Comparison of peptide score distributions 2012_PGNEXUS_proteome_con_sp.canonical.isoforms_junc.exons 2012_PGNEXUS_proteome_con.sp.canonical.isoforms 2012_PGNEXUS_proteome_junc.exons 200 250 3300 350 5500 5500 100 20 100 150 20 20 2012_PGNEXUS_proteome_sp.canonical.isoforms_junc.exons 2020_phosphoproteome_OBseries_con_sp.hsa.canonical.isoforms 2020_phosphoproteome_OBseries_junc.exons Frequency (normalised) Peptide Hit Type Swissprot hits Exons from 3FT Junctions from 3FT Contaminant Reversed sequence 100 20 2020_phosphoproteome_OBseries_sp.hsa.canonical.isoforms_junc.exons 90 100

Score_{MaxQuant} + 1