

Supplementary Materials

Appendix S1. Sampling locations and their landscape type categories and coordinates.

Sampling location	Category	Coordinates (decimal degrees)
Donald Mclean Summit Track	Heavily forested	-37.0146, 174.5401
Home Track	Heavily forested	-36.9509, 174.5171
Upper Huia Dam Track	Heavily forested	-36.9463, 174.5336
Upper Nihotupu Dam Walk	Heavily forested	-36.9379, 174.5585
Slip Track	Heavily forested	-36.9467, 174.6054
Clark Bush Track	Semi-urban	-36.9381, 174.6428
Atkinson Park	Semi-urban	-36.9407, 174.6575
Rahui Kahika Reserve	Semi-urban	-36.9338, 174.6651
Craigavon Park	Urban	-36.9261, 174.6932
Gittos Domain	Urban	-36.9258, 174.7046
Wattle Reserve	Urban	-36.9326, 174.7255

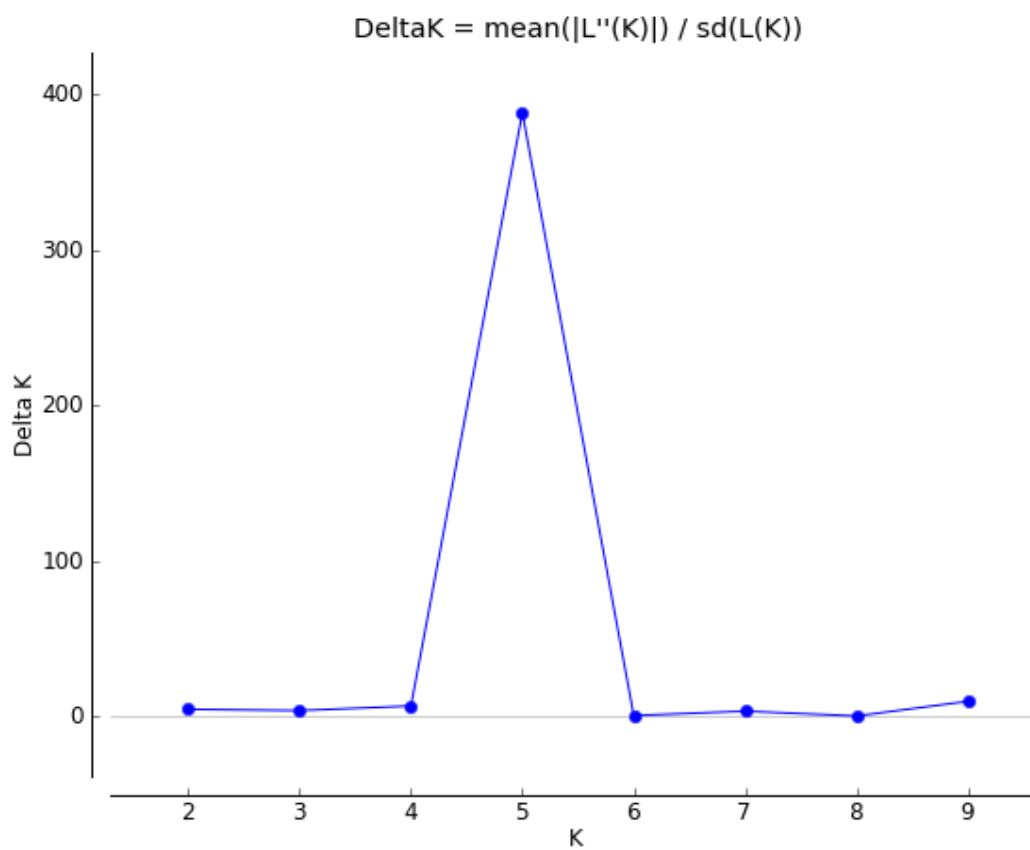
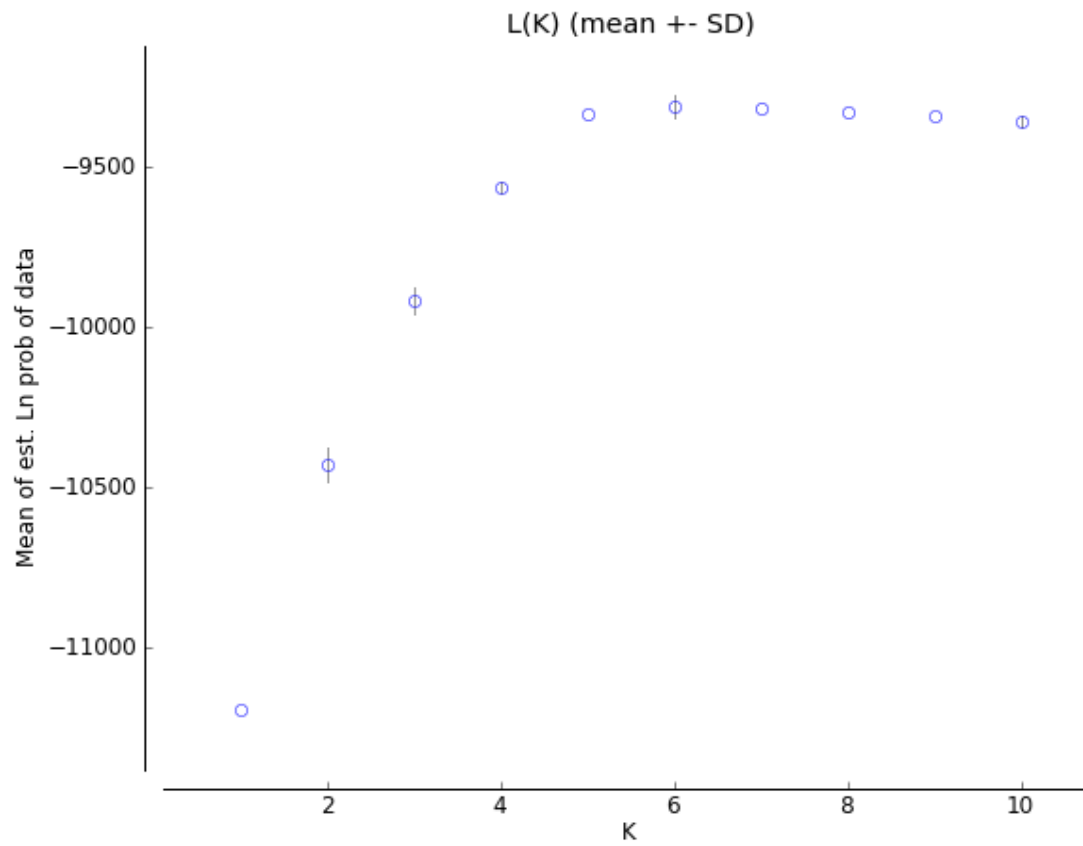
Appendix S2. A summary of the number of *Geochus inaequalis*, *G. politus*, and *G. similis* specimens collected at each sampling location, including the number of site visits that were undertaken.

Sampling location name	No. site visits	No. specimens collected		
		<i>Geochus inaequalis</i>	<i>Geochus politus</i>	<i>Geochus similis</i>
Slip Track	1	2	33	0
Upper Nihotupu Dam Walk	2	0	20	25
Upper Huia Dam Track	1	0	26	45
Home Track	3	0	20	45
Donald Mclean Summit Track	2	8	48	6
Clark Bush Track	2	8	35	1
Atkinson Park	2	0	27	7
Rahui Kahika Reserve	2	0	100+	1
Craigavon Park	1	0	0	0
Gittos Domain	1	29	0	0
Wattle Reserve	2	0	44	0

Appendix S3. Marker information for those included in multiplexes, including marker name, multiplex number, fluorescent tag, final concentration of forward and reverse primers in multiplex reactions, forward (F) and reverse (R) primer sequences (5'-3'), microsatellite repeat motif including the number of repeats that were observed in the Illumina sequencing data, number of alleles per marker (N_A), and size ranges of alleles per marker.

Marker Name	Multiplex	Tag	[Primer] (μ M)	Primer (F)	Primer (R)	Repeat Motif	N_A	Size Range
GP26	1	VIC	0.1	ACCCGCTCCTTCA GCAAC	AGACGCGTTTCG CTTTGAG	(TTA) ₁₄	18	127–184
GP30	1	PET	0.3	GCAGAGCGCTTCG TTATGG	TCTACCAATGTC AGCTCGTAATC	(TAA) ₁₂	17	160–208
GP20	1	6-FAM	0.1	AATGGGCTGGCTC GTAGAC	TCCACCAAGTAT CGGCTCAC	(ATT) ₁₄	17	183–225
GP7	1	6-FAM	0.2	TGGCATGTTTCTC TGCTTAAC	TTTCTGACATTGT TCCACATCC	(TAGA) ₁₄	21	219–352
GP3	2	6-FAM	0.2	CATGTTGGATTAT TCCCAGTGTC	TGGTAGTACGCT GGTTACAGG	(CA) ₄ , (CACG) ₁₂	23	137–206
GP27	2	NED	0.3	ACAGCAGCTAGTT TGTGGC	CTCGCCTAGATG TTCAAACCG	(ATT) ₁₅	13	131–175
GP21	2	VIC	0.2	GGGCCAACCTGTT ATTGGAC	AGCCAGAACCTT TCCACTTG	(TAAA) ₁₉	15	215–274
GP24	2	PET	0.3	GGTCAGGTTAAGA ATAATGCCCG	GCGCCTTTGAGG CTATCAAG	(TCGAA) ₁₈	26	189–313
GP4	2	NED	0.2	AGAGGAGGATTC AGCTTTCG	CGGGATCCACAC CATAGAGG	(ATAG) ₁₀	14	275–309

Appendix S4. Plots of $\ln \Pr(X|K)$ and ΔK vs K generated by Structure Harvester v 0.6.94 (Earl 2012) to estimate the most likely K value.



Appendix S5. Plot of genetic distance vs geographic distance, as implemented in the R package PopGenReport (Adamack & Gruber, 2014).

