Supplemental Tables

Supplemental Table S1. **Overall protein identifications after QuantFusion analysis**

Table displaying protein accession number, posterior error probability (PEP), number of unique peptides and list of peptide sequences identified for each protein

Supplemental Table S2. **Protein identifications reported with single peptides**

Table displaying identified peptide sequence, modified sequence, m/z, charge, Andromeda score and posterior error probability (PEP)

Supplemental Table S3. **Comparisons of LFQ, RoR and QuantFusion quantitative methods**

Table displaying identification number: (ID), UniProt protein accession, RoR, RoR-SE, RoR-Q, RoR-posterior, LFQ, LFQ-SE, LFQ-Q, LFQ-posterior, QuantFusion, QuantFusion-SE, QuantFusion-Q, QuantFusion-posterior and posterior error probability for protein identification. Note: LFQ: Label-free Quantitation ratio of log2(WHIM2/WHIM16), RoR: Ratio of Ratios of log2(WHIM2/WHIM16), SE: Standard error, Q: q-value, posterior: posterior probability

Supplemental Table S4. **Missing quantitative values in LFQ and RoR analysis**

Table displaying quantitative methods shown in Supplement Table 3 with the inclusion of missing quantitative values observed in either LFQ or RoR

Supplemental Table S5. **List of proteins rescued by QuantFusion for LFQ**

This table lists proteins not significantly differentially expressed (or not quantifiable or not identified) in LFQ but were in QuantFusion.

Table displaying Protein: UniProt protein accession, QF: QuantFusion fold change log2(WHIM2/WHIM16), QF_Q: q-value for QuantFusion, LFQ: LFQ fold change log2(WHIM2/WHIM16), LFQ_Q: q-value for LFQ, RoR: RoR fold change log2(WHIM2/WHIM16), RoR_Q: q-value for RoR. Columns QF_DIFF_EXPRESS, LFQ_DIFF_EXPRESS, ROR_DIFF_EXPRESS indicate whether or not the protein is significantly differentially expressed in QuantFusion, LFQ, RoR respectively: ‘+’ indicates that the protein is significantly differentially expressed, ‘-‘ indicates that the protein is not significantly differentially expressed, blank indicates that the protein was not quantifiable or not identified.

Supplemental Table S6. **List of proteins rescued by QuantFusion for RoR**

This table lists proteins not significantly differentially expressed (or not quantifiable or not identified) in RoR but were in QuantFusion.

Table displaying Protein: UniProt protein accession, QF: QuantFusion fold change log2(WHIM2/WHIM16), QF_Q: q-value for QuantFusion, LFQ: LFQ fold change log2(WHIM2/WHIM16), LFQ_Q: q-value for LFQ, RoR: RoR fold change log2(WHIM2/WHIM16), RoR_Q: q-value for RoR. Columns QF_DIFF_EXPRESS, LFQ_DIFF_EXPRESS, ROR_DIFF_EXPRESS indicate whether or not the protein is significantly differentially expressed in QuantFusion, LFQ, RoR respectively: ‘+’ indicates that the protein is significantly differentially expressed, ‘-‘ indicates that the protein is not significantly differentially expressed, blank indicates that the protein was not quantifiable or not identified.

Supplemental Table S7. **List of proteins rescued by QuantFusion for both LFQ and RoR**

This table lists proteins not significantly differentially expressed (or not quantifiable or not identified) in both LFQ and RoR but were in QuantFusion.

Table displaying Protein: UniProt protein accession, QF: QuantFusion fold change log2(WHIM2/WHIM16), QF_Q: q-value for QuantFusion, LFQ: LFQ fold change log2(WHIM2/WHIM16), LFQ_Q: q-value for LFQ, RoR: RoR fold change log2(WHIM2/WHIM16), RoR_Q: q-value for RoR. Columns QF_DIFF_EXPRESS, LFQ_DIFF_EXPRESS, ROR_DIFF_EXPRESS indicate whether or not the protein is significantly differentially expressed in QuantFusion, LFQ, RoR respectively: ‘+’ indicates that the protein is significantly differentially expressed, ‘-‘ indicates that the protein is not significantly differentially expressed, blank indicates that the protein was not quantifiable or not identified.