

## Supplementary Information

### *IGF1* Gene Is Associated With Triglyceride Levels In Subjects With Family History Of Hypertension From The SAPPHIRe And TWB Projects

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**Supplementary Table S1.** *IGF1* single-nucleotide polymorphisms (SNPs) genotyped in the Stanford Asian Pacific Program in Hypertension and Insulin Resistance (SAPPHIRE) sample

SNP	Chromosome position <sup>a</sup>	Gene region	Allele type Minor/Major	MAF	<i>p</i> for HWE test	Number of subject successfully genotyped
rs2288377 <sup>b</sup>	102874762	Promoter	<i>A/T</i>	0.30	0.39	972 (99.3%)
rs2195239	102462924	Intron 2	<i>G/C</i>	0.45	0.42	973 (99.4%)
rs978458 <sup>b</sup>	102408461	Intron 3	<i>A/G</i>	0.44	0.77	956 (97.7%)
rs1520220	102402744	Intron 3	<i>G/C</i>	0.45	0.73	976 (99.7%)
rs6220	102400737	3'UTR	<i>C/T</i>	0.44	0.91	946 (96.6%)
rs6217 <sup>b</sup>	102400008	3'UTR	<i>G/T</i>	0.28	0.10	952 (97.2%)
rs6218	102399855	3'UTR	<i>C/T</i>	0.27	0.46	930 (95.0%)
rs6214 <sup>b</sup>	102399791	3'UTR	<i>A/G</i>	0.47	0.11	964 (98.5%)
rs6219 <sup>b</sup>	102396414	3'UTR	<i>A/G</i>	0.17	0.55	977 (99.8%)

<sup>a</sup> GRCh38.p7.

<sup>b</sup> The tag-SNPs.

MAF, minor allele frequency; HWE, Hardy-Weinberg equilibrium.

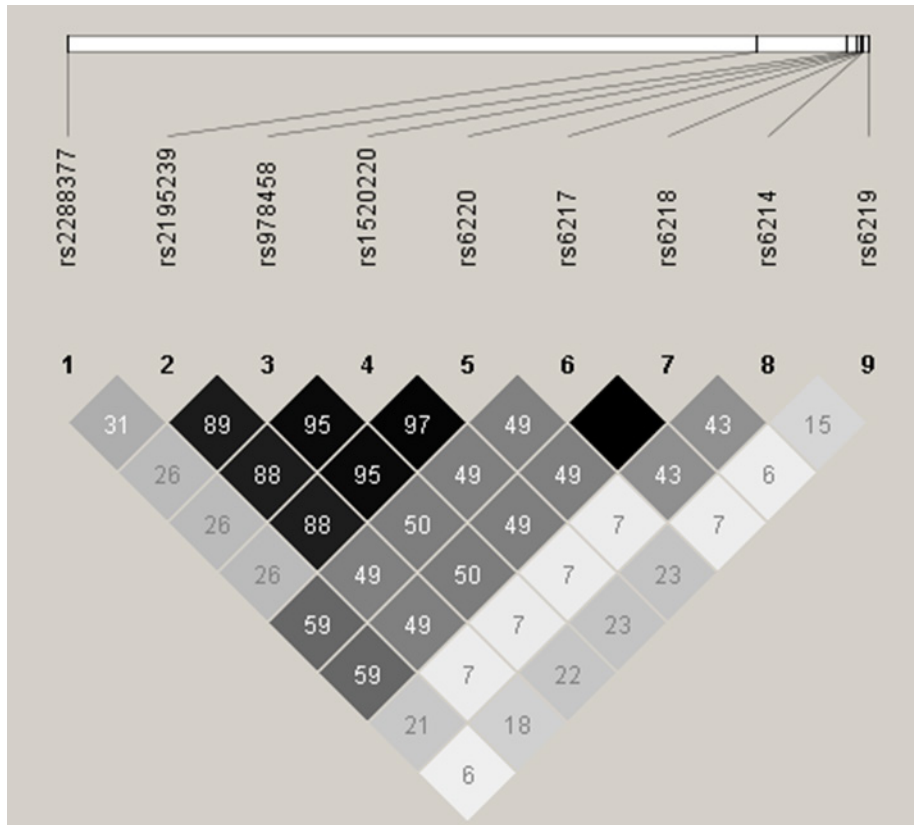
**Supplementary Table S2.** Comparison of genotype distribution of rs978458 in different

subsets of the Taiwan biobank (TWB) sample

Genotype	Non-hypertensive subjects without a family history (%)	Non-hypertensive subjects with a family history (%)	Hypertensive subjects without a family history (%)	Hypertensive subjects with a family history (%)	<i>p</i>
<i>GG</i>	2690 (28.59%)	335 (27.06%)	250 (29.00%)	465 (29.87%)	0.22
<i>AG</i>	4703 (49.92%)	642 (51.86%)	422 (48.96%)	799 (51.32%)	
<i>AA</i>	2025 (21.49%)	261 (21.08%)	190 (22.04%)	293 (18.82%)	

**Supplementary Table S3.** Distribution of the number of hypertensive members in the Stanford Asian Pacific Program in Hypertension and Insulin Resistance (SAPPHIRE) families

Number of hypertensive members	Number of families (%)
1	182 (45.84%)
2	120 (30.23%)
3	60 (15.11%)
4	23 (5.79%)
5	8 (2.02%)
6	3 (0.76%)
7	1 (0.25%)



**Supplementary Figure S1.** Linkage disequilibrium (LD) structure of the *IGF1* SNPs

genotyped in the SAPHIRE sample. The pair-wise LD levels were measured by  $r^2$  and were estimated using the Haploview (v. 4.2) program.