

Table S6 Male (co)variance components. Within-sex variances (diagonal), covariances (lower off diagonal) and correlations (upper off diagonal) between male life history traits ($\pm 1SE$) from a multivariate model of all male traits simultaneously. Genetic parameters do not have associated significances or standard errors as they are calculated from a second order FA model where significance values and errors are given on factor estimates not on the subsequently recovered **G**-matrix. Non-genetic matrices were estimated as variance-covariance matrices as these models proved more stable than unstructured variance-covariance models (Gilmour *et al.* 2009) and thus there are no standard errors on covariances. The permanent env/residual section of the table presents permanent environment (PE) variances in the upper row and residual variances in the lower row. AFR is multiplied by -1 to make any trade-offs negative in sign. Variances are presented for comparison with estimates from univariate models, but year of measurement variance was not significant for any trait and was thus not fit in the multivariate model of male traits.

	SBA	AFR	L	ABS
Genetic				
SBA	0.0386	0.110	1.00	0.708
AFR	0.0172	0.626	0.104	0.781
L	0.0774	0.0323	0.155	0.703
ABS	0.0380	0.167	0.0756	0.0746
Permanent env/ Residual				
SBA	X 0.727±0.045	NA NA	NA NA	NA NA
AFR	NA NA	0.471±0.212 X	0.339±0.232* NA	0.238±0.225* NA
L	NA NA	0.221 NA	0.829±0.135 X	0.204±0.156* NA
ABS	NA NA	0.0508 NA	0.0490 NA	0.129±0.032 0.649±0.023
Birth year				
SBA	0.0846±0.0279	NA	NA	NA
AFR	NA	X	NA	NA
L	NA	NA	X	NA
ABS	NA	NA	NA	X
Maternal				
SBA	0.0624±0.0282	NA	NA	NA
AFR	NA	X	NA	NA
L	NA	NA	X	NA
ABS	NA	NA	NA	X

Bold values are significantly different from 0 ($P < 0.05$), X term not fit see methods for details. NA covariance or correlation not applicable. *covariance is between PE for ABS and residual for other traits, estimated by forcing residual variance into permanent environment variance as detailed in the methods.