Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:48:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063521.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_SRR6063521 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063521.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:48:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063521.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,470,074
Mapped reads	4,229,257 / 94.61%
Unmapped reads	240,817 / 5.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,118 / 0.65%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	528,035 / 11.81%
Duplication rate	10.41%
Clipped reads	2,261,069 / 50.58%

2.2. ACGT Content

Number/percentage of A's	69,406,011 / 25.64%
Number/percentage of C's	48,653,115 / 17.97%
Number/percentage of T's	88,343,670 / 32.63%
Number/percentage of G's	64,290,521 / 23.75%
Number/percentage of N's	29,483 / 0.01%
GC Percentage	41.72%

2.3. Coverage

Mean	0.0875

Standard Deviation	0.9547

2.4. Mapping Quality

Mean Mapping Quality	44.87

2.5. Mismatches and indels

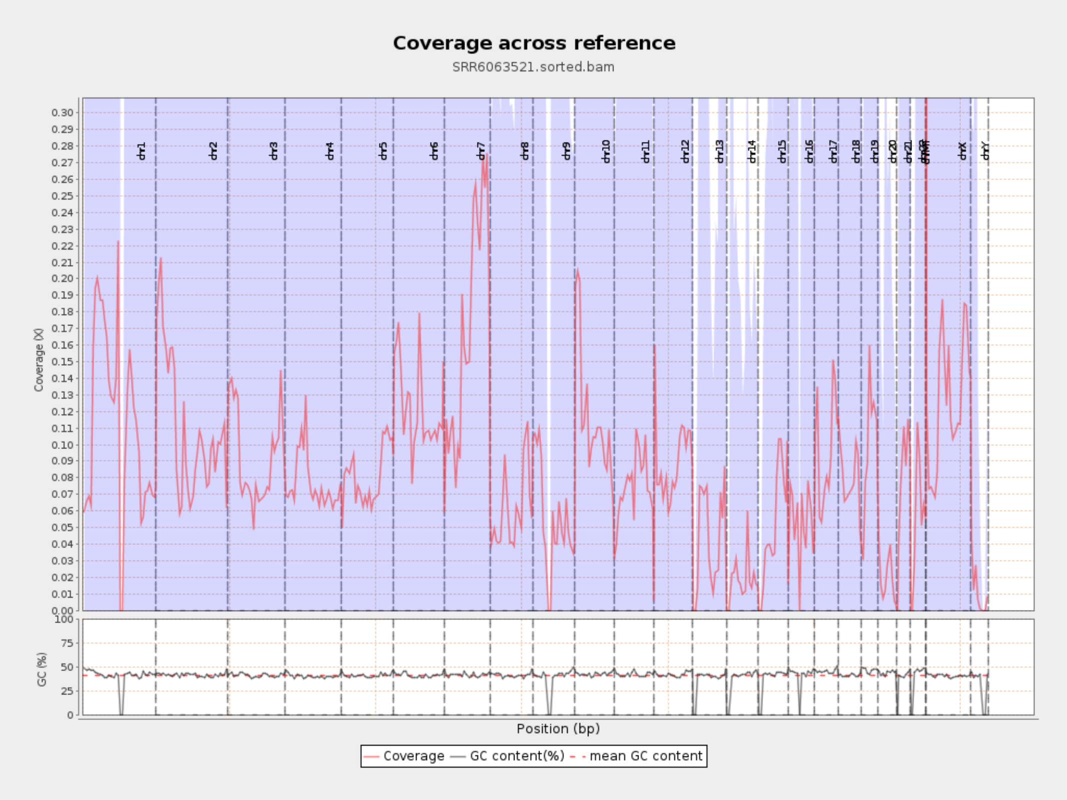
General error rate	0.54%
Mismatches	1,427,227
Insertions	15,865
Mapped reads with at least one insertion	0.37%
Deletions	65,294
Mapped reads with at least one deletion	1.53%
Homopolymer indels	44.2%

