predict for labels = new.grps kendall linear 0.6 x\_prefix 0.4 -RNAseq\_all\_genes rnaseq\_effector\_path\_vals rnaseq\_metabolic\_mod\_activities acc rnaseq\_metabolic\_mod\_genevalues rnaseq\_metabolic\_mod\_nodevalues rnaseq\_path\_vals rnaseq\_signaling\_genes 0.2 -0.0 x\_prefix