Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:53:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063522.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_SRR6063522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063522.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:53:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,702,773
Mapped reads	4,504,593 / 95.79%
Unmapped reads	198,180 / 4.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,868 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	477,513 / 10.15%
Duplication rate	8.77%
Clipped reads	1,894,095 / 40.28%

2.2. ACGT Content

Number/percentage of A's	82,779,942 / 27.51%
Number/percentage of C's	54,875,299 / 18.24%
Number/percentage of T's	97,106,827 / 32.27%
Number/percentage of G's	66,132,505 / 21.98%
Number/percentage of N's	36,202 / 0.01%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0973

Standard Deviation	1.0146

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

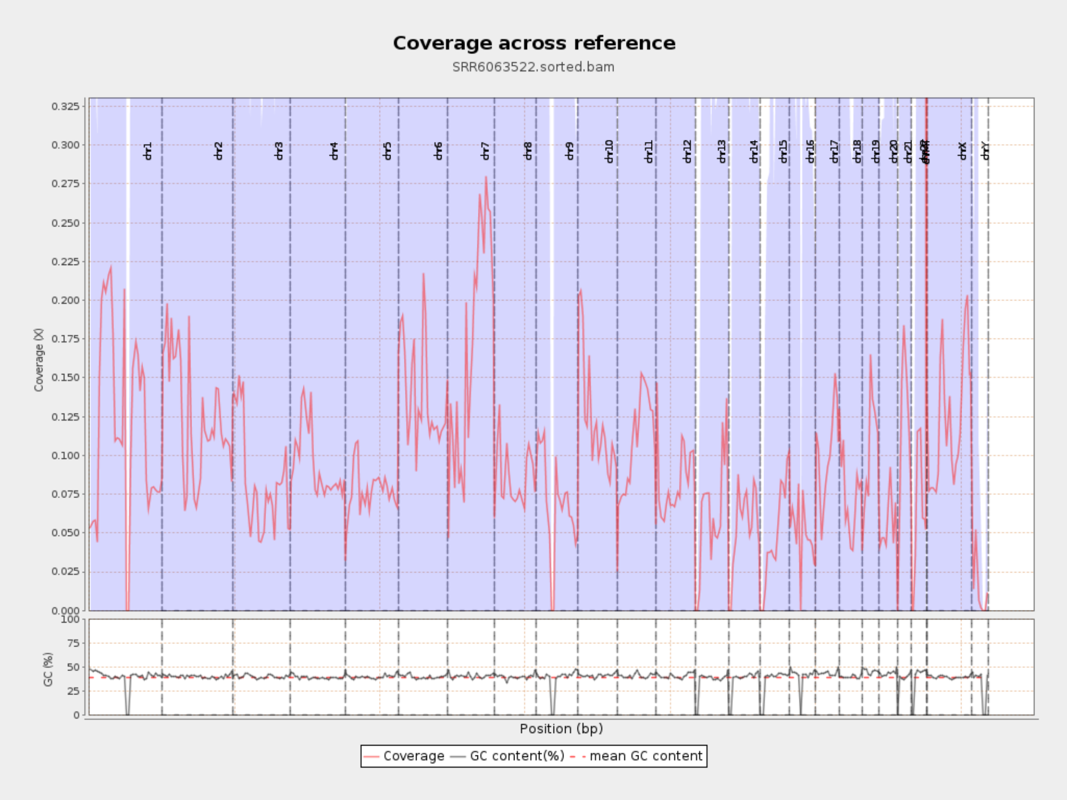
General error rate	0.54%
Mismatches	1,579,881
Insertions	19,761
Mapped reads with at least one insertion	0.43%
Deletions	78,285
Mapped reads with at least one deletion	1.72%
Homopolymer indels	45.13%

