APPENDICES

APPENDIX A

Doyle & Doyle CTAB Procedure.

1. Add 2-mercaptoethanol (5µl/tube) to CTAB buffer and preheat at 65^{o}C
2. Add 100mg of grind or cut sample to 2ml tube.
3. Pipette 500µl of preheat CTAB into 2ml tube containing the samples.
4. Add 10µl of proteinase K for each tube
5. Incubate 65^{o}C for 30min, shake
6. Add 500µl chloroform:isoamyl alcohol (24:1). Mix gently, thoroughly for 15min.
7. Spin at 14000xg, 10 min, 4^{o}C
8. Take the top phase into a new tube
9. Pipette 20µl/tube RNase and incubate at 37^{o}C for 30min
10. Add equal volume of isopropanol (-20^{o}C), mix gently to precipitate DNA
11. Place in -20^{o}C for 1-3 hours
12. Spin at 15000xg at 4^{o}C and then discard the isopropanol
13. Pipette 1ml of wash buffer to each tube
14. Spin for 12000xg, 10min at 4oC and throw the supernatant
15. Pipette 1ml of 70% ethanol for each tube
16. Spin for 12000xg, 10min at 4^{o}C and throw the supernatant
17. Dry the pellet at room temperature
18. After it dries, pipette 50µl of dH_20 of TE Buffer (pH 8.0) to dissolve the pellet

APPENDIX B

Table 1 : Characterization of CSF-335 primers according to its annotated protein classes and its functional classification

CODE	PCR_PRODUCT_SIZE	LEFT_PRIMER	RIGHT_PRIMER	MICROSATELLITE	REPEAT_TYPE	UNIT	REPEAT_LENGTH	NR_ID	SWISSPROT_ID	GENE_ID	CCDS_ID
63_UVR_1	300-400	CTGCTTCCATCCAGTCTCTTCTT	TGGGTGCTGGTGGTTCTGTTG	perfect UTR	Trinucleotide	gga	3	gi|[illegible]	CCDS[illegible]	gga-[illegible]	-
63_UVR_2	100-200	ACACCTGGGCACGGGACATTCTG	GGGGATGGGTTTGTTCATGGTTG	perfect UTR	Trinucleotide	aaa	3	gi|[illegible]	CCDS[illegible]	Tax-[illegible]	aaCCCCC_2
63_UVR_3	100-200	CCACGGTTGGTCTGGTTCCTCTT	GCCATCGCCCAACGTCACTCATCA	perfect UTR	Trinucleotide	tca	3	gi|[illegible]	CCDS[illegible]	Tax-[illegible]	ZFAACCCCCCCCC
63_UVR_4	100-200	TCCGGTTTTCCTGGTTCCTCTCC	CCTTCCATTTCCTTCATGGTTCG	perfect UTR	Trinucleotide	tca	3	gi|[illegible]	CCDS[illegible]	spa-[illegible]	ACCCCCCC
63_UVR_5	100-200	TTCCCCCAACTGCTTCTCTCTC	CCCCCCCCCCTCCTTGTTGTTCC	perfect UTR	Trinucleotide	tca	0	gi|[illegible]	CCDS[illegible]	gln-[illegible]	-
63_UVR_6	100-200	CTGTTTTTGCCCCCCCCTCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	gC	0	gi|[illegible]	-	arna-[illegible]	-
63_UVR_7	100-200	CTCACCCCCCCCCCTTGGTCC	GTTTCCCCCTTCCCCCCCCCCCT	perfect UTR	Trinucleotide	agg	0	gi|[illegible]	PCR_CCC	rn-s-hit-NCR_y1g-[illegible]	-
63_UVR_8	100-200	ACTTCTTCCCTTCCCCCCCCCCT	TCCCCCTCCCCCCCCCCCCCCCT	perfect UTR	Trinucleotide	tca	0	gi|[illegible]	CCDS[illegible]	Tax-[illegible]	YCCL1-CCx
63_UVR_9	100-200	CCTCCCTCCCCTCCCTTCCCCT	CCCTCCCCCCCCCTTCCCCCCCC	perfect UTR	Trinucleotide	gga	0	gi|[illegible]	CCDS[illegible]	arna-[illegible]	ZFZFZFZCCCCx
63_UVR_10	100-200	CCCCCCCCCCCCTCCCCCCCCC	CTCCTCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	tca	0	gi|[illegible]	CCDS[illegible]	Tax-[illegible]	ZFZCCCCCCCCC
63_UVR_11	100-200	CTCCCCCCCCCCCCCCCCCCCC	CCTCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaa	0	gi|[illegible]	CCDS[illegible]	rn-[illegible]	-
63_UVR_12	100-200	CTCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaa	0	gi|[illegible]	PCR_CCC	Gene-Cterm_[illegible]	VCCCCCC
63_UVR_13	100-200	TGGGCCCCTCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	tca	7	gi|[illegible]	CCDS_CCC	[illegible]	CCCCCCC
63_UVR_14	100-200	CTCTCCCTTCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aC	7	gi|[illegible]	CCDS_PCR	Tax-[illegible]	CCCCCCCCCCCCC
63_UVR_15	100-200	TGGTCCTTCCCCCCCCCCCCCCC	CCCTTCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aC	8	gi|[illegible]	PCR_CCC	Gene-Cterm_[illegible]	VCCCCCC
63_UVR_16	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	tgg	3	gi|[illegible]	CCTTCCC	arna-[illegible]	-
63_UVR_17	100-200	TCCCCCCCCCCCCCCCCCCCCCC	CCCTCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	gga	3	gi|[illegible]	PCR_CCC	aag-Cterm_CCCCCCCCCCCCCCC	PCCCCCCCCCCCCCC
63_UVR_18	100-200	GTCCCCCCCCCCCCCCCCCCCC	CTTTCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	tca	9	gi|[illegible]	CCCTTCC	Gene-[illegible]	YCCCCCCCCCCCCCC_2
63_UVR_19	100-200	TCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	tca	9	gi|[illegible]	PCR_CCC	arna-[illegible]	-
63_UVR_20	100-200	CCCCCCCCCCCCCCCCCCCCCCC	TCCTCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaa	10	gi|[illegible]	CCDS_CCC	Gene-Cterm_[illegible]	ZFCCCCCCCCCCCCCCC
63_UVR_21	100-200	TTCCCCCCCCCCCCCCCCCCCCC	TTCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	agg	10	gi|[illegible]	CCDS_CCC	arna-[illegible]	-
63_UVR_22	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aC	10	gi|[illegible]	CCCCCCC	Gene-[illegible]	YCCCCCCCCCCCCCC_2
63_UVR_23	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	tca	10	gi|[illegible]	PCR_CCC	Tax-[illegible]	YCCCCCCCCCCCCCC_2
63_UVR_24	100-200	ACTCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	agca	3	gi|[illegible]	PCR_CCC	aag-Cterm_CCCCCCCCCCCCCCC	ZFCCCCCCCCCCCCCCC
63_UVR_25	100-200	CTCCCCCCCCCCCCCCCCCCCCC	TCCCTCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aag	3	gi|[illegible]	CCDS_CCC	Tax-[illegible]	-
63_UVR_26	100-200	CTTTCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tax	3	gi|[illegible]	CCDS_CCC	Tax-[illegible]	-
63_UVR_27	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CTTTCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	gTg	3	gi|[illegible]	CCCCCCC	Tax-[illegible]	ZFCCCCCCCCCCCCCCC
63_UVR_28	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCTCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaa	3	gi|[illegible]	PCR_CCC	Gene-[illegible]	-
63_UVR_29	100-200	TCCCCCCCCCCCCCCCCCCCCCC	TCCTTCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tax	3	gi|[illegible]	CCDS_CCC	arna-[illegible]	ZFCCCCCCCCCCCCCCC
63_UVR_30	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CT CCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tga	3	gi|[illegible]	CCDS_CCC	Tax-[illegible]	-
63_UVR_31	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	TCg	3	gi|[illegible]	CCDS_CCC	Tax-[illegible]	YCCCCCCCCCCCCCC_2
63_UVR_32	100-200	CCCCCCCCCCCCCCCCCCCCCCC	TTCCTCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaa	3	gi|[illegible]	PCR_CCC	Tax-[illegible]	-
63_UVR_33	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aCa	3	gi|[illegible]	CCTCCCT	aag-[illegible]	ZFCCCCCCCCCCC
63_UVR_34	100-200	TCCCCCCCCCCCCCCCCCCCCCT	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	agca	3	gi|[illegible]	CCCCCCC	Tax-[illegible]	-
63_UVR_35	100-200	TGTCTCTCCCCCCCCCCCCCCCC	TCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aCa	3	gi|[illegible]	CCCCCCC	Tax-[illegible]	-
63_UVR_36	100-200	CCCCTCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	gCg	0	gi|[illegible]	CCDS_CCC	aag-[illegible]	ZFCCCCCCCCCCC
63_UVR_37	100-200	CTTCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	gaC	0	gi|[illegible]	CCDS_CCC	arna-[illegible]	-
63_UVR_38	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aTg	0	gi|[illegible]	PCR_CCC	Tax-[illegible]	-
63_UVR_39	100-200	TCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tax	0	gi|[illegible]	CCDS_CCC	Tax-[illegible]	YCCCCCCCCCCCCCC
63_UVR_40	100-200	TCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tax	0	gi|[illegible]	CCTCCCC	Gene-Cterm_[illegible]	YCCCCCCCCCCCCCC
63_UVR_41	100-200	TCCTCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tax	0	gi|[illegible]	CCCCCCC	Gene-Cterm_[illegible]	aCCCCCCC_2
63_UVR_42	100-200	CCCCTCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	Tgg	0	gi|[illegible]	CCCCCCC	aag-Cterm_CCCCCCCCCCCCCCC	-
63_UVR_43	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	agC	0	gi|[illegible]	CCCCCCC	Tgc-[illegible]	ZFCCCCCCCCCCCCCCC
63_UVR_44	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aCC	0	gi|[illegible]	CCCCCCC	Gene-[illegible]	-
63_UVR_45	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaa	0	gi|[illegible]	CCCCCCC	Gene-Cterm_[illegible]	-
63_UVR_46	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aC	7	gi|[illegible]	CCCCCCC	-	-
63_UVR_47	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CT CCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aCC	7	gi|[illegible]	CCDV_CC	aag-Cterm_CP_CCCCCCC	VCCCCC
63_UVR_48	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	Tax	7	gi|[illegible]	CCCCCCC	gCa-[illegible]	YCCCCCCCCCCCCCC
63_UVR_49	100-200	TGGGCTCCTCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaC	7	gi|[illegible]	CCCP_CCC	Tax-[illegible]	ZFCCCCCCCCCCCCCC
63_UVR_50	100-200	CCCCTCCCCCCCCCCCCCCCCCC	TTCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaa	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_51	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	perfect UTR	Trinucleotide	aaa	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_52	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaa	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_53	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_54	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_55	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_56	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_57	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_58	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_59	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC
63_UVR_60	100-200	CCCCCCCCCCCCCCCCCCCCCCC	CCCCCCCCCCCCCCCCCCCCCCC	predicted CCDS	Trinucleotide	aaC	7	gi|[illegible]	CCCCCCC	[illegible]	CCCCCCCCCCCCCCC

code	
	gi record
	chromosome
	cds/transcription
	linkage map
	mapping
	peptide
	Cross
	chromosome [illegible] from Kegg

APPENDIX C

Table 2: Genotypic scoring for all individuals based on seven microsatellites loci

npops = 4														
nloci = 7														
	estmr5		estmr8		estmr13		estmr14		estmr37		estmr41		estmr51	
pop = Sg Timun														
b1	169	177	192	200	153	159	163	165	156	156	182	191	142	151
b2	169	177	202	202	159	161	163	165	156	156	191	194	151	151
b3	169	177	192	200	151	159	165	167	156	156	176	191	151	151
b4	177	179	202	202	159	159	163	165	156	156	191	194	151	151
b5	177	177	202	202	159	161	165	167	156	156	191	191	142	151
b6	169	177	202	202	159	159	163	169	150	159	191	191	151	151
b7	169	177	192	202	159	159	163	165	156	159	191	194	148	151
b8	169	177	202	202	159	159	165	165	156	156	191	191	142	151
b9	177	177	202	202	159	159	163	169	156	156	191	191	151	151
b10	161	177	202	202	147	159	165	167	156	156	179	191	151	151
j1	177	177	202	202	151	159	163	169	156	156	191	194	136	136
j2	165	177	202	202	159	159	163	165	156	156	191	191	151	151
j3	169	177	192	202	161	161	163	165	156	156	191	194	142	151
j4	169	177	192	202	159	159	163	165	156	156	182	191	151	151
j5	169	177	192	200	159	161	165	165	150	156	191	194	151	154
j6	169	177	202	202	159	159	163	165	156	156	191	191	151	151
j7	177	177	202	202	159	159	163	163	150	156	191	194	151	151
j8	177	177	202	202	159	159	163	165	147	159	182	191	142	151
j9	169	177	202	202	159	159	157	165	156	156	191	194	151	151
j10	177	177	202	202	159	159	163	163	156	159	191	194	151	151
j11	177	177	202	202	159	159	163	165	156	156	182	191	142	151
j12	177	179	202	202	159	161	163	165	156	159	191	191	151	151
j13	169	177	202	202	159	159	163	165	156	156	191	194	142	151

j14	169	177	200	202	151	159	163	163	150	156	191	194	151	151
j15	169	177	202	202	159	159	163	165	147	159	182	191	151	151
j16	169	177	202	202	159	161	163	165	156	159	176	191	142	151
j17	169	177	202	202	159	159	155	163	156	159	191	194	142	151
j18	169	177	202	202	151	159	163	165	156	156	191	191	151	151
j19	177	179	202	202	159	161	163	165	156	159	191	191	139	151
j20	177	179	202	202	159	161	163	165	156	159	191	191	151	151
pop = Kedah														
k1	177	177	202	202	161	161	163	165	156	156	194	194	136	136
k2	169	177	202	202	159	161	163	165	156	156	191	194	151	151
k3	169	177	202	202	159	161	165	167	156	159	191	194	142	151
k4	169	177	202	202	159	159	163	165	150	156	191	191	151	151
k5	169	177	202	202	159	161	165	167	156	156	182	191	142	151
k6	169	177	182	202	159	161	157	165	147	156	182	191	151	151
k7	169	177	200	200	153	161	165	165	156	156	176	191	151	151
k8	177	177	202	202	161	161	165	167	156	156	191	194	151	151
k9	177	177	202	202	159	161	163	165	150	156	191	194	151	151
k10	169	177	202	202	159	161	157	165	156	156	194	197	151	151
k11	177	177	202	202	159	161	165	165	156	156	176	191	151	151
k12	177	177	202	202	159	161	165	165	156	156	191	194	142	148
k13	169	177	202	202	?	?	157	165	156	156	185	185	142	151
k14	169	177	202	202	161	161	165	165	156	156	182	191	151	151
k15	169	177	202	202	159	161	163	165	156	156	191	191	139	151
k16	177	177	202	202	159	159	163	165	156	156	182	191	136	151
k17	177	177	202	202	159	159	165	167	156	156	191	194	151	154
k18	169	177	202	202	159	161	155	163	156	156	191	194	151	151
k19	169	177	202	202	159	161	165	167	150	156	194	194	133	151
k20	177	177	202	202	159	159	155	163	156	156	194	194	142	151
k21	177	177	202	202	159	161	165	167	150	156	191	191	151	151
k22	177	177	202	202	159	161	165	169	156	156	191	194	151	151

