IncRNA genes as max trans in sample Cell Type Expression:(top transcripts per gene) filled by category of transcript cell-type specificity of A549.longNonPolyA A549.longPolyA 0.6 0.2 0.4 0.1 0.2 0.0 0.0 AG04450.longNonPolyA AG04450.longPolyA 0.6 0.3 0.4 0.2 0.2 0.1 0.0 0.0 BJ.longNonPolyA BJ.longPolyA 0.3 0.4 0.3 0.2 0.2 0.1 0.1 0.0 0.0 GM12878.longNonPolyA GM12878.longPolyA 0.2 0.2 0.1 0.1 0.0 0.0 H1.HESC.longNonPolyA H1.HESC.longPolyA 0.2 0.2 0.1 0.1 0.0 0.0 HELA.S3.longNonPolyA HELA.S3.longPolyA 0.3 0.2 0.2 0.1 0.1 0.0 0.0 HEPG2.longNonPolyA HEPG2.longPolyA 0.3 0.20 0.2 0.15 0.10 0.1 0.05 0.0 0.00 HMEC.longNonPolyAHMEC.longPolyA 0.3 0.2 0.2 0.1 0.1 ctsCat 0.0 0.0 cell-type-other HSMM.longPolyA HSMM.longNonPolyAcell-type-this 0.2 0.2 -0.1 0.1 0.0 0.0 HUVEC.longNonPolyA HUVEC.longPolyA 0.25 0.20 0.20 0.15 0.15 0.10 0.10 0.05 0.05 0.00 0.00 K562.longNonPolyAK562.longPolyA 0.3 0.2 0.2 0.1 0.1 0.0 0.0 MCF.7.longNonPolyA MCF.7. Iong Poly A0.2 0.2 0.1 0.1 0.0 0.0 NHEK.longNonPolyA NHEK.longNonPolyA.1 0.5 0.20 0.4 0.15 0.3 0.10 0.2 0.05 0.1 0.0 0.00 NHEK.longPolyA NHEK.longPolyA.1 0.3 0.2 0.2 0.1 0.1 0.0 0.0 NHLF. long Non Poly ANHLF.longPolyA0.3 0.3 0.2 0.2 0.1 0.1 0.0 0.0 SK.N.SH_RA.longNonPolyA SK.N.SH_RA.longPolyA 0.3 0.2 0.2 0.1 0.1 0.0 -5 -10 -10 -5 log(value)