transcript pulldown RPKM comparisons facet over bin where bin=range of transcript expr sum in sample Transcripts: lpaOnly (1e-05,0.000364] (0.000364,0.00075] (0.00075,0.00136] 500 (0.00136,0.00235] (0.00235, 0.0042]transcriptTypePulldown (0.0042, 0.0075]IncRNA.longNonPolyA 100 IncRNA.longPolyA mRNA.longNonPolyA mRNA.longPolyA (0.0075,0.0141] (0.0141,0.0298] (0.0298, 0.0847]80 (0.0847, 258]5 N N 1 --10 log(RPKM)