IncRNA genes as max trans in sample Cell Type Expression:(top transcripts per gene) filled by category of transcript cell-type JSD(0.6) specificity of A549.longNonPolyA A549.longPolyA 0.6 0.4 0.3 0.4 0.2 -0.2 0.1 0.0 0.0 AG04450.longNonPolyA AG04450.longPolyA 0.5 0.6 0.4 0.3 -0.4 0.2 -0.2 0.1 0.0 0.0 BJ.longNonPolyA BJ.longPolyA 0.4 0.4 0.3 -0.3 0.2 -0.2 0.1 0.1 0.0 0.0 GM12878.longPolyA GM12878.longNonPolyA 0.3 0.3 0.2 0.2 0.1 0.1 0.0 0.0 H1.HESC.longNonPolyA H1.HESC.longPolyA 0.3 -0.2 0.2 -0.1 0.1 -0.0 0.0 HELA.S3.longPolyA HELA.S3.longNonPolyA 0.4 0.3 -0.3 0.2 0.2 0.1 0.1 0.0 0.0 HEPG2.longNonPolyA HEPG2.longPolyA 0.3 0.4 0.3 0.2 -0.2 0.1 -0.1 0.0 0.0 HMEC.longPolyA HMEC.longNonPolyA 0.3 -0.3 0.2 0.2 0.1 0.1 jsdCat density 0.0 -0.0 cell-type-other HSMM.longNonPolyA HSMM.longPolyA cell-type-this none 0.3 0.2 0.2 -0.1 0.1 -0.0 0.0 HUVEC. Iong Non Poly AHUVEC. Iong Poly A0.25 -0.20 -0.2 0.15 -0.10 -0.1 0.05 -0.00 0.0 K562.longNonPolyA K562. Iong Poly A0.5 0.3 -0.4 0.2 -0.3 0.2 0.1 -0.1 0.0 0.0 MCF.7.longNonPolyA MCF.7.longPolyA 0.4 0.2 0.3 -0.2 -0.1 0.1 -0.0 0.0 -NHEK.longNonPolyA NHEK.longNonPolyA.1 0.5 0.4 0.2 -0.3 -0.2 -0.1 0.1 -0.0 0.0 NHEK.longPolyA NHEK.longPolyA.1 0.4 0.3 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 ${\sf SK.N.SH_RA.longNonPolyA}$ ${\sf SK.N.SH_RA.longPolyA}$ 0.3 0.3 -0.2 0.2 -0.1 0.1 0.0 -5 -5 -10 -10 log(value)