chromosome 1

q43

breakpoint1
1:243255040

breakpoint2
1:244053788

chromosome 1

q44

Coverage 170

0

19 | 18 17 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1

1 | 2

CEP170
ENST00000366544.5

ZBTB18
ENST00000358704.4

1 | 2

GCGACGC...TCCCTCTCTCCACGGTAAGGGGTTATGAAGACAGTATGGAGTTTCCAGACC

3 kbp
introns not to scale

No protein domains retained in fusion.

CEP170
ZBTB18

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 1

translocation   deletion
duplication   inversion

chromosome 2

q21.3

breakpoint1
2:136118046

Coverage
9497
0

CXCR4
ENST00000241393.3

chromosome 2

q37.1

breakpoint2
2:231711348

PTMA
ENST00000409321.5

AGAACCAGCGGTTACCATGGAGGGGATCAGTGACTTAAAGGAGAAGAAGGAAGTTGTGGAA
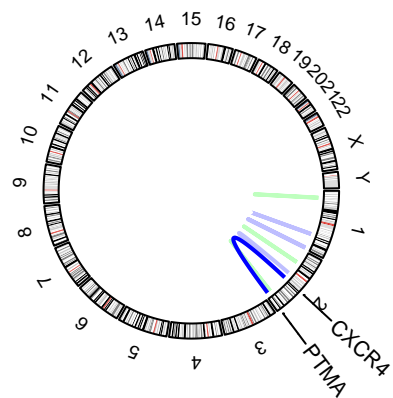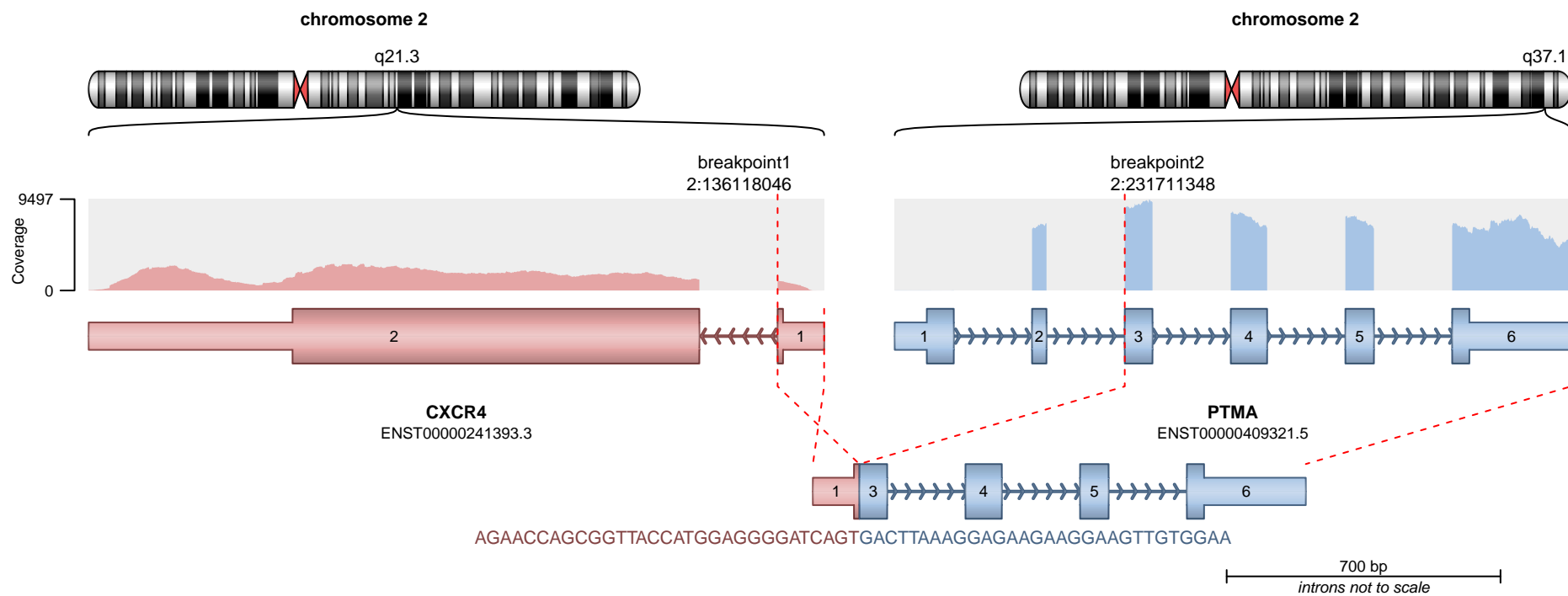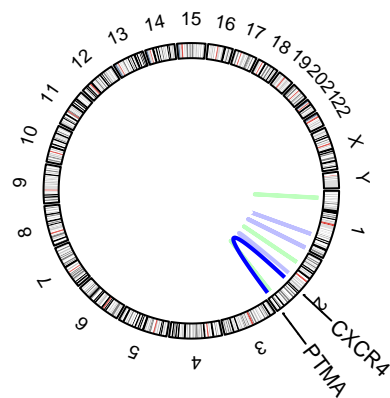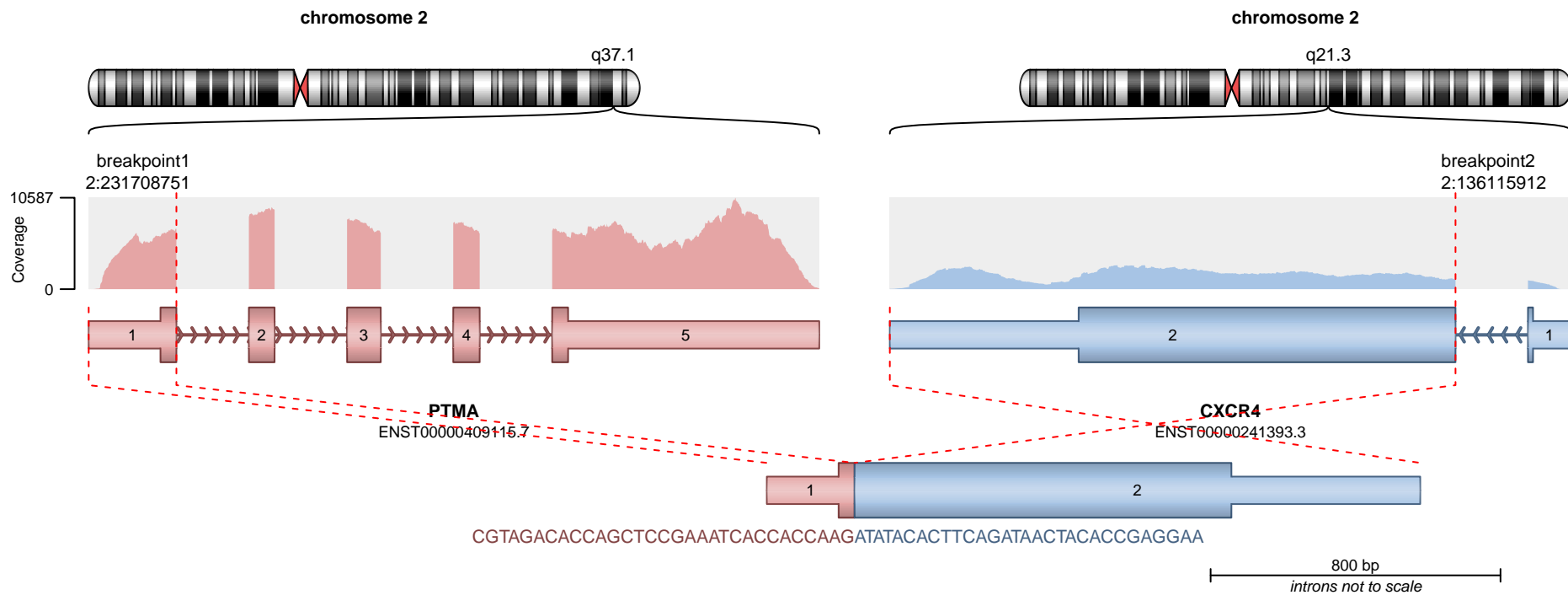
700 bp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 7
Discordant mates = 0

translocation   deletion
duplication   inversion

chromosome 2

q37.1

breakpoint1
2:231708751

Coverage

10587

0

PTMA
ENST00000409115.7

chromosome 2

q21.3

breakpoint2
2:136115912

CXCR4
ENST00000241393.3

CGTAGACCAGCTCCGAAATCACCACCAAGATATACACTTCAGATAACTACACCGAGGAA
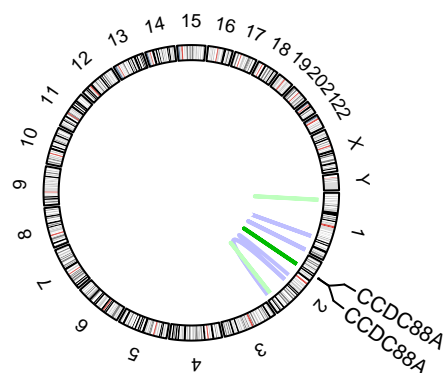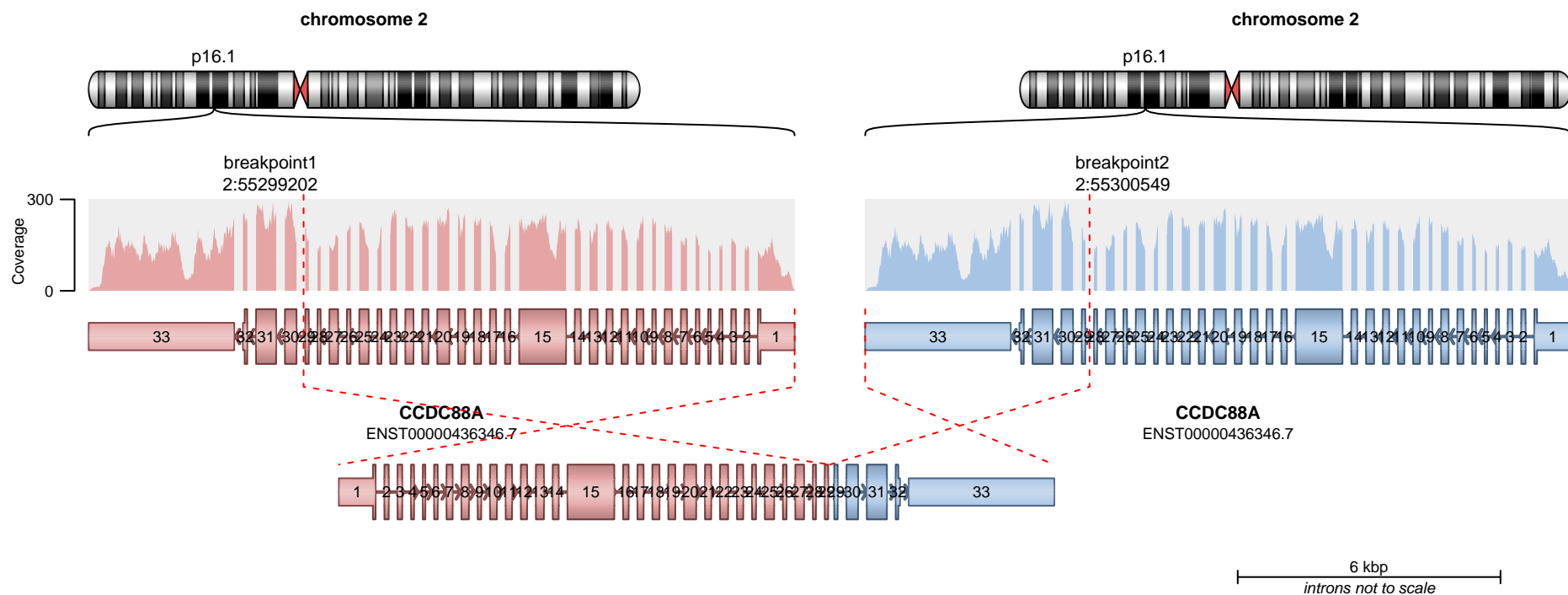
800 bp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 0
Discordant mates = 0

translocation   deletion
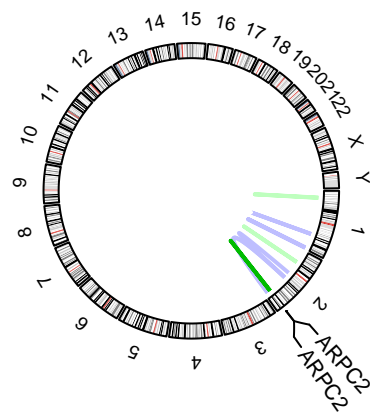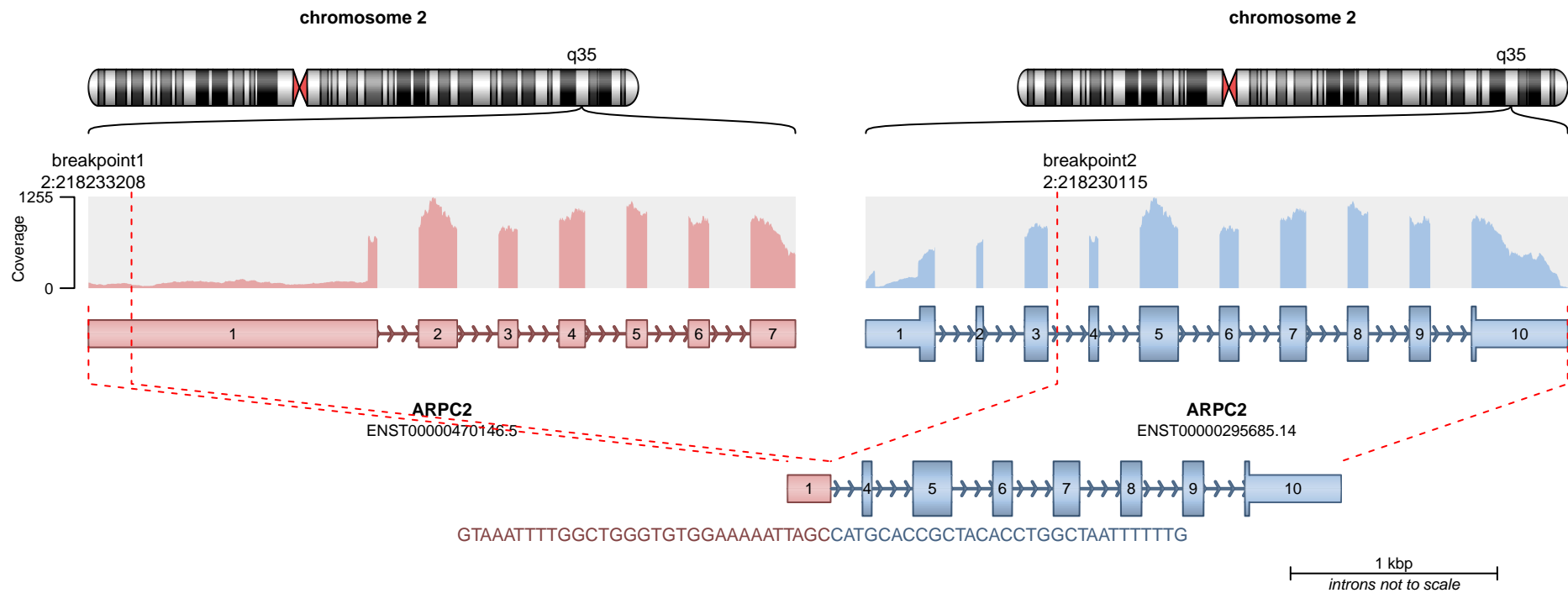duplication   inversion

chromosome 2

chromosome 2

p16.1

p16.1

breakpoint1
2:55299202

breakpoint2
2:55300549

Coverage

300

0

33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

CCDC88A
ENST00000436346.7

CCDC88A
ENST00000436346.7

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32   33

6 kbp
introns not to scale

11 12 13 14 15 16 17 18 19 20 21 22
X
Y
1
2
CCDC88A
CCDC88A
3
4
5
6
7
8
9
10

SUPPORTING READ COUNT

Failed to determine retained protein domains due to lack of strand information.

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 2
Discordant mates = 2

translocation   deletion
duplication   inversion

chromosome 2

q35

breakpoint1
2:218233208

Coverage

1255

0

1 2 3 4 5 6 7

ARPC2
ENST00000470146.5

chromosome 2

q35

breakpoint2
2:218230115

1 2 3 4 5 6 7 8 9 10

ARPC2
ENST00000295685.14

1 4 5 6 7 8 9 10

GTAAATTTTGGCTGGGTGTGGAAAAATTAGCCATGCACCGCTACACCTGGCTAATTTTTTG
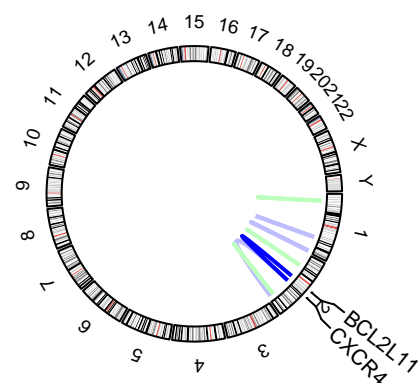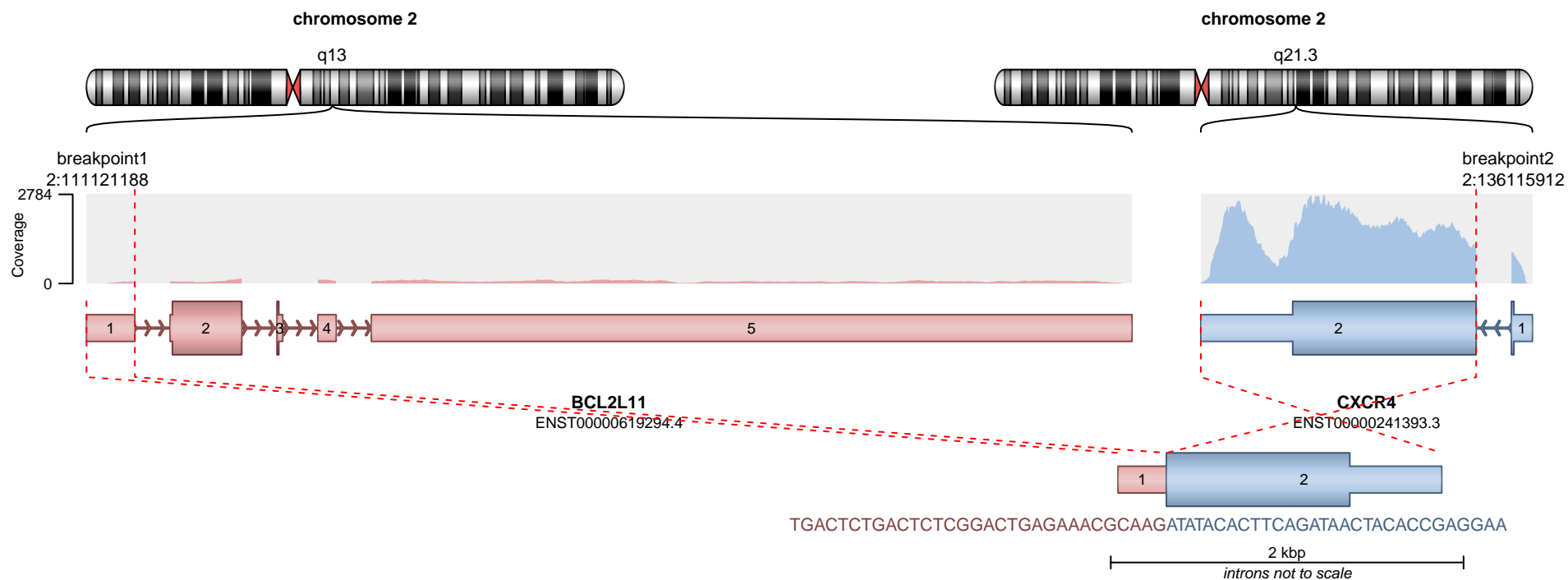
1 kbp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 3
Discordant mates = 2
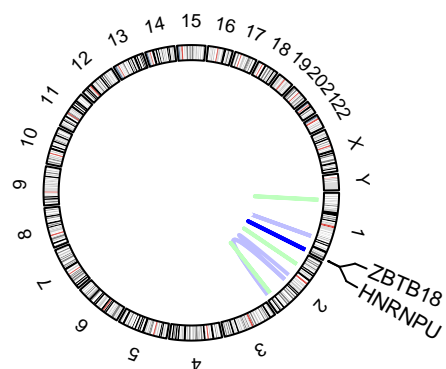
translocation   deletion
duplication   inversion

ARPC2
ARPC2

chromosome 2

q13

breakpoint1
2:111121188

chromosome 2

q21.3

breakpoint2
2:136115912

2784

Coverage

0

1   2   3   4   5

2   1

BCL2L11
ENST00000619294.4

CXCR4
ENST00000241393.3

1   2

TGACTCTGACTCTCGGACTGAGAAACGCAAGATATACACTTCAGATAACTACACCGAGGAA

2 kbp
introns not to scale

No protein domains retained in fusion.

12 13 14 15 16 17 18 19 20 21 22 X

11

10

Y

9

1

8

7

2

6

3

5   4

BCL2L11

CXCR4

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 2
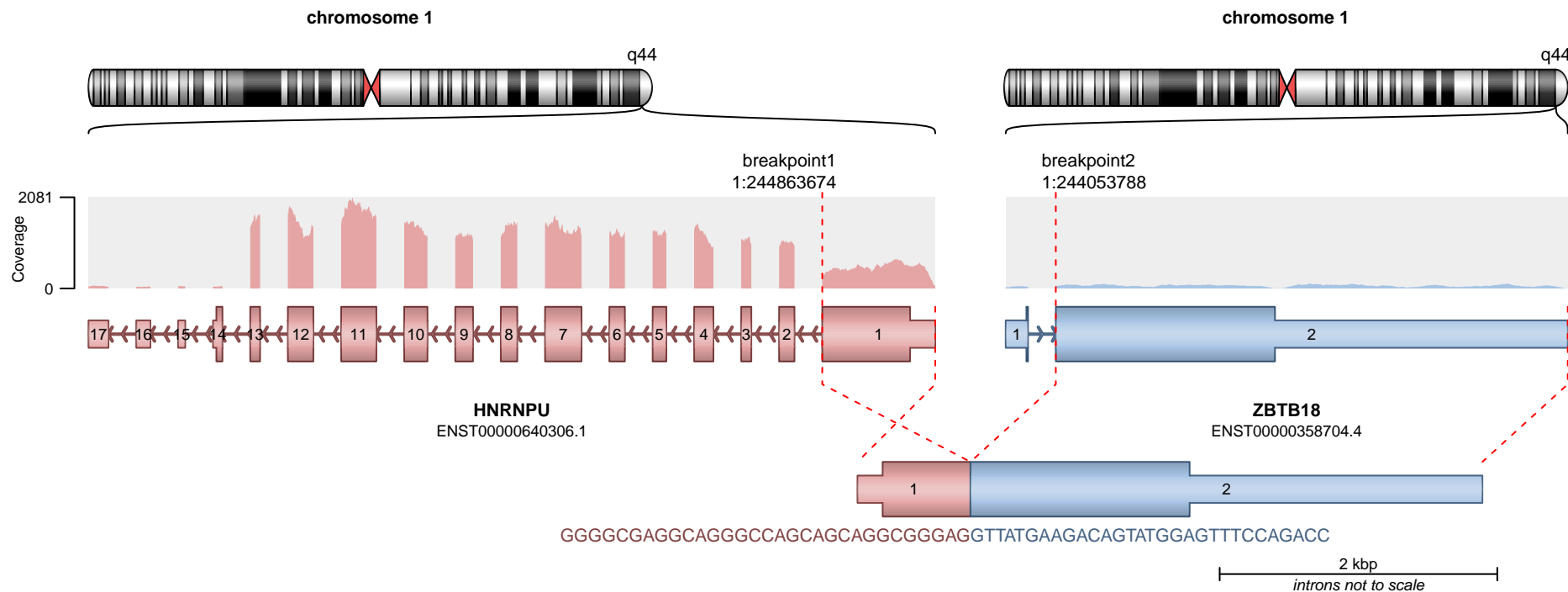
—— translocation   —— deletion
—— duplication   —— inversion

chromosome 1

q44

breakpoint1
1:244863674

breakpoint2
1:244053788

2081

Coverage

0

17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

1 2

HNRNPU
ENST00000640306.1

ZBTB18
ENST00000358704.4

1 2

GGGGCGAGGCAGGGCCAGCAGCAGGCGGGAGGTTATGAAGACAGTATGGAGTTTCCAGACC

2 kbp

introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
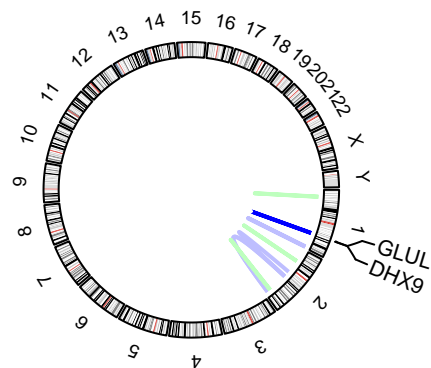Split reads at breakpoint2 = 0
Discordant mates = 1

ZBTB18
HNRNPU

translocation   deletion
duplication   inversion

chromosome 1

q25.3

chromosome 1

q25.3

breakpoint1
1:182839456

1902

Coverage

0

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28

breakpoint2
1:182388750

8 7 6 5 4 3 2 1

DHX9
ENST00000367549.4

GLUL
ENST00000642379.1

1 3 4 5 6 7 8

CTAAGAGCTGGGCACCAGGAAGCGAAGGCTGAACACCTTCCACCATGACCACCTCAGCAAG

3 kbp

introns not to scale

11 12 13 14 15 16 17 18 19 20 21 22 X Y
10 9 8 7 6 5 4 3 2 1

GLUL
DHX9

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
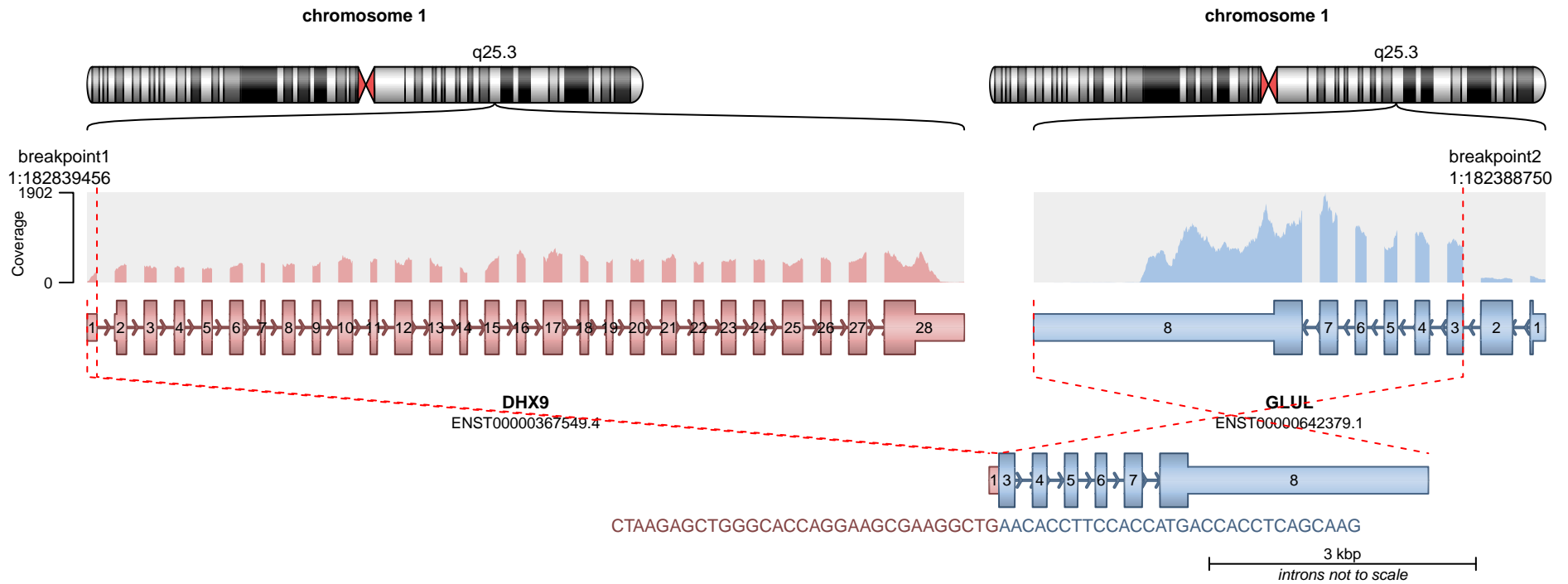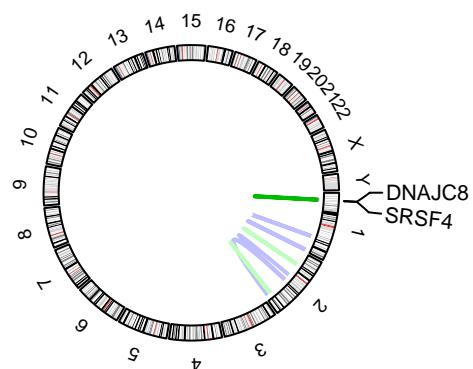Split reads at breakpoint2 = 1
Discordant mates = 0

translocation   deletion
duplication   inversion

chromosome 1

p35.3

chromosome 1

p35.3

Coverage

686

0

breakpoint1
1:28228922

breakpoint2
1:29154910

9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1

6 | 5 | 4 | 3 | 2 | 1

DNAJC8
ENST00000263697.6

SRSF4
ENST00000373795.7

1 | 2 | 4 | 5 | 6

TTCCTCTTACTTCAATTTGAACCCATTTGAGGATTATATGCGTCAGGCAGGAGAAGTGACT

1 kbp
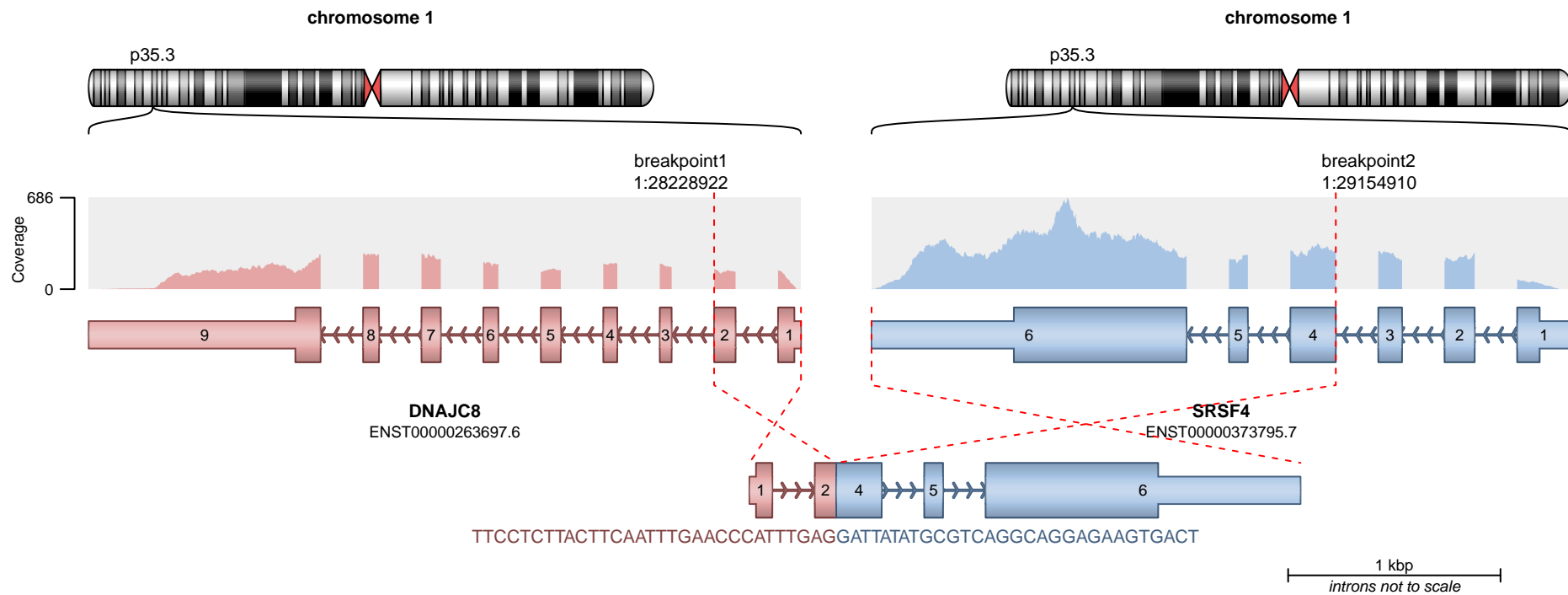*introns not to scale*

DNAJC8
SRSF4

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 1
Discordant mates = 0
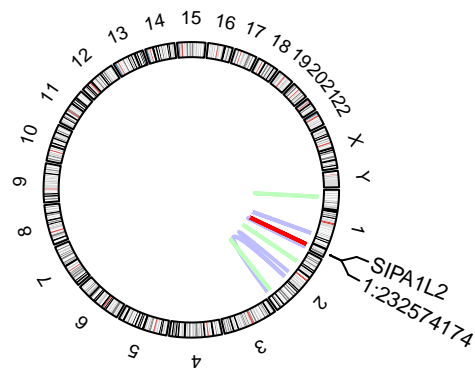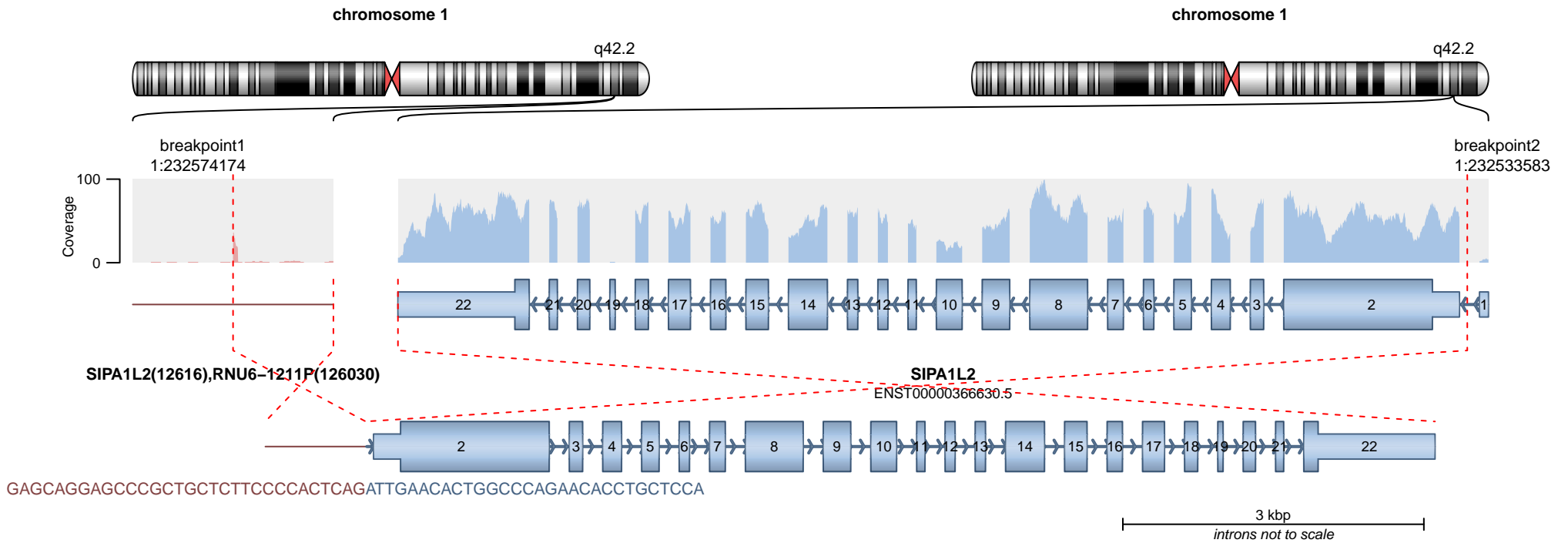
translocation   deletion
duplication   inversion

chromosome 1

q32.1

breakpoint1
1:204621122

breakpoint2
1:204597112

447

Coverage

0

LRRN2
ENST00000367175.1

1

RNA5SP74(34591),AL512306.3(5923)

1

CTGCCAGGCTGTTGGGAAAGGAGAAACACTCCTCAGTCGATCTCTCCTTCCAAGTAAAGCA

1 kbp
introns not to scale

1:204597112
LRRN2

No coding regions retained in fusion transcript.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 9
Split reads at breakpoint2 = 7
Discordant mates = 2

translocation   deletion
duplication   inversion

chromosome 1   chromosome 1

q42.2   q42.2

breakpoint1
1:232574174

breakpoint2
1:232533583

Coverage

100

0

22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

SIPA1L2(12616),RNU6−1211P(126030)

SIPA1L2
ENST00000366630.5

2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

GAGCAGGAGCCCGCTGCTCTTCCCCACTCAGATTGAACACTGGCCCAGAACACCTGCTCCA

3 kbp
introns not to scale

11 12 13 14 15 16 17 18 19 20 21 22 X
10   Y
9
8   1
7
6   2
5 4 3   SIPA1L2
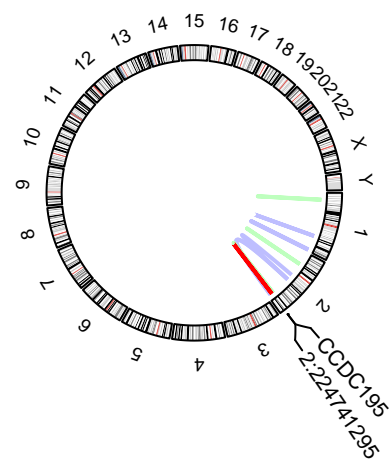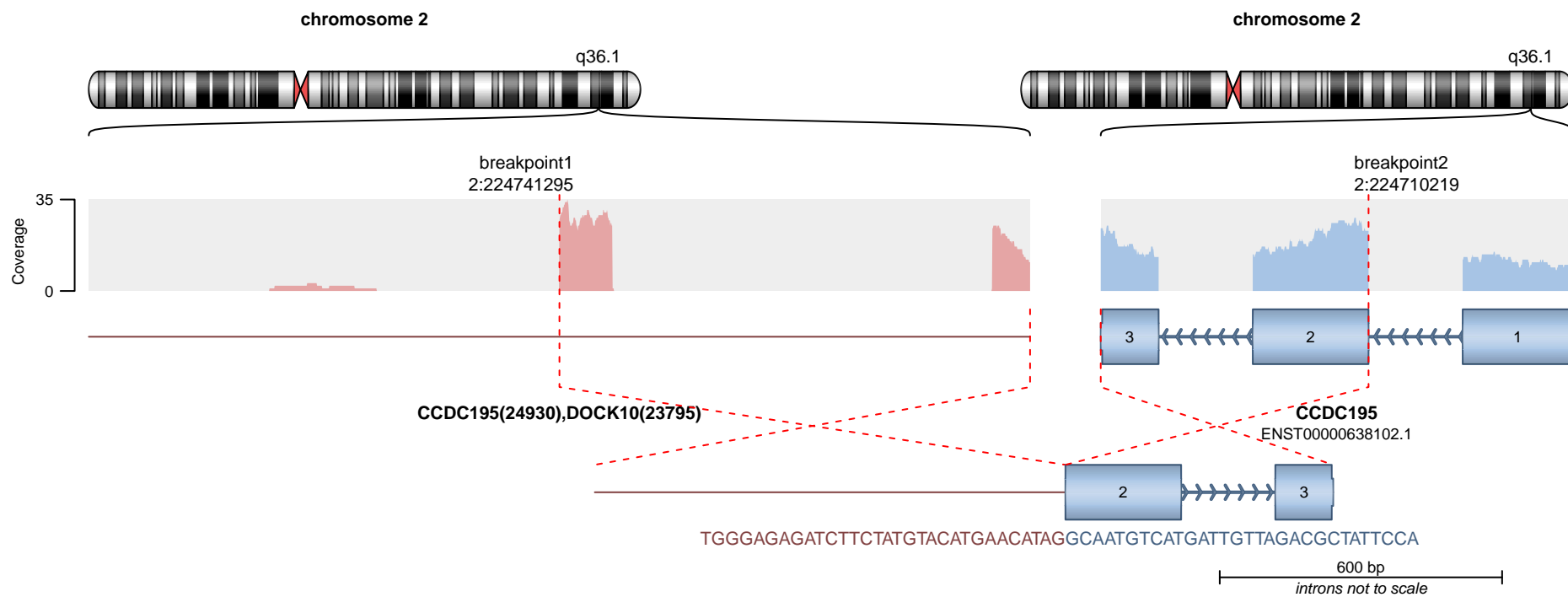   1:232574174

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 4
Discordant mates = 3

—— translocation   —— deletion
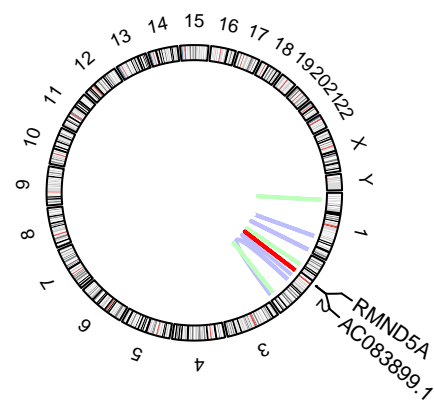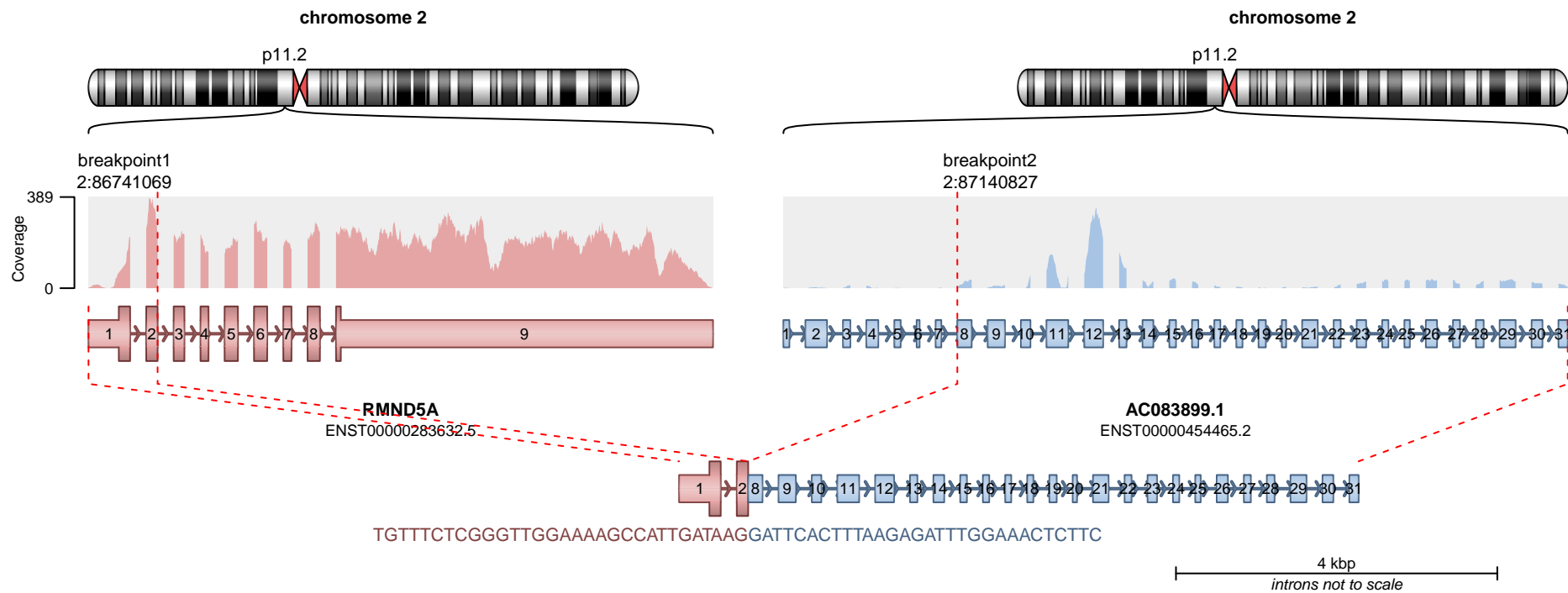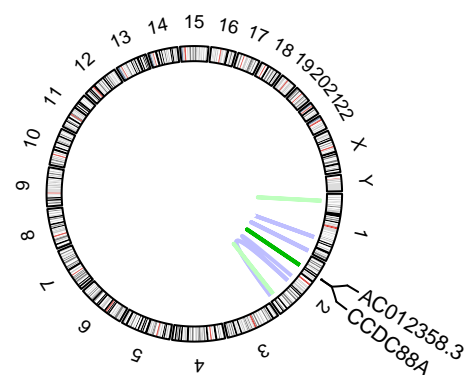—— duplication   —— inversion

chromosome 2

q36.1

breakpoint1
2:224741295

breakpoint2
2:224710219

Coverage 35

0

CCDC195(24930),DOCK10(23795)

CCDC195
ENST00000638102.1

3   2   1

2   3

TGGGAGAGATCTTCTATGTACATGAACATAG GCAATGTCATGATTGTTAGACGCTATTCCA

600 bp
introns not to scale

No protein domains retained in fusion.

CCDC195
2:224741295

SUPPORTING READ COUNT

Split reads at breakpoint1 = 4
Split reads at breakpoint2 = 3
Discordant mates = 2

translocation   deletion
duplication   inversion

chromosome 2

p11.2

chromosome 2

p11.2

breakpoint1
2:86741069

breakpoint2
2:87140827

389

Coverage

0

1 2 3 4 5 6 7 8 9

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31

RMND5A
ENST00000283632.5

AC083899.1
ENST00000454465.2

1 2 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31

TGTTTCTCGGGTTGGAAAAGCCATTGATAAGGATTCACTTTAAGAGATTTGGAAACTCTTC

4 kbp
introns not to scale

11 12 13 14 15 16 17 18 19 20 21 22 X Y 1

10

9

8

7

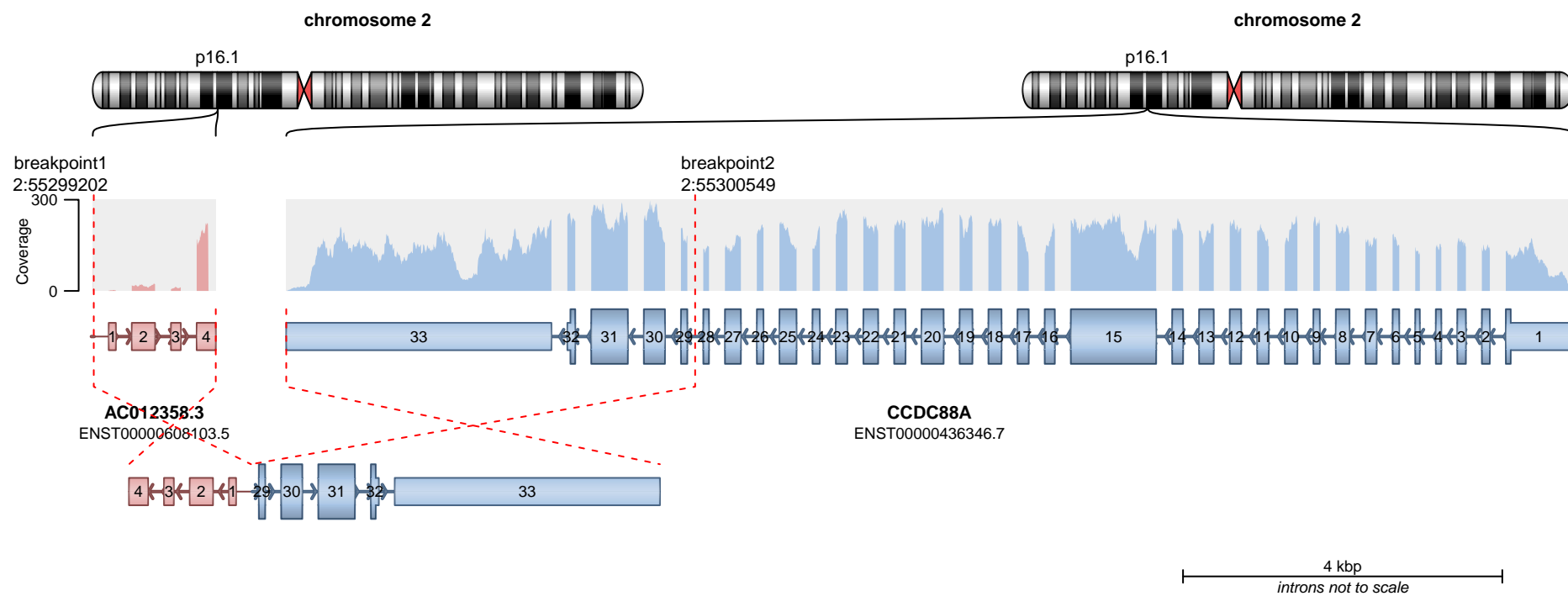6 5 4 3 2

RMND5A
AC083899.1

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 1
Discordant mates = 5

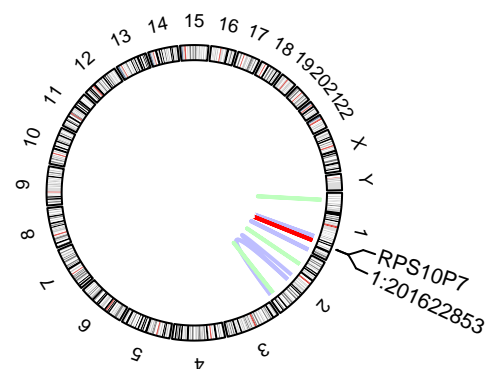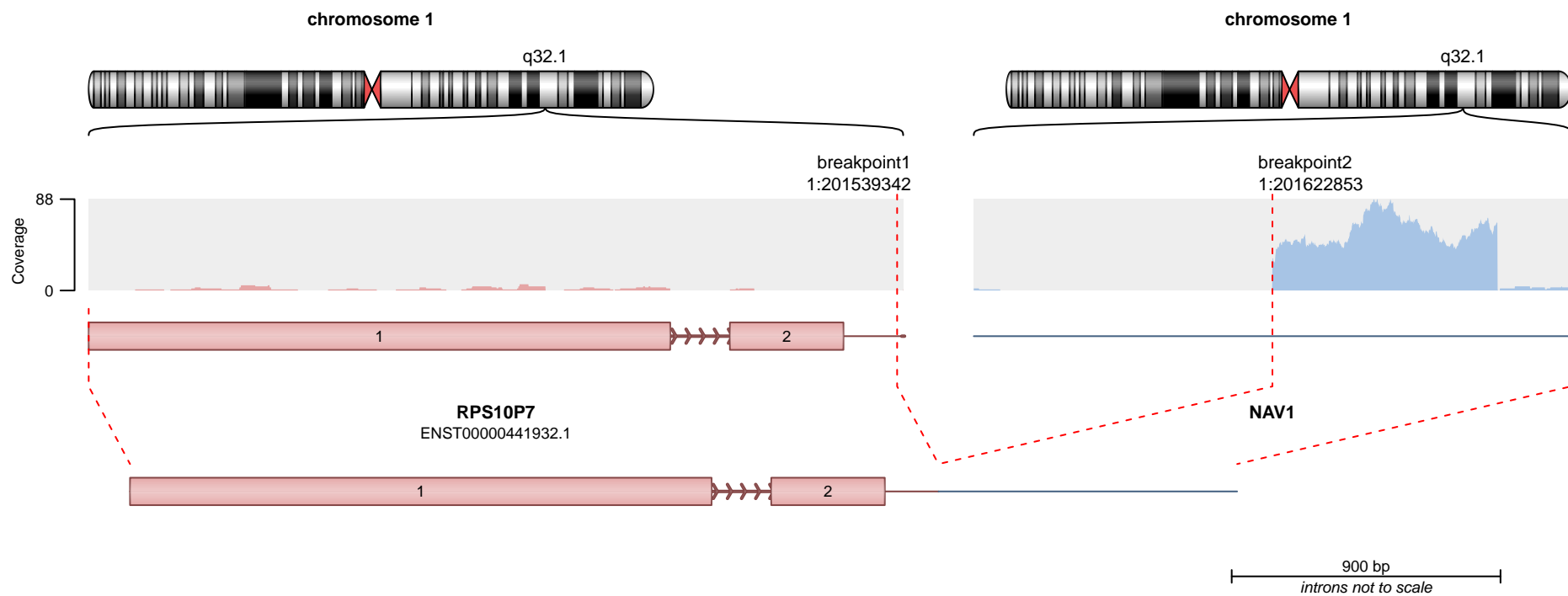translocation   deletion
duplication   inversion

chromosome 2   **chromosome 2**

p16.1   p16.1

breakpoint1
2:55299202

Coverage 300

0

AC012358.3
ENST00000608103.5

breakpoint2
2:55300549

CCDC88A
ENST00000436346.7

4 kbp
introns not to scale

SUPPORTING READ COUNT

Failed to determine retained protein domains due to lack of strand information.

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 2
Discordant mates = 2

AC012358.3
CCDC88A

translocation   deletion
duplication   inversion

chromosome 1

q32.1

breakpoint1
1:201539342

chromosome 1

q32.1

breakpoint2
1:201622853

88

Coverage

0

1

2

RPS10P7
ENST00000441932.1

NAV1

1

2

900 bp
introns not to scale
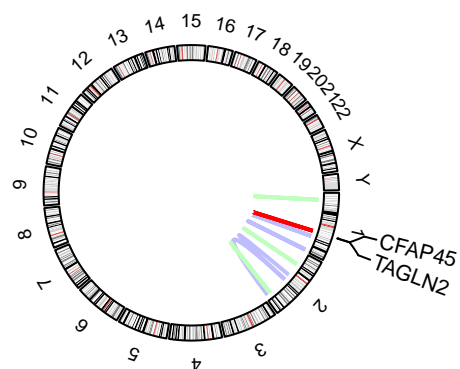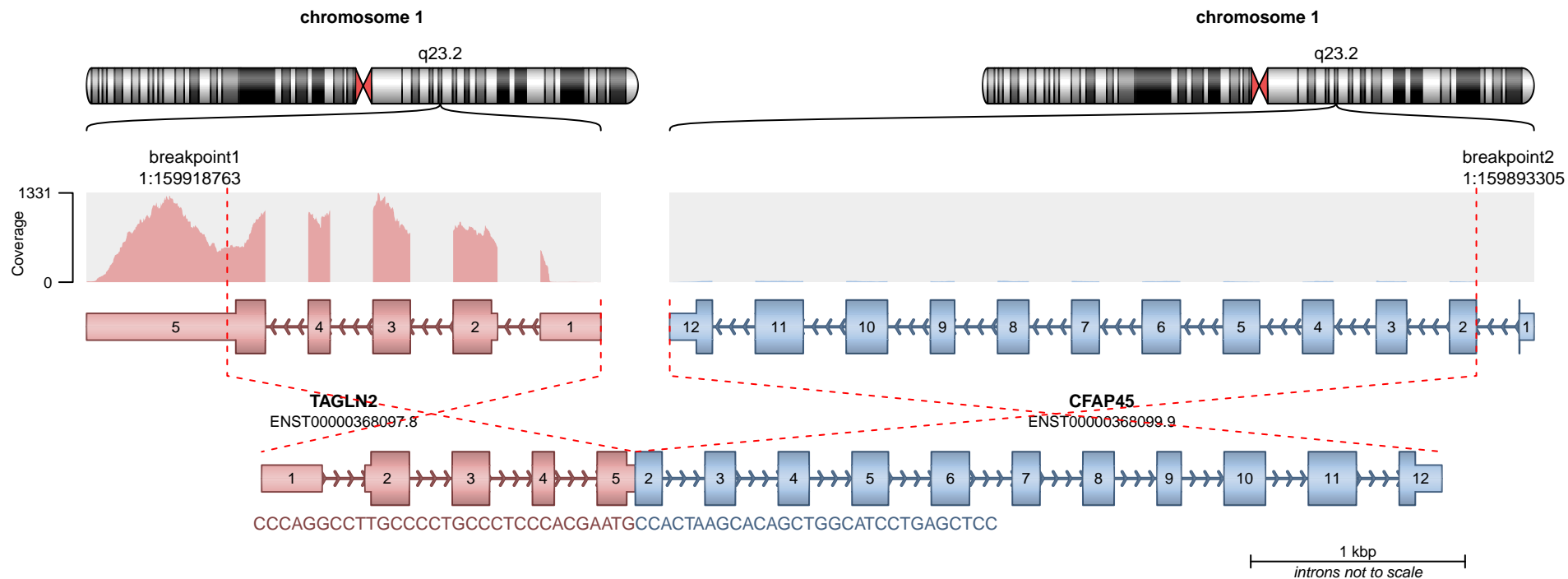
RPS10P7
1:201622853

Genes are not protein−coding.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 5
Discordant mates = 0

— translocation   — deletion
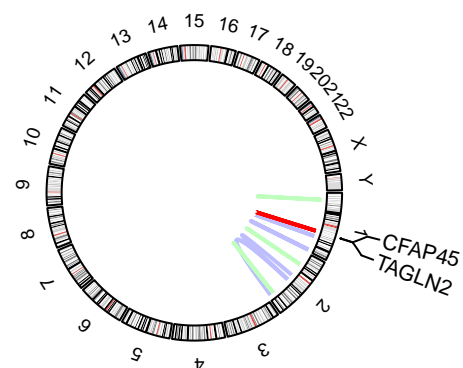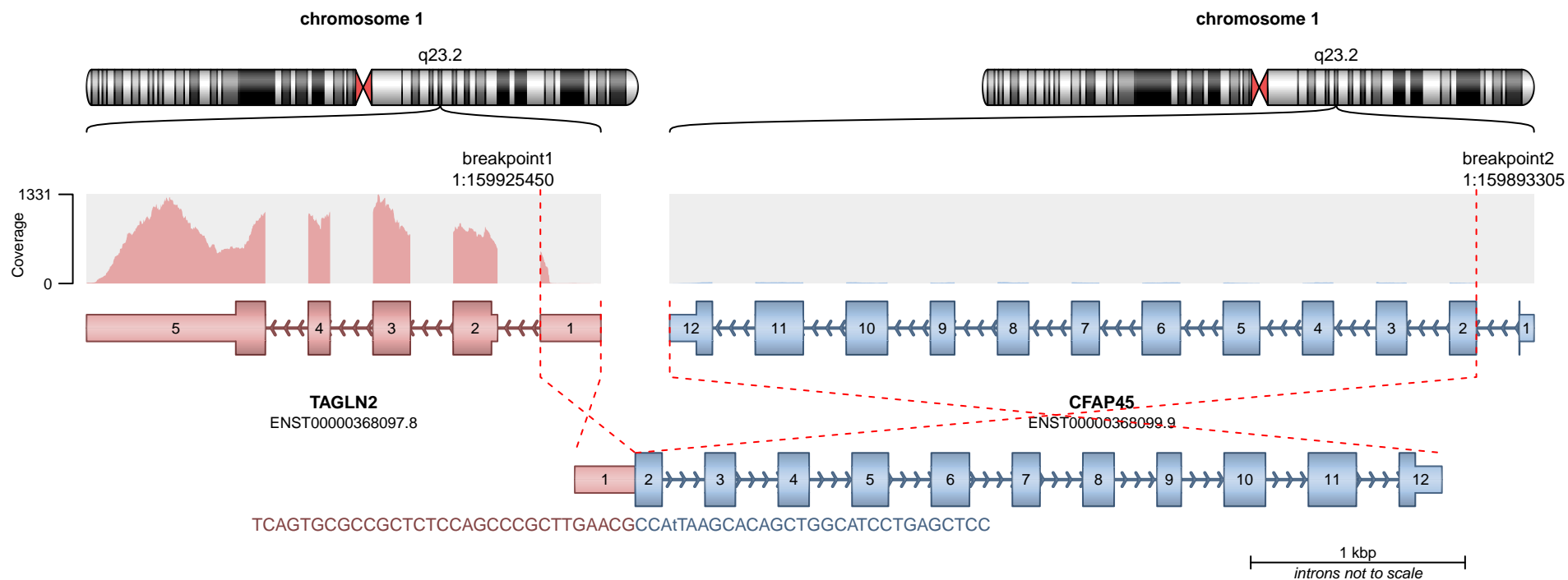— duplication   — inversion

chromosome 1

chromosome 1

q23.2

q23.2

breakpoint1
1:159918763

breakpoint2
1:159893305

1331

Coverage

0

| 5 | 4 | 3 | 2 | 1 |

| 12 | 11 | 10 | 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 |

TAGLN2
ENST00000368097.8

CFAP45
ENST00000368099.9

| 1 | 2 | 3 | 4 | 5 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 |

CCCAGGCCTTGCCCCTGCCCTCCCACGAATGCCACTAAGCACAGCTGGCATCCTGAGCTCC

1 kbp

introns not to scale

13 14 15 16 17 18 19 20 21 22
12
11
10
9
8
7
6
5
4
3
2
X
Y
CFAP45
TAGLN2

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 2
Discordant mates = 0
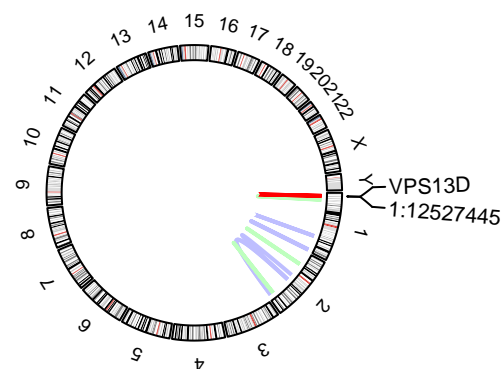
translocation   deletion
duplication   inversion

chromosome 1

q23.2

chromosome 1

q23.2

breakpoint1
1:159925450

breakpoint2
1:159893305

Coverage

1331

0

5 4 3 2 1

12 11 10 9 8 7 6 5 4 3 2 1

TAGLN2
ENST00000368097.8

CFAP45
ENST00000368099.9

1 2 3 4 5 6 7 8 9 10 11 12

TCAGTGCGCCGCTCTCCAGCCCGCTTGAACGCCAtTAAGCACAGCTGGCATCCTGAGCTCC
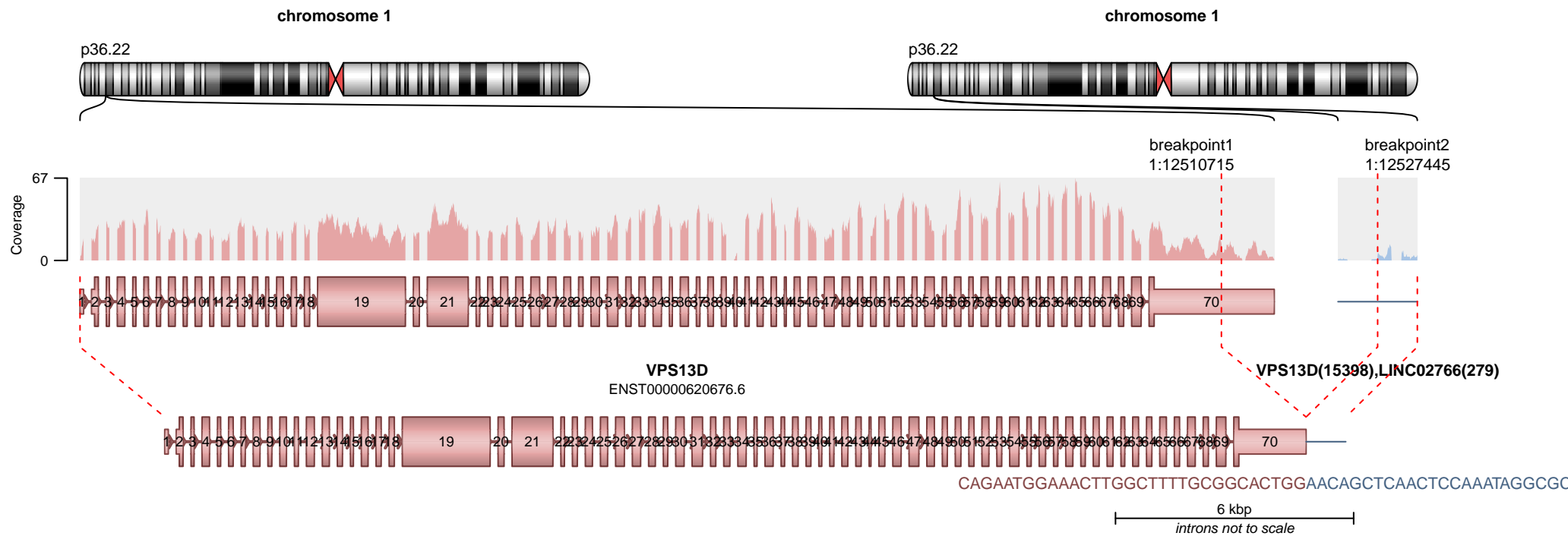
1 kbp

introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

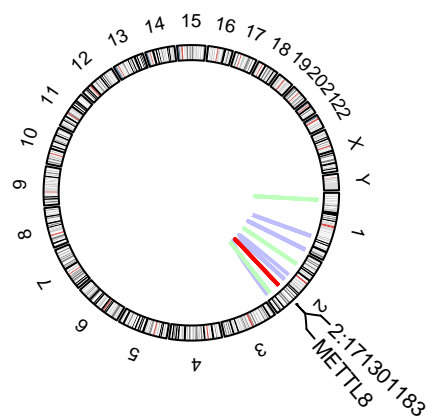translocation   deletion
duplication   inversion

CFAP45
TAGLN2

chromosome 1 **chromosome 1**

p36.22 p36.22

breakpoint1
1:12510715

breakpoint2
1:12527445

Coverage

67

0

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 | 19 | 20 | 21 | 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 | 70

VPS13D
ENST00000620676.6

VPS13D(15398),LINC02766(279)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 | 19 | 20 | 21 | 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 | 70

CAGAATGGAAACTTGGCTTTTGCGGCACTGGAACAGCTCAACTCCAAATAGGCGC

6 kbp

introns not to scale

VPS13D
1:12527445

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 3
Split reads at breakpoint2 = 1
Discordant mates = 0
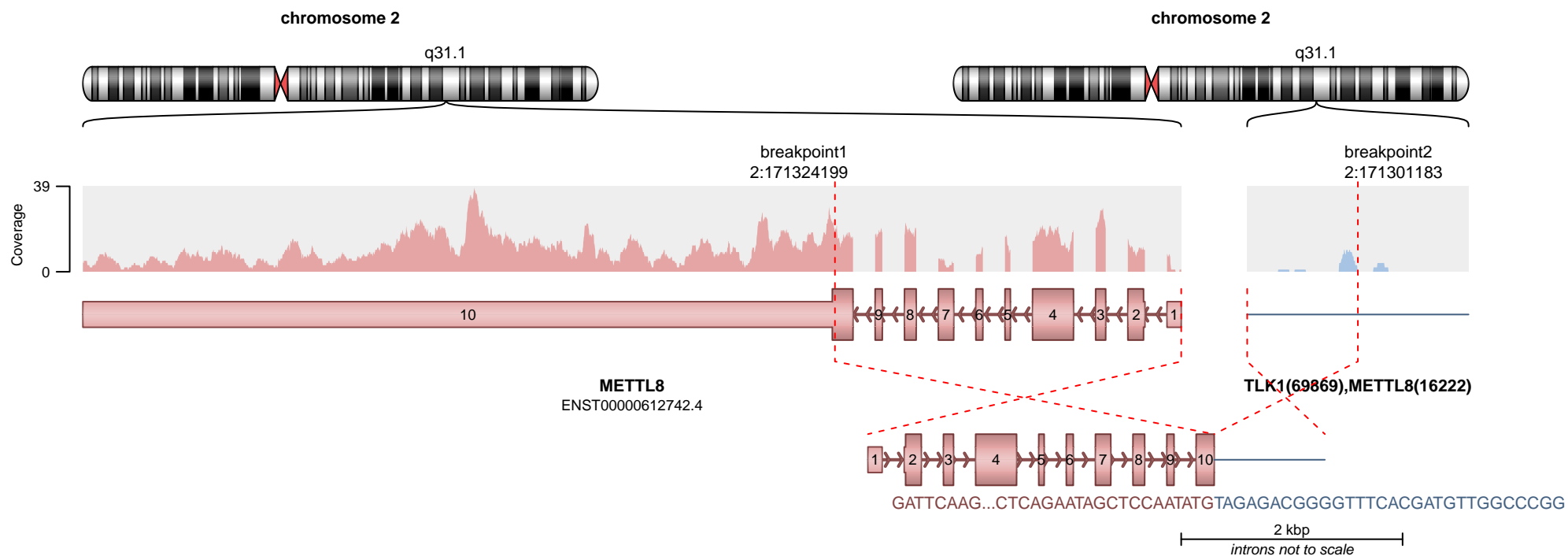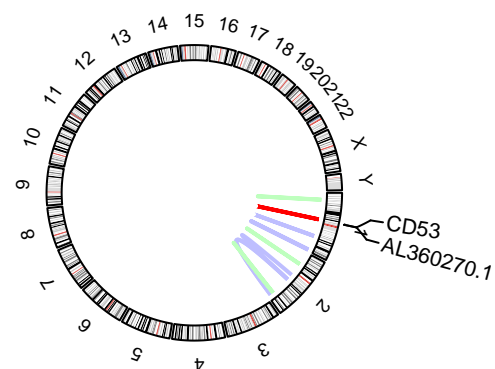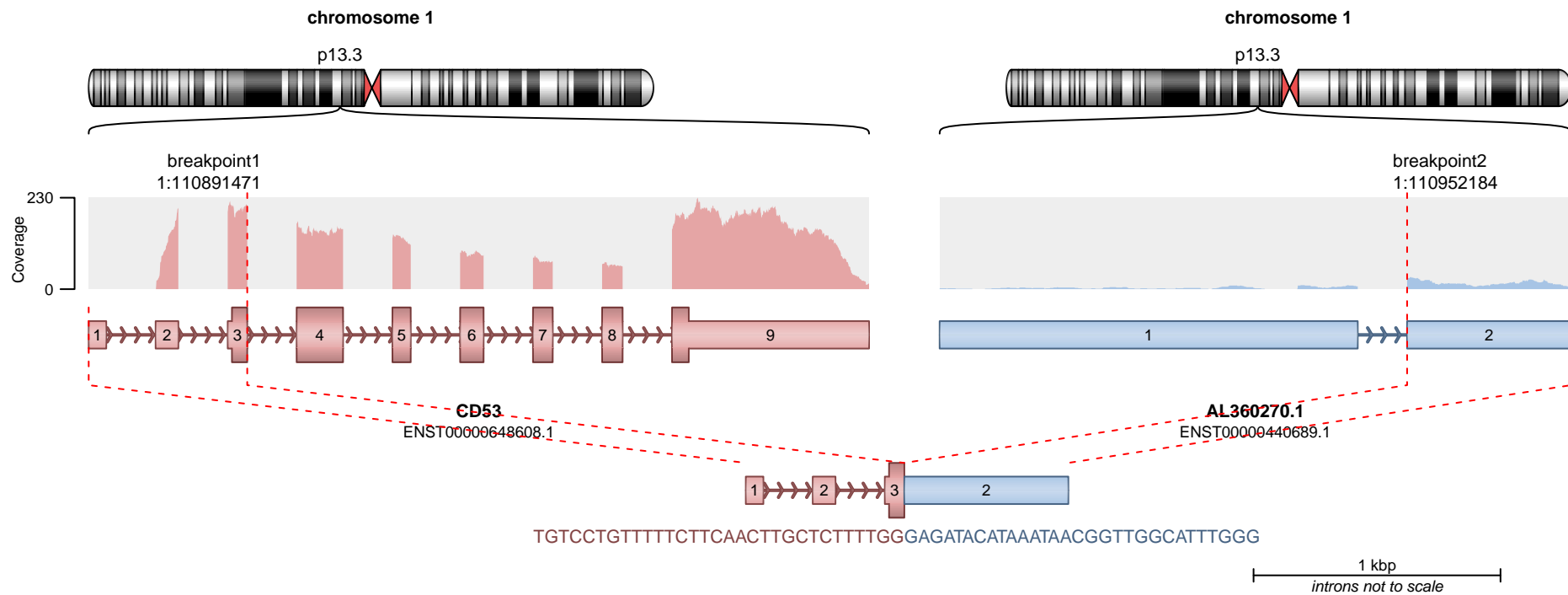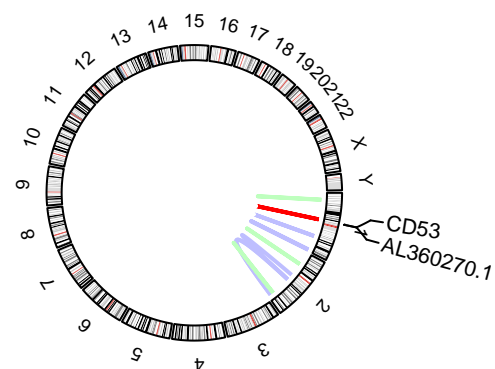
translocation deletion
duplication inversion

chromosome 2

q31.1

chromosome 2

q31.1

breakpoint1
2:171324199

breakpoint2
2:171301183

Coverage

39

0

10

9 8 7 6 5 4 3 2 1

METTL8
ENST00000612742.4

TLK1(69869),METTL8(16222)

1 2 3 4 5 6 7 8 9 10

GATTCAAG...CTCAGAATAGCTCCAATATGTAGAGACGGGGTTTCACGATGTTGGCCCGG

2 kbp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 2

2:171301183
METTL8

translocation   deletion
duplication   inversion

chromosome 1

p13.3

breakpoint1
1:110891471

CD53
ENST00000648608.1

Coverage
230
0

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |

chromosome 1

p13.3

breakpoint2
1:110952184

AL360270.1
ENST00000440689.1

| 1 | 2 |

| 1 | 2 | 3 | 2 |

TGTCCTGTTTTTCTTCAACTTGCTCTTTTGGGAGATACATAAATAACGGTTGGCATTTGGG

1 kbp
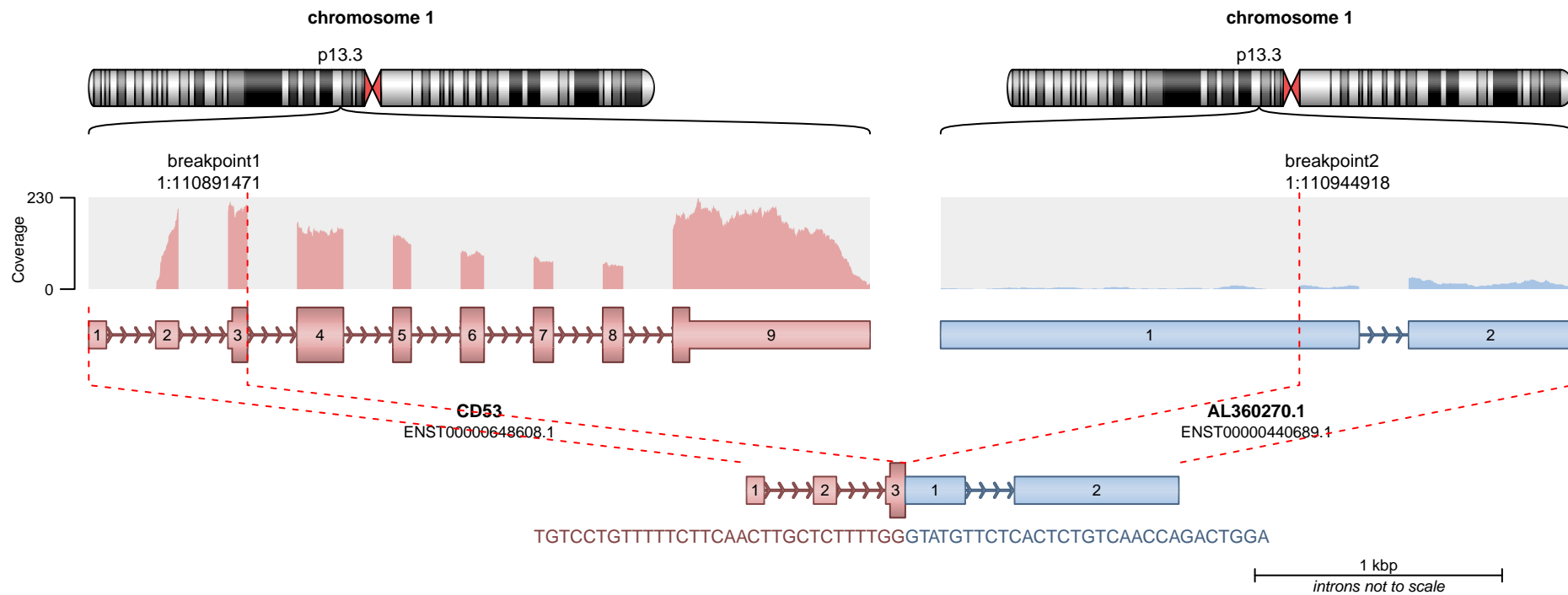*introns not to scale*

CD53
AL360270.1

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 0
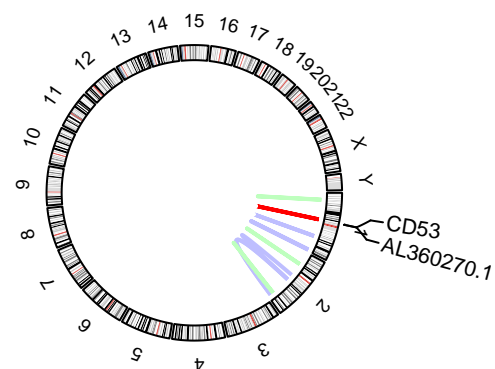
translocation
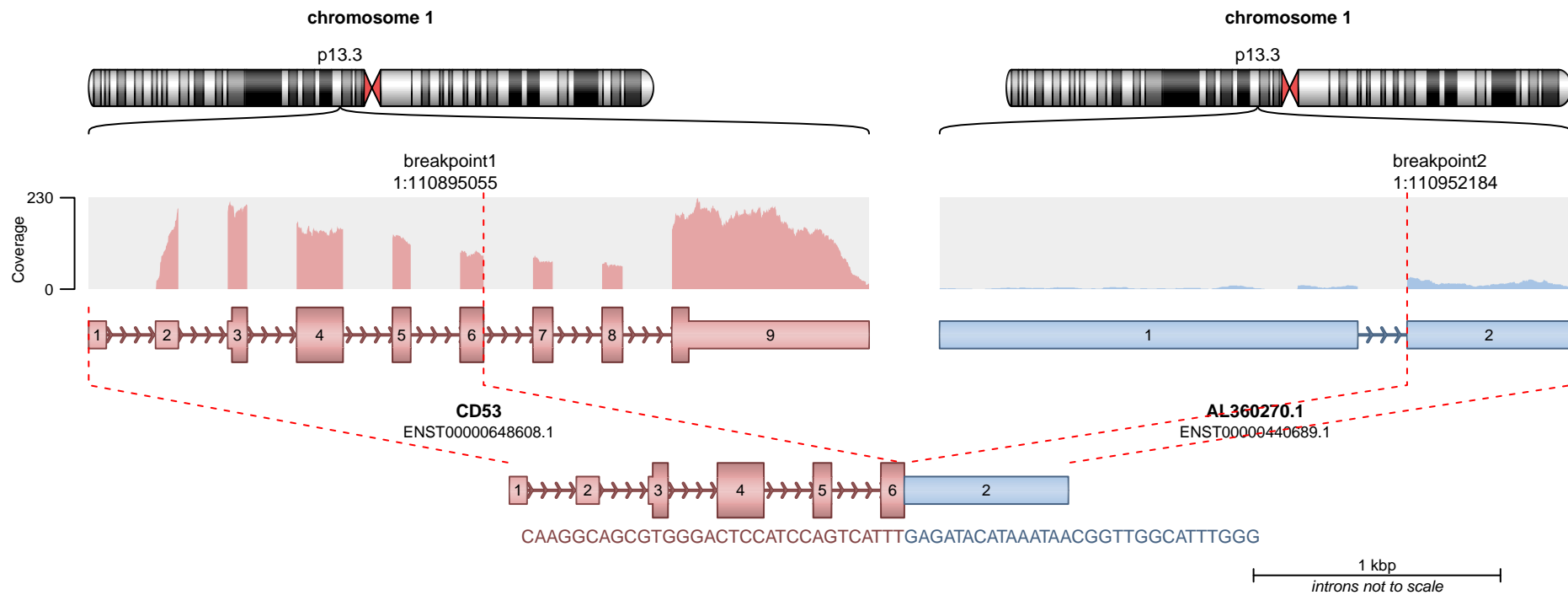deletion
duplication
inversion

chromosome 1

p13.3

breakpoint1
1:110891471

Coverage
230
0

chromosome 1

p13.3

breakpoint2
1:110944918

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |

| 1 | 2 |

CD53
ENST00000648608.1

AL360270.1
ENST00000440689.1

| 1 | 2 | 3 | 1 | 2 |

TGTCCTGTTTTTCTTCAACTTGCTCTTTTGGGTATGTTCTCACTCTGTCAACCAGACTGGA

1 kbp
introns not to scale

CD53
AL360270.1

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 0

— translocation   — deletion
— duplication   — inversion

chromosome 1

chromosome 1

p13.3

p13.3

breakpoint1
1:110895055

breakpoint2
1:110952184

Coverage

230

0

1 2 3 4 5 6 7 8 9

1 2

CD53
ENST00000648608.1

AL360270.1
ENST00000440689.1

1 2 3 4 5 6 2

CAAGGCAGCGTGGGACTCCATCCAGTCATTT GAGATACATAAATAACGGTTGGCATTTGGG

1 kbp
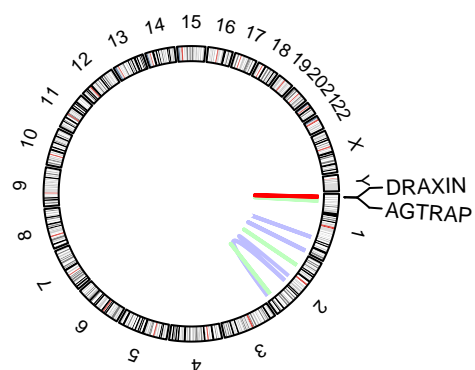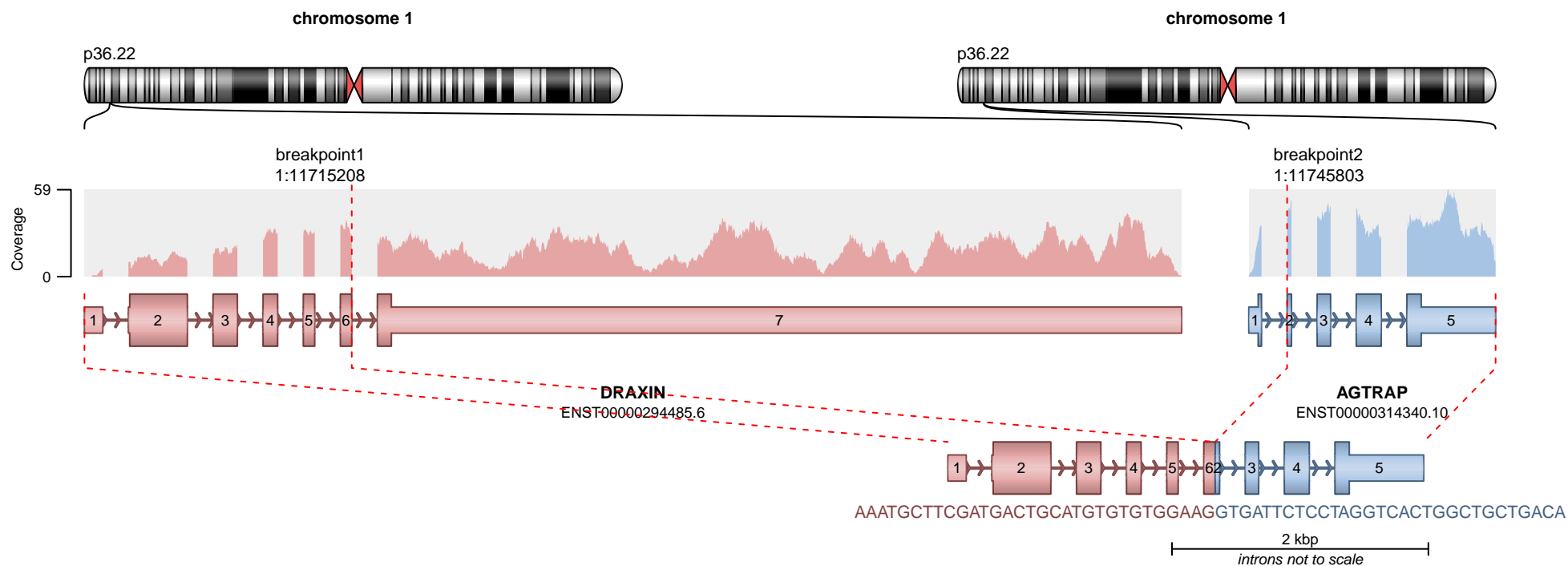*introns not to scale*

CD53
AL360270.1

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 1

translocation   deletion
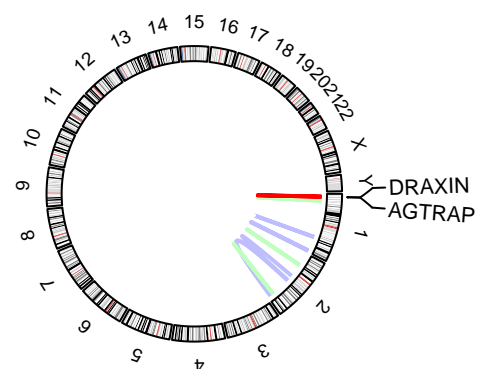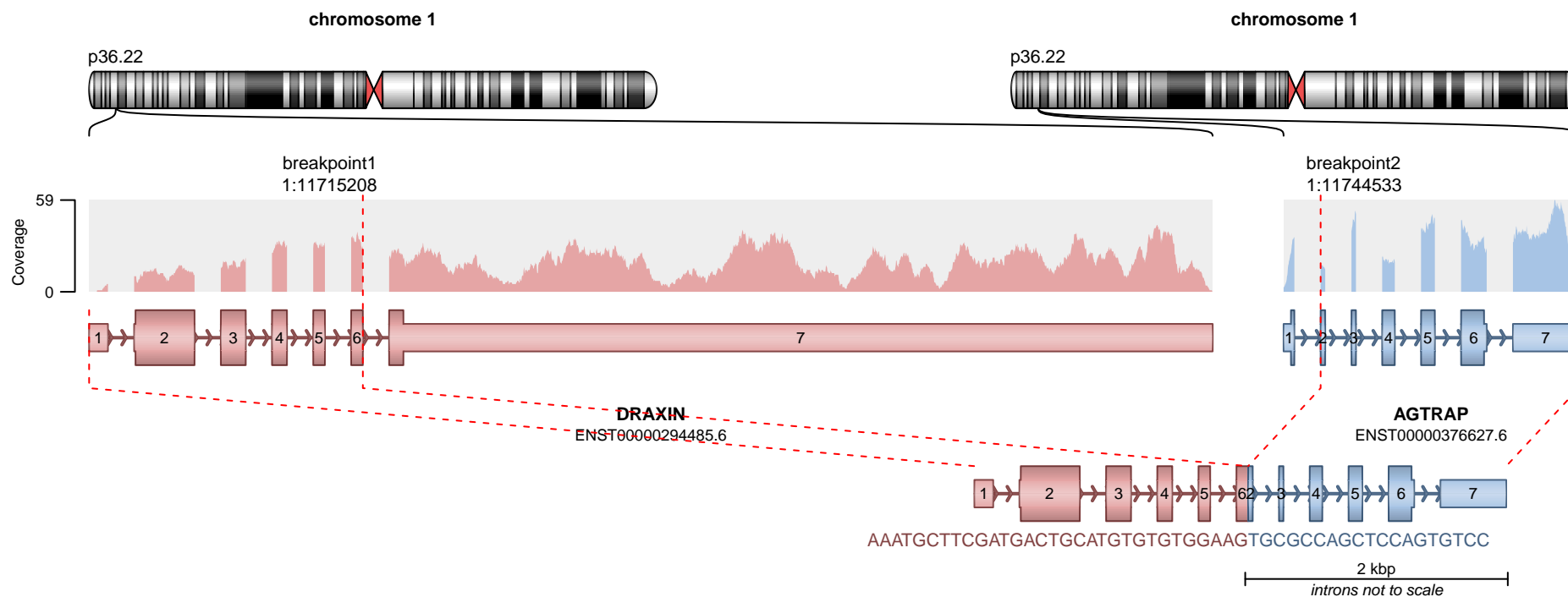duplication   inversion

chromosome 1

chromosome 1

p36.22

p36.22

breakpoint1
1:11715208

breakpoint2
1:11745803

Coverage

59

0

1 2 3 4 5 6 7

1 2 3 4 5

DRAXIN
ENST00000294485.6

AGTRAP
ENST00000314340.10

1 2 3 4 5 62 3 4 5

AAATGCTTCGATGACTGCATGTGTGTGGAAGGTGATTCTCCTAGGTCACTGGCTGCTGACA

2 kbp

introns not to scale

DRAXIN
AGTRAP

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 3
Discordant mates = 0

— translocation — deletion
— duplication — inversion

chromosome 1

chromosome 1

p36.22

p36.22

breakpoint1
1:11715208

breakpoint2
1:11744533

Coverage

59

0

1 2 3 4 5 6 7

1 2 3 4 5 6 7

DRAXIN
ENST00000294485.6

AGTRAP
ENST00000376627.6

1 2 3 4 5 62 3 4 5 6 7

AAATGCTTCGATGACTGCATGTGTGTGGAAGTGCGCCAGCTCCAGTGTCC

2 kbp

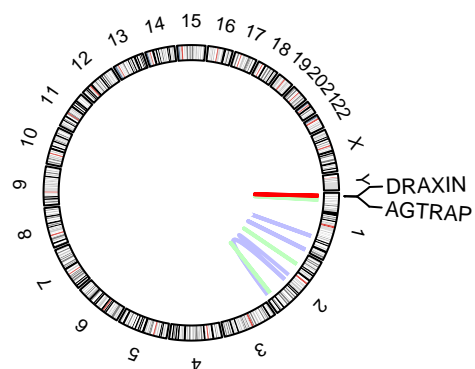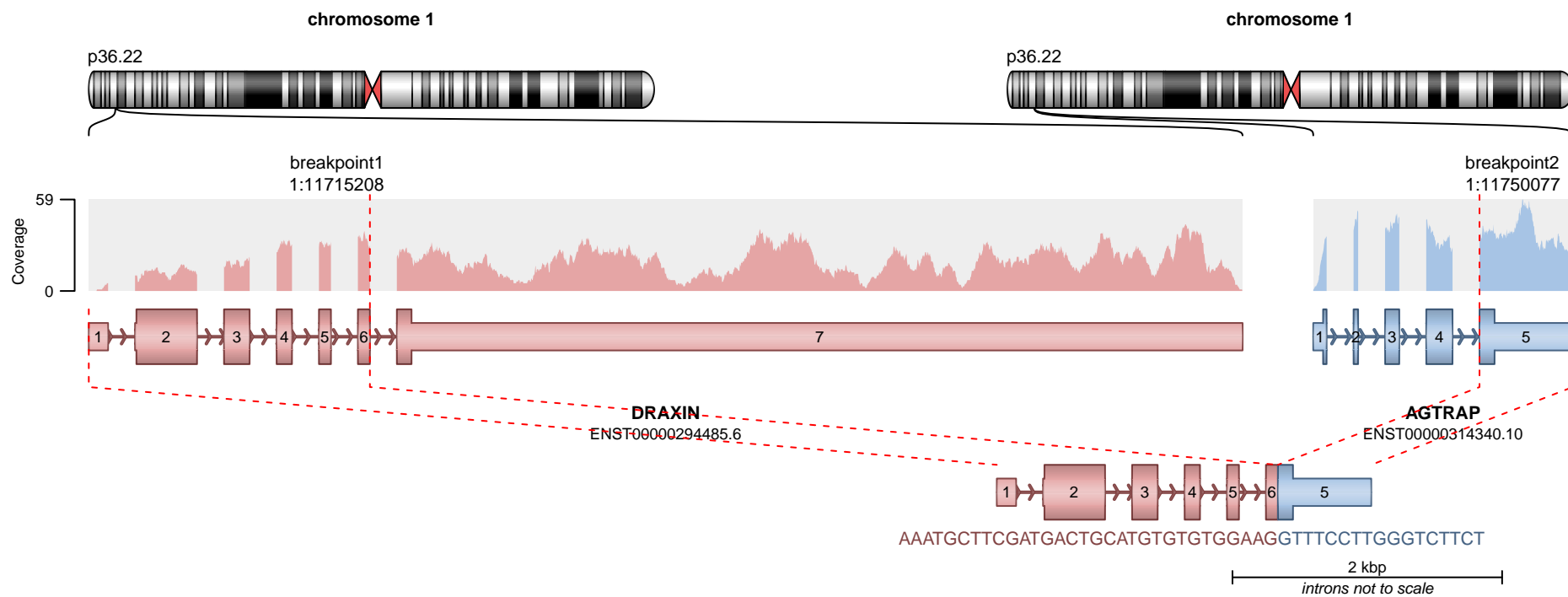*introns not to scale*

DRAXIN
AGTRAP

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 0

translocation   deletion
duplication   inversion

chromosome 1

chromosome 1

p36.22

p36.22

breakpoint1
1:11715208

breakpoint2
1:11750077

59

Coverage

0

1 2 3 4 5 6 7

1 2 3 4 5

DRAXIN
ENST00000294485.6

AGTRAP
ENST00000314340.10

1 2 3 4 5 6 5

AAATGCTTCGATGACTGCATGTGTGTGGAAGGTTTCCTTGGGTCTTCT

2 kbp
introns not to scale

DRAXIN
AGTRAP

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 0
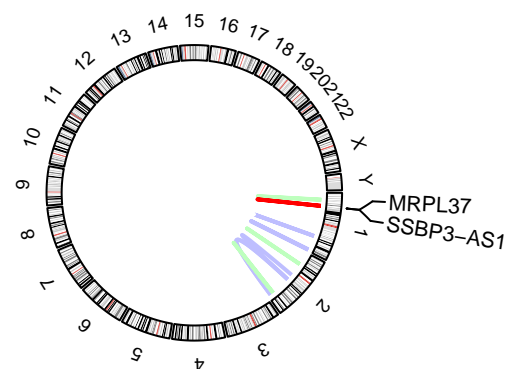
translocation   deletion
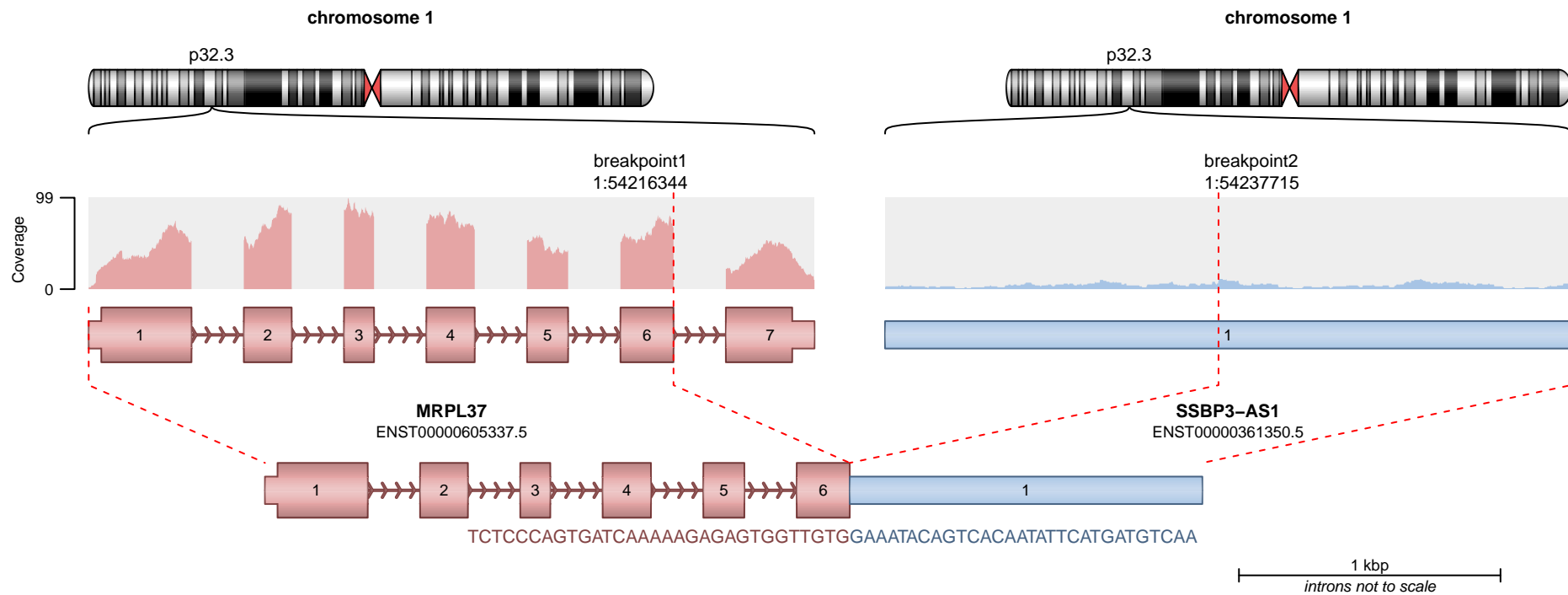duplication   inversion

chromosome 1

p32.3

chromosome 1

p32.3

breakpoint1
1:54216344

breakpoint2
1:54237715

99

Coverage

0

1 2 3 4 5 6 7

1

MRPL37
ENST00000605337.5

SSBP3−AS1
ENST00000361350.5

1 2 3 4 5 6

1

TCTCCCAGTGATCAAAAAGAGAGTGGTTGTGGGAAATACAGTCACAATATTCATGATGTCAA

1 kbp
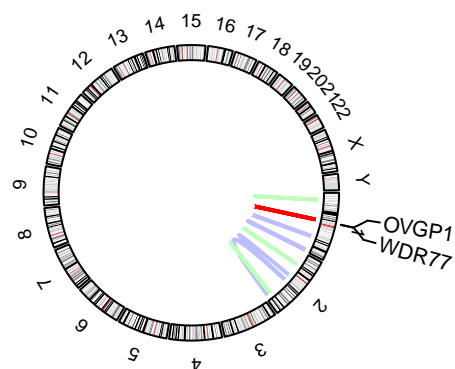*introns not to scale*

MRPL37
SSBP3−AS1

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 2
Discordant mates = 0

translocation   deletion
duplication   inversion

chromosome 1

p13.3

breakpoint1
1:111441211

Coverage
43

0

10 9 8 7 6 5 4 3 2 1

WDR77
ENST00000235090.10

chromosome 1

p13.3

breakpoint2
1:111427091

11 10 9 8 7 6 5 4 3 2 1

OVGP1
ENST00000369732.4

1 2 3 4 5 6 7 8 9 10 2 3 4 5 6 7 8 9 10 11

GTTACTGAGTAGATTGGATTTAAGACAAAAAGGCTGGTTCTTGTGCTGAAACACCACGATG

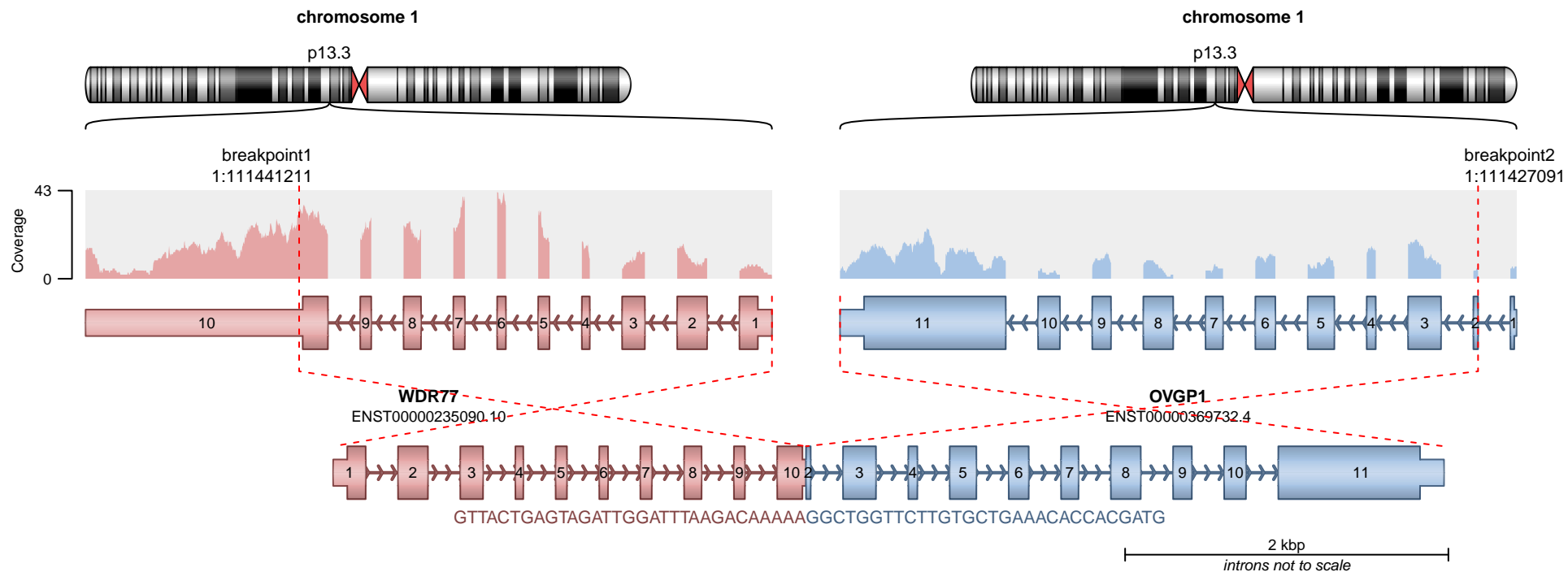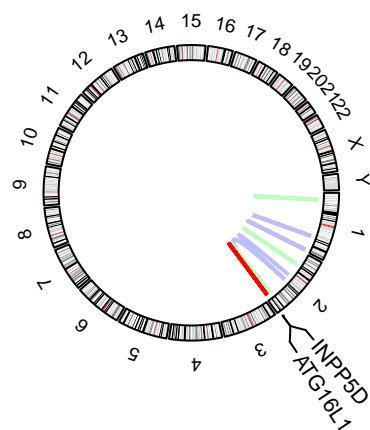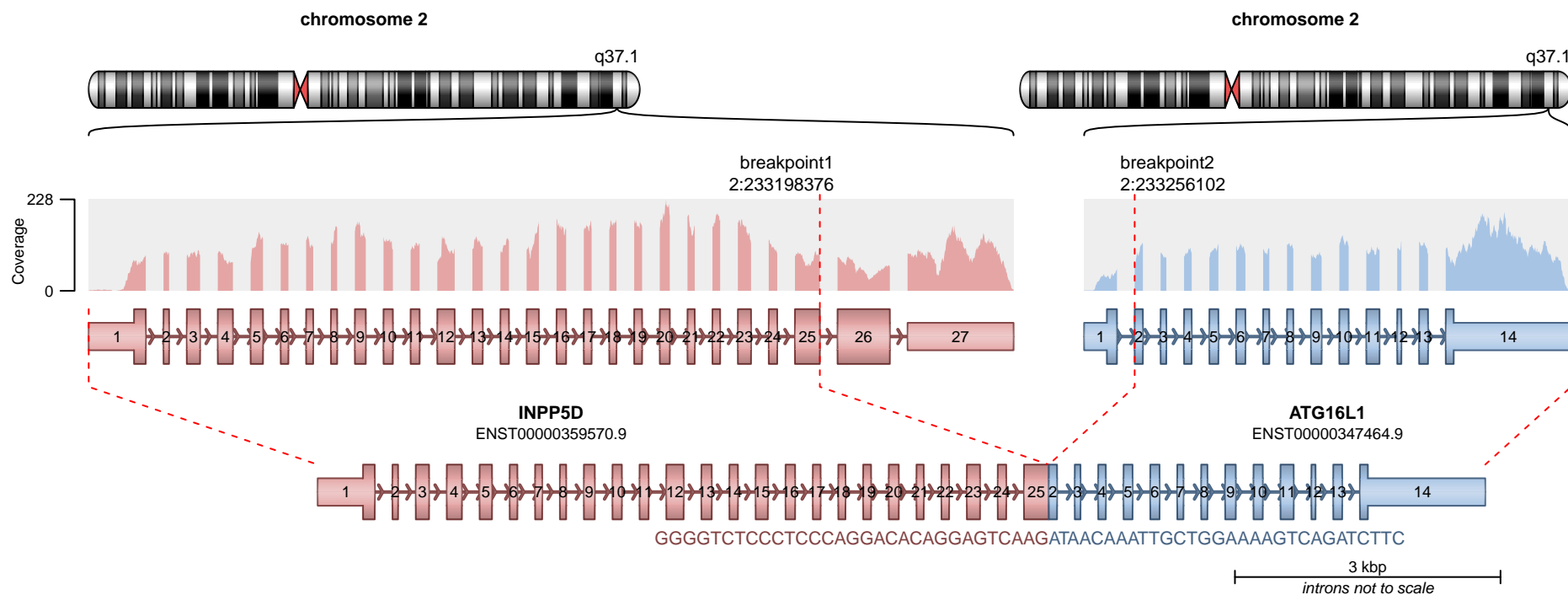2 kbp

introns not to scale

OVGP1
WDR77

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 1
Discordant mates = 1

translocation   deletion
duplication   inversion

chromosome 2

chromosome 2

q37.1

q37.1

breakpoint1
2:233198376

breakpoint2
2:233256102

Coverage

228

0

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27

1 2 3 4 5 6 7 8 9 10 11 12 13 14

INPP5D
ENST00000359570.9

ATG16L1
ENST00000347464.9

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 2 3 4 5 6 7 8 9 10 11 12 13 14

GGGGTCTCCCTCCCAGGACACAGGAGTCAAG ATAACAAATTGCTGGAAAAGTCAGATCTTC

3 kbp
introns not to scale

12 13 14 15 16 17 18 19 20 21 22 X Y
11 1
10 2
9 3
8 4
7 5
6 INPP5D
ATG16L1

RETAINED PROTEIN DOMAINS
out−of−frame fusion

RNB domain

INPP5D

ATG16L1

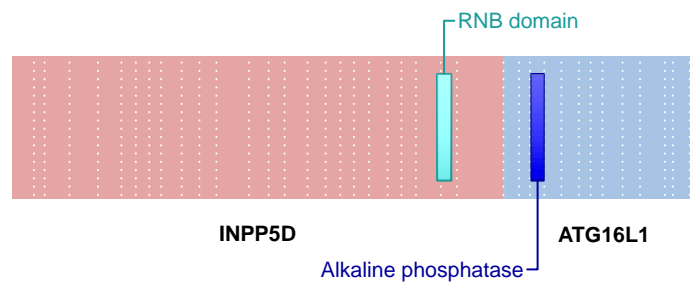Alkaline phosphatase

SUPPORTING READ COUNT

Split reads at breakpoint1 = 2
Split reads at breakpoint2 = 0
Discordant mates = 0

translocation   deletion
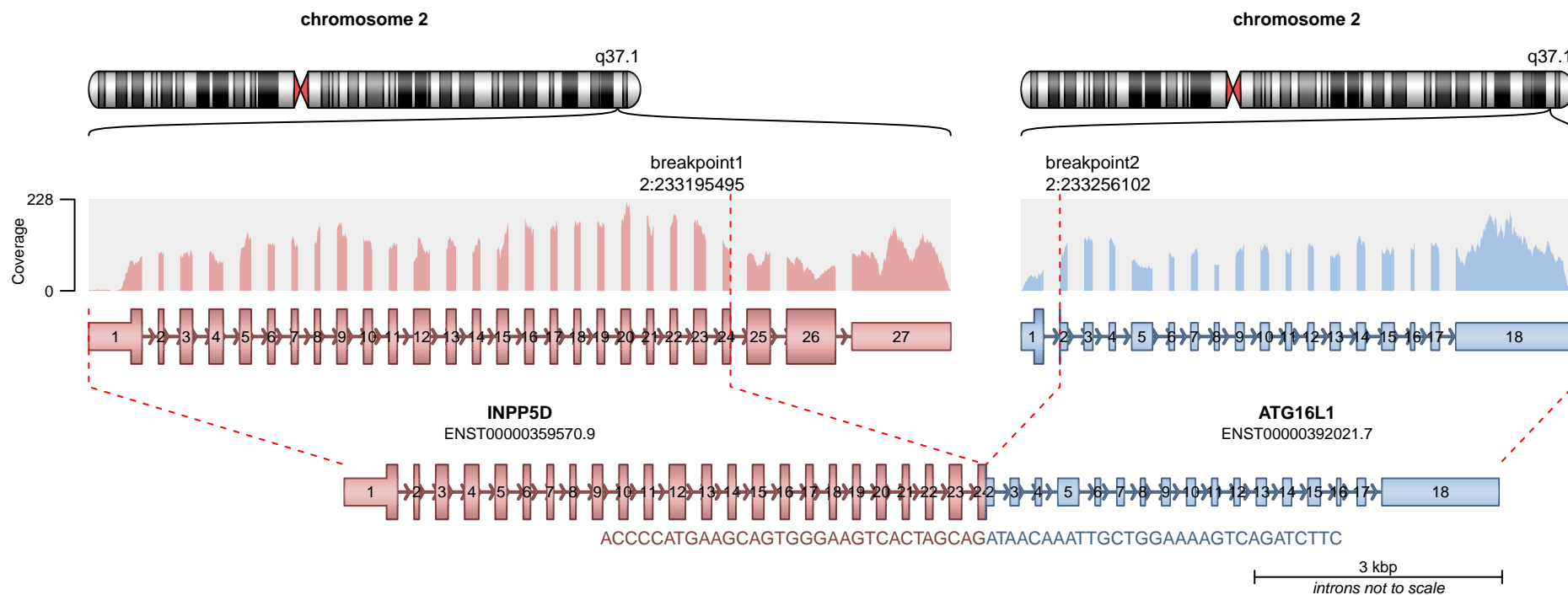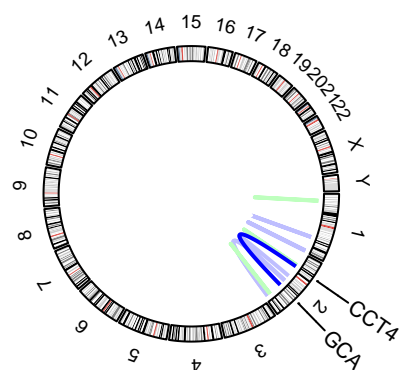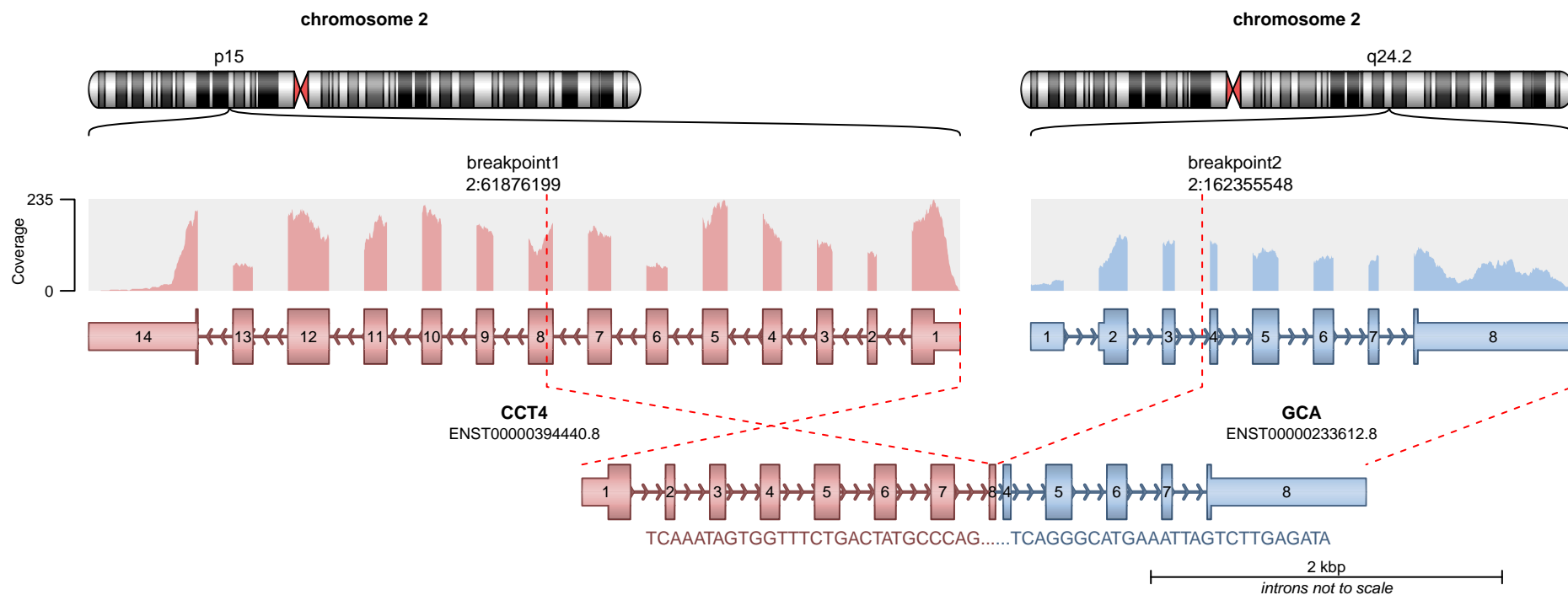duplication   inversion

chromosome 2

q37.1

breakpoint1
2:233195495

228

Coverage

0

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27

INPP5D
ENST00000359570.9

chromosome 2

q37.1

breakpoint2
2:233256102

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

ATG16L1
ENST00000392021.7

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

ACCCCATGAAGCAGTGGGAAGTCACTAGCAG ATAACAAATTGCTGGAAAAGTCAGATCTTC

3 kbp
introns not to scale

RETAINED PROTEIN DOMAINS
out−of−frame fusion

RNB domain

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

INPP5D   **ATG16L1**

INPP5D
ATG16L1

translocation   deletion
duplication   inversion

chromosome 2

p15

breakpoint1
2:61876199

Coverage
235
0

14 13 12 11 10 9 8 7 6 5 4 3 2 1

CCT4
ENST00000394440.8

chromosome 2

q24.2

breakpoint2
2:162355548

1 2 3 4 5 6 7 8

GCA
ENST00000233612.8

1 2 3 4 5 6 7 8 4 5 6 7 8

TCAAATAGTGGTTTCTGACTATGCCCAG......TCAGGGCATGAAATTAGTCTTGAGATA

2 kbp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 0
Discordant mates = 2

CCT4
GCA

translocation   deletion
duplication   inversion

chromosome 2

q22.3

chromosome 2

q21.3

breakpoint1
2:144517278

breakpoint2
2:136115912

2784

Coverage

0

| 9 | 8 | 7 | 6 | 5 | 4 | 3 | 2 | 1 |

| 2 | 1 |

ZEB2
ENST00000558170.6

CXCR4
ENST00000241393.3

| 1 | 2 |

CGCAAACAAGCCAATCCCAGGAGGAAAAACGATATACACTTCAGATAACTACACCGAGGAA
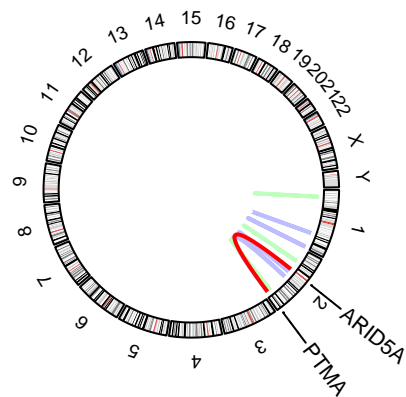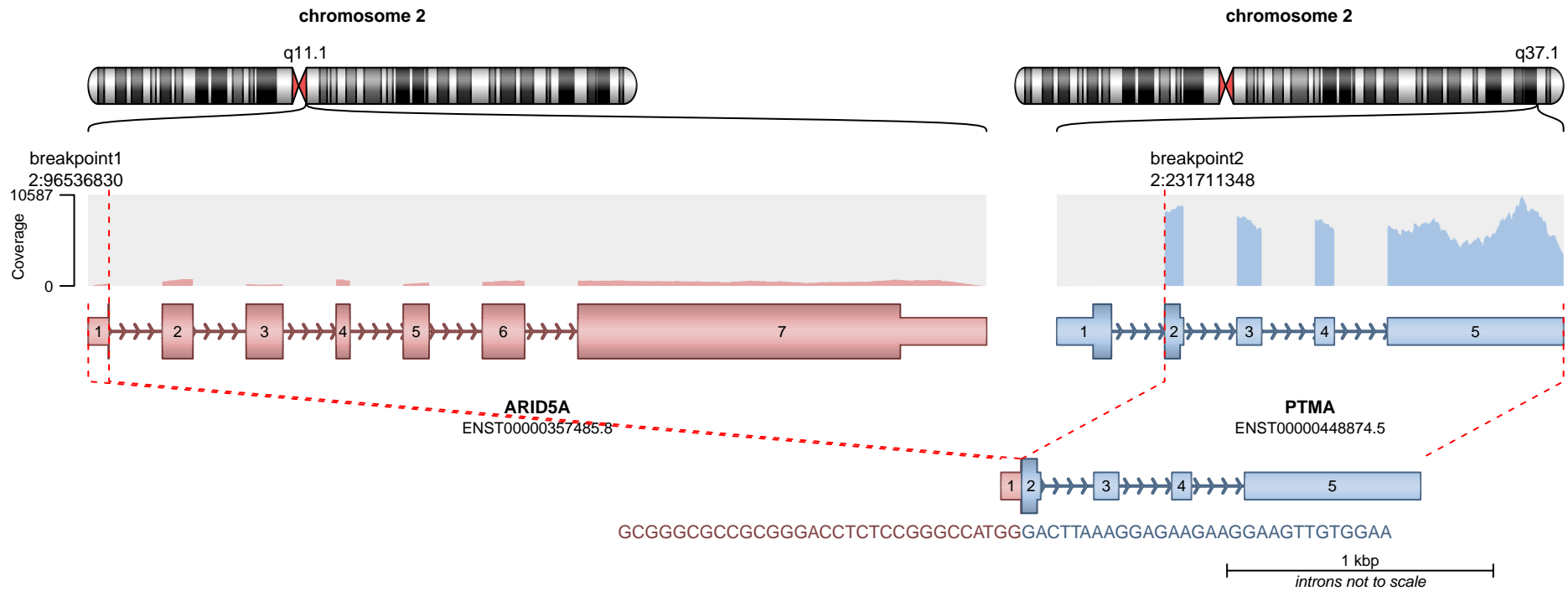
1 kbp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 1

CXCR4
ZEB2

translocation   deletion
duplication   inversion

chromosome 2

q11.1

breakpoint1
2:96536830

Coverage
10587

0

1 2 3 4 5 6 7

ARID5A
ENST00000357485.8

chromosome 2

q37.1

breakpoint2
2:231711348

1 2 3 4 5

PTMA
ENST00000448874.5

1 2 3 4 5

GCGGGCGCCGCGGGACCTCTCCGGGCCATGGGACTTAAAGGAGAAGAAGGAAGTTGTGGAA
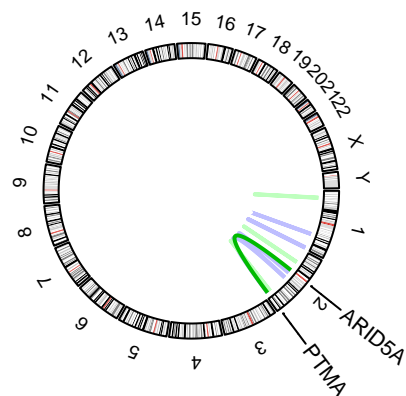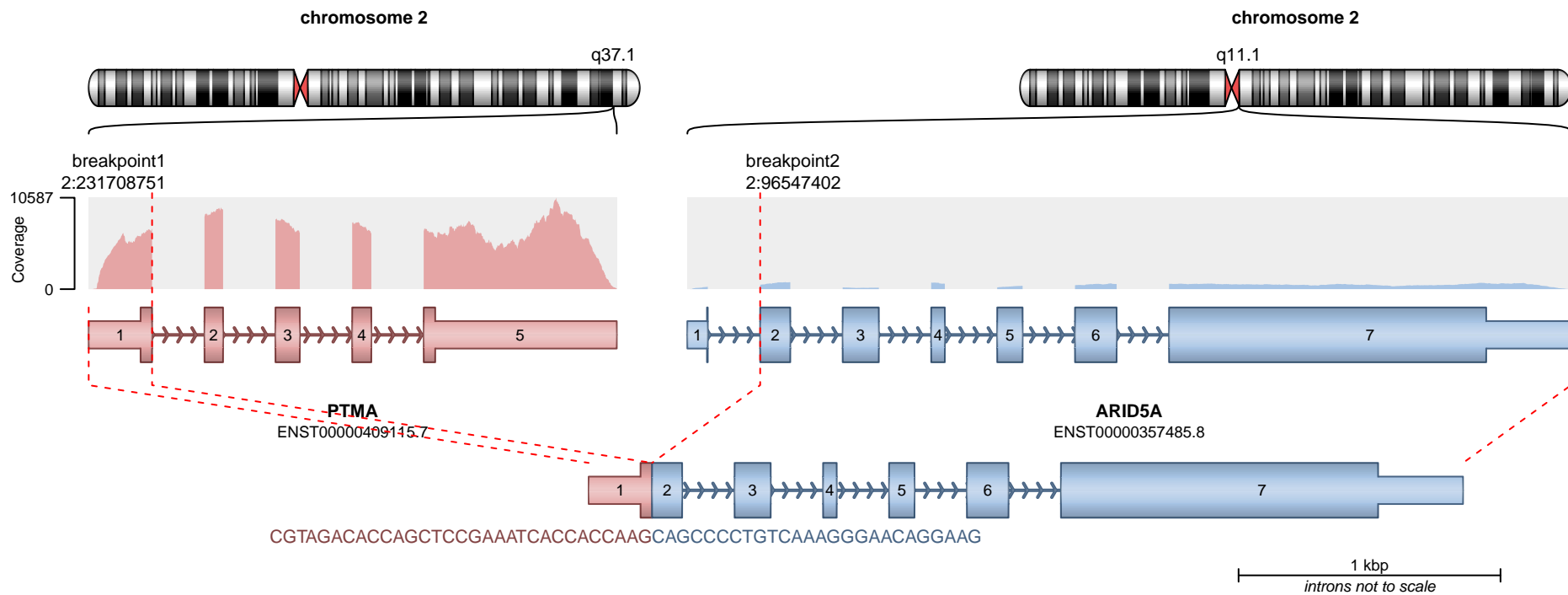
1 kbp
introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 2
Discordant mates = 0

ARID5A

PTMA

translocation   deletion
duplication   inversion

chromosome 2   chromosome 2

q37.1   q11.1

breakpoint1   breakpoint2
2:231708751   2:96547402

10587

Coverage

0

PTMA   ARID5A
ENST00000409115.7   ENST00000357485.8

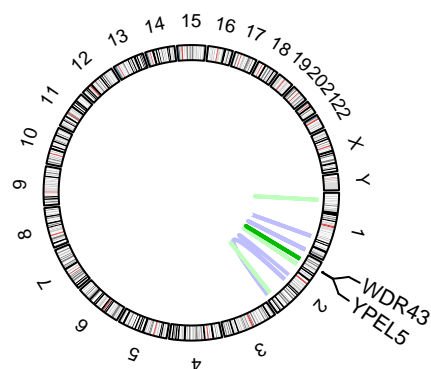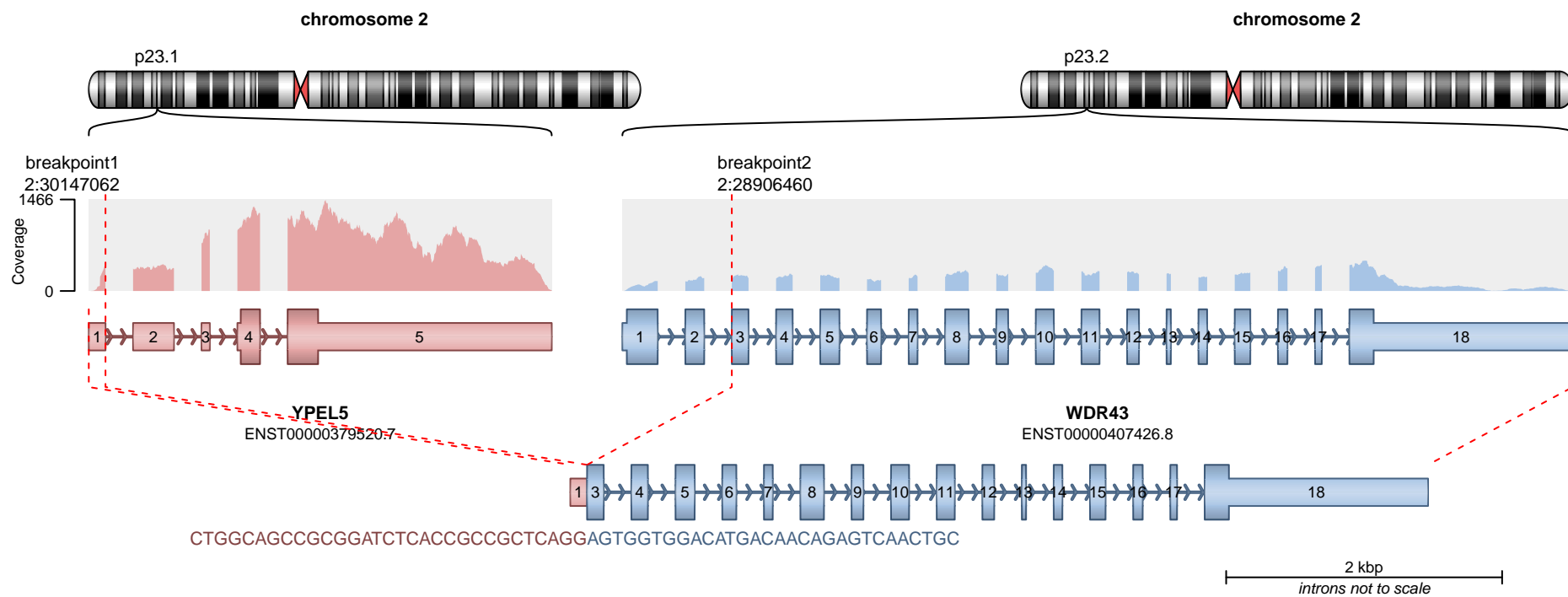CGTAGACACCAGCTCCGAAATCACCACCAAGCAGCCCCTGTCAAAGGGAACAGGAAG

1 kbp

introns not to scale

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 1
Split reads at breakpoint2 = 0
Discordant mates = 0

ARID5A
PTMA

translocation   deletion
duplication   inversion

chromosome 2

chromosome 2

p23.1

p23.2

breakpoint1
2:30147062

breakpoint2
2:28906460

1466

Coverage

0

1 2 3 4 5

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

YPEL5
ENST00000379520.7

WDR43
ENST00000407426.8

1 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

CTGGCAGCCGCGGATCTCACCGCCGCTCAGGAGTGGTGGACATGACAACAGAGTCAACTGC

2 kbp
introns not to scale

11 12 13 14 15 16 17 18 19 20 21 22 X Y

10

9

8

7

6

5

4

3

2

1

WDR43
YPEL5

No protein domains retained in fusion.

SUPPORTING READ COUNT

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation   — deletion
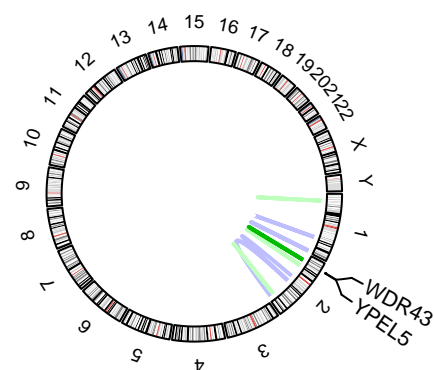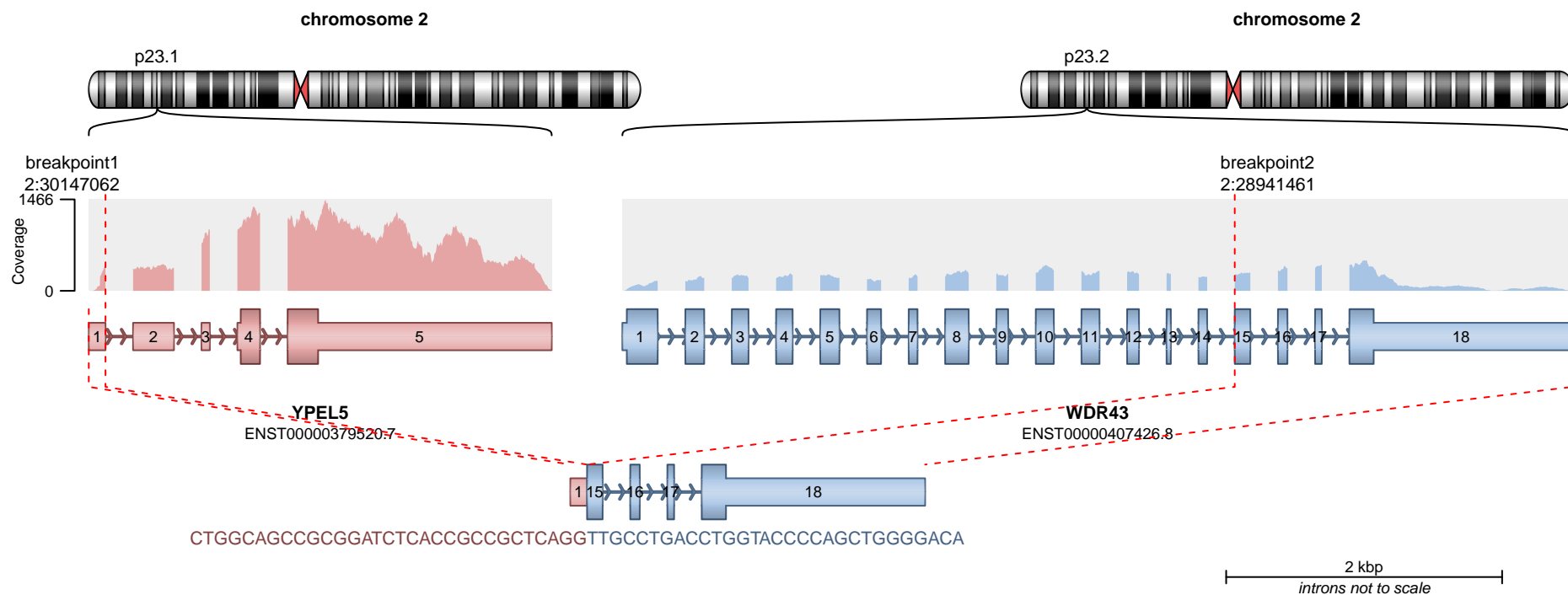— duplication   — inversion

chromosome 2

chromosome 2

p23.1

p23.2

breakpoint1
2:30147062

breakpoint2
2:28941461

1466

Coverage

0

1 2 3 4 5

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18

YPEL5
ENST00000379520.7

WDR43
ENST00000407426.8

1 15 16 17 18

CTGGCAGCCGCGGATCTCACCGCCGCTCAGGTTGCCTGACCTGGTACCCCAGCTGGGGACA

2 kbp

introns not to scale

WDR43
YPEL5

SUPPORTING READ COUNT

No protein domains retained in fusion.

Split reads at breakpoint1 = 0
Split reads at breakpoint2 = 1
Discordant mates = 0

— translocation   — deletion
— duplication   — inversion