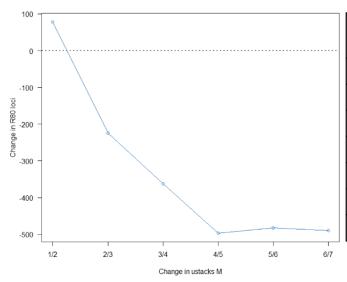**Appendix 1.** We used the R80 method to make a *de novo* assembly in our ddRAD-sequencing data without using genome reference information (Paris et al., 2017). To optimize the parameters M and n which define the *de novo* assembly of loci for *Stacks*, R80 method was used. When we set the values M and n = 2, we can find the 'Change in R80 loci' approaches zero. Then, if more than 3 values after the value is below zero keep below zero this indicates M/n = 2 is the optimal value for *de novo* assembly in our dataset (Rivera-Colón and Catchen, 2022). The plot and the value of 'Change in R80 loci' were presented below.

M/n	Number of R80 Loci	Change in R80 Loci
1	42,504	-
2	42,583	79
3	42,395	-224
4	41,997	-362
5	41,500	-497
6	41,018	-482
7	40,528	-490