Supporting Information for:

Elbers JP, Clostio RW and Taylor SS (2016) Population genetic inferences using immune gene SNPs mirror patterns inferred by microsatellites. Molecular Ecology Resources.

Table S1 Sequencing metrics for *Gopherus polyphemus* samples. Percent UR for percent of total reads that were unique, Percent URA for percent of unique reads that were alignable, Mean coverage for mean number of reads across the target region, Percent 20x for percent of bases in target region with greater than 20x coverage, No. genes for number of genes, and No. exons for number of exons.

	Sample	Total reads	Percent UR	Percent URA	Mean coverage	Percent 20x	No. genes	No. exons
1	AL102	3,212,450	42.5489	98.7624	64.702327	70.9051	592	4,107
2	AL103	4,465,410	41.6559	98.7366	86.236747	74.194	598	4,238
3	AL106	3,359,715	45.6208	98.8027	71.663432	71.6972	600	4,156
4	AL108	2,819,070	46.9525	98.4416	61.437226	72.4334	600	4,222
5	FL846	3,053,761	48.2949	98.7728	68.408722	69.2006	594	4,120
6	FL855	3,001,641	49.9861	98.8119	70.02287	70.426	587	4,162
7	FL857	4,126,014	48.3302	98.7755	91.599757	73.6741	595	4,209
8	FL880	2,495,515	47.5824	98.5998	55.003413	67.7526	592	4,140
9	GA1044	2,735,000	50.4835	98.8161	64.467663	69.2348	594	4,135
10	GA1435	3,114,664	48.0062	98.8188	69.54348	69.2231	593	4,088
11	GA1835	3,160,564	47.5032	98.8015	69.893149	70.4834	595	4,135
12	GA462	1,692,328	50.9997	98.7798	40.600786	61.147	586	3,934
13	LA62	2,490,648	47.5604	98.7996	55.582373	67.2087	592	4,032
14	LA66	2,366,268	48.6917	98.6262	53.254455	65.3586	592	3,992
15	LA77	3,449,116	46.1951	98.7934	74.612173	72.2789	600	4,162
16	LA78	1,920,641	55.6212	98.8716	50.102979	63.859	596	3,899

Table S2 All genes with di-allelic, polymorphic SNPs from 16 *Gopherus polyphemus* samples.

Gene
1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1-like
16 kDa beta-galactoside-binding lectin-like
25-hydroxyvitamin D-1 alpha hydroxylase, mitochondrial
3-phosphoinositide dependent protein kinase 1
4-hydroxy-2-oxoglutarate aldolase 1
A.superbus venom factor 1-like
acetylcholinesterase-like
active BCR-related
adenosine A2b receptor
adenosine A3 receptor
ADP-ribosylation factor-like 13B
alpha-2-macroglobulin
alpha-2-macroglobulin-like
alpha-2-macroglobulin-like 1
alpha-2-macroglobulin-like protein 1
angiogenin-2-like
ankyrin repeat and death domain containing 1A
annexin A3
antigen-presenting glycoprotein CD1d1-like
apolipoprotein A-IV
apoptosis-associated speck-like protein containing a CARD
aquaporin 4
arrestin, beta 2
ATPase, Cu++ transporting, alpha polypeptide
autophagy related 5
B-cell CLL/lymphoma 10
B-cell CLL/lymphoma 2
B-cell CLL/lymphoma 3
B-cell receptor-associated protein 29
B-cell receptor-associated protein 31
B-cell scaffold protein with ankyrin repeats 1
B and T lymphocyte associated
B lymphoid tyrosine kinase
bactericidal permeability-increasing protein-like
bactericidal/permeability-increasing protein
basic leucine zipper transcription factor, ATF-like
beta-2-microglobulin
bone morphogenetic protein 6
bone morphogenetic protein receptor, type IA
breakpoint cluster region
butyrophilin-like protein 9
butyrophilin subfamily 1 member A1-like
butyrophilin subfamily 2 member A1-like
butyrophilin subfamily 3 member A2-like
butyrophilin subfamily 3 member A3-like
C-C chemokine receptor type 5-like
C-C motif chemokine 5-like
C-type lectin domain family 1 member A-like
C-type lectin domain family 2 member B-like

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Gene
C-type lectin domain family 2 member D-like
C-type lectin domain family 4 member D-like
C-type lectin domain family 4 member E-like
C-type lectin domain family 4 member G-like
C-X-C motif chemokine 10-like
C3a anaphylatoxin chemotactic receptor-like
C4b-binding protein alpha chain-like
C5a anaphylatoxin chemotactic receptor 1-like
cactin, spliceosome C complex subunit
calcium binding and coiled-coil domain 2
calcium channel, voltage-dependent, beta 3 subunit
calcium channel, voltage-dependent, beta 4 subunit
calcium/calmodulin-dependent protein kinase IV
calicin
cardiotrophin-like cytokine factor 1
caspase recruitment domain family, member 9
cathepsin G-like
Cbl proto-oncogene B, E3 ubiquitin protein ligase
CD14 molecule
CD180 molecule
CD226 molecule
CD247 molecule
CD274 molecule
CD36 molecule (thrombospondin receptor)
CD37 molecule
CD3e molecule, epsilon (CD3-TCR complex)
CD40 molecule, TNF receptor superfamily member 5
CD74 molecule, major histocompatibility complex, class II invariant chain
CD79a molecule, immunoglobulin-associated alpha
CD79b molecule, immunoglobulin-associated beta
CD82 molecule
cell adhesion molecule 1
cell adhesion molecule 4
cell division cycle 37
cell division cycle 37-like 1
centromere protein F, 350/400kDa
chemokine (C-C motif) receptor 7
chemokine (C-X3-C motif) receptor 1
chromosome unknown open reading frame, human C9orf84
cis-aconitate decarboxylase-like
class I histocompatibility antigen, F10 alpha chain-like
class II histocompatibility antigen, M alpha chain
class II, major histocompatibility complex, transactivator
coagulation factor II (thrombin) receptor-like 1
coagulation factor XIII, B polypeptide
coenzyme Q10 homolog B (S. cerevisiae)
coiled-coil domain containing 142
coiled-coil domain containing 151
coiled-coil domain containing 170

