

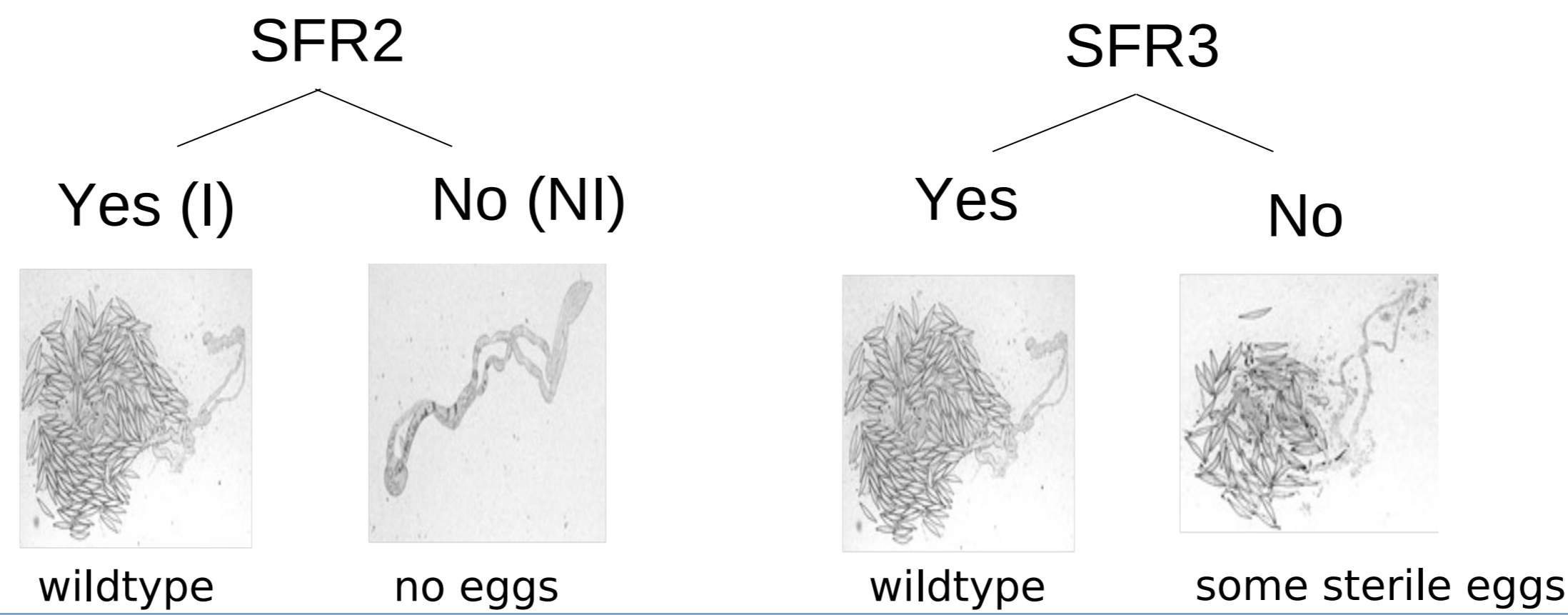
## Experimental design

*A. tabida* requires the intracellular bacterium *Wolbachia* for oogenesis, but the ovarian phenotype without *Wolbachia* is variable.

*Asobara tabida* lineages

*Wolbachia* infection

Ovarian phenotype

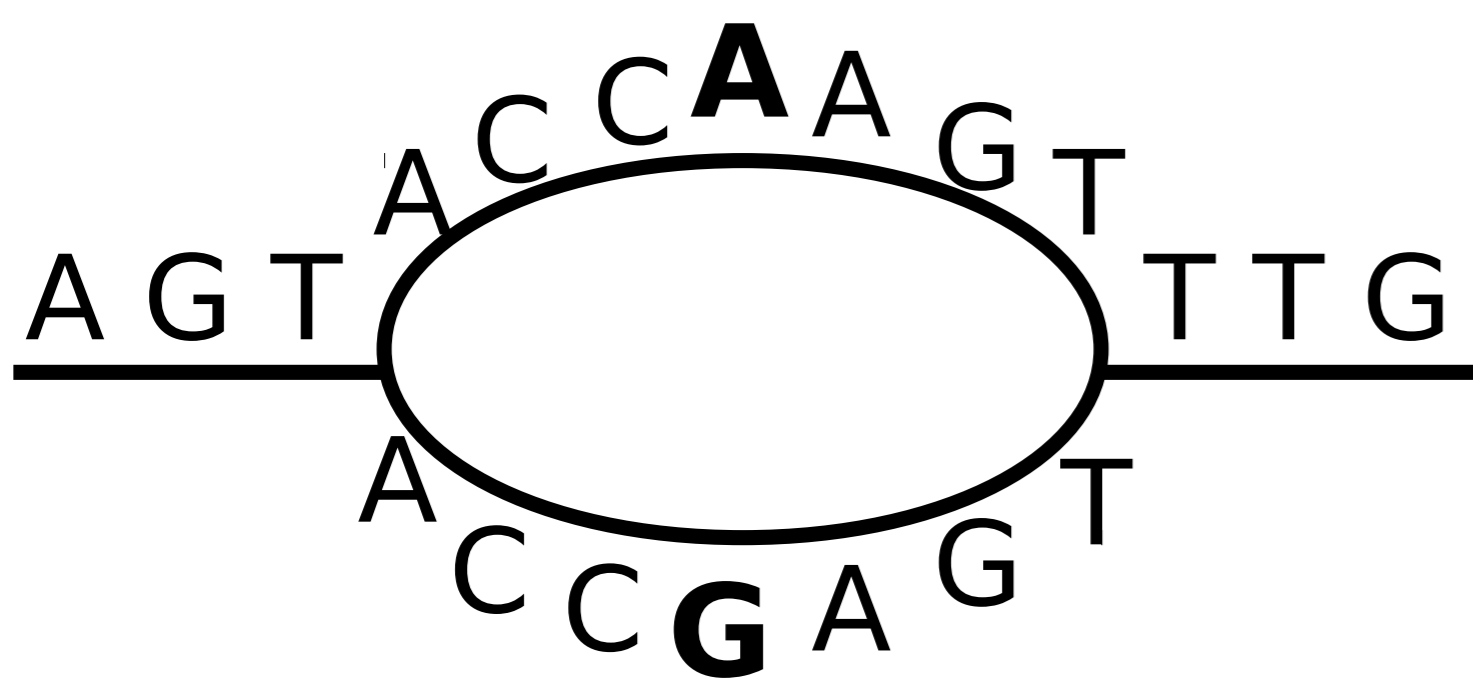


2 replicates per condition  
(8 lanes in total)

## SNP detection : KissSplice<sup>[4]</sup>

- De-Bruijn graph construction
- Graph traversal and search for bubbles

# reads(SFR2) / # reads (SFR3)



# reads(SFR2) / # reads (SFR3)

	SFR2	SFR3
Upper path	570	0
Lower path	0	339

Detection of specific SNPs of each lineage

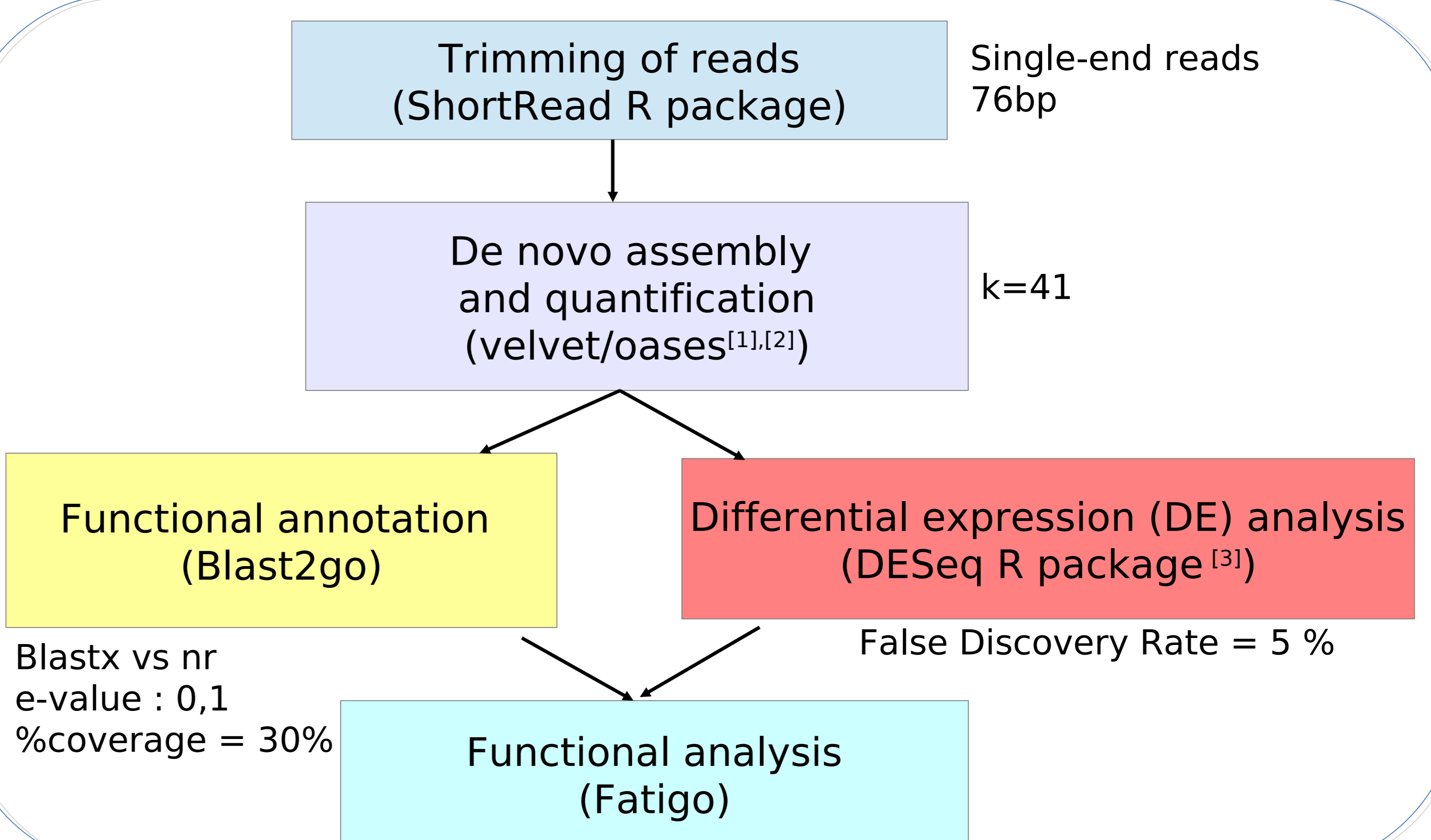
## Results

### Differentially represented SNP

SFR2i_vs_SFR3i	SFR2ni_vs_SFR3ni
2742	3195
2596	2596

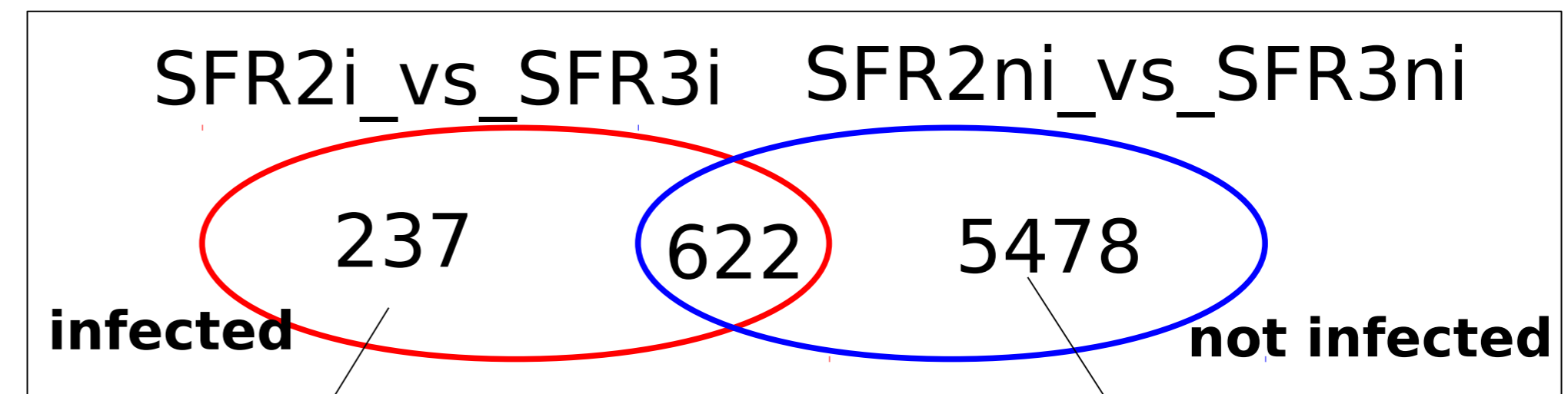
infected (left), not infected (right)

## RNA-Seq analysis (without reference genome)



## Results

Differentially expressed locus



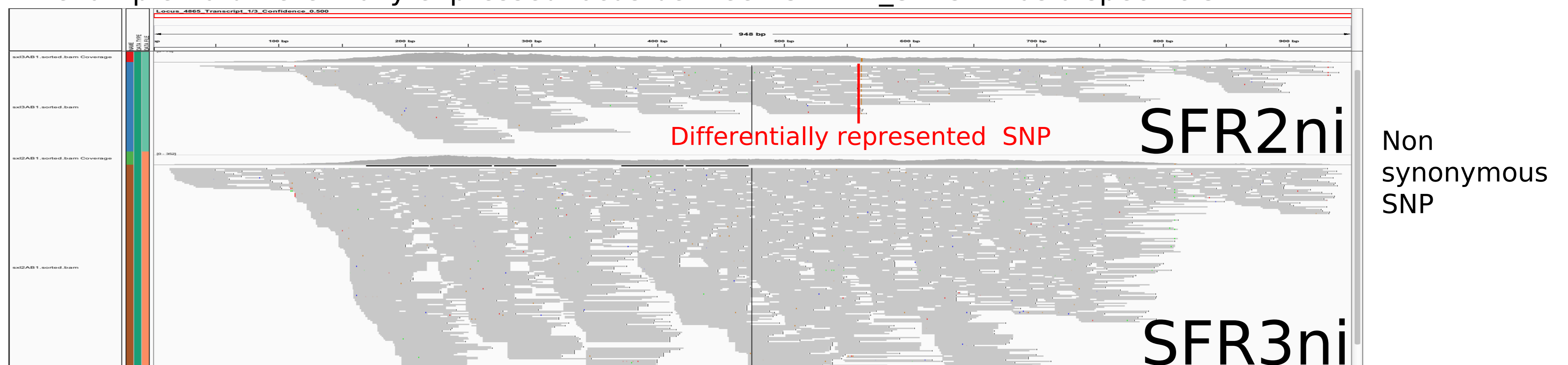
Function overexpressed

Apoptosis

Oxido-reduction regulation  
Apoptosis  
Autophagy

## Linking SNPs and differential expression

An example : a differentially expressed locus between SFR2ni\_SFR3ni has a specific SNP



## Conclusion

From RNA-Seq data, without reference genome :

- Detection of differentially expressed genes
- Detection of polymorphism between 2 different lineages
- Proposition of candidate to explain the phenotype

## Future Work

- Improvement of statistical test for differentially represented SNP detection
- Find mutation patterns (i.e. synonymous and non synonymous mutations)

## References

- [1] D. Zerbino and E. Birney, Gen. Res., 2008.
- [2] M.H. Schulz et al., Bioinformatics, 2012.
- [3] S. Anders and W. Huber, Gen. Biol., 2010.
- [4] Sacomoto et al., BMC Bioinformatics, 2012.