Figure Legends

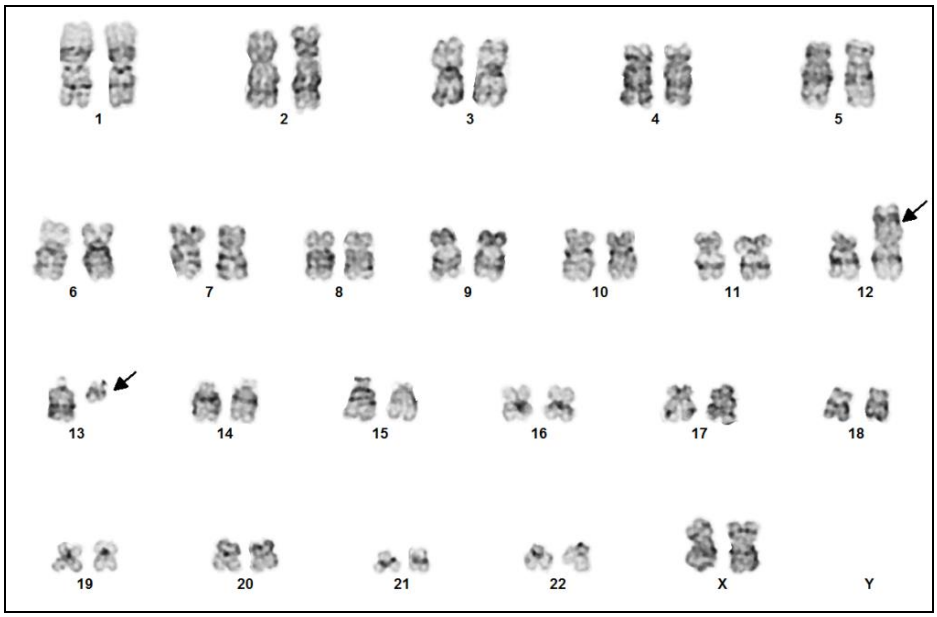
Figure 1. Identification of the *ETV6-FLT3* fusion gene. RT-PCR using *ETV6* exon-5 forward primer and *FLT3* exon-15 reverse primer results in an amplicon of 1050 base pairs, confirming the identity of the two fusion partners (center lane). RT-PCR conducted on an *ETV6-FLT3*-negative control patient sample using forward *ETV6* exon-5 primer and reverse *FLT3* exon-15 primer, fails to generate an amplicon (right lane).

Supplemental Figure 1. **Conventional and molecular cytogenetic analysis performed at the time of referral.** (A) Female karyotype with a t(12;13)(p13;q12). The abnormal chromosomes, indicated by the arrows, are derived from a non-reciprocal translocation involving chromosomes 12p13 and 13q12; (B) Fluorescent *in-situ* hybridization (FISH) was positive for an *ETV6* rearrangement. A dual-color break-apart FISH probe, showing normal and abnormal signal patterns was used. Left panel: two normal fusion signals in two normal interphase cells. Right panel: abnormal FISH signal (1 fusion, 1 red, and 1 green) in two interphase cells and one metaphase cell.

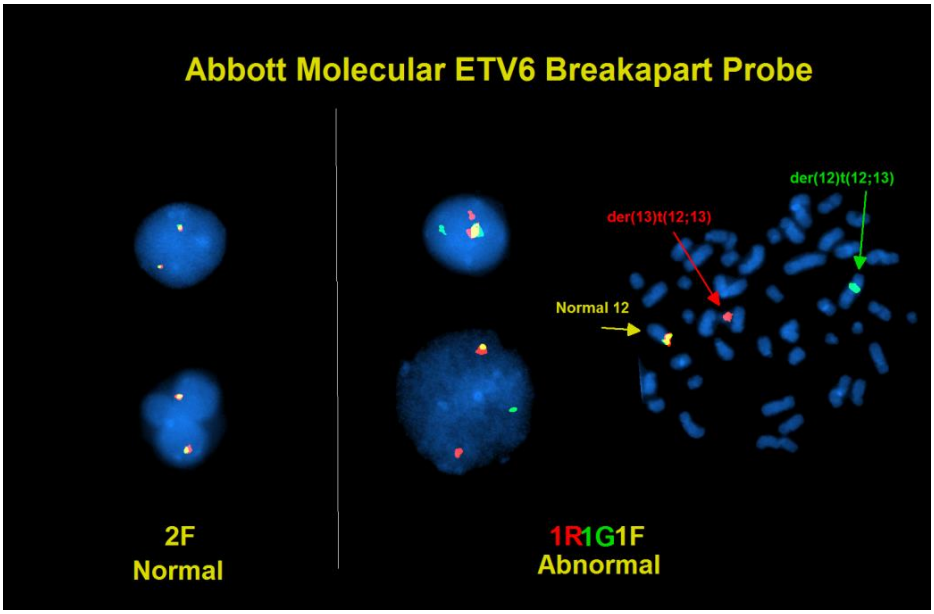
Supplemental Figure 2. Identification of the *ETV6-FLT3* fusion gene. (A) 3'-Rapid Amplification of cDNA Ends (RACE)-polymerase chain reaction (PCR) for *ETV6* was performed with mRNA derived from the patient's sample to generate cDNA as previously described,(3) resulting in a 1800 base pairs amplicon (B) Nested RT-PCR using forward primer in *ETV6* exon 5 and universal adapter primer as reverse primer, resulted in a 1200 base pairs amplicon.

Supplemental Figures

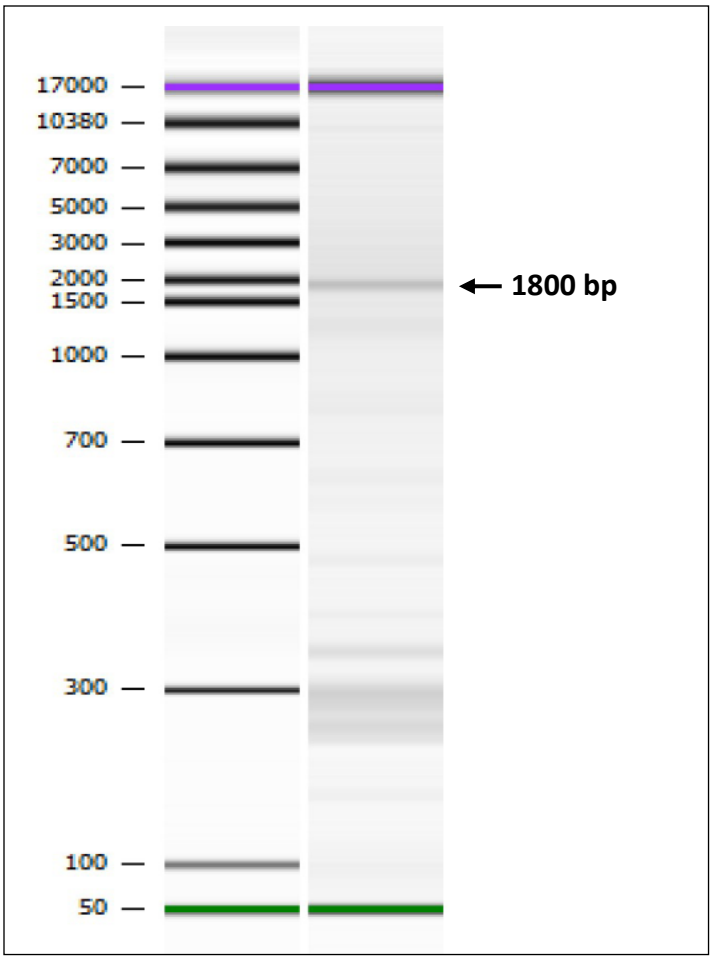
Supplemental Figure 1A.



Supplemental Figure 1B.



Supplemental Figure 2A.



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13 **Supplemental Figure 2B.**

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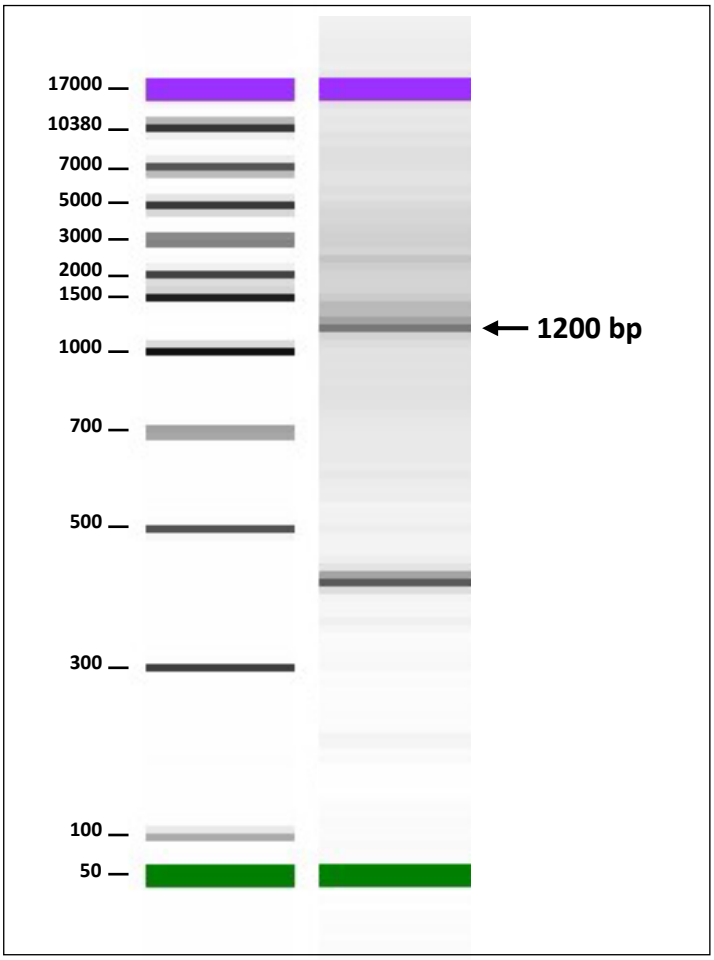

Supplemental Tables.

Supplemental Table 1. Next generation sequencing–based analysis for the detection of cancer-associated mutations in a panel of 53 genes.

Coverage by gene and codon(s) tested for adequate amplicons	
Gene	**Exons (codons) tested**
ABL1	4 (243-274), 5 (275-303), 6 (303-321), 6 (321-362), 7 (395-424)
AKT1	3 (16-49)
ALK	23 (1172-1175), 25 (1248-1275)
APC	16 (875-918), 16 (1113-1153), 16 (1257-1297), 16 (1288-1328), 16 (1318-1357), 16 (1349-1386), 16 (1377-1416), 16 (1416-1456), 16 (1456-1494), 16 (1493-1530), 16 (1530-1575)
ATM	8 (353-355), 9 (409-412), 12 (601-633), 17 (846-880), 26 (1308-1331), 34 (1678-1719), 35 (1741-1773), 36 (1792-1832), 39 (1940-1973), 50 (2441-2479), 54 (2665-2670), 55 (2694-2717), 56 (2725-2756), 59 (2889-2891), 61 (2946-2950), 63 (3007-3051)
BRAF	11 (439-471), 15 (581-606)
CDH1	3 (77-117), 8 (369-379), 9 (399-439)
CSF1R	7 (297-301), 22 (926-970)
CTNNB1	3 (12-50)
DNMT3A	23 (866-913)
EGFR	3 (108-142), 7 (288-297), 15 (598-627), 18 (708-728), 19 (729-761), 20 (762-775), 20 (775-817), 21 (857-875)
ERBB2	19 (754-769), 20 (772-818), 21 (839-883)
ERBB4	3 (98-140), 4 (153-186), 6 (208-244), 7 (248-287), 8 (295-306), 9 (333-350), 15 (579-619), 23 (907-936)
EZH2	16 (613-644)
FBXW7	5 (243-278), 8 (375-394), 9 (429-471), 10 (473-508), 11 (549-583)
FGFR1	4 (120-126), 7 (247-250)
FGFR2	7 (250-273), 7 (273-311), 7 (302-313), 9 (362-382), 12 (521-550)
FGFR3	7 (247-288), 9 (379-422), 18 (792-807)
FLT3	11 (437-456), 14 (569-605), 16 (648-683), 20 (807-843)
GNA11	4 (172-202), 6 (255-297), 7 (297-304), 7 (304-349)
GNAQ	4 (159-202), 5 (202-210), 5 (210-245), 5 (241-245), 6 (246-263), 6 (263-297), 6 (291-297), 7 (297-324), 7 (324-360), 7 (355-360)
GNAS	8 (200-220)
HNF1A	3 (205-238), 4 (271-314)
HRAS	2 (1-15), 3 (38-63)
IDH1	4 (90-132)
IDH2	4 (125-178)
JAK2	14 (615-622)
JAK3	13 (568-573), 16 (683-723)
KDR	6 (220-248), 7 (267-276), 11 (471-476), 19 (872-874), 21 (946-985), 26 (1135-1146), 27 (1171-1211), 30 (1308-1352), 30 (1352-1357)
KIT	2 (51-93), 9 (502-514), 10 (514-547), 10 (540-549), 11 (550-550), 11 (550-592), 13 (641-664), 14 (670-712), 15 (714-745), 17 (815-828), 18 (838-866)
KLHL6	1 (1-13), 1 (13-73), 1 (73-98)
KRAS	2 (1-22), 3 (38-63), 4 (103-147)
MET	2 (168-209), 2 (375-400), 14 (1008-1028), 16 (1110-1132), 19 (1247-1284)
MLH1	12 (383-426)
MPL	10 (514-522)

NOTCH1	26 (1562-1601), 27 (1673-1679)
NPM1	11 (283-295)
NRAS	2 (1-18), 3 (38-62)
PDGFRA	12 (552-592), 14 (659-668), 15 (673-717), 18 (823-854)
PIK3CA	2 (83-118), 5 (345-353), 8 (418-445), 10 (538-555), 14 (701-729), 21 (988-1027), 21 (1027-1069)
PTEN	1 (5-27), 3 (67-70), 6 (170-210), 7 (212-221), 7 (221-266), 8 (287-332), 8 (332-342)
PTPN11	3 (59-104), 13 (501-533)
RB1	4 (127-158), 6 (199-203), 11 (357-376), 18 (570-605), 20 (659-700), 21 (703-733), 22 (746-775)
RET	10 (610-627), 11 (628-667), 13 (766-798), 15 (880-910), 16 (918-934)
SMAD4	3 (119-142), 5 (167-208), 6 (243-263), 8 (310-319), 9 (329-373), 10 (385-424), 11 (443-480), 12 (496-535)
SMARCB1	2 (39-78), 4 (156-167), 5 (199-210), 9 (381-386)
SMO	3 (197-242), 5 (323-366), 11 (639-646)
STK11	1 (36-77), 6 (261-288), 8 (332-370)
TP53	2 (1-12), 4 (69-112), 5 (126-147), 5 (147-186), 5 (181-187), 6 (187-192), 6 (187-223), 6 (214-224), 7 (225-253), 8 (267-306), 10 (332-342)
VHL	1 (88-114), 2 (129-155), 3 (157-200)
XPO1	14 (501-522), 15 (523-539), 15 (539-575)
Coverage by gene and codon(s) tested for indeterminate amplicons	
Gene	**Exons (codons) tested**
CDKN2A	2 (51-70)
FGFR3	14 (639-653), 15 (654-659), 16 (692-723)
GNA11	4 (159-172), 5 (202-216), 7 (349-360)
NOTCH1	34 (2467-2526)
RB1	17 (550-565)
SMO	6 (403-422), 9 (533-551)
SRC	14 (530-537)
STK11	4 (193-199), 5 (200-211)

Supplemental Table 2. Primer sequences used in this patient study.

Primer	**Primer sequence**
ETV6 Exon 4 F	5’-GTGATGTGCTCTATGAACTC-3’
ETV6 Exon 5F	5’-CAGGCCATCCGTGGATAATG-3’
ETV6 Exon 8R	5’-TGTCTAAGGTGCTCCAGGGTC-3’