2.6. Chromosome stats

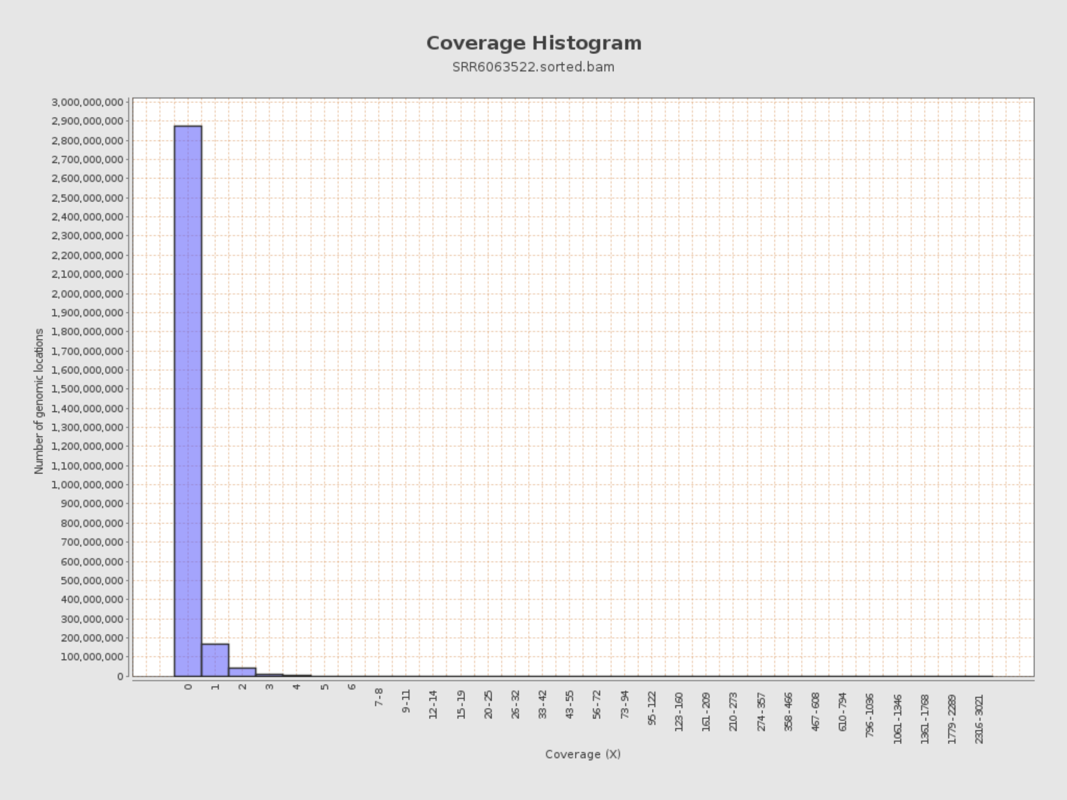
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29735539	0.1193	2.3542
chr2	243199373	30406897	0.125	0.9225
chr3	198022430	16739038	0.0845	0.3752
chr4	191154276	18100204	0.0947	0.431
chr5	180915260	14113339	0.078	0.3611
chr6	171115067	23975728	0.1401	0.5869
chr7	159138663	27258870	0.1713	1.4036

chr8	146364022	12651668	0.0864	1.7661
chr9	141213431	9811412	0.0695	0.7187
chr10	135534747	16920969	0.1248	0.7204
chr11	135006516	14660073	0.1086	0.5991
chr12	133851895	11226602	0.0839	0.4207
chr13	115169878	7144004	0.062	0.3288
chr14	107349540	5900845	0.055	0.4028
chr15	102531392	4900602	0.0478	0.3047
chr16	90354753	4431309	0.049	0.3626
chr17	81195210	8232223	0.1014	0.4501
chr18	78077248	5744747	0.0736	1.3447
chr19	59128983	6190787	0.1047	1.49
chr20	63025520	3549131	0.0563	0.3646
chr21	48129895	5456807	0.1134	0.4681
chr22	51304566	3096013	0.0603	0.3058
chrMT	16571	626337	37.7972	19.1052
chrX	155270560	19304410	0.1243	0.5641
chrY	59373566	894140	0.0151	0.5882

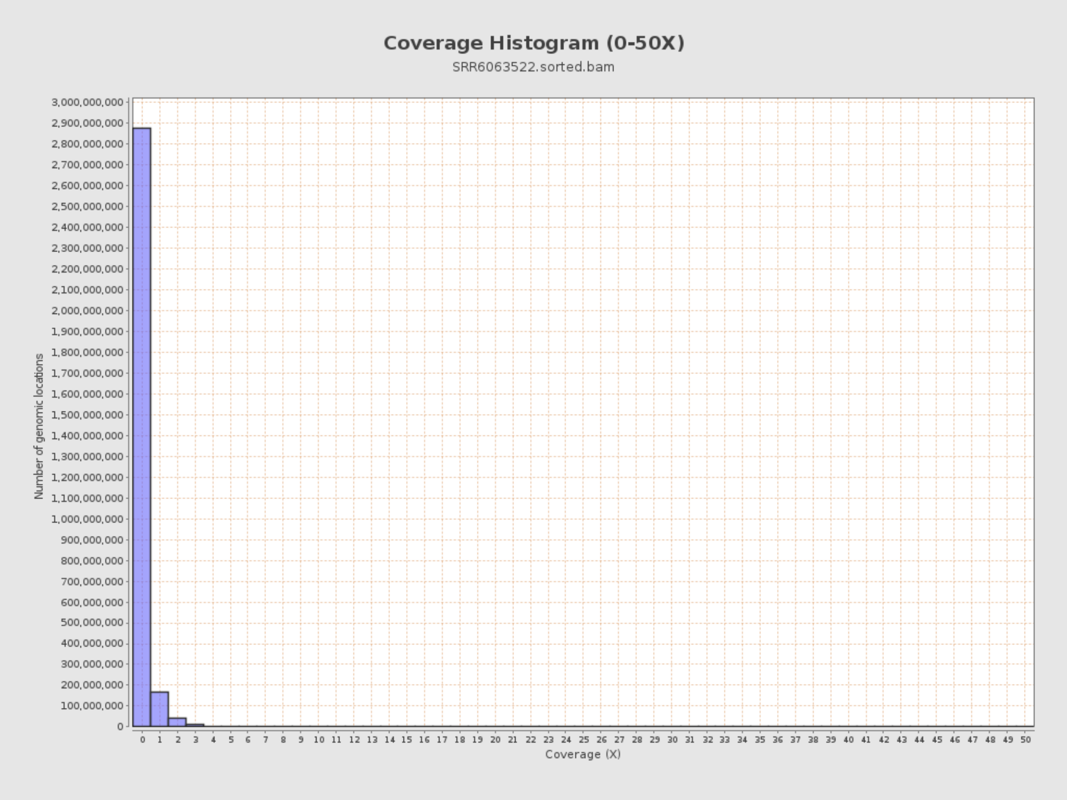
3. Results : Coverage across reference



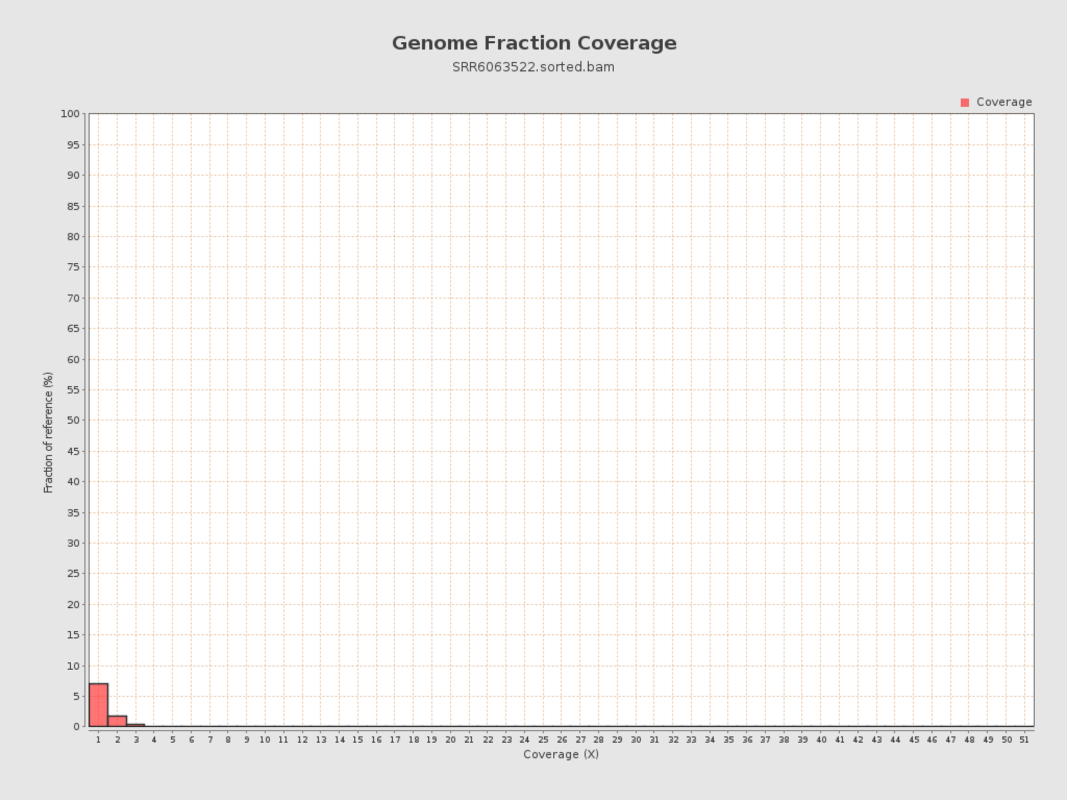
