Somatic Mutations Predict Poor Outcome in Myelodysplastic Syndrome Patients after Hematopoietic Stem Cell Transplantation

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Supplementary Tables and Figures

Supplemental Table 1: Summary of transplant regimens received by patients in the cohort.

Protocol Type	N	Conditioning Regimen	Stem Cell Source*	GVHD Prophylaxis	NOTES
RIC	35	Flu-Bu	PBSC	Tac-Mtx-Rap	
RIC	7	Flu-Bu	PBSC	Tac-Mtx	GVAX Vaccine
RIC	2	Flu-Bu	PBSC	Rap-Tac-Mtx	
RIC	1	Flu-Bu	PBSC	Tac-Mtx	CD8-depleted
RIC	3	Flu-Bu	PBSC	Tac-Rap-Vel	
RIC	2	Flu-Bu	PBSC	Rap-MMF	
Full	9	Cy-TBI	BM vs.PBSC	Tac-Mtx	ATG in some
Full	10	Cy-TBI	PBSC	Variable	Off study**
Full	6	Cy-TBI	PBSC (or BM)	Rap-Tac	
Full	4	Cy-TBI	PBSC (or BM)	Tac-Mtx	
Full	3	Cy-TBI	PBSC	Tac-(Rap vs. Mtx)	
Full	2	Bu-Cy	PBSC (or BM)	Tac-Mtx	
Full	2	Cy-TBI	PBSC	Tac-Mtx-Rap	
Full	1	Cy-TBI	PBSC	Rap-Tac	

* The term "vs." indicates that patients were randomized to one of two options. The term (or BM) indicates that PBSC was the default, but BM was acceptable if preferred by the donor.

** These patients were not transplanted as part of a clinical trial.

Abbreviations: **N**-number of patients in each group, **RIC**-reduced intensity conditioning, **Full**-full intensity conditioning, **GVHD**-graft versus host disease, **Flu**-fludarabine, **Bu**-busulfan, **Cy**-Cyclophosphamide, **TBI**-total body irradiation, **ATG**-anti-thymocyte globulin, **PBSC**-peripheral blood stem cells, **BM**-bone marrow, **Rap**-rapamycin, **Tac**-tacrolimus, **Mtx**-methotrexate, **MMF**- mycophenolate mofetil.

Supplemental Table 2: A) Selected target regions included coding exons of recurrently mutated genes plus an additional 10 nucleotides on either side to encompass consensus splicing sequences. B) Coordinates and ID of SNPs used for fingerprint genotyping.

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr1	43814924	43815040	*MPL*	e10
chr1	115251142	115251281	*NRAS*	e5
chr1	115252180	115252359	*NRAS*	e4
chr1	115256411	115256609	*NRAS*	e3
chr1	115258661	115258791	*NRAS*	e2
chr2	25457138	25457299	*DNMT3A*	e23
chr2	25458566	25458704	*DNMT3A*	e22
chr2	25459795	25459884	*DNMT3A*	e21
chr2	25461989	25462094	*DNMT3A*	e20
chr2	25463161	25463329	*DNMT3A*	e19
chr2	25463499	25463609	*DNMT3A*	e18
chr2	25464421	25464586	*DNMT3A*	e17
chr2	25466757	25466861	*DNMT3A*	e16
chr2	25467014	25467217	*DNMT3A*	e15
chr2	25467399	25467531	*DNMT3A*	e14
chr2	25468112	25468211	*DNMT3A*	e13
chr2	25468879	25468943	*DNMT3A*	e12
chr2	25469019	25469188	*DNMT3A*	e11
chr2	25469479	25469655	*DNMT3A*	e10
chr2	25469910	25470037	*DNMT3A*	e9
chr2	25470450	25470628	*DNMT3A*	e8
chr2	25470896	25471131	*DNMT3A*	e7
chr2	25497800	25497966	*DNMT3A*	e6
chr2	25498359	25498422	*DNMT3A*	e5
chr2	25505300	25505590	*DNMT3A*	e4
chr2	25522998	25523122	*DNMT3A*	e3
chr2	25536772	25536863	*DNMT3A*	e2
chr2	198257017	198257195	*SF3B1*	e25
chr2	198257686	198257922	*SF3B1*	e24
chr2	198260770	198261062	*SF3B1*	e23
chr2	198262699	198262850	*SF3B1*	e22
chr2	198263175	198263315	*SF3B1*	e21
chr2	198264769	198264900	*SF3B1*	e20
chr2	198264966	198265168	*SF3B1*	e19
chr2	198265429	198265670	*SF3B1*	e18
chr2	198266114	198266259	*SF3B1*	e17
chr2	198266456	198266622	*SF3B1*	e16
chr2	198266699	198266864	*SF3B1*	e15
chr2	198267270	198267560	*SF3B1*	e14
chr2	198267663	198267769	*SF3B1*	e13
chr2	198268299	198268498	*SF3B1*	e12
chr2	198269790	198269911	*SF3B1*	e11
chr2	198269989	198270206	*SF3B1*	e10
chr2	198272712	198272853	*SF3B1*	e9
chr2	198273083	198273315	*SF3B1*	e8
chr2	198274484	198274741	*SF3B1*	e7
chr2	198281455	198281645	*SF3B1*	e6
chr2	198283223	198283322	*SF3B1*	e5
chr2	198285142	198285276	*SF3B1*	e4
chr2	198285743	198285867	*SF3B1*	e3

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr2	198288522	198288708	*SF3B1*	e2
chr2	198299686	198299733	*SF3B1*	e1
chr2	209113083	209113394	*IDH1*	e4
chr3	105438881	105439104	*CBLB*	e10
chr3	105452843	105452994	*CBLB*	e9
chr3	128199852	128200171	*GATA2*	e6
chr3	128200652	128200797	*GATA2*	e5
chr3	128202693	128202858	*GATA2*	e4
chr3	128204560	128205221	*GATA2*	e3
chr3	128205636	128205884	*GATA2*	e2
chr4	55593572	55593718	*KIT*	e11
chr4	55599226	55599368	*KIT*	e17
chr4	106155090	106158518	*TET2*	e3
chr4	106162486	106162596	*TET2*	e4
chr4	106163981	106164094	*TET2*	e5
chr4	106164717	106164945	*TET2*	e6
chr4	106180766	106180936	*TET2*	e7
chr4	106182906	106183015	*TET2*	e8
chr4	106190757	106190914	*TET2*	e9
chr4	106193711	106194085	*TET2*	e10
chr4	106196195	106197686	*TET2*	e11
chr5	170834694	170834788	*NPM1*	e10
chr5	170837521	170837579	*NPM1*	e11
chr7	139044998	139045078	*LUC7L2*	e1
chr7	139060798	139060912	*LUC7L2*	e2
chr7	139083335	139083453	*LUC7L2*	e3
chr7	139086873	139087003	*LUC7L2*	e4
chr7	139090380	139090543	*LUC7L2*	e5
chr7	139091910	139092106	*LUC7L2*	e6
chr7	139094299	139094410	*LUC7L2*	e7
chr7	139097287	139097336	*LUC7L2*	e8
chr7	139102274	139102485	*LUC7L2*	e9
chr7	139106899	139107096	*LUC7L2*	e10
chr7	140453065	140453203	*BRAF*	e15
chr7	148504728	148504808	*EZH2*	e20
chr7	148506153	148506257	*EZH2*	e19
chr7	148506392	148506492	*EZH2*	e18
chr7	148507415	148507516	*EZH2*	e17
chr7	148508707	148508822	*EZH2*	e16
chr7	148511041	148511239	*EZH2*	e15
chr7	148511996	148512141	*EZH2*	e14
chr7	148512588	148512648	*EZH2*	e13
chr7	148513766	148513880	*EZH2*	e12
chr7	148514304	148514493	*EZH2*	e11
chr7	148514959	148515219	*EZH2*	e10
chr7	148516678	148516789	*EZH2*	e9
chr7	148523536	148523734	*EZH2*	e8
chr7	148524246	148524368	*EZH2*	e7
chr7	148525822	148525982	*EZH2*	e6
chr7	148526810	148526950	*EZH2*	e5
chr7	148529716	148529852	*EZH2*	e4
chr7	148543552	148543700	*EZH2*	e3
chr7	148544264	148544400	*EZH2*	e2
chr9	5073688	5073795	*JAK2*	e14
chr11	32410594	32410735	*WT1*	e10

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr11	32413508	32413620	*WT1*	e9
chr11	32414202	32414311	*WT1*	e8
chr11	32417793	32417963	*WT1*	e7
chr11	32421484	32421600	*WT1*	e6
chr11	32438026	32438096	*WT1*	e5
chr11	32439113	32439210	*WT1*	e4
chr11	32449492	32449614	*WT1*	e3
chr11	32450033	32450175	*WT1*	e2
chr11	32456236	32456901	*WT1*	e1
chr11	85956262	85956395	*EED*	e1
chr11	85961328	85961500	*EED*	e2
chr11	85963180	85963292	*EED*	e3
chr11	85966254	85966339	*EED*	e4
chr11	85967419	85967564	*EED*	e5
chr11	85968547	85968648	*EED*	e6
chr11	85975204	85975315	*EED*	e7
chr11	85977115	85977268	*EED*	e8
chr11	85979488	85979613	*EED*	e9
chr11	85988012	85988190	*EED*	e10
chr11	85988950	85989043	*EED*	e11
chr11	85989431	85989577	*EED*	e12
chr11	119148866	119149017	*CBL*	e8
chr11	119149210	119149433	*CBL*	e9
chr12	11803052	11803104	*ETV6*	e1
chr12	11905374	11905523	*ETV6*	e2
chr12	11992064	11992248	*ETV6*	e3
chr12	12006351	12006505	*ETV6*	e4
chr12	12022348	12022913	*ETV6*	e5
chr12	12037369	12037531	*ETV6*	e6
chr12	12038850	12038970	*ETV6*	e7
chr12	12043865	12043990	*ETV6*	e8
chr12	25368365	25368504	*KRAS*	e5
chr12	25378538	25378717	*KRAS*	e4
chr12	25380158	25380356	*KRAS*	e3
chr12	25398198	25398328	*KRAS*	e2
chr12	50024381	50024418	*PRPF40B*	e1
chr12	50025174	50025337	*PRPF40B*	e2
chr12	50025633	50025718	*PRPF40B*	e3
chr12	50026369	50026416	*PRPF40B*	e4
chr12	50026628	50026673	*PRPF40B*	e5
chr12	50026787	50026917	*PRPF40B*	e6
chr12	50027200	50027340	*PRPF40B*	e7
chr12	50027410	50027454	*PRPF40B*	e8
chr12	50027659	50027885	*PRPF40B*	e9
chr12	50028105	50028248	*PRPF40B*	e10
chr12	50028311	50028395	*PRPF40B*	e11
chr12	50028872	50029056	*PRPF40B*	e12
chr12	50029138	50029266	*PRPF40B*	e13
chr12	50029616	50029786	*PRPF40B*	e14
chr12	50030489	50030642	*PRPF40B*	e15
chr12	50031243	50031377	*PRPF40B*	e16
chr12	50031506	50031617	*PRPF40B*	e17
chr12	50035681	50035817	*PRPF40B*	e18
chr12	50036008	50036165	*PRPF40B*	e19
chr12	50036353	50036468	*PRPF40B*	e20

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr12	50036700	50036809	*PRPF40B*	e21
chr12	50036996	50037190	*PRPF40B*	e22
chr12	50037464	50037545	*PRPF40B*	e23
chr12	50037634	50037797	*PRPF40B*	e24
chr12	50037873	50037985	*PRPF40B*	e25
chr12	112856906	112856939	*PTPN11*	e1
chr12	112884070	112884212	*PTPN11*	e2
chr12	112888112	112888326	*PTPN11*	e3
chr12	112890989	112891201	*PTPN11*	e4
chr12	112892358	112892494	*PTPN11*	e5
chr12	112893744	112893877	*PTPN11*	e6
chr12	112910738	112910854	*PTPN11*	e7
chr12	112915445	112915544	*PTPN11*	e8
chr12	112915651	112915829	*PTPN11*	e9
chr12	112919868	112920019	*PTPN11*	e10
chr12	112924269	112924443	*PTPN11*	e11
chr12	112926237	112926324	*PTPN11*	e12
chr12	112926818	112926989	*PTPN11*	e13
chr12	112939938	112940070	*PTPN11*	e14
chr12	112942489	112942578	*PTPN11*	e15
chr13	28592594	28592736	*FLT3*	e20
chr13	28608014	28608138	*FLT3*	e15
chr13	28608209	28608361	*FLT3*	e14
chr15	90631809	90631989	*IDH2*	e4
chr17	1554086	1554260	*PRPF8*	e43
chr17	1554392	1554614	*PRPF8*	e42
chr17	1554698	1554857	*PRPF8*	e41
chr17	1554932	1555092	*PRPF8*	e40
chr17	1556826	1556987	*PRPF8*	e39
chr17	1557061	1557320	*PRPF8*	e38
chr17	1558634	1558847	*PRPF8*	e37
chr17	1559676	1559869	*PRPF8*	e36
chr17	1559932	1560065	*PRPF8*	e35
chr17	1561537	1561685	*PRPF8*	e34
chr17	1561810	1562067	*PRPF8*	e33
chr17	1562641	1562852	*PRPF8*	e32
chr17	1563125	1563305	*PRPF8*	e31
chr17	1563716	1563882	*PRPF8*	e30
chr17	1563982	1564131	*PRPF8*	e29
chr17	1564277	1564466	*PRPF8*	e28
chr17	1564555	1564710	*PRPF8*	e27
chr17	1564895	1565094	*PRPF8*	e26
chr17	1565190	1565457	*PRPF8*	e25
chr17	1576365	1576501	*PRPF8*	e24
chr17	1576641	1576871	*PRPF8*	e23
chr17	1577030	1577196	*PRPF8*	e22
chr17	1577726	1577984	*PRPF8*	e21
chr17	1578436	1578643	*PRPF8*	e20
chr17	1578904	1579116	*PRPF8*	e19
chr17	1579212	1579358	*PRPF8*	e18
chr17	1579491	1579674	*PRPF8*	e17
chr17	1579789	1580015	*PRPF8*	e16
chr17	1580260	1580476	*PRPF8*	e15
chr17	1580849	1580998	*PRPF8*	e14
chr17	1581802	1581956	*PRPF8*	e13

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr17	1582046	1582185	*PRPF8*	e12
chr17	1582301	1582510	*PRPF8*	e11
chr17	1582575	1582714	*PRPF8*	e10
chr17	1582893	1583103	*PRPF8*	e9
chr17	1584010	1584135	*PRPF8*	e8
chr17	1584213	1584358	*PRPF8*	e7
chr17	1584762	1584994	*PRPF8*	e6
chr17	1585104	1585342	*PRPF8*	e5
chr17	1585413	1585597	*PRPF8*	e4
chr17	1586817	1587005	*PRPF8*	e3
chr17	1587756	1587875	*PRPF8*	e2
chr17	7572917	7573018	*TP53*	e11
chr17	7573917	7574043	*TP53*	e10
chr17	7576843	7576936	*TP53*	e9
chr17	7577009	7577165	*TP53*	e8
chr17	7577489	7577618	*TP53*	e7
chr17	7578167	7578299	*TP53*	e6
chr17	7578361	7578564	*TP53*	e5
chr17	7579302	7579600	*TP53*	e4
chr17	7579690	7579731	*TP53*	e3
chr17	7579829	7579922	*TP53*	e2
chr17	7748863	7749019	*KDM6B*	e4
chr17	7749180	7749298	*KDM6B*	e5
chr17	7749386	7749625	*KDM6B*	e6
chr17	7749708	7749820	*KDM6B*	e7
chr17	7749887	7750068	*KDM6B*	e8
chr17	7750127	7750344	*KDM6B*	e9
chr17	7750413	7750780	*KDM6B*	e10
chr17	7750854	7753056	*KDM6B*	e11
chr17	7753129	7753275	*KDM6B*	e12
chr17	7753380	7753505	*KDM6B*	e13
chr17	7754329	7754554	*KDM6B*	e14
chr17	7754638	7754722	*KDM6B*	e15
chr17	7754786	7754877	*KDM6B*	e16
chr17	7754956	7755124	*KDM6B*	e17
chr17	7755259	7755393	*KDM6B*	e18
chr17	7755457	7755664	*KDM6B*	e19
chr17	7755803	7755964	*KDM6B*	e20
chr17	7756308	7756454	*KDM6B*	e21
chr17	7756518	7756849	*KDM6B*	e22
chr17	29422318	29422397	*NF1*	e1
chr17	29482991	29483154	*NF1*	e2
chr17	29486018	29486121	*NF1*	e3
chr17	29490194	29490404	*NF1*	e4
chr17	29496899	29497025	*NF1*	e5
chr17	29508430	29508517	*NF1*	e6
chr17	29508718	29508813	*NF1*	e7
chr17	29509516	29509693	*NF1*	e8
chr17	29527430	29527623	*NF1*	e9
chr17	29528045	29528187	*NF1*	e10
chr17	29528419	29528513	*NF1*	e11
chr17	29533248	29533399	*NF1*	e12
chr17	29541459	29541613	*NF1*	e13
chr17	29546013	29546146	*NF1*	e14
chr17	29548858	29548957	*NF1*	e15

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr17	29550452	29550595	*NF1*	e16
chr17	29552103	29552278	*NF1*	e17
chr17	29553443	29553712	*NF1*	e18
chr17	29554226	29554319	*NF1*	e19
chr17	29554531	29554634	*NF1*	e20
chr17	29556033	29556493	*NF1*	e21
chr17	29556843	29557002	*NF1*	e22
chr17	29557268	29557410	*NF1*	e23
chr17	29557850	29557953	*NF1*	e24
chr17	29559081	29559217	*NF1*	e25
chr17	29559708	29559909	*NF1*	e26
chr17	29560010	29560241	*NF1*	e27
chr17	29562619	29562800	*NF1*	e28
chr17	29562926	29563049	*NF1*	e29
chr17	29575992	29576147	*NF1*	e30
chr17	29579946	29580028	*NF1*	e31
chr17	29585352	29585530	*NF1*	e32
chr17	29586040	29586157	*NF1*	e33
chr17	29587377	29587543	*NF1*	e34
chr17	29588719	29588885	*NF1*	e35
chr17	29592237	29592367	*NF1*	e36
chr17	29652828	29653280	*NF1*	e37
chr17	29654507	29654867	*NF1*	e38
chr17	29657304	29657526	*NF1*	e39
chr17	29661846	29662059	*NF1*	e40
chr17	29663341	29663501	*NF1*	e41
chr17	29663643	29663942	*NF1*	e42
chr17	29664376	29664610	*NF1*	e43
chr17	29664827	29664908	*NF1*	e44
chr17	29665033	29665167	*NF1*	e45
chr17	29665712	29665833	*NF1*	e46
chr17	29667513	29667673	*NF1*	e47
chr17	29670017	29670163	*NF1*	e48
chr17	29676128	29676279	*NF1*	e49
chr17	29677191	29677346	*NF1*	e50
chr17	29679265	29679442	*NF1*	e51
chr17	29683468	29683610	*NF1*	e52
chr17	29683968	29684118	*NF1*	e53
chr17	29684277	29684397	*NF1*	e54
chr17	29685488	29685650	*NF1*	e55
chr17	29685977	29686043	*NF1*	e56
chr17	29687495	29687731	*NF1*	e57
chr17	29701021	29701183	*NF1*	e58
chr17	30264256	30264549	*SUZ12*	e1
chr17	30267295	30267361	*SUZ12*	e2
chr17	30267431	30267515	*SUZ12*	e3
chr17	30274626	30274714	*SUZ12*	e4
chr17	30293156	30293225	*SUZ12*	e5
chr17	30300155	30300260	*SUZ12*	e6
chr17	30302491	30302742	*SUZ12*	e7
chr17	30303530	30303643	*SUZ12*	e8
chr17	30310008	30310133	*SUZ12*	e9
chr17	30315329	30315526	*SUZ12*	e10
chr17	30320251	30320362	*SUZ12*	e11
chr17	30320874	30321037	*SUZ12*	e12

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr17	30321573	30321750	*SUZ12*	e13
chr17	30322573	30322791	*SUZ12*	e14
chr17	30323807	30323906	*SUZ12*	e15
chr17	30325667	30326032	*SUZ12*	e16
chr17	74732233	74732556	*SRSF2*	e2
chr17	74732871	74733252	*SRSF2*	e1
chr19	33792234	33793330	*CEBPA*	e1
chr19	56166461	56166529	*U2AF2*	e1
chr19	56170566	56170721	*U2AF2*	e2
chr19	56171533	56171597	*U2AF2*	e3
chr19	56171872	56171995	*U2AF2*	e4
chr19	56172394	56172565	*U2AF2*	e5
chr19	56173858	56173994	*U2AF2*	e6
chr19	56174962	56175120	*U2AF2*	e7
chr19	56179863	56179962	*U2AF2*	e8
chr19	56180026	56180168	*U2AF2*	e9
chr19	56180439	56180557	*U2AF2*	e10
chr19	56180800	56181068	*U2AF2*	e11
chr19	56185290	56185444	*U2AF2*	e12
chr20	30946569	30946645	*ASXL1*	e1
chr20	30954177	30954279	*ASXL1*	e2
chr20	30956808	30956936	*ASXL1*	e4
chr20	31015921	31016061	*ASXL1*	e5
chr20	31016118	31016235	*ASXL1*	e6
chr20	31017131	31017244	*ASXL1*	e7
chr20	31017694	31017866	*ASXL1*	e8
chr20	31019114	31019297	*ASXL1*	e9
chr20	31019376	31019492	*ASXL1*	e10
chr20	31020673	31020798	*ASXL1*	e11
chr20	31021077	31021730	*ASXL1*	e12
chr20	31022225	31025151	*ASXL1*	e13
chr20	42295914	42295953	*MYBL2*	e1
chr20	42302436	42302549	*MYBL2*	e2
chr20	42310414	42310505	*MYBL2*	e3
chr20	42311424	42311536	*MYBL2*	e4
chr20	42315482	42315722	*MYBL2*	e5
chr20	42320787	42320969	*MYBL2*	e6
chr20	42328387	42328694	*MYBL2*	e7
chr20	42331120	42331553	*MYBL2*	e8
chr20	42333849	42334008	*MYBL2*	e9
chr20	42338593	42338712	*MYBL2*	e10
chr20	42340118	42340251	*MYBL2*	e11
chr20	42341632	42341756	*MYBL2*	e12
chr20	42343764	42343933	*MYBL2*	e13
chr20	42344589	42344737	*MYBL2*	e14
chr20	57484395	57484488	*GNAS*	e8
chr20	57484566	57484644	*GNAS*	e9
chr21	36164422	36164917	*RUNX1*	e8
chr21	36171588	36171769	*RUNX1*	e7
chr21	36206697	36206908	*RUNX1*	e6
chr21	36231761	36231885	*RUNX1*	e5
chr21	36252844	36253020	*RUNX1*	e4
chr21	36259130	36259403	*RUNX1*	e3
chr21	36265212	36265270	*RUNX1*	e2
chr21	36421129	36421206	*RUNX1*	e1

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chr21	44513202	44513369	*U2AF1*	e8
chr21	44514571	44514683	*U2AF1*	e7
chr21	44514755	44514908	*U2AF1*	e6
chr21	44515538	44515656	*U2AF1*	e5
chr21	44515794	44515863	*U2AF1*	e4
chr21	44521466	44521552	*U2AF1*	e3
chr21	44524415	44524522	*U2AF1*	e2
chr21	44527551	44527614	*U2AF1*	e1
chr22	30730573	30730694	*SF3A1*	e16
chr22	30731446	30731537	*SF3A1*	e15
chr22	30731631	30731752	*SF3A1*	e14
chr22	30733005	30733179	*SF3A1*	e13
chr22	30733669	30733896	*SF3A1*	e12
chr22	30734768	30735033	*SF3A1*	e11
chr22	30735109	30735250	*SF3A1*	e10
chr22	30736175	30736380	*SF3A1*	e9
chr22	30736674	30736811	*SF3A1*	e8
chr22	30737671	30737884	*SF3A1*	e7
chr22	30738179	30738349	*SF3A1*	e6
chr22	30738784	30738878	*SF3A1*	e5
chr22	30740912	30741189	*SF3A1*	e4
chr22	30742291	30742518	*SF3A1*	e3
chr22	30748930	30749071	*SF3A1*	e2
chr22	30752709	30752791	*SF3A1*	e1
chrX	15808609	15808669	*ZRSR2*	e1
chrX	15809047	15809146	*ZRSR2*	e2
chrX	15817985	15818086	*ZRSR2*	e3
chrX	15821801	15821929	*ZRSR2*	e4
chrX	15822224	15822330	*ZRSR2*	e5
chrX	15826346	15826404	*ZRSR2*	e6
chrX	15827313	15827451	*ZRSR2*	e7
chrX	15833790	15834023	*ZRSR2*	e8
chrX	15836700	15836775	*ZRSR2*	e9
chrX	15838320	15838449	*ZRSR2*	e10
chrX	15840844	15841375	*ZRSR2*	e11
chrX	76763819	76764117	*ATRX*	e35
chrX	76776256	76776404	*ATRX*	e34
chrX	76776871	76776986	*ATRX*	e33
chrX	76777731	76777876	*ATRX*	e32
chrX	76778720	76778889	*ATRX*	e31
chrX	76812912	76813126	*ATRX*	e30
chrX	76814130	76814327	*ATRX*	e29
chrX	76829705	76829833	*ATRX*	e28
chrX	76845294	76845420	*ATRX*	e27
chrX	76849156	76849329	*ATRX*	e26
chrX	76854870	76855059	*ATRX*	e25
chrX	76855191	76855299	*ATRX*	e24
chrX	76855893	76856043	*ATRX*	e23
chrX	76872071	76872208	*ATRX*	e22
chrX	76874264	76874459	*ATRX*	e21
chrX	76875853	76876010	*ATRX*	e20
chrX	76888685	76888882	*ATRX*	e19
chrX	76889044	76889210	*ATRX*	e18
chrX	76890075	76890204	*ATRX*	e17
chrX	76891396	76891557	*ATRX*	e16

Chromosome	Coordinate Start	Coordinate End	Gene Name	Exon #
chrX	76907594	76907853	*ATRX*	e15
chrX	76909578	76909700	*ATRX*	e14
chrX	76912040	76912153	*ATRX*	e13
chrX	76918861	76919057	*ATRX*	e12
chrX	76920124	76920277	*ATRX*	e11
chrX	76931711	76931803	*ATRX*	e10
chrX	76937002	76940095	*ATRX*	e9
chrX	76940421	76940508	*ATRX*	e8
chrX	76944301	76944430	*ATRX*	e7
chrX	76949303	76949436	*ATRX*	e6
chrX	76952055	76952202	*ATRX*	e5
chrX	76953061	76953133	*ATRX*	e4
chrX	76954052	76954127	*ATRX*	e3
chrX	76972598	76972730	*ATRX*	e2
chrX	77041458	77041497	*ATRX*	e1
chrX	133511638	133511795	*PHF6*	e2
chrX	133512025	133512146	*PHF6*	e3
chrX	133527521	133527674	*PHF6*	e4
chrX	133527929	133527992	*PHF6*	e5
chrX	133547511	133547697	*PHF6*	e6
chrX	133547843	133548006	*PHF6*	e7
chrX	133549036	133549160	*PHF6*	e8
chrX	133551189	133551342	*PHF6*	e9
chrX	133559221	133559370	*PHF6*	e10

Fingerprint Variant Coordinates

Chromosome	Coordinate Start	Coordinate End	SNP ID
chr1	14096751	14096891	rs1210110
chr1	14804804	14804944	rs7555566
chr2	8178665	8178805	rs1364054
chr2	67241104	67241244	rs6734275
chr2	223845872	223846012	rs7584993
chr3	17077198	17077338	rs17272796
chr3	37627042	37627182	rs1155741
chr3	151899634	151899774	rs161792
chr4	27162408	27162548	rs11940551
chr5	88416284	88416424	rs9293511
chr6	79424363	79424503	rs9352613
chr6	153344461	153344601	rs685449
chr7	86983645	86983785	rs7808249
chr8	71012741	71012881	rs1106334
chr10	129200894	129201034	rs11017876
chr13	35252812	35252952	rs9572094
chr14	96103029	96103169	rs4905366
chr15	47873479	47873619	rs4775699
chr16	51098357	51098497	rs1528601
chr17	20851665	20851805	rs11655512
chr17	43131410	43131550	rs4793172
chr22	33229760	33229900	rs242076
chrX	320510	320650	rs6603251

Supplemental Table 3: Frequency of mutations in targeted genes with one or more mutations.

Gene	N Mutations (%)	No. achieving CR N (%)
Any gene mutated	80(92)	52 (65)
No gene mutated	7(8)	7 (100)
ASXL1	25 (29)	18 (72)
TP53	18 (21)	7 (39)
DNMT3A	16 (18)	10 (63)
RUNX1	14 (16)	11 (79)
U2AF1	12 (14)	11 (92)
TET2	11 (13)	6 (55)
SRSF2	9 (10)	7 (78)
SF3B1	8 (9)	6 (75)
PRPF8	8 (9)	6 (75)
NRAS	7 (8)	5 (71)
SUZ12	6 (7)	3 (50)
CBL	6 (7)	3 (50)
KDM6B	6 (7)	4 (67)
PRPF40B	5 (6)	3 (60)
WT1	5 (6)	5 (100)
JAK2	5 (6)	4 (80)
ZRSR2	5 (6)	4 (80)
GATA2	4 (5)	1 (25)
PHF6	4 (5)	4 (100)
NF1	4 (5)	3 (75)
KRAS	3 (3)	3 (100)
EZH2	3 (3)	2 (67)
ETV6	3 (3)	2 (67)
IDH1	3 (3)	2 (67)
IDH2	2 (2)	2 (100)
NCSTN	2 (2)	1 (50)
MAML1	2 (2)	2 (100)
EED	2 (2)	2 (100)
ATRX	2 (2)	1 (50)
LUC7L2	2 (2)	2 (100)
PTPN11	2 (2)	1 (50)
SF3A1	1 (1)	1 (100)
BRAF	1 (1)	0 (0)
CEPBA	1 (1)	1 (100)
U2AF2	1 (1)	0 (0)
FLT3	1 (1)	1 (100)
MYBL2	1 (1)	1 (100)
CBLB	1 (1)	0 (0)

Supplemental Table 4: The hazard ratio for disease progression associated with clinical features and mutations in univariate and adjusted analyses.

Variable	Univariate HR (95% CI)	p-value	Adjusted† HR (95% CI)	p-value
Blast %				
≥5% vs. <5%	**2.14 (1.24, 3.68)**	**0.006**		
Conditioning Regimen				
Non-Myeloablative vs. Ablative	**2.35 (1.24, 4.46)**	**0.009**		
Karyotype				
Complex vs. Other	**2.23 (1.30, 3.81)**	**0.004**		
Donor Type				
Unrelated vs. Related	1.62 (0.90, 2.92)	0.11		
Gene Mutation (Present vs. Absent)				
TP53	**3.97 (2.22, 7.10)**	**<0.001**	**2.48 (1.25, 4.94)**	**0.01**
DNMT3A	1.76 (0.98, 3.19)	0.061	**2.56 (1.27, 5.16)**	**0.009**
NOTCH2	1.67 (0.60, 4.65)	0.33	1.66 (0.55, 4.97)	0.37
TET2	1.30 (0.61, 2.75)	0.49	1.82 (0.82, 4.03)	0.14
PRPF8	1.27 (0.54, 2.97)	0.58	1.11 (0.46, 2.65)	0.82
ZRSR2	1.11 (0.40, 3.06)	0.85	1.13 (0.39, 3.23)	0.83
SF3B1	0.94 (0.37, 2.35)	0.89	2.30 (0.83, 6.42)	0.11
CBL	0.92 (0.33, 2.54)	0.87	0.74 (0.26, 2.12)	0.57
AXSL1	0.83 (0.47, 1.48)	0.53	0.74 (0.40, 1.37)	0.34
NRAS	0.81 (0.32, 2.02)	0.65	0.65 (0.25, 1.67)	0.37
U2AF1	0.76 (0.34, 1.67)	0.49	1.07 (0.45, 2.52)	0.88
SRSF2	0.76 (0.30, 1.90)	0.55	0.84 (0.33, 2.14)	0.71
SUZ12	0.70 (0.22, 2.24)	0.54	1.08 (0.30, 3.94)	0.9
RUNX1	0.69 (0.31, 1.51)	0.35	0.71 (0.31, 1.63)	0.42
PRPF40B	0.47 (0.11, 1.92)	0.29	0.43 (0.10, 1.86)	0.26
WT1	0.40 (0.10, 1.64)	0.20	0.45 (0.11, 1.88)	0.27
JAK2	0.19 (0.03, 1.36)	0.10	0.24 (0.03, 1.78)	0.16

† Adjusted for blast %, conditioning regimen, complex karyotype, and donor type

Supplemental Table 5: Characteristics of Patients with and without TP53 Mutations

	N (%)	TP53 no Mutation	TP53 Mutation	p-value
No. of Patients	87	69	19	
Age, median (range)	58 (19, 73)	58 (18, 73)	58 (41, 70)	0.57
Age, ≥60 yrs.	34 (39)	26 (38)	8 (44)	0.60
Sex, Male	60 (69)	45 (65)	15 (83)	0.16
FAB at Transplant†				
RA	24 (28)	20 (29)	4 (22)	0.41
RARS	7 (8)	7 (10)	0 (0)	
RAEB	42 (48)	32 (46)	10 (56)	
RAEB-t	1 (1)	0 (0)	1 (6)	
CMML	5 (6)	4 (6)	1 (6)	
MDS-U	1 (1)	1 (1)	0 (0)	
Other/Unknown	7 (8)	5 (7)	2 (11)	
Karyotype				
-7/7q- or +1 (+/- other)	15 (17)	14 (20)	1 (6)	<0.001
Normal	28 (32)	28 (41)	0 (0)	
Complex	28 (32)	12 (17)	16 (89)	
Other (any not listed above)	8 (9)	8 (12)	0 (0)	
Unknown	8 (9)	7 (10)	1 (6)	
Blast %, median (range)	5 (0, 23)	4 (0, 17)	10 (1, 23)	0.064
< 5%	42 (48)	37 (54)	5 (28)	0.14
5 - 10%	32 (37)	22 (32)	10 (56)	
11 - 30%	13 (15)	10 (14)	3 (17)	
Hemoglobin, median (range)	9.9 (7.1, 16.2)	9.9 (7.1, 16.2)	9.7 (7.1, 15.6)	0.75
< 8.0 (gm/dl)	12 (14)	9 (13)	3 (17)	0.83
8.0 – 9.99 (gm/dl)	32 (37)	26 (38)	6 (33)	
10.0 – 11.99 (gm/dl)	24 (28)	20 (29)	4 (22)	
≥12.0 (gm/dl)	19 (22)	14 (20)	5 (28)	
Absolute Neutrophil Count (ANC), median (range)	1,233 (14, 57,288)	1,320 (14, 57,288)	1,020 (68, 9,583)	0.11
< 500 (cells/mm^3)	22 (25)	15 (22)	7 (39)	0.57
500 – 1,499 (cells/mm^3)	28 (32)	22 (32)	6 (33)	
1,500 - 9,999 (cells/mm^3)	32 (37)	27 (39)	5 (28)	
≥10,000 (cells/mm^3)	4 (5)	4 (6)	0 (0)	
Unknown	1 (1)	1 (1)	0 (0)	
Platelets, median (range)	64 (4, 290)	66 (4, 290)	53 (12, 127)	0.038
< 50 K	28 (32)	20 (29)	8 (44)	0.21
50 – 149 K	50 (57)	40 (58)	10 (56)	
≥ 150 K	9 (10)	9 (13)	0 (0)	
Patient-Donor Sex Matching				
M-M	34 (39)	23 (33)	11 (61)	0.12
M-F	26 (30)	22 (32)	4 (22)	
F-M	9 (10)	7 (10)	2 (11)	
F-F	18 (21)	17 (25)	1 (6)	
Type of Conditioning Regimen				
Myeloablative	25 (29)	23 (33)	2 (11)	0.082

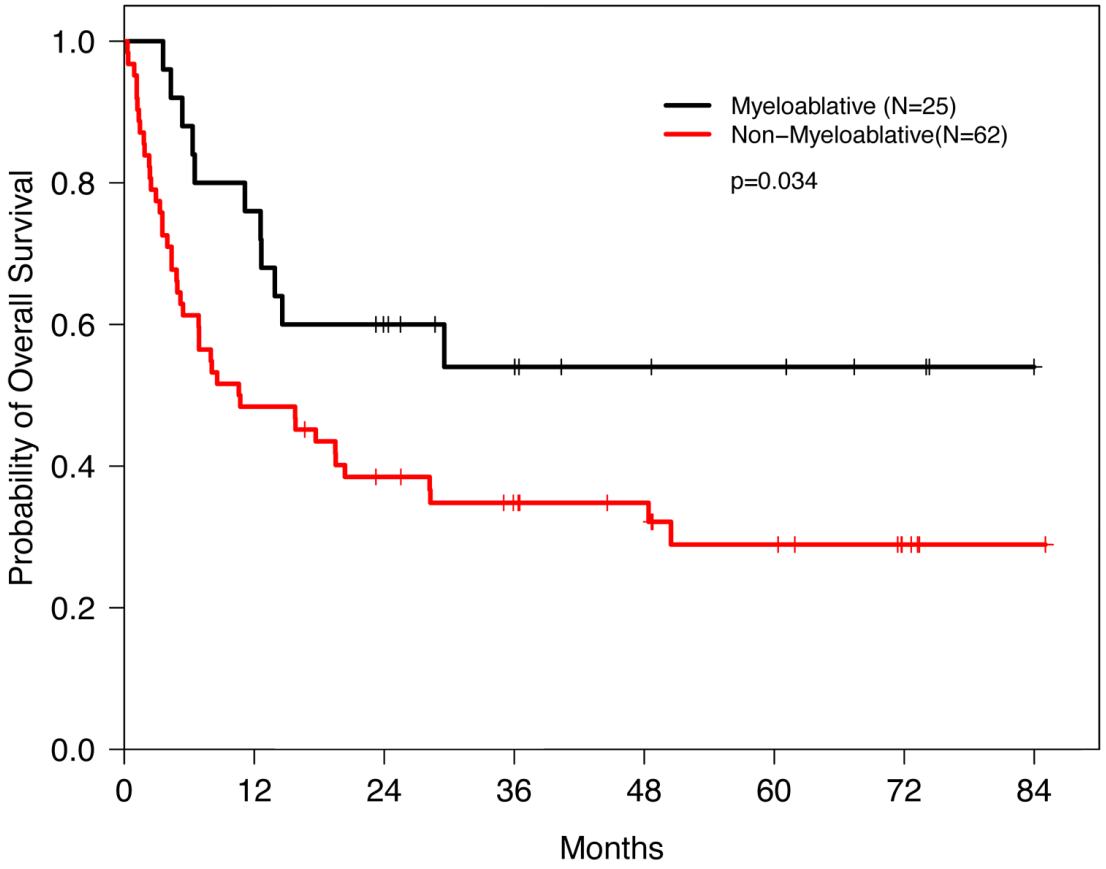
	N (%)	TP53 no Mutation	TP53 Mutation	p-value
Non-myeloablative	62 (71)	46 (67)	16 (89)	
Conditioning Regimen				
Bu/Flu +/-Other	53 (61)	39 (57)	14 (77)	0.14
Cy/TBI	30 (34)	27 (39)	3 (17)	
Other	4 (5)	3 (4)	1 (6)	
Donor Cell Source				
PBSC	80 (92)	62 (90)	18 (100)	0.34
BM	7 (8)	7 (10)	0 (0)	
HLA Matching (6/6) and Donor Relation				
MUD	53 (61)	39 (57)	14 (78)	0.011
MMURD	7 (8)	4 (6)	3 (17)	
MRD	27 (31)	26 (38)	1 (6)	

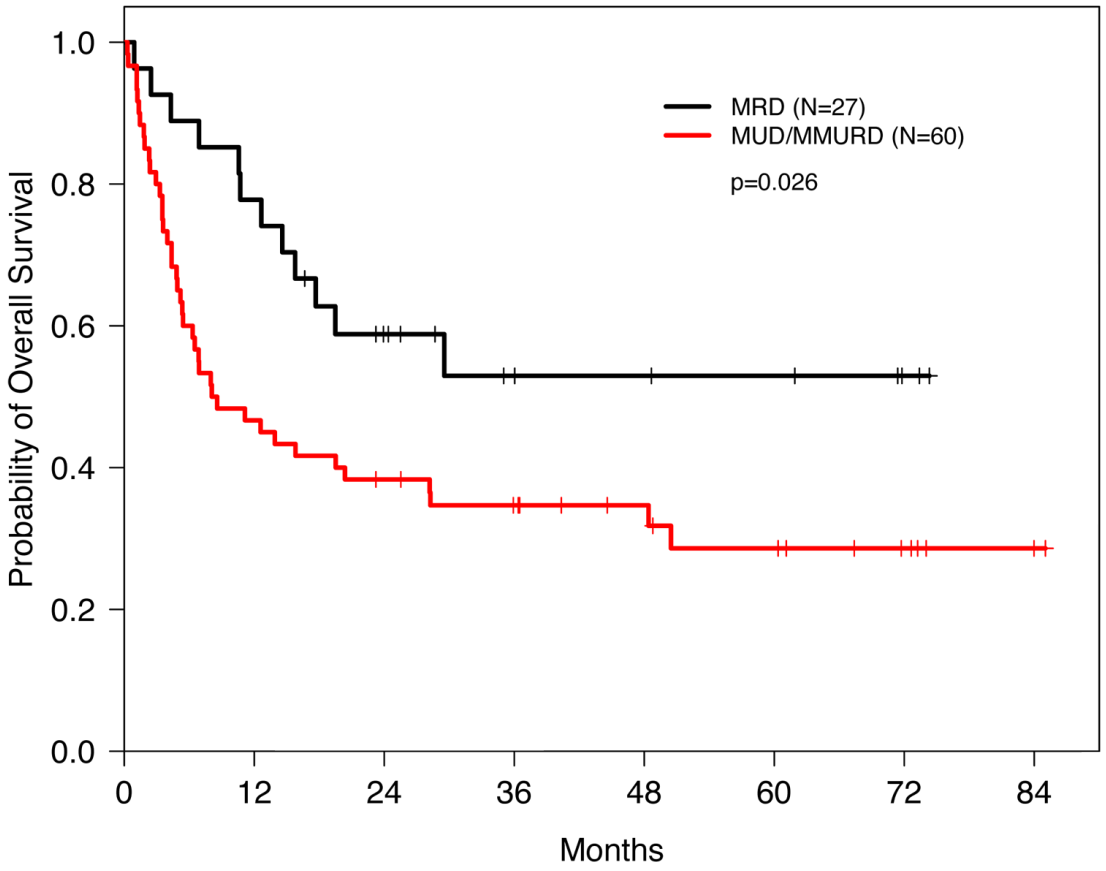
Supplemental Table 6: Characteristics of TP53 mutation identified in this cohort.

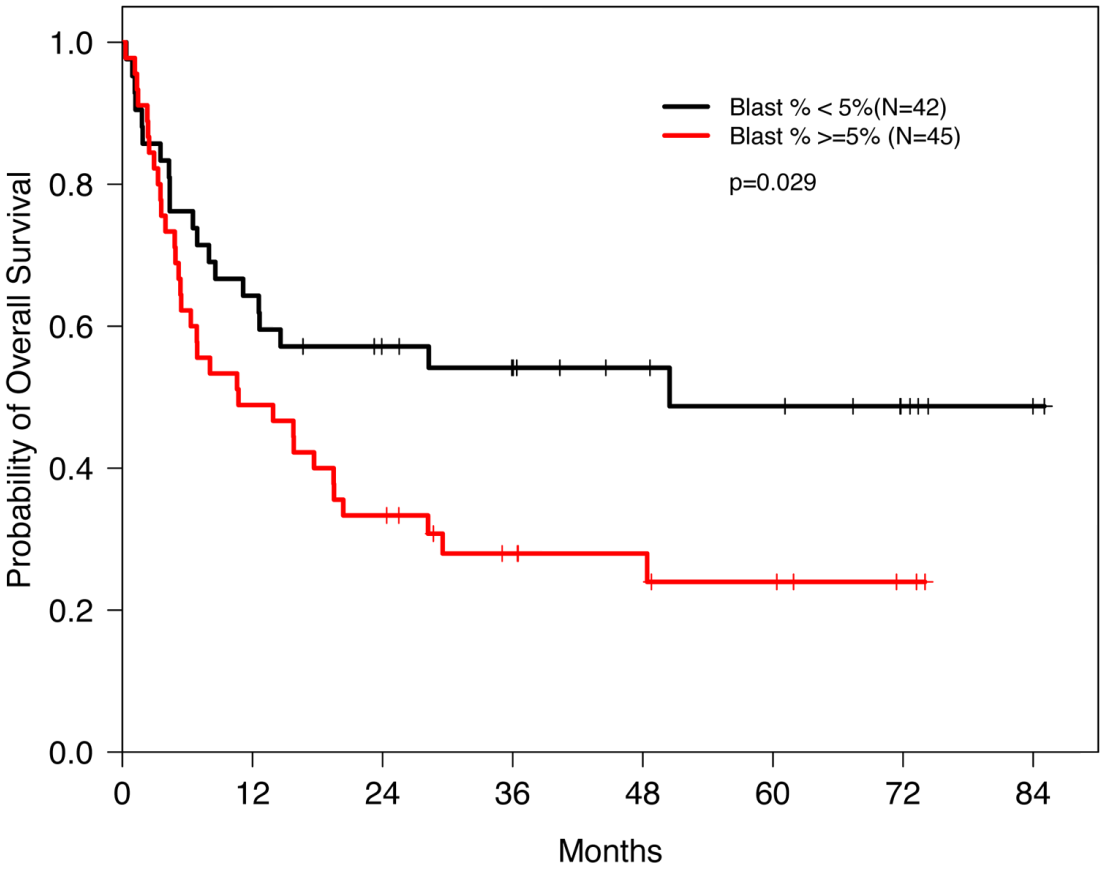
Protein Effect of Variant	Variant Allele Fraction	Reported as Somatic in COSMIC	Sift Predicted Impact
p.C176Y	48%	Yes	Damaging
p.A161T	34%	Yes	Damaging
p.S241Y	3%	Yes	Damaging
p.Y220C	7%	Yes	Damaging
p.C176F	81%	Yes	Damaging
p.A159P	26%	No	Damaging
p.P36fs	14%	Yes*	N/A*
p.R273L	87%	Yes	Damaging
p.C135R	63%	Yes	Damaging
p.P151T	37%	Yes	Damaging
p.C275Y	67%	Yes	Damaging
p.R273H	71%	Yes	Damaging
p.C238Y	2%	Yes	Damaging
p.E258K	14%	Yes	Damaging
p.R283P	12%	Yes	Damaging
p.I195T	8%	Yes	Damaging
p.P151T	15%	Yes	Damaging
p.R273H	45%	Yes	Damaging
p.Y205C	65%	Yes	Damaging
p.V173M	3%	Yes	Damaging
p.C238Y	80%	Yes	Damaging
p.L43fs	17%	Yes*	N/A*
p.S33_splice	11%	No	Unknown

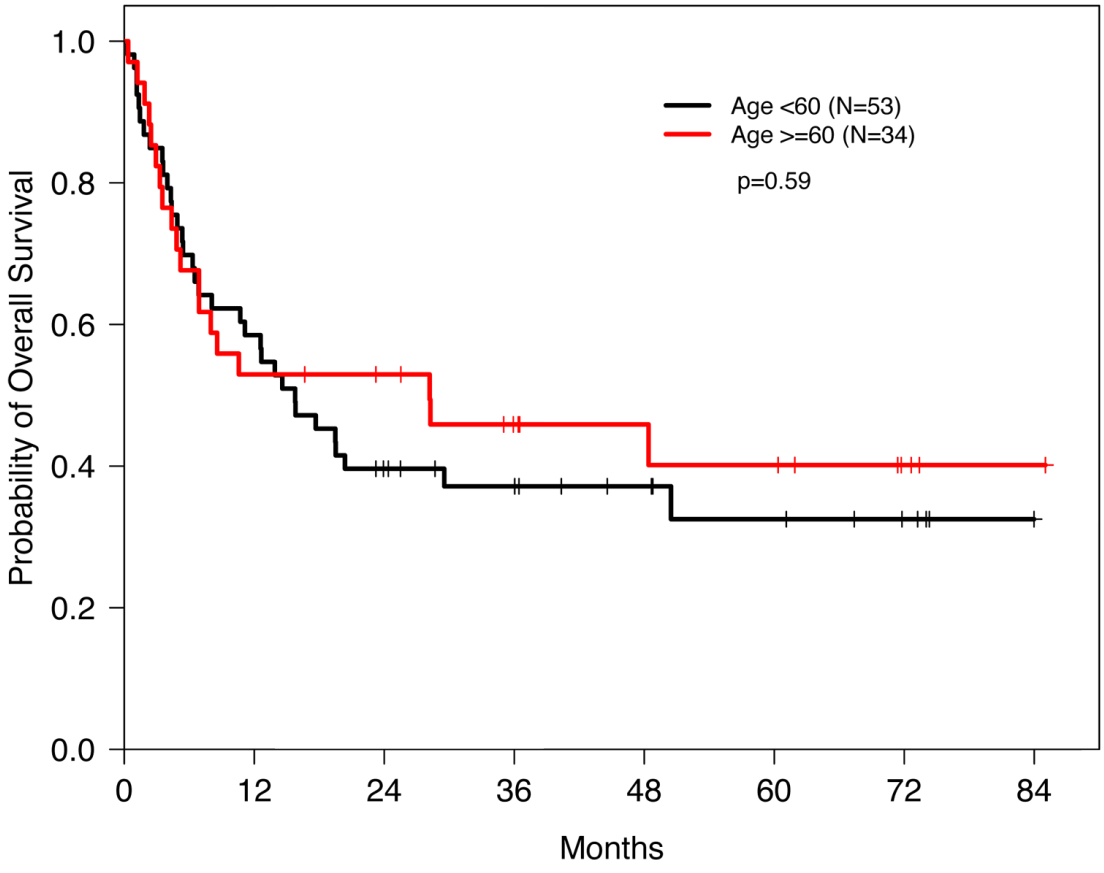
* Non-identical out-of-frame somatic mutation identified at this position assumed to be damaging.

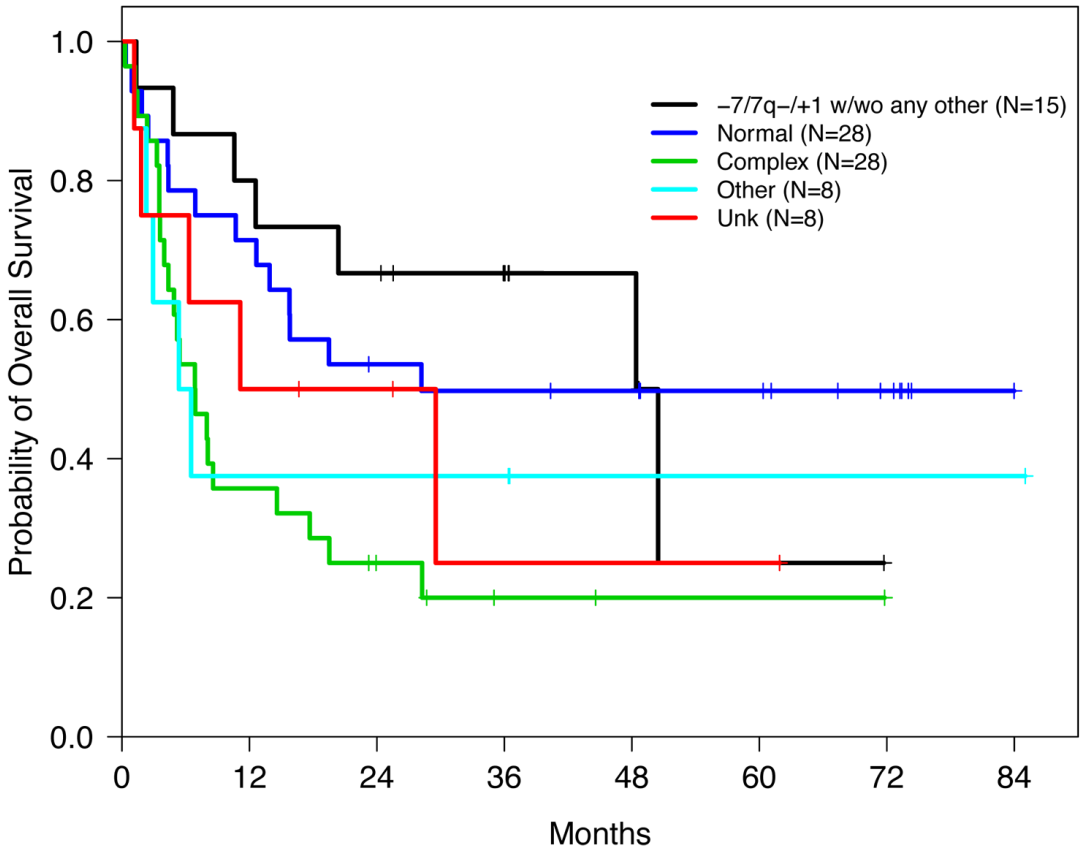
Supplemental Figure 1: Kaplan-Meier curves for overall survival associated with clinical measures.

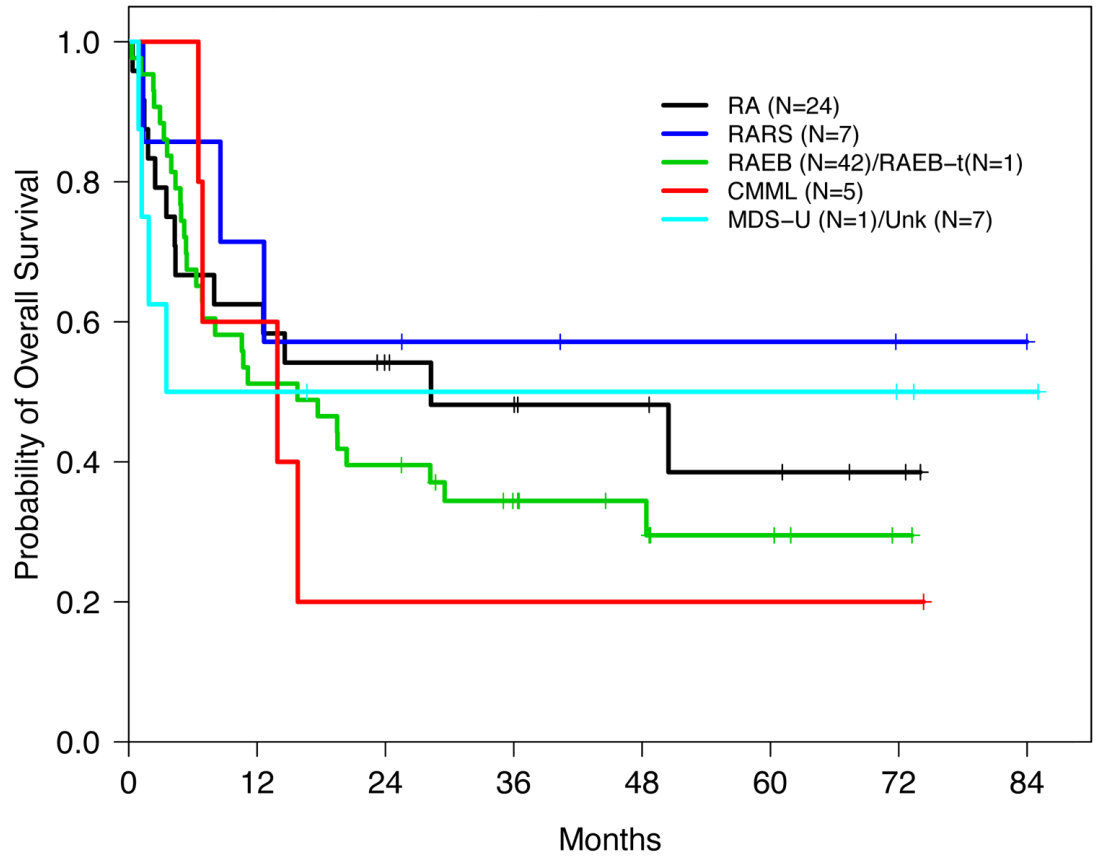




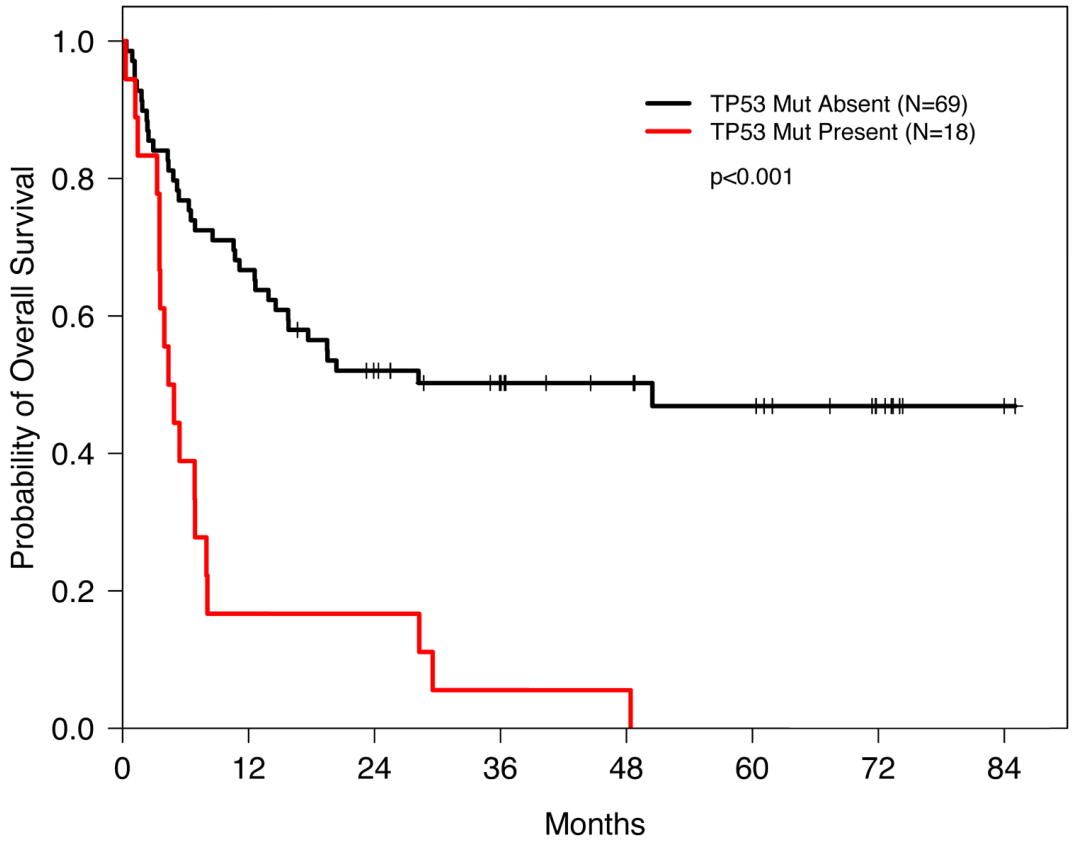

Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months
Blast % < 5%(N=42)
Blast % >=5% (N=45)
p=0.029

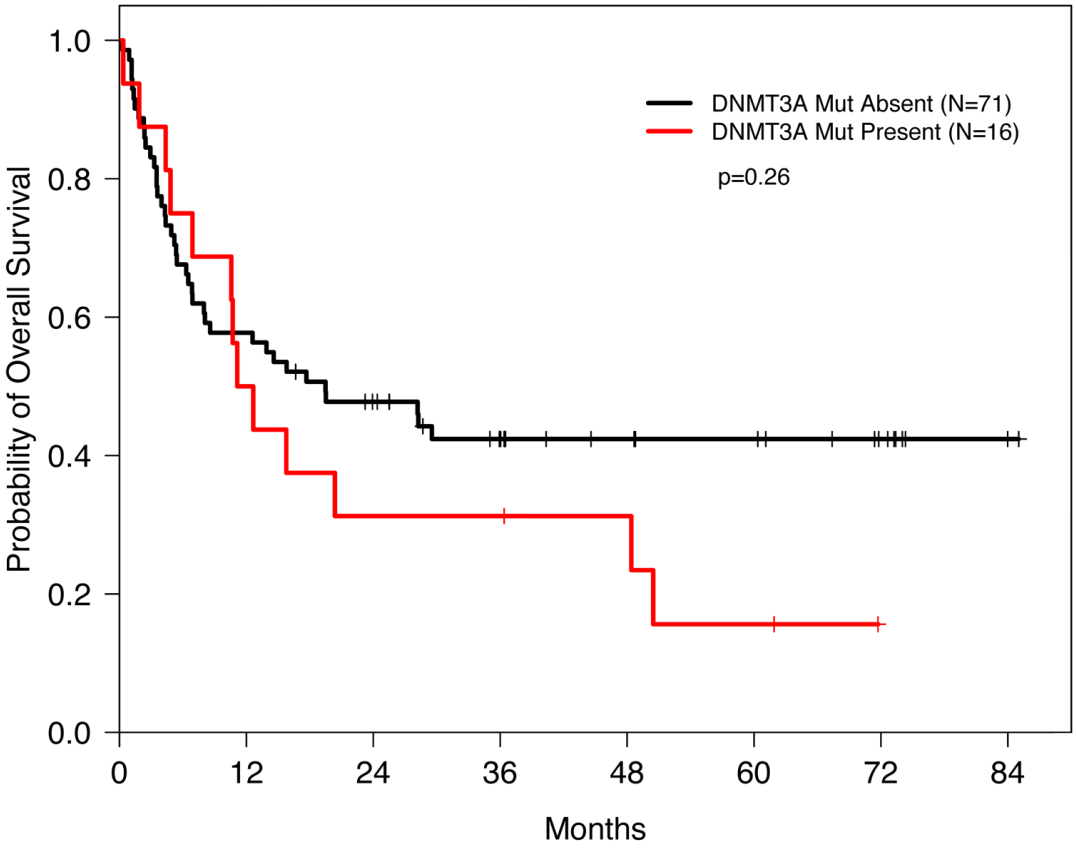

Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months
Age <60 (N=53)
Age >=60 (N=34)
p=0.59

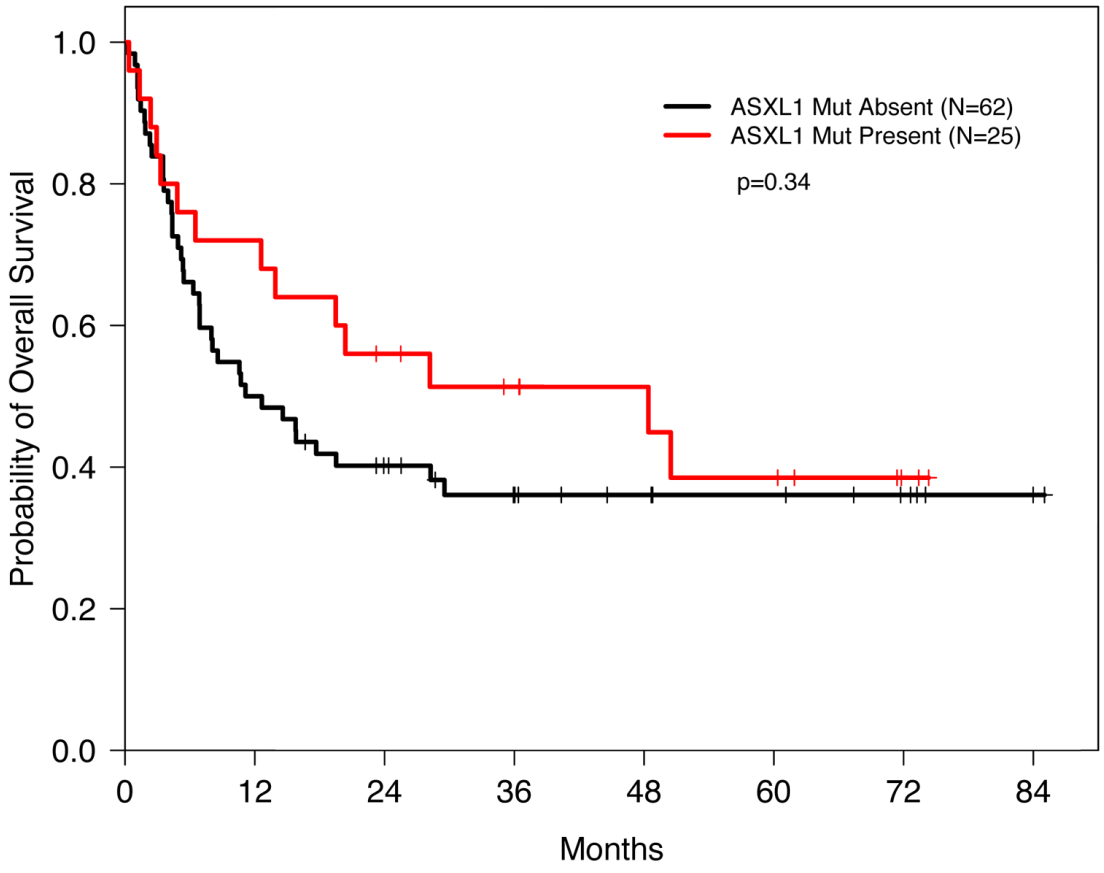

Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months
−7/7q−/+1 w/wo any other (N=15)
Normal (N=28)
Complex (N=28)
Other (N=8)
Unk (N=8)

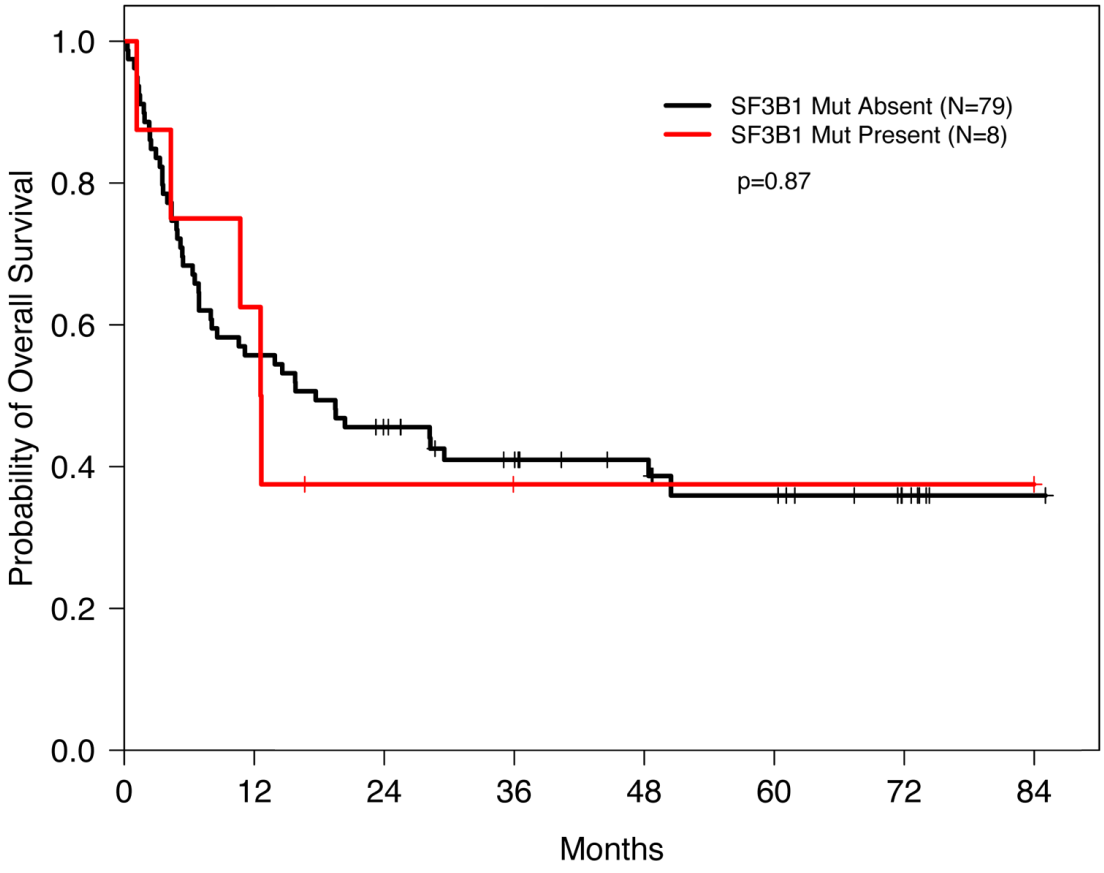

Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months
RA (N=24)
RARS (N=7)
RAEB (N=42)/RAEB−t(N=1)
CMML (N=5)
MDS−U (N=1)/Unk (N=7)

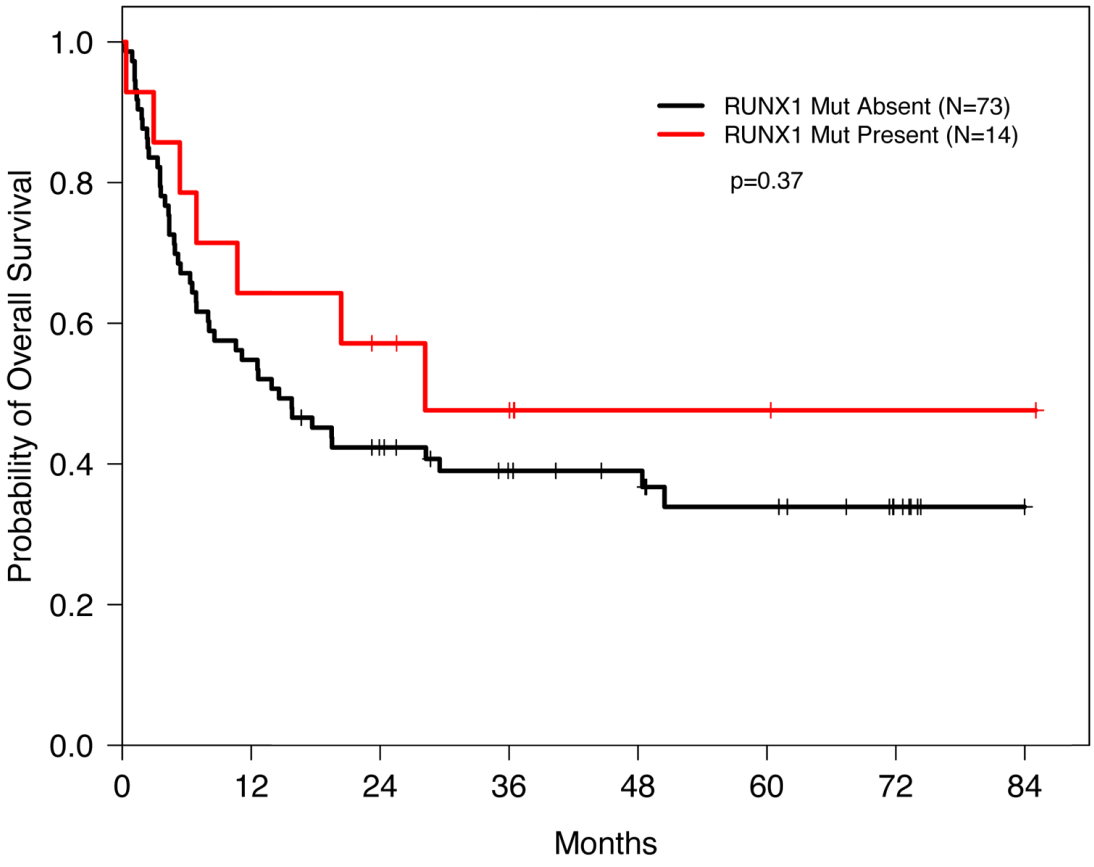
Supplemental Figure 2: Kaplan-Meier curves for overall cohort showing overall survival associated with frequently mutated genes.

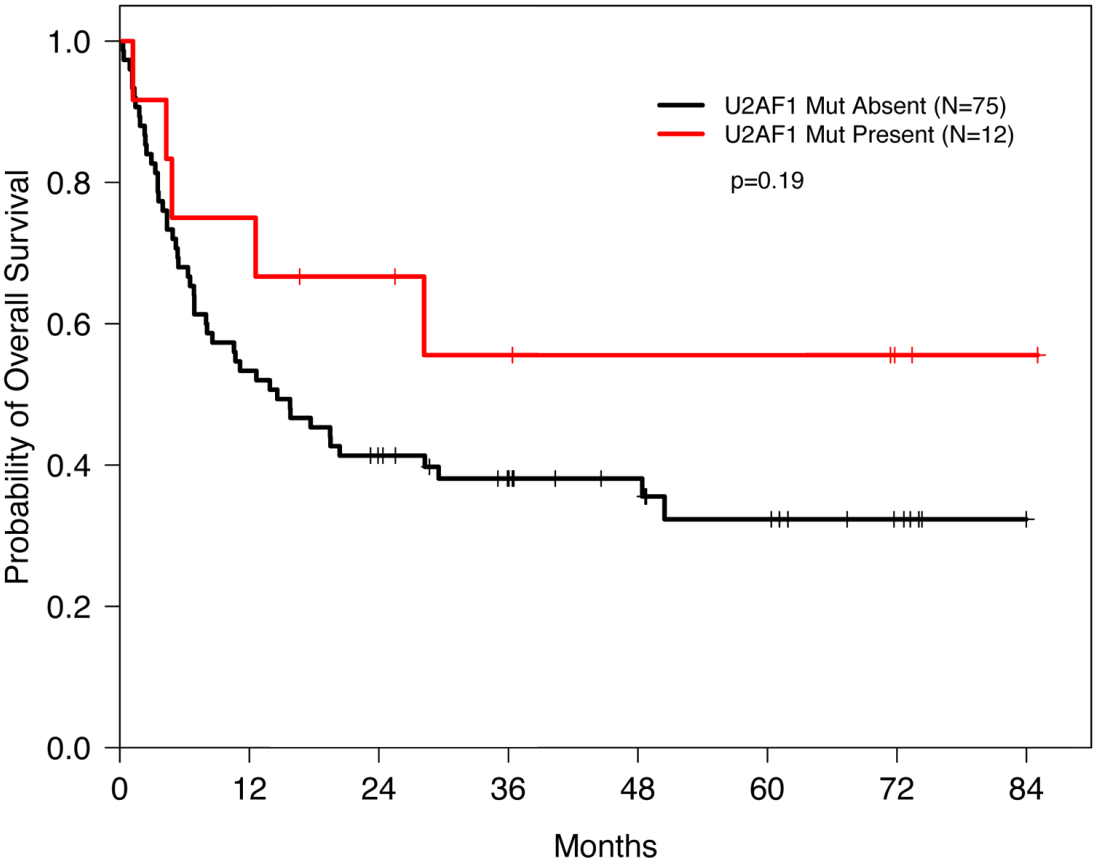


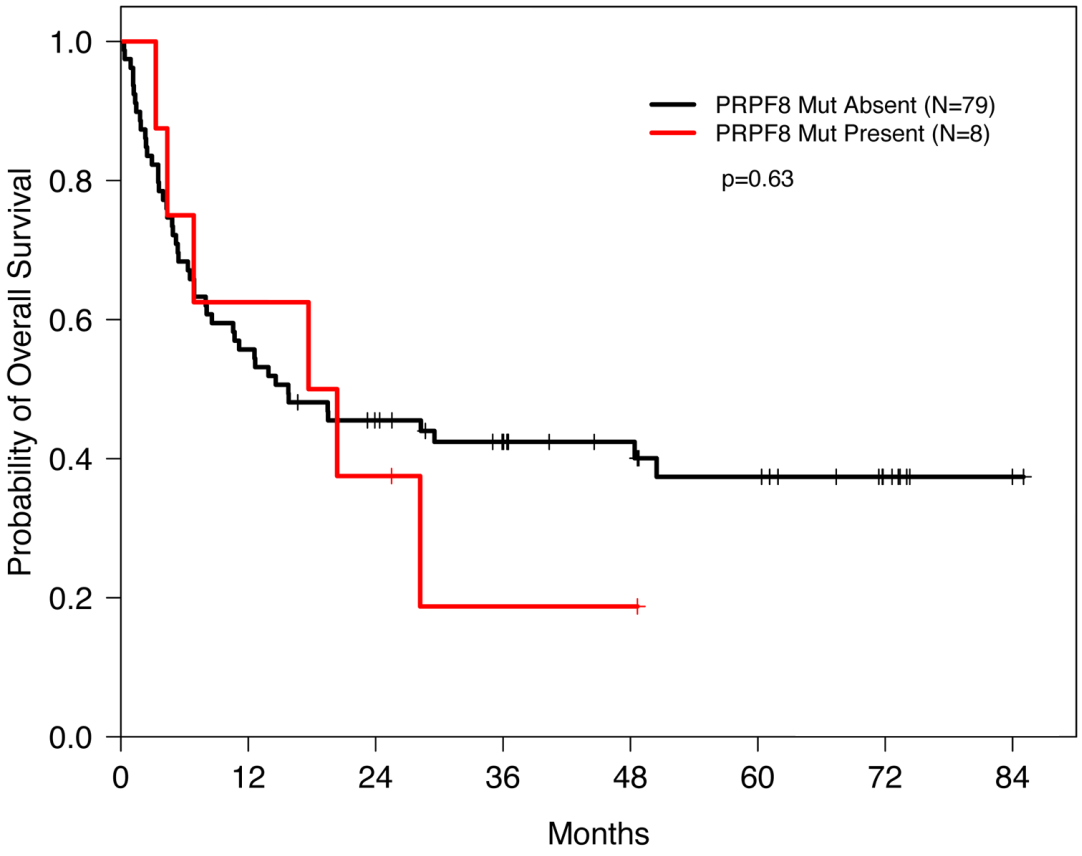


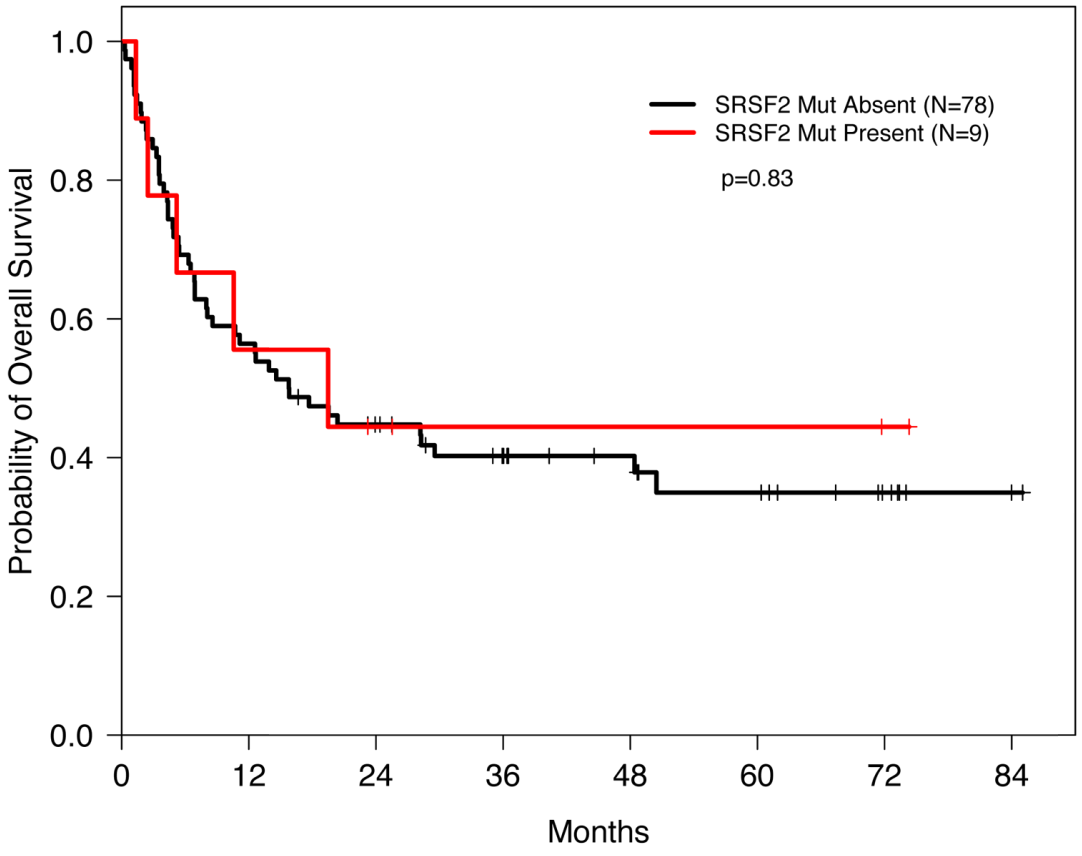

1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
ASXL1 Mut Absent (N=62)
ASXL1 Mut Present (N=25)
p=0.34
0
12
24
36
48
60
72
84
Months


1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
SF3B1 Mut Absent (N=79)
SF3B1 Mut Present (N=8)
p=0.87
0
12
24
36
48
60
72
84
Months

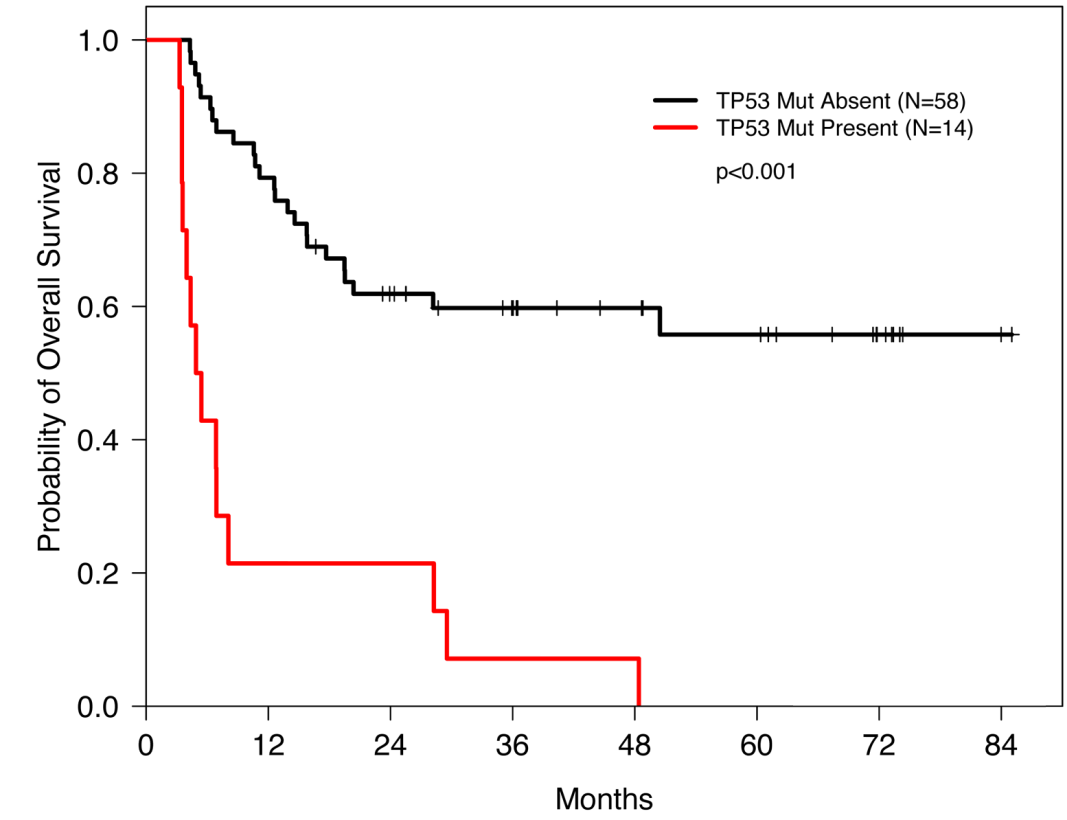

1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
RUNX1 Mut Absent (N=73)
RUNX1 Mut Present (N=14)
p=0.37
0
12
24
36
48
60
72
84
Months

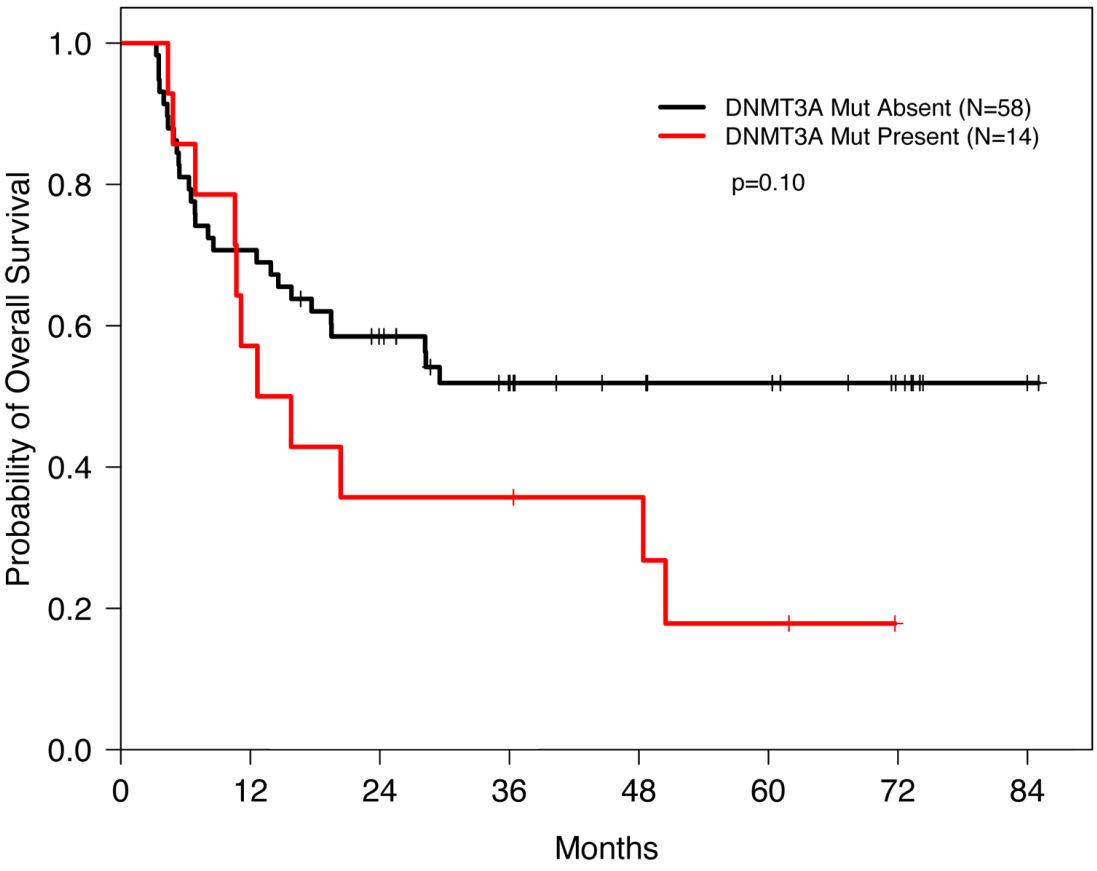

1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
U2AF1 Mut Absent (N=75)
U2AF1 Mut Present (N=12)
p=0.19
0
12
24
36
48
60
72
84
Months

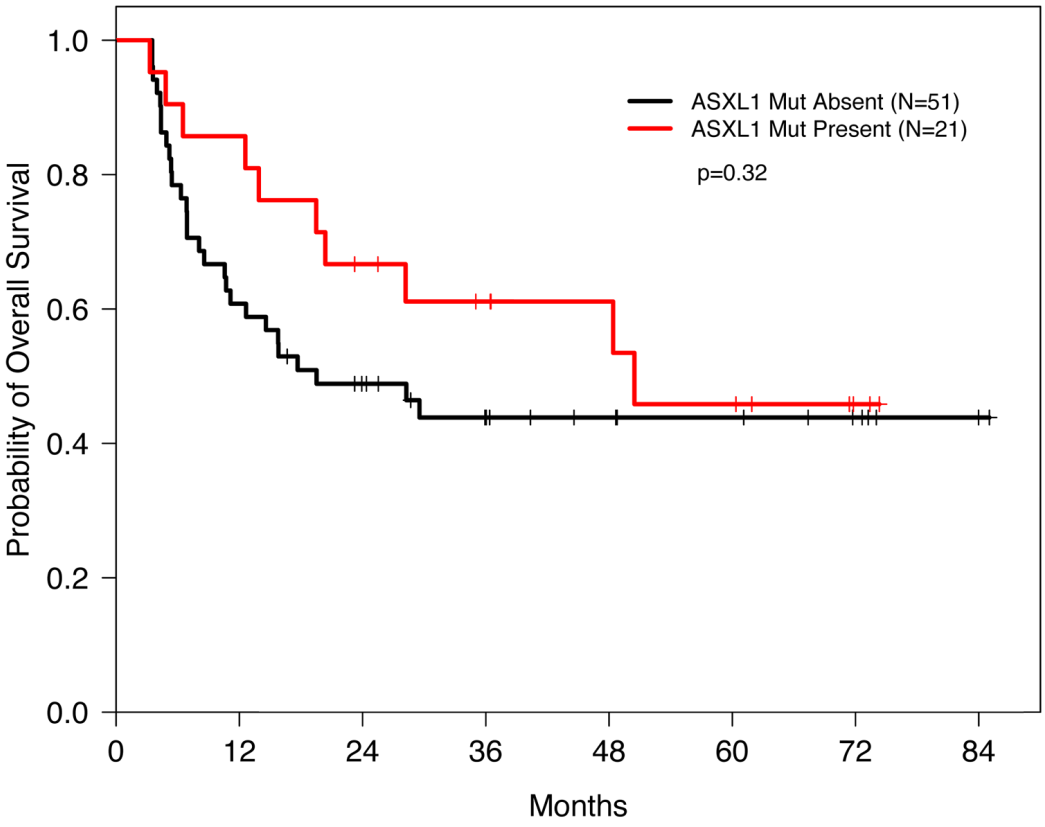

PRPF8 Mut Absent (N=79)
PRPF8 Mut Present (N=8)
p=0.63
Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months

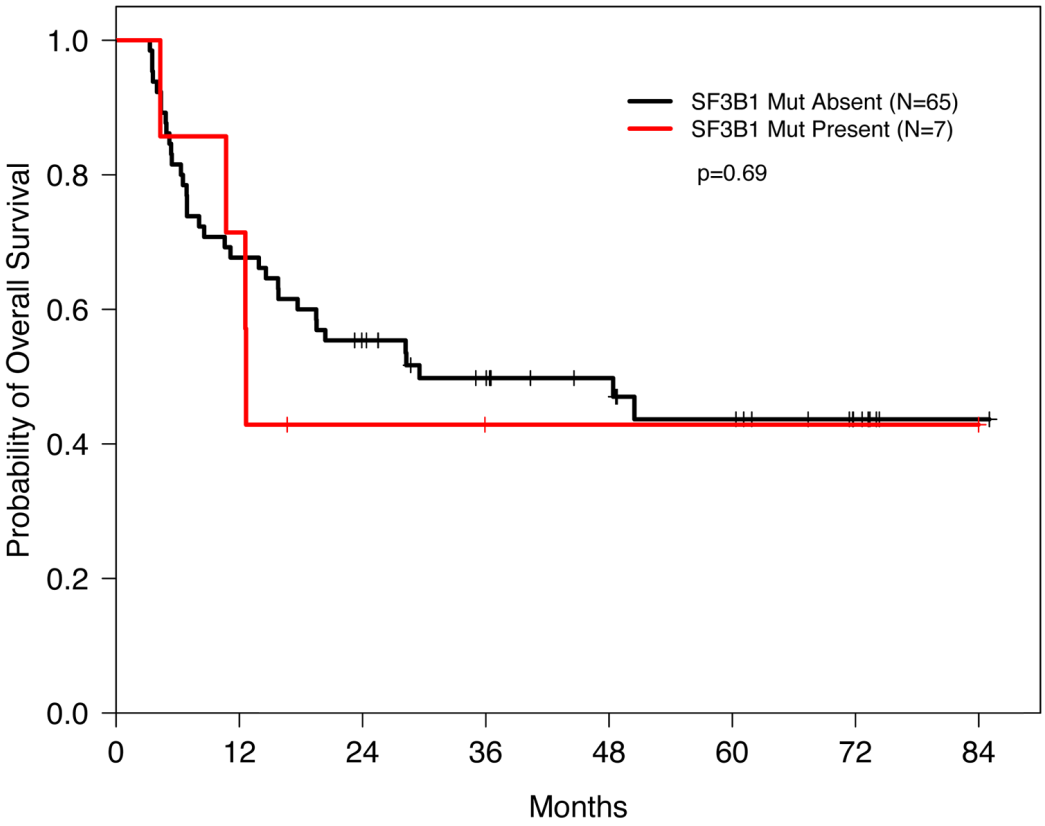

SRSF2 Mut Absent (N=78)
SRSF2 Mut Present (N=9)
p=0.83
Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months

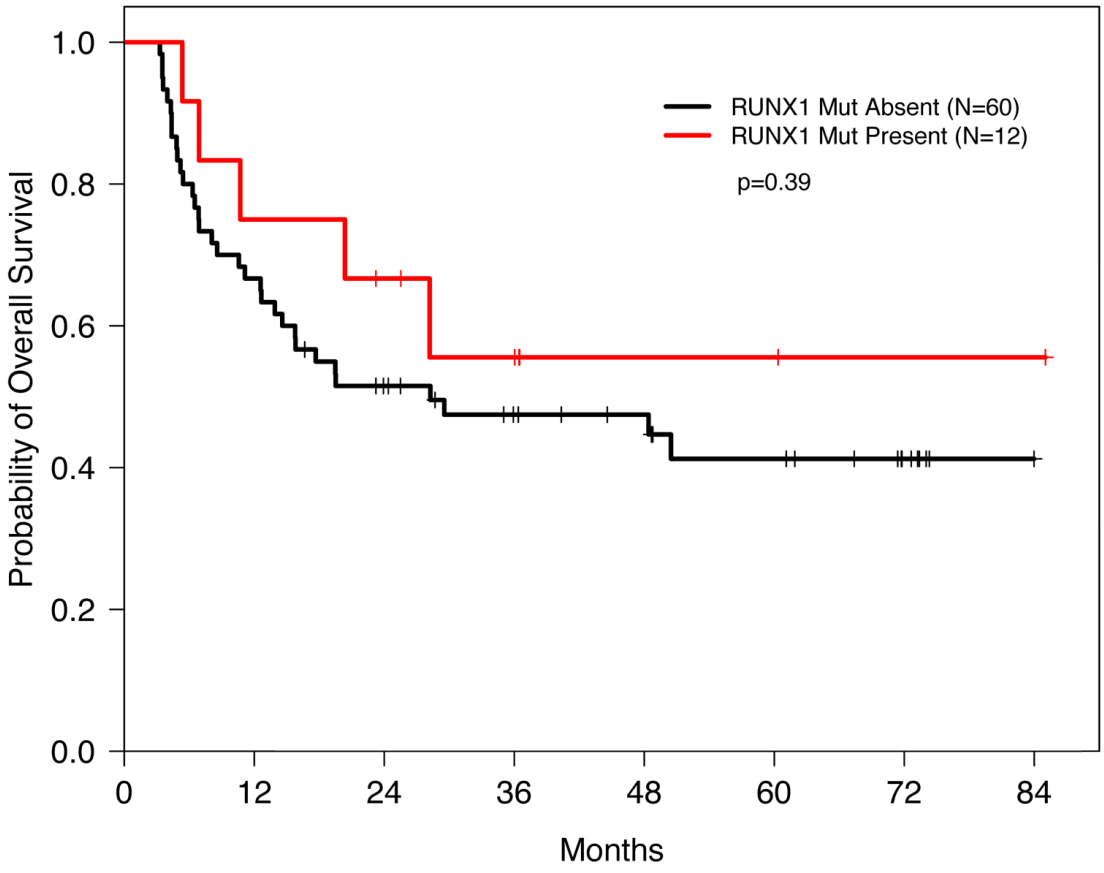
Supplemental Figure 3: Kaplan-Meier curves from day 100 landmark analysis showing overall survival associated with frequently mutated genes.

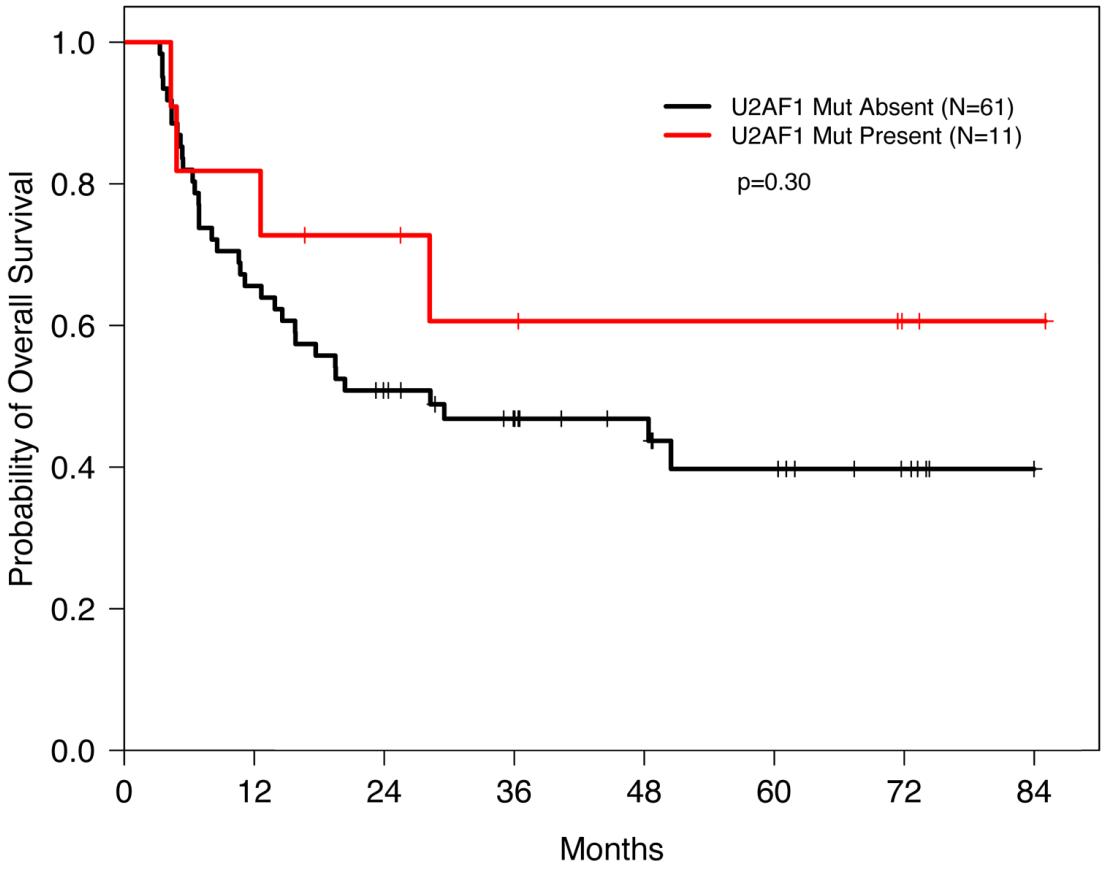


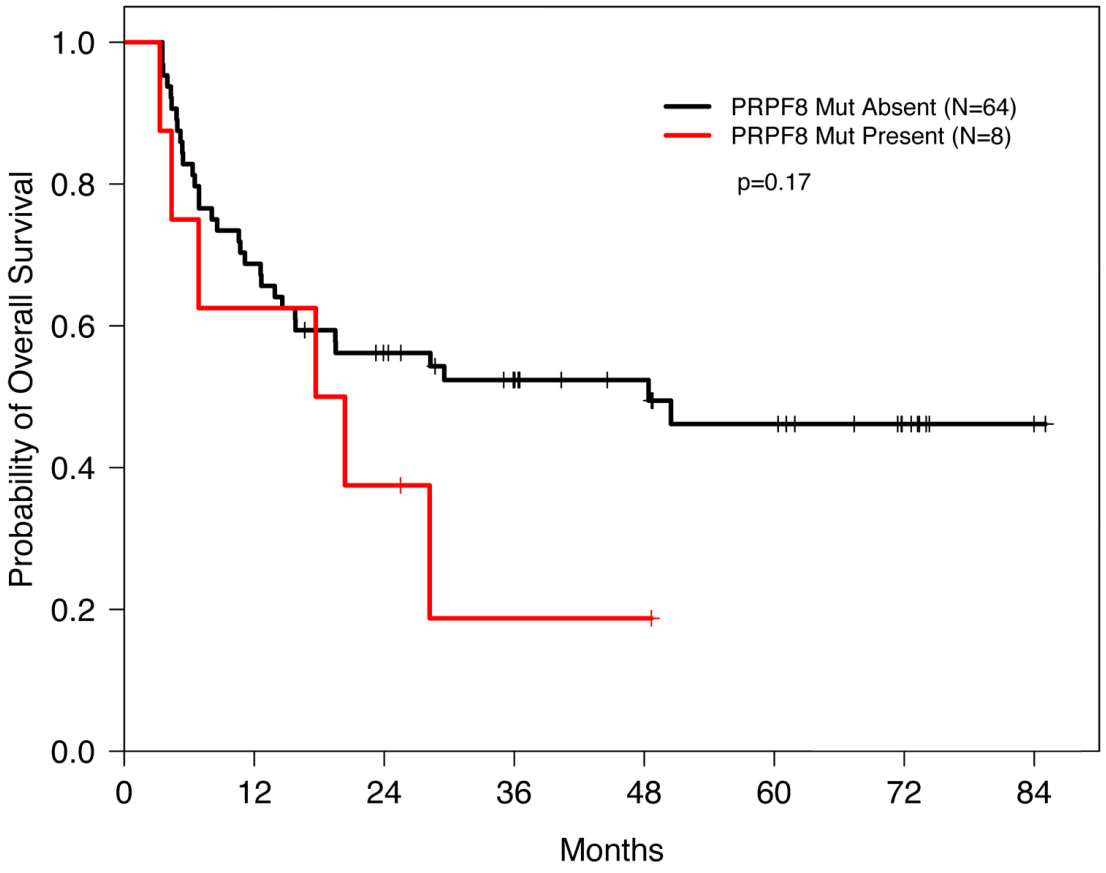


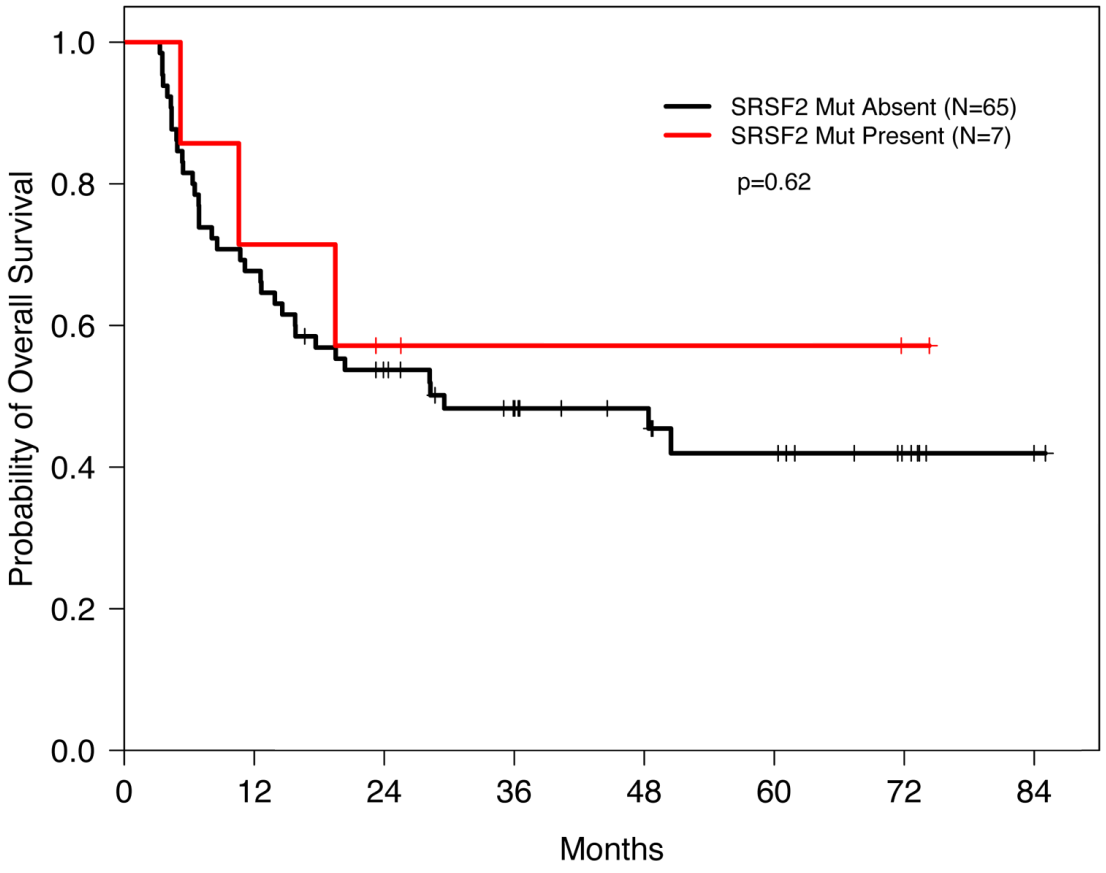

1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
ASXL1 Mut Absent (N=51)
ASXL1 Mut Present (N=21)
p=0.32
0
12
24
36
48
60
72
84
Months


1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
SF3B1 Mut Absent (N=65)
SF3B1 Mut Present (N=7)
p=0.69
0
12
24
36
48
60
72
84
Months


1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
RUNX1 Mut Absent (N=60)
RUNX1 Mut Present (N=12)
p=0.39
0
12
24
36
48
60
72
84
Months


1.0
0.8
0.6
0.4
0.2
0.0
Probability of Overall Survival
U2AF1 Mut Absent (N=61)
U2AF1 Mut Present (N=11)
p=0.30
0
12
24
36
48
60
72
84
Months


PRPF8 Mut Absent (N=64)
PRPF8 Mut Present (N=8)
p=0.17
Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months


SRSF2 Mut Absent (N=65)
SRSF2 Mut Present (N=7)
p=0.62
Probability of Overall Survival
1.0
0.8
0.6
0.4
0.2
0.0
0
12
24
36
48
60
72
84
Months