transcript pulldown RPKM comparisons facet over bin where bin=range of transcript expr sum in sample Transcripts: InpaOnly (1e-05,0.000364] (0.000364,0.00075] (0.00075,0.00136] (0.00136,0.00235] (0.00235, 0.0042]transcriptTypePulldown (0.0042, 0.0075]IncRNA.longNonPolyA count IncRNA.longPolyA mRNA.longNonPolyA mRNA.longPolyA (0.0075,0.0141] (0.0141,0.0298] 10 -(0.0298, 0.0847](0.0847, 258]N N -10 log(RPKM)