

ADDITIONAL FILE 7: SUPPLEMENTARY TABLES

Genetic Determinants Of Anti-Malarial Acquired Immunity In A Large Multi-Centre Study

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Additional Table ST3A: Details of linear regression models used to investigate effect of non-genetic factors on logged antibody levels. All covariates were categorical except for parasite density, which was continuous.

Additional Table ST3B: Details of site-specific linear regression models used to investigate SNP-antibody associations. Models were formulated for each site separately based on data collected by site. Models were run for each SNP-antibody combination separately using four genetic models (additive, dominant, heterozygote and recessive) and results were combined using meta-analysis to give an overall beta and p-value for SNP effect. All covariates were categorical.

Additional Table ST3C: Details of logistic regression model used to investigate effect of SNPs with significant SNP-antibody associations on malaria infection. All covariates were categorical.

Additional Table ST3D: Details of linear regression model used to investigate effect of SNPs with significant SNP-antibody associations on parasite density. All covariates were categorical except for parasite density, which was continuous.

Additional Table ST3A: Details of linear regression models used to investigate effect of non-genetic factors on logged antibody levels. All covariates were categorical except for parasite density, which was continuous.

Regression model type	Data used	Outcome	Full model
Linear	<i>All data</i>	antibody levels	$\beta_1\text{age} + \beta_2\text{gender} + \beta_3\text{malaria status} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month} + \beta_7\text{study}$
	<i>BJ, KM, TG, TP, SL</i>	antibody levels	$\beta_1\text{age} + \beta_2\text{gender} + \beta_3\text{malaria status} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month} + \beta_7\text{study} + \beta_8\text{bednet use}$
	<i>DP, DQ, BJ, TN, TG, TP</i>	antibody levels	$\beta_1\text{age} + \beta_2\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month} + \beta_7\text{study} + \beta_8\text{parasite density}$

Additional Table ST3B: Details of site-specific linear regression models used to investigate SNP-antibody associations. Models were formulated for each site separately based on data collected by site. Models were run for each SNP-antibody combination separately using four genetic models (additive, dominant, heterozygote and recessive) and results were combined using meta-analysis to give an overall beta and p-value for SNP effect. All covariates were categorical.

Regression model type	Data used	Outcome	Full model
Linear	<i>SE</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village}$
	<i>DP</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month}$
	<i>DQ</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{village}$
	<i>BJ</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{village} + \beta_7\text{month}$
	<i>SA</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village}$
	<i>KM</i>	antibody levels	$\beta_1\text{SNP} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{month}$
	<i>TN</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{village} + \beta_7\text{month}$
	<i>TG</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{village} + \beta_7\text{month}$
	<i>TP</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{ethnicity} + \beta_6\text{village}$
<i>SL</i>	antibody levels	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{malaria status} + \beta_5\text{village} + \beta_6\text{month}$	

Additional Table ST3C: Details of logistic regression model used to investigate effect of SNPs with significant SNP-antibody associations on malaria infection. All covariates were categorical.

Regression model type	Data used	Outcome	Full model
Logistic	<i>DQ, BJ, KM, TN, TG, TP</i>	malaria infection	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month} + \beta_7\text{study}$

Additional Table ST3D: Details of linear regression model used to investigate effect of SNPs with significant SNP-antibody associations on parasite density. All covariates were categorical except for parasite density, which was continuous.

Regression model type	Data used	Outcome	Full model
Linear	<i>DP, DQ, BJ, TN, TG, TP</i>	parasite density	$\beta_1\text{SNP} + \beta_2\text{age} + \beta_3\text{gender} + \beta_4\text{ethnicity} + \beta_5\text{village} + \beta_6\text{month} + \beta_7\text{study}$