**Protein .tsv**

***proteinName:***protein identifier

***proteinDescription:***protein description

***idScore:***protein identification score. Calculated as the summed PSM

identification score.

***idQValue:*** protein identification score q-value. Ratio of the number of decoy and target database identifications at given idScore threshold.

***nbPeptides:*** the number of confidently identified peptides for a give protein.

***allAccessions:*** accession numbers of proteins sharing a peptide with this protein.

***sample\_S:*** summed normalized intensity (AUC)

***medianInt\_condition\_C:*** median intensity of replicate measurements.

***cv\_condition\_C:*** Intensity coefficient of variance across replicate intensities.

***log2ratio\_condition\_C:*** median log2 intensity ratio (condition X / CTRL)

***pValue\_condition\_C:*** moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

***qValue\_condition\_C:*** Multiple-testing correction using Benjamini-Hochberg FDR procedure.

***log2\_pairedRatio\_sample\_S***: Ratios of all paired samples. Only exported when Correlated Samples (--EC option) experimental design is specified.

**Peptide .tsv**

***peptide:*** peptide sequnece

***proteinName:***protein identifier

***proteinDescription:***protein description

***idScore:***peptide identification score. Calculated as the summed PSM

identification score.

***idQValue:*** peptide identification score q-value. Ratio of the number of decoy and target database identifications at given idScore threshold.

***retentionTime:*** retention time (min)

***ptm:*** post-translational modification

***nbPtmsPerPeptide:*** number of PTMs per peptide

***motifX:*** amino acid sequence surrounding PTM site***.***

***modifCoord:*** distance (number of residues) from n-term of PTM site.

***allAccessions:*** accession numbers of proteins sharing a peptide with this protein.

***sample\_S:*** summed normalized intensity (AUC)

***medianInt\_condition\_C:*** median intensity of replicate measurements.

***cv\_condition\_C:*** Intensity coefficient of variance across replicate intensities.

***log2ratio\_condition\_C:*** median log2 intensity ratio (condition X / CTRL)

***pValue\_condition\_C:*** moderated t-statistic p-value comparing (condition X vs CTRL). Calculated using empirical Bayes method (Smyth, 2004).

***qValue\_condition\_C:*** Multiple-testing correction using Benjamini-Hochberg FDR procedure.

***log2\_pairedRatio\_sample\_S***: Ratios of all paired samples. Only exported when Correlated Samples (--EC option) experimental design is specified.