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Supplemental Data

Genes for Good: Engaging the Public in Genetics Research via Social Media

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Table S1. Comparison of Genes for Good cohort (genotyped diabetes cases and controls) to NHANES[1] cohort.

Diabetes Cases and Controls, Genotyped Samples				
	GfG Cases (N=948)	GfG Controls (N=16,581)	NHANES Cases (N=809)	NHANES Controls (N=4,796)
BMI	35.71 (8.63)	29.11 (7.79)	32.58 (7.75)	28.80 (6.83)
Underweight	1.0%	1.9%	0.5%	1.7%
Normal weight	8.4%	34.6%	12.5%	30.0%
Overweight	17.0%	27.4%	29.0%	32.0%
Obese	73.6%	36.1%	58.0%	36.3%
Age				
<21	1.1%	6.3%	0.1%	7.0%
21-30	8.1%	40.0%	2.8%	19.1%
31-40	21.3%	28.3%	5.7%	18.3%
41-50	20.1%	11.7%	12.0%	16.4%
51-60	27.7%	8.2%	21.5%	14.9%
61-70	16.5%	4.3%	31.1%	12.3%
>70	5.2%	1.1%	26.7%	11.8%
Sex				
Female	65.8%	68.5%	45.7%	52.8%
Male	34.2%	31.5%	54.3%	47.2%
Race				
Hispanic	7.4%	8.4%	38.1%	29.8%
Asian	1.0%	3.9%	8.9%	12.5%
Black	3.1%	2.6%	23.6%	20.8%
White	79.8%	76.2%	26.1%	33.1%
Multiracial/Other	8.7%	8.9%	3.3%	3.9%
Income				
<$35K	33.7%	26.6%	50.6%	38.7%
$35K-$75K	38.0%	38.1%	30.3%	31.6%
$75K-$100K	14.4%	15.3%	6.9%	10.8%
>$100K	13.9%	20.0%	12.2%	19.0%
Education				
No HS	3.5%	2.0%	32.8%	22.7%
HS Diploma	16.3%	11.3%	21.9%	23.0%
Some college or Associate's degree	45.8%	41.3%	27.6%	29.6%
Bachelor's or higher	34.5%	45.5%	17.7%	26.2%

Table S2. Genome-wide significant hits for various pigmentation and health phenotypes.
Note: This table is large and therefore is included as an Excel file.
All associations are consistent with findings in previous studies[2] except for the hair texture hits at rs1918719 and rs7499783. CHR, chromosome; POS38, build 38 chromosome position; EA, effect allele; EAF, effect allele frequency; N, number of participants included in analysis; SE, standard error.
* Associations not reported in previous studies.

Table S3. Comparison of Genes for Good top GWAS hits to previously reported results.
Note: This table is large and therefore is included as an Excel file.
* Associations not reported in previous studies.
Replications of the top three hits from various studies of pigmentation and health traits[3-11].
Direction of effect for all variants is consistent between the reference studies and Genes for Good, and most Genes for Good results attain at least nominal significance ($p < 0.05$).
EA, effect allele; N, number of participants included in analysis; OR, odds (log-additive) ratio.

Table S4. Comparison of Genes for Good asthma results to previously reported results.
Note: This table is large and therefore is included as an Excel file.
* Associations not reported in previous studies.
Genes for Good replications of eighteen asthma hits found in Demenais et al.[11].
Adjustments to odds ratios (OR) and sample sizes were made using the approach of Duffy et al.[12] to correct for response misclassification. Power calculations were made at the 0.05 significance level using the Genes for Good adjusted sample size, disease frequencies and relative risk values from Demenais et al.[11] control samples, 7.7% population prevalence, and an additive disease model. EA, effect allele; N, number of participants included in analysis.

Figure S1. GWAS panel of common traits in Genes for Good.

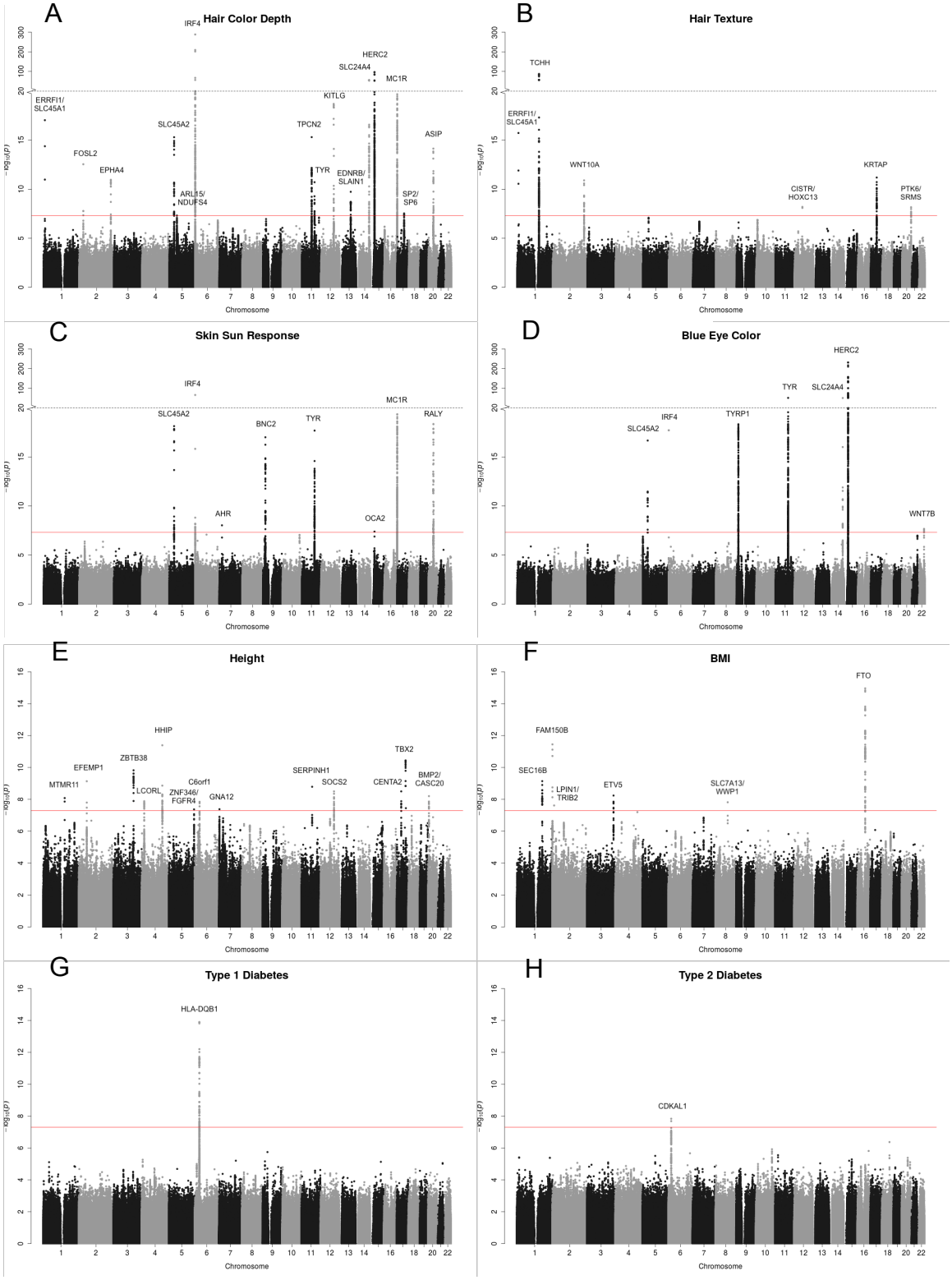
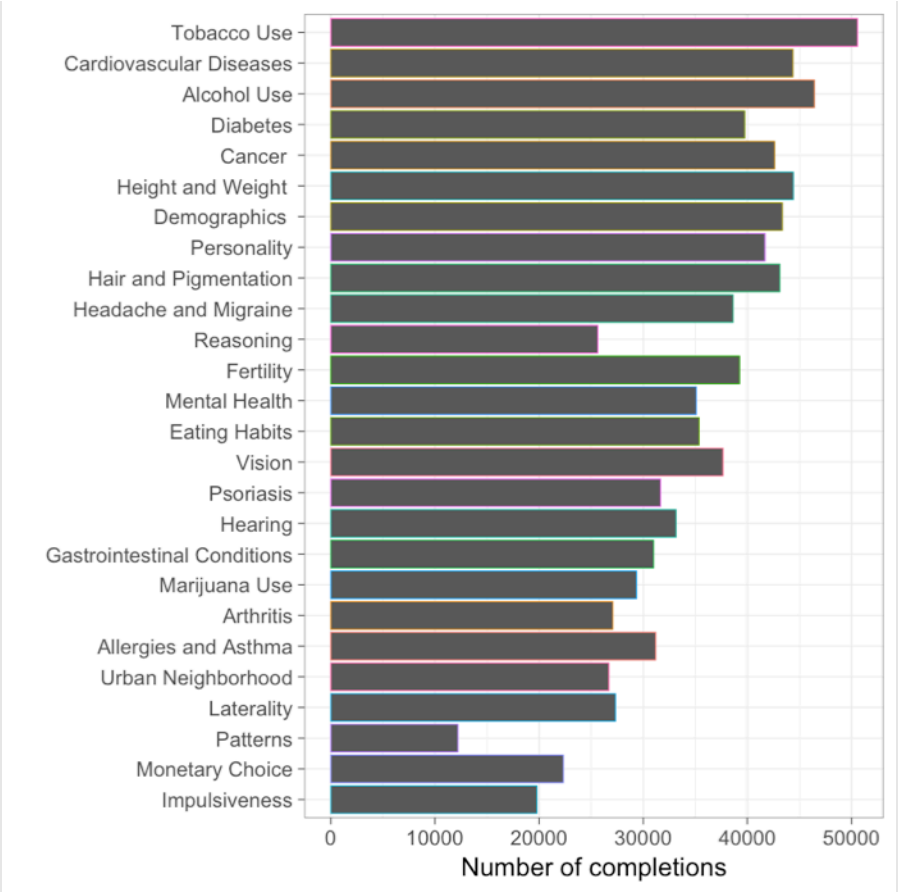


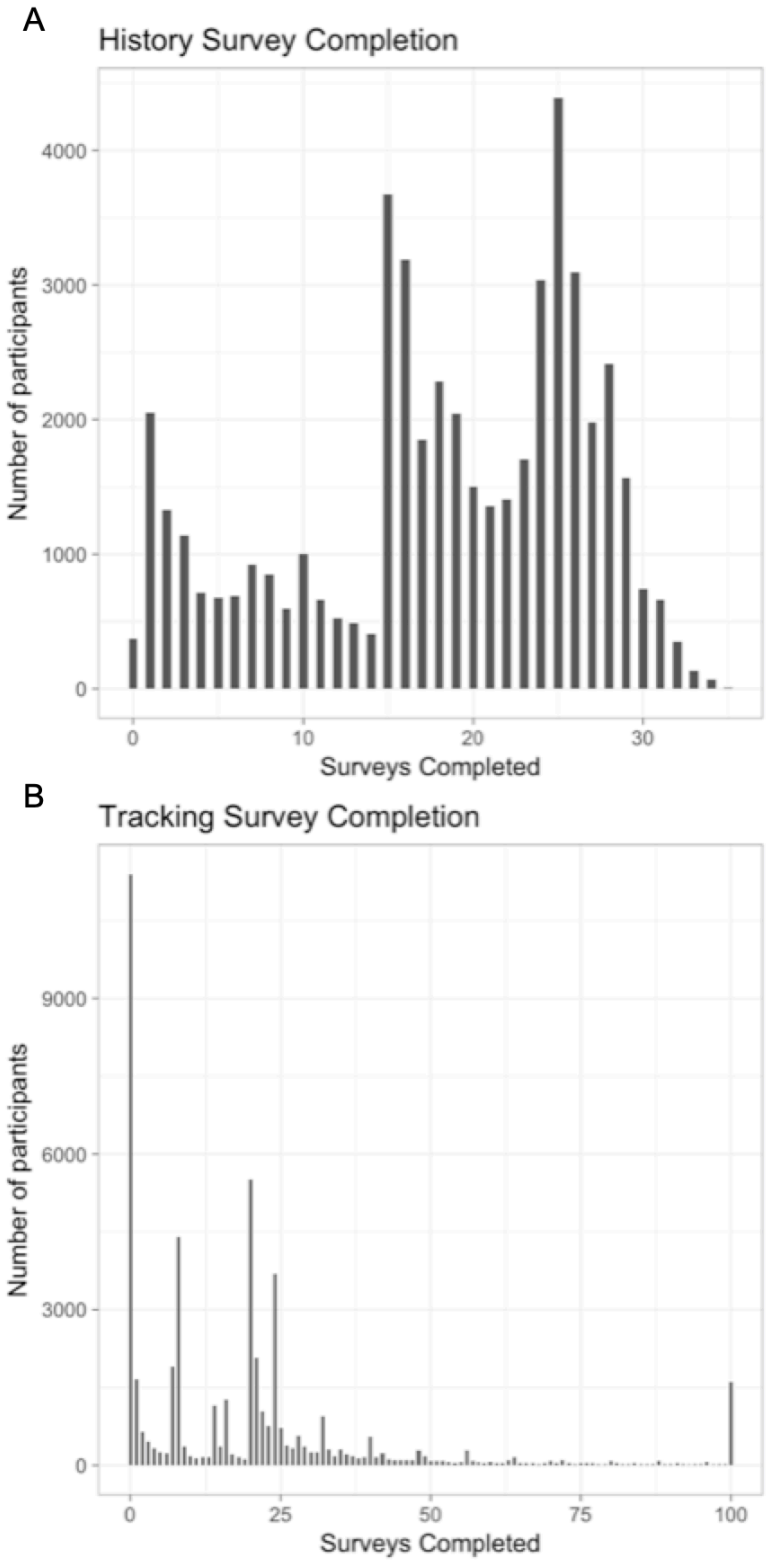
Figure S1. Manhattan plots for GWAS analysis of various pigmentation and health traits. The x-axis indicates chromosomal location. The y-axis represents $-\log_{10}$(p-value). The red line indicates genome-wide significance ($p = 5\times10^{-8}$). Each genome-wide significant locus is labeled with the gene nearest to it.

Figure S2. Survey completion count for Health History surveys available in Genes for Good.



Survey completion count for Genes for Good surveys. Surveys are ordered by date implemented, with the oldest surveys at the top. The first ten surveys were all available at launch. The Reasoning and Patterns surveys are known to be on the longer side.

Figure S3. Histogram of Health History and Daily Tracking survey completion.



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