

Supplementary Information for

The Landscape of submicroscopic structural variants at the OPN1LW/OPN1MW gene cluster on Xq28 underlying Blue Cone Monochromacy: Evidence for the instability of gene clusters with increased copy number

Bernd Wissinger*, Britta Baumann, Elena Buena-Atienza, Zeinab Ravesh, Artur V. Cideciyan, Katarina Stingl, Isabelle Audo, Isabelle Meunier, Beatrice Bocquet, Elias I. Traboulsi, Alison J. Hardcastle, Jessica C. Gardner, Michel Michaelides, Kari E. Branham, Thomas Rosenberg, Sten Andreasson, H el ene Dollfus, David Birch, Andrea L. Vincent, Loreto Martorell, Jaume Catal a Mora, Ulrich Kellner, Klaus R uther, Birgit Lorenz, Markus N. Preising, Emanuela Manfredini, Yuri A. Zarate, Raymon Vijzelaar, Eberhart Zrenner, Samuel G. Jacobson, and Susanne Kohl

* corresponding author: Bernd Wissinger
Email: wissinger@uni-tuebingen.de

This PDF file includes:

Figures S1 to S8
Table S1 to S2

Other supplementary materials for this manuscript include the following:

Dataset S1

Fig. S1. (below). Breakpoint sequences of SVs.

Sanger sequencing electropherograms were obtained from PCR amplicons covering the SV breakpoints. Breakpoint junctions are indicated by stippled vertical lines and the physical coordinates of the last nucleotide upstream and the first nucleotide downstream of the junction are indicated. The mutant allele sequence (SV-seq) is given below and aligned with the centromeric and telomeric reference sequences flanking the breakpoint. Matching reference sequence upstream and downstream of the breakpoint in bold. Sequence homologies at the breakpoint junctions are highlighted in yellow. Inserted sequences at the breakpoint junctions are indicated by red letters and additional deletions by dashes. Note that the breakpoint sequences of SVar1, SVar20, SVar38, and SVar42 are shown in Figures S2-S4.

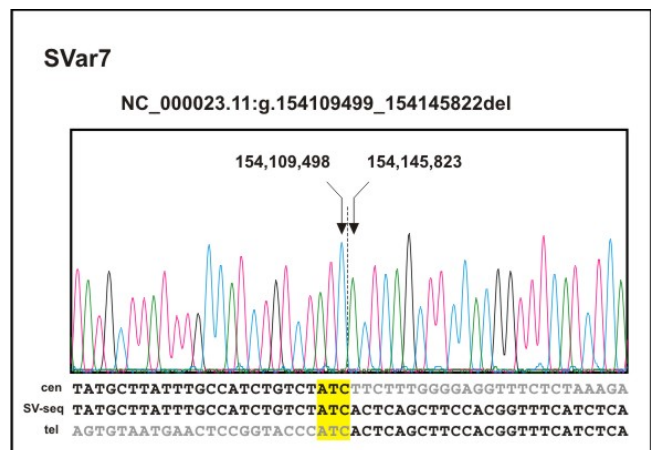
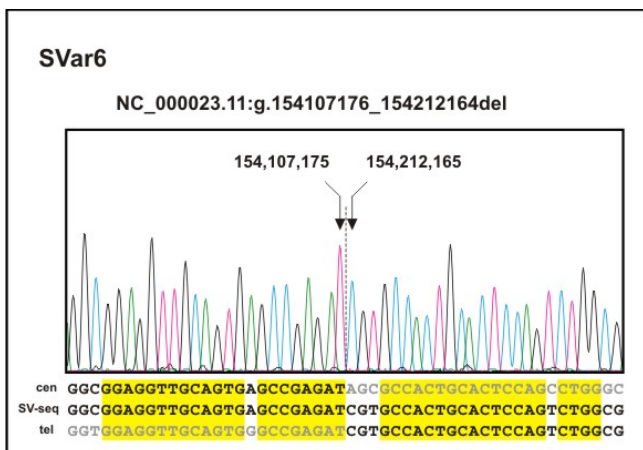
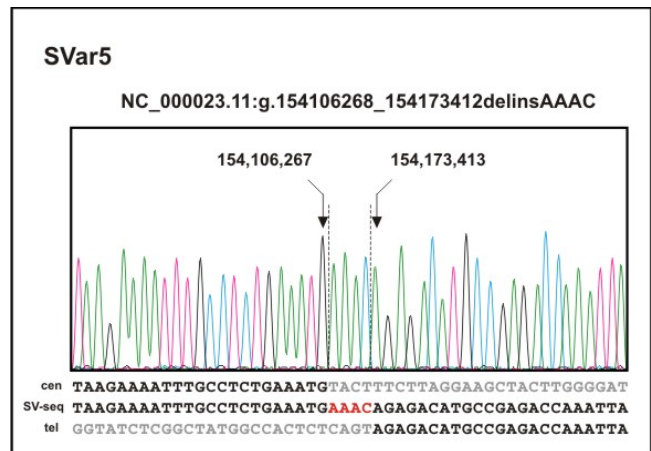
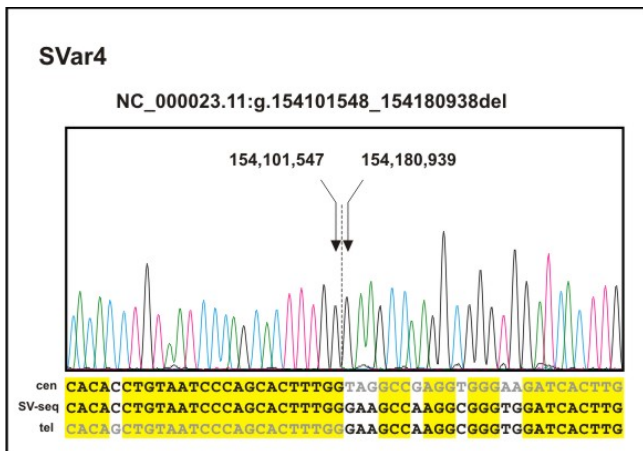
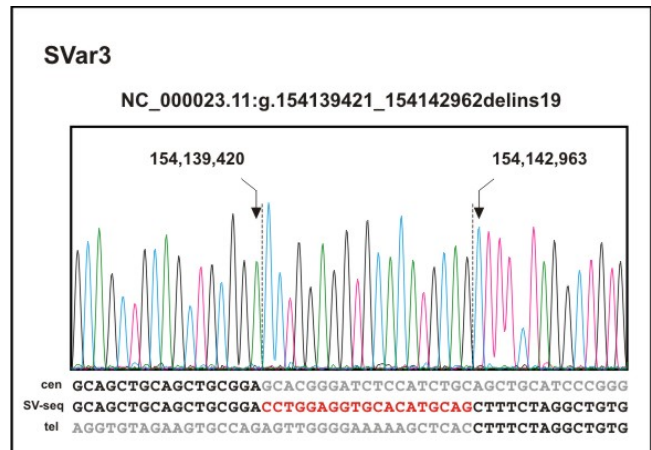
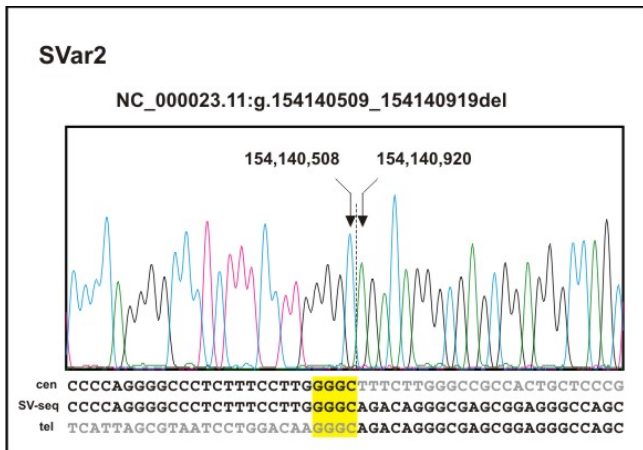


Fig. S1. (continued)

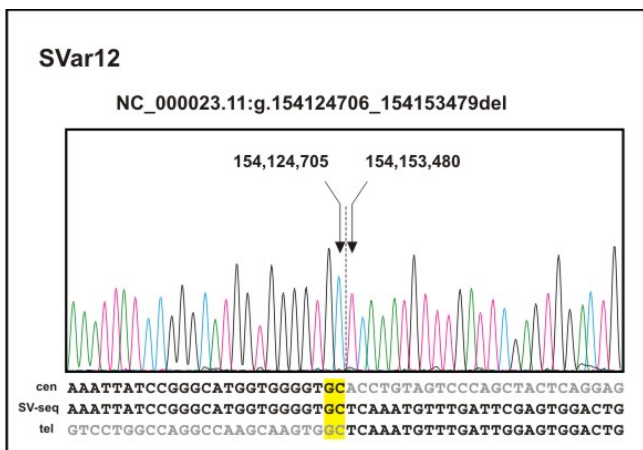
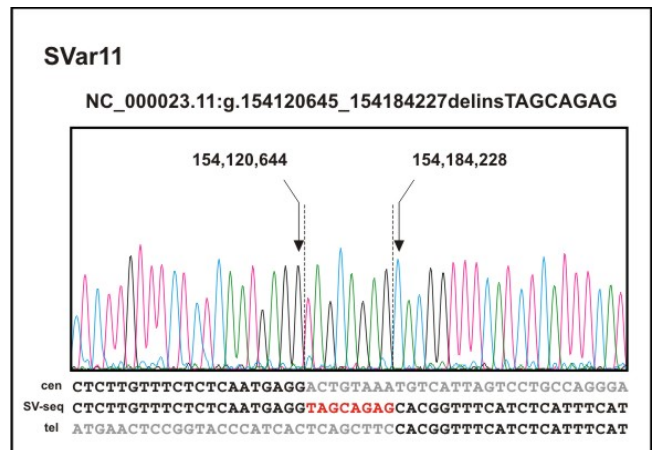
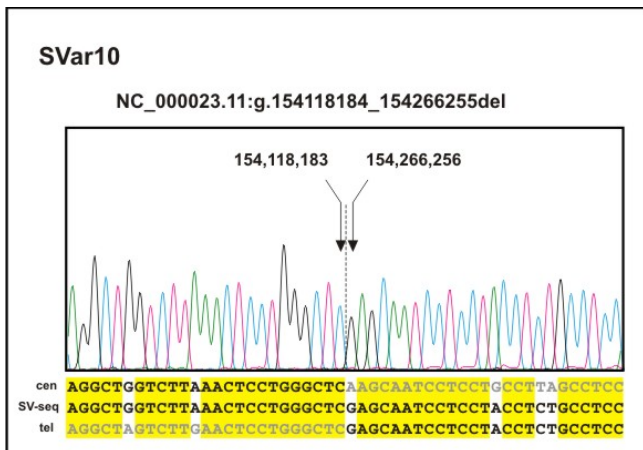
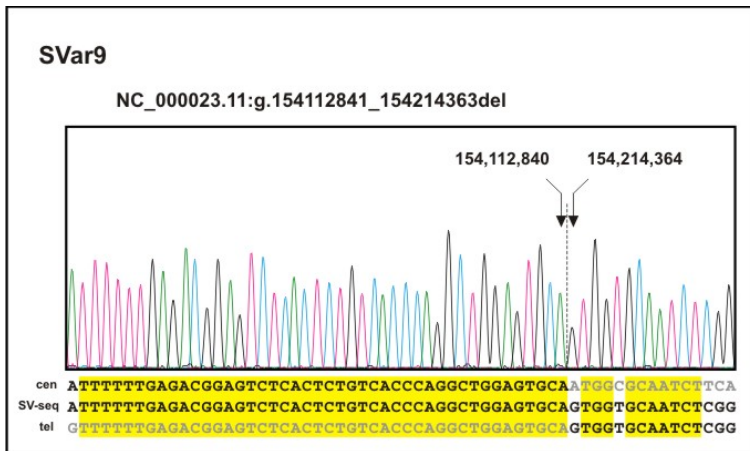
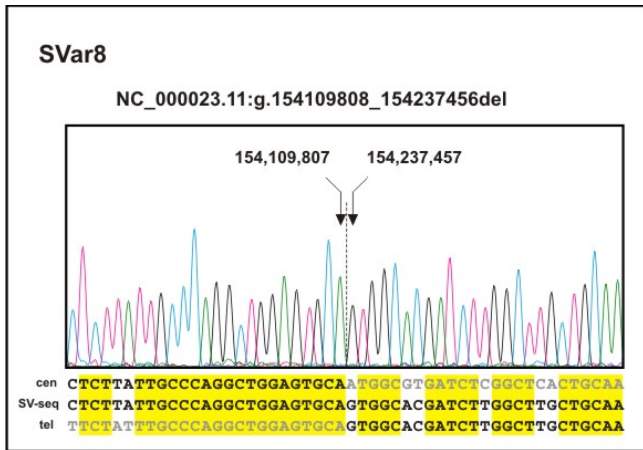


Fig. S1. (continued)

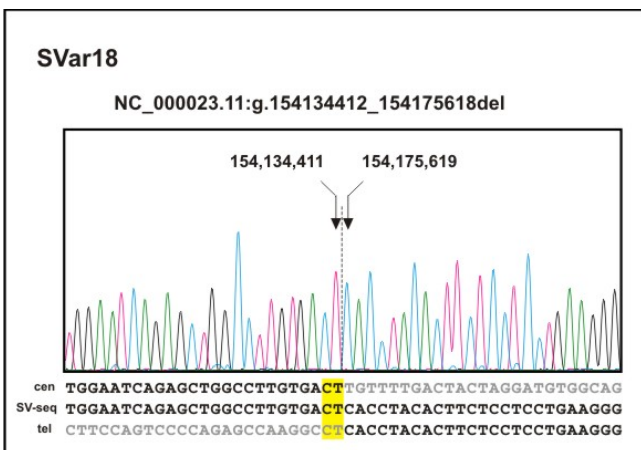
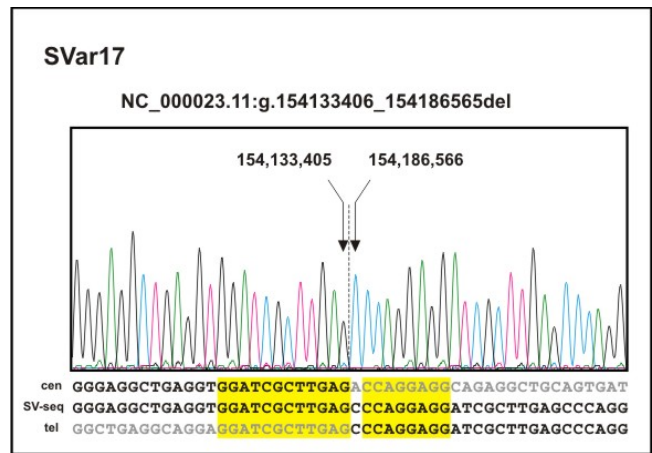
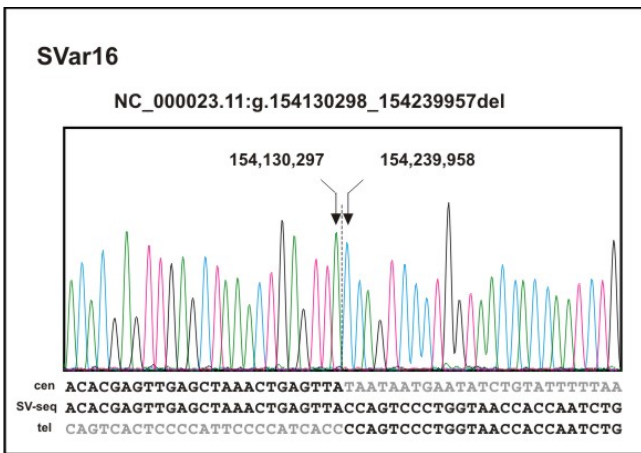
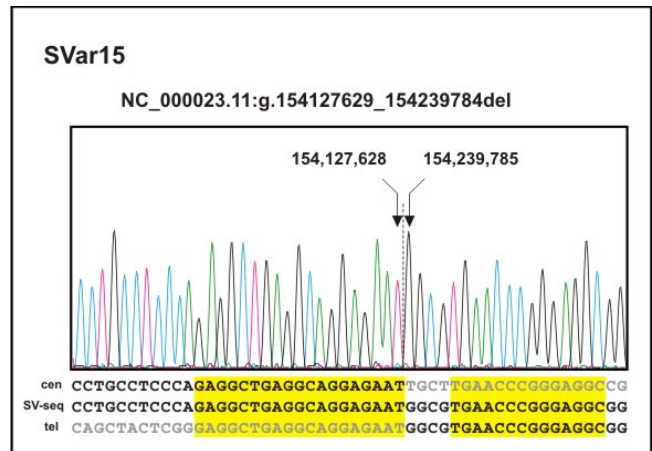
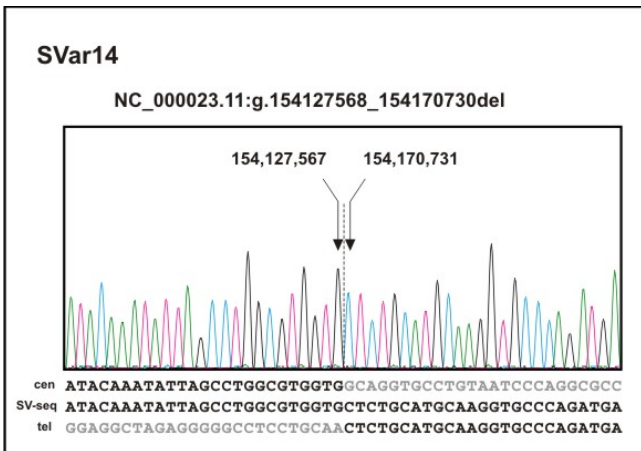
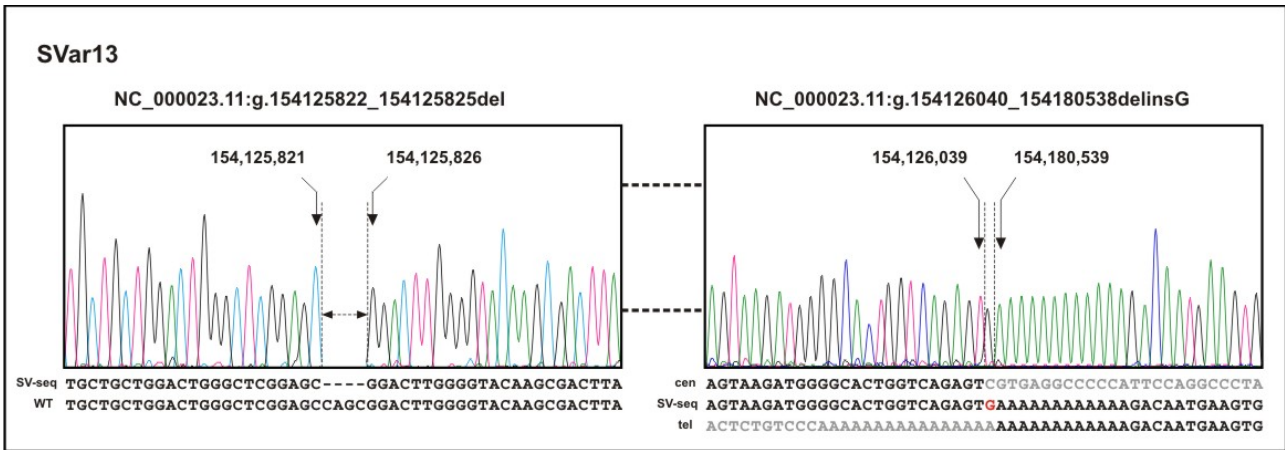


Fig. S1. (continued)

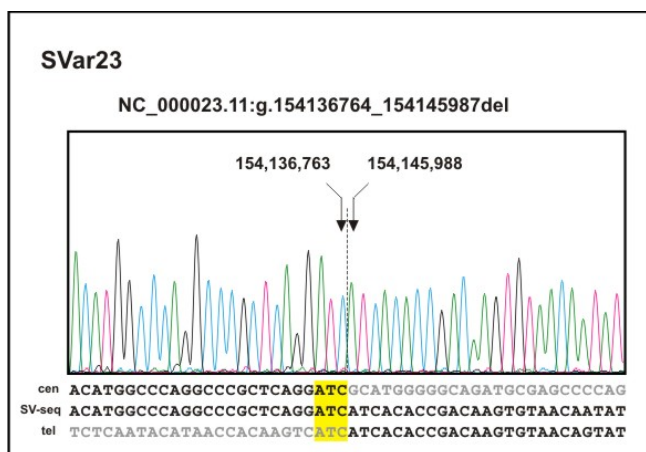
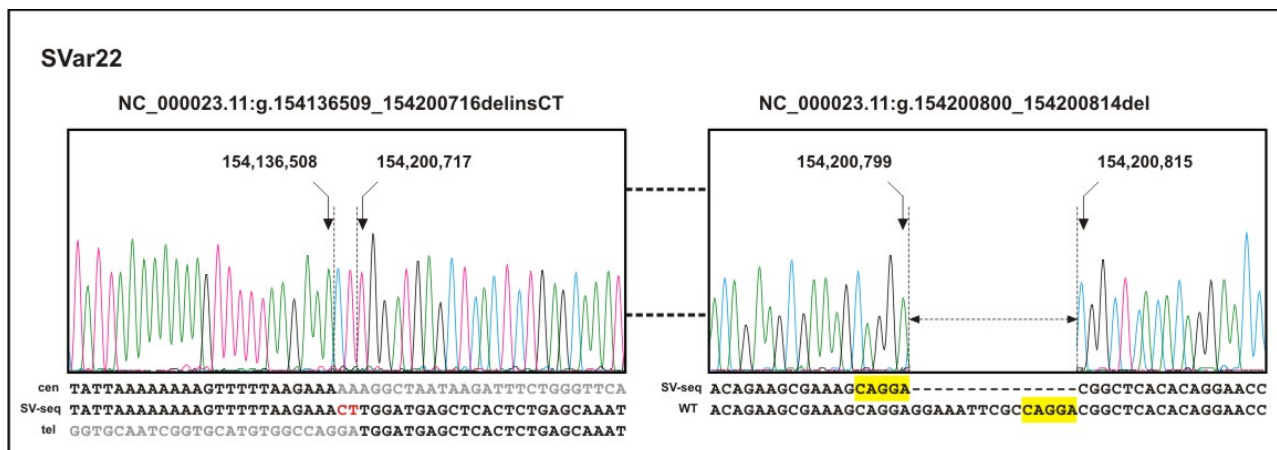
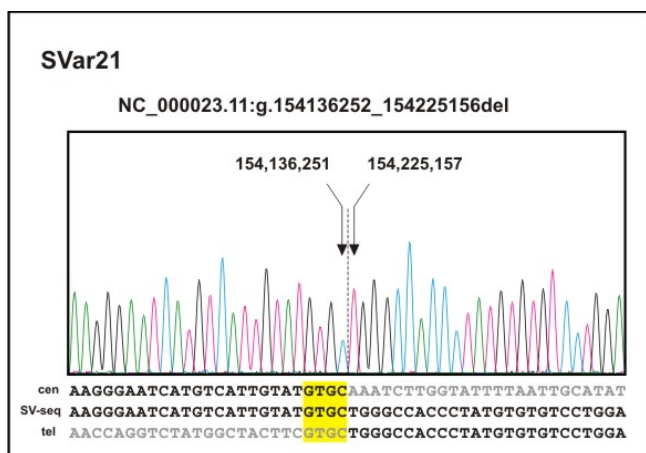
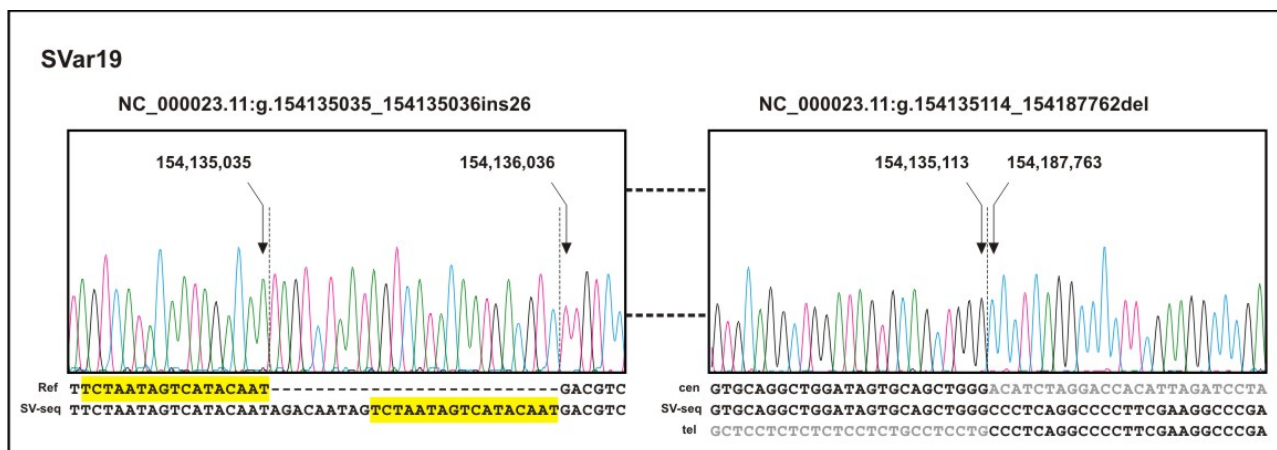


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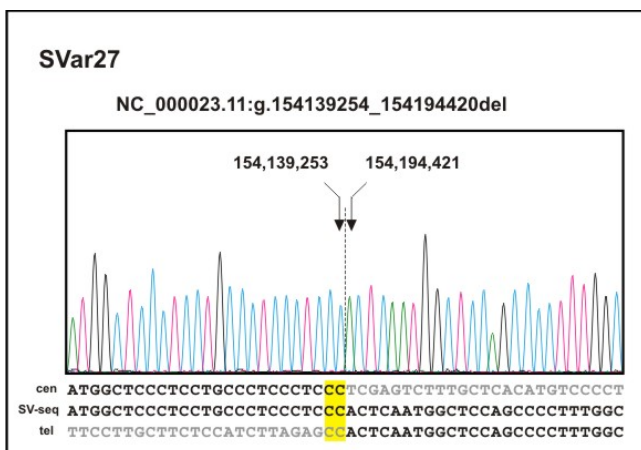
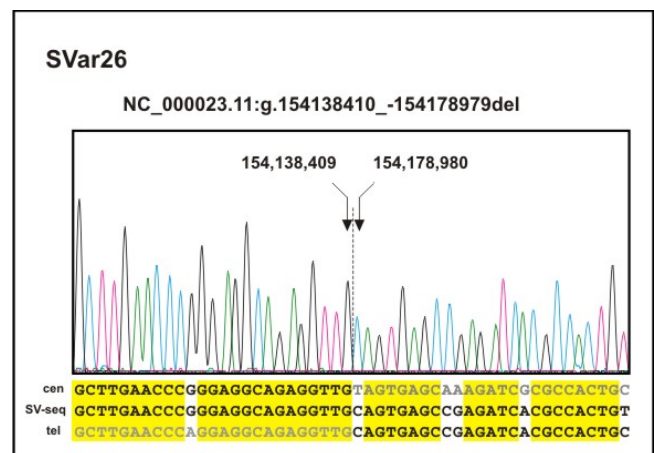
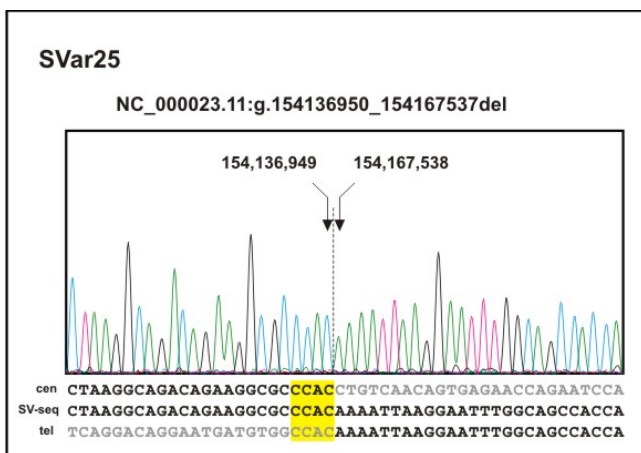
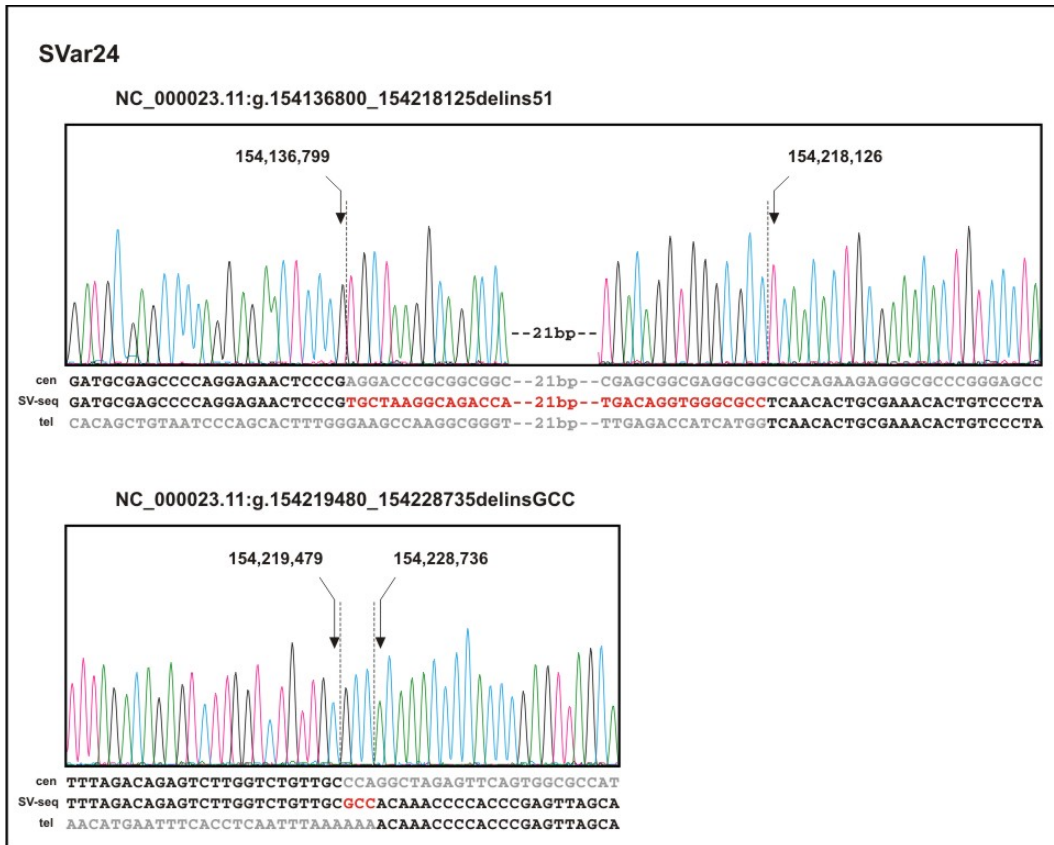


Fig. S1. (continued)

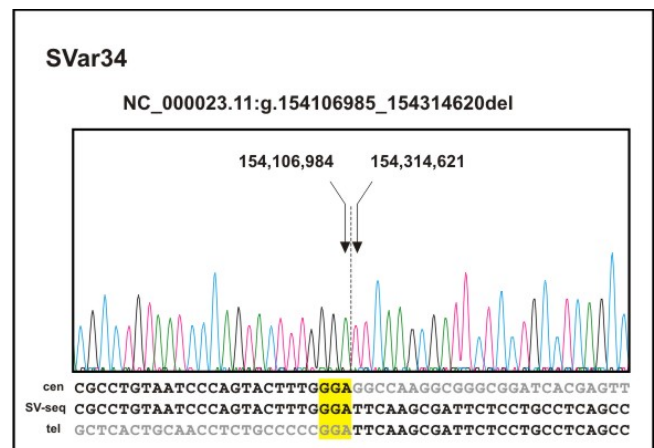
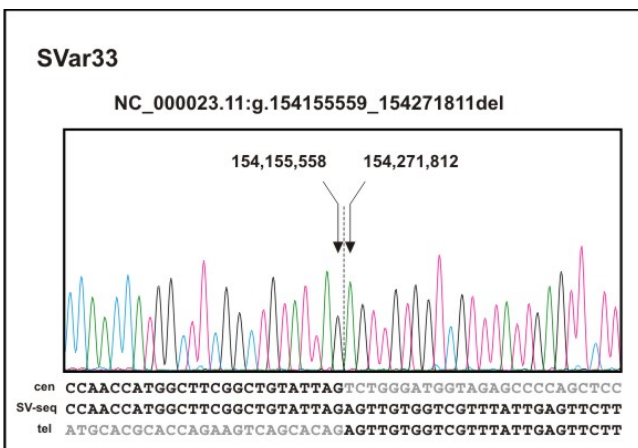
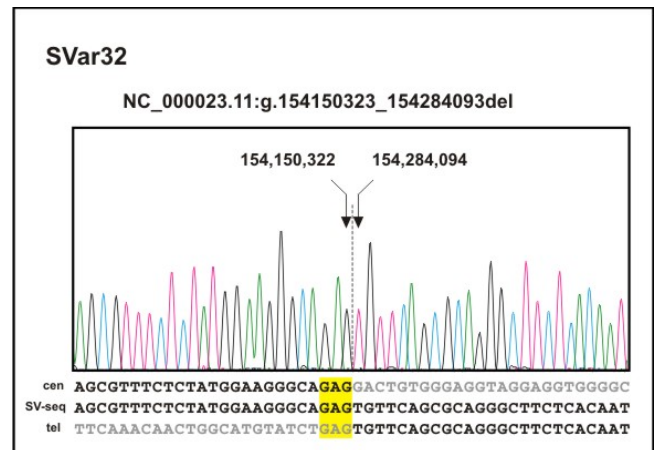
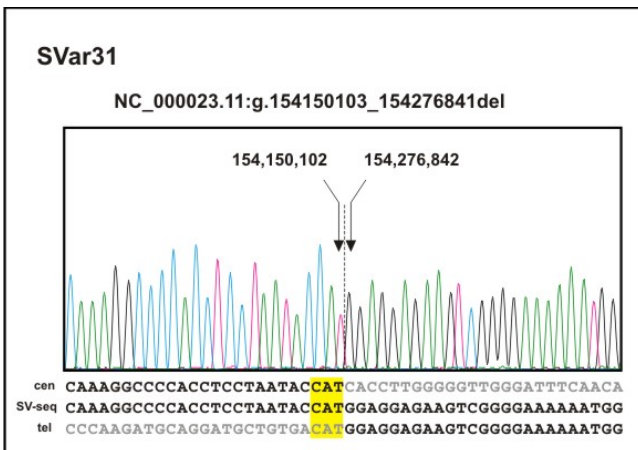
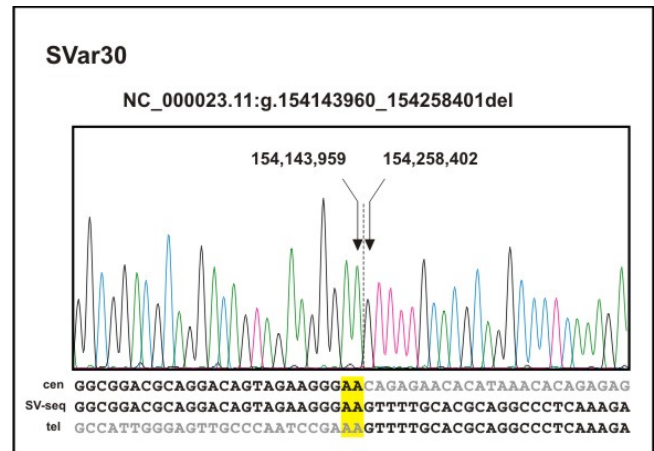
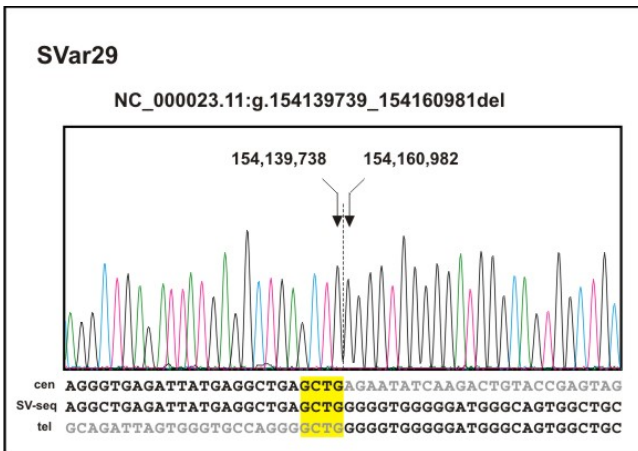
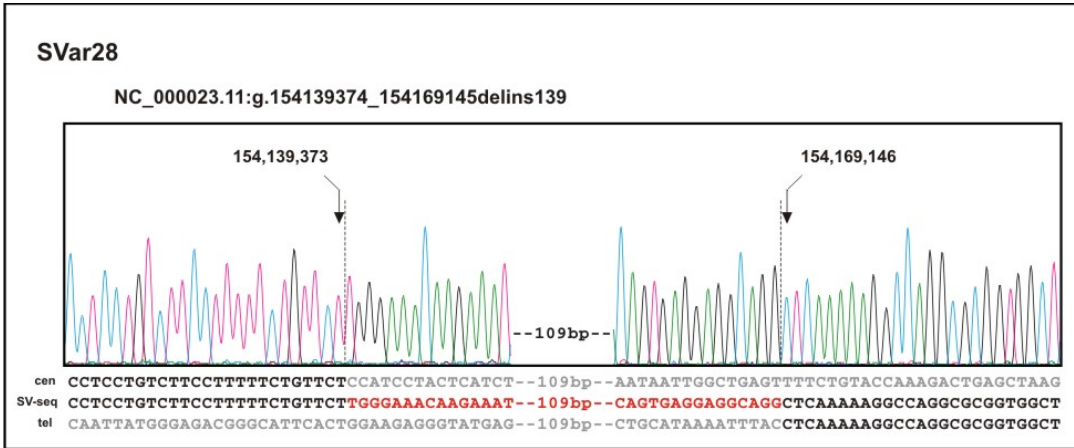


Fig. S1. (continued)

