Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2025/01/22 08:43:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR618671.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_SRR618671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR618671_1.fastq.gz SRR618671_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jan 22 08:43:58 CST 2025
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR618671.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	218,866,816
Mapped reads	211,990,830 / 96.86%
Unmapped reads	6,875,986 / 3.14%
Mapped paired reads	211,990,830 / 96.86%
Mapped reads, first in pair	105,977,378 / 48.42%
Mapped reads, second in pair	106,013,452 / 48.44%
Mapped reads, both in pair	209,102,344 / 95.54%
Mapped reads, singletons	2,888,486 / 1.32%
Secondary alignments	0
Supplementary alignments	557,159 / 0.25%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	34,905,342 / 15.95%
Duplication rate	12.03%
Clipped reads	26,689,816 / 12.19%

2.2. ACGT Content

Number/percentage of A's	6,091,541,037 / 29.58%
Number/percentage of C's	4,232,420,186 / 20.55%
Number/percentage of T's	6,064,296,266 / 29.44%
Number/percentage of G's	4,205,637,997 / 20.42%
Number/percentage of N's	2,309,437 / 0.01%

GC Percentage	40.97%

2.3. Coverage

Mean	6.6551
Standard Deviation	62.9692

2.4. Mapping Quality

Mean Mapping Quality	53.69

2.5. Insert size

Mean	42,150.46
Standard Deviation	1,965,218.49
P25/Median/P75	227 / 256 / 295

2.6. Mismatches and indels

General error rate	1.04%
Mismatches	209,334,740
Insertions	2,300,475
Mapped reads with at least one insertion	1.06%
Deletions	2,628,068
Mapped reads with at least one deletion	1.21%
Homopolymer indels	41.3%

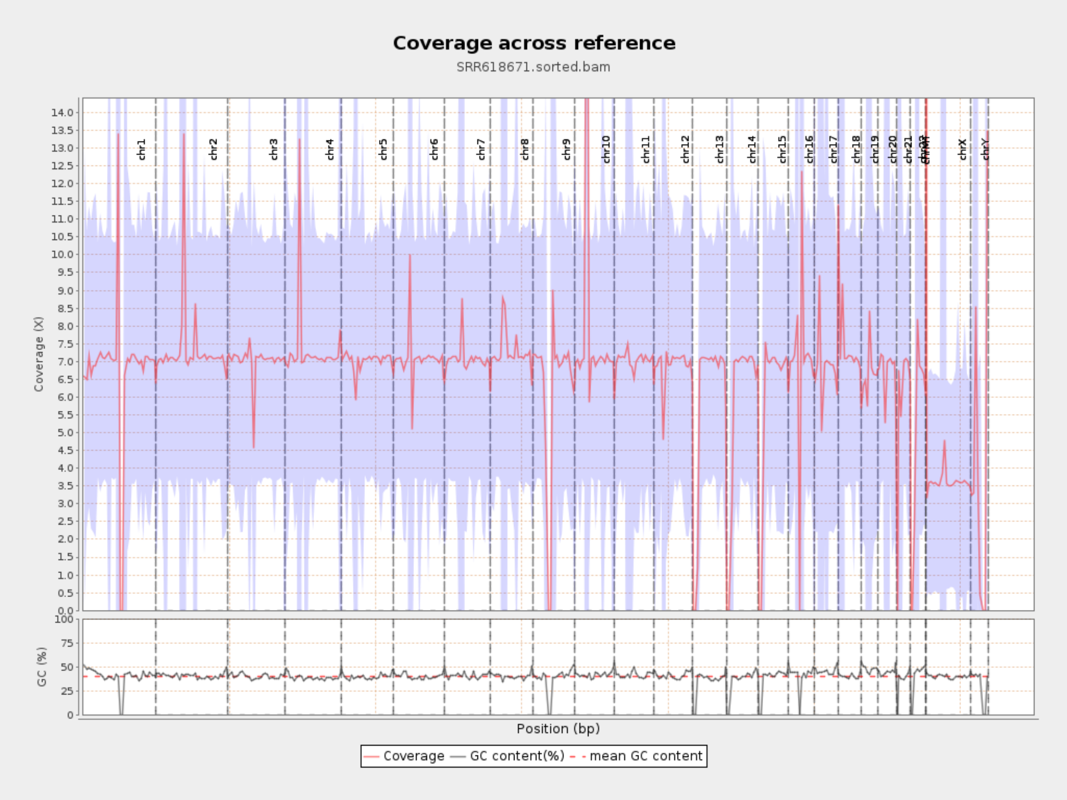
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

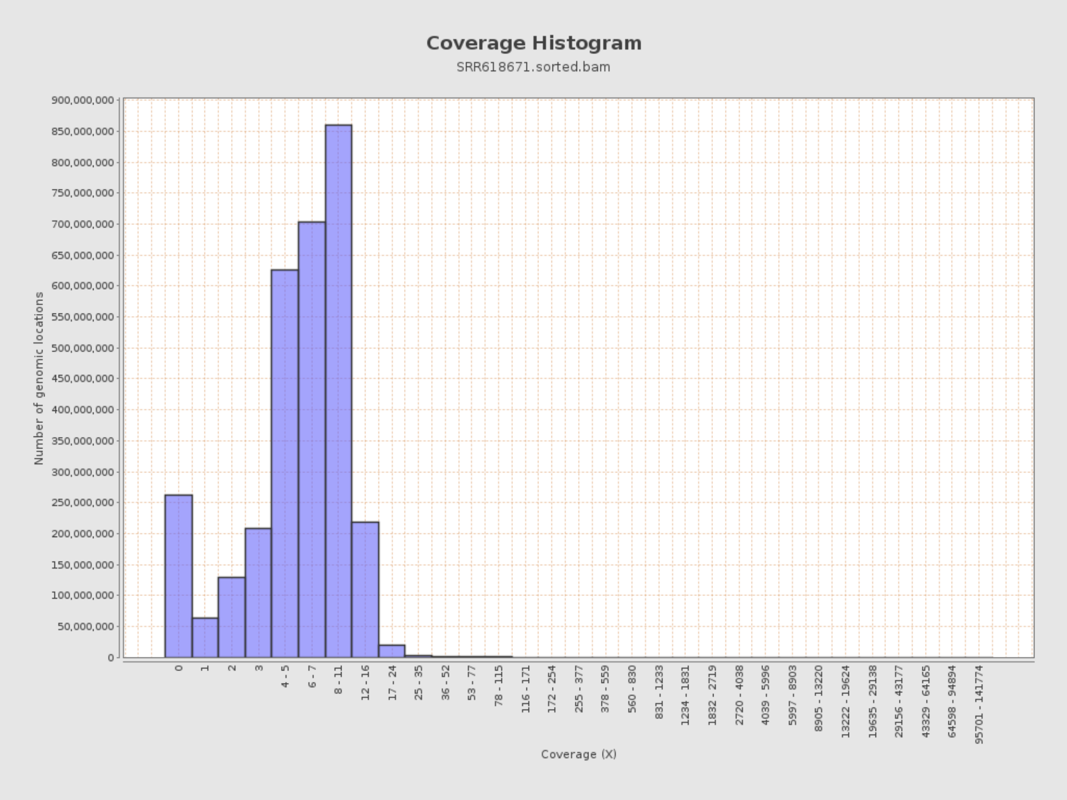
		bases	**coverage**	**deviation**
chr1	249250621	1684914951	6.7599	148.486
chr2	243199373	1786477599	7.3457	39.1741
chr3	198022430	1390322867	7.021	4.5359
chr4	191154276	1406242894	7.3566	44.6172
chr5	180915260	1268550056	7.0118	6.0821
chr6	171115067	1214047376	7.0949	34.0449
chr7	159138663	1128236706	7.0896	44.358
chr8	146364022	1066499029	7.2866	99.172
chr9	141213431	875487293	6.1997	65.2279
chr10	135534747	1065746077	7.8633	115.5358
chr11	135006516	949485727	7.0329	29.8578
chr12	133851895	922802815	6.8942	5.5432
chr13	115169878	675877047	5.8685	4.2073
chr14	107349540	627034946	5.8411	5.9102
chr15	102531392	595403962	5.807	4.6573
chr16	90354753	627544615	6.9453	43.5329
chr17	81195210	559272046	6.888	36.0523
chr18	78077248	583360256	7.4716	84.559
chr19	59128983	394478119	6.6715	67.821
chr20	63025520	425916592	6.7578	13.5396
chr21	48129895	289676754	6.0186	26.5619
chr22	51304566	250363848	4.88	33.0002
chrMT	16571	5971743	360.3731	46.6889
chrX	155270560	564288266	3.6342	12.6595

chrY	59373566	244284015	4.1144	69.0438

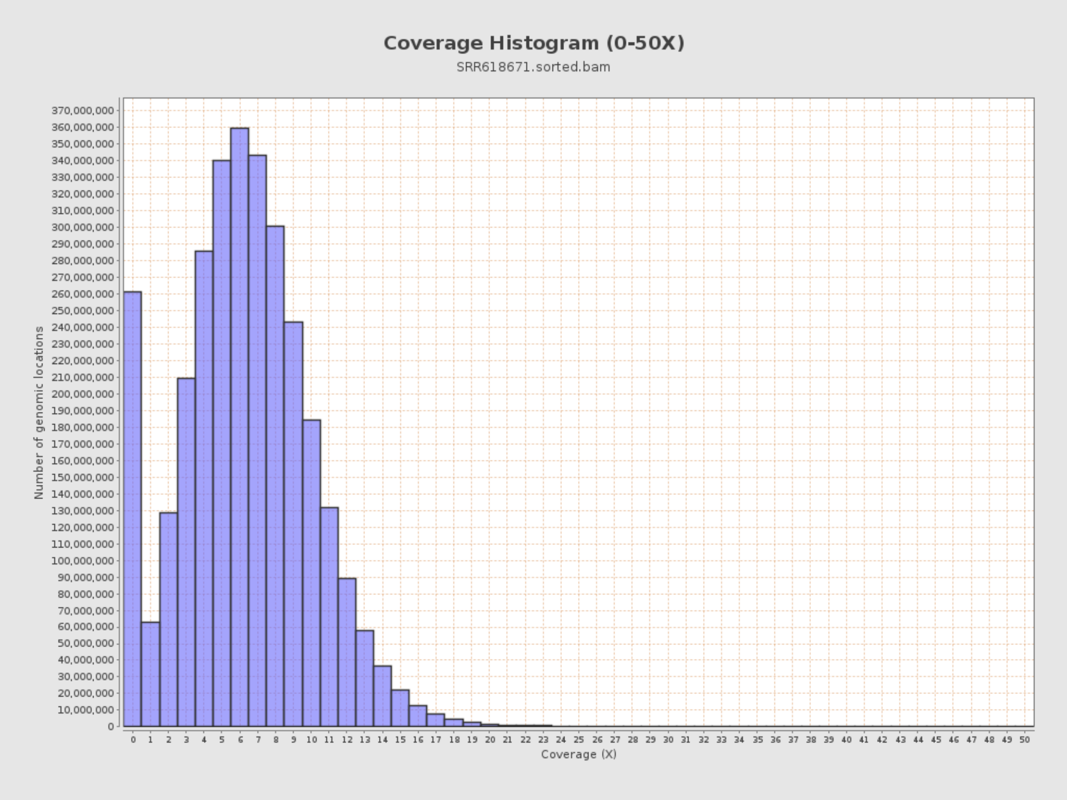
3. Results : Coverage across reference



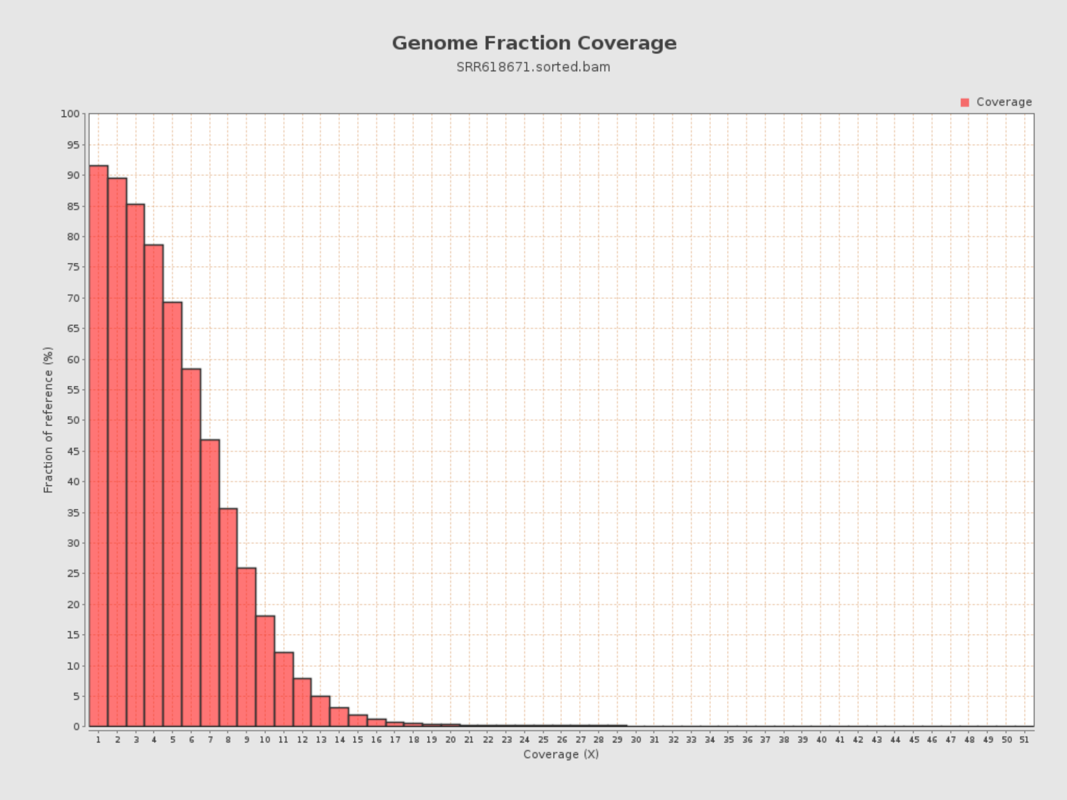
4. Results : Coverage Histogram



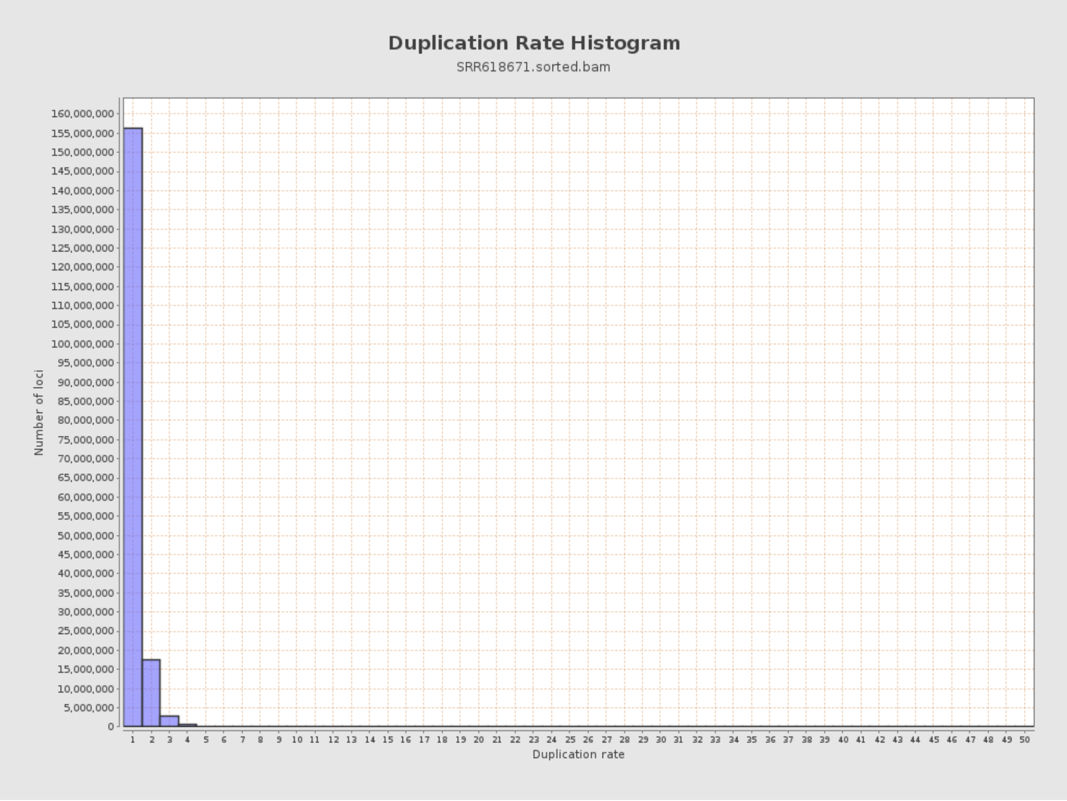
5. Results : Coverage Histogram (0-50X)



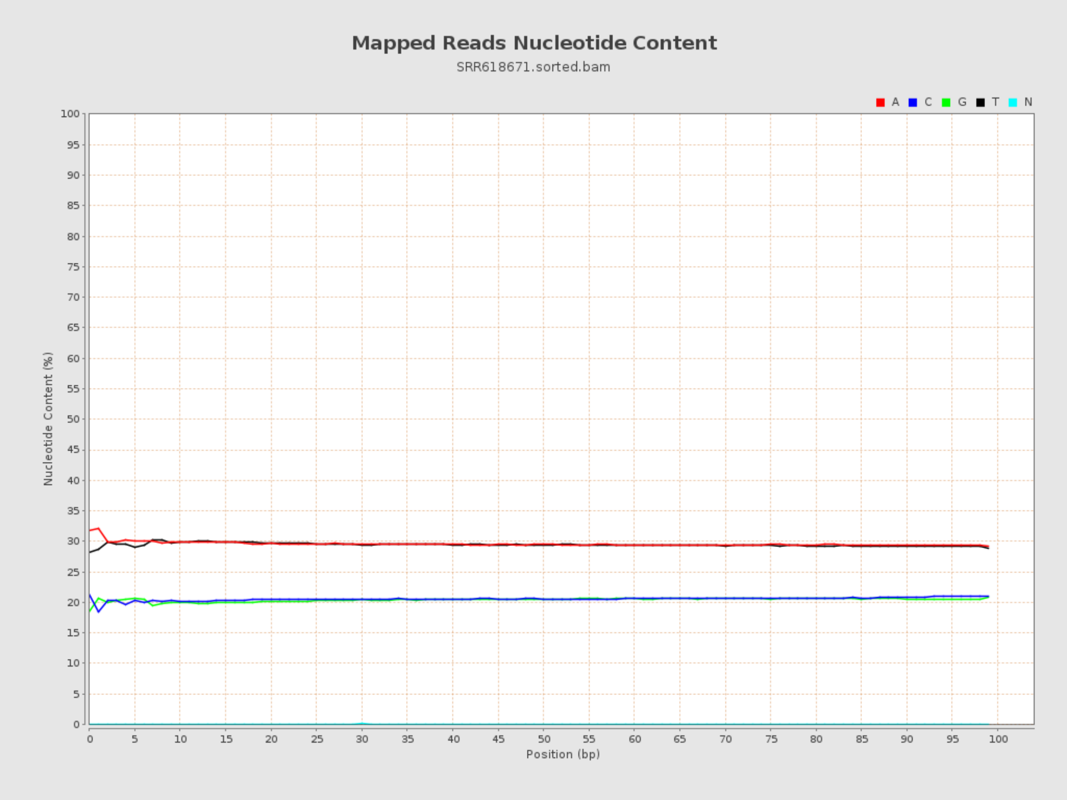
6. Results : Genome Fraction Coverage



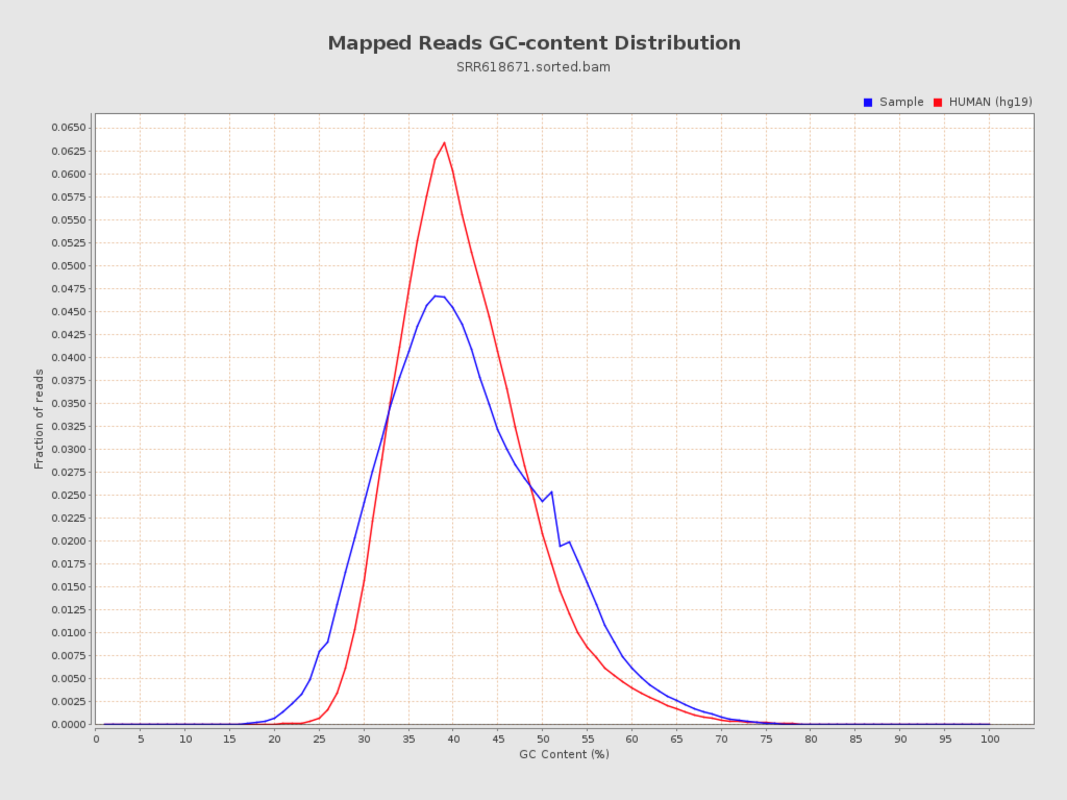
7. Results : Duplication Rate Histogram



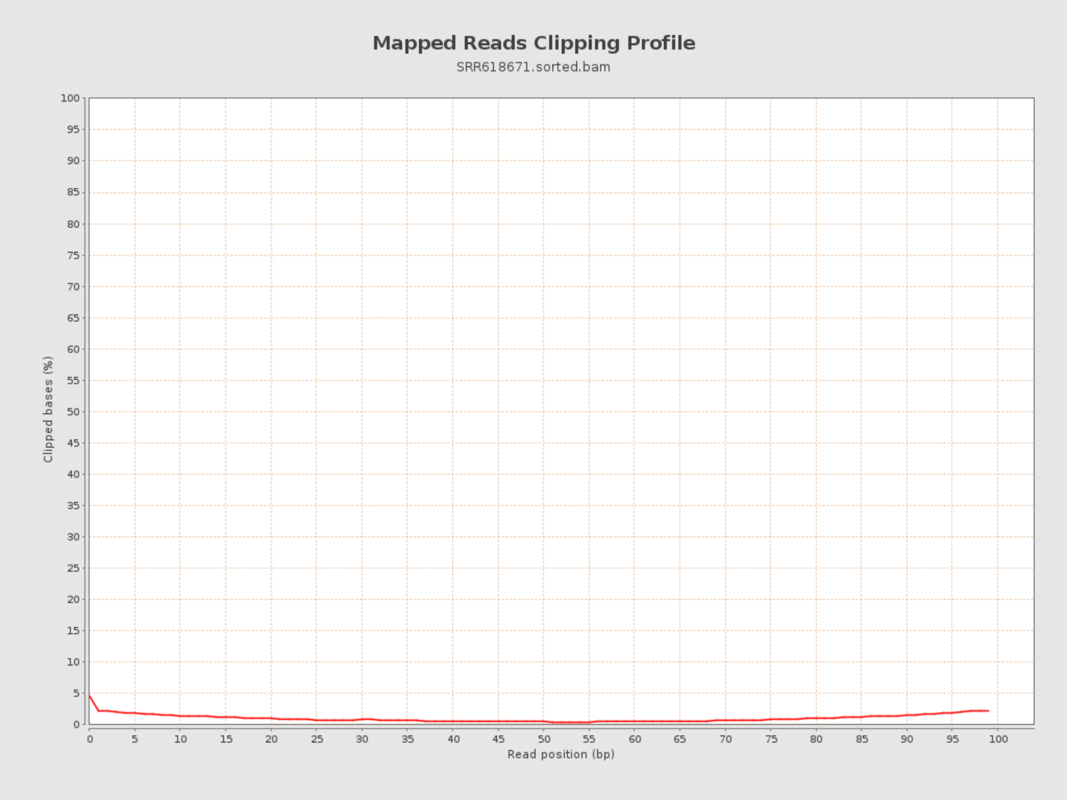
8. Results : Mapped Reads Nucleotide Content



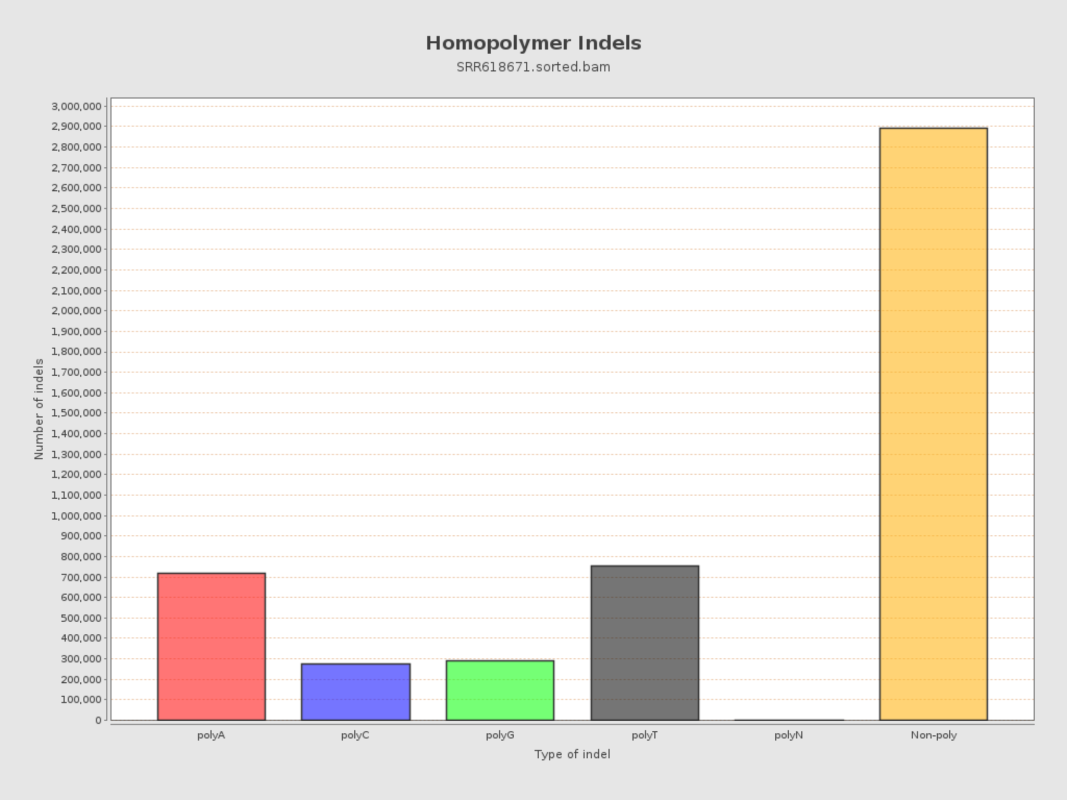
9. Results : Mapped Reads GC-content Distribution



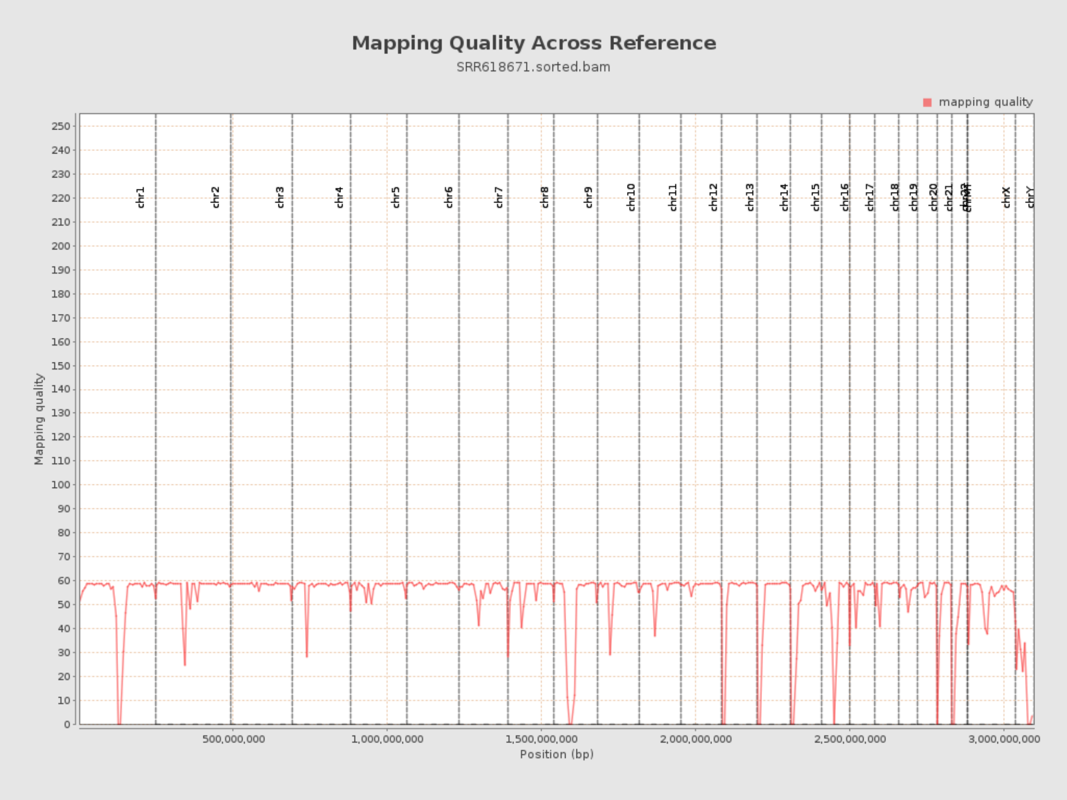
10. Results : Mapped Reads Clipping Profile



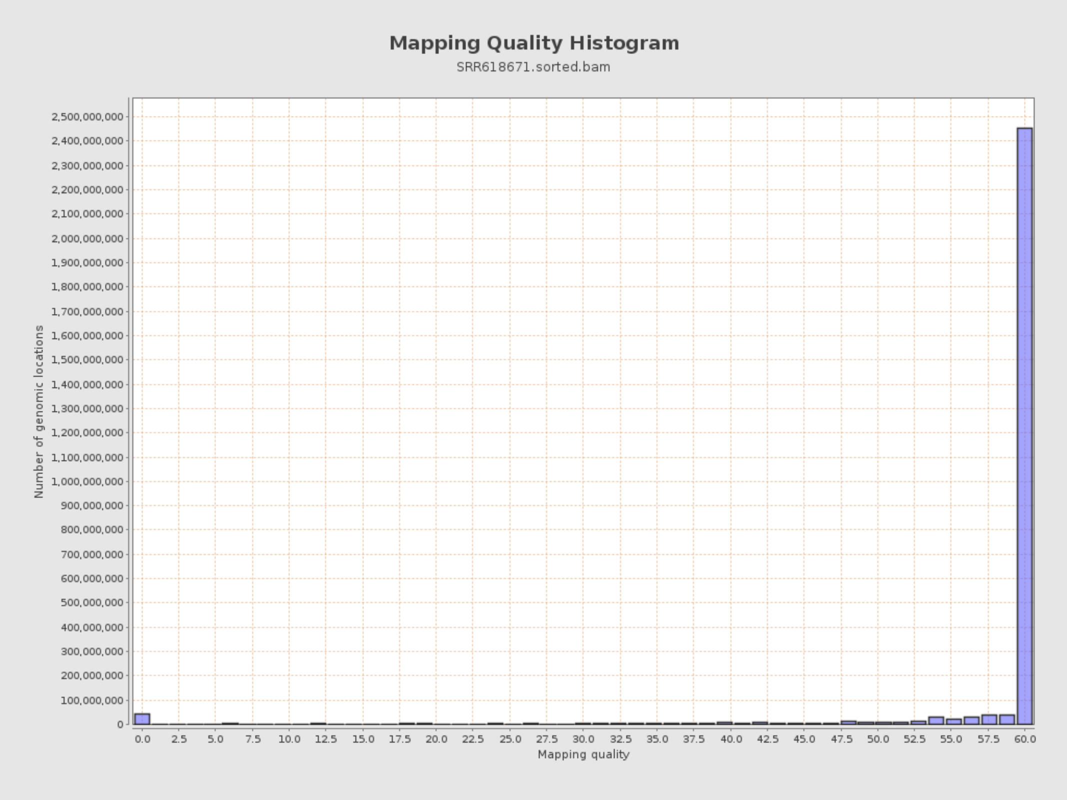
11. Results : Homopolymer Indels



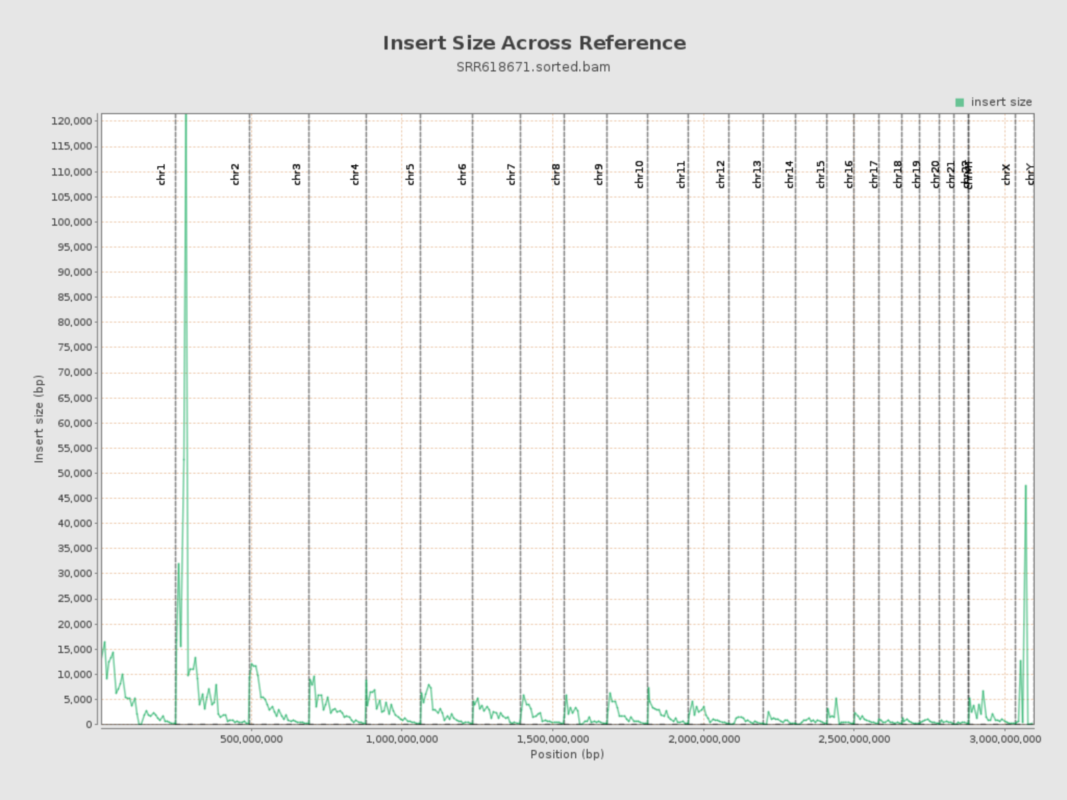
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram