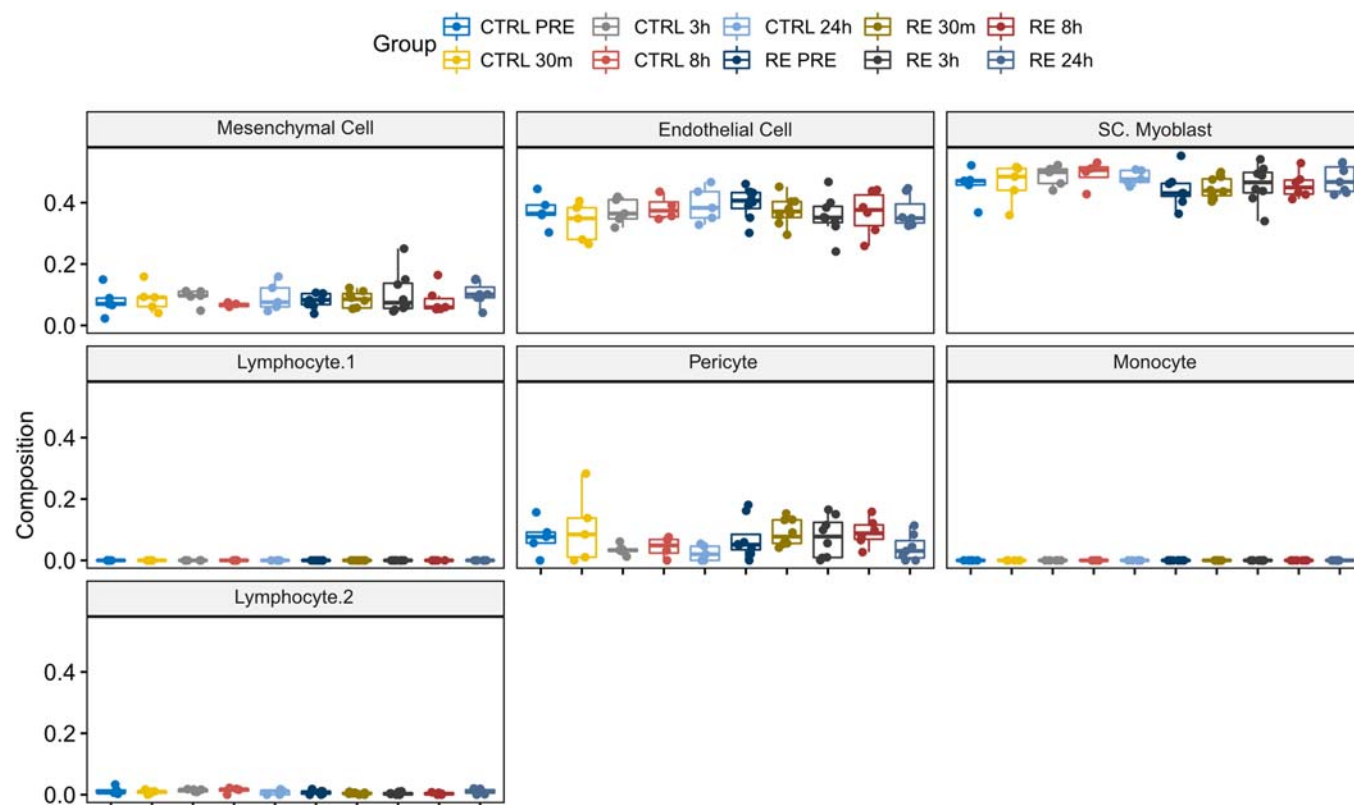
