Comparison of peptide p − value (PEP) distributions (PEP ≤ 0.05 only)

Figure axes: x-axis labeled "PEP", y-axis labeled "Frequency density (smoothed)"

Panel titles:
- 2012_PGNEXUS_proteome_con_sp.canonical.isoforms_junc.exons
- 2012_PGNEXUS_proteome_con.sp.canonical.isoforms
- 2012_PGNEXUS_proteome_junc.exons
- 2012_PGNEXUS_proteome_sp.canonical.isoforms_junc.exons
- 2020_phosphoproteome_OBseries_con_sp.hsa.canonical.isoforms
- 2020_phosphoproteome_OBseries_junc.exons
- 2020_phosphoproteome_OBseries_sp.hsa.canonical.isoforms_junc.exons

Legend — Peptide Hit Type:
- Swissprot hits
- Exons from 3FT
- Junctions from 3FT
- Contaminant
- Reversed sequence