Comparison of peptide p – value (PEP) distributions (PEP \leq 0.05 only) 2012_PGNEXUS_proteome_con_sp.canonical.isoforms_junc.exons 2012_PGNEXUS_proteome_junc.exons 2012_PGNEXUS_proteome_con.sp.canonical.isoforms 4e+07 1e+06 3e+07 4e+05 2e+07 5e+05 2e+05 1e+07 0e+00 0e+00 0.015 0,0,0 0.015 0.040 0,010 0.020 0.040 0.0A5 0.020 0.025 0.030 0.035 0,000 0.005 0.025 0.030 0.035 0,040 0,000 0.00% 0,010 0.015 0.020 0.025 0.030 0.035 2020_phosphoproteome_OBseries_con_sp.hsa.canonical.isoforms 2020_phosphoproteome_OBseries_junc.exons 2012_PGNEXUS_proteome_sp.canonical.isoforms_junc.exons 2.0e+07 6e+08 Peptide Hit Type 9e+05 Swissprot hits 1.5e+07 Exons from 3FT 4e+08 6e+05 Junctions from 3FT 1.0e+07 Contaminant 2e+08 3e+05 Reversed sequence 5.0e+06 0.0e+00 0e+00 0.01/2 0,0,0 0.020 0,010 0.015 0.020 0.035 0,040 0,010 0.015 0.020 0.040 0.025 0.030 0.035 0,040 0.005 0.025 0.030 0.025 0.030 0.035 2020_phosphoproteome_OBseries_sp.hsa.canonical.isoforms_junc.exons 7.5e+07

Frequency (smoothed)

5.0e+07

2.5e+07

0.0e+00

0,0,10

0.015

0,020

0.025

0.030

0.035

0,040