Whole Genome Sequencing Report

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1 Interprétation

LAL-T avec surexpression mono-allélique de ***TAL1***.

Couverture insuffisante pour assurer une excellente sensibilité (12x).

Réarrangements

— t(11;14) avec point de cassure sur le chromosome 11 en 3' et en 5' (pour le dérivatif) de ***LMO2*** et sur le 14 en TRD-J1 (également vu par sv-finder sur l'oncoT).

Délétions

— 9p de 168 kb (chr9:21,839,796-22,008,181) impliquant ***CDKN2A***.
— 16q de 3.7 mb (chr16:8,371,132-12,069,580).

Faux-sens

— ***NOTCH1*** (hotspot NP_060087.3:p.Leu1585Pro 46%).
— ***FBXW7*** (hotspot NP_060785.2:p.Arg385His 43%).
— ***ELF5*** (NP_001413.1:p.Ser91Ile 75%, ETS family transcription factor).
— ***GDF5*** (NP_000548.2:p.Arg259Gln 47%, TGF-beta).

L'ensemble des mutations somatiques de structure ont été annotées ainsi que l'ensemble des mutations somatiques codantes.

2 Sample identity

BECERRA

3 Alignement

Diagnostic sample

Id	BECERRA
Time Point	diag
Reference Genome	hs1
Bam Type	WGS
Modified Date (UTC)	2024/04/29 17h19
Number Of Reads	9.4 M
Yield Gb	36.71
Mean Coverage	11.78
N50	6.4 k
Median Length	3382
Mean Length	3922
Median Identity	98.96
Mean Identity	108.67
Run(s)	42ad1: 100%

MRD sample

Id	BECERRA
Time Point	mrd
Reference Genome	hs1
Bam Type	WGS
Modified Date (UTC)	2024/05/31 09h00
Number Of Reads	12.4 M
Yield Gb	52.42
Mean Coverage	16.82
N50	6.6 k
Median Length	3684
Mean Length	4223
Median Identity	99.18
Mean Identity	113.03
Run(s)	5f68e: 38% 7367a: 46% bc14a: 16%

Values computed by cramino v0.14.5

3.1 Normalized read count by chromosome

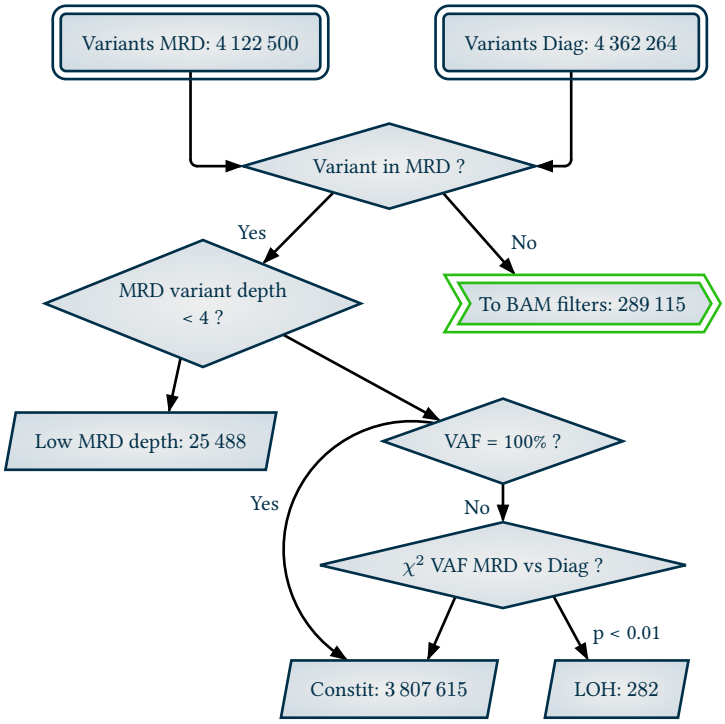
	chr1	chr2	chr3	chr4	chr5	chr6	chr7	chr8	chr9	chr10	chr11	chr12	chr13
diag	1	1.02	1	0.97	1	0.99	1	0.99	0.89	1.03	1.01	1.02	0.94
mrd	0.99	1.03	1.02	1.02	1.02	1.02	1.01	1	0.91	1.01	1	1.03	0.97

	chr14	chr15	chr16	chr17	chr18	chr19	chr20	chr21	chr22	chrX	chrY	chrM
diag	1.01	0.97	0.95	1.06	0.97	1.03	1.03	1.05	1.01	0.49	0.33	148.53
mrd	1	0.94	0.92	0.98	0.98	0.92	0.99	1.03	0.97	0.51	0.38	85.74

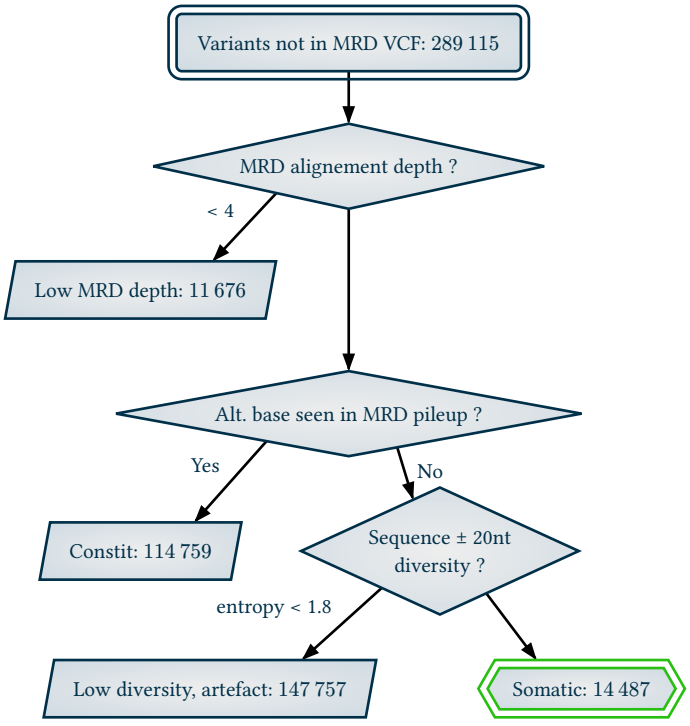
4 Variants

4.1 Variants calling

VCF filters

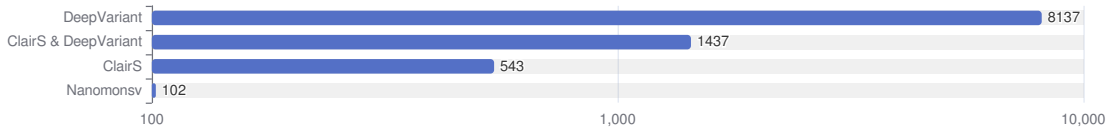


BAM filters

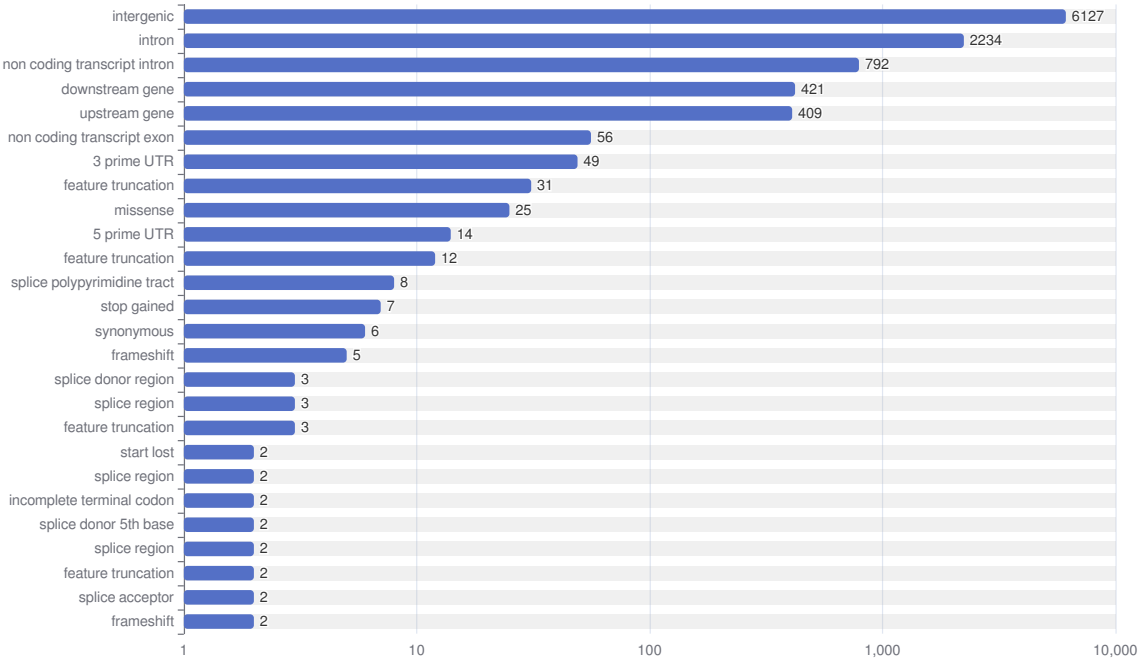


4.2 Somatic variants

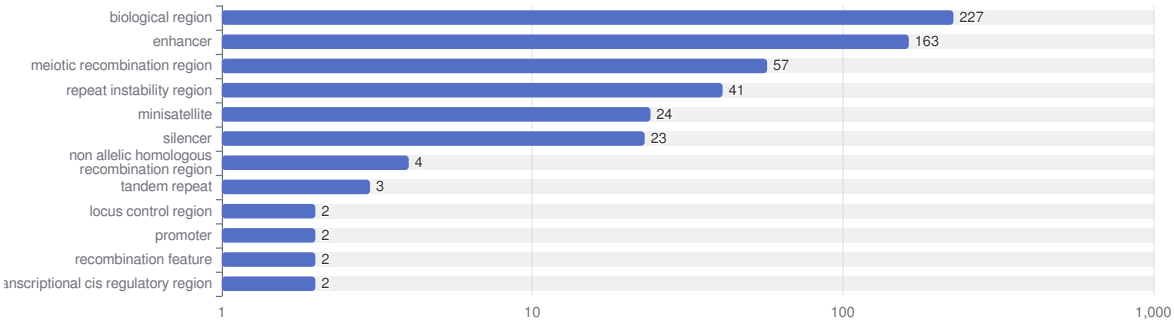
Callers



Consequences (VEP)



