Table S1 Whole genome sequencing of pooled DNA from wild-type zebrafish strains

Wild-type pool	# reads[a] (millions)	Genome coverage	# SNPs[b] (per kb)	% het[c]
Tü[B]	97	5.1x	2.6	88
Tü[G]	81	4.1x	2.5	89
WIK[B]	96	4.1x	2.9	64
WIK[G]	81	4.0x	3.5	73
AB	90	4.6x	3.3	79
TLF	91	3.8x	2.9	56

[a]Number of 100 bp reads obtained by Illumina single end sequencing. [b]Number of positions at which at least one read representing an alternate allele was observed. Only positions at the 7.6 million SNP sites identified in this study were considered. [d]Percentage of SNPs that were heterogeneous (i.e., both reference-genome and alternate alleles were represented)