4. Results : Coverage Histogram



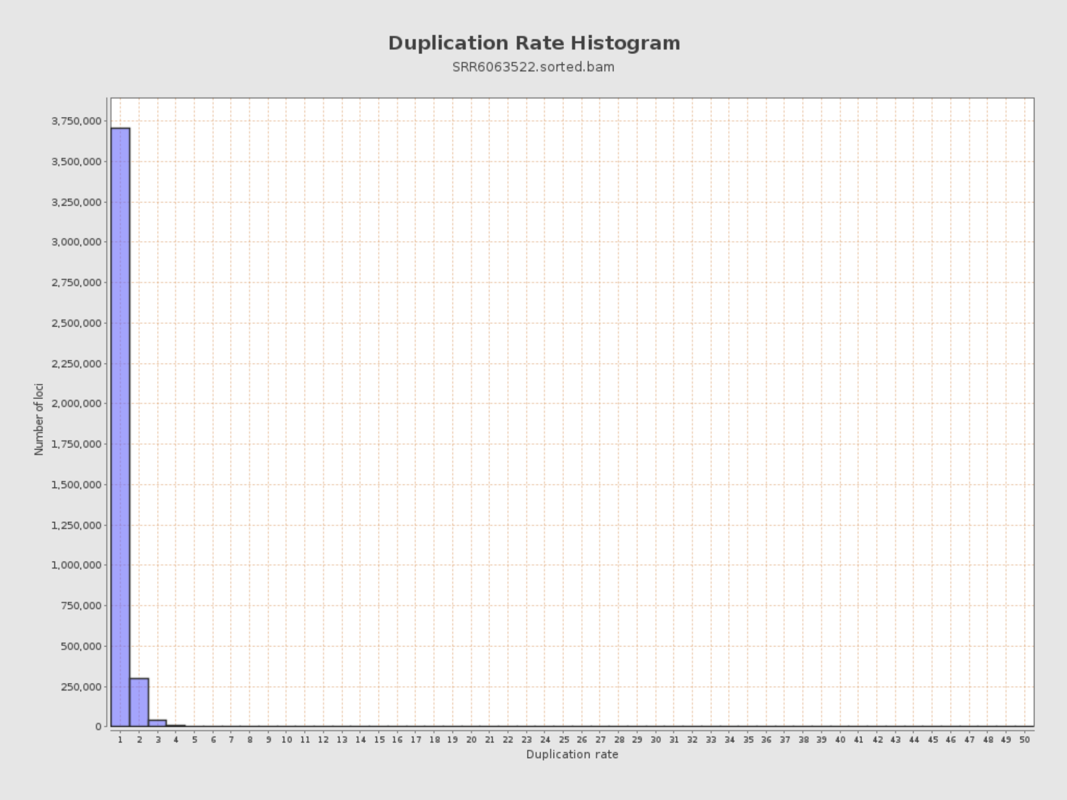
5. Results : Coverage Histogram (0-50X)



