Table S1. Pipeline Stacks Results

| Barcode | Filename | Fastqc | | | Process_radtags | | | Tsv2bam | gstacks | | | |
| | | | | | | | | | effective_coverages_per_sample | | | |
		Total sequence	Sequence length	%GC	Total RAD	Low Quality	Retained Reads	sample loci to catalog loci	n_loci	n_used_fw_reads	mean_cov	mean_cov_ns
GCAATATACATGCAG	cor_1	28.784	117	54	2.878.859	230	2.878.629	233.846	233.579	2.400.847	10.279	11.671
AAGAATTCGGTGCAG	cor_2	18.399	117	59	1.966.710	142	1.966.568	177.946	15.419	98.047	6.359	6.427
TCGGCAGTCGTGCAG	cor_3	15.499	117	50	1.528.291	123	1.528.168	147.894	243.357	1.888.196	7.759	8.312
AGTTCCATTGTGCAG	corsib_1	59.528	117	53	4.426.504	370	4.426.134	391.320	60.923	425.681	6.987	6.838
TTCTTGCGCTTGCAG	corsib_2	8.995	117	51	487.158	50	487.108	58.964	656.060	6.967.417	10.620	13.184
AGCAATCTAATGCAG	corsib_3	20.077	117	48	1.436.769	121	1.436.648	149.444	185.500	1.666.463	8.984	10.116
GAATTGTCGCTGCAG	corsib_4	2.565	117	49	187.174	20	187.154	23.805	836.628	10.159.803	12.144	16.230
CTTCGACATATGCAG	corsib_5	5.086	117	45	379.166	28	379.138	49.265	167.002	1.113.703	6.669	7.153
GAGATATGGTTGCAG	sib_1	60.973	117	52	3.072.204	230	3.071.974	15.467	177.802	1.714.945	9.645	10.186
CTCCTTGGAGTGCAG	sib_2	2.760	117	48	123.302	10	123.292	243.825	147.689	1.288.288	8.723	9.901
GTGTCTCTTGTGCAG	sib_3	33.497	117	52	2.366.944	167	2.366.777	310.503	390.768	3.784.425	9.685	10.188
TGCAGTTATCTGCAG	pal_1	6.821	117	53	531.273	34	531.239	61.028	58.864	395.432	6.718	6.763
TTCTGGAATATGCAG	pal_2	125.833	117	55	10.714.124	877	10.713.247	657.154	149.235	1.152.516	7.723	8.985
ACGCAACACATGCAG	pal_3	19.015	117	51	1.945.096	138	1.944.958	185.713	23.740	146.828	6.185	6.323
ACTGCCTCAATGCAG	pal_4	215.429	117	53	14.414.533	1.057	14.413.476	838.144	49.036	294.042	5.996	6.144
ACATCAATATTGCAG	pal_5	18.690	117	50	1.404.006	106	1.403.900	167.378	310.155	2.649.635	8.543	9.166