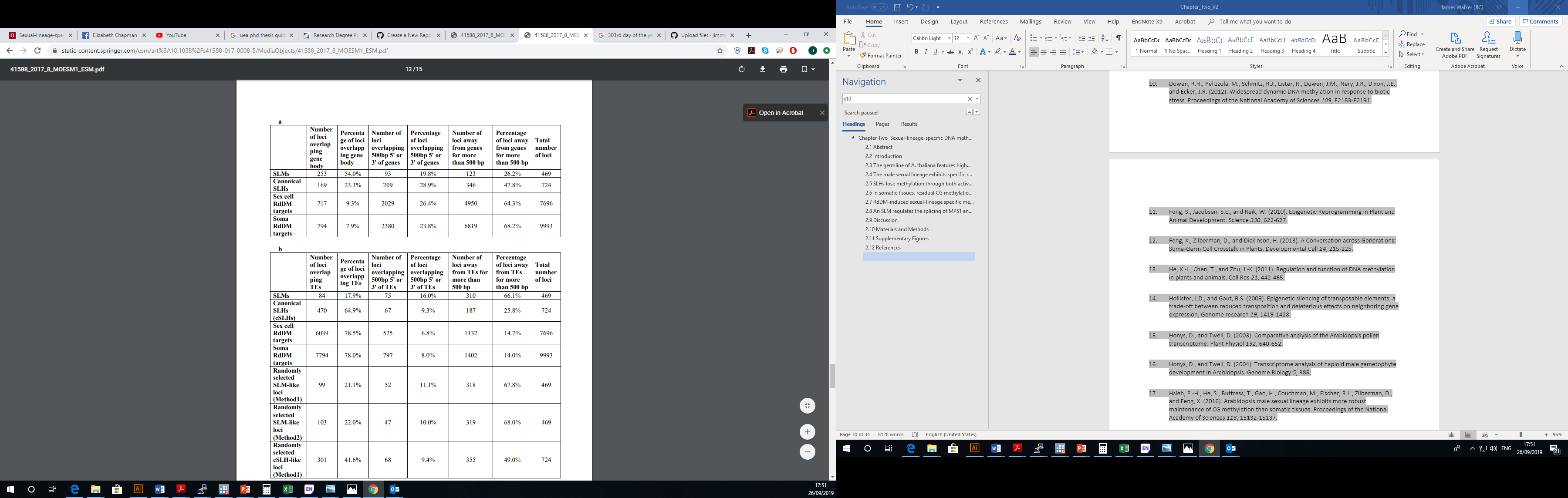
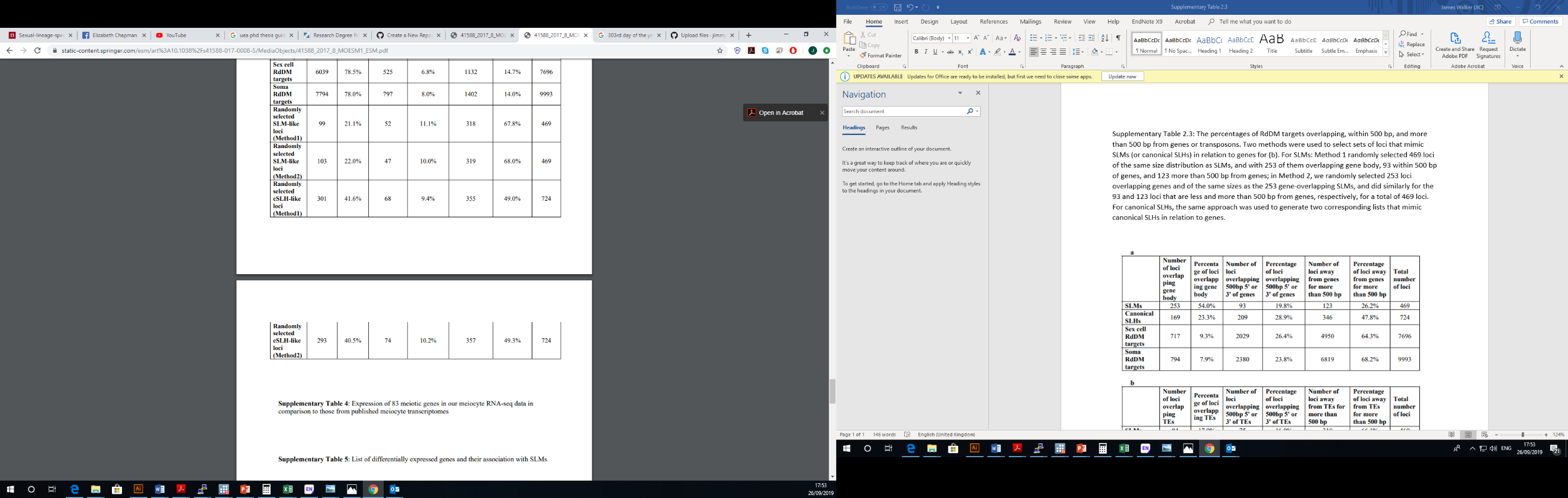
Supplementary Table 2.1: Sequencing summary statistics for bisulfite sequencing libraries. Mean DNA methylation (Met) was calculated by averaging methylation of individual cytosines in each context, and chloroplast CHH methylation was used as a measure of cytosine nonconversion and other errors.

Supplementary Table 2.3: The percentages of RdDM targets overlapping, within 500 bp, and more than 500 bp from genes or transposons. Two methods were used to select sets of loci that mimic SLMs (or canonical SLHs) in relation to genes for (b). For SLMs: Method 1 randomly selected 469 loci of the same size distribution as SLMs, and with 253 of them overlapping gene body, 93 within 500 bp of genes, and 123 more than 500 bp from genes; in Method 2, we randomly selected 253 loci overlapping genes and of the same sizes as the 253 gene-overlapping SLMs, and did similarly for the 93 and 123 loci that are less and more than 500 bp from genes, respectively, for a total of 469 loci. For canonical SLHs, the same approach was used to generate two corresponding lists that mimic canonical SLHs in relation to genes.



A screenshot of a computer

Description automatically generatedSupplementary Table 2.6: pre-tRNA genes hypermethylated by RdDM in the sexual lineage. Tables list the anticodons of the 24 pre-tRNA genes overlapping SLMs (a) and a complete list of 84 pre-tRNA genes methylated in the sexual lineage by RdDM (b).

A computer screen shot of a computer screen

Description automatically generatedSupplementary Table 2.7. Primers used in this study.