

Figure S1

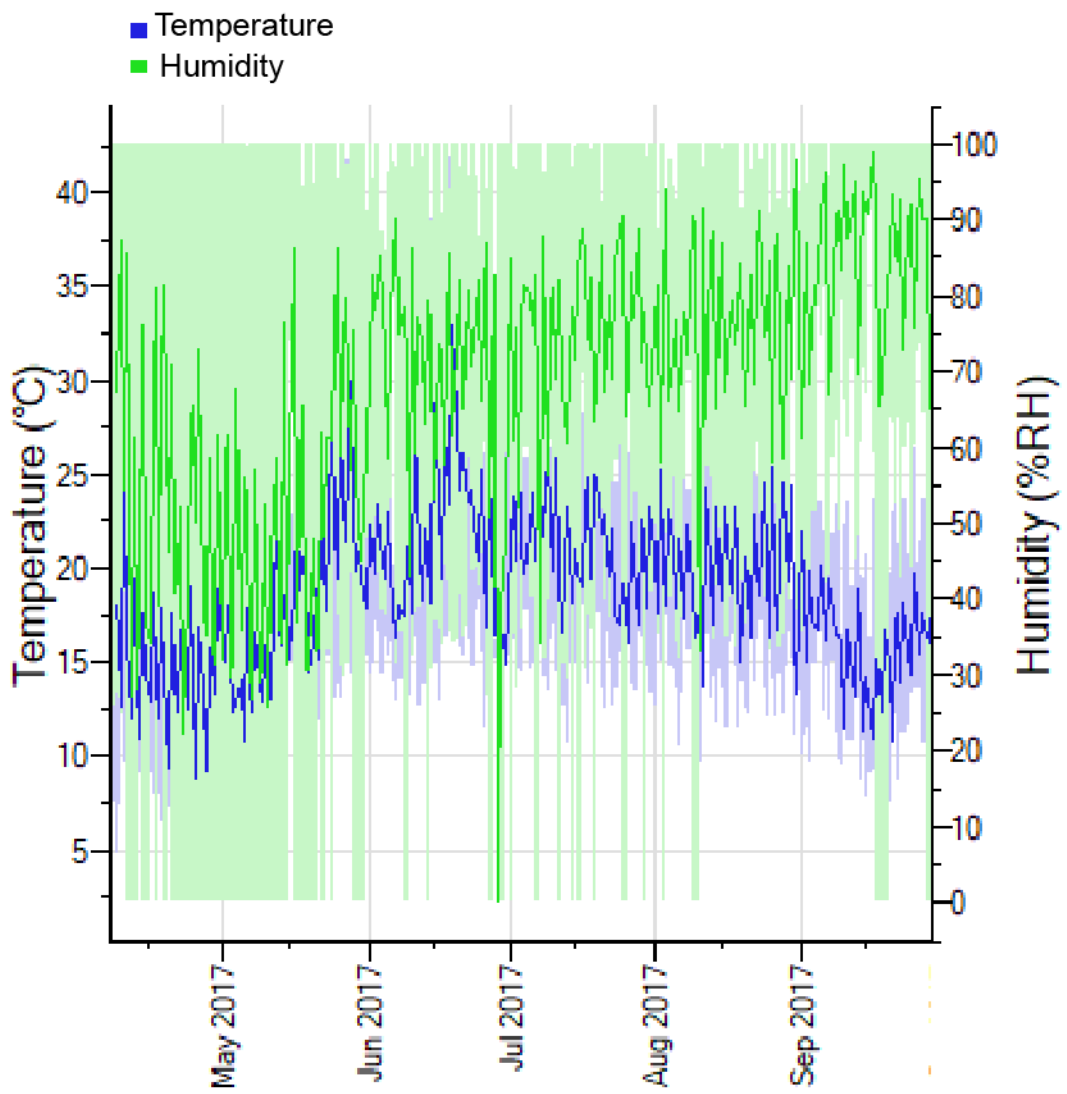


Figure S2

