Table S2 Classifying SNPs identified by whole genome sequencing of pooled DNA from zebrafish mutants

Mutant pool	SNP genotype[a] (average per kb)				Parental origin of alleles[b] (average per kb)	
	Het	Hom		n/d	Mapping strain allele	Reference genome allele
		Non-ref	Ref			
moto	1.6	0.9	1.8	1.3	0.6	0.6
wdd	1.0	0.4	2.1	2.2	0.3	0.3
hlw	1.7	0.4	2.4	1.0	0.4	0.8
frnt	2.1	0.6	2.1	0.7	0.6	0.7
sump	1.8	1.1	2.0	0.6	0.7	0.6

[a]Calculated for the 7.6 million SNP sites identified in this study. SNPs were defined as heterogeneous (Het) for sites at which both a reference genome allele (Zv9) and an alternate allele were observed in the WGS of pooled DNA. SNPs were defined as homogeneous (Hom) for sites at which only the alternate allele (non-ref) or the reference genome allele (ref) were observed; sites that were covered by less than 2 sequencing reads were deemed uninformative (n/d). [b]Calculated for all SNP sites at which an alternate allele was present in the TLF or WIK mapping strain, but not in the Tü strain (0.7 million and 1.2 million sites respectively); Mapping strain allele = at least one read representing the alternate allele was observed in a mutant pool; Reference genome allele = all reads in a mutant pool represented the reference genome allele. Note that the reference genome is based on the Tü strain.