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 <https://github.com/LittleFrogHill/Mites-assembly/blob/main/README.md>



## Evolutionary innovation in the long-term absence of sex in the oribatid mite *Platynothrus peltifer*

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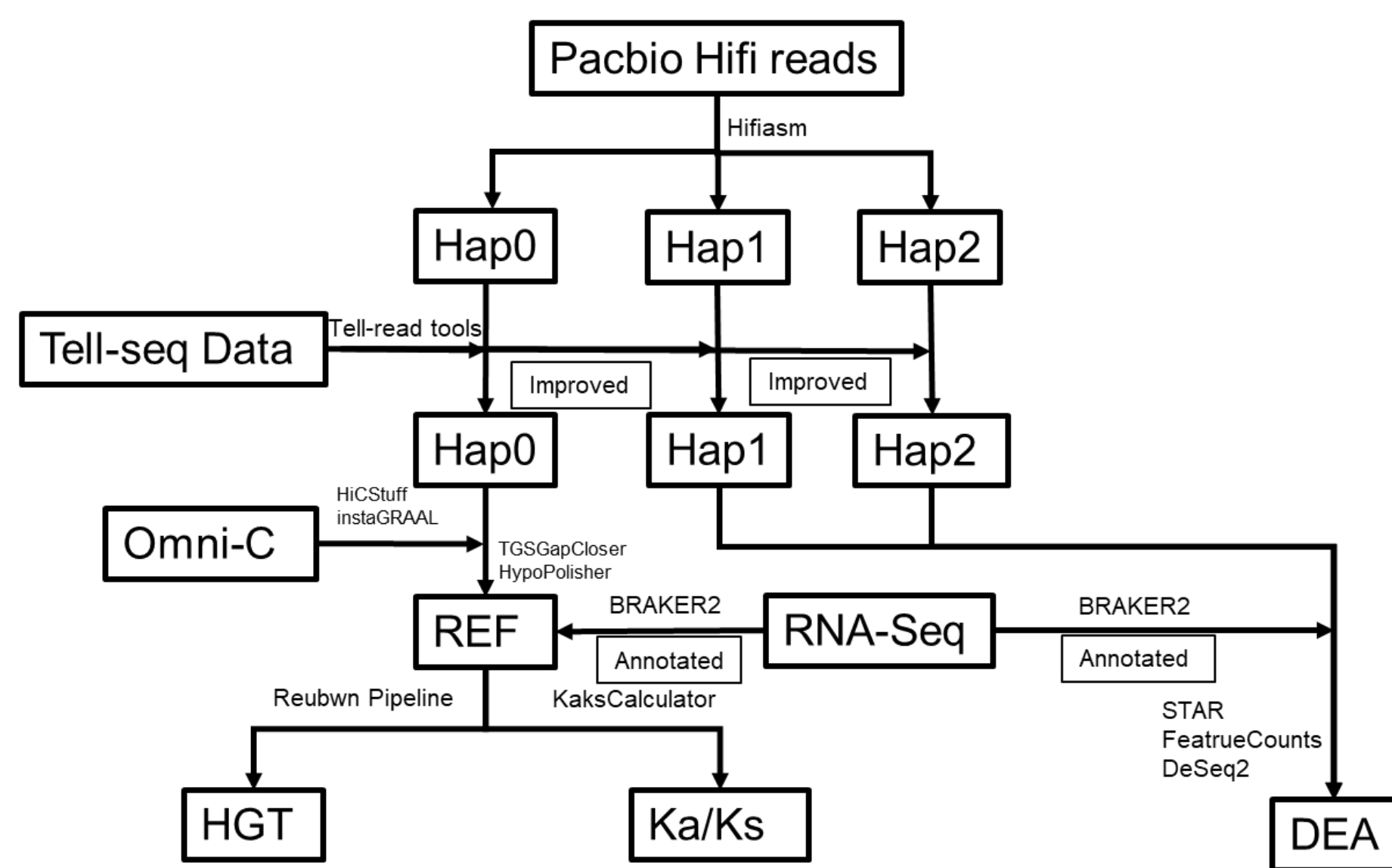
### Highlight

- Single individual chromosome-level scale reference genome and two high quality haplotypes assemblies.
- $K_A/K_S$  of DEA relatively higher EEA genes.
- 10% single copy genes between two haplotypes show DEA
- 77.5% HGT with intron and 1.8% HGT show DEA

### Introduce

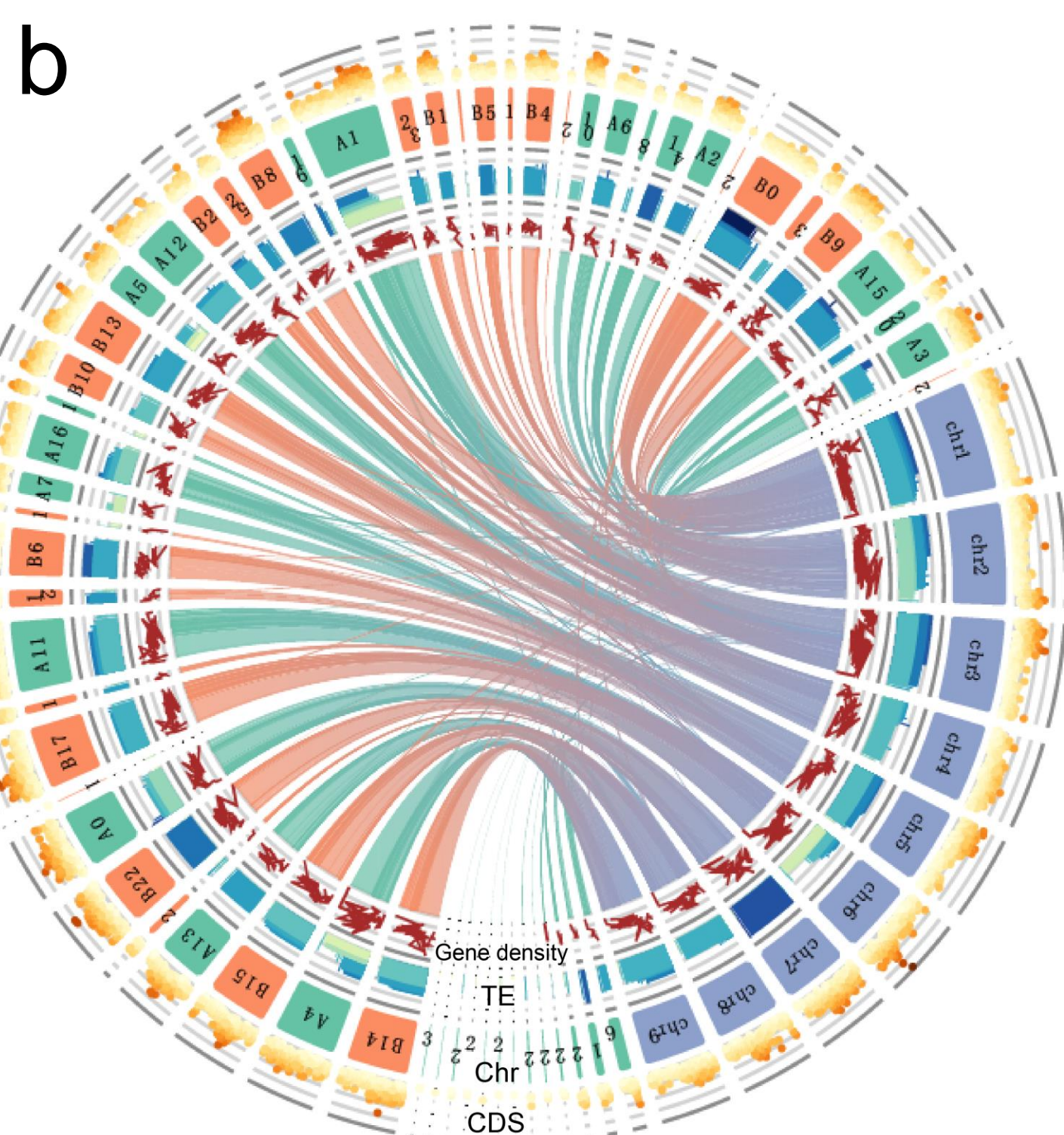
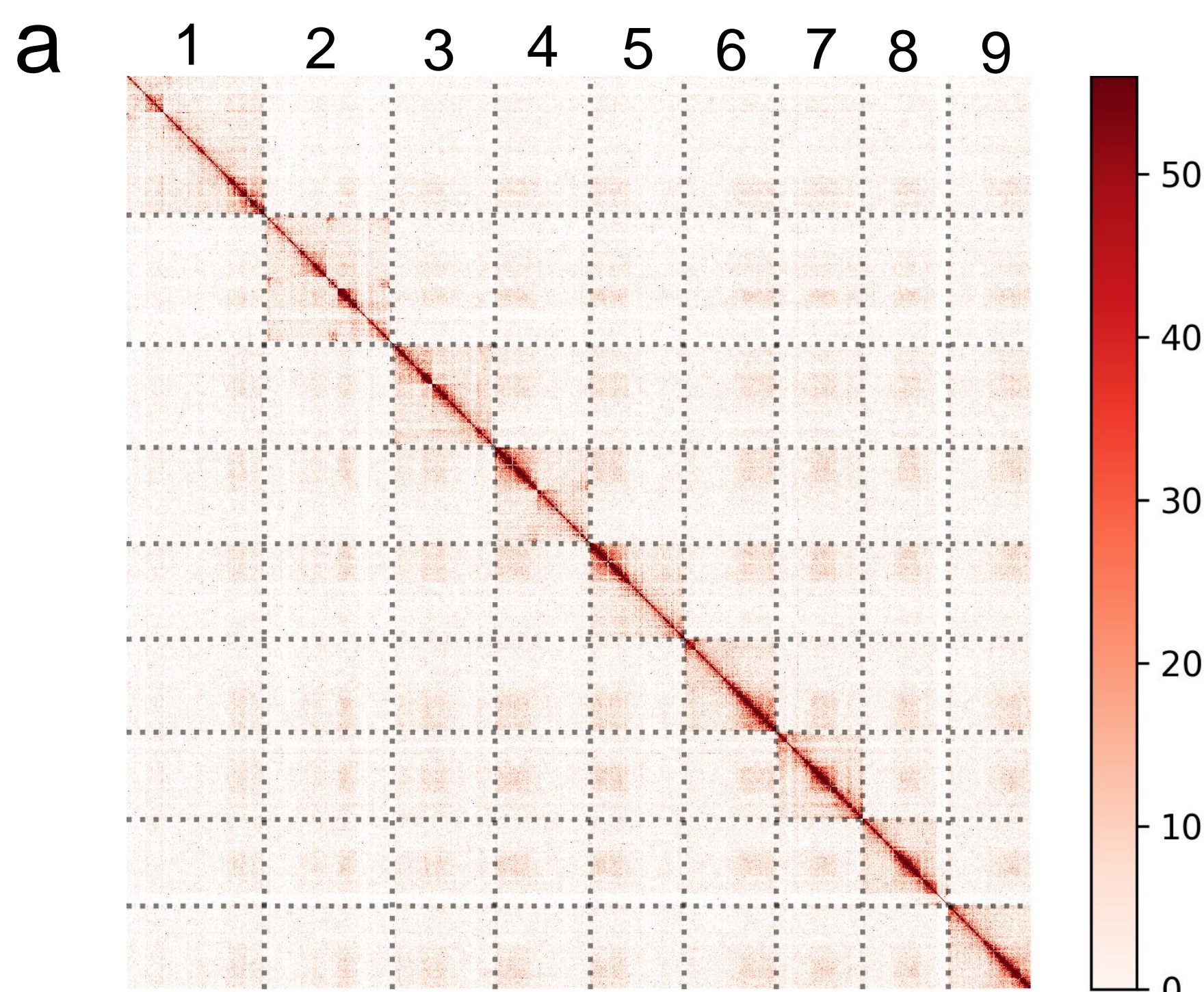
Asexuality is considered an evolutionary dead-end, but some ‘ancient asexual organisms’, like oribatid mites, have persisted and diversified over time. Very little is known about the processes that could generate evolutionary novelty and adaptability in the absence of sex. We analyzed potential genomic footprints of innovation in the haplotype-resolved, chromosome-scale genome of the ancient asexual oribatid mite *Platynothrus peltifer*. Large-scale structural variants might not play a major role, as there are few rearrangements within and between chromosomes as well as between haplotypes. However, heterozygosity is maintained and divergent haplotypes, as well as **differential allele expression (DEA)** with an functional enrichment in e.g. metabolic pathways, resource uptake and immune system. We further analyzed the evolutionary trajectories of these alleles, as these processes might contribute to adaptation and evolutionary novelty in the absence of sex. Moreover, **Horizontal Gene Transfer (HGT)** could supply the substrate for novelty via modulating gene regulation of these mites. Overall, identifying such signatures of evolutionary innovation will help to understand why some asexual can escape the dead-end fate and to identify the benefits of sex vice-versa.

### Workflow



*Platynothrus peltifer*

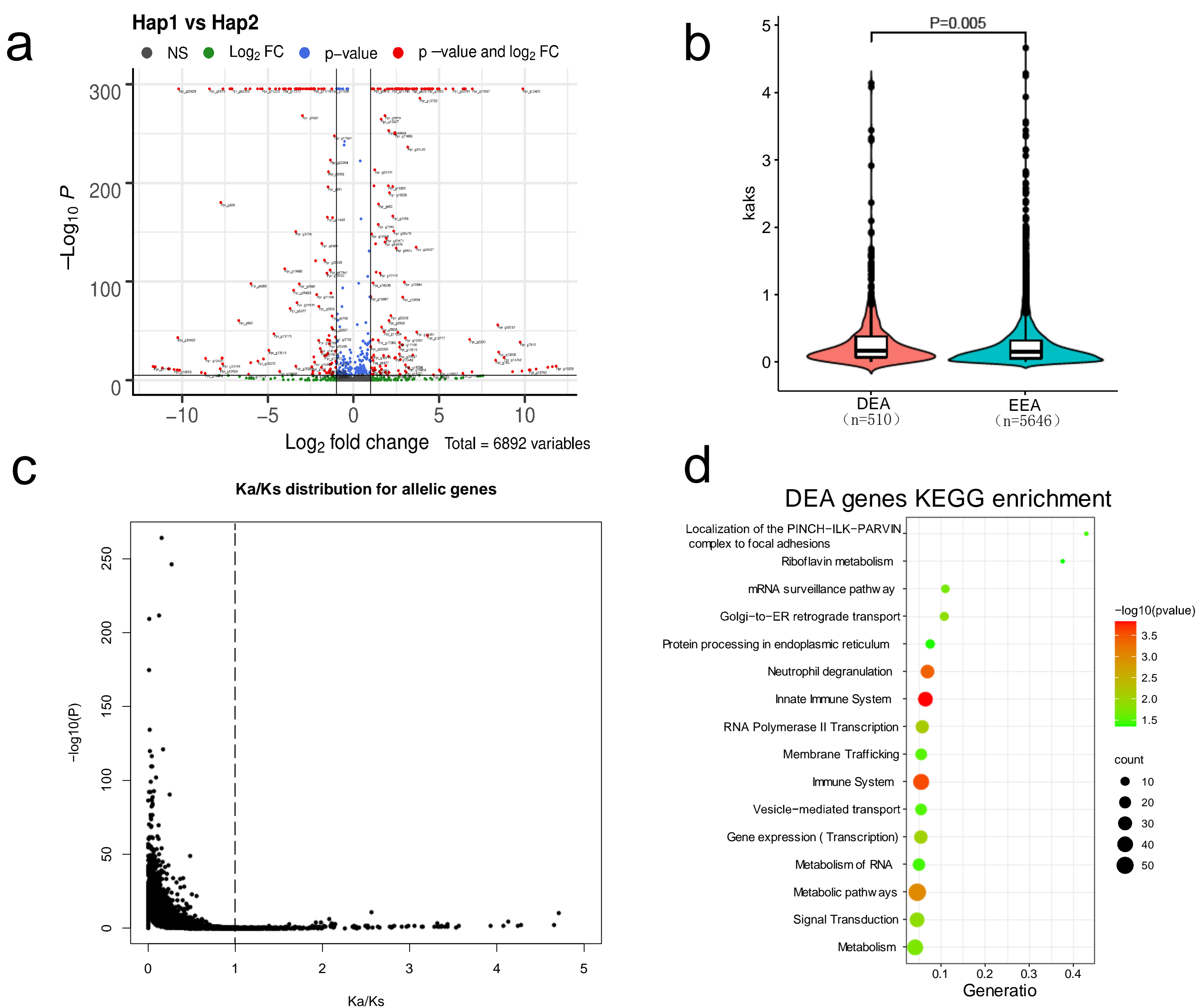
### Subtitle 1. Genome assembly



**Fig. 1:** Genome assembly

**a**, Contact map of Hi-C links among 9 chromosomes. **b**, Synteny alignment of the *Platynothrus peltifer* and genomic features.

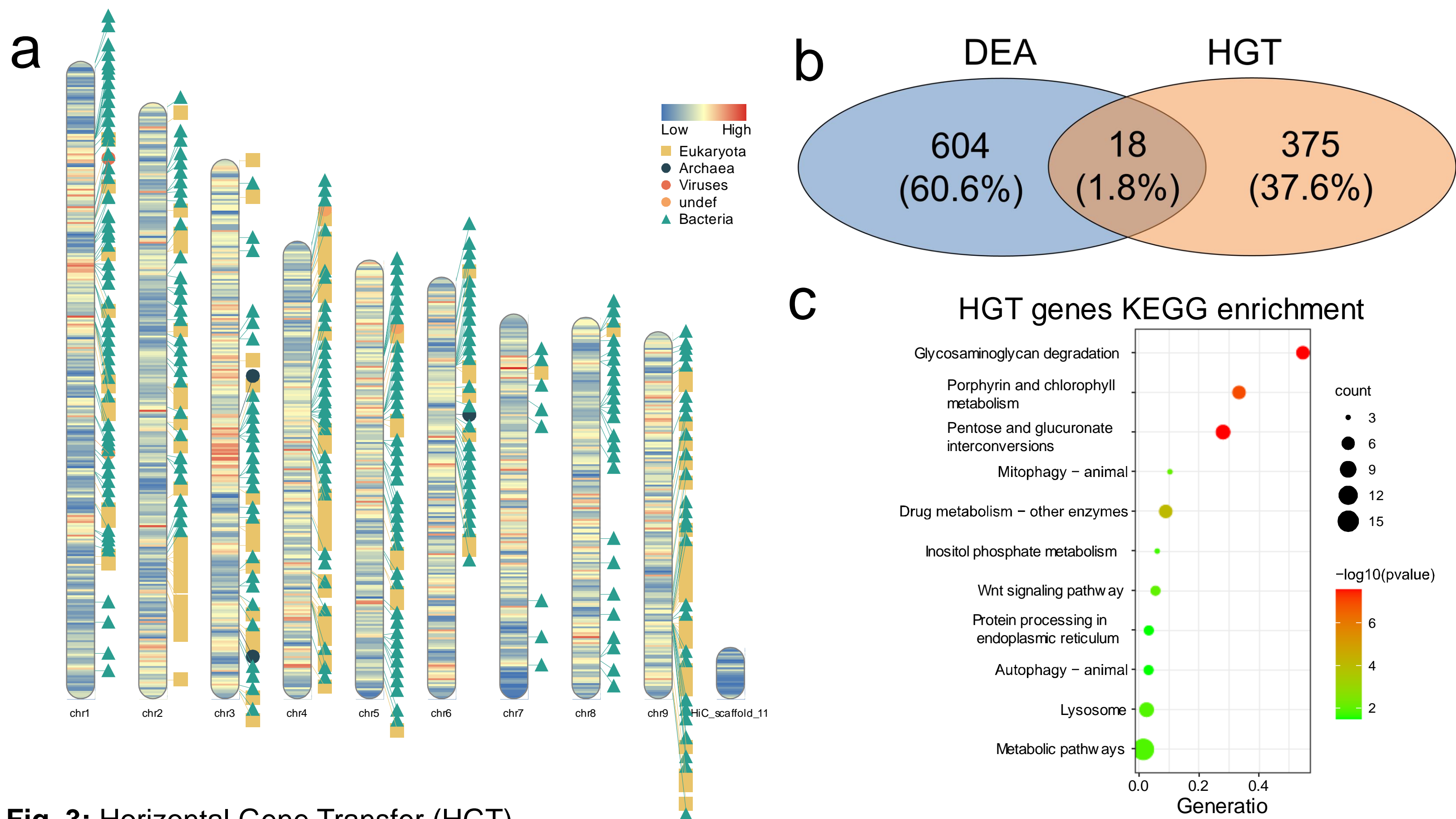
### Subtitle 2. Differential expression of alleles(DEA)



**Fig. 2:** Differential expression of alleles (DEA)

**a**, Volcano plot of the all DEA genes **b**, DEAs are of relatively lower Ka/Ks value. P values were calculated with Wilcoxon's t-test. **c**, Pairwise comparison of the Ka/Ks distribution for allelic genes. **d**, KEGG enrichment of DEA genes ( $P_{\text{adjust}} < 0.05$ ).

### Subtitle 3. Horizontal Gene Transfer (HGT)



**Fig. 3:** Horizontal Gene Transfer (HGT)

**a**, Landscape of the HGT genes in the reference genome. **b**, Venn plot of the DEA and HGT genes. **c**, KEGG enrichment of HGT genes ( $P_{\text{adjust}} < 0.05$ ).