Supplemental Tables

Supplemental Table 1. Complete list of somatic mutations detected in 99 adrenocortical adenomas by whole-exome sequencing.

ID	Diagnosis	n mut/sample	Genesymbol	Class	Function
AD1	overt Cushing	4	DHCR7	snp	missense
AD1	overt Cushing		FRY	snp	missense
AD1	overt Cushing		SNED1	snp	missense
AD1	overt Cushing		GNAS	snp	missense
AD2	overt Cushing	2	PTPN22	snp	missense
AD2	overt Cushing		HECA	snp	missense
AD3	overt Cushing	26	MASP2	snp	missense
AD3	overt Cushing		CRNN	snp	missense
AD3	overt Cushing		FCRL2	snp	missense
AD3	overt Cushing		COL17A1	snp	missense
AD3	overt Cushing		TBC1D10C	snp	missense
AD3	overt Cushing		IQSEC3	snp	missense
AD3	overt Cushing		NELL2	snp	missense
AD3	overt Cushing		EFS	snp	missense
AD3	overt Cushing		C14orf80	snp	missense
AD3	overt Cushing		NAPG	snp	missense
AD3	overt Cushing		CLIP3	snp	missense
AD3	overt Cushing		GTDC1	snp	missense
AD3	overt Cushing		SYNJ1	snp	missense
AD3	overt Cushing		CTNNB1	snp	missense
AD3	overt Cushing		CTNNB1	snp	missense
AD3	overt Cushing		CPN2	snp	missense
AD3	overt Cushing		BHMT	snp	missense
AD3	overt Cushing		PCDHA6	snp	missense
AD3	overt Cushing		RANBP9	deletion	indel
AD3	overt Cushing		E2F3	indel	frameshift
AD3	overt Cushing		ZAN	snp	missense
AD3	overt Cushing		PRSS58	snp	missense
AD3	overt Cushing		MED30	deletion	frameshift
AD3	overt Cushing		PTENP1	snp	missense
AD3	overt Cushing		MAGEB4	snp	missense
AD3	overt Cushing		NDP	snp	missense
AD3	overt Cushing		ATRX	snp	missense
AD4	subclinical Cushing	2	OR1D2	snp	missense
AD4	subclinical Cushing		CTNNB1	snp	missense
AD5	subclinical Cushing	1	CTNNB1	snp	missense
AD6	inactive	10	FMN2	indel	frameshift
AD6	inactive		ARNTL	snp	splice
AD6	inactive		RASGRP2	snp	missense
AD6	inactive		ARID2	snp	missense
AD6	inactive		PRR12	snp	missense
AD6	inactive		CTNNB1	snp	missense
AD6	inactive		GMPPB	snp	missense
AD6	inactive		PCDHA12	snp	missense
AD6	inactive		CADPS2	indel	frameshift
AD6	inactive		ATP6V1C1	snp	missense
AD7	inactive	7	THYN1	snp	missense
AD7	inactive		COL4A1	snp	missense

AD7	inactive		MIA2	snp	syn
AD7	inactive		ZNF99	snp	missense
AD7	inactive		MYLK2	snp	missense
AD7	inactive		CTNNB1	snp	missense
AD7	inactive		POP1	snp	missense
AD8	subclinical Cushing	16	MAST2	snp	missense
AD8	subclinical Cushing		HIF1AN	snp	missense
AD8	subclinical Cushing		PHRF1	snp	missense
AD8	subclinical Cushing		TMEM131A	snp	missense
AD8	subclinical Cushing		HEPHL1	snp	missense
AD8	subclinical Cushing		H2AFJ	indel	frameshift
AD8	subclinical Cushing		RYR3	snp	splice
AD8	subclinical Cushing		ASIC2	snp	missense
AD8	subclinical Cushing		FUT1	snp	missense
AD8	subclinical Cushing		CTNNB1	snp	missense
AD8	subclinical Cushing		QTRTD1	snp	missense
AD8	subclinical Cushing		LETM1	snp	missense
AD8	subclinical Cushing		GRIA2	snp	missense
AD8	subclinical Cushing		DNAH5	snp	missense
AD8	subclinical Cushing		PCDHGA11	snp	missense
AD8	subclinical Cushing		TEX10	snp	missense
AD9	subclinical Cushing	1	PKP2	snp	missense
AD10	inactive	3	TP53I13	snp	missense
AD10	inactive		HIRA	snp	missense
AD10	inactive		ZC3H12D	snp	missense
AD11	overt Cushing	9	TCN1	snp	missense
AD11	overt Cushing		ACAN	snp	missense
AD11	overt Cushing		ZNF205	snp	missense
AD11	overt Cushing		INO80D	deletion	frameshift
AD11	overt Cushing		OXT	snp	missense
AD11	overt Cushing		CTNNB1	snp	missense
AD11	overt Cushing		APC	snp	missense
AD11	overt Cushing		NAPRT1	snp	nonsense
AD11	overt Cushing		TFDP3	snp	missense
AD12	overt Cushing	9	CAPNS2	snp	missense
AD12	overt Cushing		WDR16	snp	missense
AD12	overt Cushing		KIDINS220	snp	missense
AD12	overt Cushing		ARMC9	snp	missense
AD12	overt Cushing		GNAS	snp	missense
AD12	overt Cushing		CTNNB1	snp	missense
AD12	overt Cushing		ZNF354C	snp	missense
AD12	overt Cushing		ETV7	snp	missense
AD12	overt Cushing		LCN1	snp	nonsense
AD13	subclinical Cushing	6	TRIM33	snp	missense
AD13	subclinical Cushing		KRT84	snp	missense
AD13	subclinical Cushing		MCF2L	snp	missense
AD13	subclinical Cushing		PHACTR3	snp	missense
AD13	subclinical Cushing		CTNNB1	snp	missense
AD13	subclinical Cushing		PCDHGA5	snp	missense

AD14	overt Cushing	2	SLC25A52	snp	missense
AD14	overt Cushing		GADD45B	indel	frameshift
AD15	subclinical Cushing	5	PALD1	indel	frameshift
AD15	subclinical Cushing		CEP290	snp	missense
AD15	subclinical Cushing		HPN	snp	missense
AD15	subclinical Cushing		CTNNB1	snp	missense
AD15	subclinical Cushing		DMD	indel	frameshift
AD16	overt Cushing	13	CHF	snp	missense
AD16	overt Cushing		IPO9	snp	missense
AD16	overt Cushing		MICAL2	snp	missense
AD16	overt Cushing		HERC1	snp	missense
AD16	overt Cushing		ARMC5	snp	missense
AD16	overt Cushing		FASN	snp	missense
AD16	overt Cushing		CEP76	snp	missense
AD16	overt Cushing		FASTKD5	snp	missense
AD16	overt Cushing		CSF2RB	snp	missense
AD16	overt Cushing		PDCHA8	snp	missense
AD16	overt Cushing		DSP	snp	splice
AD16	overt Cushing		CEP57L	snp	missense
AD16	overt Cushing		SCL46A2	snp	missense
AD17	overt Cushing	39	SKI	snp	missense
AD17	overt Cushing		GPATCH3	snp	missense
AD17	overt Cushing		PTGFR	snp	missense
AD17	overt Cushing		KLHL12	snp	missense
AD17	overt Cushing		PM20D1	snp	missense
AD17	overt Cushing		CRTAC1	snp	nonsense
AD17	overt Cushing		C10orf2	snp	missense
AD17	overt Cushing		ACCS	snp	missense
AD17	overt Cushing		MGAT4C	snp	missense
AD17	overt Cushing		SIX4	snp	missense
AD17	overt Cushing		EXD2	snp	missense
AD17	overt Cushing		ESRRB	snp	missense
AD17	overt Cushing		TRPM7	snp	nonsense
AD17	overt Cushing		KBTBD13	snp	missense
AD17	overt Cushing		TBC1D2B	snp	missense
AD17	overt Cushing		TPSG1	snp	missense
AD17	overt Cushing		KCTD19	snp	missense
AD17	overt Cushing		BCAR1	snp	missense
AD17	overt Cushing		SCARF1	snp	missense
AD17	overt Cushing		RPS15	snp	missense
AD17	overt Cushing		MAP2K2	snp	missense
AD17	overt Cushing		PEX11G	snp	missense
AD17	overt Cushing		BCL3	snp	missense
AD17	overt Cushing		IAH1	snp	missense
AD17	overt Cushing		DUSP2	snp	missense
AD17	overt Cushing		CUL3	snp	missense
AD17	overt Cushing		GNAS	snp	missense
AD17	overt Cushing		OLIG1	snp	missense
AD17	overt Cushing		TNFRSF13C	snp	missense

AD17	overt Cushing		FLNB	snp	missense
AD17	overt Cushing		SI	snp	missense
AD17	overt Cushing		PAPSS1	snp	missense
AD17	overt Cushing		PDE5A	snp	nonsense
AD17	overt Cushing		FGF2	snp	missense
AD17	overt Cushing		DHX29	snp	missense
AD17	overt Cushing		LTC4S	snp	nonsense
AD17	overt Cushing		TTBK1	snp	missense
AD17	overt Cushing		COL4A6	snp	missense
AD18	overt Cushing	1	PRSS50	snp	missense
AD19	overt Cushing	1	AQP12B	snp	missense
AD20	subclinical Cushing	1	CTNNB1	snp	missense
AD21	inactive	10	AGRN	snp	missense
AD21	inactive		CACNA1E	snp	splice
AD21	inactive		PCDH15	snp	missense
AD21	inactive		TENC1	snp	missense
AD21	inactive		UGGT2	indel	frameshift
AD21	inactive		CAMSAP2	snp	missense
AD21	inactive		MFI2	snp	missense
AD21	inactive		HELQ	indel	indel
AD21	inactive		RAET1E	snp	missense
AD21	inactive		EXTL3	snp	missense
AD22	inactive	9	SEZ6L2	snp	missense
AD22	inactive		TP53	indel	frameshift
AD22	inactive		ARHGAP23	snp	missense
AD22	inactive		GLS	snp	missense
AD22	inactive		PLK1S1	snp	missense
AD22	inactive		SLC6A11	snp	missense
AD22	inactive		LNP1	snp	missense
AD22	inactive		TRIM26	snp	missense
AD22	inactive		COL5A1	snp	missense
AD23	subclinical Cushing	12	HTR6	indel	frameshift
AD23	subclinical Cushing		ANAPC16	snp	missense
AD23	subclinical Cushing		DRD2	snp	missense
AD23	subclinical Cushing		ABCC9	snp	missense
AD23	subclinical Cushing		NID2	snp	missense
AD23	subclinical Cushing		ELAVL1	snp	missense
AD23	subclinical Cushing		ELAVL1	snp	nonsense
AD23	subclinical Cushing		RYR1	snp	missense
AD23	subclinical Cushing		DGCR6L	snp	missense
AD23	subclinical Cushing		CTNNB1	snp	missense
AD23	subclinical Cushing		PCDHB12	snp	nonsense
AD23	subclinical Cushing		EFHC2	snp	missense
AD24	overt Cushing	14	NFYC	snp	splice
AD24	overt Cushing		TNNT2	snp	missense
AD24	overt Cushing		TMEM63A	snp	missense
AD24	overt Cushing		CUZD1	snp	missense
AD24	overt Cushing		ABTB2	snp	missense
AD24	overt Cushing		RNF214	snp	missense

AD24	overt Cushing		EEA1	snp	missense
AD24	overt Cushing		MAGEL2	snp	missense
AD24	overt Cushing		ARHGAP11A	snp	missense
AD24	overt Cushing		BTBD17	snp	missense
AD24	overt Cushing		COL5A3	snp	missense
AD24	overt Cushing		PVRL2	snp	missense
AD24	overt Cushing		SEPT2	snp	missense
AD24	overt Cushing		DPY19L1	snp	missense
AD25	inactive	7	POLE2	snp	missense
AD25	inactive		ATXN3	snp	syn
AD25	inactive		SCARF2	snp	missense
AD25	inactive		CTNNB1	snp	missense
AD25	inactive		ZNF197	snp	missense
AD25	inactive		CDH9	snp	missense
AD25	inactive		DST	snp	missense
AD25	inactive		CARD11	snp	missense
AD26	subclinical Cushing	6	SBK1	snp	missense
AD26	subclinical Cushing		MYOCD	snp	missense
AD26	subclinical Cushing		GNAS	snp	missense
AD26	subclinical Cushing		TAF4	snp	missense
AD26	subclinical Cushing		PAX4	snp	missense
AD26	subclinical Cushing		ZHX1	snp	missense
AD27	overt Cushing	4	KIAA0754	snp	missense
AD27	overt Cushing		CATSPERG	snp	missense
AD27	overt Cushing		C2orf54	snp	missense
AD27	overt Cushing		BICD2	snp	missense
AD28	subclinical Cushing	11	ASH1L	snp	nonsense
AD28	subclinical Cushing		BBOX1	snp	missense
AD28	subclinical Cushing		LCMT2	snp	missense
AD28	subclinical Cushing		CSPG4	snp	missense
AD28	subclinical Cushing		LPPR3	snp	missense
AD28	subclinical Cushing		ZNF433	snp	missense
AD28	subclinical Cushing		ZNF566	snp	missense
AD28	subclinical Cushing		PPP6R1	snp	missense
AD28	subclinical Cushing		CTNNB1	snp	missense
AD28	subclinical Cushing		PCDH1	snp	missense
AD28	subclinical Cushing		KIAA0141	snp	missense
AD29	subclinical Cushing	11	SLC6A9	snp	missense
AD29	subclinical Cushing		ALDH9A1	snp	missense
AD29	subclinical Cushing		ARHGAP21	snp	missense
AD29	subclinical Cushing		CLEC9A	snp	missense
AD29	subclinical Cushing		PSG1	snp	missense
AD29	subclinical Cushing		AGFG1	snp	missense
AD29	subclinical Cushing		ATP9A	snp	missense
AD29	subclinical Cushing		ZNF35	snp	missense
AD29	subclinical Cushing		GRIA1	snp	missense
AD29	subclinical Cushing		DST	snp	missense
AD29	subclinical Cushing		DAPK1	snp	missense
AD30	overt Cushing	9	PLCZ1	snp	missense

AD30	overt Cushing		PRKACA	snp	missense
AD30	overt Cushing		ADCY3	snp	nonsense
AD30	overt Cushing		URB1	snp	nonsense
AD30	overt Cushing		PCGF3	snp	missense
AD30	overt Cushing		CMAHP	snp	missense
AD30	overt Cushing		PKD1L1	snp	missense
AD30	overt Cushing		TSTD2	indel	frameshift
AD30	overt Cushing		GPC4	snp	missense
AD31	subclinical Cushing	12	BMS1	snp	missense
AD31	subclinical Cushing		COL13A1	snp	missense
AD31	subclinical Cushing		OR9G9	snp	missense
AD31	subclinical Cushing		KBTBD7	snp	missense
AD31	subclinical Cushing		SOX15	snp	missense
AD31	subclinical Cushing		ZNF407	snp	missense
AD31	subclinical Cushing		MBP	snp	nonsense
AD31	subclinical Cushing		THSD7B	snp	missense
AD31	subclinical Cushing		CTNNB1	snp	missense
AD31	subclinical Cushing		MITF	snp	missense
AD31	subclinical Cushing		PRPS1L1	snp	missense
AD31	subclinical Cushing		LRP12	snp	missense
AD32	subclinical Cushing	7	KIAA1279	snp	missense
AD32	subclinical Cushing		GRIP1	snp	missense
AD32	subclinical Cushing		VPS33B	indel	splice
AD32	subclinical Cushing		CUX1	indel	frameshift
AD32	subclinical Cushing		PLXNA4	snp	splice
AD32	subclinical Cushing		TRPA1	snp	missense
AD32	subclinical Cushing		ZDHHC12	snp	missense
AD33	subclinical Cushing	2	GNAS	snp	missense
AD33	subclinical Cushing		MORC2	snp	missense
AD34	inactive	3	RYR1	snp	missense
AD34	inactive		CTNNB1	snp	missense
AD34	inactive		CTNNB1	snp	missense
AD35	inactive	7	MTHFR	snp	missense
AD35	inactive		PDZRN4	snp	missense
AD35	inactive		SLC5A8	snp	missense
AD35	inactive		RIMBP2	snp	missense
AD35	inactive		ANKRD62	snp	nonsense
AD35	inactive		TGM6	snp	missense
AD35	inactive		CTNNB1	snp	missense
AD36	overt Cushing	8	IGFN1	snp	missense
AD36	overt Cushing		TMEM170	snp	missense
AD36	overt Cushing		MAU2	snp	missense
AD36	overt Cushing		PLEKHF1	snp	missense
AD36	overt Cushing		IL36B	snp	missense
AD36	overt Cushing		CTSO	snp	missense
AD36	overt Cushing		EGFL8	snp	missense
AD36	overt Cushing		ATG9B	snp	frameshift
AD37	overt Cushing	6	TUBA1A	snp	missense
AD37	overt Cushing		IRX5	snp	missense

AD37	overt Cushing		PRKAR1A	indel	frameshift
AD37	overt Cushing		LOC728810	snp	missense
AD37	overt Cushing		CTNNB1	snp	missense
AD37	overt Cushing		ZAR1	snp	missense
AD38	subclinical Cushing	9	LEPREL2	snp	missense
AD38	subclinical Cushing		VAT1L	snp	missense
AD38	subclinical Cushing		POLG2	snp	missense
AD38	subclinical Cushing		ZCCHC2	snp	missense
AD38	subclinical Cushing		GRIN3B	snp	missense
AD38	subclinical Cushing		DNAJB3	snp	missense
AD38	subclinical Cushing		CTNNB1	snp	missense
AD38	subclinical Cushing		PCDHA10	snp	missense
AD38	subclinical Cushing		GPR64	snp	missense
AD39	overt Cushing	8	DAP3	deletion	splice
AD39	overt Cushing		ADAMTS15	snp	missense
AD39	overt Cushing		SLC46A3	snp	missense
AD39	overt Cushing		MAN2C1	indel	frameshift
AD39	overt Cushing		GNAS	snp	missense
AD39	overt Cushing		TBX18	snp	missense
AD39	overt Cushing		IFT74	snp	nonsense
AD39	overt Cushing		VSIG4	snp	missense
AD40	inactive	12	EPHX1	snp	missense
AD40	inactive		TTC40	snp	missense
AD40	inactive		KMT2D	snp	missense
AD40	inactive		MMP17	snp	missense
AD40	inactive		PABPC3	snp	missense
AD40	inactive		PRKD1	snp	missense
AD40	inactive		CEP95	snp	nonsense
AD40	inactive		CYP4F11	snp	splice
AD40	inactive		ZHX3	snp	missense
AD40	inactive		MIOX	snp	syn
AD40	inactive		DHX30	snp	missense
AD40	inactive		IER5L	snp	missense
AD41	inactive	14	RUNX3	snp	missense
AD41	inactive		DMBT1	snp	missense
AD41	inactive		SWAP70	snp	missense
AD41	inactive		NXN	snp	missense
AD41	inactive		DCXR	snp	missense
AD41	inactive		TNFRSF13C	snp	missense
AD41	inactive		CTNNB1	snp	missense
AD41	inactive		LGI2	snp	missense
AD41	inactive		AFAP1L1	snp	splice
AD41	inactive		CADPS2	snp	missense
AD41	inactive		LOC100289341	snp	missense
AD41	inactive		MSL3	snp	missense
AD41	inactive		EIF1AX	snp	splice
AD41	inactive		SPANXE	snp	missense
AD42	subclinical Cushing	2	CYP17A1	indel	indel
AD42	subclinical Cushing		TM9SF4	snp	missense

AD43	inactive	5	ASB13	snp	missense
AD43	inactive		CTNNB1	snp	missense
AD43	inactive		NBEAL2	indel	indel
AD43	inactive		MYO10	snp	missense
AD44	inactive	1	RNF32	snp	missense
AD45	inactive	19	CFH	snp	missense
AD45	inactive		PTPRC	snp	missense
AD45	inactive		ADARB2	snp	missense
AD45	inactive		ZNF511	snp	missense
AD45	inactive		KCNC1	snp	missense
AD45	inactive		MCAM	snp	missense
AD45	inactive		AGAP2	snp	missense
AD45	inactive		NEDD1	snp	missense
AD45	inactive		ATP8B4	snp	missense
AD45	inactive		IFT140	snp	missense
AD45	inactive		DSC1	snp	missense
AD45	inactive		MAST1	snp	missense
AD45	inactive		MAST1	snp	missense
AD45	inactive		ZNF208	snp	missense
AD45	inactive		EPB41L5	snp	missense
AD45	inactive		SLC11A1	snp	missense
AD45	inactive		CTNNB1	snp	missense
AD45	inactive		PCDH10	snp	missense
AD45	inactive		PCDHB16	snp	missense
AD46	subclinical Cushing	1	RGS14	snp	missense
AD47	subclinical Cushing	2	CEP192	snp	missense
AD47	subclinical Cushing		CTNNB1	snp	missense
AD48	overt Cushing	8	OR5B2	snp	missense
AD48	overt Cushing		ANAPC5	snp	missense
AD48	overt Cushing		TSR1	snp	missense
AD48	overt Cushing		WDR18	snp	missense
AD48	overt Cushing		GNAS	snp	missense
AD48	overt Cushing		SERINC5	snp	missense
AD48	overt Cushing		TUBE1	snp	missense
AD48	overt Cushing		MTMR9	snp	missense
AD49	overt Cushing	1	GRM6	snp	missense
AD50	overt Cushing	5	MIA3	snp	missense
AD50	overt Cushing		MMP12	snp	missense
AD50	overt Cushing		CHRNB4	snp	missense
AD50	overt Cushing		FOXA2	snp	missense
AD50	overt Cushing		MUC17	indel	frameshift
AD51	inactive	3	DDB2	snp	missense
AD51	inactive		TBC1D1	snp	missense
AD51	inactive		COL5A1	snp	missense
AD52	inactive	6	FBLIM1	snp	missense
AD52	inactive		STAP2	snp	missense
AD52	inactive		SOGA1	snp	nonsense
AD52	inactive		CTNNB1	snp	missense
AD52	inactive		GPR174	snp	missense

