Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:34:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004065.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_SRR6004065 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004065.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:34:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004065.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,168,426
Mapped reads	969,356 / 82.96%
Unmapped reads	199,070 / 17.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,344 / 0.71%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	30,547 / 2.61%
Duplication rate	2.47%
Clipped reads	449,620 / 38.48%

2.2. ACGT Content

Number/percentage of A's	18,472,278 / 28.8%
Number/percentage of C's	11,339,790 / 17.68%
Number/percentage of T's	20,550,528 / 32.05%
Number/percentage of G's	13,724,161 / 21.4%
Number/percentage of N's	42,239 / 0.07%
GC Percentage	39.08%

2.3. Coverage

Mean	0.0207

Standard Deviation	0.2237

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

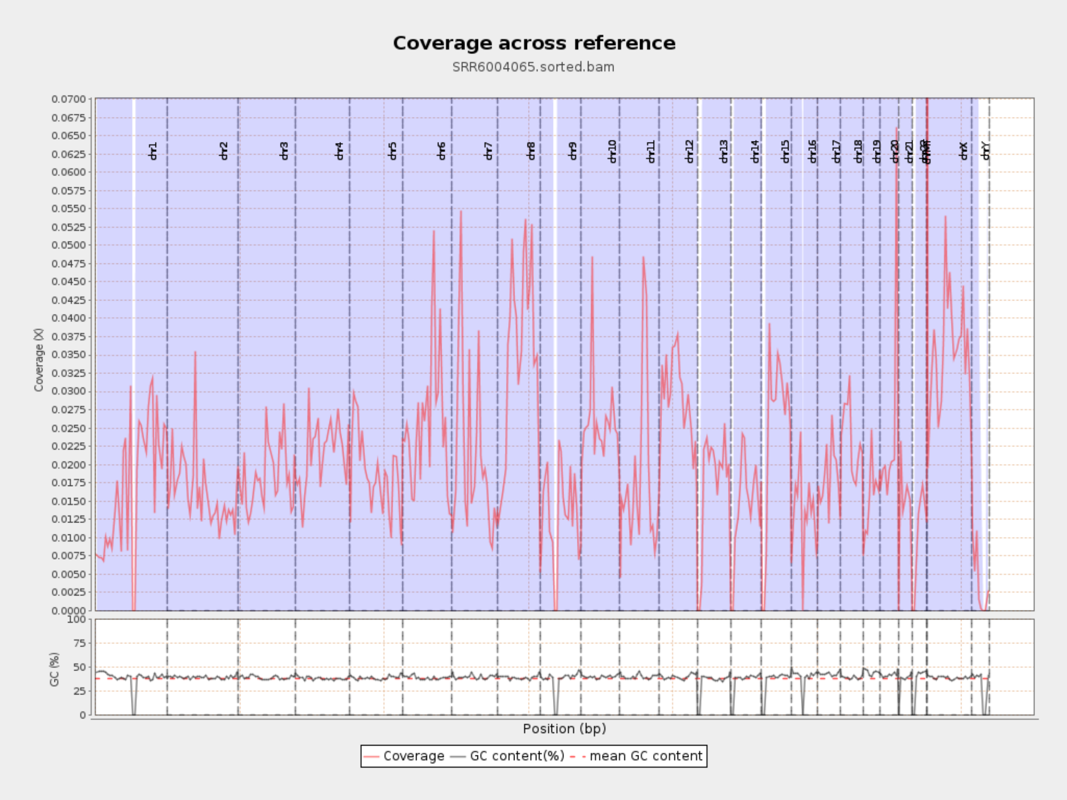
General error rate	1.05%
Mismatches	660,840
Insertions	5,318
Mapped reads with at least one insertion	0.54%
Deletions	26,014
Mapped reads with at least one deletion	2.64%
Homopolymer indels	43.88%

