

Table S1. *SF3B1* sequencing oligonucleotides

Exon	Direction	Oligonucleotide		
Exon 1	Forward	5'	GGATTCCTGGGTCACCAC	3'
Exon 1	Reverse	5'	GGCTTTTATTAGGCTAGCAACG	3'
Exon 2	Forward	5'	TGGGAGTTCTTTTGGAAAGTG	3'
Exon 2	Reverse	5'	CAGATGGCTGCAACAAAAGT	3'
Exon 3	Forward	5'	TTTTGAATCTTTGCATATTCTTTCTAA	3'
Exon 3	Reverse	5'	TGGGAACTCAGACATTCACCTTTT	3'
Exon 4	Forward	5'	TGTGCTTTATGGTGTTCTGATTTT	3'
Exon 4	Reverse	5'	TCAAAGGGCTAAAGACAACCTAAT	3'
Exon 5	Forward	5'	AGAGCAGGGCAGATAAATCA	3'
Exon 5	Reverse	5'	ACCTAACAGTCTCTCAATCACAACCT	3'
Exon 6	Forward	5'	TGGTAGAAAAATACATTGAAAGCA	3'
Exon 6	Reverse	5'	GCAGACTAATACAGTCCATAACAGAAA	3'
Exon 1	Forward	5'	TTTCTGTGTGGGTGTGTGAA	3'
Exon7	Reverse	5'	TTCAGTCTGTAAACATATCACTCAACA	3'
Exon8	Forward	5'	AATGGGTCACCATTTTAGGAA	3'
Exon8	Reverse	5'	AACAATTATGTCCAATGAGACAGTTC	3'
Exon9	Forward	5'	AGCAAATAATAGGATTGATCTTAACTG	3'
Exon9	Reverse	5'	TCCTAAATACCACCTCATTCAA	3'
Exon10	Forward	5'	TGCAAATATTGTTTATTATGCTGTT	3'
Exon10	Reverse	5'	TGTTAAGGGAAGTTGAAATGTTATGA	3'
Exon11	Forward	5'	TCATAACATTTCAACTCCCTTAACA	3'
Exon11	Reverse	5'	AAGCAACAAACATGACAATTTAACA	3'
Exon12	Forward	5'	GAAACCACACCTATTACTCTGCTC	3'
Exon12	Reverse	5'	AAGGAAAAGGTCTAGGAGAATATGT	3'
Exon13	Forward	5'	CATGAGCATTTCATCAGTAATTG	3'
Exon13	Reverse	5'	TCAACCATTTCTTTCCATAATCAA	3'
Exon14a	Forward	5'	CCAACCTCATGACTGTCCTTTCTT	3'
Exon14a	Reverse	5'	GGGCAACATAGTAAGACCCTGT	3'
Exon14b	Forward	5'	TCTGTTTATGGAATTGATTATGGAA	3'
Exon14b	Reverse	5'	CAACTTACCATGTTCAATGATTTT	3'
Exon15	Forward	5'	TTGGGGCATAGTTAAAACCTG	3'
Exon15	Reverse	5'	AAATCAAAGGTAATTGGTGGA	3'
Exon16	Forward	5'	TCTTCATTAAAGTTAAGGCGACA	3'
Exon16	Reverse	5'	CCAGTTTACATTAACAAATCTGGAA	3'
Exon17	Forward	5'	AAATCACGTAATCAGCAATGAGT	3'
Exon17	Reverse	5'	TGAGTTGAAAGGACTTTTGAGAA	3'
Exon18	Forward	5'	TTGGTTTTTCATGATGTTGCTTT	3'
Exon18	Reverse	5'	GCAATGTGCCATAATAGTTTTTCAT	3'

