

Supplementary Table 1. Recurrently reported mutational hotspots across the 48 somatic landscape studies. Listed are 434 hotspots reported to have splice-site or protein-altering mutations in 3 or more patients at diagnosis of ALL, AML, CML, CMML, JMML, MPN, or MDS across the 48 NGS studies. All original reported mutations were mapped to the single transcript per gene shown. The last column contains reference numbers from the main paper and hyperlinks to the original articles.

Gene	AA locus	No. patients*	No. hemat. disorders†	No. studies‡	Transcript§	Studies observed in
<i>DNMT3A</i>	p.R882	517	6	20	NM_022552	33,36,38,44,49,56,57,53,52,47,39,32,15,50,16,34,26,29,46,41
<i>NPM1</i>	p.W288	411	2	4	NM_002520	38,55,25,34
<i>NRAS</i>	p.G12	345	6	35	NM_002524	18,24,36,38,44,49,55,56,53,45,40,31,14,12,52,32,15,11,17,20,37,3,51,50,16,34,26,30,35,21,28,27,46,48,41
<i>JAK2</i>	p.V617	282	5	14	NM_004972	36,38,44,56,57,31,52,23,25,50,34,35,27,46
<i>NRAS</i>	p.Q61	210	5	21	NM_002524	24,33,36,38,44,49,40,31,15,17,3,51,34,26,30,35,21,28,27,48,41
<i>IDH2</i>	p.R140	201	5	19	NM_002168	24,33,36,38,44,55,57,53,12,52,32,50,16,34,35,29,28,46,41
<i>IDH1</i>	p.R132	185	5	16	NM_005896	24,33,36,38,56,57,12,52,32,15,3,50,34,26,46,41
<i>FLT3</i>	p.D835	177	2	15	NM_004119	24,33,36,38,31,19,15,37,34,26,30,35,21,29,27
<i>SRSF2</i>	p.P95	172	4	15	NM_003016	33,38,44,55,57,53,45,52,50,34,35,29,28,46,41
<i>NRAS</i>	p.G13	158	5	26	NM_002524	18,24,33,36,38,49,55,53,31,19,12,52,15,11,17,25,37,16,34,30,35,21,27,46,48,41
<i>KRAS</i>	p.G12	135	5	27	NM_033360	18,24,36,38,44,49,55,45,31,19,14,15,11,25,37,3,51,50,16,26,30,35,21,27,46,48,41
<i>KIT</i>	p.D816	108	4	13	NM_000222	24,36,38,40,31,50,16,34,26,30,27,46,41
<i>NPM1</i>	p.L287	79	4	8	NM_002520	38,44,52,32,51,34,46,48
<i>U2AF1</i>	p.S34	72	5	16	NM_001025203	24,33,36,38,44,57,53,52,32,3,50,16,34,29,46,41
<i>PTPN11</i>	p.E76	67	4	8	NM_002834	24,38,49,55,31,21,48,41
<i>KRAS</i>	p.G13	65	3	18	NM_033360	24,36,38,49,19,15,11,17,3,16,34,30,35,21,29,27,48,41
<i>IDH2</i>	p.R172	59	1	6	NM_002168	36,38,32,34,29,41
<i>SF3B1</i>	p.K700	55	4	11	NM_012433	36,38,57,53,52,32,25,50,28,46,41
<i>PTPN11</i>	p.A72	45	4	14	NM_002834	24,33,36,38,49,55,19,15,51,34,35,21,48,41
<i>FBXW7</i>	p.R465	44	2	5	NM_033632	38,13,12,17,16
<i>PTPN11</i>	p.D61	37	4	11	NM_002834	24,36,38,49,55,19,51,50,30,48,41
<i>ASXL1</i>	p.H630	33	5	10	NM_015338	38,44,49,57,43,42,34,28,27,46
<i>KIT</i>	p.N822	31	1	7	NM_000222	24,38,40,34,26,30,27
<i>U2AF1</i>	p.Q157	31	4	10	NM_001025203	36,38,44,57,53,45,52,54,50,46
<i>ASXL1</i>	p.G643	27	3	8	NM_015338	44,45,34,35,29,28,46,48
<i>SF3B1</i>	p.K666	27	3	8	NM_012433	33,38,52,32,50,34,46,41
<i>TP53</i>	p.R273	27	5	12	NM_000546	36,38,44,56,57,52,11,3,50,34,35,22
<i>FLT3</i>	p.N676	26	3	7	NM_004119	24,33,38,11,37,50,30
<i>MYC</i>	p.P74	25	2	5	NM_002467	24,36,38,23,26
<i>PTPN11</i>	p.G503	25	3	8	NM_002834	24,33,38,49,31,30,46,48
<i>RPL10</i>	p.R98	25	1	3	NM_001303625	13,17,16
<i>RUNX1</i>	p.R201	25	4	9	NM_001754	24,36,38,44,52,32,17,50,41
<i>NOTCH1</i>	p.L1678	24	1	2	NM_017617	13,16
<i>FBXW7</i>	p.R479	23	1	3	NM_033632	12,17,16
<i>WT1</i>	p.R462	23	3	9	NM_024426	24,36,38,31,52,37,16,28,41
<i>NOTCH1</i>	p.L1600	22	1	3	NM_017617	13,12,16
<i>RUNX1</i>	p.R166	22	4	7	NM_001754	38,44,32,15,50,34,41

TP53	p.R248	21	3	8	NM_000546	24,36,38,53,52,3,50,22
JAK3	p.M511	20	2	7	NM_000215	36,13,12,15,17,16,27
RUNX1	p.R162	20	5	10	NM_001754	24,36,38,44,56,50,16,34,27,41
WT1	p.S381	20	3	12	NM_024426	24,38,55,31,12,52,32,17,37,16,28,27
ASXL1	p.R693	19	5	10	NM_015338	38,44,53,42,23,51,50,16,46,41
FLT3	p.I836	19	2	5	NM_004119	38,19,15,3,27
FLT3	p.V491	19	2	4	NM_004119	24,38,37,16
KRAS	p.Q61	19	3	9	NM_033360	24,36,38,49,11,37,34,48,41
NOTCH1	p.L1585	19	1	3	NM_017617	13,12,16
PTPN11	p.S502	19	3	7	NM_002834	36,38,44,15,34,28,41
KIT	p.Y418	18	1	5	NM_000222	24,36,26,30,27
KRAS	p.A146	18	4	10	NM_033360	18,36,38,44,31,19,11,17,37,50
PTPN11	p.G60	18	3	10	NM_002834	36,38,49,31,19,3,30,28,48,41
SETBP1	p.D868	18	4	8	NM_015559	36,44,49,55,51,46,48,41
FBXW7	p.R505	17	2	4	NM_033632	38,13,12,16
FLT3	p.D839	17	2	9	NM_004119	24,36,38,32,15,11,34,26,27
RUNX1	p.R204	17	4	7	NM_001754	24,33,38,42,16,34,46
WHSC1	p.E1099	17	1	8	NM_133330	18,19,14,15,23,11,17,3
WT1	p.R370	17	2	10	NM_024426	33,38,13,32,17,37,16,34,26,27
NF1	p.T676	16	3	4	NM_001042492	49,52,34,48
SRSF2	p.S101	16	1	1	NM_003016	38
TP53	p.R175	16	3	4	NM_000546	38,52,15,22
WT1	p.R458	16	2	8	NM_024426	24,38,32,37,16,30,28,41
RUNX1	p.D198	15	3	8	NM_001754	24,33,36,38,52,34,28,46
SETBP1	p.G870	15	4	6	NM_015559	36,44,49,52,51,48
FLT3	p.A680	14	1	3	NM_004119	24,38,34
KIT	p.D419	14	1	4	NM_000222	24,26,30,27
NOTCH1	p.F1592	14	1	2	NM_017617	12,16
NOTCH1	p.I1680	14	1	3	NM_017617	13,12,16
NOTCH1	p.R1598	14	1	3	NM_017617	13,12,16
PTEN	p.R406	14	2	4	NM_001304717	38,12,16,27
TP53	p.Y220	14	4	5	NM_000546	38,44,52,34,22
CSF3R	p.T618	13	3	5	NM_156039	24,36,44,3,41
DHX15	p.R222	13	1	5	NM_001358	24,40,31,30,27
DNMT3A	p.G543	13	2	6	NM_022552	33,38,53,52,39,41
FLT3	p.N841	13	1	4	NM_004119	24,38,37,27
PHF6	p.R116	13	2	6	NM_001015877	24,38,13,12,23,16
PHF6	p.R274	13	3	6	NM_001015877	38,13,52,15,23,16
CALR	p.E364	12	1	1	NM_004343	57
CEBPA	p.V314	12	1	1	NM_004364	38
EZH2	p.R690	12	3	7	NM_004456	24,36,38,56,57,52,54
WT1	p.D464	12	1	3	NM_024426	24,38,27
