Table S6 Details of sequence coverage for the additional inbred medaka lines. The table provides percent read alignment for each of the libraries sequenced for each inbred strain. Total coverage of the genome and median read depth is given for the total sequence for all libraries from that strain.

Strain	**HNI**	**HSOK**	**Kaga**	**Nilan**
Aligned reads by library type (%)				
3kb mate-pair 100bp reads	50	59,7	56,2	56.2
54bp reads	69,3	66	60,9	60.9
300bp paired-end	82,5	81	77,3	77.3
500bp paired-end	82,4	81	76,5	76.5
Coverage of reference genome (%)	78,4	77,8	78,4	76,9
Median coverage at locations covered at least once	113	108	119,0	125