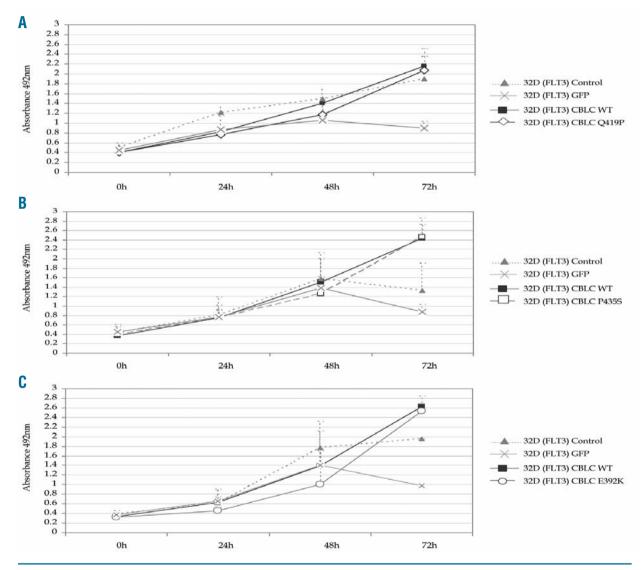
CBL mutations in myeloproliferative neoplasms are also found in the gene's proline-rich domain and in patients with the V617FJAK2

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Online Supplementary Figure S1. MTS cell proliferation assays corresponding to four different transfections for *CBLC* mutants. Two negative controls (cells mock-transfected and cells transfected with GFP control vector) were included. (A) Assay corresponding to the *CBLC* mutation p.Q419PfsX81 compared to wild-type (t-test, P>0.05). (B) Assay corresponding to *CBLC* p.P435S mutation (t-test, P>0.05). (C) Assay corresponding to *CBLC* p.E392K mutation (t-test, P>0.05).

Online Supplementary Table S1. dHPLC primers and conditions used for the mutational screening of *CBL* genes. Two primers were used to amplify each exon (Fw and Rv). Another primer with a base change was used for every exon (Fwm or Rvm) to amplify a mutated fragment, which was used as a mutant control to validate the dHPLC analyses.

	(4)		Primers	dHPLC conditions			
CBL	Exon	Size (bp)		% Buffer A	% Buffer B	Temp. (°C)	
			Fw:GCCCTTCTTTTTCATTTGTTG	39.0	61.1	56.7	
	(N-adaptor)	319	Rv:GGCAGTCACAGACCTGCATA	39.0	61.1	58.0	
	(iv-adaptor)		Fwm GCCCTTCTTCTTCATTTGTTG	46.5	53.6	60.7	
			Fw:ATGGTGAATTTGGTGCATTT		50.7		
	(EF-hand like)	324	Rv:TTTTCTCAGAGTTCCCAAATTTTA	41.4 43.9	58.7 56.2	56.5 58.7	
	(EF-Hand like)		Fwm ATGGTGAATGTGGTGCATTT	43.9	36.2	36.7	
			Fw:GCTCTCCTTCCTTGA	20.0	co. 2	22101	
	4 (EF-hand like)	290	Rv:TCACCGAAGTAGCAGTAACCAG	39.9 42.4	60.2 57.7	57.1 60.7	
	(ET-Hand like)		Fwm GCTCTCCTTCCTGTCCTTGA	42.4	37.7	00.7	
	2		Fw:TGCCCTCTGAGTTGGTTGTA				
	5 (SH2 adaptor)	291	Rv:AACCTTGGCTATTGCGAAAC	39.8	60.3	59.8	
	(STI2 adaptor)		Fwm TGCCCTCTGAATTGGTTGTA				
	2		Fw:TATCTTGCCTTGCCTTCCAC				
	(SH2 adaptor)	265	Rv:AGGTTGGACAGCCCCTAAGT	40.7	59.4	57.5	
	(SH2 adaptor)		Rvm:AGGTTGGAAAGCCCCTAAGT				
	1,425		Fw:ACACCACGTTGCCCTTTTAG				
	(SH2 adaptor)	243	Rv:AAGCTTGTGTCCAGTGATATGG	41.5	58.6	58.5	
