Genetic identification of crustacean species (penaeid shrimps) using ddRADseq

Genome-wide SNP genotype data (double-digest restriction-site associated DNA sequencing)

1. Dataset description

A total of 61 crustacean samples belonging to five shrimp species of the family Penaeidae (Crustacea: Decapoda) were genotyped with double-digest restriction-site associated DNA sequencing (ddRADseq) for species identification. Most samples were of the Mediterranean caramote prawn (*Melicertus kerathurus*, n = 43); four other species that are commercially important or are imported to the European market were included for comparison. SNPs were identified with the dDocent pipeline. The dataset contains 15,326 biallelic variants (12,996 SNPs and 2,330 multi-nucleotide or complex variants) located on 3,407 RAD loci (contigs).

Taxa	Crustacea, Decapoda, Penaeidae – 5 species
Samples	61
Method	ddRADseq; SNP calling with dDocent
Markers	15,326 biallelic variants (SNPs and complex variants) on 3,407 RAD loci
Data format	PLINK (.ped/.map) genotype files
Missing genotypes	15.5% overall

2. Species summary

Table 1. Samples, genotyping success and genetic variation per species

Species	Common name	n	Call rate, % (range)	Observed heterozygosity	SNPs genotyped	Polymorphic SNPs	Diagnostic SNPs*
Farfantepenaeus aztecus	Northern brown shrimp	5	63.7 (50.5–73.7)	0.092	15,021	7,370	2
Litopenaeus vannamei	Whiteleg shrimp	5	58.6 (49.4–67.6)	0.094	14,705	7,228	14
Melicertus kerathurus	Caramote prawn	43	95.5 (58.4–99.8)	0.056	15,326	11,329	51
Parapenaeus longirostris	Deep-water rose shrimp	4	57.8 (29.1–80.6)	0.126	14,162	7,025	168
Penaeus notialis	Southern pink shrimp	4	52.1 (39.8–62.8)	0.069	13,641	4,256	3
Total		**61**	**84.5 (29.1–99.8)**	**0.068**	**15,326**		

** SNPs fixed for one allele in the species and fixed for the alternative allele in all other species (≥ 3 genotyped samples in the species and ≥ 2 in each of the others).*

Table 2. Mean pairwise genetic distance (proportion of allelic differences) within (diagonal) and between species

Species	*F. aztecus*	*L. vannamei*	*M. kerathurus*	*P. longirostris*	*P. notialis*
F. aztecus	**0.245**	0.320	0.389	0.440	0.257
L. vannamei	0.320	**0.275**	0.396	0.434	0.302
M. kerathurus	0.389	0.396	**0.074**	0.374	0.404
P. longirostris	0.440	0.434	0.374	**0.296**	0.446
P. notialis	0.257	0.302	0.404	0.446	**0.197**

Distances calculated from SNPs genotyped in both samples of each pair.

3. Sample information

Table 3. Genotyping call rate, observed heterozygosity and nearest-neighbour species for each sample

Sample ID	Call rate (%)	Observed heterozygosity	Nearest-neighbour species
Farfantepenaeus aztecus **(n = 5)**			
FA_FA1	50.5	0.072	*F. aztecus*
FA_FA2	69.1	0.102	*F. aztecus*
FA_FA3	61.7	0.086	*F. aztecus*
FA_FA4	63.7	0.092	*F. aztecus*
FA_FA5	73.7	0.108	*F. aztecus*
Litopenaeus vannamei **(n = 5)**			
LV_LV1	60.9	0.101	*L. vannamei*
LV_LV2	49.4	0.071	*L. vannamei*
LV_LV3	67.6	0.120	*L. vannamei*
LV_LV4	57.9	0.095	*L. vannamei*
LV_LV5	57.0	0.085	*L. vannamei*
Melicertus kerathurus **(n = 43)**			
MK_MK1	99.3	0.025	*M. kerathurus*
MK_MK2	98.8	0.025	*M. kerathurus*
MK_MK3	98.7	0.023	*M. kerathurus*
MK_MK4	99.3	0.021	*M. kerathurus*
MK_MK5	99.8	0.022	*M. kerathurus*
MK_MK6	99.3	0.025	*M. kerathurus*
MK_MK7	98.4	0.022	*M. kerathurus*
MK_MK8	98.6	0.022	*M. kerathurus*
MK_MK9	99.1	0.023	*M. kerathurus*
MK_MK10	98.7	0.022	*M. kerathurus*
MK_MK11	98.5	0.025	*M. kerathurus*
MK_MK12	98.5	0.023	*M. kerathurus*
MK_MK13	96.1	0.024	*M. kerathurus*
MK_MK14	98.1	0.027	*M. kerathurus*
MK_MK15	98.8	0.028	*M. kerathurus*
MK_MK16	98.9	0.028	*M. kerathurus*
MK_MK17	99.5	0.025	*M. kerathurus*
MK_MK18	99.1	0.025	*M. kerathurus*
MK_MK19	98.7	0.022	*M. kerathurus*
MK_MK20	99.2	0.024	*M. kerathurus*
MK_MK21	96.1	0.031	*M. kerathurus*
MK_MK22	99.5	0.022	*M. kerathurus*
MK_MK23	99.1	0.024	*M. kerathurus*
MK_MK24	97.5	0.087	*M. kerathurus*
MK_MK25	97.2	0.087	*M. kerathurus*
MK_MK26	95.4	0.116	*M. kerathurus*
MK_MK27	92.9	0.100	*M. kerathurus*

Sample ID	Call rate (%)	Observed heterozygosity	Nearest-neighbour species
MK_MK28	94.3	0.053	*M. kerathurus*
MK_MK29	95.8	0.092	*M. kerathurus*
MK_MK30	90.4	0.084	*M. kerathurus*
MK_MK31	88.6	0.068	*M. kerathurus*
MK_MK32	83.4	0.126	*M. kerathurus*
MK_MK33	84.3	0.082	*M. kerathurus*
MK_MK34	89.6	0.062	*M. kerathurus*
MK_MK35	90.7	0.075	*M. kerathurus*
MK_MK36	94.2	0.073	*M. kerathurus*
MK_MK37	98.1	0.188	*M. kerathurus*
MK_MK38	94.2	0.110	*M. kerathurus*
MK_MK39	98.0	0.080	*M. kerathurus*
MK_MK40	96.5	0.102	*M. kerathurus*
MK_MK41	98.6	0.074	*M. kerathurus*
MK_MK42	58.4	0.075	*M. kerathurus*
MK_MK43	97.4	0.130	*M. kerathurus*
***Parapenaeus longirostris* (n = 4)**			
PL_PL1	68.9	0.128	*P. longirostris*
PL_PL2	52.8	0.087	*P. longirostris*
PL_PL3	80.6	0.236	*P. longirostris*
PL_PL5	29.1	0.053	*P. longirostris*
***Penaeus notialis* (n = 4)**			
PN_PN1	39.8	0.050	*P. notialis*
PN_PN2	61.2	0.094	*P. notialis*
PN_PN3	62.8	0.084	*P. notialis*
PN_PN4	44.6	0.048	*P. notialis*

Nearest-neighbour species: species of the genetically closest sample in the dataset. All 61 samples clustered with samples of their own species.

4. Raw genotype data

The complete genotype data (61 samples × 15,326 variants) are given in Appendix B. Appendix B contains all the information of the PLINK genotype files of the dataset:

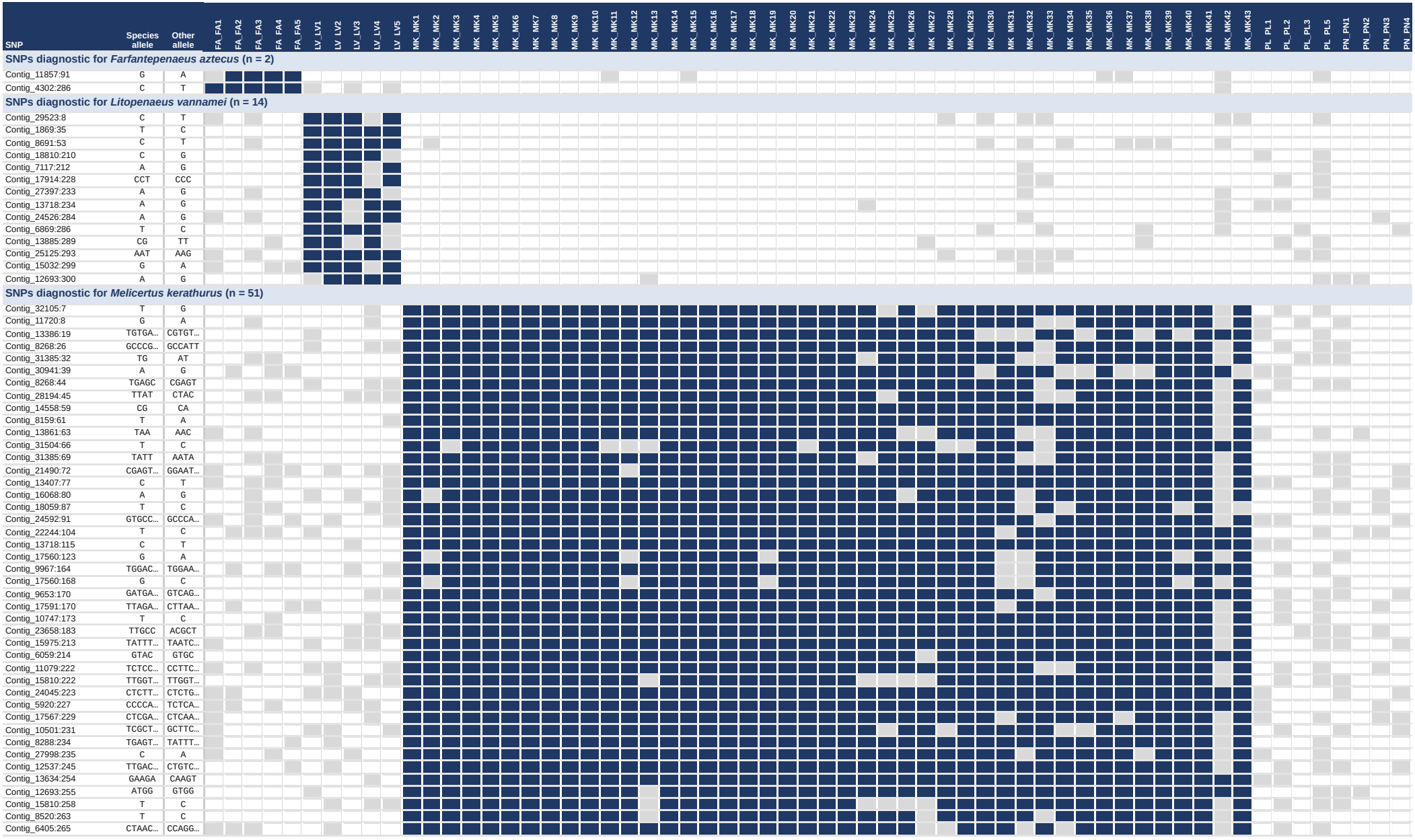
shrimp.map — Variant information: RAD locus (dDocent contig) and position of each variant (column "Variant" in Appendix B)

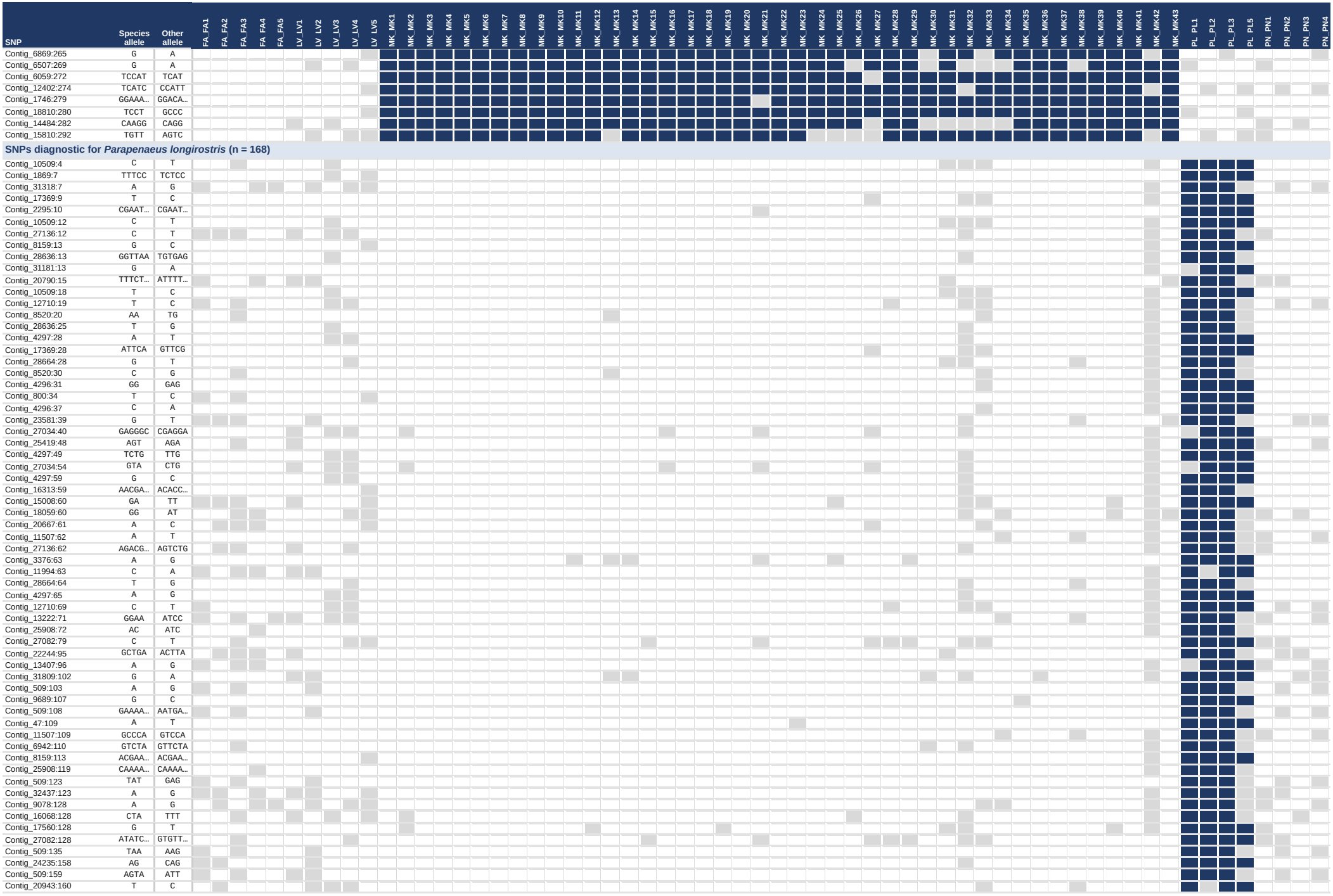
shrimp.ped — Sample information (species, sample ID) and the two alleles of each sample at each variant (columns "Allele 1", "Allele 2" and the sample genotypes in Appendix B)

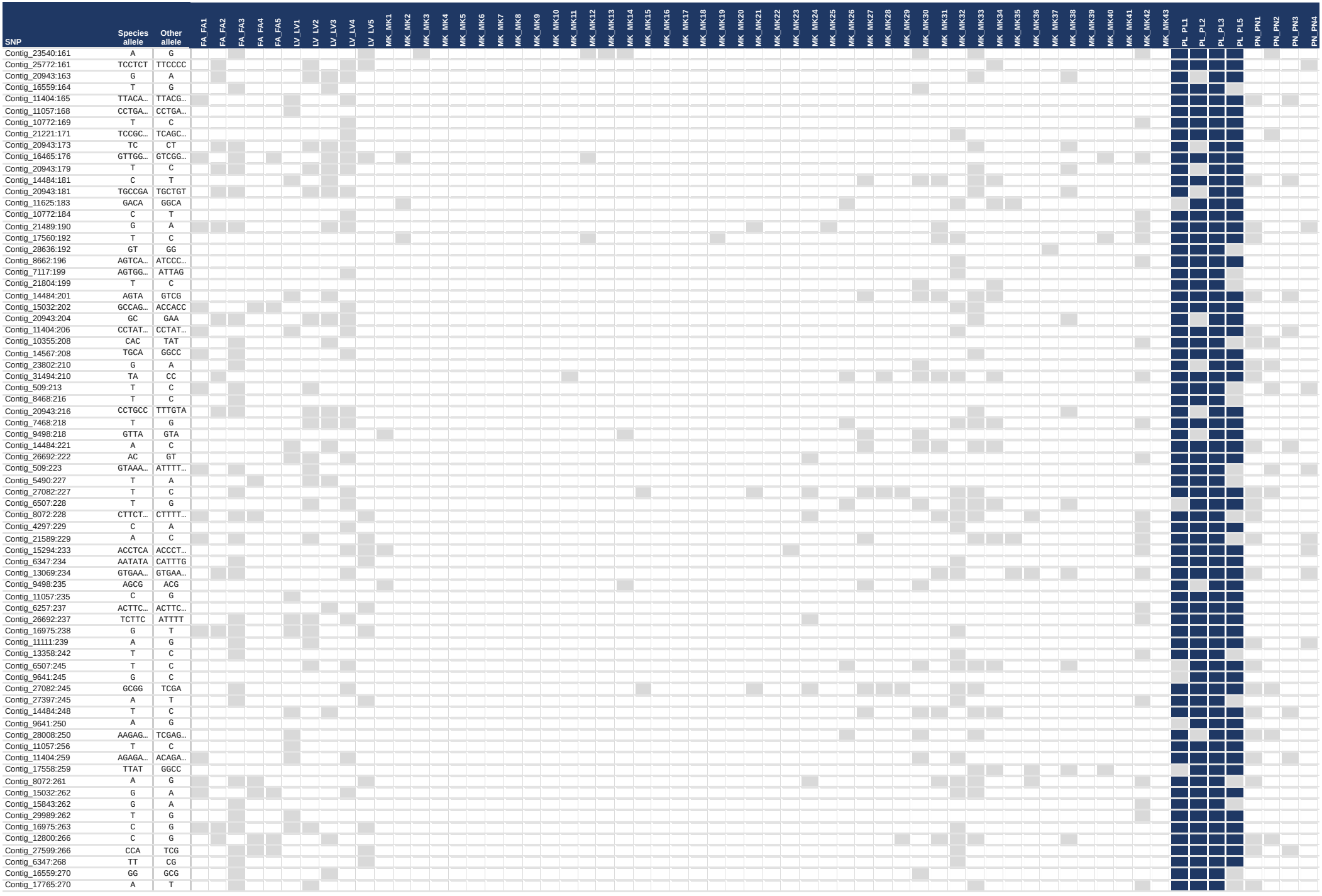
In Appendix B, genotypes are coded as 0 = homozygous for allele 1, 1 = heterozygous, 2 = homozygous for allele 2 and . = missing. Appendix A lists the genotypes of all samples at the 238 species-diagnostic SNPs.

Appendix A. Genotypes at species-diagnostic SNPs

Genotypes (alleles) of all 61 samples at the SNPs that distinguish each species from all others. Dark blue = homozygous for the species allele (the allele fixed in the species named in the section heading); light blue = heterozygous; white = homozygous for the other allele; grey = missing. Long alleles are truncated (…); full alleles are given in Appendix B. SNP name: RAD locus (dDocent contig) : position.




SNP
Species allele
Other allele
FA_FA1
FA_FA2
FA_FA3
FA_FA4
FA_FA5
LV_LV1
LV_LV2
LV_LV3
LV_LV4
LV_LV5
MK_MK1
MK_MK2
MK_MK3
MK_MK4
MK_MK5
MK_MK6
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MK_MK39
MK_MK40
MK_MK41
MK_MK42
MK_MK43
PL_PL1
PL_PL2
PL_PL3
PL_PL5
PN_PN1
PN_PN2
PN_PN3
PN_PN4
Contig_6869:265 G A
Contig_6507:269 G A
Contig_6059:272 TCCAT TCAT
Contig_12402:274 TCATC CCATT
Contig_1746:279 GGAAA… GGACA…
Contig_18810:280 TCCT GCCC
Contig_14484:282 CAAGG CAGG
Contig_15810:292 TGTT AGTC
SNPs diagnostic for Parapenaeus longirostris (n = 168)
Contig_10509:4 C T
Contig_1869:7 TTTCC TCTCC
Contig_31318:7 A G
Contig_17369:9 T C
Contig_2295:10 CGAAT… CGAAT…
Contig_10509:12 C T
Contig_27136:12 C T
Contig_8159:13 G C
Contig_28636:13 GGTTAA TGTGAG
Contig_31181:13 G A
Contig_20790:15 TTTCT… ATTTT…
Contig_10509:18 T C
Contig_12710:19 T C
Contig_8520:20 AA TG
Contig_28636:25 T G
Contig_4297:28 A T
Contig_17369:28 ATTCA GTTCG
Contig_28664:28 G T
Contig_8520:30 C G
Contig_4296:31 GG GAG
Contig_800:34 T C
Contig_4296:37 C A
Contig_23581:39 G T
Contig_27034:40 GAGGGC CGAGGA
Contig_25419:48 AGT AGA
Contig_4297:49 TCTG TTG
Contig_27034:54 GTA CTG
Contig_4297:59 G C
Contig_16313:59 AACGA… ACACC…
Contig_15008:60 GA TT
Contig_18059:60 GG AT
Contig_20667:61 A C
Contig_11507:62 A T
Contig_27136:62 AGACG… AGTCTG
Contig_3376:63 A G
Contig_11994:63 C A
Contig_28664:64 T G
Contig_4297:65 A G
Contig_12710:69 C T
Contig_13222:71 GGAA ATCC
Contig_25908:72 AC ATC
Contig_27082:79 C T
Contig_22244:95 GCTGA ACTTA
Contig_13407:96 A G
Contig_31809:102 G A
Contig_509:103 A G
Contig_9689:107 G C
Contig_509:108 GAAAA… AATGA…
Contig_47:109 A T
Contig_11507:109 GCCCA GTCCA
Contig_6942:110 GTCTA GTTCTA
Contig_8159:113 ACGAA… ACGAA…
Contig_25908:119 CAAAA… CAAAA…
Contig_509:123 TAT GAG
Contig_32437:123 A G
Contig_9078:128 A G
Contig_16068:128 CTA TTT
Contig_17560:128 G T
Contig_27082:128 ATATC… GTGTT…
Contig_509:135 TAA AAG
Contig_24235:158 AG CAG
Contig_509:159 AGTA ATT
Contig_20943:160 T C


SNP
Species allele
Other allele
FA_FA1
FA_FA2
FA_FA3
FA_FA4
FA_FA5
LV_LV1
LV_LV2
LV_LV3
LV_LV4
LV_LV5
MK_MK1
MK_MK2
MK_MK3
MK_MK4
MK_MK5
MK_MK6
MK_MK7
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MK_MK42
MK_MK43
PL_PL1
PL_PL2
PL_PL3
PL_PL5
PN_PN1
PN_PN2
PN_PN3
PN_PN4
Contig_23540:161 A G
Contig_25772:161 TCCTCT TTCCCC
Contig_20943:163 G A
Contig_16559:164 T G
Contig_11404:165 TTACA… TTACG…
Contig_11057:168 CCTGA… CCTGA…
Contig_10772:169 T C
Contig_21221:171 TCCGC… TCAGC…
Contig_20943:173 TC CT
Contig_16465:176 GTTGG… GTCGG…
Contig_20943:179 T C
Contig_14484:181 C T
Contig_20943:181 TGCCGA TGCTGT
Contig_11625:183 GACA GGCA
Contig_10772:184 C T
Contig_21489:190 G A
Contig_17560:192 T C
Contig_28636:192 GT GG
Contig_8662:196 AGTCA… ATCCC…
Contig_7117:199 AGTGG… ATTAG
Contig_21804:199 T C
Contig_14484:201 AGTA GTCG
Contig_15032:202 GCCAG… ACCACC
Contig_20943:204 GC GAA
Contig_11404:206 CCTAT… CCTAT…
Contig_10355:208 CAC TAT
Contig_14567:208 TGCA GGCC
Contig_23802:210 G A
Contig_31494:210 TA CC
Contig_509:213 T C
Contig_8468:216 T C
Contig_20943:216 CCTGCC TTTGTA
Contig_7468:218 T G
Contig_9498:218 GTTA GTA
Contig_14484:221 A C
Contig_26692:222 AC GT
Contig_509:223 GTAAA… ATTTT…
Contig_5490:227 T A
Contig_27082:227 T C
Contig_6507:228 T G
Contig_8072:228 CTTCT… CTTTT…
Contig_4297:229 C A
Contig_21589:229 A C
Contig_15294:233 ACCTCA ACCCT…
Contig_6347:234 AATATA CATTTG
Contig_13069:234 GTGAA… GTGAA…
Contig_9498:235 AGCG ACG
Contig_11057:235 C G
Contig_6257:237 ACTTC… ACTTC…
Contig_26692:237 TCTTC ATTTT
Contig_16975:238 G T
Contig_11111:239 A G
Contig_13358:242 T C
Contig_6507:245 T C
Contig_9641:245 G C
Contig_27082:245 GCGG TCGA
Contig_27397:245 A T
Contig_14484:248 T C
Contig_9641:250 A G
Contig_28008:250 AAGAG… TCGAG…
Contig_11057:256 T C
Contig_11404:259 AGAGA… ACAGA…
Contig_17558:259 TTAT GGCC
Contig_8072:261 A G
Contig_15032:262 G A
Contig_15843:262 G A
Contig_29989:262 T G
Contig_16975:263 C G
Contig_12800:266 C G
Contig_27599:266 CCA TCG
Contig_6347:268 TT CG
Contig_16559:270 GG GCG
Contig_17765:270 A T

| SNP | Species allele | Other allele | FA_FA1 | FA_FA2 | FA_FA3 | FA_FA4 | FA_FA5 | LV_LV1 | LV_LV2 | LV_LV3 | LV_LV4 | LV_LV5 | MK_MK1 | MK_MK2 | MK_MK3 | MK_MK4 | MK_MK5 | MK_MK6 | MK_MK7 | MK_MK8 | MK_MK9 | MK_MK10 | MK_MK11 | MK_MK12 | MK_MK13 | MK_MK14 | MK_MK15 | MK_MK16 | MK_MK17 | MK_MK18 | MK_MK19 | MK_MK20 | MK_MK21 | MK_MK22 | MK_MK23 | MK_MK24 | MK_MK25 | MK_MK26 | MK_MK27 | MK_MK28 | MK_MK29 | MK_MK30 | MK_MK31 | MK_MK32 | MK_MK33 | MK_MK34 | MK_MK35 | MK_MK36 | MK_MK37 | MK_MK38 | MK_MK39 | MK_MK40 | MK_MK41 | MK_MK42 | MK_MK43 | PL_PL1 | PL_PL2 | PL_PL3 | PL_PL5 | PN_PN1 | PN_PN2 | PN_PN3 | PN_PN4 |
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Appendix B. Complete genotype data (PLINK shrimp.ped / shrimp.map)

61 samples x 15,326 variants. Genotype codes: 0 = homozygous for allele 1; 1 = heterozygous; 2 = homozygous for allele 2; . = missing. Variant: RAD locus (dDocent contig) : position.

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