mdx Vehicle+dnMstn vs. D2.mdx Vehicle only) and (B) combining prednisolone (Pred) with myostatin inhibition (D2.mdx Pred+dnMstn vs. D2.mdx Vehicle+dnMstn). Genes of these analyses were enriched from genes having normalized expression levels greater than or equal to 11. Targeted clustered analysis showing absolute expression patterns of significantly changed genes associated with (C) inflammation and immune cells and (D) TGFβ superfamily activation from wild-type DBA/2J, D2.mdx vehicle, D2.mdx vehicle+dnMstn, and D2.mdx Pred+dnMstn groups. Gene expression levels are displayed as log<sub>10</sub>(normalized expression).