Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 01:25:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063541.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_SRR6063541 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063541.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 01:25:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063541.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,776,858
Mapped reads	3,418,524 / 90.51%
Unmapped reads	358,334 / 9.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,857 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	194,777 / 5.16%
Duplication rate	4.32%
Clipped reads	1,817,435 / 48.12%

2.2. ACGT Content

Number/percentage of A's	59,849,911 / 26.98%
Number/percentage of C's	40,702,777 / 18.35%
Number/percentage of T's	69,967,281 / 31.54%
Number/percentage of G's	51,300,787 / 23.13%
Number/percentage of N's	4,402 / 0%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0717

Standard Deviation	0.6308

2.4. Mapping Quality

Mean Mapping Quality	43.58

2.5. Mismatches and indels

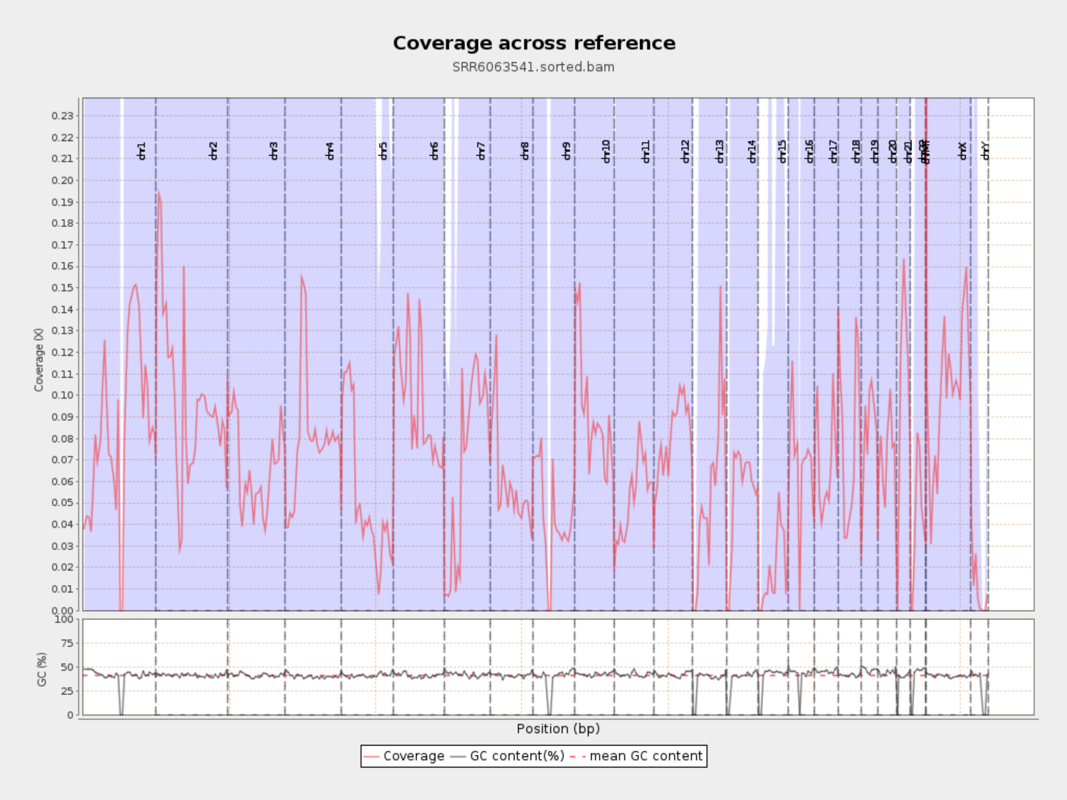
General error rate	0.8%
Mismatches	1,752,999
Insertions	16,487
Mapped reads with at least one insertion	0.48%
Deletions	60,935
Mapped reads with at least one deletion	1.76%
Homopolymer indels	45.72%

