

Supplementary Data

***Alu*-mediated diverse and complex pathogenic copy-number variants within human chromosome 17 at p13.3**

Shen Gu¹, Bo Yuan¹, Ian M. Campbell¹, Christine R. Beck¹, Claudia M.B. Carvalho¹, Sandesh C.S. Nagamani^{1,2}, Ayelet Erez^{1,5}, Ankita Patel¹, Carlos A. Bacino^{1,2}, Chad A. Shaw¹, Paweł Stankiewicz¹, Sau Wai Cheung¹, Weimin Bi¹ and James R. Lupski^{1,2,3,4,*}

¹Department of Molecular & Human Genetics, Baylor College of Medicine, Houston, TX 77030, USA.

²Texas Children's Hospital, Houston, TX 77030, USA.

³Department of Pediatrics, Baylor College of Medicine, Houston, TX 77030, USA.

⁴Human Genome Sequencing Center, Baylor College of Medicine, Houston, TX 77030, USA.

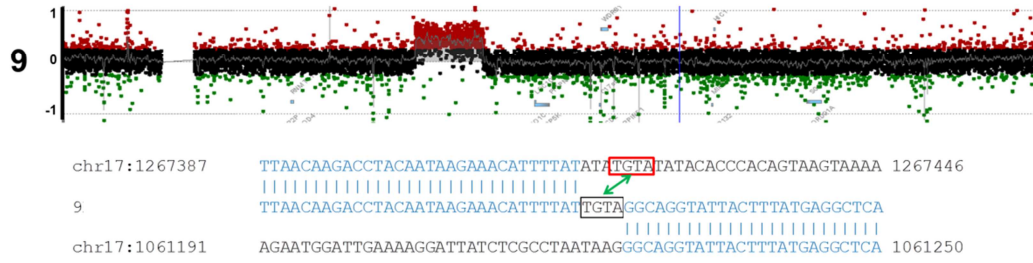
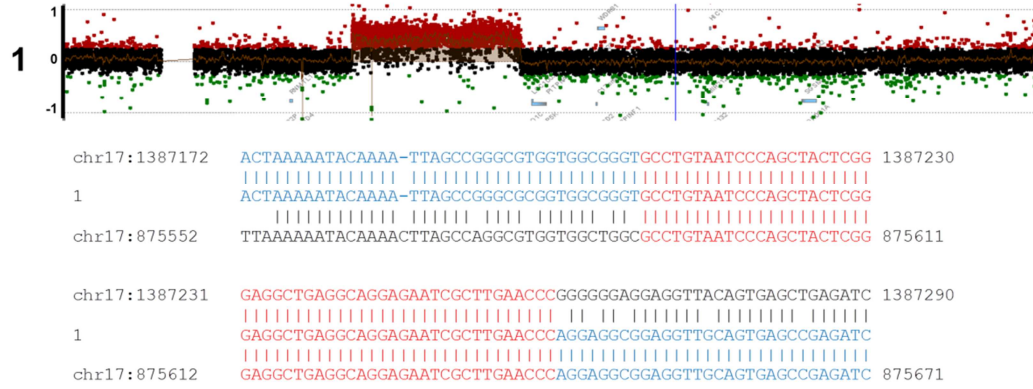
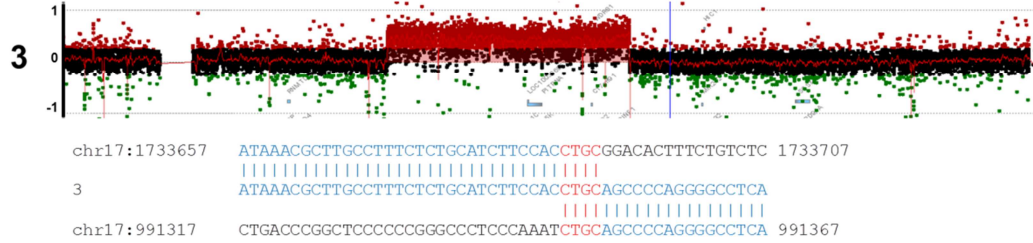
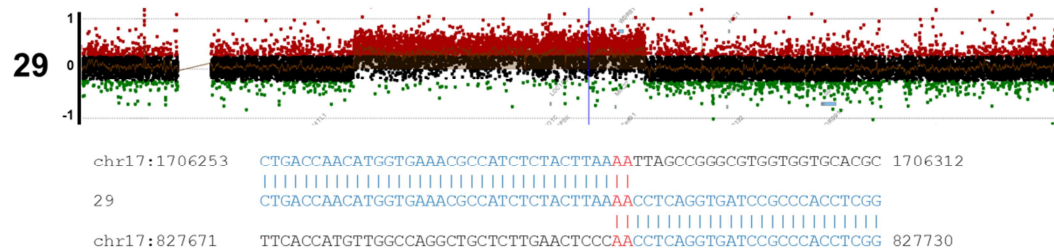
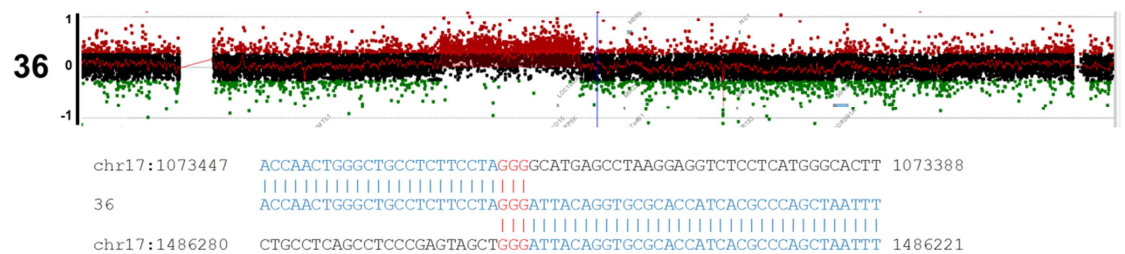
⁵Department of Biological Regulation, Weizmann Institute of Science, Rehovot, Israel.

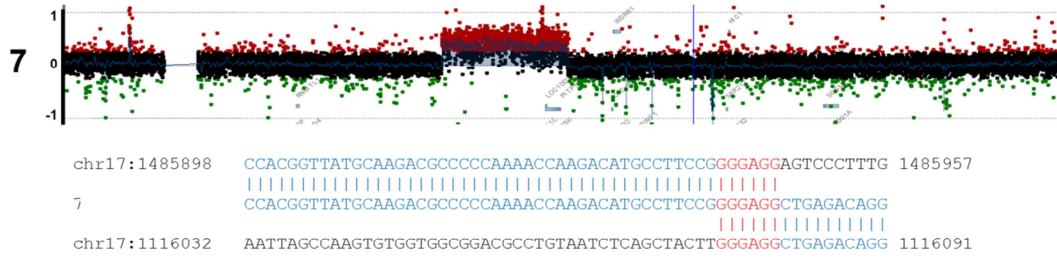
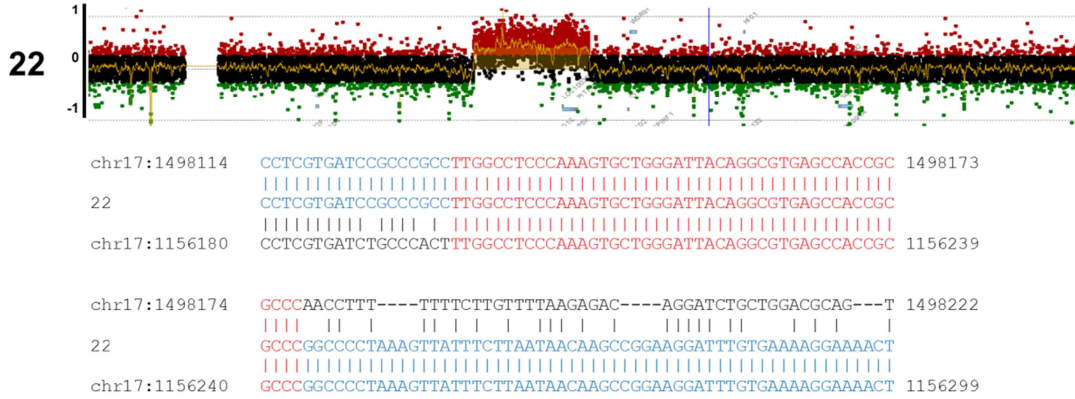
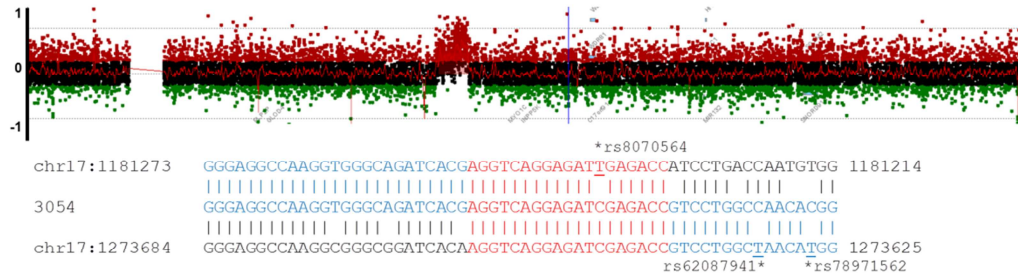
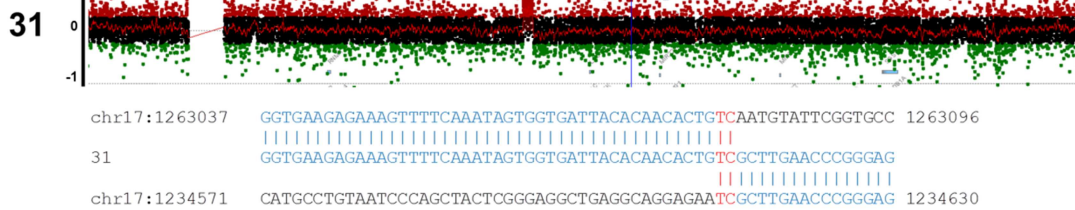
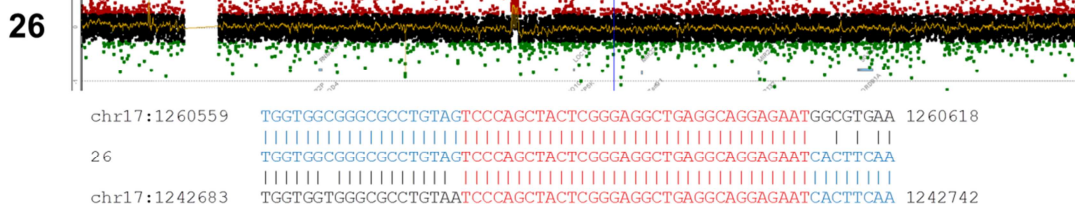
* To whom correspondence should be addressed.

