transcript pulldown RPKM comparisons facet over bin where bin=range of transcript expr sum in sample Transcripts: both (2e-06,0.000517] (0.000517,0.00137] (0.00137,0.00278] (0.00278, 0.00506](0.00506, 0.0089]transcriptTypePulldown (0.0089, 0.0155]IncRNA.longNonPolyA count IncRNA.longPolyA mRNA.longNonPolyA mRNA.longPolyA (0.0155, 0.028](0.028, 0.0562]25000 -(0.0562, 0.15](0.15,258]20000 -0 --5 log(RPKM) -10 -15