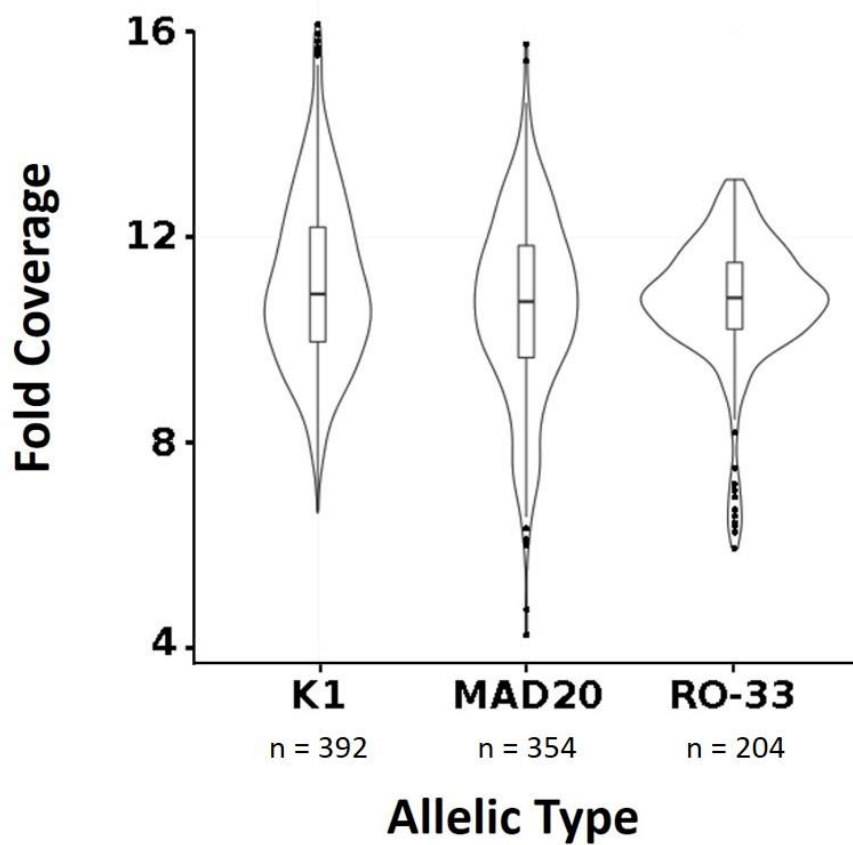


Additional file 8.



Distribution of coverage by allelic type after alignment of dummy reads to reference library. 100 bp dummy reads created from *msp1* block 2 long read sequences (Appendix files 1 and 2) were aligned to the reference library of 15 allelic sequences (Appendix file 4) using BWA-MEM. Coverage was calculated for each alignment and is shown for each major allelic type, showing no bias in the coverage among the types.