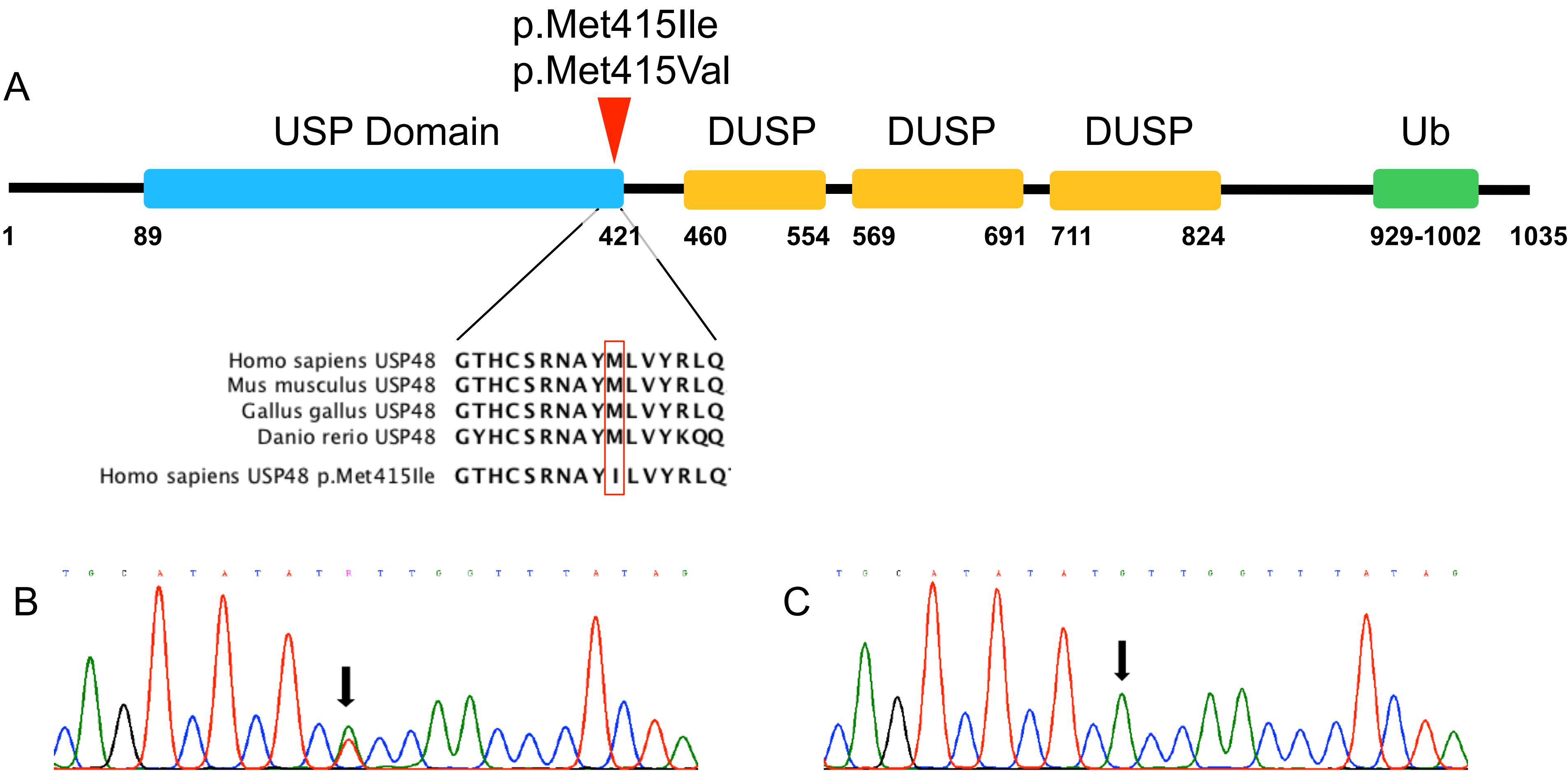
Supplementary Figures and Tables

Total: 237 CD DNA samples

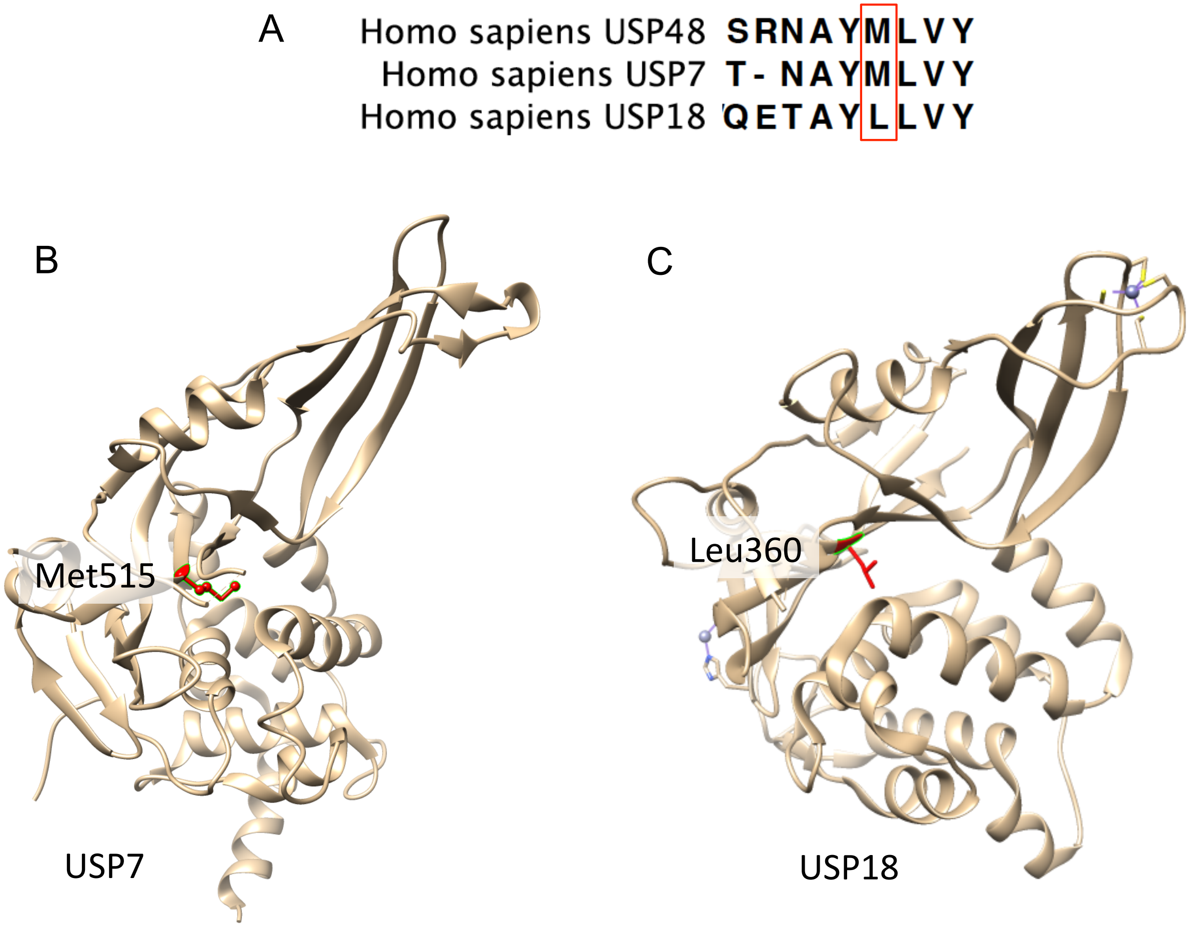
New cryo cohort (n=44)	New FFPE cohort (n=80)	JCEM 2015 cohort (n=62)[18]	Clin Endo 2018 cohort (n=38)[21]	EJE 2018 cohort (n=13)[19]	Total	
44	80	62*	33*	13*	232	USP8 Sanger
18 (USP8 wt)	0	0	0	0	18	Exome seq
5	57	62	38	13	175	USP48 Sanger
8	6	62	18	0	94	BRAF Sanger
0	0	62	0	0	62	FAT1 Sanger

Supplementary figure 1. **Usage of different DNA material from different patient cohorts for different sequencing analyses.**