Exon	Direction	Oligonucleotide		
Exon19	Forward	5'	TCAACTGTGCAGTCATAAACCA	3'
Exon19	Reverse	5'	TTTGGGGAAGAAGTAAGAATTTG	3'
Exon20	Forward	5'	GCTGTTGTCATGAAGACTTGTC	3'
Exon20	Reverse	5'	TCTTATGTAACCAGCAAATTCCA	3'
Exon21	Forward	5'	AAGGAAAGTGAACAAAAGTTGC	3'
Exon21	Reverse	5'	AATTGAATACAAAGTGGCCAAA	3'
Exon22	Forward	5'	TCATGTTTTTGAAGACTGAATTTGC	3'
Exon22	Reverse	5'	TGGAAGTATTTTCCAATACCACA	3'
Exon23	Forward	5'	CAGCTTGTTGACCCATTTGTT	3'
Exon23	Reverse	5'	TTCACGATGTTCTAAAATGAAGGA	3'
Exon24a	Forward	5'	TTTAAGGATTTTTCCCCCTTTC	3'
Exon24a	Reverse	5'	CCCTCTAGGGCTCCCAT AAC	3'
Exon24b	Forward	5'	TCGCTGAATCACTTGTTGAA	3'
Exon24b	Reverse	5'	GCAGGGCTTAAAACCTAGATG	3'
Exon25a	Forward	5'	AAAATTGAAATAATGTAACCGTTCAA	3'
Exon25a	Reverse	5'	TGACCAGTTCTACTGATCTGC	3'

Table S2. Indexing oligonucleotides

Index	Oligonucleotide		
Forward 1	5'	AACGTGAT	3'
Forward 2	5'	ACCACTGT	3'
Forward 3	5'	ACAAGCTA	3'
Forward 4	5'	AACCGAGA	3'
Forward 5	5'	ACGTATCA	3'
Forward 6	5'	CAATGGAA	3'
Forward 7	5'	GCCACATA	3'
Forward 8	5'	TATCAGCA	3'
Reverse 1	5'	ATGCCTAA	3'
Reverse 2	5'	AGTGGTCA	3'
Reverse 3	5'	ACATTGGC	3'
Reverse 4	5'	CATCAAGT	3'
Reverse 5	5'	CGCTGATC	3'
Reverse 6	5'	AGTACAAG	3'
Reverse 7	5'	ACGCTCGA	3'
Reverse 8	5'	CAGATCTG	3'
Reverse 9	5'	AACGCTTA	3'
Reverse 10	5'	AGATCGCA	3'
Reverse 11	5'	ACCTCCAA	3'
Reverse 12	5'	AAGACGGA	3'

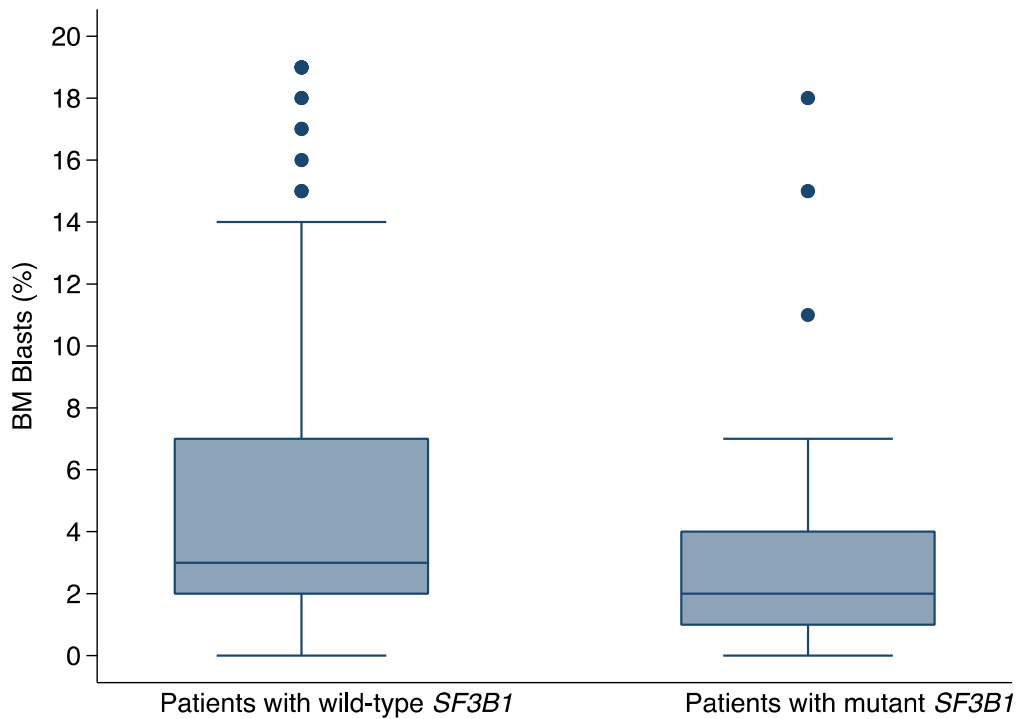


Figure S1. Relationship between *SF3B1* mutation status and proportion of bone marrow (BM) blasts

Although median values were close (3% in patients without *SF3B1* mutation vs. 2% in those with *SF3B1* mutation), comparison of the two groups by means of the Mann-Whitney test showed a significant lower proportion of bone marrow blasts in patients with *SF3B1* mutation ($P < .001$). Data are shown in a box plot depicting the smallest and largest observation (lowest and highest line, respectively), lower and upper quartile with median value (box), and outliers (dots).

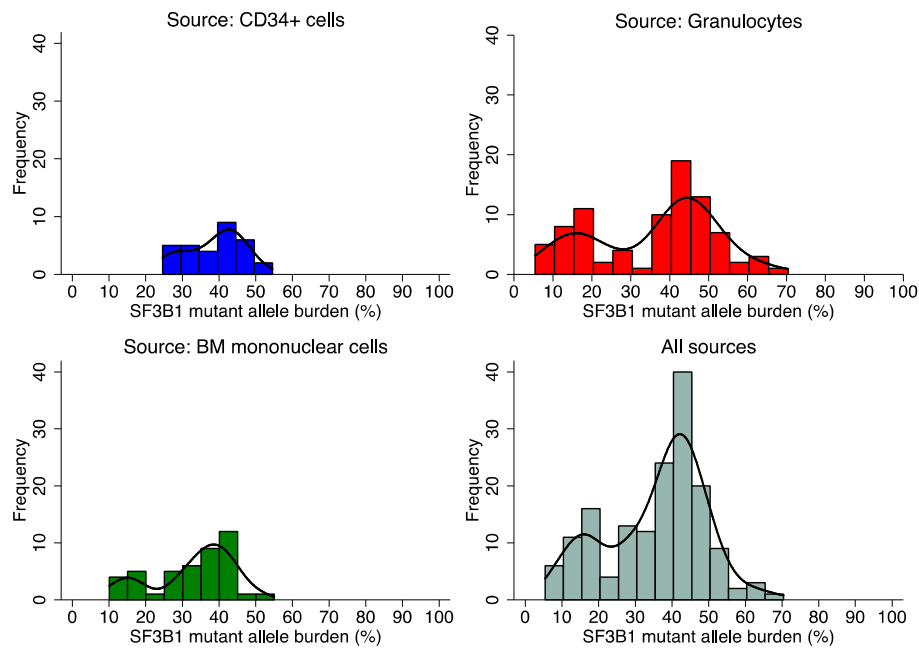


Figure S2. Histogram of *SF3B1* mutant allele burden in DNA samples from different sources

Median values for *SF3B1* mutant allele burden were 40.6% (24.6-52.1%) in the CD34-positive cell DNA subgroup, 40.9% (7.5-70.3%) in the granulocyte DNA subgroup, and 35.7% (10.1-51.1%) in the bone marrow DNA subgroup. Kruskal–Wallis one-way analysis of variance by ranks showed no significant difference in *SF3B1* mutant allele burden between these subgroups ($P=.077$). In each group, the bimodal distribution has been highlighted by adding a Gaussian kernel density plot to the histogram.