2.6. Chromosome stats

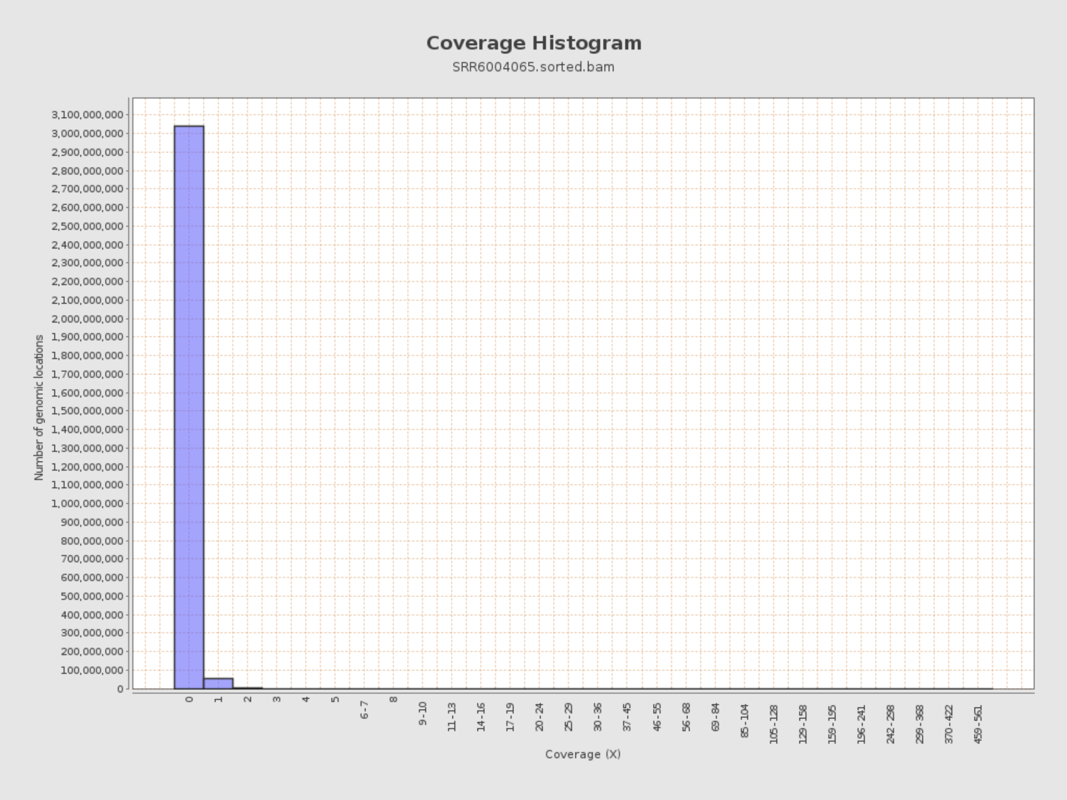
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4257009	0.0171	0.3631
chr2	243199373	3952293	0.0163	0.2046
chr3	198022430	3620198	0.0183	0.1475
chr4	191154276	4137803	0.0216	0.1633
chr5	180915260	3405609	0.0188	0.1487
chr6	171115067	4407742	0.0258	0.1912
chr7	159138663	3379394	0.0212	0.2494

chr8	146364022	5147554	0.0352	0.3958
chr9	141213431	1877286	0.0133	0.1849
chr10	135534747	3502412	0.0258	0.2563
chr11	135006516	2403636	0.0178	0.1747
chr12	133851895	3895707	0.0291	0.1849
chr13	115169878	1985751	0.0172	0.1406
chr14	107349540	1546745	0.0144	0.1374
chr15	102531392	2551281	0.0249	0.1724
chr16	90354753	1195551	0.0132	0.1514
chr17	81195210	1494555	0.0184	0.1535
chr18	78077248	1830273	0.0234	0.363
chr19	59128983	928225	0.0157	0.2467
chr20	63025520	1615826	0.0256	0.1787
chr21	48129895	691619	0.0144	0.136
chr22	51304566	535172	0.0104	0.1091
chrMT	16571	25881	1.5618	1.6576
chrX	155270560	5569449	0.0359	0.2201
chrY	59373566	216339	0.0036	0.0912

