

## Supplementary File 2:

### Differential Cysteine Labelling and Global Label-Free Quantification Reveals an Altered Metabolic State in Skeletal Muscle Aging.

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## MS Data Analysis and Search Parameters

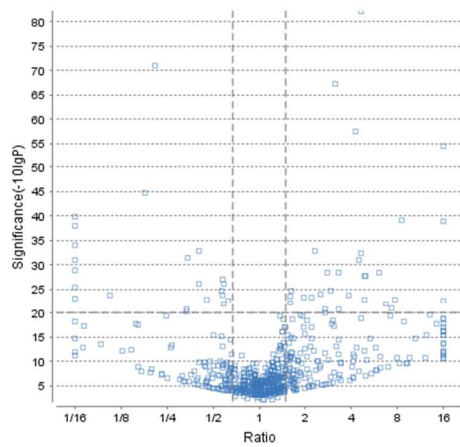


Figure 1. Volcano plot for proteins.

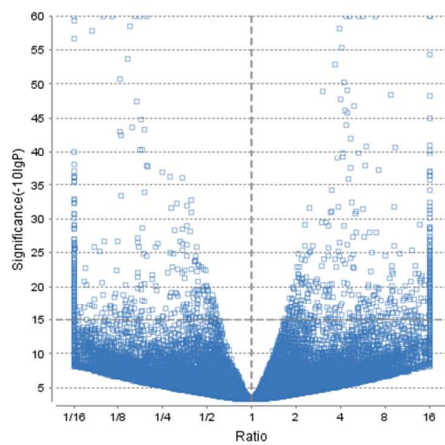


Figure 2. Volcano plot for peptides

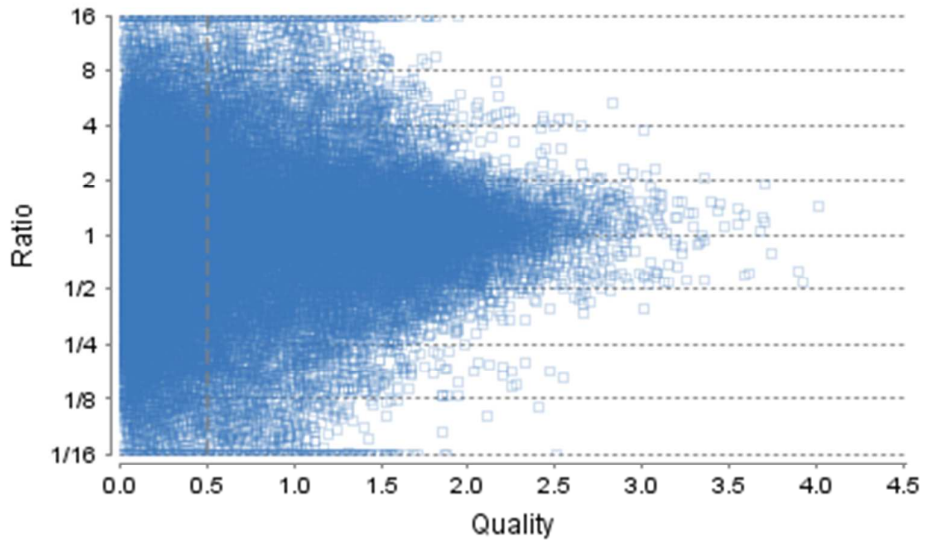


Figure 3. The distribution of feature vector ratio by quality.

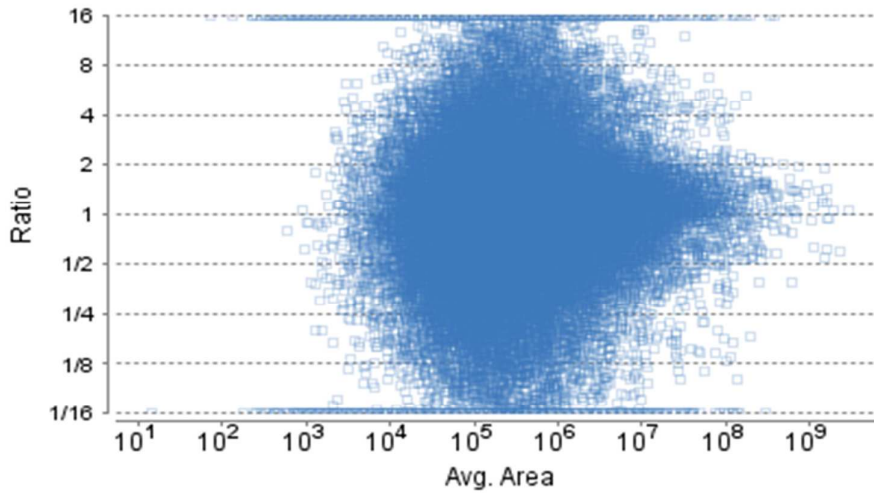


Figure 4. The distribution of feature vector ratio by intensity.

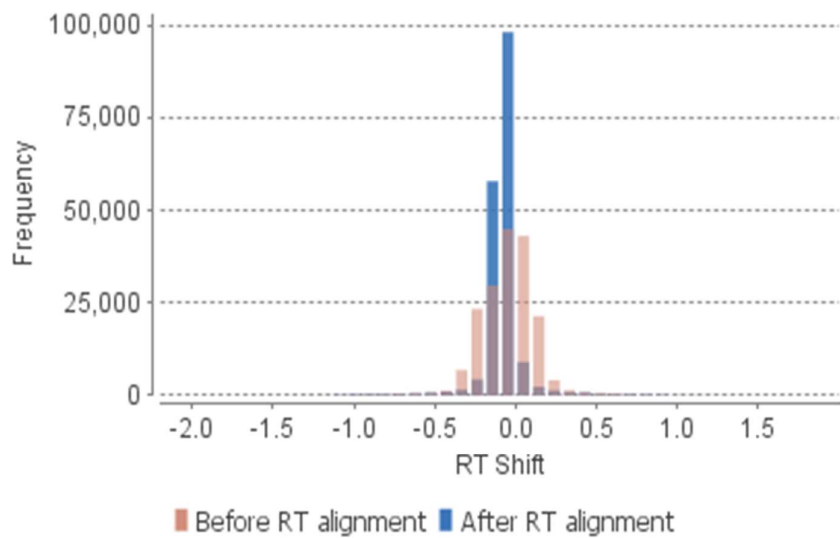


Figure 5. Retention time shift distribution

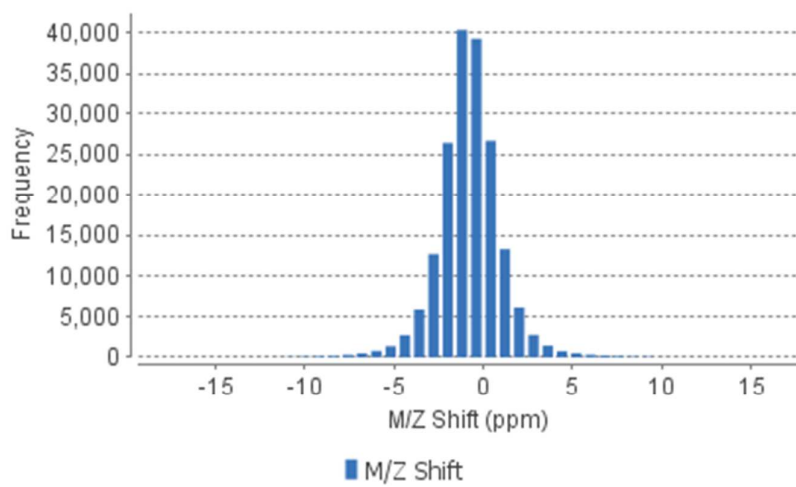


Figure 6. M/Z Shift Distribution

**Table 1.** Result filtration parameters.

Retention time	$\geq 0$
Retention time	$\leq 110$
Feature fold change	$\geq 1$
Quality	$\geq 0.5$
Avg. Area	$\geq 0E0$
Charge	$\geq 2$
Charge	$\leq 5$
Confident sample number	$\geq 1$
With peptide ID	true
Normalization	Use TIC
Protein significance	$\geq 20$
Protein fold change	$\geq 1.5$
Confident unique supports	$\geq 1$

**Table 2.** Statistics of filtered result.

Features	2194
Features with ID	1735
Feature vectors	293
Feature vectors with ID	293
Protein groups	50

**Table 3.** Search Parameters

Quantification type: Label free quantification  
Mass Error Tolerance: 10.0 ppm  
Retention Time Shift Tolerance: 1.0 min  
Dependent on PID: 24,25  
FDR Threshold: 1%  
Samples: 9 samples in 2 groups  
: Adult\_1 Adult\_2 Adult\_3 Adult\_4  
: Adult\_5 Aged\_1 Aged\_2 Aged\_3  
: Aged\_4  
Reference Sample: Aged\_2 (auto detected)  
Training Samples: Adult\_3, Adult\_5 (auto detected)