

Supplementary Online Content

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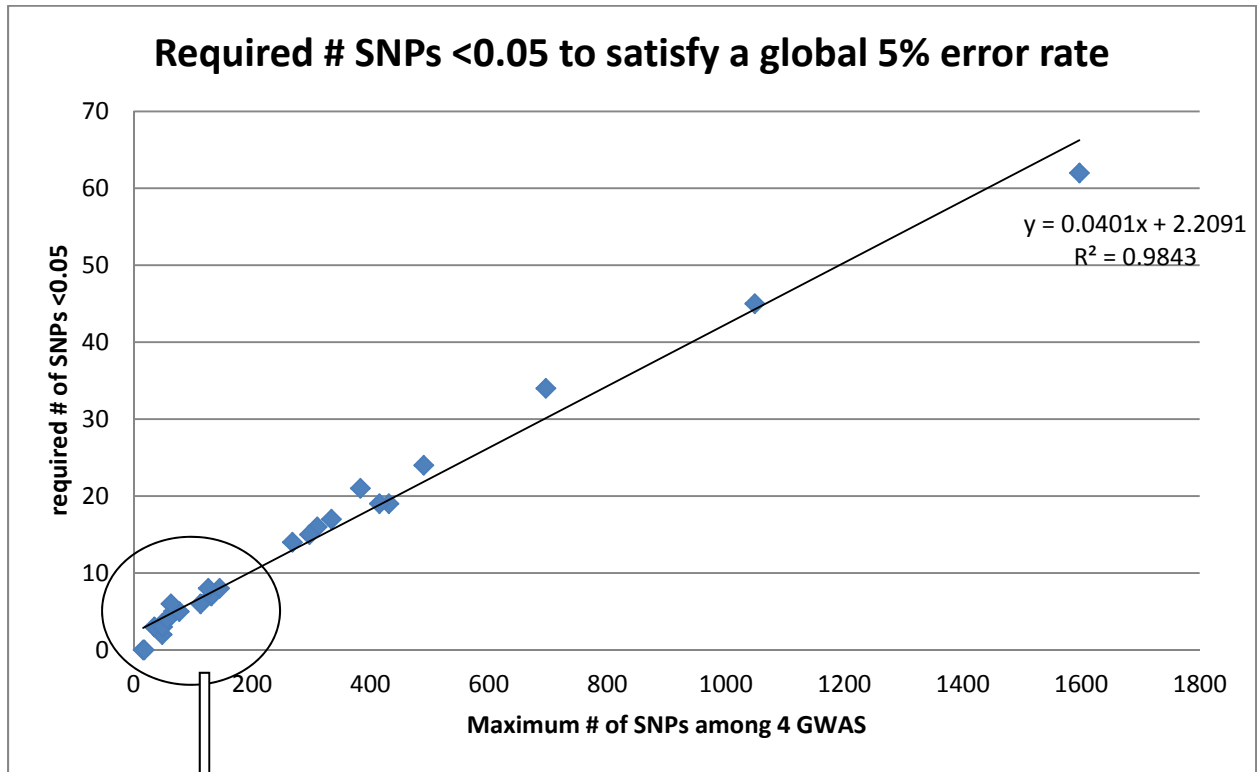
eBox. Summary of Steps in Pathway Analysis

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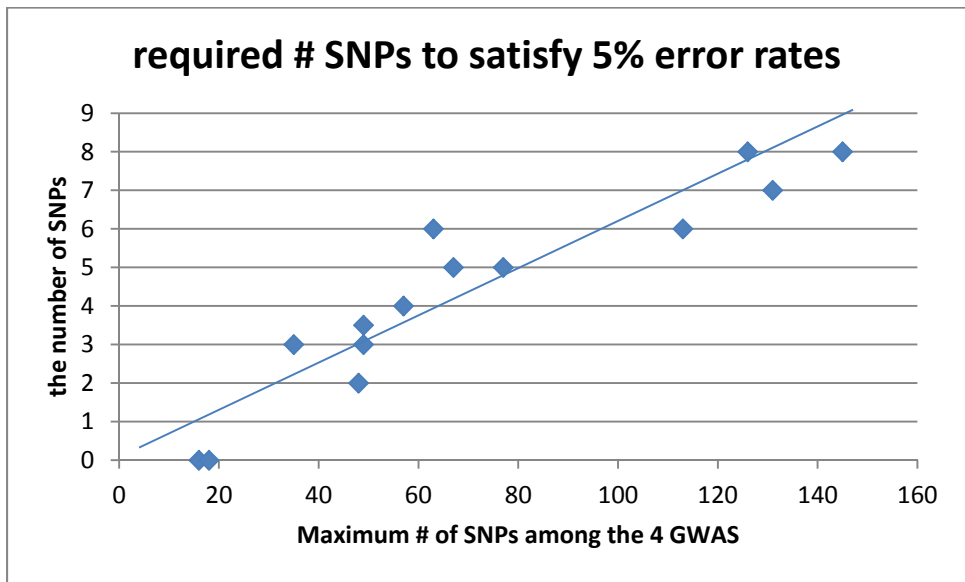
This supplementary material has been provided by the authors to give readers additional information about their work.

eFigure 1. Threshold for Study Entry Is Related to Gene Size

A



B



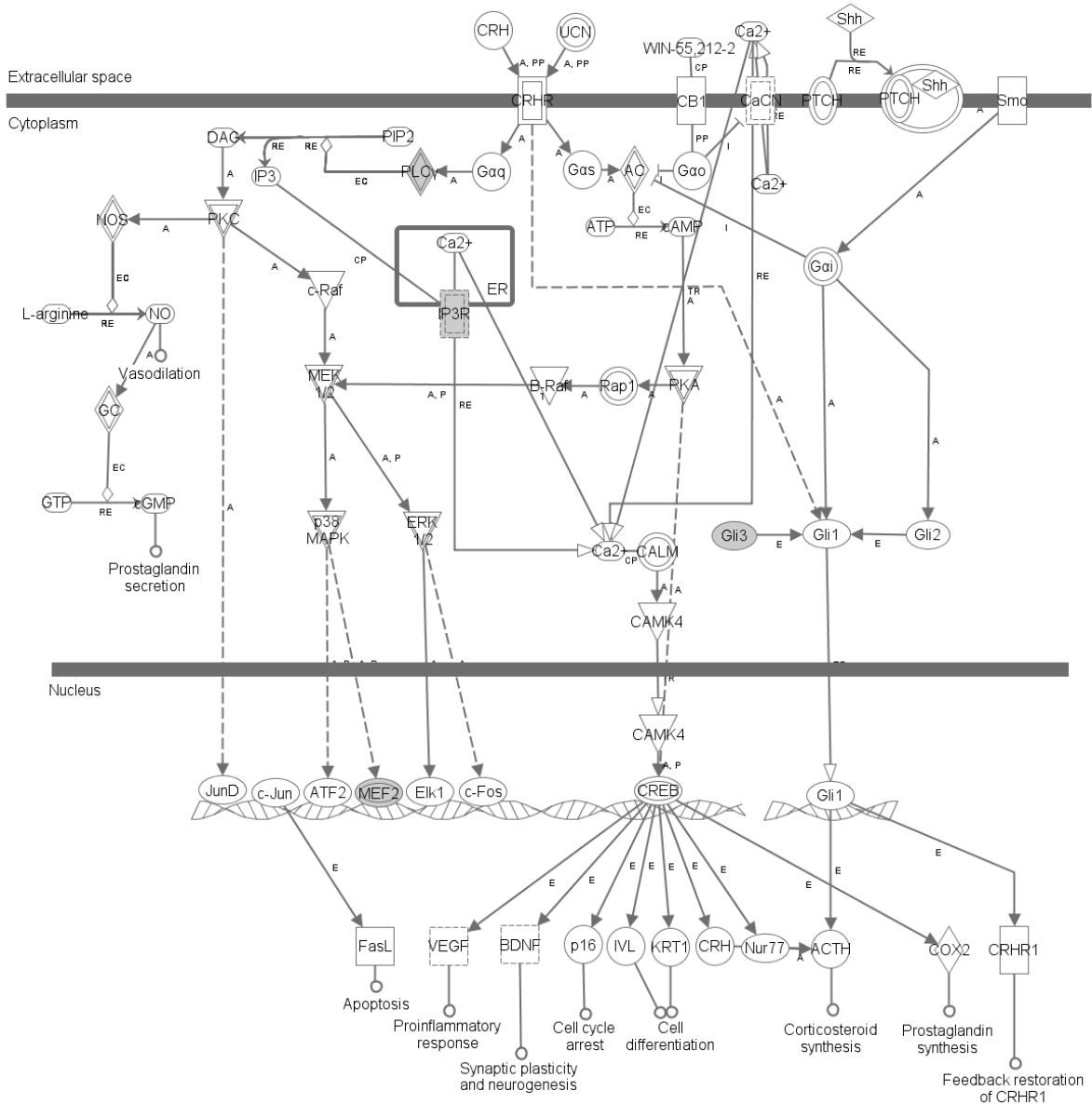
eFigure 1A shows the derivation of a regression equation to determine the empirical p value threshold for each gene entered into the pathway analysis. Four GWAS studies were simulated using 10,000

replications per study and permuting case and control status. The number of times that SNPs from a particular gene were found to reach a nominal p value of $\leq .05$ in 3 out of 4 GWAS datasets was found to be directly related to the maximum number of SNPs tested in that gene in any GWAS (an indirect measure of gene size). The relationship between maximum number of SNPs tested in a gene and the number of SNPs at nominal $p \leq .05$ necessary to achieve an empirical $p \leq .05$ is given by the regression line. eFigure 1B provides an expansion of that relationship to more precisely define the threshold for smaller genes.

eFigures 2-7. These figures show the Canonical Pathway Diagrams for each of the selected pathways, as designated in Ingenuity Systems. The shaded molecules in each diagram indicate the specific genes, or gene-families, tagged by genes in the list of 226 in the Box of the present report.

eFigure 2. Corticotropin-Releasing Hormone Signaling

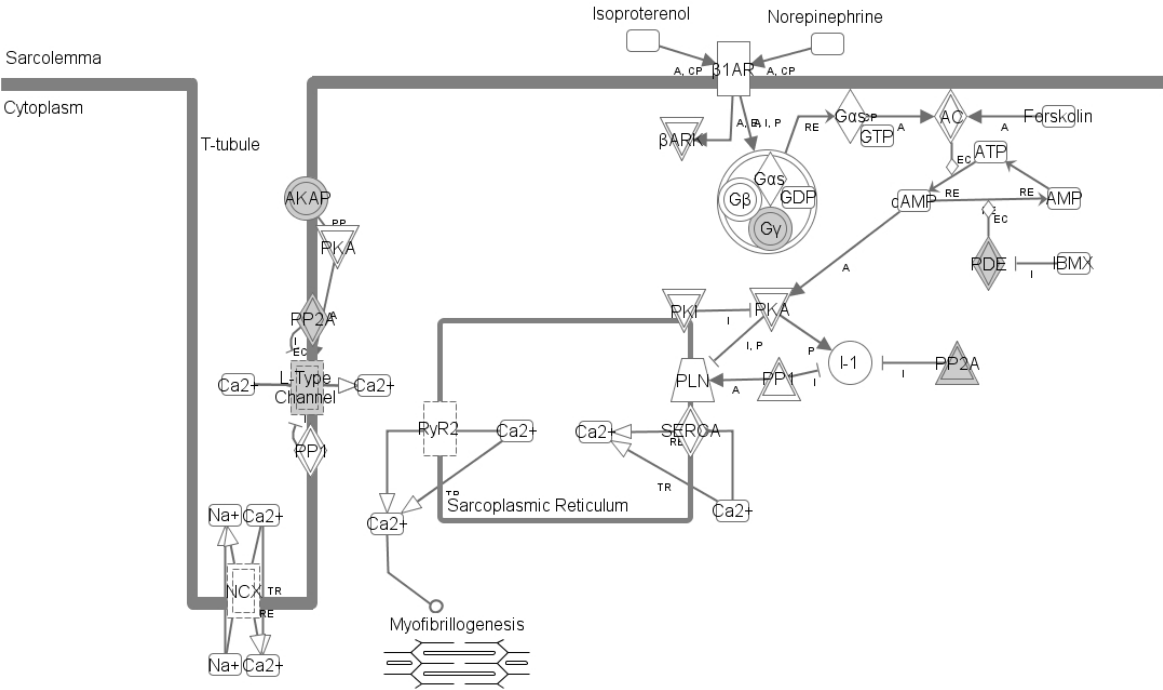
Corticotropin Releasing Hormone Signaling



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eFigure 3. Cardiac β -Adrenergic Signaling

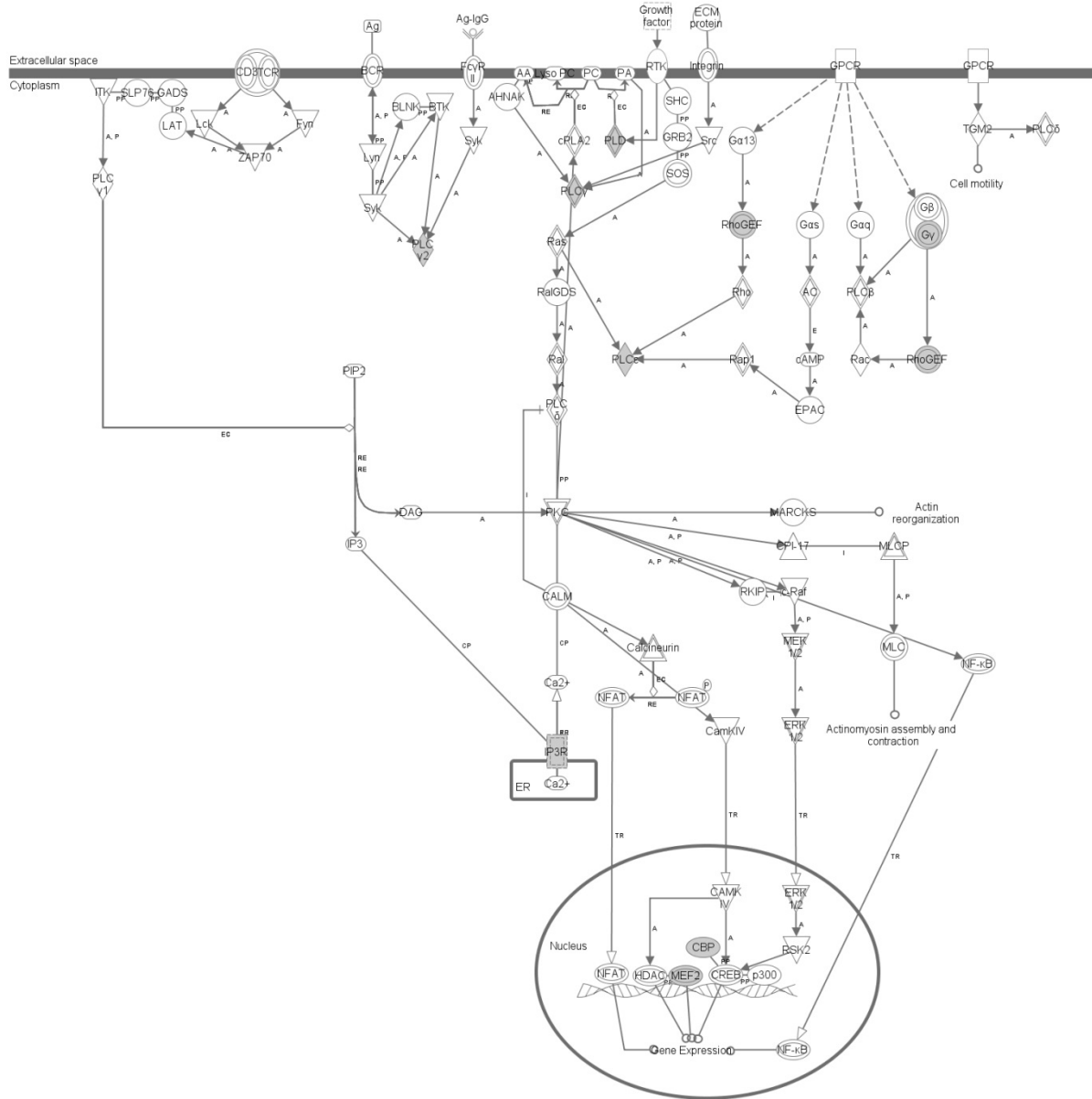
Cardiac β -adrenergic Signaling



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eFigure 4. Phospholipase C Signaling

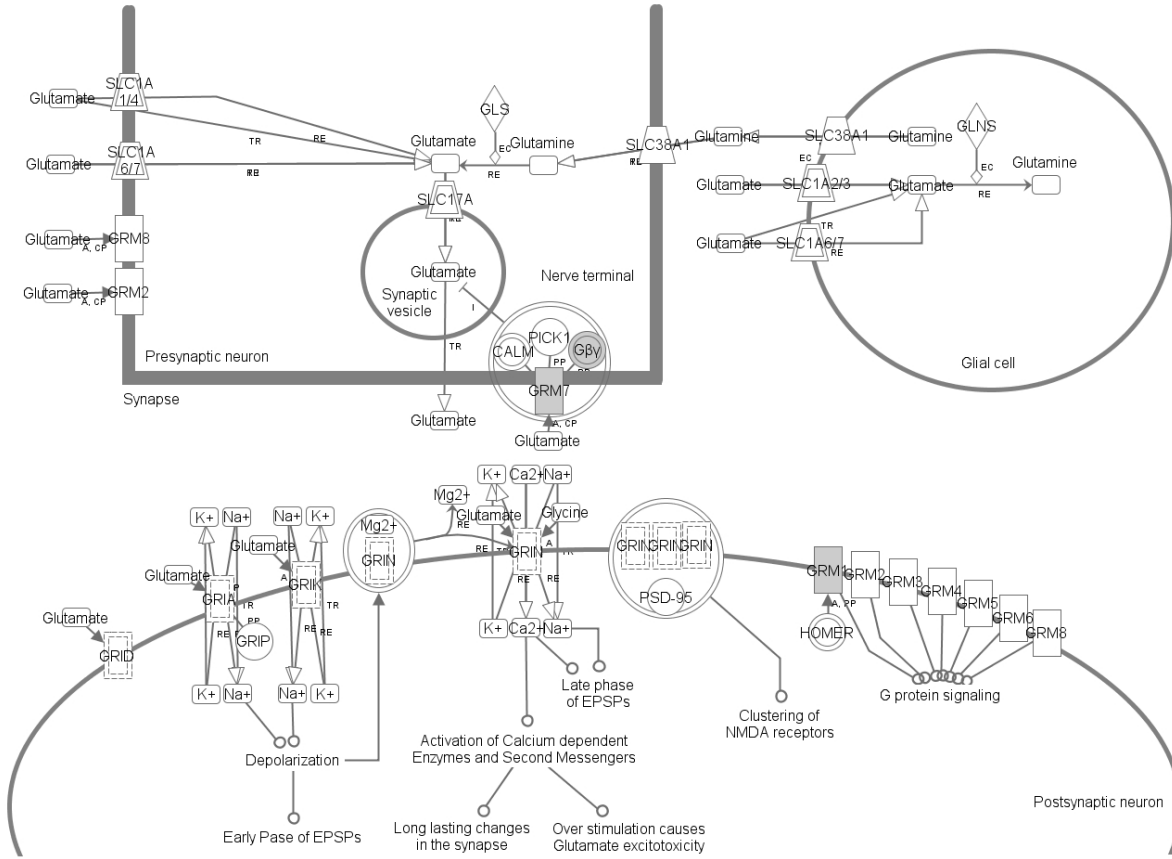
Phospholipase C Signaling



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eFigure 5. Glutamate Receptor Signaling

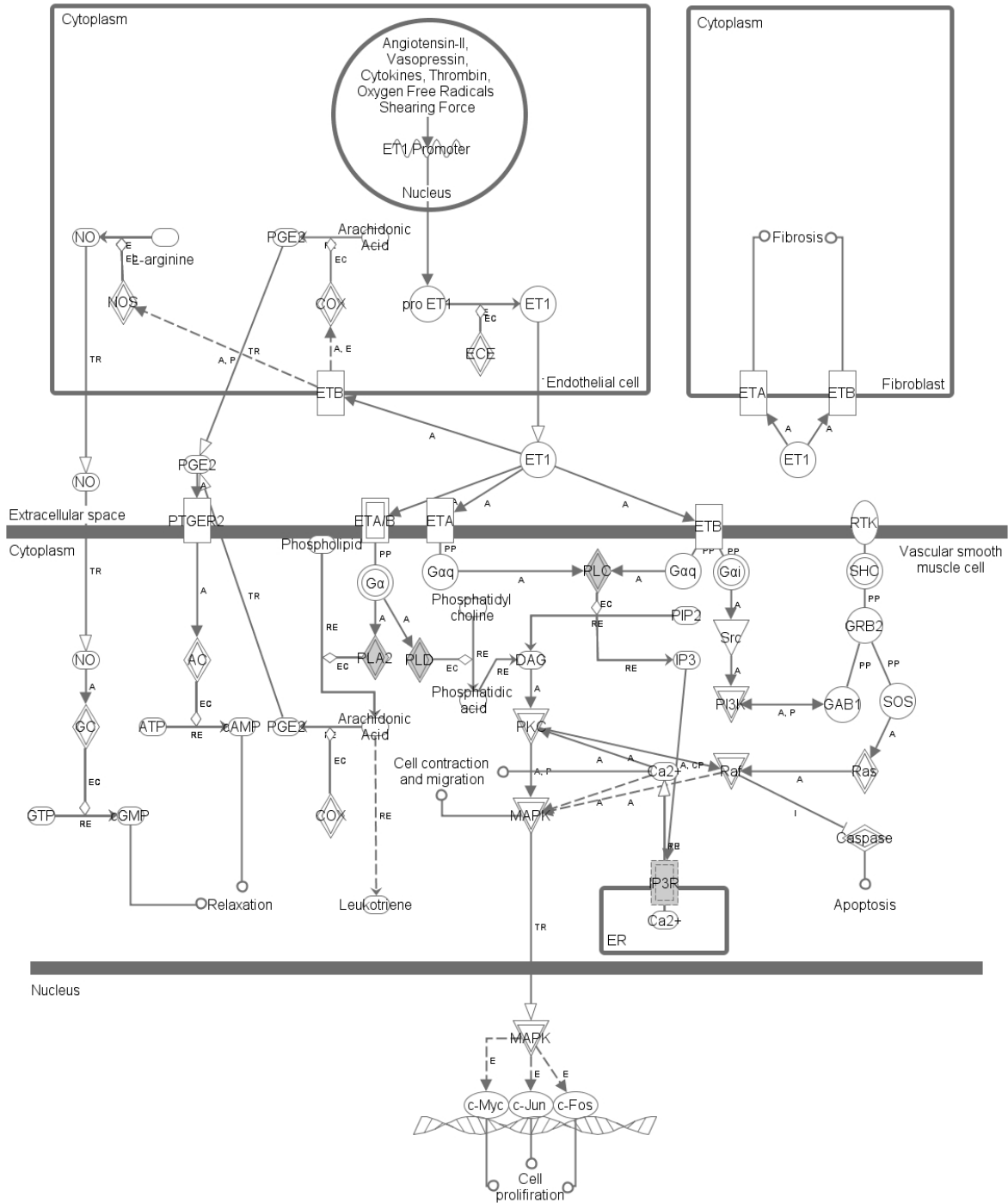
Glutamate Receptor Signaling



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eFigure 6. Endothelin 1 Signaling

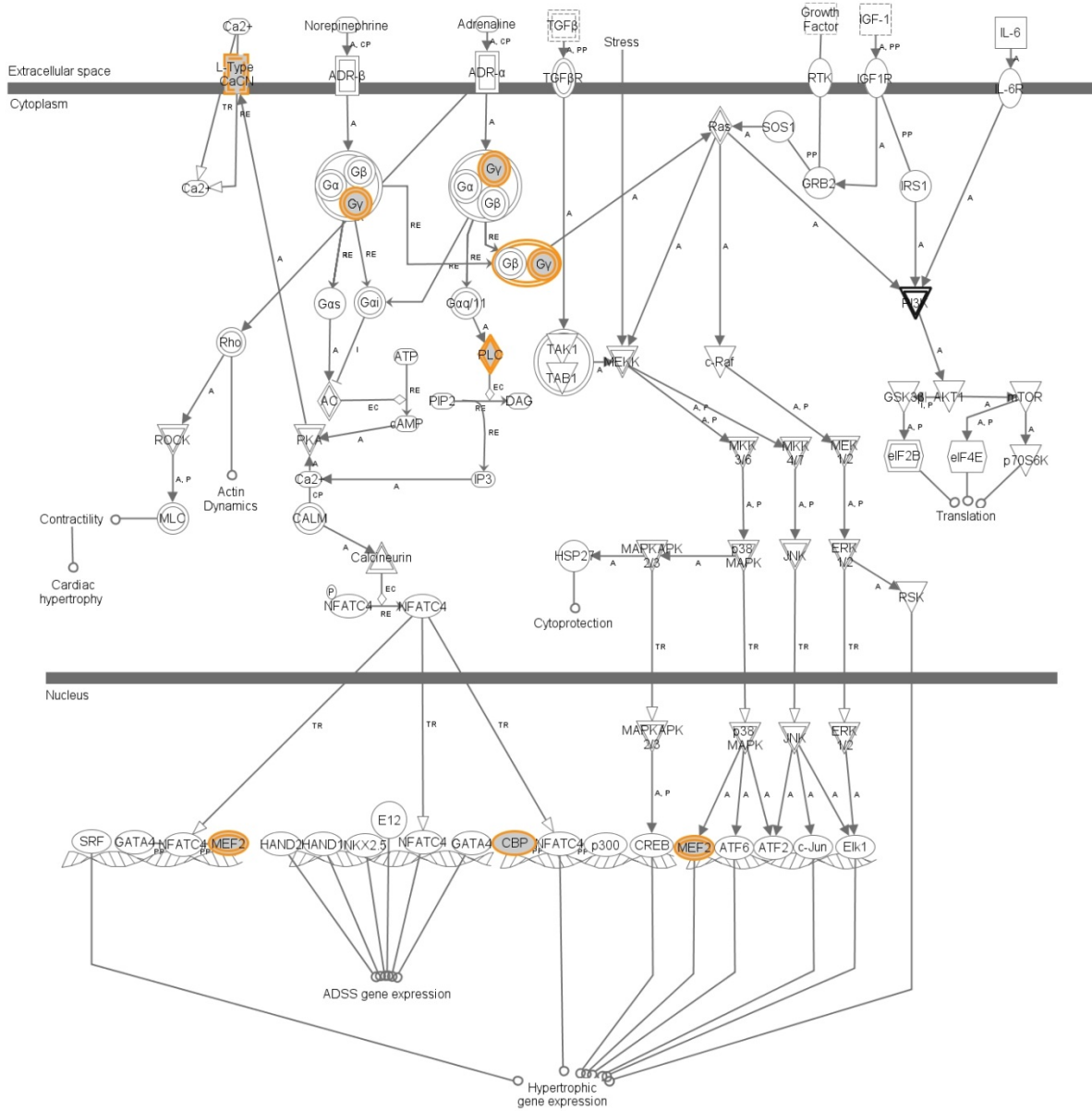
Endothelin-1 Signaling



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eFigure 7. Cardiac Hypertrophy Signaling

Cardiac Hypertrophy Signaling



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eTable. Characteristics of 25 Genes Included in Simulation to Determine the Relationship Between Gene Size and Empirical *P* Value

Gene	GAIN	STEP	Wellcome	German	GENE_SIZE(bp)	mean # of SNPs among 4 GWAS	Maximum # of SNPs among 4 GWAS	the required # of SNPs <0.05 for a global 5% FPE
<i>A2BP1</i>	1049	544	614	856	1,694,208	766	1049	45
<i>ADCY2</i>	131	74	82	116	433,851	101	131	7
<i>CNTNAP2</i>	696	372	438	558	2,304,637	516	696	34
<i>CSMD1</i>	1420	685	793	1597	2,059,453	1124	1597	62
<i>DLG2</i>	383	206	233	366	2,172,259	297	383	21
<i>GRM7</i>	334	182	210	300	880,416	257	334	17
<i>KCNMA1</i>	310	178	203	217	768,218	227	310	16
<i>NPAS3</i>	431	209	235	370	864,923	311	431	19
<i>OPCML</i>	415	192	222	413	1,117,528	311	415	19
<i>PARK2</i>	490	247	283	456	1,380,244	369	490	24
<i>PTPRG</i>	268	137	170	236	733,330	203	268	14
<i>SLIT3</i>	297	160	177	267	635,062	225	297	15
<i>CDK6</i>	49	25	33	42	231,706	37	49	3.5
<i>DDEF2/ASAP2</i>	48	26	38	31	198,918	36	48	2
<i>FER1L3/MYOF</i>	67	33	59	63	175,888	56	67	5
<i>TP53I11</i>	35	20	26	33	18,709	29	35	3
<i>C15ORF53</i>	16	8	8	9	3,440	10	16	1
<i>CHST8</i>	49	33	38	46	151,553	42	49	3
<i>FBN2</i>	77	43	53	71	280,134	61	77	5
<i>LGMN</i>	18	7	9	18	44,895	13	18	1
<i>MYLK4</i>	63	38	38	56	87,291	49	63	6
<i>NCAM1</i>	145	94	103	93	317,163	109	145	8
<i>NTNG1</i>	113	55	80	81	341,846	82	113	6
<i>PLA2R1</i>	57	38	47	45	121,109	47	57	4
<i>PRKCB</i>	126	69	88	97	384,632	95	126	8

eBox. Summary of Steps in Pathway Analysis

- 1) We derived a list of 966 genes with 2 SNPs at $p < 0.05$ in 3 out of four GWAS datasets (N = 5253 cases and 6874 controls).
- 2) We used 10,000 permutations of phenotype in the four GWAS datasets in order to extract 226 genes from the 966 that were each empirically significant at $p < 0.05$.
- 3) We ran the 226 genes through an Ingenuity pathway analysis and obtained 16 pathways.
- 4) We ran the 16 pathways in a separate GWAS dataset (PGC2, an independent set of several thousand cases and controls). 6/16 pathways showed $p < .05$ and $FDR < .05$.
- 5) We compared gene-level results from a multicenter gene expression analysis (N=919 genes) with the gene-level results from our own analysis (N=226 genes), observing an overlap of 9 genes, three of which were among the genes driving the pathway results (chi-square $p < 0.005$).

eAppendix. Psychiatric Genomics Consortium Bipolar Group Members and Affiliations

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