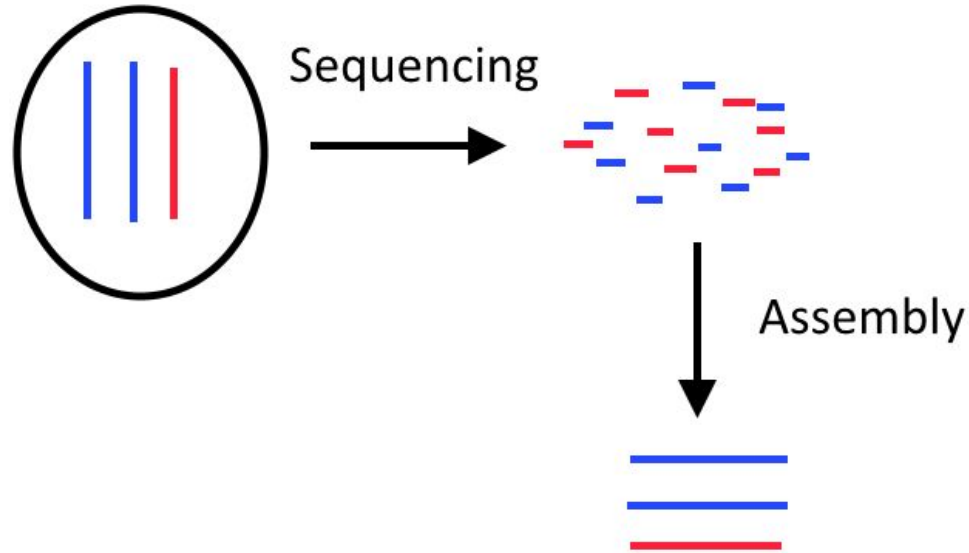


nPhase and hybrid polyploid considerations

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If one of the haplotypes is very different from the others...

nPhase will struggle to distinguish between the haplotypes that are comparatively closer



Solution: SNP density strategy

The **1n** portion of the hybrid genome will account for **many more (or fewer)** het positions

We may be able to separate 2n and 1n reads based on **SNP density**

SNP density strategy

The **1n** portion of the hybrid genome might account for **most** het positions

We may be able to separate 2n and 1n reads based on **SNP density**

When aligned to a reference, long reads should be long enough to accumulate:

A low density of heterozygous positions for the **diploid** part of the hybrid

A high density of heterozygous positions for the **haploid** part of the hybrid

SNP density strategy

The **1n** portion of the hybrid genome might account for **most** het positions

We may be able to separate 2n and 1n reads based on **SNP density**

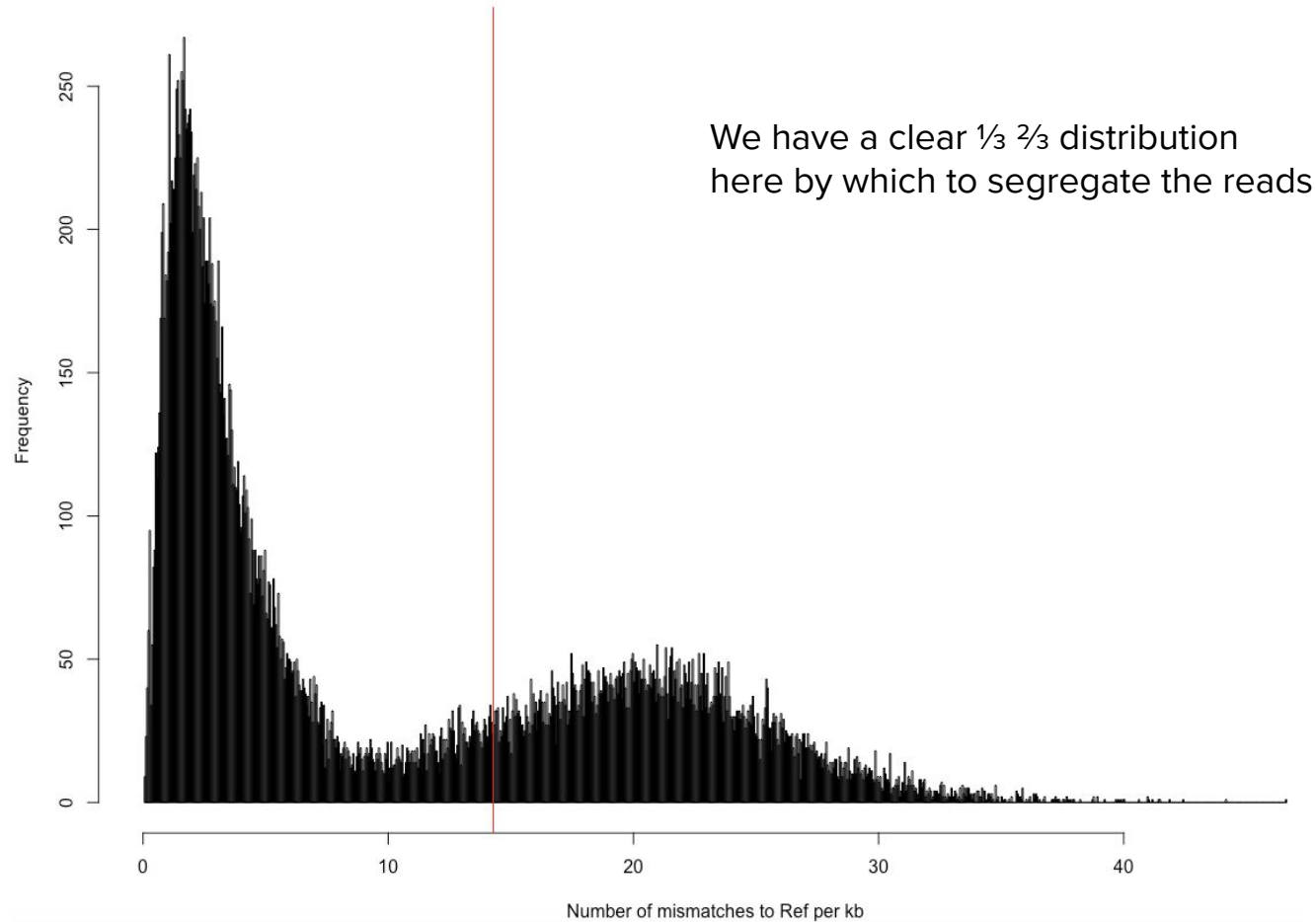
When aligned to a reference, long reads should be long enough to accumulate:

A low density of heterozygous positions for the **diploid** part of the hybrid

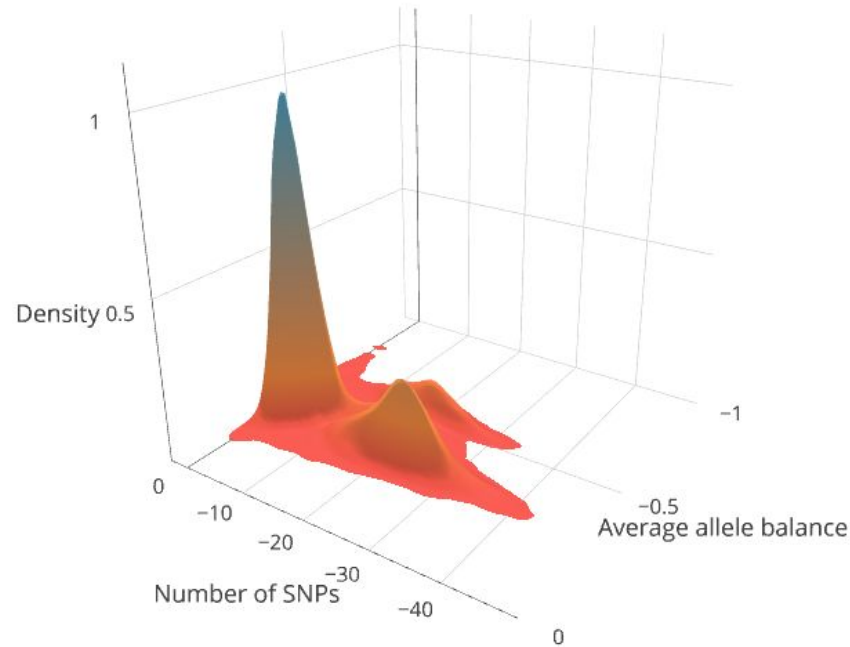
A high density of heterozygous positions for the **haploid** part of the hybrid

(If the **1n** accounts for the least amount of het positions we simply invert the logic)

Distribution of SNP density in 30350 reads > 3500 bp

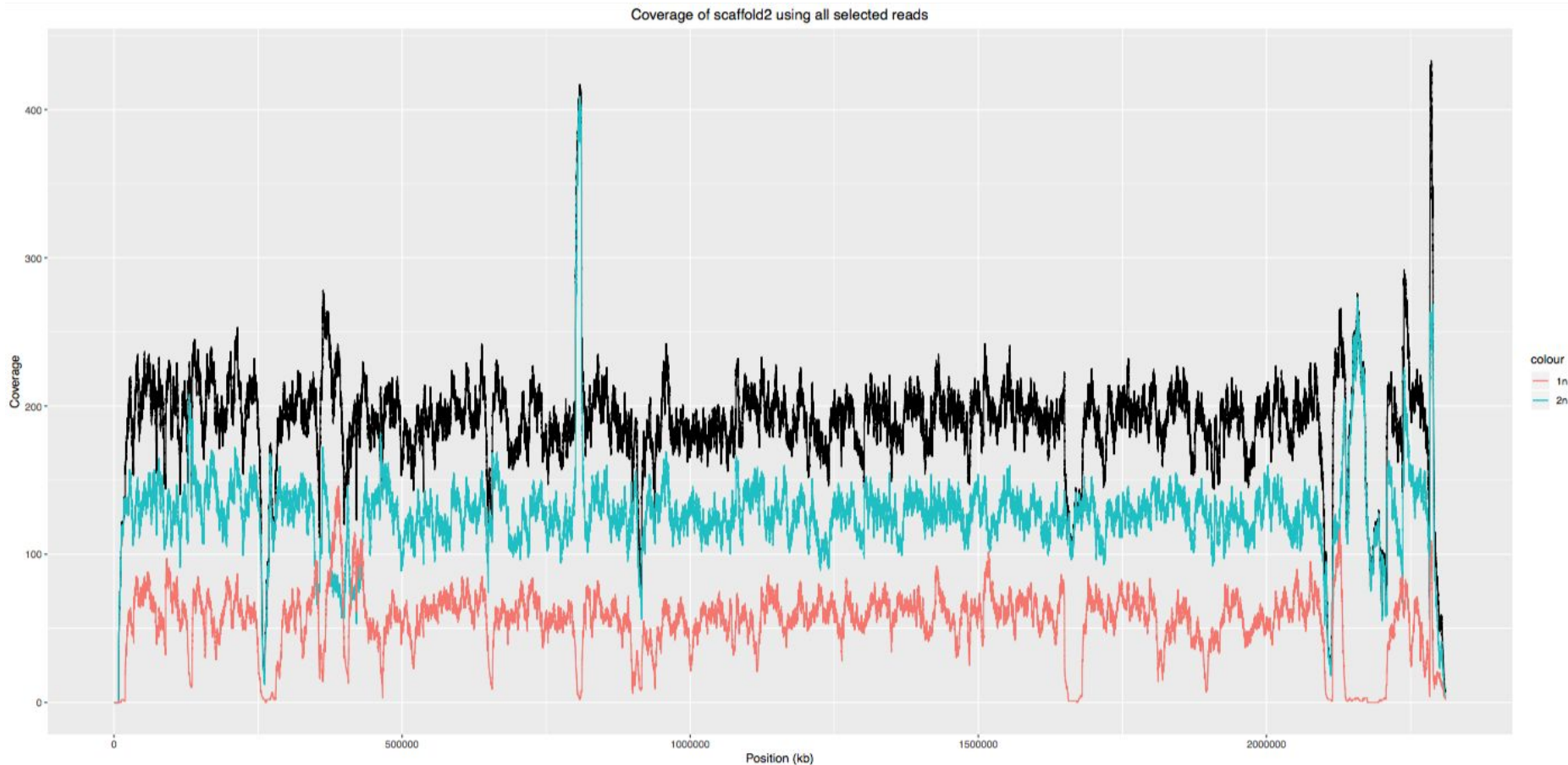


SNP density and average allele balance 3D plot

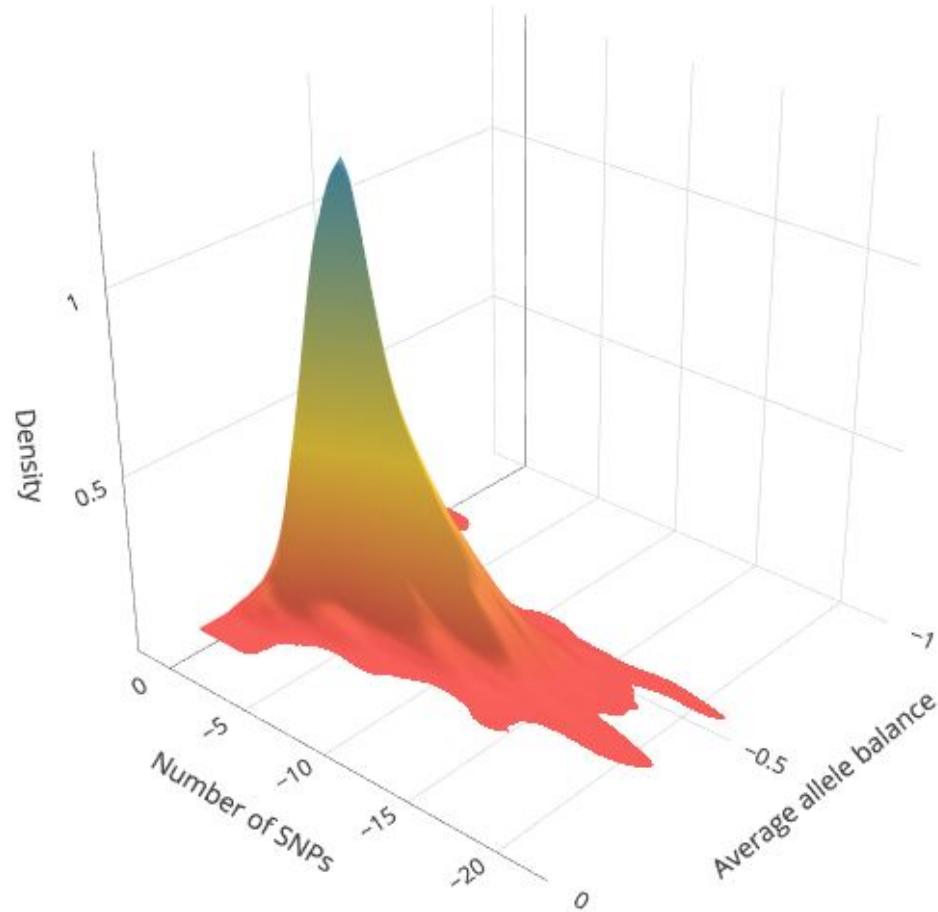


<http://rpubs.com/oabousaada/437878>

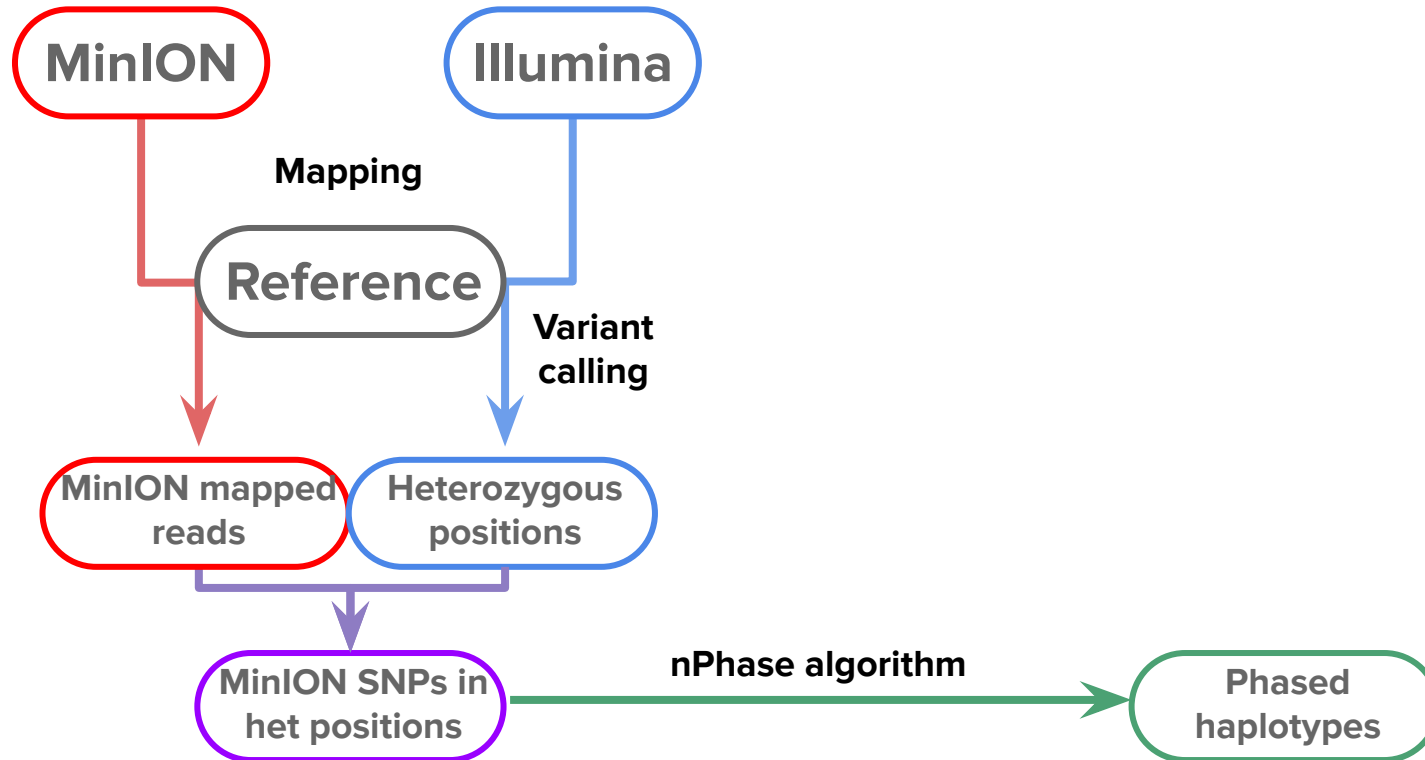
Remapping reads reveals a consistent $\frac{2}{3}$ $\frac{1}{3}$ distribution



If all reads have the same **SNP** density...



Then use nPhase: Polyploid phasing pipeline



Thank you for your attention



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