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

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