Correlation of rover insertions with Modencode tracks for S2

Assay Factor (y-axis, top to bottom): ACF1, ASH-1, PCL, ORC2, NURF301, MSL-1, MRG15, MOF, MLE, MCM2-7, MBD-R2, LSD1, KDM4A, JIL-1, JHDM1, ISWI, HP4, HP2, HP1c, POF, PR-Set7, Pc, Su(var)3-7, dmTopo-II, dSFMBT, dRING, dMi-2, ZW5, WDS, Su(var)3-9, Su(Hw), Pho, Smc3, SPT16, Rhino, Replication-Origin, RPD3, Psc, PolII, HP1b, HP1a, H4acTetra, H2Av, H3K27me1, H3K27ac, H3K23ac, H3K18ac, H3, H2Bubi, H2BK5ac, H1, H3K27me3, GAF, Enhancer-of-zeste, Chriz, CTCF, CP190, CG10630, BEAF-32, H3K27me2, H3K36me1, H4K8ac, H3K9me1, H4K5ac, H4K20me1, H4K16ac, H4K12ac, H4, H3K9me3, H3K9me2, H3K9acS10P, H3K36me3, H3K9ac, H3K79me3, H3K79me2, H3K79me1, H3K4me3, H3K4me2, H3K4me1, mod(mdg4)

Each row value: 0

x-axis: -log10 p-value, values 0, 20, 40 (log2_enrichment)