Supplemental table S1. Clinical characteristics of the patients with STAT3 mutations.

Exome sequencing	Variant	VAF	Sex	Age	Hb	Leuk	Lymph	Neut	Throm	Vbeta	Concominant disorders
Patient 1 T-LGL	H410R	49% CD8+	M	60	85,0	10,2	1,6	1,4	203,0	vb.17: 95%	Anemia, neutropenia, B-cell dyscracia, hyper-gammaglobulinemia
Amplicon sequencing											
Patient 2 T-LGL	H410R	9% MNC	F	75	127,0	4,2	3,7	0,0	260,0	NA	Neutropenia
Patient 3 T-LGL	S381Y	7% MNC	F	20	108,0	7,0	4,7	2,0	181,0	NA	Anemia
Patient 4 T-LGL	F174S	54% CD8+	M	68	95,0	8,6	7,2	1,1	211,0	NA	Anemia, neutropenia

Abbreviations: M, male; F, female; VAF, variant allele frequency; Hb, hemoglobin; Leuk, leukocytes; Lymph, lymphocytes; Neut, neutrophils; Throm, thrombocytes

Supplemental table S2. Exome sequencing results from index patient E1 and patients E2-E7.

Index patient 1

chrom	pos	ref	var	Gene	Effect	Effect Impact	Codon Change	Amino Acid Change	Normal reads[1]	Normal reads[2]	Normal var_freq	Tumor Reads[3]
chr17	40481576	T	C	STAT3	NON_SYNONYMOUS_CODING	MODERATE	cAc/cGc	H410R	81	1	1,22	68
chr6	26285607	G	C	HIST1H4H	NON_SYNONYMOUS_CODING	MODERATE	Cgc/Ggc	R41G	89	1	1,11	74
chr19	48640278	G	A	LIG1	NON_SYNONYMOUS_CODING	MODERATE	Cgg/Tgg	R440W	68	1	1,45	52
chr10	18789769	G	T	CACNB2	NON_SYNONYMOUS_CODING	MODERATE	cGa/cTa	R162L	45	1	2,17	50
chr19	50910609	C	T	POLD1	NON_SYNONYMOUS_CODING	MODERATE	cCc/cTc	P571L	44	0	0	25
chr3	38616913	C	T	SCN5A	NON_SYNONYMOUS_CODING	MODERATE	Gtg/Atg	V1181M	38	1	2,56	63
chr21	10934987	C	T	TPTE	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R269Q	91	0	0	118
chr6	39869697	C	T	DAAM2	NON_SYNONYMOUS_CODING	MODERATE	Cgc/Tgc	R1031C	37	0	0	31
chr14	100743840	A	G	YY1	NON_SYNONYMOUS_CODING	MODERATE	tAt/tGt	Y383C	39	0	0	45
chr16	1129599	G	A	SSTR5	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R244Q	9	0	0	2
chr19	46215222	C	T	FBXO46	NON_SYNONYMOUS_CODING	MODERATE	gGc/gAc	G511D	22	0	0	20
chr5	71495673	C	T	MAP1B	NON_SYNONYMOUS_CODING	MODERATE	cCg/cTg	P2164L	28	0	0	28
chr5	176308804	C	T	HK3	NON_SYNONYMOUS_CODING	MODERATE	cGc/cAc	R761H	30	0	0	32
chr14	57947415	G	A	C14orf105	NON_SYNONYMOUS_CODING	MODERATE	Cca/Tca	P184S	19	0	0	21
chr16	89805925	G	C	FANCA	NON_SYNONYMOUS_CODING	MODERATE	cCg/cGg	P1324R	15	0	0	15
chr14	58813218	G	A	ARID4A	NON_SYNONYMOUS_CODING	MODERATE	Gac/Aac	D357N	10	0	0	13
chr20	17640518	G	A	RRBP1	NON_SYNONYMOUS_CODING	MODERATE	gCt/gTt	A212V	20	0	0	13
chr15	63901315	C	T	HERC1	NON_SYNONYMOUS_CODING	MODERATE	Gtg/Atg	V4851M	34	0	0	48
chr12	49436629	G	A	MLL2	STOP_GAINED	HIGH	Cag/Tag	Q1893*	39	0	0	81