2.6. Chromosome stats

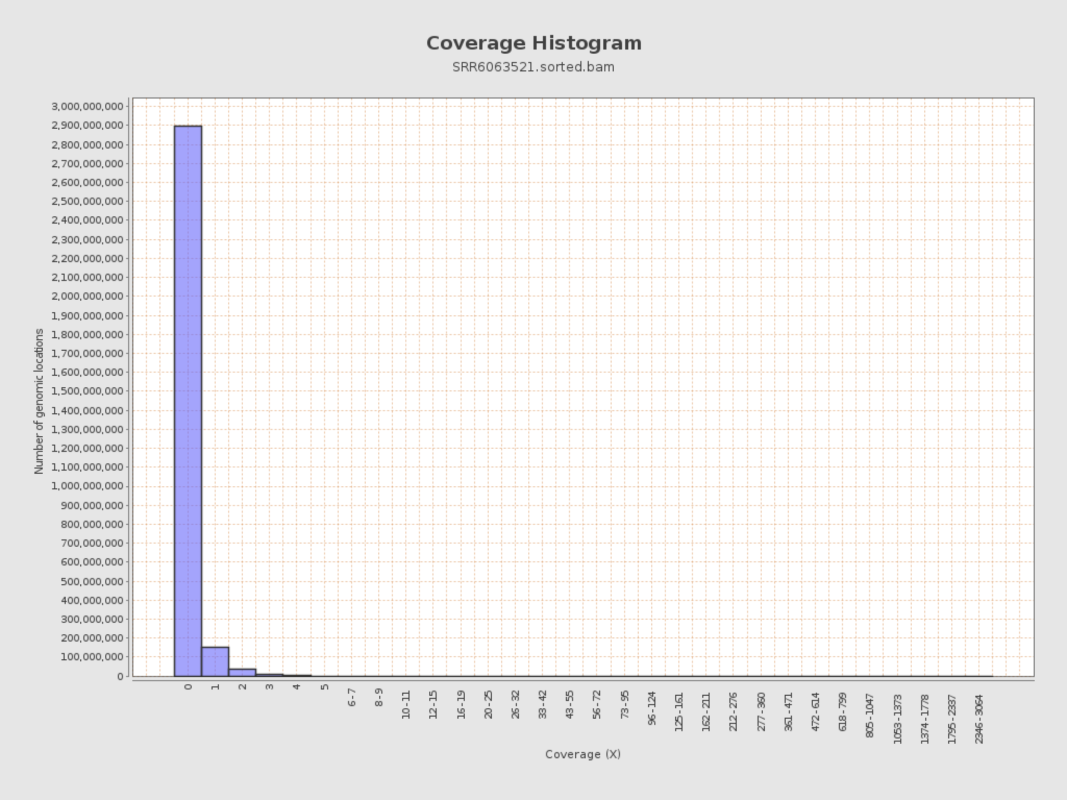
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27934672	0.1121	2.325
chr2	243199373	26995562	0.111	1.4255
chr3	198022430	18188447	0.0919	0.3946
chr4	191154276	14745453	0.0771	0.375
chr5	180915260	14587776	0.0806	0.3715
chr6	171115067	21026436	0.1229	0.6487
chr7	159138663	27383177	0.1721	1.236

chr8	146364022	9011917	0.0616	0.7728
chr9	141213431	7707889	0.0546	0.5044
chr10	135534747	15907606	0.1174	0.6541
chr11	135006516	10102361	0.0748	0.4974
chr12	133851895	12069909	0.0902	0.4318
chr13	115169878	4949634	0.043	0.3347
chr14	107349540	2054881	0.0191	0.2667
chr15	102531392	5150542	0.0502	0.3558
chr16	90354753	4609497	0.051	0.3301
chr17	81195210	7890885	0.0972	0.4341
chr18	78077248	6348744	0.0813	1.0285
chr19	59128983	5806872	0.0982	1.3894
chr20	63025520	1208180	0.0192	0.2176
chr21	48129895	3799640	0.0789	0.3706
chr22	51304566	2815128	0.0549	0.2975
chrMT	16571	498345	30.0733	15.2302
chrX	155270560	19387458	0.1249	0.5529
chrY	59373566	657053	0.0111	0.2249

