

**Table S1:** Selected baseline genes and coefficients of variation

Gene	Mean Coverage (DMD-relative)	Coefficient of Variation ( $\sigma/\mu$ )	Region
FH	9.521	0.037	1:241661107-241683042
GFM1	5.358	0.041	3:158362403-158409276
FASTKD2	7.239	0.045	2:207631397-207656546
ACADM	8.042	0.045	1:76190464-76228468
AGL	2.997	0.050	1:100316578-100387227
SLC35D1	9.892	0.050	1:67470002-67519716
ALG6	6.794	0.052	1:63836628-63902711
Aggregate	0.880	0.040	

Mean and coefficient of variation for aggregate baseline are calculated based on total coverage across all baseline genes, such that  $\mu_A = \frac{1}{38} \sum \frac{C_{DMD}}{\sum_i C_i}$ . Note that the total number of baseline genes selected was limited so as to keep  $\mu_A$  relatively close to 1, while holding  $\sigma_A/\mu_A$  low. Specific genomic regions for each of the 112 targets comprising these genes can be found at <http://github.com/vkozareva/geneCNV/>.