Patient E2

chrom	pos	ref	var	Gene	Effect	Effect Impact	Codon Change	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tum read
chr19	58385748	G	A	ZNF814	NON_SYNONYMOUS_CODING	MODERATE	gCt/gTt	A337V	189	1	0,53	25
chr13	38266376	T	C	TRPC4	NON_SYNONYMOUS_CODING	MODERATE	Aca/Gca	T332A	65	1	1,52	26
chr2	120438592	G	A	TMEM177	NON_SYNONYMOUS_CODING	MODERATE	Gct/Act	A55T	53	0	0	29
chr15	45386840	G	A	DUOX2	NON_SYNONYMOUS_CODING	MODERATE	aCg/aTg	T1482M	38	0	0	31
chr7	70236631	G	C	AUTS2	SPLICE_SITE_DONOR	HIGH			47	1	2,08	28
chr1	42914260	T	A	ZMYND12	NON_SYNONYMOUS_CODING	MODERATE	gAa/gTa	E101V	42	2	4,55	25
chr22	29885598	AAGGAAG	A	NEFH	CODON_DELETION	MODERATE	aaggaagag/aag	KEE657K	50	2	3,85	76
chr3	137956387	T	C	ARMC8	NON_SYNONYMOUS_CODING	MODERATE	aTt/aCt	I250T	60	2	3,23	37
chr5	171766472	G	A	SH3PXD2B	NON_SYNONYMOUS_CODING	MODERATE	aCg/aTg	T546M	28	1	3,45	24
chr15	68642973	T	C	ITGA11	NON_SYNONYMOUS_CODING	MODERATE	Aga/Gga	R348G	63	1	1,56	73
chr20	61467852	G	A	COL9A3	NON_SYNONYMOUS_CODING	MODERATE	cGc/cAc	R524H	28	0	0	30
chr4	122831309	C	T	TRPC3	NON_SYNONYMOUS_CODING	MODERATE	Gct/Act	A598T	28	1	3,45	17
chr4	52862277	C	T	LRRC66	NON_SYNONYMOUS_CODING	MODERATE	cGc/cAc	R304H	23	0	0	14
chr9	71002447	A	G	PGM5	NON_SYNONYMOUS_CODING	MODERATE	Aag/Gag	K214E	66	1	1,49	45
chr21	46604883	G	A	ADARB1	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R521Q	40	1	2,44	42
chr5	151047138	C	A	SPARC	STOP_GAINED	HIGH	Gag/Tag	E159*	14	0	0	10
chr11	102056815	A	G	YAP1	NON_SYNONYMOUS_CODING	MODERATE	aAg/aGg	K252R	68	3	4,23	70
chr11	16340159	C	T	SOX6	NON_SYNONYMOUS_CODING	MODERATE	cGa/cAa	R93Q	25	1	3,85	22
chr3	180322347	G	C	TTC14	NON_SYNONYMOUS_CODING	MODERATE	gGt/gCt	G218A	93	0	0	90
chr9	116268683	G	A	RGS3	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R332Q	20	0	0	27
chr19	58385906	G	C	ZNF814	NON_SYNONYMOUS_CODING	MODERATE	ttC/ttG	F284L	196	2	1,01	13
chr1	89449029	A	G	RBMXL1	NON_SYNONYMOUS_CODING	MODERATE	Tct/Cct	S161P	276	12	4,17	37
chr16	30531243	C	CG	ITGAL	FRAME_SHIFT	HIGH	-/G	-1099	10	0	0	8
chr1	152681692	CTGTGGT	C	LCE4A	CODON_DELETION	MODERATE	tgtggt/-	CG48-	45	1	2,17	61
chr7	19184746	C	CTCT	FERD3L	CODON_INSERTION	MODERATE	gag/gAGAag	E80EK	8	1	11,11	7

Patient E3

chrom	pos	ref	var	Gene	Effect	Effect Impact	Codon Change	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tumor reads1
chr4	86844810	G	A	ARHGAP24	NON_SYNONYMOUS_CODING	MODERATE	cGa/cAa	R93Q	91	3	3,19	31
chr1	176734840	C	T	PAPPA2	NON_SYNONYMOUS_CODING	MODERATE	cCg/cTg	P1397L	66	1	1,49	34
chr1	183093952	G	A	LAMC1	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R863Q	63	0	0	33
chr5	32052757	C	T	PDZD2	NON_SYNONYMOUS_CODING	MODERATE	aCg/aTg	T569M	80	1	1,23	45
chr1	19505624	G	T	UBR4	NON_SYNONYMOUS_CODING	MODERATE	Cgc/Agc	R759S	81	1	1,22	66
chr15	41861215	G	A	TYRO3	NON_SYNONYMOUS_CODING	MODERATE	cGt/cAt	R416H	68	2	2,86	29
chr10	68857522	C	T	LRRTM3	STOP_GAINED	HIGH	Cga/Tga	R572*	77	4	4,94	52
chr12	122406062	A	T	WDR66	STOP_GAINED	HIGH	Aaa/Taa	K920*	42	1	2,33	23
chr6	108985555	C	T	FOXO3	NON_SYNONYMOUS_CODING	MODERATE	Cgg/Tgg	R507W	180	0	0	179
chr1	156449103	C	G	MEF2D	NON_SYNONYMOUS_CODING	MODERATE	Gga/Cga	G215R	50	2	3,85	35
chr7	82452006	C	T	PCLO	SPLICE_SITE_ACCEPTOR	HIGH			22	1	4,35	9
chr22	20130876	G	T	ZDHHC8	NON_SYNONYMOUS_CODING	MODERATE	Gac/Tac	D575Y	25	1	3,85	17
chr19	57175488	C	T	ZNF835	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R382Q	26	1	3,7	21
chr17	54431314	G	A	ANKFN1	NON_SYNONYMOUS_CODING	MODERATE	Gag/Aag	E173K	57	2	3,39	40
chr3	53226178	C	T	PRKCD	NON_SYNONYMOUS_CODING	MODERATE	Cgc/Tgc	R643C	28	0	0	21
chr2	197537109	C	T	CCDC150	NON_SYNONYMOUS_CODING	MODERATE	gCa/gTa	A326V	57	2	3,39	40
chr15	88472429	T	C	NTRK3	NON_SYNONYMOUS_CODING	MODERATE	tAt/tGt	Y709C	20	0	0	22
chr5	140605446	G	A	PCDHB14	NON_SYNONYMOUS_CODING	MODERATE	cGa/cAa	R790Q	151	1	0,66	162
chr16	23692270	G	A	PLK1	NON_SYNONYMOUS_CODING	MODERATE	Ggg/Agg	G205R	65	1	1,52	49
chr16	21416379	A	G	NPIPL3	NON_SYNONYMOUS_CODING	MODERATE	cTt/cCt	L171P	151	2	1,31	132
chr6	49494368	G	A	GLYATL3	STOP_GAINED	HIGH	tGg/tAg	W203*	106	0	0	64
chr1	27332626	G	C	FAM46B	NON_SYNONYMOUS_CODING	MODERATE	Cgc/Ggc	R363G	24	0	0	23
chr2	1926367	G	A	MYT1L	NON_SYNONYMOUS_CODING	MODERATE	Cgg/Tgg	R392W	93	0	0	109

