**Methylomes**

Whole genome bisulfite sequencing from *F. vesca* Hawaii-4 (NCBI SRA: SRR3286267) [1] was mapped to the v2 and v4 genomes and methylated sites called using previously described methods [1, 2]. Custom python scripts were used to plot DNA methylation across chromosomes and gene bodies ( available at: <https://github.com/chadn737/Fvesca-v4-genome-paper>) . Briefly, for chromosome plots, the weighted methylation level [3] was calculated for 100 Kbs sliding windows with a 50 Kbs step size. For gene metaplots, the gene body and 2000 bps upstream and downstream were each divided into 20 windows and methylation data mapped to the windows. For the gene bodies, only methylation within coding sequences was used as methylation of transposons located in UTR and intronic sequences can inflate methylation levels. These were then plotted in R using ggplot2.

1. Niederhuth CE, Bewick AJ, Ji L, Alabady MS, Kim KD, Li Q, et al. Widespread natural variation of DNA methylation within angiosperms. Genome biology. 2016;17(1):194. doi: 10.1186/s13059-016-1059-0. PubMed PMID: 27671052.

2. Schultz MD, He Y, Whitaker JW, Hariharan M, Mukamel EA, Leung D, et al. Human body epigenome maps reveal noncanonical DNA methylation variation. Nature. 2015. doi: 10.1038/nature14465.

3. Schultz MD, Schmitz RJ, Ecker JR. 'Leveling' the playing field for analyses of single-base resolution DNA methylomes. Trends in genetics : TIG. 2012;28(12):583-5. Epub 2012/11/08. doi: 10.1016/j.tig.2012.10.012. PubMed PMID: 23131467; PubMed Central PMCID: PMC3523709.