

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/19 07:04:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618611.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR618611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618611_1.fastq.gz SRR618611_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Jan 19 07:04:16 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	46,595,358
Mapped reads	45,156,555 / 96.91%
Unmapped reads	1,438,803 / 3.09%
Mapped paired reads	45,156,555 / 96.91%
Mapped reads, first in pair	22,786,283 / 48.9%
Mapped reads, second in pair	22,370,272 / 48.01%
Mapped reads, both in pair	44,437,424 / 95.37%
Mapped reads, singletons	719,131 / 1.54%
Secondary alignments	0
Supplementary alignments	150,241 / 0.32%
Read min/max/mean length	30 / 100 / 100.13
Duplicated reads (estimated)	15,486,870 / 33.24%
Duplication rate	27.99%
Clipped reads	10,469,609 / 22.47%

2.2. ACGT Content

Number/percentage of A's	1,162,873,021 / 27.45%
Number/percentage of C's	908,624,211 / 21.45%
Number/percentage of T's	1,180,549,232 / 27.86%
Number/percentage of G's	984,792,838 / 23.24%
Number/percentage of N's	150,749 / 0%

GC Percentage	44.69%
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2.3. Coverage

Mean	1.3696
Standard Deviation	5.8112

2.4. Mapping Quality

Mean Mapping Quality	51.77
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2.5. Insert size

Mean	65,216.88
Standard Deviation	2,543,385.66
P25/Median/P75	154 / 183 / 223

2.6. Mismatches and indels

General error rate	1.23%
Mismatches	51,107,748
Insertions	774,083
Mapped reads with at least one insertion	1.68%
Deletions	2,159,755
Mapped reads with at least one deletion	4.66%
Homopolymer indels	52.68%

