Gene	Chromosomal location	Number of mutated samples	%	Genetic variants	cDNA level	Protein level
FBXW7	chr4	4	8%	chr4_153247289_G/- (3pts)	NM_033632.3:c.1513delC	p.(Arg505Alafs*19)
				chr4_153247162_A/T	NM_033632.3:c.1640T>A	p.(Leu547Ter)
CLTC	chr17	3	6%	chr17_57743859_G/-	NM_001288653.1:c.1814delG	p.(Gly605Alafs*27)
				chr17_57760140_C/T	NM_001288653.1:c.3763C>T	p.(Arg1255Ter)
				chr17_57758839_G/A	NM_001288653.1:c.3508G>T	p.(Glu1170Ter)
NEXN	chr1	3	6%	chr1_78392479_C/T	NM_144573.3:c.766C>T	p.(Arg256Ter)
				chr1_78407759_CA/-	NM_144573.3:c.1527_1528delCA	p.(His509Glnfs*7)
				chr1_78390900_G/T	NM_144573.3:c.475G>T	p.(Glu159Ter)
ZNF750	chr17	3	6%	chr17_80788075_C/T	NM_024702.2:c.721G>T	p.(Glu241Ter)
				chr17_80789802_C/A	NM_024702.2:c.529G>T	p.(Glu177Ter)
				chr17_80789503_G/C	NM_024702.2:c.828C>G	p.(Tyr276Ter)
ARHGAP21	chr10	2	4%	chr_10_24880815_C/T	NM_020824.3:c.4002+1G>A	Not predictable
				chr_10_24909599_G/A	NM_020824.3:c.1225C>T	p.(Gln409Ter)
CNOT7	chr8	2	4%	chr_8_17088237_G/A (2 pts)	NM_001322093.1:c.916C>T	p.(Gln306Ter)
COG1	chr17	2	4%	chr17_71196845_ -/GGGGGGG (2 pts)	NM_018714.2:c.1212_1213insGGGGGGG	p.(Arg405Gly*22)
FAT1	chr4	2	4%	chr4_187519130_G/A	NM_005245.3:c.12253C>T	p.(Gln4085Ter)
				chr4_187524567_G/A	NM_005245.3:c.11113C>T	p.(Gln3705Ter)
KIAA0753	chr17	2	4%	chr17_6483132_G/-	NM_014804.2:c.2839delC	p.(Gln947Argfs*17)
				chr17_6493938_G/C	NM_014804.2:c.2453C>G	p.(Ser818Ter)
KMT2C	chr7	2	4%	chr7:151873303_G/A	NM_170606.2:c.9235C>T	p.(Arg3079Ter)
				chr7_151851141_G/C	NM_170606.2:c.12230C>G	p.(Ser4077Ter)
NSD1	chr5	2	4%	chr5_176637894_A/T	NM_022455.4:c.2494A>T	p.(Lys832Ter)
				chr5_176687170_G/A	NM_022455.4:c.5146+1G>A	Not predictable
RHBG	chr1	2	4%	chr1_156339093_TG/-	NM_020407.4:c.55_56delTG	p.(Cys19Profs*33)
				chr1_156351694_ -/CATTG	NM_020407.4:c.937_938insCATTG	p.(Leu313Serfs*69)
SRRM3	chr7	2	4%	chr7_75914935_-/C (2 pts)	NM_001291831.1:c.1815-1dupC	p.(Gln606Alafs*19)
SYNE2	chr14	2	4%	chr14_64518696_C/T	NM_182914.2:c.8065C>T	p.(Gln2689Ter)
				chr14_64625496_ -/ATGAGGAAAGGAGGAT	NM_182914.2:c.15945_15946ins(16)	p.(Gln5316Metfs*16)
TRAF3IP1	chr2	2	4%	chr2_239261562_C/T	NM_015650.3:c.1546C>T	p.(Gln516Ter)
				chr2_239261523_ AATG/-	NM_015650.3:c.1509_1512delTGAA	p.(Asn503Lysfs*23)

Supp. Table 2: High impact genetic variants identified in more than one patient.