Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:56:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240047.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_SRR6240047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:56:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,931,566
Mapped reads	1,589,689 / 82.3%
Unmapped reads	341,877 / 17.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,162 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	156,376 / 8.1%
Duplication rate	8.2%
Clipped reads	995,304 / 51.53%

2.2. ACGT Content

Number/percentage of A's	27,129,018 / 27.49%
Number/percentage of C's	17,440,096 / 17.67%
Number/percentage of T's	32,050,982 / 32.47%
Number/percentage of G's	22,016,610 / 22.31%
Number/percentage of N's	64,820 / 0.07%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.3117

2.4. Mapping Quality

Mean Mapping Quality	45.45

2.5. Mismatches and indels

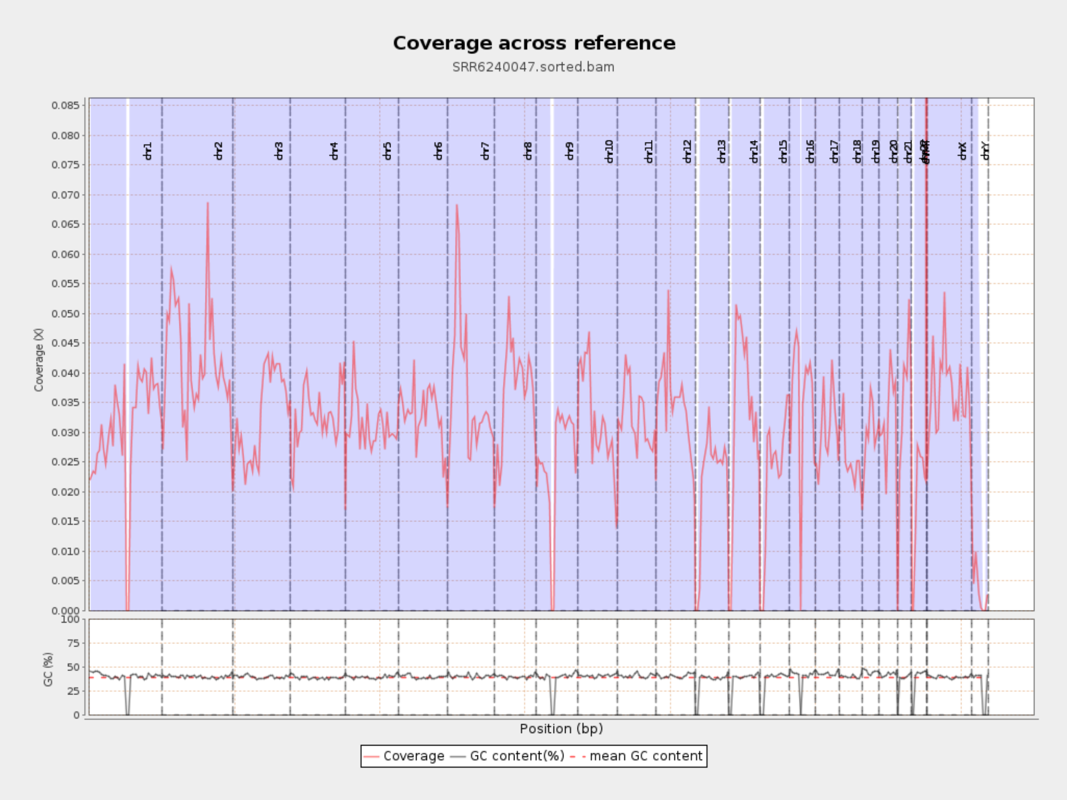
General error rate	0.95%
Mismatches	927,739
Insertions	7,058
Mapped reads with at least one insertion	0.44%
Deletions	28,337
Mapped reads with at least one deletion	1.76%
Homopolymer indels	48.57%

2.6. Chromosome stats

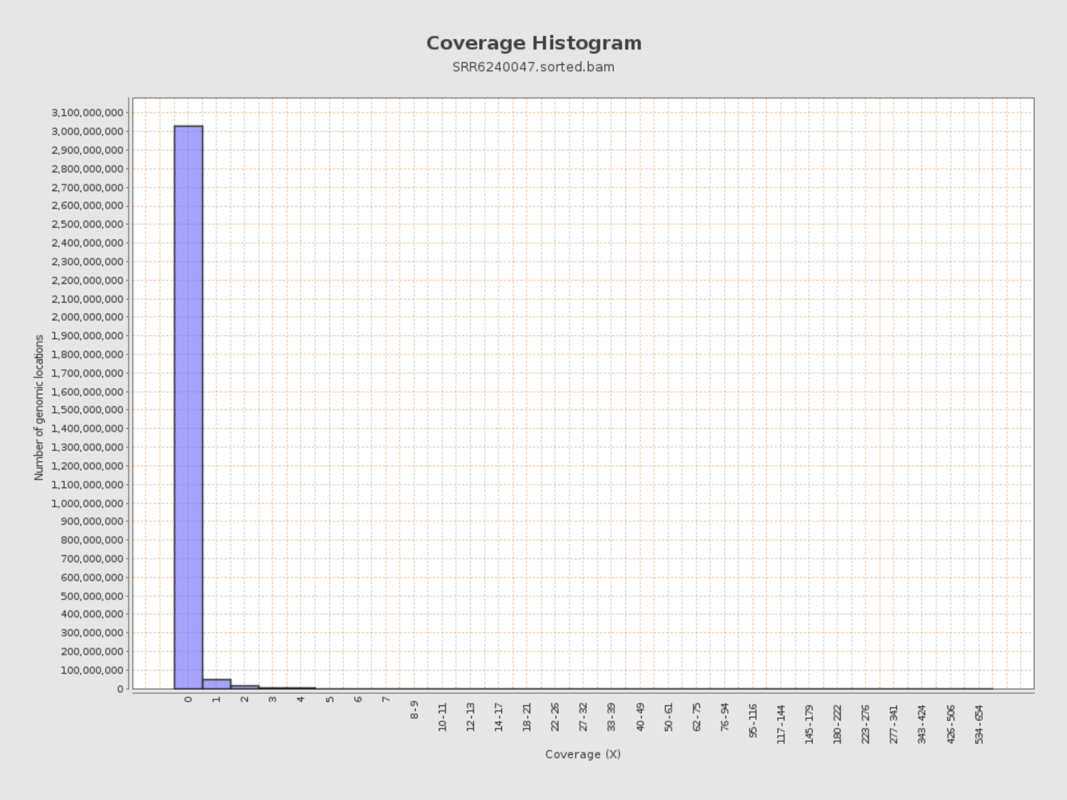
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7671741	0.0308	0.4453
chr2	243199373	10260812	0.0422	0.38
chr3	198022430	6493096	0.0328	0.2474
chr4	191154276	6258749	0.0327	0.2525
chr5	180915260	5656297	0.0313	0.2438
chr6	171115067	5641493	0.033	0.2839
chr7	159138663	5923502	0.0372	0.3835

