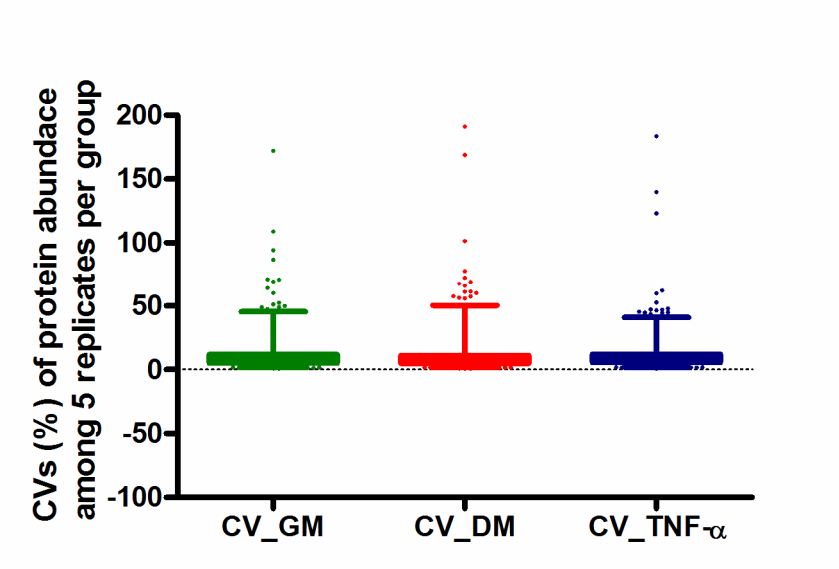
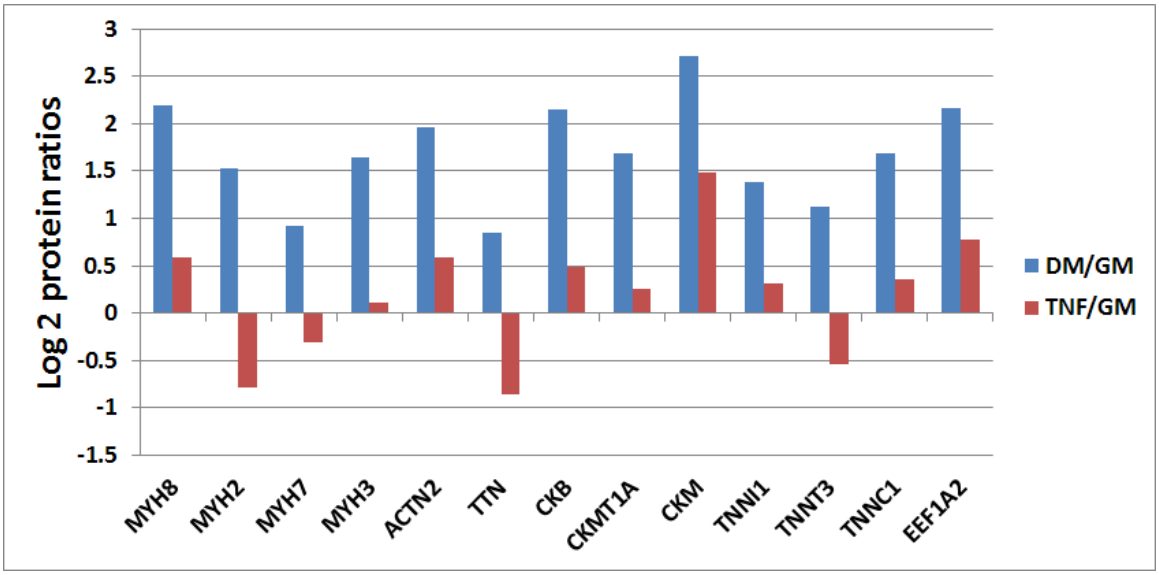
Supplemental Figure 1.



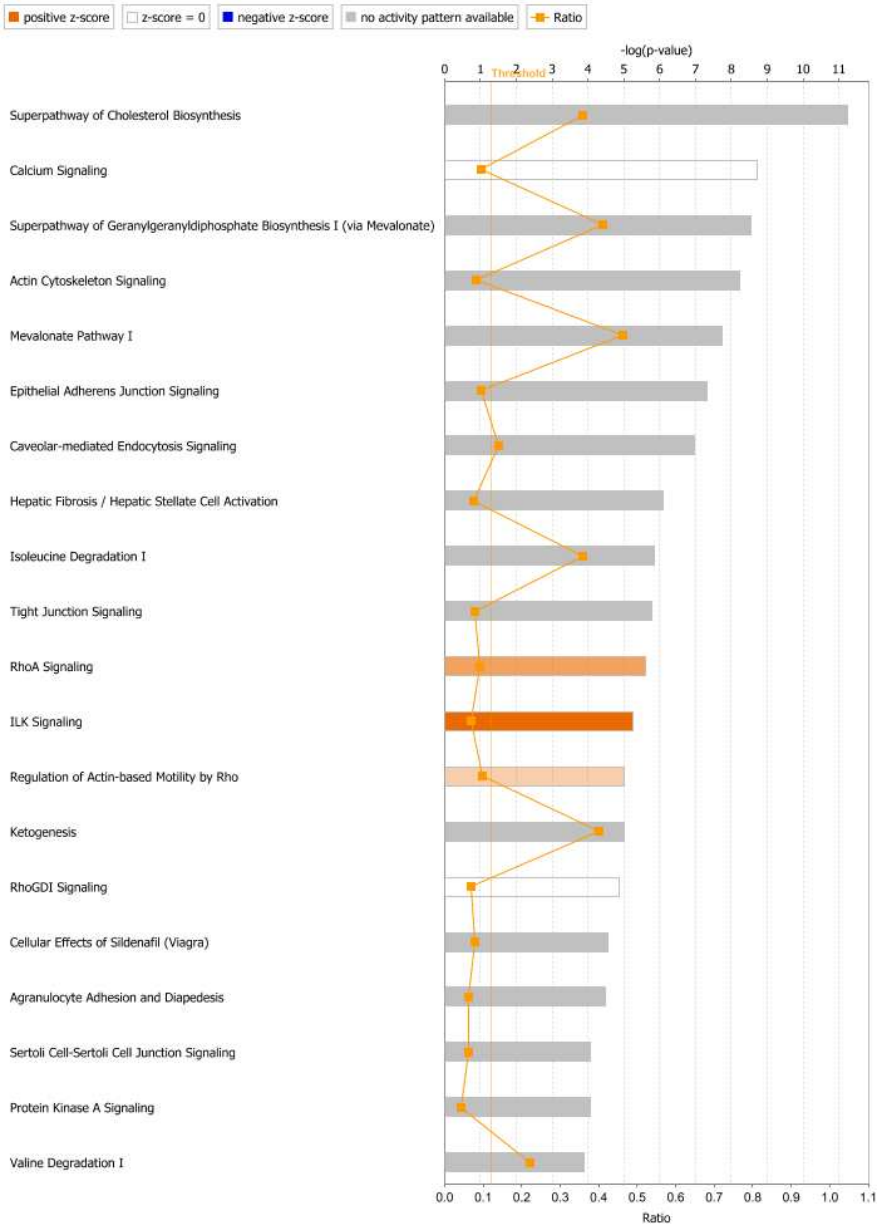
Supplemental Figure 1. The evaluation of reproducibility of protein abundance values among 5 replicates in each group. Box-and-whisker plot analysis was employed to show the spread of protein CVs around the median value (the horizontal line inside the box); bottom and top of the boxes correspond to the top 25th and 75th percentile of the CV distribution and whiskers to the top 1st and 99th percentile of the CV distribution.

Supplemental Figure 2



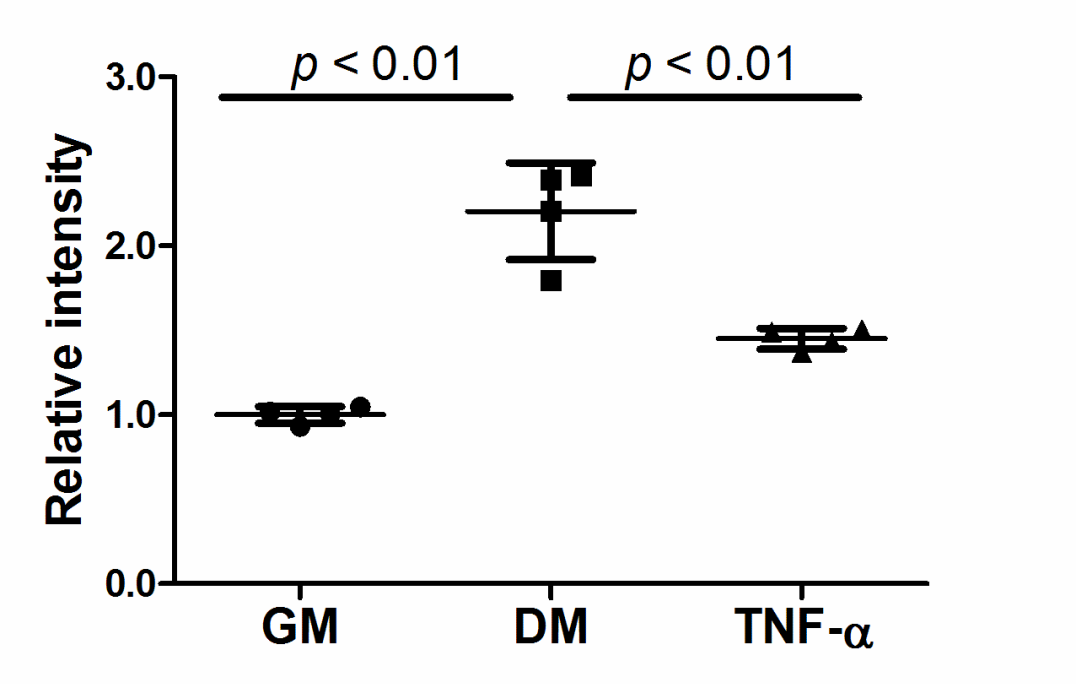
Supplemental Figure 2. The relative expression of known markers of myogenic differentiation dysregulated by TNF-α treatment. Myosin heavy chains (MYH2/3/7/8), alpha-actinin-2 (ACTN2), titin(TTN), creatine kinase (CKM, CKB, CKMT1A), elongation factor 1-alpha 2 (EEF1A2) and troponins (TNNI1, TNNT3, TNNC1) were presented. The expression of these proteins elevated during myogenic differentiation, but not change or change in the opposite direction of cultures with TNF-α treatment.

Supplemental Figure 3



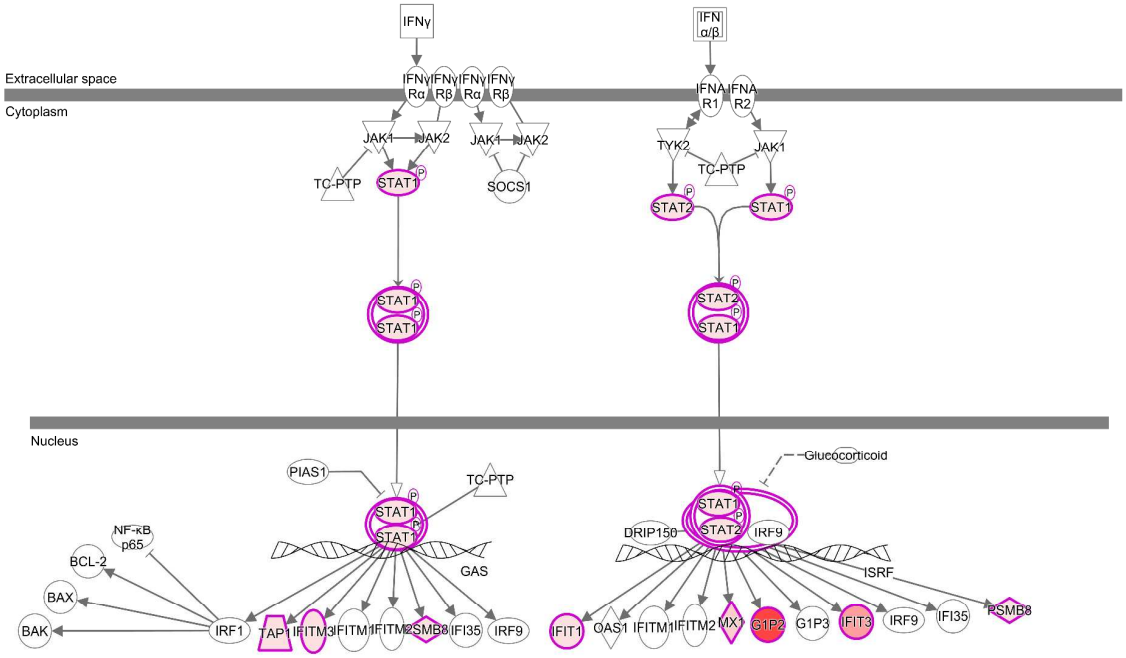
Supplemental Figure 3, Top-20 pathways for the differentiated proteins during myogenic differentiation.

Supplemental Figure 4



Supplemental Figure 4. Densitometry calculations for Western-blot data of cleaved caspase-3. ImagJ (v1.44p) was used to calculate the intensities of bands. Data of cleaved caspase-3 for each band were normalized against the intensities of GAPDH from respective band. We also set the mean intensities of cleaved caspase-3 from GM group as 1 and serve as control group. The mean and standard deviation for each group were presented. Student's t-test was also performed for adjacent groups.

Supplemental Figure 5.



Supplemental Figure 5. Activated interferon signaling pathway in muscle precursor cells undergoing serum starvation and TNF-α treatment.