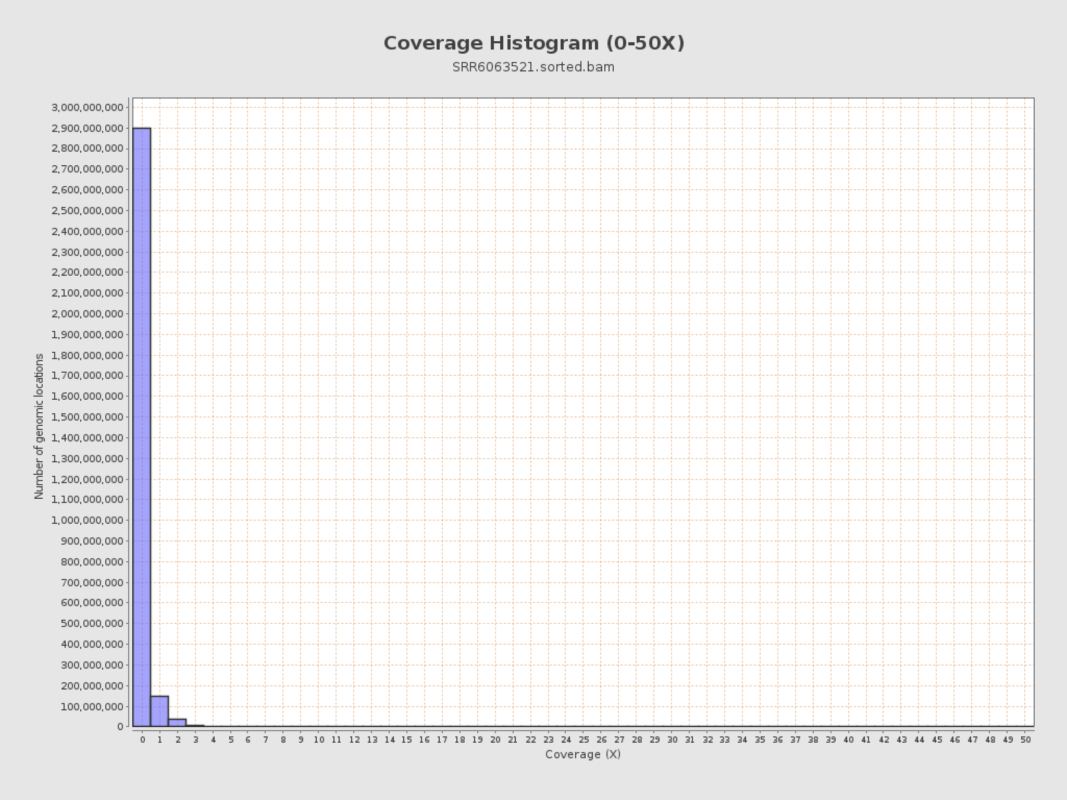
3. Results : Coverage across reference



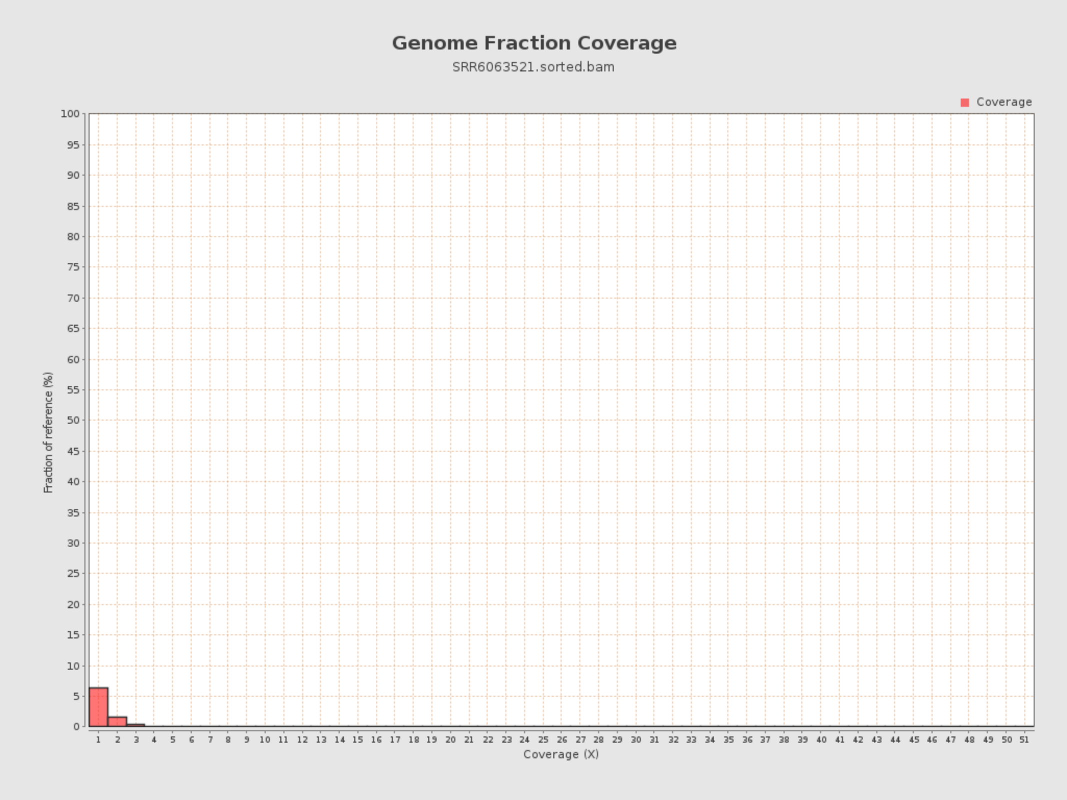
4. Results : Coverage Histogram



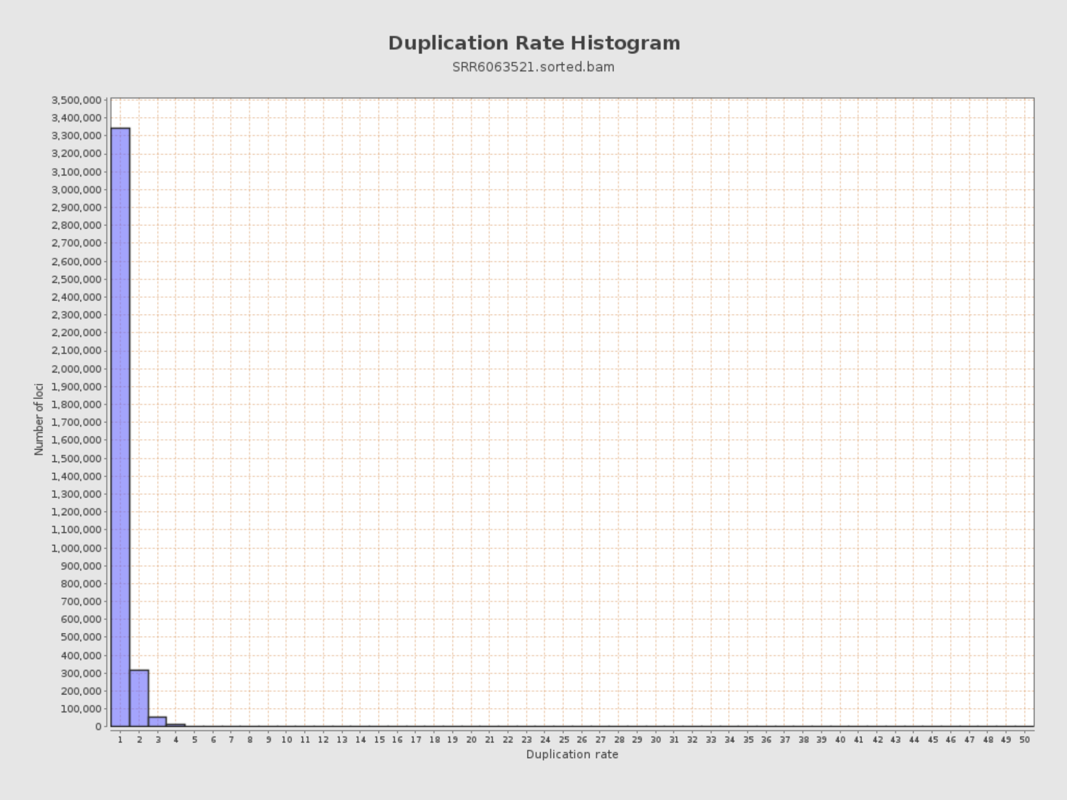
5. Results : Coverage Histogram (0-50X)



