

```

1. DATA ZIKV;
2. INPUT progeny sire dam orig tvalue trait$;
3. CARDS;
      1      41      4      660000      5.820      SG
      1      41      4      19.8      1.318      Sal
      2      41      4      264000      5.422      SG
      2      41      4      0      0.000      Sal
4. ;
5.      /* Salivary glands pfu;
6.      PROC MIXED data = ZIKVcovtest asycov;
7.      class sire dam;
8.      where TRAIT = "SG";
9.      model tvalue = /solution;
10.     random Sire Dam(Sire);
11.     run;
12.     PROC MIXED data = ZIKVcovtest asycov;
13.     class sire dam;
14.     where TRAIT = "SG";
15.     model tvalue = /solution;
16.     random dam(sire);
17.     run;
18.     PROC MIXED data = ZIKVcovtest asycov;
19.     class sire dam;
20.     where TRAIT = "SG";
21.     model tvalue = /solution;
22.     random sire;
23.     run;
24.     /* Saliva pfu;
25.     PROC MIXED data = ZIKVcovtest asycov;
26.     class sire dam;
27.     where TRAIT = "Sal";
28.     model tvalue = /solution;
29.     random Sire Dam(Sire);
30.     run;
31.     PROC MIXED data = ZIKVcovtest asycov;
32.     class sire dam;
33.     where TRAIT = "Sal";
34.     model tvalue = /solution;
35.     random Dam(Sire);
36.     run;
37.     PROC MIXED data = ZIKVcovtest asycov;
38.     class sire dam;
39.     where TRAIT = "Sal";
40.     model tvalue = /solution;
41.     random Sire;
42.     run;

```

Figure S1. The SAS code for performing REML analyses.