

Appendix 2: post-filtering results/iterations using *populations* output with settings *-p 1 -r 0.5*

| | | Nind rem. | Final SNPs | Genotyping rate | NOTES: |
|---|---|--------------|---------------|--------------------|---|
| <i>Pseudacris</i> 37597 loci 132 ind | Test 1 (geno 0.5 + mind 0.5) | 49 | 5513 | 0.782942 | <i>No mainland retained</i> |
| | Test 2(geno 0.4 +mind 0.5) | 30 | 2693 | 0.804 | <i>Retains SINGLE mainland</i> 1688 SNPs after MAF filter <0.02 |
| | Test 3(geno 0.5 +mind 0.4) | 58 | 5513 | 0.812 | <i>No mainland, few of SRI</i> |
| | Test 4(geno 0.3 +mind 0.5) | 22 | 318 | 0.821 | |
| | Test 5 (geno 0.7 +mind 0.5) | 70 | 37597 | 0.691 | |
| | Test 6 (geno 0.35 +mind 0.5)** | 33 | 855 | 0.817 | <i>**most "conservative" clean matrix</i> 1150 SNPs after MAF filter <0.02 |
| <i>Xantusia</i> 83445 loci 141 ind | Test 1 (geno 0.5 + mind 0.5) | 55 | 12861 | 0.823 | <i>No mainland</i> |
| | Test 2(geno 0.4 +mind 0.5) | 49 | 3145 | 0.815 | <i>** most "conservative" clean matrix, retains 5 mainland</i> 1118 SNPs after MAF filter <0.02 |
| | Test 3(geno 0.5 +mind 0.4) | 59 | 12861 | 0.836 | <i>No mainland</i> |
| | Test 4(geno 0.3 +mind 0.5) | 22 | 324 | 0.796 | <i>MOST mainland retained (16!)</i> |
| | Test 5 (geno 0.7 +mind 0.5) | 70 | 41500 | 0.748 | <i>No mainland, few SBI</i> |
| | Test 6 (geno 0.35 +mind 0.5)** | 39 | 1023 | 0.808 | <i>retains 10 mainland</i> 389 SNPs after MAF filter <0.02 |