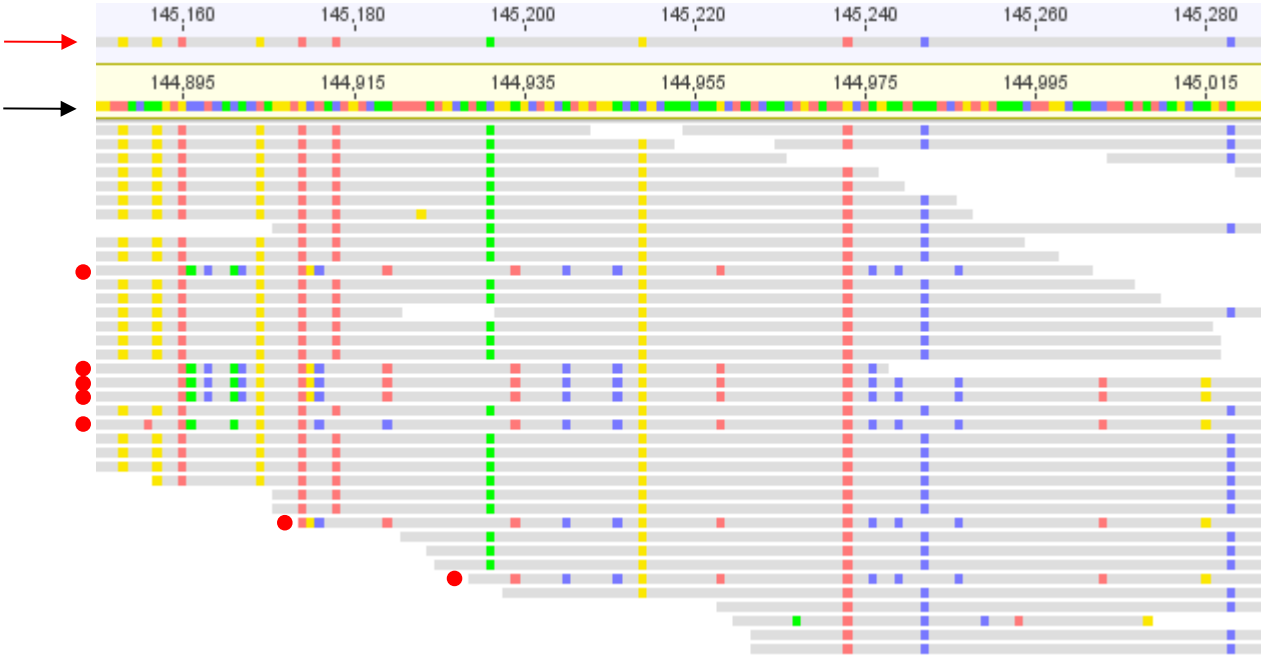
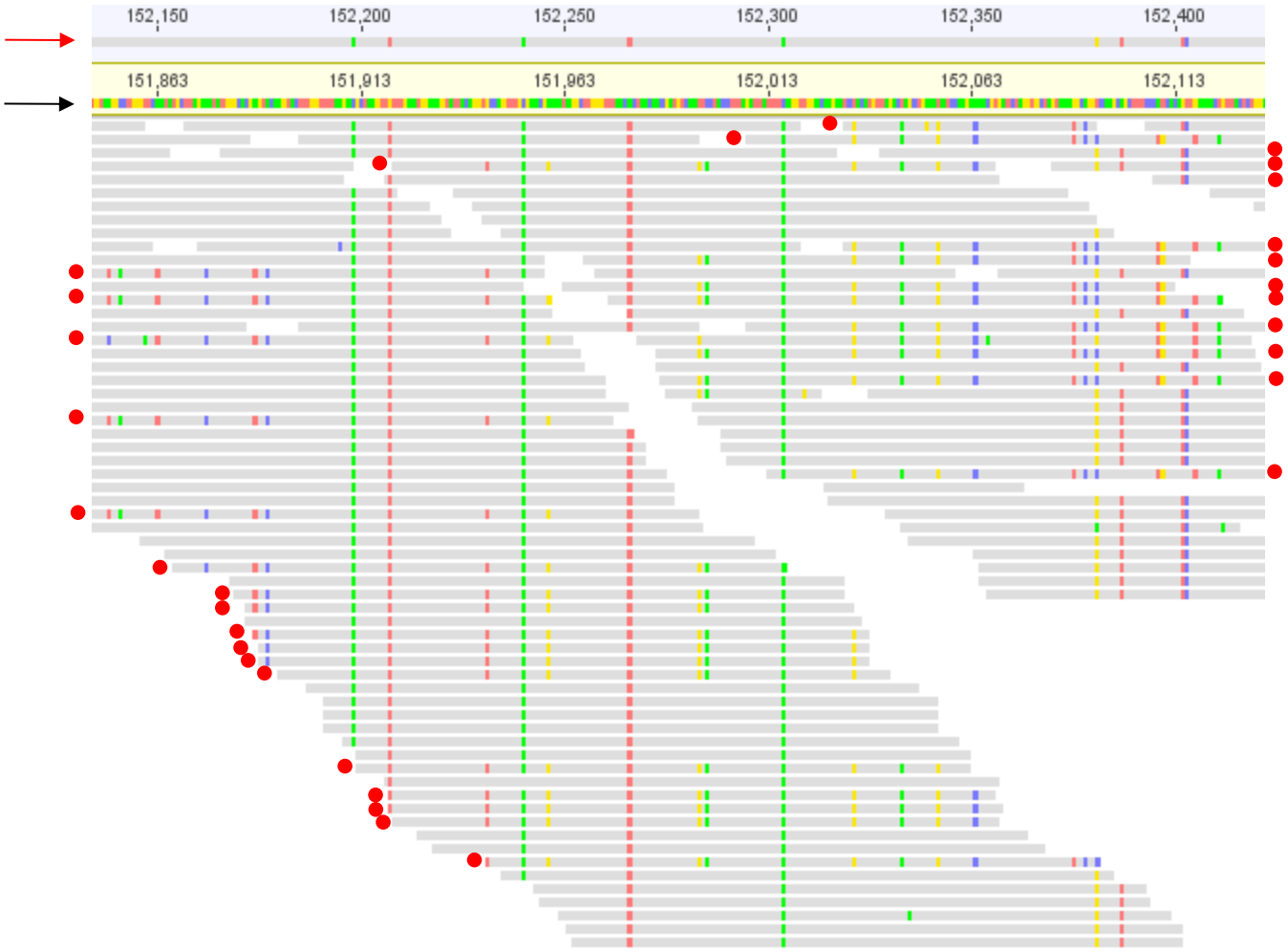
Supplement Figure 1: Visualization of reads originating from *Oxalis polyphylla* J11-44 mapped to the "pseudoreference" (black arrow) using Geneious. A – locus 11 339, exon 3. B – locus 11 386, exon 2. Polymorphic single nucleotide polymorphisms (SNPs) compared to the pseudoreference are highlighted in form of coloured squares compared to agreements with the pseudoreference marked as gray bars. The majority of reads (31× coverage in A, 42× coverage in B) are relatively similar to the pseudoreference (11 SNPs in A, 9 SNPs in B), whereas the alternative reads (paralogs or alleles; 7× coverage in A, 20× coverage in B) show a much higher number of SNPs compared to the pseudoreference (around 21 SNPs in A, around 26 SNPs in B). These reads of lower abundance are marked with red dots. Only the dominant variants influence the resulting consensus sequence (red arrow), which is used in subsequent analyses.



A


152,150
152,200
152,250
152,300
152,350
152,400
151,863
151,913
151,963
152,013
152,063
152,113

B