Supplemental Material

Title:

Novel human *ABCC9/SUR2* brain expressed transcripts and an eQTL relevant to hippocampal sclerosis of aging

Abbreviated title:

ABCC9/SUR2 in brain

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Supplemental Figure Legends

Supplemental Figure 1. Transcript-specific primers enables PCR to test for the presence of *SUR2A* transcripts with the novel *SUR2A*-specific 3'UTR portion in human tissues. Primers were developed which span exon junctions to enable transcript subtype-specific PCR (see cartoon at the bottom of the figure and Table 3 for specific primer sequences). Representative PCR results (agarose gel stained with SYBR green stain) from human cerebellar cortex (CECTX), frontal cortex (FCTX), hippocampus (Hippo; in brain), superior and middle temporal gyrus (SMTG), heart, and skeletal muscle. NTC is a control lacking cDNA input. This amplicon is approximately 1.2 kilobases. The "Case" identifications in this figure are not the same as in Table 2, these represent a convenience sample that were previously described (Wang et al. 2014).

Supplemental Figure 2. RT-PCR was performed using additional transcript-specific primers (arrows indicate locations) to test for the presence of *SUR2A, SUR2B, and SUR2Ab* transcripts including the novel *SUR2A*-specific 3'UTR portion in human tissues.

Supplemental Figure 3. Correlations between qPCR results from the four primer pairs shown in Fig. 9. For this study, data from all the samples shown in Table 2 were included and correlated with each other. The top number is correlation coefficient (r) and the bottom number is the result of the statistical test using linear regression (p value, if $p<0.05$). The level of SUR2B/Exon39 portion was positively correlated with the level of the proximal 3'UTR, but negatively correlated with the level of the distal 3'UTR.

Supplemental Table 1. PCR primers used in current study

Primer	Sequence (5'>3')	Target	Application or Comment
SUR2A-F	GTCTTTTCTGAGGGTATTTTAGTGGAGTGTGATACTGTCC	Exon38	3' RACE
SUR2B-F	GAATATGACACTCCAGAAAGCCTCTTGGCTCAGGAAAATG	Exon39	3' RACE
SUR2A-F1	CCGTGTCTCTTCTATTATGGATGCAGG	Exon38	qPCR
SUR2A-R	CTACTTGTTGGTCATCACCAAAGTGGAAAAG	Exon38	qPCR
SUR2B-F1	CGAGTACACACTATTCTGACGGCAGG	Exon39	qPCR
SUR2B-R	TCACATGTCTGCGCGAACAAAAGAAGCAA	Exon39	qPCR
UTR-A-F	GCTTGACCTCTGTAAAGTGGCATC	Proximal *SUR2B* 3'UTR	qPCR
UTR-A-R	CCTTCCAATAACCTCTGGAGACTC	Proximal *SUR2B* 3'UTR	qPCR
UTR-E-F	AGGTGCTGGAGAGGATGTGGAGA	Distal *SUR2B* 3'UTR	qPCR
UTR-E-R	AGTTACTTAGAGGGTCTTCTGG	Distal *SUR2B* 3'UTR	qPCR
2A-Sp-F	GGTGACAATAGCTCACCGTGTCTCTT	*SUR2A* and *SUR2Ab*	Span Exon 37/39 junction
2B-Sp-F	GGTGACAATAGCTCATCGAGTACACA	*SUR2B*	Span Exon 38/39 junction
bUTR-R	CAGGAATGGAAGTGTCAATGAGTAGTCAG	Proximal *SUR2B* 3'UTR	
SUR2AUTR 1049-R	CTAGGTATCCTAGTGGCCACGTTCAC	*SUR2A*	

Supplemental information about databases:

The Genotype-Tissue Expression (GTEx) Project: from—

http://www.gtexportal.org/home/documentationPage

GTEx was supported by the Common Fund of the Office of the Director of the National Institutes of Health. Additional funds were provided by the NCI, NHGRI, NHLBI, NIDA, NIMH, and NINDS. Donors were enrolled at Biospecimen Source Sites funded by NCI\SAIC-Frederick, Inc. (SAIC-F) subcontracts to the National Disease Research Interchange (10XS170), Roswell Park Cancer Institute (10XS171), and Science Care, Inc. (X10S172). The Laboratory, Data Analysis, and Coordinating Center (LDACC) was funded through a contract (HHSN268201000029C) to The Broad Institute, Inc. Biorepository operations were funded through an SAIC-F subcontract to Van Andel Institute (10ST1035). Additional data repository and project management were provided by SAIC-F (HHSN261200800001E). The Brain Bank was supported by a supplements to University of Miami grants DA006227 & DA033684 and to contract N01MH000028. Statistical Methods development grants were made to the University of Geneva (MH090941 & MH101814), the University of Chicago (MH090951, MH090937, MH101820, MH101825), the University of North Carolina - Chapel Hill (MH090936 & MH101819), Harvard University (MH090948), Stanford University (MH101782), Washington University St Louis (MH101810), and the University of Pennsylvania (MH101822). The data used for the analyses described in this manuscript were obtained from: [insert, where appropriate] the GTEx Portal on MM/DD/YY and/or dbGaP accession number phs000424.vN.pN on MM/DD/YYYY.

BRAINEAC: from –

http://www.braineac.org/

and

http://www.nature.com/neuro/journal/v17/n10/full/nn.3801.html#acknowledgments

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SNPExp: SNPexp v1.2, from –

http://app3.titan.uio.no/biotools/help.php?app=snpexp

General description: SNPexp provides a convenient and platform-independent way to calculate and visualize the correlation between the HapMap genotypes in a genomic region of interest and gene expression levels. Gives a hint of which SNPs that are associated with a change in gene expression. Both the SNP gentypes and the gene expression levels for the same individuals are publicly available: The HapMap project: Genome-wide SNP genotyping in 270 individuals from 4 populations. GENEVAR - GENe Expression VARiation: Analysis of gene expression variation in the HapMap samples using genome-wide expression arrays (47294 transcripts) from EBV-transformed lymphoblastoid cell lines from the same 270 HapMap individuals. The tool SNPexp provides an easy way to combine the information in these two datasets. It uses the whole genome association analysis toolset PLINK to calculate correlation (p-values) between genotypes for a chosen range of SNPs and the expression value for a gene of interest. The result can be visualized as a custom track on the UCSC Genome Browser.