Figure S3: Covariance estimation error Plot of typical percent error across covariance matrix with $k = 79$, estimated from 35 simulated samples at coverage of 60,000 read pairs. Original covariance values derived from parameter estimates using training set of 38 samples as described in Methods. Target names represent primary transcript exons in *DMD* ordered by genomic position. Note that a small number of covariance terms have very high proportional error; the position of these terms is not consistent between different simulated instantiations of training cohorts.