Electronic Supplementary Material_6; Data file S2

Sequential lipidomic, metabolomic and proteomic analyses of serum, liver and heart tissue specimens from peroxisomal biogenesis factor 11α knockout mice

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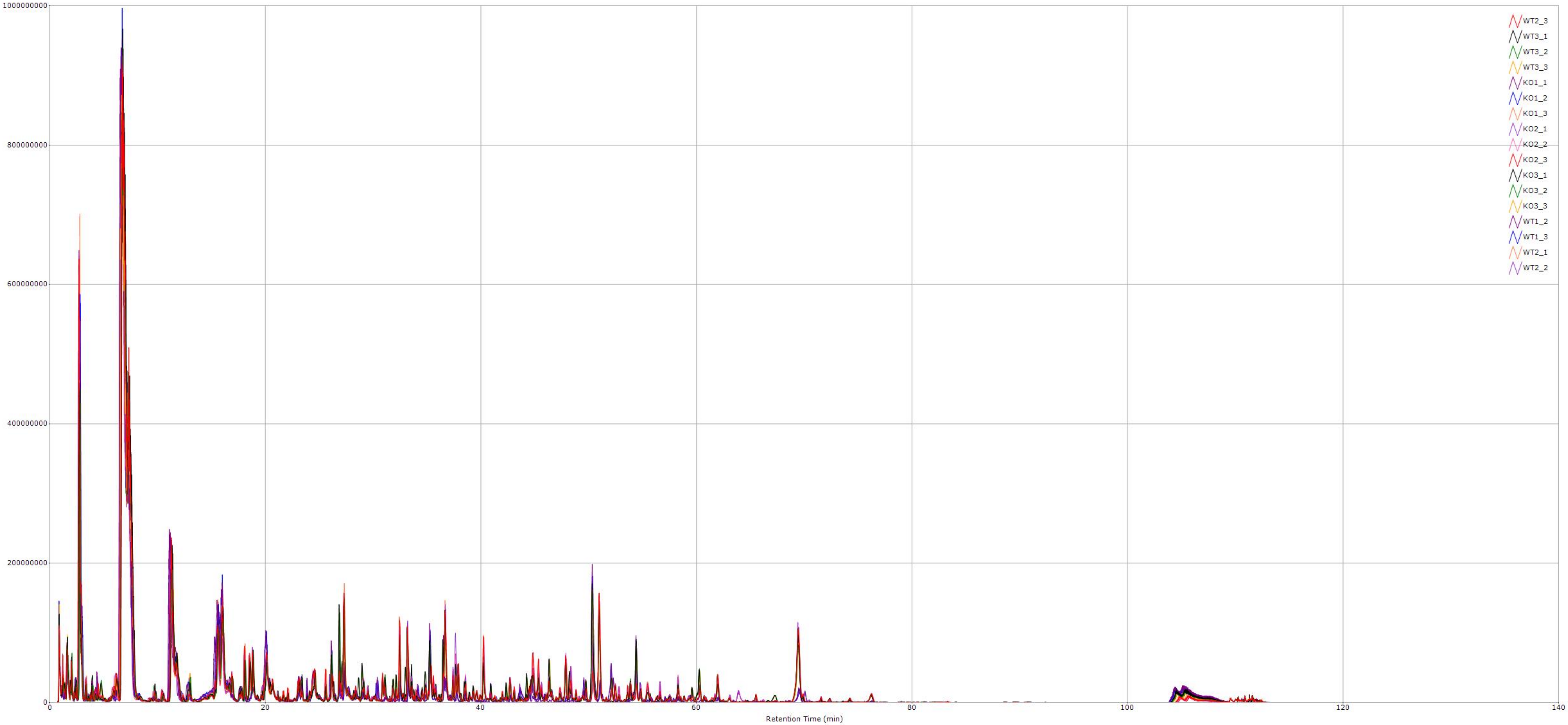
Proteomics raw data quality evaluation using RawMeat (v2.1) software

