

Supplementary Materials: *POLRMT* as a Novel Susceptibility Gene for Cardiotoxicity in Epirubicin Treatment of Breast Cancer Patients

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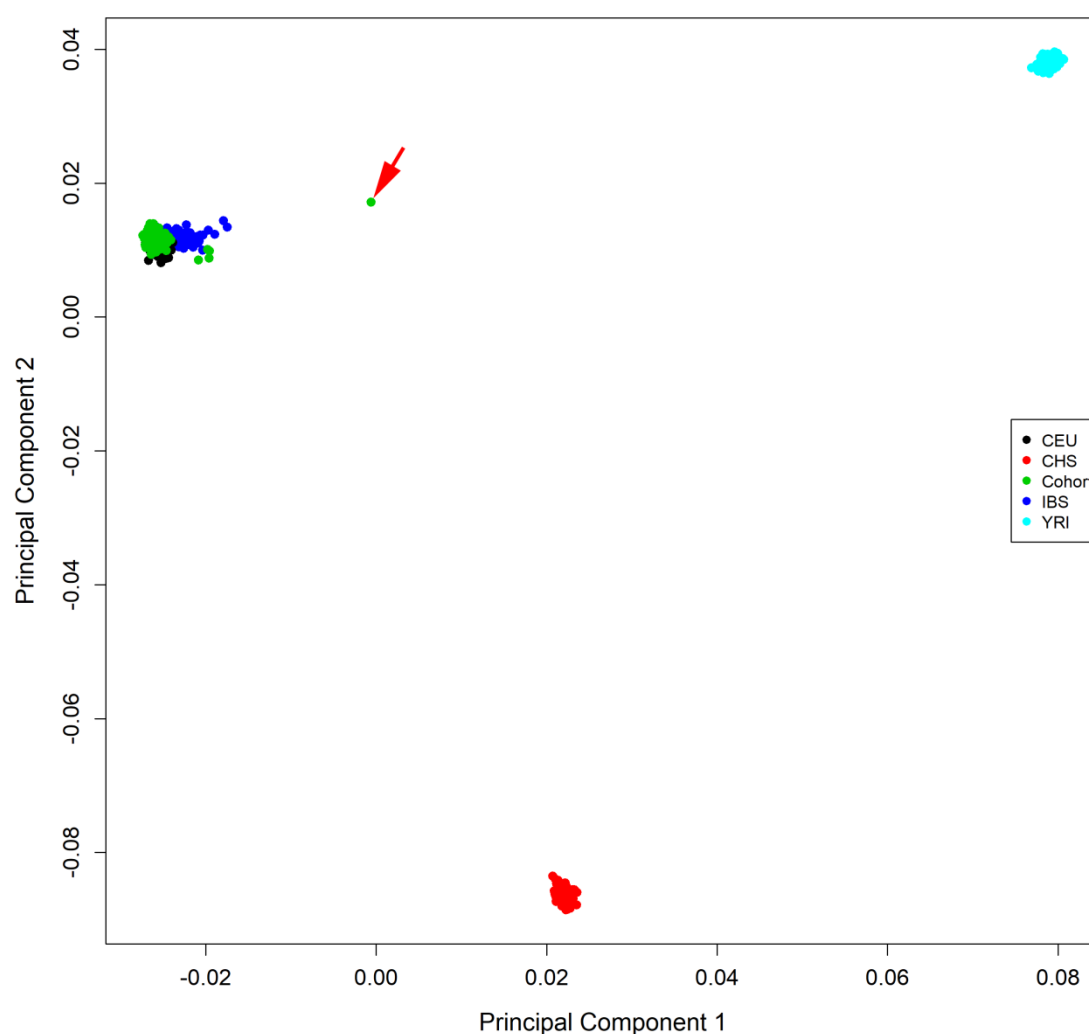


Figure S1. Principal Component Analysis (PCA) of genetic data for the 227 samples from the discovery cohort (green dots) for the 725,785 SNVs that passed quality control, including CEU (black dots), IBS (dark blue dots), CHS (red dots) and YRI (light blue dots) populations from the 1000 Genomes project (<https://www.internationalgenome.org/>, access on 06 July 2016). Principal components 1 and 2 were plotted. The sample indicated by a red arrow was excluded from further analysis.

Table S1. Previously described variants and their association to Anthracycline-Induced Cardiotoxicity in our cohorts via logistic regression analysis.

SNV	Gene	Discovery Cohort				Replication Cohort			
		Case-Control ¹		Extreme Phenotypes ¹		Case-Control ¹		Extreme Phenotypes ¹	
		<i>p</i> -Value	OR	<i>p</i> -Value	OR	<i>p</i> -Value	OR	<i>p</i> -Value	OR
rs1056892	CBR3	0.659	0.91	0.599	0.86	0.160	1.49	0.706	0.779
rs7542939	PRMD2	0.882	0.96	0.716	0.87	0.186	0.59	0.303	0.33
rs28714259	Intergenic	0.953	0.98	0.700	1.17	0.311	0.63	0.515	1.62
rs79338777	ETFB	0.149	0.53	0.404	0.63	0.355	1.51	0.628	1.47

¹ Case-Control (Controls against Mild and Severe Cases, Discovery Cohort *N* = 226, Replication Cohort *N* = 123), Extreme Phenotypes (Controls against Severe Cases, Discovery Cohort *N* = 135, Replication Cohort *N* = 77), Abbreviations: OR, Odds Ratio; *N*, Sample Size. Cumulative dose is used as covariate in each analysis. Significant *p*-values (*p*-val < 0.05) are highlighted in bold.