Patient E4

chrom	pos	ref	var	Gene	Effect	Effect Impact	Codon Change	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tum reads
chr13	28624291	T	C	FLT3	NON_SYNONYMOUS_CODING	MODERATE	gAc/gGc	D228G	108	3	2,7	44
chr5	96320849	C	G	LNPEP	NON_SYNONYMOUS_CODING	MODERATE	cCa/cGa	P309R	84	3	3,45	49
chr8	133144498	C	T	KCNQ3	NON_SYNONYMOUS_CODING	MODERATE	Gta/Ata	V605I	115	6	4,96	59
chr4	55981173	T	C	KDR	NON_SYNONYMOUS_CODING	MODERATE	Aga/Gga	R176G	86	2	2,27	41
chr18	28934818	C	T	DSG1	STOP_GAINED	HIGH	Cga/Tga	R887*	83	4	4,6	51
chr4	17707473	G	A	FAM184B	NON_SYNONYMOUS_CODING	MODERATE	Cgg/Tgg	R358W	86	4	4,44	47
chr1	79121071	G	A	IFI44	NON_SYNONYMOUS_CODING	MODERATE	Ggg/Agg	G239R	63	3	4,55	40
chr16	22926721	G	GA	HS3ST2	FRAME_SHIFT	HIGH	aaa/Aaaa	K315K	36	0	0	24
chr6	110620294	TGCA	T	C6orf186	CODON_CHANGE	MODERATE	gtgcat/gat	VH205D	73	4	5,19	33
chr4	122682824	C	T	TMEM155	NON_SYNONYMOUS_CODING	MODERATE	atG/atA	M27I	69	1	1,43	53
chr1	152732566	C	T	KPRP	NON_SYNONYMOUS_CODING	MODERATE	Cgt/Tgt	R168C	45	2	4,26	14
chr17	80788031	G	A	ZNF750	NON_SYNONYMOUS_CODING	MODERATE	gCc/gTc	A720V	24	0	0	14
chr22	50633332	A	G	TRABD	NON_SYNONYMOUS_CODING	MODERATE	Atc/Gtc	I95V	24	1	4	6
chr9	99404121	T	G	C9orf21	NON_SYNONYMOUS_CODING	MODERATE	Aaa/Caa	K201Q	74	1	1,33	41
chr14	23744800	ACAT	A	RP11-124D2.6.1	CODON_CHANGE	MODERATE	gatgtg/gtg	DV547V	13	0	0	9
chr12	42512938	T	A	GXYLT1	NON_SYNONYMOUS_CODING	MODERATE	cAt/cTt	H117L	40	0	0	32
chr17	72324574	G	A	KIF19	NON_SYNONYMOUS_CODING	MODERATE	cGg/cAg	R17Q	20	0	0	9
chr12	42512924	C	T	GXYLT1	NON_SYNONYMOUS_CODING	MODERATE	Gcc/Acc	A122T	41	0	0	37
chr15	33192236	G	T	FMN1	NON_SYNONYMOUS_CODING	MODERATE	Caa/Aaa	Q1200K	89	1	1,11	71
chr5	140188559	C	T	PCDHA4	NON_SYNONYMOUS_CODING	MODERATE	gCg/gTg	A596V	22	1	4,35	6
chr2	215854314	G	T	ABCA12	NON_SYNONYMOUS_CODING	MODERATE	gCa/gAa	A1219E	66	0	0	66

Patient E5

chrom	position	ref	var	Gene	Effect	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tumor reads1	Tumor reads2	Tumo var_fr
8	6366477	T	C	ANGPT2	missense	K436E	73	0	0	56	29	34,12
11	20948885	T	A	NELL1	nonsense	L264*	67	0	0	60	22	26,83
4	156760015	C	T	ACCN5	missense	G339E	83	0	0	66	18	21,43
13	36878743	G	A	SPG20	missense	T587I	47	1	2,08	34	15	30,61
7	14758275	G	A	DGKB	missense	R120W	36	0	0	23	10	30,3

Patient E6

chrom	position	ref	var	Gene	Effect	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tumor reads1	Tumor reads2	Tumo var_fr
8	56711628	T	G	TGS1	missense	N566K	100	0	0	62	38	38
17	56276945	C	T	EPX	missense	R443W	57	0	0	23	26	53,06
14	99723858	T	C	BCL11B	missense	H126R	33	0	0	21	22	51,16
14	21360276	G	A	RNASE3	missense	R144Q	46	0	0	35	22	38,6
14	25043007	C	T	CTSG	missense	G202R	32	0	0	18	17	48,57
8	117868903	C	T	RAD21	missense	E266K	63	1	1,56	43	16	27,12
2	218954691	C	A	RUFY4	missense	L544I	27	0	0	10	8	44,44

Patient E7

chrom	position	ref	var	Gene	Effect	Amino Acid Change	Normal reads1	Normal reads2	Normal var_freq	Tumor reads1	Tumor reads2	Tumo var_fr
2	125284860	A	T	CNTNAP5	splice-3	-	80	1	1,23	34	24	41,38
4	20543120	G	A	SLIT2	stop-gained	W674*	46	1	2,13	19	23	54,76
15	41352080	T	A	INO80	missense	R609S	55	0	0	21	16	43,24
10	33510758	C	T	NRP1	missense	V391M	59	0	0	27	16	37,21
16	20355365	C	T	UMOD	missense	A438T	36	0	0	22	15	40,54
11	3050595	T	C	CARS	missense	I294V	25	0	0	9	9	50
10	5436190	C	A	TUBAL3	missense	V171L	42	0	0	20	6	23,08
15	42059521	A	T	MGA	utr-3	-	8	1	11,11	2	7	77,78
16	71317453	A	T	FTSJD1	utr-3	-	14	0	0	6	5	45,45
13	27256838	G	A	WASF3	missense	V360I	26	1	3,7	14	7	33,33

Abbreviations: var, variant base; ref, reference base
[1] Sequencing reads supporting reference allele in normal sample
[2] Sequencing reads supporting variant allele in normal sample
[3] Sequencing reads supporting reference allele in tumor sample
[4] Sequencing reads supporting variant allele in tumor sample
* Somatic p-value for somatic/loss of heterozygosity events

Supplemental table S3. Primers for qPCR

Target gene	Sequence	PCR fragment size
GAPDH-F	AGCACCCCTGGCCAAGGTCA	108bp
GAPDH-R	CCGGAGGGGCCATCCACAGT	
SOCS3-F	CTTCGATTCGGGACCAGCCCCC	135bp
SOCS3-R	GGCGGCGGGAAACTTGCTGT	
STAT3-F	AGCGAGGACTGAGCATCGAGCA	125bp
STAT3-R	GCCCTTGCCAGCCATGTTTTCTTTG	
MYC-F	CAGCTGCTTAGACGCTGGATT	131bp
MYC-R	GTAGAAATACGGCTGCACCGA	
JAK2-F	GCTCAGTGGCGGCATGAT	87bp
JAK2-R	CACTGCCATCCCAAGACATTC	
JUNB-F	TGGTGGCCTCTCTCTACACGA	66bp
JUNB-R	GGGTCGGCCAGGTTGAC	
CCL2-F	GTCTCTGCCGCCCTTCTGT	76bp
CCL2-R	TTGCATCTGGCTGAGCGAG	
BCL3-F	CCACAGACGGTAATGTGGTG	143bp
BCL3-R	TATTGCTGTGGTGCAGGGTA	
PGK1-F	CCCAGCTGTATTTCCAAAATGTCGC	148bp
PGK1-R	ACAGCAGCCTTAATCCTCTGGTTGT	
LDHA-F	CTCTGAAGACTCTGCACCCA	124bp
LDHA-R	GCCCAGGATGTGTAGCCTTT	
NONO-F	GCTCTGGACAGATGCAGTGAA	150bp
NONO-R	CTGCTCTCGTTCCTTGTGAA	