2.6. Chromosome stats

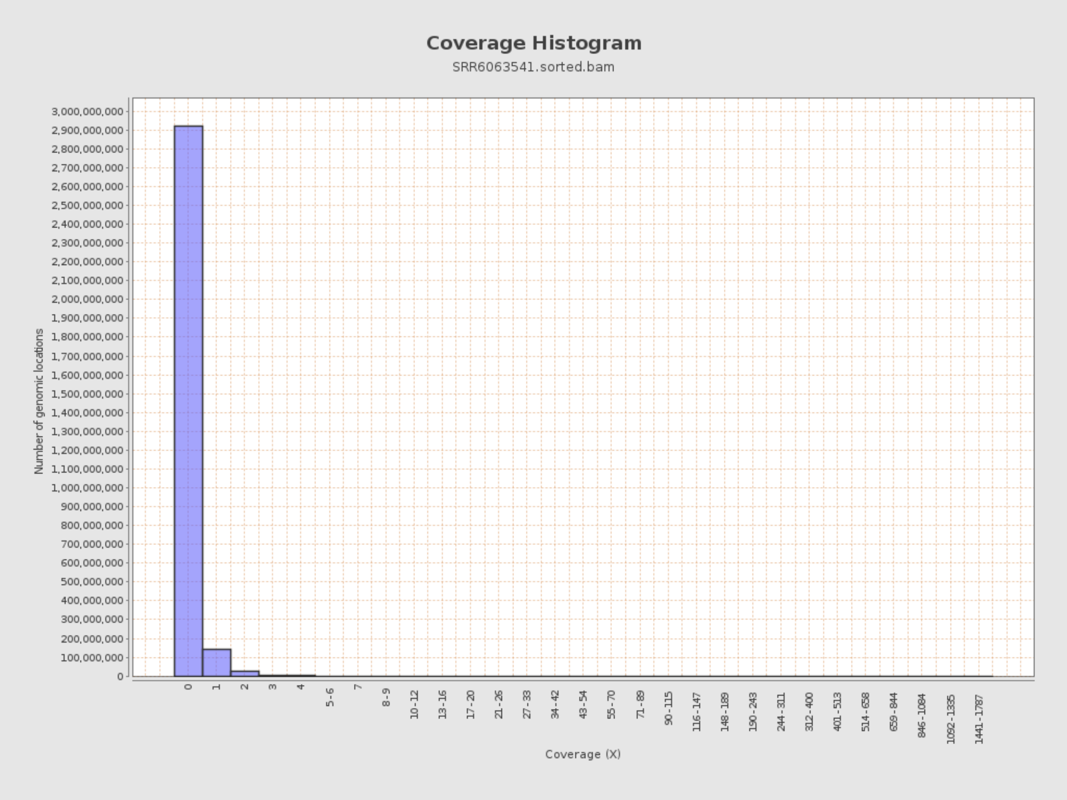
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21306651	0.0855	1.1426
chr2	243199373	24111992	0.0991	1.0165
chr3	198022430	13201067	0.0667	0.3153
chr4	191154276	15425267	0.0807	0.3615
chr5	180915260	9613527	0.0531	0.2838
chr6	171115067	16687168	0.0975	0.5046
chr7	159138663	10966008	0.0689	0.7435

chr8	146364022	8702523	0.0595	0.938
chr9	141213431	6167278	0.0437	0.5486
chr10	135534747	12506342	0.0923	0.5184
chr11	135006516	7193693	0.0533	0.3989
chr12	133851895	10907056	0.0815	0.3722
chr13	115169878	6515623	0.0566	0.2967
chr14	107349540	5925752	0.0552	0.3616
chr15	102531392	1828972	0.0178	0.2236
chr16	90354753	6084304	0.0673	0.3603
chr17	81195210	5657234	0.0697	0.3453
chr18	78077248	6156513	0.0789	0.888
chr19	59128983	4911587	0.0831	0.8678
chr20	63025520	4579442	0.0727	0.3609
chr21	48129895	4906212	0.1019	0.4095
chr22	51304566	2154230	0.042	0.2462
chrMT	16571	26571	1.6035	1.8815
chrX	155270560	15781227	0.1016	0.4872
chrY	59373566	607123	0.0102	0.1876

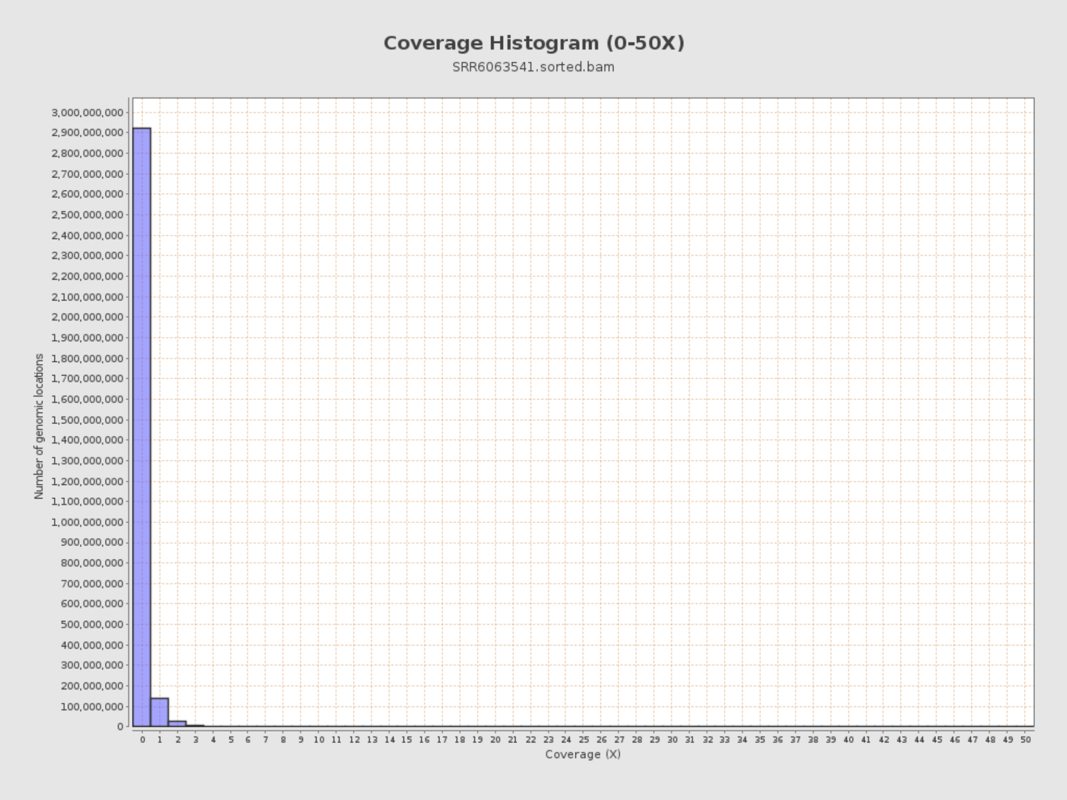
3. Results : Coverage across reference



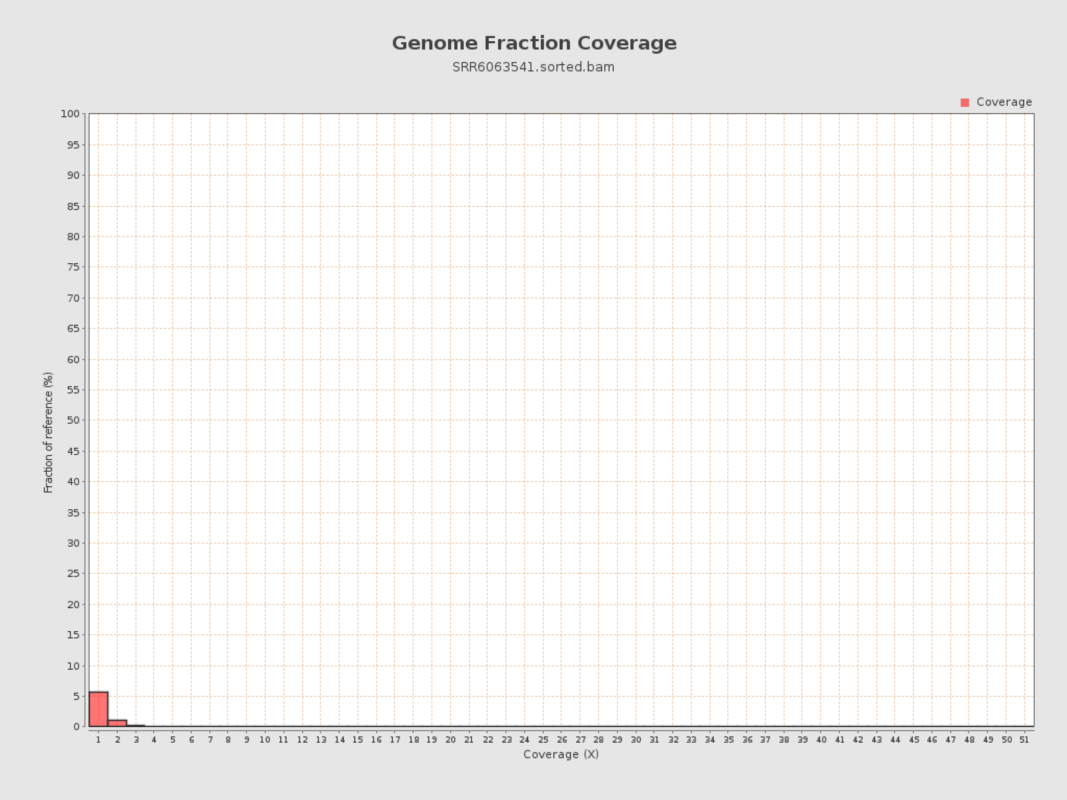
4. Results : Coverage Histogram



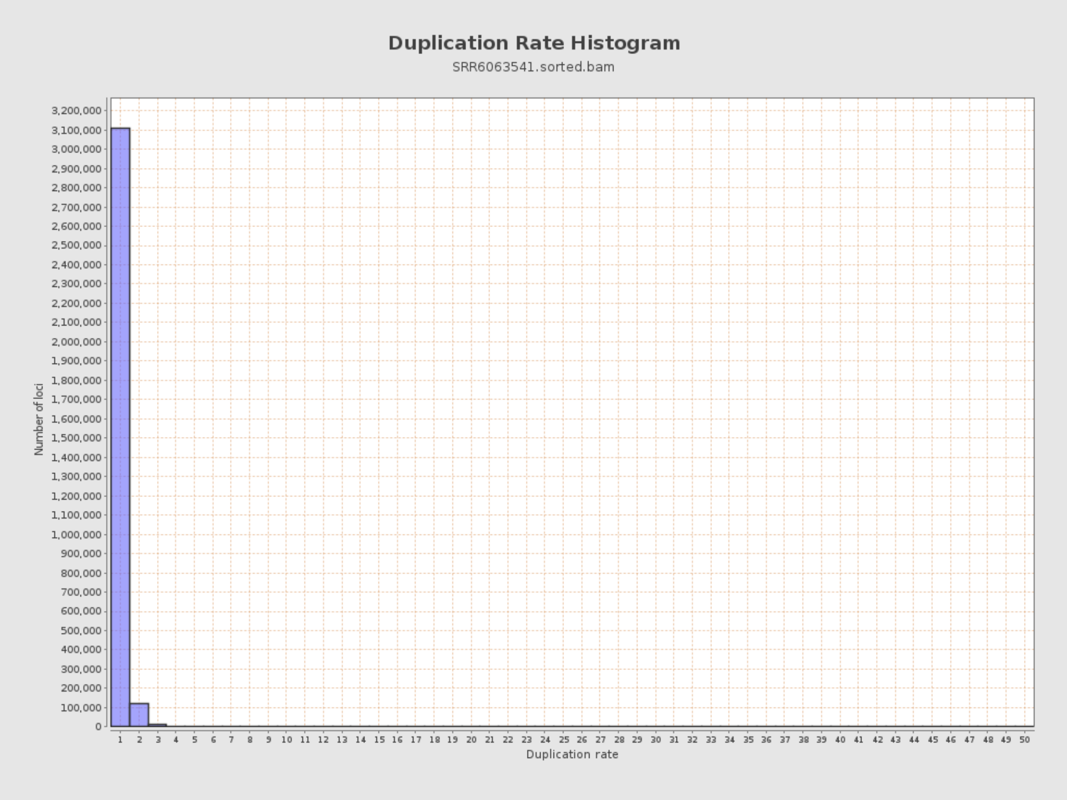
5. Results : Coverage Histogram (0-50X)



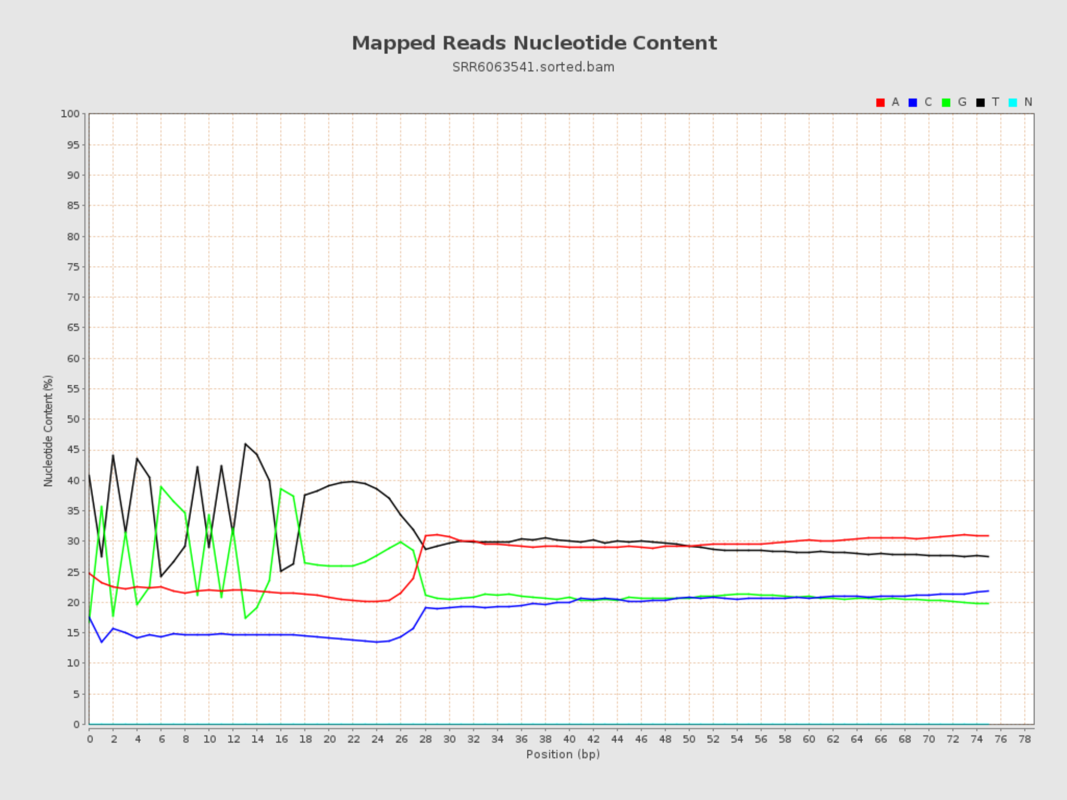
6. Results : Genome Fraction Coverage



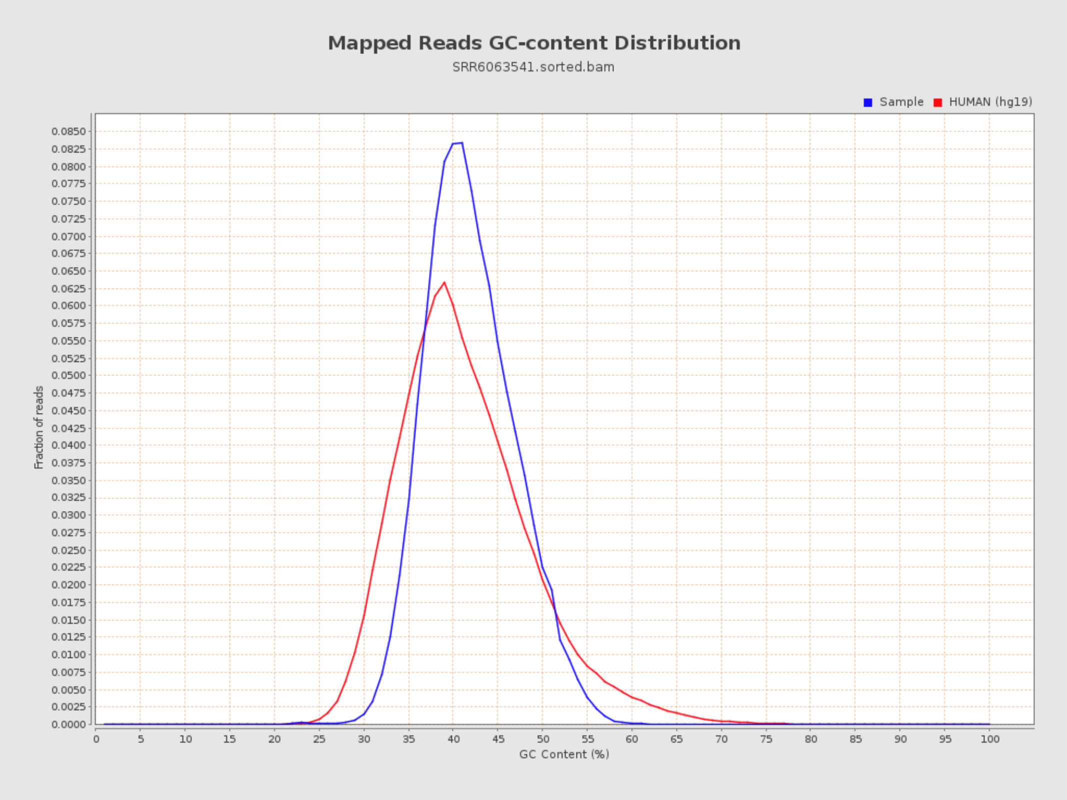
7. Results : Duplication Rate Histogram



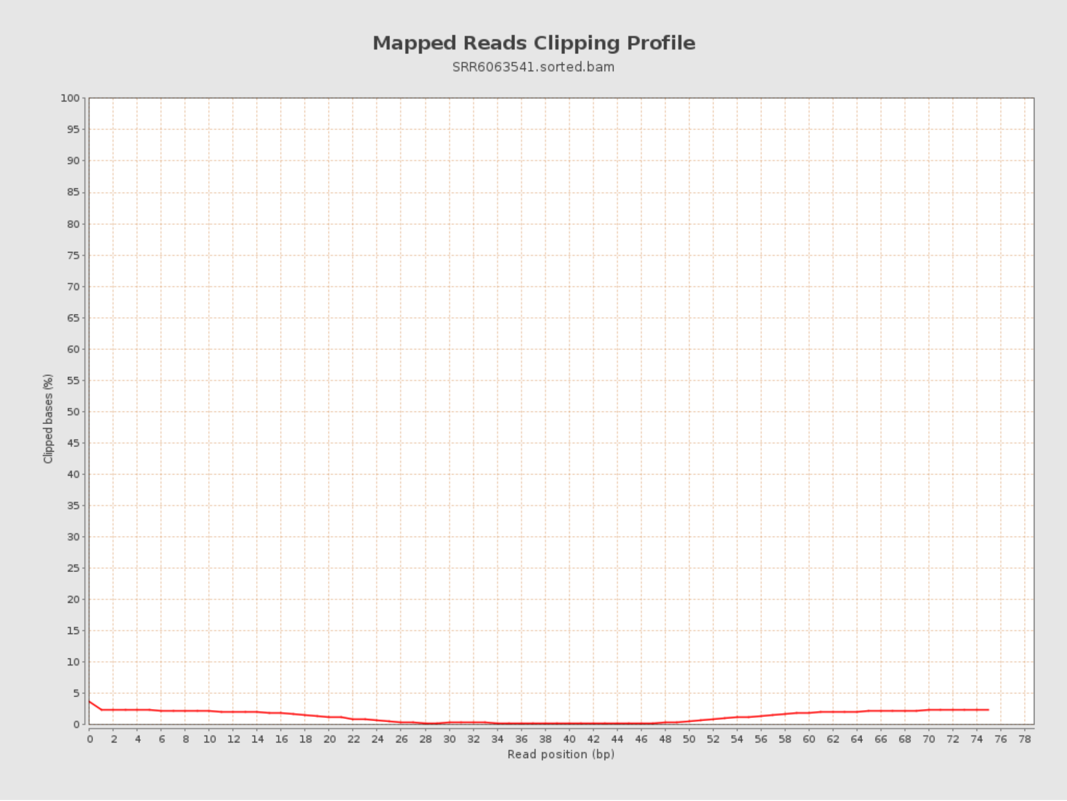
8. Results : Mapped Reads Nucleotide Content



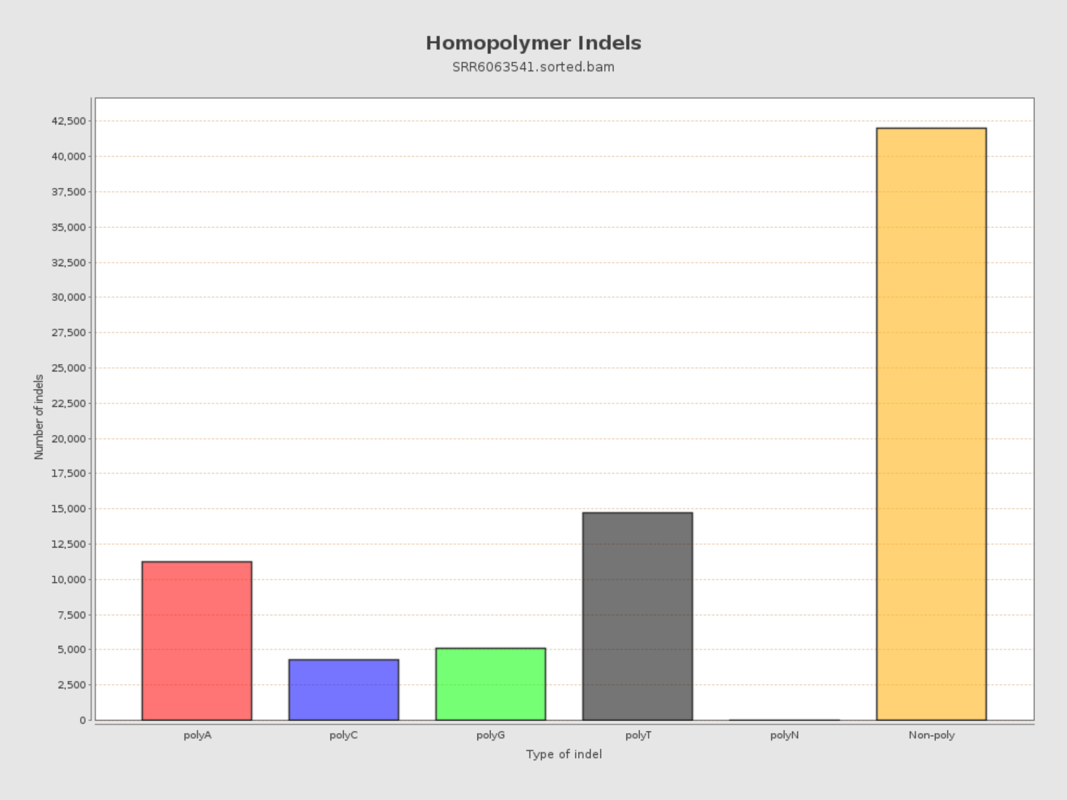
9. Results : Mapped Reads GC-content Distribution



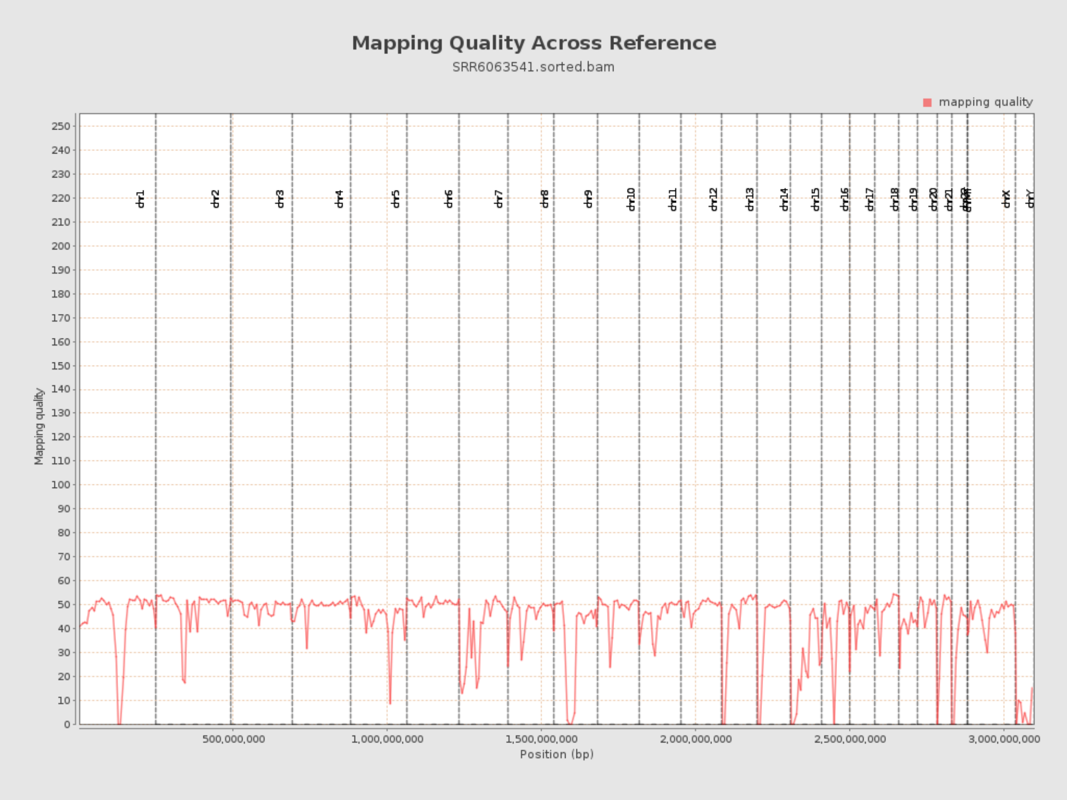
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram