

SUPPLEMENTARY MATERIALS

SUPPLEMENTARY TABLES

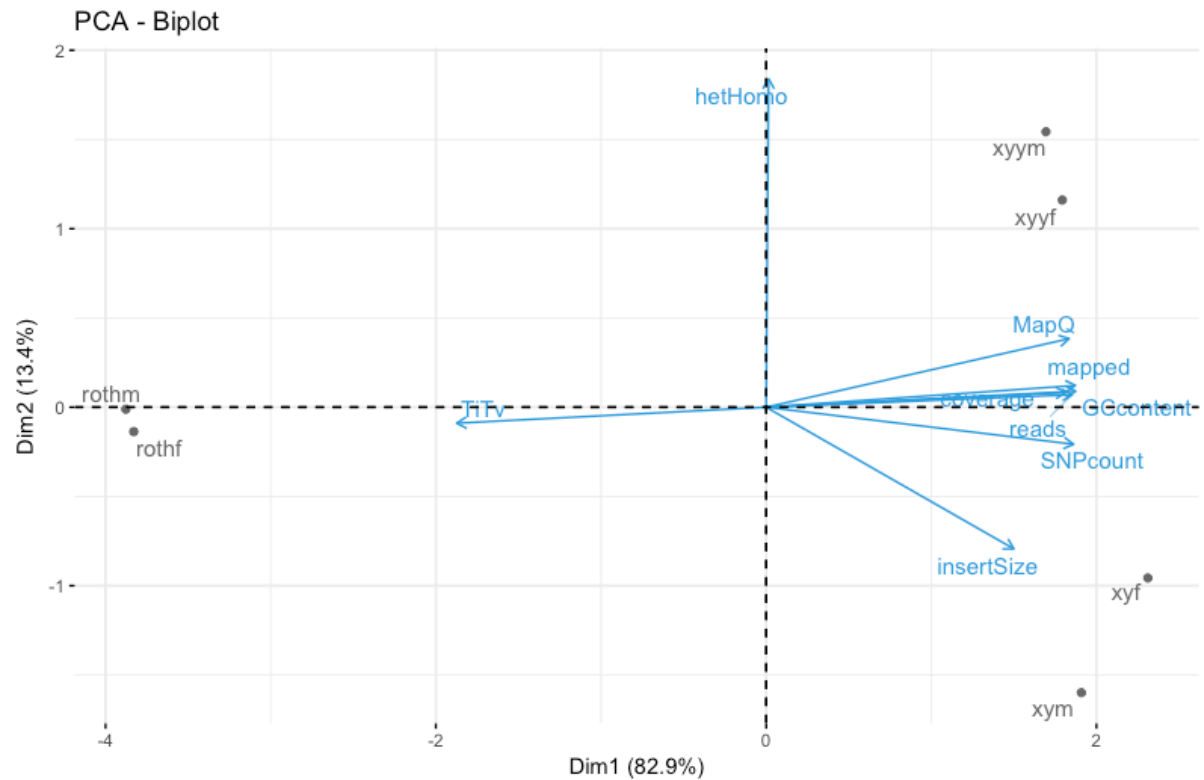
Supplementary Table 1. Read and mapping quality metrics for genomic samples of *Rumex hastatulus* XY and XYY and of *R. rothschildianus*

| Sample | # of reads | % mapped | Coverage | %GC | Tl/Tv | SNP count | Het/Homo | Insert Size | MapQ |
|-------------|------------|----------|----------|-----|-------|-----------|----------|-------------|-------|
| XY male | 272382436 | 82 | 49.12 | 41 | 1.45 | 710574 | 3.26 | 469 | 45.07 |
| XY female | 317774830 | 82.6 | 71.52 | 41 | 1.45 | 741370 | 3.17 | 363 | 46.56 |
| XYY male | 287355336 | 82.1 | 57.29 | 41 | 1.45 | 666867 | 5.32 | 349 | 46.85 |
| XYY female | 289203274 | 83 | 57.88 | 41 | 1.45 | 637476 | 4.97 | 357 | 47.41 |
| roth male | 156949772 | 69.4 | 14.85 | 40 | 1.54 | 325501 | 4.12 | 271 | 38.78 |
| roth female | 160974028 | 69 | 16.29 | 40 | 1.54 | 332486 | 4.02 | 273 | 38.8 |

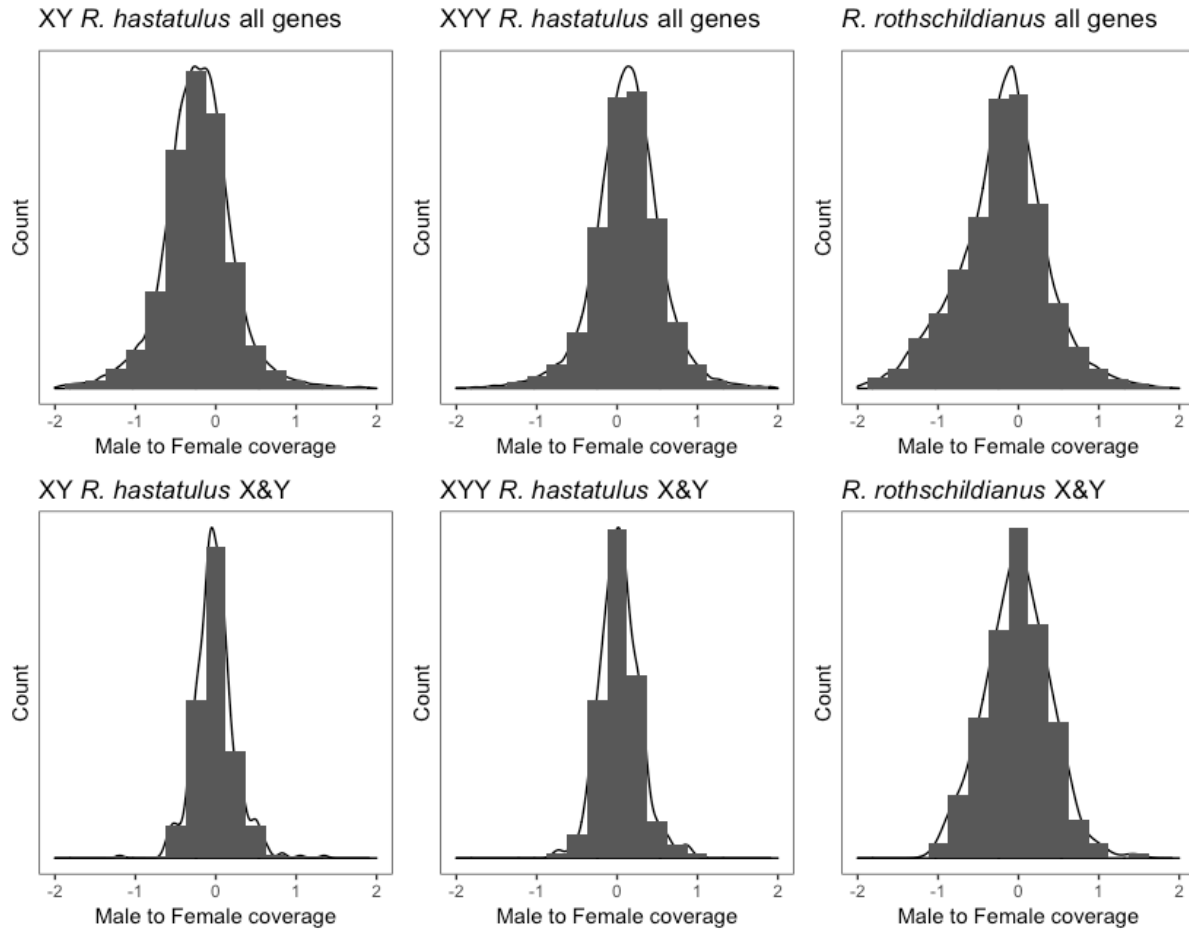
Supplementary Table 2. Counts of silenced and deleted genes and percentage of silenced genes for the XY and XYY karyotypes of *Rumex hastatulus* given filtering with a range of MapQ cutoff scores.

| MapQ cutoff | XY karyotype | | | XYY karyotype | | |
|-------------|--------------|---------|------------|---------------|---------|------------|
| | Silenced | Deleted | % Silenced | Silenced | Deleted | % Silenced |
| 10 | 49 | 55 | 47 | 51 | 66 | 44 |
| 30 | 49 | 55 | 47 | 48 | 69 | 41 |
| 50 | 48 | 56 | 46 | 48 | 69 | 41 |

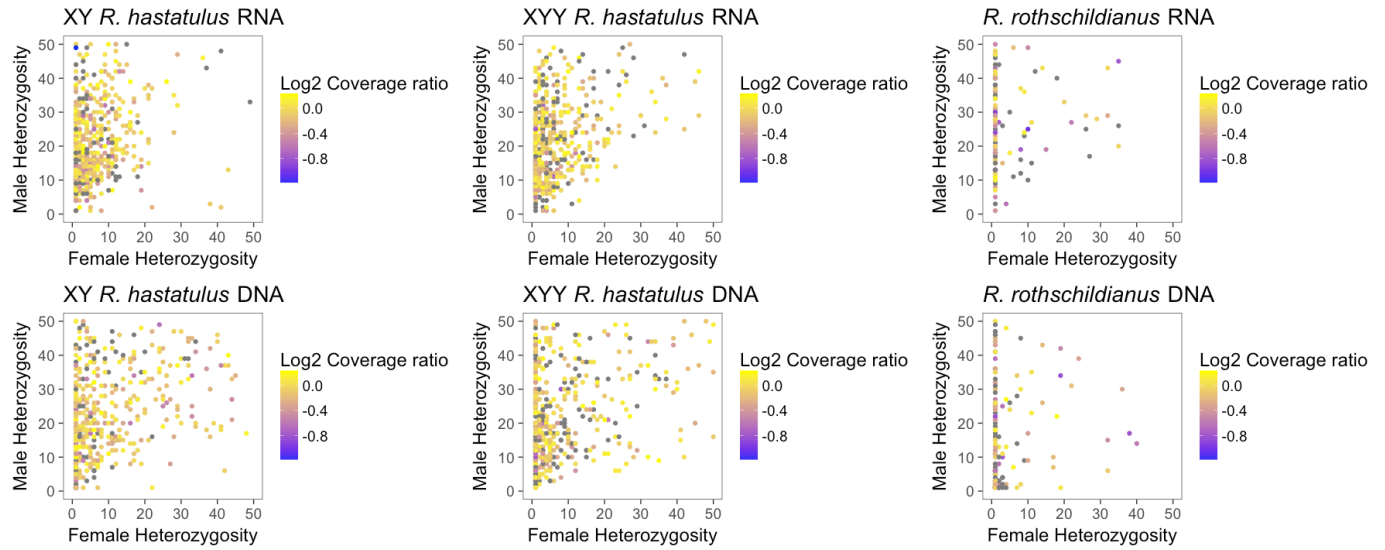
SUPPLEMENTARY FIGURES



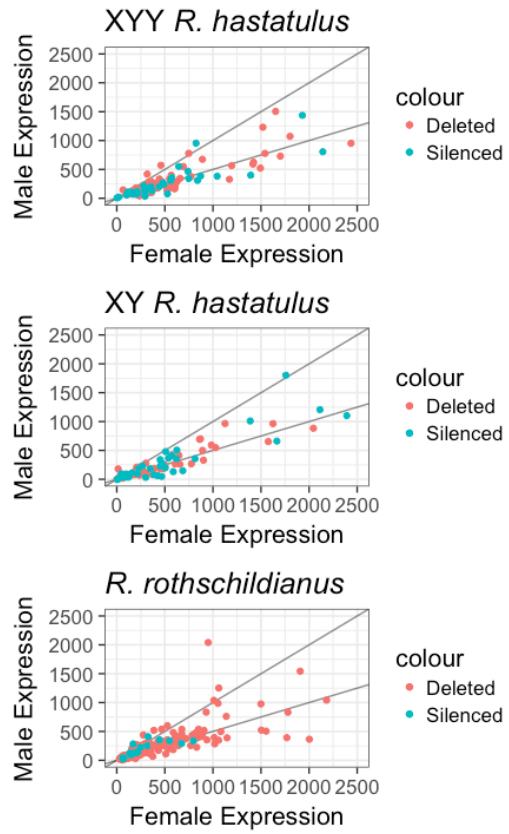
Supplementary figure 1. Principle component analysis (PCA) of read and mapping quality metrics of *R. hastatus* XY and XYY and *R. rothschildianus* genomic sequences to assess batch effects. Included metrics are read count, % of reads mapped, median coverage, GC content, Transition/Transversion ratio, SNP count, heterozygous/homozygous SNP ratio, insert size mean, and mean mapping quality (MapQ score).



Supplementary figure 2. Distribution of \log_2 of the male to female genomic coverage ratio across genes for *Rumex hastatulus* XY karyotype, for *R. hastatulus* XYY karyotype, and for *R. rothschildianus* for all, and for X&Y genes. Sex linkage was determined using SNP segregation patterns. Bars represent histograms, while curves in read ratio plots represent kernel density estimates.



Supplementary figure 3. Number of heterozygous SNPs in males vs. females for X&Y genes the XY and XYY karyotypes of *R. hastatulus* and for *Rumex rothschildianus* in RNA reads and in DNA reads. Shapes are coloured according to their values of \log_2 of male to female genomic coverage ratio: more yellow is unbiased genomic coverage and blue is female biased.



Supplementary figure 4. Male to female gene expression for deleted (red) and silenced (blue) genes in the *Rumex hastatulus* XYY and XY karyotypes and for *R. rothschildianus*.