File S1

Library PCR-primers

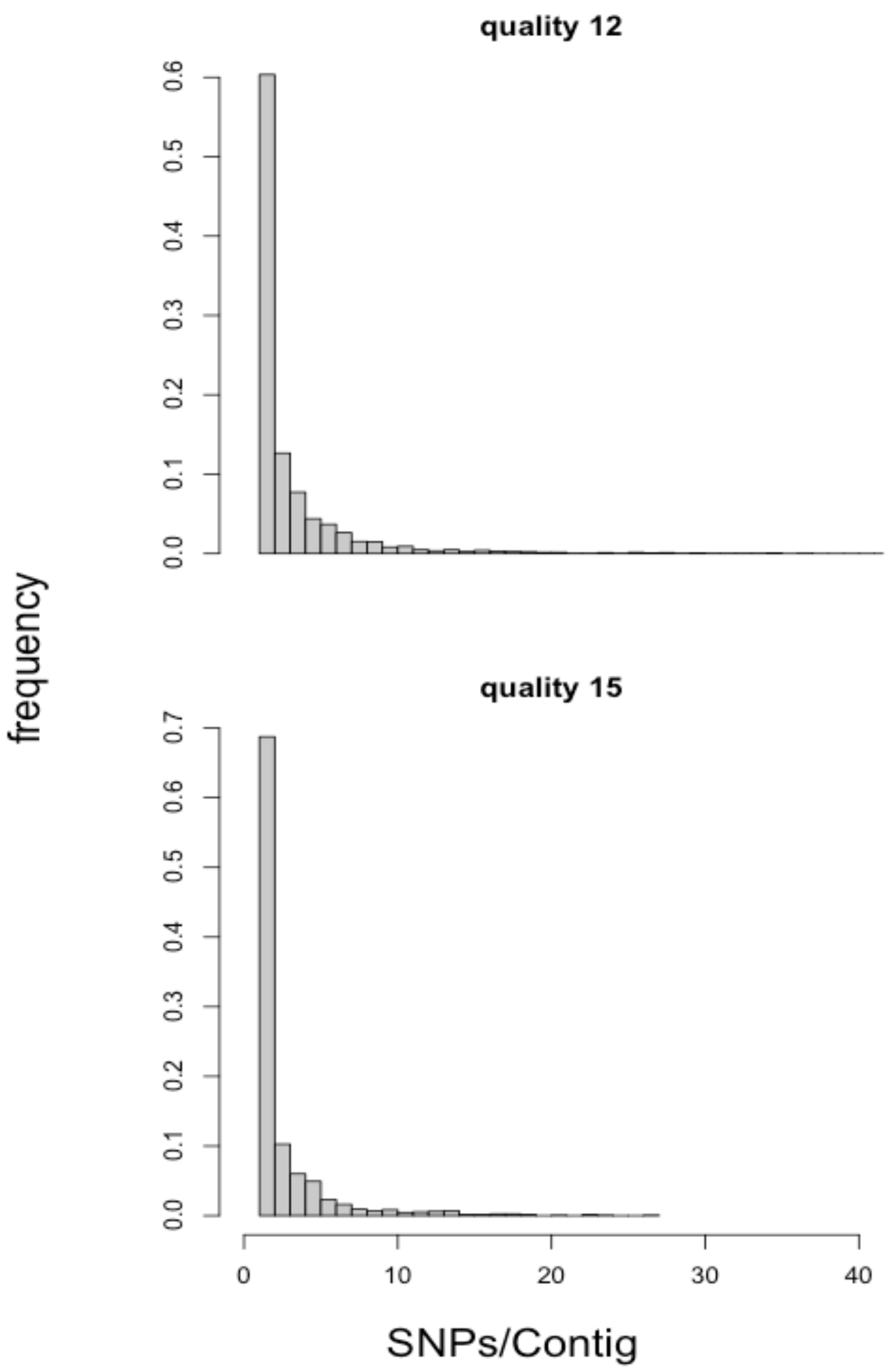
```
>TI-MID-B_plusT.seq
CCTATCCCCTGTGTGCCTTGGCAGTCTCAGT

>Ti-MID1-A_plusT.seq
CCATCTCATCCCTGCGTGTCTCCGACTCAGACGAGTGCGTT
```

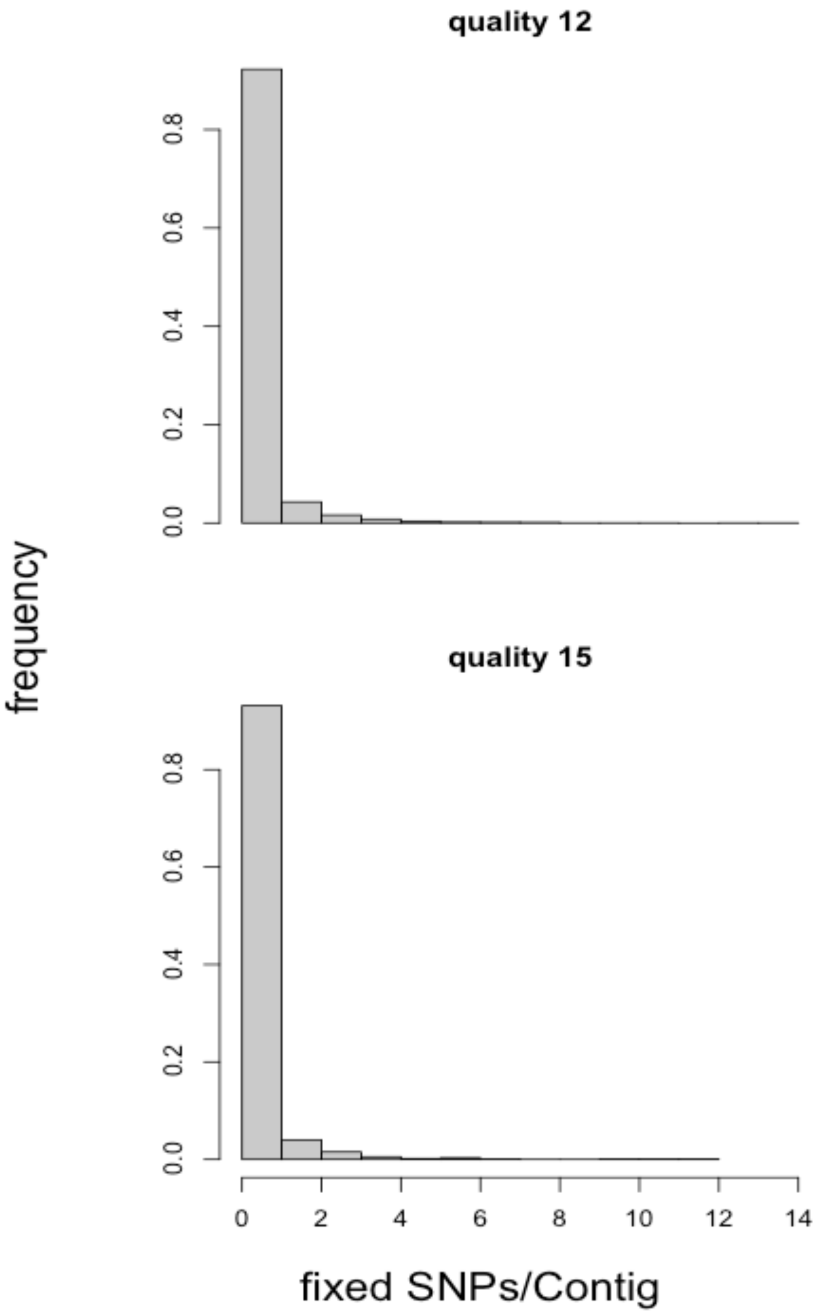
File S2

List of highly divergent contigs

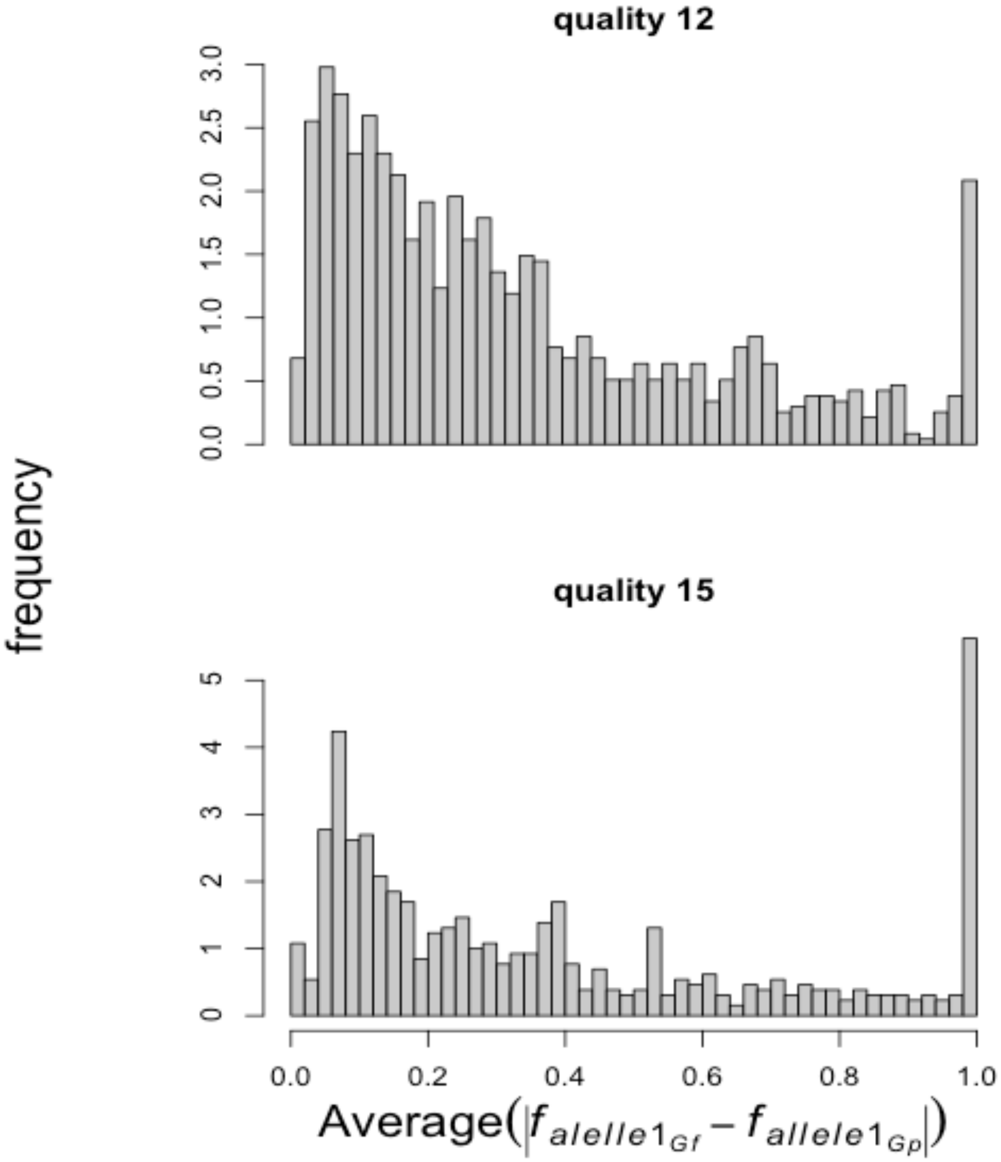
SNPs/contig



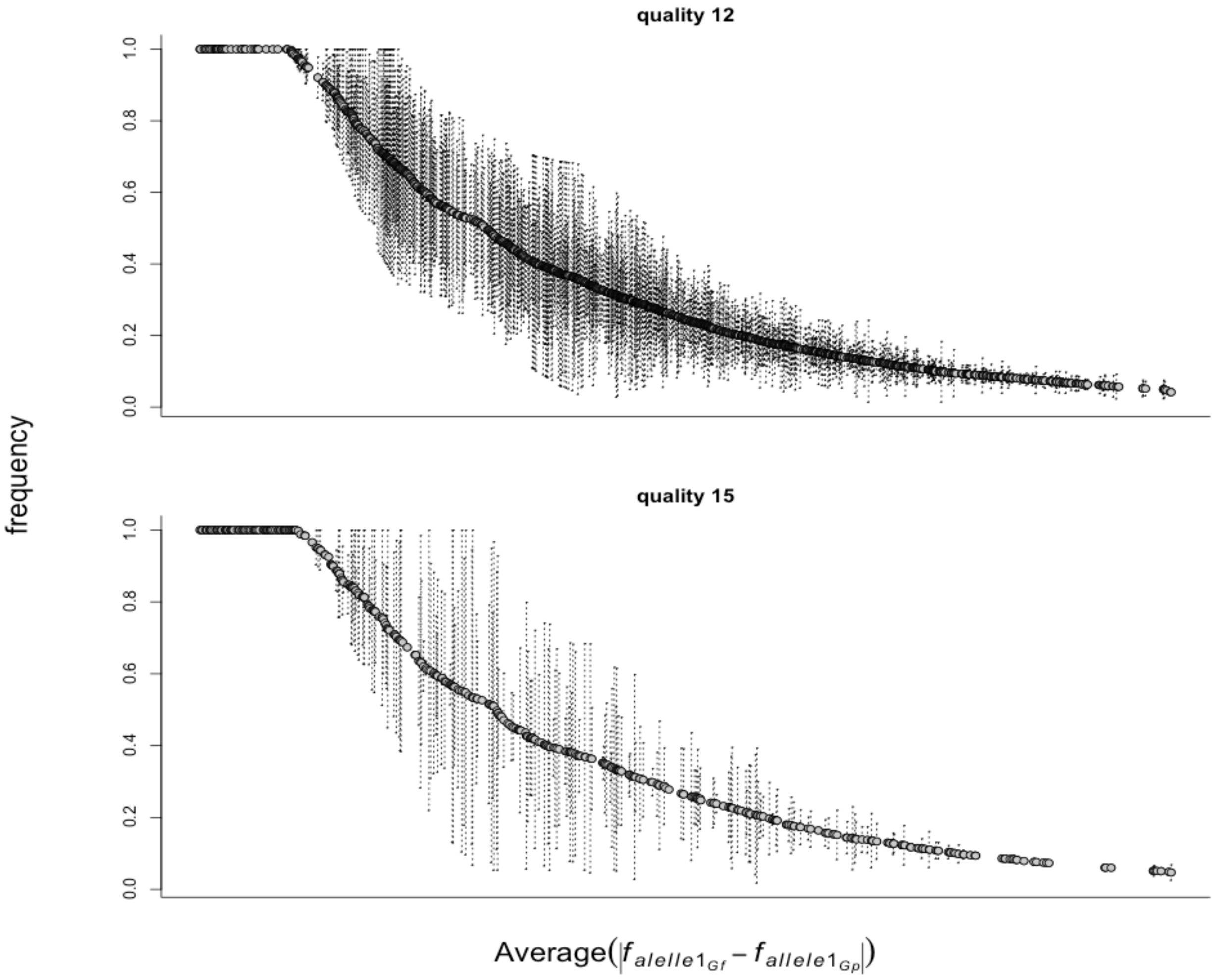
fixed SNPs/Contig



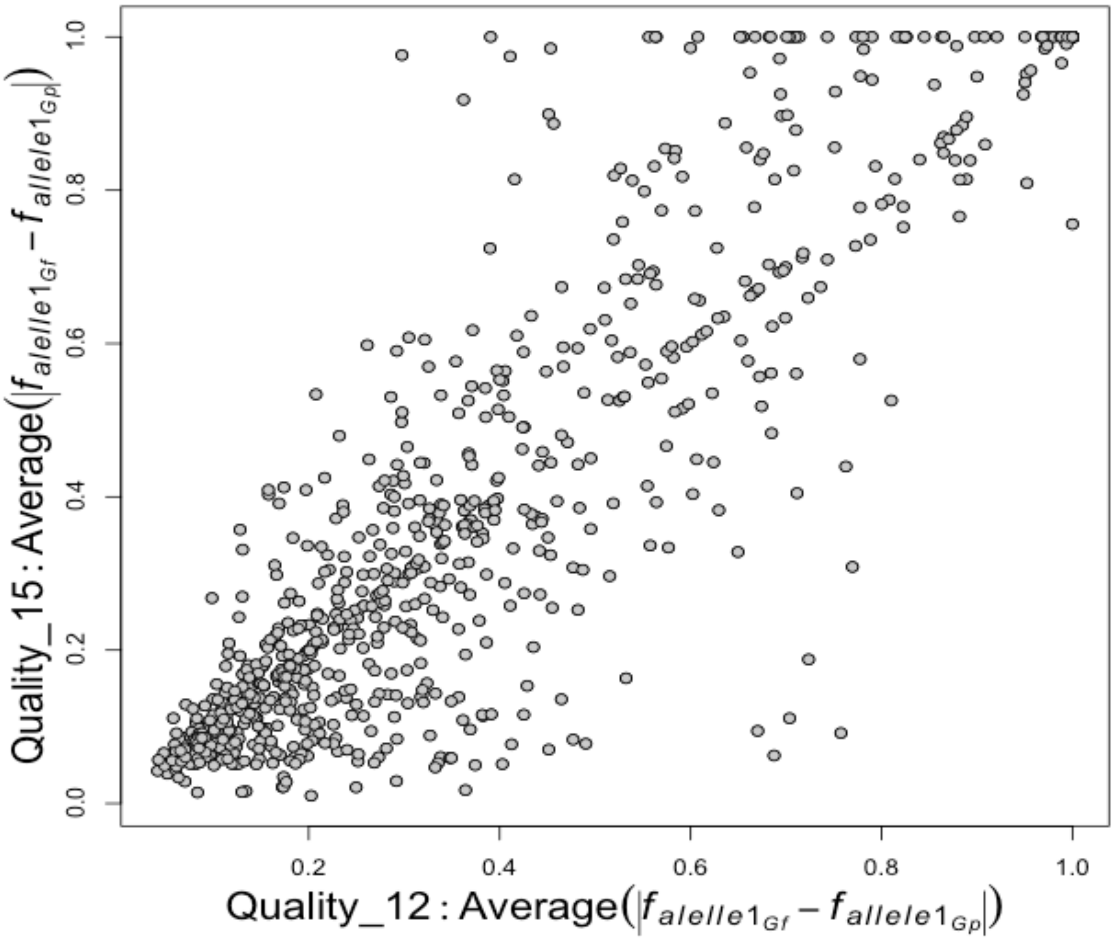
Dmean (for contigs with at least 3 SNPs



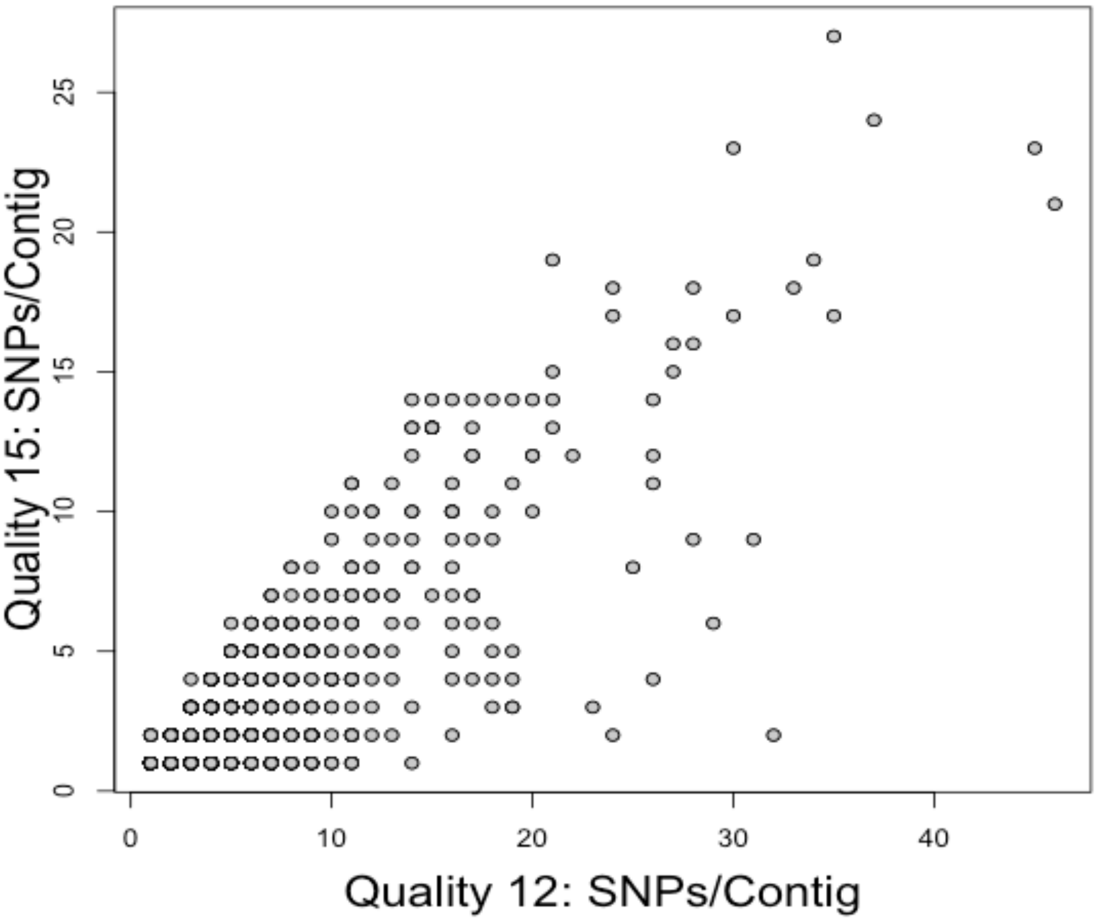
D mean (and STError)



Correlation between Dmean (qual 12 and qual 15)



Correlation between # of SNPs (qual 12 and 15)



File S3

Individual sequencing genotypes

Available for download as an excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.142299/-/DC1.

Table S1 Annotated list of genes

Available for download as an excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.142299/-/DC1.

Table S2 Annotation of the contigs showing at least 3 fixed (D>0.98) differences between *G. firmus* and *G. pennsylvanicus*.

Contigs in bold correspond to mitochondrial loci.

Contig	$\overline{D}$	SNPs		TBLAXT similarity
		N	Fixed	
80	0.909	20	14	Similar to eukaryotic translation initiation factor 3 subunit 1
625	0.865	18	13	Transcription initiation factor
432	0.865	14	11	Similar to *Tribolium castaneum* LOC398543 protein
70	1.000	10	10	**Cytochrome b**
310	0.998	9	9	**NADH dehydrogenase subunit 2 (*ND2*)**
7153	0.899	9	8	Proliferating cell nuclear antigen (*PCNA*)
142	0.898	9	8	*Gryllus pennsylvanicus* putative accessory gland
3104	0.825	11	8	Similar to Charged multivesicular body protein 2B
1313	0.757	11	8	Similar to pacifastin light chain
2733	0.882	9	7	Similar to *Gryllus bimaculatus* mRNA, GBcontig25049
136	0.882	9	7	Mn-Superoxide dismutase (*Sod2*)
1002	0.855	9	7	**Hypothetical protein. Mitochondrial?**
448	0.790	9	7	**tRNA-Lys, partial ATPase 8 (ATP8). Mitochondrial**
94	0.710	11	7	Similar to *Gryllus bimaculatus* mRNA, GBcontig18903
454	1.000	6	6	**Teleogryllus emma mitochondrion**
755	1.000	6	6	#N/A
656	0.893	9	6	**Teleogryllus emma mitochondrion**
665	0.879	7	6	**Teleogryllus emma mitochondrion**
6023	0.867	7	6	ns
5214	0.865	7	6	ns

618	1.000	5	5	Conserved protein (similar to Cyclin-D1-binding protein 1)
1341	1.000	5	5	Citrate lyase beta-like protein
1699	1.000	5	5	Similar to *Tribolium castaneum* ADP ribosylation factor 79F
1774	1.000	5	5	ns
1903	1.000	5	5	#N/A
1978	1.000	5	5	similar to conserved hypothetical protein
5368	1.000	5	5	ns
543	0.823	7	5	Similar to *Gryllus bimaculatus* mRNA, GBcontig05368
280	0.800	15	5	Ubiquinol-cytochrome c reductase
2185	0.717	13	5	ns
1414	0.682	8	5	Similar to mitochondrial ribosomal protein L36
1309	1.000	4	4	Similar *Tribolium castaneum* similar to B52 CG10851-PA
1412	1.000	4	4	Insect conserved protein
1721	1.000	4	4	Similar to Gryllus bimaculatus mRNA, GBcontig28218
5711	1.000	4	4	GalNAc transferase 6-like
7164	1.000	4	4	ns
14713	1.000	4	4	ns
855	0.956	7	4	Similar to *Tribolium castaneum* AGAP003463-PA
2020	**0.877**	**6**	**4**	***Prumna arctica* mitochondrion, complete genome**
267	0.825	6	4	Conserved hypothetical protein
730	0.823	5	4	Conserved hypothetical protein
874	**0.821**	**5**	**4**	**ES1 protein homolog, mitochondrial-like**
1231	0.816	5	4	Glutathione S-transferase
4679	0.810	5	4	Conserved hypothetical protein (zinc finger protein)

7046	0.777	8	4	ns
1847	0.773	9	4	Flap endonuclease-1
1177	0.773	6	4	Small nucleolar RNA
3433	0.704	6	4	Similar to zinc finger protein
989	0.688	8	4	*Gryllus pennsylvanicus* hypothetical accessory gland
99	0.667	8	4	Similar to extracellular proteinase inhibitor
726	0.609	11	4	Similar to Gryllus bimaculatus mRNA, GBcontig01128
2864	0.605	12	4	Conserved hypothetical protein
5727	0.524	9	4	Similar to CSL-type zinc finger protein
2989	0.444	14	4	#N/A
87	1.000	3	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig31800
580	1.000	3	3	Similar to *Nasonia vitripennis* p15-2a protein
937	1.000	3	3	Dynactin subunit 4 (*Dctn4*)
963	1.000	3	3	Similar to growth hormone-inducible soluble protein
1101	1.000	3	3	#N/A
1275	1.000	3	3	Protease regulatory subunit S10B
1306	1.000	3	3	Similar to translocase of outer membrane 7
1374	1.000	3	3	Conserved protein: unknown
1415	1.000	3	3	Myosin essential light chain
1513	1.000	3	3	UBX domain-containing protein
1667	1.000	3	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig12028
2182	1.000	3	3	Histone h2a
2658	1.000	3	3	ns
3084	1.000	3	3	Similar to *Glossina morsitans* mRNA

3432	1.000	3	3	Similar to *DnaJ* (*Hsp40*)
3566	1.000	3	3	ns
3758	1.000	3	3	**NADH dehydrogenase. Mitochondrial**
3843	1.000	3	3	Translation initiation factor 4 gamma
4655	1.000	3	3	Conserved protein: unknown
5777	1.000	3	3	Similar to transport and Golgi organization 1 (*Tango1*)
6030	1.000	3	3	Ethanolaminephosphotransferase
8373	1.000	3	3	Asparagine synthetase
9851	1.000	3	3	ns
14741	1.000	3	3	Similar to eritrophin-like protein 1
6271	0.995	3	3	ns
6026	0.994	3	3	Omega-amidase (*NIT2-B*)
4450	0.989	3	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig24459
861	0.980	4	3	Ribulose-5-phosphate-3-epimerase mRNA
586	0.974	4	3	ns
1147	0.969	4	3	protein ERGIC-53-like
1392	0.952	4	3	delta-coatomer protein
1369	0.950	5	3	Acyrthosiphon pisum outer dense fiber protein 3-like
827	0.826	5	3	aspartate aminotransferase
1790	0.790	6	3	ns
3732	0.788	4	3	#N/A
1084	**0.778**	**4**	**3**	**Cytochrome oxidase I (*COI*). Mitochondrial**
2100	0.773	4	3	Fructose-1,6-bisphosphatase
2292	0.700	7	3	Similar to Monodelphis domestica ORF

2	0.673	7	3	#N/A
5131	0.652	5	3	Golgi-associated microtubule-binding protein (*HOOK3*)
367	0.635	6	3	Similar to Tm-139 signal peptidase complex
4914	0.630	5	3	ns
541	0.630	5	3	Similar to *Tribolium castaneum* predicted protein
1372	0.624	8	3	ns
5067	0.618	6	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig12980
6557	0.605	6	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig07377
4913	0.426	16	3	Similar to Anopheles gambiae mRNA
2570	0.424	13	3	Similar to *Gryllus bimaculatus* mRNA, GBcontig26520