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Supplementary Table 1: List of proteins identified and quantified in OXN/TEBT1-dioxin exposure and OXN/TEBT1-Paracetamol exposure using TMT-based quantitative proteomics approach

Table with 26 columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Unique_Peptide, AA, MS, cal. sd, Abundance Ratio (OXN/TEBT1-Paracetamol/BC), Abundance Ratio (OXN/TEBT1-dioxin/BC), Abundance Ratio (OXN/TEBT1-Paracetamol/dioxin), Sequence, PSMs, Proteins, Modification, Abundance Ratio (OXN/TEBT1-dioxin/TEBT1-Paracetamol/BC), Abundance Ratio (OXN/TEBT1-dioxin/TEBT1-Paracetamol/BC), Abundance Ratio (OXN/TEBT1-dioxin/TEBT1-Paracetamol/BC), Score, Missed_Cleavage, Theo. MS1, seq. ID#, DeNovo Peptide, Peptide (Da), RT (min)

Supplementary Table 1. List of protein identified and quantified in OXN/TER1-Shiba vaccine and OXN/TER1-Parasol vaccine using TMT-based quantitative proteomics approach.

Table with 25 columns: Accession, Gene Symbol, Description, Coverage, Peptides, PSMs, Enzyme, Pylar, AA, MW, pI, Abundance Ratio (OXN/TER1-Shiba / OXN/TER1-Parasol), Abundance Ratio (OXN/TER1-Shiba / OXN/TER1-Parasol), Abundance Ratio (OXN/TER1-Shiba / OXN/TER1-Parasol), Score, Missed, Charge, Theor. MS, exp. MS, Dec-M, Mass (Da), RT (min).

Supplementary Table 1: List of protein identified and quantified in OXN/TER11-shikonin and OXN/TER11-paracetamol using TMT-based quantitative proteomics approach

Table with 27 columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Uniq. Pept. IDs, AA, MS, cal. pt., Abundance Ratio (OXN/TER11-Paracetol) B1, Abundance Ratio (OXN/TER11-Shikonin) B2, Abundance Ratio (OXN/TER11-Shikonin) B3, Sequence, PSMs, Protein, Modification, Abundance Ratio (OXN/TER11-Paracetol) B4, Abundance Ratio (OXN/TER11-Shikonin) B5, Abundance Ratio (OXN/TER11-Shikonin) B6, Score, Mascot, Chovav, Theo. MS, MS/MS, DeNovo, DeNovo (Da), RT (min)

Supplementary Table 3: List of proteins identified and quantified in OXN/TERT1-Shikimic acid and OXN/TERT1-Paracetamol variants using TMT-based quantitative proteomics approach

Table with columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Unique_Pept Size, AA, MS, MS/MS, calc. id, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Sequence, PSMs, Protein, Modification, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Abundance Ratio: OXN/TERT1-Shikimic acid / OXN/TERT1-Paracetamol, Score, Method, Charge, Mass, MW, pI, DeNovo, Labeled, RT (min)

Supplementary Table 1. List of proteins identified and quantified in OMS/TER11-Shiba coculture and OMS/TER11-Paracetamol coculture using TMT-based quantitative proteomic approach

Table with columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Unique_Peptid, AA, MS, col. id, Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Sequence, PSMs, Proteins, Modification, Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Abundance Ratio (OxMS/TER11-Shiba / OMS/TER11-Paracetamol), Score, Mascot, Charge, Thres. MS/MS, MS/MS, Delim.Delimit, Delimit.Delimit, RT (min)

Supplementary Table 1: List of proteins identified and quantified in OXN/TERT1-Sludge coculture and OXN/TERT1-Paracetamol coculture using TMT-based quantitative proteomics approach

Table with columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Unique_Pept., AA, MS, MS/MS, Abundance Ratio (OXN/TERT1-Sludge/Paracetamol), Abundance Ratio (OXN/TERT1-Sludge/COB/TCDF), Abundance Ratio (OXN/TERT1-Sludge/COB/TCDF/Paracetamol), Sequence, PSMs, Protein, Modification, Abundance Ratio (OXN/TERT1-Sludge/Paracetamol), Abundance Ratio (OXN/TERT1-Sludge/COB/TCDF), Abundance Ratio (OXN/TERT1-Sludge/COB/TCDF/Paracetamol), Score, Missed_Cleavage, Theor. MW, MW (Da), pI, Mol. Wt. (Da), pI (kDa)

Supplementary Table 1. List of proteins identified and quantified in OXN/TERT1-Shikais neurons and OXN/TERT1-Paraxons using TMT-based quantitative proteomic approach

Table with columns: Accession, Gene_Symbol, Description, Coverage, Peptides, PSMs, Uniq. Pept, AA, MS, MS/MS, Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons), Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons) K1, Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons) K2, Sequence, PSMs, Protein, Modification, Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons) K1, Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons) K2, Abundance Ratio (OXN/TERT1-Shikais / OXN/TERT1-Paraxons) K3, Score, Method, Charge, Thr. MB, p1, p2, p3, p4, p5, p6, p7, p8, p9, p10.