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Table S2 – *Continued from previous page*

Gene
collagen, type III, alpha 1
collectin-46-like
collectin sub-family member 12
complement C1r-B subcomponent-like
complement C2-like
complement C3-like
complement component 1, q subcomponent binding protein
complement component 1, q subcomponent, A chain
complement component 1, r subcomponent
complement component 1, s subcomponent
complement component 8, alpha polypeptide
complement decay-accelerating factor-like
complement factor B
complement factor H
complement factor properdin
complement receptor type 2-like
CUB and Sushi multiple domains 1
cyclic GMP-AMP synthase-like
cytochrome P450 27C1
cytotoxic and regulatory T cell molecule
cytotoxic T-lymphocyte-associated protein 4
DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
death-associated protein kinase 1
death-associated protein kinase 2-like
death-associated protein kinase 3
death-associated protein kinase 3-like
dedicator of cytokinesis 2
dedicator of cytokinesis protein 2-like
DEXH (Asp-Glu-X-His) box polypeptide 58
discs, large homolog 1 (Drosophila)
dispanin subfamily A member 2b
DLA class II histocompatibility antigen, DR-1 beta chain-like
DnaJ (Hsp40) homolog, subfamily A, member 3
docking protein 6
dual specificity phosphatase 10
duodenase-1-like
dynactin 1
E3 ubiquitin-protein ligase TRIM39-like
E3 ubiquitin-protein ligase TRIM39 pseudogene
E3 ubiquitin-protein ligase TRIM56-like
eomesodermin
epiregulin
excision repair cross-complementation group 1
exonuclease 1
exosome component 3
extracellular matrix protein 1
family with sequence similarity 105, member A
family with sequence similarity 177, member A1
family with sequence similarity 83, member E

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Table S2 – *Continued from previous page*

Gene
Fanconi anemia, complementation group F
Fas cell surface death receptor
Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
feline Gardner-Rasheed sarcoma viral oncogene homolog
feline sarcoma oncogene
fer (fps/fes related) tyrosine kinase
ficolin-1-like
ficolin-2-like
ficolin (collagen/fibrinogen domain containing) 3
fucokinase
FYN oncogene related to SRC, FGR, YES
G-protein coupled receptor 183-like
G patch domain and KOW motifs
gastrula zinc finger protein XlCGF57.1-like
GATA binding protein 3
glucosaminyl (N-acetyl) transferase 3, mucin type
glutamyl-prolyl-tRNA synthetase
glutathione peroxidase 1
glutathione peroxidase 2 (gastrointestinal)
glycosylphosphatidylinositol specific phospholipase D1
granzyme-like protein 2
GRB2-associated binding protein 2
growth arrest-specific 6
GTP cyclohydrolase 1
GTP cyclohydrolase 1-like
H-2 class II histocompatibility antigen, A-R alpha chain-like
H-2 class II histocompatibility antigen, E-S beta chain-like
H2.0-like homeobox
heat shock 60kDa protein 1 (chaperonin)
hemopexin
heparan sulfate (glucosamine) 3-O-sulfotransferase 4
HLA class II histocompatibility antigen, DP alpha 1 chain-like
HLA class II histocompatibility antigen, DR alpha chain-like
HLA class II histocompatibility antigen, DR beta 5 chain-like
HLA class II histocompatibility antigen, DRB1-15 beta chain-like
immunoresponsive 1 homolog (mouse)
importin 11
indoleamine 2,3-dioxygenase 1
inositol polyphosphate-5-phosphatase, 145kDa
insulin-like growth factor 1 receptor
integrin alpha-L-like
interferon-induced guanylate-binding protein 1
interferon-induced guanylate-binding protein 1-like
interferon-induced protein 44-like
interferon-induced protein with tetratricopeptide repeats 1-like
interferon-induced protein with tetratricopeptide repeats 5
interferon induced transmembrane protein 5
interferon kappa-like
interferon regulatory factor 3

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Table S2 – *Continued from previous page*

Gene
interferon regulatory factor 7
interferon regulatory factor 8
interferon, kappa
interleukin-1 receptor-associated kinase 1
interleukin-36 receptor antagonist protein
interleukin 1 receptor-like 1
interleukin 12 receptor, beta 1
interleukin 12A
interleukin 12B
interleukin 18
interleukin 18 receptor 1
interleukin 20 receptor beta
interleukin 23 receptor
interleukin 27 receptor, alpha
interleukin 4 receptor
interleukin 6
interleukin 7 receptor
ISG15 ubiquitin-like modifier
Janus kinase 2
Janus kinase 3
kelch-like family member 24
kelch-like family member 35
kelch-like family member 38
kelch-like family member 6
kelch repeat and BTB (POZ) domain containing 8
keratin, type II cytoskeletal 1-like
killer cell lectin-like receptor subfamily B member 1B allele C
killer cell lectin-like receptor subfamily F member 1
killer cell lectin-like receptor subfamily G member 1
kynureninase
lectin, galactoside-binding, soluble, 2
lectin, galactoside-binding, soluble, 8
leucine rich repeat (in FLII) interacting protein 2
leucine rich repeat containing 70
lymphocyte-specific protein tyrosine kinase
lymphocyte cytosolic protein 1 (L-plastin)
lymphotoxin alpha
lysosomal trafficking regulator
Mab-21 domain containing 1
macrophage migration inhibitory factor
major histocompatibility complex class I-related gene protein-like
mannan-binding lectin serine peptidase 1
mannan-binding lectin serine peptidase 2
mast cell protease 1A-like
mast cell protease 3-like
mediator of RNA polymerase II transcription subunit 1-like
melanotransferrin-like
membrane-associated ring finger (C3HC4) 1, E3 ubiquitin protein ligase
membrane cofactor protein-like

