Supplementary Figures

Fig S1. The age and gender distribution of ACP and PCP group.

Fig S2. The correlation between somatic mutation number and age.

Fig S3. Structure alterations called in each patient.

Fig S4. Kataegis analysis of somatic mutations (SNVs and InDels) in each patient.

Fig S5. The proportion of 96 different extending possible base-pair substitutions of all SNVs identified in ACPs and 10 PCPs.

Fig S6. Schematics for genes listed in Fig. 3a indicating the location of the identified mutations.

Fig S7. IGV graphic report for the alignment of deletion in CTNNB1 CP111 tumor and normal blood sample.

Fig S8. IGV graphic report for the alignment of nonsense mutation of W425X in FBXW7 of CP22 tumor and normal blood sample.

Fig S9. CTNNB1 mRNA stability in CTNNB1-WT/Mut 293T/HCT116 cells.

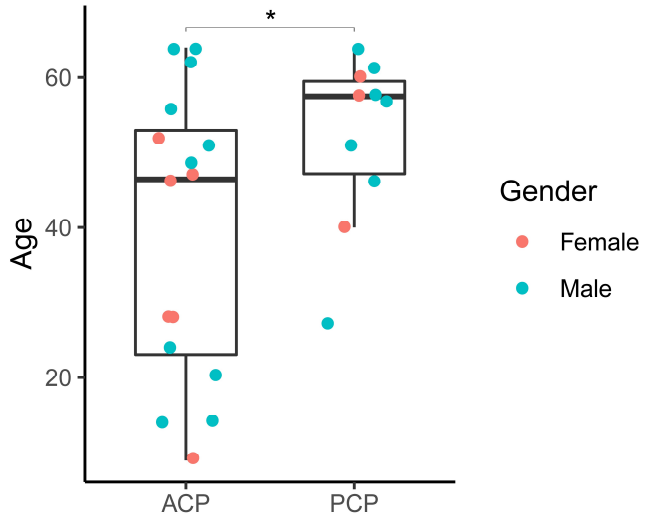


Fig S1. The age and gender distribution of ACP and PCP group.

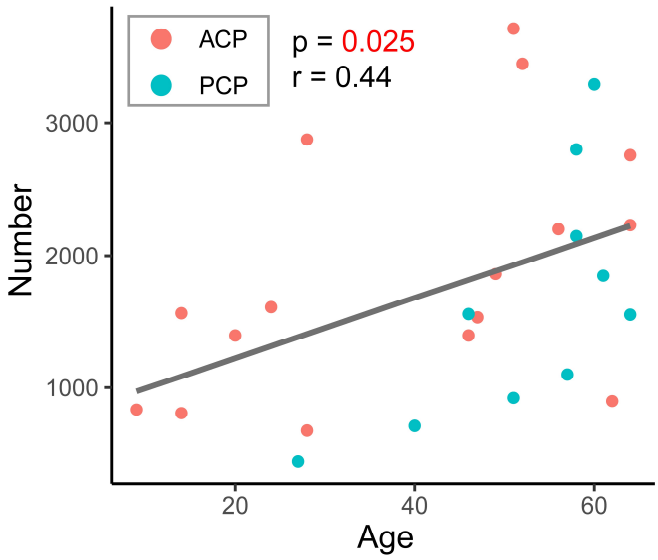
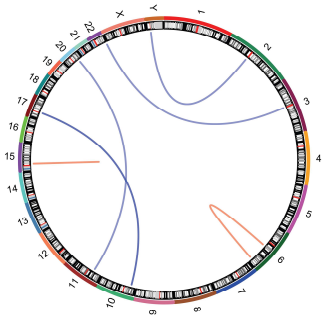


Fig S2. The correlation between somatic mutation number and age.

CP1-2



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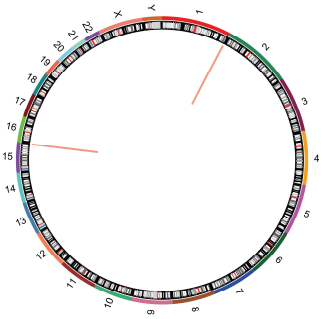

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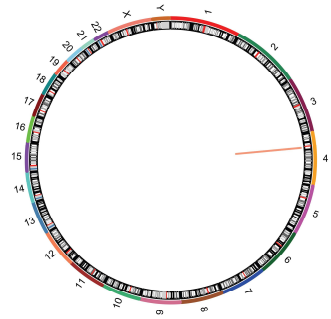

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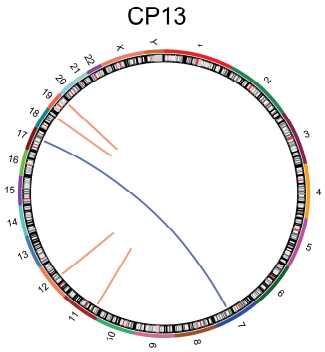

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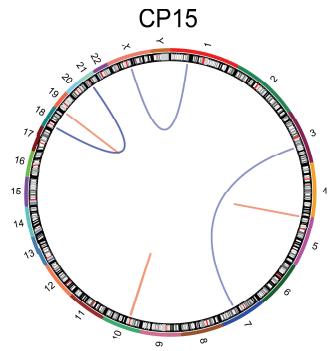

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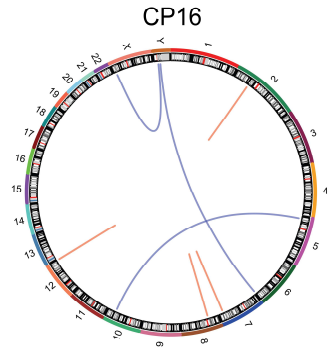

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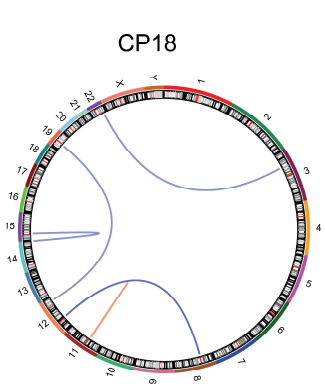

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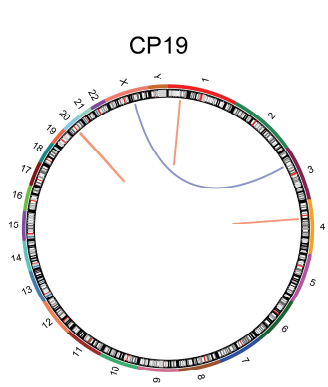

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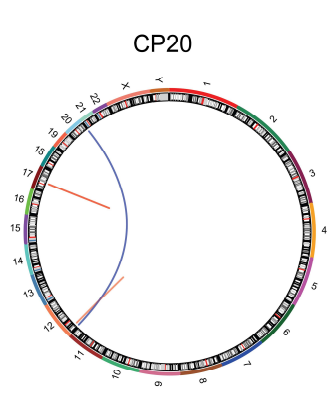

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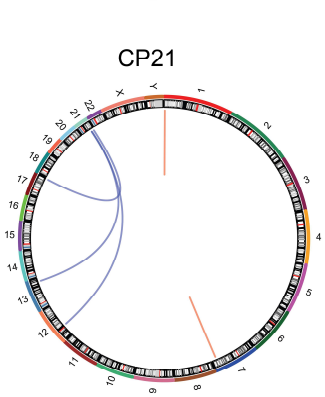

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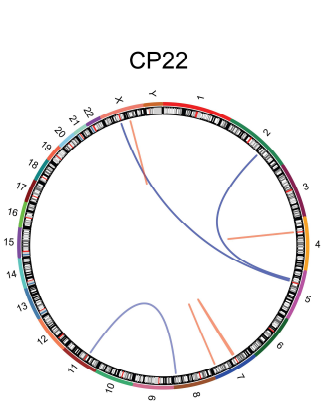

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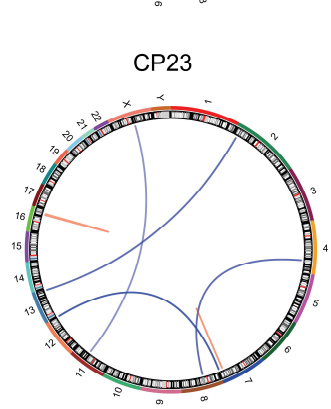

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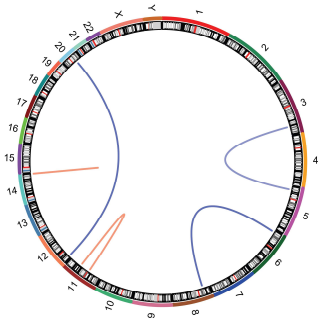

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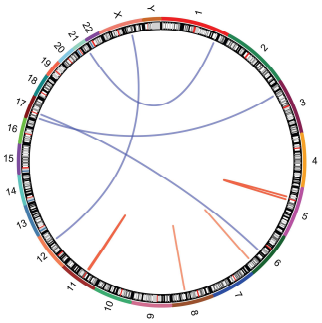

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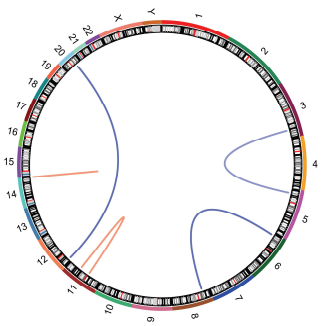

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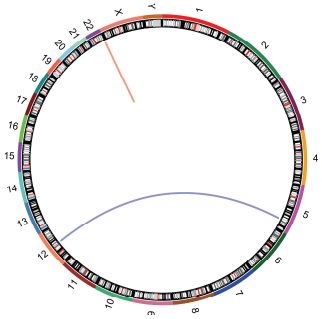

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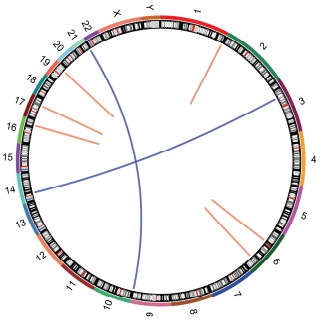

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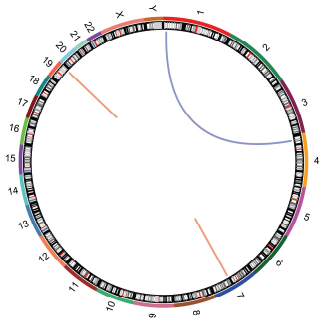

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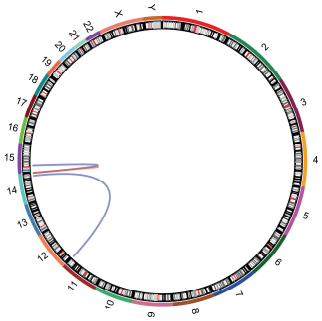

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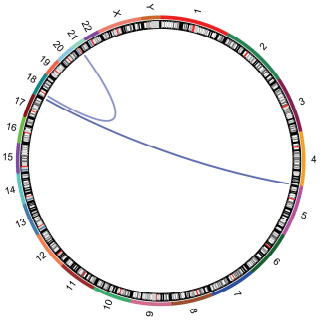

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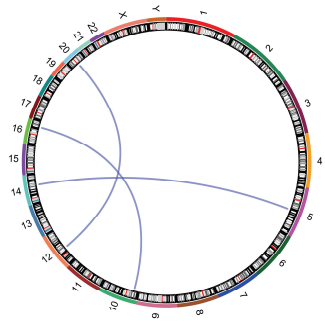

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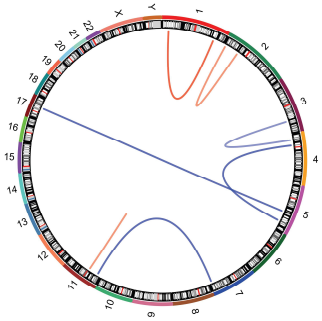

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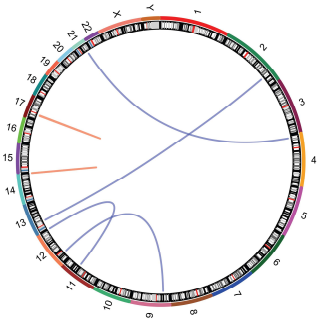

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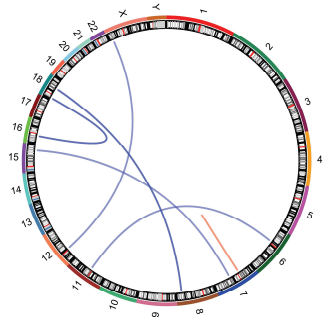


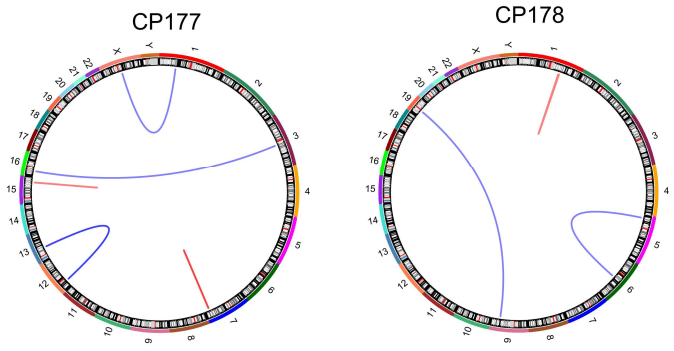
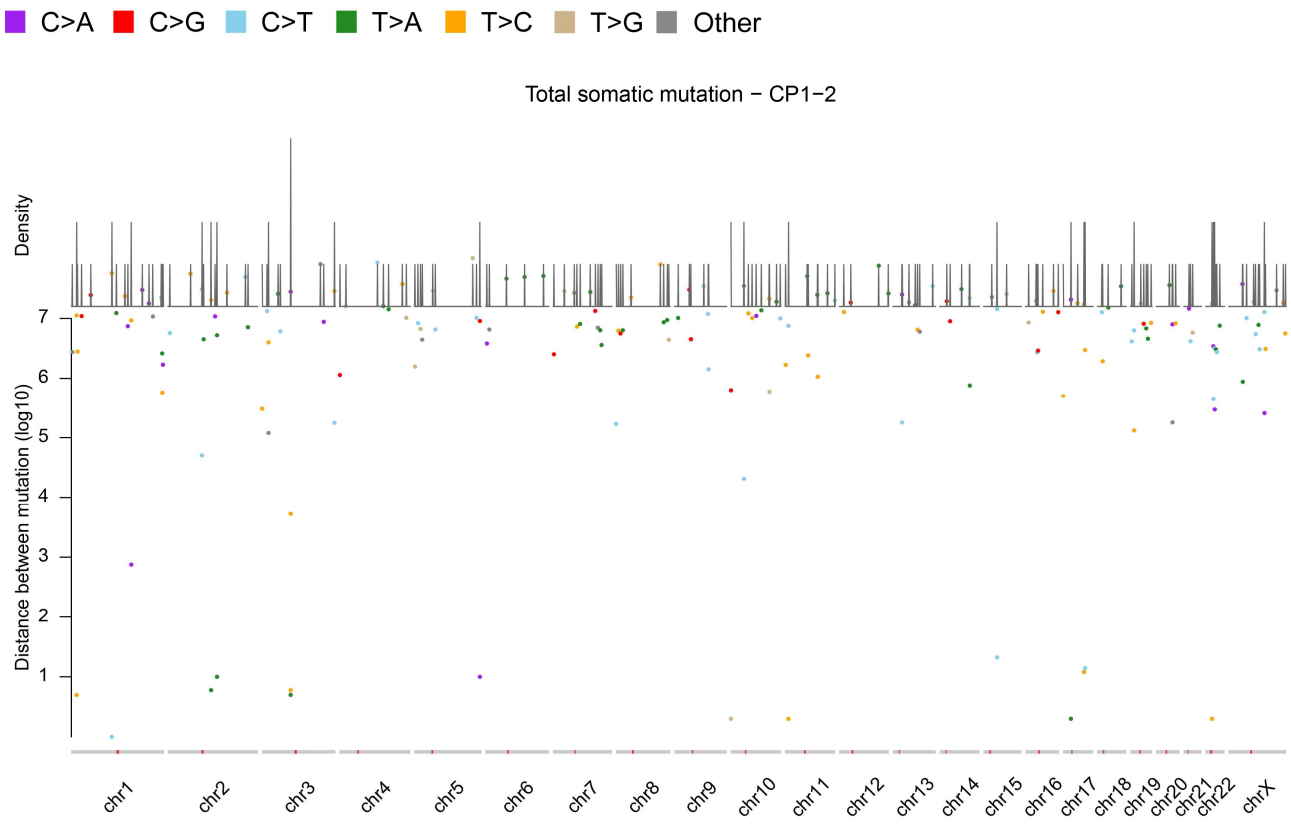
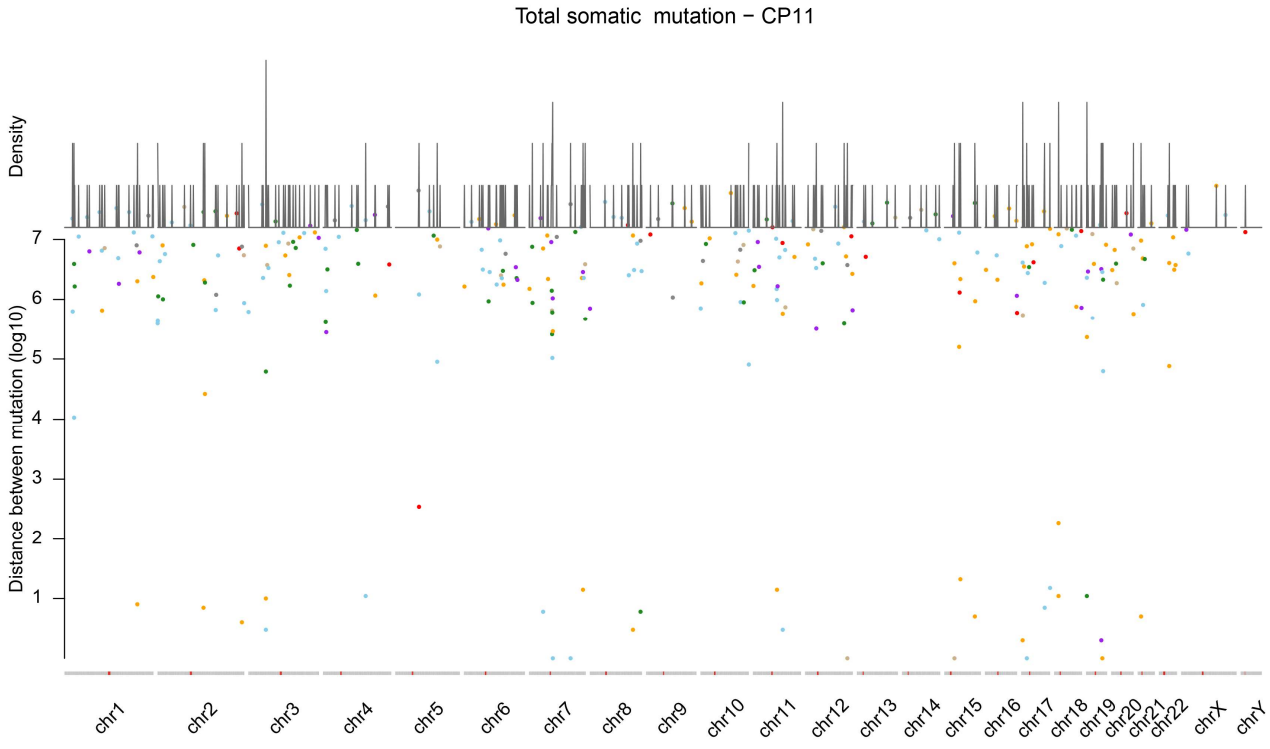


Fig S3. Structure alterations called in each patient.




