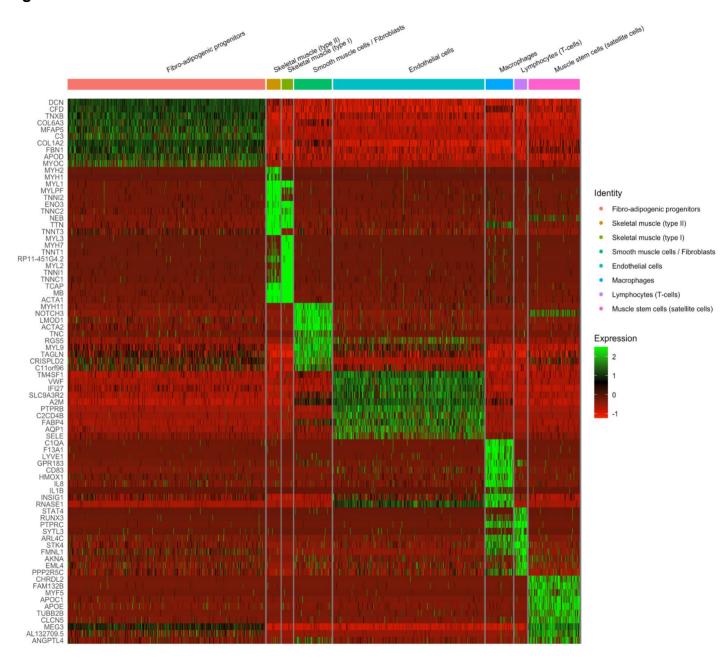
Supplementary

Fig. S1:



GO: Cellular Component mitochondrial inner membrane	FDR=3.7e-10
mitochondrial respiratory chain complex I-	FDR=7.6e-8
mitochondrian respiratory ename complex r	FDR=7.0e-6
mitochondrial respiratory chain complex IV	FDR=7.5e-3
	FDR=4.6e-2
proteasome core complex - extracellular matrix -	FDR=4.6e-2
cortical actin cytoskeleton -	FDR=4.7e-2
mitochondrial respiratory chain complex III-	FDR=5.1e-2
protein-DNA complex-	FDR=5.1e-2
chylomicron -	FDR=5.9e-2
	Enrichment significance: –log ₁₀ (FDR)
GO: Biological process mitochondrial electron transport, NADH to ubiquinone	FDR=2.8e-7
mitochondrial respiratory chain complex I assembly	FDR=5.0e-6
negative regulation of ERK1 and ERK2 cascade	FDR=1.6e-3
positive regulation of transcription from RNA polymerase II promoter	FDR=1.6e-3
negative regulation of G2/M transition of mitotic cell cycle	FDR=2.0e-3
hydrogen ion transmembrane transport-	FDR=2.0e-3
regulation of transcription from RNA polymerase II promoter in response to hypoxia	FDR=2.0e-3
proteasome-mediated ubiquitin-dependent protein catabolic process	FDR=2.0e-3
mitochondrial electron transport, cytochrome c to oxygen	FDR=2.8e-3
transcription from RNA polymerase II promoter	FDR=3.4e-3
	Enrichment significance: -log ₁₀ (FDR)
GO: Molecular Function	
NADH dehydrogenase (ubiquinone) activity	FDR=1.7e-7
cytochrome-c oxidase activity-	FDR=1.9e-4
transcriptional activator activity, RNA polymerase II core promoter proximal region	FDR=3.6e-3
ubiquitin protein ligase activity -	FDR=2.6e-2
threonine-type endopeptidase activity-	FDR=3.6e-2
mRNA 3'-UTR AU-rich region binding -	FDR=3.9e-2
cyclin-dependent protein serine/threonine kinase inhibitor activity -	FDR=4.4e-2
RNA polymerase binding -	FDR=5.7e-2
AU-rich element binding -	FDR=5.7e-2
cullin family protein binding -	FDR=5.7e-2

Enrichment significance: -log₁₀(FDR)

GO: Cellular Component extracellular matrix - 15 FDR=4.0e-14 focal adhesion FDR=3.2e-9 endoplasmic reticulum lumen proteinaceous extracellular matrix FDR=6.2e-9 10 extracellular space FDR=5.8e-8 FDR=1.0e-6 midbody FDR=7.2e-6 spindle microtubule •5 stress fiber FDR=2.3e-5 kinetochore FDR=3.0e-5 membrane FDR=3.0e-5 - 0 Enrichment significance: $-\log_{10}(FDR)$

GO: Biological process extracellular matrix organization

cell adhesion angiogenesis cell migration cell division collagen fibril organization mitotic cell cycle collagen catabolic process DNA replication mitotic sister chromatid segregation
 FDR=5.9e-10
 FDR=5.9e-10

 FDR=4.6e-10
 15

 FDR=1.4e-9
 10

 FDR=1.6e-9
 10

 FDR=5.9e-9
 5

 FDR=1.7e-7
 5

 FDR=1.4e-6
 0

 FDR=3.4e-6
 0

 Enrichment significance: -log₁₀(FDR)
 0

GO: Molecular Function

collagen binding collagen binding integrin binding extracellular matrix binding laminin binding chromatin binding heparin binding actin binding protein kinase binding -

FDR=2.8e-9	
FDR=8.8e-7	-7.5
FDR=2.4e-5	
FDR=7.5e-5	
FDR=8.7e-5	-5.0
FDR=1.4e-4	
FDR=2.2e-4	-2.5
FDR=2.5e-4	2.0
FDR=4.7e-4	
FDR=4.8e-4	-0.0
Enrichment significance: - log. (EDR)	

Enrichment significance: - log₁₀(FDR)

Supplementary figure legends:

Fig. S1: Heatmap of top 10 differentially expressed markers of each cluster from single cell transcriptomic data. Expression is ranged from -1 to 2. (n=1).

Fig. S2: Effect of pre-culturing on Muscle Stem Cell (MuSC) transcriptome. Gene Ontology analysis (GO) of Cellular Components, Biological Processes, and Molecular Function of direct isolated cells (red) and cells pre-cultured for 7 days before isolation (blue).

Methods for Supplementary figures are a part of the main manuscript.