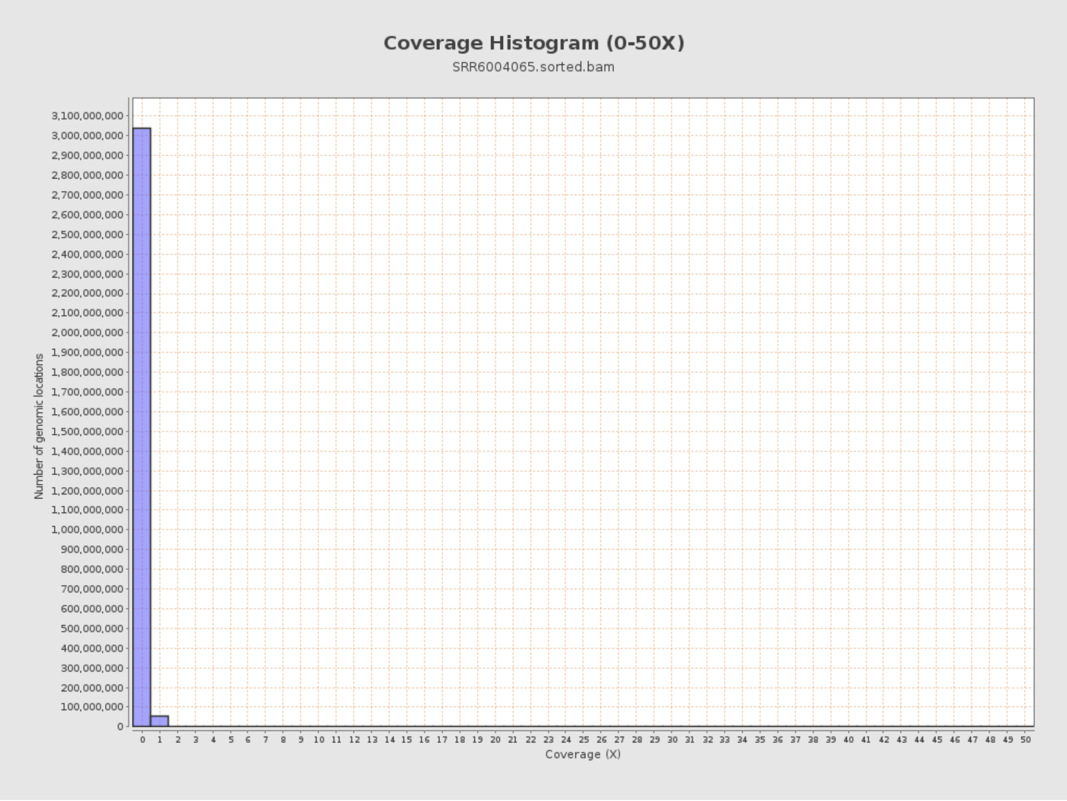
3. Results : Coverage across reference



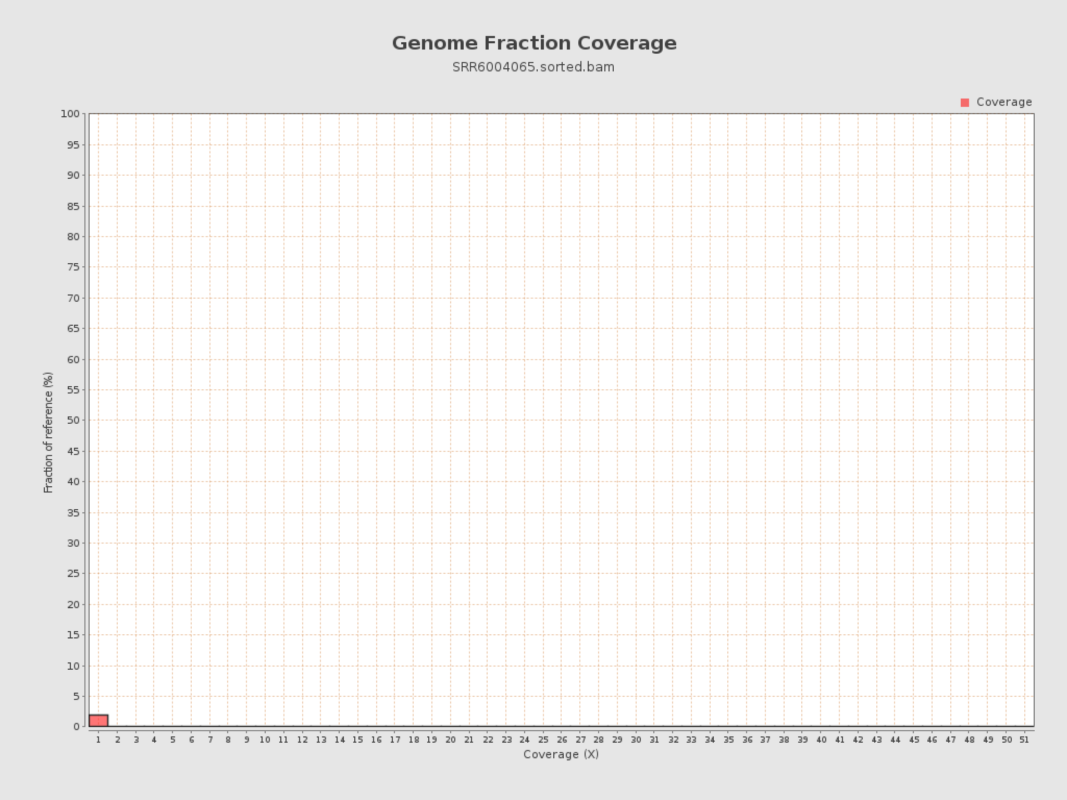