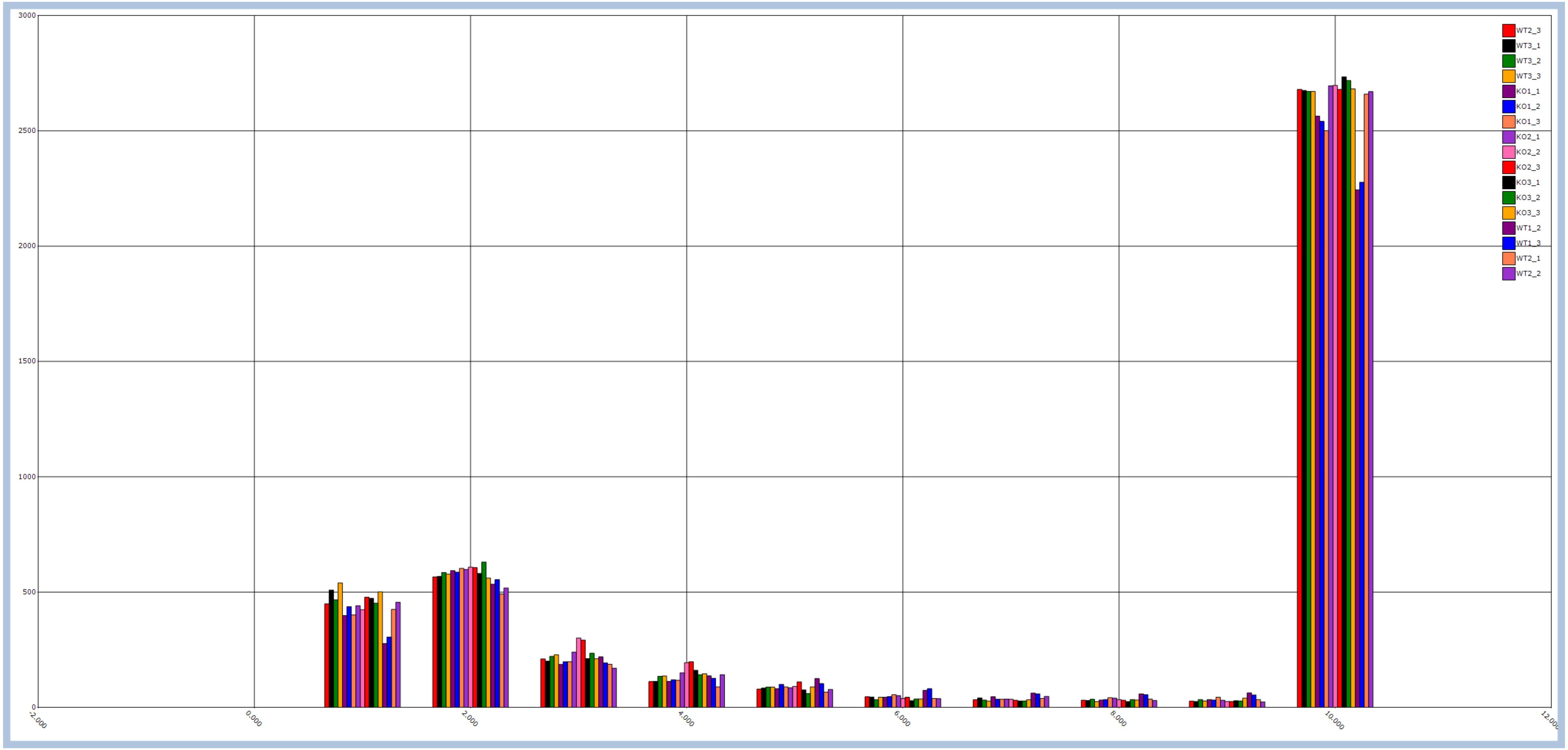
Wild type control and peroxisomal biogenesis factor 11α knockout mouse liver proteome

Base peak intensity from full MS scans as a function of retention time



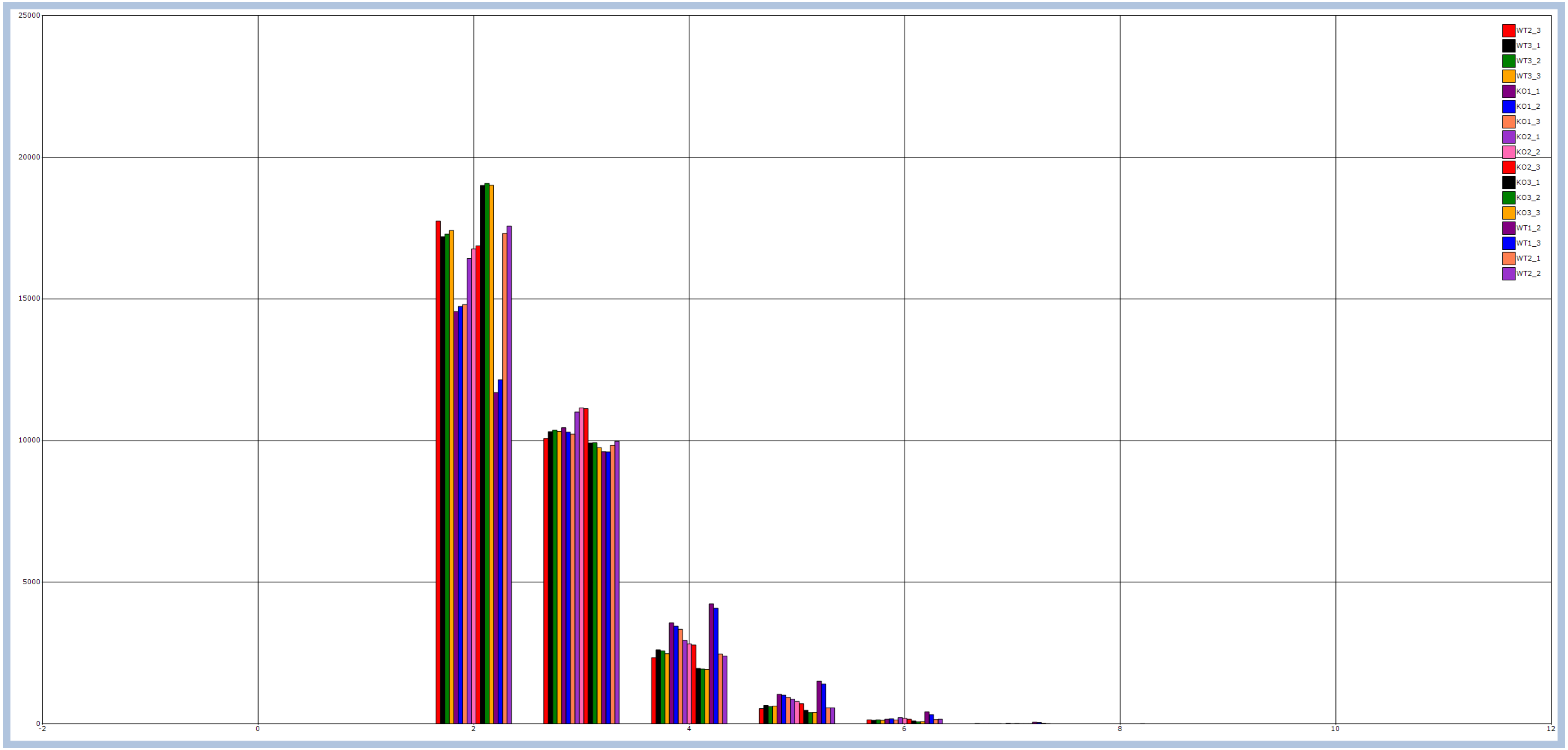
Horizontal axis (X-axis): Retention time in minutes; Vertical axis (Y-axis): Base peak intensity per full MS scans

Number of MS2 scans in between consecutive scans



Horizontal axis (X-axis): Number of MS2 scans in between consecutive scans; Vertical axis (Y-axis): Frequency

