Fastq files:

RNA-seq from scion or rootstock

1 23R

2 23S

3 31R

4 31S

5 C3309Root-25-2009

6 C3309Root-35-2009

7 CabSavBuds-2535-2008

8 CabSavLeaf-25-2009

9 CabSavLeaf-2535-2008

10 CabSavLeaf-35-2009

11 P1

12 P10

13 P11

14 P12

15 P13

16 P14

17 P15

18 P16

19 P17

20 P18

21 P2

22 P3

23 P4

24 P7

25 P8

26 P9

C: driver has no grape grafting fastq files

My passport (G:) has no grape grafting fastq files

Penguin backup (E:) has no grape grafting fastq files

WD white I:\data files\GraftingDataSets\GenomicLibrary

I:\data files\GraftingDataSets\InVitroRNASeq

I:\data files\GraftingDataSets\RNAseq

E:\data backup\Riesling (fq files, boyce backup)

Melon, wwz, boyce has no fastq files

(penguin)

10194013\_428KRAAXX\_s\_4\_sequence[1].txt.gz 10194013\_428KRAAXX\_s\_6\_sequence[1].txt.gz

DNA-seq fastq files

(penguin server) Zhong\_genome:

1380-P15\_R1.fastq.gz 1380-P15\_R2.fastq.gz 2228-P16\_R1.fastq.gz 2228-P16\_R2.fastq.gz

From Dr. Fei

|  |  |
| --- | --- |
| P1 | 1380-2week scion |
| P3 | 1380-4week scion |
| P8 | 2228-2week rootstock |
| P10 | 2228-4week rootstock |
| P2 | 1380-2week rootstock |
| P4 | 1380-4week rootstock |
| P7 | 2228-2week scion |
| P9 | 2228-4week scion |

1. Remove loci with exactly same genotype between 1380 and 2228, or either is heterozygous, or either is not covered by at least 7 reads or the ratio of secondary allele to the first allele greater than 0.1 (keep those loci that are homozygous in both genotype and show polymorphism).
2. Remove loci at which P1 (RNA) bases are same as the 1380 genome bases, or P1 is “N”, or P1 bases do not contain the base of 2228. For example:

chr pos base DNA-1380 DNA-2228 P1

chr1 573681 A A(13) C(10) A(38)G(1)

We don’t know where the “G” comes from, so this locus is removed.

1. A locus is transmitted if 1) supported by at least two reads; or 2) supported by at least a flanking SNP coming from the same read; or 3) supported by at least another SNP from the same gene (see picture below).