Tel: 1-713-798-6530

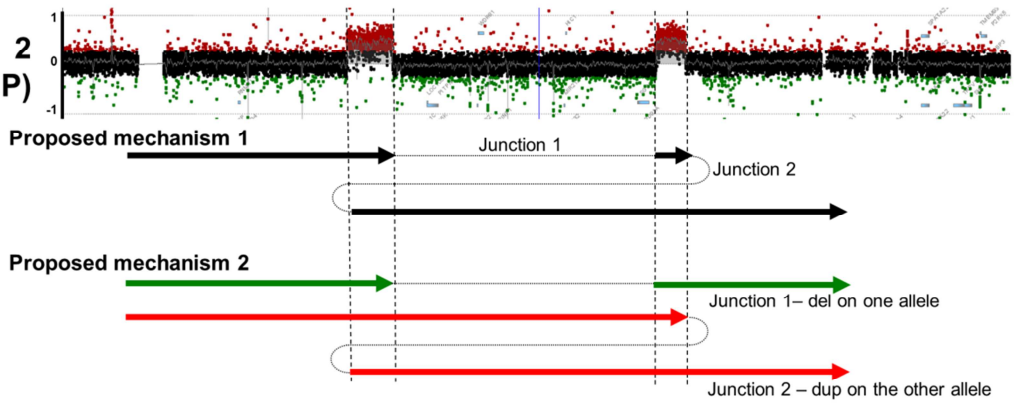
Fax: 1-713-798-5073

E-mail: jlupski@bcm.edu

A**B****C****D****E**

F**G****H****BAB3054****I****J**

A
(DUP-NML-DUP)



Junction 1

```

                                *rs77376275
chr17:1287744  GGGAGGCCAAGCGGGCGGATCACAACGTCAGGAGATCAAGACCATCCTGGCTAACACGG 1287803
2_1          GGGAGGCCAAGCGGGCGGATCACAACGTCAGGAGATCAAGACCATCCTGGCTAACACGG
chr17:2311717  GGGAGGCCGAGTGGCGGATCAGAGTCAAGACCATCCTGGCTAACACGG 2311776

chr17:1287804  TGAAACCCGTGCTCTACTAAAAATACAAAAAATAGCCAGGCATGGTGGCAGGCACCT 1287863
2_1          TGAAACCCCGTCTCTACTAAAAATACAAAAA---TTAGCCGGGCGTGGTGGCAGGCACCT
chr17:2311777  TGAAACCCCGTCTCTACTAAAAATACAAAAA---TTAGCCGGGCGTGGTGGCAGGCACCT 2311833
                                *rs12452380          rs12450730*   *rs12450250

```

Junction 2

```

chr17:1108955  AA-----CGGTCCGCGCCGCCGAGTGGGACATTAGGTCGTGAGACCCCTCCGGGT 1109006
2_2          AATTTTTTATCCGGTCCGCCGCCGAGTGGGACATTAGGTCGTGAGACCCCTCCGGGT
chr17:2426932  AATTTTTTATCCGGTCCGCCGCCGAGTGGGACATTAGGTCGTGAGACCCCTCCGGTT 2426991

```


references and color-matched. Microhomology at the breakpoint is indicated in red. Sequence in purple indicates inserted sequences at the breakpoint junction.

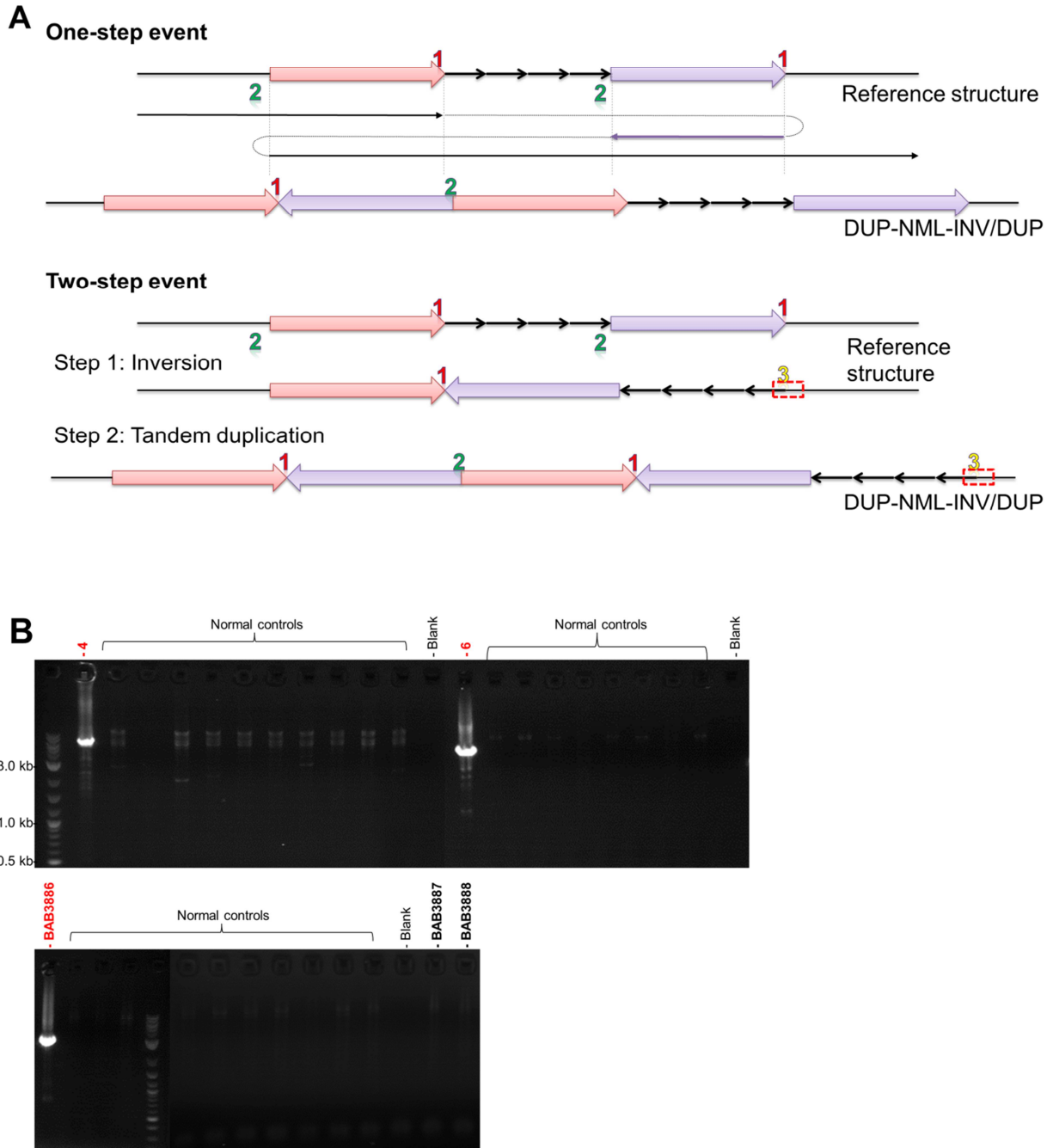


Figure S4. (A). Two possible rearrangements to generate the DUP-NML-INV/DUP pattern in samples 4F, 6M and BAB3886. (B). Long-range PCR detected “breakpoint junction 1” as shown in Figure S4A only existed in proband 4F, 6M and BAB3886, but not in any of the available parental samples (BAB3887 and BAB3888 as mother and father of BAB3886, respectively) or normal individuals (“Normal controls”).

A

Junction 1

```
chr17:4334048 AGTTCAAGACCAGCCTGGCGAAGACAGTGAAACCCCTGTCTCTACTAAAACACAAAAAATTA 4333986
|||||
23_1 AGTTCAAGACACATTTGCCCTGTGTTTTGGATCAGTGTGTCGCGATGATCACAATGCCTTTTTT
|||||
chr17:99539 GCAGCGATGGAGCTTGGTTTAAACCTAGTGCTTTTCAAGAGTATGTGATTAGAAACCTTTTTT 99477
```

Junction 2

```
chr17:4359046 CCCAGGGTCCATTCTCCCCGAATGCCAGATGACATGCATCTGAGTGTCTTAAAGAC 4359101
|||||
23_2 CCCAGGGTCCATTCTGACCAGCAGCCTCCCAAAGCGCTAGGATTACAGGCGTGAGC
|||||
chr17:5986795 GTGACCTTTATAACTGACCAGCAGCCTCCCAAAGCGCTAGGATTACAGGCGTGAGC 5986850
```

Junction 3

```
chr17:6000851 TCTCAGTCGCGACACAAAAGTGCTTTCTCATTCTTTTTTACCATTGCACGGAGGTCCTAT 6000910
|||||
23_3 TCTCAGTCGCGACACAAAAGCAACCTGTTTGTGTCCTGGAACCACACTTCCCAACAAG
|||||
chr17:1966846 AAAGAAAGTTCTGAGGCTGGGGTGGGGCCAGCAGTCCCTGGAACCACACTTCCCAACAAG 1966905
```

Junction 4

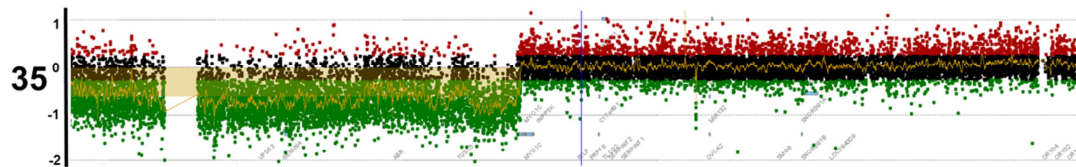
```
chr17:6451754 TTACCACAAGGGATGACTCTAGAGTTGCTCGGCTGGGACTAGCCTCACGGGGGCGAGAA 6451813
|||||
23_4 TTACCACAAGGGATGACTCTAGAGTTGCTCGGGCCACCGAGAGGCTCAGGCTCCCCAA
|||||
chr17:7697573 AAATGTTCTGATGGCTGCCATGGGCCCCCTGGGGTGGACGGACTGTCTCTCCCAA 7697632
CGGGCCACCGAGAGGCTCAGG : chr17:8958078-8958057
```

Junction 5

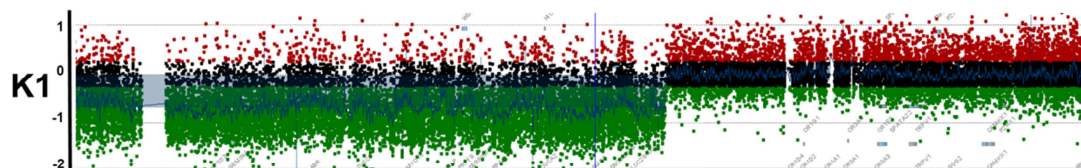
```
chr17:9856287 *rs142763445
TCGACCCAGCAATCCCATTACTGGGTATATACCCAAAGGAATATAAATCTTCCACATA 9856346
|||||
23_5 TCGACCCAGCAAGCCATTACTGGGTATATACCCAAAGGAATATAAATA_TAAAAGAAA
|||||
chr17:9845519 CAAGACTGCCAACTACACTCCAGCCTGGATGACAGAGCGAGACTCTGTCTAAAAGAAA 9845578
```

Junction 6

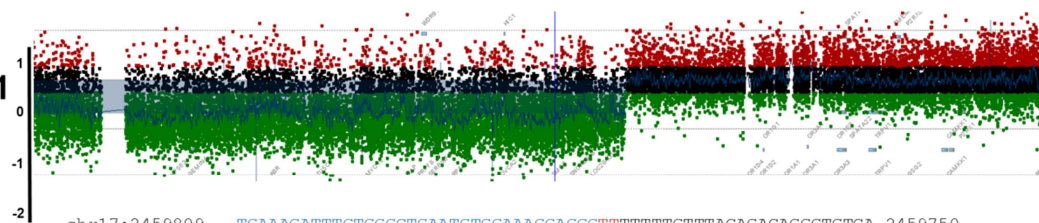
```
chr17:10091013 TGGCTGTTTCCAAAAAATCAAATCCACCCTCAAAGACAAAGATTGCTGTTACT 10091070
|||||
23_6:1 TGGCTGTTTCCAAA_CAGACTGAGGCTATGTTTTAAAGAGGAATGACATGGCACTGGAA 58
|||||
chr17:1512390 TCGTTTTTCATAGGATCAGAGTGGCTATGTTTTAAAGAGGAATGACATGGCACTGGAA 1512447
GAGACTGAGGCTATGTTTTAAAGAGGAATGACATGGCACTGGAA
23_6:59 GGGACATGGAGGAAAAGACACTCTGTACACGTACTCGTGTACGTGCTGGTGGGC 99
|||||
chr17:1512448 GGGACATGGAGGAAAAGACACTC-----GTGTACGTGCTGGTGGGC 1512488
```


A

chr17:1964448 TCTCGCCTGGGGACGCAGCCACTTTCCTCCAGTGGAGACAGGGCAGGGGTTCTGAGTTTCCGTCA 1964385
 35 TCTCGCCTGGGGACGCAGCCACTTTCCTCCAGTGGAGACAGGGTTAGGGTTAGGGTTAGGGTTAG
 TEL TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAG

B

chr17:2455955 TTTTTTTTTTTGAGATGGAGTTTCGCTCTTGTTCACAGGC TGGAGTGCAATGGCATAATCT 2455893
 K1 TTTTTTTTTTTGAGATGGAGTTTCGCTCTTGTTCACAGGC TAGGGTTAGGGTTAGGGTTA
 TEL TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTA

C**BAB3291**

chr17:2459809 TGAAAGATTTGTGGGCTGAATGTGGAAGGAGGGTTTTTTTTGTTTACAGACAGGGTGTC 2459750
 BAB3291 TGAAAGATTTGTGGGCTGAATGTGGAAGGAGGGTTAGGGTTAGGGTTAGGGTTAGGGTT
 TEL AGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTT

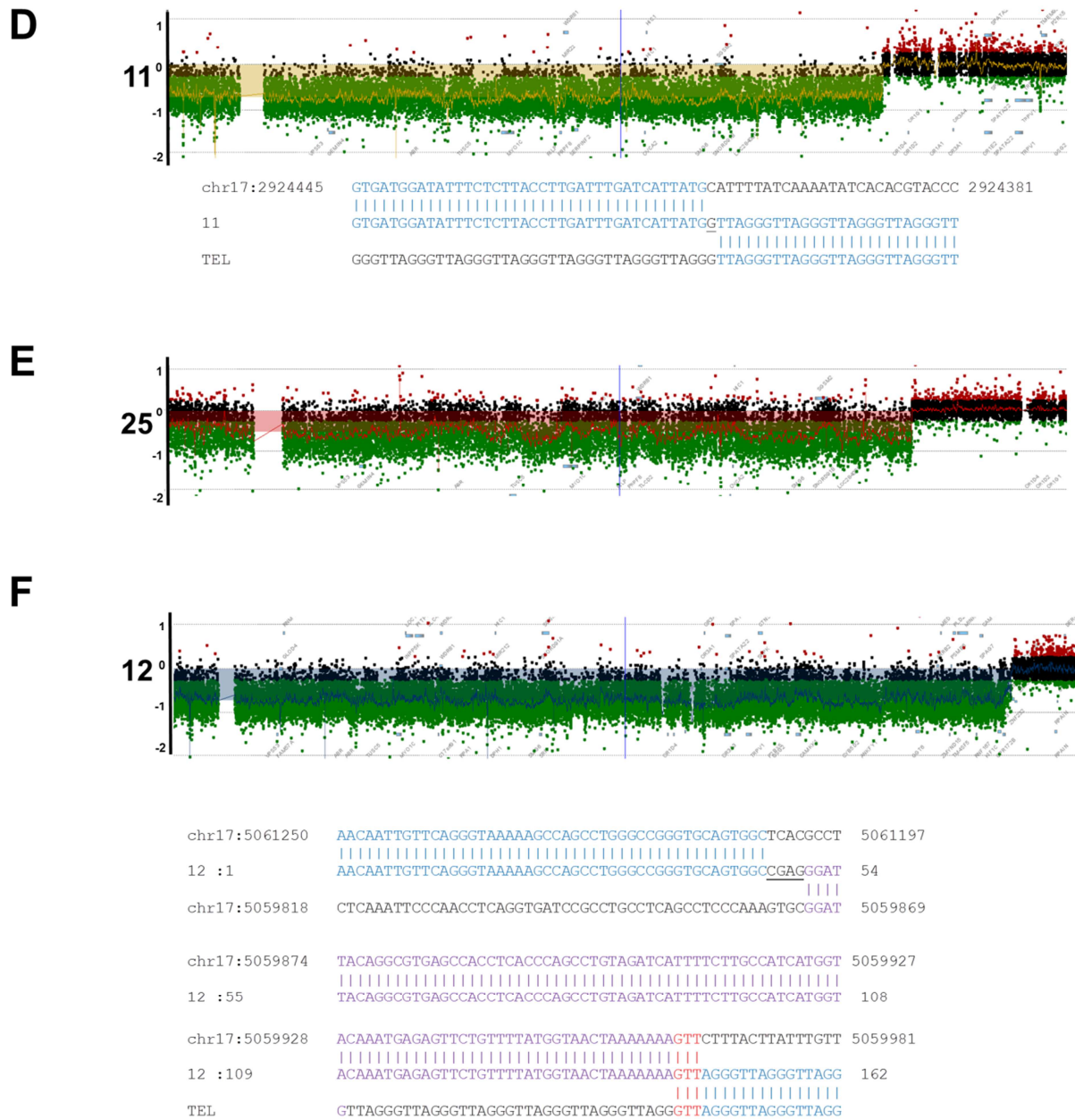


Figure S7. Array plots and breakpoint sequences of additional cases with terminal deletion (refer to Figure 6). Breakpoint junction sequence is aligned to the proximal and distal genomic references and color-matched. Microhomology at the breakpoint is indicated in red.