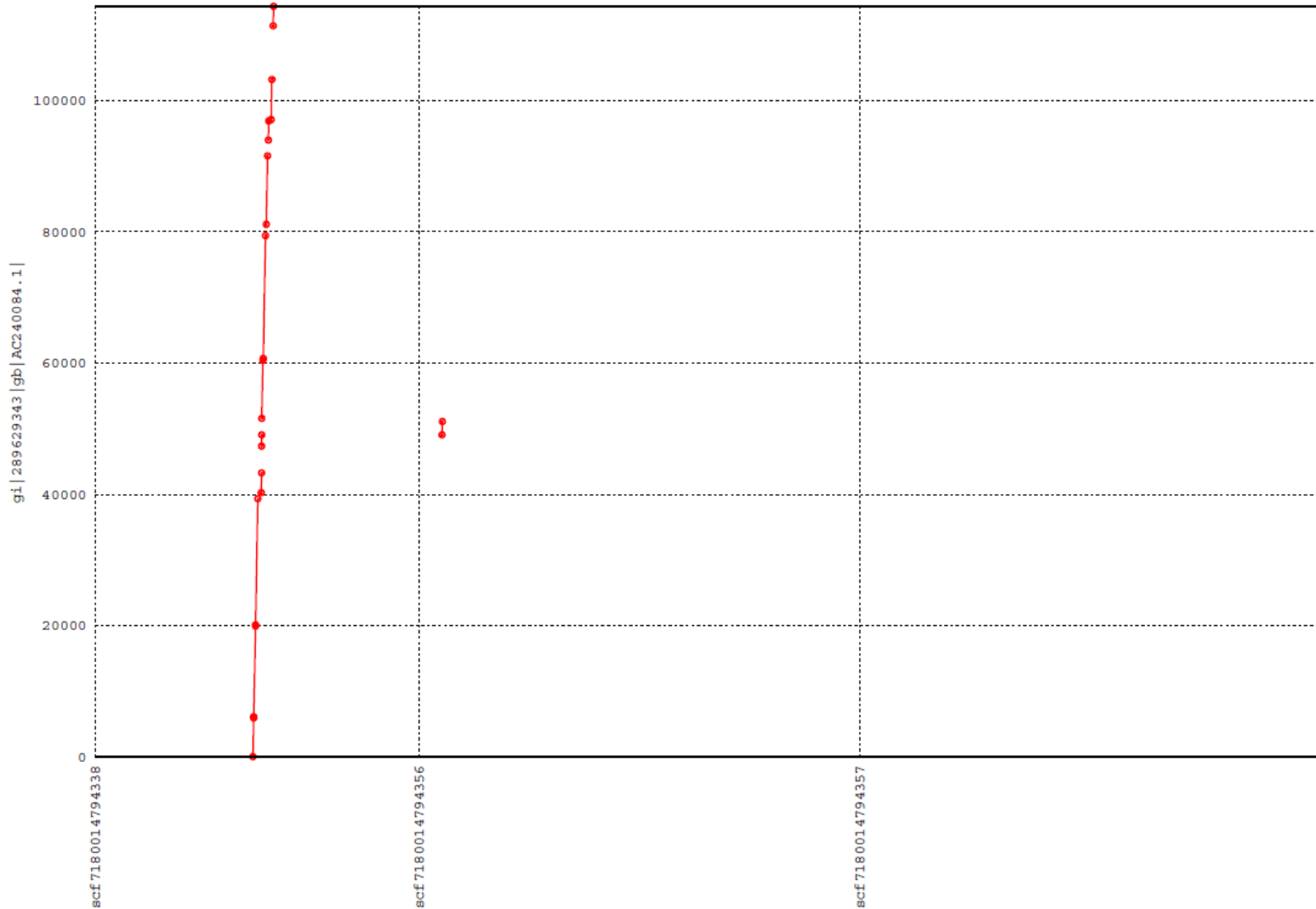


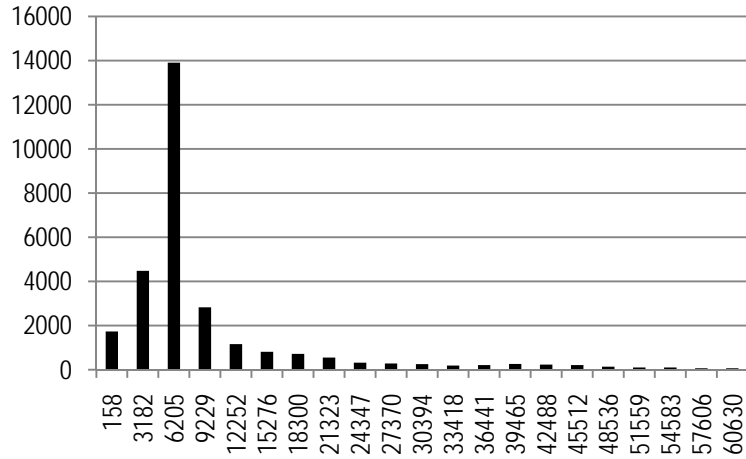
# C genome sequencing

# Examples of *B. oleracea* TO1000 version 3 assembly alignment with

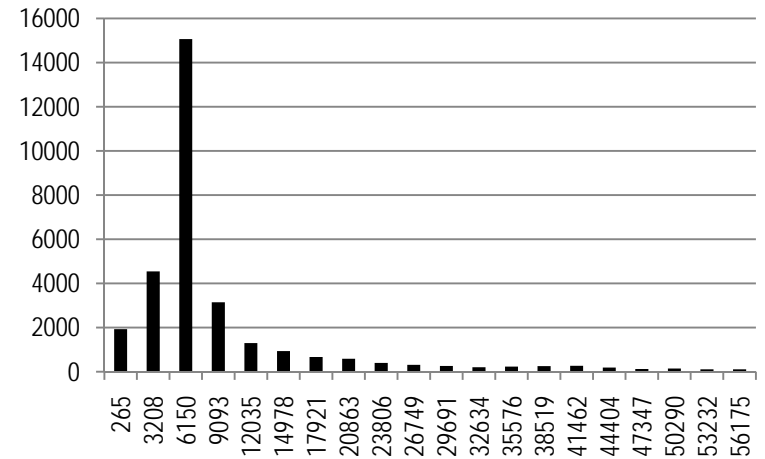


# 454 / Roche mate libraries – 8kb

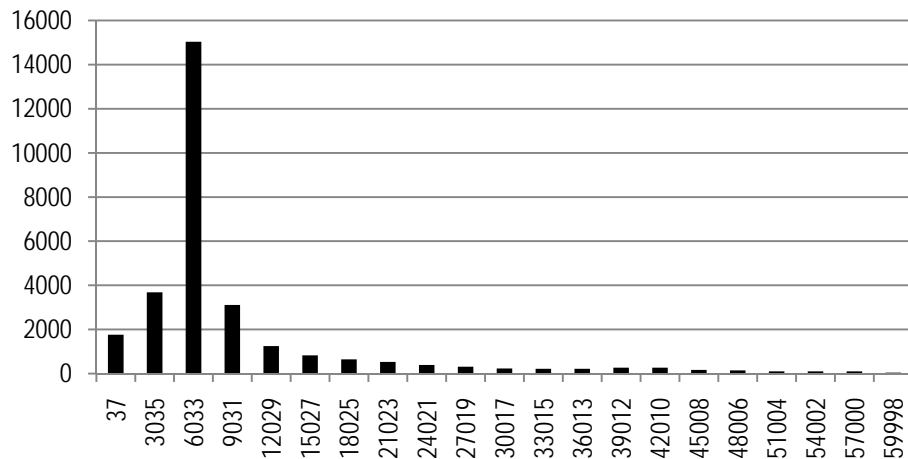
## APZ\_AOTA\_GG3RUF002 - 8kb



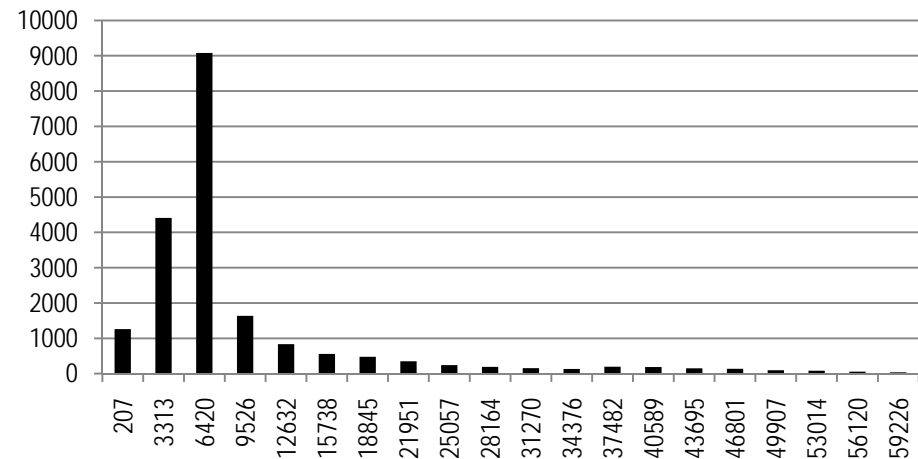
## APZ\_AOTA\_GILAAW301 - 8kb



## APZ\_AOTA\_GILAAW302 - 8kb

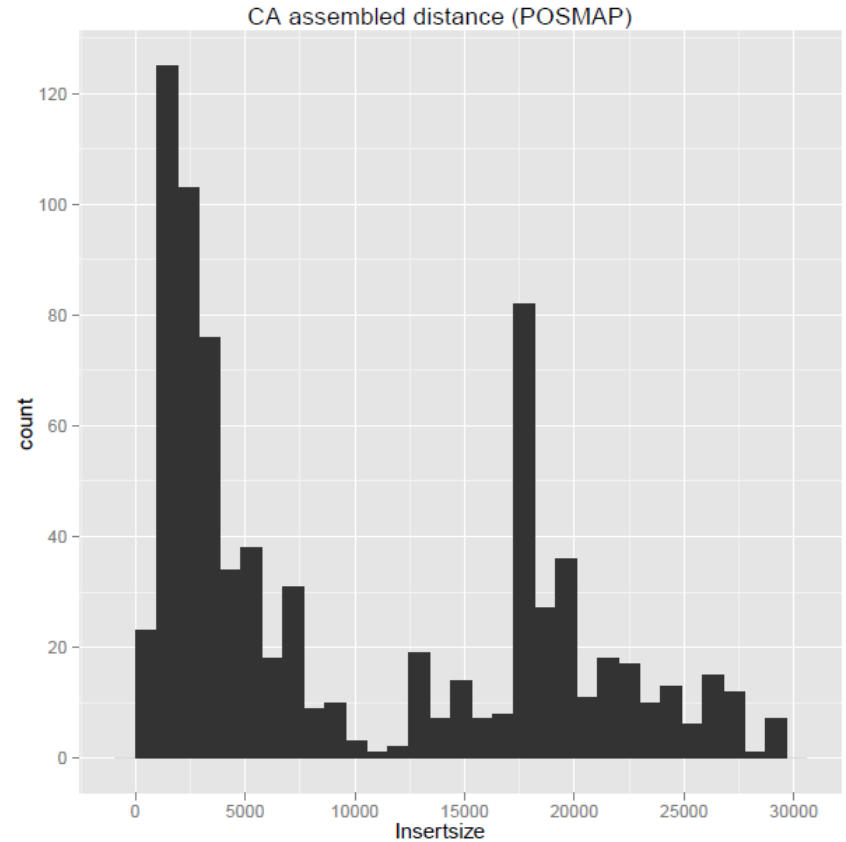
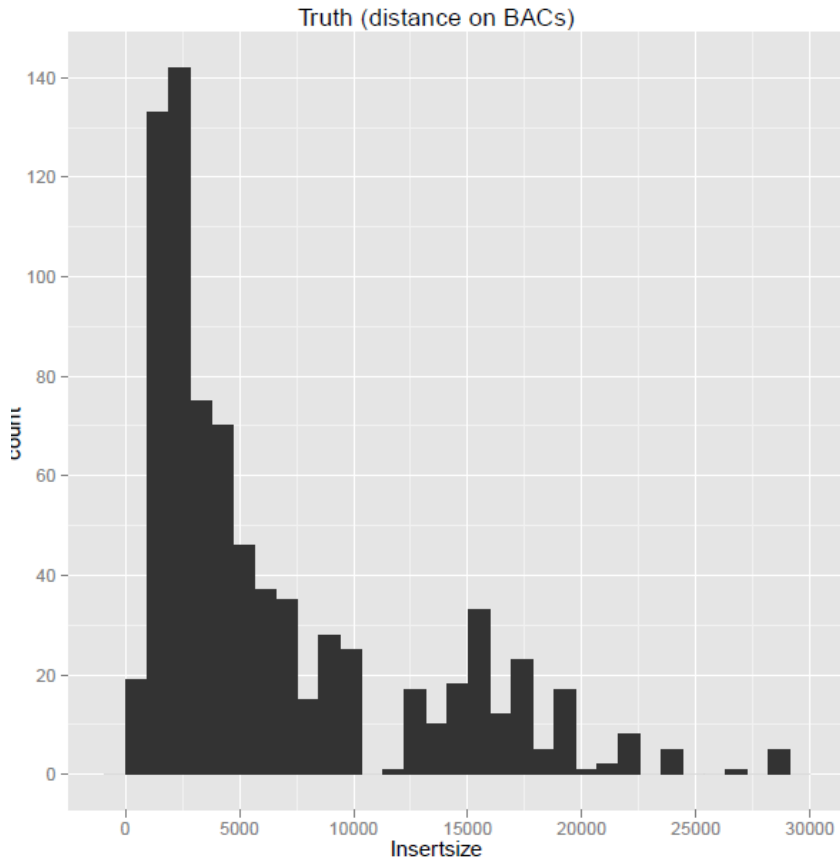


## F7QNI9P01 - 8kb



# Shifting peaks

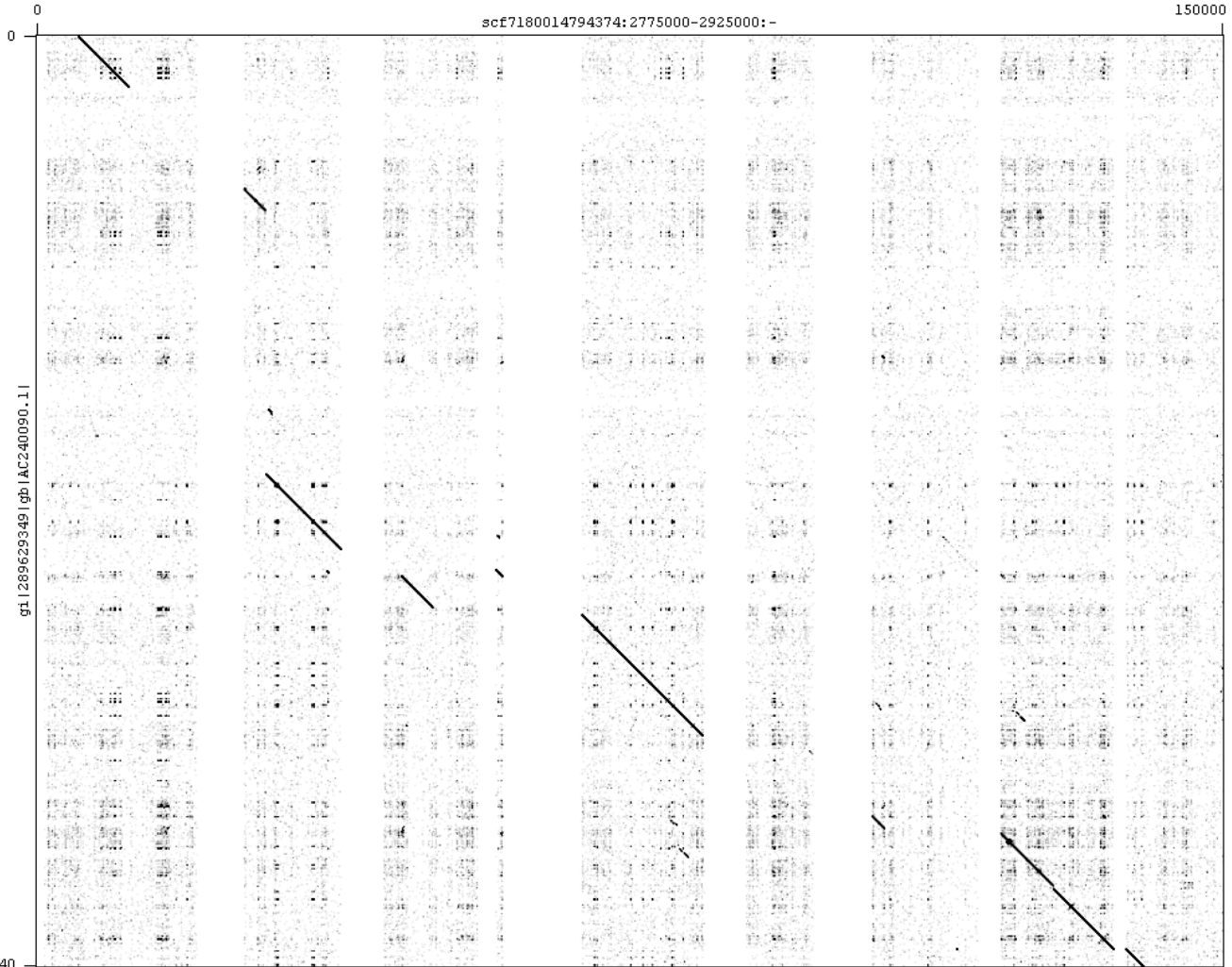
20kb peak got boosted



- For the same mate pair sets, CA creates an “artificial peak” around 20Kb

# Sequences displaced

scf7180014794374:2775000-2925000:- vs. gi|289629349|gb|AC240090.1|  
Zoom: 157 : 1  
Word length: 10 GC ratio seq1: 0.2431  
Window size: 0 GC ratio seq2: 0.3570  
Matrix: DNA Program: Gepard (1.30)



Missing sequences on other scaffolds (interleaving)

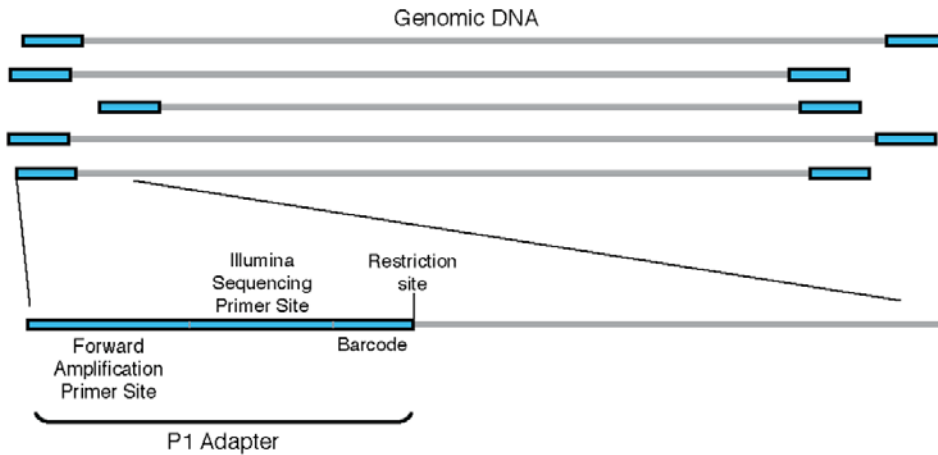
# Summary of SNPs mapped in AGDH and TBDH *B. oleracea* maps

| LG           | AGDH       | Joint      | TBDH       |
|--------------|------------|------------|------------|
| C1           | 19         | 15         | 43         |
| C2           | 23         | 15         | 46         |
| C3           | 37         | 32         | 84         |
| C4           | 25         | 19         | 51         |
| C5           | 33         | 28         | 58         |
| C6           | 28         | 18         | 30         |
| C7           | 27         | 24         | 51         |
| C8           | 32         | 25         | 56         |
| C9           | 38         | 27         | 56         |
| <b>Total</b> | <b>262</b> | <b>203</b> | <b>475</b> |

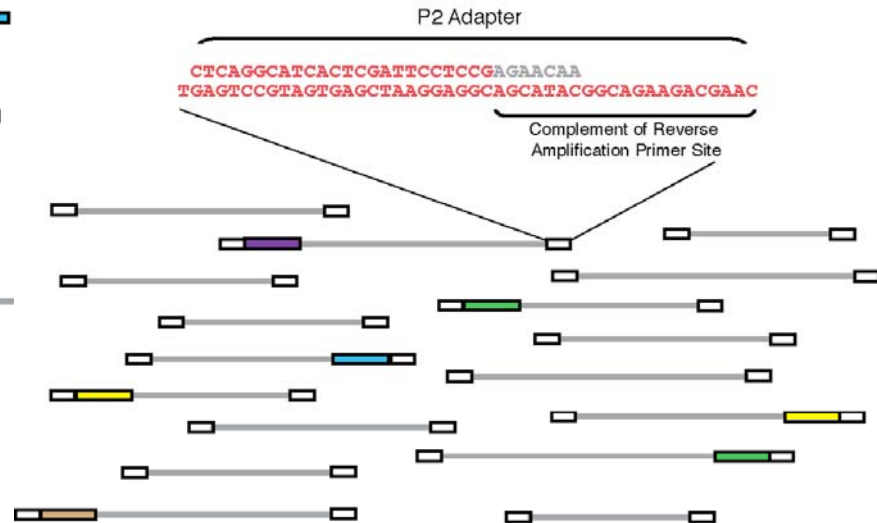
A further 1536 SNP have now been designed and are awaiting genotyping

# Rad-Tag sequencing

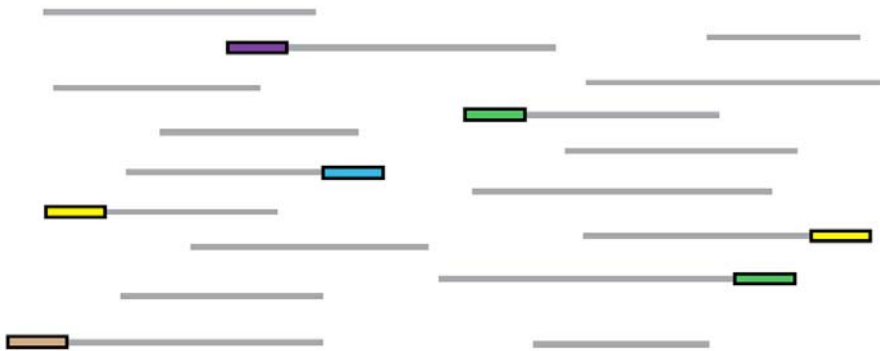
## A *Ligate P1 Adapter to digested genomic DNA*



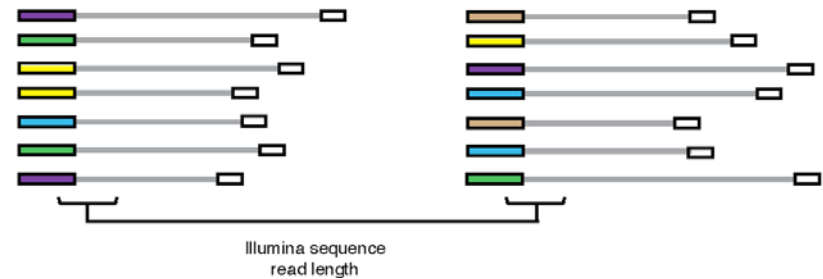
## C *Ligate P2 Adapter to sheared fragments*



## B *Pool barcoded samples and shear*



## D *Selectively amplify RAD tags*



Step C is important as ligation of this adaptor (**P2, white boxes**) prevents amplification of genomic fragments lacking a P1 adapter.

(Reproduced from Baird et al., PLoS One 2008)

# An example from *Brassica oleracea*

|              | <b>Num sites<br/>in<br/>reference</b> | <b>TO1000DH</b> | <b>EarlyBig</b> | <b>Shared<br/>(S)</b> | <b>Num<br/>Contigs<br/>covered<br/>by S</b> | <b>%Conti<br/>gs<br/>covere<br/>d by S</b> | <b>%bases<br/>in<br/>reference</b> |
|--------------|---------------------------------------|-----------------|-----------------|-----------------------|---|--|------------------------------------|
| <b>EcoRI</b> | 83,167                                | 78,489          | 57,513          | 56,632                | 32,616                                      | 37%  | 59%                                |





Hydroponic culture of *B.oleracea*  
DFFS lines for transcriptome  
analysis of roots and leaves

