Supplemental Information for:

Susceptibility to a sexually transmitted disease in a wild koala population shows heritable genetic variance but no inbreeding depression

Romane H Cristescu**§**, Kasha Strickland**§***, Anthony J Schultz, Loeske E B Kruuk, Deidre de Villiers, Céline H Frère

§ These authors contributed equally to the work

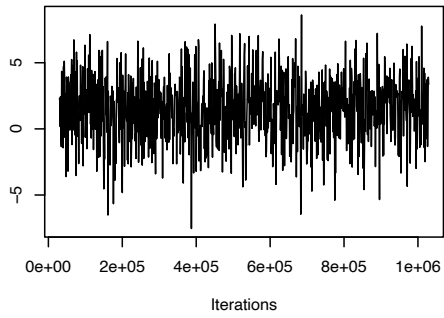* Corresponding author: kasha.strickland@ed.ac.uk
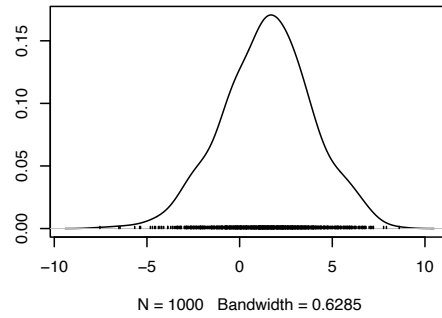
Table of Contents:

Figure S1. Trace and density plots showing posterior distribution of parameter estimates for a model used to investigate the effect of internal relatedness, additive genetic effects, and shared environment effect on probability of testing positive for *C. pecorum*. "IR_new" is internal relatedness, "Name" refers to the additive genetic effects, "Name2" refers to the shared environment effect. Residual variance ("Units") was fixed at one.
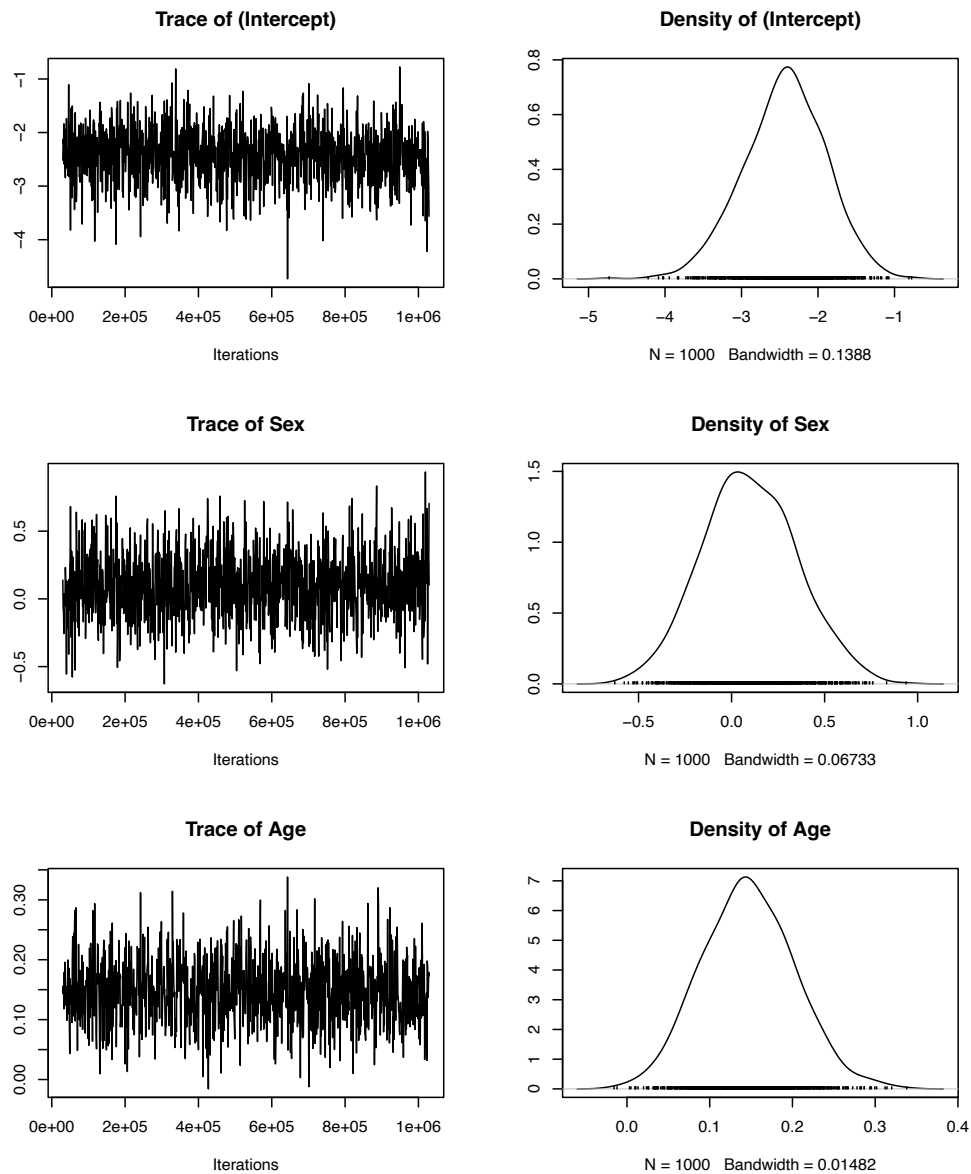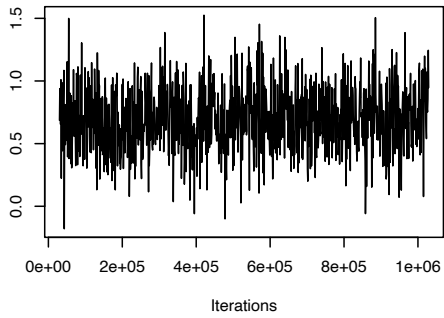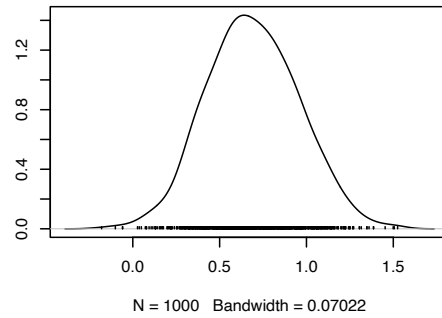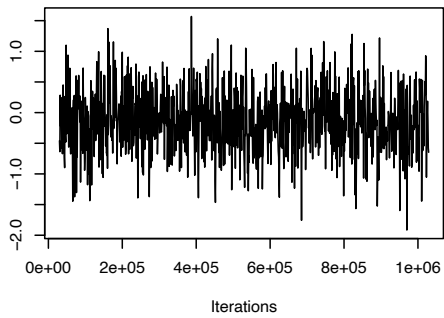
Trace of IR_new

Density of IR_new

N = 1000   Bandwidth = 0.6285

Trace of Breeding

Density of Breeding

N = 1000   Bandwidth = 0.07022

Trace of Age:IR_new

Density of Age:IR_new

N = 1000   Bandwidth = 0.134

3

Trace of Name

Density of Name

N = 1000   Bandwidth = 0.188
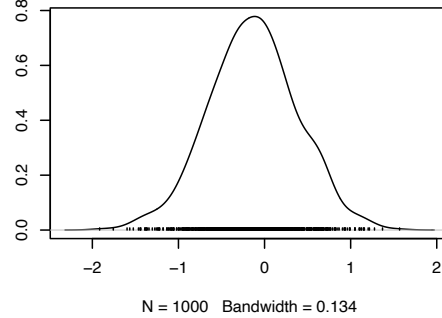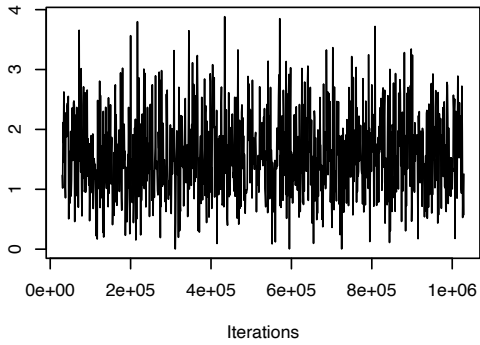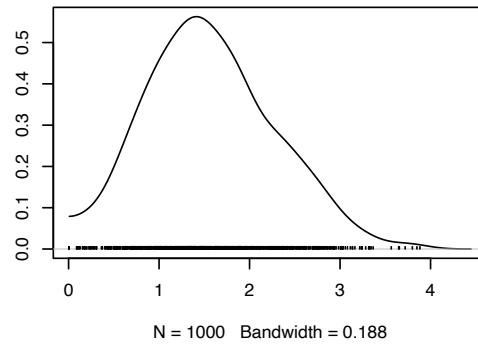
Trace of Name2

Density of Name2

N = 1000   Bandwidth = 0.0003357
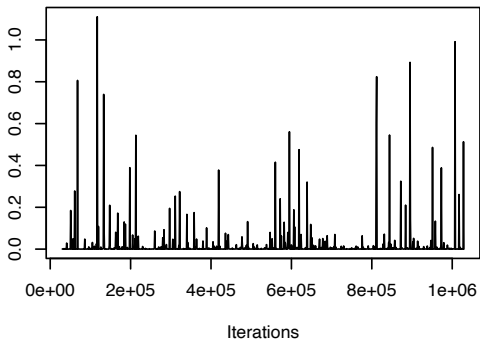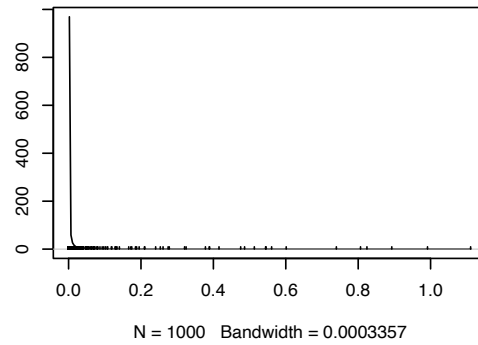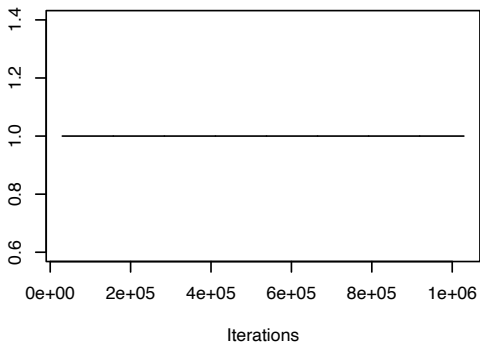
Trace of units

Density of units

Figure S2. Trace and density plots showing posterior distribution of parameter estimates for a model used to investigate the effect of internal relatedness, additive genetic effects, and maternal effect on probability of testing positive for *C. pecorum*. "IR_new" is internal relatedness, "Name" refe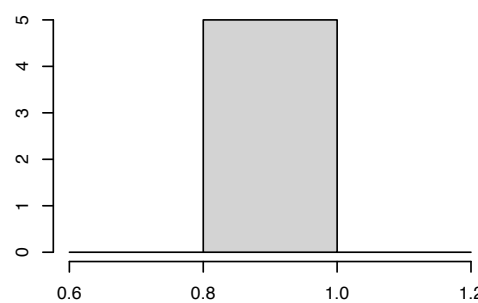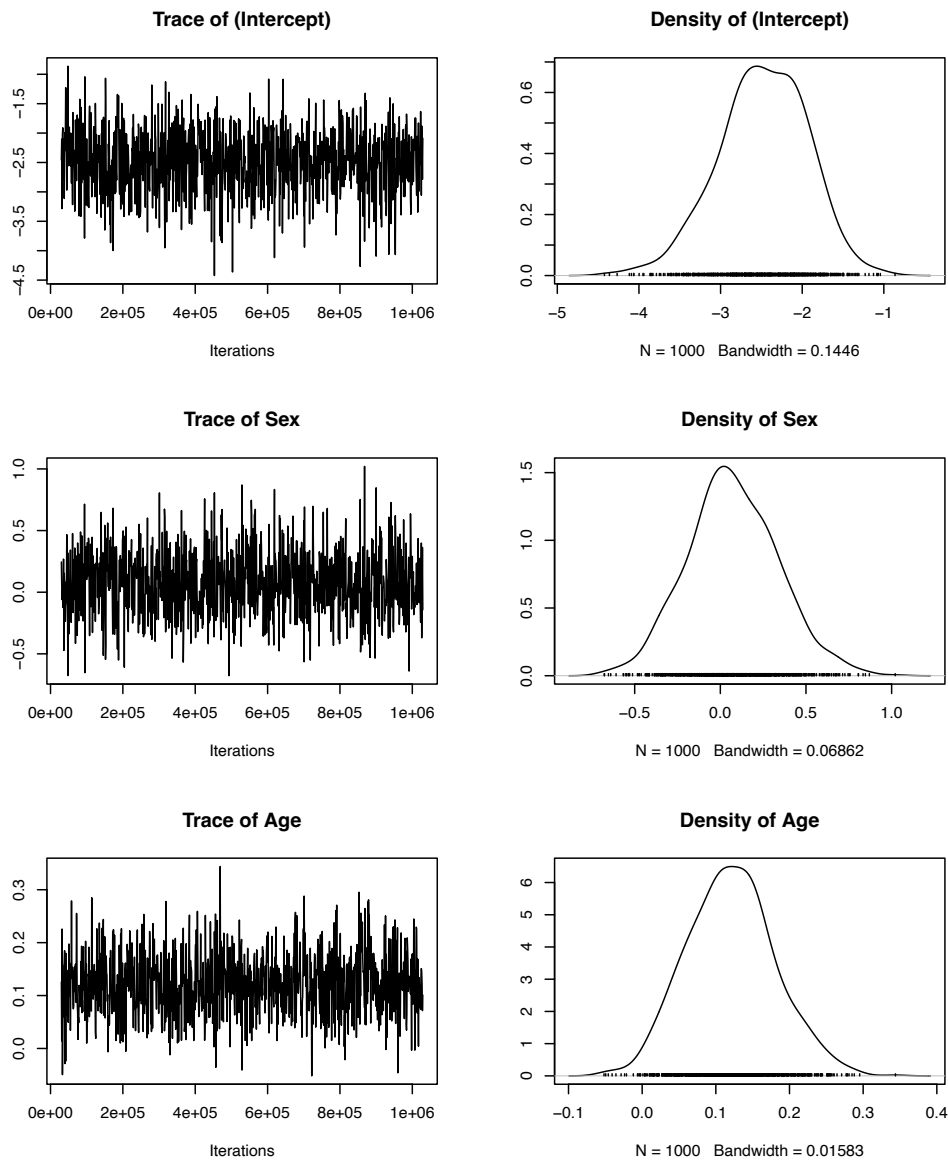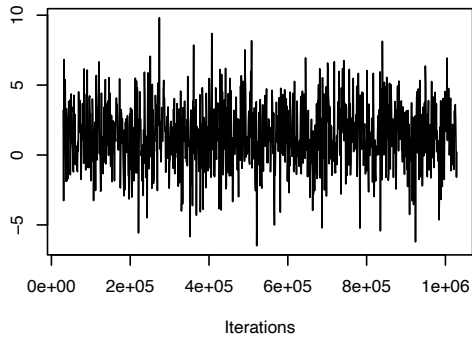rs to the additive genetic effects, "maternal_id" refers to the shared environment effect. Residual variance ("Units") was fixed at one.

Trace of IR_new

Density of IR_new

N = 1000   Bandwidth = 0.6279

Trace of Breeding

Density of Breeding

N = 1000   Bandwidth = 0.07011

Trace of Age:IR_new

Density of Age:IR_new

N = 1000   Bandwidth = 0.1372

Trace of Name

Density of Name

N = 1000   Bandwidth = 0.1863
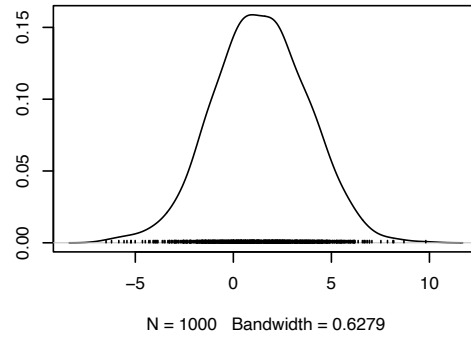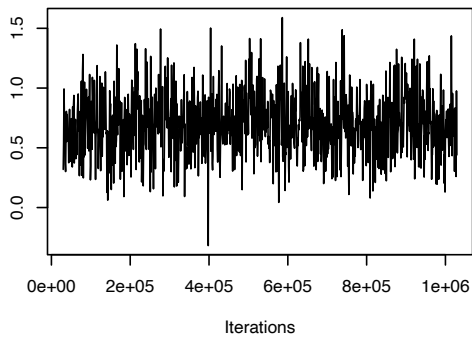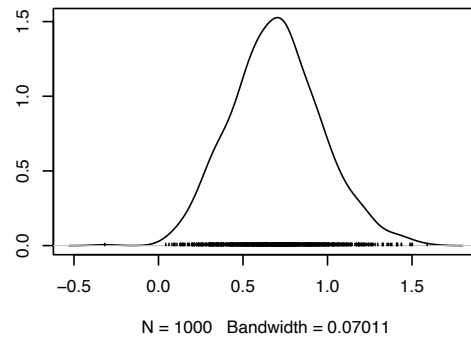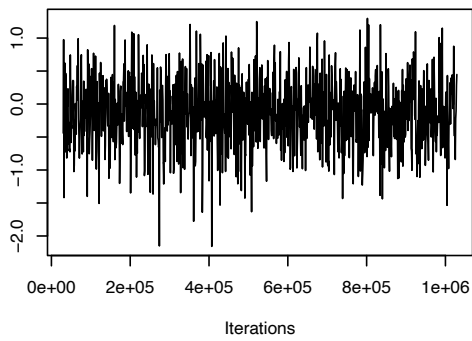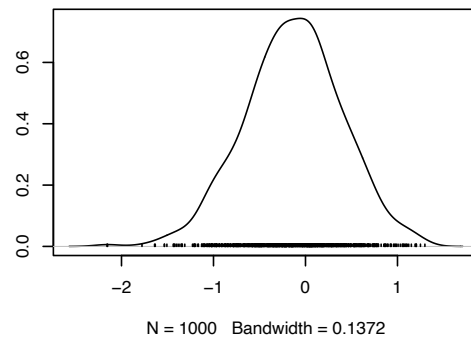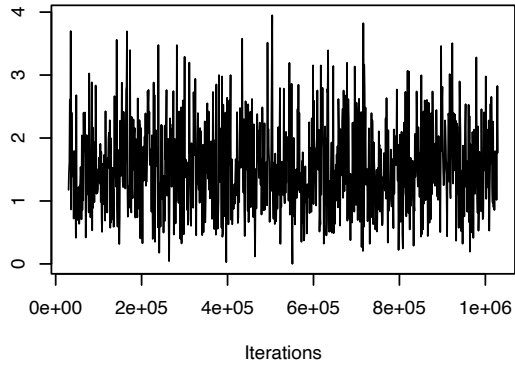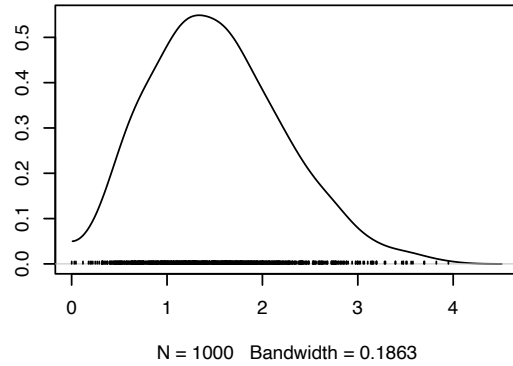
Trace of maternal_id
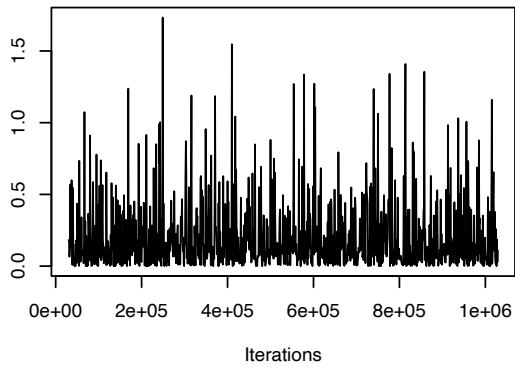
Density of maternal_id

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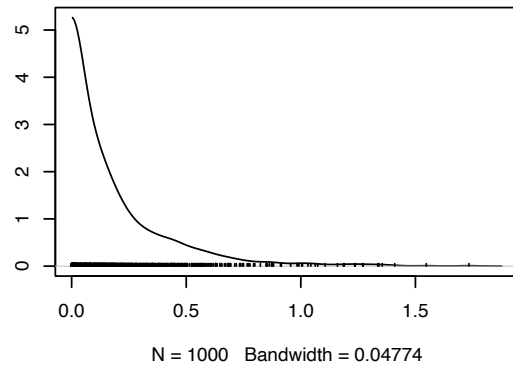
Trace of units
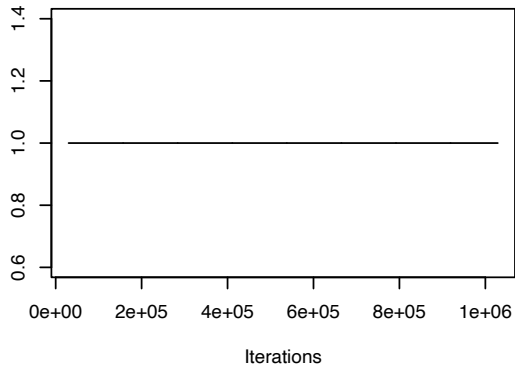
Density of units

Table S1. Estimates for both fixed and random effects from a model used to investigate additive genetic effects for the probability of koalas testing positive for *Chlamydia pecorum*. Values in brackets are 95% credible intervals. Random effect variance estimates and genetic heritability (h^2) are both presented on both latent and observed data-scale are presented. Parameters estimates were converted to the observed data-scale using QG_{GLMM} package.

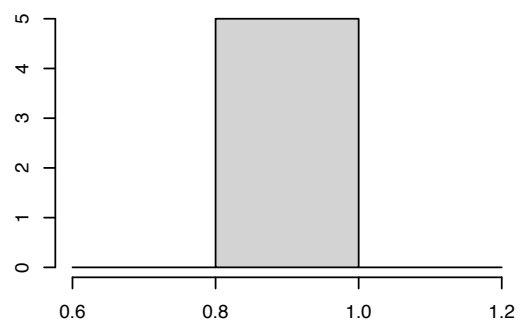|			*Posterior distribution*			
			mode	*mean*	*CI5%*	*CI95%*
Fixed effects	β	Intercept	-2.292	-2.439	-3.441	-1.4
		Sex_{FEMALE}	0.094	0.084	-0.396	0.59
		Age	0.145	0.152	0.045	0.262
		IR	1.527	1.427	-3.293	5.912
		$Season_{BREEDING}$	0.601	0.678	0.119	1.2
		Age*IR	-0.057	-0.136	-1.189	0.829
Random effects	Latent	V_A	1.614	1.627	0.339	2.957
	Data-scale	V_A	0.006	0.015	0.003	0.034
	Latent	h^2	0.634	0.588	0.336	0.741
	Data-scale	h^2	0.101	0.145	0.066	0.243

Table S2. Estimates for both fixed and random effects from a model used to investigate maternal effects for the probability of koalas testing positive for *Chlamydia pecorum*. Values in brackets are 95% credible intervals. Random effect variance estimates presented on both latent and observed data-scale are presented. Parameters estimates were converted to the observed data-scale using QG_{GLMM} package.

			Posterior distribution			
			mode	mean	CI5%	CI95%
		Intercept	-1.779	-1.861	-2.592	-1.194
		Sex_{FEMALE}	0.081	0.121	-0.204	0.477
Fixed effects	β	Age	0.084	0.069	-0.006	0.141
		IR	0.671	1.253	-1.645	4.754
		$Season_{BREEDING}$	0.59	0.516	0.179	0.869
		Age*IR	-0.061	-0.162	-0.835	0.431
Random effects	Latent	V_{ME}	0.004	0.221	<0.001	0.804
	Data-scale	V_{ME}	<0.001	0.003	<0.001	0.011
	Latent	ICC_{ME}	0.003	0.151	0.003	0.445
	Data-scale	ICC_{ME}	0.001	0.031	0.001	0.097