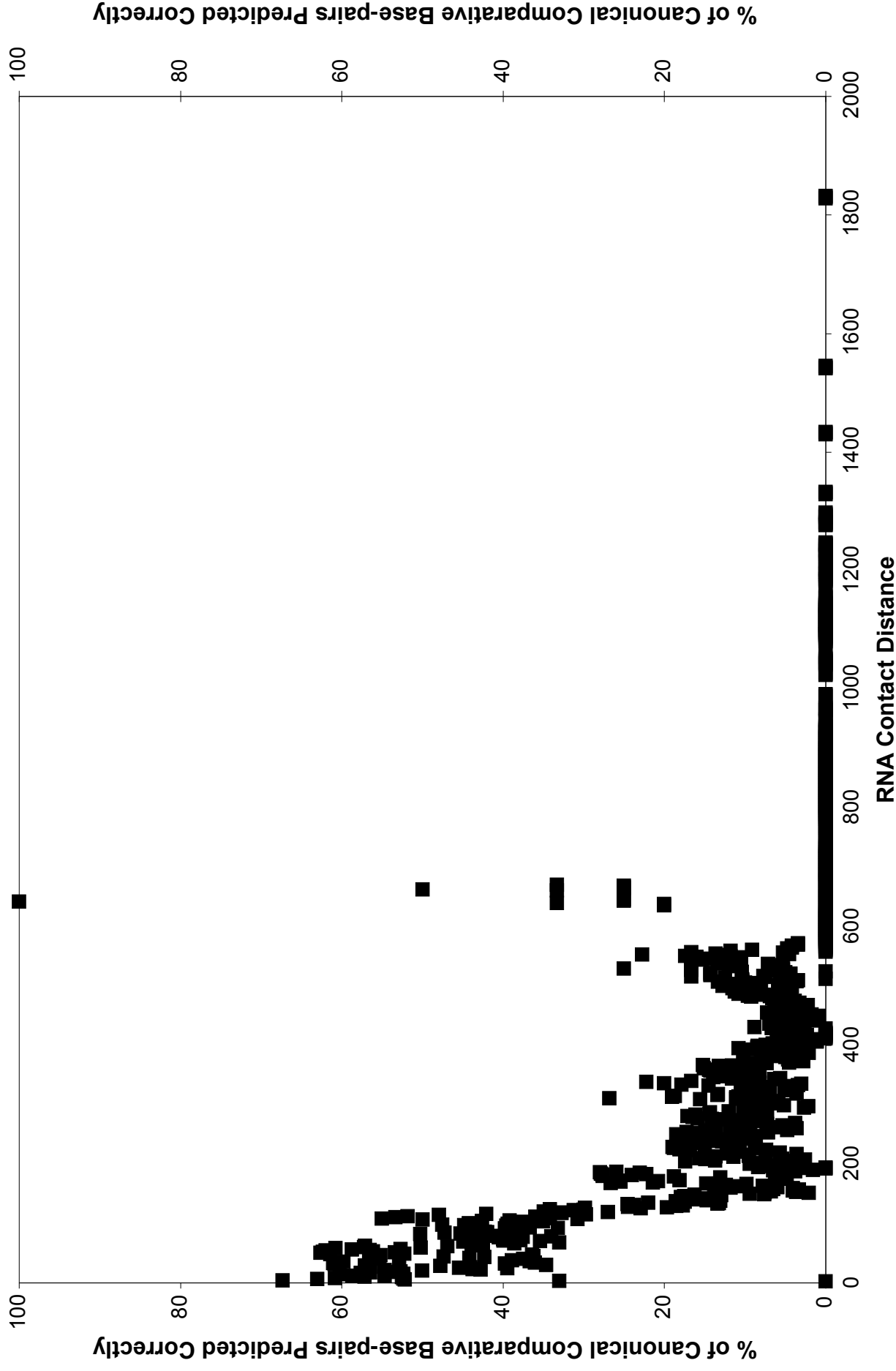


Prediction Accuracy for 191,994 Comparative, Canonical Base-pairs (from 496 16S rRNA Structures)



This chart shows the prediction accuracy for 191,994 comparative, canonical base-pairs by RNA Contact Distance. The base-pairs are taken from the 496 16S rRNA secondary structures in our dataset. The base-pairs range in contact distance from a minimum of 3 to a maximum of 1833. See the RNA Contact Distance distribution plot (Figure 2A) for the number of comparative base-pairs observed for each contact distance value. Folding parameters for Mfold 3.1 were window size (W)=1, max suboptimal (MAX)=750, percent suboptimality (P)=5% and efn2 re-evaluation and re-ordering of predicted folds.