Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:44:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063547.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_SRR6063547 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063547.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:44:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063547.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,722,585
Mapped reads	1,536,734 / 89.21%
Unmapped reads	185,851 / 10.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,567 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	84,868 / 4.93%
Duplication rate	4.4%
Clipped reads	815,563 / 47.35%

2.2. ACGT Content

Number/percentage of A's	26,693,880 / 26.87%
Number/percentage of C's	17,704,461 / 17.82%
Number/percentage of T's	32,192,639 / 32.4%
Number/percentage of G's	22,766,895 / 22.91%
Number/percentage of N's	2,530 / 0%
GC Percentage	40.73%

2.3. Coverage

Mean	0.0321

Standard Deviation	0.3614

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

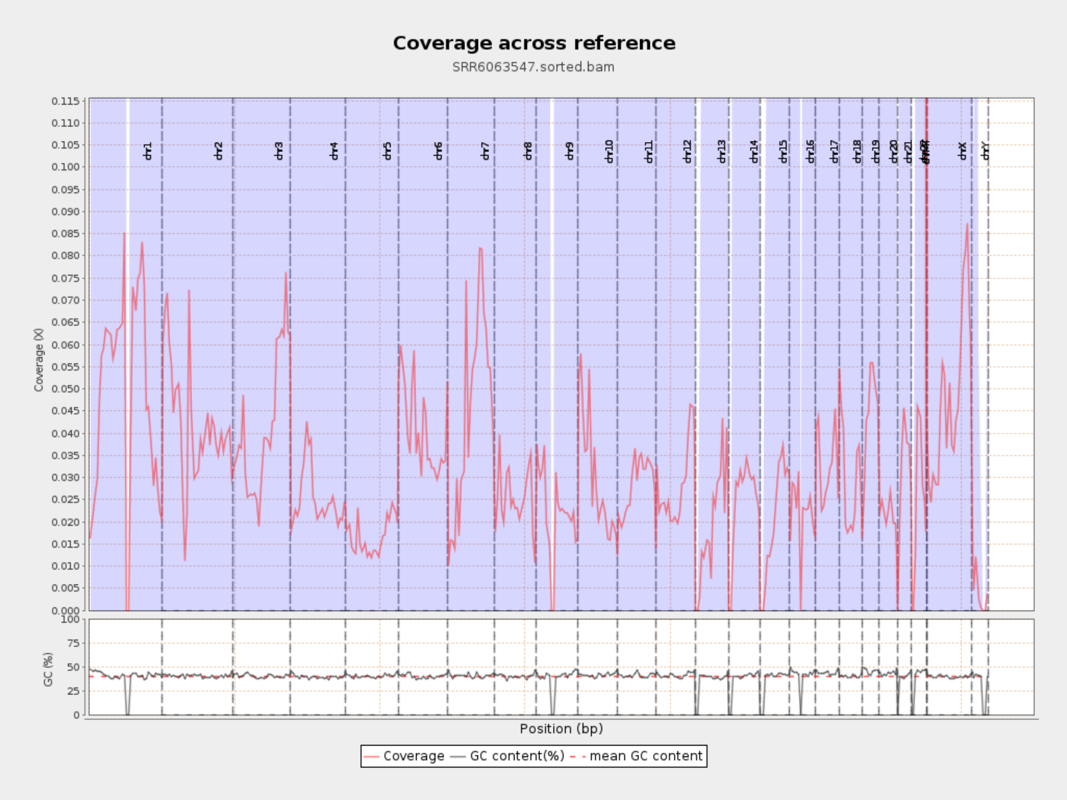
General error rate	0.83%
Mismatches	814,539
Insertions	7,600
Mapped reads with at least one insertion	0.49%
Deletions	27,784
Mapped reads with at least one deletion	1.79%
Homopolymer indels	46.36%

