ON-LINE TABLES AND LEGENDS

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On-line Table 1. SHP selection strategy for follow-up after pooled GWAS.

In Excel → PDF format.

Relative Allele Scores (RAS) were calculated in the highest versus lowest BP groups, which were then ranked for each SNP. SNP loci with RAS values most different between extreme cases and extreme controls, for both the Affymetrix-5.0 and Illumina HumanHap300, were pursued further. First, we ranked all SNPs by their allele frequency differences between the two blood pressure groups. Second, we took the top 250 SNPs from each array (Affymetrix and Illumina) and computed the absolute (bp) distances between each neighboring SNP in these top lists. For those SNPs that were on different arrays but were ranked in the top 250 SNPs, and had a nearby neighbor SNP from the opposite array, we ranked (supplemental Table 1) and selected candidates for follow up replication genotyping, resulting in 5 selected SNP pairs.

On-line Table 2. Positions and LD of all SNPs evaluated in this study (SLC35F3, Intron-2).

In Excel → PDF format.

Chromosomal positions of SNPs were derived from NCBI dbSNP <http://www.ncbi.nlm.nih.gov/SNP/>, while LD was determined from HapMap-3 at <http://hapmap.ncbi.nlm.nih.gov/>. SNP positions in different releases of the human genome (e.g., hg19) were determined at <http://genome.ucsc.edu/>.

On-line Table 3: Amino acid sequence alignment and homology between human SLC35F3 (UniProt Q8IY50; 421 amino acids) and yeast (S. cerevisiae) THI74 (UniProt Q04083; thiamine-repressible mitochondrial transport protein; 370 amino acids). Alignment by CLUSTAL 2.0.11 at <http://www.ebi.ac.uk/Tools/msa/clustalw2/>. (Score: 15. Pairwise score is the number of identities between the two sequences, divided by the length of the alignment, and represented as a percentage). *(asterisk): indicates positions which have a single, fully conserved residue. :(colon): indicates conservation between groups of strongly similar properties - scoring >0.5 in the Gonnet PAM 250 matrix. .(period): indicates conservation between groups of weakly similar properties - scoring =<0.5 in the Gonnet PAM 250 matrix.

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Hum_Transporter      MKKHSARVAPLSACNSPVLTLTKVEGEERPRDSPGPAEAQAPAGVEAGGRASRRCWTCSR 60
Yeast_Thi            MNRVGIDVDHMIGVLLLAVVVVFWVG----------ASCLTNELLETN--------AYNK 42
                     *:: .  *  : .    .:.:.   *          *.. :   :*:.        : .:

Hum_Transporter      AQLKKIFWGVAVVLCVCSSWAGSTQLAKLTFRKFDAPFTLTWFATNWNFLFFPLYYVGHV 120
Yeast_Thi            PFFLTYLNISSFALYLTPDLWRIIQSRRKSLQER-TERTLPIHTQESFSEFLPLLSSTPS 101
                     . : . :   :..* : ..     *  : ::::  :  **. .: :    *:**

Hum_Transporter      CKSTEKQSVKQRYRECCRFFGDNGLTLKVFFTKAAPFGVLWTLTNYLYLHAIKKINTTDV 180
Yeast_Thi            TSSNLSSIADTKVKDTMRLS--------------LLFCVLWFVANLAANAALSYTTVASS 147
                      .*. .. .. : ::  *:                 * *** ::*     *:.  ..:.

Hum_Transporter      SVLFCCNKAFVFLLSWIVLRDRFMGVRIVAAILAIAGIVMMTYADGFHSHSV------IG 234
Yeast_Thi            TILSSTSSFFTLFLATSLGIETFSTKKLLGLFVSLFGIILIVMQSSKQQDSVSASSFLVG 207
                     ::* . .. *.::*:  :  : *   :::. :::: **:::.  .. :..**      :*

Hum_Transporter      IALVVASASMSALYKVLFKLLLGSAKFG-EAALFLSILGVFNILFITCIPIILYFTKVEY 293
Yeast_Thi            NTLALLGSLGYSVYTTLLKYEISSKGLRLDIQMFLGYVGIFTFLLFWPILIILDITHMET 267
                      :*.: .:   ::*..*:*  :.*  :  :  :**. :*:*.:*::  * *** :*::*

Hum_Transporter      WSSFDDIPWGNLCGFS-VLLLTFNIVLNFGIAVTYPTLMSLGIVLSIPVNAVIDHYTSQI 352
Yeast_Thi            FELPSNFHISFLVMLNCIIIFVSDYFWCKALILTSPLVVTVALTFTIPLAMFADFVWREA 327
                     :.  .::  . *  :. ::::. : .   .: :* * ::::.:.::**:  . *.   :

Hum_Transporter      VFNGVRVIAIIIIGLGFLLLLLPEEWDVWLIKLLTRLKVRKKEEPAEGAADLSSGPQSKN 412
Yeast_Thi            FFTPWYIIGVIFIFVSFFLVNH-----------------RGESAVEKDCAAVEKGPILDA 370
                     .*.   :*.:*:* :.*:*:                   * :.   :..* :..**  .

Hum_Transporter      RRARPSFAR 421
Yeast_Thi            ---------
```

On-line Table 4. Allelic Expression Imbalance (AEI) at the human *SLC35F3* locus: SNPs on the same DNA strand with transcripts differentially expressed in 53 CEU lymphoblastoid cell lines.

Cell panel	**Gene**	**RefSeq**	**Chr**	**Start**	**End**	**SNP**	**Location**	**P-value**	**R^2 (effect size)**	**Allele**	**Slope**
CEU	SLC35F3	NM_173508	1q42	232107301	232526885	rs10910399	232,458,663 (Intron-2)	**4.80E-07**	0.4005	C	0.1801
"	"	"	"	"	"	rs12029247	232,459,164 (Intron-2)	**5.92E-07**	0.3956	A	-0.1793

Slope: +ve value indicates that allele in preceding column is relatively overexpressed.
CEU: CEPH (Caucasian, European ancestry) 53 lymphoblastoid cell line DNAs and transcripts.

ON-LINE/SUPPLEMENTARY FIGURES.

On-line Figure 1. BP associations across the *SLC35F3* locus for the ICBP. In these LocusZoom plots, the upper panel illustrates SBP associations, while the lower panel gives DBP associations. The Exon/Intron structure of SLC35F3 is given beneath the bottom panel. 617 SNPs were scored across the ~420 kbp locus. Results are shown for SBP/DBP in >27,000 adults from North America or Western Europe (see Table 1). The position of peak SBP SNP rs16842784 (within Intron-2) is identified in each plot. Left vertical axis: Significance of the association, as reciprocal of Log[10] of the p-value. Right vertical axis: Recombination frequency in cM/Mb, as estimated by marker-on-marker correlations. Pseudocolor scale: Marker-on-marker correlations (R^2) within the trait-associated regions, referenced to the peak SNP (diamond) for the particular trait.

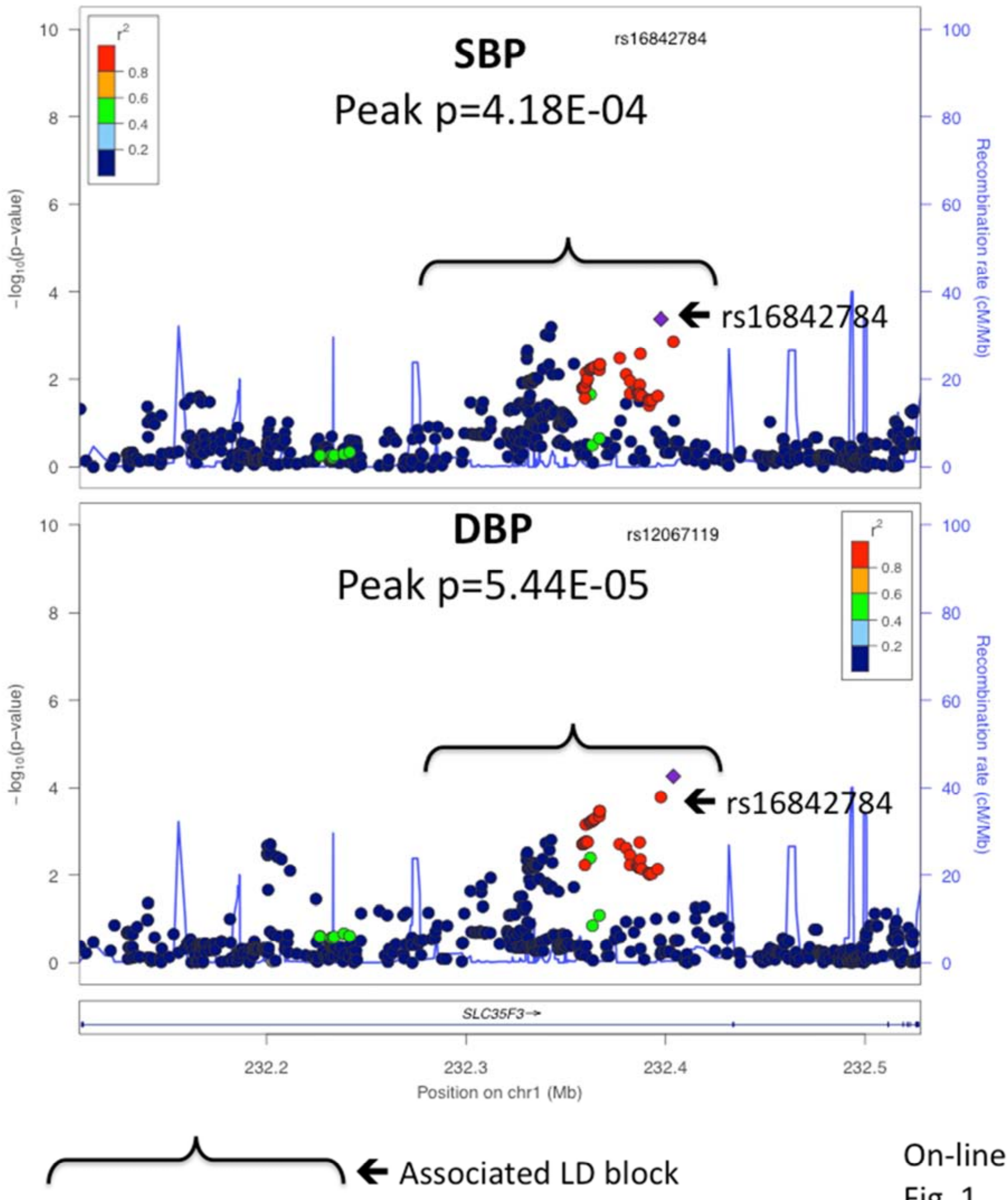
On-line Figure 2. Amino acid sequence homologies between human SLC35F3 and yeast Thi74, within TCDB (Transporter Classification DataBase).

2A: Secondary structure prediction of human SLC35F3.

2B: Secondary structure prediction of yeast Thi74.

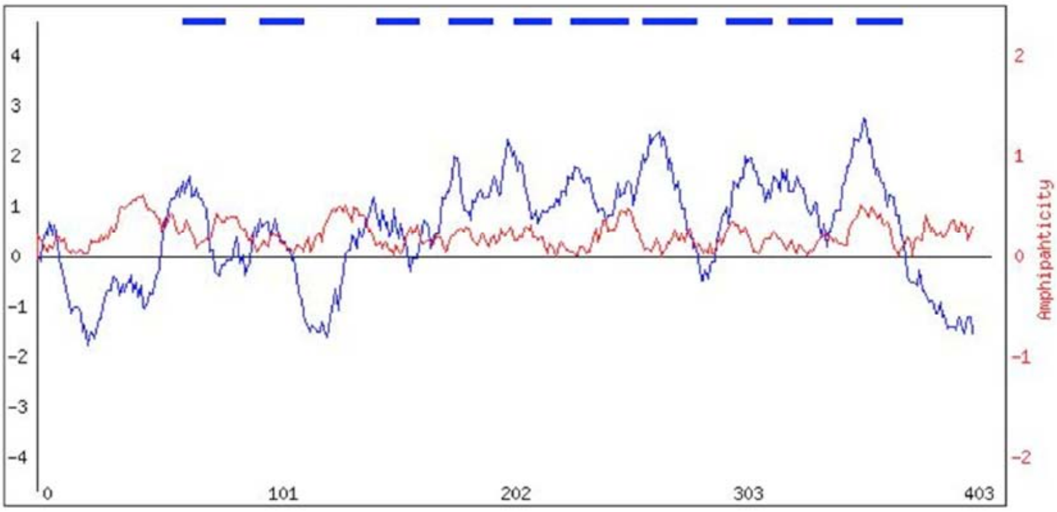
On-line Figure 3. Alternative splicing of the human *SLC35F3* mRNA. Results are based on EST alignments (and deduced splicing) at the *SLC35F3* locus performed at <http://ccg.vital-it.ch/tromer>, and viewed at <http://genome.ucsc.edu>.

SLC35F3*: Association with SBP and DBP in ICBP-GWAS



On-line
Fig. 1

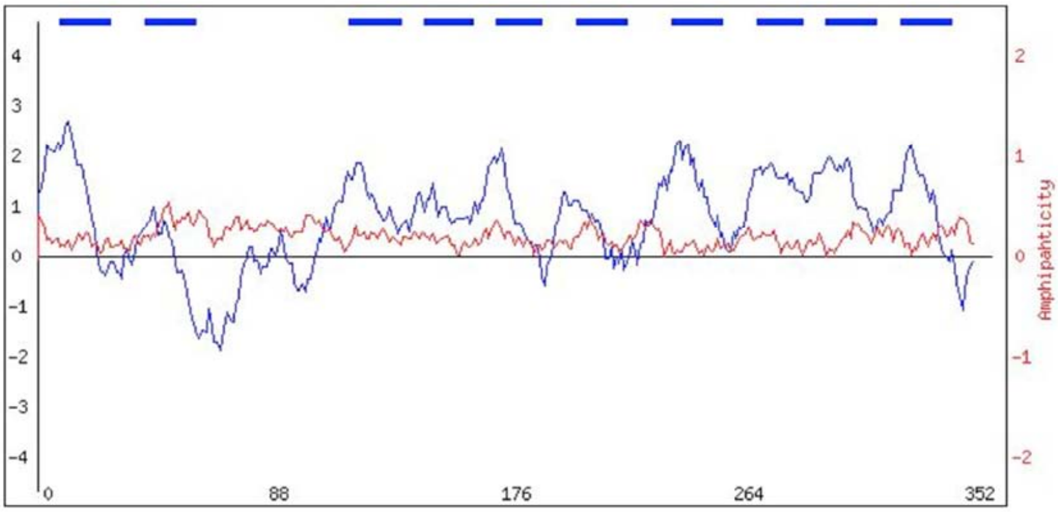
Hydropathy plot on human Q8IY50 (SLC35F3) at TCDB.org:



Blue Curve = Hydropathy
Red Curve = Hydrophobic Moment (Amphipathicity)
Blue Bars = putative transmembrane segments (TMSs)
Putative TMSs can be clicked to plot a helical wheel diagram of the TMS

On-line Figure 2A

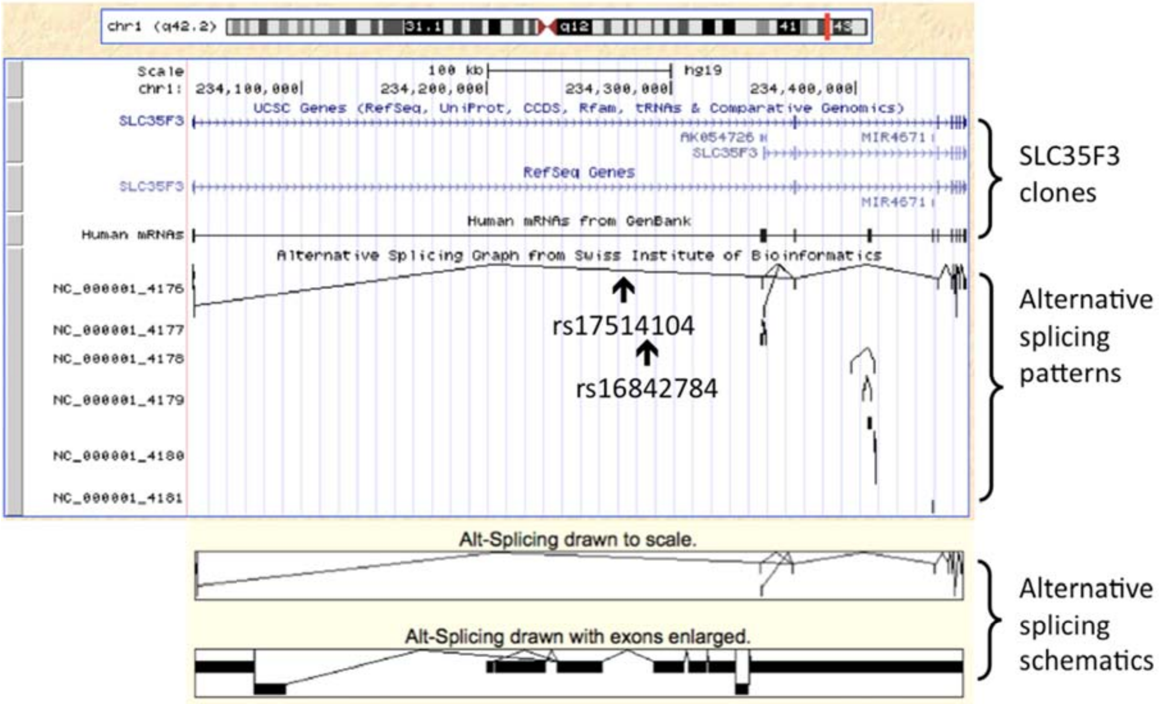
Hydropathy plot on yeast Q04083, Thi74, 2.A.7.24.1, at TCDB.org:



Blue Curve = Hydropathy
Red Curve = Hydrophobic Moment (Amphipathicity)
Blue Bars = putative transmembrane segments (TMSs)
Putative TMSs can be clicked to plot a helical wheel diagram of the TMS

On-line Figure 2B

Human *SLC35F3*: Alternative splicing patterns deduced from spliced ESTs



<http://genome.ucsc.edu>
<http://ccg.vital-it.ch/tromer>

Supplemental Figure 3