predict for labels = effect.grps kendall linear 0.4 -0.3 x_prefix RNAseq_all_genes rnaseq_effector_path_vals rnaseq_metabolic_mod_activities Se 0.2 rnaseq_metabolic_mod_genevalues rnaseq_metabolic_mod_nodevalues rnaseq_path_vals rnaseq_signaling_genes 0.1 -0.0 -

x_prefix