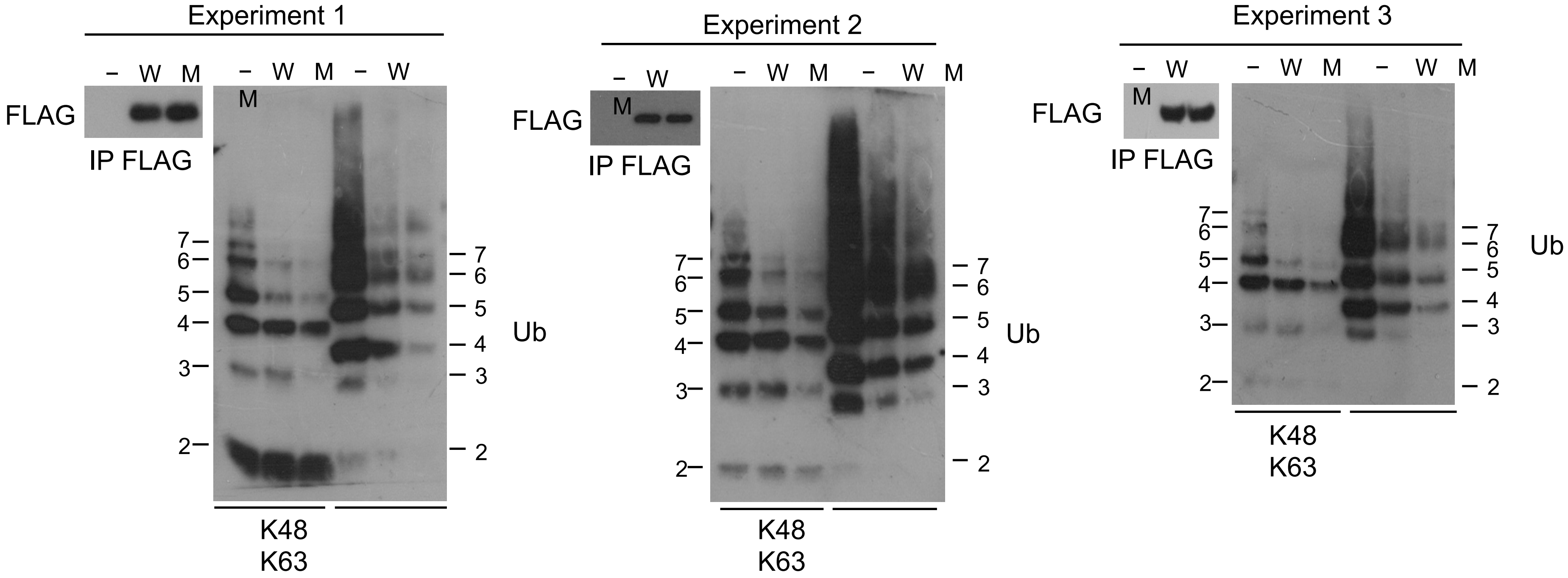
**USP8* Sanger sequencing has been performed and published before (see main text)



Supplementary figure 2. Localization of somatic hotspot mutations in the USP48 gene. Localisation of the identified mutations and alignment with the human USP48 functional regions. The affected amino-acid is highly conserved between species (A). Somatic heterozygous c.G1245A hotspot mutation in USP48 gene resulting in p.Met415Ile substitution by Sanger sequencing (B). The mutations were not present in corresponding normal leukocyte DNA (C). USP= Ubiquitin Specific Protease Domain; DUSP= Domain present in Ubiquitin-Specific Proteases; Ub= Ubiquitin-like domain.



Supplementary Fig. 3. Localization of the corresponding amino-acids to the Met415 of USP48 in the 3D structure of the human USP18 and USP7. Alignment of the region around the Met415 of USP48 with the protein sequences of the two closest related USP family genes, USP18 and USP7, revealed that a small sequence around the site is similar between the three proteins (A). The amino-acids corresponding to the Met415 of USP48 were Leu360 for USP18 (B) and Met515 for USP7 (C) and both had the same localisation on the beta-sheet of the “palm” region towards the helix of the “thumb”.



Supplementary Fig. 4. K-48 and K-63 Deubiquitinating activity of USP48 WT and p.Met415Ile mutant. Results of three independent deubiquitination assay with immunopurified FLAG-tagged USP48 variants and purified K48- or K63-linked ubiquitin chains, containing 2 to 7 ubiquitin moieties. The big panels show immunoblots of the deubiquitination reactions using anti-ubiquitin antibodies. The small panels show total amount of purified USP48 proteins used in the experiment. - =naive cells, W=cells transfected with USP48 wt and M= cells transfected with USP48 Met415Ile mutant.

Supplementary Table 1. Clinical and genetic characteristics of the 18 CD cases analysed by exome sequencing

#	Sex (F/M)	Age (years)	Max tum diam (mm)	Type of adenoma	Clinical diagnosis (CD/NS)	BMI (kg/m^2)	Plasma ACTH (pg/ml)	Serum cortisol after 1 mg Dex (ng/ml)	TSS (n)	Histo	ACTH (ir)	USP8	USP48	TP53
S1	F	38	8	Micro	CD	30.2	94	212	1	DG, Ki67 1-2%	++++	wt	c.1245C>T; p.Met415Ile	WT
S2	F	44	15	Macro	CD	24.8	48	43	1	DG, Ki67 1-2%	+++	wt	WT	WT
S3	M	32	9	Micro	CD	29.4	403	na	1	DG, Ki67 1-2%	++++	wt	WT	WT
S4	M	59	8	Micro	CD	29.9	54	261	2	DG, KI67 7%	+++	wt	WT	chr17:g.7577548G>A; c.733G>A; p.Gly245Ser; rs28934575
S5	F	58	22	Macro	CD	36.0	40	na	1	SG, KI67 1-2%	++	wt	WT	WT
S6	F	69	3	Micro	CD	29.7	63	175	1	Crooke cells, Ki67 3%	++++	wt	c.1245C>T; p.Met415Ile	WT
S7	M	30	16	Macro	CD	38.4	81	6	2	DG, Ki67 1-2%	++++	wt	WT	WT
S8	F	59	27	Macro	CD	36.4	82	386	3	SG, KI67 5%	++++	wt	WT	WT
S9	M	63	39	Macro	CD	22.4	122	4	1	DG, Ki67 1-2%	+++	wt	WT	WT
S10	F	56	37	Macro	CD	28.2	52	163	2	SG, KI67 1-2%	++	wt	WT	chr17:g.7578227G>C; c.622G>C; p.Asp208His
S11	F	39	6	Micro	CD	36.7	70	78	1	DG, Ki67 1-2%	+++	wt	WT	WT
S12	F	57	9	Micro	CD	34.7	62	204	1	DG, Ki67 1-2%	+++	wt	c.1245C>T; p.Met415Ile	WT
S13	F	76	26	Macro	CD	31.2	25	11	1	SG, KI67 1-2%	+	wt	WT	WT
S14	F	58	27	Macro	CD	32.4	55	7.4	2	Atypical, Ki67 10%	+	wt	WT	chr17:g.7577120G>A; c.818G>A; p.Arg273His; rs28934576
S15	M	51	13	Macro	CD	22.9	184	35 (2mgDex)	3	SG, Ki76 5-6%	++	wt	WT	WT
S16	F	59	43	Macro	NS	27.8	48000	na	3	SG, KI67 3%	+++	wt	WT	chr17:g.7576876-7577303del (CNV)
S17	F	49	40	Macro	NS	26.7	na	na	>3	Ki67 5-6%	++++	wt	WT	chr17:g.7577127C>A; p.Glu271Stop
S18	F	69	13	Macro	NS	35.0	3160	na	3	Basophilic	na	wt	WT	chr17:g.7577567A>T; p.Cys238Stop

F, Female, M, Male; Age is at diagnosis; Max tum diam, maximal tumour diameter in millimetres; Micro, microadenoma (<10mm); Macro, macroadenoma (≥ 10mm); BMI, body mass index; TSS, transsphenoidal surgery (number of TSS is indicated); DG, densely granulated; SG, sparsely granulated; ir, immunoreactivity; WT, wild type

Supplementary table 2. Primer sequences used for targeted sequencing

Name	**Sequence (5’ – 3’)**
USP8 for	TTCTTGACCCAATCACTGG
USP8 rev	GAAATTTCCAACTCCCTGACAC
USP48 for	GCCCCGCTAAAGAATAAACA
USP48 rev	TGCCTGCTATAATCCTGGAAA
BRAF for	TGCTTGCTCTGATAGGAAAATG
BRAF rev	AGCATCTCAGGGCCAAAAAT
FAT1 (exon 21) for	GTTTTCCCACAGAATTGGATAG
FAT1 (exon 21) rev	GTCTAAAACTTGTACAGGCATC
FAT1 (exon 25) for	TCATCAAGGAGGGATTAGTCTT
FAT1 (exon 25) rev	CATACGGATTTCAGTCTGAGC
FAT1 (exon 26) for	GCATGGTGTGTCTCAGGATT
FAT1 (exon 26) rev	GCTATTTTCCCCAGCAGACAT
FAT1 (exon 27) for	CGAGGAATTTCCAGTGGTGAAC
FAT1 (exon 27) rev	CACTGCTGCAAAGAACAGC

FAT1 sequencing primers

Exon	**Forward (5’ – 3’)**	**Reverse (5’ – 3’)**
21	ATATGCTTAAACTTGGTTCTGGTT	GGTTTGAAAGTCTTCCACTAAGATG
25	GGATTGAGCCTGACATACG	CACACATTTTGACTGGACAGA
26	GGTGAACAAAACCGTCTTGG	TGGTGAGGCTTTAAGGGTAG
27	TAAATGCGGTTGCATCTTTG	ACAGCGCGGATTACTCACAT

Supplementary Table 3. List of all somatic mutations identified by exome sequencing in our samples cohort

Patient no.	Gene symbol	chromosomal region affected	base exchange	amino acid exchange	Genotype	Inheritance
S1	USP48	chr1:22056252-22056252	1245C->T	Met415Ile	heterozygous	somatic
	HELZ	chr17:65074680-65074694	5503_5517delGGGTTTGACAGTCTT	1835-1839delKTVKP	heterozygous	somatic
	LTN1	chr21:30316141-30316141	4206delT	Phe1404fs*	heterozygous	somatic
	NAF1	chr4:164069540-164069540	587A->G	Ile196Thr	heterozygous	somatic
	MYO1G	chr7:45005453-45005453	1450G->A	Arg484Trp	heterozygous	somatic
	PSMC2	chr7:103007956-103007956	941A->G	Asn314Ser	heterozygous	somatic
	SULF1	chr8:70539531-70539531	1937T->C	Ile646Thr	heterozygous	somatic
	MXRA5	chrX:3242393-3242393	1333G->A	Gln445Stop	heterozygous	somatic
	CSAG1	chrX:151903872-151903872	128C->G	Pro43Arg	heterozygous	somatic
S2	HRAS	chr11:534286-534286	37C->G	Gly13Arg	heterozygous	somatic
	PRKAB1	chr12:120110187-120110187	241G->A	Val81Met	heterozygous	somatic
S3	C1orf123	chr1:53683845-53683845	260T->C	Asn87Ser	heterozygous	somatic
	TMEM72	chr10:45430277-45430277	523C->G	Leu175Val	heterozygous	somatic
	DNHD1	chr11:6584456-6584456	2330C->G	Ser777Stop	heterozygous	somatic
	SSR1	chr6:7299024-7299027	576delTTGA	Asn191fs*	heterozygous	somatic
	REPS1	chr6:139238701-139238701	1511G->C	Thr504Ser	heterozygous	somatic
	SYTL3	chr6:159086507-159086507	191C->T	Ala64Val	heterozygous	somatic
S4	ATG13	chr11:46686971-46686971	1038_1038delT	Ser346fs*	heterozygous	somatic
	TP53	chr17:7577548-7577548	733C->T	Gly245Ser	heterozygous	somatic
	PCDH7	chr4:30921854-30921854	3254G->A	Ser1085Asn	heterozygous	somatic
	DAXX	chr6:33287404-33287405	1692_1693delGA	Gln565fs*	heterozygous	somatic
	TXN	chr9:113013130-113013130	159T->C	Ile53Met	heterozygous	somatic
S5	FAM89B	chr11:65340225-65340225	85G->A	Gly29Ser	heterozygous	somatic
	MYO5A	chr15:52643512-52643512	44T->A	Lys15Met	heterozygous	somatic
	NLRC3	chr16:3613299-3613299	1639C->A	Ala547Ser	heterozygous	somatic
	ANGPT2	chr8:6371226-6371226	1172T->C	Tyr391Cys	heterozygous	somatic
S6	USP48	chr1:22056252-22056252	1245C->T	Met415Ile	heterozygous	somatic
	SYTL1	chr1:27679830-27679830	1364G->T	Arg455Leu	heterozygous	somatic
	INPP5A	chr10:134521818-134521818	476G->A	Cys159Tyr	heterozygous	somatic
	PIK3C2A	chr11:17153475-17153475	2219T->C	Lys740Arg	heterozygous	somatic
	DENND5B	chr12:31568332-31568332	2626T->C	Thr876Ala	heterozygous	somatic
	MGA	chr15:42059270-42059270	8990C->G	Ala2997Gly	heterozygous	somatic
	PSTPIP1	chr15:77317899-77317899	308G->A	Arg103Gln	heterozygous	somatic
	NT5C1B	chr2:18767525-18767525	253C->T	Ala85Thr	heterozygous	somatic
	MAGI1	chr3:65342189-65342189	4253C->T	Arg1418Lys	heterozygous	somatic
	MAST4	chr5:66445281-66445281	3159T->A	Asp1053Glu	heterozygous	somatic
	ZDHHC14	chr6:157803204-157803204	151T->G	Cys51Gly	heterozygous	somatic
	SUMF2	chr7:56142358-56142358	521A->G	Tyr174Cys	heterozygous	somatic
S7	KIN	chr10:7811298-7811298	679G->A	Pro227Se	heterozygous	somatic
	SOX6	chr11:16119165-16119165	1007A->G	Leu336Ser	heterozygous	somatic
	KIAA1468	chr18:59888475-59888475	712C->G	Arg238Gly	heterozygous	somatic
	FBL	chr19:40331259-40331259	179C->T	Gly60Asp	heterozygous	somatic
S8	PAX7	chr1:18960926-18960926	215T->A	Ile72Asn	heterozygous	somatic
	IQGAP3	chr1:156509302-156509302	2920T->C	Ile974Val	heterozygous	somatic
	GFRA1	chr10:118029030-118029030	403C->T	Val135Ile	heterozygous	somatic
	ADAM12	chr10:127806704-127806704	515A->T	Leu172Gln	heterozygous	somatic
	FREM2	chr13:39266238-39266238	4757C->T	Thr1586Ile	heterozygous	somatic
	BCL6B	chr17:6927165-6927165	175T->C	Cys59Arg	heterozygous	somatic
	LRFN1	chr19:39798620-39798620	1969C->T	Glu657Lys	heterozygous	somatic
	PROM1	chr4:16077370-16077370	160delT	Ile54fs*	heterozygous	somatic
	ADH1C	chr4:100257928-100257928	1106C->A	Arg369Leu	heterozygous	somatic
	FBXL7	chr5:15937167-15937167	1348G->C	Ala450Pro	heterozygous	somatic
	PDLIM7	chr5:176918109-176918112	332_335delTGCT	Ser111fs*	heterozygous	somatic
	CPNE5	chr6:36713279-36713279	338T->C	Glu113Gly	heterozygous	somatic
S9	DLG5	chr10:79556322-79556322	1460T->C	Gln487Arg	heterozygous	somatic
	MYO1C	chr17:1374547-1374547	2048C->G	Gly683Ala	heterozygous	somatic
	DLG4	chr17:7100350-7100350	629T->C	Asn210Ser	heterozygous	somatic
S10	C8A	chr1:57341789-57341789	371G->A	Gly124Asp	heterozygous	somatic
	ACADM	chr1:76198596-76198596	275C->T	Pro92Leu	heterozygous	somatic
	FCAMR	chr1:207134037-207134037	929G->A	Thr310Met	heterozygous	somatic
	MUC5B	chr11:1260185-1260185	3382G->A	Ala1128Thr	heterozygous	somatic
	MEN1	chr11:64577330-64577333	249_252delAGAC	Leu83fs*	heterozygous	somatic
	POLE	chr12:133218264-133218264	1759C->T	Asp587Asn	heterozygous	somatic
	ZNF605	chr12:133502033-133502033	1945C->G	Gly649Arg	heterozygous	somatic
	TP53	chr17:7578227-7578227	622C->G	Asp208His	heterozygous	somatic
	CACNA1A	chr19:13339572-13339572	1117G->A	Arg373Stop	heterozygous	somatic
	FSIP2	chr2:186667454-186667454	13688G->C	Arg4563Thr	heterozygous	somatic
	APCDD1L	chr20:57088894-57088894	61T->C	Ile21Val	heterozygous	somatic
	TERT	chr5:1293731-1293731	1270C->T	Gly424Ser	heterozygous	somatic
	LOC100131257	chr7:7136039-7136039	253G->C	Leu85Val	heterozygous	somatic
	KCP	chr7:128519845-128519845	3590A->G	Val1197Ala	heterozygous	somatic
	NOBOX	chr7:144098546-144098546	437A->T	Val146Asp	heterozygous	somatic
	TAF1L	chr9:32631721-32631721	3857C->T	Cys1286Tyr	heterozygous	somatic
	ASTN2	chr9:119976939-119976939	713C->T	Arg238His	heterozygous	somatic
	TSPYL2	chrX:53115057-53115057	1483A->G	Asn495Asp	heterozygous	somatic
	ATRX	chrX:76939666-76939669	1079_1082delTCAA	Ile360fs*	heterozygous	somatic
S11	CSMD2	chr1:34208884-34208885	2169_2170insA	Gly723fs*	heterozygous	somatic
	LRRC41	chr1:46744867-46744867	2206G->A	Gln736Stop	heterozygous	somatic
	WNT11	chr11:75907712-75907712	134C->T	Cys45Tyr	heterozygous	somatic
	MAPKBP1	chr15:42113141-42113141	2593G->A	Asp865Asn	heterozygous	somatic

	B3GNTL1	chr17:80915309-80915309	454C->A	Ala152Ser	heterozygous	somatic
	APMAP	chr20:24959495-24959495	236A->C	Leu79Arg	heterozygous	somatic
	FYB	chr5:39202975-39202975	88A->C	Ser30Ala	heterozygous	somatic
	MAGED2	chrX:54837432-54837432	716G->A	Arg239Gln	heterozygous	somatic
S12	USP48	chr1:22056252-22056252	1245C->T	Met415Ile	heterozygous	somatic
	LDHB	chr12:21807506-21807506	100T->C	Met34Val	heterozygous	somatic
	SRSF6	chr20:42088773-42088773	95G->A	Arg32His	heterozygous	somatic
	TTK	chr6:80749459-80749459	2177A->T	Tyr726Phe	heterozygous	somatic
	OFD1	chrX:13786877-13786877	2969C->T	Thr990Me	heterozygous	somatic
	ATP11C	chrX:138850445-138850445	2374G->C	Arg792Gly	heterozygous	somatic
S13	HRNR	chr1:152193920-152193920	185T->C	Asp62Gly	heterozygous	somatic
	CANX	chr5:179149977-179149977	1460A->G	Asn487Ser	heterozygous	somatic
	DPP7	chr9:140008388-140008388	484G->A	Arg162Cys	heterozygous	somatic
S14	MXRA8	chr1:1290110-1290110	901delG	Arg301fs*	heterozygous	somatic
	IFI16	chr1:159024632-159024634	2131_2133delAAG	Lys711del	heterozygous	somatic
	TP53	chr17:7577120-7577120	818C->T	Arg273His	heterozygous	somatic
	CIC	chr19:42797780-42797780	3832G->A	Val1278Ile	heterozygous	somatic
	HSP90AB1	chr6:44218796-44218798	969_971delAGA	Glu324del	heterozygous	somatic
	ROS1	chr6:117681119-117681120	3500_3501insA	Asn1167fs*	heterozygous	somatic
	EGFR	chr7:55240789-55240789	2033C->T	Thr678Met	heterozygous	somatic
S15	FAM46B	chr1:27332938-27332938	775C->A	Glu259Stop	heterozygous	somatic
	CCDC18	chr1:93687201-93687202	1998_1999delTA	Lys666fs*	heterozygous	somatic
	PIGR	chr1:207110959-207110959	526C->G	Val176Leu	heterozygous	somatic
	FAM160B1	chr10:116603630-116603630	947T->C	Leu316Pro	heterozygous	somatic
	TRIM3	chr11:6478975-6478975	466C->A	Glu156Stop	heterozygous	somatic
	OR10Q1	chr11:57996014-57996014	334C->T	Gly112Ser	heterozygous	somatic
	P4HA3	chr11:73984594-73984594	1394A->T	Ile465Asn	heterozygous	somatic
	WNK1	chr12:990889-990889	3923C->T	Ala1308Val	heterozygous	somatic
	USP30	chr12:109505421-109505421	376delT	Ala126fs*	heterozygous	somatic
	CCDC63	chr12:111296461-111296461	251G->A	Arg84Lys	heterozygous	somatic
	GPR137C	chr14:53100572-53100572	1020delC	His340fs*	heterozygous	somatic
	MAPK6	chr15:52350949-52350949	820C->T	Pro274Ser	heterozygous	somatic
	FURIN	chr15:91422705-91422705	1085A->T	Glu362Val	heterozygous	somatic
	C18orf63	chr18:72009289-72009289	634A->C	Asn212His	heterozygous	somatic
	ANKRD27	chr19:33135387-33135387	367T->C	Ser123Ala	heterozygous	somatic
	CD22	chr19:35827050-35827050	524A->T	Gln175Leu	heterozygous	somatic
	ZNF614	chr19:52519903-52519907	944_948delCACAT	Phe315fs*	heterozygous	somatic
	ZNF417	chr19:58420839-58420841	805_807delATC	Glu269del	heterozygous	somatic
	CDC42EP1	chr22:37964151-37964151	500C->T	Pro167Leu	heterozygous	somatic
	P2RY1	chr3:152554379-152554379	808G->T	Ala270Ser	heterozygous	somatic
	GAK	chr4:876550-876550	1054T->C	Ile352Val	heterozygous	somatic
	BMP3	chr4:81967143-81967143	568T->G	Ser190Ala	heterozygous	somatic
	MAP3K5	chr6:137017185-137017185	521G->A	Ser174Phe	heterozygous	somatic
	NFE2L3	chr7:26224537-26224537	1219G->C	Asp407His	heterozygous	somatic
	DPP6	chr7:154677424-154677424	2023C->G	Leu675Val	heterozygous	somatic
	HIATL1	chr9:97200758-97200758	343G->A	Gly115Ser	heterozygous	somatic
	PORCN	chrX:48371104-48371104	683G->C	Arg228Pro	heterozygous	somatic
	SLC6A14	chrX:115588824-115588824	1664C->T	Ala555Val	heterozygous	somatic
S16	LIPM	chr10:90568137-90568137	230G->A	Arg77Lys	heterozygous	somatic
	NRAP	chr10:115388708-115388708	46G->C	Gln16Glu	heterozygous	somatic
	CLEC1B	chr12:10149777-10149777	265C->G	Glu89Gln	heterozygous	somatic
	AX747187	chr12:97023975-97023975	1148T->C	Ile383Thr	heterozygous	somatic
	C12orf55	chr12:97023975-97023975	1148T->C	Ile383Thr	heterozygous	somatic
	KIAA1033	chr12:105540892-105540892	2482C->T	Arg828Stop	heterozygous	somatic
	ASB7	chr15:101170073-101170073	643C->T	Gln215Stop	heterozygous	somatic
	TP53	chr17:7576876-7577303	cnv,DEL	cnv,DEL	heterozygous	somatic
	CALCOCO2	chr17:46923842-46923842	218T->C	Leu73Pro	heterozygous	somatic
	PDE8B	chr5:76715693-76715693	2231A->G	Asn744Ser	heterozygous	somatic
	MAPK9	chr5:179663524-179663524	1135C->T	Ala379Thr	heterozygous	somatic
	DDR1	chr6:30866967-30866967	2525G->A	Gly842Asp	heterozygous	somatic
	HEMGN	chr9:100692983-100692983	694T->A	Met232Leu	heterozygous	somatic
	CRB2	chr9:126132765-126132765	1433A->G	Asn478Ser	heterozygous	somatic
S17	C10orf90	chr10:128158701-128158701	1562G->A	Ser521Phe	heterozygous	somatic
	MADD	chr11:47295481-47295481	16A->T	Lys6Stop	heterozygous	somatic
	KRT72	chr12:52992683-52992683	640T->A	Arg214Trp	heterozygous	somatic
	AKAP6	chr14:33015930-33015930	2062A->G	Thr688Ala	heterozygous	somatic
	TP53	chr17:7577127-7577127	811C->A	Glu271Stop	heterozygous	somatic
	MROH2B	chr5:41018798-41018798	1333A->C	Phe445Val	heterozygous	somatic
	ATRX	chrX:76939369-76939369	1379G->C	Ser460Stop	heterozygous	somatic
S18	ECM1	chr1:150483380-150483380	180C->A	Ser60Arg	heterozygous	somatic
	MFSD5	chr12:53647526-53647526	1228A->G	Thr410Ala	heterozygous	somatic
	RBM19	chr12:114395714-114395714	713T->C	Glu238Gly	heterozygous	somatic
	TMEM132B	chr12:125834599-125834599	324C->G	Phe108Leu	heterozygous	somatic
	CKAP2	chr13:53049162-53049164	1935_1937delTCC	Ser646del	heterozygous	somatic
	ZFYVE26	chr14:68234443-68234443	5768C->T	Arg1923Gln	heterozygous	somatic
	RBM25	chr14:73543059-73543059	139A->T	Met47Leu	heterozygous	somatic
	NR2E3	chr15:72105875-72105875	894G->A	Met298Ile	heterozygous	somatic
	TP53	chr17:7577567-7577567	714A->T	Cys238Stop	heterozygous	somatic
	RAVER1	chr19:10433949-10433949	1001G->A	Ala334Val	heterozygous	somatic
	CYP4F11	chr19:16025584-16025584	1237C->T	Val413Ile	heterozygous	somatic
	AAK1	chr2:69734553-69734553	2164C->G	Gly722Arg	heterozygous	somatic
	KLHL18	chr3:47324546-47324546	91A->G	Ile31Val	heterozygous	somatic
	TECRL	chr4:65180408-65180408	509T->A	Asp170Val	heterozygous	somatic

NUP155	chr5:37310655-37310655	2450T->G		Lys817Thr	heterozygous	somatic
PKHD1	chr6:51798952-51798952	152C->A		Gly51Val	heterozygous	somatic
FYN	chr6:112021340-112021340	829G->C		Leu277Val	heterozygous	somatic
UTRN	chr6:144803397-144803397	3560A->G		Asp1187Gly	heterozygous	somatic
PCMTD1	chr8:52758300-52758300	331T->G		Ile111Leu	heterozygous	somatic
GPR64	chrX:19027788-19027788	1330A->G		Phe444Leu	heterozygous	somatic