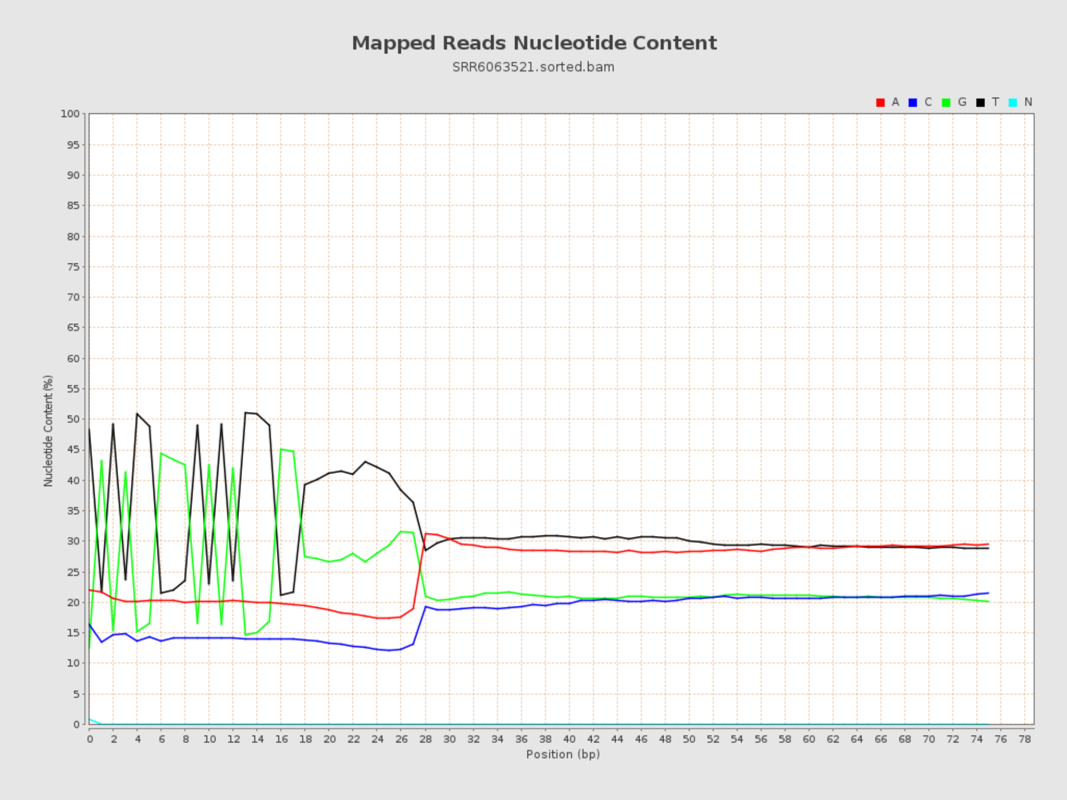
6. Results : Genome Fraction Coverage



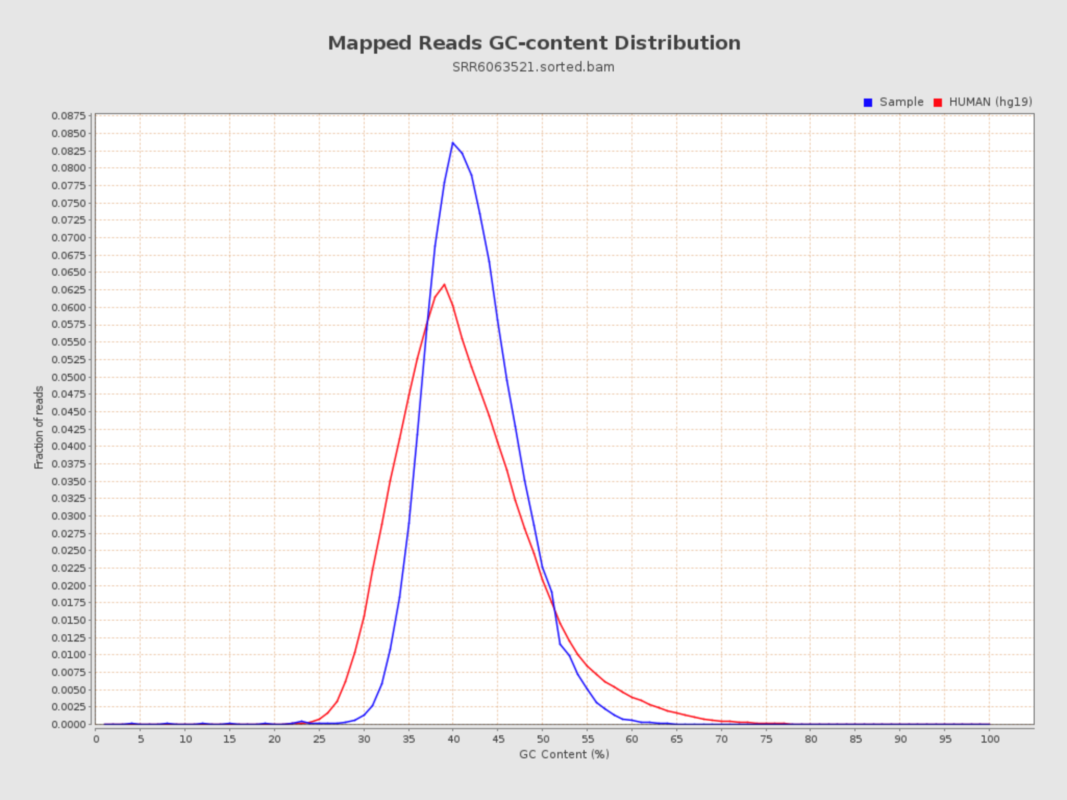
