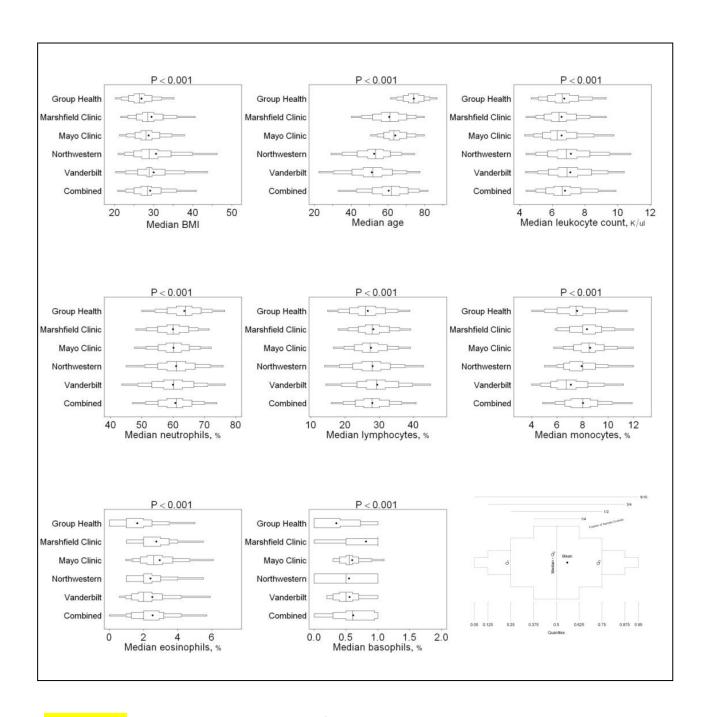
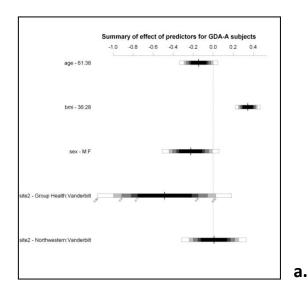
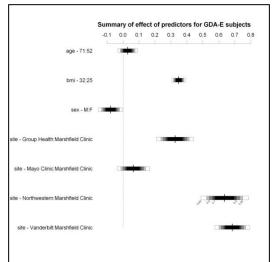


Supplemental Figure S1: Plots of eigenvectors 1 and 2 using PCA. Principal components analysis of 17,150 eMERGE subjects from all field centers, anchored by HapMap controls. Color-coding is according to self-identified or self-observed race.



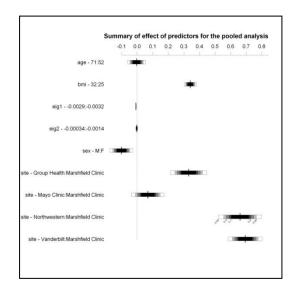
Supplemental Figure S2: Box-percentile plots of median age, median BMI, median leukocyte count and median differentials. The bottom right plot is an annotated example showing the layout of the box-percentile plots. P-values listed are from the Kruskal-Wallis test as listed in Table 2.



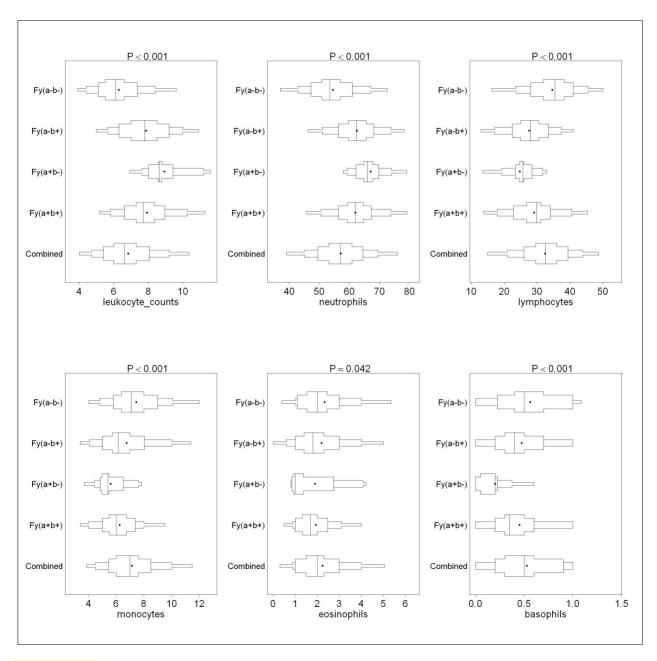


b.

c.



Supplemental Figure S3: Summary of effects of predictors on WBC in the (a.) AA, (b.) EE and (c.) pooled models. Continuous variables are compared using default ranges (interquartile).



Supplemental Figure S4: Box-percentile plots of median leukocyte count and median differentials by Duffy phenotype (Fya+b+, Fya+b-, Fya-b+, Fya-b-) in the subjects of African ancestry. The bottom right plot in Figure 1 is an annotated example showing the layout of the box-percentile plots. P-values listed are from the Kruskal-Wallis test.

## Supplemental Table 1: Summary of effects of loci that reached genome-wide significance for the pooled analyses by study site.

	<b>Group Health</b>		Marshfield		Mayo		Northwestern		Vanderbilt	
	ß	p-value	ß	p-value	ß	p-value	ß	p-value	ß	p-value
1q21, <i>DARC</i>										
					-					
	0.0	6.30E-	-	8.37E-	0.0			2.27E-		
rs12075	2	01	0.06	02	7	9.42E-02	0.10	01	0.10	5.69E-02
17q21.1, GSDMA										
	0.0	3.50E-		5.06E-	0.1			1.27E-		
rs3894194	4	01	0.09	03	1	1.06E-02	0.19	02	0.12	7.70E-03
	0.0	2.48E-		3.36E-	0.2			1.68E-		
rs3859192	9	02	0.10	03	0	3.37E-06	0.18	02	0.13	4.06E-03
17q21.1, PSMD3										
	0.1	5.27E-		1.64E-	0.1			1.81E-		
rs4065321	4	04	0.10	03	5	7.60E-04	0.19	02	0.15	3.95E-04
17q21.1, MED24										
	-				-					
	0.1	9.49E-	-	8.41E-	0.1			1.29E-		
rs9916158	1	03	0.13	05	8	4.58E-05	-0.13	01	-0.09	6.79E-02