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MANUSCRIPT DATA IDENTIFICATION FORM

Title: Muscle Transcriptional Networks Underlying Hypertrophic Response Heterogeneity

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Manuscript Table/Figure

Table 1: Participant Characteristics

Table 2: PLIER Latent Variables with relationship to outcomes of interest

Figure 1: Methodological flowchart showing complementary application of WGCNA and PLIER analysis pipelines

Figure 2: Top pathways associated with PLIER latent variables (LVs) for which an acceptably robust (adjusted P<0.05) pathway association was found (16 of 25 LVs).

Figure 3: Heterogeneity in change in thigh muscle area (cm²) as measured by CT following 14-wk resistance exercise training

Figure 4: Heatmap showing Pearson correlation R values (and associated P-values) for relationship between wholemuscle hypertrophy module eigengenes in WGCNA Prediction analysis

Figure 5: Prediction analysis red module

Figure 6: Prediction analysis magenta module

Figure 7: Representative heatmap for PLIER prediction analysis

Figure 8: Response LVs that changed following RT independently of changes in muscle phenotype.

Figure 9: Normalized relative gene expression for two exercise responsive LVs.

Data in Text (Section/¶)

Program or Chunk Name

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Chunk 9: bring in histology
Chunk 12: sample RIN summary
Chunk 42: basal approach
Chunk 97: calculate the change index
Chunk 50: load pathways
Chunk 67: test module sensitivity for Prediction modules
Chunk 11: participant table 1
Chunk 57: look at basal network
Chunk 59: prediction heatmap
Chunk 57: look at basal network & Chunk 81: mod LV check
Chunk 73: prediction effect Im & Chunk 79: sensitivity checks for plier prediction
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Chunk 83: bring in CT LV files and compare to red magenta genes
Chunk 86: exercise effect for sensitivity check
Chunk 119: use idoverlaps & Chunk 122: connections to mods of interest for AT
Chunk 93: look at paired network
Chunk 102: plasticity heatmap
Chunk 113: sensitivity test for plier cbi lvs
Chunk 66: calculate R value for red magenta salmon & Chunk 68: intramodular scatterplot
Chunk 66: calculate R value for red
magenta salmon &

^{*}All analyses were run between 06/29/20 and 10/31/20. Revisions were performed between 01/18/2021 and 02/11/21.

Newly-Derived Variables

The following variables are generated by running the pipeline.

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Special Files: Generated Outside Main Program Program Name

Subject Characteristics (Table 1)	Microsoft Word
Computational Pipeline (Figure 1)	Microsoft PowerPoint
Fiber type-specific Gene Marker/Pathway Association Matrix	R
MetaMEx Gene / Pathway Association Matrix	R
Network Maps (Prediction: red, magenta)	Cytoscape
Table S15: directional changes in MetaMEx database	Microsoft Excel
Number of genes in PLIER-identified LVs	Manually assessed