7. Results : Duplication Rate Histogram



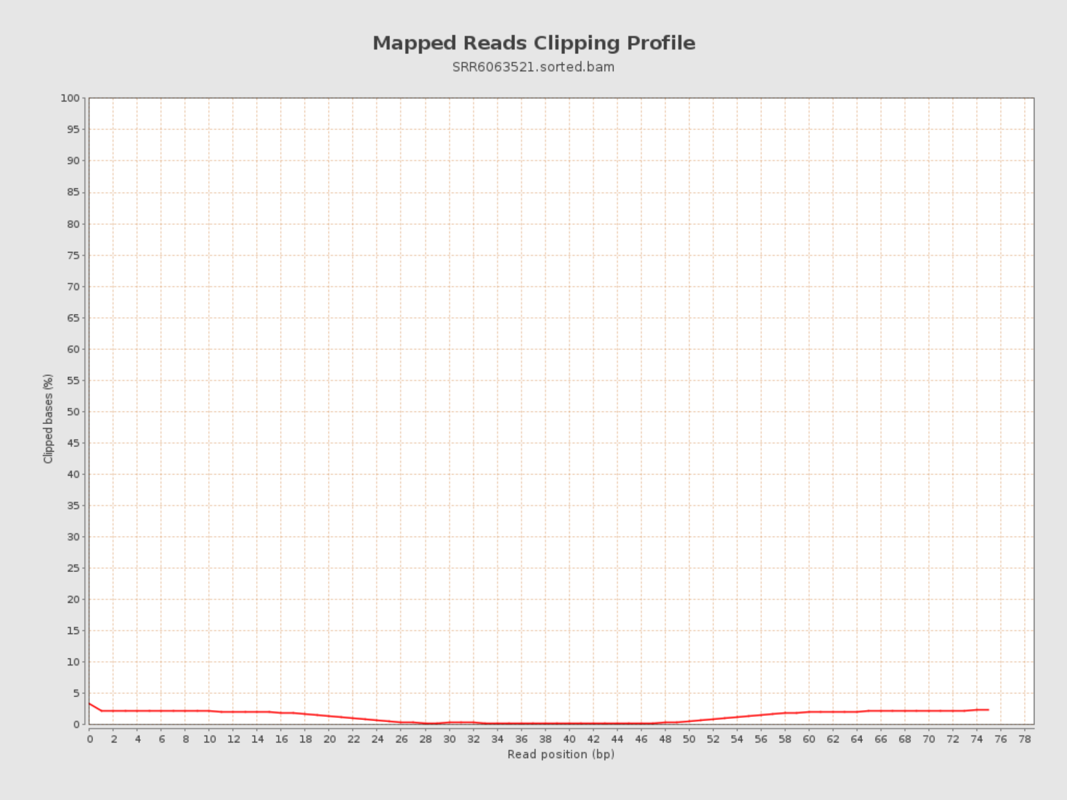
8. Results : Mapped Reads Nucleotide Content



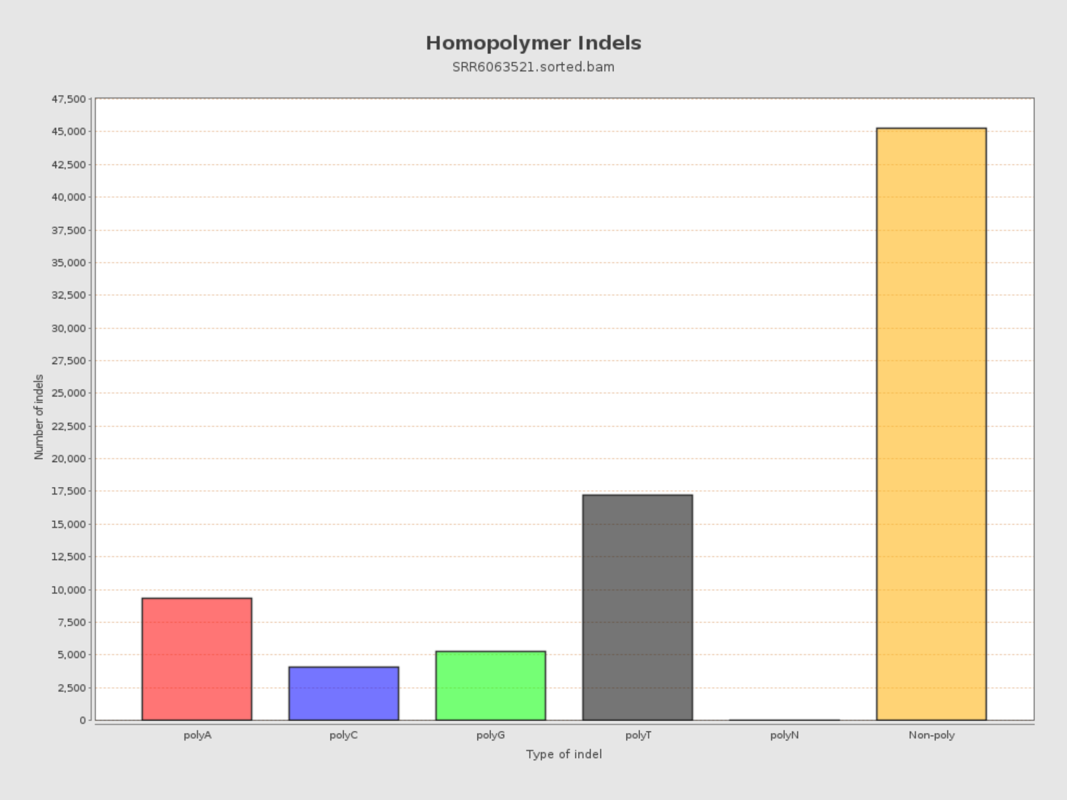
9. Results : Mapped Reads GC-content Distribution



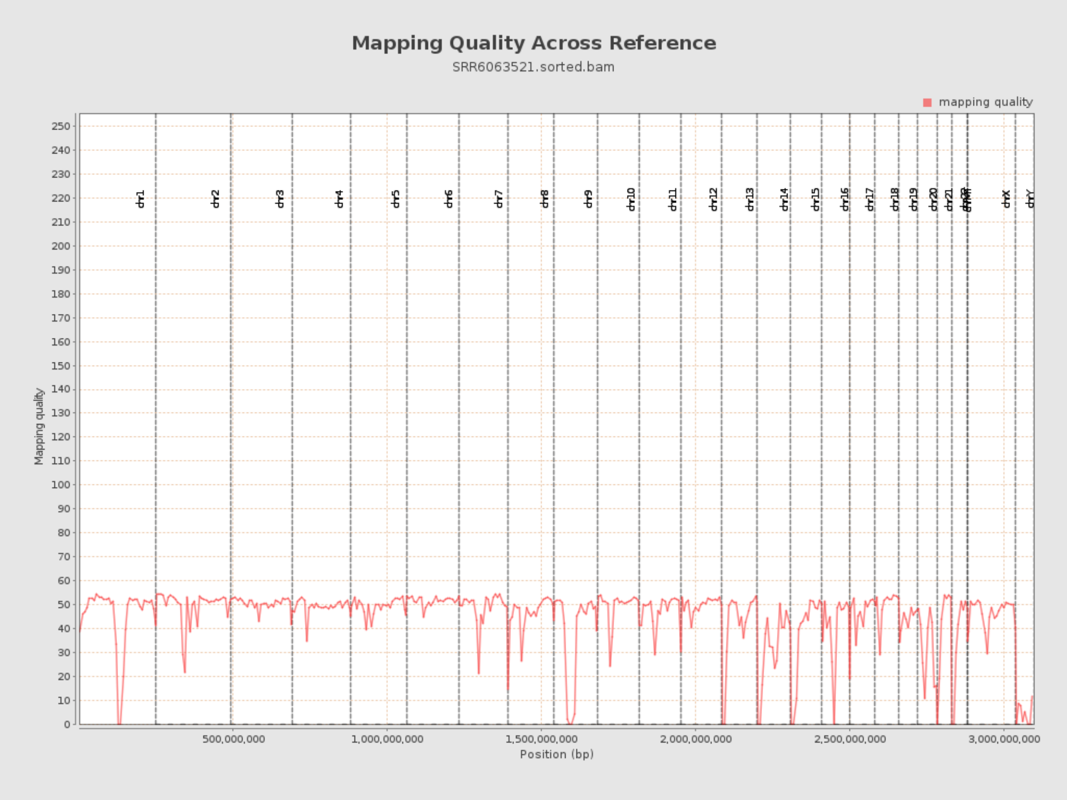
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram