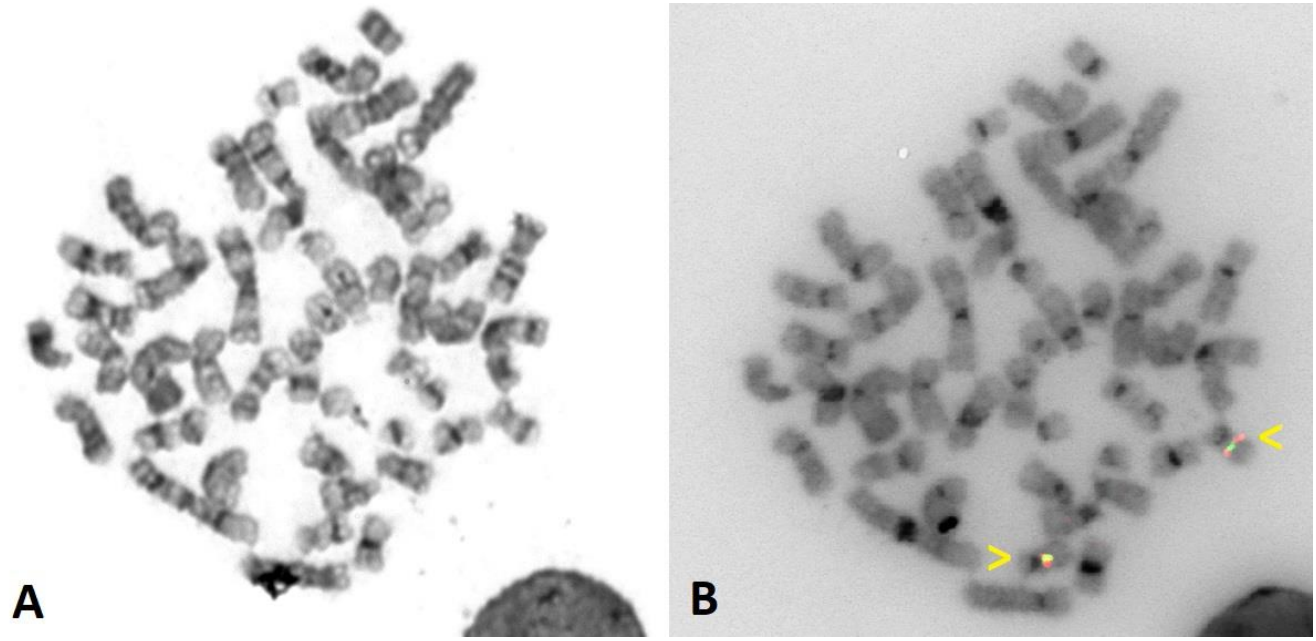
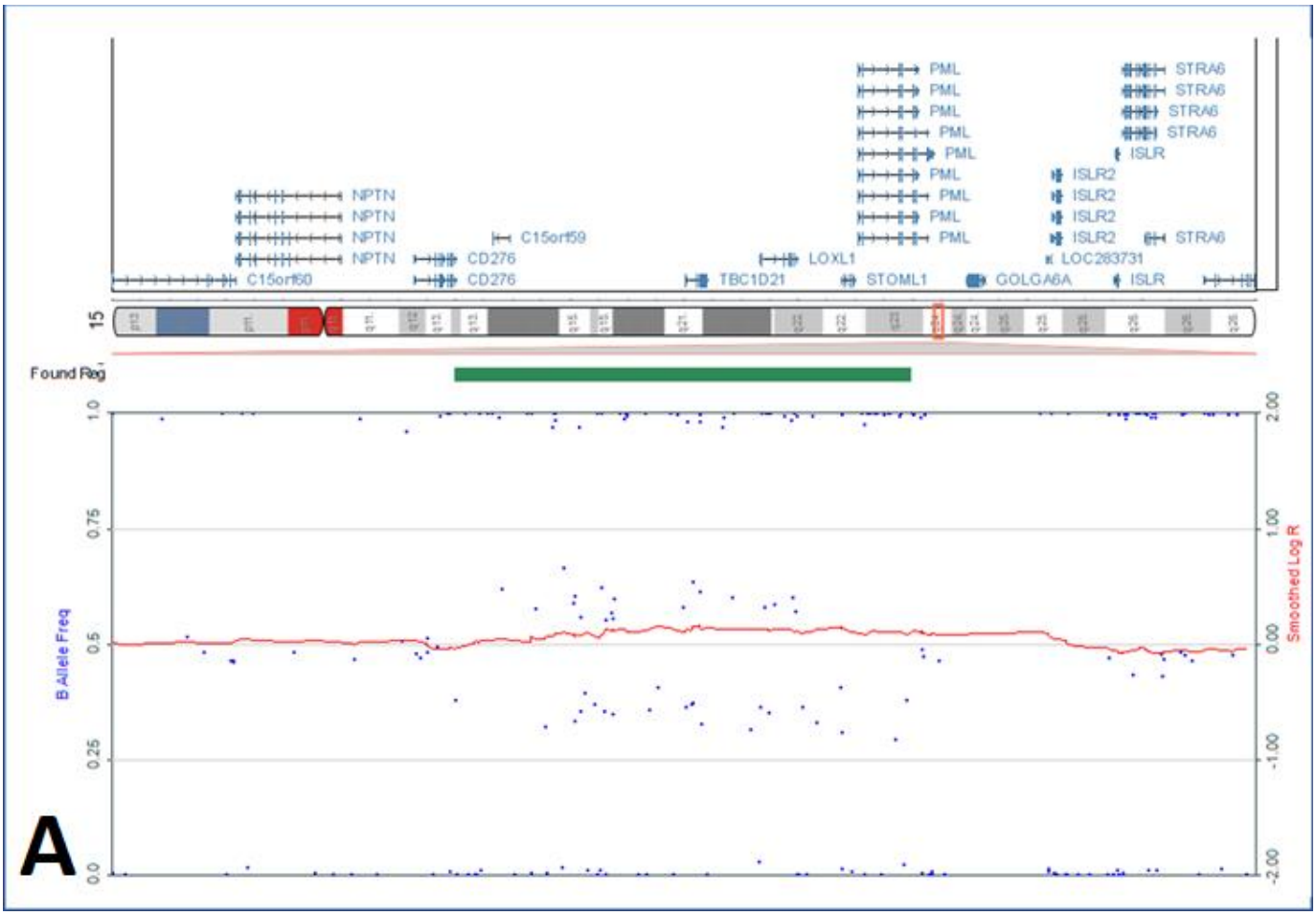
Supplemental materials include Supplemental Figure S1-S2 and Supplemental Table S1-S2



Supplementary Figure S1. Metaphase FISH for RARA break apart, demonstrating the two in-tact fusion signals are present on the two copies of chromosome 17. **A:** G-banded metaphase displaying a normal female karyotype. **B:** Inverted DAPI image of metaphase RARA FISH, with yellow arrows indicating fusions.


PML
PML
PML
PML
PML
PML
PML
PML
PML
STRA6
STRA6
STRA6
STRA6
ISLR
ISLR2
ISLR2
ISLR2
ISLR2
STRA6
NPTN
NPTN
NPTN
NPTN
C15orf59
CD276
CD276
C15orf60
LOXL1
TBC1D21
STOML1
GOLGA6A
LOC283731
ISLR
15
Found Reg
B Allele Freq
Smoothed Log R
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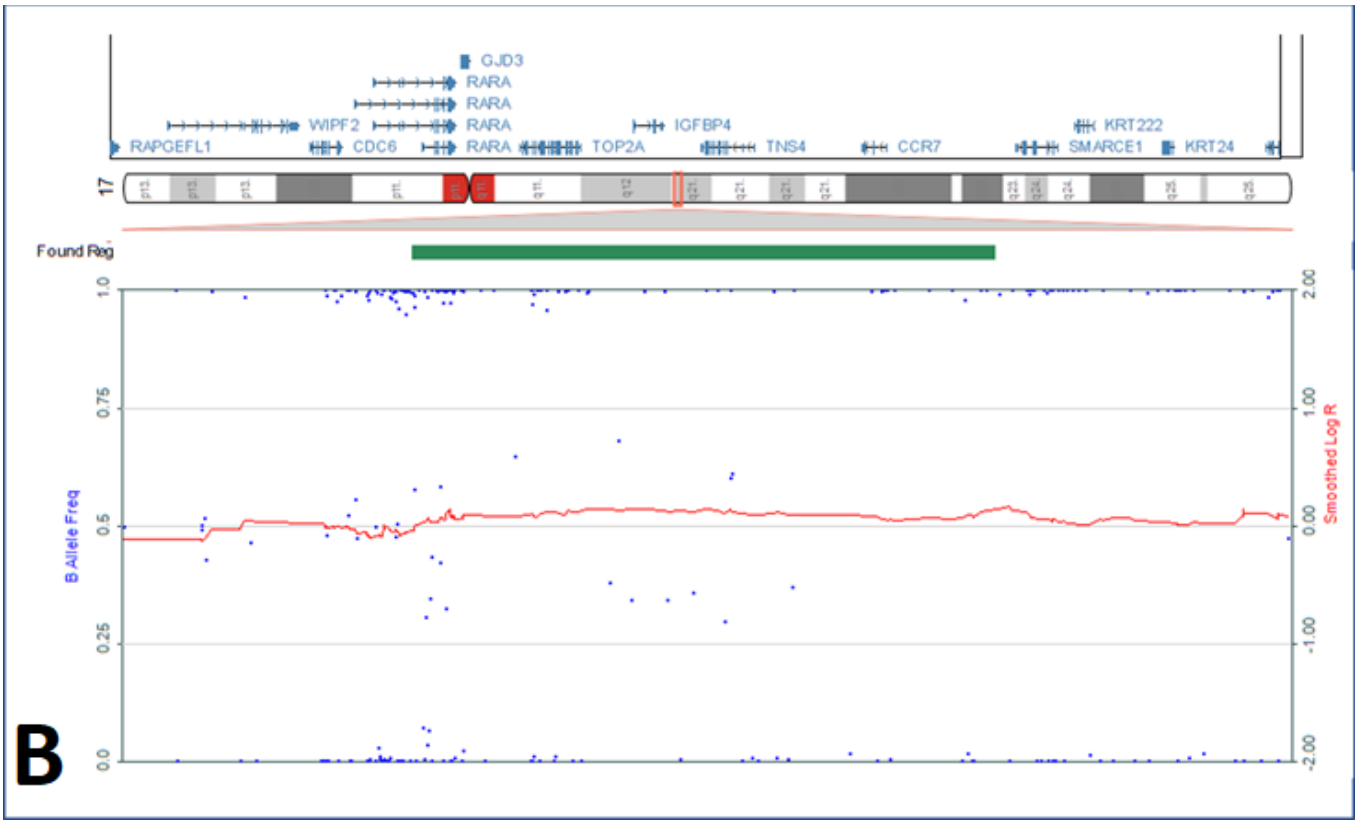
0.75
0.5
0.25
0.0
2.00
1.00
0.00
-1.00
-2.00
A



Supplementary Figure S2: SNP microarray plots displaying genotype information using the B-allele frequency data (blue dots) and the intensity data for the average LogR value (red line). The horizontal green bar indicates the regions of gain identified by microarray which are demonstrated by an increase in intensity data as well as the absence of heterozygous genotypes noted by the B-allele frequency data. Specifically, microarray showed **A:** 319 kilobase gain on 15q24.1 within the *PML* gene (ending within exon 5, NM_033238, arr[GRCh38] 15q24.1(73,713,259-74,032,683)x3) and **B:** a 282 kilobase gain on 17q21.2 within the *RARA* gene (starting within intron 2; NM_000964, arr[GRCh38] 17q21.2(40,332,287-40,614,034)x3).

Supplemental Table S1: list of covered cancer genes in the targeted NGS assay

ABL1	NM_005157	**NF1**	NM_000267
ASXL1	NM_015338	**NFE2**	NM_006163
ATM	NM_000051	**NLRP1**	NM_033004
ATRX	NM_000489	**NOTCH1**	NM_017617
BCL2	NM_000633	**NOTCH2**	NM_024408
BCL6	NM_001706	**NPM1**	NM_002520
BCOR	NM_017745	**NRAS**	NM_002524
BCORL1	NM_021946	**NSD1**	NM_022455
BRAF	NM_004333	**NUP98**	NM_016320
BTK	NM_000061	**PAX5**	NM_016734

CALR	NM_004343	**PDGFRA**	NM_006206
CARD11	NM_032415	**PHF6**	NM_032458
CBL	NM_005188	**PIGA**	NM_002641
CBLB	NM_170662	**PIM1**	NM_001243186, NM_002648
CD79A	NM_001783	**PLCG2**	NM_002661
CD79B	NM_000626	**POT1**	NM_015450
CDKN2A	NM_000077	**PPM1D**	NM_003620
CEBPA	NM_004364	**PRDM1**	NM_001198
CHEK2	NM_007194	**PTEN**	NM_000314
CREBBP	NM_004380	**PTPN11**	NM_002834
CSF3R	NM_156039	**RAD50**	NM_005732
CXCR4	NM_001008540	**RECQL4**	NM_004260
DDX41	NM_016222	**RHOA**	NM_001664
DNMT3A	NM_022552	**RHOH**	NM_004310
EP300	NM_001429	**RUNX1**	NM_001754,
ERBB2	NM_004448	**SAMD9**	NM_017654
ETV6	NM_001987	**SAMD9L**	NM_152703
EZH2	NM_004456	**SETBP1**	NM_015559
FAS	NM_000043	**SF3B1**	NM_012433
FBXW7	NM_033632	**SGK1**	NM_005627
FLT3	NM_004119	**SRSF2**	NM_003016
FOXO1	NM_002015	**STAG2**	NM_006603
GATA1	NM_002049	**STAT3**	NM_139276
GATA2	NM_032638	**STAT5B**	NM_012448
GNA13	NM_006572	**STAT6**	NM_003153
GNAS	NM_000516	**TERT promoter**	NM_198253
IDH1	NM_005896	**TET2**	NM_001127208
IDH2	NM_002168	**TNFAIP3**	NM_001270507
IKZF1	NM_006060	**TNFRSF14**	NM_003820
JAK2	NM_004972	**TP53**	NM_000546
KDM2B	NM_032590	**U2AF1**	NM_006758
KDM6A	NM_021140	**UBA1**	NM_003334
KIT	NM_000222	**WT1**	NM_024426
KMT2A	NM_001197104	**ZRSR2**	NM_005089
KMT2D/MLL2	NM_003482		
KRAS	NM_004985		
MEF2B	NM_001145785		
MPL	NM_005373		
MYC	NM_002467		
MYD88	NM_002468		

Supplemental Table S2: key lab test results of peripheral blood and bone marrow aspirate

Blood Results		
D-Dimer (mg/L FEU)	11.01	H
Fibrinogen, Quant., Superstat (mg/dL)	101	L

INR, Protime	1.5	H
Prothrombin Time (sec)	15.3	H
APTT (sec)	25.2	
White Blood Cell Count (K/cu mm)	4.02	L
Red Blood Cell Count (M/cu mm)	2.21	L
Hemoglobin (g/dL)	7.2	L
Hematocrit %	21.1	L
Mean Corpuscular Volume (fL)	95.5	
Mean Corpus Hgb (pg)	32.6	
Mean Corpus Hgb Conc (g/dL)	34.1	
Mean Platelet Volume (fL)	12.1	
RBC Distribution Width (%)	15.8	H
Platelet Count (K/cu mm)	34	L
Nucleated RBC Number (K/cu mm)	0	
Neutrophils %	16	L
Lymphocyte %	11	L
Monocyte %	3	
Eosinophil %	1	
Basophil %	0	
Myelocyte %	1	H
Blasts %	46	HH
Promyelocyte %	20	H
ANC-Absolute Neut Count (K/cu mm)	0.64	L
Lymphocytes Absolute,Manual (K/cu mm)	0.44	L

L = Data is abnormally low

H = Data is abnormally high

HH = Data is critically high

Bone Marrow Results		
Plasma Cells %	0	
Blast %	0.5	
Promyelocytes %	84.5	H
Myelocytes %	1.5	L
Metamyelocytes %	0	L
Bands %	0	L
Neutrophils %	1	L
Lymphocytes %	4	L
Monocytes %	0	
Eosinophils %	0.5	L
Basophils %	2	H
Early Erythroid Precursors %	0	

Late Erythroid Precursors %	6	
Histiocytes %	0	L
Others %	0	
Megakaryocytes	Absent	
Cellularity	Normocellular	
Stromal Elements	Absent	
Myeloid Erythroid Ratio	15	
Comments, Bone Marrow: 200 nucleated cells identified on 2 coverslips scanned.		

L = Data is abnormally low

H = Data is abnormally high