WT1	p.R369	12	2	7	NM_024426	24,38,13,17,37,16,29
CALR	p.K385	11	1	1	NM_004343	57
DNMT3A	p.R736	11	1	4	NM_022552	33,36,38,34

<i>DNMT3A</i>	p.S714	11	2	4	NM_022552	33,38,52,39
<i>KRAS</i>	p.K117	11	2	6	NM_033360	24,38,19,15,11,37
<i>MPL</i>	p.W515	11	1	2	NM_005373	56,57
<i>WT1</i>	p.R380	11	1	6	NM_024426	24,33,34,26,30,27
<i>ZRSR2</i>	p.S439	11	3	4	NM_005089	49,29,27,46
<i>ASXL2</i>	p.T740	10	2	3	NM_018263	23,30,27
<i>JAK3</i>	p.R657	10	3	6	NM_000215	49,12,16,30,27,48
<i>NOTCH1</i>	p.L1574	10	1	2	NM_017617	12,16
<i>RUNX1</i>	p.S141	10	5	9	NM_001754	36,38,52,43,32,16,26,46,41
<i>TET2</i>	p.Q916	10	4	6	NM_001127208	36,38,56,52,46,41
<i>TET2</i>	p.R550	10	3	5	NM_001127208	36,38,50,34,46
<i>TP53</i>	p.G245	10	4	5	NM_000546	38,52,42,25,22
<i>TP53</i>	p.M237	10	3	4	NM_000546	38,52,17,22
<i>U2AF1</i>	p.R156	10	2	4	NM_001025203	24,38,44,31
<i>WT1</i>	p.H465	10	1	4	NM_024426	24,36,38,37
<i>CBL</i>	p.C404	9	4	6	NM_005188	38,44,56,50,35,46
<i>CBL</i>	p.Y371	9	3	3	NM_005188	38,44,49
<i>CEBPA</i>	p.E309	9	1	1	NM_004364	36
<i>CEBPA</i>	p.K313	9	1	1	NM_004364	38
<i>DNMT3A</i>	p.P904	9	2	4	NM_022552	38,52,39,41
<i>FLT3</i>	p.S451	9	1	5	NM_004119	24,33,38,34,30
<i>JAK2</i>	p.R683	9	2	5	NM_004972	15,17,20,3,27
<i>PTPN11</i>	p.E69	9	4	7	NM_002834	38,49,52,15,11,3,51
<i>TET2</i>	p.R1216	9	2	5	NM_001127208	24,36,38,34,46
<i>TP53</i>	p.I195	9	2	5	NM_000546	36,38,25,34,22
<i>WT1</i>	p.P376	9	2	5	NM_024426	24,16,34,30,35
<i>ARIH1</i>	p.G79	8	1	1	NM_005744	44
<i>CBL</i>	p.C396	8	3	5	NM_005188	38,44,52,46,41
<i>CBL</i>	p.splice_E366	8	3	6	NM_005188	24,36,38,44,30,48
<i>CNOT3</i>	p.R57	8	1	3	NM_014516	13,12,16
<i>KIT</i>	p.T417	8	1	4	NM_000222	31,34,30,27
<i>MYC</i>	p.P75	8	2	4	NM_002467	24,33,38,17
<i>NOTCH1</i>	p.L1593	8	1	3	NM_017617	13,12,16
<i>PIK3CD</i>	p.E1021	8	1	2	NM_005026	12,16
<i>PTPN11</i>	p.F71	8	2	5	NM_002834	24,36,38,31,16
<i>TET2</i>	p.C1271	8	4	8	NM_001127208	38,56,57,53,25,50,34,46
<i>TET2</i>	p.R1261	8	5	6	NM_001127208	38,44,57,15,50,34
<i>TP53</i>	p.C275	8	4	5	NM_000546	38,57,52,34,22
<i>TP53</i>	p.R282	8	2	6	NM_000546	14,11,3,16,34,22
<i>WT1</i>	p.A382	8	3	7	NM_024426	38,52,32,17,34,26,27
<i>WT1</i>	p.R434	8	2	2	NM_024426	38,16
<i>WT1</i>	p.V379	8	3	6	NM_024426	12,52,16,26,30,27
<i>ASXL1</i>	p.Y591	7	5	6	NM_015338	44,49,56,57,42,50
<i>BRAF</i>	p.V600	7	2	3	NM_004333	33,38,21
<i>DNMT3A</i>	p.S770	7	3	4	NM_022552	38,57,52,41

<i>DNMT3A</i>	p.W893	7	2	3	NM_022552	38,56,41
<i>EZH2</i>	p.E745	7	3	6	NM_004456	24,33,38,44,13,16
<i>FBXW7</i>	p.R689	7	1	3	NM_033632	12,17,16
<i>FLT3</i>	p.F594	7	1	6	NM_004119	24,33,36,38,37,30
<i>FLT3</i>	p.L576	7	2	5	NM_004119	38,14,15,37,3
<i>GATA2</i>	p.A318	7	1	3	NM_032638	24,38,34
<i>GATA2</i>	p.A372	7	1	3	NM_032638	24,38,31
<i>GATA2</i>	p.L321	7	2	3	NM_032638	38,49,28
<i>KDM6A</i>	p.V1113	7	2	5	NM_021140	38,13,23,16,30
<i>NOTCH1</i>	p.P2514	7	1	1	NM_017617	16
<i>NRAS</i>	p.A59	7	4	7	NM_002524	33,49,57,52,50,26,48
<i>PIK3R1</i>	p.N564	7	1	2	NM_181523	14,16
<i>PTPN11</i>	p.P491	7	1	3	NM_002834	24,36,38
<i>PTPN11</i>	p.Q510	7	2	4	NM_002834	36,38,13,34
<i>PTPN11</i>	p.T73	7	2	2	NM_002834	38,49
<i>SF3B1</i>	p.R625	7	2	4	NM_012433	38,52,50,41
<i>STAG2</i>	p.R216	7	2	4	NM_001042749	24,38,34,46
<i>STAT5B</i>	p.N642	7	1	3	NM_012448	12,17,16
<i>TET2</i>	p.C1298	7	3	5	NM_001127208	38,44,52,50,41
<i>TET2</i>	p.I274	7	3	4	NM_001127208	38,44,50,46
<i>TET2</i>	p.R1359	7	3	6	NM_001127208	33,38,44,52,50,34
<i>TET2</i>	p.R1516	7	2	4	NM_001127208	36,38,44,45
<i>TP53</i>	p.S241	7	2	2	NM_000546	38,22
<i>WT1</i>	p.R430	7	3	5	NM_024426	33,38,52,37,16
<i>ASXL1</i>	p.G642	6	2	3	NM_015338	33,52,51
<i>BRAF</i>	p.D594	6	3	4	NM_004333	38,55,16,35
<i>CCND2</i>	p.P281	6	1	2	NM_001759	30,27
<i>CEBPA</i>	p.R300	6	1	2	NM_004364	36,38
<i>EZH2</i>	p.R684	6	2	5	NM_004456	24,38,13,16,41
<i>FLT3</i>	p.M664	6	1	3	NM_004119	24,38,34
<i>FLT3</i>	p.Y591	6	2	4	NM_004119	38,32,15,30
<i>GATA2</i>	p.N317	6	2	4	NM_032638	24,38,49,34
<i>MYCN</i>	p.P44	6	1	1	NM_001293228	16
<i>NF1</i>	p.R1534	6	3	4	NM_001042492	38,49,14,34
<i>NOTCH1</i>	p.V1676	6	2	2	NM_017617	16,34
<i>PHF6</i>	p.R225	6	2	4	NM_001015877	38,17,16,34
<i>RIT1</i>	p.M90	6	4	5	NM_006912	36,44,55,15,3
<i>RUNX1</i>	p.G165	6	1	3	NM_001754	33,38,34
<i>RUNX1</i>	p.R107	6	3	3	NM_001754	38,50,46
<i>RUNX1</i>	p.R169	6	2	2	NM_001754	38,52
<i>SMC1A</i>	p.G1131	6	2	5	NM_006306	40,23,30,29,27
<i>TET2</i>	p.H1380	6	4	4	NM_001127208	38,56,50,46
<i>TET2</i>	p.R544	6	5	5	NM_001127208	38,56,43,50,46
<i>TET2</i>	p.splice_E1137	6	3	4	NM_001127208	38,57,34,46
<i>TP53</i>	p.C176	6	2	5	NM_000546	36,38,14,3,22

TP53	p.C238	6	3	4	NM_000546	38,52,50,22
TP53	p.V143	6	3	4	NM_000546	38,52,22,41
TP53	p.V272	6	3	3	NM_000546	38,52,22
U2AF1	p.R35	6	2	3	NM_001025203	24,38,16
AKT1	p.E17	5	1	2	NM_001014432	12,16
ASXL1	p.R965	5	3	4	NM_015338	44,56,52,54
CBL	p.L380	5	2	2	NM_005188	38,46
CCND2	p.T280	5	1	2	NM_001759	26,27
CCND3	p.A269	5	1	1	NM_001760	16
CEBPA	p.Q311	5	1	1	NM_004364	38
CREBBP	p.R1446	5	1	3	NM_004380	19,3,16
CRLF2	p.F232	5	1	1	NM_022148	3
CTCF	p.T204	5	2	3	NM_006565	12,25,16
DNMT3A	p.R635	5	2	4	NM_022552	38,52,39,41
EZH2	p.R288	5	3	4	NM_004456	49,56,57,34
GATA2	p.G320	5	1	3	NM_032638	24,38,26
GATA2	p.R330	5	2	3	NM_032638	24,38,49
GATA2	p.R362	5	1	1	NM_032638	38
GATA2	p.R398	5	1	2	NM_032638	24,38
JAK1	p.R724	5	1	2	NM_002227	12,16
KIT	p.D820	5	1	4	NM_000222	24,38,30,27
MYC	p.T73	5	2	3	NM_002467	38,15,3
NOTCH1	p.I1616	5	1	1	NM_017617	16
NOTCH1	p.Q2503	5	1	1	NM_017617	16
PHF6	p.C242	5	2	3	NM_001015877	36,38,23
PHF6	p.R319	5	3	5	NM_001015877	55,23,17,16,46
PTPN11	p.F285	5	2	3	NM_002834	18,38,34
PTPN11	p.N308	5	3	4	NM_002834	24,33,44,50
SF3B1	p.H662	5	2	2	NM_012433	38,50
SMC1A	p.R586	5	2	5	NM_006306	36,55,30,27,41
SMC3	p.R661	5	1	5	NM_005445	24,36,30,27,41
STAG2	p.R1045	5	2	3	NM_001042749	36,38,52
STAG2	p.R259	5	1	1	NM_001042749	38
TET2	p.F868	5	1	1	NM_001127208	42
TET2	p.H1912	5	2	3	NM_001127208	38,44,34
TET2	p.I1873	5	3	4	NM_001127208	33,44,57,46
TET2	p.L1322	5	3	4	NM_001127208	38,56,52,41
TET2	p.Q958	5	3	4	NM_001127208	38,44,31,50
TP53	p.R283	5	2	2	NM_000546	38,22
TP53	p.splice_Y126	5	2	4	NM_000546	36,38,52,25
TP53	p.V216	5	3	3	NM_000546	56,52,22
TP53	p.Y234	5	3	3	NM_000546	38,50,22
TRIM24	p.R910	5	1	2	NM_015905	24,36
USP7	p.D482	5	1	2	NM_003470	17,16
ASXL1	p.P808	4	3	4	NM_015338	38,57,52,41

ASXL1	p.Q588	4	1	1	NM_015338	38
ASXL1	p.Q733	4	3	3	NM_015338	36,44,57
BCL11B	p.R471	4	1	1	NM_001282237	16
BCL11B	p.T449	4	1	3	NM_001282237	13,17,16
BCOR	p.N1425	4	2	2	NM_017745	24,16
CBL	p.C384	4	3	4	NM_005188	24,49,45,48
CBL	p.C401	4	2	3	NM_005188	33,38,57
CBL	p.E366	4	2	3	NM_005188	24,45,30
CBL	p.F418	4	1	2	NM_005188	38,41
CEBPA	p.D301	4	1	1	NM_004364	38
CEBPA	p.N307	4	1	1	NM_004364	38
CEBPA	p.Q312	4	1	1	NM_004364	38
CEBPA	p.Q83	4	1	2	NM_004364	24,38
CEBPA	p.R297	4	1	1	NM_004364	38
DNMT3A	p.C497	4	1	3	NM_022552	36,38,39
DNMT3A	p.I705	4	3	4	NM_022552	38,57,42,32
DNMT3A	p.L547	4	1	1	NM_022552	38
DNMT3A	p.N879	4	2	3	NM_022552	38,50,41
DNMT3A	p.Q842	4	1	1	NM_022552	38
DNMT3A	p.R320	4	2	3	NM_022552	36,38,47
DNMT3A	p.R598	4	3	4	NM_022552	38,56,47,41
DNMT3A	p.R729	4	1	3	NM_022552	33,36,38
DNMT3A	p.R771	4	2	4	NM_022552	38,52,50,28
DNMT3A	p.W581	4	2	2	NM_022552	38,12
DNMT3A	p.W860	4	2	4	NM_022552	33,32,25,50
ETV6	p.R105	4	2	2	NM_001987	38,14
EZH2	p.S695	4	2	4	NM_004456	38,23,26,30
FBXW7	p.G423	4	2	2	NM_033632	38,16
FLT3	p.V592	4	2	3	NM_004119	38,19,15
JAK2	p.N542	4	1	2	NM_004972	56,57
KIT	p.L416	4	1	2	NM_000222	30,27
KRAS	p.A59	4	2	4	NM_033360	24,36,12,15
NF1	p.R1276	4	3	4	NM_001042492	36,44,49,46
NOTCH1	p.V1721	4	1	2	NM_017617	13,16
NPM1	p.Q289	4	1	1	NM_002520	38
PHF6	p.R129	4	1	2	NM_001015877	23,16
PTEN	p.P419	4	1	1	NM_001304717	16
PTPN11	p.N58	4	2	2	NM_002834	38,21
RAD21	p.R586	4	1	2	NM_006265	38,30
RUNX1	p.L56	4	1	1	NM_001754	46
RUNX1	p.R346	4	2	3	NM_001754	38,50,34
RUNX1	p.splice_G170	4	2	4	NM_001754	24,36,38,52
SMC1A	p.R711	4	2	3	NM_006306	33,30,46
SMC3	p.R381	4	1	3	NM_005445	24,36,41
SRSF2	p.P96	4	2	3	NM_003016	38,44,34

STAG2	p.R1033	4	1	2	NM_001042749	38,41
STAG2	p.S1065	4	1	1	NM_001042749	38
TET2	p.A912	4	2	3	NM_001127208	38,23,30
TET2	p.E1178	4	3	3	NM_001127208	38,44,50
TET2	p.F653	4	2	3	NM_001127208	38,44,45
TET2	p.R1262	4	2	3	NM_001127208	38,52,34
TET2	p.R1404	4	3	3	NM_001127208	38,50,46
TET2	p.R1465	4	2	3	NM_001127208	38,44,41
TET2	p.splice_E1268	4	2	3	NM_001127208	44,52,50
TET2	p.splice_E1318	4	2	2	NM_001127208	38,50
TP53	p.H179	4	2	4	NM_000546	36,56,25,34
TP53	p.K132	4	2	2	NM_000546	38,22
TP53	p.R158	4	3	4	NM_000546	38,52,26,22
TP53	p.R267	4	3	3	NM_000546	38,52,22
USP7	p.R340	4	1	2	NM_003470	23,16
ZEB2	p.H1038	4	2	3	NM_014795	33,15,3
ASXL1	p.L775	3	3	3	NM_015338	38,50,48
ASXL1	p.Q695	3	2	2	NM_015338	38,44
ASXL1	p.Q708	3	3	3	NM_015338	56,52,46
ASXL1	p.R417	3	2	3	NM_015338	38,56,57
ASXL1	p.R634	3	1	1	NM_015338	46
ASXL1	p.Y974	3	2	3	NM_015338	38,56,57
ASXL2	p.R591	3	1	2	NM_018263	24,27
ASXL2	p.R719	3	1	1	NM_018263	27
ASXL2	p.S524	3	2	3	NM_018263	23,30,27
BCL11B	p.Y454	3	1	1	NM_001282237	16
BRAF	p.N581	3	2	3	NM_004333	15,50,16
CBL	p.C381	3	3	3	NM_005188	33,50,46
CBL	p.L370	3	2	3	NM_005188	38,44,30
CBL	p.Q367	3	1	3	NM_005188	36,38,30
CEBPA	p.A295	3	1	2	NM_004364	38,34
CEBPA	p.A303	3	1	1	NM_004364	38
CEBPA	p.A66	3	1	1	NM_004364	38
CEBPA	p.E316	3	1	2	NM_004364	38,41
CEBPA	p.E59	3	1	2	NM_004364	36,38
CEBPA	p.L317	3	1	1	NM_004364	38
CEBPA	p.N321	3	1	1	NM_004364	38
CEBPA	p.P43	3	1	2	NM_004364	38,34
CEBPA	p.V308	3	1	2	NM_004364	24,38
CEBPA	p.Y67	3	1	1	NM_004364	38
CHD4	p.R1162	3	2	3	NM_001273	24,15,17
DDX41	p.R525	3	1	2	NM_016222	36,34
DNM2	p.R770	3	1	3	NM_001005360	13,17,16
DNMT3A	p.A910	3	2	3	NM_022552	47,34,41
DNMT3A	p.F731	3	3	3	NM_022552	44,57,34

<i>DNMT3A</i>	p.F902	3	1	3	NM_022552	38,26,27
<i>DNMT3A</i>	p.G707	3	2	2	NM_022552	38,49
<i>DNMT3A</i>	p.L773	3	1	2	NM_022552	38,34
<i>DNMT3A</i>	p.M880	3	1	3	NM_022552	33,38,32
<i>DNMT3A</i>	p.R749	3	1	2	NM_022552	38,32
<i>DNMT3A</i>	p.R803	3	1	2	NM_022552	36,38
<i>DNMT3A</i>	p.splice_F827	3	1	1	NM_022552	38
<i>DNMT3A</i>	p.splice_R556	3	2	3	NM_022552	36,38,12
<i>EP300</i>	p.C1201	3	1	1	NM_001429	38
<i>ETV6</i>	p.F102	3	2	3	NM_001987	38,55,31
<i>EZH2</i>	p.E249	3	2	3	NM_004456	38,52,54
<i>EZH2</i>	p.G648	3	1	2	NM_004456	38,30
<i>EZH2</i>	p.I131	3	2	2	NM_004456	38,52
<i>EZH2</i>	p.V626	3	2	2	NM_004456	56,32
<i>FBXO28</i>	p.R348	3	1	1	NM_015176	16
<i>FLT3</i>	p.L601	3	3	3	NM_004119	55,32,11
<i>FLT3</i>	p.T582	3	3	3	NM_004119	19,32,46
<i>GATA2</i>	p.L359	3	2	2	NM_032638	38,16
<i>GATA2</i>	p.P304	3	1	2	NM_032638	36,38
<i>GATA2</i>	p.R307	3	1	1	NM_032638	41
<i>GATA3</i>	p.A287	3	1	1	NM_001002295	16
<i>GATA3</i>	p.R276	3	1	2	NM_001002295	13,12
<i>GIGYF2</i>	p.R792	3	1	1	NM_001103147	30
<i>GNAS</i>	p.R201	3	2	2	NM_000516	38,50
<i>GNB1</i>	p.D76	3	1	2	NM_002074	3,16
<i>GNB1</i>	p.K57	3	2	2	NM_002074	36,52
<i>HDAC7</i>	p.R116	3	1	2	NM_015401	23,16
<i>IKZF1</i>	p.N159	3	3	3	NM_006060	55,31,16
<i>JAK3</i>	p.L857	3	1	2	NM_000215	13,16
<i>JAK3</i>	p.V674	3	1	1	NM_000215	16
<i>KDM6A</i>	p.R1111	3	2	3	NM_021140	31,23,16
<i>KMT2C</i>	p.C391	3	1	2	NM_170606	32,37
<i>MED12</i>	p.R82	3	1	2	NM_005120	12,17
<i>MPL</i>	p.R592	3	3	3	NM_005373	38,44,57
<i>MPL</i>	p.S505	3	1	1	NM_005373	25
<i>MYC</i>	p.A59	3	1	1	NM_002467	38
<i>NF1</i>	p.R2258	3	2	2	NM_001042492	38,49
<i>NF1</i>	p.R2637	3	2	3	NM_001042492	24,16,30
<i>NF1</i>	p.R461	3	2	3	NM_001042492	24,38,14
<i>NF1</i>	p.R711	3	1	2	NM_001042492	38,30
<i>NF1</i>	p.S2309	3	1	2	NM_001042492	38,30
<i>NOTCH1</i>	p.C1528	3	1	1	NM_017617	16
<i>NOTCH1</i>	p.I1718	3	1	2	NM_017617	13,16
<i>NOTCH1</i>	p.P2458	3	1	1	NM_017617	16
<i>NOTCH1</i>	p.Q2391	3	1	1	NM_017617	16

<i>NOTCH1</i>	p.Q2395	3	1	2	NM_017617	12,16
<i>NOTCH1</i>	p.Q2459	3	1	3	NM_017617	13,12,16
<i>NOTCH1</i>	p.S2461	3	1	1	NM_017617	16
<i>NOTCH1</i>	p.T2466	3	1	2	NM_017617	12,16
<i>NRAS</i>	p.G60	3	3	3	NM_002524	52,16,46
<i>NSD1</i>	p.Y1971	3	1	3	NM_022455	33,32,26
<i>PAX5</i>	p.P80	3	1	1	NM_016734	15
<i>PAX5</i>	p.V26	3	1	3	NM_016734	14,15,20
<i>PHF6</i>	p.C20	3	2	2	NM_001015877	38,46
<i>PHF6</i>	p.E139	3	2	3	NM_001015877	36,23,16
<i>PHF6</i>	p.F263	3	2	2	NM_001015877	38,23
<i>PHF6</i>	p.G275	3	2	2	NM_001015877	38,12
<i>PHF6</i>	p.H239	3	2	3	NM_001015877	38,23,16
<i>PHF6</i>	p.I314	3	3	3	NM_001015877	38,13,52
<i>PHF6</i>	p.M243	3	2	3	NM_001015877	38,17,27
<i>PHF6</i>	p.S246	3	1	2	NM_001015877	23,16
<i>PHF6</i>	p.splice_M278	3	2	2	NM_001015877	38,16
<i>PHF6</i>	p.splice_R196	3	1	3	NM_001015877	24,36,38
<i>PIK3CA</i>	p.C420	3	1	2	NM_006218	11,16
<i>PPP4C</i>	p.D54	3	1	3	NM_002720	12,23,3
<i>PTEN</i>	p.L420	3	1	1	NM_001304717	16
<i>PTEN</i>	p.T405	3	1	2	NM_001304717	12,16
<i>PTPN11</i>	p.A461	3	1	2	NM_002834	38,28
<i>PTPN11</i>	p.E139	3	2	2	NM_002834	38,49
<i>RAD21</i>	p.A20	3	1	2	NM_006265	38,30
<i>RAD21</i>	p.Q432	3	1	2	NM_006265	38,26
<i>RAD21</i>	p.R65	3	1	3	NM_006265	24,33,38
<i>RAD21</i>	p.splice_D441	3	1	1	NM_006265	38
<i>RAD21</i>	p.V32	3	1	1	NM_006265	38
<i>RUNX1</i>	p.A142	3	1	2	NM_001754	38,34
<i>RUNX1</i>	p.D160	3	2	2	NM_001754	38,16
<i>RUNX1</i>	p.G168	3	1	2	NM_001754	38,32
<i>RUNX1</i>	p.L98	3	2	2	NM_001754	38,50
<i>RUNX1</i>	p.P200	3	2	2	NM_001754	38,46
<i>RUNX1</i>	p.S226	3	1	2	NM_001754	38,41
<i>RUNX1</i>	p.S322	3	3	3	NM_001754	38,42,50
<i>RUNX1</i>	p.splice_D269	3	1	1	NM_001754	38
<i>RUNX1</i>	p.splice_R205	3	3	3	NM_001754	38,49,50
<i>SETBP1</i>	p.I871	3	3	3	NM_015559	44,55,25
<i>SETD2</i>	p.S1572	3	2	3	NM_014159	15,23,30
<i>SF3B1</i>	p.D781	3	2	3	NM_012433	38,52,41
<i>SF3B1</i>	p.G742	3	2	3	NM_012433	38,16,41
<i>SMARCA2</i>	p.G1202	3	2	3	NM_003070	23,25,28
<i>SPI1</i>	p.R231	3	1	3	NM_001080547	24,40,35
<i>SRSF2</i>	p.F57	3	1	2	NM_003016	38,32

<i>STAG2</i>	p.R1012	3	2	2	NM_001042749	38,53
<i>STAG2</i>	p.R110	3	1	2	NM_001042749	24,38
<i>STAG2</i>	p.R614	3	2	3	NM_001042749	36,38,52
<i>STAG2</i>	p.Y636	3	2	2	NM_001042749	38,50
<i>TET2</i>	p.C1193	3	1	2	NM_001127208	38,41
<i>TET2</i>	p.C1273	3	1	1	NM_001127208	38
<i>TET2</i>	p.E1874	3	2	3	NM_001127208	38,44,34
<i>TET2</i>	p.F1377	3	2	2	NM_001127208	38,46
<i>TET2</i>	p.L1212	3	2	3	NM_001127208	33,38,46
<i>TET2</i>	p.L1872	3	1	2	NM_001127208	38,41
<i>TET2</i>	p.Q654	3	3	3	NM_001127208	38,52,46
<i>TET2</i>	p.Q705	3	2	2	NM_001127208	38,57
<i>TET2</i>	p.Q749	3	3	3	NM_001127208	38,56,53
<i>TET2</i>	p.Q810	3	2	2	NM_001127208	38,56
<i>TET2</i>	p.Q886	3	3	3	NM_001127208	38,57,50
<i>TET2</i>	p.Q913	3	3	3	NM_001127208	23,50,30
<i>TET2</i>	p.R1452	3	2	3	NM_001127208	36,38,50
<i>TET2</i>	p.S1848	3	3	3	NM_001127208	38,44,50
<i>TET2</i>	p.S217	3	3	3	NM_001127208	57,50,46
<i>TET2</i>	p.S825	3	2	3	NM_001127208	53,50,41
<i>TET2</i>	p.splice_I1349	3	2	2	NM_001127208	38,50
<i>TET2</i>	p.splice_W1198	3	2	3	NM_001127208	44,45,50
<i>TET2</i>	p.W954	3	3	3	NM_001127208	38,56,46
<i>TP53</i>	p.A276	3	2	3	NM_000546	38,11,22
<i>TP53</i>	p.C242	3	2	2	NM_000546	38,22
<i>TP53</i>	p.K164	3	2	2	NM_000546	38,22
<i>TP53</i>	p.N239	3	2	2	NM_000546	38,56
<i>TP53</i>	p.R337	3	2	2	NM_000546	36,22
<i>TP53</i>	p.S215	3	1	2	NM_000546	36,38
<i>TP53</i>	p.V173	3	2	3	NM_000546	38,52,41
<i>TP53</i>	p.Y163	3	2	2	NM_000546	38,52
<i>TRRAP</i>	p.E3136	3	2	3	NM_001244580	24,19,15
<i>WT1</i>	p.L294	3	1	2	NM_024426	38,37
<i>WT1</i>	p.splice_G447	3	1	3	NM_024426	24,36,38
<i>WT1</i>	p.T377	3	1	1	NM_024426	30
<i>WT1</i>	p.V371	3	2	3	NM_024426	32,17,41
<i>ZRSR2</i>	p.R452	3	1	1	NM_005089	38

AA = amino acid. *Number of patients across the 48 studies reported to have a protein-altering or splice-site mutation at the given locus. †Number of hematologic malignancies for which a protein-altering or splice-site mutation was reported in at least one diagnostic patient sample at the given locus (of the seven types assessed: ALL, AML, CML, CMML, JMML, MDS, and MPN). ‡Number of studies of the total 48 in which a protein-altering or splice-site mutation was reported in at least one diagnostic patient at the given locus. §Mutations reported across the studies were harmonized to a single transcript (listed) for each gene.