Total somatic mutation − CP11
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Distance between mutation (log10)
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2
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chr8
chr9
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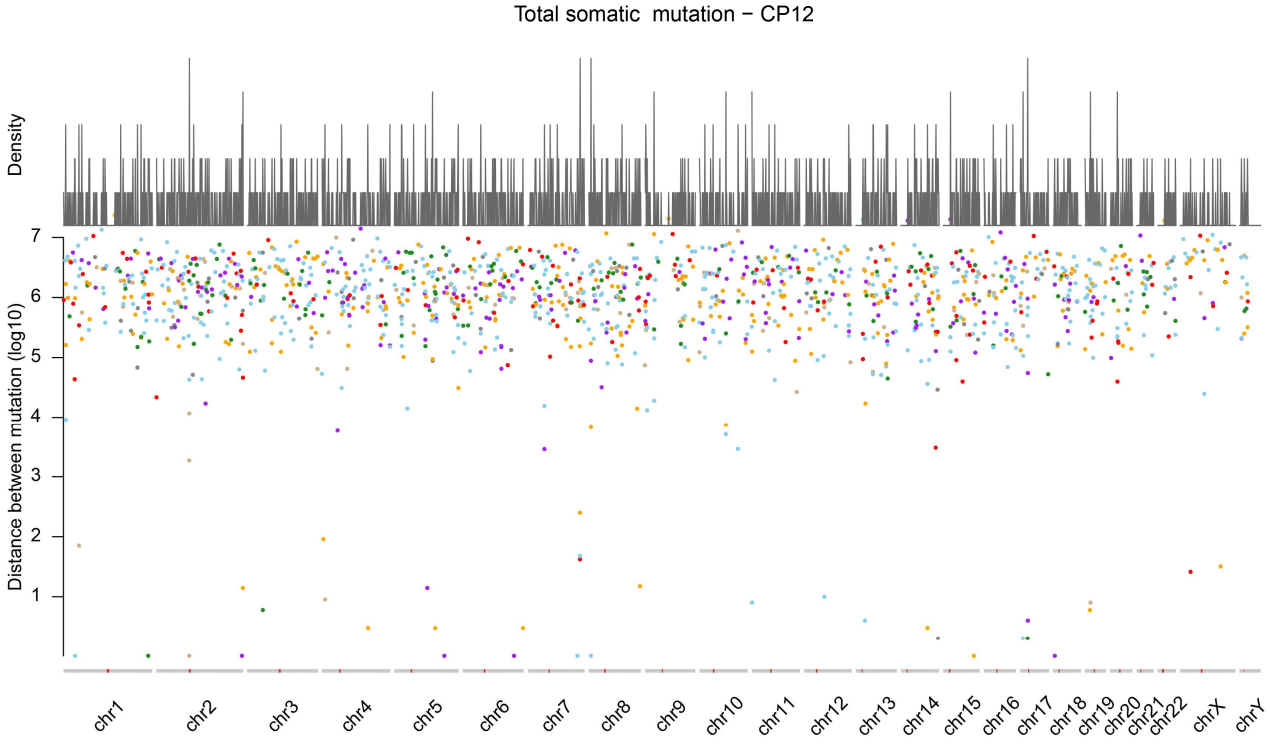
Total somatic mutation − CP12
Density
Distance between mutation (log10)
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chr3
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chr8
chr9
chr10
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chr14
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chr17
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chr19
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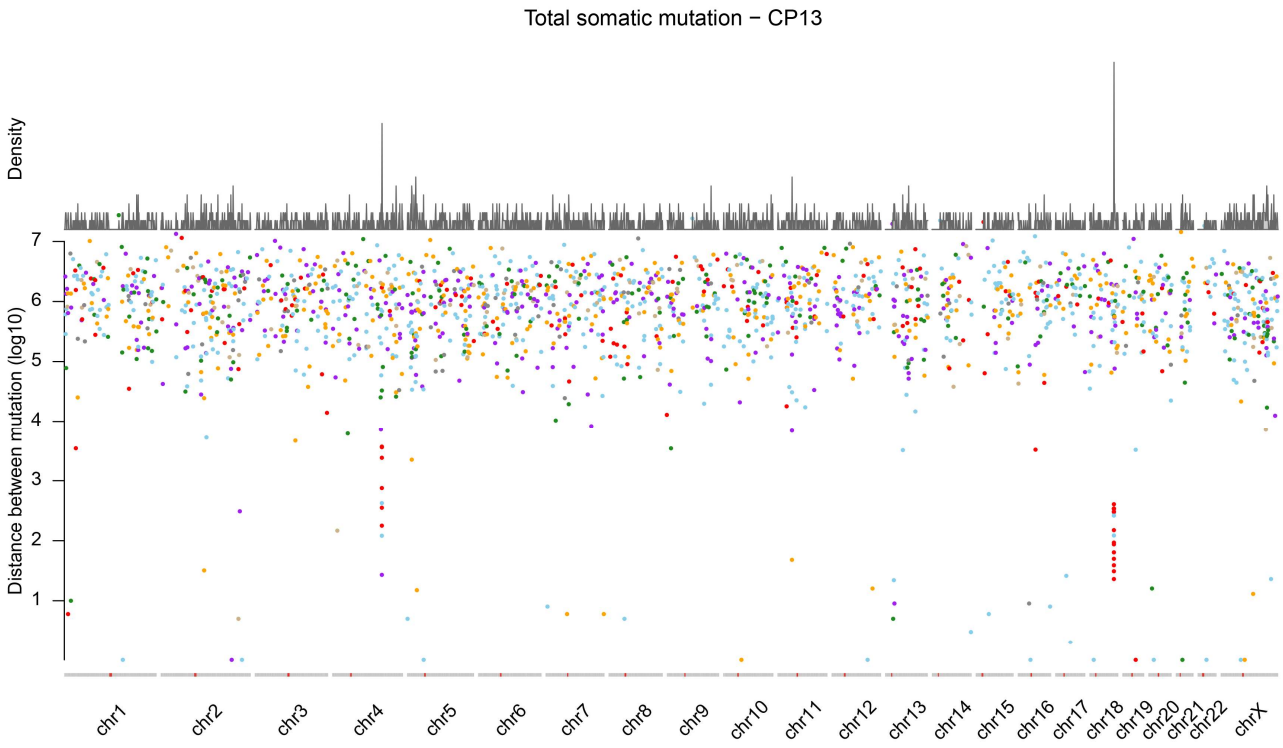
chr21
chr22
chrX
chrY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Density
Distance between mutation (log10)
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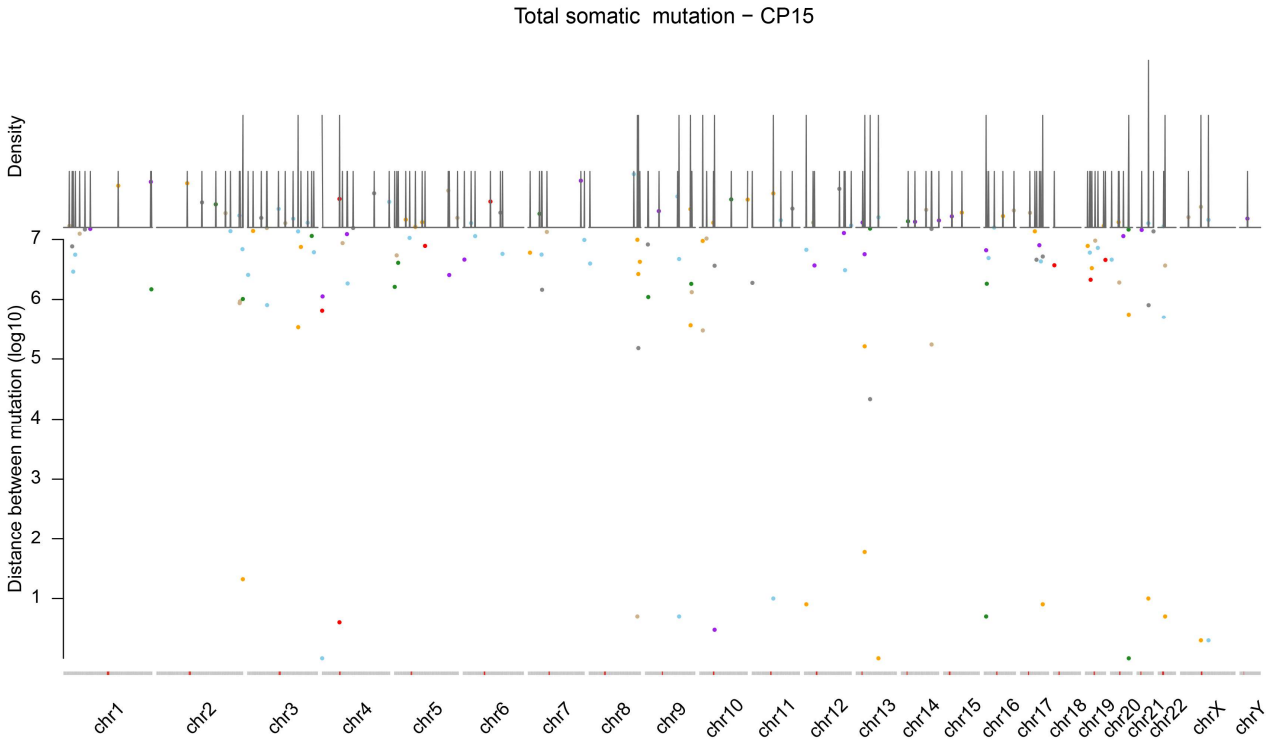
Total somatic mutation − CP15
Density
Distance between mutation (log10)
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chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP16
Density
Distance between mutation (log10)
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6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
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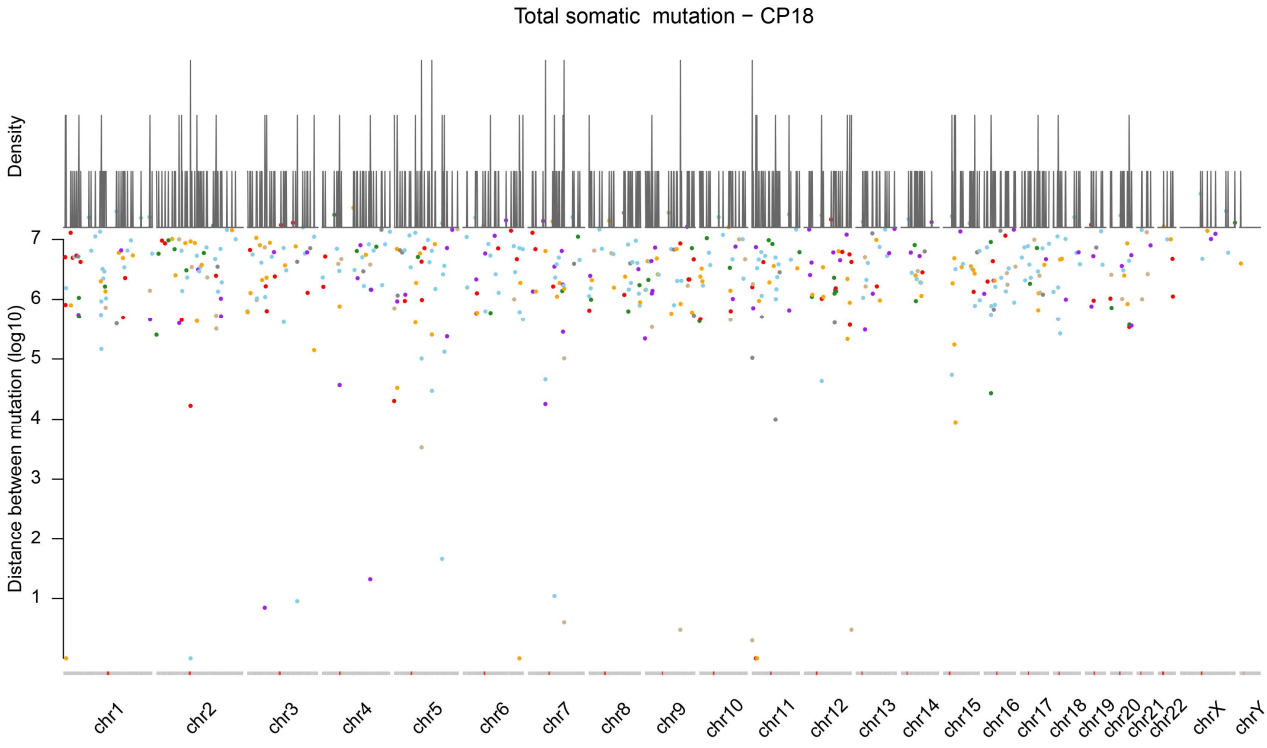
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Distance between mutation (log10)
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chr9
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chr11
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chr14
chr15
chr16
chr17
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chr19
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chr21
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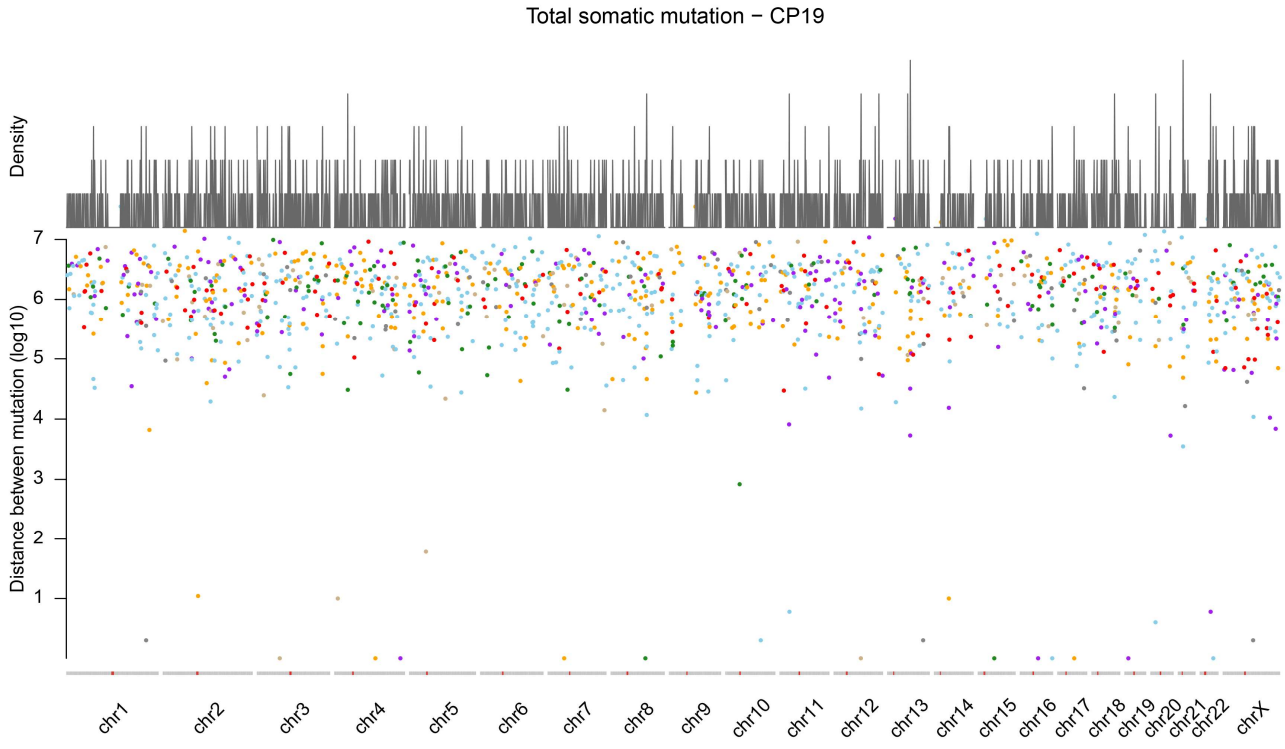
Total somatic mutation − CP19
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Distance between mutation (log10)
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4
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chr1
chr2
chr3
chr4
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chr7
chr8
chr9
chr10
chr11
chr12
chr13
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chr15
chr16
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chr18
chr19
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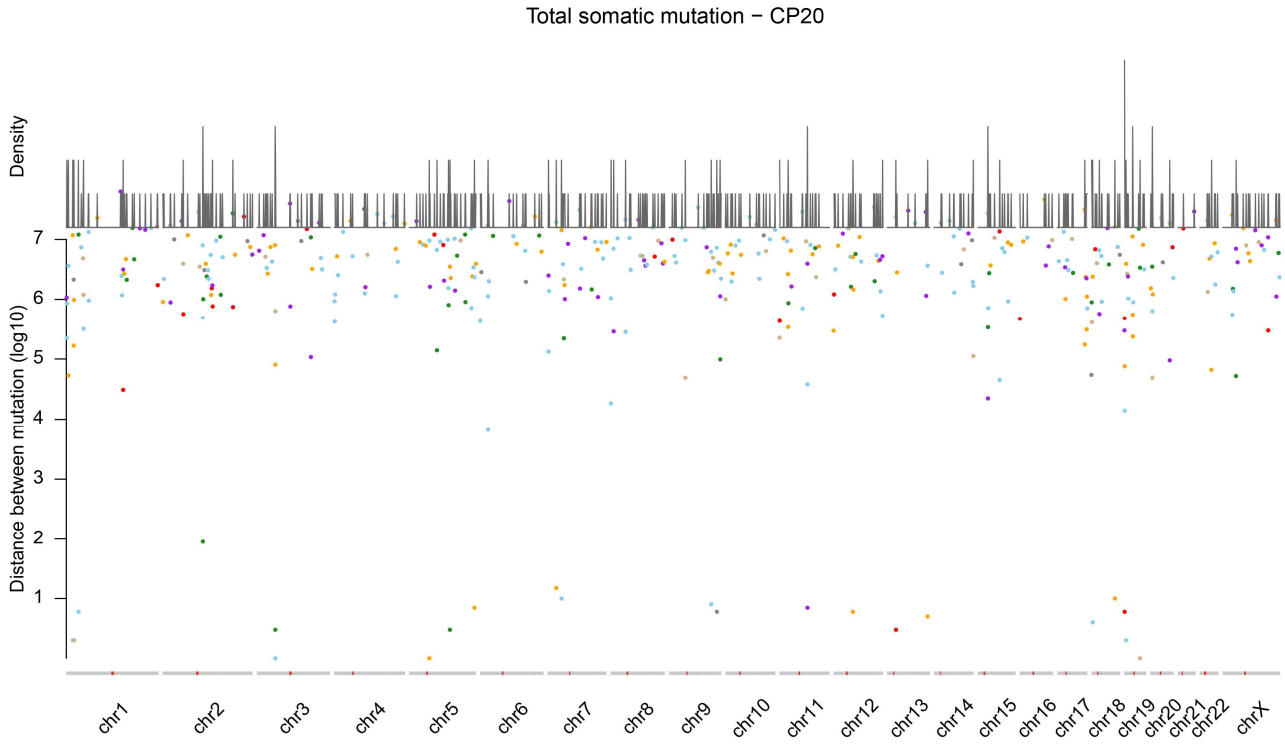
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Distance between mutation (log10)
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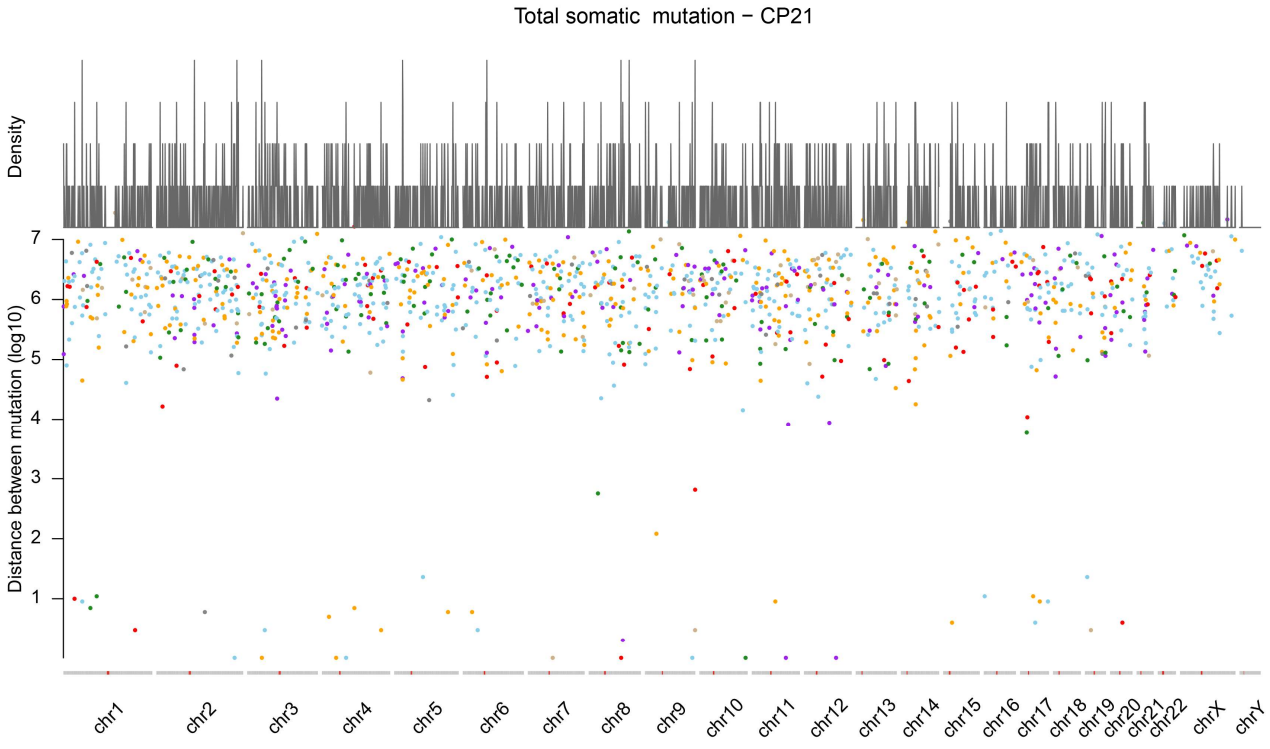
Total somatic mutation − CP21
Density
Distance between mutation (log10)
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chr8
chr9
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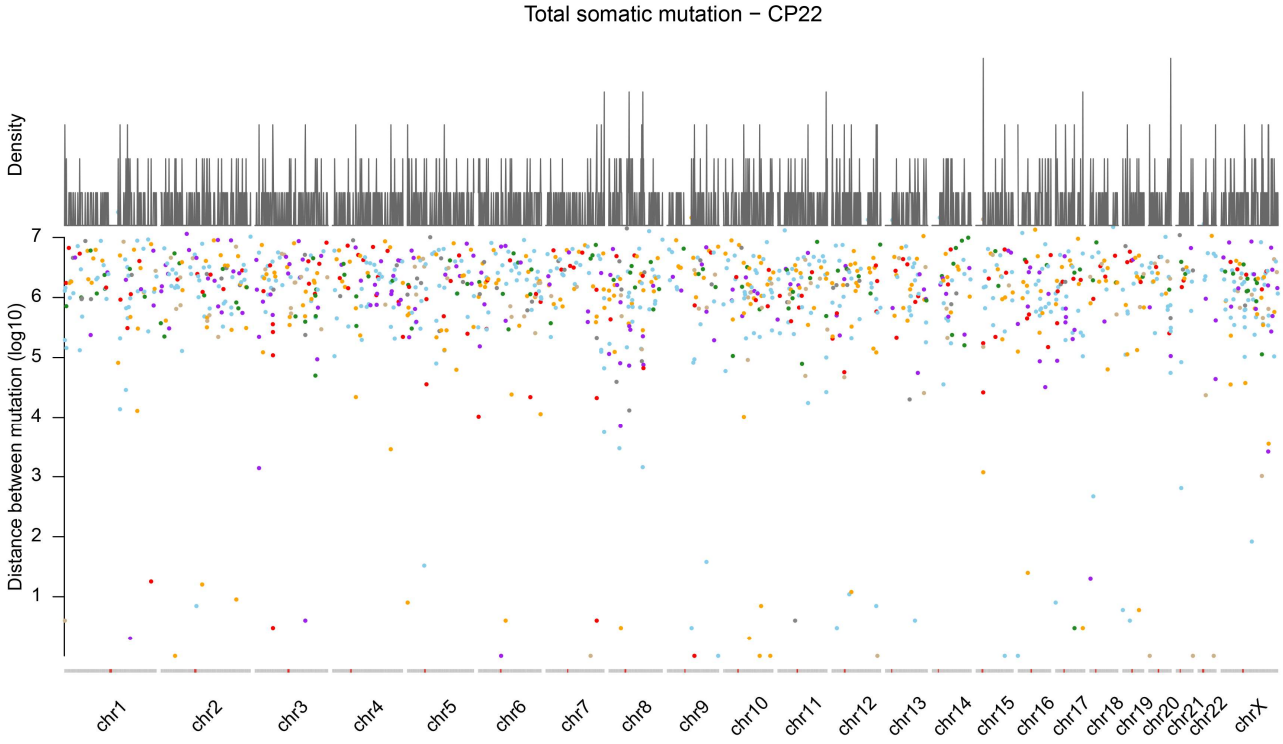
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Distance between mutation (log10)
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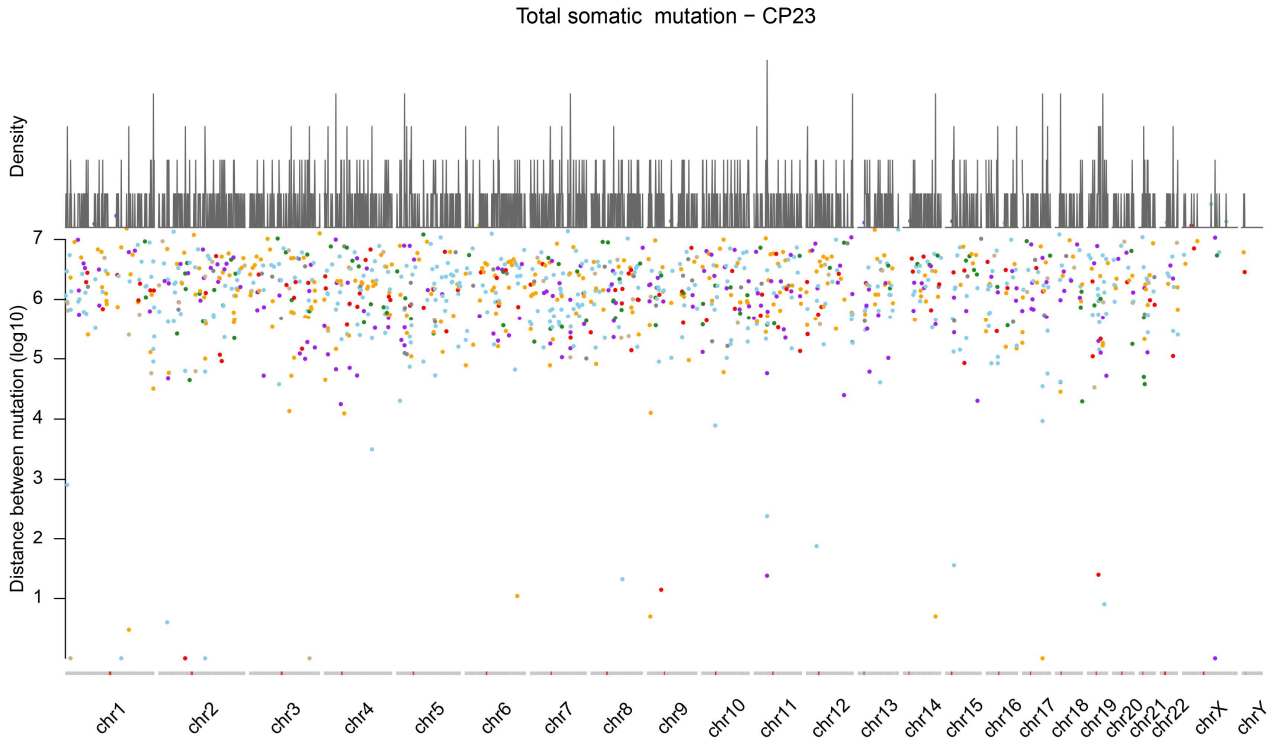
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Distance between mutation (log10)
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chr9
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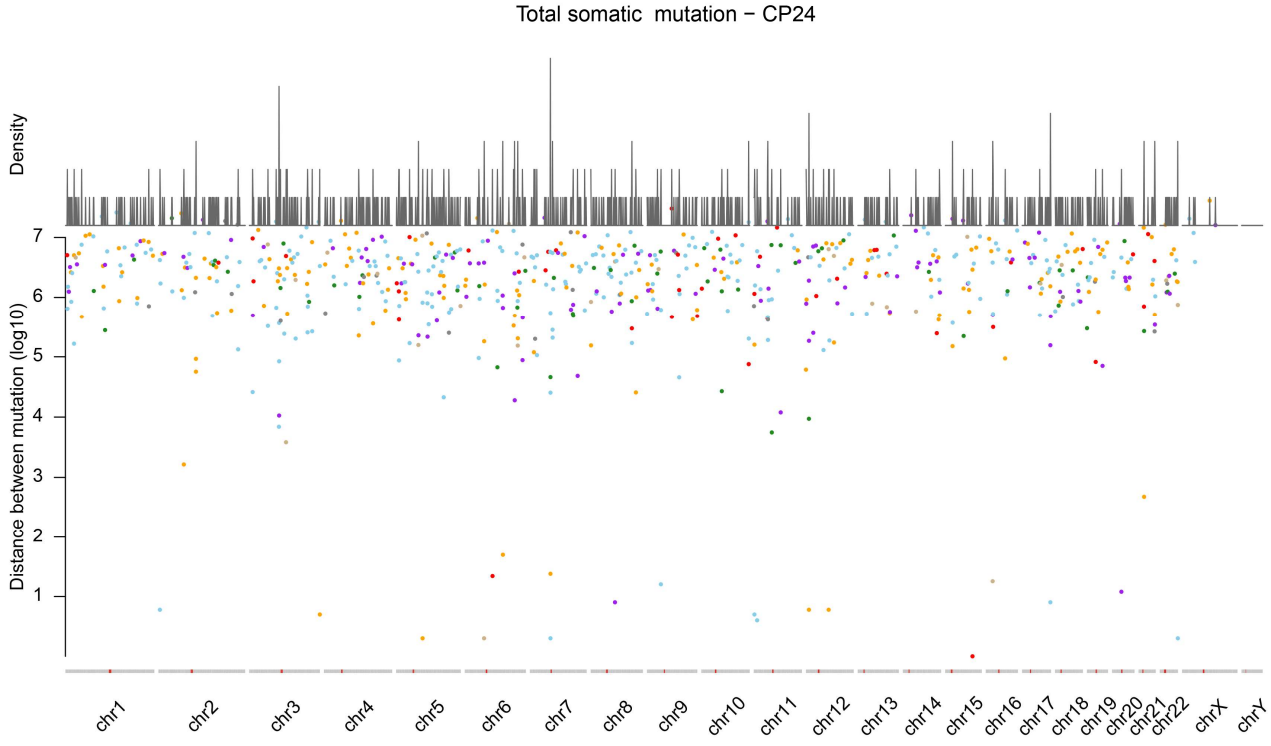
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Density
Distance between mutation (log10)
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chr9
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chr19
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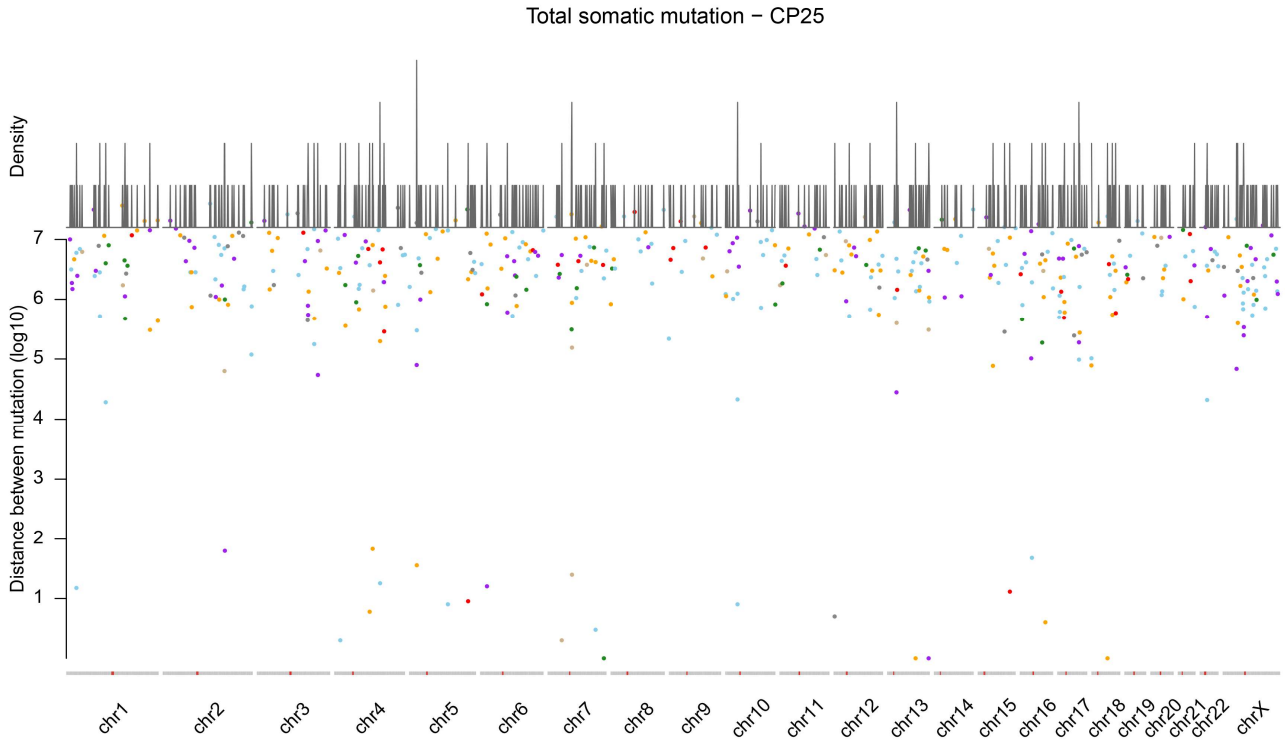
Total somatic mutation − CP25
Density
Distance between mutation (log10)
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chr7
chr8
chr9
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chr16
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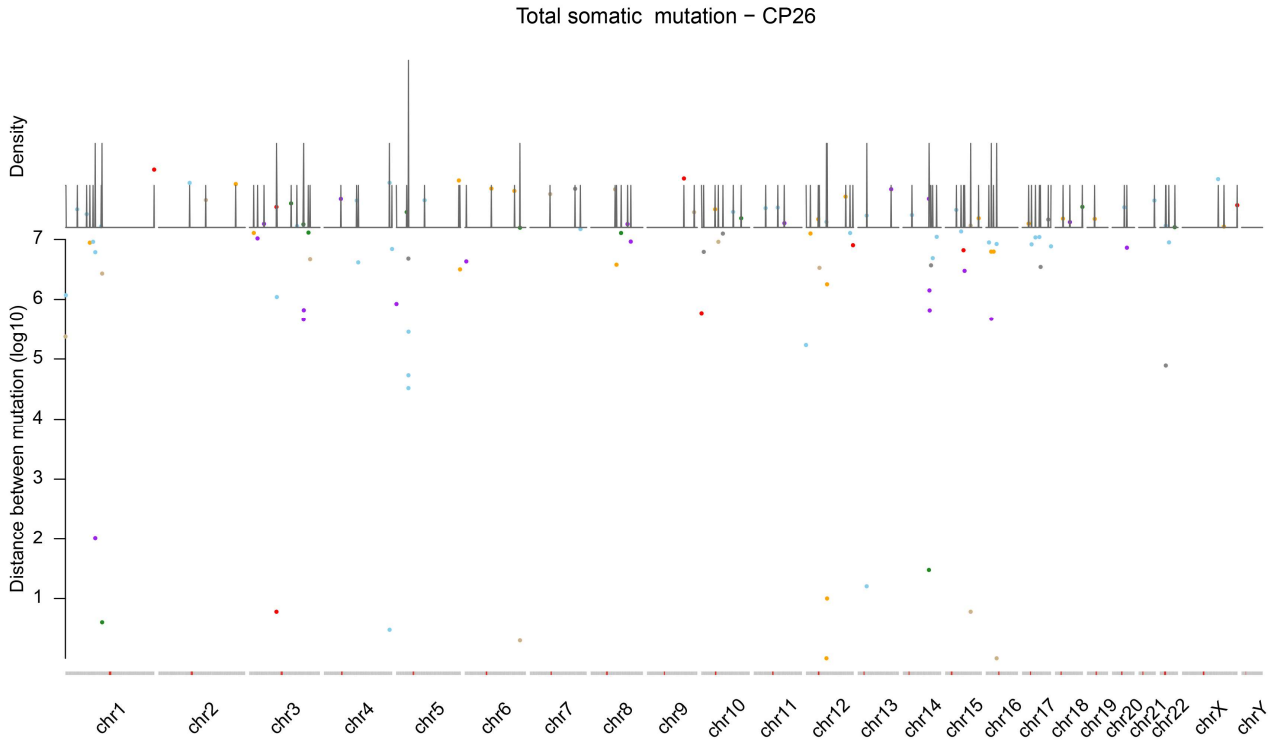
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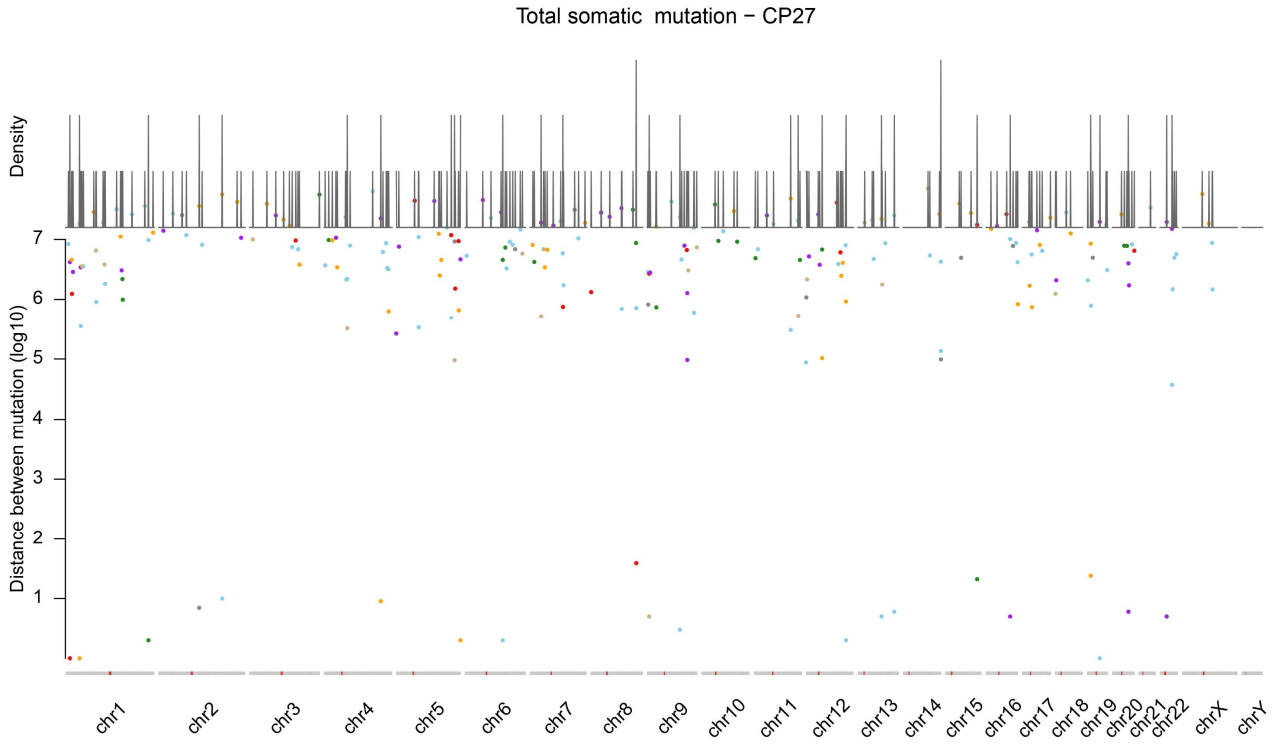
Total somatic mutation − CP27
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Distance between mutation (log10)
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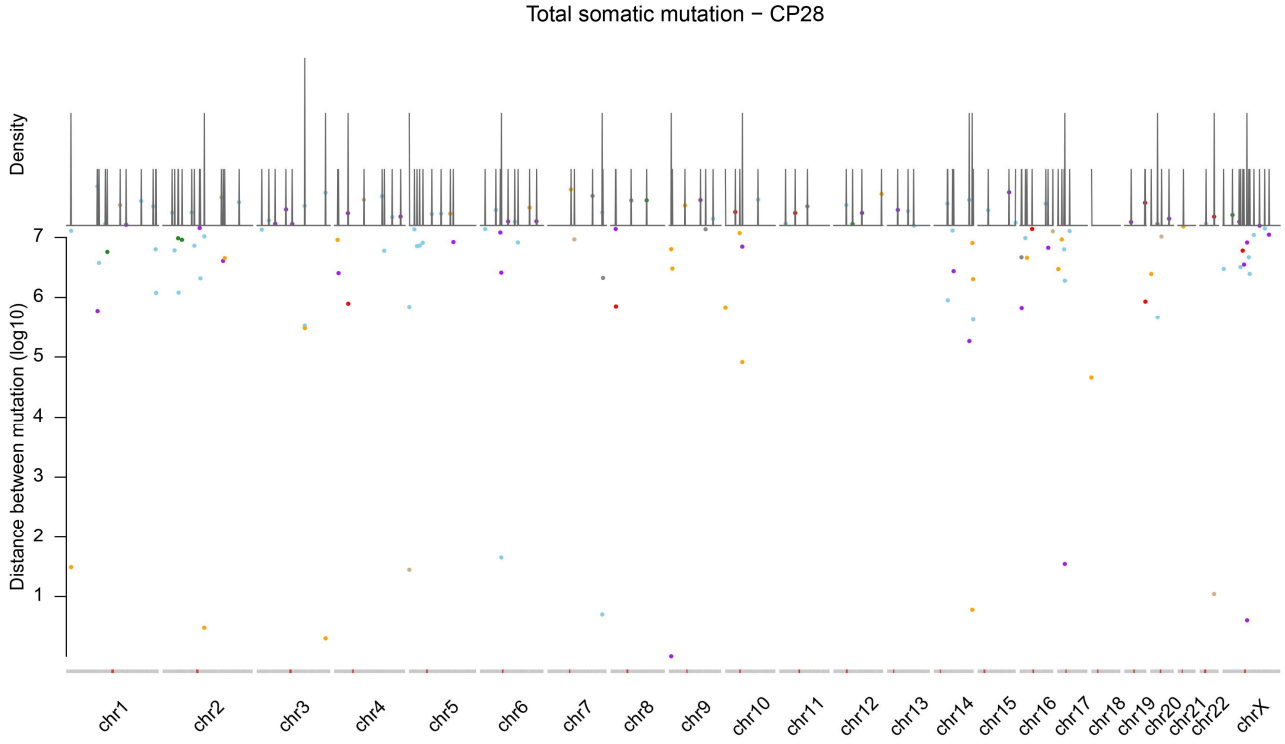
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Distance between mutation (log10)
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chr14
chr15
chr16
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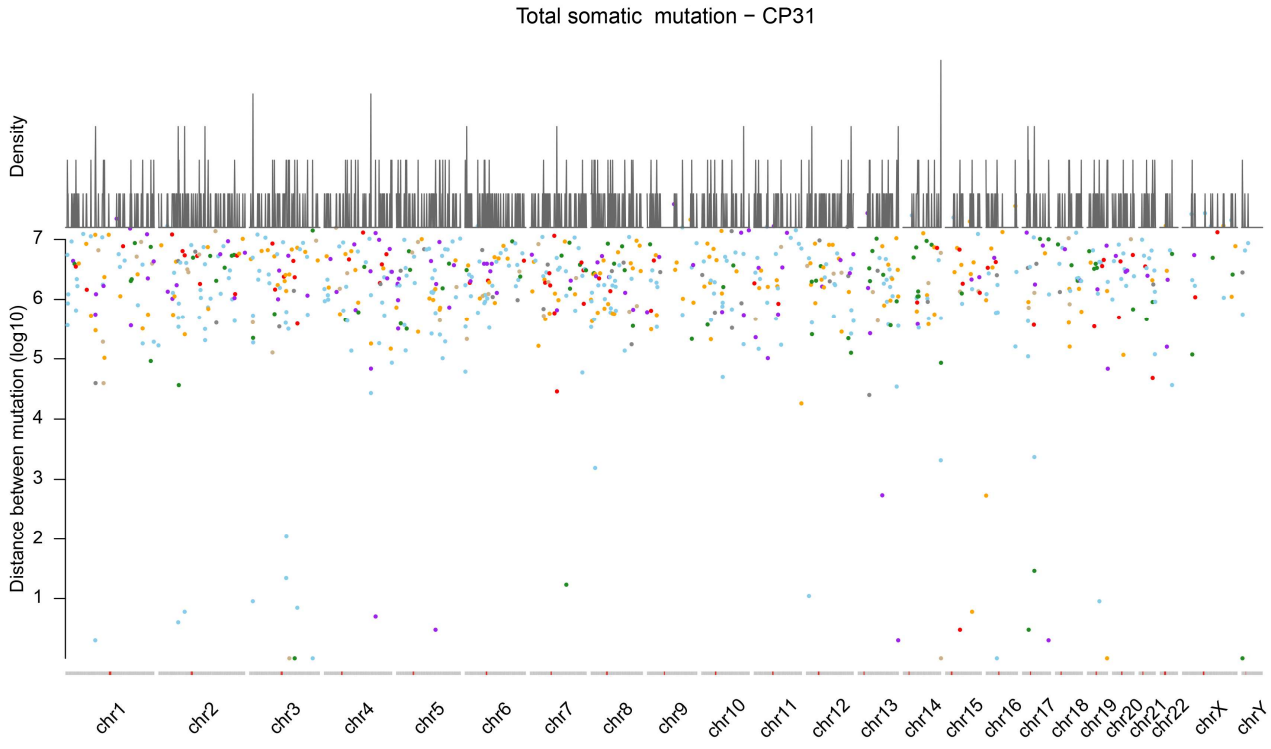
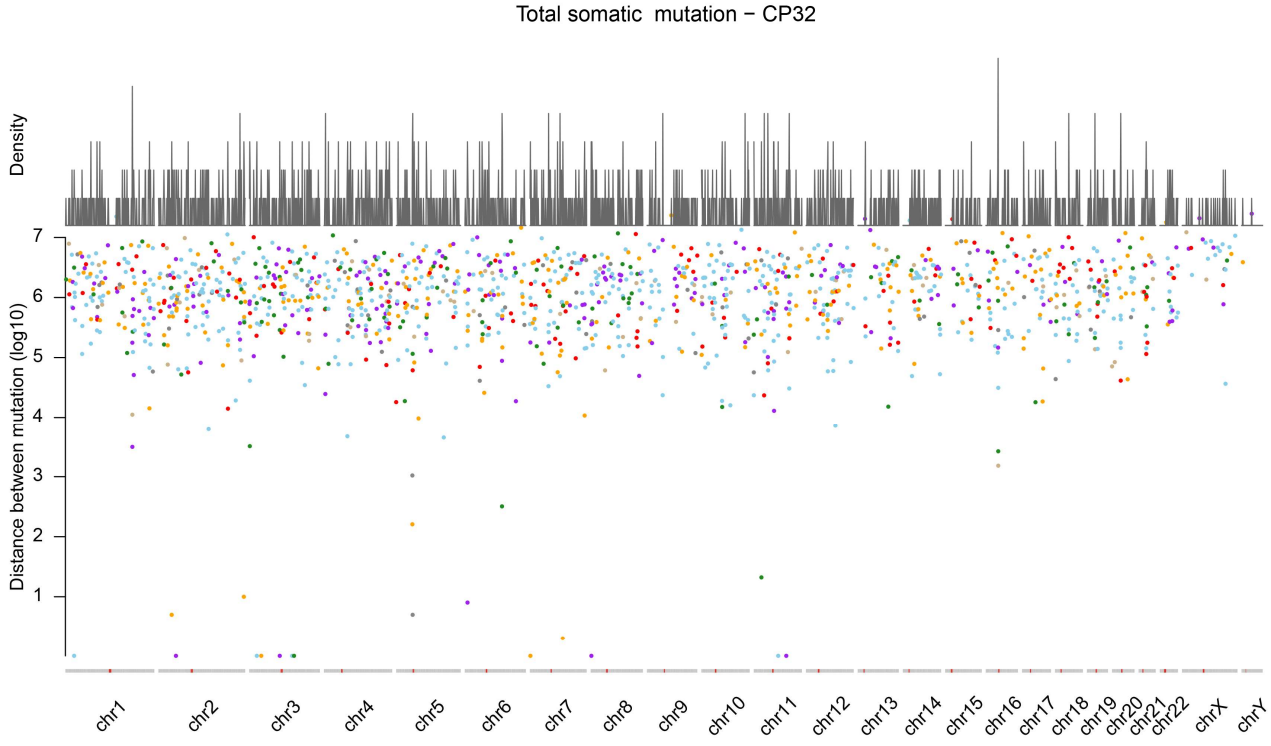
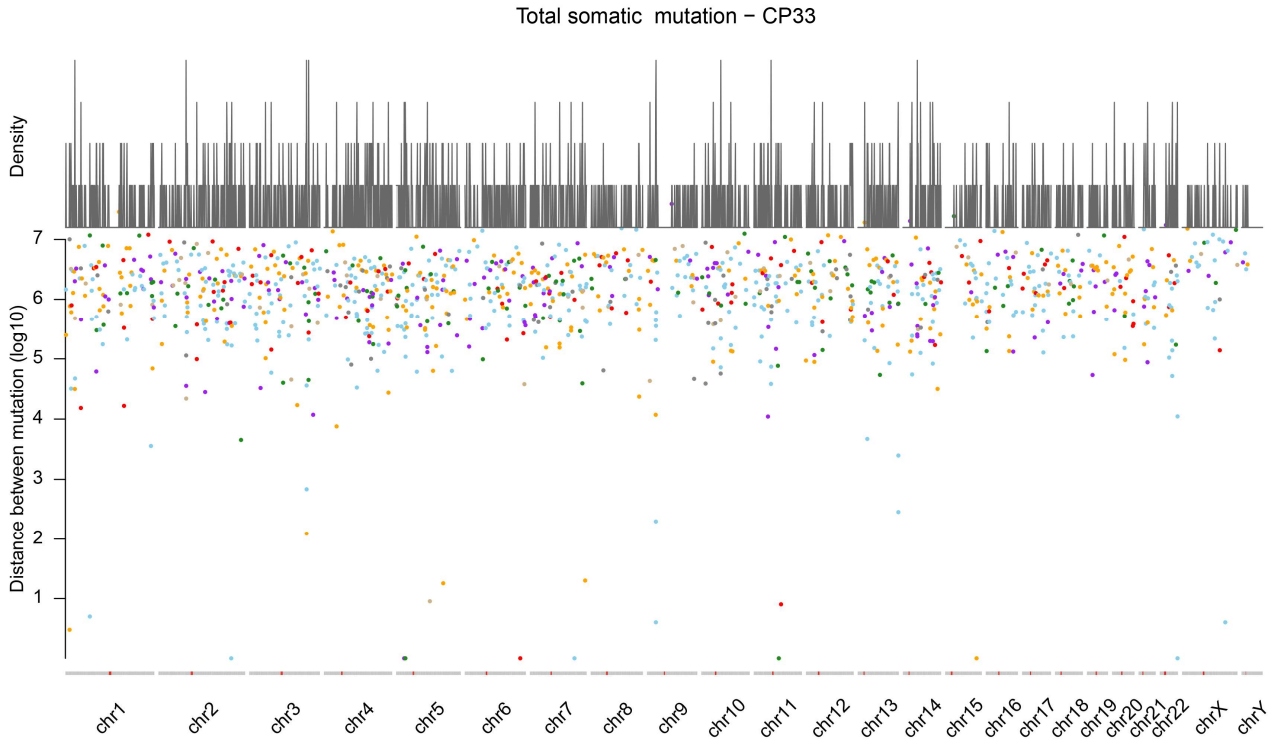
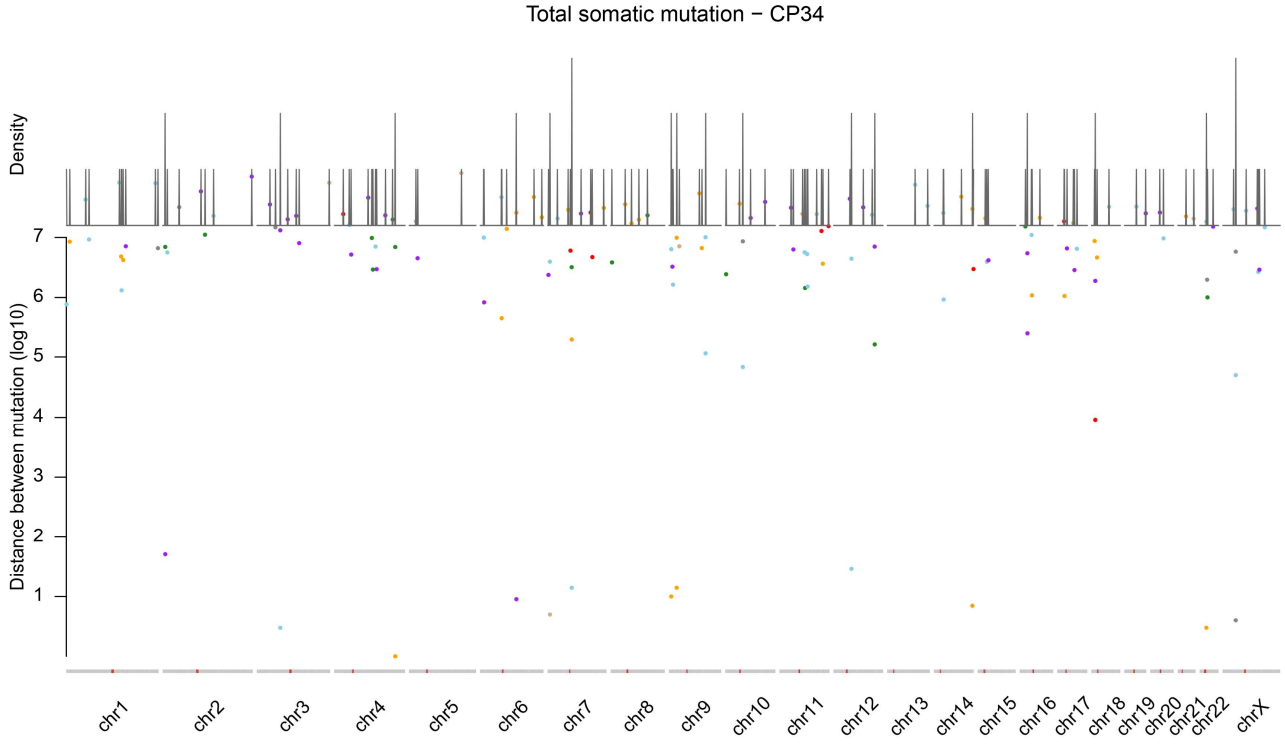
chr19
chr20
chr21
chr22
chrX


Total somatic mutation − CP31
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP32
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP33
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP34
Density
Distance between mutation (log10)
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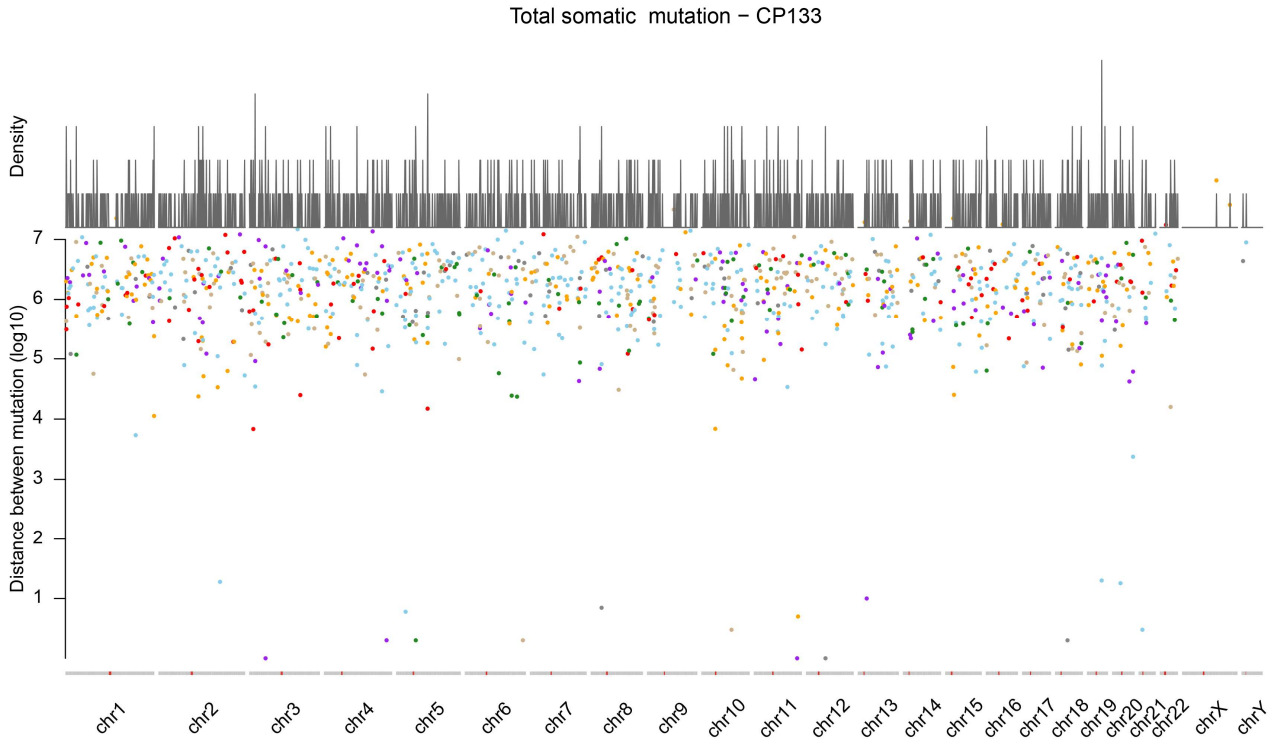
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX


Total somatic mutation − CP111
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP133
Density
Distance between mutation (log10)
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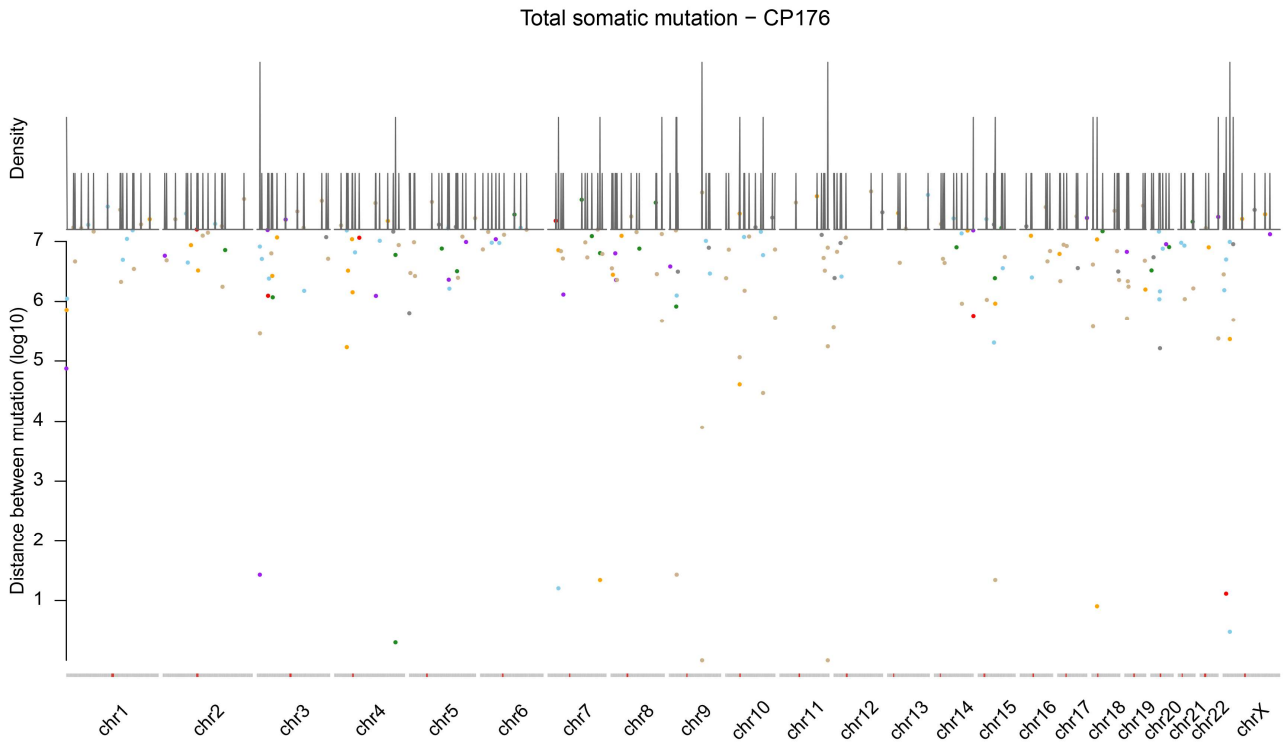
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY


Total somatic mutation − CP176
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX

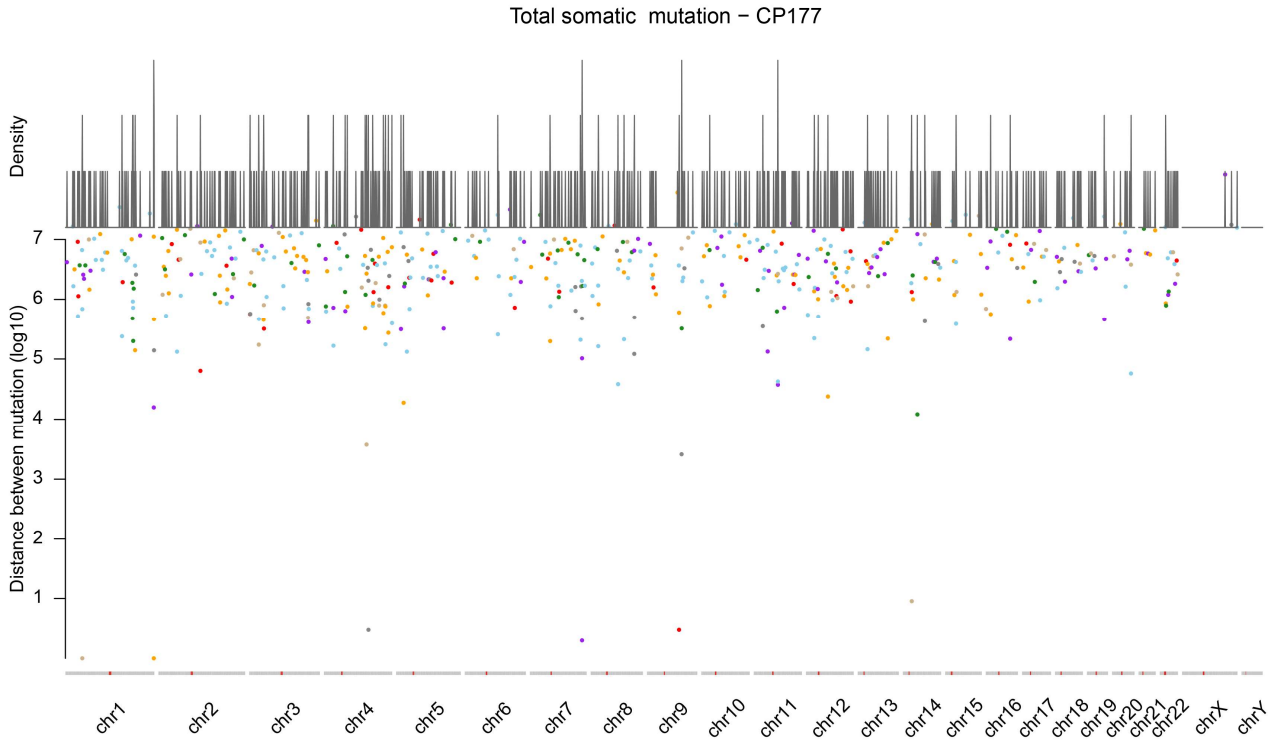

Total somatic mutation − CP177
Density
Distance between mutation (log10)
7
6
5
4
3
2
1
chr1
chr2
chr3
chr4
chr5
chr6
chr7
chr8
chr9
chr10
chr11
chr12
chr13
chr14
chr15
chr16
chr17
chr18
chr19
chr20
chr21
chr22
chrX
chrY

Fig S4. Kataegis analysis of somatic mutations (SNVs and InDels) in each patient.

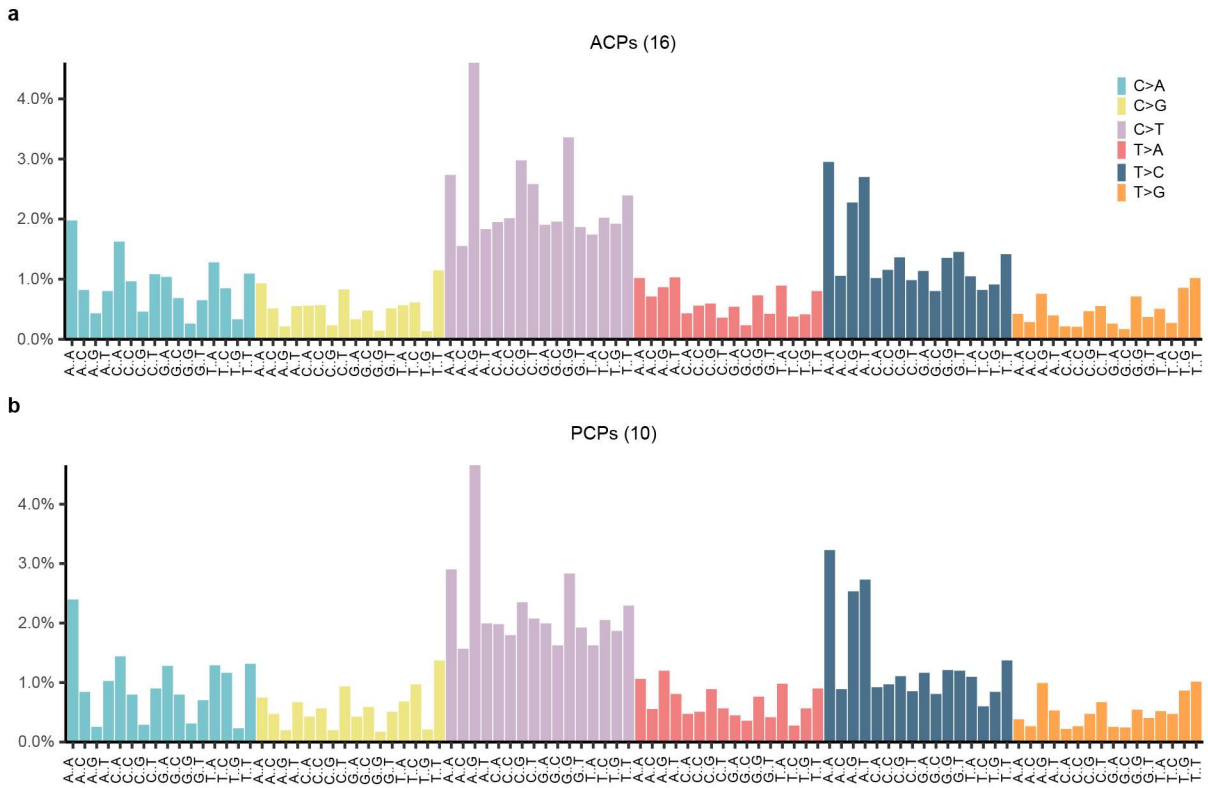


Fig S5. The proportion of 96 different extending possible base-pair substitutions of all SNVs identified in 16 ACPs and 10 PCPs.