MS2 charge distribution

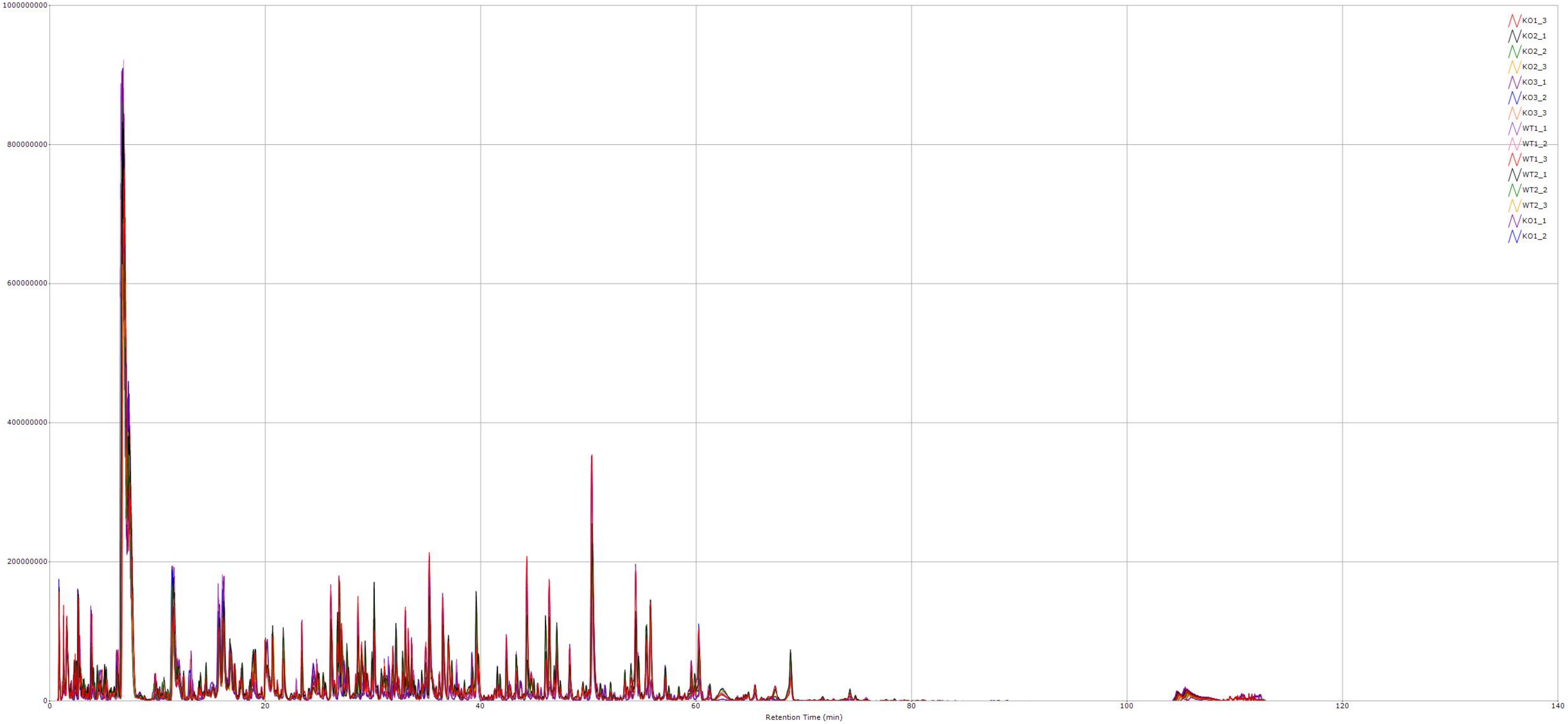


Horizontal axis (X-axis): Precursor ion charge; Vertical axis (Y-axis): Counts per charge

Proteomics raw data quality evaluation using RawMeat (v2.1) software

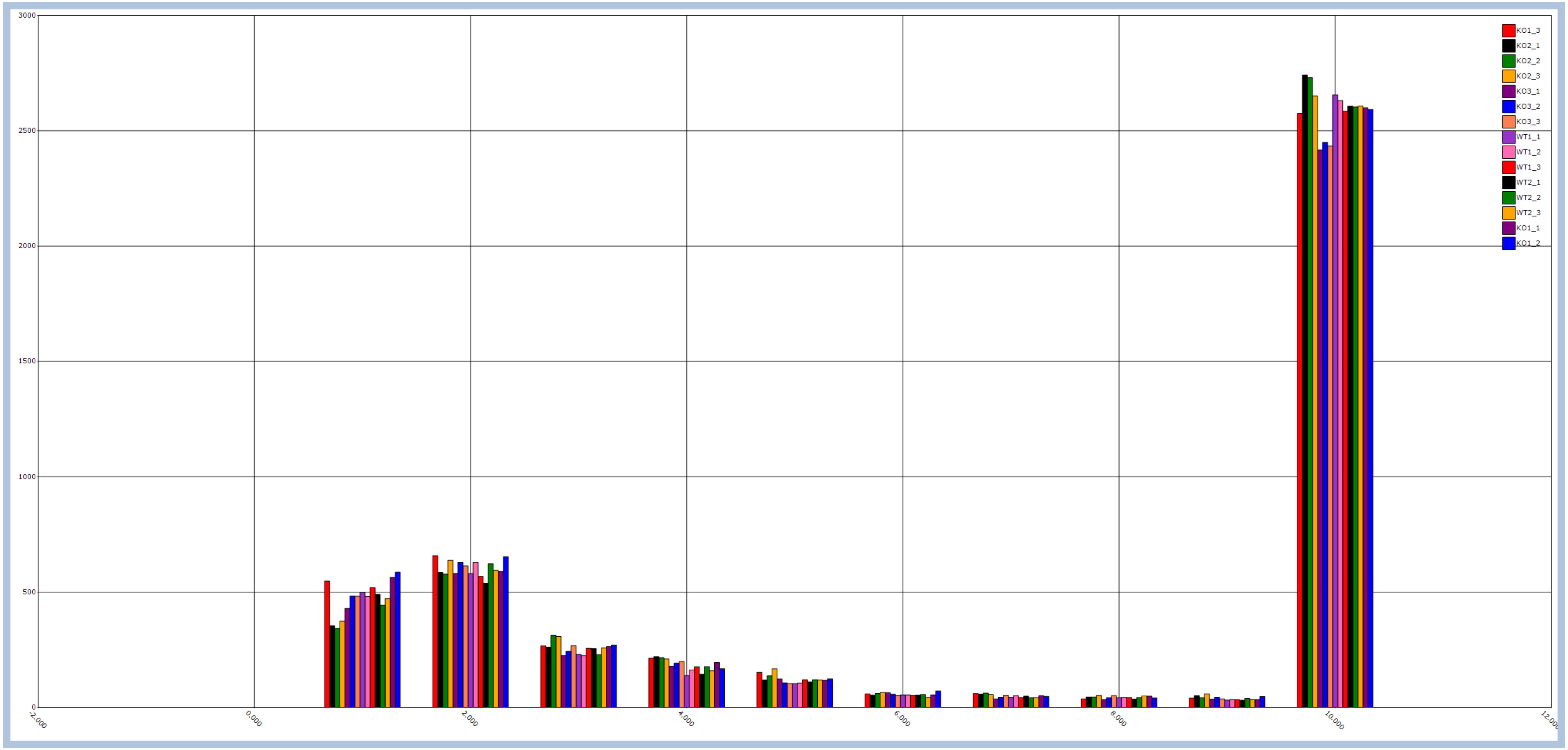
Wild type control and peroxisomal biogenesis factor 11α knockout mouse heart proteome

Base peak intensity from full MS scans as a function of retention time



Horizontal axis (X-axis): Retention time in minutes; Vertical axis (Y-axis): Base peak intensity per full MS scans

Number of MS2 scans in between consecutive scans



Horizontal axis (X-axis): Number of MS2 scans in between consecutive scans; Vertical axis (Y-axis): Frequency

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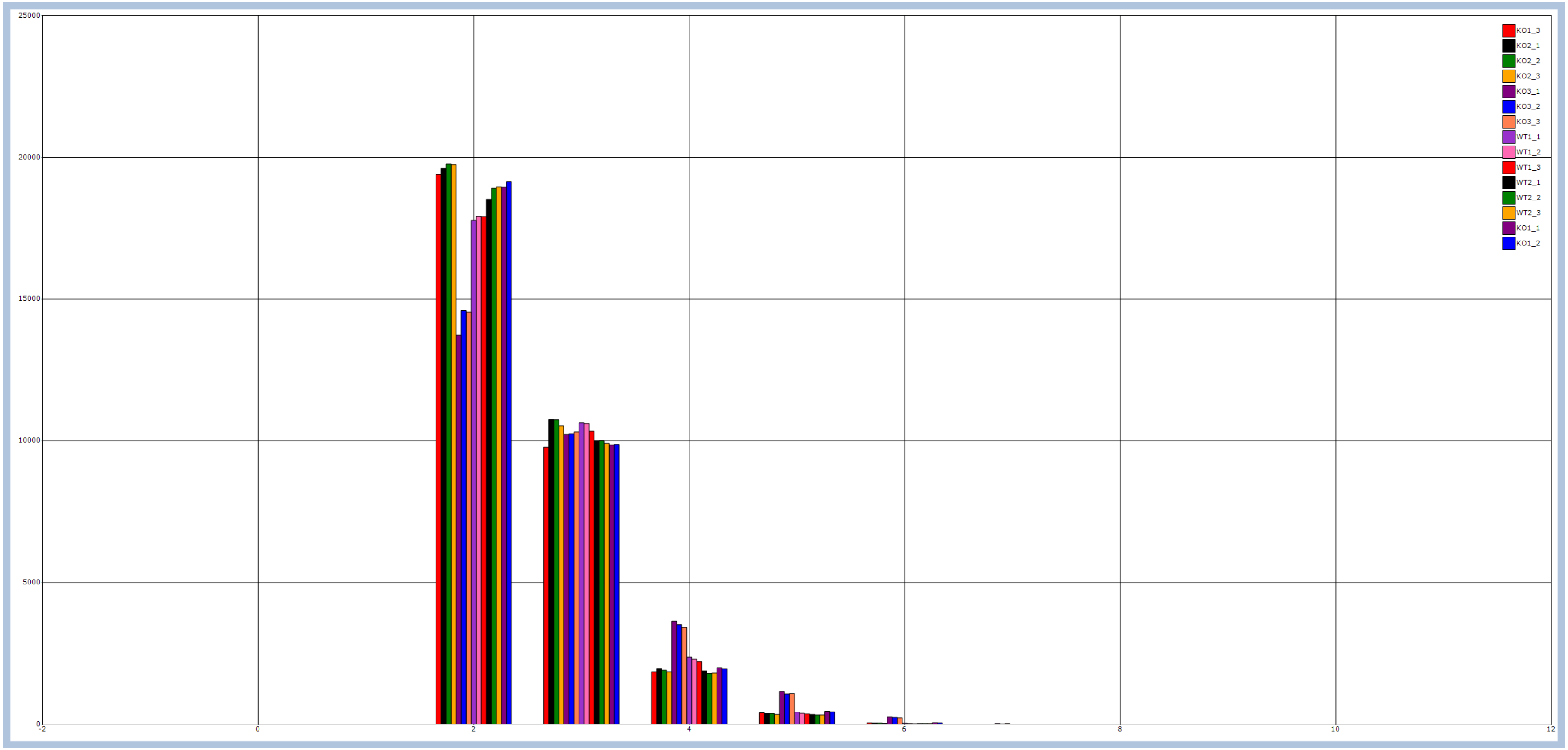
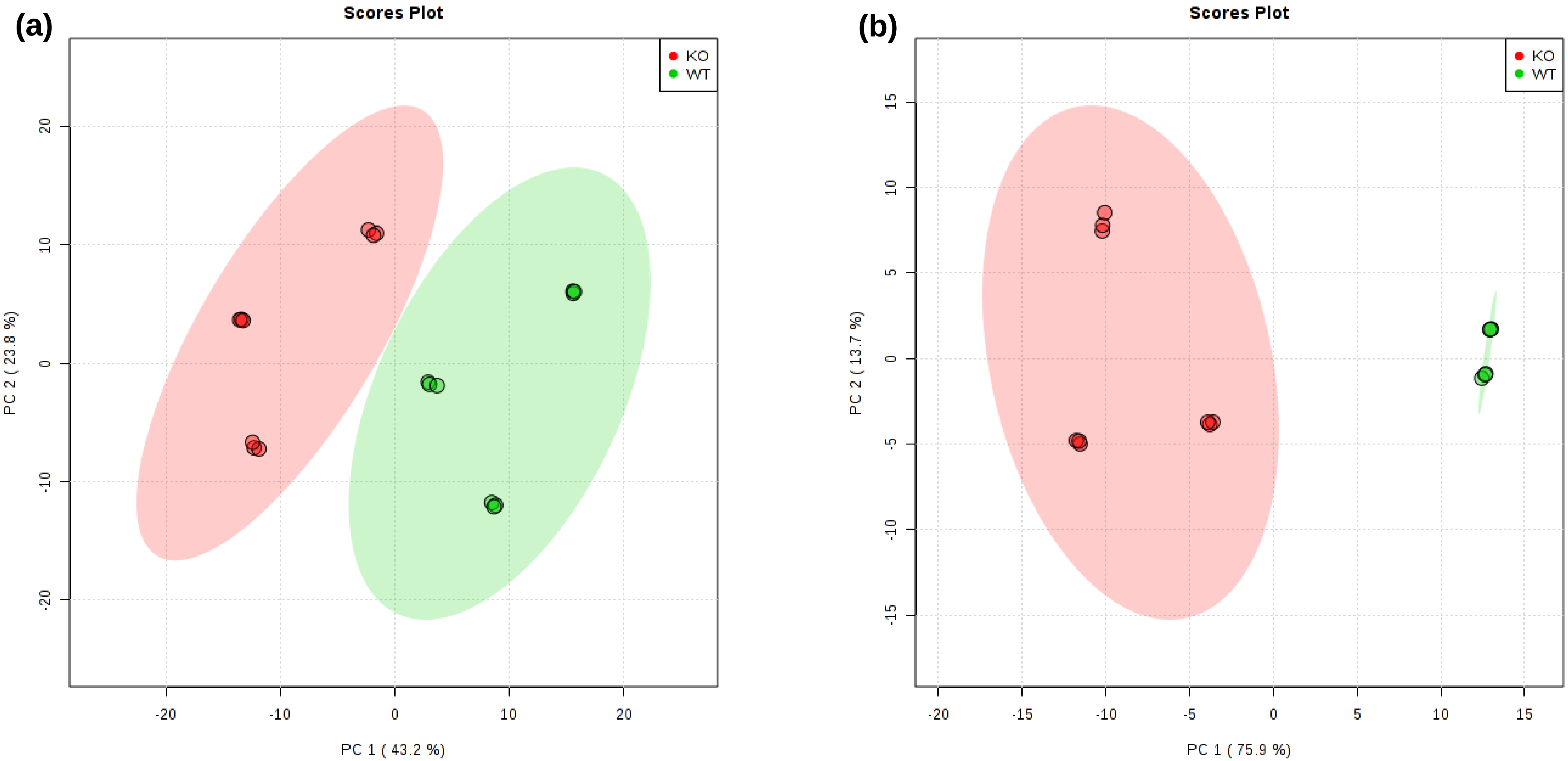


Horizontal axis (X-axis): Precursor ion charge; Vertical axis (Y-axis): Counts per charge

Principal component analysis



Principal component analysis of proteomics data obtained from wild type control (WT; $Pex11\alpha^{+/+}$) and peroxisomal biogenesis factor 11α knockout (KO; $Pex11\alpha^{-/-}$) mouse a) liver and b) heart tissue homogenates