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## **Supplemental Data**

### **Joint Linkage and Association Analysis**

#### **with Exome Sequence Data**

#### **Implicates *SLC25A40* in Hypertriglyceridemia**

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## **ESP Groups**

<sup>1</sup>Anthropometry Project Team, <sup>2</sup>Blood Count/Hematology Project Team, <sup>3</sup>Blood Pressure Project Team, <sup>4</sup>Data Flow Working Group, <sup>5</sup>Early MI Project Team, <sup>6</sup>ELSI Working Group, <sup>7</sup>Executive Committee, <sup>8</sup>Family Study Project Team, <sup>9</sup>Lipids Project Team, <sup>10</sup>Lung Project Team, <sup>11</sup>Personal Genomics Project Team, <sup>12</sup>Phenotype and Harmonization Working Group, <sup>13</sup>Population Genetics and Statistical Analysis Working Group, <sup>14</sup>Publications and Presentations Working Group, <sup>15</sup>Quantitative Analysis Ad Hoc Task Group, <sup>16</sup>Sequencing and Genotyping Working Group, <sup>17</sup>Steering Committee, <sup>18</sup>Stroke Project Team, <sup>19</sup>Structural Variation Working Group, <sup>20</sup>Subclinical/Quantitative Project Team

## **ESP Cohorts**

<sup>21</sup>Acute Lung Injury (ALI), <sup>22</sup>Atherosclerosis Risk in Communities Study (ARIC), <sup>23</sup>Cardiovascular Health Study (CHS), <sup>24</sup>Chronic Obstructive Pulmonary Disease (COPD)Gene), <sup>25</sup>Coronary Artery Risk Development in Young Adults (CARDIA), <sup>26</sup>Cystic Fibrosis (CF), <sup>27</sup>Early Pseudomonas Infection Control (EPIC), <sup>28</sup>Framingham Heart Study (FHS), <sup>29</sup>Jackson Heart Study (JHS), <sup>30</sup>Lung Health Study (LHS), <sup>31</sup>Multi-Ethnic Study of Atherosclerosis (MESA), <sup>32</sup>Pulmonary Arterial Hypertension (PAH), <sup>33</sup>Severe Asthma Research Program (SARP), <sup>34</sup>Women's Health Initiative (WHI)

## Supplemental Figures

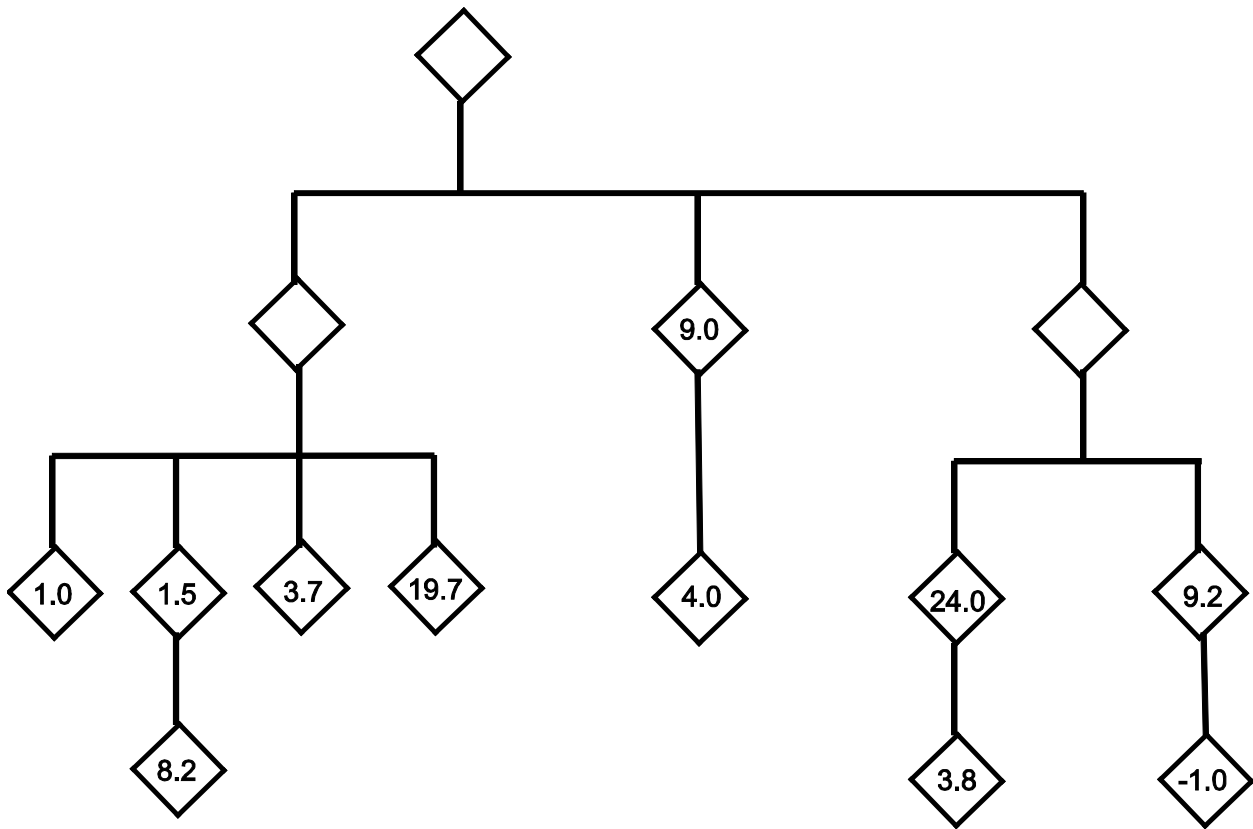


Figure S1: Portion of the pedigree containing all carriers of the novel *SLC25A40* variant. The numbers within each symbol are the standard deviations away from the age and sex normalized TG in the population, using 1980plus data.

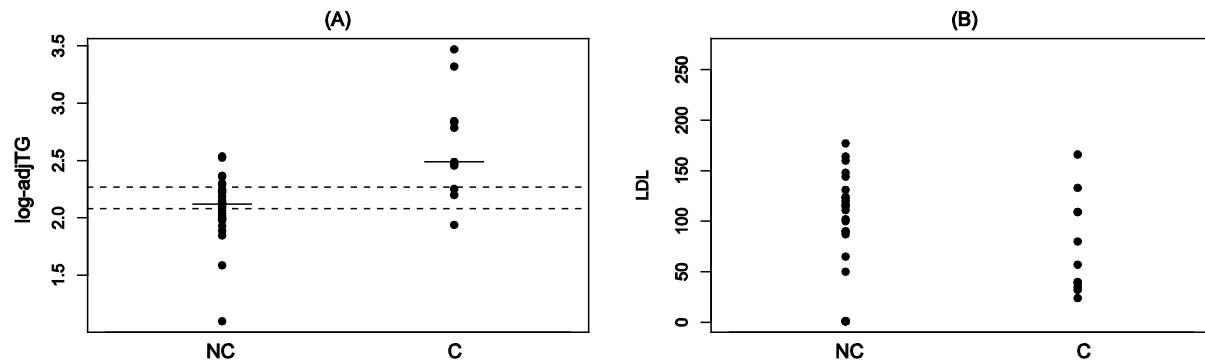


Figure S2: Distribution of (A) log-adjTG and (B) LDL, using 1980plus data, for non-carriers (NC) and carriers (C) of the novel *SLC25A40* variant in the pedigree. The top most dashed line shows the 95<sup>th</sup> percentile for log of age and sex adjusted TG. The lower dashed line shows the 50<sup>th</sup> percentile for log of age and sex adjusted TG. The solid horizontal lines show the median log-adjTG for non-carriers and carriers. Log-adjTG is significantly associated with carrier status (0.0001) adjusting for pedigree structure, which controls for shared genetic background. LDL is not significantly associated with carrier status, adjusting for pedigree structure.

## Supplemental Tables

Gene	Chromosome	SNV
<i>COBLL1</i>	2	rs10195252
<i>IRS1</i>	2	rs2943645
<i>MAP3K1</i>	5	rs9686661
<i>TIMD4</i>	5	rs1553318
<i>HLA</i>	6	rs2247056
<i>TYW1B</i>	7	rs13238203
<i>TBL2</i>	7	rs7811265
<i>PINX1</i>	8	rs11776767
<i>NAT2</i>	8	rs1495741
<i>NAT2</i>	8	rs1495743
<i>JMJD1C</i>	10	rs10761731
<i>APOA5</i>	11	rs964184
<i>LRP1</i>	12	rs11613352
<i>ZNF664</i>	12	rs12310367
<i>CAPN3</i>	15	rs2412710
<i>FRMD5</i>	15	rs2929282

Table S1: SNVs reported to be associated with TG and which are neither on the CVD chip nor have a proxy on the CVD chip. Gene names are from NCBI and aliases are as follows: *DOCK7*=*ANGPTL3*, *AFF1* = *KHL8*, *TBL2* = *MLXIPL*, *SUGP1* = *CILP2*.

Gene	# SNVs	# Carriers	Mean (Min, Max) log(TG) among carriers	Mean (Min, Max) log(TG) among non- carriers	Beta	p-value
SLC25A40	5	8	5.2 (4.4,6.2)	4.7 (1.8,7.2)	0.42	0.03
PLD2	22	64	6.6 (3.6,6.6)	4.8 (1.8,7.2)	0.04	0.48
WSCD1	16	29	4.6 (3.1,5.8)	4.8 (1.8,7.2)	-0.13	0.19
MNT	3	3	4.8 (4.3,5.1)	4.8 (1.8,7.2)	0.08	0.81
SMTNL2	7	47	4.8 (3.7,6.0)	4.8 (1.8,7.2)	-0.01	0.87

Table S2: Distribution of log(TG) by carrier status in each of 5 genes, as well as model coefficients and p-value after adjusting for age, sex and race in the ESP cohort.