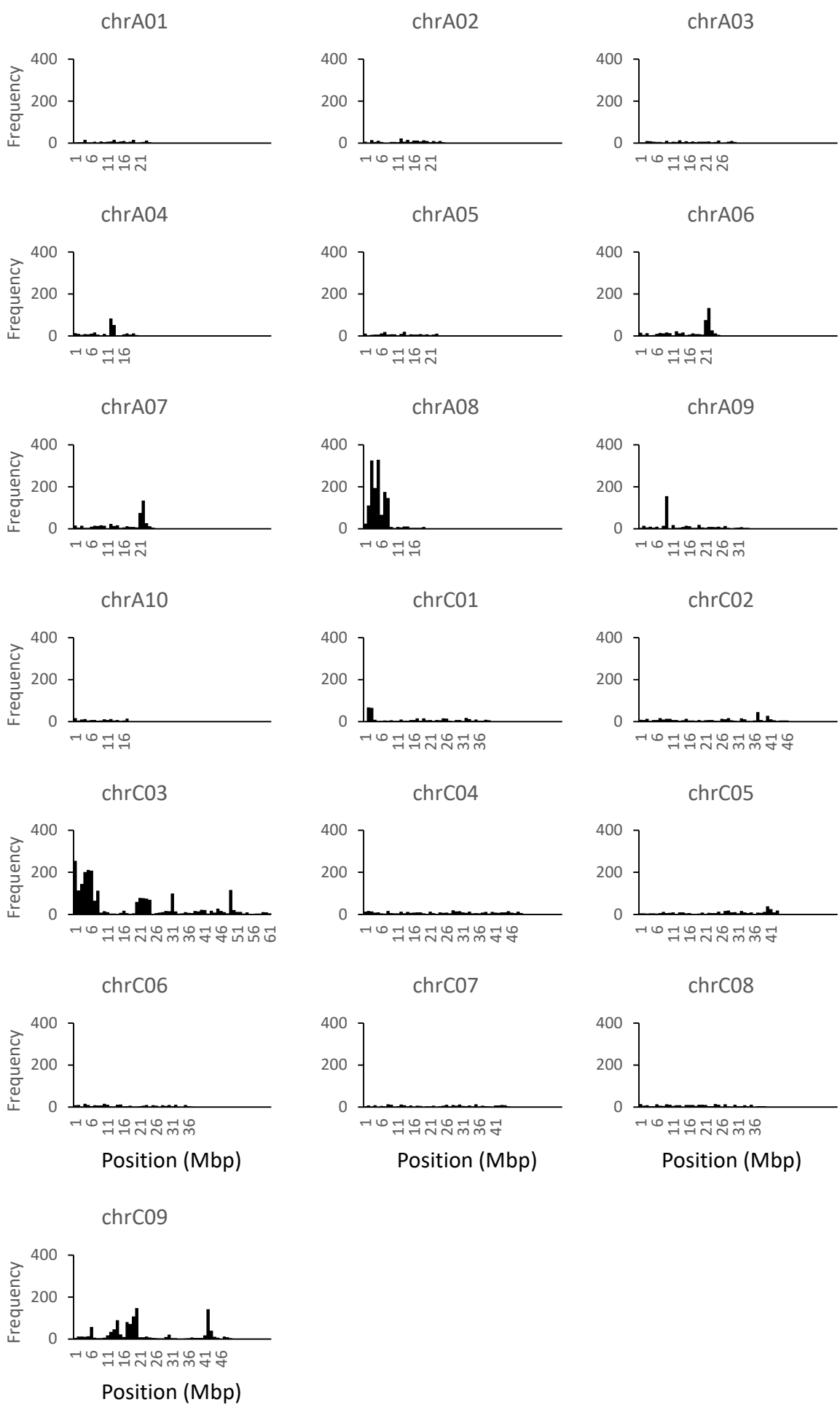


Figure S3

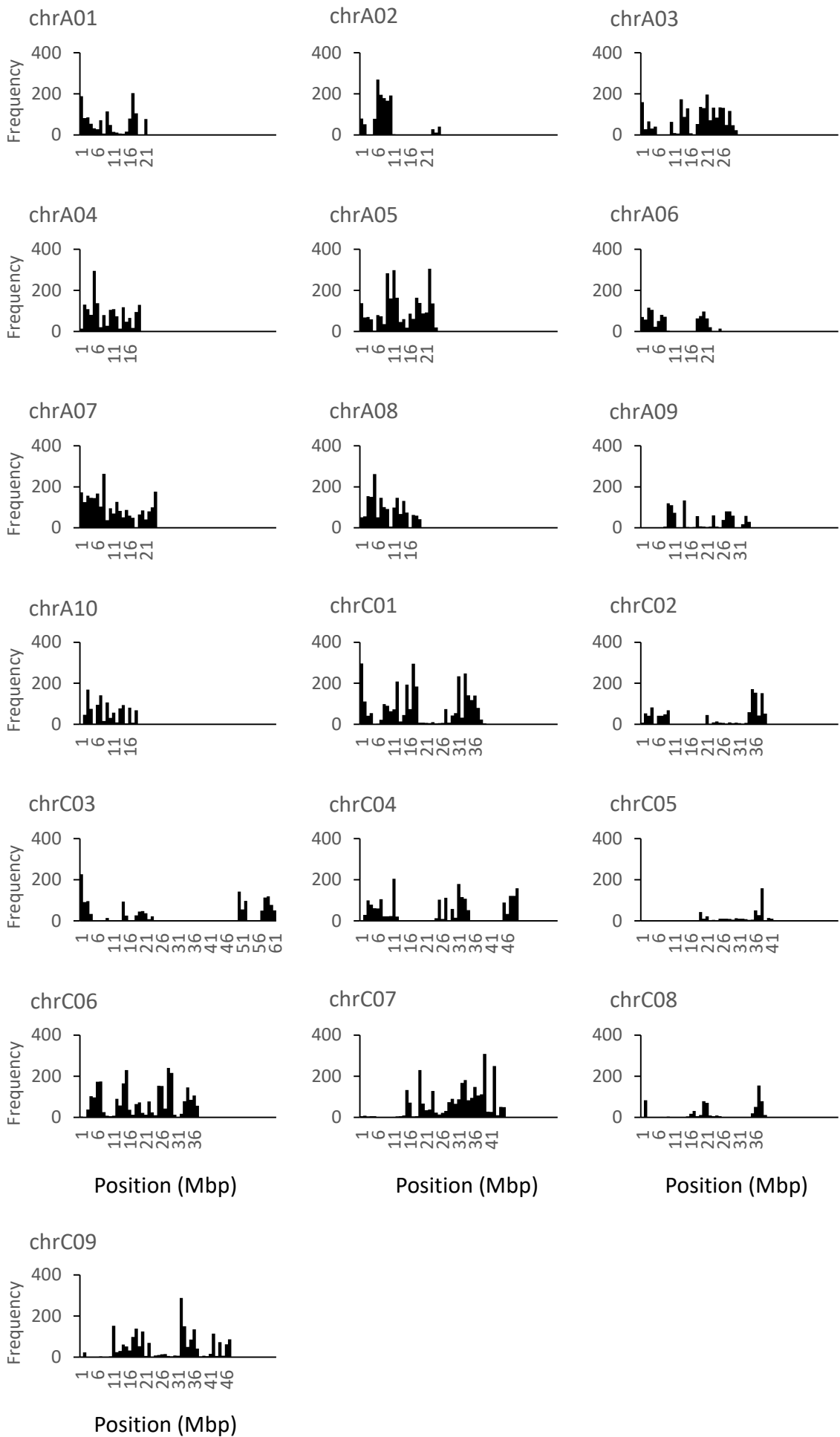


Figure S4

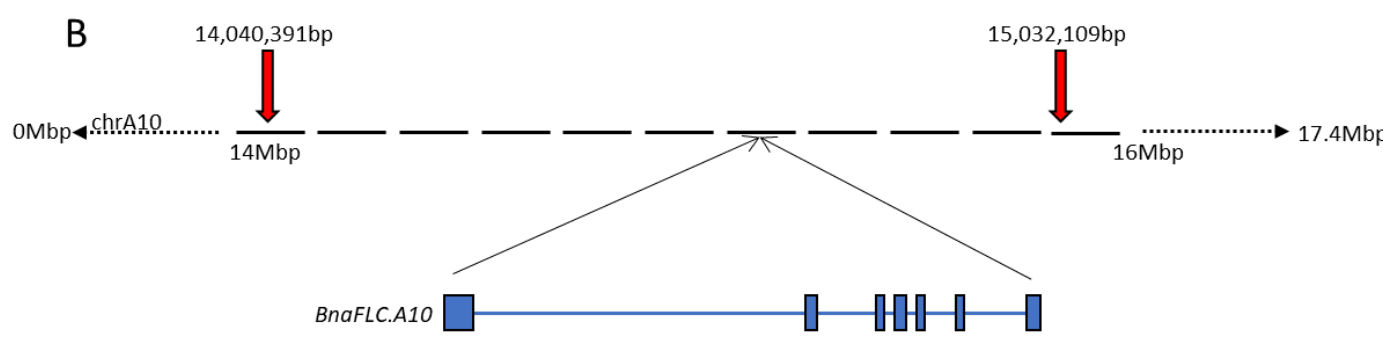
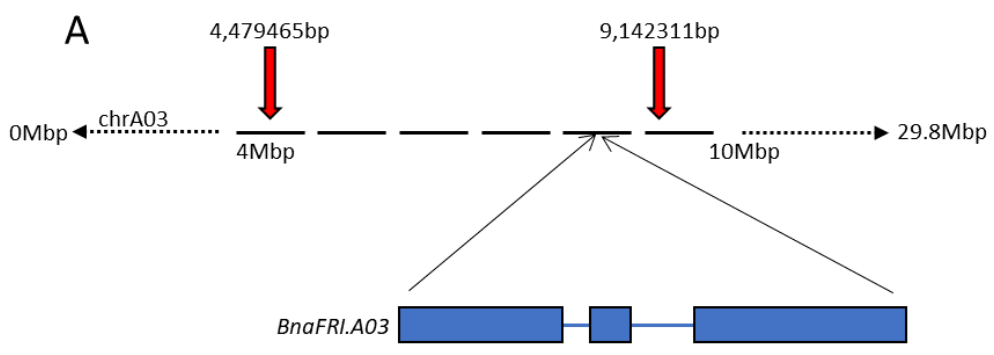


Figure S5

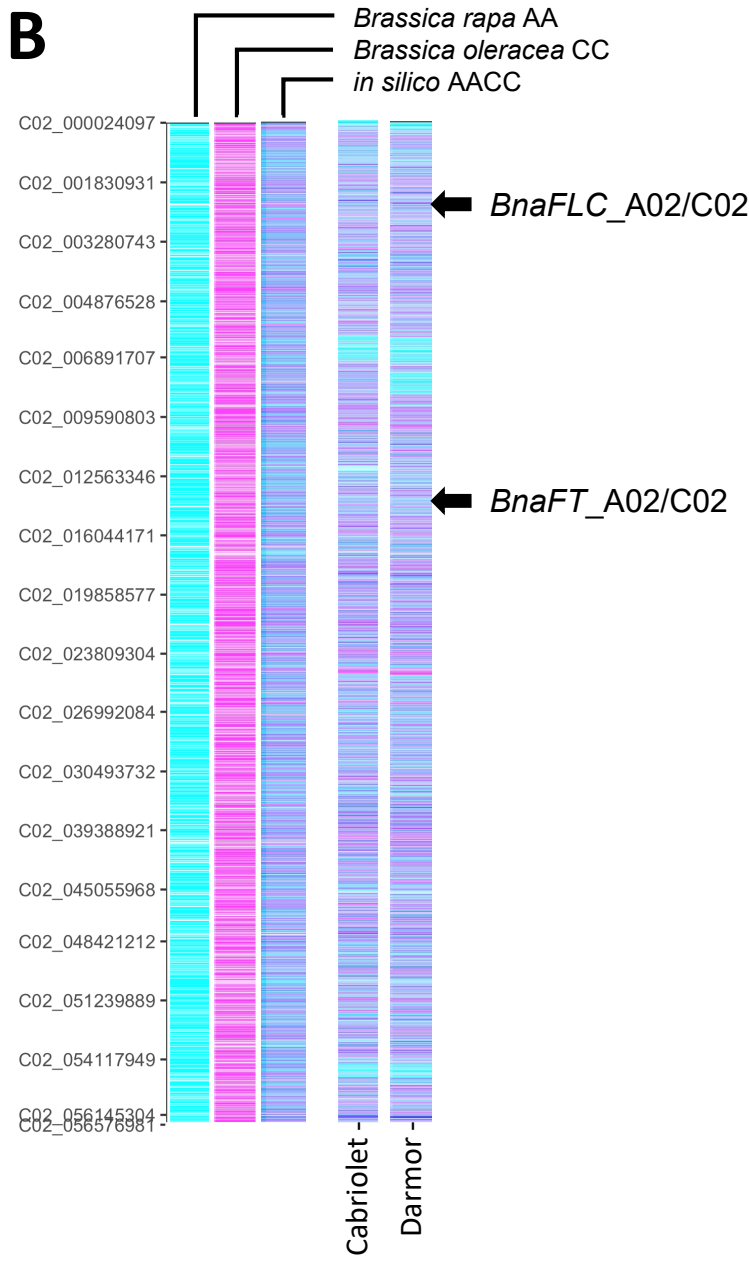
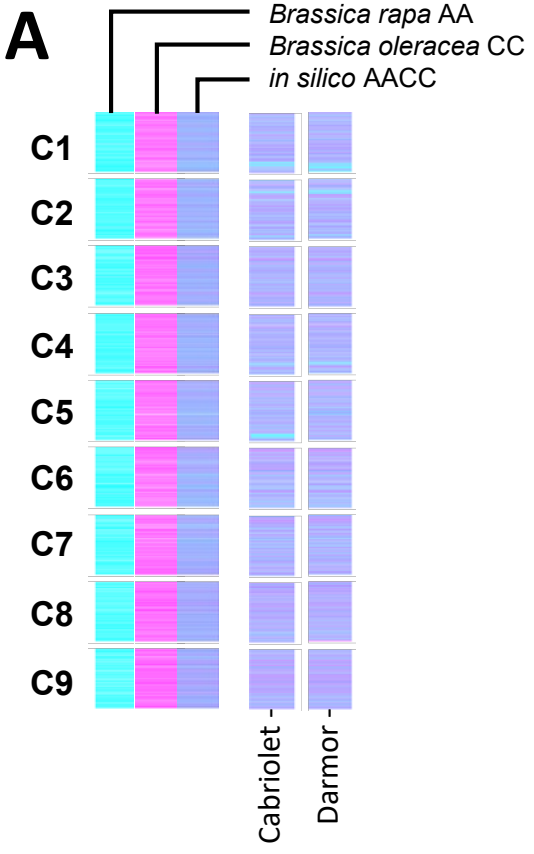
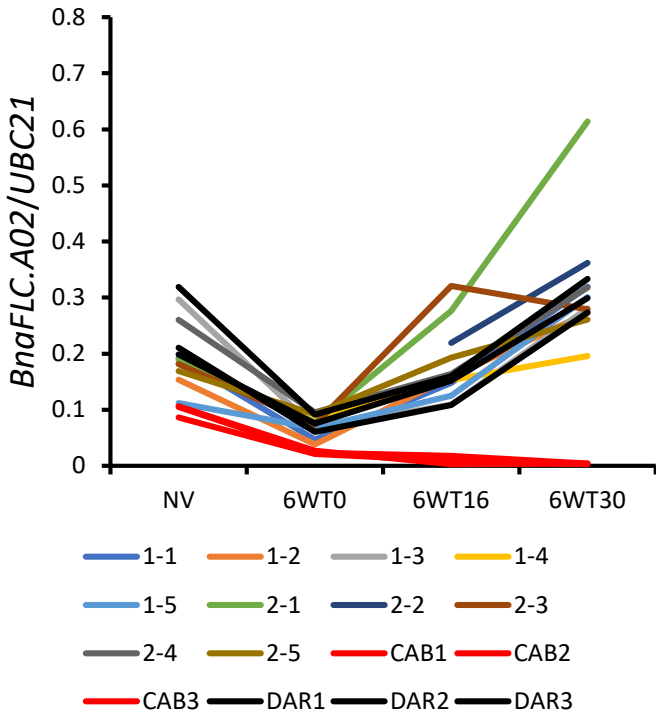


Figure S6

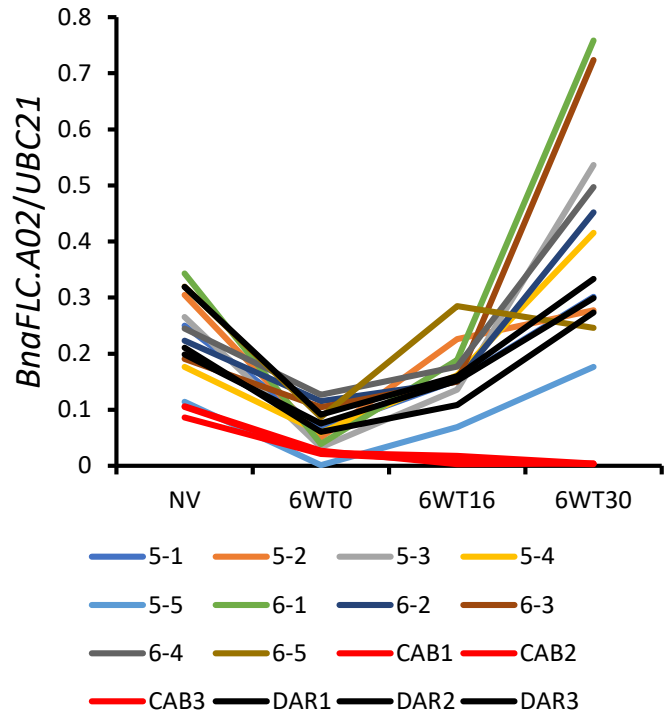
A

BnaFLC.A02-Dar/BnaFT.A02-Dar



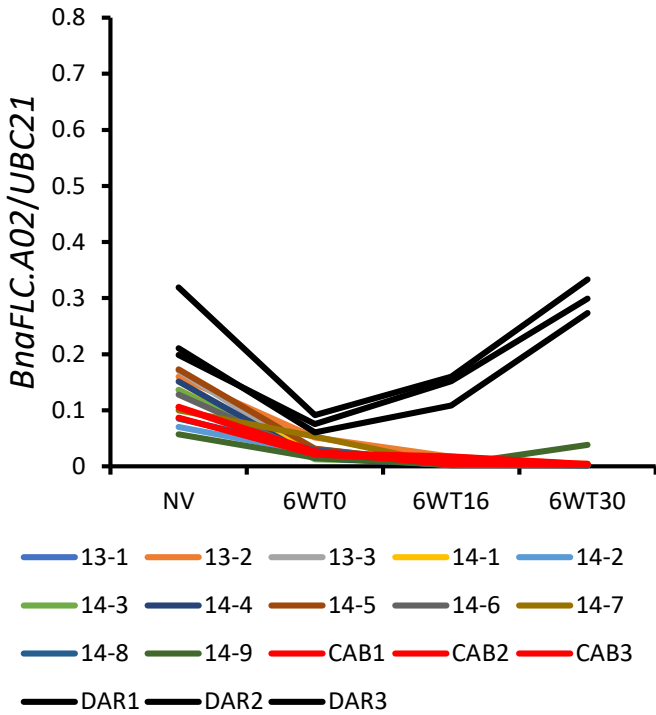
B

BnaFLC.A02-Dar/BnaFT.A02-Cab



C

BnaFLC.A02-Cab/BnaFT.A02-Dar



D

BnaFLC.A02-Cab/BnaFT.A02-Cab

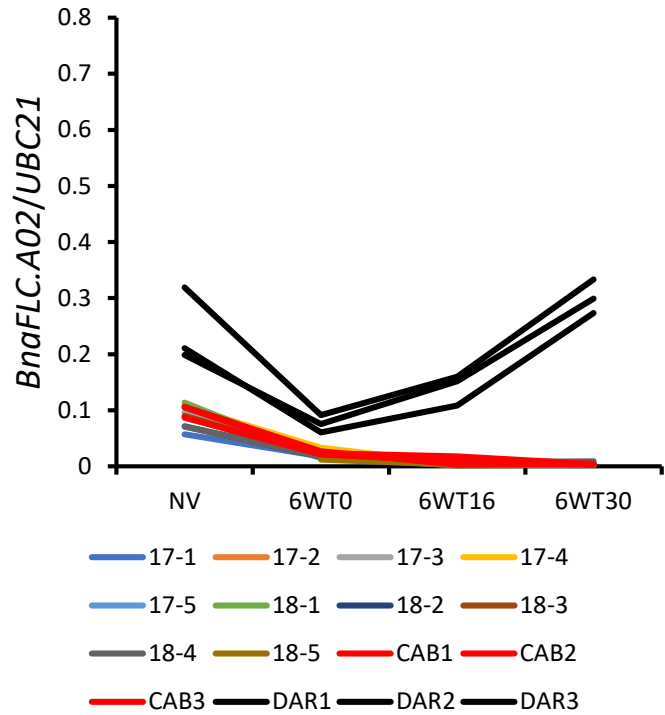
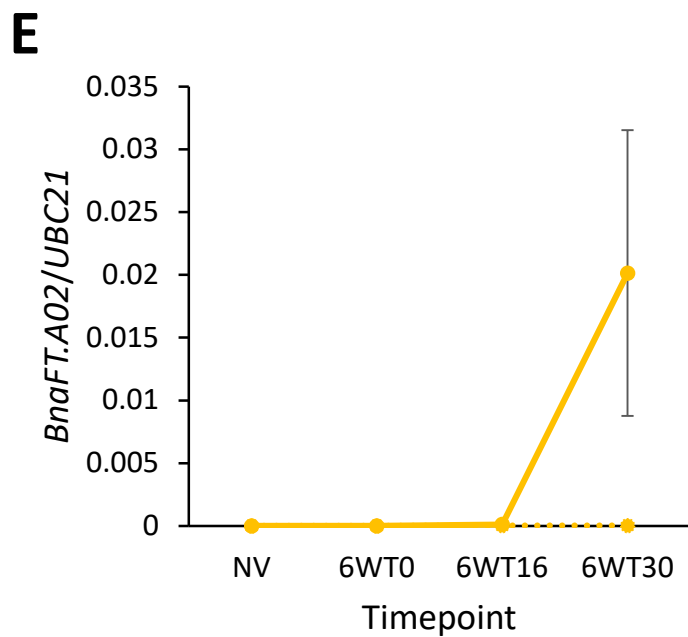
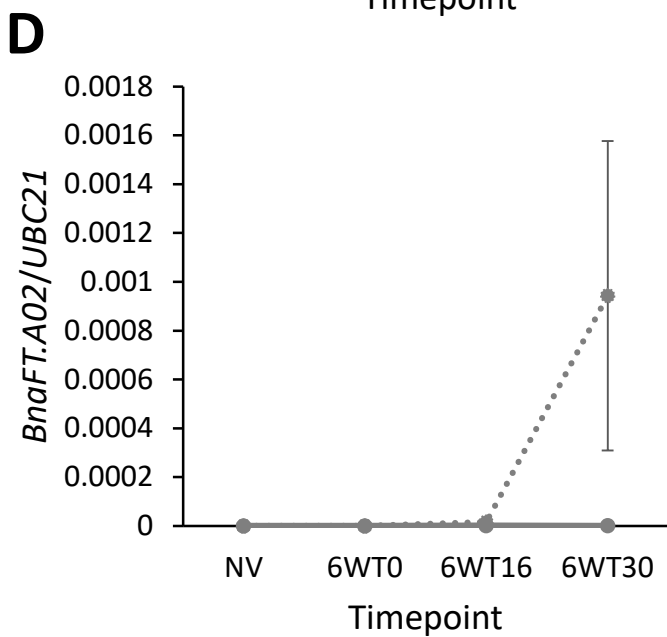
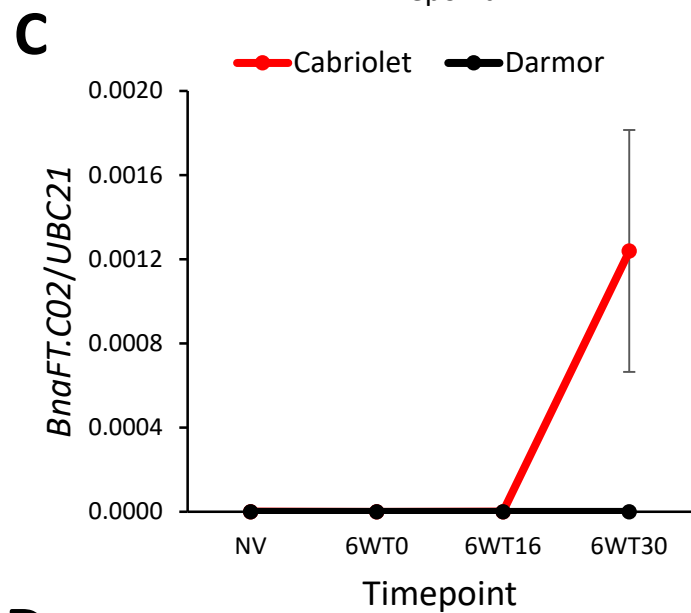
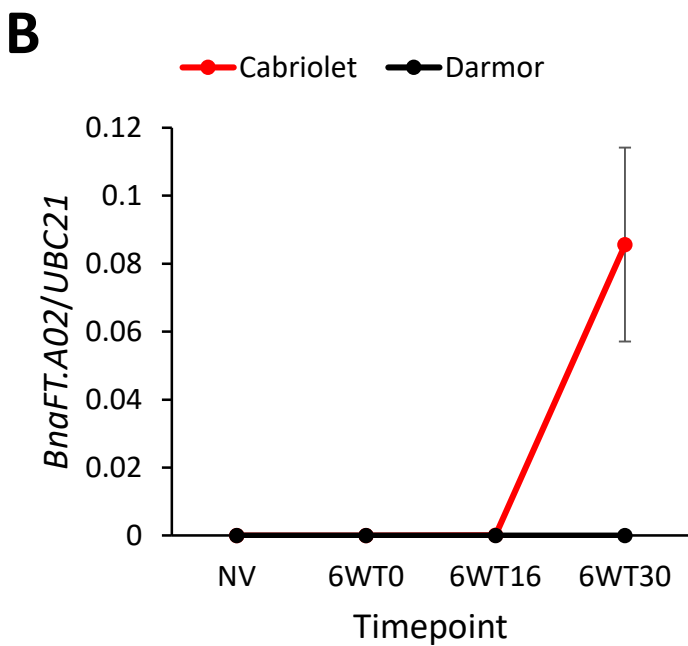
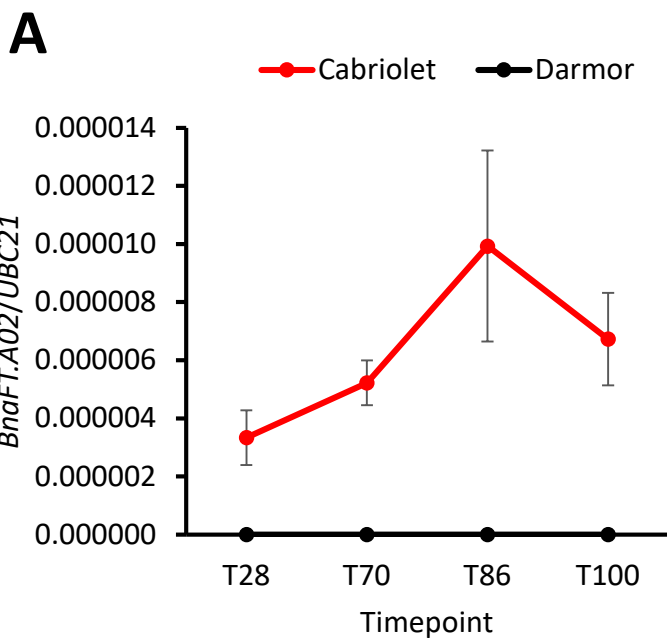


Figure S7



—●— $BnaFLC.A02-Dar:BnaFT.A02-Dar$

····●···· $BnaFLC.A02-Cab:BnaFT.A02-Dar$

····●···· $BnaFLC.A02-Dar:BnaFT.A02-Cab$

—●— $BnaFLC.A02-Cab:BnaFT.A02-Cab$

Figure S8

Percentage of genomic positions with adequate sequence read depth coverage

