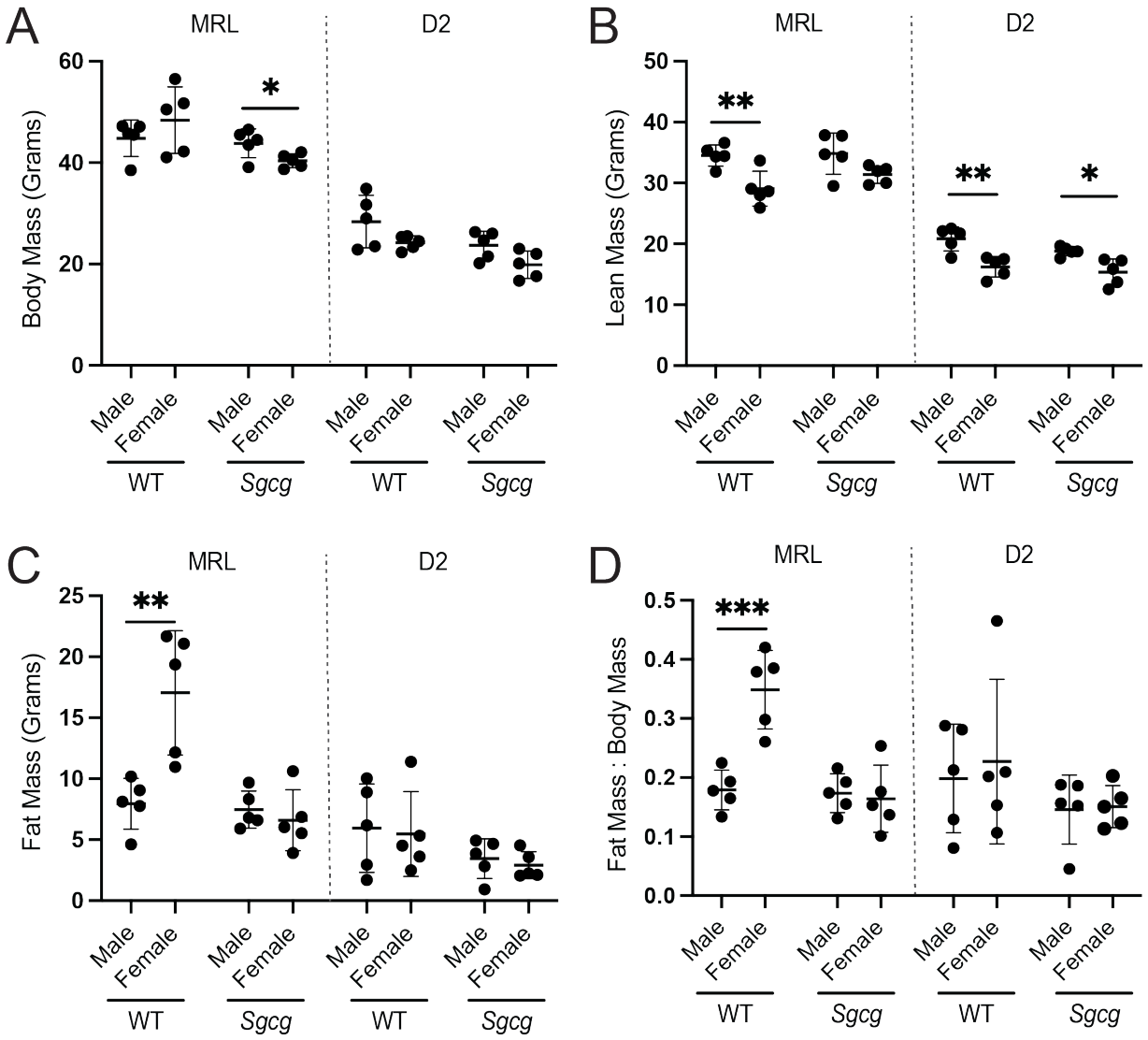
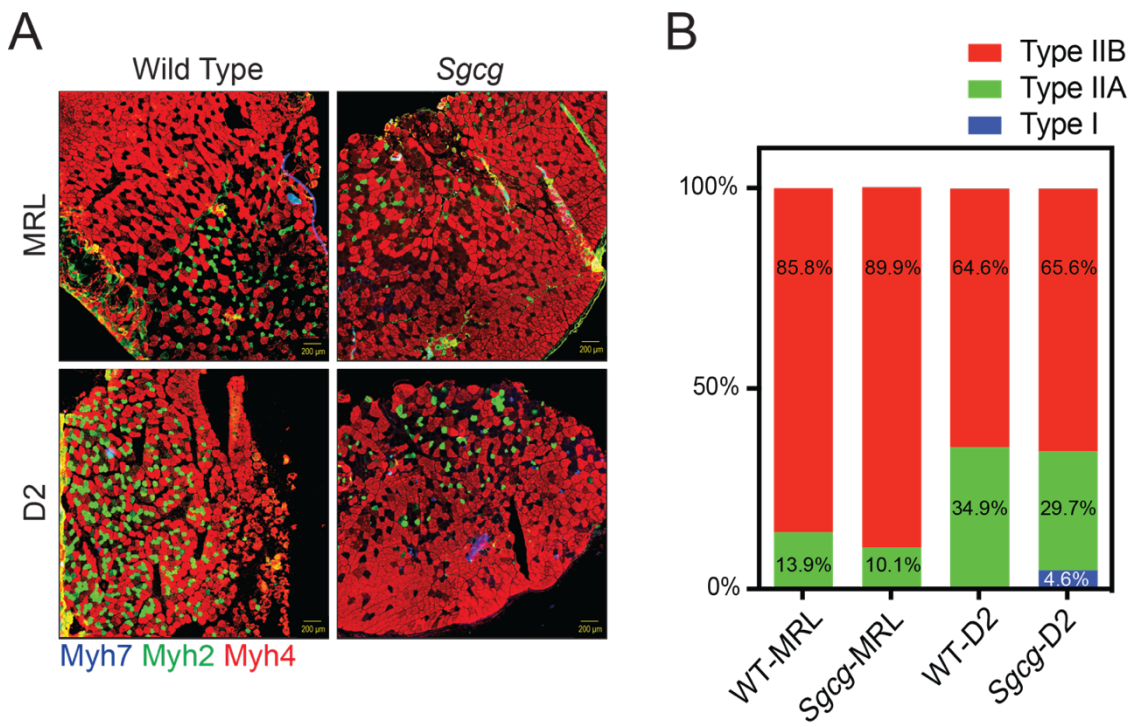
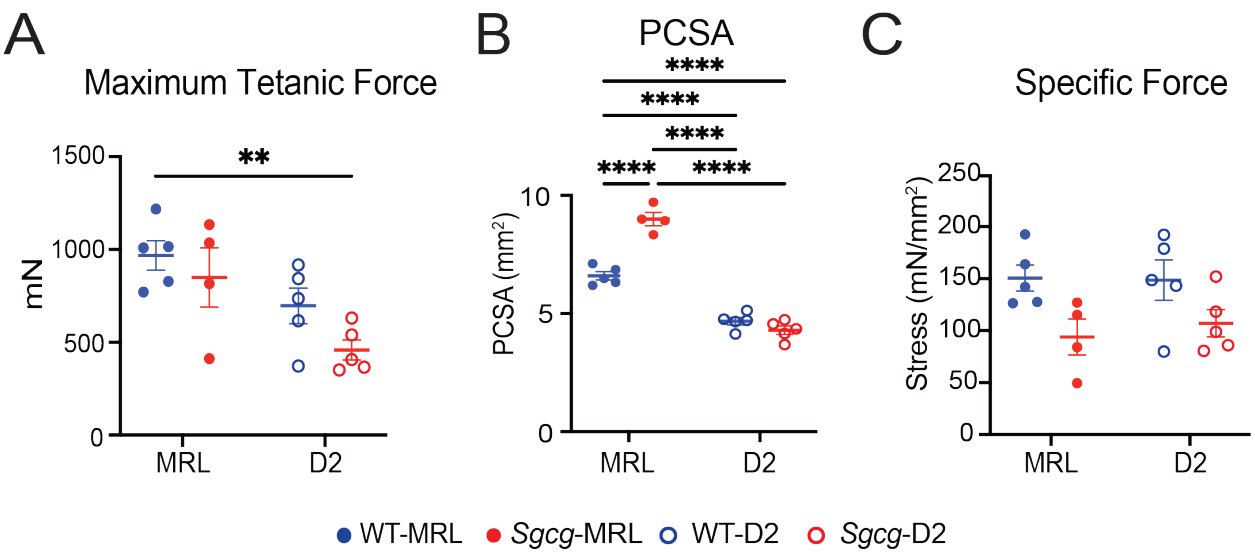
SUPPLEMENTAL INFORMATION



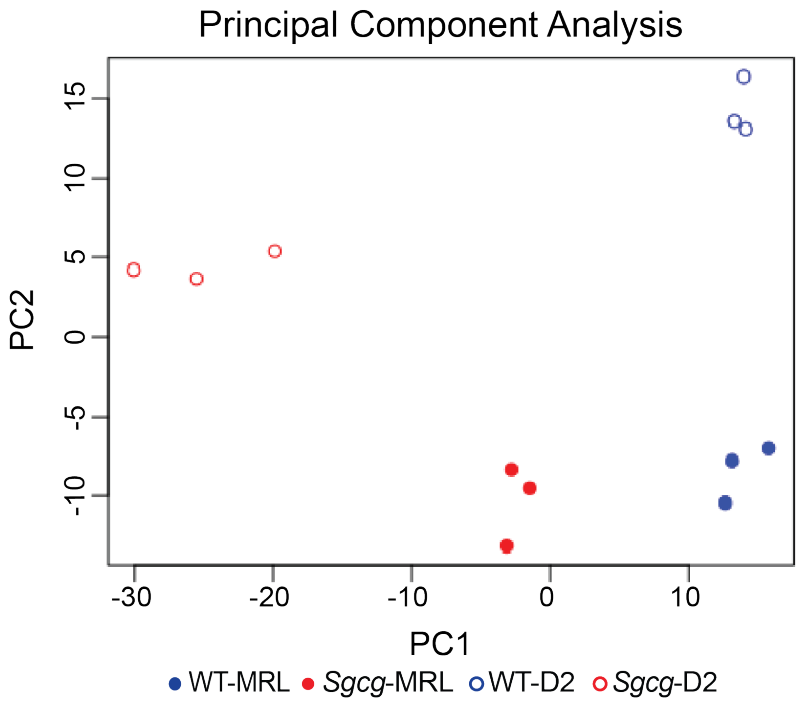
Supplemental Figure 1. MRL mice were larger than DBA/2J (D2) mice. Whole body mass and body mass composition analysis is shown from 5 male and 5 female mice at 20 weeks. (**A**) Body mass of the MRL strain was significantly higher than the D2 strain, and female *Sgcg*-MRL were lighter than their male counterparts. (**B**) Lean mass was less in female mice compared to male mice, except for *Sgcg*-MRL mice, where this difference was not significant. (**C**) Fat mass of the WT-MRL female MRL mice was significantly greater than WT-MRL male mice. Fat mass remained unchanged between sexes in all other cohorts. (**D**) Fat Mass: Body Mass ratio of the WT-MRL cohort was significantly greater in the females than the males in WT-MRL mice. Graphical quantification of mean ± SD. Student's t-test was used was used to determine statistical significance. * $p<0.05$, ** $p<0.01$, *** $p<0.001$, **** $p<0.0001$.



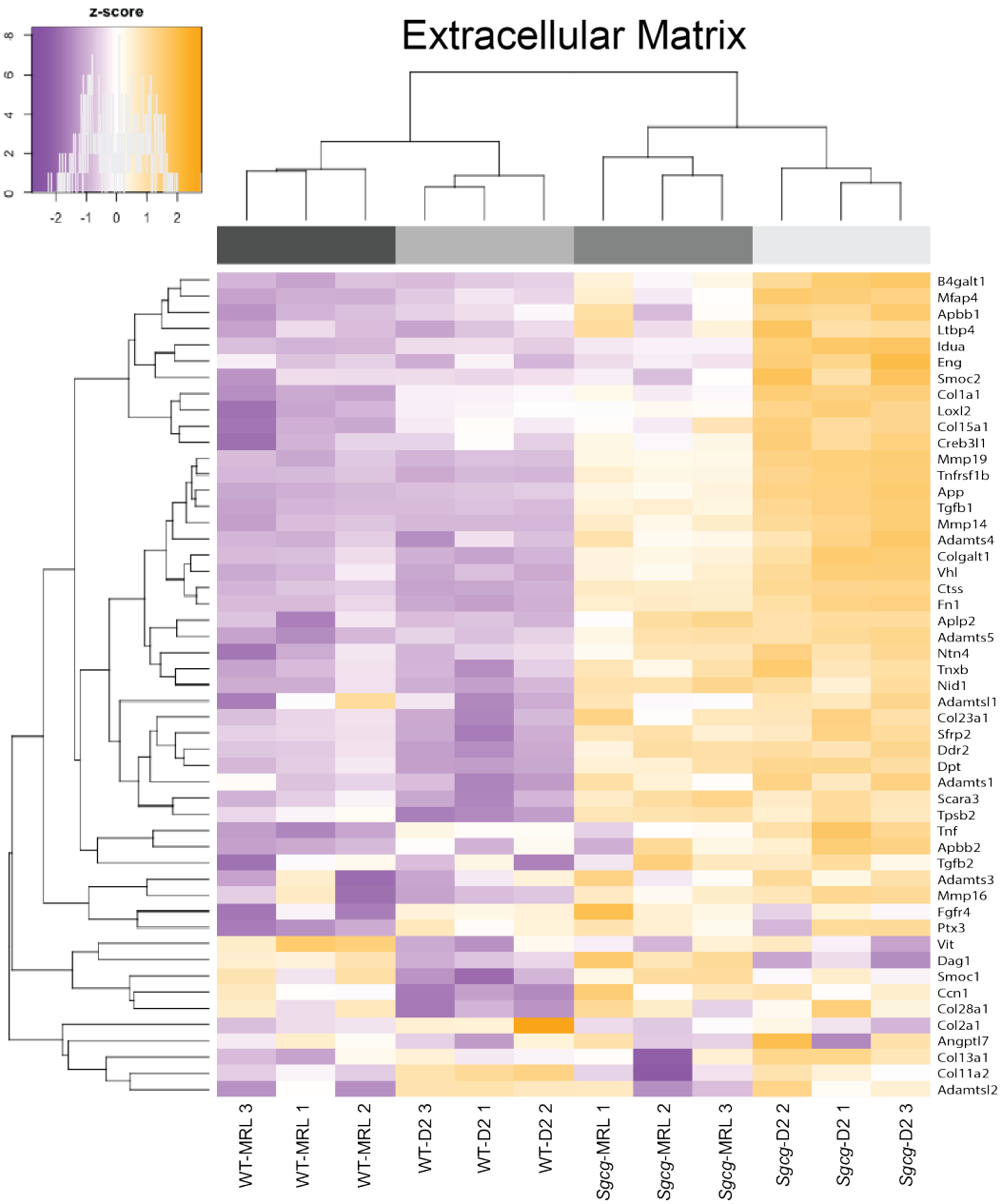
Supplemental Figure 2. Type I fibers in *Sgcg*-D2 mice were suppressed by the MRL background. *Tibialis anterior* (TA) muscles were harvested from 3 male mice, cryosectioned, and co-stained with antibodies to Myh7, Myh2 and Myh4. (**A**) Representative images of muscles showed a higher proportion of Myh4 positive fibers in the MRL background and a small percentage of Type I fibers in the *Sgcg*-D2 mice. (**B**) Quantified data confirms higher Myh4, lower Myh2 and lower Myh7 positive fibers in the MRL background.



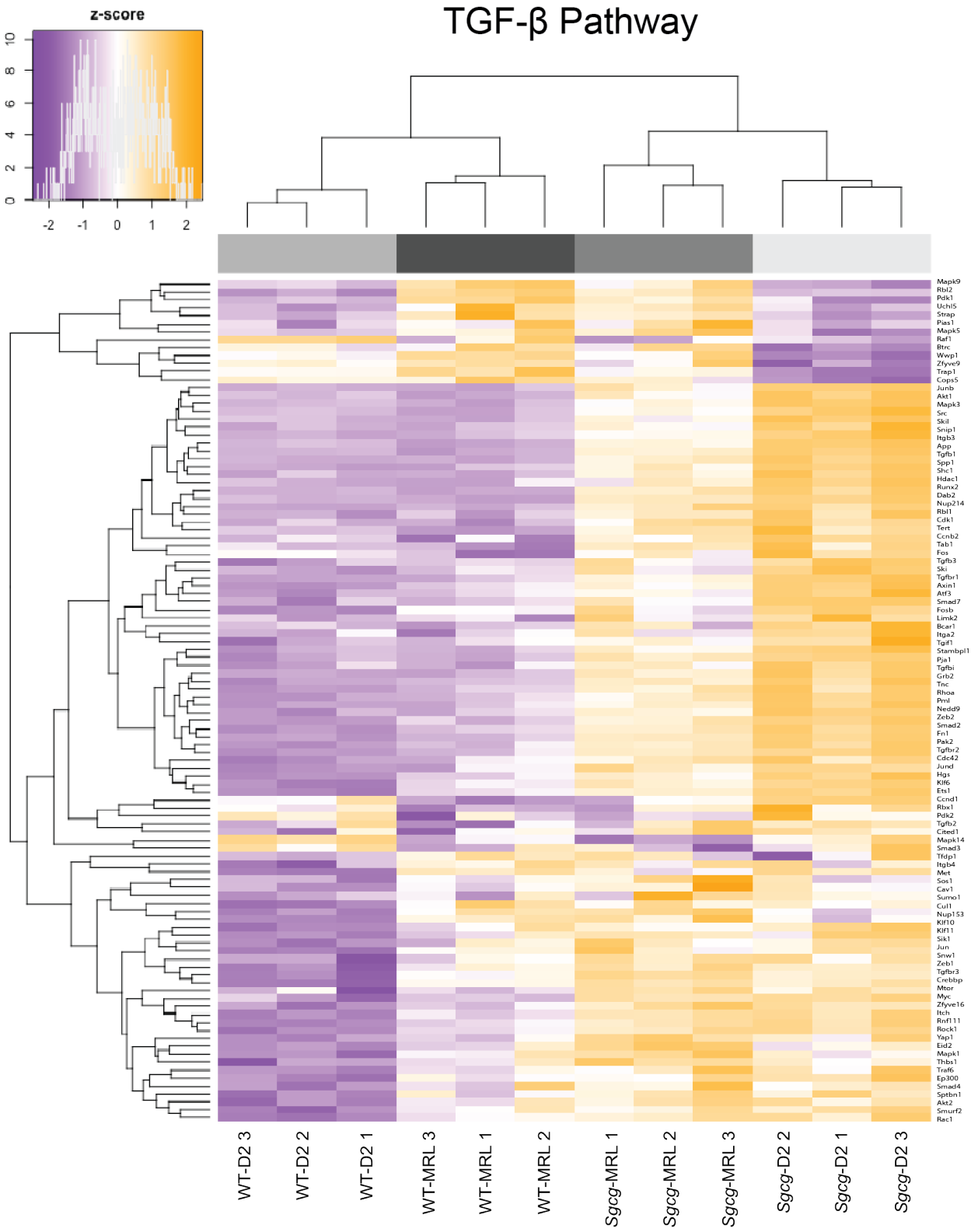
Supplemental Figure 3. Muscle force measurements demonstrate high variability and no significant differences in force production in *Sgcg* mice from either background strain. Muscle force mechanics were conducted on five female mice, 20 weeks of age. (**A**) The maximum tetanic force in the MRL background trended higher than D2 but did not reach significance. (**B**) Physiological Cross-Sectional Area (PCSA) of the MRL background was significantly larger. **C**. Specific force did not differ by strain or genotype. Graphical quantification of mean ± SD. Two-way ANOVA was used to determine statistical significance. * p<0.05, ** p<0.01, *** p<0.001, **** p< 0.0001.



Supplemental Figure 4. Principal component analysis (PCA) of RNA sequencing shows distinct clustering of phenotypic cohorts.



Supplemental Figure 5. Clustered heatmap indicates upregulation of ECM genes in the *Sgcg*-D2 muscle.



Supplemental Figure 6. Clustered heatmap illustrating the differential regulation of TGF-β genes in *Sgcg*-MRL compared to *Sgcg*-D2