

# F1D-SNP

All variants: 8,373,559



6,391,052



2,261,115



1,659,117



1,658,845



85,352



68,172 (including 3,275 from LG0)



23,190 (19,915 + 3,275)



17,534



Candidates submitted: 17,518 (including 3,275 from LG0)

## Pipeline steps

1. Exclude indels.
2. Min. variant read count ( $x=3$ ).
3. BothSafe (24 +/-) in F1D.
3. SNP site read depth  $\geq 20$ .
4. SNP  $\geq 3$  reads.
5. Heterozygosity check;  
~1:1 ratio alternate alleles.
6. A/T – G/C exclusion.
7. CDS (except in LG0).
8. BothSafe (24 +/-) in GDP.
9. Exclude redundant codon based.