AD52	inactive		FGF13	snp	missense
AD53	overt Cushing	4	ZIC5	snp	missense
AD53	overt Cushing		TRIM65	snp	missense
AD53	overt Cushing		FAM168B	snp	missense
AD53	overt Cushing		CASD1	snp	nonsense
AD54	subclinical Cushing	6	SF1	indel	indel
AD54	subclinical Cushing		LAMA3	snp	missense
AD54	subclinical Cushing		SPHK2	snp	missense
AD54	subclinical Cushing		GSTA1	snp	splice
AD54	subclinical Cushing		SYNE1	snp	missense
AD54	subclinical Cushing		C5	snp	missense
AD55	inactive	6	FMO1	snp	missense
AD55	inactive		SMCHD1	snp	missense
AD55	inactive		CTNNB1	snp	missense
AD55	inactive		CTNNB1	snp	missense
AD55	inactive		PALLD	snp	missense
AD55	inactive		PCDHGA8	indel	frameshift
AD56	subclinical Cushing	16	MUC5B	snp	missense
AD56	subclinical Cushing		SC5D	snp	missense
AD56	subclinical Cushing		GUCY1B2	indel	frameshift
AD56	subclinical Cushing		SPG7	snp	missense
AD56	subclinical Cushing		FAM69C	snp	missense
AD56	subclinical Cushing		DNAAF3	snp	missense
AD56	subclinical Cushing		CTNNB1	snp	missense
AD56	subclinical Cushing		MED12L	snp	missense
AD56	subclinical Cushing		DCHS2	snp	missense
AD56	subclinical Cushing		DCHS2	snp	missense
AD56	subclinical Cushing		MCIDAS	snp	missense
AD56	subclinical Cushing		FAT2	snp	nonsense
AD56	subclinical Cushing		SDK1	snp	missense
AD56	subclinical Cushing		GLDC	snp	missense
AD56	subclinical Cushing		BCAP31	indel	frameshift
AD57	subclinical Cushing	11	UROD	indel	frameshift
AD57	subclinical Cushing		LYPD8	snp	missense
AD57	subclinical Cushing		PDZD7	snp	nonsense
AD57	subclinical Cushing		P2RX2	snp	missense
AD57	subclinical Cushing		SEC1P	snp	missense
AD57	subclinical Cushing		REM1	snp	nonsense
AD57	subclinical Cushing		CSE1L	snp	missense
AD57	subclinical Cushing		CTNNB1	snp	missense
AD57	subclinical Cushing		AFF1	snp	missense
AD57	subclinical Cushing		PCDHGA6	snp	missense
AD57	subclinical Cushing		PLOD3	snp	missense
AD58	subclinical Cushing	11	CNST	snp	missense
AD58	subclinical Cushing		CDH23	snp	missense
AD58	subclinical Cushing		ARHGAP9	snp	missense
AD58	subclinical Cushing		KIF5C	snp	missense
AD58	subclinical Cushing		RIPPLY3	snp	missense
AD58	subclinical Cushing		CTNNB1	snp	missense

AD58	subclinical Cushing		FXR1	snp	missense
AD58	subclinical Cushing		C4orf21	snp	splice
AD58	subclinical Cushing		FBXL13	snp	missense
AD58	subclinical Cushing		ZC3HC1	indel	frameshift
AD58	subclinical Cushing		GRIN1	snp	missense
AD59	inactive	7	FIGNL2	snp	nonsense
AD59	inactive		TMEM88	snp	missense
AD59	inactive		KIAA1715	snp	missense
AD59	inactive		CTNNB1	snp	missense
AD59	inactive		PCDHGB3	snp	missense
AD59	inactive		TMEM24 8	snp	nonsense
AD59	inactive		ZNF252P	snp	missense
AD60	inactive	8	KMT2D	snp	missense
AD60	inactive		KCNE1	snp	missense
AD60	inactive		CTNNB1	snp	missense
AD60	inactive		CCRN4L	deletion	frameshift
AD60	inactive		PCDHGA6	snp	missense
AD60	inactive		TAF1L	snp	missense
AD60	inactive		PTBP3	snp	missense
AD61	inactive	6	RYR3	indel	frameshift
AD61	inactive		OXSM	snp	missense
AD61	inactive		CTNNB1	snp	missense
AD61	inactive		RBM5	indel	frameshift
AD61	inactive		KIAA1456	snp	missense
AD61	inactive		NGFRAP1	snp	missense
AD62	inactive	3	TFAP2C	snp	missense
AD62	inactive		SCUBE1	snp	missense
AD62	inactive		CRAT	snp	missense
AD63	inactive	3	BIRC6	snp	missense
AD63	inactive		INHA	snp	nonsense
AD63	inactive		MFHAS1	snp	missense
AD64	inactive	3	E2F2	snp	missense
AD64	inactive		ACADVL	snp	missense
AD64	inactive		SYDE1	snp	missense
AD65	overt Cushing	2	TEKT2	snp	missense
AD65	overt Cushing		MYL1	snp	missense
AD66	overt Cushing	6	RASGRF1	snp	missense
AD66	overt Cushing		PLEKHM1	snp	missense
AD66	overt Cushing		GNAS	snp	missense
AD66	overt Cushing		FCHO2	snp	nonsense
AD66	overt Cushing		HIST1H4C	snp	missense
AD66	overt Cushing		KIAA2026	snp	missense
AD67	overt Cushing	7	ARHGAP2 0	snp	missense
AD67	overt Cushing		SPTA1	snp	missense
AD67	overt Cushing		STRA6	snp	missense
AD67	overt Cushing		APC2	deletion	indel
AD67	overt Cushing		PRKACA	snp	missense
AD67	overt Cushing		FAM193B	snp	missense
AD67	overt Cushing		ANKMY2	snp	missense

AD68	overt Cushing	24	RABGGTB	snp	missense
AD68	overt Cushing		AMPD1	snp	missense
AD68	overt Cushing		PRR9	snp	missense
AD68	overt Cushing		CD84	snp	missense
AD68	overt Cushing		NAV1	snp	missense
AD68	overt Cushing		ABCG4	snp	missense
AD68	overt Cushing		MON2	snp	missense
AD68	overt Cushing		RCBTB1	snp	missense
AD68	overt Cushing		MYH2	snp	missense
AD68	overt Cushing		LPPR3	snp	missense
AD68	overt Cushing		MKNK2	snp	missense
AD68	overt Cushing		ZNF676	snp	missense
AD68	overt Cushing		GPATCH1	snp	missense
AD68	overt Cushing		CACNG8	snp	missense
AD68	overt Cushing		NCKAP5	snp	missense
AD68	overt Cushing		SCN1A	snp	missense
AD68	overt Cushing		ERG	snp	missense
AD68	overt Cushing		RNF123	snp	missense
AD68	overt Cushing		ITIH3	snp	missense
AD68	overt Cushing		MECOM	snp	missense
AD68	overt Cushing		NDST3	snp	nonsense
AD68	overt Cushing		ARID1B	deletion	frameshift
AD68	overt Cushing		EXOSC4	snp	missense
AD68	overt Cushing		MAGEB5	snp	missense
AD69	overt Cushing	58	TMEM51	snp	nonsense
AD69	overt Cushing		PPP1R12B	snp	nonsense
AD69	overt Cushing		RYR2	snp	missense
AD69	overt Cushing		CARNS1	snp	missense
AD69	overt Cushing		ZNF259	snp	missense
AD69	overt Cushing		CACNA1C	snp	nonsense
AD69	overt Cushing		CPM	snp	missense
AD69	overt Cushing		CKAP4	snp	missense
AD69	overt Cushing		C12orf52	snp	nonsense
AD69	overt Cushing		DPF3	snp	nonsense
AD69	overt Cushing		NDUFB1	snp	missense
AD69	overt Cushing		AQR	snp	nonsense
AD69	overt Cushing		PPP1R14D	snp	missense
AD69	overt Cushing		TGM5	snp	missense
AD69	overt Cushing		ADAMTS17	snp	missense
AD69	overt Cushing		HEATR3	snp	missense
AD69	overt Cushing		SREBF1	snp	splice
AD69	overt Cushing		SRCIN1	snp	nonsense
AD69	overt Cushing		SDK2	snp	missense
AD69	overt Cushing		PTBP1	snp	missense
AD69	overt Cushing		DOHH	snp	missense
AD69	overt Cushing		SPRED3	snp	missense
AD69	overt Cushing		PPFIA3	snp	missense
AD69	overt Cushing		SSFA2	snp	missense
AD69	overt Cushing		PGAP1	snp	missense

AD69	overt Cushing		ALS2CR11	snp	syn
AD69	overt Cushing		NINL	snp	missense
AD69	overt Cushing		REM1	snp	missense
AD69	overt Cushing		RBBP8NL	snp	missense
AD69	overt Cushing		STMN3	snp	missense
AD69	overt Cushing		UPB1	snp	missense
AD69	overt Cushing		PKDREJ	snp	missense
AD69	overt Cushing		SCN5A	snp	nonsense
AD69	overt Cushing		ZNF502	snp	missense
AD69	overt Cushing		PRSS46	snp	missense
AD69	overt Cushing		NT5DC2	snp	missense
AD69	overt Cushing		PHLDB2	snp	missense
AD69	overt Cushing		MME	snp	missense
AD69	overt Cushing		DGKQ	snp	missense
AD69	overt Cushing		CASP3	snp	missense
AD69	overt Cushing		PLEKHG4B	snp	splice
AD69	overt Cushing		IRX1	snp	missense
AD69	overt Cushing		RASGEF1C	snp	splice
AD69	overt Cushing		HIVEP1	snp	missense
AD69	overt Cushing		ZSCAN12	snp	missense
AD69	overt Cushing		TTLL2	snp	nonsense
AD69	overt Cushing		TRRAP	snp	missense
AD69	overt Cushing		VGF	snp	missense
AD69	overt Cushing		CPA2	snp	missense
AD69	overt Cushing		SSPO	snp	missense
AD69	overt Cushing		MROH5	snp	missense
AD69	overt Cushing		C9orf66	snp	missense
AD69	overt Cushing		MEGF9	snp	nonsense
AD69	overt Cushing		SOWAHD	snp	missense
AD69	overt Cushing		XPNPEP2	snp	missense
AD70	subclinical Cushing	10	TRPM5	snp	missense
AD70	subclinical Cushing		WASF3	snp	missense
AD70	subclinical Cushing		MYH4	snp	missense
AD70	subclinical Cushing		RTN4	snp	missense
AD70	subclinical Cushing		CHD6	snp	missense
AD70	subclinical Cushing		DIDO1	snp	missense
AD70	subclinical Cushing		CTNNB1	snp	missense
AD70	subclinical Cushing		ASTN2	snp	missense
AD70	subclinical Cushing		RBM10	snp	missense
AD70	subclinical Cushing		MED12	snp	missense
AD71	subclinical Cushing	9	C1orf170	snp	missense
AD71	subclinical Cushing		C1orf106	snp	missense
AD71	subclinical Cushing		OR5A2	snp	missense
AD71	subclinical Cushing		SLC15A3	snp	missense
AD71	subclinical Cushing		B3GNT3	snp	missense
AD71	subclinical Cushing		CTNNB1	snp	missense
AD71	subclinical Cushing		CTNNB1	snp	missense
AD71	subclinical Cushing		DEF6	snp	missense
AD72	subclinical Cushing	12	ELK4	snp	nonsense

AD72	subclinical Cushing		WAPAL	indel	frameshift
AD72	subclinical Cushing		NRXN3	snp	missense
AD72	subclinical Cushing		TP53BP1	snp	nonsense
AD72	subclinical Cushing		GGT6	snp	missense
AD72	subclinical Cushing		MBP	snp	missense
AD72	subclinical Cushing		CREB1	snp	missense
AD72	subclinical Cushing		SERPINE2	snp	missense
AD72	subclinical Cushing		HELZ2	snp	missense
AD72	subclinical Cushing		CTNNB1	snp	missense
AD72	subclinical Cushing		HNRNPAB	indel	frameshift
AD72	subclinical Cushing		ZNF451	snp	missense
AD72	subclinical Cushing		DOCK4	snp	missense
AD73	overt Cushing	2	SFXN4	snp	splice
AD73	overt Cushing		PCDHB11	snp	missense
AD74	overt Cushing	9	TSGA10IP	snp	missense
AD74	overt Cushing		WFIKKN1	snp	missense
AD74	overt Cushing		TSEN54	snp	missense
AD74	overt Cushing		PRKACA	indel	indel
AD74	overt Cushing		IAH1	snp	missense
AD74	overt Cushing		IFT172	indel	frameshift
AD74	overt Cushing		GRIK2	snp	missense
AD74	overt Cushing		CSMD1	snp	missense
AD74	overt Cushing		DGAT2L6	snp	splice
AD75	overt Cushing	11	DDX20	snp	missense
AD75	overt Cushing		ITGA8	snp	missense
AD75	overt Cushing		SLC25A16	snp	missense
AD75	overt Cushing		LSP1	snp	missense
AD75	overt Cushing		NID2	snp	missense
AD75	overt Cushing		PHKB	snp	missense
AD75	overt Cushing		XIRP2	snp	missense
AD75	overt Cushing		FSIP2	snp	missense
AD75	overt Cushing		MYH9	indel	indel
AD75	overt Cushing		CTNNB1	snp	missense
AD75	overt Cushing		GRM3	snp	missense
AD76	overt Cushing	17	ASH1L	snp	missense
AD76	overt Cushing		CYP17A1	snp	nonsense
AD76	overt Cushing		KRT81	snp	nonsense
AD76	overt Cushing		ALDH2	snp	missense
AD76	overt Cushing		CREBBP	snp	missense
AD76	overt Cushing		MYO15B	snp	splice
AD76	overt Cushing		PODNL1	snp	missense
AD76	overt Cushing		AGPS	snp	missense
AD76	overt Cushing		TSHZ2	snp	missense
AD76	overt Cushing		MICAL3	snp	missense
AD76	overt Cushing		CTNNB1	snp	missense
AD76	overt Cushing		SORCS2	snp	missense
AD76	overt Cushing		TENM3	snp	missense
AD76	overt Cushing		CYP21A2	snp	missense
AD76	overt Cushing		GRM4	snp	missense

AD76	overt Cushing		HEY2	snp	missense
AD76	overt Cushing		DOCK5	snp	nonsense
AD77	overt Cushing	4	RHOT2	snp	missense
AD77	overt Cushing		APOBR	snp	missense
AD77	overt Cushing		SEC14L1	snp	missense
AD77	overt Cushing		CTNNB1	deletion	splice
AD78	overt Cushing	2	OBSCN	snp	missense
AD78	overt Cushing		SLC35F3	snp	missense
AD79	subclinical Cushing	1	ASXL2	snp	missense
AD80	overt Cushing	2	VENTX	snp	nonsense
AD80	overt Cushing		COL5A1	snp	missense
AD81	subclinical Cushing	10	TROVE2	snp	missense
AD81	subclinical Cushing		GRID1	snp	missense
AD81	subclinical Cushing		C12orf63	snp	missense
AD81	subclinical Cushing		SYNE2	snp	missense
AD81	subclinical Cushing		MYOM1	snp	splice
AD81	subclinical Cushing		ASPDH	snp	missense
AD81	subclinical Cushing		MERTK	indel	frameshift
AD81	subclinical Cushing		H1F0	snp	missense
AD81	subclinical Cushing		CTNNB1	snp	missense
AD81	subclinical Cushing		SEPT6	snp	missense
AD82	overt Cushing	4	CYP2A13	snp	missense
AD82	overt Cushing		EIF4ENIF1	snp	missense
AD82	overt Cushing		VPS13A	snp	splice
AD82	overt Cushing		DCAF12L1	snp	missense
AD83	overt Cushing	9	CUBN	snp	missense
AD83	overt Cushing		CEP76	snp	missense
AD83	overt Cushing		HOOK2	snp	missense
AD83	overt Cushing		SLC4A5	snp	missense
AD83	overt Cushing		COL6A3	snp	missense
AD83	overt Cushing		FRS3	snp	missense
AD83	overt Cushing		C6orf132	snp	missense
AD83	overt Cushing		COL26A1	snp	missense
AD83	overt Cushing		APBA1	snp	missense
AD84	overt Cushing	1	MTHFR	snp	missense
AD85	overt Cushing	9	CLDN2	snp	missense
AD85	overt Cushing		RNF175	snp	missense
AD85	overt Cushing		ADAMTS18	snp	missense
AD85	overt Cushing		TDRD1	snp	missense
AD85	overt Cushing		SASH1	snp	missense
AD85	overt Cushing		CLEC4M	snp	missense
AD85	overt Cushing		APLP2	snp	missense
AD85	overt Cushing		OR2T1	snp	missense
AD85	overt Cushing		COL16A1	snp	missense
AD86	overt Cushing	8	RP1	snp	missense
AD86	overt Cushing		SYNE2	snp	missense
AD86	overt Cushing		XIRP2	snp	missense
AD86	overt Cushing		CDC73	snp	missense
AD86	overt Cushing		MED25	snp	missense

AD86	overt Cushing		FAT4	snp	missense
AD86	overt Cushing		SHOC2	snp	missense
AD86	overt Cushing		GIT1	snp	nonsense
AD87	overt Cushing	18	RICTOR	snp	missense
AD87	overt Cushing		OR7D4	snp	missense
AD87	overt Cushing		B4GALNT1	snp	missense
AD87	overt Cushing		MYH14	snp	missense
AD87	overt Cushing		OR4A15	snp	missense
AD87	overt Cushing		PRDM4	snp	missense
AD87	overt Cushing		KIF11	snp	missense
AD87	overt Cushing		TIAM1	snp	missense
AD87	overt Cushing		OR6C76	snp	missense
AD87	overt Cushing		HTRA2	snp	missense
AD87	overt Cushing		EFR3B	snp	missense
AD87	overt Cushing		NBAS	snp	missense
AD87	overt Cushing		CALB1	snp	missense
AD87	overt Cushing		KCNB2	snp	missense
AD87	overt Cushing		GDAP2	snp	missense
AD87	overt Cushing		MEAF6	snp	nonsense
AD87	overt Cushing		KCNQ1	deletion	indel
AD87	overt Cushing		LRWD1	snp	splice
AD88	overt Cushing	4	WDR3	snp	missense
AD88	overt Cushing		CTNNB1	snp	missense
AD88	overt Cushing		SLC2A5	snp	missense
AD88	overt Cushing		ATP2C2	snp	nonsense

Base change	**Genomic position**
A>G	chr11:g.71146602A>G
C>T	chr13:g.32747670C>T
A>G	chr2:g.242004771A>G
G>A	chr20:g.57484421G>A
T>G	chr1:g.114380930T>G
C>A	chr6:g.139456772C>A
C>A	chr1:g.11103529C>A
T>C	chr1:g.152382789T>C
G>T	chr1:g.157718696G>T
G>T	chr10:g.105796271G>T
G>T	chr11:g.67176484G>T
G>T	chr12:g.208364G>T
T>C	chr12:g.44915832T>C
C>T	chr14:g.23826574C>T
G>T	chr14:g.105963752G>T
A>G	chr18:g.10526119A>G
T>G	chr19:g.36518111T>G
C>A	chr2:g.144765096C>A
T>A	chr21:g.34011237T>A
C>G	chr3:g.41266133C>G
T>C	chr3:g.41266136T>C
A>T	chr3:g.194063083A>T
T>A	chr5:g.78411627T>A
C>G	chr5:g.140209037C>G
insGCTGCTGCTGCTGTT	chr6:g.13711682_13711683insGCTGCTGCTGCTGTT
delC	chr6:g.20488408delC
G>A	chr7:g.100377217G>A
A>G	chr7:g.141952335A>G
delCCTTC	chr8:g.118533159_118533163delCCTTC
A>G	chr9:g.33676439A>G
G>A	chrX:g.30261205G>A
C>T	chrX:g.43809062C>T
C>G	chrX:g.76938262C>G
G>A	chr17:g.2995927G>A
T>C	chr3:g.41266136T>C
T>G	chr3:g.41266136T>G
delT	chr1:g.240374511_240374511delT
G>A	chr11:g.13407339G>A
C>T	chr11:g.64503102C>T
A>G	chr12:g.46244670A>G
C>T	chr19:g.50100303C>T
T>C	chr3:g.41266136T>C
A>C	chr3:g.49761060A>C
C>A	chr5:g.140255073C>A
insTA	chr7:g.122303533_122303534insTA
A>G	chr8:g.104075427A>G
C>A	chr11:g.134118838C>A
C>G	chr13:g.110828836C>G

T>C	chr14:g.39706219T>C
C>G	chr19:g.22942226C>G
C>T	chr20:g.30408070C>T
C>T	chr3:g.41266137C>T
T>C	chr8:g.99161128T>C
G>C	chr1:g.46489629G>C
C>T	chr10:g.102300420C>T
G>T	chr11:g.608913G>T
G>T	chr11:g.66062315G>T
T>C	chr11:g.93796680T>C
delACAG	chr12:g.14927499_14927502delACAG
A>G	chr15:g.34080417A>G
G>T	chr17:g.31439018G>T
A>G	chr19:g.49253797A>G
C>T	chr3:g.41266137C>T
C>G	chr3:g.113798838C>G
A>C	chr4:g.1838256A>C
G>T	chr4:g.158254056G>T
C>T	chr5:g.13717570C>T
A>G	chr5:g.140803156A>G
T>A	chr9:g.103092333T>A
G>A	chr12:g.32949197G>A
G>T	chr17:g.27899916G>T
C>A	chr22:g.19340906C>A
G>T	chr6:g.149772525G>T
C>T	chr11:g.59620785C>T
C>G	chr15:g.89401505C>G
G>C	chr16:g.3165454G>C
delGCCGTGC	chr2:g.206921116_206921122delGCCGTGC
A>G	chr20:g.3052769A>G
T>C	chr3:g.41266136T>C
A>G	chr5:g.112154826A>G
C>A	chr8:g.144657236C>A
C>T	chrX:g.132351911C>T
G>C	chr16:g.55600684G>C
A>G	chr17:g.9546435A>G
C>G	chr2:g.8871987C>G
C>T	chr2:g.232156120C>T
A>C	chr20:g.57470699A>C
C>G	chr3:g.41266137C>G
A>G	chr5:g.178506619A>G
A>C	chr6:g.36334694A>C
C>T	chr9:g.138415818C>T
G>A	chr1:g.114952872G>A
C>G	chr12:g.52774875C>G
G>A	chr13:g.113741732G>A
G>T	chr20:g.58381134G>T
T>C	chr3:g.41266136T>C
G>A	chr5:g.140745836G>A

G>A	chr18:g.29340456G>A
insAACC	chr19:g.2477485_2477486insAACC
delCG	chr10:g.72298096_72298097delCG
T>C	chr12:g.88465077T>C
T>C	chr19:g.35556497T>C
C>T	chr3:g.41266137C>T
delCTCA	chrX:g.31645970_31645973delCTCA
G>A	chr1:g.196711064G>A
T>C	chr1:g.201836070T>C
C>T	chr11:g.12225917C>T
T>C	chr15:g.63955319T>C
C>T	chr16:g.31477999C>T
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C>A	chr20:g.61541329C>A
T>C	chr3:g.41266136T>C
C>T	chr9:g.119976918C>T
G>C	chrX:g.47044552G>C
C>T	chrX:g.70354957C>T
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C>T	chr19:g.17918884C>T
C>G	chr3:g.41266133C>G
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delATTT	chr10:g.88277340_88277343delATTT
C>T	chr14:g.80327444C>T
G>A	chr15:g.43730553G>A
G>T	chr17:g.4461524G>T
G>T	chr18:g.74721832G>T
A>G	chr2:g.208440035A>G
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C>A	chr20:g.62200334C>A
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delG	chr5:g.177632955delG
G>C	chr6:g.57006863G>C
C>G	chr7:g.111368574C>G
G>T	chr10:g.120923642G>T
G>A	chr5:g.140581307G>A
G>A	chr11:g.65727397G>A
G>C	chr16:g.683203G>C
T>C	chr17:g.73519787T>C
delCATAGATCTGGATGG	chr19:g.14208193_14208207delCATAGATCTGGATGG
C>G	chr2:g.9628412C>G
delT	chr2:g.27695123_27695123delT
C>T	chr6:g.102376409C>T
T>C	chr8:g.3165951T>C
T>A	chrX:g.69424368T>A
T>C	chr1:g.112302173T>C
C>A	chr10:g.15639248C>A
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A>G	chr11:g.1908726A>G
C>A	chr14:g.52535501C>A
G>A	chr16:g.47674946G>A
C>T	chr2:g.168107251C>T
A>G	chr2:g.186656511A>G
delCTT	chr22:g.36688041_36688043delCTT
C>T	chr3:g.41266113C>T
C>T	chr7:g.86493608C>T
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C>T	chr10:g.104597113C>T
G>T	chr12:g.52680246G>T
C>T	chr12:g.112235943C>T
G>T	chr16:g.3929860G>T
G>T	chr17:g.73592981G>T
G>A	chr19:g.14047184G>A
A>T	chr2:g.178285007A>T
C>T	chr20:g.51870953C>T
C>G	chr22:g.18379082C>G
G>A	chr3:g.41275669G>A
G>T	chr4:g.7194539G>T
C>G	chr4:g.183721295C>G
C>A	chr6:g.32007331C>A
G>A	chr6:g.34101096G>A

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C>T	chr8:g.25200014C>T
C>T	chr16:g.722092C>T
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A>G	chr17:g.75189584A>G
del	chr3:g.41264756_41266357del
G>A	chr1:g.228475581G>A
T>C	chr1:g.234367415T>C
C>T	chr2:g.25972825C>T
C>T	chr10:g.135053574C>T
C>A	chr9:g.137622092C>A
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C>T	chr10:g.87407069C>T
C>A	chr12:g.97137817C>A
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T>C	chr18:g.3116327T>C
G>A	chr19:g.51016646G>A
delACCACAC	chr2:g.112686772_112686778delACCACAC
G>C	chr22:g.38201682G>C
T>C	chr3:g.41266136T>C
G>T	chrX:g.118797464G>T
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C>G	chr22:g.31843418C>G
G>C	chr9:g.79898462G>C
C>A	chrX:g.125686219C>A
C>T	chr10:g.16949618C>T
C>G	chr18:g.12697401C>G
T>C	chr19:g.12874362T>C
G>C	chr2:g.74531748G>C
C>T	chr2:g.238303518C>T
A>C	chr6:g.41740659A>C
C>G	chr6:g.42074830C>G
G>A	chr7:g.101196619G>A
A>G	chr9:g.72047579A>G
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C>A	chrX:g.106171480C>A
G>T	chr4:g.154636670G>T
G>T	chr16:g.77325291G>T
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G>C	chr19:g.7831083G>C
A>G	chr11:g.129991699A>G
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C>T	chr8:g.55533611C>T
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C>G	chr5:g.38964904C>G
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G>C	chr19:g.50771447G>C
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G>T	chr12:g.108145505G>T
A>C	chr10:g.94381218A>C
C>A	chr21:g.32554838C>A
G>A	chr12:g.55820323G>A
A>G	chr2:g.74758526A>G
A>G	chr2:g.25359466A>G
C>A	chr2:g.15417090C>A
C>T	chr8:g.91094286C>T
T>A	chr8:g.73849064T>A
T>A	chr1:g.118461227T>A
C>A	chr1:g.37980296C>A
del	chr11:g.2683268_2683288del
A>G	chr7:g.102108507A>G
C>T	chr1:g.118486222C>T
T>C	chr3:g.41266136T>C
G>A	chr1:g.9098036G>A
C>T	chr16:g.84402288C>T

Transcript	cDNA level	Protein level	pph2
NM_001360.2	c.1247T>C	p.Leu416Pro	probably damaging
NM_023037.2	c.2318C>T	p.Ala773Val	benign
NM_001080437.1	c.2770A>G	p.Ile924Val	benign
NM_000516.4	c.602G>A	p.Arg201His	probably damaging
NM_012411.4	c.927A>C	p.Lys309Asn	benign
NM_016217.2	c.239C>A	p.Ala80Glu	benign
NM_006610.3	c.608G>T	p.Arg203Leu	benign
NM_016190.2	c.769A>G	p.Thr257Ala	benign
NM_030764.3	c.1362C>A	p.Asp454Glu	benign
NM_000494.3	c.3397C>A	p.Arg1133Ser	benign
NM_198517.3	c.679G>T	p.Gly227Cys	possibly damaging
NM_015232.1	c.607G>T	p.Asp203Tyr	
NM_006159.2	c.2126A>G	p.Tyr709Cys	probably damaging
NM_005864.3	c.1547G>A	p.Arg516Gln	benign
NM_001134875.1	c.743G>T	p.Arg248Leu	probably damaging
NM_003826.2	c.20A>G	p.Asn7Ser	benign
NM_015526.2	c.229A>C	p.Thr77Pro	possibly damaging
NM_024659.4	c.528G>T	p.Met176Ile	benign
NM_003895.3	c.4013A>T	p.Glu1338Val	benign
NM_001904.3	c.130C>G	p.Pro44Ala	possibly damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_001080513.2	c.349T>A	p.Phe117Ile	probably damaging
NM_001713.2	c.71T>A	p.Ile24Asn	probably damaging
NM_018909.2	c.1361C>G	p.Ala454Gly	benign
NM_005493.2	c.55_56insAACAGCAGCAGCAGC	p.Gln14_Gln18dup	
NM_001949.4	c.1064delC	p.Thr355Metfs*7	
NM_003386.2	c.6466G>A	p.Arg2155His	benign
NM_001001317.3	c.533T>C	p.Met178Thr	probably damaging
NM_080651.2	c.44_48delCCTTC	p.Pro15Argfs*65	
NR_023917.1	n.980T>C		probably damaging
NM_002367.3	c.953G>A	p.Arg318Gln	benign
NM_000266.3	c.385G>A	p.Glu129Lys	probably damaging
NM_000489.3	c.2486G>C	p.Ser829Thr	benign
NM_002548.2	c.364C>T	p.Arg122Cys	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_001904.3	c.133T>G	p.Ser45Ala	benign
NM_020066.4	c.4041delT	p.Ile1348Serfs*13	
NM_001030272.1	c.1717+1G>A		
NM_153819.1	c.1208G>A	p.Arg403Gln	benign
NM_152641.2	c.2764A>G	p.Thr922Ala	benign
NM_020719.1	c.2711C>T	p.Ser904Leu	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_013334.3	c.100T>G	p.Leu34Val	benign
NM_018903.2	c.16C>A	p.Pro6Thr	benign
NM_017954.10	c.543_544insTA	p.Glu182*	
NM_001695.4	c.799A>G	p.Arg267Gly	benign
NM_014174.2	c.496G>T	p.Val166Phe	probably damaging
NM_001845.4	c.2993G>C	p.Ser998Thr	possibly damaging

NM_054024.3	c.209T>C	p.Val70Ala	benign
NM_001080409.2	c.485G>C	p.Arg162Thr	benign
NM_033118.3	c.194C>T	p.Thr65Ile	benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_015029.2	c.1796T>C	p.Leu599Ser	probably damaging
NM_015112.2	c.1757G>C	p.Cys586Ser	probably damaging
NM_017902.2	c.458C>T	p.Thr153Ile	possibly damaging
NM_020901.2	c.3454G>T	p.Ala1152Ser	benign
NM_153266.3	c.598G>T	p.Val200Phe	probably damaging
NM_001098672.1	c.422T>C	p.Leu141Pro	probably damaging
NM_177925.2	c.95_98delACAG	p.Arg33Cysfs*46	
NM_001036.3	c.9590-2A>G		
NM_001094.4	c.623C>A	p.Thr208Lys	probably damaging
NM_000148.3	c.742T>C	p.Trp248Arg	probably damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_024638.3	c.832C>G	p.Gln278Glu	benign
NM_012318.2	c.638T>G	p.Leu213Arg	probably damaging
NM_000826.3	c.968G>T	p.Arg323Leu	benign
NM_001369.2	c.12559G>A	p.Ala4187Thr	benign
NM_018914.2	c.2362A>G	p.Lys788Glu	possibly damaging
NM_017746.3	c.1369A>T	p.Ile457Leu	benign
NM_004572.3	c.2335C>T	p.Pro779Ser	possibly damaging
NM_138349.2	c.1156G>T	p.Gly386Cys	probably damaging
NM_003325.3	c.2821G>T	p.Val941Phe	benign
NM_207360.2	c.878C>A	p.Ala293Asp	probably damaging
NM_001062.3	c.1131G>A	p.Met377Ile	benign
NM_001135.3	c.5689C>G	p.Leu1897Val	possibly damaging
NM_003456.2	c.156G>C	p.Glu52Asp	probably damaging
NM_000915.3	c.167A>G	p.Asn56Ser	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_000038.5	c.1097A>G	p.Asp366Gly	benign
NM_145201.4	c.1474G>T	p.Glu492*	
NM_016521.2	c.377G>A	p.Gly126Glu	probably damaging
NM_032330.1	c.16G>C	p.Ala6Pro	benign
NM_145054.4	c.1783A>G	p.Ile595Val	benign
NM_020738.2	c.4179G>C	p.Gln1393His	probably damaging
NM_025139.4	c.1681C>T	p.Arg561Cys	benign
NM_000516.4	c.172A>C	p.Lys58Gln	probably damaging
NM_001904.3	c.134C>G	p.Ser45Cys	probably damaging
NM_014594.1	c.1186A>G	p.Ile396Val	benign
NM_016135.3	c.866T>G	p.Leu289Arg	probably damaging
NM_002297.3	c.385C>T	p.Arg129*	
NM_015906.3	c.2128C>T	p.Pro710Ser	benign
NM_033045.3	c.1192G>C	p.Ala398Pro	benign
NM_024979.4	c.2551G>A	p.Glu851Lys	probably damaging
NM_080672.4	c.1213G>T	p.Val405Leu	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_018918.2	c.1939G>A	p.Glu647Lys	benign

NM_001034172.2	c.199C>T	p.Arg67Trp	probably damaging
NM_015675.2	c.370-1_370insAACC	p.Pro125Glnfs*	
NM_014431.2	c.1384_1385delCG	p.Arg462Profs*94	
NM_025114.3	c.6005A>G	p.Tyr2002Cys	possibly damaging
NM_002151.2	c.962T>C	p.Val321Ala	benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_000109.3	c.8010_8013delTGAG	p.Glu2673Leufs*44	
NM_000186.3	c.3016G>A	p.Asp1006Asn	benign
NM_018085.4	c.1838T>C	p.Phe613Ser	probably damaging
NM_014632.2	c.385C>T	p.Leu129Phe	probably damaging
NM_003922.3	c.8765A>G	p.Tyr2922Cys	probably damaging
NM_001105247.1	c.2597C>T	p.Pro866Leu	benign
NM_004104.4	c.2555A>G	p.Asn852Ser	benign
NM_024899.3	c.827C>T	p.Thr276Ile	benign
NM_021826.4	c.130C>G	p.Pro44Ala	probably damaging
NM_000395.2	c.2608G>T	p.Val870Phe	possibly damaging
NM_018911.2	c.914G>A	p.Arg305Gln	benign
NM_004415.2	c.423-1G>T		
NM_173830.4	c.568A>G	p.Lys190Glu	possibly damaging
NM_033051.3	c.637G>A	p.Val213Met	probably damaging
NM_003036.3	c.19G>T	p.Gly7Cys	benign
NM_022078.2	c.1361G>T	p.Gly454Val	probably damaging
NM_000959.3	c.545C>T	p.Ser182Leu	possibly damaging
NM_021633.2	c.1518G>T	p.Met506Ile	probably damaging
NM_152491.4	c.624G>T	p.Arg208Ser	possibly damaging
NM_018058.6	c.122C>G	p.Ser41*	
NM_021830.4	c.1570C>A	p.His524Asn	benign
NM_032592.3	c.385C>A	p.Leu129Met	possibly damaging
NM_013244.3	c.68G>T	p.Arg23Leu	benign
NM_017420.4	c.2099C>T	p.Ser700Phe	benign
NM_018199.3	c.1330C>A	p.Gln444Lys	benign
NM_004452.3	c.937C>A	p.Arg313Ser	possibly damaging
NM_017672.4	c.3535G>T	p.Glu1179*	
NM_001101362.2	c.55C>A	p.Gln19Lys	benign
NM_015079.5	c.79G>A	p.Gly27Arg	benign
NM_012467.3	c.509G>T	p.Gly170Val	probably damaging
NM_001100915.1	c.2092G>A	p.Gly698Arg	benign
NM_001170715.1	c.13G>T	p.Gly5Cys	benign
NM_003693.3	c.464G>T	p.Trp155Leu	benign
NM_001018.3	c.45C>A	p.Phe15Leu	benign
NM_030662.3	c.649G>T	p.Gly217Cys	probably damaging
NM_080662.3	c.437G>T	p.Trp146Leu	benign
NM_005178.4	c.968C>A	p.Pro323Gln	benign
NM_001039613.1	c.529G>T	p.Val177Leu	possibly damaging
NM_004418.3	c.56G>T	p.Arg19Leu	possibly damaging
NM_003590.4	c.56G>T	p.Arg19Leu	possibly damaging
NM_000516.4	c.601C>T	p.Arg201Cys	probably damaging
NM_138983.2	c.696C>A	p.Phe232Leu	benign
NM_052945.3	c.91C>A	p.His31Asn	benign

NM_001457.3	c.5423C>A	p.Pro1808His	probably damaging
NM_001041.3	c.4405G>T	p.Asp1469Tyr	benign
NM_005443.4	c.1068G>T	p.Trp356Cys	probably damaging
NM_001083.3	c.1027G>T	p.Glu343*	
NM_002006.4	c.221C>A	p.Pro74Gln	benign
NM_019030.2	c.1238G>T	p.Arg413Met	possibly damaging
NM_145867.1	c.421G>T	p.Gly141*	
NM_032538.1	c.1434G>T	p.Met478Ile	benign
NM_001847.2	c.3784G>T	p.Gly1262Trp	probably damaging
NM_013270.4	c.295G>A	p.Asp99Asn	benign
NM_001102467.1	c.362G>T	p.Gly121Val	probably damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_198576.3	c.3331G>C	p.Gly1111Arg	probably damaging
NM_000721.3	c.4329+1G>A		
NM_033056.3	c.2057T>A	p.Leu686Gln	probably damaging
NM_015319.2	c.3794C>T	p.Pro1265Leu	benign
NM_020121.3	c.2585delA	p.Asp862Valfs*19	
NM_020902.1	c.1511G>A	p.Gly504Glu	probably damaging
NM_005929.5	c.1246G>A	p.Asp416Asn	probably damaging
NM_133636.2	c.201_203delACT	p.Leu68del	
NM_139165.2	c.19A>T	p.Thr7Ser	benign
NM_001440.3	c.599A>G	p.Asp200Gly	benign
NM_012410.3	c.1416C>G	p.Asp472Glu	probably damaging
NM_000546.5	c.532_533insC	p.His178Profs*3	
NM_020876.1	c.953A>G	p.Asp318Gly	benign
NM_014905.4	c.32G>A	p.Arg11Gln	benign
NM_018474.4	c.708G>A	p.Met236Ile	benign
NM_014229.1	c.1261G>A	p.Ala421Thr	possibly damaging
NM_001085451.1	c.397A>G	p.Ser133Gly	benign
NM_003449.4	c.943G>A	p.Val315Ile	benign
NM_000093.4	c.3023C>A	p.Thr1008Lys	probably damaging
NM_000871.1	c.477delC	p.Leu160Cysfs*54	
NM_173473.3	c.172G>A	p.Val58Ile	possibly damaging
NM_000795.3	c.460G>A	p.Val154Ile	possibly damaging
NM_005691.2	c.1484C>T	p.Thr495Ile	possibly damaging
NM_007361.3	c.893G>A	p.Arg298His	benign
NM_001419.2	c.623G>T	p.Gly208Val	benign
NM_001419.2	c.622G>T	p.Gly208*	
NM_000540.2	c.9652G>T	p.Val3218Leu	probably damaging
NM_033257.3	c.628C>A	p.Gln210Lys	benign
NM_001904.3	c.122C>A	p.Thr41Asn	possibly damaging
NM_018932.3	c.1464C>A	p.Tyr488*	
NM_025184.3	c.1334A>T	p.Lys445Ile	possibly damaging
NM_014223.4	c.561+2T>A		
NM_000364.3	c.538G>C	p.Asp180His	probably damaging
NM_014698.2	c.2059T>G	p.Phe687Val	benign
NM_022034.5	c.897T>A	p.Asn299Lys	benign
NM_145804.2	c.2879A>C	p.Lys960Thr	probably damaging
NM_207343.3	c.1138T>C	p.Tyr380His	possibly damaging

NM_003566.3	c.694C>A	p.Gln232Lys	probably damaging
NM_019066.4	c.547C>T	p.Pro183Ser	
NM_014783.3	c.2002T>C	p.Cys668Arg	benign
NM_001080466.1	c.1154G>T	p.Arg385Leu	probably damaging
NM_015719.3	c.1318G>T	p.Gly440Cys	probably damaging
NM_002856.2	c.1100G>A	p.Gly367Glu	probably damaging
XM_005247009.1	c.56C>T	p.Ala19Val	benign
NM_015283.1	c.1708A>G	p.Ile570Val	benign
NM_002692.3	c.541G>A	p.Ala181Thr	benign
NM_004993.5	c.27A>G	p.Gln9Gln	
NM_153334.4	c.238T>C	p.Cys80Arg	probably damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_006991.3	c.394C>A	p.Pro132Thr	benign
NM_016279.3	c.476T>C	p.Phe159Ser	probably damaging
NM_015548.4	c.13451T>G	p.Met4484Arg	possibly damaging
NM_032415.4	c.2009C>T	p.Thr670Met	benign
NM_001024401.2	c.169C>T	p.Arg57Trp	probably damaging
NM_153604.2	c.443C>A	p.Thr148Lys	benign
NM_000516.4	c.602G>A	p.Arg201His	probably damaging
NM_003185.3	c.3256T>C	p.*1086Arg	
NM_006193.2	c.971G>T	p.Ser324Ile	benign
NM_007222.4	c.1330A>G	p.Thr444Ala	benign
NM_015038.1	c.2720C>T	p.Ala907Val	benign
NM_021185.4	c.2909G>A	p.Arg970His	probably damaging
NM_024861.2	c.524C>A	p.Pro175Gln	probably damaging
NM_015250.3	c.1637A>G	p.Asn546Ser	probably damaging
NM_018489.2	c.2902A>T	p.Lys968*	
NM_003986.2	c.880G>A	p.Ala294Thr	benign
NM_014793.4	c.988C>T	p.Pro330Ser	benign
NM_001897.4	c.6112G>A	p.Val2038Ile	benign
NM_024888.2	c.703C>T	p.Arg235Cys	benign
NM_001080411.1	c.221T>G	p.Phe74Cys	benign
NM_032838.4	c.488T>G	p.Ile163Ser	benign
NM_014931.3	c.954C>A	p.His318Gln	benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_002587.4	c.1105G>A	p.Ala369Thr	benign
NM_014773.3	c.142G>A	p.Asp48Asn	benign
NM_006934.3	c.1064A>G	p.Tyr355Cys	probably damaging
NM_000696.3	c.28C>G	p.Leu10Val	benign
NM_020824.3	c.2724C>G	p.Ile908Met	benign
NM_207345.2	c.565C>A	p.Gln189Lys	possibly damaging
NM_006905.2	c.1067C>T	p.Ala356Val	possibly damaging
NM_004504.4	c.621C>G	p.Ile207Met	probably damaging
NM_006045.1	c.2103C>A	p.His701Gln	probably damaging
NM_003420.3	c.1256A>C	p.Asp419Ala	possibly damaging
NM_000827.3	c.2467G>T	p.Val823Phe	possibly damaging
NM_001723.5	c.6112C>G	p.Pro2038Ala	benign
NM_004938.2	c.2713G>C	p.Asp905His	possibly damaging
NM_033123.3	c.1372A>G	p.Ile458Val	probably damaging

NM_002730.3	c.589T>C	p.Trp197Arg	probably damaging
NM_004036.3	c.2839G>T	p.Glu947*	
NM_014825.2	c.6688C>T	p.Gln2230*	
NM_006315.4	c.722T>C	p.Leu241Ser	possibly damaging
NR_002174.2	n.267G>C		benign
NM_138295.3	c.4839T>G	p.Phe1613Leu	probably damaging
NM_001448.2	c.1103A>G	p.His368Arg	benign
NM_014753.3	c.615G>T	p.Arg205Ser	possibly damaging
NM_005203.3	c.1526G>A	p.Gly509Asp	probably damaging
NM_001005213.1	c.700C>T	p.Leu234Phe	possibly damaging
NM_032138.4	c.1422C>A	p.Phe474Leu	benign
NM_006942.1	c.569G>A	p.Cys190Tyr	benign
NM_017757.2	c.3859C>T	p.Arg1287Cys	benign
XR_245459.1	n.912G>A		
NM_001080427.1	c.3121T>A	p.Cys1041Ser	probably damaging
NM_001904.3	c.134C>A	p.Ser45Tyr	probably damaging
NM_000248.3	c.188C>T	p.Pro63Leu	benign
NM_175886.2	c.122G>A	p.Cys41Tyr	benign
NM_013437.4	c.328A>G	p.Ile110Val	probably damaging
NM_015634.3	c.98A>G	p.Tyr33Cys	probably damaging
NM_021150.3	c.1213A>G	p.Ser405Gly	probably damaging
NM_018668.3	c.700_700+2delGGT		
NM_181552.3	c.3771delG	p.Ala1258Argfs*2	
NM_020911.1	c.3253-1C>A		
NM_007332.2	c.1731C>A	p.Asn577Lys	probably damaging
NM_032799.4	c.374A>G	p.His125Arg	probably damaging
NM_000516.4	c.601C>T	p.Arg201Cys	probably damaging
NM_014941.1	c.277C>T	p.Arg93Trp	possibly damaging
NM_000540.2	c.4405C>G	p.Arg1469Gly	probably damaging
NM_001904.3	c.130C>G	p.Pro44Ala	possibly damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_005957.4	c.1219T>C	p.Tyr407His	benign
NM_013377.3	c.1247G>A	p.Arg416Lys	probably damaging
NM_145913.3	c.493G>A	p.Ala165Thr	benign
NM_015347.4	c.1275C>A	p.Asn425Lys	probably damaging
XM_292717.9	c.1741C>T	p.Gln581*	
NM_198994.2	c.1214A>G	p.His405Arg	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_001164586.1	c.1436C>G	p.Ala479Gly	
NM_207379.1	c.499T>C	p.Tyr167His	probably damaging
NM_015329.3	c.1333A>T	p.Asn445Tyr	possibly damaging
NM_024310.4	c.9C>G	p.Asp3Glu	benign
NM_014438.4	c.357C>A	p.Phe119Leu	benign
NM_001334.2	c.396C>G	p.Cys132Trp	probably damaging
NM_030652.3	c.451A>T	p.Ser151Cys	possibly damaging
NM_173681.5	c.2447_2466delGGGGCCAGAAGC	p.Gly816Alafs*31	
NM_006009.3	c.628T>C	p.Tyr210His	probably damaging
NM_005853.5	c.606C>G	p.Asp202Glu	benign

NM_002734.4	c.617delT	p.Tyr207Metfs*15	
NM_001101330.1	c.241G>A	p.Glu81Lys	
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_175619.2	c.1027T>G	p.Tyr343Asp	probably damaging
			possibly damaging
NM_020927.1	c.295C>G	p.Pro99Ala	probably damaging
NM_007215.3	c.1141A>G	p.Ile381Val	benign
NM_017742.4	c.391G>A	p.Gly131Ser	probably damaging
NM_138690.1	c.2089G>A	p.Val697Met	probably damaging
NM_001001394.3	c.203A>G	p.Tyr68Cys	benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_018901.2	c.357C>G	p.Asp119Glu	benign
NM_005756.3	c.2864A>G	p.Asn955Ser	benign
NM_004632.3	c.473-6_499del		
NM_139055.2	c.2333C>T	p.Pro778Leu	possibly damaging
NM_181785.3	c.887T>C	p.Phe296Ser	benign
NM_006715.3	c.1787_1788delAT	p.Tyr596*	
NM_000516.4	c.601C>A	p.Arg201Ser	probably damaging
NM_001080508.2	c.493G>C	p.Gly165Arg	probably damaging
NM_025103.2	c.439C>T	p.Gln147*	
NM_007268.2	c.273G>C	p.Lys91Asn	benign
NM_000120.3	c.629A>G	p.Lys210Arg	probably damaging
NM_001200049.2	c.4297G>T	p.Val1433Leu	
NM_003482.3	c.16211C>T	p.Ser5404Phe	probably damaging
NM_016155.4	c.1777G>A	p.Ala593Thr	benign
NM_030979.2	c.1243G>C	p.Ala415Pro	benign
NM_002742.2	c.1100A>T	p.Asp367Val	benign
NM_138363.1	c.1298C>G	p.Ser433*	
NM_021187.3	c.986-1C>T		
NM_015035.3	c.1931G>T	p.Arg644Leu	probably damaging
NM_017584.5	c.528C>T	p.Leu176Leu	benign
NM_014966.3	c.2113G>A	p.Val705Met	probably damaging
NM_203434.2	c.1057A>T	p.Ile353Phe	probably damaging
NM_007329.2	c.1838G>A	p.Gly613Asp	probably damaging
NM_015055.2	c.1043A>G	p.Asn348Ser	probably damaging
NM_022463.4	c.866C>T	p.Thr289Met	probably damaging
NM_016286.3	c.718G>A	p.Gly240Ser	probably damaging
NM_052945.3	c.266T>C	p.Leu89Pro	probably damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_018176.3	c.215C>A	p.Thr72Lys	benign
NM_152406.2	c.1810+2T>C		
NM_017954.10	c.58C>T	p.Arg20Cys	benign
XM_002344207.1	c.346C>A	p.Pro116Thr	benign
NM_006800.3	c.559C>A	p.Arg187Ser	probably damaging
NM_001412.3	c.338-2T>A		
NM_032417.2	c.116C>T	p.Pro39Leu	probably damaging
NM_000102.3	c.979_981delAAG	p.Lys327del	
NM_014742.3	c.1176T>G	p.Phe392Leu	possibly damaging

NM_024701.3	c.104T>A	p.Leu35Gln	probably damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_015175.2	c.2536_2538delCTC	p.Leu847del	
NM_012334.2	c.5254G>C	p.Asp1752His	benign
NM_030936.3	c.761G>A	p.Cys254Tyr	possibly damaging
NM_000186.3	c.2444C>A	p.Pro815His	probably damaging
NM_002838.4	c.2426G>T	p.Arg809Ile	probably damaging
NM_018702.3	c.568G>T	p.Val190Leu	benign
NM_145806.2	c.175C>T	p.Leu59Phe	benign
NM_004976.4	c.123C>G	p.Asp41Glu	benign
NM_006500.2	c.1738T>C	p.Tyr580His	probably damaging
NM_014770.3	c.952C>G	p.Arg318Gly	probably damaging
NM_152905.3	c.886T>A	p.Cys296Ser	possibly damaging
NM_024837.3	c.1274C>G	p.Thr425Arg	benign
NM_014714.3	c.1309G>T	p.Ala437Ser	benign
NM_004948.3	c.1667G>A	p.Gly556Asp	probably damaging
NM_014975.2	c.927C>A	p.His309Gln	benign
NM_014975.2	c.928G>A	p.Ala310Thr	possibly damaging
NM_007153.3	c.1874C>A	p.Thr625Asn	probably damaging
NM_001184938.1	c.1402C>G	p.Pro468Ala	benign
XM_005246794.1	c.3G>A		benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_020815.1	c.1237T>A	p.Tyr413Asn	probably damaging
NM_020957.1	c.886C>A	p.Pro296Thr	benign
NM_006480.4	c.224C>A	p.Pro75Gln	probably damaging
NM_032142.3	c.6800C>T	p.Pro2267Leu	possibly damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_001005566.2	c.600G>A	p.Met200Ile	benign
NM_016237.4	c.1102G>T	p.Ala368Ser	benign
NM_018128.4	c.976A>G	p.Met326Val	benign
NM_024100.3	c.780C>A	p.Asp260Glu	benign
NM_000516.4	c.601C>A	p.Arg201Ser	probably damaging
NM_178276.5	c.920A>G	p.Tyr307Cys	possibly damaging
NM_016262.4	c.235G>C	p.Gly79Arg	probably damaging
NM_015458.3	c.1225C>T	p.Arg409Cys	benign
NM_000843.3	c.325G>T	p.Ala109Ser	benign
NM_198551.2	c.1661C>T	p.Ser554Leu	benign
NM_002426.4	c.373A>C	p.Met125Leu	benign
NM_000750.3	c.296G>T	p.Gly99Val	probably damaging
NM_021784.4	c.478A>C	p.Ser160Arg	benign
NM_001040105.1	c.133delG	p.Asp46Thrfs*3	
NM_000107.2	c.737C>T	p.Thr246Met	probably damaging
NM_015173.3	c.1142A>G	p.Lys381Arg	benign
NM_000093.4	c.2809G>A	p.Gly937Arg	probably damaging
NM_017556.2	c.418C>A	p.Pro140Thr	benign
NM_017720.2	c.1175G>T	p.Ser392Ile	benign
NM_080627.2	c.76G>T	p.Glu26*	
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_032553.1	c.25A>G	p.Arg9Gly	benign

NM_001139500.1	c.187G>A	p.Val63Ile	benign
NM_033132.3	c.1056G>T	p.Gln352His	benign
NM_173547.3	c.344G>T	p.Ser115Ile	benign
NM_001009993.2	c.329C>G	p.Ala110Gly	possibly damaging
NM_022900.4	c.108C>A	p.Cys36*	
NM_004630.3	c.529_531delATC	p.Ile177del	
NM_000227.3	c.2275G>C	p.Asp759His	probably damaging
NM_020126.4	c.1591T>A	p.Trp531Arg	probably damaging
NM_145740.3	c.414+2A>C		
NM_033071.3	c.2351G>A	p.Ser784Asn	benign
NM_001735.2	c.1207G>A	p.Asp403Asn	benign
NM_002021.1	c.1208G>A	p.Ser403Asn	benign
NM_015295.2	c.2890C>A	p.Pro964Thr	probably damaging
NM_001904.3	c.99T>C	p.Ser33Ser	
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
XM_005262861.1	c.2222A>T	p.Gln741Leu	possibly damaging
NM_014004.2	c.561delT	p.Asn187Lysfs*4	
NM_002458.2	c.3344C>T	p.Ala1115Val	probably damaging
NM_006918.4	c.119T>C	p.Val40Ala	benign
NR_003923.2	n.962delT		
NM_003119.2	c.965G>A	p.Arg322His	possibly damaging
NM_001044369.2	c.332G>A	p.Arg111Gln	benign
NM_178837.4	c.694C>T	p.Pro232Ser	benign
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_053002.4	c.2738A>C	p.Lys913Thr	probably damaging
NM_017639.3	c.6644A>T	p.Tyr2215Phe	probably damaging
NM_001142552.1	c.1306G>T	p.Val436Leu	possibly damaging
XR_040412.2	n.247G>A		
NM_001447.2	c.11059G>T	p.Glu3687*	
NM_152744.3	c.6604G>A	p.Ala2202Thr	benign
NM_000170.2	c.2405C>A	p.Ala802Glu	possibly damaging
NM_005745.7	c.147_148insT	p.Thr50Tyrfs*25	
NM_000374.4	c.709delA	p.Ile237Serfs*8	
			benign
NM_001195263.1	c.1627C>T	p.Gln543*	
NM_012226.3	c.141G>T	p.Glu47Asp	possibly damaging
NR_004401.2	n.1020G>A		possibly damaging
NM_014012.5	c.700G>T	p.Glu234*	
NM_001316.3	c.431A>G	p.His144Arg	possibly damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_005935.2	c.287C>G	p.Pro96Arg	probably damaging
NM_018919.2	c.1868C>T	p.Thr623Met	probably damaging
NM_001084.4	c.1264G>A	p.Gly422Ser	benign
NM_152609.2	c.1120C>T	p.His374Tyr	possibly damaging
NM_001171932.1	c.1180G>T	p.Asp394Tyr	benign
NM_032496.2	c.685C>A	p.Arg229Ser	benign
			benign
NM_018962.2	c.17C>A	p.Ala6Glu	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging

NM_005087.3	c.1838A>T	p.Glu613Val	benign
NM_018392.4	c.103-2T>A		
NM_145032.3	c.140G>A	p.Cys47Tyr	benign
NM_016478.3	c.444_451delGTGTACTG	p.Leu148Phefs*3	
NM_000832.6	c.1035C>A	p.Asp345Glu	possibly damaging
NM_001013690.4	c.814G>T	p.Glu272*	
NM_203411.1	c.68A>G	p.Asp23Gly	probably damaging
NM_030650.1	c.506G>A	p.Arg169Gln	possibly damaging
NM_001904.3	c.134C>T	p.Ser45Phe	probably damaging
NM_018924.2	c.5G>C	p.Gly2Ala	possibly damaging
NM_017994.4	c.919G>T	p.Glu307*	
NR_023392.1	n.1608A>G		benign
NM_003482.3	c.62C>T	p.Ala21Val	benign
NM_000219.4	c.94C>T	p.Arg32Cys	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_012118.3	c.408_414del	p.Cys136*	
NM_018919.2	c.331G>C	p.Glu111Gln	possibly damaging
NM_153809.2	c.5083A>G	p.Ile1695Val	benign
NM_005156.6	c.1144T>G	p.Tyr382Asp	probably damaging
NM_001036.3	c.13538delG	p.Lys4514Serfs*26	
NM_017897.2	c.563C>T	p.Ala188Val	possibly damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_005778.3	c.330_331delAG	p.Ser112Argfs*64	
NM_020844.2	c.291T>A	p.Phe97Leu	probably damaging
NM_014380.1	c.314A>G	p.Asp105Gly	benign
NM_003222.3	c.66C>G	p.Ser22Arg	benign
NM_173050.3	c.860T>A	p.Leu287Gln	benign
NM_000755.3	c.1372C>T	p.Arg458Cys	probably damaging
NM_016252.3	c.9940A>G	p.Asn3314Asp	probably damaging
NM_002191.3	c.870C>A	p.Tyr290*	
NM_004225.2	c.2332G>A	p.Glu778Lys	benign
NM_004091.3	c.155C>T	p.Thr52Met	benign
NM_000018.3	c.1097G>T	p.Arg366Leu	probably damaging
NM_033025.4	c.1619C>T	p.Ser540Phe	probably damaging
NM_014466.2	c.815T>C	p.Met272Thr	benign
NM_079420.2	c.505G>C	p.Glu169Gln	possibly damaging
NM_002891.4	c.3476T>C	p.Ile1159Thr	benign
NM_014798.2	c.2238C>G	p.Phe746Leu	probably damaging
NM_000516.4	c.602G>A	p.Arg201His	probably damaging
NM_138782.2	c.1294G>T	p.Gly432*	
NM_003542.3	c.35G>T	p.Gly12Val	
NM_001017969.2	c.2347G>A	p.Glu783Lys	possibly damaging
NM_004815.3	c.2688G>T	p.Met896Ile	benign
NM_003126.2	c.4266C>A	p.Asp1422Glu	benign
NM_022369.3	c.1964G>A	p.Arg655His	probably damaging
NM_005883.2	c.567_596del	Leu	
NM_002730.3	c.95A>T	p.Glu32Val	benign
NM_019057.3	c.554C>T	p.Ala185Val	possibly damaging
NM_020319.2	c.998C>T	p.Ser333Leu	probably damaging

NM_004582.3	c.99G>C	p.Lys33Asn	benign
NM_000036.2	c.431C>T	p.Thr144Ile	benign
NM_001195571.1	c.98G>A	p.Cys33Tyr	
NM_003874.3	c.763G>A	p.Ala255Thr	possibly damaging
NM_020443.4	c.4018G>C	p.Glu1340Gln	possibly damaging
NM_022169.4	c.1809G>C	p.Gln603His	benign
NM_015026.2	c.4414A>G	p.Ile1472Val	benign
NM_018191.3	c.1492C>T	p.His498Tyr	probably damaging
NM_017534.5	c.4523A>G	p.Asn1508Ser	probably damaging
NM_024888.2	c.428C>A	p.Ala143Asp	probably damaging
NM_017572.3	c.887T>C	p.Val296Ala	benign
NM_001001411.2	c.793G>A	p.Val265Ile	benign
NM_018025.2	c.1279A>C	p.Ile427Leu	benign
NM_031895.5	c.605A>G	p.Tyr202Cys	probably damaging
NM_207363.2	c.404A>G	p.Glu135Gly	benign
NM_006920.4	c.257A>G	p.Asn86Ser	benign
NM_004449.4	c.400G>A	p.Val134Met	probably damaging
NM_022064.3	c.625C>G	p.Leu209Val	benign
NM_002217.3	c.915G>T	p.Glu305Asp	benign
NM_004991.3	c.808C>A	p.Gln270Lys	benign
NM_004784.2	c.1069G>T	p.Gly357*	
NM_020732.3	c.1195_1220del	p.Ala399Profs*127	
NM_019037.2	c.265C>G	p.Arg89Gly	probably damaging
XM_293407.7	c.104C>T	p.Ser35Leu	
NM_018022.2	c.505G>T	p.Glu169*	
NM_002481.3	c.1999G>T	p.Glu667*	
NM_001035.2	c.6792G>C	p.Lys2264Asn	probably damaging
NM_020811.1	c.963C>A	p.His321Gln	benign
NM_003904.3	c.26C>A	p.Pro9Gln	benign
NM_000719.6	c.5989G>T	p.Glu1997*	
NM_001874.4	c.948G>T	p.Lys316Asn	probably damaging
NM_006825.3	c.73C>A	p.Pro25Thr	benign
NM_032848.1	c.241G>T	p.Glu81*	
NM_012074.4	c.289G>T	p.Glu97*	
NM_004545.3	c.144G>T	p.Met48Ile	possibly damaging
NM_014691.2	c.4366G>T	p.Glu1456*	
NM_017726.7	c.140A>G	p.Lys47Arg	benign
NM_004245.3	c.373G>T	p.Asp125Tyr	probably damaging
NM_139057.2	c.786C>A	p.Asn262Lys	possibly damaging
NM_182922.2	c.1508C>A	p.Pro503Gln	possibly damaging
NM_004176.4	c.1786-1C>A		
NM_025248.2	c.1847C>A	p.Ser616*	
NM_001144952.1	c.2687G>T	p.Gly896Val	probably damaging
NM_002819.4	c.1312C>A	p.Gln438Lys	benign
NM_031304.4	c.763C>A	p.Leu255Met	benign
XM_005258942.1	c.457C>A	p.Pro153Thr	probably damaging
NM_003660.3	c.1244G>T	p.Arg415Leu	benign
NM_006751.5	c.3356G>A	p.Gly1119Asp	benign
NM_024989.3	c.2335G>T	p.Val779Leu	benign

NM_152525.5	c.1509G>T	p.Val503Val	benign
NM_025176.4	c.1810G>T	p.Gly604Cys	probably damaging
NM_014012.5	c.796C>A	p.Gln266Lys	benign
NM_080833.2	c.1509G>T	p.Gln503His	benign
NM_015894.3	c.524G>T	p.Arg175Leu	benign
NM_016327.2	c.884C>A	p.Pro295Gln	benign
NM_006071.1	c.2327G>A	p.Arg776His	benign
NM_000335.4	c.1805C>A	p.Ser602*	
NM_033210.4	c.652A>C	p.Lys218Gln	possibly damaging
NM_001205271.1	c.223C>A	p.His75Asn	
NM_022908.2	c.411C>A	p.His137Gln	possibly damaging
NM_145753.2	c.2177A>G	p.Lys726Arg	probably damaging
NM_000902.3	c.1309A>G	p.Lys437Glu	possibly damaging
NM_001347.3	c.346G>T	p.Val116Phe	probably damaging
NM_004346.3	c.511G>T	p.Gly171Cys	probably damaging
NM_052909.3	c.1582-1G>T		
NM_024337.3	c.319G>A	p.Ala107Thr	benign
NM_175062.3	c.177+1C>A		
NM_002114.2	c.2930A>G	p.His977Arg	probably damaging
NR_028077.1	n.828A>G		benign
NM_031949.4	c.277G>T	p.Glu93*	
NM_003496.3	c.5889G>T	p.Leu1963Phe	benign
NM_003378.3	c.1135G>T	p.Gly379Trp	possibly damaging
NM_001869.2	c.1244G>T	p.Arg415Leu	benign
NM_198455.2	c.1742C>A	p.Ser581Tyr	possibly damaging
NM_207414.2	c.1445G>T	p.Cys482Phe	probably damaging
NM_152569.2	c.671C>T	p.Pro224Leu	benign
NM_001080497.2	c.301G>T	p.Glu101*	
NM_001105576.2	c.734G>T	p.Trp245Leu	benign
NM_003399.5	c.338C>A	p.Thr113Asn	probably damaging
NM_014555.3	c.2095C>T	p.Arg699Trp	benign
NM_006646.5	c.767A>G	p.His256Arg	possibly damaging
NM_017533.2	c.5533C>T	p.Arg1845Cys	probably damaging
NM_020532.4	c.1606A>G	p.Thr536Ala	benign
NM_032221.4	c.1804A>G	p.Arg602Gly	probably damaging
NM_022105.4	c.883G>T	p.Asp295Tyr	probably damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_014010.4	c.734G>A	p.Ser245Asn	probably damaging
NM_005676.4	c.2049G>C	p.Glu683Asp	benign
NM_005120.2	c.4879C>T	p.Arg1627Cys	probably damaging
NR_027693.1	n.226C>T		benign
NM_018265.3	c.1300G>A	p.Ala434Thr	benign
NM_001001954.1	c.235G>T	p.Ala79Ser	benign
NM_016582.2	c.866G>A	p.Arg289His	benign
NM_014256.3	c.268C>T	p.Arg90Cys	probably damaging
NM_001904.3	c.130C>G	p.Pro44Ala	possibly damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_022047.3	c.1367G>A	p.Arg456Gln	probably damaging
NM_001973.3	c.55C>T	p.Gln19*	

NM_015045.2	c.484_487delAAAT	p.Lys162*	
XM_005268218.1	c.4192C>T	p.Arg1398Cys	possibly damaging
NM_005657.2	c.3145C>T	p.Arg1049*	
NM_153338.2	c.1172C>A	p.Thr391Asn	possibly damaging
NM_002385.2	c.228C>A	p.Ser76Arg	benign
NM_004379.3	c.545A>G	p.Asn182Ser	benign
NM_006216.3	c.190A>T	p.Met64Leu	benign
NM_001037335.2	c.1107G>T	p.Gln369His	benign
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_004499.3	c.322delG	p.Gly108Aspfs*21	
NM_015555.2	c.974G>C	p.Arg325Pro	possibly damaging
NM_014705.3	c.5657G>C	p.Ser1886Thr	benign
NM_213649.1	c.177+1C>A		
NM_018931.2	c.1960G>A	p.Ala654Thr	benign
NM_152762.2	c.1657G>A	p.Glu553Lys	benign
NM_053284.2	c.793G>C	p.Ala265Pro	probably damaging
NM_207346.2	c.1357T>C	p.Tyr453His	possibly damaging
NM_002730.3	c.731_745delCCATCCAGATCTATG	p.Pro244_Glu249delinsGln	
NM_001039613.1	c.701C>G	p.Ala234Gly	benign
NM_015662.1	c.1518delA	p.Lys506Asnfs*16	
NM_021956.4	c.1987C>T	p.Arg663Cys	probably damaging
NM_033225.5	c.3706A>G	p.Thr1236Ala	benign
NM_198512.1	c.859+2T>A		
NM_007204.4	c.548T>C	p.Ile183Thr	probably damaging
NM_003638.1	c.2169G>T	p.Met723Ile	benign
NM_152707.3	c.566A>G	p.Tyr189Cys	probably damaging
NM_002339.2	c.953A>G	p.Tyr318Cys	probably damaging
NM_007361.3	c.212G>T	p.Arg71Leu	benign
NM_000293.2	c.1459G>A	p.Gly487Ser	probably damaging
NM_152381.5	c.9349C>T	p.Arg3117Cys	possibly damaging
NM_173651.2	c.4915A>G	p.Lys1639Glu	
NM_002473.4	c.4333_4335delAAG	p.Lys1445del	
NM_001904.3	c.110C>T	p.Ser37Phe	probably damaging
NM_000840.2	c.1504C>T	p.His502Tyr	benign
NM_018489.2	c.6706C>T	p.Arg2236Trp	probably damaging
NM_000102.3	c.6G>A	p.Trp2*	
NM_002281.3	c.1311C>A	p.Cys437*	
NM_000690.3	c.1145C>T	p.Ala382Val	probably damaging
NM_004380.2	c.58C>A	p.Pro20Thr	probably damaging
NR_003587.2	n.3291+1G>T		
NM_024825.3	c.155C>T	p.Pro52Leu	benign
NM_003659.3	c.271A>T	p.Met91Leu	benign
NM_173485.5	c.956C>T	p.Pro319Leu	probably damaging
NM_015241.2	c.1252G>C	p.Ala418Pro	possibly damaging
NM_001904.3	c.1564G>A	p.Ala522Thr	benign
NM_020777.2	c.166G>T	p.Gly56Trp	possibly damaging
NM_001080477.1	c.7891C>G	p.Arg2631Gly	benign
NM_000500.7	c.558C>A	p.Asn186Lys	benign
NM_000841.2	c.178C>T	p.Arg60Trp	possibly damaging

NM_012259.2	c.683C>T	p.Thr228Met	possibly damaging
NM_024940.6	c.2608C>T	p.Arg870*	
NM_138769.2	c.1106C>T	p.Thr369Ile	probably damaging
NM_018690.3	c.2756C>T	p.Ala919Val	benign
NM_003003.3	c.427A>G	p.Thr143Ala	benign
NM_052843.3	c.9731G>A	p.Arg3244Gln	possibly damaging
NM_173508.2	c.536T>C	p.Leu179Ser	probably damaging
NM_018263.4	c.1600G>A	p.Glu534Lys	benign
NM_014468.2	c.541C>T	p.Gln181*	
NM_000093.4	c.935C>A	p.Pro312Gln	benign
NM_004600.5	c.1439C>A	p.Ala480Asp	probably damaging
NM_017551.2	c.2083G>A	p.Gly695Ser	probably damaging
NM_198520.2	c.2852C>A	p.Thr951Lys	benign
NM_015180.4	c.17381T>A	p.Met5794Lys	benign
NM_003803.3	c.3303+2A>G		
NM_001114598.1	c.80C>T	p.Ala27Val	benign
NM_006343.2	c.137_143delACCACAC	p.His47Argfs*15	
NM_005318.3	c.131G>C	p.Gly44Ala	probably damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_015129.5	c.322C>A	p.Gln108Lys	possibly damaging
NM_000766.4	c.427C>G	p.Arg143Gly	probably damaging
NM_019843.3	c.1982G>C	p.Arg661Thr	benign
NM_015186.3	c.3236-1G>C		
NM_178470.4	c.373G>T	p.Val125Leu	probably damaging
NM_001081.3	c.7594G>A	p.Val2532Ile	benign
NM_024899.3	c.527G>C	p.Gly176Ala	benign
NM_013312.2	c.1990A>G	p.Ile664Val	probably damaging
NM_021196.3	c.139C>G	p.Gln47Glu	benign
NM_004369.3	c.421G>A	p.Gly141Arg	probably damaging
NM_006653.4	c.292T>G	p.Phe98Val	probably damaging
XM_930012.4	c.820G>C	p.Ala274Pro	
NM_133457.3	c.1036G>A	p.Val346Met	benign
NM_001163.3	c.2315T>C	p.Met772Thr	probably damaging
NM_005957.4	c.152G>T	p.Arg51Leu	probably damaging
NM_020384.3	c.22C>A	p.Leu8Ile	benign
			benign
NM_199355.2	c.3274C>A	p.Pro1092Thr	benign
NM_198795.1	c.3016T>A	p.Phe1006Ile	benign
NM_015278.3	c.2606C>A	p.Pro869Gln	benign
NM_014257.4	c.774G>C	p.Lys258Asn	benign
NM_001642.2	c.707A>G	p.Tyr236Cys	possibly damaging
NM_030904.1	c.860C>T	p.Ala287Val	probably damaging
NM_001856.3	c.3826G>T	p.Gly1276Cys	probably damaging
NM_006269.1	c.85C>T	p.Leu29Phe	benign
NM_015180.4	c.16534C>A	p.Leu5512Ile	benign
NM_152381.5	c.6237G>T	p.Met2079Ile	benign
NM_024529.4	c.911C>T	p.Thr304Met	possibly damaging
NR_040037.1	n.2049C>G		possibly damaging

NM_024582.4	c.10675A>T	p.Ser3559Cys	probably damaging
NM_007373.3	c.1736G>A	p.Arg579His	probably damaging
NM_014030.3	c.985C>T	p.Arg329*	
NM_152756.3	c.1390G>C	p.Glu464Gln	benign
NM_001005191.2	c.57T>A	p.Asp19Glu	benign
NM_001276469.1	c.731G>A	p.Arg244Lys	benign
NM_024729.3	c.2733G>C	p.Glu911Asp	benign
NM_001005275.1	c.371G>A	p.Gly124Asp	benign
NM_012406.3	c.813C>A	p.Asp271Glu	benign
NM_004523.3	c.1205A>C	p.Glu402Ala	benign
NM_003253.2	c.2787G>T	p.Glu929Asp	benign
NM_001005183.1	c.286G>A	p.Ala96Thr	benign
			benign
NM_014971.1	c.1559A>G	p.Lys520Arg	possibly damaging
NM_015909.3	c.5274G>T	p.Arg1758Ser	probably damaging
NM_004929.2	c.124G>A	p.Glu42Lys	probably damaging
NM_004770.2	c.1474T>A	p.Trp492Arg	probably damaging
NM_017686.3	c.308A>T	p.Lys103Ile	probably damaging
NM_022756.5	c.52G>T	p.Glu18*	
NM_000218.2	c.1471_1491del	p.Leu491_Leu497del	
NM_006784.2	c.1301C>T	p.Ala434Val	possibly damaging
NM_001904.3	c.133T>C	p.Ser45Pro	possibly damaging
NM_003039.2	c.1222C>T	p.Arg408Trp	probably damaging
NM_014861.2	c.67C>T	p.Gln23*	

pph2 prob	Sift	Genotype	SNV Qual	Map Qual	Depth	%Var	Cases	Controls
0.989	0.04	heterozygous	194	60	115	25	1	0
0.033	0.26	heterozygous	37	60	15	20	1	0
0.338	0.28	heterozygous	132	60	194	23	1	0
1	0	heterozygous	173	60	208	25	6	0
0.064	0.53	heterozygous	59	60	101	15	1	0
0.023	0.33	heterozygous	34	60	16	19	2	0
0.018	0.07	heterozygous	115	60	36	28	2	0
0.006	0.8	heterozygous	89	60	165	18	1	0
0.033	0.94	heterozygous	96	60	64	20	1	0
0.268	0.15	heterozygous	206	60	137	26	1	0
0.794	0.04	heterozygous	82	60	23	26	1	1
	0.05	heterozygous	109	60	112	19	1	0
1	0.09	heterozygous	197	60	279	28	1	0
0.004	0.06	heterozygous	220	60	83	29	1	0
0.909	0.25	heterozygous	154	60	85	24	1	1
0.005	0.73	heterozygous	206	60	94	27	1	0
0.5	0	heterozygous	107	60	264	23	1	0
0.007	0.39	heterozygous	64	60	185	18	1	0
0.287 9	0.01	heterozygous	203	60	202	28	1	0
0.643	0.07	heterozygous	225	60	102	50	3	0
0.905	0	heterozygous	225	60	101	50	23	0
0.939	0.01	heterozygous	225	60	140	31	1	0
0.994	0	heterozygous	211	60	261	29	1	0
0.211	0.03	heterozygous	76	58	111	16	1	0
		heterozygous	999	999	16	25	4	0
		heterozygous	169	60	94	29	1	0
0.005	0.56 0	heterozygous	225	60	139	28	1	0
0.96	0	heterozygous	144	60	230	24	1	0
		heterozygous	999	999	56	21	1	0
0.999		heterozygous	79	58	265	21	1	0
0.004	0.18	heterozygous	225	60	280	35	1	0
0.989	1 0.02	heterozygous	209	60	165	27	1	0
0.197	0.33	heterozygous	203	60	99	26	1	0
0.04	0	heterozygous	64	60	82	17	3	0
0.905	0	heterozygous	216	60	94	28	23	0
0.403	0	heterozygous	84	60	119	16	1	0
		heterozygous	36	60	66	14	1	0
		heterozygous	195	60	53	28	1	0
0.001	0.11	heterozygous	97	60	54	24	1	0
0	1	heterozygous	74	60	585	22	3	6
0.016	0.16	heterozygous	159	59	83	25	1	0
0.905	0	heterozygous	171	60	100	22	23	0
0.1	0.26	heterozygous	111	60	231	22	1	0
0.003	0.09	heterozygous	149	59	204	23	1	0
		heterozygous	118	60	361	12	1	0
0.309	0.03	heterozygous	37	60	28	18	1	0
0.935	0.09	heterozygous	83	60	159	20	1	0
0.852	0.56	heterozygous	189	60	148	27	1	0

0.066		heterozygous	154	60	183	23	1	0
0.401	0.57	heterozygous	130	60	82	20	1	0
0.004	0.23	heterozygous	146	60	119	21	1	0
0.928	0	heterozygous	27	60	126	13	15	0
0.998	0	heterozygous	40	60	101	14	1	0
0.994	0	heterozygous	134	60	267	23	1	0
0.548	0.21	heterozygous	213	60	231	29	1	0
0.003	0.57	heterozygous	225	60	129	29	1	0
0.969	0.12	heterozygous	225	60	110	30	1	0
0.997	0.29	heterozygous	208	59	143	31	1	0
		heterozygous	217	59	193	22	1	0
		heterozygous	159	60	146	26	1	0
0.967	0.08	heterozygous	164	60	62	26	1	0
0.98	0.11	heterozygous	225	60	158	30	1	0
0.928	0	heterozygous	225	60	152	32	15	0
0.027	0.01	heterozygous	158	60	108	23	1	0
1	0.07	heterozygous	156	60	194	24	1	0
0.002	0.02	heterozygous	225	60	134	29	1	0
0.079	0.41	heterozygous	220	60	73	29	1	0
0.721	0.11	heterozygous	225	59	198	30	1	0
0.001	1	heterozygous	127	60	541	24	1	0
0.748	0.23	heterozygous	33	59	143	15	1	0
0.999	0	heterozygous	31	60	17	18	1	0
0.069	0.07	heterozygous	45	60	12	25	1	0
0.996	0.01	heterozygous	37	60	15	20	1	0
0.004	0.37	heterozygous	225	60	112	38	1	0
0.897	0.29	heterozygous	225	60	196	32	1	0
0.981	0.21	heterozygous	54	60	110	15	1	0
		heterozygous	999	999	170	22	1	0
0.01	1	heterozygous	41	59	32	16	1	0
0.905	0	heterozygous	225	60	89	56	23	0
0.033	0.26	heterozygous	169	60	81	25	1	0
	0.03	heterozygous	133	60	80	20	1	0
0.993	0	heterozygous	225	60	54	35	1	0
0.403	0	heterozygous	102	59	20	40	1	0
0.338	0.34	heterozygous	140	60	182	23	1	0
0.999	0.12	heterozygous	223	60	164	28	1	0
0.134	0.07	heterozygous	225	60	211	34	1	0
0.987	0	heterozygous	79	60	68	22	1	0
0.95	0	heterozygous	225	60	100	28	1	0
0.001	0.48	heterozygous	225	60	288	35	1	0
1	0.73	heterozygous	80	60	152	20	1	0
	0.49	heterozygous	206	60	173	27	1	0
0.18	0.13	heterozygous	44	60	90	14	1	0
0.013	0	heterozygous	83	60	204	19	1	0
0.998	0.14 0.05	heterozygous	99	60	105	17	1	0
0.347	0.55	heterozygous	144	60	165	24	1	0
0.905	0	heterozygous	189	60	155	25	23	0
0.007	0.9	heterozygous	107	60	123	19	1	0

0.998	0	heterozygous	207	58	88	27	1	0
		heterozygous	217	59	123	16	1	0
		heterozygous	30	60	37	11	1	0
0.616	0.06	heterozygous	84	60	48	21	1	0
0.157	0.65	heterozygous	51	60	197	17	1	0
0.928	0	heterozygous	206	60	82	27	15	0
		heterozygous	144	60	43	14	1	0
0		heterozygous	166	60	52	25		
0.92		heterozygous	77	60	180	18		
0.968		heterozygous	218	59	157	27		
0.994		heterozygous	171	60	155	23		
0.006		heterozygous	80	60	43	19		
0		heterozygous	94	60	73	16		
0.001		heterozygous	42	60	18	22		
1		heterozygous	225	60	193	33		
0.608		heterozygous	211	60	115	26		
0.018		heterozygous	188	46	76	26		
		heterozygous	185	60	56	25		
0.575		heterozygous	126	60	24	29		
0.961		heterozygous	225	60	105	40		
0.157	0.01	heterozygous	52	60	9	33	1	0
1	0	heterozygous	36	59	25	16	1	0
0.56	0.12	heterozygous	67	60	197	18	1	0
0.988	0	heterozygous	79	60	22	27	1	0
0.771	0.02	heterozygous	31	60	54	13	1	0
	0.37	heterozygous	221	60	88	28	1	0
0.229	0.51	heterozygous	54	60	56	14	1	0
0.612	0.03	heterozygous	36	60	33	15	1	0
0.187	0.14	heterozygous	220	60	67	30	1	0
0.259	0	heterozygous	192	60	194	26	1	0
0 0.002	0.66	heterozygous	49	60	18	22	1	0
0.805	0.11	heterozygous	40	60	14	21	1	0
	0.02	heterozygous	31	60	38	13	1	0
0.001	0.7	heterozygous	45	60	11	27	1	0
0.001		heterozygous	34	58	14	21	1	0
0.99	0.08	heterozygous	36	60	24	17	1	0
0.034	0.01	heterozygous	224	60	112	30	1	1
0.109	0.05	heterozygous	46	60	23	17	1	0
0.159	0.08	heterozygous	52	60	10	30	1	0
0.059	0.04	heterozygous	61	60	18	22	2	0
1	0.04	heterozygous	50	47	30	17	1	0
0.339	0.61	heterozygous	39	60	51	14	1	0
0.008	0.01	heterozygous	31	60	17	18	1	0
0.576	0.03	heterozygous	225	60	102	39	1	0
0.782	0.02	heterozygous	66	60	14	29	2	1
0.82 0.433	0.08	heterozygous	36	60	45	13	1	0
1	0	heterozygous	225	60	206	35	9	0
0.013	0.81	heterozygous	42	60	12	25	1	0
0.001	1	heterozygous	48	60	9	33	1	0

1	0	heterozygous	31	60	28	14	2	0
0.13	0.05	heterozygous	31	60	38	13	1	0
0.997	0	heterozygous	39	60	23	17	1	0
	0.05	heterozygous	31	60	38	13	1	0
0.093	0	heterozygous	47	60	18	22	1	0
0.594	0.01	heterozygous	63	60	27	19	1	0
	0.46	heterozygous	37	60	13	23	1	2
0.001	0.17	heterozygous	40	60	14	21	1	0
1	0	heterozygous	43	60	21	19	1	1
0.053		heterozygous	33	60	19	21		
1		heterozygous	42	60	5	100		
0.905	0	heterozygous	225	60	98	36	23	0
0.999	0.01	heterozygous	131	60	88	20	1	0
		heterozygous	101	60	54	20	1	0
1	0	heterozygous	73	60	289	21	1	0
0.007	0.81	heterozygous	206	60	104	26	1	0
		heterozygous	217	60	136	30	1	0
0.998	0.07	heterozygous	187	60	325	28	1	0
1	0	heterozygous	225	60	90	37	1	0
		heterozygous	217	58	347	31	1	0
0.025	0.89	heterozygous	171	60	108	23	1	0
0.243		heterozygous	135	60	348	24	1	0
0.997	0.1	heterozygous	203	60	162	27	1	0
		heterozygous	98	60	73	45	1	0
0.055	0.13	heterozygous	225	60	188	50	1	0
0.356	0.1 0	heterozygous	57	60	19	79	1	0
0.014		heterozygous	225	60	388	34	1	0
0.826	0	heterozygous	118	60	56	79	1	0
0.003	0.86	heterozygous	219	60	78	58	1	0
0.194	0.6	heterozygous	92	59	53	26	1	0
0.995	0.29	heterozygous	114	60	76	21	1	0
		heterozygous	151	60	55	27	1	0
0.893	0	heterozygous	225	60	132	33	1	0
0.771	0.32	heterozygous	225	60	159	34	1	0
0.672	0.1	heterozygous	204	60	60	40	1	0
0 0.001	0.31	heterozygous	193	60	126	26	1	0
0.032	0.63	heterozygous	163	60	31	42	1	0
	0.37	heterozygous	165	60	32	41	1	0
0.984	0.41	heterozygous	138	59	37	27	1	0
0	0.26	heterozygous	31	55	17	18	1	1
0.468	0.04	heterozygous	223	60	73	30	1	0
	1	heterozygous	51	60	9	67	1	0
0.646	0.15 0.24	heterozygous	225	60	77	32	1	0
		heterozygous	108	60	20	30	1	0
0.965	0	heterozygous	102	60	77	18	1	0
0.101	0.85	heterozygous	144	60	139	25	1	0
0.265	0.51	heterozygous	108	58	114	23	1	0
0.928	0	heterozygous	145	60	66	21	1	0
0.564	0.37	heterozygous	101	59	126	17	1	0

0.93	0.42	heterozygous	94	60	175	18	1	0
		heterozygous	90	60	50	20	1	0
0.002	0.46	heterozygous	155	59	79	22	1	0
0.997	0.47	heterozygous	51	60	58	14	1	0
1	0	heterozygous	225	60	95	32	1	0
1	0.06	heterozygous	150	60	70	23	1	0
0.001	0.14	heterozygous	66	60	96	21	1	0
0.002	0.28	heterozygous	72	60	21	29	1	0
0	0.29	heterozygous	60	60	51	16	1	0
		heterozygous	45	59	90	18	1	0
0.996	0	heterozygous	52	57	63	16	1	0
0.928	0	heterozygous	225	60	63	32	15	0
0.202	0.31	heterozygous	55	60	63	14	1	0
0.998		heterozygous	129	60	140	19	1	0
0.622	0.11	heterozygous	76	59	79	15	1	0
0.032	0.18	heterozygous	52	60	77	14	2	0
0.991	0	heterozygous	223	60	77	29	1	1
0.039	0.92	heterozygous	55	60	109	15	1	0
1	0	heterozygous	203	60	210	27	6	0
		heterozygous	43	60	105	15	1	0
0.025	0.39	heterozygous	225	59	38	47	1	0
0	0.53	heterozygous	63	60	154	16	1	0
0.055	0.04	heterozygous	225	60	99	67	1	0
0.992	0.03	heterozygous	74	59	81	19	1	2
0.999	0	heterozygous	77	60	144	17	1	0
0.997	0.28	heterozygous	225	60	42	43	1	0
	1	heterozygous	225	60	107	32	2	0
0.008	0.39	heterozygous	225	60	146	38	2	0
0.036	0.48	heterozygous	225	60	137	34	2	0
0.038	0.39	heterozygous	225	60	206	41	2	0
0.001		heterozygous	225	60	90	36	2	0
0.001	0.2	heterozygous	225	60	137	39	2	0
0.017	0.16	heterozygous	225	60	200	36	2	0
0.154	0.48	heterozygous	225	60	60	37	2	0
0.928	0	heterozygous	225	60	90	44	15	0
0.406	0.11	heterozygous	225	60	175	45	2	0
0.015	0.05	heterozygous	225	59	203	38	2	0
0.999	0	heterozygous	214	60	91	30	1	0
0.007	0.6	heterozygous	135	60	91	29	1	0
0.311	0.12	heterozygous	97	60	48	29	1	0
0.629	0.07	heterozygous	178	59	122	27	1	0
0.458	0.03	heterozygous	225	48	174	35	1	1
0.978 0.983 0.99 0.897	0.23	heterozygous	223	60	201	31	1	0
0.99 0.969	0.01	heterozygous	225	60	69	35	1	0
0.855	0.04	heterozygous	154	60	138	23	1	0
0.885	0	heterozygous	110	60	89	18	1	0
0.002	0.16	heterozygous	156	60	240	27	1	0
0.888	0.03	heterozygous	225	60	100	36	1	0
0.994		heterozygous	225	60	248	38		

0.969		heterozygous	210	60	267	30		
		heterozygous	194	60	54	30		
		heterozygous	133	60	78	21		
0.478		heterozygous	225	60	55	38		
0.367		heterozygous	137	60	30	27		
0.996		heterozygous	225	60	147	33		
		heterozygous	217	60	72	31		
0.056		heterozygous	160	60	45	27		
0.682	0	heterozygous	214	59	285	29	1	0
0.998	0	heterozygous	225	60	93	32	1	0
0.9	0.7	heterozygous	34	55	182	16	1	0
0.039	1	heterozygous	225	60	178	33	1	0
0.181	0.69 1	heterozygous	207	59	57	37	1	0
0	0.09	heterozygous	219	60	167	29	1	0
	1	heterozygous	225	60	226	31	1	0
0.999	0.02	heterozygous	223	60	169	28	1	0
0.95	0	heterozygous	225	60	56	57	1	0
0.062		heterozygous	225	60	86	49	1	0
0.133	0.21	heterozygous	225	60	462	32	1	0
0.956	0.01	heterozygous	118	60	179	24	1	0
0.956	0.01	heterozygous	102	60	228	22	1	0
0.997		heterozygous	80	60	31	26	1	0
		heterozygous	217	59	165	20	1	0
		heterozygous	114	60	234	26	1	0
		heterozygous	142	60	83	23	1	0
0.998	0.06	heterozygous	189	60	65	37	1	0
0.996	0	heterozygous	225	60	135	33	1	0
1	0	heterozygous	30	60	251	19	9	0
0.828	0.11	heterozygous	73	60	29	21	1	0
0.987	0.03	heterozygous	126	60	72	29	1	0
0.643	0.07	heterozygous	130	60	78	19	3	0
0.905	0	heterozygous	120	60	76	18	23	0
0.027	0.24	heterozygous	103	60	152	20	1	0
0.961	0.02	heterozygous	225	60	171	30	1	0
0.037	0.18	heterozygous	39	60	189	16	1	2
0.992	0.05	heterozygous	88	60	163	18	1	0
	0.01	heterozygous	104	57	139	18	1	0
0.068	0.63	heterozygous	56	60	170	18	3	0
0.905	0	heterozygous	225	60	87	43	23	0
		heterozygous	152	60	88	22		
0.998		heterozygous	192	60	221	26		
0.742		heterozygous	161	60	31	42		
0.338		heterozygous	225	60	123	33		
0		heterozygous	225	60	118	37		
1		heterozygous	175	60	36	53		
0.526		heterozygous	225	60	291	33		
		heterozygous	999	0	11	0		
0.989	0	heterozygous	161	56	49	29	1	0
0.059	0.39	heterozygous	68	59	160	18	1	0

		heterozygous	71	60	123	20	1	0
		heterozygous	50	60	188	18	1	0
0.905	0	heterozygous	211	60	78	28	23	0
1	0	heterozygous	85	60	123	17	1	0
0.787	0.01	heterozygous	210	60	143	28	1	0
0.999	0	heterozygous	138	60	127	20	1	0
0.009	1	heterozygous	189	60	77	25	1	0
0.982	0	heterozygous	161	60	55	25	1	0
0.983	0	heterozygous	206	59	84	27	1	0
0.167		heterozygous	188	59	195	27	1	0
0.928	0	heterozygous	164	60	90	23	15	0
0.01	1	heterozygous	212	59	208	31	1	0
0.014	0.24	heterozygous	213	60	242	29	1	0
		heterozygous	999	999	118	31	1	0
0.71	0.02	heterozygous	133	59	159	23	1	0
0.398	0.4	heterozygous	225	60	117	30	1	0
		heterozygous	217	60	140	20	1	0
1	0	heterozygous	225	60	241	34	3	0
1	0	heterozygous	191	60	117	25	1	0
	0.17	heterozygous	180	60	95	23	1	0
0.016	0.49	heterozygous	211	60	115	26	1	0
0.964	0.2	heterozygous	225	59	74	46	1	0
	0.26	heterozygous	99	60	49	24	1	0
0.997	0	heterozygous	225	60	171	31	1	0
0.001	0.42	heterozygous	186	59	49	39	1	1
0.002	0.58	heterozygous	225	59	133	43	1	0
0.006	0.17	heterozygous	225	60	211	39	1	0
	0.28	heterozygous	188	60	30	37	1	0
		heterozygous	225	60	98	34	1	0
0.991	0.01	heterozygous	225	60	166	33	1	0
0		heterozygous	225	60	97	38	1	0
0.992	0	heterozygous	225	60	52	35	1	0
0.995	0	heterozygous	220	60	101	28	1	0
		heterozygous	225	60	241	36	1	0
1	0	heterozygous	205	59	49	37	1	0
0.985	0.27	heterozygous	125	60	31	45	1	0
0.994	0	heterozygous	225	60	49	39	1	0
1		heterozygous	225	60	114	35	1	0
0.996	0.01	heterozygous	225	59	62	42	1	0
0.928	0	heterozygous	225	59	81	36	15	0
0.012	0.55	heterozygous	71	60	53	17	1	0
		heterozygous	99	60	39	21	1	0
0.064	0.05	heterozygous	85	60	28	21	1	0
0		heterozygous	225	60	39	38	1	0
0.97	0.26	heterozygous	225	60	148	39	1	0
		heterozygous	225	60	73	30	1	0
0.999	1	heterozygous	42	52	121	15	1	0
		heterozygous	122	60	129	11	1	0
0.516	0.34	heterozygous	100	60	177	19	1	0

0.992	0.02	heterozygous	30	60	36	14	1	0
0.905	0	heterozygous	225	60	108	33	23	0
		heterozygous	217	59	195	15	1	0
0.06	0.01	heterozygous	51	60	169	17	1	0
0.753	0.03	heterozygous	106	60	207	21	1	0
0.995	0.11	heterozygous	184	60	79	29	1	0
0.999	0	heterozygous	175	59	90	27	1	0
0.035	0.01	heterozygous	113	60	235	23	1	0
0.363	0.04	heterozygous	98	60	37	22	1	0
0.315	1	heterozygous	222	60	122	28	1	0
1	0	heterozygous	145	60	174	24	1	0
0.975	0	heterozygous	91	60	190	20	1	0
0.814	1	heterozygous	166	60	180	25	1	0
0.005	0.54	heterozygous	155	60	51	25	1	0
0.184	0.74	heterozygous	194	60	90	29	1	0
1	0.23	heterozygous	116	60	139	22	1	0
0.023	0.47	heterozygous	182	60	132	25	1	0
0.726	0	heterozygous	203	60	129	26	1	0
0.933	0.53	heterozygous	123	54	95	19	1	0
0.002	0.07	heterozygous	138	60	79	23	1	0
0	0.19 0.02	heterozygous	73	60	43	23	1	0
0.928	0	heterozygous	196	60	127	25	15	0
0.996	0	heterozygous	137	60	419	23	1	0
0.014	0.28	heterozygous	156	60	250	26	1	0
0.944	0.1	heterozygous	49	60	11	27	2	0
0.806	0.32	heterozygous	126	60	155	23	3	3
0.928	0	heterozygous	87	60	80	16	15	0
0	0.76	heterozygous	225	60	82	32	1	0
0.012	0.44	heterozygous	225	60	264	32	1	0
0	0.58	heterozygous	221	60	144	28	1	0
0.005	1	heterozygous	225	55	99	35	1	0
1	0	heterozygous	225	60	249	38	3	0
0.806	0.17	heterozygous	225	60	161	35	1	0
0.974	0	heterozygous	153	59	28	36	1	0
0.033	0.04 0.15	heterozygous	225	60	164	39	1	1
0.02	1	heterozygous	38	60	22	18	1	1
0.001	1	heterozygous	225	60	199	34	1	0
0.003		heterozygous	225	60	186	31	1	0
0.995 1	0	heterozygous	225	60	265	34	1	0
0.326	0	heterozygous	225	59	127	37	1	0
		heterozygous	119	60	77	35	1	0
0.971	0.23	heterozygous	207	60	243	29	1	1
0.077	0.35	heterozygous	34	60	27	15	1	0
0.997	0	heterozygous	225	60	231	30	1	0
0.006	0.59	heterozygous	30	54	12	25	1	1
0.354	0	heterozygous	37	58	13	23	2	0
	0.84	heterozygous	34	60	15	20	2	1
0.905	0	heterozygous	225	60	73	37	23	0
0	0.4	heterozygous	225	60	70	61	1	0

0.052	0.14	heterozygous	141	60	53	25	1	0
0	0.63	heterozygous	42	58	12	25	1	1
0.173	0.4	heterozygous	34	60	16	19	1	0
0.627	0.07	heterozygous	112	60	124	19	1	0
	0.17	heterozygous	74	60	12	33	1	1
		heterozygous	217	59	166	37	1	0
0.974	0.02	heterozygous	185	60	329	26	1	0
0.997	0	heterozygous	142	60	113	22	1	0
		heterozygous	225	59	273	31	1	0
0.192	0.35	heterozygous	66	60	246	22	1	0
0.081	0.49	heterozygous	44	60	306	21	1	0
0.015	0.48	heterozygous	42	60	61	13	1	0
0.996	0.07	heterozygous	55	60	103	15	1	0
		heterozygous	225	60	140	30	1	0
0.905	0	heterozygous	225	60	122	29	23	0
0.477	0.08	heterozygous	34	60	48	15	1	0
		heterozygous	126	60	112	21	1	0
0.994	0	heterozygous	225	60	118	33	1	0
0.08	0.15	heterozygous	220	60	236	29	1	0
		heterozygous	119	60	250	28	1	0
0.703	0.01	heterozygous	225	60	60	32	1	0
0.001	1	heterozygous	218	60	216	29	1	0
0.147	0.27	heterozygous	73	60	30	20	1	3
0.928	0	heterozygous	225	60	130	32	15	0
0.987	0	heterozygous	225	60	484	37	1	0
0.988	0.06	heterozygous	225	60	134	34	1	0
0.723	0.04	heterozygous	225	60	268	36	1	0
	0.01	heterozygous	201	60	75	39	1	0
	0.31	heterozygous	225	60	329	35	1	0
0.001	0.12	heterozygous	225	60	41	41	1	0
0.882	0	heterozygous	208	59	84	36	1	0
		heterozygous	214	60	141	27	1	0
		heterozygous	210	60	166	29	1	0
0.018		heterozygous	213	60	289	29	1	0
	0.83	heterozygous	175	60	58	29	1	0
0.595	0 0.46	heterozygous	208	60	209	28	1	0
0.688		heterozygous	225	60	176	35	1	0
	0.01	heterozygous	216	60	106	28	1	0
0.741	0.54	heterozygous	97	60	258	22	1	0
0.928	0	heterozygous	225	60	120	28	15	0
0.995	0.05	heterozygous	225	60	256	37	1	0
0.957	0	heterozygous	225	56	58	38	1	0
0.288	0.17	heterozygous	130	60	143	20	1	0
0.883	0	heterozygous	62	60	144	15	1	0
0.092		heterozygous	225	60	81	33	1	0
0.413	0	heterozygous	152	60	82	22	1	0
0.004		heterozygous	120	60	137	19	1	0
0.256	0.23	heterozygous	126	60	18	39	1	2
0.905	0	heterozygous	225	60	111	32	23	0

0.017	0.04	heterozygous	135	60	92	34	1	0
		heterozygous	217	60	73	29	1	0
0	1	heterozygous	221	60	228	30	1	0
		heterozygous	48	57	84	14	1	0
0.896	0.1	heterozygous	225	60	143	49	1	0
		heterozygous	225	60	57	47	1	1
0.998	0.27	heterozygous	124	60	43	30	1	0
0.629	0	heterozygous	210	60	48	38	1	0
0.928	0	heterozygous	225	60	117	36	15	0
0.81		heterozygous	46	60	83	17	1	0
	0	heterozygous	170	59	124	23	1	0
0.078	0.57	heterozygous	140	60	39	26	1	0
0.196	0	heterozygous	197	60	65	28	1	0
0.022	0.03	heterozygous	225	60	265	30	3	0
0.905	0	heterozygous	140	60	99	20	23	0
		heterozygous	999	999	101	22	1	0
0.892	0.01	heterozygous	225	60	180	29	1	0
0.009	0.46	heterozygous	157	60	95	27	1	0
0.995	0	heterozygous	99	60	80	19	1	0
		heterozygous	101	60	42	24	1	0
0.525	0.25	heterozygous	137	60	340	25	1	0
0.905	0	heterozygous	147	60	115	22	23	0
		heterozygous	217	60	103	30	1	0
0.957	0.12	heterozygous	118	60	78	19	1	0
0.042	0.03	heterozygous	199	60	103	29	1	0
0.235	0.06	heterozygous	82	60	62	18	1	0
0.001	0.64 0.54	heterozygous	69	60	171	18	1	0
1	0	heterozygous	42	60	122	15	1	0
0.971	0.35	heterozygous	37	59	136	15	1	0
		heterozygous	185	60	255	28	1	0
0.031	0.23	heterozygous	48	60	126	15	1	0
0.062	0.25	heterozygous	225	60	122	29	1	0
1	0	heterozygous	62	60	36	17	1	0
0.968	0.1	heterozygous	117	60	372	22	1	0
0.002	1	heterozygous	69	60	103	16	1	0
0.892	0	heterozygous	225	60	367	33	1	0
0.173	0	heterozygous	154	60	162	25	1	0
0.997	0	heterozygous	166	27	63	48	1	0
1	0	heterozygous	225	60	252	38	6	0
	0.11	heterozygous	187	60	74	27	1	0
	0	heterozygous	85	60	108	17	1	0
0.832	0.12	heterozygous	173	60	49	31	1	0
0 0.001	0.19	heterozygous	225	60	267	33	1	0
0.192	0.51	heterozygous	225	60	165	30	1	0
0.999	0	heterozygous	223	60	150	31	1	0
		heterozygous	999	999	38	29	1	0
0.064	0.04	heterozygous	48	60	32	16	1	0
0.475	0.28	heterozygous	33	58	29	17	1	0
0.986	0	heterozygous	225	60	180	30	1	0

0.001	0.47	heterozygous	107	60	78	19	1	0
0.056	0.19	heterozygous	199	60	144	26	1	0
	0	heterozygous	225	60	141	33	1	0
0.797	0.55	heterozygous	72	60	177	18	1	0
0.9	0	heterozygous	211	60	258	29	1	0
0.081	0.08	heterozygous	225	60	72	33	1	0
0.002		heterozygous	225	60	179	29	1	0
0.974	0	heterozygous	211	60	72	28	1	0
0.999	0	heterozygous	225	60	113	31	1	0
0.994	0	heterozygous	225	59	107	30	1	0
0.403	0.56	heterozygous	144	60	34	29	1	0
0.089	0.15	heterozygous	225	56	111	32	1	0
0	1	heterozygous	221	60	97	28	1	0
0.999	0	heterozygous	225	60	199	32	1	0
0.007	0.21	heterozygous	203	60	180	28	1	0
0.144	0.03	heterozygous	171	60	44	34	1	0
0.991	0	heterozygous	172	59	76	32	1	0
0.094	0.25	heterozygous	225	60	192	31	1	0
0.026	0.36	heterozygous	75	60	38	21	1	0
0.132	1	heterozygous	141	60	73	29	1	0
	0	heterozygous	164	60	410	28	1	0
		heterozygous	999	999	96	25	1	0
0.977	0.07	heterozygous	225	60	202	36	1	0
	0.66	heterozygous	211	60	220	29	1	0
	0.06	heterozygous	111	60	142	20	1	0
	0.43	heterozygous	34	59	16	19	1	0
0.996	0	heterozygous	142	60	136	20	1	0
0.001	1	heterozygous	58	60	8	38	1	0
0.132	0.04	heterozygous	50	60	10	30	1	0
	0.48	heterozygous	85	60	157	17	1	0
0.998		heterozygous	31	60	17	18	1	0
0.305	0.01	heterozygous	44	58	10	30	2	0
	0.12	heterozygous	59	60	50	16	1	0
	0.02	heterozygous	40	60	35	14	1	0
0.623	0.1	heterozygous	35	55	26	15	1	0
	0.56	heterozygous	225	59	117	37	1	0
0.008	0.34	heterozygous	225	60	84	29	1	0
0.945	0.02	heterozygous	33	60	25	16	1	0
0.478	0.01	heterozygous	40	60	14	21	1	0
0.694	0.57	heterozygous	88	60	18	28	1	0
		heterozygous	37	60	15	20	1	0
	1	heterozygous	33	58	15	20	1	0
0.997	0.01	heterozygous	39	60	13	23	1	0
0.005	0.16	heterozygous	54	60	9	33	1	1
0.196	0.2	heterozygous	30	60	17	18	1	0
0.969	0.12	heterozygous	42	60	12	25	1	0
0.423	0.01	heterozygous	49	60	11	27	1	0
0.344	0.03	heterozygous	162	60	149	23	1	0
0.001	0.83	heterozygous	34	60	16	19	1	0

0.226	0.02	heterozygous	34	60	16	19	2	1
0.981	0.03	heterozygous	34	60	16	19	1	0
0.001	1	heterozygous	34	60	15	20	1	0
0.258	0.14	heterozygous	35	60	19	21	1	0
0.009	0.32	heterozygous	33	56	15	20	1	2
0.058	0.02	heterozygous	48	60	31	16	1	0
0.006	0.13	heterozygous	151	60	206	23	1	0
	1	heterozygous	101	60	73	19	1	0
0.736	0.01	heterozygous	153	59	41	27	1	0
		heterozygous	40	60	14	21	1	0
0.574	0.2	heterozygous	30	60	17	18	1	0
0.999	0.12	heterozygous	193	60	121	24	1	0
0.841	0	heterozygous	176	60	109	25	1	0
0.927	0.01	heterozygous	31	60	17	18	1	1
1	0	heterozygous	31	60	16	19	2	0
		heterozygous	49	57	8	38	1	0
0.27	0.49	heterozygous	139	60	93	20	1	0
		heterozygous	33	60	16	19	1	0
0.997		heterozygous	134	60	217	24	1	0
0	0.58	heterozygous	225	60	187	30	1	0
	0.38	heterozygous	85	59	78	17	1	0
0.358	0.96	heterozygous	34	60	16	19	1	0
0.61	0.03	heterozygous	38	60	10	30	1	1
0.008	0.99	heterozygous	43	59	72	19	1	0
0.642		heterozygous	38	60	8	38	2	2
0.952		heterozygous	58	59	29	17	1	0
0.373	0	heterozygous	100	60	53	19	1	0
	0.01	heterozygous	130	59	33	27	1	0
0.006	0.5	heterozygous	34	60	37	14	1	0
1	0	heterozygous	55	60	20	20	1	0
0.001	0.02	heterozygous	225	60	51	49	1	0
0.814	0.55	heterozygous	221	60	477	31	1	0
0.997	0	heterozygous	180	60	374	31	1	2
0	0.36	heterozygous	76	60	274	20	1	0
0.998	0	heterozygous	34	60	282	21	1	0
1	0	heterozygous	225	60	232	33	1	0
0.905	0	heterozygous	225	60	103	31	23	0
0.921		heterozygous	225	60	302	46	1	0
0.055	0.24	heterozygous	211	60	115	29	1	0
0.943	0	heterozygous	200	60	60	30	1	0
0.047	0.01	heterozygous	57	60	38	16	1	0
0.046	0.51	heterozygous	101	60	129	19	1	0
0.07	0.13	heterozygous	79	60	148	17	1	0
0	0.56 0.4	heterozygous	118	60	139	22	1	0
0.999	0	heterozygous	172	60	88	23	1	0
0.643	0.07	heterozygous	225	60	99	34	3	0
0.905	0	heterozygous	225	60	97	34	23	0
0.992	0.01	heterozygous	126	60	207	22	1	0
	0.85	heterozygous	217	60	108	26	1	0

		heterozygous	217	59	149	34	1	0
0.893		heterozygous	225	60	279	38	1	1
	0.71	heterozygous	177	60	168	24	1	0
0.571	0.14	heterozygous	225	60	96	33	1	0
0.006	0.49	heterozygous	125	60	59	20	1	0
0.033	0.1	heterozygous	225	60	182	35	1	0
0.209 0.281	0.02	heterozygous	197	60	128	30	1	0
0.088	0.12	heterozygous	225	60	85	29	1	0
0.905	0	heterozygous	225	60	94	52	23	0
		heterozygous	217	60	86	34	1	0
0.853	0.04	heterozygous	169	60	185	24	1	0
0.001	0.46	heterozygous	223	60	306	32	1	0
		heterozygous	37	57	73	15	1	0
0.075	0.11	heterozygous	46	52	17	24	2	1
0.125		heterozygous	225	59	51	45	1	0
0.995	0	heterozygous	225	60	124	33	1	0
0.869	0.06	heterozygous	225	60	131	34	1	0
		heterozygous	33	56	86	17	1	0
0.019	0.08	heterozygous	205	60	247	30	1	0
		heterozygous	113	60	47	32	1	0
1	0	heterozygous	126	60	258	24	1	0
0.001	1	heterozygous	208	59	44	34	1	0
		heterozygous	97	60	21	38	1	0
0.997	0	heterozygous	225	60	106	40	1	0
0.038	0.41	heterozygous	32	60	315	18	1	0
1	0	heterozygous	144	60	121	21	1	0
0.998	0	heterozygous	191	60	108	25	1	0
0.019	0.32	heterozygous	99	60	223	22	1	0
0.947		heterozygous	112	60	188	22	1	0
0.457	0.01	heterozygous	151	60	448	27	1	0
	0.01	heterozygous	109	60	222	22	1	0
		heterozygous	217	59	86	26	1	0
1	0	heterozygous	207	60	67	28	1	0
0.001	1	heterozygous	209	60	119	28	1	0
0.999	0	heterozygous	72	60	36	81	1	0
	1	heterozygous	225	60	58	53	1	0
	1	heterozygous	86	60	33	21	1	0
0.972	0	heterozygous	225	60	268	51	1	0
0.96	0.01	heterozygous	225	60	236	49	1	0
		heterozygous	140	59	72	21	1	0
0	0.33	heterozygous	205	59	90	39	1	0
0	1	heterozygous	94	60	59	81	1	0
0.998	0.11	heterozygous	159	60	88	77	1	0
0.893	0	heterozygous	225	60	188	39	1	0
0.098	0.35	heterozygous	95	60	67	82	1	0
0.482	0.02	heterozygous	40	60	13	23	1	3
0	0.46	heterozygous	225	60	84	40	1	0
0.173	0.99	heterozygous	187	52	146	93	1	0
0.849	0	heterozygous	119	60	60	78	1	0

0.451	0.01	heterozygous	113	60	300	76	1	0
	0.76	heterozygous	185	59	216	27	1	0
0.956	0	heterozygous	195	60	108	27	1	0
0.003	1	heterozygous	225	60	147	38	1	0
0.023	0.61	heterozygous	200	60	155	35	1	0
		heterozygous	999	999	25	24	1	0
0.47	0.62	heterozygous	164	60	201	25	1	0
0.93	0	heterozygous	143	60	161	23	1	0
0.057	0.61	heterozygous	225	60	173	36	1	0
	0.39	heterozygous	146	59	26	35	1	2
0.001	0.6	heterozygous	32	59	27	15	1	0
0.922	0.15	heterozygous	205	60	110	29	1	0
1	0	heterozygous	186	60	165	26	1	0
0.015	0.08	heterozygous	225	60	138	36	1	0
0.001	0.06	heterozygous	225	60	141	30	1	0
		heterozygous	61	60	18	28	1	0
0.063	0.28	heterozygous	199	60	113	33	1	0
		heterozygous	84	55	81	23	1	0
0.961	0.01	heterozygous	225	60	391	33	1	0
0.905	0	heterozygous	225	60	86	31	23	0
0.904	0.17	heterozygous	93	60	53	28	1	0
0.948	0.01	heterozygous	115	60	104	21	1	0
0.409	0.08	heterozygous	98	60	19	32	1	0
		heterozygous	36	60	86	13	1	0
0.988	0.26	heterozygous	96	60	166	19	1	0
0.007	0.19	heterozygous	92	60	22	36	1	0
0.002	0.83	heterozygous	89	60	75	29	1	0
0.987	1	heterozygous	106	60	198	21	1	0
0.014	0.34	heterozygous	219	60	96	28	1	0
0.964	0.3	heterozygous	225	60	133	32	1	0
0.999	0.02	heterozygous	177	60	62	29	1	0
	0.39	heterozygous	225	59	151	32	1	1
0.018	0.11	heterozygous	225	60	147	31	1	0
0.961	0.04	heterozygous	98	60	191	20	1	0
0.997		heterozygous	194					
0.212		heterozygous	220					
0.024		heterozygous	137					
0.085		heterozygous	190					
0.053		heterozygous	154					
0.36		heterozygous	225					
0.359		heterozygous	225					
0.518		heterozygous	79					
1		heterozygous	157					
1		heterozygous	150					
0.289		heterozygous	175					
0.361		heterozygous	150					
0.003		heterozygous	188					
0.494		heterozygous	225					
0.827		heterozygous	142					

0.997		heterozygous	146					
0.982		heterozygous	186					
		heterozygous	38					
0.02		heterozygous	225					
0.001		heterozygous	120					
0.003		heterozygous	225					
0.012		heterozygous	59					
0.374		heterozygous	225					
0.002		heterozygous	225					
0.012		heterozygous	225					
0.001		heterozygous	142					
0.002		heterozygous	225					
0.025		heterozygous	225					
0.73		heterozygous	191					
0.998		heterozygous	225					
0.986		heterozygous	209					
0.973		heterozygous	225					
0.942		heterozygous	90					
		heterozygous	33					
		heterozygous	999					
		heterozygous	105					
0.52		heterozygous	116					
0.905		heterozygous	225					
1		heterozygous	38					
		heterozygous	35					

Supplemental Table 2. Canonical pathway analysis by Gene Set Enrichment Analysis including all the somatic mutations observed in 99 adrenocortical adenomas (n=605 genes associated with Gene Ontology terms)

Set Name [number of genes]	**Description**	**Genes in overlap**	**p-value**	**FDR q-value**
KEGG calcium signaling pathway [178]	Calcium signaling pathway	16	$2.33\ e^{-9}$	$1.55\ e^{-6}$
REACTOME collagen formation [58]	Genes involved in collagen formation	10	$4.37\ e^{-9}$	$1.94\ e^{-6}$
REACTOME extracellular matrix organization [87]	Genes involved in extracellular matrix organization	11	$2.17\ e^{-8}$	$7.21\ e^{-6}$
KEGG MAPK signaling pathway [267]	MAPK signaling pathway	17	$1.26\ e^{-7}$	$2.39\ e^{-5}$
REACTOME developmental biology [396]	Genes involved in developmental biology	20	$4.28e^{-7}$	$5.69e^{-5}$

FDR: false discovery rate.

Supplemental Table 3. Gene family analysis by Gene Set Enrichment Analysis including all the somatic mutations observed in 99 adrenocortical adenomas (n=605 genes associated with Gene Ontology terms)

Cytokines and growth factors	Transcription factors	Protein kinases	Cell differentiation markers	Translocated cancer genes	Oncogenes	Tumor suppressor genes
C5 *FGF13* *FGF2* *IL36B* *INHA* *NDP* *OXT* *VGF*	*AFF1, ARID1B* *ARNTL, ASH1L* *ATRX, BCL3,* *CHD6, CREB1* *CREBBP* *CTNNB1* *CUX1, DIDO1* *DPF3, E2F2* *E2F3, ELK4* *ERG, ESRRB* *ETV7, FOXA2* *HEY2, HIRA* *HIVEP1* *IFT172* *IRX1, IRX5* *MECOM* *MED12, MITF,* *NFYC, OLIG1,* *PAX4, PCGF3* *PHRF1,* *PRDM4* *RUNX3* *SF1, SIX4* *SOX15* *SREBF1* *TAF4, TBX18* *TFAP2C* *TFDP3, TP53* *TP53I13* *TRIM26* *TRIM33* *TSHZ2, VENTX* *ZAR1, ZHX1* *ZHX3, ZIC5* *ZNF197* *ZNF205* *ZNF208* *ZNF259* *ZNF35* *ZSCAN12*	*DAPK1* *MAP2K2* *MAST1* *MAST2* *MERTK* *MKNK2* *MYLK2* *OBSCN* *PRKACA* *PRKD1* *SBK1* *TAF1L* *TRIM33* *TRPM7* *TRRAP* *TTBK1*	*CD84* *CLEC4M* *CSF2RB* *MCAM* *MFI2* *MME* *PSG1* *PTPRC* *PVRL2* *TNFRSF13C*	*AFF1* *BCL3* *CREB1* *CREBBP* *CTNNB1* *ELK4* *ERG* *MECOM* *MYH9* *PRKAR1A* *SEPT6* *TRIM33*	*AFF1* *BCL3* *CARD11* *CREB1* *CREBBP* *CTNNB1* *ELK4* *ERG* *GNAS* *MECOM* *MITF* *MYH9* *SEPT6* *TRIM33*	*APC* *CDC73* *DDB2* *TP53*

Supplemental Table 4. Patients´ classification according to the known or potential functional consequences of the most recurrent somatic mutations.

Group	**Gene**	**Number of patients**
Wnt/beta-catenin	*CTNNB1*	23
	CTNNB1 + PCDHx	13
	CTNNB1 + CDHx	2
	CTNNB1 + APC	1
	PCDHx	3
	APC2	1
	PKP2	1
cAMP/PKA	*GNAS*	8
	PRKACA	2
	PRKACA + ADCY3	1
	PRKAR1A	1
	GRM3	1
	GRM4+ CREBBP	1
	GRM6	1
	CREB1	1
Ca^{2+}-dependent signaling	*RYR1*	2
	RYR3	1
	RYR3 + GRIA2	1
	RYR2 + CACNA1C	1
	CACNA1E	1
	CACNG8	1
	GRIA1	1
	GRID1	1
	GRIK2	1
	GRIN1	1
	GRIN3B	1
	GRIP1	1

PCDHx: genes of the protocadherin superfamily, CDHx: genes of the cadherin superfamily, PKA: protein kinase A.

Supplemental Table 5. General characteristics, clinical, and hormonal data of patients classified according to the potential functional consequences of the most recurrent somatic mutations.

	no Wnt/β-catenin mutations (n=55)	**Wnt/β-catenin mutations (n=44)**	**P value**		**no cAMP-PKA mutations (n=83)**	**cAMP-PKA mutations (n=16)**	**P value**		**no Ca^{++}-channels mutations (n=86)**	**Ca^{++}-channels mutations (n=13)**	**P value**
General characteristics											
Age (yrs)	45.0 (35.0-60.0)	57.0 (51.0-67.0)	0.001		55.0 (42.8-63.0)	40.0 (35.0-45.0)	0.009		52.0 (39.0-62.3)	55.0 (47.0-60.5)	0.424
Sex (M/F)	17/37	12/32	0.665		29/53	0/16	0.002		24/61	5/8	0.518
Diagnosis (EIA/SCS/CS)	11/15/29	14/20/10	0.010		25/32/26	0/3/13	0.001		22/28/36	3/7/3	0.288
Number of mutations	3.0 (1.0-8.0)	7.5 (5.0-11.0)	<0.001		5.0 (2.0-10.0)	8.0 (6.0-10.5)	0.060		4.5 (1.8-9.0)	10.0 (8.0-13.5)	0.001
Clinical and hormonal data											
Tumor diameter (mm)	35.0 (27.5-40.0)	43.0 (35.0-51.5)	0.001		39.5 (30.0-48.0)	35.0 (29.5-46.3)	0.518		36.0 (30.0-48.0)	43.0 (40.0-48.0)	0.137
Cortisol after DST (µg/dL)	11.6 (3.1-18.3)	2.9 (2.0-7.0)	0.024		3.2 (2.2-12.8)	15.1 (13.5-20.3)	0.007		4.5 (2.3-15.4)	3.2 (2.9-7.5)	0.699
ACTH (pg/mL)	5.0 (2.0-7.3)	6.2 (3.0-13.7)	0.225		5.0 (2.0-10.3)	3.5 (2.0-6.0)	0.321		5.0 (2.0-9.0)	5.0 (3.9-10.0)	0.512
UFC ULN>2 (n/total)	22/32	10/25	0.036		24/48	8/9	0.063		27/48	5/9	1.000
Midnight cortisol ULN>2 (n/total)	7/9	6/15	0.105		12/22	1/2	1.000		11/21	2/3	1.000

Data are expressed as median with interquartile range in parenthesis or frequencies. PKA: protein kinase A, EIA: endocrine inactive adenoma, SCS: subclinical Cushing´s syndrome, CS: Cushing´s syndrome, DST: 1-mg dexamethasone suppression test, UFC: urinary free cortisol, ULN upper limit of normal.

Supplemental Table 6. Integrative comparison analysis including adrenocortical adenomas and carcinomas investigated by whole-exome sequencing (present study and previous literature).

					cAMP signalling			Wnt/beta catenin signalling			Calcium signalling			Others	
Paper	**N**	**CS/SCS**	***PRKACA* mutated**	***PRKACA* WT**	***GNAS***	***PRKAR1A***	**mGluRs**	***CTNNB1***	***APC***	**PCDH family**	**RYR family**	**iGluRs**	**Ca channels**	***TP53***	***RB1***
CPA	**143**	**100/43**	**49 (35%)**	**94 (65%)**	**13 (14%)**	**2 (2%)**	**4 (4%)**	**32 (34%)**	**2 (2%)**	**12 (13%)**	**3 (3%)**	**8 (9%)**	**2 (2%)**	**3 (3%)**	**2 (2%)**
literature[2]	69	61/8	46 (67%)	23 (33%)	5 (22%)	1 (4%)	1 (4%)	8 (35%)	1 (4%)	3 (9%)	0	1 (4%)	0	3 (13%)	2 (9%)
present study	74	39/35	3[1]	71[1]	8 (11%)	1 (1%)	3 (4%)	26 (35%)	1 (1%)	9 (12%)	3 (4%)	7 (9%)	2 (3%)	0	0
EIA present study	**25**		**0**	**25**	**0**	**0**	**0**	**13 (52%)**	**0**	**6 (24%)**	**3 (12%)**	**0**	**1 (4%)**	**1 (4%)**	**0**
ACC literature[3]	**176**		**0**	**176**	**1 (0.6%)**	**8 (5%)**	**6 (3.5%)**	**25 (15%)**	**4 (2%)**	**26 (15%)**	**6 (3%)**	**13 (7%)**	**6 (3%)**	**37 (22%)**	**9 (5%)**

Percentages are calculated referring to *PRKACA* p.L206R WT cases. CS: Cushing´s syndrome, SCS: Subclinical Cushing´s syndrome, CPA: cortisol-producing adenomas, EIA: endocrine inactive adenomas, ACC: adrenocortical carcinomas, mGluRs: metabotropic glutamate receptors, iGluRs: ionotropic glutamate receptors, NA: not applicable.

[1] Pre-screening for p.Arg206Leu PRKACA mutation. Three new *PRKACA* mutations detected.

[2] Data collected from previous studies (9, 10, 12, 13)

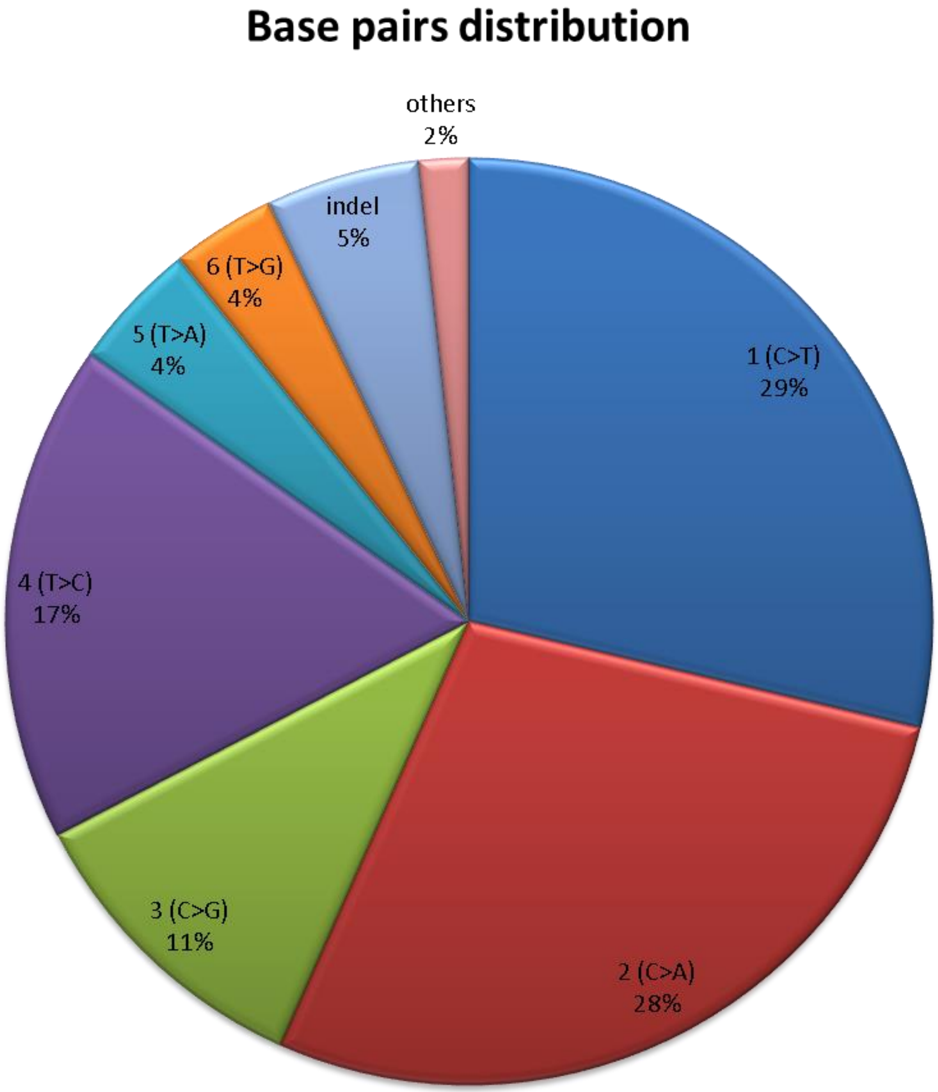
[3] Data collected from previous studies (12, 20, 21)

Supplemental Table 7. Canonical pathway analysis by Gene Set Enrichment Analysis (REACTOME and KEGG gene sets) including all the somatic mutations observed in 169 adrenocortical adenomas (99 from the present study and 79 from previous literature), including 144 cortisol-producing adenomas (CPA) and 25 endocrine inactive adenomas.

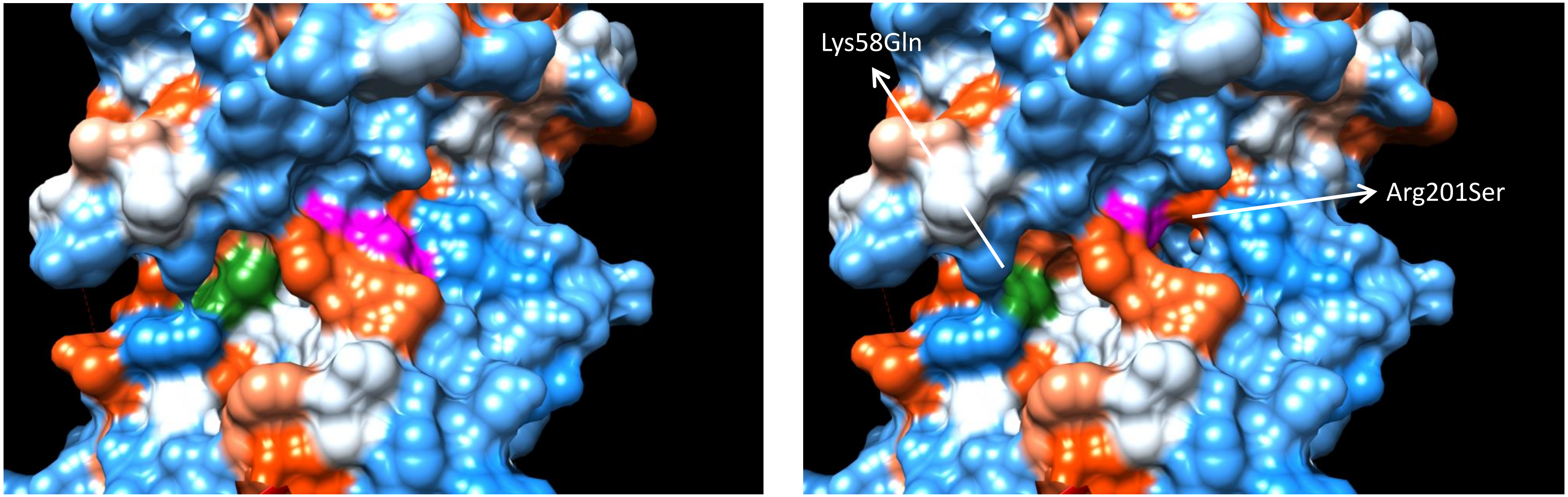
Set Name	Description	Genes in Overlap	p-value	FDR q-value
All ACA (n=169)				
KEGG	**Pathways in cancer**	28	1.55 e^{-10}	1.34 e^{-7}
KEGG	**Calcium signaling pathway**	19	3.59 e^{-9}	1.54 e^{-6}
REACTOME	**Genes involved in Collagen formation**	11	1.78 e^{-8}	5.11 e^{-6}
REACTOME	Genes involved in Developmental Biology	27	4.03 e^{-8}	8.67 e^{-6}
KEGG	MAPK signaling pathway	21	1.21 e^{-7}	2.01 e^{-5}
REACTOME	Genes involved in Metabolism of lipids and lipoproteins	29	1.57 e^{-7}	2.01 e^{-5}
REACTOME	**Genes involved in Extracellular matrix organization**	12	1.63 e^{-7}	2.01 e^{-5}
KEGG	Focal adhesion	17	6.9 e^{-7}	7.15 e^{-5}
REACTOME	Genes involved in Axon guidance	19	8.52 e^{-7}	7.15 e^{-5}
KEGG	ECM-receptor interaction	11	9.09 e^{-7}	7.15 e^{-5}
CPA PRKACA WT (n=94)				
REACTOME	**Genes involved in Collagen formation**	9	3.87 e^{-8}	2.57 e^{-5}
REACTOME	**Genes involved in Extracellular matrix organization**	9	1.36 e^{-6}	3.61 e^{-4}
KEGG	Neuroactive ligand-receptor interaction	15	1.82 e^{-6}	4.04 e^{-4}
KEGG	**Calcium signaling pathway**	12	2.51 e^{-6}	4.77 e^{-4}
KEGG	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	8	4.62 e^{-6}	6.82 e^{-4}
REACTOME	Genes involved in Signaling by GPCR	29	5.34 e^{-6}	7.1 e^{-4}
KEGG	**Pathways in cancer**	15	1.72 e^{-5}	1.78 e^{-3}

REACTOME	Genes involved in Signaling by FGFR in disease	9	$3.04\ e^{-5}$	$2.52\ e^{-3}$
REACTOME	Genes involved in Developmental Biology	16	$4.1\ e^{-5}$	$3.21\ e^{-3}$
REACTOME	Genes involved in Apoptotic execution phase	6	$5.37\ e^{-5}$	$3.76\ e^{-3}$
CPA PRKACA mutated (n=50)				
KEGG	Steroid hormone biosynthesis	5	$1.4\ e^{-5}$	$5.1\ e^{-3}$
REACTOME	Genes involved in Metabolism of lipids and lipoproteins	11	$8.48\ e^{-5}$	$2.25\ e^{-2}$
KEGG	**Pathways in cancer**	9	$1.01\ e^{-4}$	$2.25\ e^{-2}$
REACTOME	Genes involved in L1CAM interactions	5	$1.22\ e^{-4}$	$2.32\ e^{-2}$
FDR: false discovery rate.				

Supplemetal Figure 1



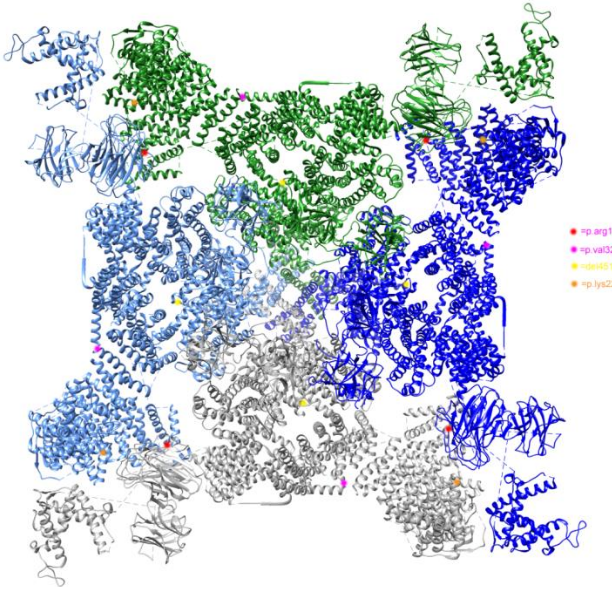
Supplemental Figure 2

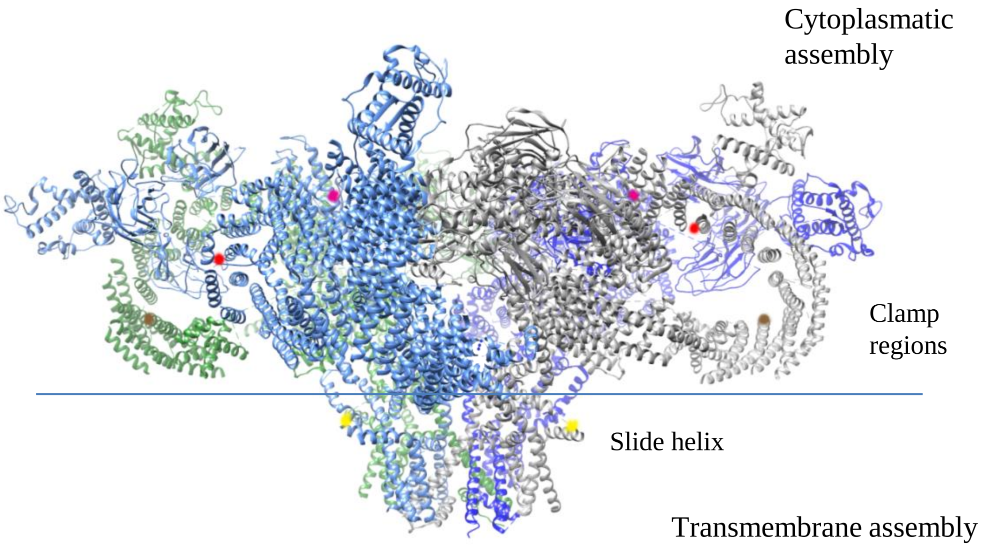


A) GNAS 15 WT

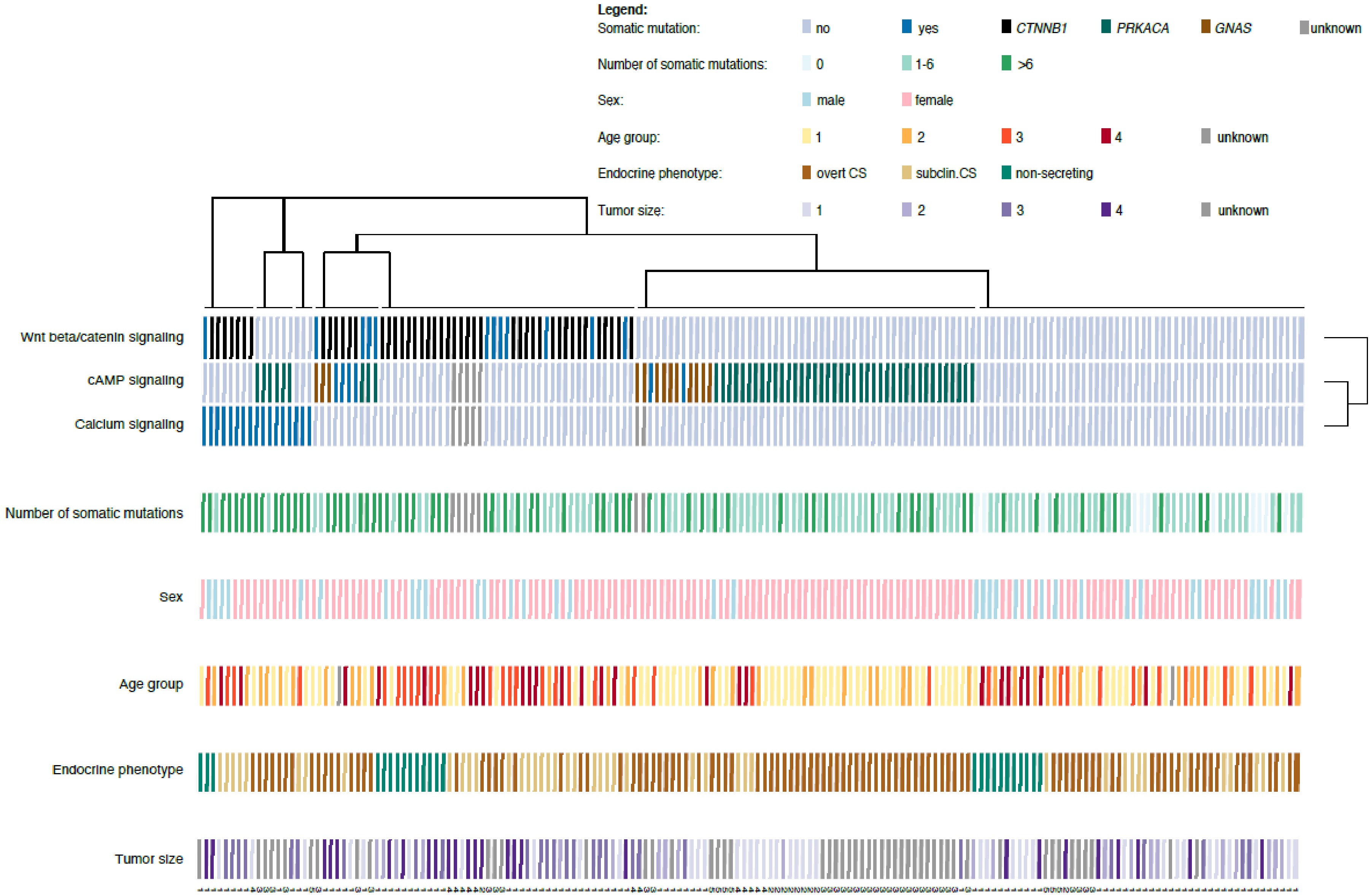
B) GNAS 15

Supplemental Figure 3

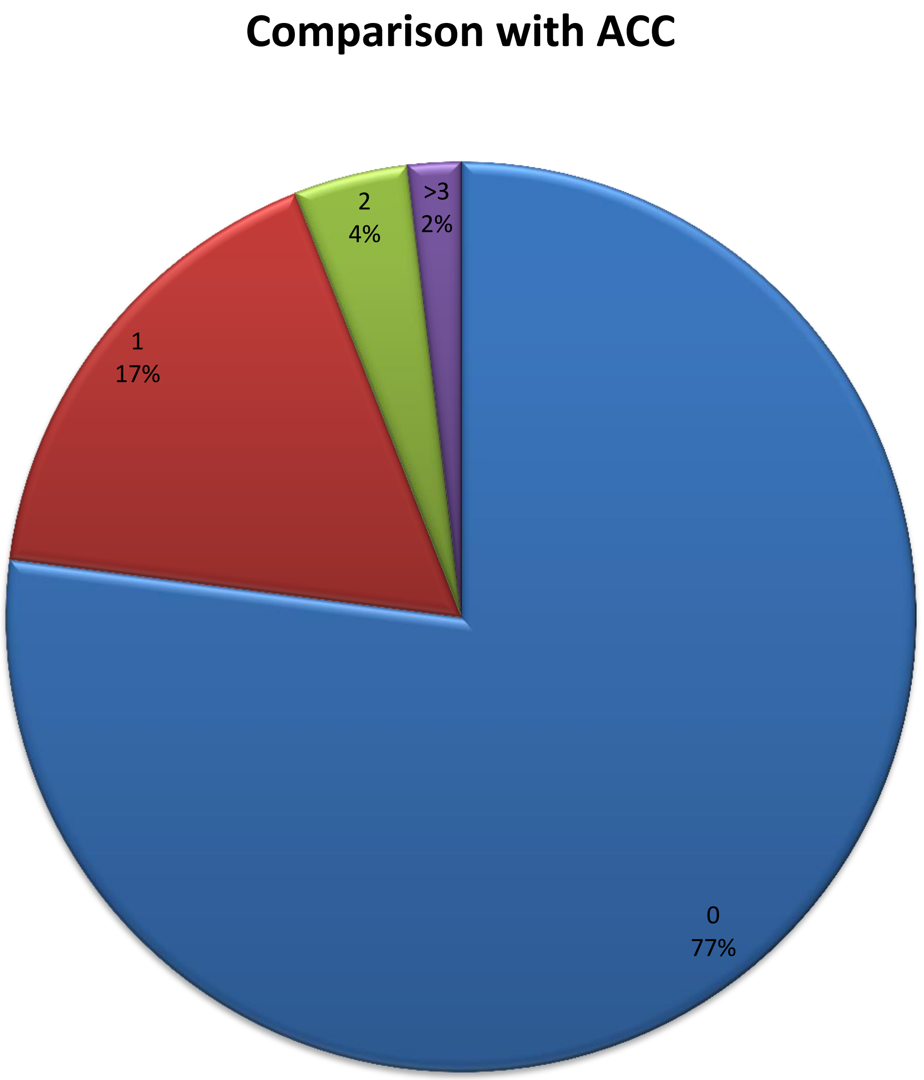




Supplemental Figure 4



Supplemental Figure 5



Supplemental Figure legend

Supplemental Figure 1. Distribution of base pairs substitutions among the detected somatic genetic alterations (n=706). The C:G>T:A transition (29% of cases) and the C:G>A:T transversion (28% of cases) were the most frequent, consistent with most cancer types.

Supplemental Figure 2. *In silico* analysis of the 3D structure change of the somatic mutations at the GNAS complex locus (variant 15, hydrophobic visualization). a) wild type; b) mutation in *GNAS* p.Lys58Gln (green) is conformational near the critical position 201 (i.e. where the known mutation p. Arg201His is located, purple).

Supplemental Figure 3. *In silico* analysis of the 3D structure change of the somatic mutations at the three members of the RYR family (chimera). The mutations in *RYR1* (p.Arg1469Gly, red, and p.Val3218Leu, purple) and *RYR2* (p.Lys2264Asn, orange) are all in the clamps regions of the cytoplasmic assembly, while the mutation in *RYR3* (del4516, yellow) was in the sliding helix region between the transmembrane and cytoplasmic assemblies.

Supplemental Figure 4. Heat map of the genetic data obtained with exome-sequencing on adrenocortical adenomas available from the present study and in the literature are included (n=168 samples). The most recurrent somatic mutations are classified according to their known or potential biological consequences, similarly to the classification showed in Figure 3: mutations in genes encoding components of Wnt-β catenin pathway, those in genes encoding members of the cAMP/PKA pathway, and mutations in genes involved in Ca^{2+} signaling. The relationship with the total number of somatic mutations and clinical parameter is also shown.

Supplemental Figure 5. Comparison between present findings on adrenocortical adenomas and genetic data available in the literature in 176 ACC (12, 20, 21). Represented are the somatic mutations reported only in ACAs (77%), those with at least one somatic mutation reported in ACAs and ACCs.

In particular, 17% of somatic mutations in ACAs were identified in at least one ACC sample, and 6% in two or more ACC samples.