4. Results : Coverage Histogram



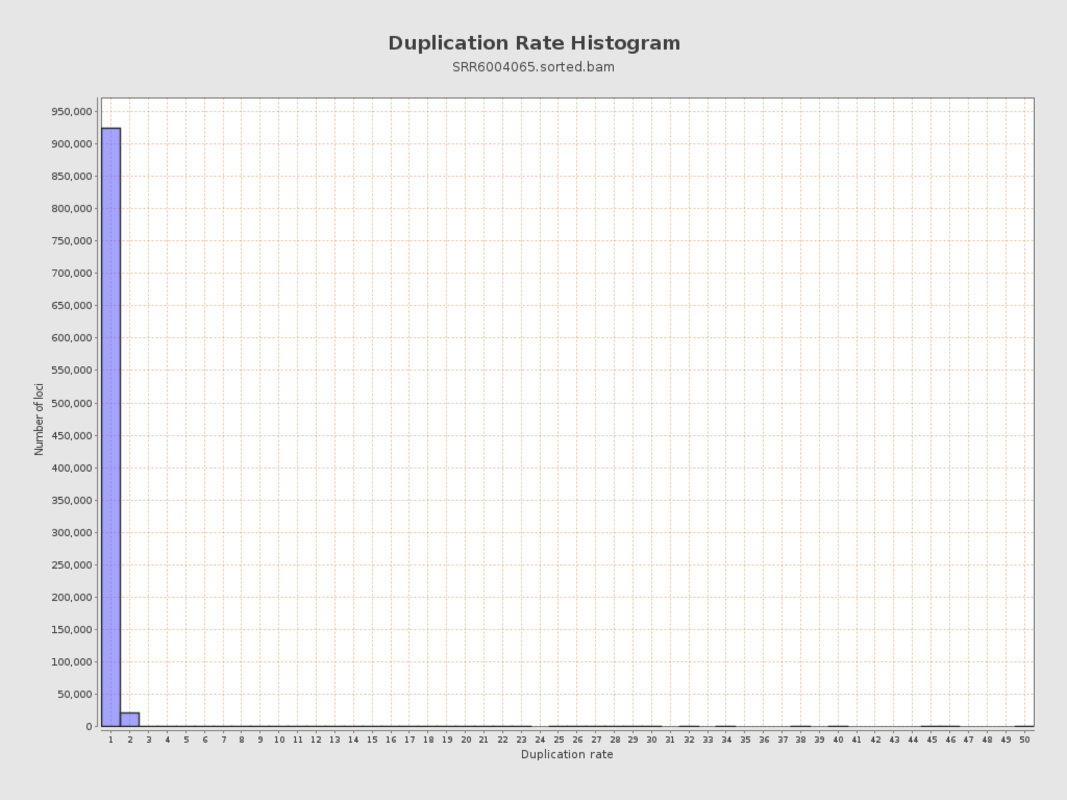
5. Results : Coverage Histogram (0-50X)



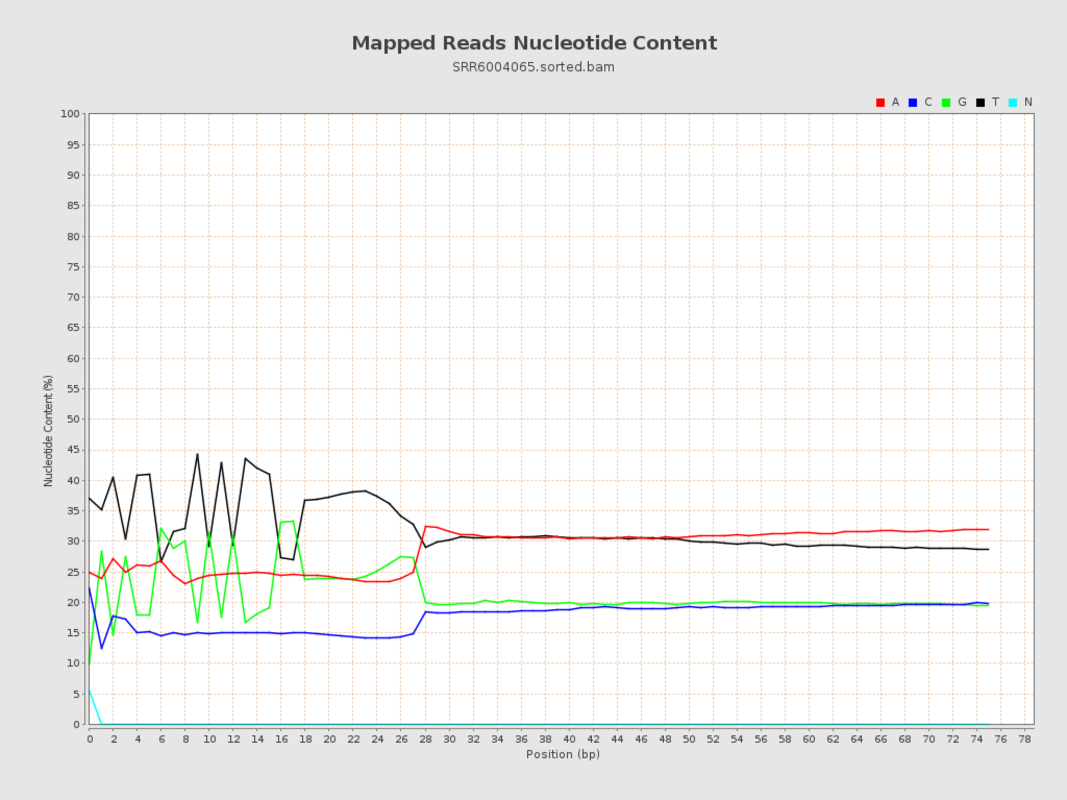
6. Results : Genome Fraction Coverage



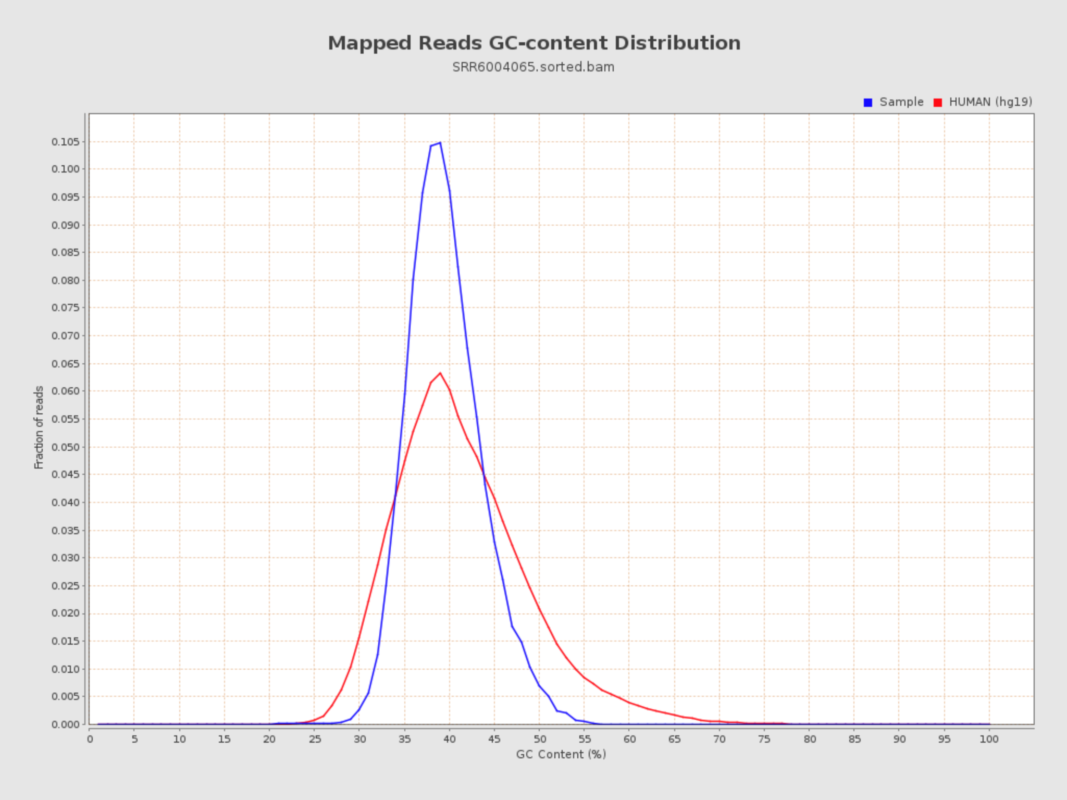
7. Results : Duplication Rate Histogram



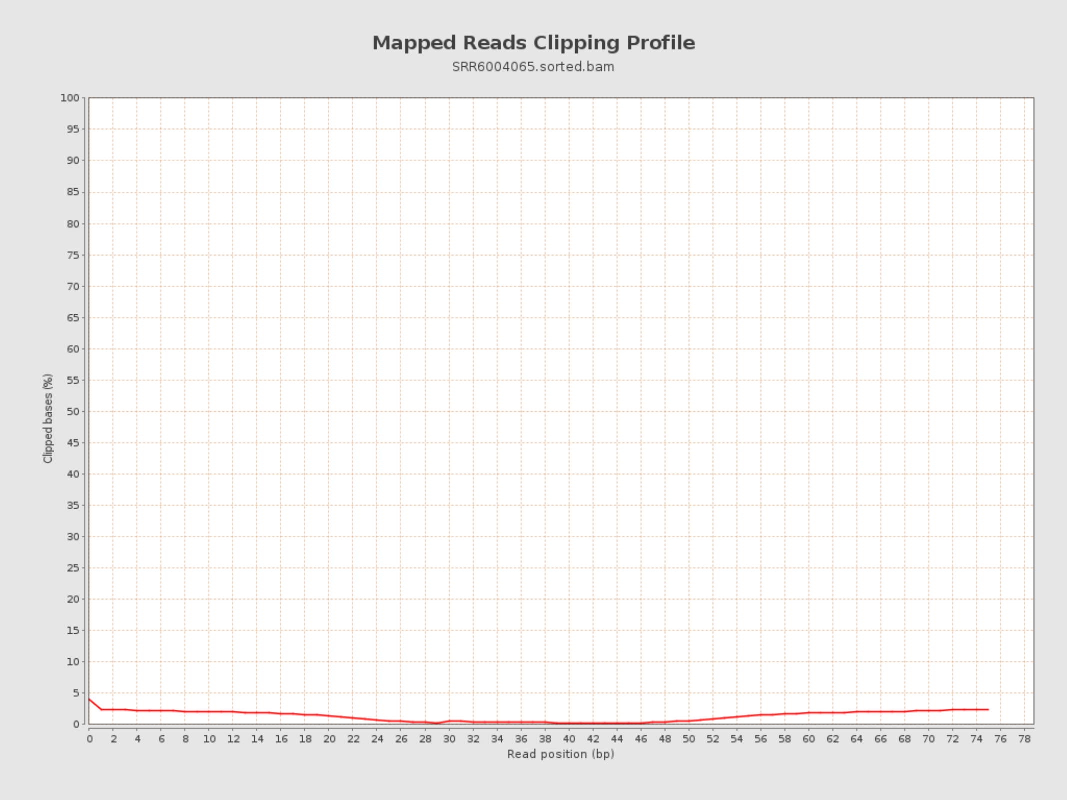
8. Results : Mapped Reads Nucleotide Content



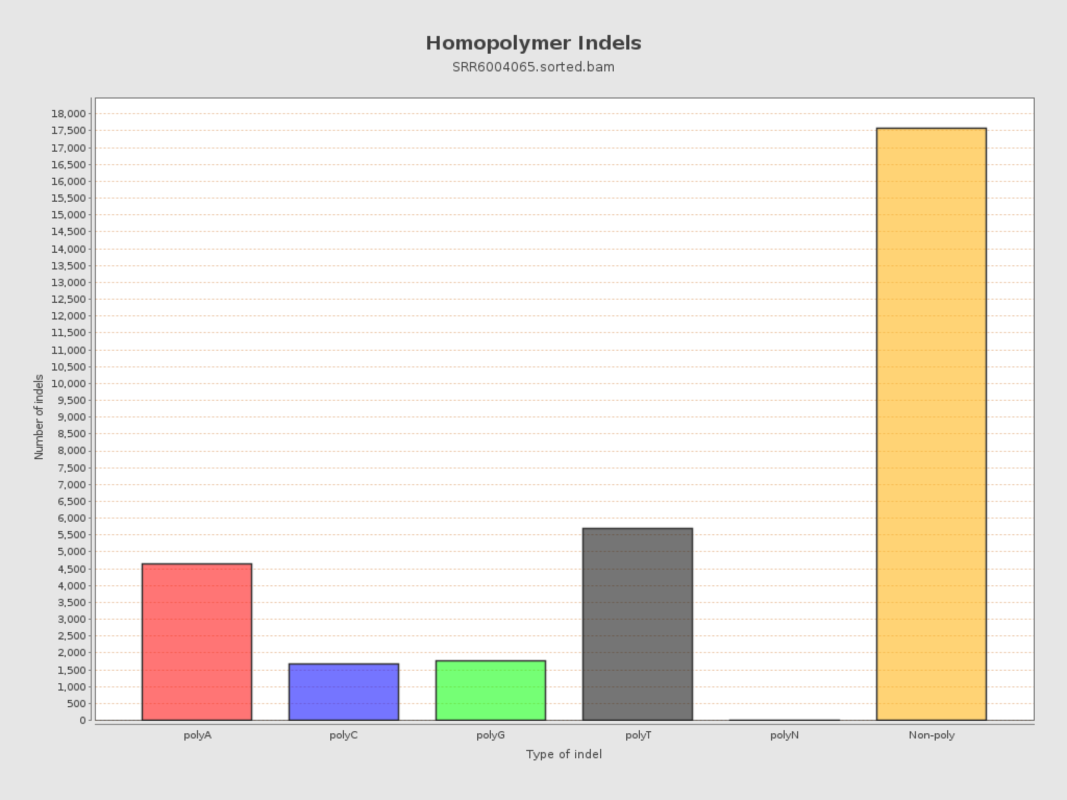
9. Results : Mapped Reads GC-content Distribution



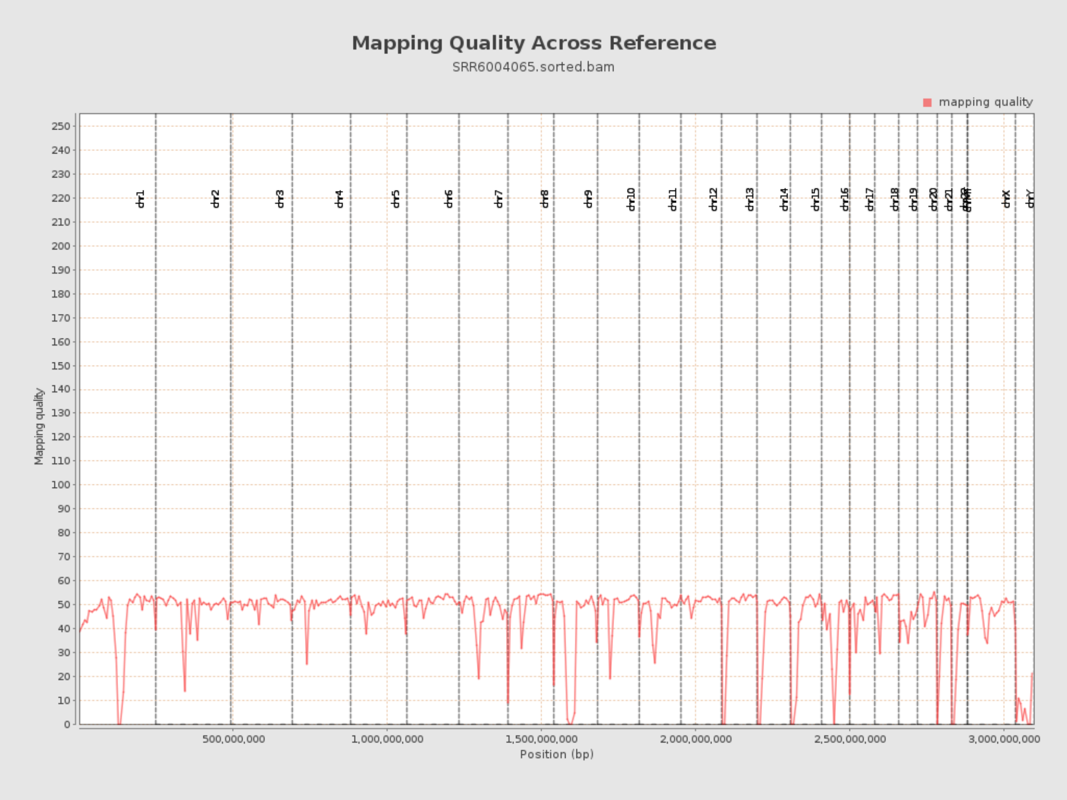
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram