Figure W1. Chromosomal view of one representative chromosome (chr 1) in 15 cortisol-secreting ACA. The heat map shows the intensity plots in each sample. Gains/amplifications are represented in red and losses/deletions in blue. The CN profile is shown for one representative case (no. 312A). Normal CN score corresponds to 2.0, whereas gains correspond to a CN score greater than 2.5 and losses to a CN score less than 1.5 in blue. The genomic segmentation (Partek GS) shows the altered regions for each sample (selected case underlined). CN gains are represented in red and CN losses in blue.

Table W1. Primers for RT-qPCR at the DNA Level (Validation) and at the mRNA Level (Gene Expression) for the Candidate Genes and for the Internal Reference Genes.

DNA RT-qPCR

Gene Symbol		Primers	Chromosome
IGF2	fw	5′-gct gac acc tgg cgg cca tt-3′	11
	rw	5′-ggc gtc ctg act ttg ccc cc-3′	
EPHA7	fw	5′-agg cct tgg cca gga agc tg-3′	6
	rw	5′-ggc ttg cac ata tcc ctt ctg ccc-3′	
SGK1	fw	5′-tgg aag ctg ctg ctg ccc ac-3′	6
	rw	5′-tgt cca tct ctg gcc ccc gg-3′	
CTNNB1	fw	5′-acg agg agg caa gtt tct cca agg-3′	3
	rw	5′-tgc gcc tct ccc cac ctc ac-3′	
CYP11B2	fw	5′-cct gtg tct tgg ggc gg-3′	8
	rw	5′-ggc ctt ggg cga cag cac at-3′	
GAPDH	fw	5′-tga cgc tgg ggc tgg cat tg-3′	12
	rw	5′-ggc ggc aga ccc tgc act tt-3′	

RNA RT-qPCR

Gene Symbol	Primer Probe Mix*	Chromosome	Amplicon Length (bp)
IGF2	Hs00171254_m1	11	94
EPHA7	Hs01033009_m1	6	88
SGK1	Hs00178612_m1	6	81
CTNNB1	Hs00994404_g1	3	93
FHIT	Hs00179987_m1	3	79
NOTCH1	Hs01062014_m1	9	80
CYP11B1	Hs01596404_m1	8	137
CYP11B2	Hs01597732_m1	8	137
HRAS	Hs00610483_m1	11	69
β-actin	Hs9999903_m1	7	171

*TaqMan Gene Expression Assays (Applied Biosystems).

Table W4. Gene Ontology Family Analysis (Performed with GSEA) Including the Genes with CNAs Observed in at Least 2 of 15 Cortisol-Secreting ACAs (Frequency, ≥13%; Total, 638 Recognized Genes).

Cytokines and Growth Factors	Transcriptional Factors	Homeodomain Proteins	Cell Differentiation Markers	Protein Kinases	Oncogenes	Tumor Suppressor Genes
CTGF	IRX4	IRX4	**CD151**	**ADCK5**	CTNNB1	**FANCA**
IGF2	**LHX3**	**LHX3**	CD24	BRSK2	DUX4	RECQL4
INS	NKX6-2	NKX6-2	IFITM1	CAMK2B	**HRAS**	TSC2
INS-IGF2	TGIF1	TGIF1	IL9R	CDK10	**NOTCH1**	FHIT
KITLG	VENTX	TGIF2LY	**L1CAM**	CDK11A	PRDM16	**H19**
PDGFA	CTNNB1	**UNCX**	RHCE	**EPHA7**	STIL	
SCT	DUX4	VENTX	TNFRSF4	EPHB2		
SLURP1	PRDM16			**IRAK1**		
	ARC			**MAPK15**		
	DEAF1			NRBP2		
	E2F2			PRKCZ		
	E4F1			PRKG1		
	FAM20C			PRKY		
	FOXH1			PTK2		
	HES4			SGK1		
	HES5					
	HEY2					
	HSF1					
	HSFY1					
	ID3					
	IRF7					
	LRRC14					
	MAFK					
	MECP2					
	MFSD3					
	NFKBIL2					
	NPAS2					
	PHRF1					
	PRDM7					
	RASSF7					
	REV3L					
	RXRA					
	SCRT1					
	SNAPC4					
	SOX8					
	SRY					
	TBL1Y					
	TP73					
	TRIP13					
	UTF1					
	ZFY					
	ZNF16					
	ZNF250					
	ZNF251					
	ZNF33B					
	ZNF696					
	ZNF7					

Red: genes with CN gains
Blue: genes with CN losses.
Underlined: genes with microalterations.
Bold: genes altered in at least three samples (frequency, ≥20%).
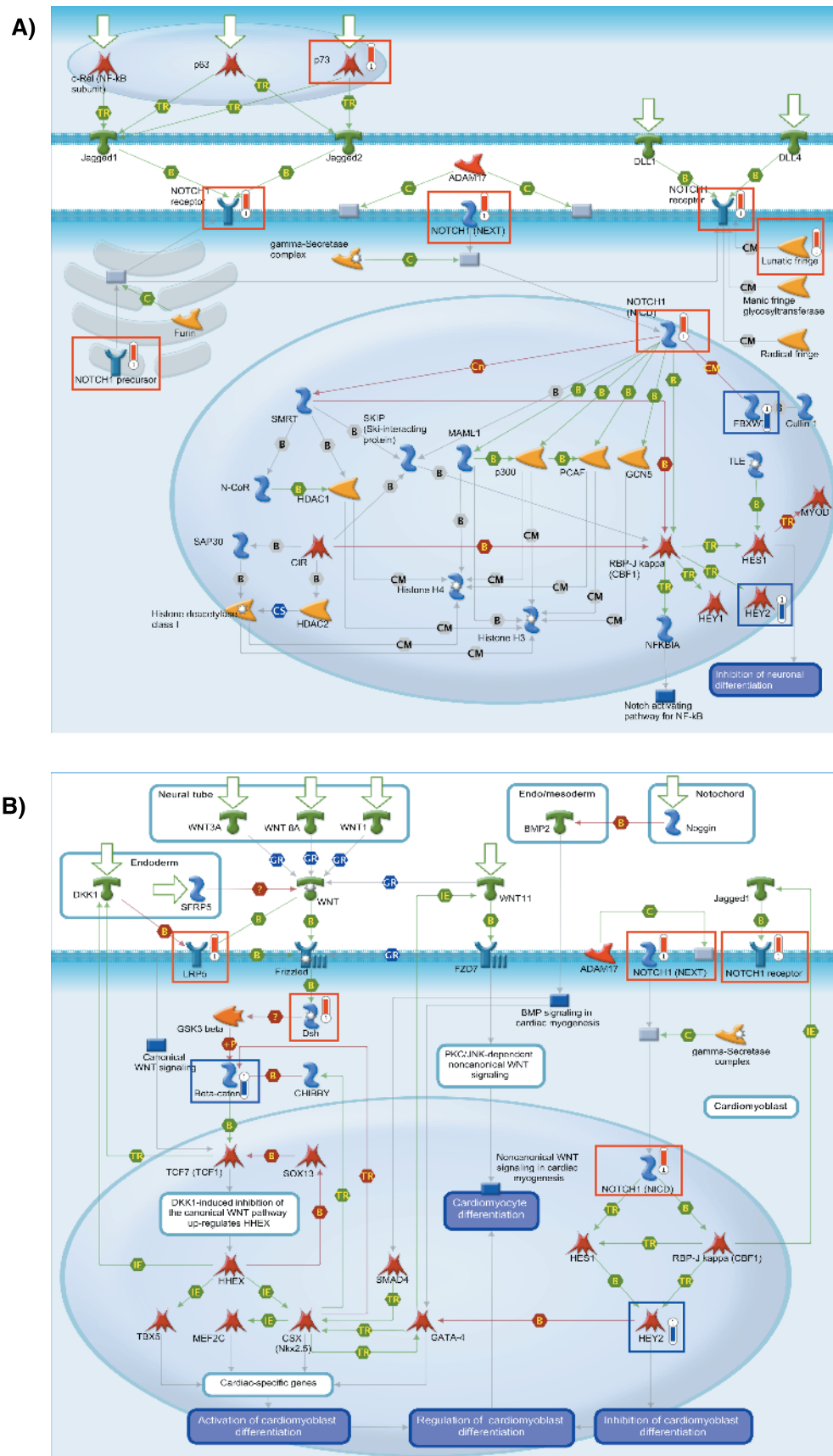
Figure W2. The Notch signaling pathway map (A, gene ontology enrichment $P = 1.494^{e-6}$) and the Wnt and Notch signaling in early cardiac myogenesis (B, gene ontology enrichment, $P = 4.287^{e-6}$) according to the GeneGo analysis (MetaCore Analytical suite) including all the genes ($n = 285$ annotated genes) with CNAs observed in at least two samples (recurrent CNA). Genes with gains are underlined in red and genes with losses in blue. Detailed legend is available at http://www.genego.com/mapsearch.php.
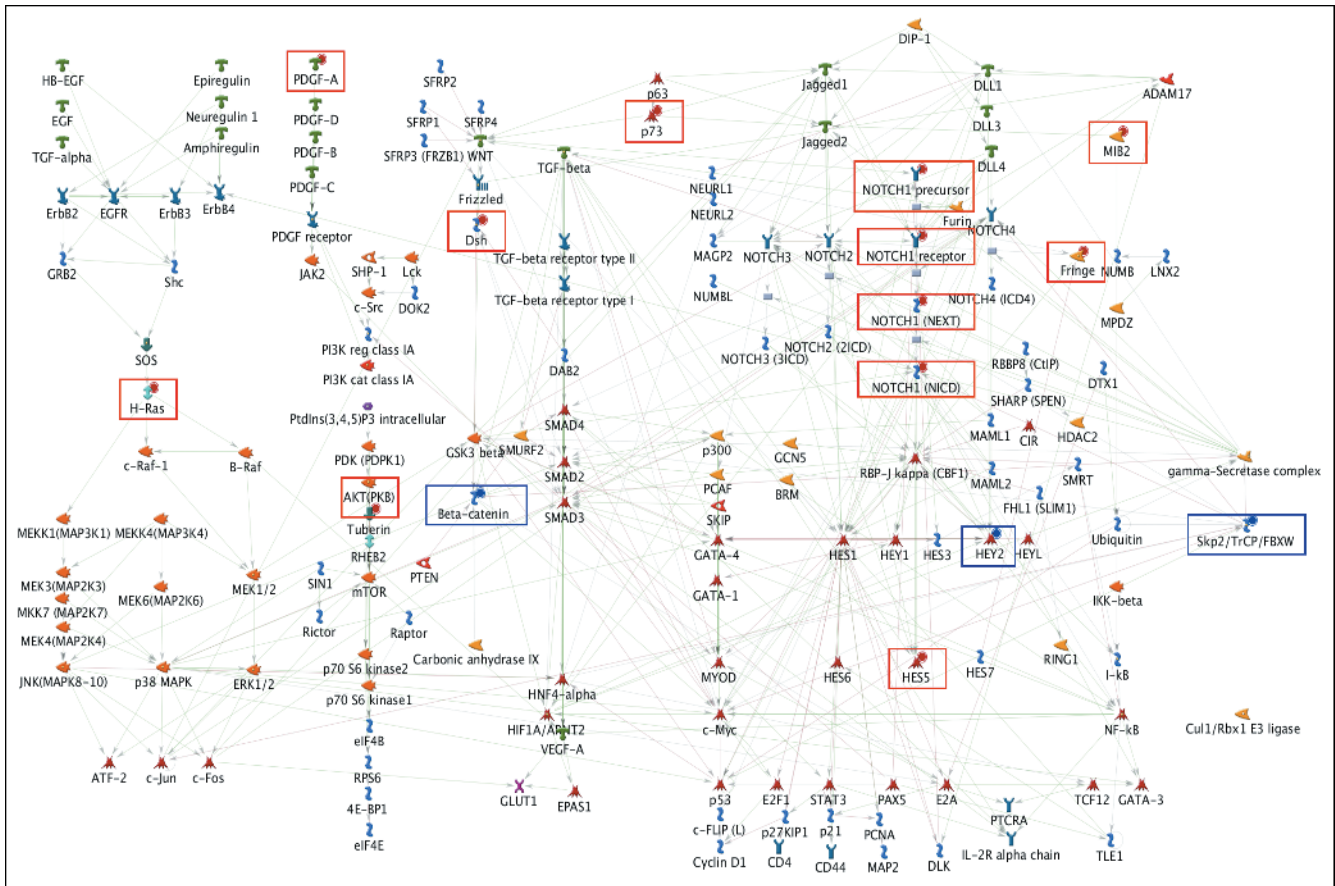
Figure W3. The entire Notch signaling gene network according to the GeneGo analysis (MetaCore Analytical suite). Detailed legend is available at http://www.genego.com/mapsearch.php.
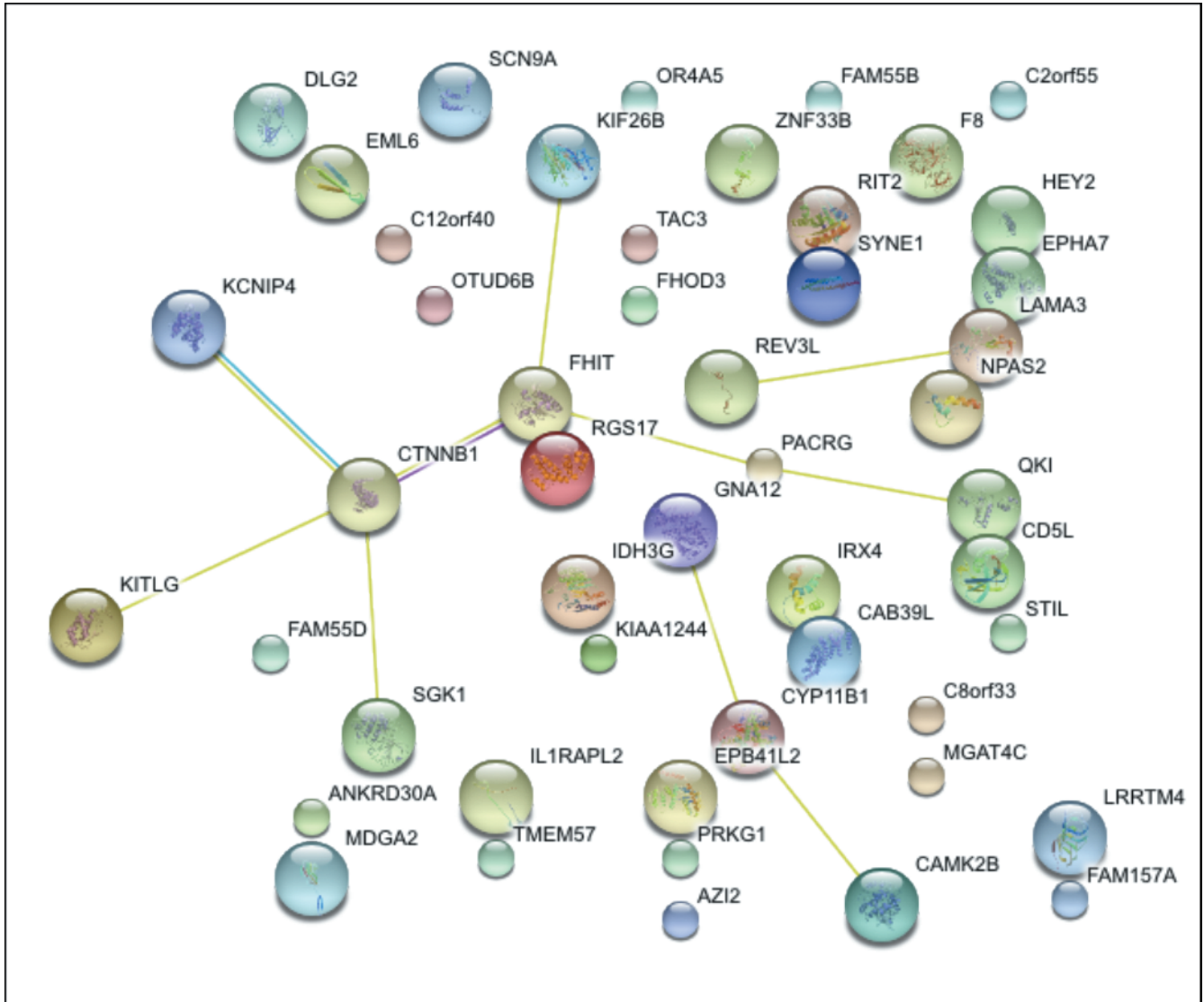
Figure W4. Graphical representation of the STRING-generated protein-protein network (action view) for the single genes with CN micro-alterations observed in at least two samples (*n* = 46 annotated genes). Modes of action are shown in different colors. Detailed legend is available at http://string-db.org/newstring_cgi/show_network_section.