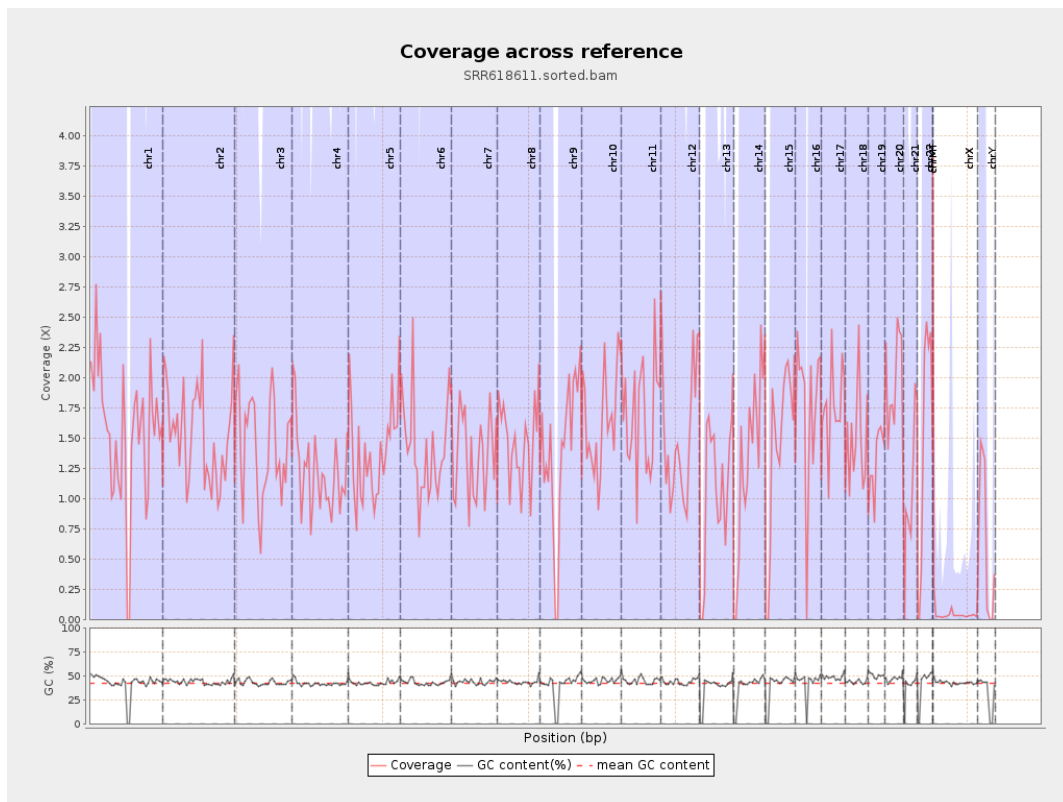
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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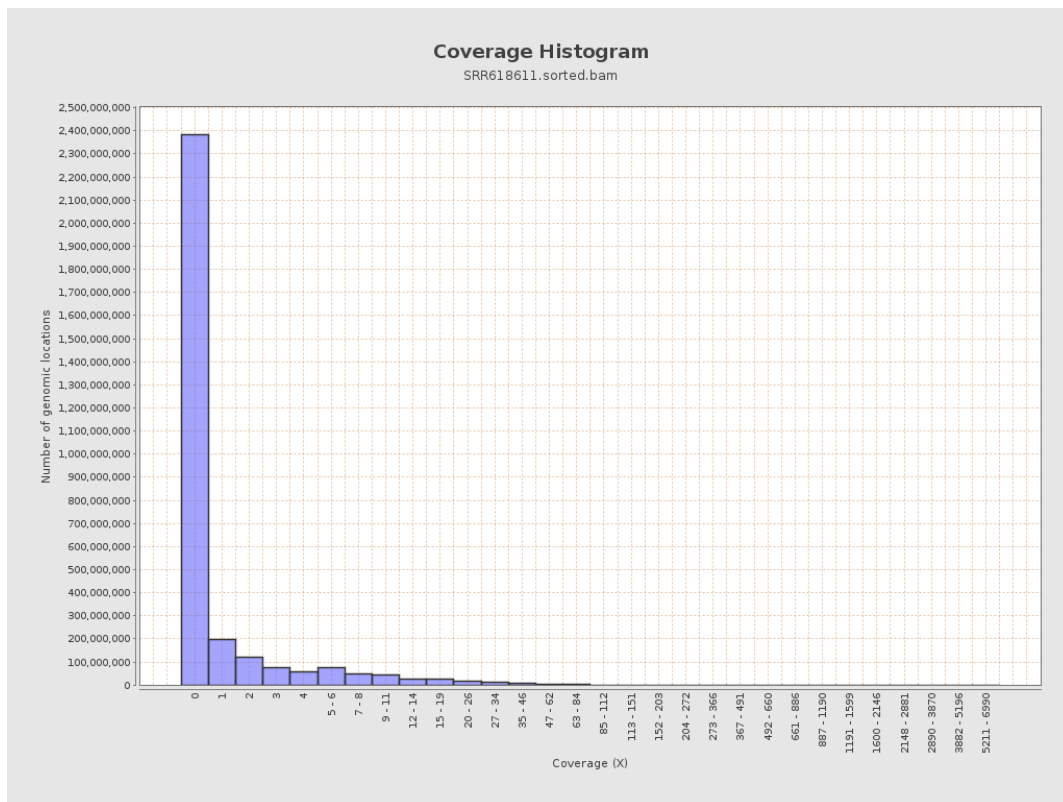
		bases	coverage	deviation
chr1	249250621	383993731	1.5406	6.2885
chr2	243199373	372033738	1.5297	7.6624
chr3	198022430	280925774	1.4187	4.6583
chr4	191154276	231854768	1.2129	4.9631
chr5	180915260	253175621	1.3994	4.7399
chr6	171115067	240169201	1.4036	4.8361
chr7	159138663	216839434	1.3626	4.7867
chr8	146364022	213620986	1.4595	4.8041
chr9	141213431	196151465	1.389	5.7989
chr10	135534747	221530624	1.6345	5.365
chr11	135006516	227508620	1.6852	6.0408
chr12	133851895	201406315	1.5047	5.3235
chr13	115169878	122286510	1.0618	3.9998
chr14	107349540	140528063	1.3091	4.7856
chr15	102531392	146537665	1.4292	5.1117
chr16	90354753	155035949	1.7159	13.1074
chr17	81195210	142834660	1.7592	6.0018
chr18	78077248	114111089	1.4615	5.5477
chr19	59128983	78072880	1.3204	5.5284
chr20	63025520	124292784	1.9721	6.1544
chr21	48129895	52680733	1.0946	7.1808
chr22	51304566	77937873	1.5191	6.0559
chrMT	16571	63499	3.8319	4.8137
chrX	155270560	6792631	0.0437	1.1877

chrY	59373566	39581249	0.6666	5.6859
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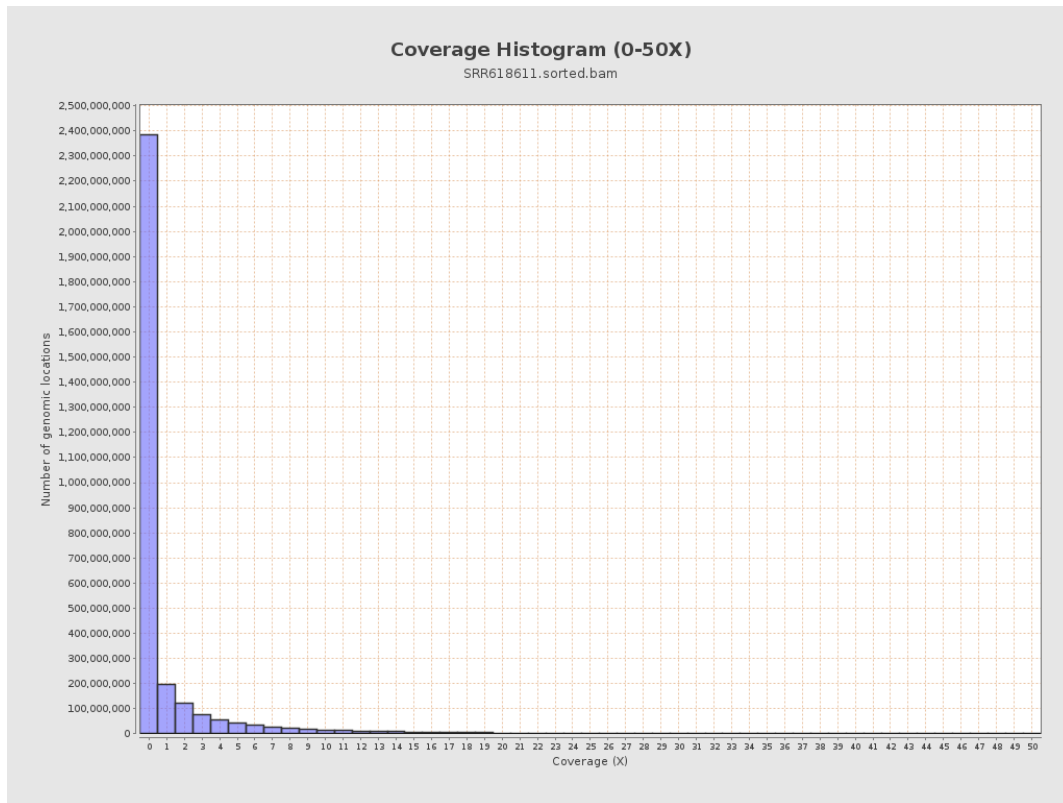
3. Results : Coverage across reference



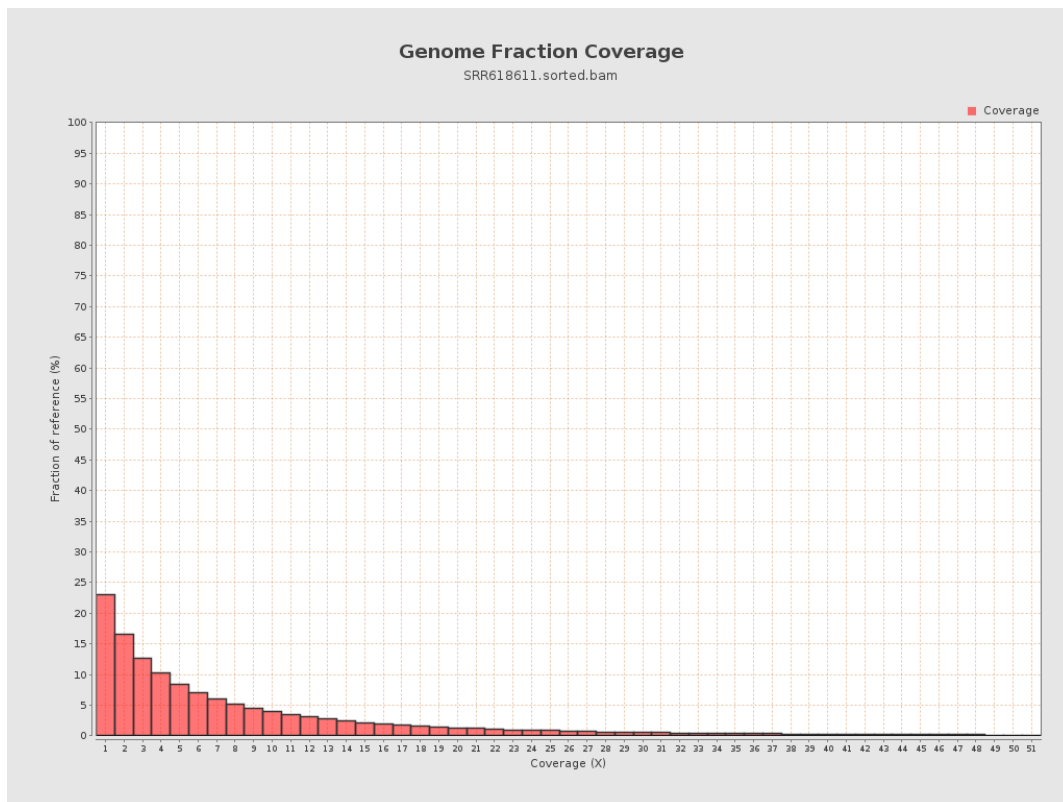
4. Results : Coverage Histogram



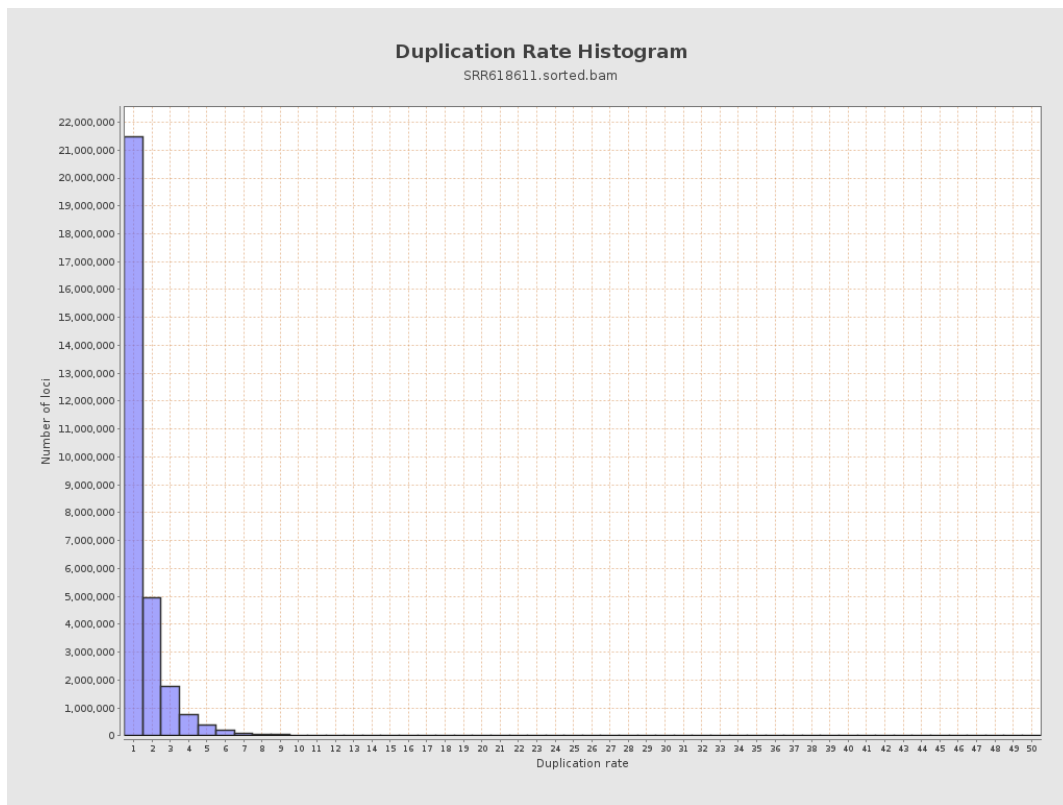
5. Results : Coverage Histogram (0-50X)



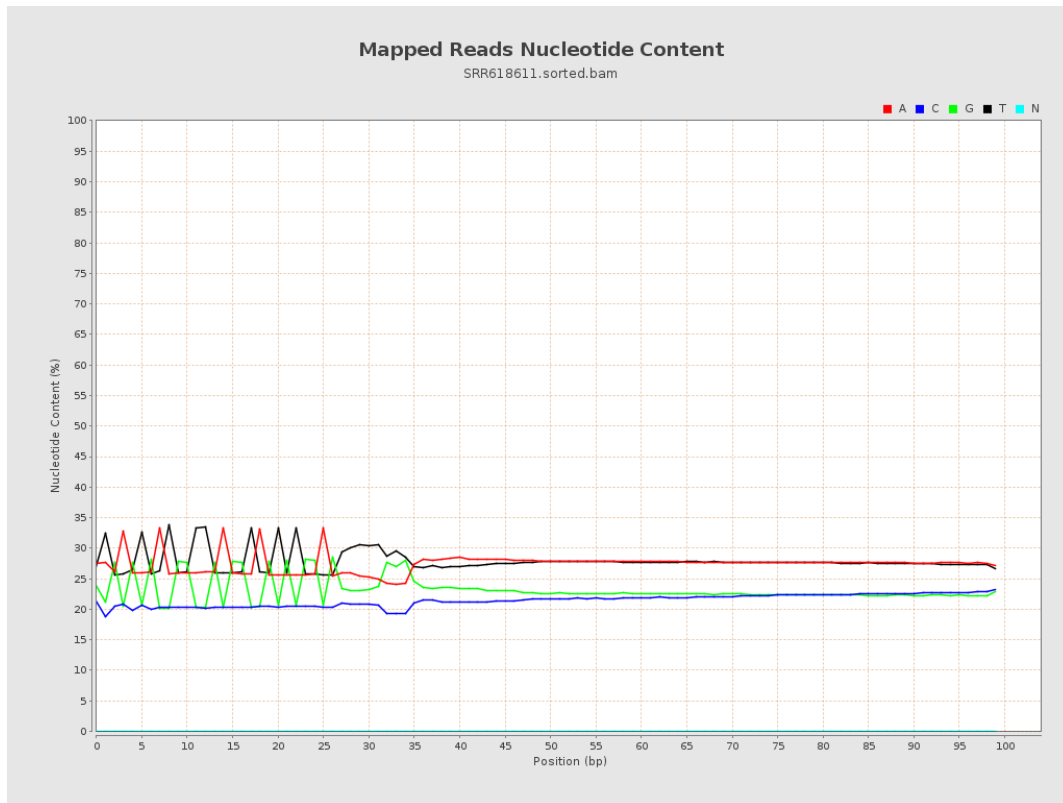
6. Results : Genome Fraction Coverage



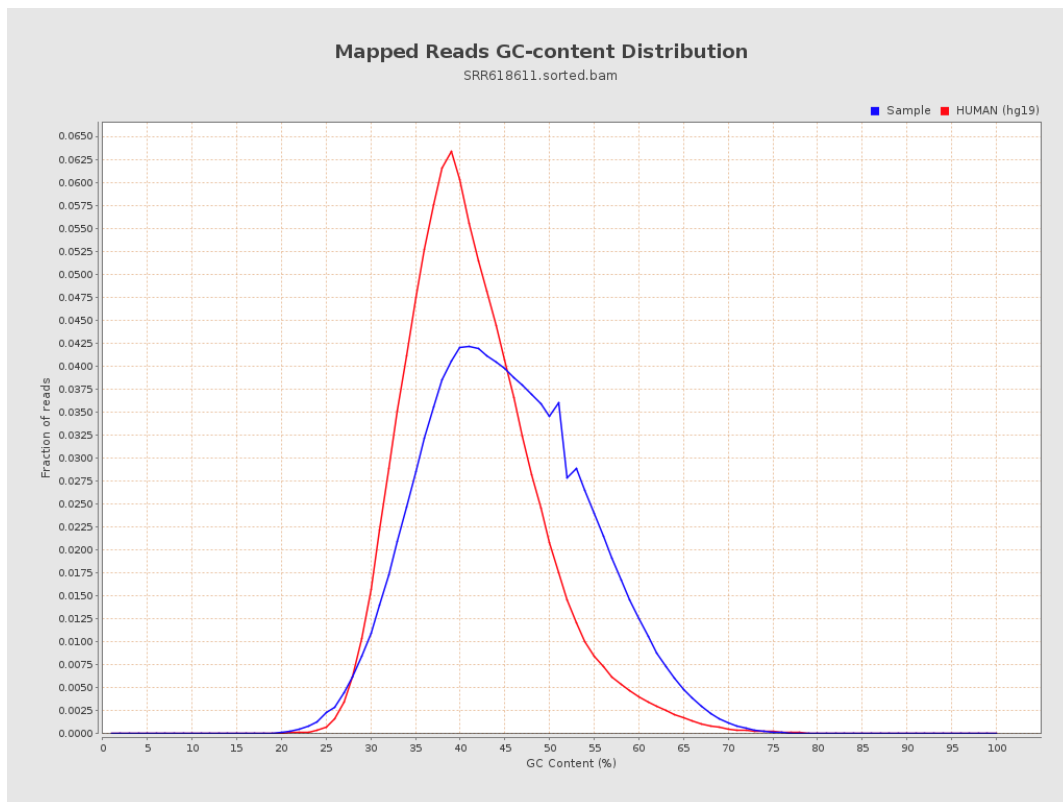
7. Results : Duplication Rate Histogram



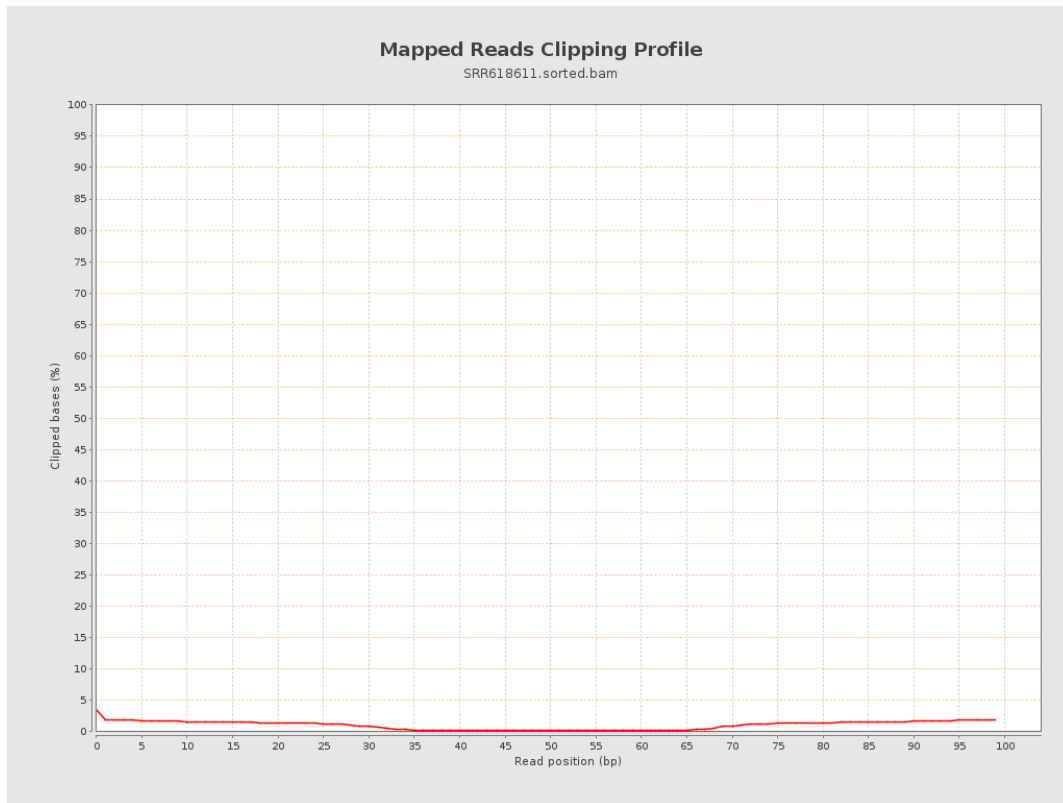
8. Results : Mapped Reads Nucleotide Content



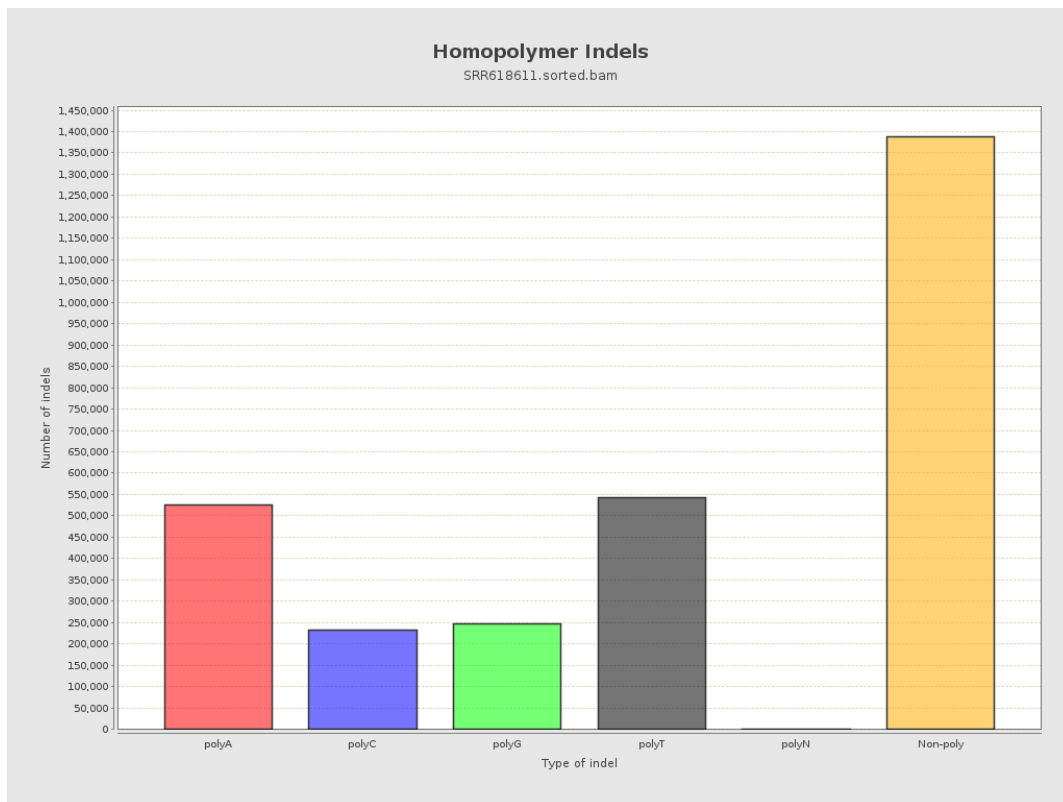
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



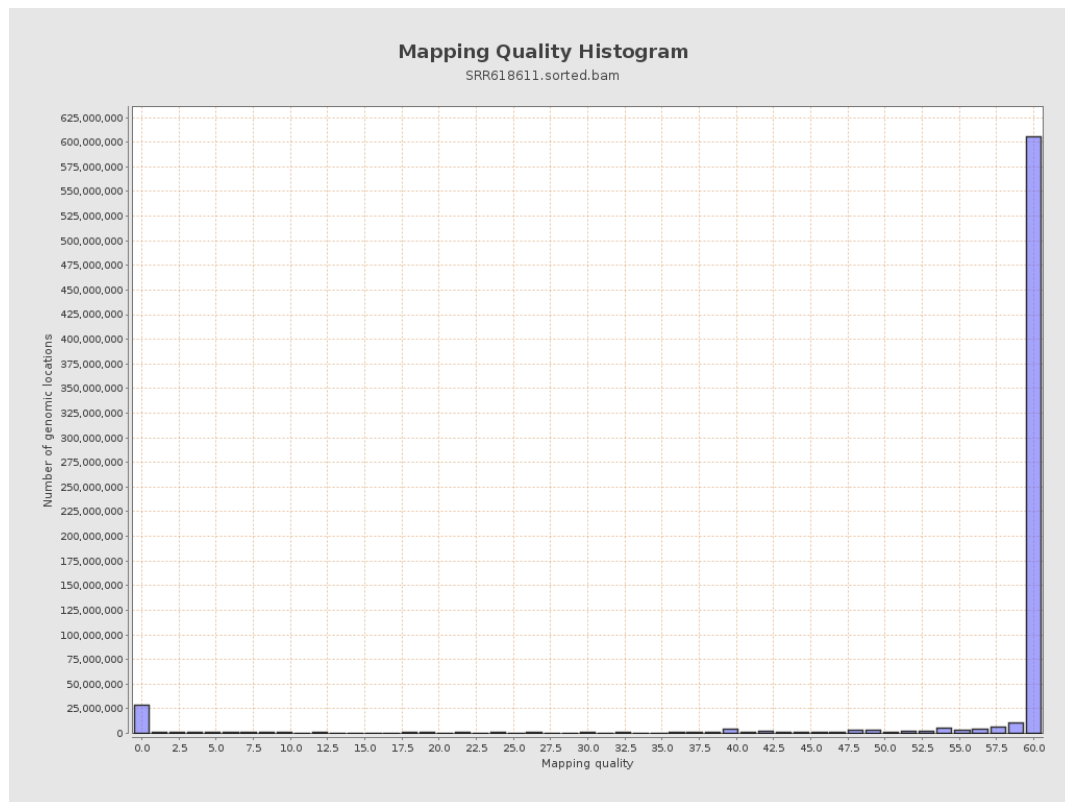
11. Results : Homopolymer Indels



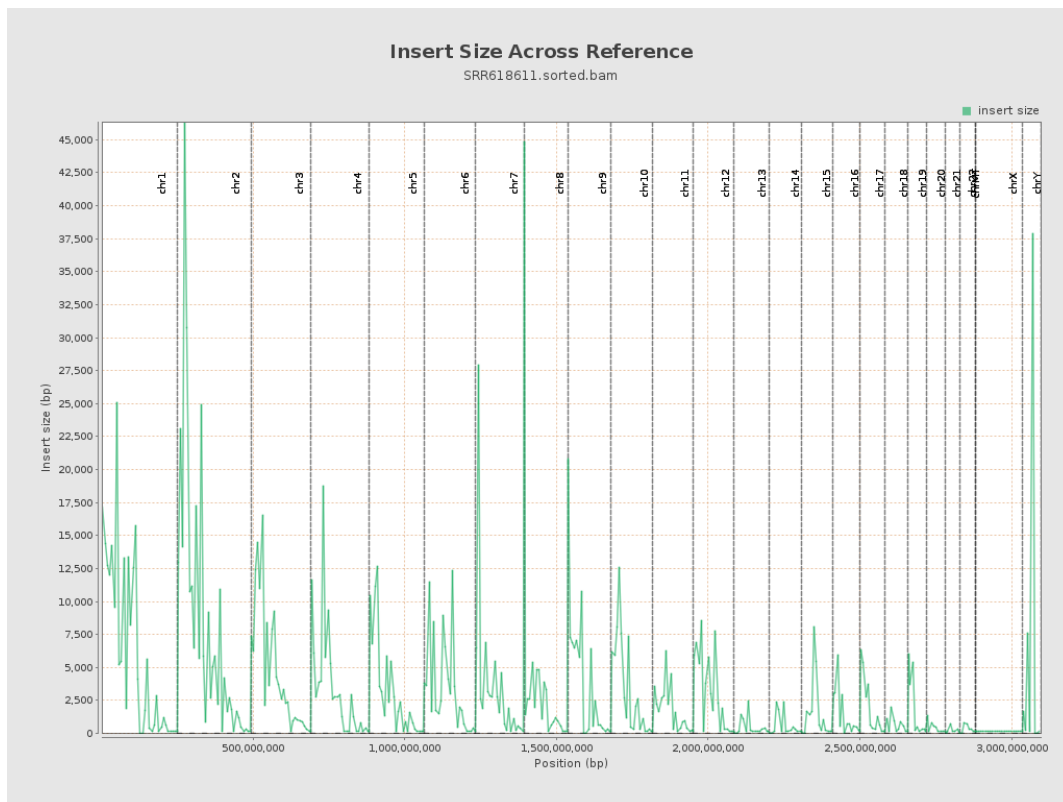
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