	(Sriz adaptor)		Rvm:AAGCTTGTGTACAGTGATATGG				
	1000		Fw:GGACCCAGACTAGATGCTTTCT	37.5	62.6	53.2	
	8	386	Rv:GGCCACCCCTTGTATCAGTA	40.0	60.1	55.5	
	(Ring finger)		Rvm:GGCCACCCCTCGTATCAGTA	45.0	55.1	59.5	
	1016		Fw:CTGGCTTTTGGGGTTAGGTT	40.5	59.6	58.5	
	9	364	RV:AATGGATTTTGCCAGTCTCC	40.5	59.6	59.5	
	(Ring finger)		RVM:AATGGATTCTGCCAGTCTCC	43.0	57.1	61.5	
	1.00%		Fw:CCATTTCCCCAAACGAAAGT	40.9	59.2	58.0	
	10	260	Rv:GCAGGGTGAAAGCAAATCAG	43.4	56.7	61.0	
	(proline-rich)		Rvm:GCAGGGTGAGAGCAAATCAG	45.9	54.2	63.8	
			Fw:CTTTCACCCTGCTTCCACAG	36.4	63.7	59.5	
	.11	452	Rv:CCTGGCCCACACATATTTCTT	36.4	63.7	60.6	
	(proline-rich)		Fwm CTTTCACCCGGCTTCCACAG	38.9	61.2	62.4	
	-		Fw:CAGAGGCTCAGCTGTGGTAA				
	12	240	Rv:ACACTTTTCTGGGTTTTCTCAA	41.7	58.4	57.5	
	(proline-rich)	2.0	Fwm CAGAGGCTCCGCTGTGGTAA	46.7	53.4	59.5	
			Fw:GGTGACATGTATTTTGCTCTGTTC				
	13	263	Rv:CCCAAAAAGGGTTGTTGTGA	43.3	56.8	60.5	
		200	Rvm:CCCAAAAAGGGCTGTTGTGA	45.8	54.3	61.5	
			Fw:TGGCAAAACGAGAAGATGAA				
	14	267		43.1	57.0	59.0	
	14	267	Rv:CAAGCTATCTCAATTGCCAAATA	45.6	54.5	60.0	
			Rvm:CAAGCTATCTCGATTGCCAAATA	2000	72200		
	772	272	Fw:GATGAAGTGCGTCAGAAGAAGA	40.5	59.6	60.0	
	15	272	Rv:CACACTGCCATTCAGGACAA	40.5	59.6	61.8 66.0	
	2		Rvm:CACACTGCCAGTCAGGACAA	48.0	52.1	50.0	
			Fw:AAATGAGGATTTCCCCAGATTT	41.3	58.8	58.1	
	16 (UBA)	249	Rv:AAGCTTTCTGGATGTCCTGGT	43.8 43.8	56.3 56.3	62.0 63.0	
	(UBA)		Rvm:AAGCTTTCTGTATGTCCTGGT	46.3	53.8	64.5	

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CBLB

	61 4 11	n .	dHPLC conditions		
Exon	Size (pb)	Primers	% Buffer A	% Buffer B	Temp (°C)
		Fw:CCCCGCCCCATGGAGGAAGATGCAGTGGT	39.1	61.0	56.0
(N-adaptor)	316	Rv:CAGGCAACGTCAGACAGAAC	41.6	58.5	59.0
(iv-adaptor)		Rvm:CAGGCAACGGCAGACAGAAC	44.1	56.0	61.5
	385	Fw:TGGAAAAATGAAGAAATAGGACA	27.5		
(N-adaptor)		Rv:TGACCTTTACACCAAAACATCTG	37.5 40.0	62.6 60.1	55.0 56.0
(iv-adaptor)		Rvm:TGACCTTTACGCCAAAACATCTG	40.0	60.1	30.0
		Fw:TTTTTCCCTTGTGCCTACAG	42.0	67.1	
(N-adaptor)	211	Rv:CCTTGAAAGATAGATCCACAGC		57.1 54.6	56.5 58.8
