**Look for homeoSNP in VCF**

*Script name:* look\_for\_homeosnp.pl

What it does: This script takes an input VCF file and two database (parents A and B) and look for homeosnp alleles

*Synopsis:*

***perl look\_for\_homeosnp.pl -i VCF\_FILENAME\_IN -a DB\_A -b DB\_B -m MAF-o OUT\_FILENAME***

*Parameters:*

-i (string): VCF file

-a (string): Database A

-b (string): Database B

-m (float): minor allele frequency

-o (string): output filename

*Output examples*

Output a tab delimited file with alleles counts for each variant position. All the cases are described in the powerpoint “useful\_snp”.

CHR POS REF ALT ITC0127B A\_ALLELES B\_ALLELES CASE

chr11 851742 C T C:9;T:18 C T 1