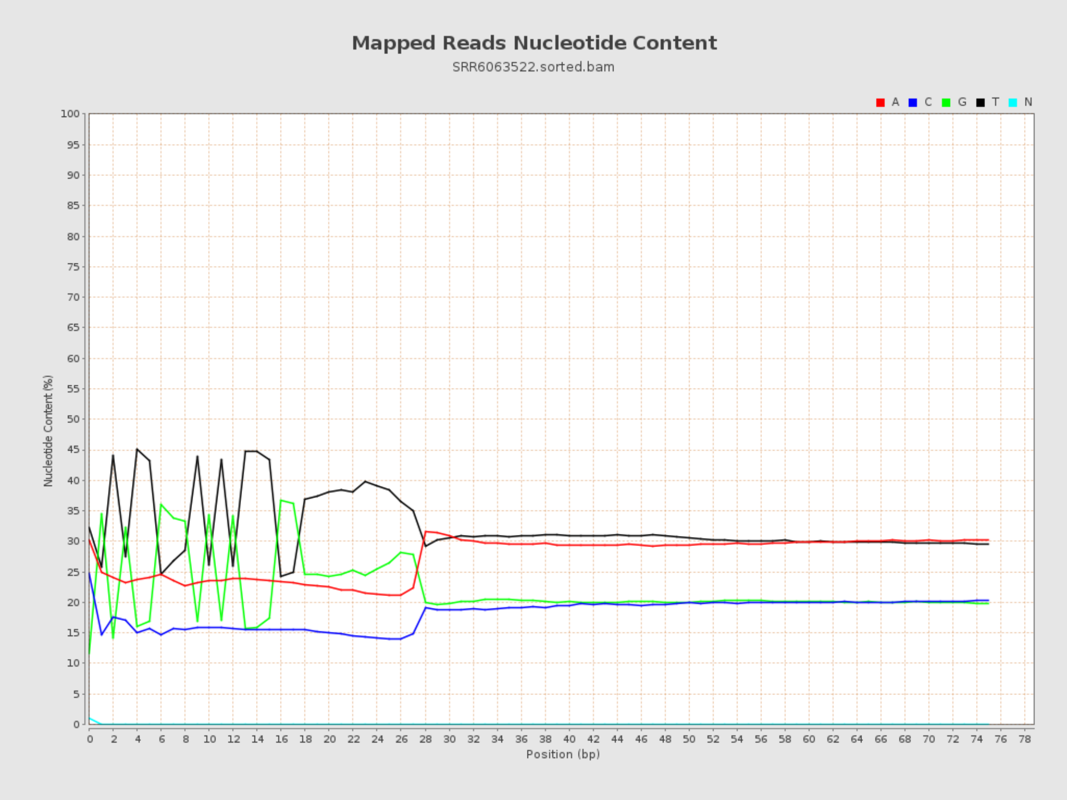
6. Results : Genome Fraction Coverage



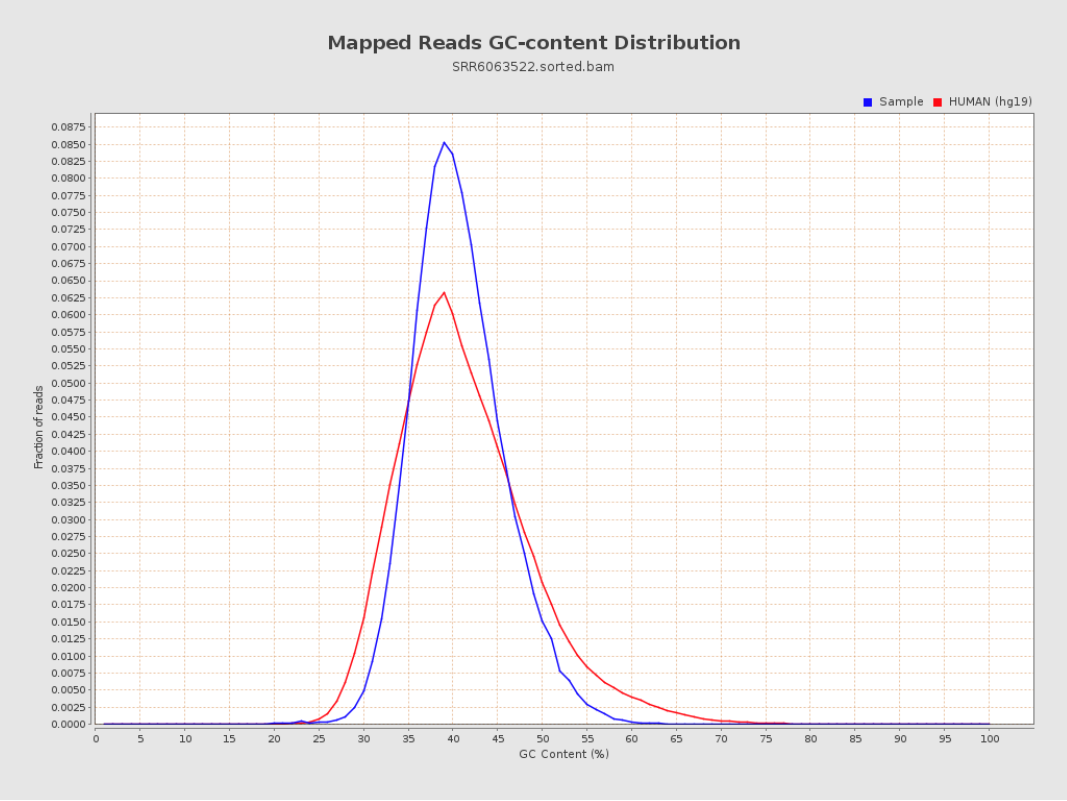
7. Results : Duplication Rate Histogram



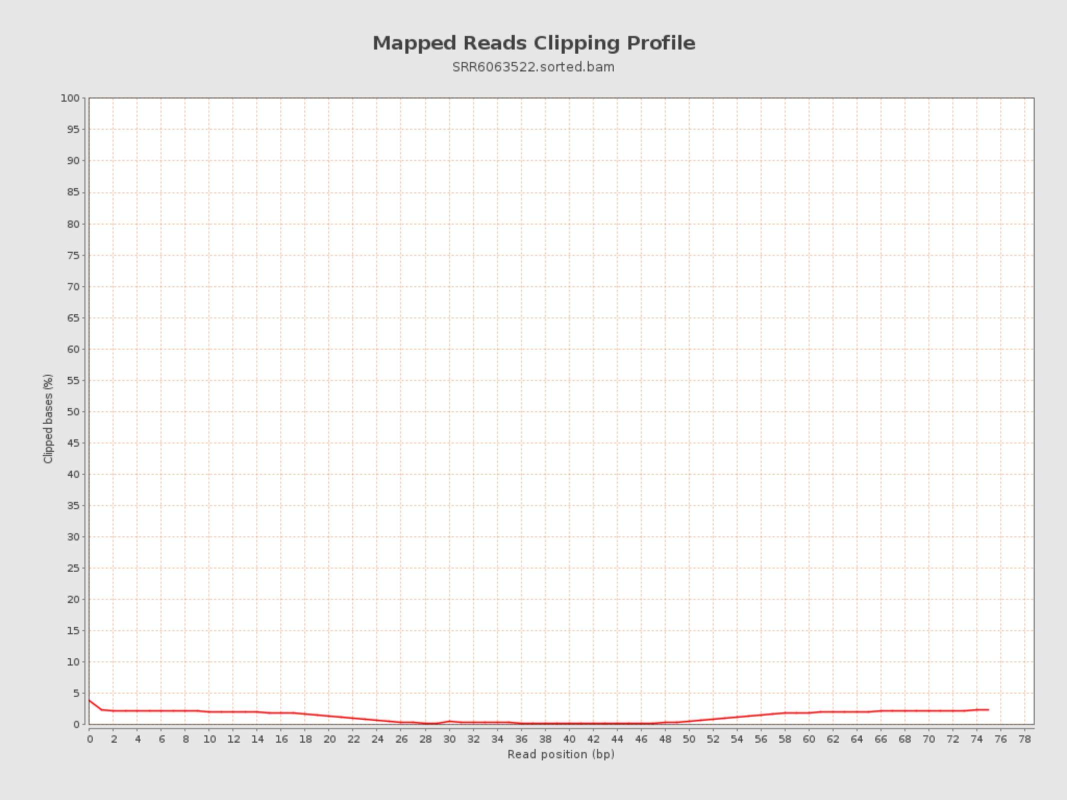
8. Results : Mapped Reads Nucleotide Content



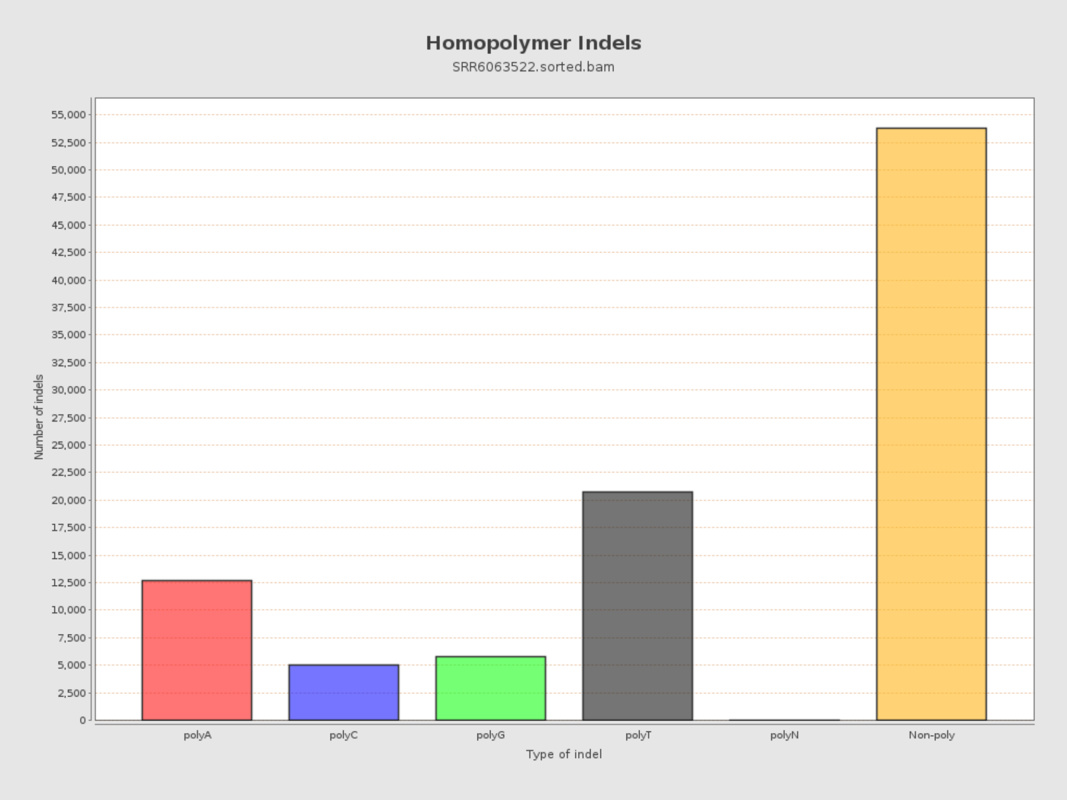
9. Results : Mapped Reads GC-content Distribution



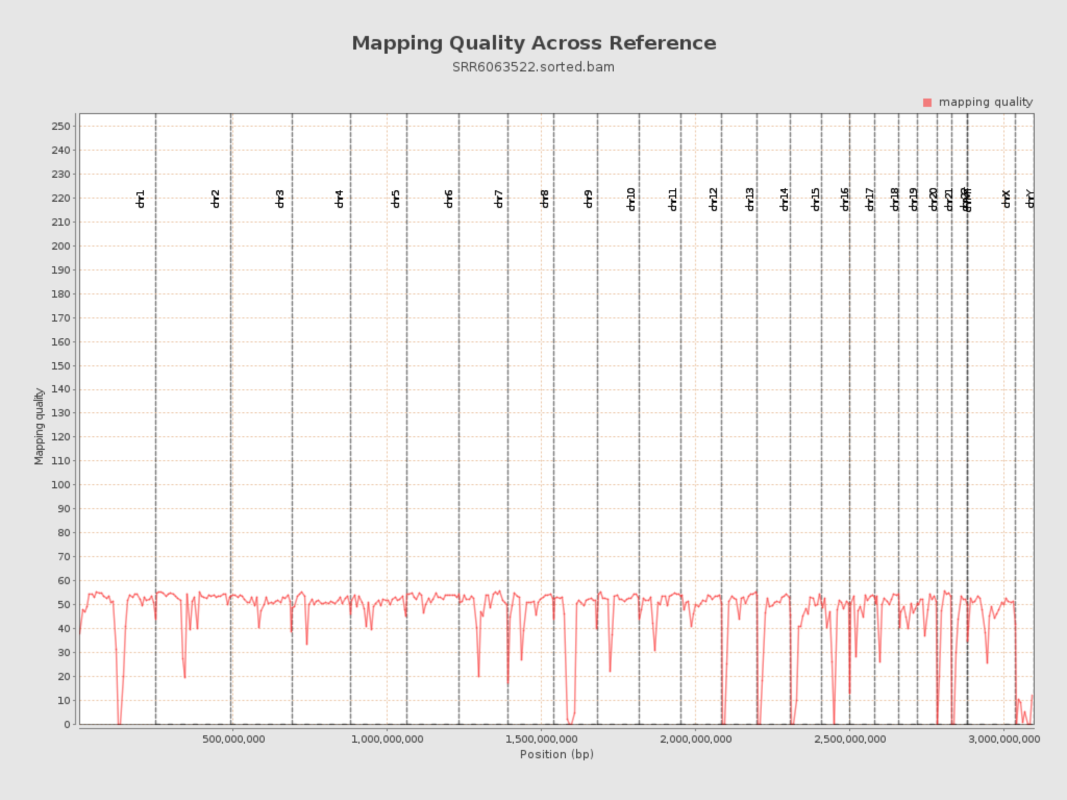
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram