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1 #!/usr/bin/perl
2 # use strict;
3 #FL1
4 #FL2
5 open(FL0, "$ARGV[0]") || die ;
6 open(FL1, ">$ARGV[1]") || die ;
7 open(FL2, ">$ARGV[2]") || die ;
8
9 # $haplotypeA='';
10 # $haplotypeB='';
11 while (<FL0>){
12 chomp;
13 @arr=split(/\t/, $_);
14 @phase = split (/\/, $arr[3]);
15 # print $phase[0], "\t", $phase[1], "\n";
16 # push (@genotype, $arr[1]);
17 # push (@genotype, $arr[2]);
18 # print $genotype[$phase[0]], "\t", $genotype[$phase[1]], "\n";
19 push (@haplotypeA, $arr[$phase[0]+1]);
20 push (@haplotypeB, $arr[$phase[1]+1]);
21 # $haplotypeA = $genotype[$phase[0]];
22 # $haplotypeB = $genotype[$phase[1]];
23 # print FL1 $haplotypeA;
24 # print FL2 $haplotypeB;
25 }
26 print FL1 @haplotypeA, "\n";
27 print FL2 @haplotypeB, "\n";

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