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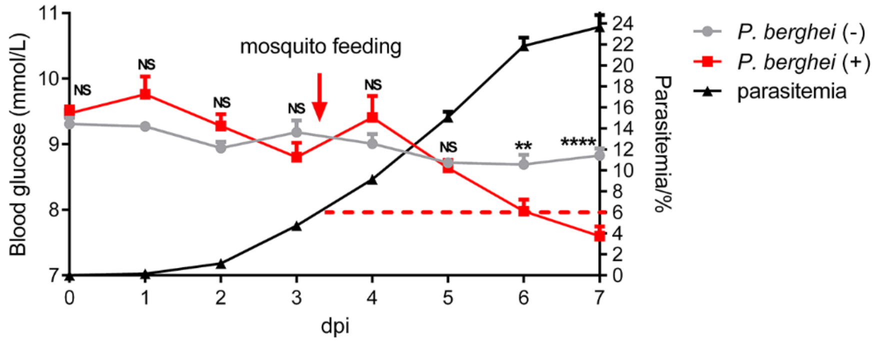

Figure S1. Daily blood glucose level and parasitemia in *P. berghei* infected mice, Related to Figure 1.

Blood glucose levels (left *y* axis) of Balb/c mice infected with *P. berghei* (red line) or without *P. berghei* (grey line), and the parasitemia (right *y* axis, black line) from 0 to 7 days post infection. Data were shown as mean ± SEM (n =10). Significance was determined by Student's *t* test. NS, not significant, **, $p < 0.01$, and ****, $p < 0.0001$

Supplementary Table 1: Significantly changed metabolites with corresponding correlation coefficients in the mosquito extract between NB and IB Group. Related to Figure 1. Lipids: R-CH_3, R-CH_2, CH_2CH_2CO, $CH_2C{=}C$, UFA: unsaturated fatty acids; PC: phosphorylcholine; GPC: glycerophosphocholine; DMA: dimethylamine; ADP: adenosine diphosphate; IMP: Inosine 5'-phosphate.

	Keys	Metabolite	NB1D vs. IB1D
Lipids	1	R-CH_3	-0.98
	2	R-CH_2	-0.99
	3	CH_2CH_2CO	-0.97
	4	$CH_2C{=}C$	-0.92
	5	UFA	-0.97
Glucose & TCA Cycles	6	trehalose	-0.85
	7	glucose	-0.88
	8	pyruvate	0.60
	9	succinate	-0.87
	10	citrate	-0.77
	11	acetate	0.85
	12	acetoacetate	0.79
Amino acids	13	tyrosine	0.69
Cholines	14	choline	0.74
	15	PC	0.79
	16	GPC	-0.96
	17	DMA	0.60
Nucleotides & Nucleosides	18	xanthurate	0.74
	19	inosine	-0.66
	20	ADP	-0.88
	21	IMP	0.61

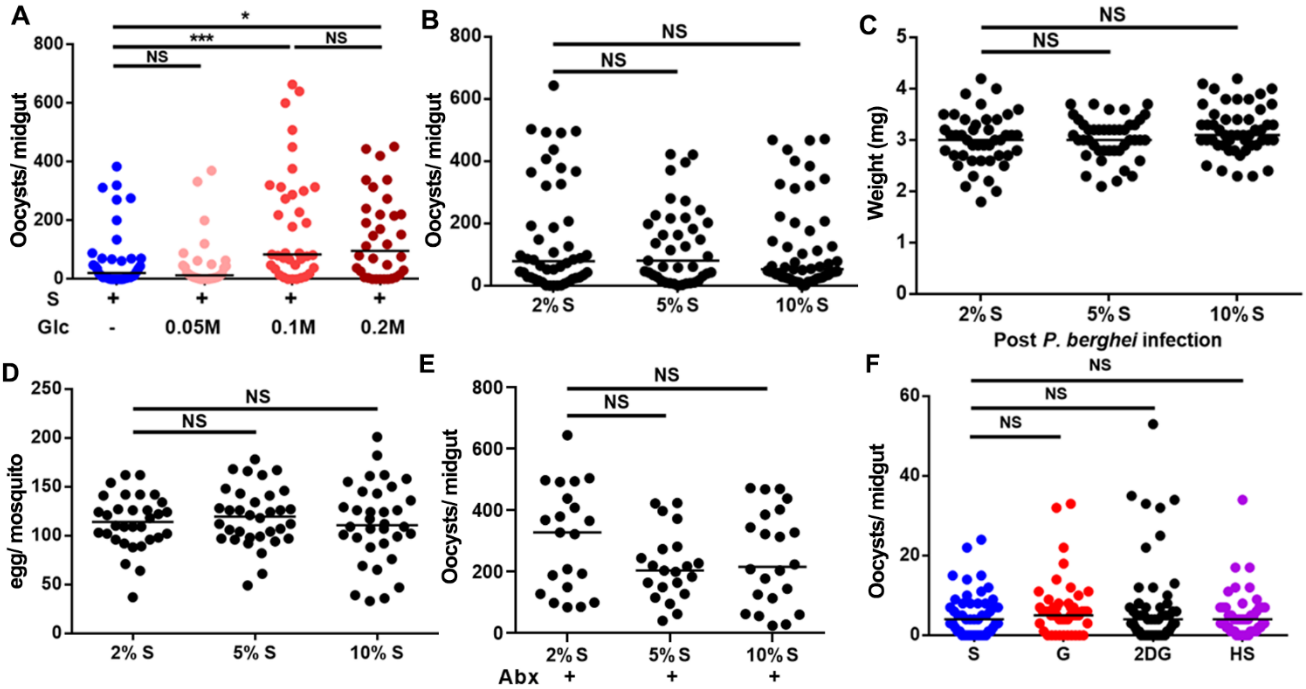

Figure S2. The influence of sugar treatments on *An. stephensi*, Related to Figure 2.

(A) *P. berghei* oocyst intensity in mosquitoes fed with 2% sucrose containing 0 M, 0.05 M, 0.1 M and 0.2 M glucose, respectively.

(B) *P. berghei* oocyst intensity in mosquitoes fed with 2%, 5%, and 10% sucrose.

(C) Weight of fully engorged mosquitoes fed with 2%, 5%, and 10% sucrose.

(D) The number of mature eggs in ovaries of mosquitoes fed with 2%, 5%, and 10% sucrose.

(E) *P. berghei* oocyst intensity in antibiotics treated mosquitoes (Abx) fed with 2%, 5%, and 10% sucrose.

(F) *P. berghei* oocyst intensity in mosquitoes fed with S, G, 2-DG and HS diets post blood meal.

Each dot represents an individual mosquito and horizontal lines represent the medians. Results shown in A-F were pooled from at least two independent experiments. Significance in A, B, E and F was determined by ANOVA with Dunn's tests. Significance in C and D was determined by ANOVA with Dunnett tests. NS, not significant, *, $p < 0.05$, and ***, $p < 0.001$. S, 2% sucrose; G, 2% sucrose + 0.1 M glucose; 2-DG, 2% sucrose + 0.1 M glucose + 5 mM 2-DG; HS, 10% sucrose.

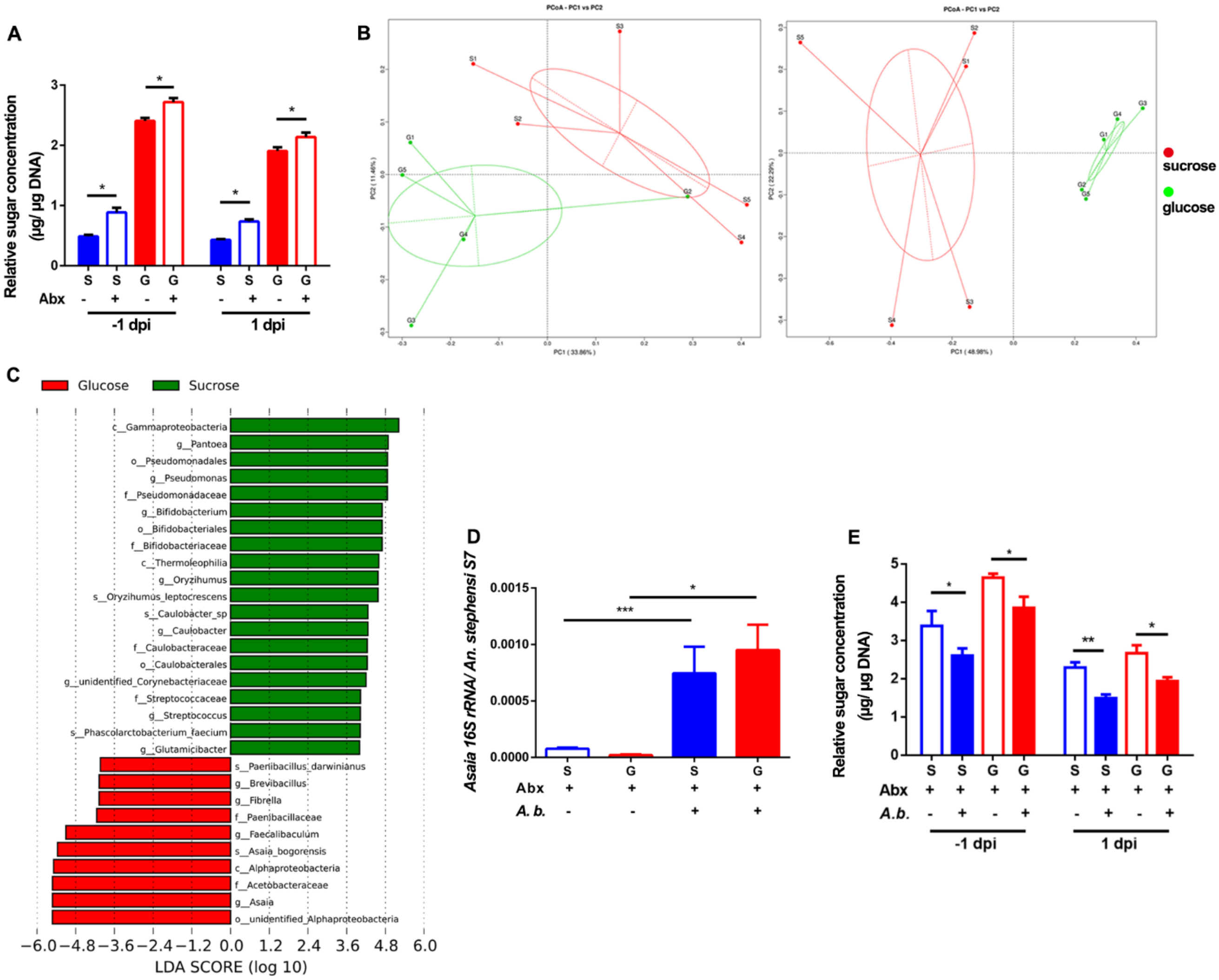

Figure S3. The influence of *A. bogorensis* on glucose consumption and *P. berghei* infection, Related to Figure 3.

(A) The relative concentration of total sugar (glucose + trehalose) in the midgut of antibiotics treated mosquitoes fed on different sugar diets 1 day prior to (-1 dpi) and 1 day (1 dpi) post infection, respectively.

(B) Principal Component Analysis (PCA) of bacterial composition by unweighted (left panel) and weighted (right panel) unifrac analyses. Each plot represents 5 midguts as a biological repeat.

(C) LEfSe analysis of midgut microbiota fed on S and G diets. LDA scores showed significant bacterial differences within groups at the different levels. Green, mosquitoes fed on 2% sucrose; Red, mosquitoes fed on 2% sucrose + 0.1 M glucose.

(D) The abundance of *A. bogorensis* in the midgut of *An. stephensi* determined by qPCR.

(E) The relative concentration of total sugar (glucose and trehalose) in the midgut of mosquitoes 1 day prior to (-1 dpi) and 1 day (1 dpi) post infection.

Glucose and trehalose concentrations in A and E were normalized to genomic DNA extracted from midgut. Significance in A, and E was determined by Student's t test, in D was determined by ANOVA with Dunnett tests. Data were shown as mean ± SEM (A and E, $n = 5$, D, $n = 10$). *, $p < 0.05$, **, $p < 0.01$, and ***, $p < 0.001$, S, 2% sucrose; G, 2% sucrose + 0.1 M glucose, Abx, antibiotics treatment, *A. b.*, *A. bogorensis* re-colonization.

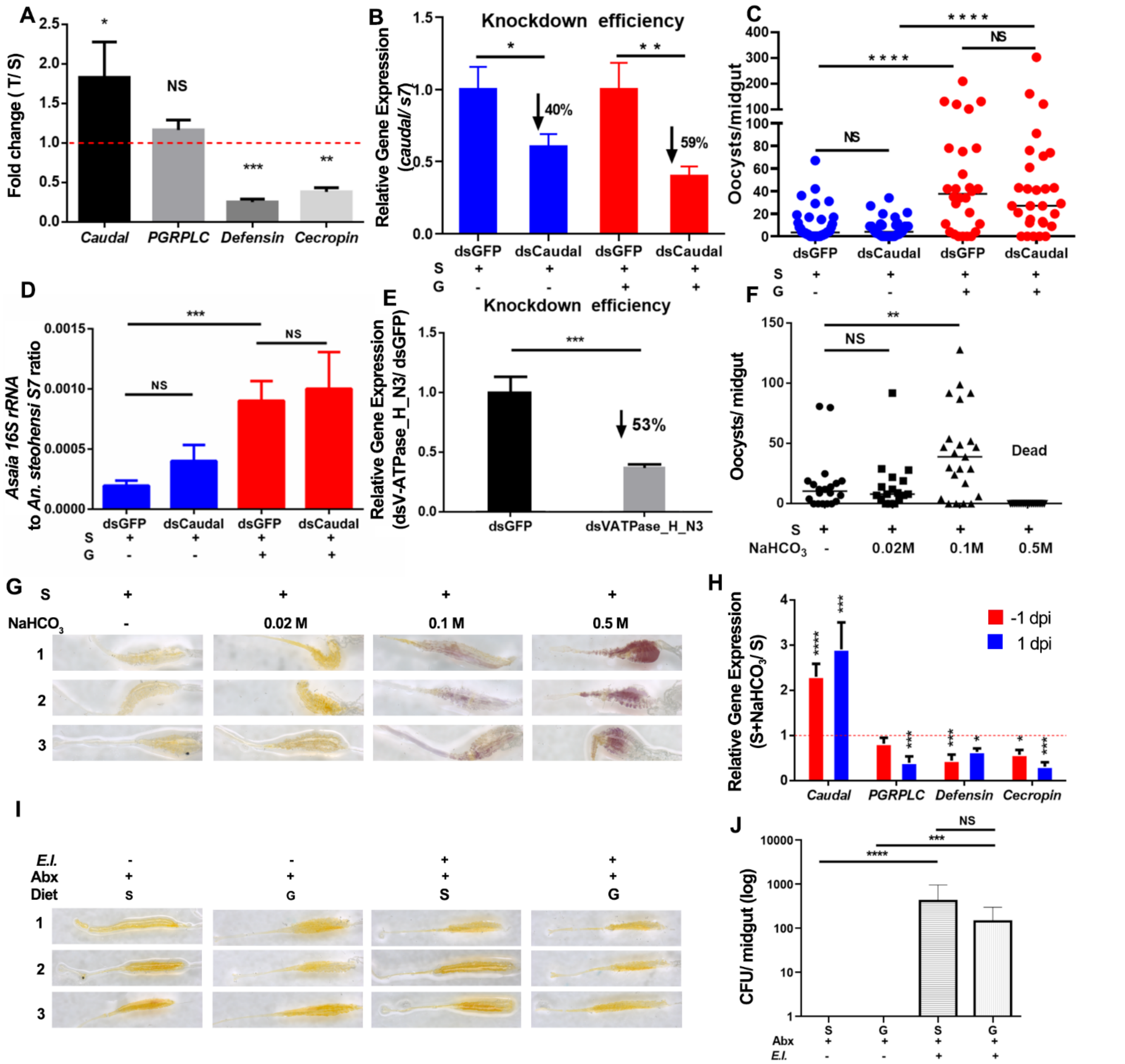

Figure S4. Influence of mosquito midgut pH on *P. berghei* infection, Related to Figures 4 and 5.

(A) The relative expression levels of *caudal, pgrp-lc, defensin,* and *cecropin* in mosquitoes fed with T at -1 dpi. The expression levels of genes in T fed mosquitoes were normalized to the gene's expression in S fed ones.

(B) *Caudal* knocking down efficiency. Relative expression level of *Caudal* was normalized to that in dsGFP control. Ribosomal gene *S7* used as an internal control. Error bars indicate standard error (n = 8). Results from one of two independent experiments are shown.

(C) *P. berghei* oocyst intensity in dsRNA treated mosquitoes fed with S and G diets, respectively.

(D) The abundance of *A. bogorensis* in the midgut of S and G fed *An. stephensi* treated with dsRNA.

(E) *V-ATPase_H_N3* knocking down efficiency. Relative expression level of *V-ATPase_H_N3* was normalized to that in dsGFP control. Ribosomal gene *S7* used as an internal control. Error bars indicate standard error of the mean (n =10). Results from one of three independent experiments are shown.

(F) *P. berghei* oocyst intensity in mosquitoes fed with S and S + 0.02 M, 0.1 M and 0.5 M $NaHCO_3$, respectively.

(G) The pH staining of mosquito midguts fed with increasing concentration of $NaHCO_3$ by m-cresol purple. Images are the three representatives of at least five individual mosquito midguts.

(H) The expression levels of *caudal, pgrp-lc, defensin,* and *cecropin* in mosquitoes fed with S + 0.1 M $NaHCO_3$ diet one day prior to (-1 dpi) and one day (1 dpi) post infection, were normalized to the gene's expression of the ones fed with S diet.

(I) Influence of *Enterobacter* sp. re-colonization on the pH of midguts by m-cresol purple. Images are three representatives of at least five individual mosquito midguts.

(J) The CFU of *Enterobacter* sp. colonized in the midgut of antibiotics treated *An. stephensi*.

Each dot in C and F represents an individual mosquito and horizontal lines represent the medians. Significance in A, B, E and H was determined by Student's *t* test. Significance in D and J was determined by ANOVA with Tukey tests. Error bars indicate standard error of the mean (A, B, E and H, n = 8; D and J, n = 10). Results shown in C and F were pooled from at least two independent experiments. Significance was determined by ANOVA with Dunn's tests. NS, not significant, *, $p < 0.05$, **, $p < 0.01$, ***, $p < 0.001$, and ****, $p < 0.0001$. T, 2% sucrose + 0.1 M trehalose; S, 2% sucrose; G, 2% sucrose + 0.1 M glucose.

Supplementary Table 3: Significantly changed metabolites in conditioned media from *A. bogorensis* grown. Related to Figure 5. S, 2% sucrose; G, 2% sucrose + 0.1 M glucose; T, 2% sucrose + 0.1 M trehalose. ***, P<0.001.

Keys	Metabolites	Fold change (G/S)	Fold change (T/S)
1	sucrose	1.93 ***	0.39 ***
2	glucose	0.45 ***	0.7 ***
3	trehalose	1.15 ***	86.11 ***
4	citrate	0.65 ***	0.5 ***
5	succinate	0.56 ***	0.65 ***
6	ethanol	0.70 ***	0.55 ***
7	valine	0.62 ***	0.48 ***
8	isoleucine	0.64 ***	0.51 ***
9	leucine	0.66 ***	0.49 ***
10	alanine	0.58 ***	0.41 ***
11	tyrosine	0.70 ***	0.53 ***
12	phenylalanine	0.69 ***	0.53 ***
13	trimethylamine	2.22 ***	0.51 ***
14	dimethylamine	0.65 ***	0.51 ***
15	inosine	1.13 ***	0.49 ***

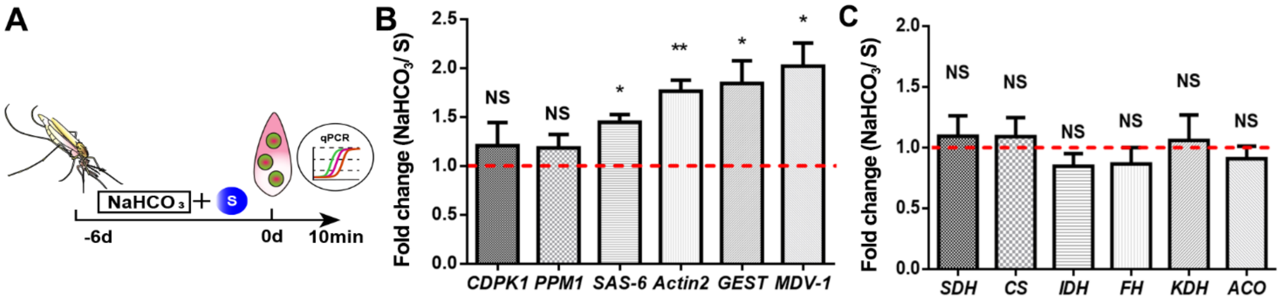

Figure S5. Addition of $NaCHO_3$ induces the expression of genes associated with microgamete development, Related to Figure 6.

(A) Workflow of $NaCHO_3$ treatment and qPCR assay.

(B) Quantification of expression levels of genes associated with male gametogenesis. The expression level of male gametogenesis related genes in $NaHCO_3$ (0.1 M) supplemented mosquitoes was normalized to that in mosquitoes fed on S diet.

(C) Quantification of expression levels of genes associated with mitochondrial energy metabolism. *SDH*, succinate dehydrogenase; *CS*, citrate synthase; *IDH*, isocitrate dehydrogenase; *FH*, fumarate hydratase; *KDH*, alpha-Ketoglutarate dehydrogenase; *ACO*, acyl-CoA oxidase. The expression level of target genes in $NaHCO_3$ (0.1 M) supplemented mosquitoes was normalized to that in mosquitoes fed on S diet.

Significance in B and C was determined by Student’s *t* test. Error bars indicate standard error of the mean (n = 8). NS, not significant, *, $p < 0.05$, and **, $p < 0.01$. S, 2% sucrose.

Supplementary Table 4: qRT-PCR primers used in this study. Related to Figure 3, Figure 6, Figure 7, Figure S2, Figure S3, Figure S4 and Figure S5.

Gene	Forward primer	Reverse primer	Reference
VATPase_H_N3	TGGCATCAGCACGCTCATCAG	TCCTTCGCACAGTCGCTCAGA	This paper
Caudal	CAAGGACCGCAAGCAGAAGAA	CGATTGACCGCCGAGACC	This paper
Ab16S rRNA	GATGACATGAACCGTGCCCTGG	ACCTCCGTCTTGATGGCGTACA	(Favia et al., 2007)
AsteS7	TGCGGAGCGTCGTATTCTGC	ACACAGCGGTGAGCGTTCG	(Salazar et al., 1993)
PbCDPK1	TGGTGGGCAAAACGATCAAGA	GCTTCCTCAGCCGTACATCT	This paper
PbPPM1	AGGGGATAGTCGCTGTGTCTT	ACCTCGGCATACTCCTAAGCAT	This paper
PbAcint2	TTCTTGATAGTGGTGATGGCGTAA	CGATTTCTCTTTCAGCGGTTGTAG	This paper
PbGEST	CTACATTCGAGAGCCATGATACTT	AAACTGTGTCACCAATTTCAAGAT	This paper
PbMDV-1	TCCAACATCAACCATAGGGTGTCT	TGCCTTGCCTCCACTTCCA	This paper
PbSAS-6	AAAGGATATGGGCGTGATGGAT	ACACTCATTAGATGTACCACCACT	This paper
Pb18S	AAGCATTAAATAAAGCGAATACATCCTTAC	GGAGATTGGTTTTGACGTTTATGTG	(Baptista et al., 2010)
PbACO	TGGCACCAGAATATGGAGCTACAA	TCTCGTCATCTCGTCCTGTTTGTT	This paper
PbKDH	ATGAACATCCAGACGCACTAG	AGGTAACAACATAACAACTCCAGA	This paper
PbIDH	GAGGGTTTGTTTGGGCGTGTAAA	GGCTTCCATATCCTTGTGCAACTG	This paper
PbCS	TTCACGAGAGCTATATTGCCGAG	TAGGGTGTGTAAATGGTGGTATGC	This paper
PbSDH	TCGCTGGATAGTTGATACAAGAGA	GCACACTGAGCAATTCATTATTCC	This paper
PbFH	GCCAACAACTGCTGGAAGA	GCCAAAGAAATTAAAGACGCATTG	This paper
AsteCec	GCTGCTCTTTCTCGTTGCG	CGGCACCTTCCACCTTCT	This paper
AsteDef	CCGCCTTGAACACGCTCCT	GCTGCCGACACCGAATCCA	This paper
AsteLC	TGTGCCATCGTAGCGGTCAT	AGCCACTCGGTTCTCGTCAC	This paper