(iv-adaptor)		Fwm TTTTTCCCTCGTGCCTACAG	45.5	34.0	50.0
		Fw:TGCTGCTTCAAAGGGAGGTA	40.3	59.8	55.5
5 (EF-hand like)	277	Rv:GGGAGAGAGAAGAAGGGAATG	42.8 5	57.3	58.0
(Li -mand fixe)		Rvm:GGGAGAGAGAGAGGAATG	45.3	54.8	59.5
3		Fw:TGACCTAAACCACATAAGGTCAGA			
6 (EF-hand like)	353	Rv:ATCAGCGGGTATTGCTGACT	40.7	59.4	57.2
(EF-Hand like)		Rvm:ATCAGCGGGTCTTGCTGACT			
		Fw:CCGCCGCATGGAGAAGTACATTGTTGCTAAA	12212	12210	
7 (SH2 adaptor)	322	Rv:GCACTCCAACTTCCATTTCTC	39.0	61.1	55.0 58.6
(Sriz adaptor)		Rvm:GCACTCCAACCTCCATTTCTC	44.0	56.1	30.0
2		Fw:TGAAAAGGAAACATCCAAATGTA	0.00	525	de a
8	296	Rv:ATTTATTTCAAGGGCATTATGG	39.7	60.4	53.7
(SH2 adaptor)		Rvm:ATTTATTTCAATGGCATTATGG	42.2	57.9	55.0
150		Fw:TCTGACAAGGTCAATTGTGAGAT	20.50	86.66	
9	348	RV:CGGCGGCCAGCATTACTTCCTAAACCAT	40.8	59.3	56.3
(Ring finger)	2.0	FWM TCTGACAAGGTTAATTGTGAGAT	43.3	56.8	58.4
V. 65.5	294	Fw:TCCATGCATTTTCTATTTGTTTAG	(585)	100000	95040
10		Rv:GCCGCCGCATCATTTCCTTTTCATATGGT	39.8	60.3	58.3
(Ring finger)		Fwm TCCATGCATTTT∆TATTTTGTTTAG	42.3	57.8	60.5
		Fw:CAGCGGCATCTTTCTCTTTT		***	302,200
11	375	Rv:CCGCCCGAATGTGGGCTCACCATAAA		59.9	58.4 61.1
		Fwm CAGCGGCATATTTCTCTTTT	45.2	54.9	01.1
		Fw:TGTCAGTGCATGGTACAACCT	77.0	50.1	
12A	256	Rv:GGGCACCATGCTTCAAGA	41.0 43.5	59.1 56.6	57.4 61.2
		Rvm:GGGCACCATACTTCAAGA	43.3	30.0	01.2
		Fw:CACCAATCCCACCAGACAAT	***	GW CA	
12B	302	Rv:GCCGCCGCTTCTGCTTTGCGTATTTCTT	39.5	60.6	60.3
		Fwm CACCAATCCTACCAGACAAT	39.5	60.6	61.5
		Fw:TTGGGCAGTGGTGAATCAT		24.2	100000000
13	301	Rv:CAAGTGATCTCCAAATTCAACAA	39.5	60.6	57.1
(proline-rich)		Rvm:CAAGTGATCTCCAGATTCAACAA	44.5	55.6	59.7
		Fw:TGTCACATCAGACTTGCCTGT			
14	242	Rv:GTGGCAAAAATCTGCCCATA	41.6	58.5	58.2
(proline-rich)		Rvm:GTGGCAAAAATTTGCCCATA			
		Fw:TTGTGGCCCTTGTAATTCTTG			
15	400	Rv:TGCCTTTAAATTCTGACCATTAAG	37.3	62.8	54.0
(proline-rich)		Rvm:TGCCTTTAAAGTCTGACCATTAAG	44.8	55.3	56.6
	248	Fw:TGGTCAGAATTTAAAGGCAAAA			
16		Rv:GCCGCCAGGGGTGGGTTGTTCAAAA	41.3	58.8	57.6
(proline-rich)		Rvm:GGCGGCAGGGGTGGGCTGTTCAAAA	43.8	56.3	61.0
	298	Fw:CTGCTGATATCGACCTTTCTTT			
17		Rv:CACCCAGGGATTTTTCTGTT	42.1	58.0	58.5
(proline-rich)		Fwm CTGCTGATATCAACCTTTCTTT	44.6	55.5	60.8
		Fw:TCAGCCAATCAACAGAGATCA			
18	207	RV:TCTTGGGTGGACAACATTCA	40.0	60.1	55.5
18	287		45.0	55.1	58.5
		Fwm:TCAGCCAAT <u>T</u> AACAGAGATCA	A27	N22-40	2000
19	1,242	Fw:TTGCCTTCATTTTTATTTCACTG	38.1	62.0	59.5
(UBA)	357	Rv:GGCGGCTTGCTTTCCATTTTGGTGTCT	38.1	62.0	60.0
17700000000000		Rvm:GGCGGCTTGCTTTCCATCTTGGTGTCT	40.6	59.5	62.0

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	Exon	Size (pb)	Primers	dHPLC conditions			
CBLC				% Buffer A	% Buffer B	Temp. (°C)	
	1 (N-adaptor)	397	Fw:GAGGCTCCCATGGCTCTG	37.3	62.8	65.0	
			Rv:ACCCCAGAGGACTTTGTTCTG	37.3	62.8	66.8	
			Fwm GAGGCTCCTATGGCTCTG	37.3	62.8	69.0	
	2 (N-adaptor)	294	Fw:CCCAAGGATAGCCAGAGTCC	39.8	60.3		
			Rv:AGCCTATGATGGGAGGGTCT			64.2	
			Fwm CCCAAGGATCGCCAGAGTCC				
	3 (EF-hand like)	264	Fw:ACCCTCCCATCATAGGCTCT	40.7 43.2	59.4 56.9	32.95	
			Rv:TCCTCCTGGACCCAAGTCTA			63.0 65.1	
			Fwm ACCCTCCCAGCATAGGCTCT				
	4 (EF-hand like)	250	Fw:AAGGAGGTGGTTGGATCCTC	41.3	58.8	63.5	
			Rv:GCAGCCTTGTTCTGCTGAG				
			Rvm:GCAGCCTTGTCCTGCTGAG				
	5 (SH2 adaptor)	300	Fw:ACAAAAGGGATGGCAGTGAC	39.6 39.6	60.5 60.5	62.0 63.2	
			Rv:GAATGGTTGCACCCTCAAAC				
			Fwm ACAAAAGGGCTGGCAGTGAC				
	0.00		Fw:TGGATTTGGGACAGATCCTC	39.2 44.2	60.9 55.9	62.5 65.0	
	6	315	Rv:AGAGCCACCAAGCCAACAT				
	(SH2 adaptor)		Rvm:AGAGCCACCGAGCCAACAT				
	7 (Ring finger)	296	Fw:CCGAGGTTTGGGATTTTCTT	39.7	60.4 55.4	63.0 65.5	
			Rv:GAGATCCTTTTGGGGCTTTC				
			Rvm:GAGATCCTTCTGGGGCTTTC 44.7	44.7			
	8 (Ring finger)	307	Fw:CGTCTCCCTTCCTCTGTCTG	39.4 41.9	60.7 58.2	64.0 64.5	
			Rv:AGGAATTTGGATTCCAGCTC				
			Rvm:AGGAATTTGTATTCCAGCTC				
	9 (proline-rich)	245	Fw:CGAGAAGAAAATGGCAGCTC	41.5	58.6	64.5	
			Rv:ATGGGTGCCAAGGATGAGT				
			Rvm:ATGGGTGCCCAGGATGAGT				
			Fw:ACAAAGGGACAGGGAAGAG	70747.03	P10450	~ 1*	
	10 (proline-rich)	243	Rv:GGAGAGAGGGGTGGGTTAGA	41.5 46.5	58.6 53.6	61.5 65.0	
			Rvm:GGAGAGAGGGGTTAGA		2310		