Illumina 9K, 90K conversion to VCF

**Converting Illumina AB into VCF**

Illumina data loaded into T3 database as Ref = A\_allele, Alt = B\_allele  
The Illumina 90K data can be combined with similar array data and analyzed with website tools but can not be used in PHG, Beagle, or merged with GBS data because the format is not aligned (strand and orientation) with reference genome

1. use samtools faidx with the IWGSC\_WGA\_v1.0 assembly to get Ref allele

2. compare Ref allele to A\_allele and B\_allele

|  |  |  |
| --- | --- | --- |
| match | Ref and Alt changes | genotypes changes |
| Ref = A\_allele | unchanged | unchanged |
| Ref = B\_allele | Ref = B\_allele, Alt = A\_allele | compliment |
| Ref = comp(A\_allele) | Ref = comp(A\_allele)  Alt = comp(B\_allele) | unchanged |
| Ref = comp(B\_allele) | Ref = comp(B\_allele)  Alt = comp(A\_allele) | compliment |

Compliment genotypes

|  |  |
| --- | --- |
| original | converted |
| 0/0 | 1/1 |
| 0/1 | 1/0 |
| 1/1 | 0/0 |
| ./. | ./. |

https://www.illumina.com/documents/products/technotes/technote\_topbot.pdf