Module	Variant	Genotype groups	N_noncarriers	N_carriers
Common variants				
10	rs227833	0 vs 1	1266	909
		0 vs 2	1266	153
	rs34472363	0 vs 1	843	1130
		0 vs 2	843	329
	rs5821892	0 vs 1	750	1150
		0 vs 2	750	414
20	rs34472363	0 vs 1	843	1130
		0 vs 2	843	329
22	rs2058084	0 vs 1	891	1116
		0 vs 2	891	316
27	rs10238953	0 vs 1	1720	565
		0 vs 2	1720	44
	rs2759661	0 vs 1	1452	776
		0 vs 2	1452	101
Low-freq variants				
10	rs151097801	0 vs 1/2	2325	4
	rs117788141	0 vs 1/2	2325	4
	rs140903666	0 vs 1/2	2319	10
	rs144863771	0 vs 1/2	2319	10
	rs147858841	0 vs 1/2	2324	5
18	rs142280455	0 vs 1/2	2324	5
	rs137852591	0 vs 1/2	2324	5
20	rs143666989	0 vs 1/2	2324	5
	rs148153989	0 vs 1/2	2325	4
22	rs149342416	0 vs 1/2	2323	6
	rs143662783	0 vs 1/2	2325	4
27	rs142863092	0 vs 1/2	2325	4
	rs137991779	0 vs 1/2	2324	5
28	rs142932029	0 vs 1/2	2326	3
	rs201095751	0 vs 1/2	2325	4

Fig S4. Magnitude of variant effect on facial modules, quantified by the Euclidean distance between averaged faces of different genotype groups. The 95% confidence interval was obtained by 5000 bootstraps. The farther away the blue (common) or red (low-freq) rectangular boxes fall from line x=0, the larger the group distances and the greater the magnitude of effects. Common variants that yielded significant GWAS association in the same cohort with the same modules are used as a comparison to low-frequency variants. Genotype groups column indicates the two groups of people of whom the faces were averaged and distance was computed. For example, 0 vs 1/2 means minor allele homozygotes vs the remaining. The following two columns indicate sizes of the two groups in comparison. Low-frequency variants had large effects compared to previously reported common variants, although this could be a result from the much smaller size of carrier group and may not reflect genuine greater effects of low-frequency variants.