2.6. Chromosome stats

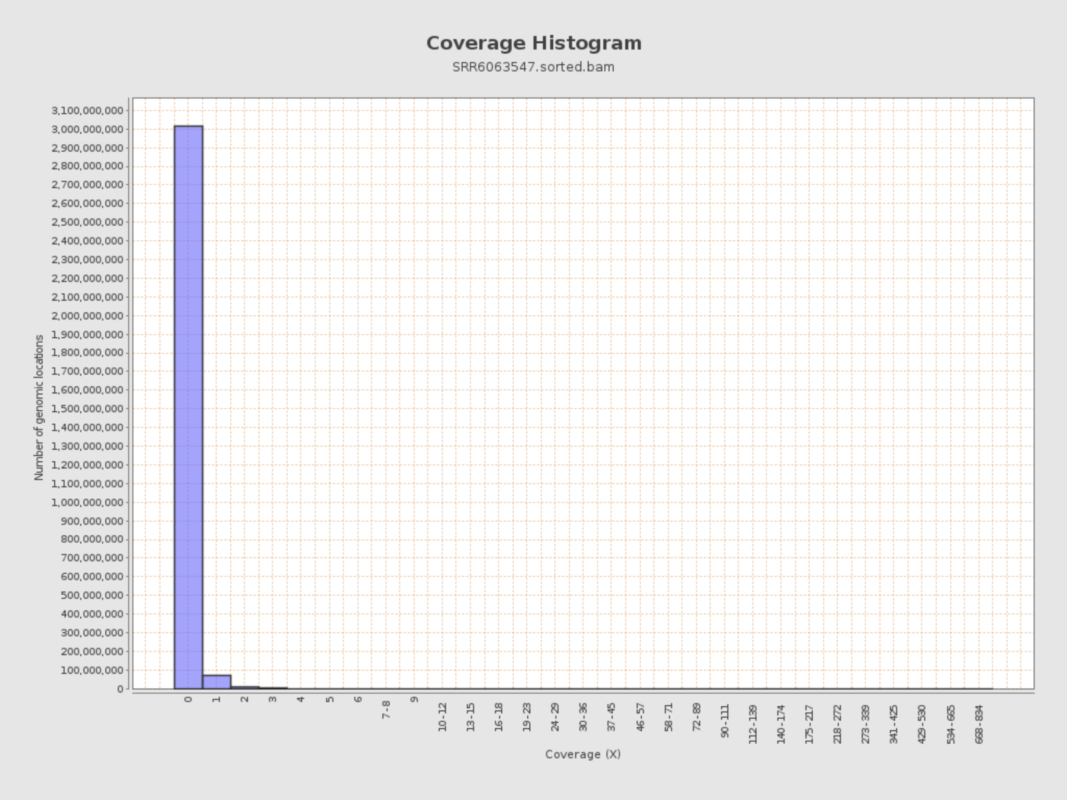
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12184243	0.0489	0.7322
chr2	243199373	10298342	0.0423	0.4771
chr3	198022430	8111237	0.041	0.2386
chr4	191154276	4807304	0.0251	0.1898
chr5	180915260	3011068	0.0166	0.1507
chr6	171115067	6985634	0.0408	0.2875
chr7	159138663	7182785	0.0451	0.5924

chr8	146364022	3697846	0.0253	0.4258
chr9	141213431	3075513	0.0218	0.2625
chr10	135534747	4131807	0.0305	0.3016
chr11	135006516	3808119	0.0282	0.2431
chr12	133851895	3760629	0.0281	0.2008
chr13	115169878	2245530	0.0195	0.1657
chr14	107349540	2640836	0.0246	0.1941
chr15	102531392	2051372	0.02	0.1761
chr16	90354753	1975564	0.0219	0.1812
chr17	81195210	2648820	0.0326	0.2239
chr18	78077248	2308103	0.0296	0.4062
chr19	59128983	2636057	0.0446	0.4464
chr20	63025520	1369679	0.0217	0.1818
chr21	48129895	1508290	0.0313	0.21
chr22	51304566	1230660	0.024	0.1777
chrMT	16571	19715	1.1897	1.3451
chrX	155270560	7456923	0.048	0.2784
chrY	59373566	259253	0.0044	0.1072

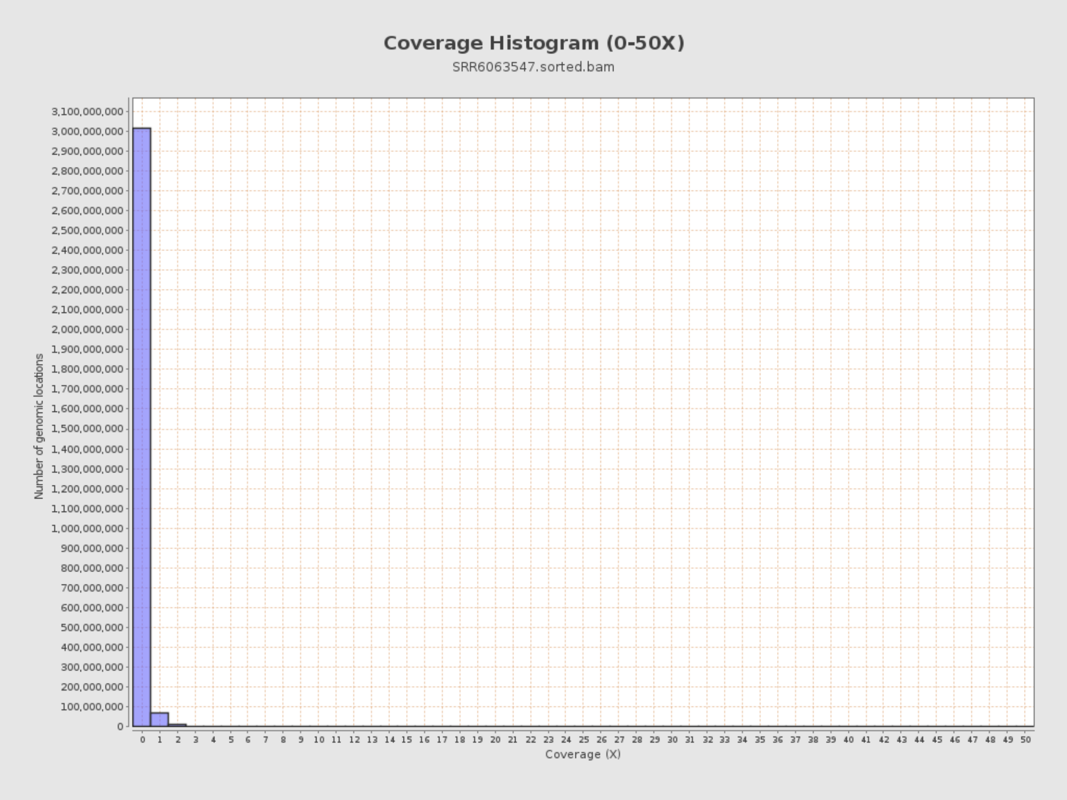
3. Results : Coverage across reference



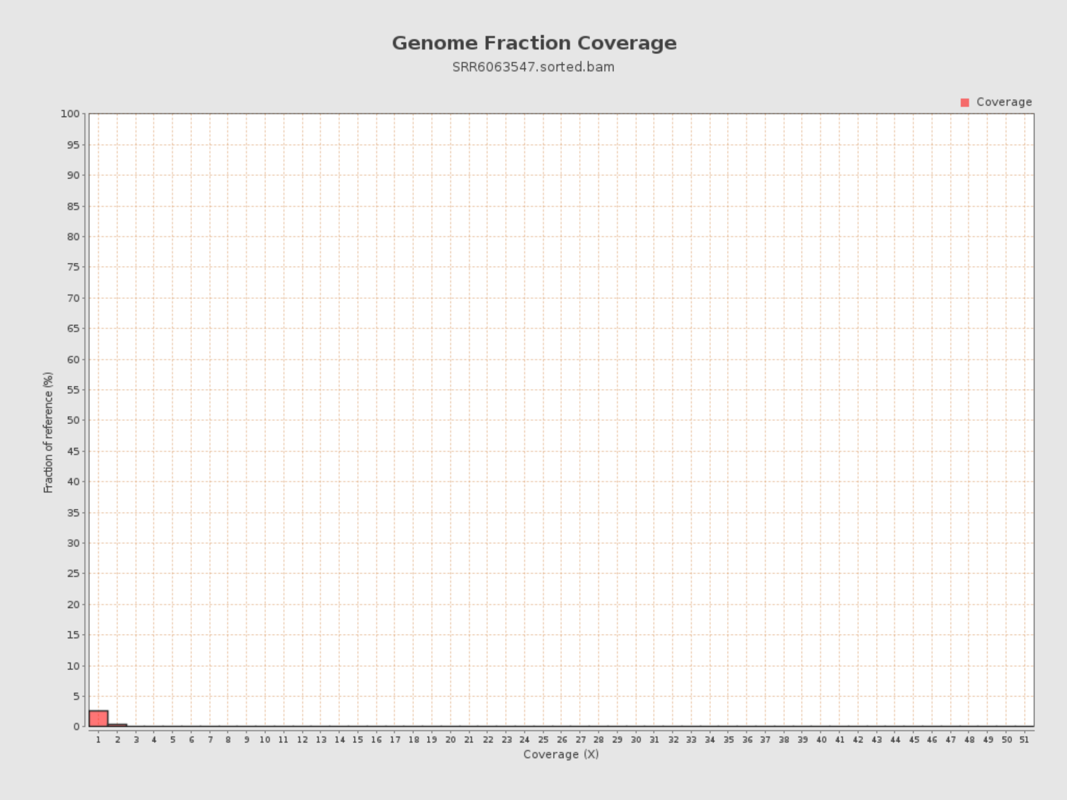
4. Results : Coverage Histogram



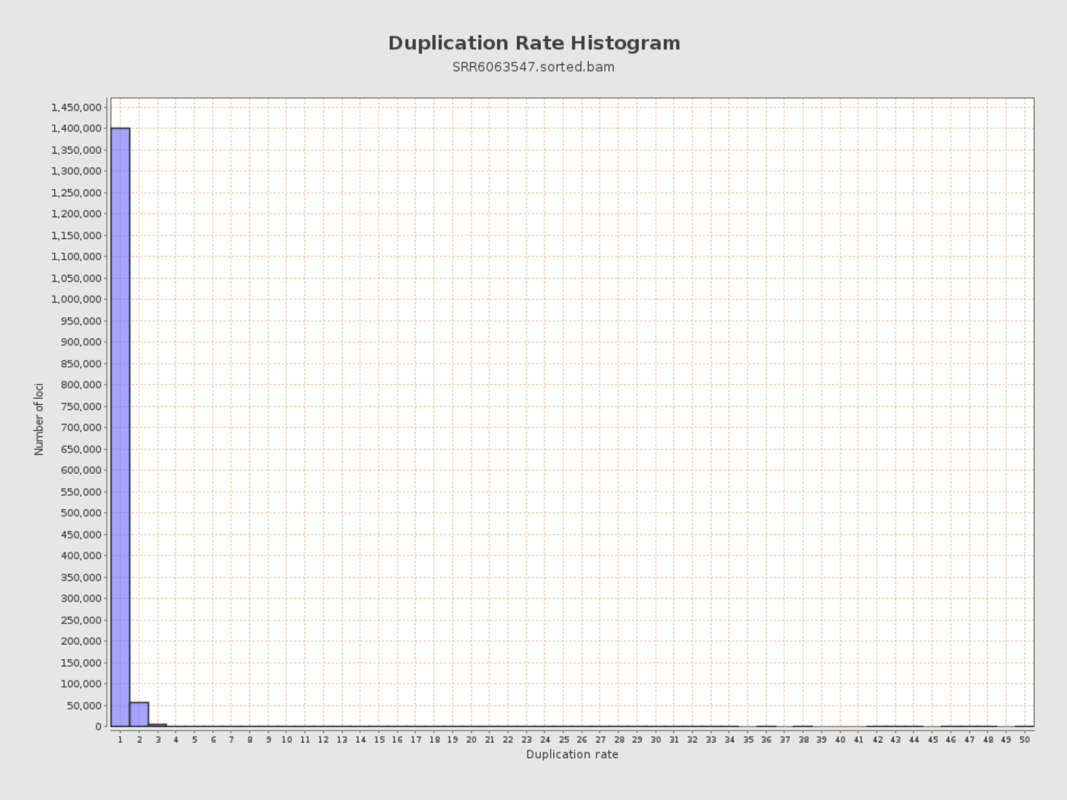
5. Results : Coverage Histogram (0-50X)



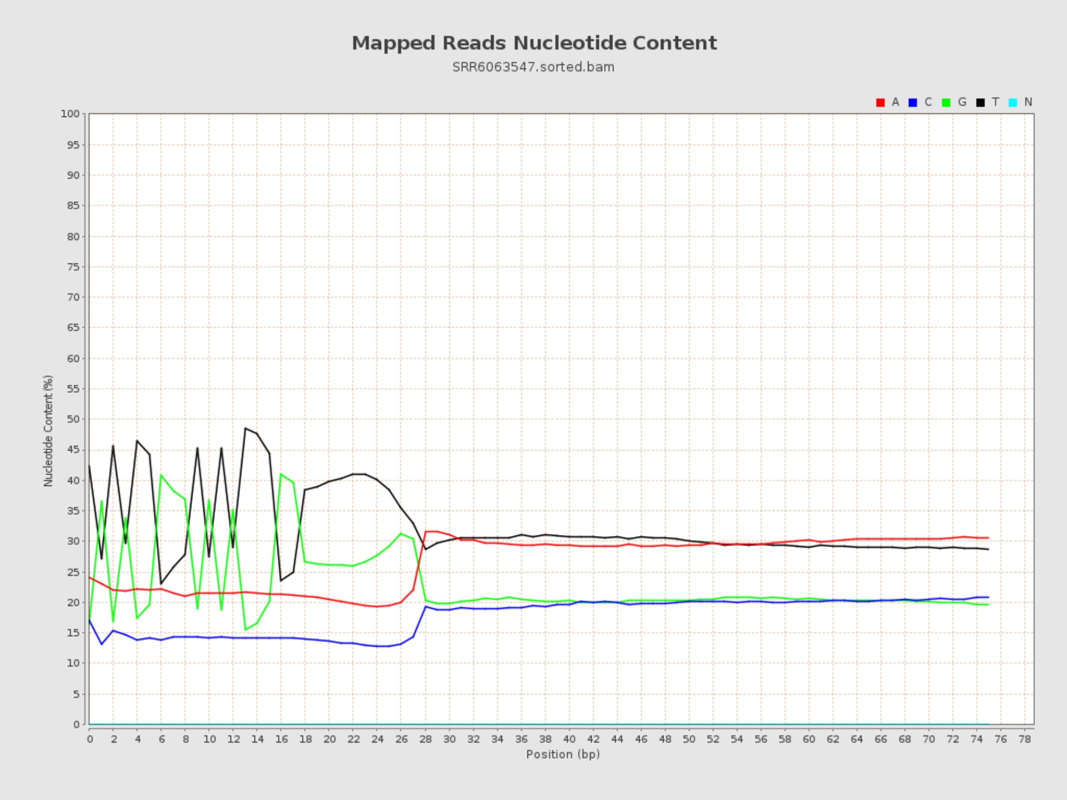
6. Results : Genome Fraction Coverage



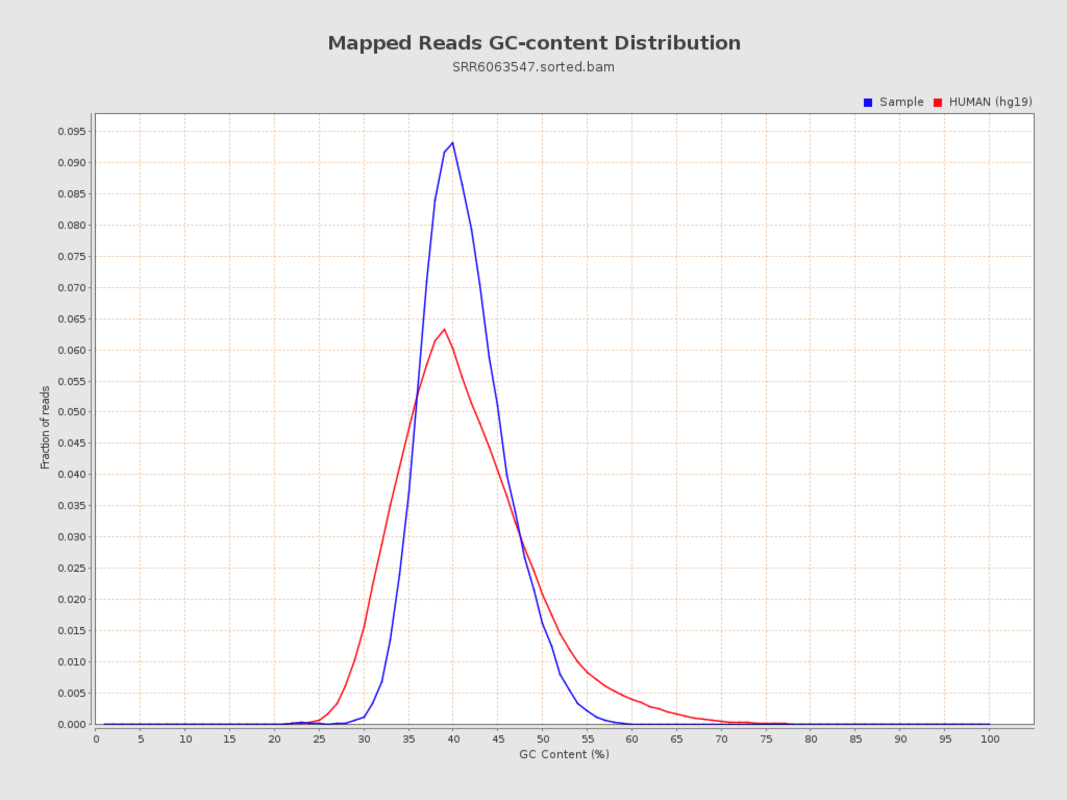
7. Results : Duplication Rate Histogram



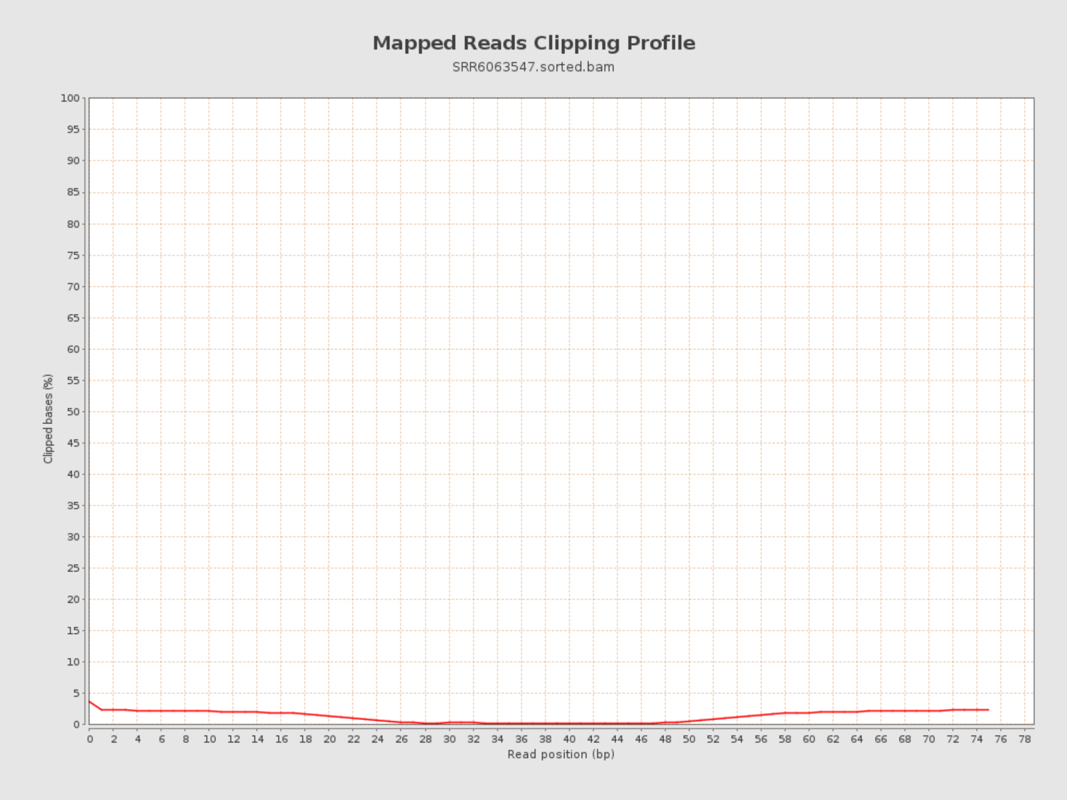
8. Results : Mapped Reads Nucleotide Content



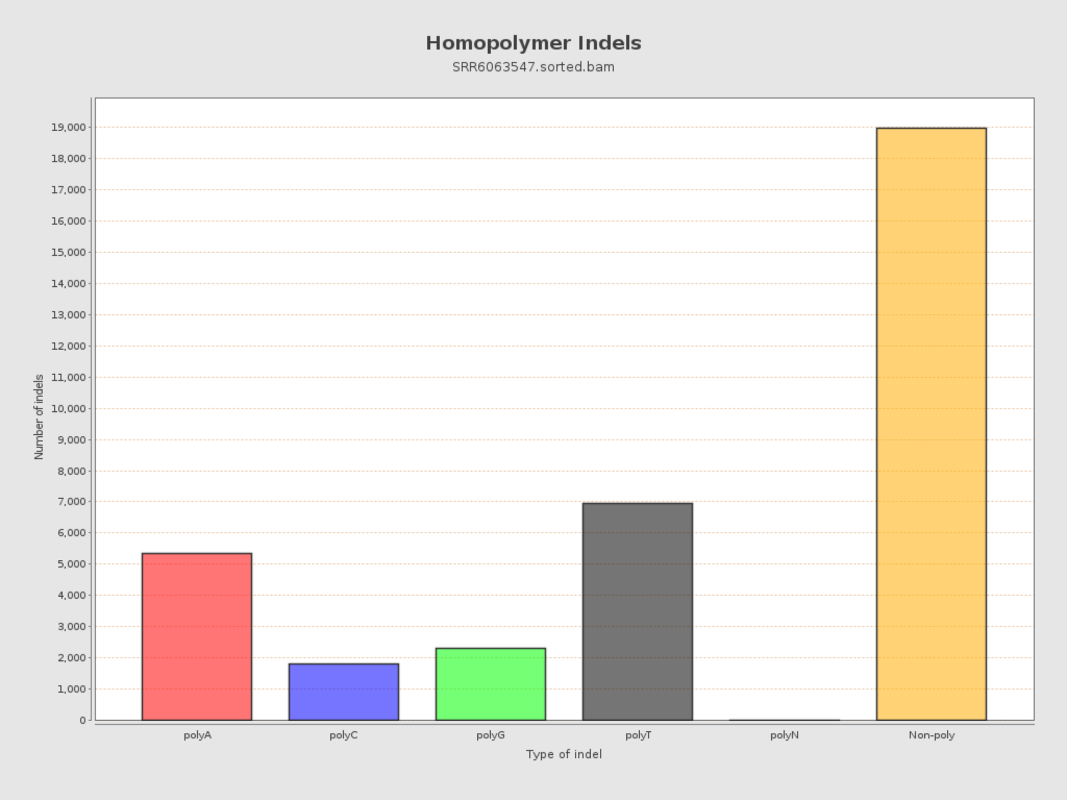
9. Results : Mapped Reads GC-content Distribution



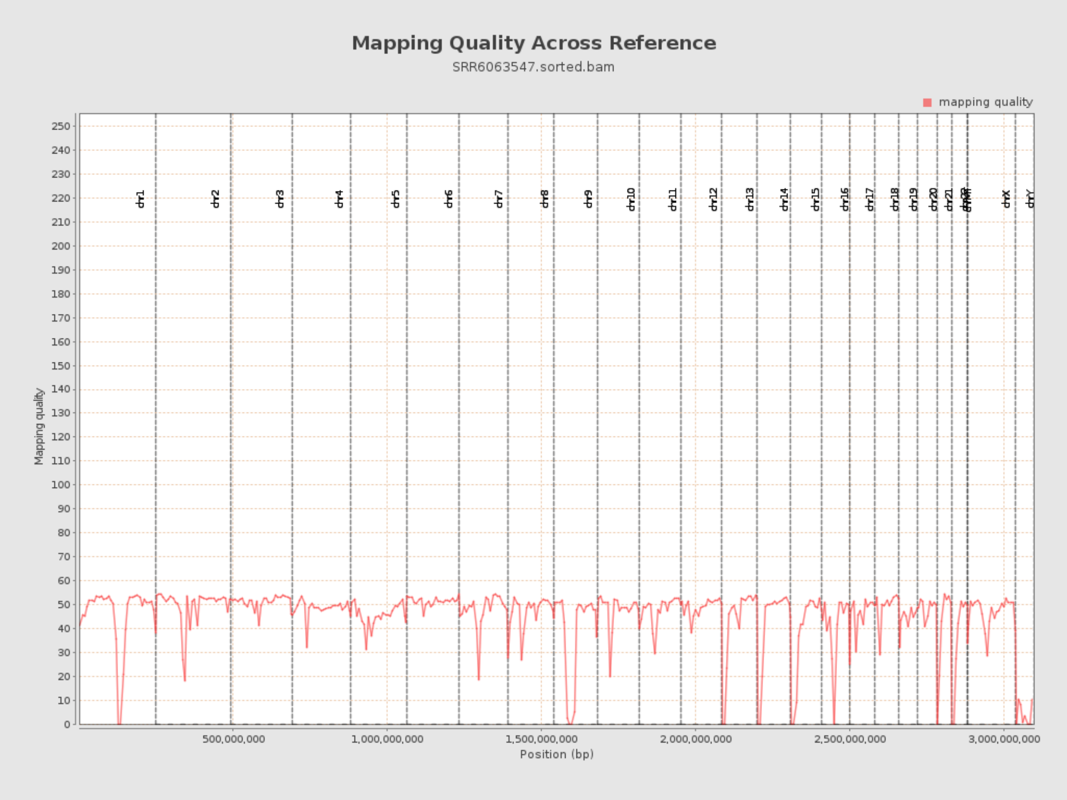
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram