



Figure S5 Minimum coverage needed for efficient mapping of zebrafish mutants. Graphs depicting the genome-wide mapping scores calculated for each mutant in 20 cM sliding windows, using either only 5 million (top) or 1 million (bottom) randomly selected Illumina sequencing reads. The actual map positions for each mutant are indicated (red arrows). When 5 million reads are used, the mapping score plots are not significantly different from those generated using all reads (>60 million) (Figure 1). The only exception is that, for *sump*, the linked region has only the 2nd highest mapping score. Even when only 1 million reads are used, in three mutants (*moto*, *frnt*, *hlw*) the linked region has the highest mapping score in the genome. For two other mutants (*wdd*, *sump*), the relative heights of the false positive peaks are significantly increased.