k23	169	177	202	202	159	161	165	167	156	156	191	191	151	151
k24	177	177	202	202	159	161	163	165	156	159	191	194	142	148
k25	177	177	202	202	159	159	165	165	156	156	191	191	151	151
k26	169	177	200	200	159	159	163	165	156	156	191	197	142	148
k27	177	177	202	202	159	159	165	167	150	156	182	191	136	151
k28	177	177	202	202	159	161	163	165	156	156	191	194	151	151
k29	169	177	202	202	161	161	159	167	150	156	191	194	151	154
k30	177	177	202	202	159	159	163	165	156	156	191	191	142	151
pop = Sarawak														
s1	177	177	202	202	161	161	163	165	156	156	182	191	151	151
s2	177	177	202	202	159	161	165	165	156	156	191	191	151	151
s3	169	177	192	202	153	161	157	165	156	156	182	191	136	151
s4	169	177	192	202	151	159	159	165	156	156	191	191	151	151
s5	177	177	202	202	159	159	165	165	150	156	191	194	151	151
s6	175	177	202	202	159	161	165	165	156	156	191	191	151	151
s7	169	177	202	202	159	161	155	163	156	159	179	191	142	151
s8	169	177	202	202	159	161	165	167	156	156	191	191	151	151
s9	177	177	202	202	159	161	163	167	150	156	191	191	151	151
s10	165	177	202	202	147	161	165	167	156	156	191	191	151	151
s11	177	177	200	200	159	161	157	157	153	156	176	191	154	160
s12	177	177	202	202	159	159	163	167	156	156	191	191	139	151
s13	169	177	202	202	159	159	163	163	156	156	182	191	151	151
s14	169	177	192	202	151	161	155	163	156	156	191	194	151	151
s15	177	177	202	202	161	161	165	165	156	156	191	191	142	151
s16	165	177	202	202	161	161	163	165	150	150	191	194	151	151
s17	177	177	202	202	159	159	165	165	156	159	191	191	151	154
s18	177	177	202	202	?	?	165	165	156	156	191	194	151	151
s19	169	177	202	202	159	161	163	165	156	156	182	191	151	151
s20	169	177	202	202	159	161	165	165	156	156	191	191	151	151
s21	177	177	202	202	151	159	163	167	150	156	191	191	133	151

s22	169	177	200	202	161	161	163	167	159	159	191	194	151	151
s23	177	177	202	202	159	159	163	163	153	156	194	194	151	157
s24	177	177	202	202	159	159	163	163	156	156	191	194	142	151
s25	177	177	202	202	161	161	163	163	156	156	191	194	151	151
s26	169	177	202	202	159	159	163	167	156	159	191	194	151	151
s27	177	177	202	202	159	159	163	165	156	159	191	191	139	151
s28	169	177	202	202	159	159	163	163	156	159	191	191	139	151
s29	177	177	202	202	159	159	163	167	156	156	191	194	151	151
s30	169	177	202	202	159	159	163	163	156	156	182	191	139	151
pop = Terengganu														
te1	169	177	202	202	159	159	163	167	156	159	182	191	136	151
te2	165	165	202	202	151	159	163	163	156	156	191	194	151	151
te3	169	177	202	202	159	159	163	163	156	156	194	194	142	148
te4	169	177	202	202	159	159	163	169	156	156	191	194	142	151
te5	177	177	202	202	?	?	163	165	150	156	191	191	151	151
te6	169	177	192	200	151	159	163	163	150	150	191	194	151	151
te7	177	177	202	202	159	159	163	167	156	159	191	194	151	151
te8	177	177	202	202	159	159	163	163	156	156	191	194	151	151
te9	169	177	200	200	151	159	153	159	156	159	188	194	142	151
te10	177	177	202	202	159	159	163	163	156	159	191	194	142	151
te11	169	177	202	202	151	159	163	167	159	159	182	191	151	151
te12	169	177	202	202	159	159	163	163	156	159	191	194	151	151
te13	169	177	202	202	159	159	163	165	159	159	191	194	151	151
te14	169	177	200	200	151	159	155	163	147	156	191	194	142	151
te15	177	177	202	202	159	159	163	169	156	159	191	191	142	151
te16	169	177	202	202	159	159	155	163	150	162	191	191	142	151
te17	169	177	200	200	151	159	163	169	156	156	185	194	151	151
te18	177	177	202	202	147	159	163	169	150	156	188	191	139	151
te19	169	177	200	200	151	159	155	163	156	159	191	191	136	151
te20	169	177	202	202	159	159	163	169	156	159	191	197	151	151

te21	169	177	202	202	159	159	163	163	156	156	191	191	136	151
te22	169	177	200	200	151	159	155	165	147	159	191	194	139	151
te23	169	177	202	202	151	159	163	167	150	156	194	194	151	151
te24	169	177	202	202	159	159	167	169	150	156	191	194	142	151
te25	161	177	202	202	159	159	155	163	156	156	191	191	142	169
te26	169	177	202	202	159	159	153	163	159	159	191	194	151	151
te27	169	177	202	202	159	159	163	165	156	159	191	191	142	151
te28	169	177	202	202	151	159	155	163	147	159	191	191	142	148
te29	169	177	202	202	151	151	163	165	150	159	191	191	151	151
te30	169	177	202	202	159	159	155	163	150	156	182	191	136	151

APPENDIX D

Table 3: Comparisons of linkage disequilibrium values for each locus pair combinations. Disequilibrium values were compared between all pairs of loci in this study, and p-values were calculated.

POP	LOCUS 1	LOCUS 2	p value	ORDER		p value	ORIG	RANK	FDR	sig?
Sg Timun	estmr5	estmr8	0.48314	a1		0.00304	a47	1	0.000595	FALSE
Sg Timun	estmr5	estmr13	0.30427	a2		0.00368	a66	2	0.00119	FALSE
Sg Timun	estmr8	estmr13	0.03116*	a3		0.01303	a45	3	0.001786	FALSE
Sg Timun	estmr5	estmr14	0.55024	a4		0.02819	a63	4	0.002381	FALSE
Sg Timun	estmr8	estmr14	0.50102	a5		0.03116	a3	5	0.002976	FALSE
Sg Timun	estmr13	estmr14	0.7051	a6		0.03406	a10	6	0.003571	FALSE
Sg Timun	estmr5	estmr37	0.87232	a7		0.03793	a50	7	0.004167	FALSE
Sg Timun	estmr8	estmr37	0.43462	a8		0.04829	a33	8	0.004762	FALSE
Sg Timun	estmr13	estmr37	0.76227	a9		0.0504	a57	9	0.005357	FALSE
Sg Timun	estmr14	estmr37	0.03406*	a10		0.05413	a62	10	0.005952	FALSE
Sg Timun	estmr5	estmr41	0.22082	a11		0.05895	a29	11	0.006548	FALSE
Sg Timun	estmr8	estmr41	0.48882	a12		0.06694	a48	12	0.007143	FALSE
Sg Timun	estmr13	estmr41	0.07827	a13		0.07827	a13	13	0.007738	FALSE
Sg Timun	estmr14	estmr41	0.30432	a14		0.09393	a56	14	0.008333	FALSE
Sg Timun	estmr37	estmr41	0.191	a15		0.11048	a24	15	0.008929	FALSE
Sg Timun	estmr5	estmr51	0.50375	a16		0.11087	a77	16	0.009524	FALSE
Sg Timun	estmr8	estmr51	0.36537	a17		0.12595	a71	17	0.010119	FALSE
Sg Timun	estmr13	estmr51	0.31991	a18		0.14092	a68	18	0.010714	FALSE
Sg Timun	estmr14	estmr51	0.31786	a19		0.15425	a65	19	0.01131	FALSE
Sg Timun	estmr37	estmr51	0.49683	a20		0.15488	a72	20	0.011905	FALSE
Sg Timun	estmr41	estmr51	0.93695	a21		0.16365	a42	21	0.0125	FALSE
Kedah	estmr5	estmr8	0.22163	a22		0.18318	a84	22	0.013095	FALSE
Kedah	estmr5	estmr13	0.34954	a23		0.18465	a43	23	0.01369	FALSE
Kedah	estmr8	estmr13	0.11048	a24		0.191	a15	24	0.014286	FALSE

Kedah	estmr5	estmr14	0.48331	a25		0.20481	a59	25	0.014881	FALSE
Kedah	estmr8	estmr14	0.53947	a26		0.21543	a49	26	0.015476	FALSE
Kedah	estmr13	estmr14	0.82442	a27		0.22082	a11	27	0.016071	FALSE
Kedah	estmr5	estmr37	1	a28		0.22163	a22	28	0.016667	FALSE
Kedah	estmr8	estmr37	0.05895	a29		0.27142	a79	29	0.017262	FALSE
Kedah	estmr13	estmr37	0.95726	a30		0.29907	a60	30	0.017857	FALSE
Kedah	estmr14	estmr37	0.3904	a31		0.30427	a2	31	0.018452	FALSE
Kedah	estmr5	estmr41	0.84585	a32		0.30432	a14	32	0.019048	FALSE
Kedah	estmr8	estmr41	0.04829*	a33		0.31786	a19	33	0.019643	FALSE
Kedah	estmr13	estmr41	0.46295	a34		0.31991	a18	34	0.020238	FALSE
Kedah	estmr14	estmr41	0.70924	a35		0.32935	a54	35	0.020833	FALSE
Kedah	estmr37	estmr41	0.9543	a36		0.3339	a46	36	0.021429	FALSE
Kedah	estmr5	estmr51	0.80704	a37		0.34309	a39	37	0.022024	FALSE
Kedah	estmr8	estmr51	0.78628	a38		0.34359	a55	38	0.022619	FALSE
Kedah	estmr13	estmr51	0.34309	a39		0.34954	a23	39	0.023214	FALSE
Kedah	estmr14	estmr51	0.90125	a40		0.35628	a82	40	0.02381	FALSE
Kedah	estmr37	estmr51	0.58591	a41		0.35666	a44	41	0.024405	FALSE
Kedah	estmr41	estmr51	0.16365	a42		0.36537	a17	42	0.025	FALSE

Sarawak	estmr5	estmr8	0.18465	a43		0.38725	a75	43	0.025595	FALSE
Sarawak	estmr5	estmr13	0.35666	a44		0.3904	a31	44	0.02619	FALSE
Sarawak	estmr8	estmr13	0.01303*	a45		0.41849	a76	45	0.026786	FALSE
Sarawak	estmr5	estmr14	0.3339	a46		0.42769	a61	46	0.027381	FALSE
Sarawak	estmr8	estmr14	0.00304*	a47		0.43462	a8	47	0.027976	FALSE
Sarawak	estmr13	estmr14	0.06694	a48		0.46295	a34	48	0.028571	FALSE
Sarawak	estmr5	estmr37	0.21543	a49		0.48314	a1	49	0.029167	FALSE
Sarawak	estmr8	estmr37	0.03793*	a50		0.48331	a25	50	0.029762	FALSE
Sarawak	estmr13	estmr37	0.85665	a51		0.48882	a12	51	0.030357	FALSE
Sarawak	estmr14	estmr37	0.84756	a52		0.49683	a20	52	0.030952	FALSE
Sarawak	estmr5	estmr41	0.7894	a53		0.50102	a5	53	0.031548	FALSE
Sarawak	estmr8	estmr41	0.32935	a54		0.50375	a16	54	0.032143	FALSE
Sarawak	estmr13	estmr41	0.34359	a55		0.53799	a73	55	0.032738	FALSE
Sarawak	estmr14	estmr41	0.09393	a56		0.53947	a26	56	0.033333	FALSE
Sarawak	estmr37	estmr41	0.0504	a57		0.55024	a4	57	0.033929	FALSE
Sarawak	estmr5	estmr51	1	a58		0.58304	a81	58	0.034524	FALSE
Sarawak	estmr8	estmr51	0.20481	a59		0.58591	a41	59	0.035119	FALSE
Sarawak	estmr13	estmr51	0.29907	a60		0.59583	a69	60	0.035714	FALSE
Sarawak	estmr14	estmr51	0.42769	a61		0.60581	a64	61	0.03631	FALSE
Sarawak	estmr37	estmr51	0.05413	a62		0.62983	a83	62	0.036905	FALSE
Sarawak	estmr41	estmr51	0.02819*	a63		0.7051	a6	63	0.0375	FALSE
Terengganu	estmr5	estmr8	0.60581	a64		0.70924	a35	64	0.038095	FALSE
Terengganu	estmr5	estmr13	0.15425	a65		0.73707	a74	65	0.03869	FALSE
Terengganu	estmr8	estmr13	0.00368*	a66		0.76227	a9	66	0.039286	FALSE
Terengganu	estmr5	estmr14	0.94713	a67		0.78628	a38	67	0.039881	FALSE
Terengganu	estmr8	estmr14	0.14092	a68		0.7894	a53	68	0.040476	FALSE
Terengganu	estmr13	estmr14	0.59583	a69		0.80704	a37	69	0.041071	FALSE
Terengganu	estmr5	estmr37	0.90352	a70		0.82442	a27	70	0.041667	FALSE
Terengganu	estmr8	estmr37	0.12595	a71		0.84585	a32	71	0.042262	FALSE

Terengganu	estmr13	estmr37	0.15488	a72		0.84756	a52	72	0.042857	FALSE
Terengganu	estmr14	estmr37	0.53799	a73		0.85665	a51	73	0.043452	FALSE
Terengganu	estmr5	estmr41	0.73707	a74		0.87232	a7	74	0.044048	FALSE
Terengganu	estmr8	estmr41	0.38725	a75		0.90125	a40	75	0.044643	FALSE
Terengganu	estmr13	estmr41	0.41849	a76		0.90352	a70	76	0.045238	FALSE
Terengganu	estmr14	estmr41	0.11087	a77		0.90613	a80	77	0.045833	FALSE
Terengganu	estmr37	estmr41	0.99425	a78		0.93695	a21	78	0.046429	FALSE
Terengganu	estmr5	estmr51	0.27142	a79		0.94713	a67	79	0.047024	FALSE
Terengganu	estmr8	estmr51	0.90613	a80		0.9543	a36	80	0.047619	FALSE
Terengganu	estmr13	estmr51	0.58304	a81		0.95726	a30	81	0.048214	FALSE
Terengganu	estmr14	estmr51	0.35628	a82		0.99425	a78	82	0.04881	FALSE
Terengganu	estmr37	estmr51	0.62983	a83		1	a28	83	0.049405	FALSE
Terengganu	estmr41	estmr51	0.18318	a84		1	a58	84	0.05	FALSE

P-value with * is significant ($p < 0.05$); p-value with ** are significant ($p < 0.05$) after False Discovery Rate (FDR) correction, whereby $\alpha=0.05$.

APPENDIX E

Table 4: Genotypic frequencies of seven microsatellites loci for all four wild populations of *Macrobrachium rosenbergii*

Locus / Population	Genotype			
	Sg Timun	**Kedah**	**Sarawak**	**Terengganu**
EST MR 5	161/177 (1) 165/177 (1) 169/177 (17) 177/177 (7) 177/179 (4)	 169/177 (15) 177/177 (15)	 165/177 (2) 169/177 (12) 175/177 (1) 177/177 (15)	161/177 (1) 165/165 (1) 169/177 (22) 177/177 (6)
EST MR 8	 192/200 (3) 192/202 (3) 200/202 (1) 202/202 (23)	182/202 (1) 200/200 (2) 202/202 (27)	 192/202 (3) 200/200 (1) 200/202 (1) 202/202 (25)	 192/200 (1) 200/200 (5) 202/202 (24)
EST MR 13	147/159 (1) 151/159 (4) 153/159 (1) 159/159 (16) 159/161 (7) 161/161 (1)	 153/161 (1) 159/159 (8) 159/161 (16) 161/161 (4)	 147/161 (1) 151/159 (2) 151/161 (1) 153/161 (1) 159/159 (11) 159/161 (8) 161/161 (5)	147/159 (1) 151/151 (1) 151/159 (10) 159/159 (17)
EST MR 14	 155/163 (1)	 155/163 (2)	 155/163 (2)	153/159 (1) 153/163 (1) 155/163 (6)

	157/165 (1) 163/163 (3) 163/165 (17) 163/169 (3) 165/165 (2) 165/167 (3)	157/165 (3) 159/167 (1) 163/165 (10) 165/165 (5) 165/167 (8) 165/169 (1)	157/157 (1) 157/165 (1) 159/165 (1) 163/163 (6) 163/165 (4) 163/167 (6) 165/165 (7) 165/167 (2)	155/165 (1) 163/163 (7) 163/165 (4) 163/167 (4) 163/169 (5) 167/169 (1)
EST MR 37	147/159 (2) 150/156 (3) 150/159 (1) 156/156 (17) 156/159 (7)	147/156 (1) 150/156 (6) 156/156 (21) 156/159 (2)	 150/150 (1) 150/156 (3) 153/156 (2) 156/156 (18) 156/159 (5) 159/159 (1)	147/156 (1) 147/159 (2) 150/150 (1) 150/156 (5) 150/159 (1) 150/162 (1) 156/156 (7) 156/159 (9) 159/159 (3)
EST MR 41	176/191 (2) 179/191 (1) 182/191 (5) 191/191 (10) 191/194 (12)	176/191 (2) 182/191 (5) 185/185 (1) 191/191 (6) 191/194 (11) 191/197 (1)	176/191 (1) 179/191 (1) 182/191 (5) 191/191 (13) 191/194 (9)	 182/191 (3) 185/194 (1) 188/191 (1) 188/194 (1) 191/191 (9) 191/194 (12) 191/197 (1)

		194/194 (3) 194/197 (1)	194/194 (1)	194/194 (2)
EST MR 51	136/136 (1) 139/151 (1) 142/151 (9) 148/151 (1) 151/151 (17) 151/154 (1)	133/151 (1) 136/136 (1) 136/151 (2) 139/151 (1) 142/148 (3) 142/151 (5) 151/151 (15) 151/154 (2)	133/151 (1) 136/151 (1) 139/151 (4) 142/151 (3) 151/151 (18) 151/154 (1) 151/157 (1) 154/160 (1)	136/151 (4) 139/151 (2) 142/148 (2) 142/151 (8) 142/169 (1) 151/151 (13)

Table 5: Allelic frequencies of seven microsatellites loci for all four wild populations of *Macrobrachium rosenbergii*

LOCUS	ALLELES	SIZE (bp)	SG TIMUN (pop 1)	KEDAH (pop 2)	SARAWAK (pop 3)	TERENGGANU (pop4)
estmr5	A	161	0.0167			0.0167
	B	165	0.0167		0.0333	0.0333
	C	169	0.2833	0.2500	0.0200	0.3667
	D	175			0.0167	
	E	177	0.6167	0.7500	0.7500	0.5833
	F	179	0.0667			
estmr8	A	182		0.0167		
	B	192	0.1000		0.0500	0.0167
	C	200	0.0667	0.0667	0.0500	0.1833
	D	202	0.8333	0.9167	0.9000	0.8000
estmr13	A	147	0.0167		0.0172	0.0172
	B	151	0.0667		0.0517	0.2069
	C	153	0.0167	0.0172	0.0172	
	D	159	0.7500	0.5517	0.5517	0.7759
	E	161	0.1500	0.4310	0.3621	
estmr14	A	153				0.0333
	B	155	0.0167	0.0333	0.0333	0.1167
	C	157	0.0167	0.0500	0.0500	
	D	159		0.0167	0.0167	0.0167
	E	161	0.4500	0.2000	0.4000	0.5667
	F	163	0.4167	0.5333	0.3667	0.0833
	G	165	0.0500	0.1500	0.1333	0.0833
	H	167	0.0500	0.0167		0.1000
estmr37	A	147	0.0333	0.0167		0.0500
	B	150	0.0667	0.1000	0.0833	0.1500
	C	153			0.0333	
	D	156	0.7333	0.8500	0.7667	0.4833

	E	159	0.1667	0.0333	0.1167	0.3000
	F	162				0.0167
estmr41	A	176	0.0333	0.0333	0.0167	
	B	179	0.0167		0.0167	
	C	182	0.0833	0.0833	0.0833	0.0500
	D	185		0.0333		0.0167
	E	188				0.0333
	F	191	0.6667	0.5167	0.7000	0.5833
	G	194	0.2000	0.3000	0.1833	0.3000
	H	197		0.0333		0.0167
estmr51	A	133		0.0167	0.0167	
	B	136	0.0333	0.0667	0.0167	0.0667
	C	139	0.0167	0.0167	0.0667	0.0333
	D	142	0.1500	0.1333	0.0500	0.1833
	E	148	0.0167	0.0500		0.0333
	F	151	0.7667	0.6833	0.7833	0.6667
	G	154	0.0167	0.0333	0.0333	
	H	157			0.0167	
	I	160			0.0167	
	J	169				0.0167

*Highlighted frequencies indicating private alleles

APPENDIX F

Table 6 : List of 22 polymorphic markers subjected for fragment analysis

CODE	PRODUCT SIZE	Ta (oC)	MICROSAT REGION	MOTIF	STATUS	PIC	He	No of allele per locus
EST MR1	300-309	63.3	predicted UTR	(Ga)5	YES	0.4491	0.5049	7
EST MR2	150-167	63.3	predicted UTR	Ca5	YES	0.4164	0.5254	3
EST MR5	150-177	55	predicted UTR	Tc6	YES	0.6094	0.5307	5
EST MR 8	150-200	55	predicted UTR	Tc6	YES	0.516	0.6011	3
EST MR13	150-160	61.4	predicted CDS	Tc7	YES	0.6351	0.6816	8
EST MR14	150-163	61.4	predicted UTR	Ct7	YES	0.739	0.784	8
EST MR18	250-284	65	predicted CDS	Tc9	YES	0.548	0.629	7
EST MR19	250-271	61.4	predicted UTR	Tc9	SIGNIFICANT STUTTERING	N/A	N/A	
EST MR32	150-184	64.5	predicted CDS	Acc5	YES	0.3867	0.4014	8
EST MR35	200-249	64.5	predicted CDS	Ata5	YES	0.2858	0.3022	4
EST MR36	150-180	64.5	predicted UTR	Gag6	YES	0.471	0.541	5
EST MR37	150-155	64.5	predicted UTR	Gct6	YES	0.631	0.6636	7
EST MR 41	150-190	63.3	predicted CDS	Tca6	YES	0.5798	0.6206	8
EST MR44	150-169	63.3	predicted CDS	Ctt6	YES	0.5603	0.6138	6
EST MR47	300-302	63.3	predicted UTR	Gga7	YES	0.62	0.655	9
EST MR51	150-150	63.3	predicted UTR	Ctt7	YES	0.6355	0.6885	7
EST MR52	200-228	63.3	predicted UTR	Tcc7	YES	0.4945	0.5376	8
EST MR53	150-159	61.4	predicted UTR	Cat7	YES	0.5199	0.5596	6
EST MR54	150-150	65	predicted UTR	Cag7	YES	0.4612	0.4937	5
EST MR55	150-166	61.4	predicted UTR	Cct7	NO AMPLIFICATION	N/A		
EST MR56	150-183	65	predicted UTR	Cct9	YES	0.4452	0.4854	6
EST MR58	300-303	65	predicted UTR	Tct24	YES	0.89	0.914	16

*PIC value of all primers were calculated using http://www.liv.ac.uk/~kempsj/pic.html (double checked with Cervus)

32 individuals were used in getting PIC value for all primers except: EST MR18 (29 individuals); EST MR47 (31 individuals); EST MR58 (30 individual