NCBI features



4.3 Selected Variants

Pathogenics

chr4:155,651,387 C›T
missense variant ***FBXW7***
NM_018315.5:c.1154G>A
NP_060785.2:p.Arg385His
VAF: 42.86% Cosmic: 245 DeepVariant: Qual: 25.3, GT: 0/1, GQ: 25, DP: 7, AD: [4, 3], VAF: 0.428571, PL: [25, 0, 49] ClairS: Qual: 14.031, GT: 0/1, GQ: 14, DP: 7, AF: 0.4286, AD: [0, 3], NAF: 0, NDP: 18, NAD: [0, 0], AU: 0, CU: 4, GU: 0, TU: 3, NAU: 0, NCU: 18, NGU: 0, NTU: 0, H, FAU: 0, FCU: 3, FGU: 0, FTU: 2, RAU: 0, RCU: 1, RGU: 0, RTU: 1

chr9:21,839,796 g›<DEL>
intergenic variant
VAF: 41.67% Nanomonsv: TR: 12, VR: 5, SVTYPE: DEL, SVLEN: −168385, END: 22008181, SVINSLEN: 4, SVINSSEQ: TCTC

chr9:148,734,037 A›G

missense variant ***NOTCH1***

NM_017617.5:c.4754T>C

NP_060087.3:p.Leu1585Pro

VAF: 45.45% Cosmic: 62

ClairS:

Qual: 14.372,

GT: 0/1, GQ: 14, DP: 11, AF: 0.4545, AD: [0, 5], NAF: 0, NDP: 16, NAD: [0, 0], AU: 6, CU: 0, GU: 5, TU: 0, NAU: 16, NCU: 0, NGU: 0, NTU: 0, H, FAU: 4, FCU: 0, FGU: 0, FTU: 0, RAU: 2, RCU: 0, RGU: 5, RTU: 0

DeepVariant:

Qual: 24.6,

GT: 0/1, GQ: 25, DP: 11, AD: [6, 5], VAF: 0.454545, PL: [24, 0, 47]

chr11:33,985,775 t›[chr14:16647835[ACTAATAAACT...

VAF: 21.74%

Nanomonsv:

TR: 23, VR: 5, SVTYPE: BND, SVINSLEN: 46, SVINSSEQ:

ACTAATAAACTAAAGTATCCCCAGTTGCACCCCTAATCTATTTTGG

, MATEID: r_24_1

chr11:34,123,069 c›cTTCGTGTGCTTTGTGCTGGACGGTCG...

VAF: 36.84%

Nanomonsv:

TR: 19, VR: 7, SVTYPE: BND, SVINSLEN: 29, SVINSSEQ:

TTCGTGTGCTTTGTGCTGGACGGTCGGCA

, MATEID: r_25_1

chr14:16,636,759 T›TTGCCGACCGTCCAGCACAAAGCACAC...
feature truncation, intron variant, non coding transcript variant ***TRD-AS1***
VAF: 36.84% Nanomonsv: TR: 19, VR: 7, SVTYPE: BND, SVINSLEN: 29, SVINSSEQ: TGCCGACCGTCCAGCACAAAGCACACGAA , MATEID: r_25_0

chr14:16,647,835 A›[chr11:33985775[CCAAAATAGAT...
coding sequence variant, feature truncation, start lost, start retained variant ***TRDJ1***
VAF: 21.74% Nanomonsv: TR: 23, VR: 5, SVTYPE: BND, SVINSLEN: 46, SVINSSEQ: CCAAAATAGATTAGGGGTGCAACTGGGGATACTTTAGTTTATTAGT , MATEID: r_24_0

Likely Pathogenics

chr11:34,630,410 C›A
missense variant ***ELF5***
NM_001422.4:c.272G>T
NP_001413.1:p.Ser91Ile
VAF: 75% DeepVariant: Qual: 20.3, GT: 0/1, GQ: 20, DP: 4, AD: [1, 3], VAF: 0.75, PL: [20, 0, 30]

chr16:8,371,132 G›<DEL>
intergenic variant
VAF: 19.05% Nanomonsv: TR: 21, VR: 4, SVTYPE: DEL, SVLEN: −3698448, END: 12069580, SVINSLEN: 5, SVINSSEQ: GTATG

chr20:37,155,500 C›T
missense variant ***GDF5***
NM_000557.5:c.776G>A
NP_000548.2:p.Arg259Gln
VAF: 47.06% Cosmic: 1 DeepVariant: Qual: 22.9, GT: 0/1, GQ: 23, DP: 17, AD: [9, 8], VAF: 0.470588, PL: [22, 0, 48] ClairS: Qual: 15.007, GT: 0/1, GQ: 15, DP: 17, AF: 0.4706, AD: [0, 8], NAF: 0, NDP: 12, NAD: [0, 0], AU: 0, CU: 9, GU: 0, TU: 8, NAU: 0, NCU: 12, NGU: 0, NTU: 0, H, FAU: 0, FCU: 3, FGU: 0, FTU: 7, RAU: 0, RCU: 6, RGU: 0, RTU: 1

Variants of uncertain significance

chr1:21,295,671 C›T
stop gained ***NBPF3***
NM_032264.6:c.634C>T
NP_115640.1:p.Gln212Ter
VAF: 46.43% DeepVariant: Qual: 27, GT: 0/1, GQ: 27, DP: 8, AD: [4, 4], VAF: 0.5, PL: [26, 0, 48] ClairS: Qual: 16.842, GT: 0/1, GQ: 16, DP: 7, AF: 0.4286, AD: [0, 3], NAF: 0, NDP: 20, NAD: [0, 0], AU: 0, CU: 4, GU: 0, TU: 3, NAU: 0, NCU: 20, NGU: 0, NTU: 0, H, FAU: 0, FCU: 2, FGU: 0, FTU: 2, RAU: 0, RCU: 2, RGU: 0, RTU: 1

chr1:89,319,247 a›[chr1:89319260[c
feature truncation, intron variant, non coding transcript variant ***LOC105378844***
VAF: 33.33% Nanomonsv: TR: 9, VR: 3, SVTYPE: BND, MATEID: r_6_1

chr1:89,319,260 c›[chr1:89319247[c
feature truncation, intron variant, non coding transcript variant ***LOC105378844***
VAF: 33.33% Nanomonsv: TR: 9, VR: 3, SVTYPE: BND, MATEID: r_6_0

chr2:10,470,368 T›A
stop gained ***ODC1***
NM_002539.3:c.1351A>T
NP_002530.1:p.Arg451Ter
VAF: 25% DeepVariant: Qual: 3.5, GT: 0/1, GQ: 4, DP: 8, AD: [6, 2], VAF: 0.25, PL: [0, 0, 38]

chr2:67,892,902 C›C]chr2:67892913]
VAF: 17.65% Nanomonsv: TR: 17, VR: 3, SVTYPE: BND, MATEID: r_72_1

chr2:67,892,913 A›A]chr2:67892902]
VAF: 17.65% Nanomonsv: TR: 17, VR: 3, SVTYPE: BND, MATEID: r_72_0

chr2:121,782,173 t›t]chr2:121782181]
feature truncation, intron variant ***CLASP1***
VAF: 18.75% Nanomonsv: TR: 16, VR: 3, SVTYPE: BND, MATEID: r_73_0

chr2:121,782,181 g›g]chr2:121782173]
feature truncation, intron variant ***CLASP1***
VAF: 18.75% Nanomonsv: TR: 16, VR: 3, SVTYPE: BND, MATEID: r_73_1

chr3:57,956,983 G›[chr3:57957061[TGAGG
feature truncation, intron variant ***SLMAP***
VAF: 21.43% Nanomonsv: TR: 14, VR: 3, SVTYPE: BND, SVINSLEN: 4, SVINSSEQ: TGAG , MATEID: r_91_1

chr3:57,957,061 G›[chr3:57956983[CTCAG
feature truncation, intron variant ***SLMAP***
VAF: 21.43% Nanomonsv: TR: 14, VR: 3, SVTYPE: BND, SVINSLEN: 4, SVINSSEQ: CTCA , MATEID: r_91_0

chr3:63,282,913 A›ACTACCATTGACACCCATCCTACCATT...
intron variant ***SYNPR***
VAF: 37.5% Nanomonsv: TR: 8, VR: 3, SVTYPE: INS, END: 63282913, SVINSLEN: 234, SVINSSEQ: CTACCATTGACACCCATCCTACCATTGTCAGGTGTGTGGTGCCCCCATCCTACCATTGTC ACCCATCCTATCATTGTCAAGTGTGTTATGCACCTACCCTACCATTGTCACCAATCCTAC CATTGCCCAGTGTGTCACACACACACACCTTACCATGAGTGCATGGTGGGATAGGTGCAT GACACACCTGACAATGGTGGAATGAGTGACAATGGTAGGATATCTGCACCATCC

chr3:82,310,545 A›AT]chr3:82310569]
feature truncation, intron variant, non coding transcript variant ***LINC02008***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, SVINSLEN: 1, SVINSSEQ: T , MATEID: r_92_1

chr3:82,310,569 g›gA]chr3:82310545]
feature truncation, intron variant, non coding transcript variant ***LINC02008***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, SVINSLEN: 1, SVINSSEQ: A , MATEID: r_92_0

chr3:142,058,265 A›G
missense variant ***LOC124909439***
XM_047449421.1:c.269T>C
XP_047305377.1:p.Leu90Pro
VAF: 44.44% DeepVariant: Qual: 32.4, GT: 0/1, GQ: 32, DP: 9, AD: [5, 4], VAF: 0.444444, PL: [32, 0, 53] ClairS: Qual: 9.909, GT: 0/1, GQ: 9, DP: 9, AF: 0.4444, AD: [0, 4], NAF: 0, NDP: 7, NAD: [0, 0], AU: 5, CU: 0, GU: 4, TU: 0, NAU: 7, NCU: 0, NGU: 0, NTU: 0, H, FAU: 2, FCU: 0, FGU: 2, FTU: 0, RAU: 3, RCU: 0, RGU: 2, RTU: 0

chr3:170,297,853 t›tATTTTTATTTTGTTTTATTAGGACTG...
intron variant ***WDR49***

VAF: 15.79%

Nanomonsv:

TR: 19, VR: 3, SVTYPE: INS, END: 170297854, SVINSLEN: 316, SVINSSEQ:

ATTTTTATTTTGTTTTATTAGGACTGAATCTCTCTCTATCTCACAGGCTGTACTGCAGTG
GTGCGATCTCAGCTTACTGCAACCTCCACTTTTCAGGATCAAGTGACTCTTGTGCTTCAG
CCTCTCAAGTAGCTAGGATTACAGGCGCCCACTACCATACCCGTCTAATTTTTGTATTTT
GAGTAGAGGCAGGGTTTCACCACGTAGGCCAGGCTGGTCTCGGACTCCTGACCTCAAGTG
ATCCACCCGCCTCAGCCTCCCAAAGCGCTGGGATTACAGGCGTGAGCCTCCACGCCCAGC
CCATAAAACAAATTTT

chr4:108,552,892 C›T
3 prime UTR variant ***TET2***
NM_017628.4:c.*4522C>T

VAF: 46.15% Cosmic: 5 GnomAD: 0.00542

ClairS:

Qual: 5.391,

GT: 0/1, GQ: 5, DP: 13, AF: 0.4615, AD: [0, 6], NAF: 0, NDP: 9, NAD: [0, 0], AU: 0, CU: 7, GU: 0, TU: 6, NAU: 0, NCU: 9, NGU: 0, NTU: 0, FAU: 0, FCU: 5, FGU: 0, FTU: 2, RAU: 0, RCU: 2, RGU: 0, RTU: 4

chr4:111,957,187 c›[chr4:111957226[g
feature truncation, intron variant ***OSTC***

VAF: 16.67%

Nanomonsv:

TR: 18, VR: 3, SVTYPE: BND, MATEID: r_101_1

chr4:111,957,226 g›[chr4:111957187[g
feature truncation, intron variant ***OSTC***

VAF: 16.67%

Nanomonsv:

TR: 18, VR: 3, SVTYPE: BND, MATEID: r_101_0

chr4:125,534,005 G›A
missense variant ***KIAA1109***
NM_015312.4:c.3056G>A
NP_056127.2:p.Arg1019Gln

VAF: 40% Cosmic: 3 GnomAD: 0.0000195

DeepVariant:

Qual: 3.7,

GT: 0/1, GQ: 4, DP: 5, AD: [3, 2], VAF: 0.4, PL: [1, 0, 24]

chr4:149,007,679 g›gCATCACACAATATATTCATGTAACAT...
intron variant ***C4orf51***

VAF: 54.55%

Nanomonsv:

TR: 11, VR: 6, SVTYPE: INS, END: 149007679, SVINSLEN: 110, SVINSSEQ:

```
CATCACACAATATATTCATGTAACATACCTGCACATGTACCCCTTGAGTCTAAAAAAAAAA
AGCCTACTAAATGTTGGTAAGGATGCCTAACAATAAGATCTCTGATATAC
```

chr4:176,653,476 A›G
missense variant ***GALNT7***
NM_017423.3:c.1485A>G
NP_059119.2:p.Ile495Met

VAF: 20%

DeepVariant:

Qual: 6.8,

GT: 0/1, GQ: 7, DP: 10, AD: [8, 2], VAF: 0.2, PL: [5, 0, 38]

chr5:1,439,645 T›[chr5:1439686[C
upstream gene variant ***LPCAT1***
VAF: 30% Nanomonsv: TR: 10, VR: 3, SVTYPE: BND, MATEID: r_105_1

chr5:1,439,686 C›[chr5:1439645[C
upstream gene variant ***LPCAT1***
VAF: 30% Nanomonsv: TR: 10, VR: 3, SVTYPE: BND, MATEID: r_105_0

chr6:75,480,432 t›t]chr6:75480451]
feature truncation, intron variant, non coding transcript variant ***LOC101928516***
VAF: 25% Nanomonsv: TR: 12, VR: 3, SVTYPE: BND, MATEID: r_115_1

chr6:75,480,451 a›a]chr6:75480432]
feature truncation, intron variant, non coding transcript variant ***LOC101928516***
VAF: 25% Nanomonsv: TR: 12, VR: 3, SVTYPE: BND, MATEID: r_115_0

chr6:108,060,177 C›[chr6:108060216[C
downstream gene variant ***LOC105377928***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, MATEID: r_117_1

chr6:108,060,216 C›[chr6:108060177[C
downstream gene variant ***LOC105377928***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, MATEID: r_117_0

chr6:117,427,892 G›A
missense variant ***NT5DC1***
NM_152729.3:c.1264G>A
NP_689942.2:p.Asp422Asn
VAF: 51.43% DeepVariant: Qual: 13, GT: 0/1, GQ: 13, DP: 7, AD: [4, 3], VAF: 0.428571, PL: [12, 0, 37] ClairS: Qual: 15.007, GT: 0/1, GQ: 15, DP: 5, AF: 0.6, AD: [0, 3], NAF: 0, NDP: 19, NAD: [0, 0], AU: 3, CU: 0, GU: 2, TU: 0, NAU: 0, NCU: 0, NGU: 19, NTU: 0, H, FAU: 0, FCU: 0, FGU: 1, FTU: 0, RAU: 3, RCU: 0, RGU: 1, RTU: 0

chr7:37,952,447 t›t]chr7:37952530]
VAF: 16.67% Nanomonsv: TR: 18, VR: 3, SVTYPE: BND, MATEID: r_121_1

chr7:37,952,530 a›a]chr7:37952447]
VAF: 16.67% Nanomonsv: TR: 18, VR: 3, SVTYPE: BND, MATEID: r_121_0

chr7:65,565,719 C›CCCACAGCCACTTTTGTGGGCCCACCT...
downstream gene variant ***ZNF736***

VAF: 46.15%

Nanomonsv:

TR: 13, VR: 6, SVTYPE: INS, END: 65565719, SVINSLEN: 101, SVINSSEQ:

```
CCACAGCCACTTTTGTGGGCCCACCTGGGCCTCCTCACTCCACTGGCCAGTGAAACCCAA
CTGGAATTCCTGAGTCCAGAATTCACATTTGGTTCTAGAAC
```

chr7:105,960,048 t›t]chr7:105960157]
feature truncation, intron variant ***LHFPL3***

VAF: 20%

Nanomonsv:

TR: 15, VR: 3, SVTYPE: BND, MATEID: r_127_1

chr7:105,960,157 g›g]chr7:105960048]
feature truncation, intron variant ***LHFPL3***

VAF: 20%

Nanomonsv:

TR: 15, VR: 3, SVTYPE: BND, MATEID: r_127_0

chr7:136,326,361 C›C]chr7:136326453]
feature truncation, intron variant ***AGBL3***

VAF: 25%

Nanomonsv:

TR: 12, VR: 3, SVTYPE: BND, MATEID: r_128_1

chr7:136,326,453 A›A]chr7:136326361]
feature truncation, intron variant ***AGBL3***
VAF: 25% Nanomonsv: TR: 12, VR: 3, SVTYPE: BND, MATEID: r_128_0

chr8:146,120,568 T›TGCTGTGGGCCTGTGTCCTGCTGTGGG...
intron variant ***ZNF16***
VAF: 41.18% Nanomonsv: TR: 17, VR: 7, SVTYPE: INS, END: 146120596, SVINSLEN: 47, SVINSSEQ: GCTGTGGGCCTGTGTCCTGCTGTGGGTCTGTATCCTGCTGTTGGGCT

chr9:23,710,958 G›A
missense variant ***ELAVL2***
NM_004432.5:c.448C>T
NP_004423.2:p.Arg150Cys
VAF: 57.78% Cosmic: 11 GnomAD: 0.000013 ClairS: Qual: 16.309, GT: 0/1, GQ: 16, DP: 9, AF: 0.5556, AD: [0, 5], NAF: 0, NDP: 17, NAD: [0, 0], AU: 5, CU: 0, GU: 4, TU: 0, NAU: 0, NCU: 0, NGU: 17, NTU: 0, H, FAU: 1, FCU: 0, FGU: 3, FTU: 0, RAU: 4, RCU: 0, RGU: 1, RTU: 0 DeepVariant: Qual: 32.9, GT: 0/1, GQ: 33, DP: 10, AD: [4, 6], VAF: 0.6, PL: [32, 0, 55]

chr9:64,107,070 g›<DUP>
intergenic variant
VAF: 14.29% Nanomonsv: TR: 28, VR: 4, SVTYPE: DUP, SVLEN: 280205, END: 64387275, SVINSLEN: 121, SVINSSEQ: GGAATGGAATGGATTCAACTTGAATGGAATGGAAAGAATGGAATCAACACGAGTGGAATGGCATGGATTGGAATGGAATGGAATGGAATCAACCCGAGTACAGGGGAATGGAATGGAATGG

chr9:118,497,472 A›<DUP>
intron variant, non coding transcript variant ***LOC107987108***
VAF: 21.88% Nanomonsv: TR: 32, VR: 7, SVTYPE: DUP, SVLEN: 5587, END: 118503059

chr11:84,243,710 a›aTCATAAAACAGA]chr11:84243766]
feature truncation, intron variant ***DLG2***
VAF: 30% Nanomonsv: TR: 10, VR: 3, SVTYPE: BND, SVINSLEN: 12, SVINSSEQ: TCATAAAACAGA , MATEID: r_28_1

chr11:84,243,766 t›tTCTGTTTTATGA]chr11:84243710]
feature truncation, intron variant ***DLG2***
VAF: 30% Nanomonsv: TR: 10, VR: 3, SVTYPE: BND, SVINSLEN: 12, SVINSSEQ: TCTGTTTTATGA , MATEID: r_28_0

chr11:93,638,403 A›G
missense variant ***CEP295***
NM_033395.2:c.5921A>G
NP_203753.1:p.Asn1974Ser
VAF: 20% DeepVariant: Qual: 4.2, GT: 0/1, GQ: 4, DP: 10, AD: [8, 2], VAF: 0.2, PL: [2, 0, 33]

chr11:123,378,828 c›[chr11:123378832[t
VAF: 20% Nanomonsv: TR: 15, VR: 3, SVTYPE: BND, MATEID: r_33_1

chr11:123,378,832 t›[chr11:123378828[t
VAF: 20% Nanomonsv: TR: 15, VR: 3, SVTYPE: BND, MATEID: r_33_0

chr12:11,920,356 A›[chr12:11920367[G
feature truncation, intron variant ***BCL2L14***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, MATEID: r_36_1

chr12:11,920,367 G›[chr12:11920356[G
feature truncation, intron variant ***BCL2L14***
VAF: 23.08% Nanomonsv: TR: 13, VR: 3, SVTYPE: BND, MATEID: r_36_0

chr12:55,807,475 A›G
missense variant ***MMP19***
NM_002429.6:c.359T>C
NP_002420.1:p.Leu120Pro
VAF: 20% DeepVariant: Qual: 5.9, GT: 0/1, GQ: 6, DP: 10, AD: [8, 2], VAF: 0.2, PL: [4, 0, 34]

chr12:58,216,365 A›A]chr12:58216387]
VAF: 25% Nanomonsv: TR: 12, VR: 3, SVTYPE: BND, MATEID: r_38_1

chr12:58,216,387 C›C]chr12:58216365]
VAF: 25% Nanomonsv: TR: 12, VR: 3, SVTYPE: BND, MATEID: r_38_0

chr13:77,949,309 A›A]chr13:77949363]

VAF: 13.64%

Nanomonsv:

TR: 22, VR: 3, SVTYPE: BND, MATEID: r_44_1

chr13:77,949,363 t›t]chr13:77949309]

VAF: 13.64%

Nanomonsv:

TR: 22, VR: 3, SVTYPE: BND, MATEID: r_44_0

chr13:108,717,066 g›gAGCATGACCGCCTGAGCTCCGCCTCC...

intergenic variant

VAF: 23.08%

Nanomonsv:

TR: 13, VR: 3, SVTYPE: INS, END: 108717066, SVINSLEN: 778, SVINSSEQ:

```
AGCATGACCGCCTGAGCTCCGCCTCCTGGTCAGATCCCAGACAGCATGACCGCCTGAGCT
CCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGATCCC
AGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGA
GCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGAT
CCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCC
TGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCA
GATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACC
GCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTG
TCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATG
ACCGCCTGAGCTCCGCCTCCTGTCACATCCCAGACAGCATGACCGCCTGAGCTCCGCCTC
CTGTCAGATCCCAGAACAGCATCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCAT
GACCGCCTGAGCTCCGCCTCCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCT
CCTGTCAGATCCCAGACAGCATGACCGCCTGAGCTCCGCCTCCTGTCAATCCCAGACA
```

chr13:112,754,534 G›C
missense variant ***TMCO3***
NM_017905.6:c.110G>C
NP_060375.4:p.Arg37Pro
VAF: 40% DeepVariant: Qual: 16.2, GT: 0/1, GQ: 16, DP: 10, AD: [6, 4], VAF: 0.4, PL: [16, 0, 45] ClairS: Qual: 13.304, GT: 0/1, GQ: 13, DP: 10, AF: 0.4, AD: [0, 4], NAF: 0, NDP: 14, NAD: [0, 0], AU: 0, CU: 4, GU: 6, TU: 0, NAU: 0, NCU: 0, NGU: 14, NTU: 0, H, FAU: 0, FCU: 2, FGU: 1, FTU: 0, RAU: 0, RCU: 2, RGU: 5, RTU: 0

chr15:63,499,976 G›A
stop gained ***DENND4A***
NM_005848.4:c.3886C>T
NP_005839.3:p.Gln1296Ter
VAF: 33.33% DeepVariant: Qual: 4.3, GT: 0/1, GQ: 4, DP: 6, AD: [4, 2], VAF: 0.333333, PL: [2, 0, 31]

chr15:70,106,668 C›A
missense variant ***CELF6***
NM_052840.5:c.455G>T
NP_443072.3:p.Arg152Leu
VAF: 40% GnomAD: 0.0000065 DeepVariant: Qual: 6, GT: 0/1, GQ: 6, DP: 5, AD: [3, 2], VAF: 0.4, PL: [4, 0, 24]

chr15:84,144,947 a›a]chr15:84144948]
feature truncation, intron variant ***AGBL1***
VAF: 10.34% Nanomonsv: TR: 29, VR: 3, SVTYPE: BND, MATEID: r_53_0

chr15:84,144,948 a›a]chr15:84144947]
feature truncation, intron variant ***AGBL1***
VAF: 10.34% Nanomonsv: TR: 29, VR: 3, SVTYPE: BND, MATEID: r_53_1

chr16:52,460,022 A›AT
frameshift variant ***VPS35***
NM_018206.6:c.1656dup
NP_060676.2:p.Trp553MetfsTer45
VAF: 75% DeepVariant: Qual: 6.5, GT: 1/1, GQ: 3, DP: 4, AD: [1, 3], VAF: 0.75, PL: [3, 1, 0]

chr16:82,597,842 G›G]chr16:82597864]
feature truncation, intron variant ***CNTNAP4***
VAF: 18.75% Nanomonsv: TR: 16, VR: 3, SVTYPE: BND, MATEID: r_58_1

chr16:82,597,864 T›T]chr16:82597842]
feature truncation, intron variant ***CNTNAP4***
VAF: 18.75% Nanomonsv: TR: 16, VR: 3, SVTYPE: BND, MATEID: r_58_0

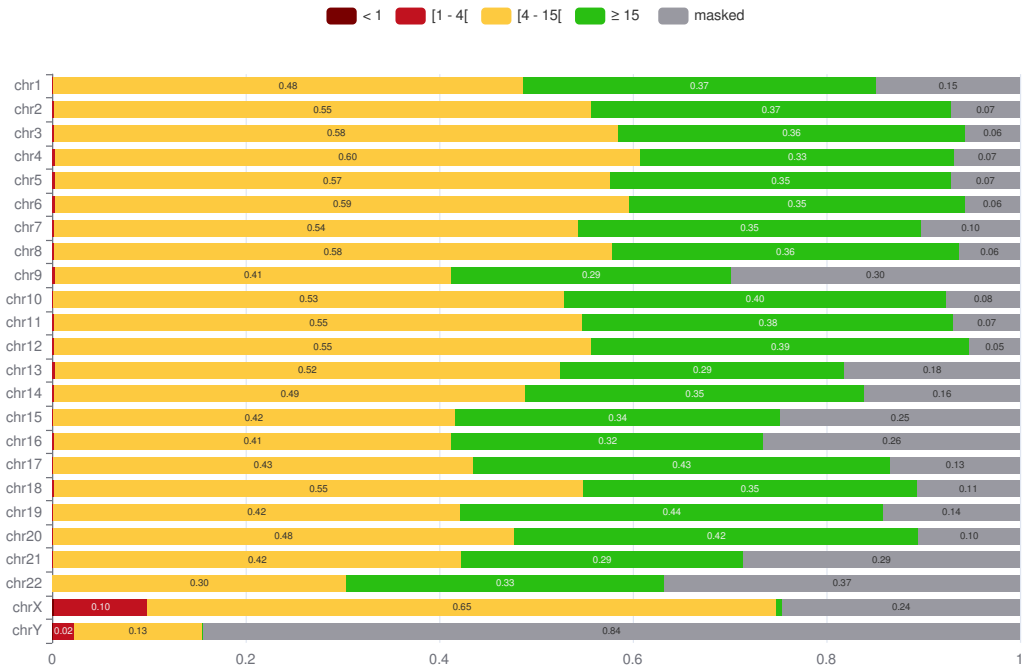
chr19:5,854,946 G›A
missense variant ***FUT5***
NM_002034.2:c.206C>T
NP_002025.2:p.Ala69Val
VAF: 40% GnomAD: 0.0000065 DeepVariant: Qual: 7.8, GT: 0/1, GQ: 8, DP: 5, AD: [3, 2], VAF: 0.4, PL: [7, 0, 31]

chr20:52,362,700 T›A
stop gained ***RIPOR3***
NM_080829.4:c.2356A>T
NP_543019.2:p.Lys786Ter
VAF: 25% DeepVariant: Qual: 3.4, GT: 0/1, GQ: 3, DP: 8, AD: [6, 2], VAF: 0.25, PL: [0, 0, 33]

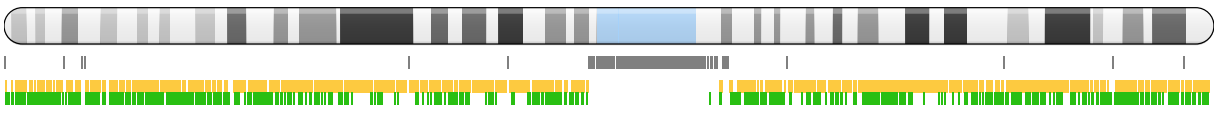
chr22:22,370,851 T>C
missense variant ***TOP3B***
NM_003935.5:c.2383A>G
NP_003926.1:p.Thr795Ala
VAF: 28.57% Cosmic: 1 GnomAD: 0.0000065 DeepVariant: Qual: 5.7, GT: 0/1, GQ: 6, DP: 7, AD: [5, 2], VAF: 0.285714, PL: [4, 0, 24]

5 Coverage by chromosome

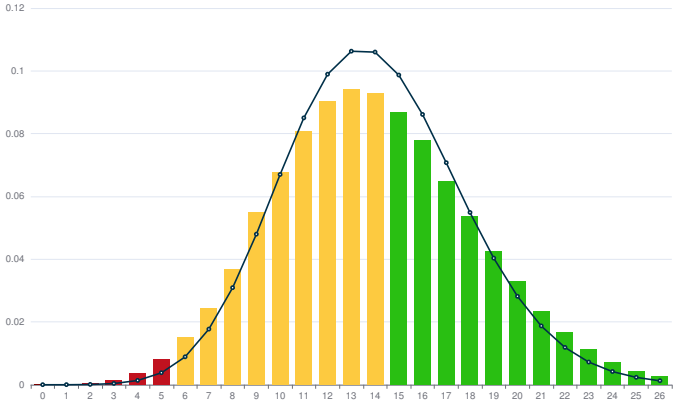
5.1 Proportion at given depth by chromosome



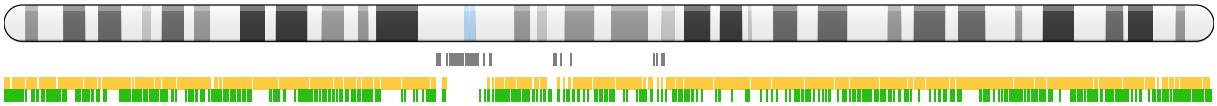
chr1



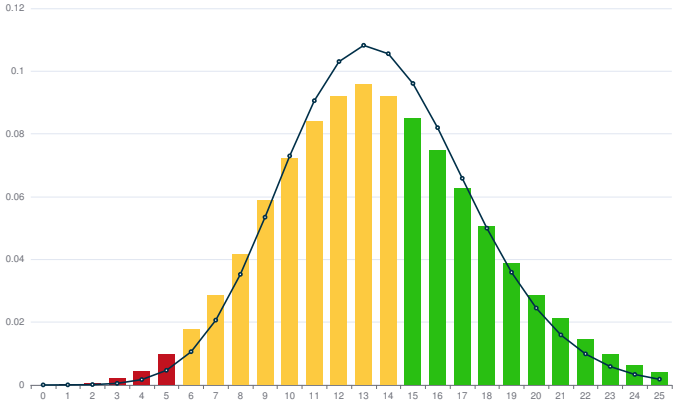
Mean	13.96
Standard dev.	4.26
< 1	0%
[1 - 4[	0.2%
[4 - 15[	56.9%
≥ 15	42.9%



chr2

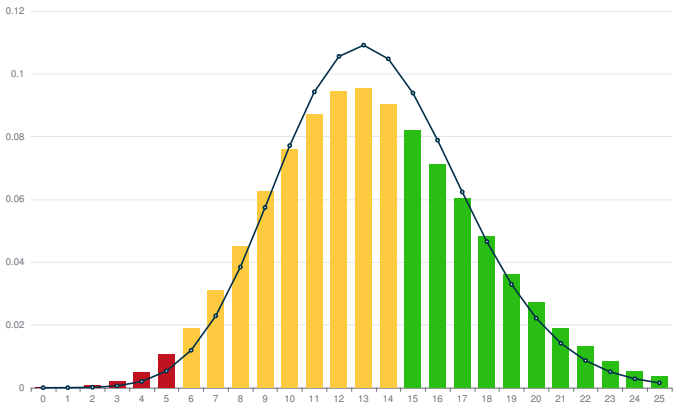


Mean	13.65
Standard dev.	4.23
< 1	0%
[1 - 4[	0.3%
[4 - 15[	59.7%
≥ 15	40.1%

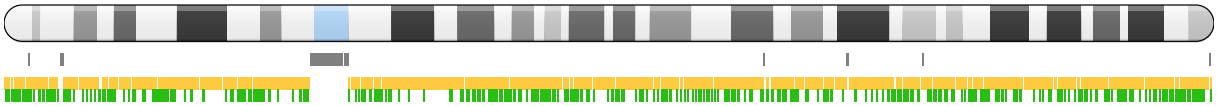


chr3

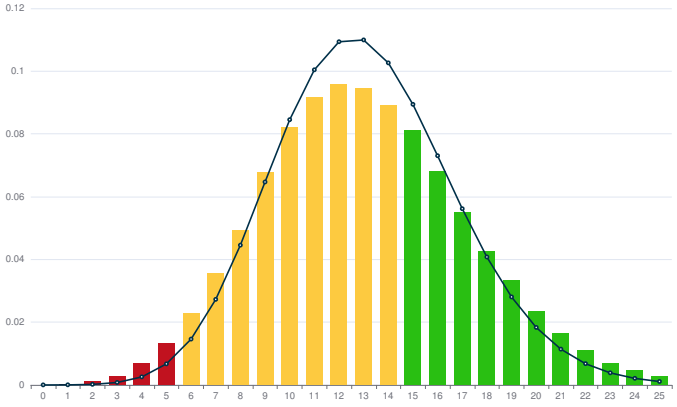
Mean	13.44
Standard dev.	4.22
< 1	0%
[1 - 4[	0.3%
[4 - 15[	61.7%
≥ 15	38%



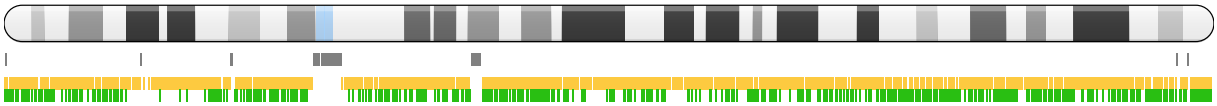
chr4



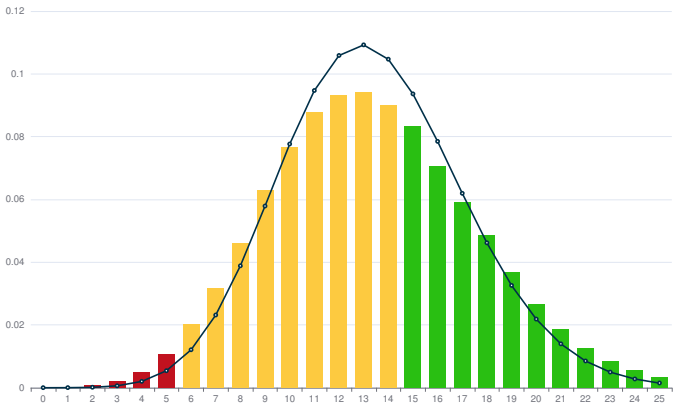
Mean	13.07
Standard dev.	4.17
< 1	0%
[1 - 4[	0.4%
[4 - 15[	64.8%
≥ 15	34.9%



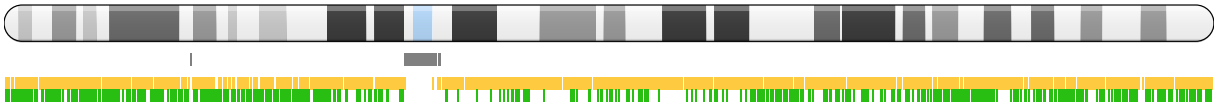
chr5



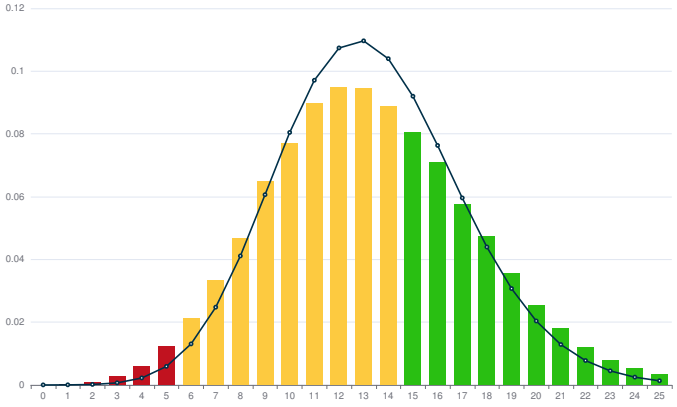
Mean	13.41
Standard dev.	4.27
< 1	0%
[1 - 4[	0.3%
[4 - 15[	61.8%
≥ 15	37.9%



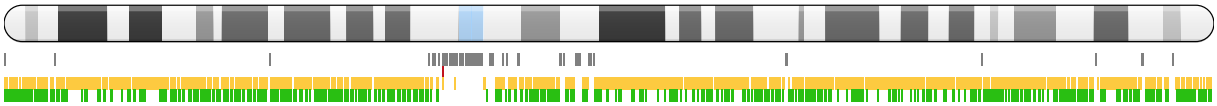
chr6



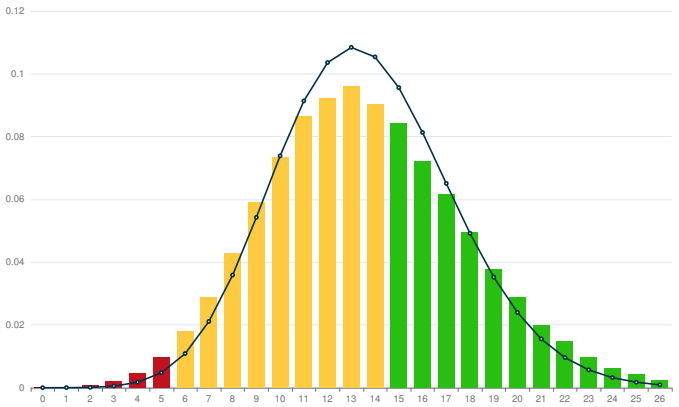
Mean	13.27
Standard dev.	4.22
< 1	0%
[1 - 4[	0.4%
[4 - 15[	62.9%
≥ 15	36.8%



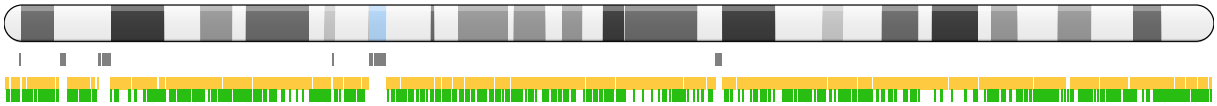
chr7



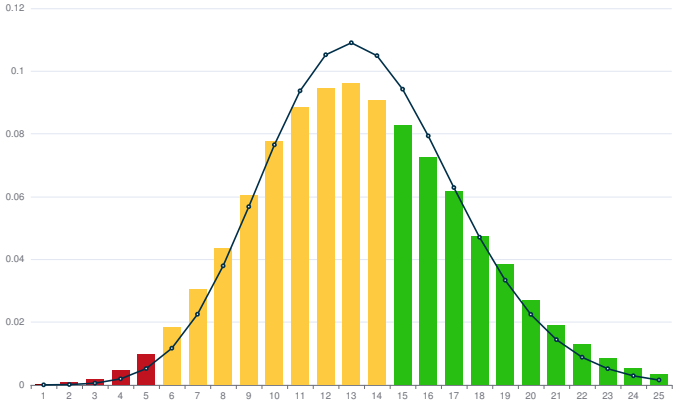
Mean	13.61
Standard dev.	4.26
< 1	0%
[1 - 4[	0.3%
[4 - 15[	60.2%
≥ 15	39.5%



chr8

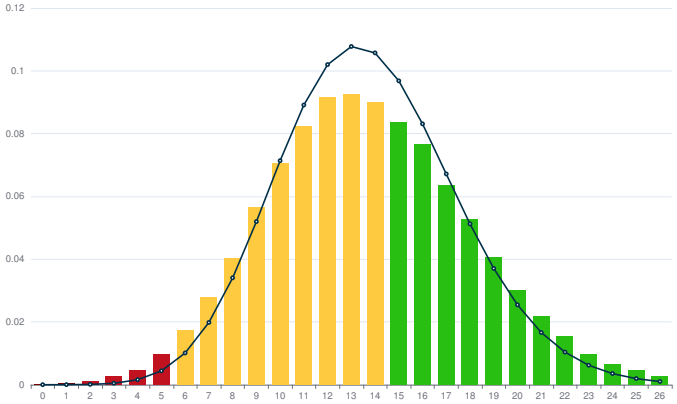


Mean	13.47
Standard dev.	4.17
< 1	0%
[1 - 4[	0.2%
[4 - 15[	61.4%
≥ 15	38.3%

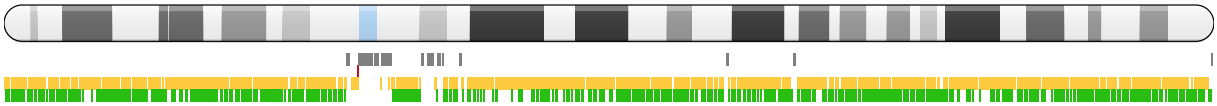


chr9

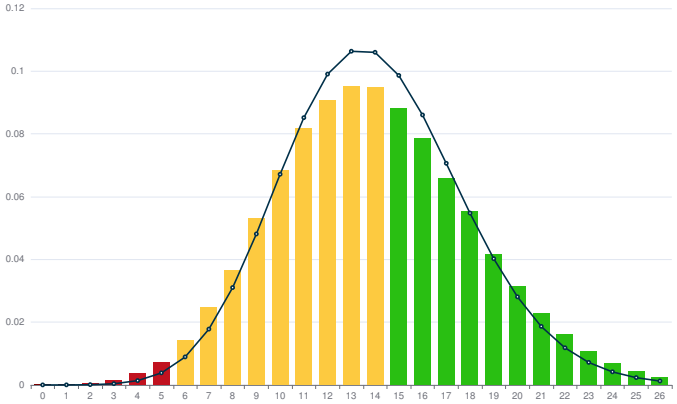
Mean	13.74
Standard dev.	4.32
< 1	0%
[1 - 4[	0.4%
[4 - 15[	58.4%
≥ 15	41.2%



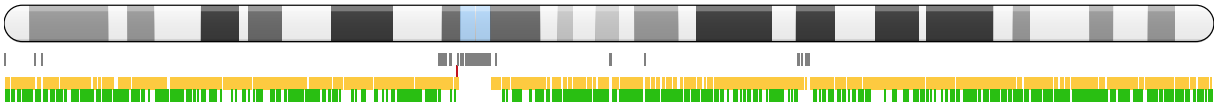
chr10



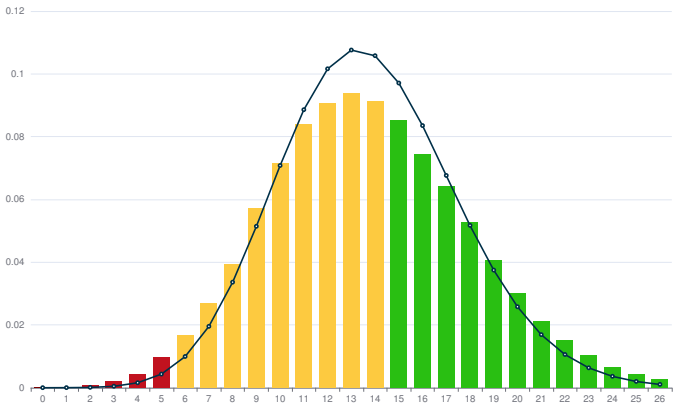
Mean	13.96
Standard dev.	4.21
< 1	0%
[1 - 4[	0.2%
[4 - 15[	57%
≥ 15	42.8%



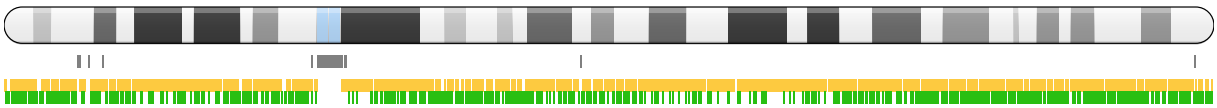
chr11



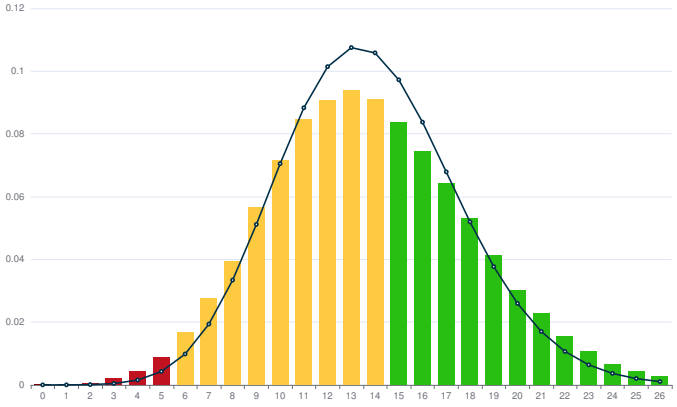
Mean	13.77
Standard dev.	4.27
< 1	0%
[1 - 4[	0.3%
[4 - 15[	58.6%
≥ 15	41.1%



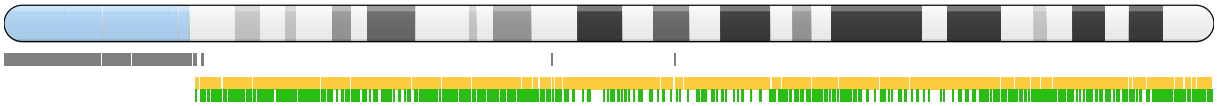
chr12



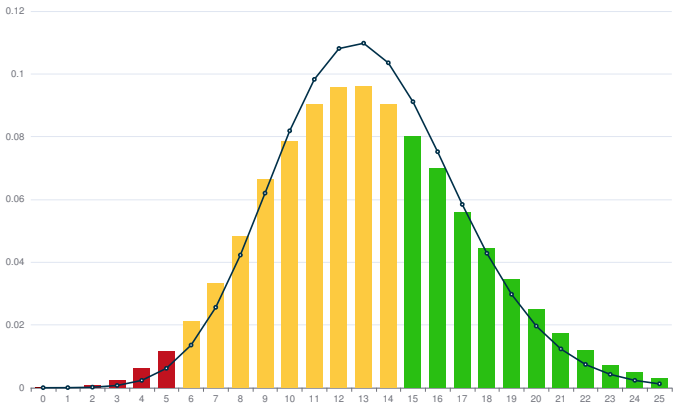
Mean	13.78
Standard dev.	4.27
< 1	0%
[1 - 4[	0.3%
[4 - 15[	58.5%
≥ 15	41.2%



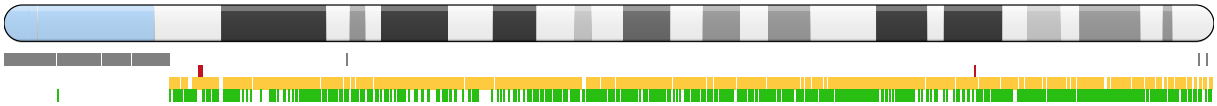
chr13



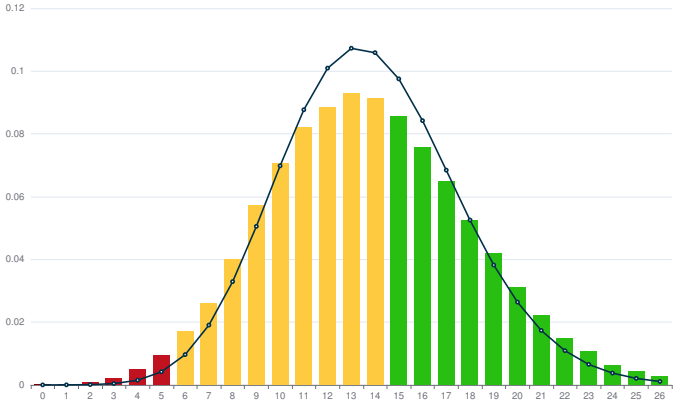
Mean	13.2
Standard dev.	4.17
< 1	0%
[1 - 4[	0.3%
[4 - 15[	63.8%
≥ 15	35.9%



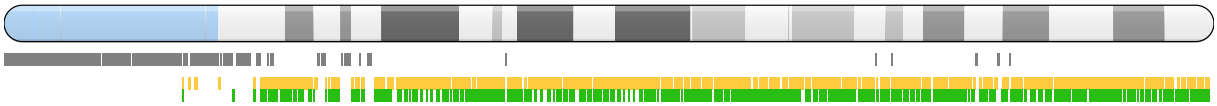
chr14



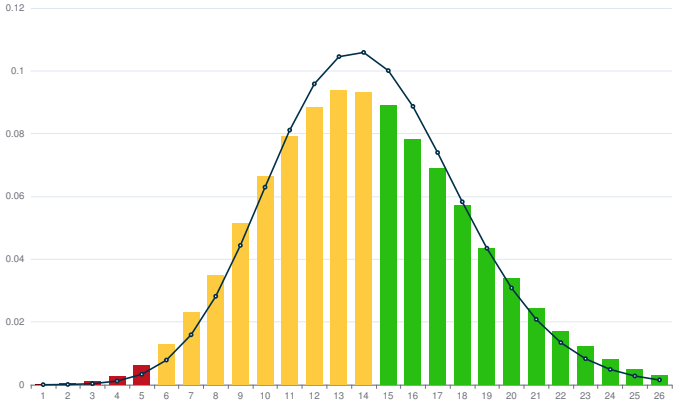
Mean	13.82
Standard dev.	4.34
< 1	0%
[1 - 4[	0.3%
[4 - 15[	58%
≥ 15	41.7%



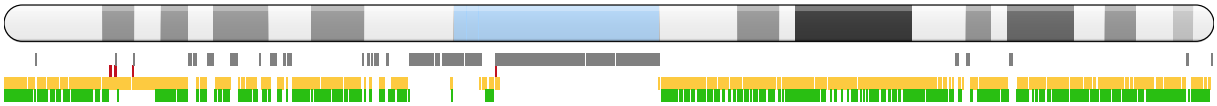
chr15



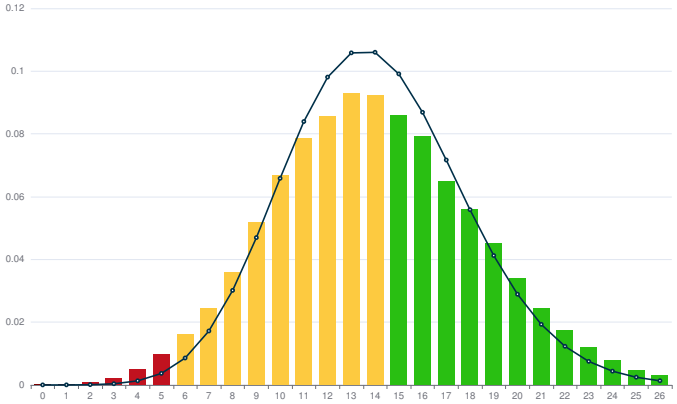
Mean	14.18
Standard dev.	4.29
< 1	0%
[1 - 4[	0.1%
[4 - 15[	55.2%
≥ 15	44.7%



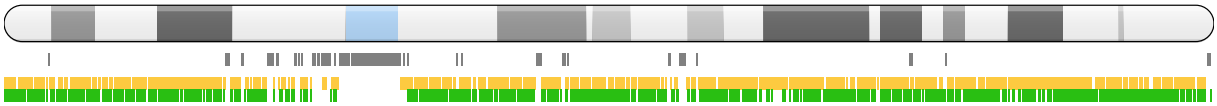
chr16



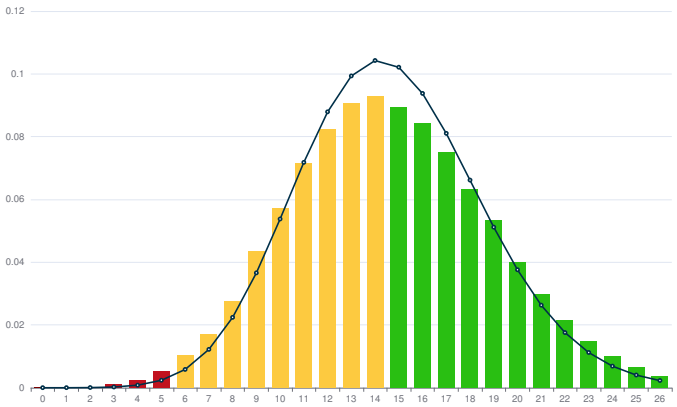
Mean	14.02
Standard dev.	4.35
< 1	0%
[1 - 4[	0.3%
[4 - 15[	55.8%
≥ 15	43.8%



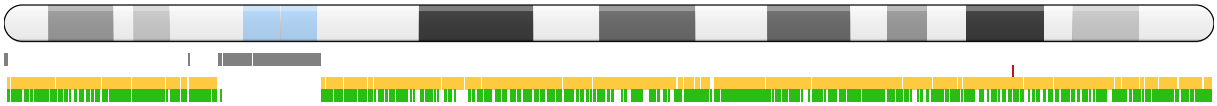
chr17



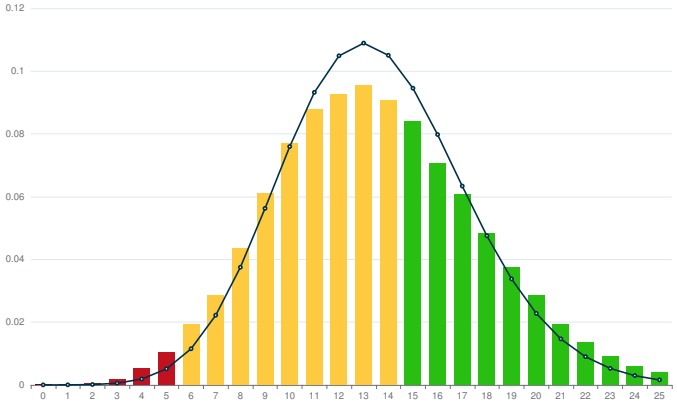
Mean	14.69
Standard dev.	4.32
< 1	0%
[1 - 4[	0.1%
[4 - 15[	50.1%
≥ 15	49.8%



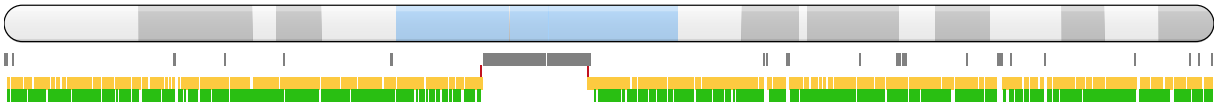
chr18



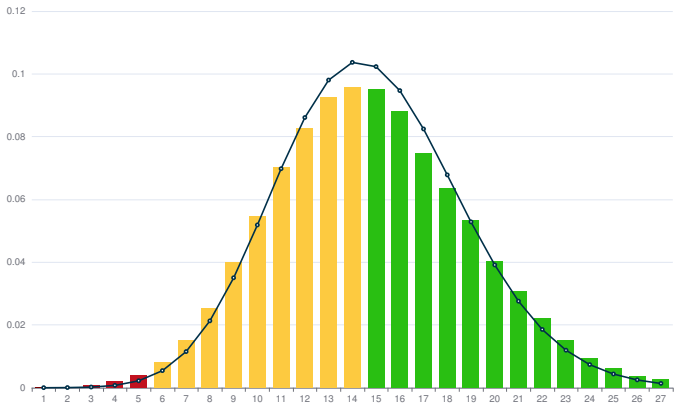
Mean	13.5
Standard dev.	4.21
< 1	0%
[1 - 4[	0.3%
[4 - 15[	61.1%
≥ 15	38.6%



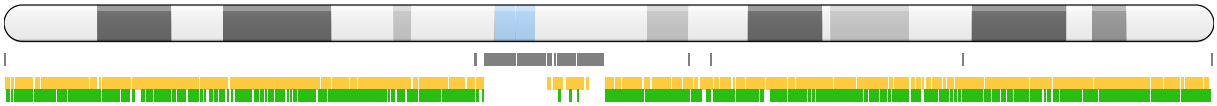
chr19



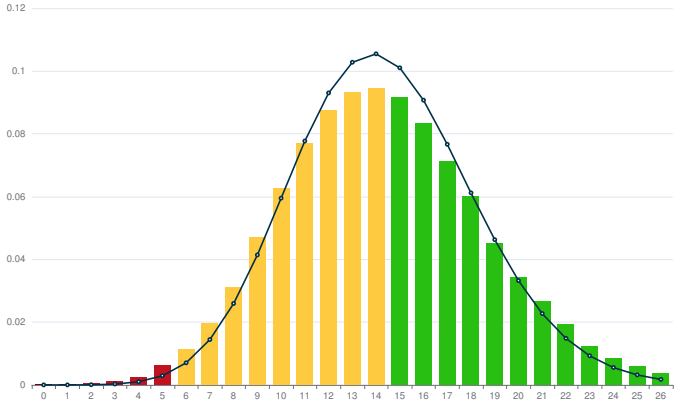
Mean	14.8
Standard dev.	4.21
< 1	0%
[1 - 4[	0.1%
[4 - 15[	49.1%
≥ 15	50.8%



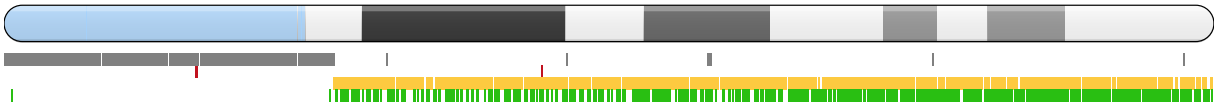
chr20



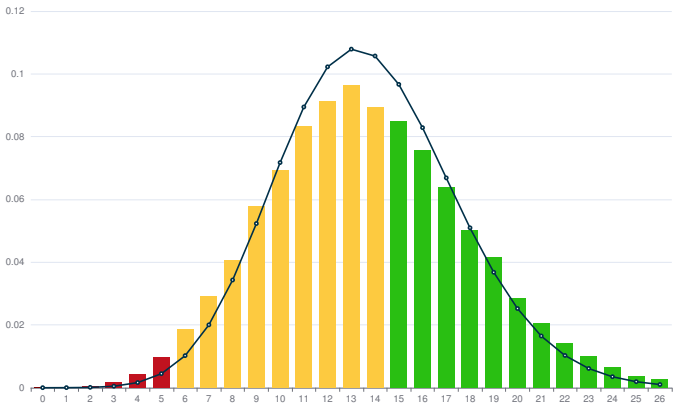
Mean	14.37
Standard dev.	4.23
< 1	0%
[1 - 4[	0.1%
[4 - 15[	53.2%
≥ 15	46.7%



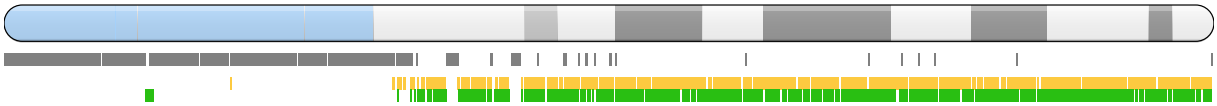
chr21



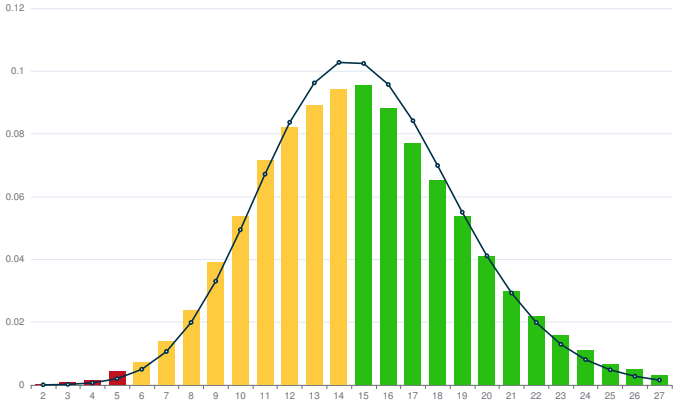
Mean	13.72
Standard dev.	4.28
< 1	0%
[1 - 4[	0.2%
[4 - 15[	59%
≥ 15	40.8%



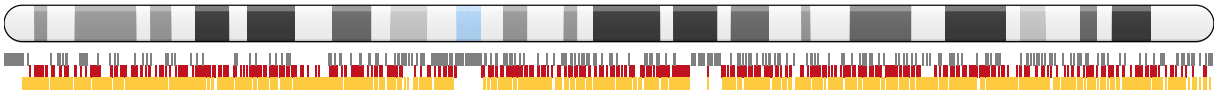
chr22



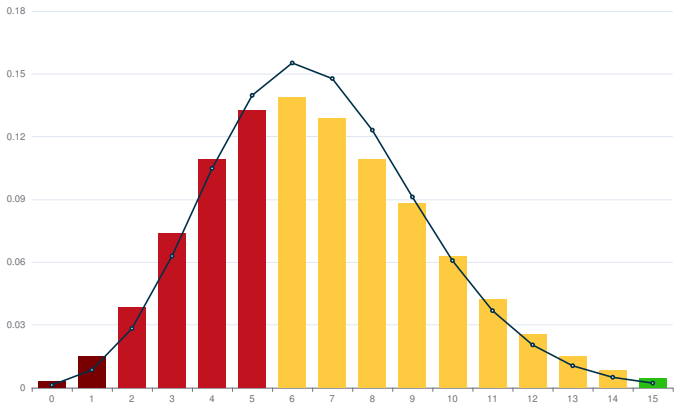
Mean	14.95
Standard dev.	4.33
< 1	0%
[1 - 4[	0.1%
[4 - 15[	48%
≥ 15	51.9%



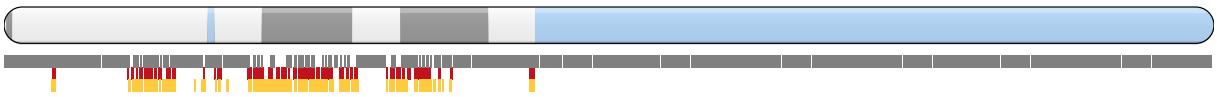
chrX



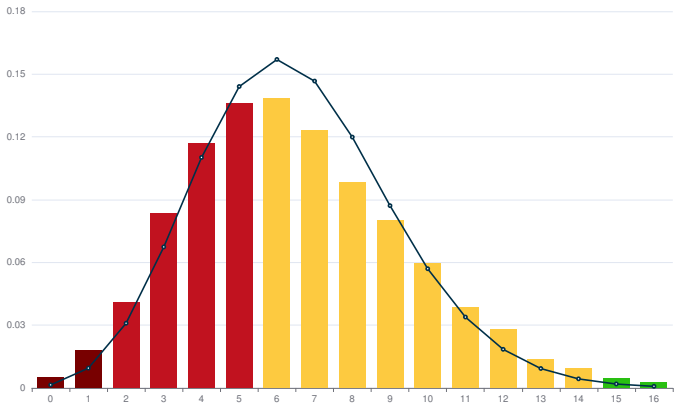
Mean	6.66
Standard dev.	2.89
< 1	0.3%
[1 - 4[	12.8%
[4 - 15[	86.1%
≥ 15	0.8%



chrY



Mean	6.54
Standard dev.	3
< 1	0.5%
[1 - 4[	14.2%
[4 - 15[	84.2%
≥ 15	1.1%



6 Method

6.1 Sample preparation and sequencing

1. DNA sampling and collection in EDTA tubes.
2. Buffy coat: pooling of multiple EDTA tubes then centrifugation (1200 rpm 10 minutes).

Values computed by Pandora development version

3. DNA extraction according to Maxwell® Promega RSC Buffy Coat DNA Kit.
4. Nanodrop DNA quantification.
5. DNA shearing: 3µg of DNA mechanically sheared by Covaris g-TUBE (8000 rpm, 1 minute).
6. DNA size qualification aiming a median of 10 kb determined by TapeStation.
7. Libary was constructed following the Oxford Nanopore Technologies Ligation Sequencing Kit V14 (SQK-LSK114) protocol with 1.5 µg as input DNA.
8. Qubit quantification
9. After evaluation of flowcell (rev 10) for pore availability (> 6000 available pores). Two distinct barcoded libraries were pooled for each flowcell.
10. sequencing run was initiated and controlled using MinKNOW software (sequencing 80 hours, data output format: Raw pod5 files).

6.2 Bioinformatic analysis

1. Orchestration and global analysis realized by in-house software (source code is accessible at Github).
2. Basecalling and alignment: dorado v0.8.2 with parameters “sup,5mC_5hmC –trim all” with alignment on hs1 genome (T2T chm13v2.0).
3. Variant calling was realized with ClairS v0.4.0, DeepVariant v1.6.1, DeepSomatic v1.7.0, Nanomonsv v0.7.2.
4. Variants filtering and merging done with in-house software.
5. Annotation: ensembl-VEP 112 with gene features defined by RefSeq Liftoff v5.1. SNP from gnomAD_4-2022_10 and Cosmic v99.
6. Interpretation and report generation performed on a local web service also published in open source.