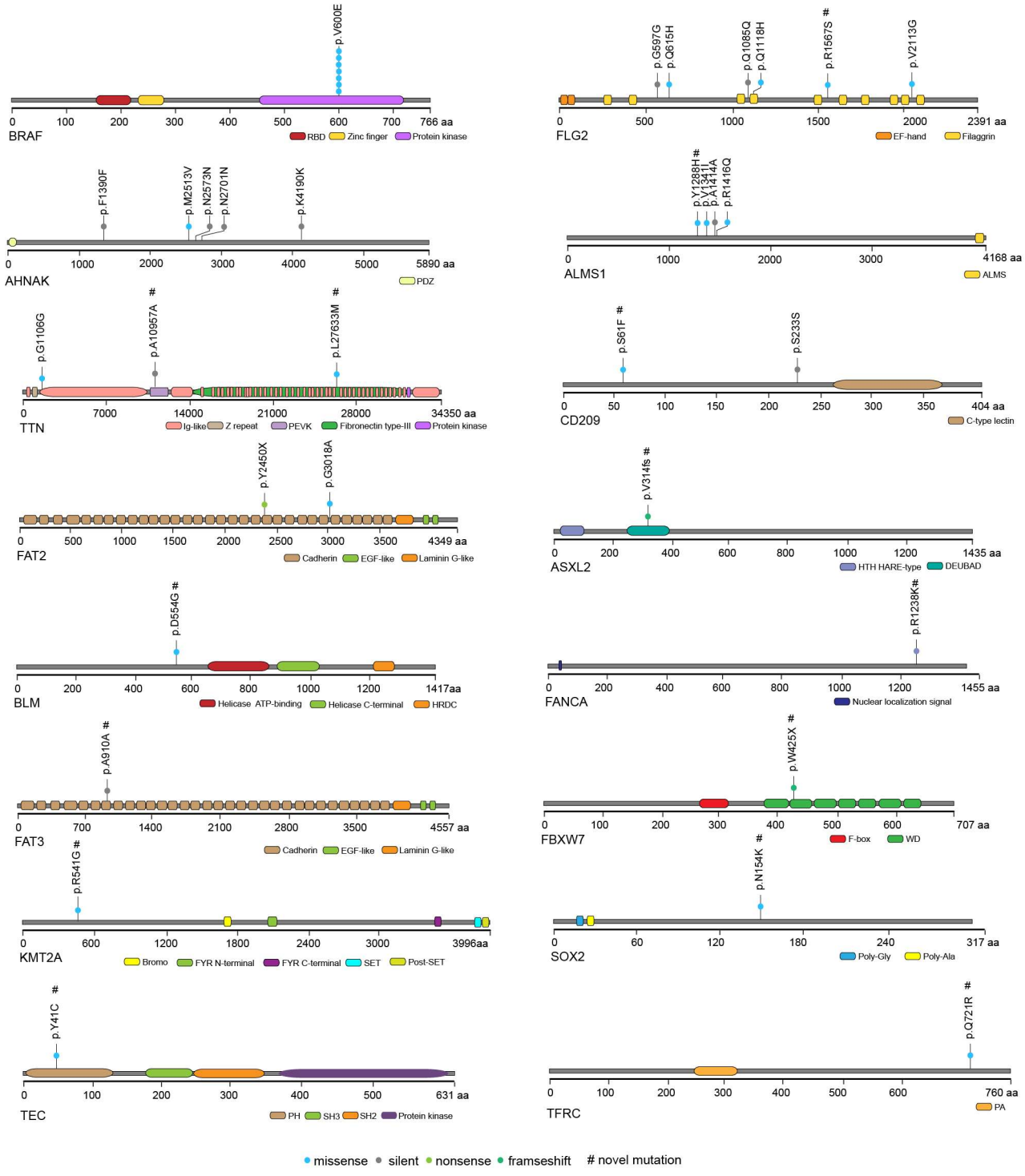


Fig S6. Schematics for genes listed in Fig. 3a indicating the location of the identified mutations.

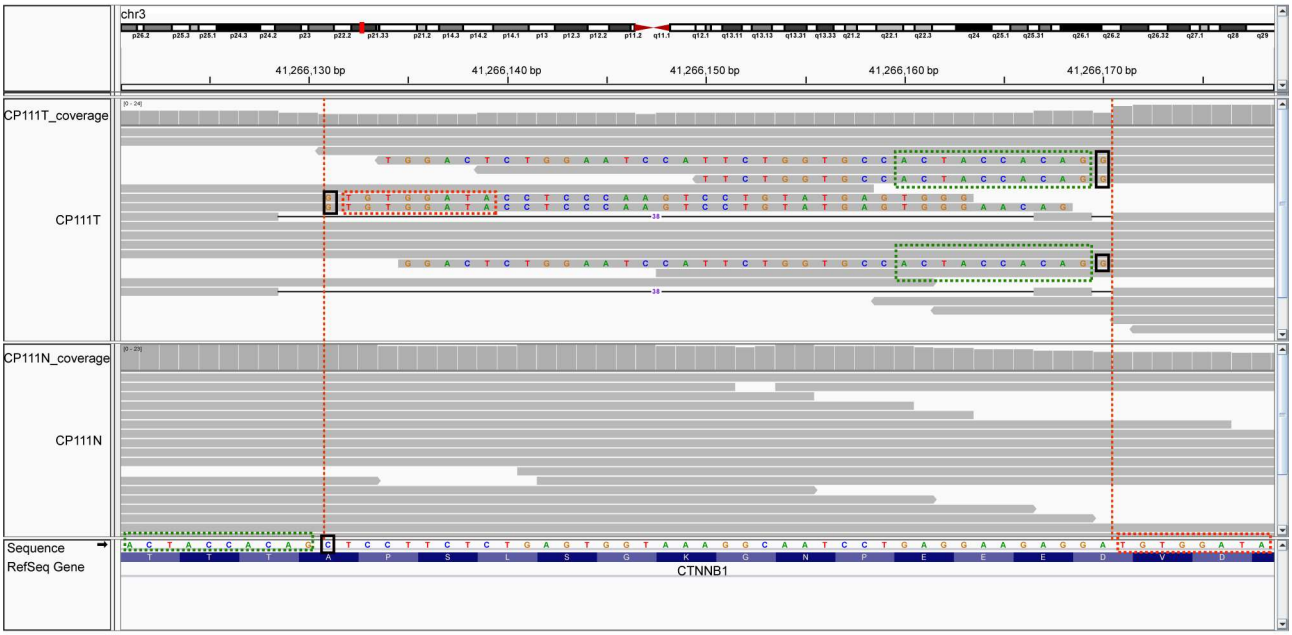


Fig S7. IGV graphic report for the alignment of deletion in CTNNB1 CP111 tumor and normal blood sample.

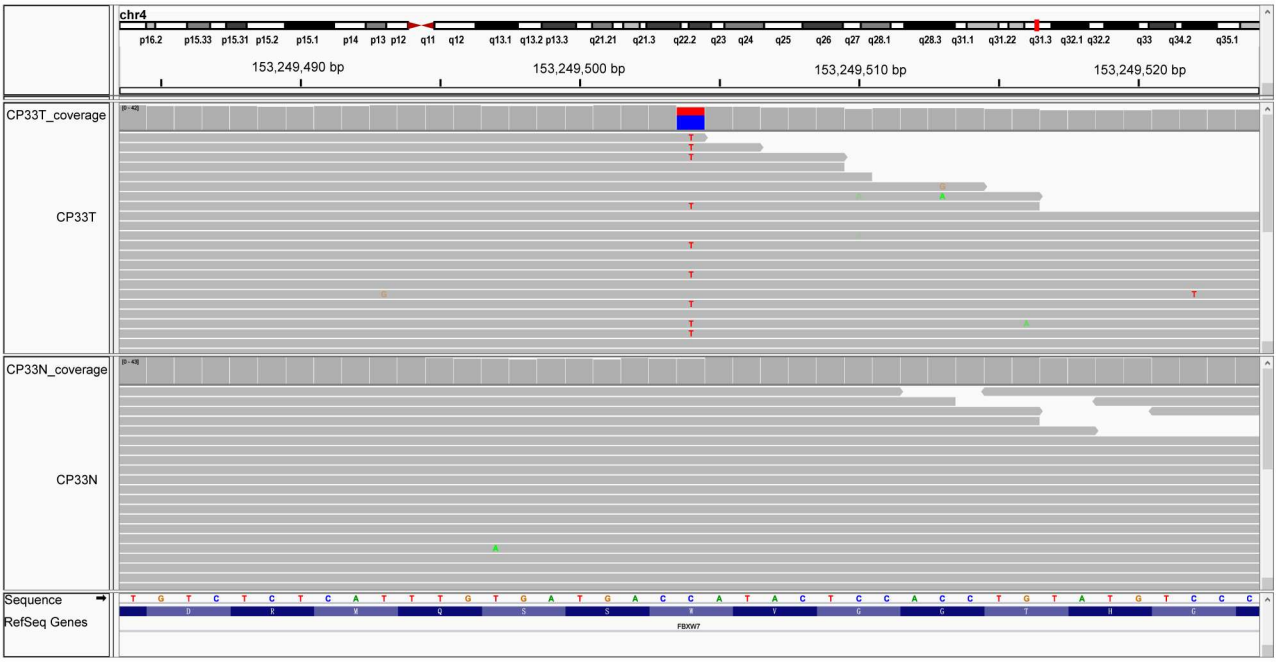


Fig S8. IGV graphic report for the alignment of nonsense mutation of W425X in FBXW7 of CP22 tumor and normal blood sample.

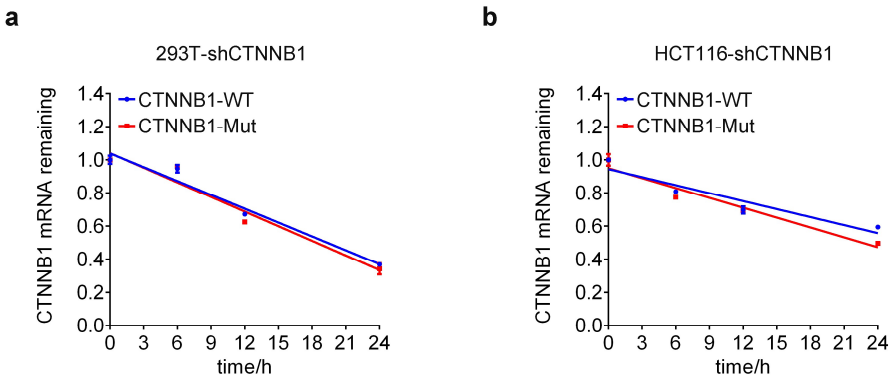


Fig S9. CTNNB1 mRNA stability in CTNNB1-WT/Mut 293T/HCT116 cells. a-b CTNNB1 mRNA stability in CTNNB1-WT/Mut 293T/HCT116 treated with 5 μg/mL actinomycin D at different time points. Actin mRNA was used as a negative control.