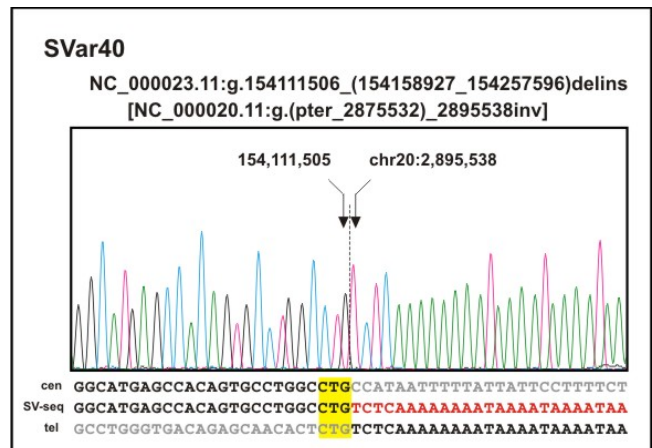
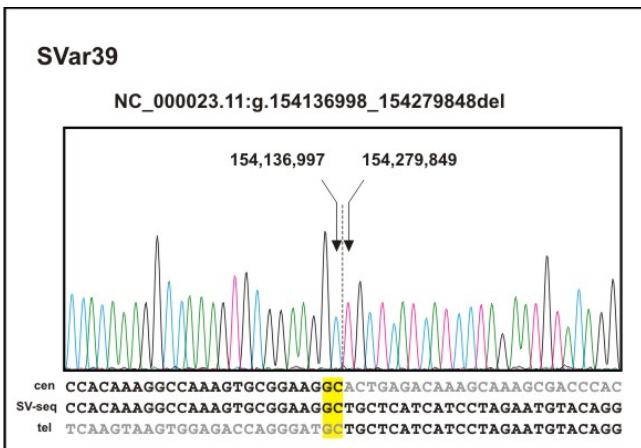
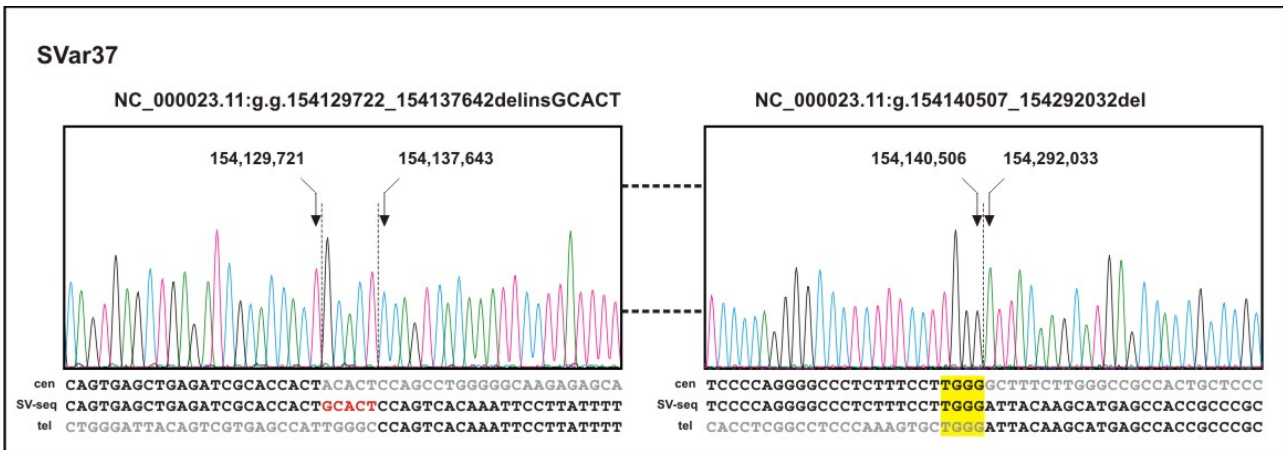
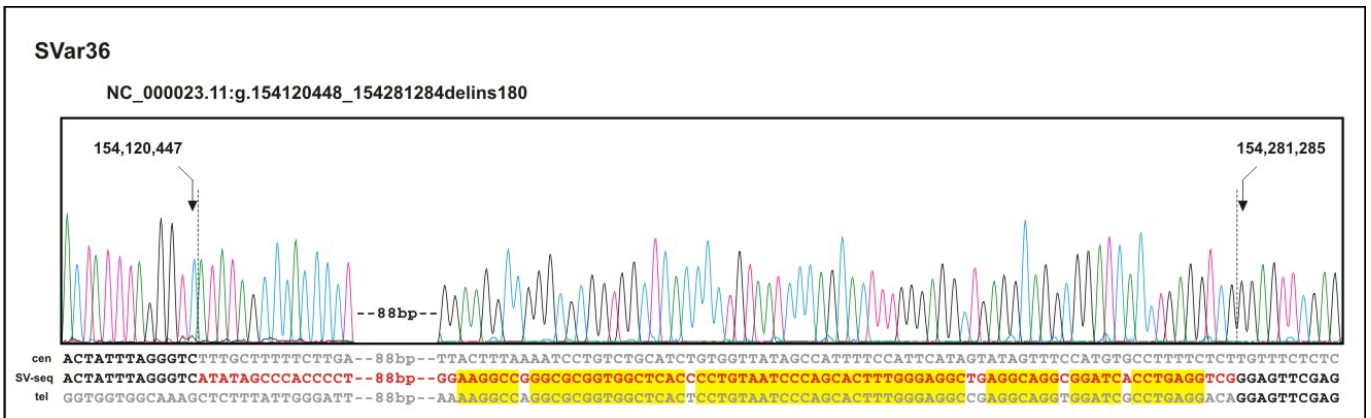
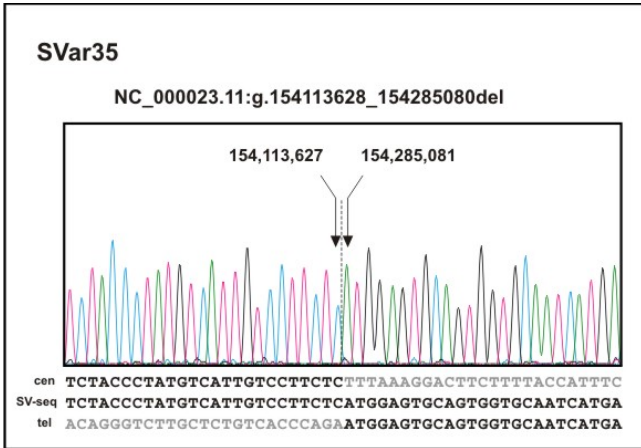
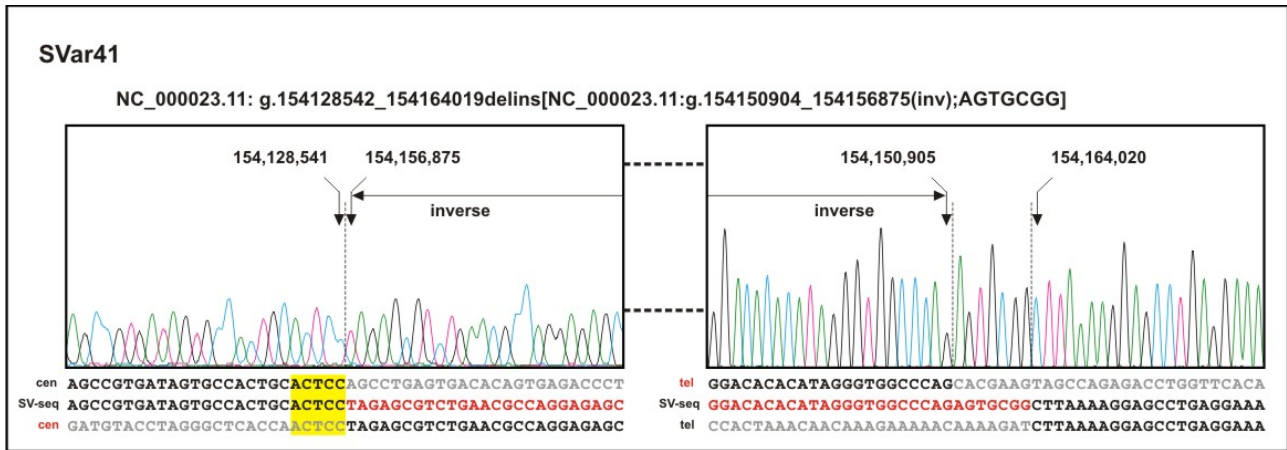


Fig. S1. (continued)



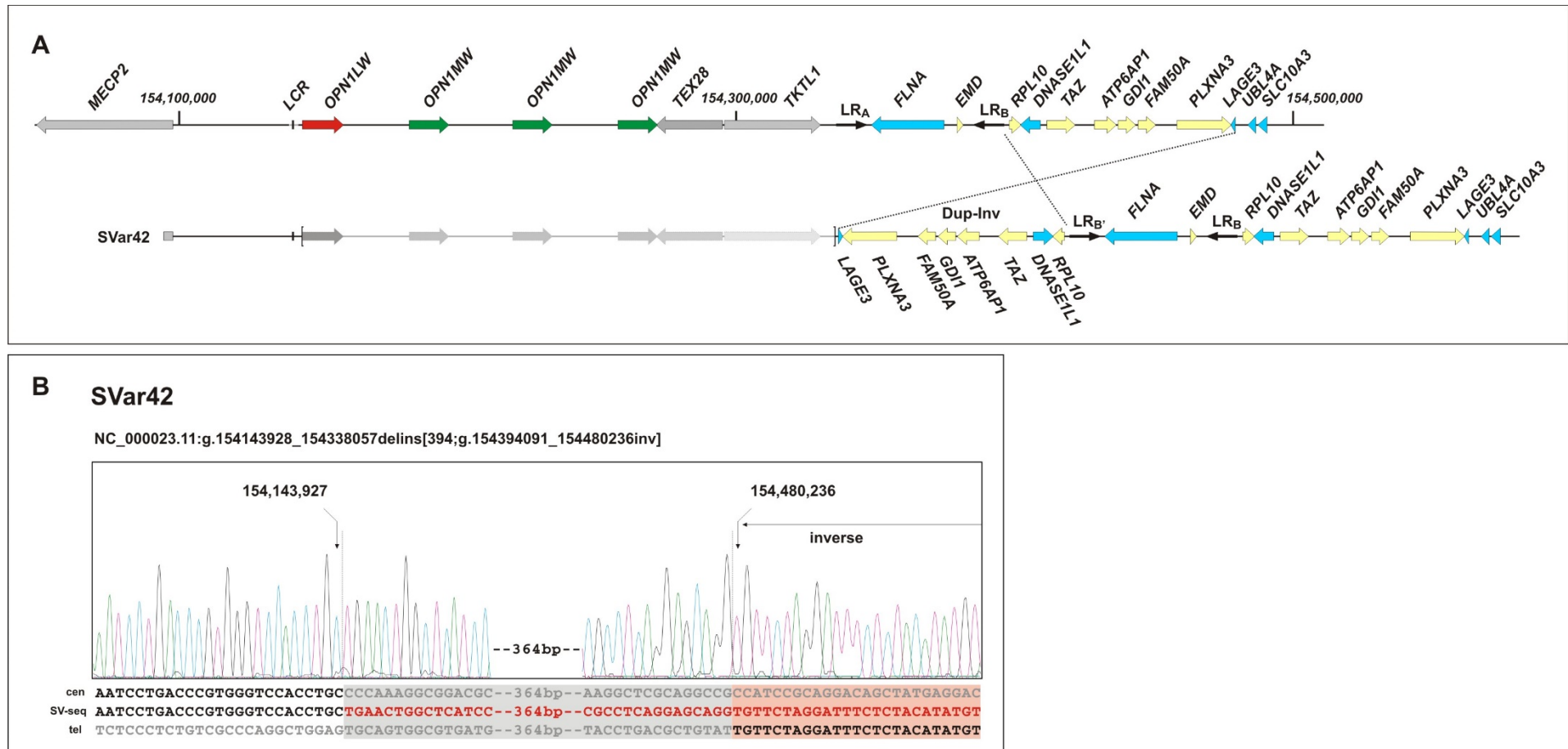


Fig. S2. Complex structure of SVar42. (A) Genomic structure of SVar42 in comparison with the normal chromosomal structure (top). SVar42 constitute a deletion of the entire *OPN1LW/MW* gene cluster downstream of the intact LCR. The deletion further includes the downstream *TEX28* and *TKTL1* genes and is combined with an interstitial inverted duplication of about 80 kb including eight annotated genes from *RPL10* to *LAGE3* (Dup-Inv). Deleted sequences are depicted in light shading and stippled lines flanked by brackets. The inverted and duplicated segment is inserted upstream of *FLNA* and *EMD* and their flanking low copy inverted repeats (LR_A and LR_B , black horizontal arrows). The telomeric repeat LR_A is thereby converted into a LR_B -like repeat copy (LR_B'). (B) Sanger sequence electropherogram of the centromeric deletion breakpoint adjunct to the 394bp insertion (derived from multiple small remnant sequences, light grey box) and the terminus of the inverted duplication (rose box).

Fig. S3. (below). Insertions at breakpoints are short remnants of *OPN1LW*/*MW* gene cluster sequences suggestive for a replication-based mechanism of SV formation. Results on the origin of breakpoint inserted sequences for SVar3, SVar24, SVar28, SVar36, and SVar42. For each SV the inserted sequence is provided with parts showing perfect or near perfect match with sequences of the *OPN1LW*/*MW* gene cluster and flanking sequences highlighted with colored boxes. The location (e.g. upstream *OPN1LW*), orientation on the sense (+) or complementary strand (-), and physical coordinates of the matching genomic sequences are provided. The 'Sbjct' sequence for the alignment is always NC_000023.11.

SVar3

NC_000023.11: g.154139421_154142962delins19

Inserted Sequence:

CCTGGAGGTGCACATGCAG

Upstream *OPN1LW*(-)

```
Query 1          GGTGCACATGCAG 13
                |||||
Sbjct 154143629 GGTGCACATGCAG 154143617
```

SVar24

NC_000023.11:g.154136800_154180989delins51

Inserted Sequence:

TGCTAAGGCAGACCAGAAGGCGCCCACTGCGCCTGTTGACAGGTGGGCGCC

Upstream *OPN1LW*(+)

```
Query 1          TGCTAAGGCAGACCAGAAGGCGCCCACT 27
                |||||
Sbjct 154136924 TGCTAAGGCAGAC.AGAAGGCGCCCACT 154136949
```

SVar28

NC_000023.11:g.154139374_154206273delins139

Inserted Sequence:

TGGGAAACAAGAAATCACAATACGGTGCTCTGTGAGCCGCAAAGTGTGGGAGAATTGGACGTGCATCTCTCC
CAATTGGCCACTGTTCCGGTTTCTGCACTGGGCGTGTGTGTCAGGGGAGCCACAGTGAGGAGGCAGG

Fig. S3. (continued)

Intergenic(+)

```
Query 1 TGGGAAACAAGAAATCACAATACGGTGCCTGTGAGCCGCAAAGTGTGGG 50
|||||
Sbjct 154176356 TGGGAAACAAGAAATCACAATACGGTGCCTGTGAGCCGCAAAGTGTGGG 154176405
Sbjct 154213494 TGGGAAACAAGAAATCACAATACGGTGCCTGTGAGCCGCAAAGTGTGGG 154213543
Sbjct 154251296 TGGGAAACAAGAAATCACAATACGGTGCCTGTGAGCCGCAAAGTGTGGG 154251345
Sbjct 154288414 TGGGAAACAAGAAATCACAATACGGTGCCTGTGAGCCGCAAAGTGTGGG 154288463
```

```
Query 51 AGAATTGGAC 60
|||||
Sbjct 154176406 AGAATTGGAC 154176415
Sbjct 154213544 AGAATTGGAC 154213553
Sbjct 154251346 AGAATTGGAC 154251355
Sbjct 154288464 AGAATTGGAC 154288473
```

Intergenic(-)

```
Query 69 TCTCCCA--ATTGGCCACTGTTCCGGTTTCTGTCACT 103
|||||
Sbjct 154168994 TCTCCATAATTGGCCACTGTTCCGGTTTCTGTCACT 154168958
Sbjct 154206122 TCTCCATAATTGGCCACTGTTCCGGTTTCTGTCACT 154206086
Sbjct 154243931 TCTCCATAATTGGCCACTGTTCCGGTTTCTGTCACT 154243895
Sbjct 154281052 TCTCCATAATTGGCCACTGTTCCGGTTTCTGTCACT 154281016
```

Intergenic(-)

```
Query 108 GTGTGTCAGGGGAGCCACAGTGAGGAGGCAG 138
|||||
Sbjct 154173338 GTGTGTCAGGGGAGCCACAGTGAGGAGGCAG 154173308
Sbjct 154210476 GTGTGTCAGGGGAGCCACAGTGAGGAGGCAG 154210446
Sbjct 154248278 GTGTGTCAGGGGAGCCACAGTGAGGAGGCAG 154248248
Sbjct 154285396 GTGTGTCAGGGGAGCCACAGTGAGGAGGCAG 154285366
```

SVar36

NC_000023.11:154120448_154281284delins180

Inserted Sequence:

```
ATATAGCCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTGGGGGGGACATGTACCCCA
TAGCAGTATGCTTAACTTTTAAGAAAGAGGAAGGCCGGCGCGGTGGCTCACCCCTGTAATCCCAGCACTTT
GGGAGGCTGAGGCAGGCCGATCACCTGAGGTGCG
```

Intergenic(-)

```
Query 7 CCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTG 56
|||||
Sbjct 154168440 CCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTG 154168391
Sbjct 154205568 CCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTG 154205519
Sbjct 154243377 CCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTG 154243328
Sbjct 154280498 CCCACCCCTTAACACCATCACATGGCCATTAAATTTCAACACGAGTTTTG 154280449
```

Fig. S3. (continued)

```

Query 57          GGGGGGACATGTACCCCATAGCAGTATGCTTAACTTTTTAAGAAAGAGGA 106
                  |||
Sbjct 154168390  GGGGGGACATGTACCCCATAGCAGTATGCTTAACTTTTTAAGAAAGAGGA 154168341
Sbjct 154205518  GGGGGGACATGTACCCCATAGCAGTATGCTTAACTTTTTAAGAAAGAGGA 154205469
Sbjct 154243327  GGGGGGACATGTACACCATAGCAGTATGCTTAACTTTTTAAGAAAGAGGA 154243278
Sbjct 154280448  GGGGGGACATGTACCCCATAGCAGTATGCTTAACTTTTTAAGAAAGAGGA 154280399

Query 107         AGGCCGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCTG 156
                  |||
Sbjct 154168340  AGGCCGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCTG 154168291
Sbjct 154205468  AGGCCGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCTG 154205419
Sbjct 154243277  AGGCCGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCTG 154243228
Sbjct 154280398  AGGCCGGGCGCGGTGGCTCACCCCTGTAATCCAGCACTTTGGGAGGCTG 154280349

Query 157         AGGCAGGCGGATCACCTGAGGTCG 180
                  |||
Sbjct 154168290  AGGCAGGCGGATCACCTGAGGTCG 154168267
Sbjct 154205418  AGGCAGGCGGATCACCTGAGGTCG 154205395
Sbjct 154243227  AGGCAGGCGGATCACCTGAGGTCG 154243204
Sbjct 154280348  AGGCAGGCGGATCACCTGAGGTCG 154280325

```

SVar42

NC_000023.11:g.154143928_154338057delins[394;g.154394091_154480236inv]

Inserted Sequence:

```

TGAACTGGCTCATCCACCAGAACGCCAAAAATTAAAAAGCCTGCCCAAAGGCGGACGCAGGACAGTA
GAAGGGAACAGAGAACACATAAACACAGCCATAGACCTGGCCCTGGGCCCCGACTGGCTTACCACACA
GGCAGCCCCCTCCCTTGGGTGTTGGGAACCAAACCTCAGACGCCCCACCCATCCCCGCCAGTGGCTTGAT
CTCAGGAGCAGCTGGGCCAGTCGCTAAAAGTATGCAGCTGGATCCTGGCAGAGACCGTCATTCACCC
TGCAAGCCCCTCCGGCCTGGGCAGCAGAGCAAGACACCACCAGGACACACATAGGGTGGCCACGACCG
AAGTAGCCAGCAAATCCCTCTGAGCCGCCCTTGCGGGCTCGCCTCAGGAGCAGG

```

Intergenic(+)

```

Query 9          CTCATCCACCAGAACGCCAAAAATTAAAAAGCCT 42
                  |||
Sbjct 154181862  CTCATCCACCAGAACGCCAAAAATTAAAAAGCCT 154181895
Sbjct 154219001  CTCATCCACCAGAACGCCAAAAATTAAAAAGCCT 154219034
Sbjct 154256805  CTCATCCACCAGAACGCCAAAAATTAAAAAGCCT 154256838
Sbjct 154293923  CTCATCCACCAGAACGCCAAAAATTAAAAAGCCT 154293956

```

Upstream *OPN1LW*(+)

```

Query 40         CCTGCCCAAAGGCGGACGCAGGACAGTAGAAGGGAACAGAGAACACATA 89
                  |||
Sbjct 154143923  CCTGCCCAAAGGCGGACGCAGGACAGTAGAAGGGAACAGAGAACACATA 154143972

Query 90         AACACAG 96
                  |||
Sbjct 154143973  AACACAG 154143979

```

Fig. S3. (continued)

***OPN1LW/MW* exon 2 & intron 2(-)**

```
Query 109 GCCTGGGCCCGACTGGCTTACCACACAGG 138
          |||
Sbjct 154150974 GCCTGGGCCCGACTGGCTTACCACACAGG 154150945
Sbjct 154188088 GCCTGGGCCCGACTGGCTTACCACACAGG 154188059
Sbjct 154225226 GCCTGGGCCCGACTGGCTTACCACACAGG 154225197
Sbjct 154263030 GCCTGGGCCCGACTGGCTTACCACACAGG 154263001
```

Upstream *OPN1LW*(-)

```
Query 158 TGGGAACCAAACCTCAGACGCCCCACCCATCCCCGCCAG 195
          |||
Sbjct 154144061 TGGGAACCAAACCTCAGACGCCCCACCCATCCCCGCCAG 154144018
```

***OPN1MW* intron 2(+)**

```
Query 263 TCATTACCCCTGCAAGCCCTCCGGCC 289
          |||
Sbjct 154188103 TCATTACCCCTGCAAGCCCTCCGGCC 154188129
Sbjct 154225241 TCATTACCCCTGCAAGCCCTCCGGCC 154225267
Sbjct 154263045 TCATTACCCCTGCAAGCCCTCCGGCC 154263071
```

Intergenic(+)

```
Query 287 GCCTGGGCAGCAGAGCAAGACACCACC 313
          |||
Sbjct 154165572 GCCTGGGCAGCAGAGCAAGACACCACC 154165598
Sbjct 154202686 GCCTGGGCAGCAGAGCAAGACACCACC 154202712
Sbjct 154240544 GCCTGGGCAGCAGAGCAAGACACCACC 154240570
Sbjct 154277630 GCCTGGGCAGCAGAGCAAGACACCACC 154277656
```

***OPN1LW* exon 2(-)**

```
Query 312 CCAGGACACACATAGGGTGGCCAGCACGAAGTAGCCAG 350
          |||
Sbjct 154150934 CCAGGACACACATAGGGTGGCCAGCACGAAGTAGCCAG 154150890
```

Upstream *OPN1LW*(+)

```
Query 347 CCAGCAAATCCCTCTGAGCCGCCCTTGCGGGCTCGCCTCAGGAGCAGG 394
          |||
Sbjct 154144053 CCAGCAAATCCCTCTGAGCCGCCCTTGCGGGCTCGCCTCAGGAGCAGG 154144100
```


A

```
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repeatMasking=none
```

```
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AGCTTTTGTCTGATTCCACTGTCTGTAAGAGTTAAAATTAATAAATAA  
ACACTTGGCTGGACCACACACTGAATTAATGATTTTAACACAAAATGAT  
ACTGAAGAGAATGTGAATGCACTAATGCCACCGAACTGTGTGTAATAA  
AACGGTTAAGATGGTAAGTTGTATGTTATGGGTATTTTACCACTATTAAA  
AAAAAGTTTTTAAGAAA || AAAGGCTAATAAGATTTCTGGGTTCAGGCAGGA SVar22  
GTAGGAAGGCAGCGAAAACCCGAATTCCCCCACTTCTCCTAAAAGAAGTC  
CAAACACAGGAAGAATGAATGAGCCCCCTCCTTGATATACTGGAGGAAA  
CCAGAACCTGTGCCATCAGAAAGCGCTAGGATGTGACAAAGCAGGGAGGG  
GACTACAAAGGGCCCCAGCGGTCCCGACCAGGATCCACCCTTTCAGGACA  
TGGCCCAGGCCCGCTCAGGATC || GCATGGGGGCAGATGCGAGCCCCAGGAG SVar23  
AACTCCCG || AGGACCCGCGGGCGCCGCGGGGGCTTCTGACGCGGAGCG SVar24  
GCGAGGCGGCGCCAGAAGAGGGCGCCCGGAGCCGAACAGGAGGCCAAAC  
CCCGGGCTTCCCGCGTTCCCGGGGTCCCCGTGCTAAGGCAGACAGAAG  
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GAAGGC || ACTGAGACAAA SVar39
```

B

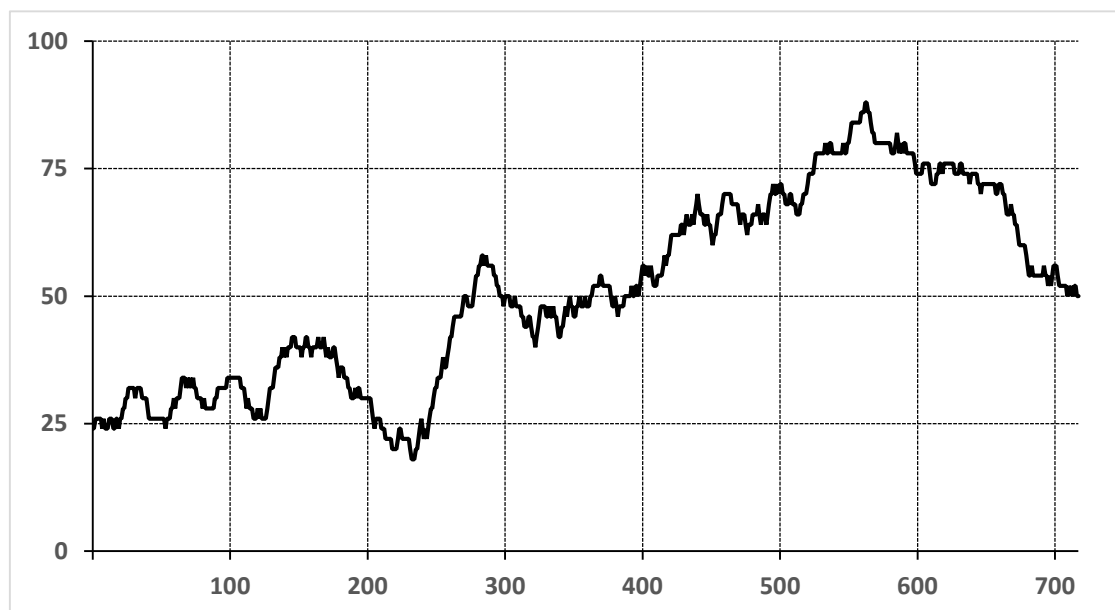


Fig. S5. GC content at the 5' breakpoint cluster at chrX:154136242_154137008.

(A) Six centromeric breakpoints (indicated by vertical yellow lines) cluster within a 750 bp region 7.2-8 kb upstream of *OPN1LW* which shows a steep increase in GC content from below 25% to higher than 75% (B). GC content (Y-axis) calculated by a sliding window of 50bp size.

< Marker	< Phys. Position (Mb)	BCM 63	BCM 127	BCM 152	BCM 157	BCM 158	BCM 162	BCM 227	BCM 264	BCM 232	BCM 128	BCM 150	BCM 141	BCM 2	BCM 18	BCM 118	BCM 124	BCM 165	BCM 213	BCM 243	BCM 294	BCM 222	BCM 156
		#15108	#20621	#22676	#22586	#22961	#23330	#27018	#28186	#27291	#20624	#22574	#21876	#6679	#9325	#20544	#20580	#23548	#26379	#27935	#29729	#26657	#22859
DXS 8011	150.69	8	8	8	8	8	8	8	7	4	8	8	5	3	1	1	1	1	1	1	1	2	7
DXS 8103	150.94	2	2	2	2	2	2	2	2	3	4	4	1	3	2	2	2	2	2	n.d.	2	2	2
DXS 1356	153.43	2	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2
DXS 8087	153.62	1	1	1	1	1	1	1	1	4	1	1	1	1	1	1	1	1	1	1	1	1	1
DXLD 15535	154.04	2	2	2	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2
DXLD 36169	154.13	3	n.d.	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	n.d.	3	3	3
L441 TA	154.51	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	n.d.	2	2	2
L441 CA	154.52	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	n.d.	1	1	1
AF277A	154.55	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	n.d.	2	2	2
AF277B	154.60	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
DXS 1073	154.60	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2



Fig. S6. (previous page). SVar26 is a founder mutation in BCM families from the United States. Eleven microsatellite markers (left column, encompassing a region of about 3.9 Mb on Xq28) were genotyped in the index patients of 22 families sharing the SVar26 deletion. Alleles (coded in numbers) of identical size are depicted as blue squares and deviant haplotype segments shown in different colors. The localization of the *OPN1LW/OPN1MW* gene cluster is indicated by the red arrow on the right. The index patients from all 22 families share a common haplotype in the vicinity of the *OPN1LW/OPN1MW* gene cluster (from DXLD36169 to DXS1073, encompassing a region of 0.47 Mb) with several recombinations telomeric to the gene cluster. n.d. – not determined

< Marker	< Phys. Position (Mb)	BCM 138	BCM 146	BCM 153
		#21475	#22040	#22677
DXS 8011	150.69	1	8	1
DXS 8103	150.94	3	2	2
DXS 1356	153.43	3	3	3
DXS 8087	153.62	2	2	2
DXLD 15535	154.04	4	4	4
DXLD 36169	154.13	1	1	1
L441 TA	154.51	2	2	2
L441 CA	154.52	1	1	1
AF277A	154.55	1	1	1
AF277B	154.60	2	2	2
DXS 1073	154.60	2	2	2



< Marker	< Phys. Position (Mb)	BCM 197	BCM 198	BCM 245
		#24863	#24872	#28091
DXS 8011	150.69	6	6	6
DXS 8103	150.94	2	2	2
DXS 1356	153.43	2	3	2
DXS 8087	153.62	1	1	1
DXLD 15535	154.04	3	3	3
DXLD 36169	154.13	1	1	1
L441 TA	154.51	1	1	1
L441 CA	154.52	1	1	1
AF277A	154.55	2	2	2
AF277B	154.60	2	2	2
DXS 1073	154.60	2	2	2



Fig. S7. SVar19 and SVar28 are founder mutations in BCM families from the US and France, respectively. Eleven microsatellite markers (left column, encompassing a region of about 3.9 Mb on Xq28) were genotyped in the index patients of three families sharing the SVar19 (left) and three families sharing SVar28 (right). Alleles (coded in numbers) of identical size are depicted as colored squares and deviant alleles are depicted as white squares. The localization of the *OPN1LW/OPN1MW* gene cluster is indicated by the red arrow on the right.

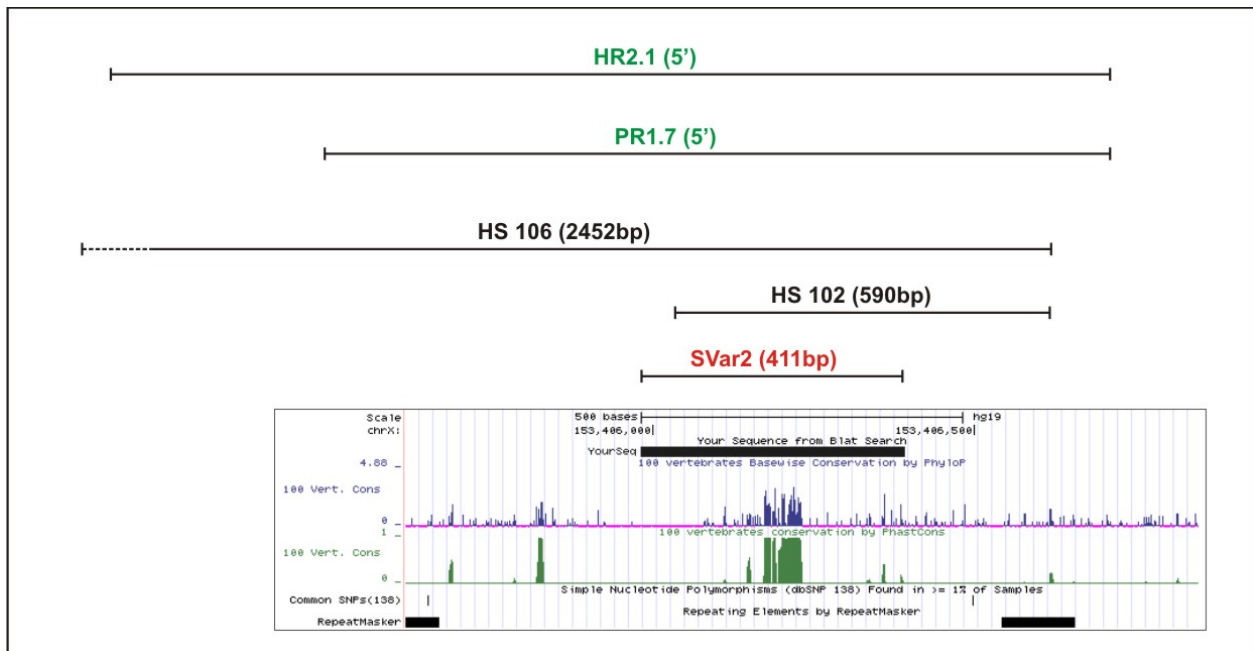


Fig. S8. Genetic refinement of the Locus Control Region. SVar2 with a deletion of 411 bp at the locus control region (LCR) is to date the smallest deletion abrogating expression of the *OPN1LW* and *OPN1MW* genes – as concluded from the BCM phenotype of the patient. SVar2 overlaps with the HS102 deletion (Nathans et al. 1989) by only 358 bp thus refining the sequence most likely crucial for enhancer activity. This coincides with the peak of sequence conservation during vertebrate evolution (UCSC genome browser snapshot depicted in the box). This refinement may actually enable shortening of enhancer/promoter sequences for cone photoreceptor transgene expression in gene therapy trials. The extent of currently used enhancer sequences in the HR2.1 and HR1.7 artificial promoters is shown above.

Table S1. Cytoscan HD probe CGH-array based CNV calls on the X chromosome for proband BCM99/#8066 carrying SVar42

<i>Aberration type</i>	<i>Copy Number State</i>	<i>Chr</i>	<i>Cytoband(s)</i>	<i>Marker boundaries</i>	<i>Size (kbp)</i>	<i>Marker Count</i>	<i>Genes in aberration</i>	<i>OMIM Genes</i>
Loss	0	chrX	q28	154,143,428-154,332,392	189	148	Count:6 Genes List:OPN1LW,OPN1MW2,OPN1MW,OPN1MW3,TEX28,TKTL1	Count:4 OMIM Genes List:OPN1LW (300822), OPN1MW (300821), TEX28 (300092), TKTL1 (300044)
Gain	2	chrX	q28	154,395,688-154,483,524	88	172	Count:11 Genes List:RPL10,SNORA70,DNAS E1L1,TAZ,CH17-340M24.3,ATP6AP1,GDI1,FAM50A,MIR6858,PLXNA3...	Count:8 OMIM Genes List:RPL10 (312173), DNASE1L1 (300081), TAZ (300394), ATP6AP1 (300197), GDI1 (300104), FAM50A (300453), PLXNA3 (300022), LAGE3 (300060)

Table S2. PCR primers for diagnostic PCRs

Variant	Forward Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	Size (bp)
SVar1	TCCAACCCCCGACTCAACTATC	ACGGTATTTTGATGTGGATCTGCT	173
SVar2	ACGTGCCACATTCACACTCTGT	TGTCCCTGTTCTGTGGATGAGA	1382
SVar3	AGGATGTCAATGGCTGTGAGG	TGTTCTCAGAGCCACGATTCTC	988
SVar4	AAATCTCGCCAGGCACCTTG	CCGTGGCTACCCTTTAATGTCT	865
SVar5	AGATAATAGGGCAATGCTTTCCA	CCTCTGGTGCATCACAACTG	286
SVar6	TATGATCCGCAAGGAGCCGT	CAGAGCTGGAAGAAGCCAAGAG	957
SVar7	ATAATGTATGATATGGAGCATCGT	CATGAACGACTTGCTTGCTTC	867
SVar8	TCTTCTTTGGGGAGGTTTCTCT	CAGAGTGAGCTCATCCATCCTG	728
SVar9	CTGCTGCTTGCTTTCTTTGAT	TCCCGCCAGTAATGATTGAG	604
SVar10	TCGACCCAGAATTAACCTCTCT	AGGAGTCTCAGTGGACTCAT	1160
SVar11	TTATAGGTGCACGCCACCAG	<i>(same as SVar7 reverse)</i>	1063
SVar12	ACATGGCAAACCTGGGTCTCT	TCACTTAGTGGCTGGAGGAT	340
SVar13	ATCACTGAAAGAGGCCGTGA	TGAATTCTTACATTTGTCAGTGGTG	815
SVar14	GAGGATCAGTCAAGCCCAAGA	CCTGGAAGGACTGTGACTGCTT	659
SVar15	<i>(same as SVar14 forward)</i>	AGGTTGATGAGCTCAGGGATT	791
SVar16	AAAAGTGACAATGGGAACACTG	<i>(same as SVar15 reverse)</i>	493
SVar17	CCAAGGCAGGAGTATCATTG	GACCACTACCCACCTCTGTCA	921
SVar18	AACATGGGAATGGATGGA	<i>(same as SVar6 reverse)</i>	295
SVar19	TCTGTGCAGGCTGGATAGTG	GAAGCCTCCAGAACCCTTCAGT	488
SVar20	<i>(same as SVar19 forward)</i>	TGCCAAAAGGGGAACCTTCATAG	1292
SVar21	<i>(same as SVar19 forward)</i>	GTGAATGAGTGGTTCCGCC	1258
SVar22	ACTTGGCTGGACCACACT	CCTTCTAAGCCCCAGTTACA	331
SVar23	CTAGCAATGAAAGACAGTTAAAGGGAATCAT	<i>(same as SVar7 reverse)</i>	773
SVar24	GAGTACAGGTATTTGCCACTAAGC	AGGAGTCTCAGTGGACTCAT	539
SVar25	<i>(same as SVar 22 forward)</i>	TACCAGTCCCACCCCTTAACAC	1520
SVar26	GGCTTTGGGGGATATATCTTTTTGAAG	CCTGCAGTCTAAAAGTCATGGT	1494
SVar27	<i>(same as SVar3 forward)</i>	TTCTCTCAGAATGTGGCAGGAC	930
SVar28	<i>(same as SVar3 forward)</i>	ATGGCAGCCAGAGGAACTC	1249
SVar29	ACGTGCCACATTCACACTCTGT	<i>(same as SVar20 reverse)</i>	1353
SVar30	CAAAGGACCTACAGCTCATGG	AAAGGAATTTGGTTGGAGGAG	417
SVar31	GATTGGGTGGCTTTTAAATGAT	TCAGACGAGGCTTGAGATAA	688
SVar32	GTAACCTCTATGTGTGACAGAAG	AGGGAGGGAGGGGTGTTATCT	723
SVar33	ACAAACCCACCCGAGTTAG	CTTCCCTCTCCTACTTTTCCATTC	1332
SVar34	TCACAGCAGGAAAACAGACCTA	CTACTTGCCCTGCTTCCC	2280
SVar35	GCAGATGCCCTAGAGTTTGC	<i>(same as SVar5 reverse)</i>	870
SVar36	CCTAGAGTTTGGTTTGAACGGA	GTTTTGCTCTTGTTGCCAGA	455
SVar37	CTAGAAGAGCCTGTCATCCAG	GGCATTGCCTTGATTTTT	780
SVar38	TCTGTGCAGGCTGGATAGTG	<i>(same as SVar20 reverse)</i>	1292
SVar39	CGCTAGGATGTGACAAAGCAG	<i>(same as SVar25 reverse)</i>	990
SVar40	GGCATAGAGTTGTTTCATAGGATTC	ACTCTTCCAGATCAGGGATTGA	480
SVar41	GCAGCCTGGACAACATAACA	CTCCCCAACCTCCCTAT	1148
SVar42	CTGGGCTTTCAAGAGAACC	GCCTGGTTGATAGAGCCAGACC	588