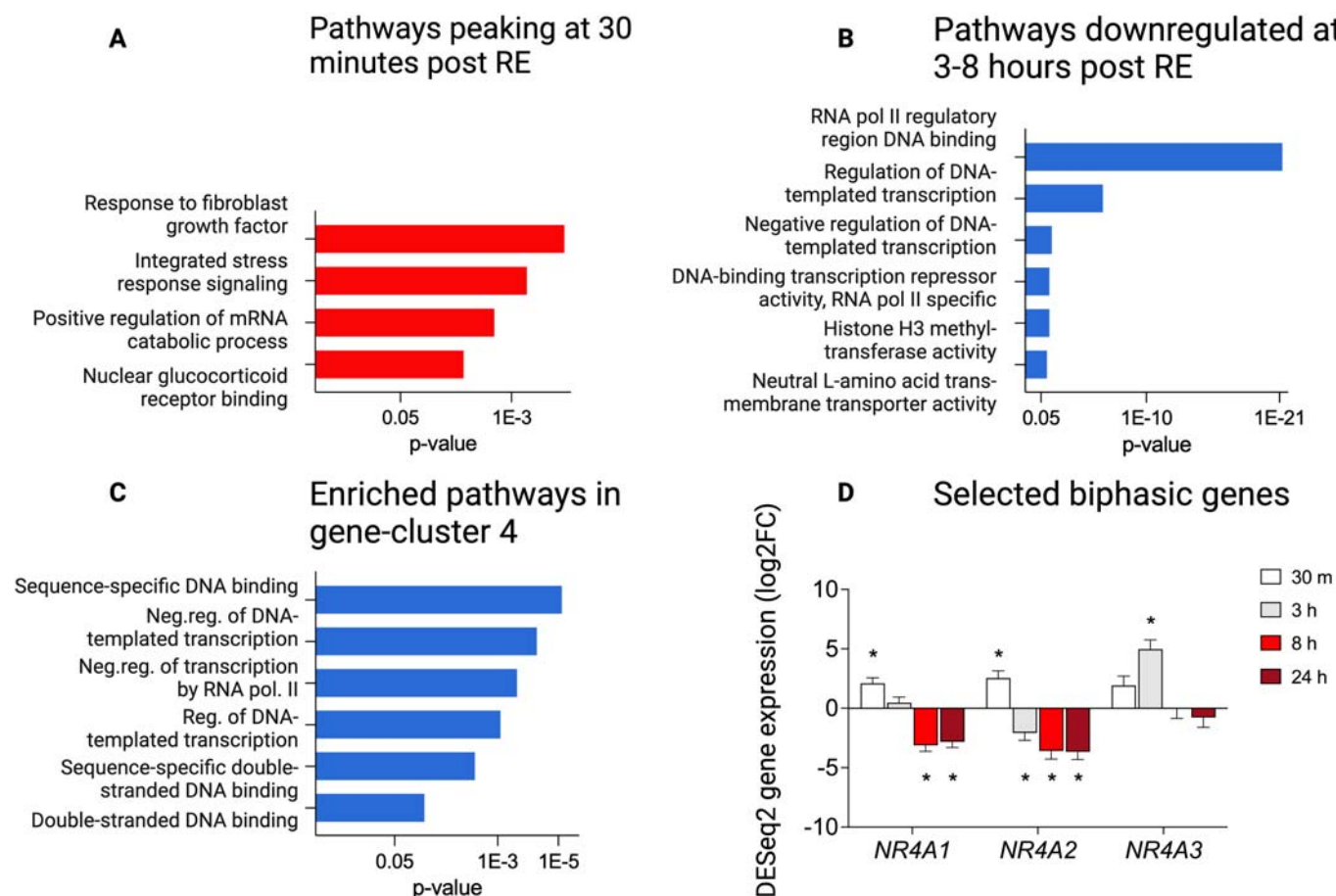


## Expanded View Figures



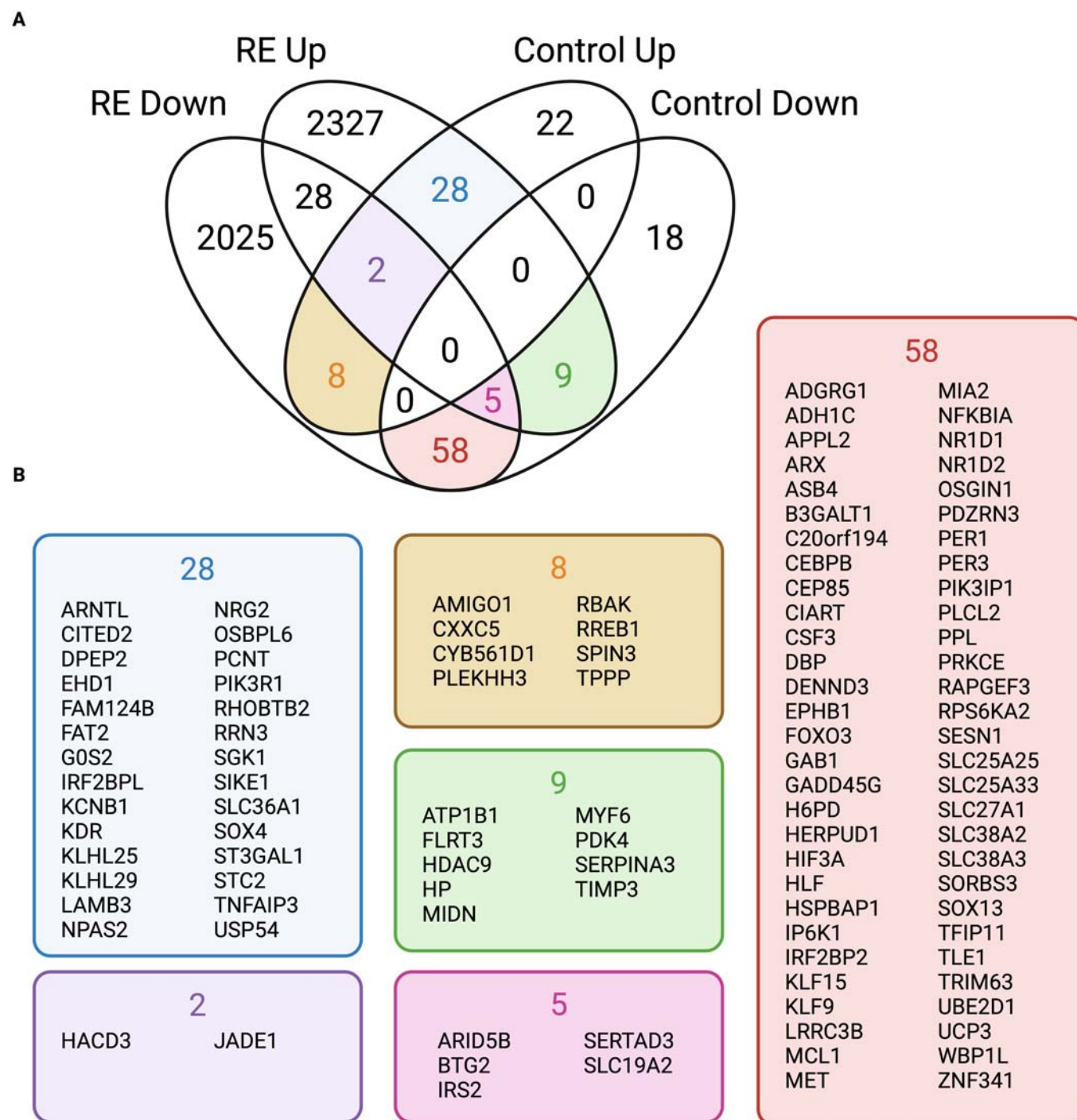
**Figure EV1. Cell composition of muscle biopsies through data deconvolution.**

Cell composition of all skeletal muscle biopsy time points excluding "myocytes" (CTRL  $n = 5$ , RE  $n = 8$ ). The box represents the 25th-75th percentile, the line represents the median, and the whiskers represent Min to Max, excluding outliers. SC satellite cell, CTRL control group, RE resistance exercise group.



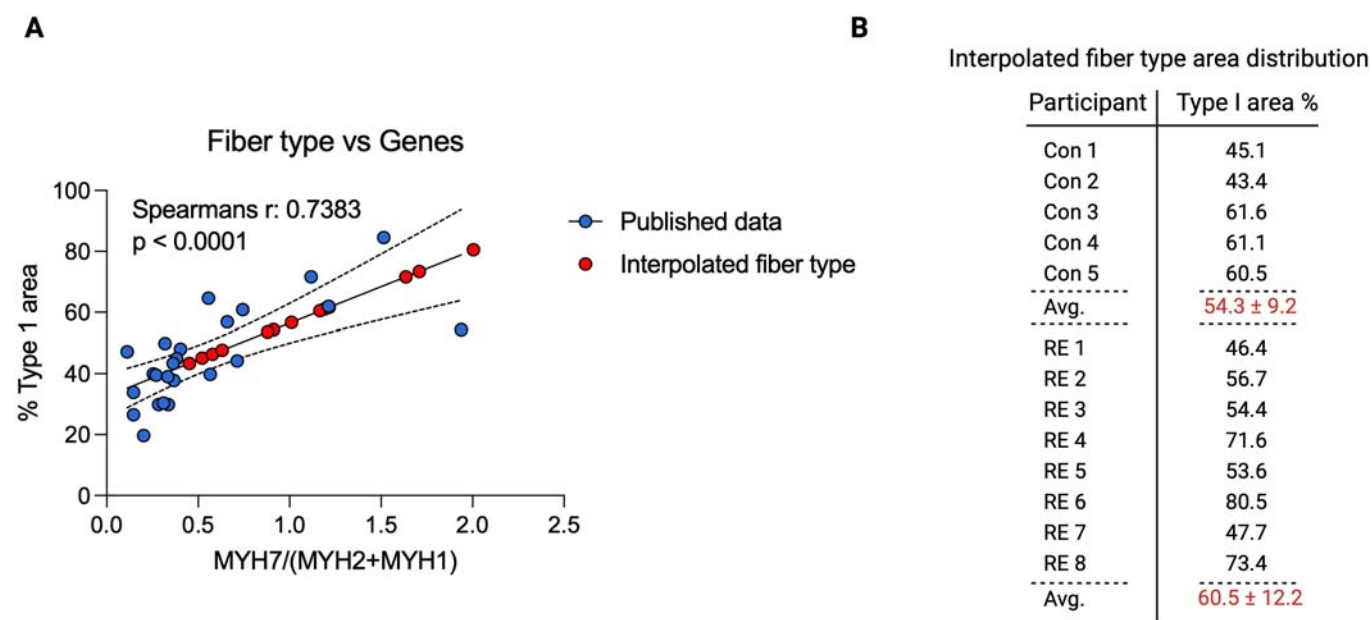
**Figure EV2. Targeted gene set enrichment analysis.**

Pooled gene ontology (GO) biological processes and molecular function gene sets. (A) Targeted analysis of gene sets peaking at 30 min post resistance exercise (RE). (B) Targeted analysis of gene sets significantly enriched in genes downregulated 3–8 h post RE. (C) Targeted analysis of biphasic DEGs composing cluster 4, as presented in Fig. 2D. NR4A1 adj.  $p = 0.0049$  at 30 min, adj.  $p = 6.5E-8$  at 8 h, adj.  $p = 1.0E-6$  at 24 h, NR4A2 adj.  $p = 0.0135$  at 30 min, adj.  $p = 0.0081$  at 3 h, adj.  $p = 4.7E-6$  at 8 h, adj.  $p = 2.4E-6$  at 24 h, NR4A3 adj.  $p = 1.8E-8$  at 8 h. (A–C) Gene ontology (GO) gene set enrichment analysis is analyzed using a Fisher exact test with Benjamini–Hochberg  $p$ -value correction. (D) Gene expression of selected genes with a biphasic gene expression pattern, up early/down late,  $n = 8$ . DESeq2 was calculated using a Wald test with a Benjamini–Hochberg  $p$ -value correction. \* $p < 0.05$  vs Pre values. Neg. negative, Reg. regulation.



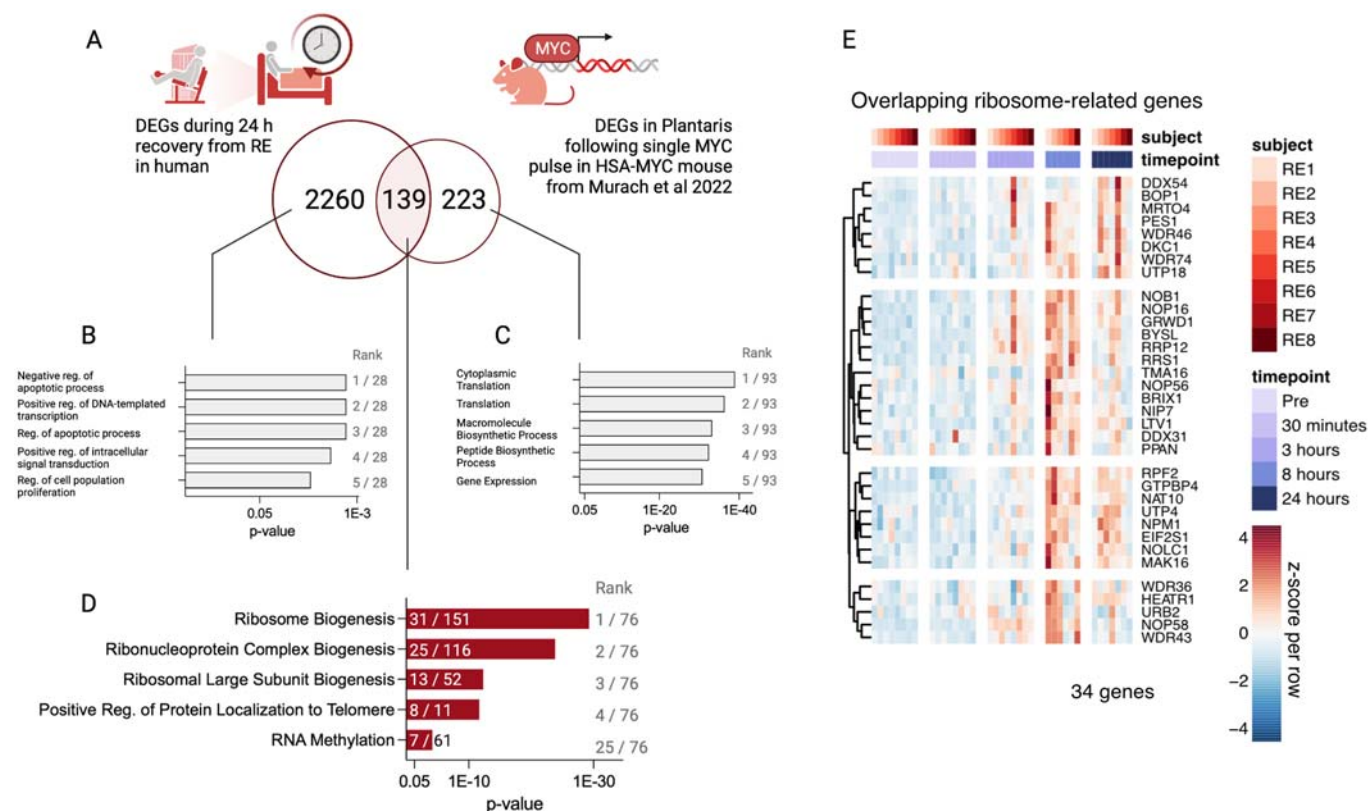
**Figure EV3. Venn diagram illustrating overlap in gene expression between the biopsy-only control group and the post-RE response at 3 and 8 h.**

(A) Venn-diagram of up and downregulated differentially expressed gene lists from the resistance exercise and control group. RE resistance exercise. (B) Genes corresponding to the overlap presented in (A).



**Figure EV4. Interpolated fiber type area distribution of muscle samples.**

(A) Correlation of gene expression data with type I fiber area asses by muscle histology ( $p = 3.0E-5$ ), data from Reitzner et al (2024). Blue dots = Data points from Reitzner et al (2024), Red dots = interpolated values based on gene data. (B) Data table of type I fiber area % in each participant.



**Figure EV5. Transcriptional similarities between human RE recovery and MYC overexpression in mouse plantaris muscle.**

(A) Comparison of upregulated DEGs across 24 h of RE recovery in humans ( $n = 8$ ) vs plantaris muscle from MYC-overexpressing mice from Murach et al (2022). (B–D) Top gene sets (GO: Biological processes) based on DEGs in (B) the human exclusive gene list, (C) MYC mouse exclusive gene list, and (D) overlapping gene list, respectively. (B–D) Gene ontology (GO) gene set enrichment analysis is analyzed using a Fisher exact test with Benjamini-Hochberg  $p$ -value correction. Gene sets are ranked according to their adj.  $p$ -values. (E) Heatmap showing DEG pattern for ribosome-related genes overlapping human RE response to a MYC response in mouse plantaris muscle. Source data are available online for this figure.