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Table S2 – *Continued from previous page*

Gene
mitochondrial carrier 2
mitogen-activated protein kinase-activated protein kinase 2
mitogen-activated protein kinase kinase 7
mitogen-activated protein kinase kinase kinase 14
mothers against decapentaplegic homolog 6-like
mucosa-associated lymphoid tissue lymphoma translocation protein 1-like
mucosa associated lymphoid tissue lymphoma translocation gene 1
mutL homolog 1
mutS homolog 6
myelin-oligodendrocyte glycoprotein-like
myosin IF
myosin light chain, phosphorylatable, fast skeletal muscle
N(alpha)-acetyltransferase 25, NatB auxiliary subunit
NACHT, LRR and PYD domains-containing protein 1-like
NACHT, LRR and PYD domains-containing protein 12-like
natural killer cells antigen CD94-like
NCK-associated protein 1-like
Nedd4 family interacting protein 1
negative regulator of ubiquitin-like proteins 1
NK2 homeobox 3
NLR family member X1
NLR family, CARD domain containing 5
nuclear factor of activated T-cells, cytoplasmic 2-like
nuclear fac. of kappa light polypep. gene enhancer in B-cells 2 (p49/p100)
nuclear fac. of kappa light polypep. gene enhancer in B-cells inhibitor, alpha
olfactomedin-4-like
olfactomedin-like
olfactomedin 4
oncoprotein induced transcript 3
opioid receptor, kappa 1
OTU deubiquitinase 7B
OTU deubiquitinase with linear linkage specificity
ovostatin-like
paired amphipathic helix protein Sin3a-like
PAX interacting (with transcription-activation domain) protein 1
peptidase domain containing associated with muscle regeneration 1
peptidoglycan recognition protein 2
peptidoglycan recognition protein 3-like
peroxisome proliferator-activated receptor gamma
phosphatidylinositol 4-kinase type 2 alpha
phosphodiesterase 4B, cAMP-specific
phosphodiesterase 4C, cAMP-specific
phosphodiesterase 4D, cAMP-specific
phosphoinositide-3-kinase adaptor protein 1
phospholipase A2, group IB (pancreas)
phospholipase A2, minor isoenzyme-like
phospholipase C, gamma 1
phospholipase D2-like
phospholipid scramblase 2

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Table S2 – *Continued from previous page*

Gene
phospholipid scramblase family, member 5
pleckstrin hom. domain contain., family A (phosphoinositide bind. spec.) member 1
poliovirus receptor-related 2 (herpesvirus entry mediator B)
poly (ADP-ribose) polymerase family, member 9
poly [ADP-ribose] polymerase 9-like
polymerase (RNA) III (DNA directed) polypeptide C (62kD)
polymerase (RNA) III (DNA directed) polypeptide D, 44kDa
polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa
polymerase (RNA) III (DNA directed) polypeptide G (32kD)
polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like
potassium channel tetramerization domain containing 7
POU class 2 homeobox 2
presenilin 2
programmed cell death 1 ligand 2-like
proteasome (prosome, macropain) subunit, beta type, 4
protein kinase C, beta
protein kinase C, delta
protein kinase C, epsilon
protein kinase C, theta
protein kinase C, zeta
protein kinase D2
protein phosphatase 2, regulatory subunit B'', gamma
protein phosphatase 3, catalytic subunit, beta isozyme
protein tyrosine phosphatase, non-receptor type 2
protein tyrosine phosphatase, non-receptor type 22 (lymphoid)
protein tyrosine phosphatase, non-receptor type 6
protein tyrosine phosphatase, receptor type, C
protein tyrosine phosphatase, receptor type, N polypeptide 2
purine nucleoside phosphorylase
purinergic receptor P2X, ligand-gated ion channel, 7
pyroglutamyl-peptidase I-like
RAB guanine nucleotide exchange factor (GEF) 1
RAB17, member RAS oncogene family
RAB27A, member RAS oncogene family
RanBP-type and C3HC4-type zinc finger containing 1
rano class II histocompatibility antigen, A beta chain-like
RAR-related orphan receptor C
RAS guanyl releasing protein 1 (calcium and DAG-regulated)
receptor-interacting serine-threonine kinase 2
receptor-interacting serine/threonine-protein kinase 2-like
regulator of cell cycle
retinoic acid receptor, alpha
Rho guanine nucleotide exchange factor (GEF) 37
RIB43A domain with coiled-coils 1
ribonuclease-like
ribosomal protein L13a
ribosomal protein S6 kinase, 90kDa, polypeptide 3
ribosomal protein S6 kinase, 90kDa, polypeptide 6
ring finger and CCCH-type domains 1

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Table S2 – *Continued from previous page*

Gene
ring finger and CCCH-type domains 2
ring finger protein 135
ring finger protein 19B
ring finger protein 31
S100 calcium binding protein A14
SAM and SH3 domain-containing protein 1
SAM and SH3 domain containing 3
SAM domain and HD domain 1
SAM domain, SH3 domain and nuclear localization signals 1
Sec61 alpha 1 subunit (S. cerevisiae)
sema domain, Ig, TM and short cytoplasmic domain, (semaphorin) 4A
sema domain, Ig, TM and short cytoplasmic domain, (semaphorin) 4B
semaphorin-7A-like
semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)
serine/threonine kinase 11
serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
SH2 domain containing 1A
SH2 domain containing 1B
SH2B adaptor protein 2
sialidase 2 (cytosolic sialidase)
signal transducer and activator of transcription 6, interleukin-4 induced
SIN3 transcription regulator family member A
sirtuin 1
SMAD family member 6
solute carrier family 26 (anion exchanger), member 6
solute carrier family 26 (anion exchanger), member 8
solute carrier family 26 (anion exchanger), member 9
solute carrier family 26, member 10
solute carrier family 30 (zinc transporter), member 8
spinster homolog 1 (Drosophila)
spinster homolog 2 (Drosophila)
spinster homolog 3 (Drosophila)
spleen tyrosine kinase
src kinase associated phosphoprotein 1
src kinase associated phosphoprotein 2
steroidogenic acute regulatory protein
steroidogenic acute regulatory protein, mitochondrial-like
stomatin (EPB72)-like 2
strawberry notch homolog 1 (Drosophila)
strawberry notch homolog 2 (Drosophila)
suppressor of cytokine signaling 5
suppressor of cytokine signaling 5-like
suppressor of Ty 6 homolog (S. cerevisiae)
suppressor of variegation 3-9 homolog 1 (Drosophila)
SWAP switching B-cell complex 70kDa subunit
synaptotagmin binding, cytoplasmic RNA interacting protein
syntaxin 11
syntaxin 19
syntaxin binding protein 2

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Table S2 – *Continued from previous page*

Gene
syntaxin binding protein 3
T-box 21
TANK-binding kinase 1
tec protein tyrosine kinase
tetraspanin 19
thaicobrin-like
thrombospondin 1
thymocyte selection associated
thymocyte selection associated family member 2
TLR4 interactor with leucine-rich repeats
TNF receptor-associated factor 1-like
TNF receptor-associated factor 2
TNF receptor-associated factor 3
TNF receptor-associated factor 6, E3 ubiquitin protein ligase
TNFAIP3 interacting protein 2
TNFAIP3 interacting protein 3
toll-interleukin 1 receptor (TIR) domain containing adaptor protein
toll-like receptor 13
toll-like receptor 2
toll-like receptor 7
toll-like receptor 8
toll-like receptor adaptor molecule 1
toll-like receptor adaptor molecule 2
transferrin
transforming growth factor, beta 2
transforming growth factor, beta 3
transforming growth factor, beta receptor III
transforming growth factor, beta receptor III-like
transient receptor potential cation channel subfamily M member 4-like
transient receptor potential cation channel, subfamily M, member 4
translation machinery associated 16 homolog (S. cerevisiae)
transmembrane protein 125
transmembrane protein 167A
tripartite motif-containing protein 10-like
tripartite motif-containing protein 7-like
tripartite motif containing 56
tumor necrosis factor (ligand) superfamily, member 13b
tumor necrosis factor receptor superfamily member 14-like
tumor necrosis factor receptor superfamily member 5-like
tumor necrosis factor receptor superfamily, member 14
tumor necrosis factor, alpha-induced protein 3
TXK tyrosine kinase
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta
UBA domain containing 2
unc-13 homolog D (C. elegans)
unc-93 homolog B1 (C. elegans)
uncharacterized LOC101938270
uncharacterized LOC101938480
uncharacterized LOC101940718

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Table S2 – *Continued from previous page*

Gene
uncharacterized LOC101941368
uncharacterized LOC101944094
uncharacterized LOC101945191
uncharacterized LOC101945921
uncharacterized LOC101945971
uncharacterized LOC101948866
uncharacterized LOC101948974
uncharacterized LOC101949200
uncharacterized LOC101949947
uncharacterized LOC101950806
uncharacterized LOC101950941
uncharacterized LOC101950982
uncharacterized LOC101951626
uncharacterized LOC103305939
uncharacterized LOC103305969
uncharacterized LOC103305996
uncharacterized LOC103306364
uncharacterized LOC103306443
uncharacterized LOC103306956
uncharacterized LOC103307015
uncharacterized protein-like
v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
v-rel avian reticuloendotheliosis viral oncogene homolog A
v-rel avian reticuloendotheliosis viral oncogene homolog B
v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
vav 1 guanine nucleotide exchange factor
vav 3 guanine nucleotide exchange factor
VCP-interacting membrane protein
veficolin-1-like
venom factor-like
wingless-type MMTV integration site family, member 5A
Wiskott-Aldrich syndrome
X-ray repair complementing defective repair in Chinese hamster cells 4
Z-DNA binding protein 1
zeta-chain (TCR) associated protein kinase 70kDa
zinc-binding protein A33-like
zinc finger and BTB domain containing 41
zinc finger protein 239-like
zinc finger protein 271-like
zinc finger protein 418-like
zinc finger protein 436-like
zinc finger protein 501-like
zinc finger protein 551-like
zinc finger protein 572-like
zinc finger protein 850-like
zinc finger protein 883-like
zinc finger protein RFP-like
zinc finger, SWIM-type containing 7
zona pellucida sperm-binding protein 3-like

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Table S2 – *Continued from previous page*

Gene
zona pellucida sperm-binding protein 4-like

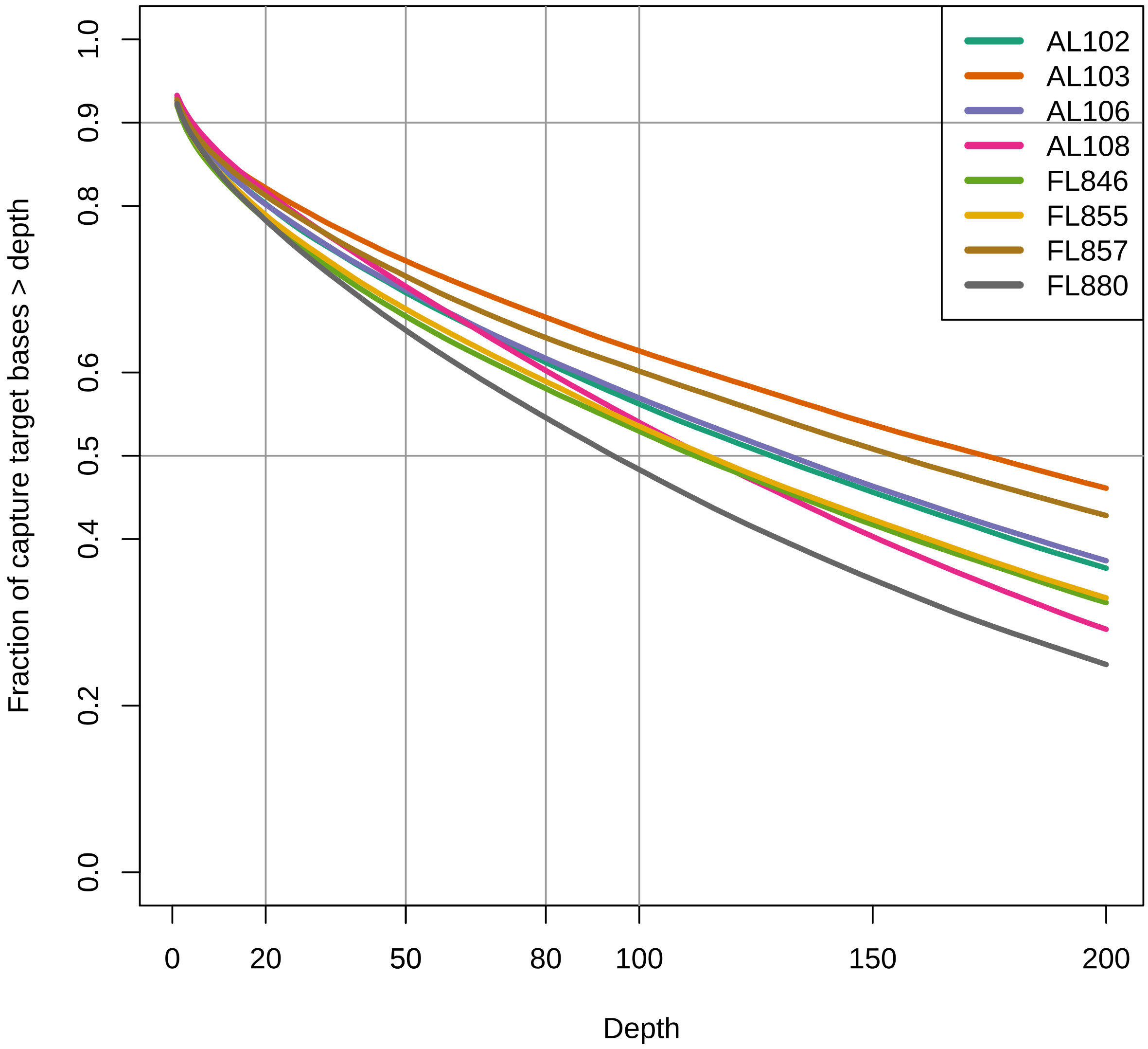

Fig. S1 Coverage plots for first eight *Gopherus polyphemus* samples showing number of sequencing reads at or above specified proportions. A value at 100 Depth and 0.5 fraction means 50 percent of bases were at or above 100X coverage.

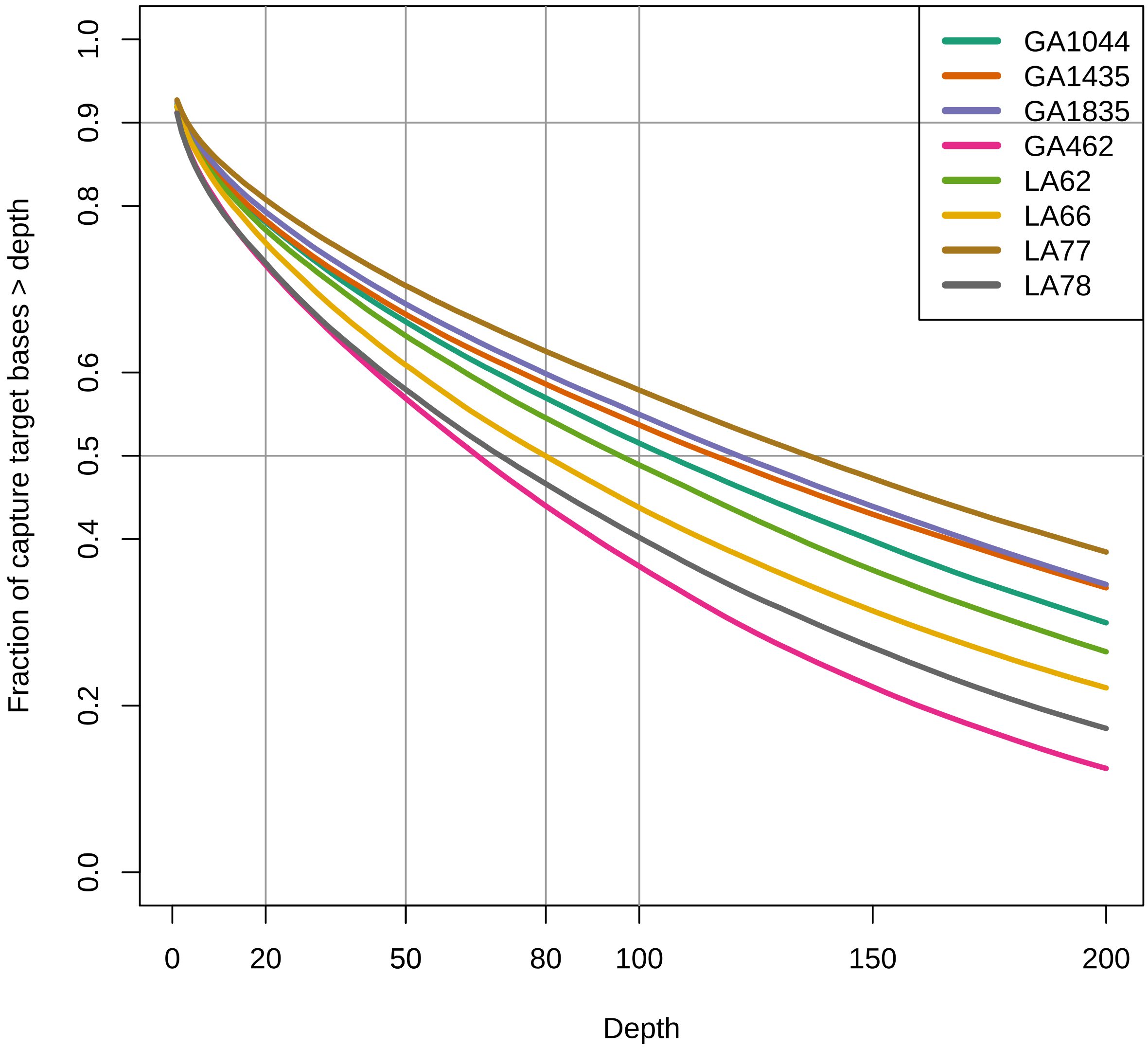

Fig. S2 Coverage plots for last eight *Gopherus polyphemus* samples showing number of sequencing reads at or above specified proportions.

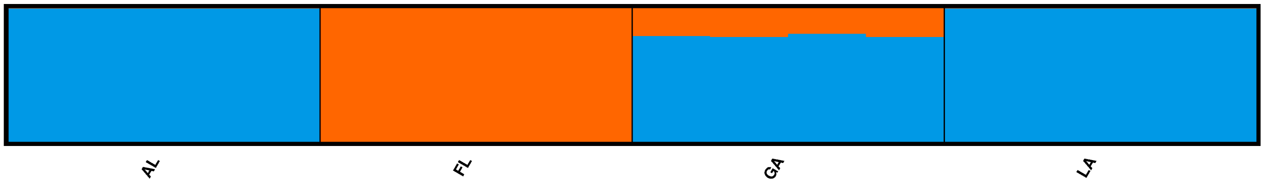

Fig. S3 `STRUCTURE` plot for 16 *Gopherus polyphemus* sequenced at 17,901 immune gene SNPs with optimum number of clusters $K = 2$ determined by `STRUCTURE HARVESTER`.

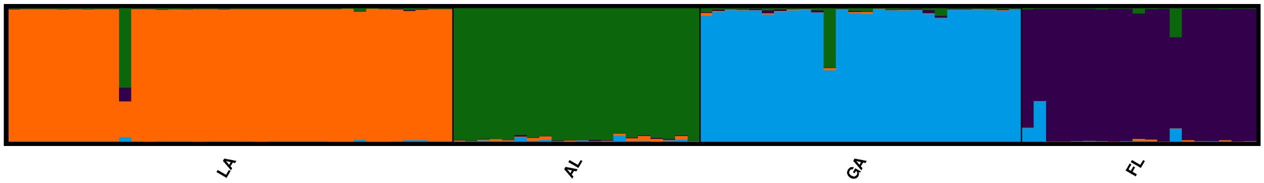

Fig. S4 `STRUCTURE` plot for the full microsatellite dataset (101 *Gopherus polyphemus* genotyped at 10 microsatellite loci) with optimum number of clusters $K = 4$ determined by `STRUCTURE HARVESTER`.

Fig. S5 `STRUCTURE` plot for the partial microsatellite dataset (16 *Gopherus polyphemus* genotyped at 10 microsatellite loci) with optimum number of clusters $K = 3$ determined by `STRUCTURE HARVESTER`.

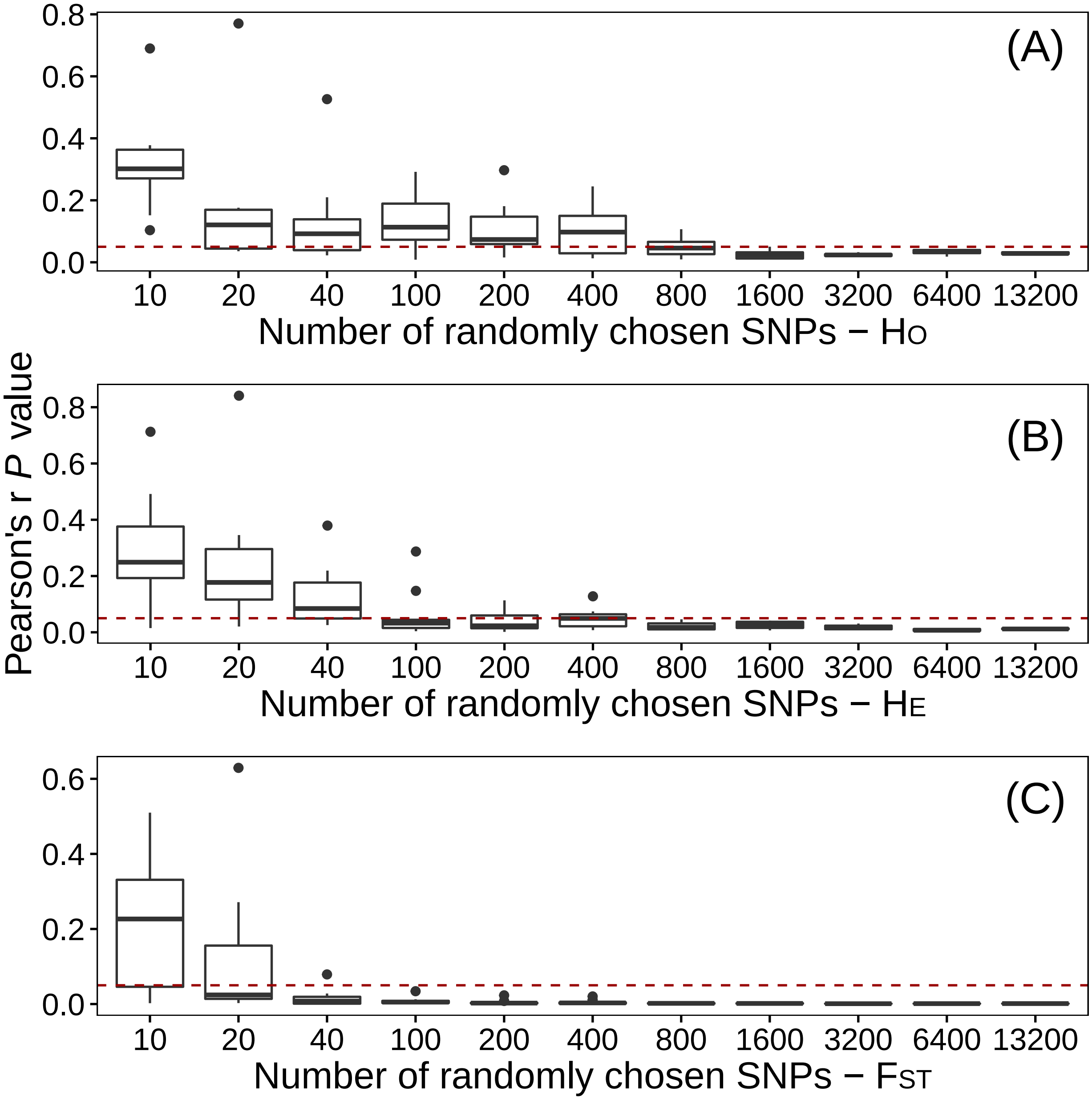

Fig. S6 Subsampling analysis showing how many randomly sampled SNP loci out of the total of 17,901 are needed in comparison to the full microsatellite dataset (101 *Gopherus polyphemus* genotyped at 10 microsatellite loci) for Pearson's r correlation coefficient to be significant at 0.05 level (dotted line) for (A) observed heterozygosity; (B) expected heterozygosity; and (C) FST. There were 10 simulations for each size class of SNPs. HO for observed heterozygosity, HE for expected heterozygosity.

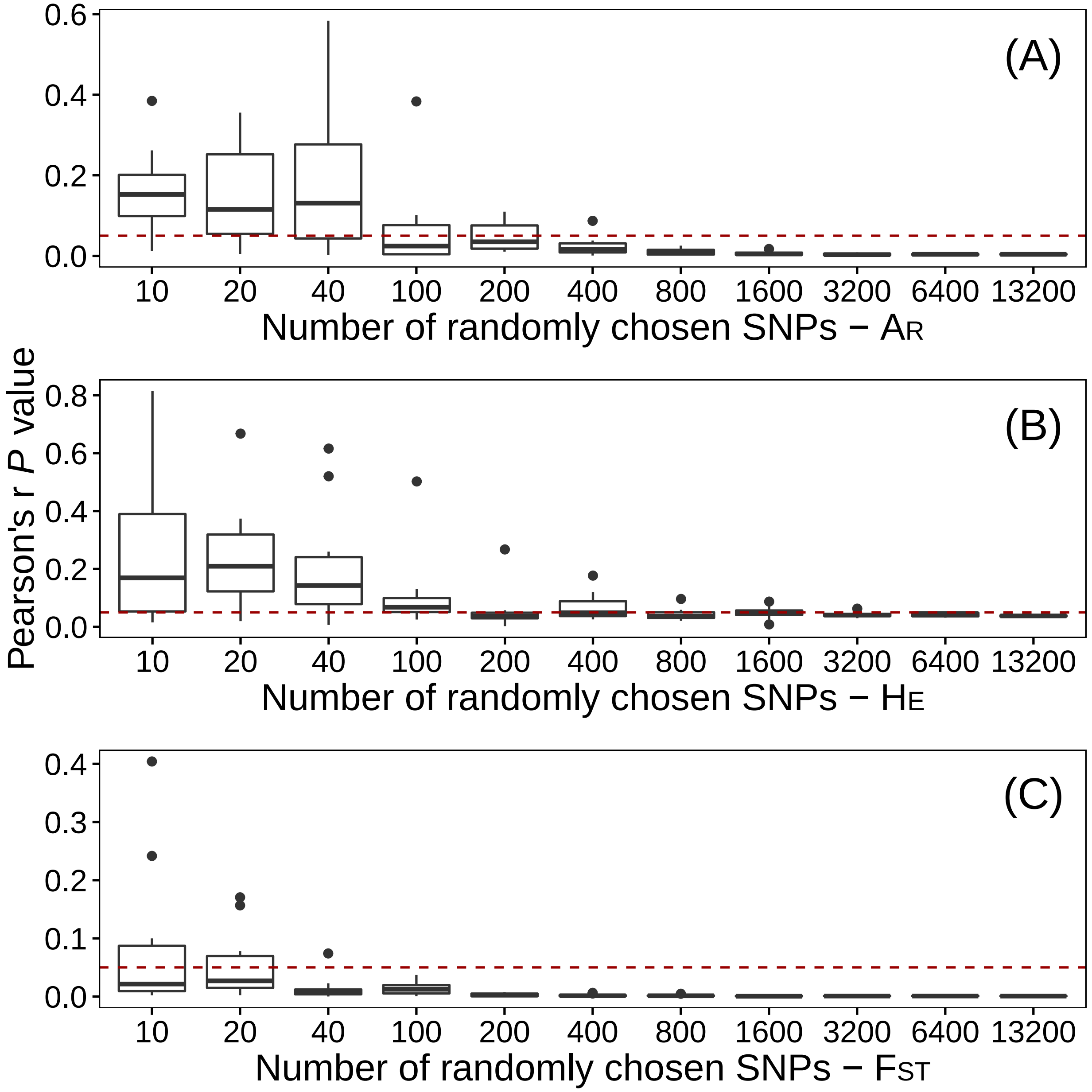

Fig. S7 Subsampling analysis showing how many randomly sampled SNP loci out of the total of 17,901 are needed in comparison to the partial microsatellite dataset (16 *Gopherus polyphemus* genotyped at 10 microsatellite loci) for Pearson's r correlation coefficient to be significant at 0.05 level (dotted line) for (A) allelic richness; (B) expected heterozygosity; and (C) F_{ST}. There were 10 simulations for each size class of SNPs. A_R for allelic richness, H_E for expected heterozygosity.

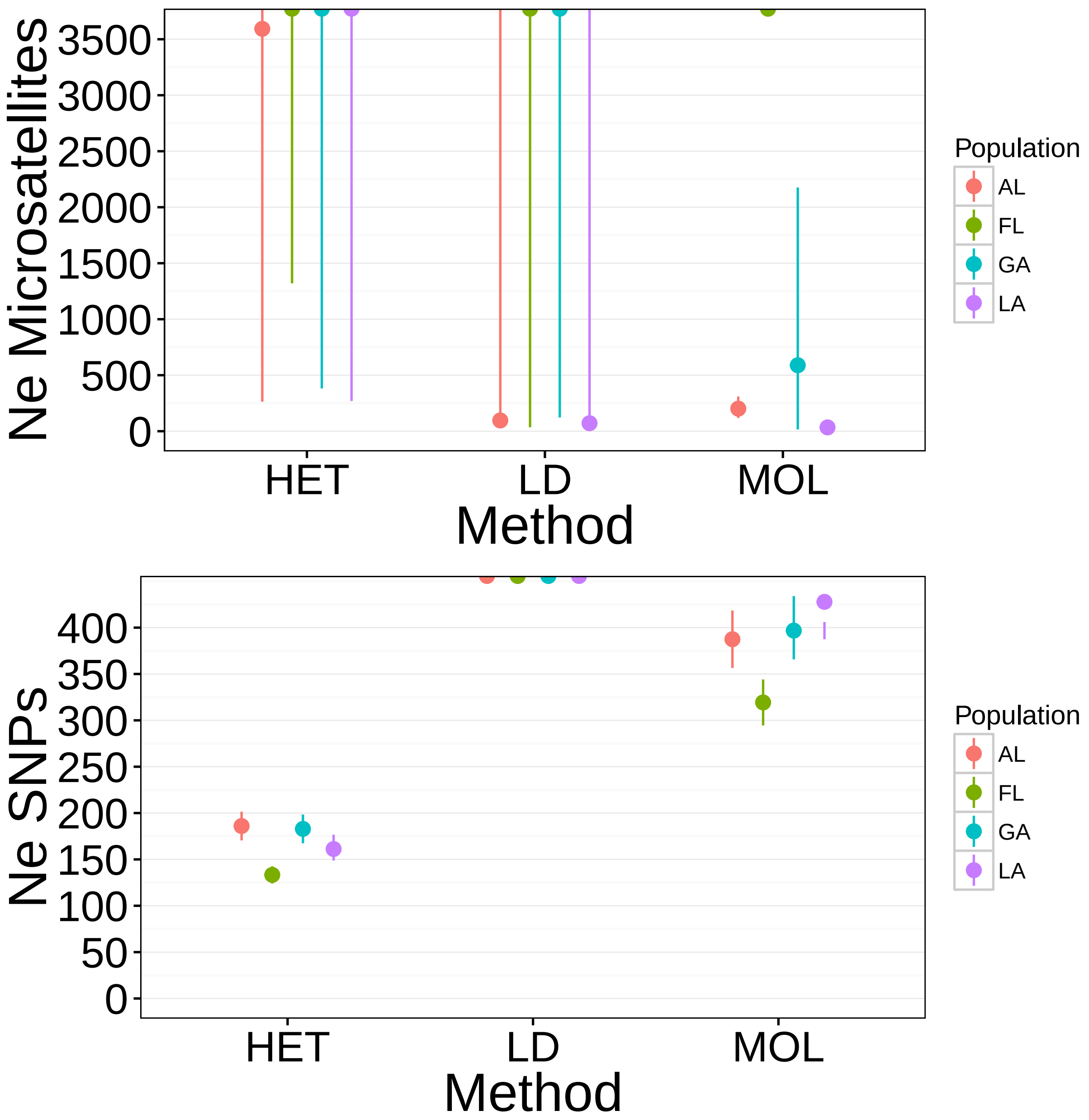

Fig. S8 Effective population sizes per generation (Ne) along with 95 % confidence intervals for *Gopherus polyphemus* samples estimated with the program `NeEstimator` using (A) the full microsatellite dataset (101 *G. polyphemus* genotyped at 10 microsatellite loci) or (B) the SNP dataset (16 *G. polyphemus* sequenced at 17,901 immune gene SNPs). Dots that are on the top of the graph represent Ne estimates of infinity, and lines that extend to the top of the graph represent upper 95 % confidence limits of infinity. LD for linkage disequilibrium method of Waples & Do (2008), HET for heterozygote-excess method of Zhdanova & Pudovkin (2008), and MOL for the molecular coancestry method of Nomura (2008). Note that the HET and MOL methods estimate the effective number of breeders per year (Nb), which were converted to Ne by multiplying Nb by the generation time of 31 years for *G. polyphemus* (Enge et al. 2006).