TABLE S4

Comparison of sequence coverage[a] and number of mutants needed to perform our cloning strategy in *fp6*

Flow cell lanes used[b]	Reads	Mutants compared	*fp6* linked region	Number of candidates[c]	true *fp6* allele identified
2	paired-end	*fp6*, *fp9*, *fp12*	5811728-10105957Mb	6	Yes
2	single-end	*fp6*, *fp9*, *fp12*	5811728-11638999Mb	6	Yes
1	paired-end	*fp6*, *fp9*, *fp12*	5811728-10105957Mb	6	Yes
1	single-end	*fp6*, *fp9*, *fp12*	3615997-10105957Mb	6	Yes
2	paired-end	*fp6*, *fp9*	5811728-10105957Mb	6	Yes
2	single-end	*fp6*, *fp9*	3468244-11638999Mb	6	Yes
1	paired-end	*fp6*, *fp9*	3615997-11638999Mb	6	Yes
1	single-end	*fp6*, *fp9*	2405323-10501170Mb	6	Yes
2	paired-end	*fp6*, *fp12*	5811728-10105957Mb	6	Yes
2	single-end	*fp6*, *fp12*	5811728-11638999Mb	6	Yes
1	paired-end	*fp6*, *fp12*	5811728-10105957Mb	6	Yes
1	single-end	*fp6*, *fp12*	3615997-10105957Mb	6	Yes

[a]Sequence coverage for each WGS scenario (number of lanes and reads used) is shown in Table S2. [b]Per mutant. The Illumina Genome Analyzer II flow cell contains 8 lanes in total. [c]In all cases, 5 missense mutations and 1 5'UTR mutation were identified in *fp6* (Table S3). We also identified obvious high-density variant regions for *fp9* (ChrX:7.74Mb-14.85Mb) and *fp12* (ChrX:4.60Mb-5.88Mb).