chr8	146364022	5401088	0.0369	0.468
chr9	141213431	3541397	0.0251	0.2769
chr10	135534747	4413809	0.0326	0.2862
chr11	135006516	4373607	0.0324	0.2974
chr12	133851895	4706999	0.0352	0.2564
chr13	115169878	2517300	0.0219	0.2019
chr14	107349540	3581308	0.0334	0.2604
chr15	102531392	2336748	0.0228	0.2123
chr16	90354753	3200517	0.0354	0.26
chr17	81195210	2469097	0.0304	0.2515
chr18	78077248	2020934	0.0259	0.4079
chr19	59128983	1771643	0.03	0.3578
chr20	63025520	2039320	0.0324	0.2457
chr21	48129895	1631030	0.0339	0.2541
chr22	51304566	925406	0.018	0.1759
chrMT	16571	42369	2.5568	2.647
chrX	155270560	5660814	0.0365	0.2736
chrY	59373566	210427	0.0035	0.0856

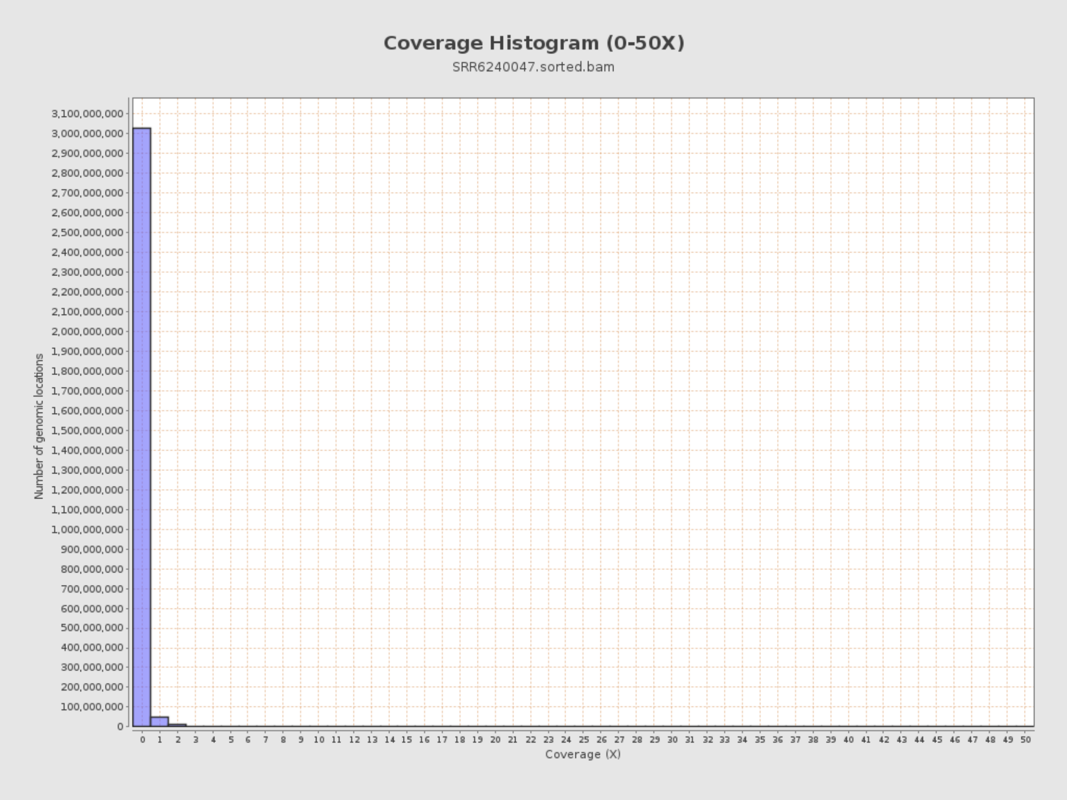
3. Results : Coverage across reference



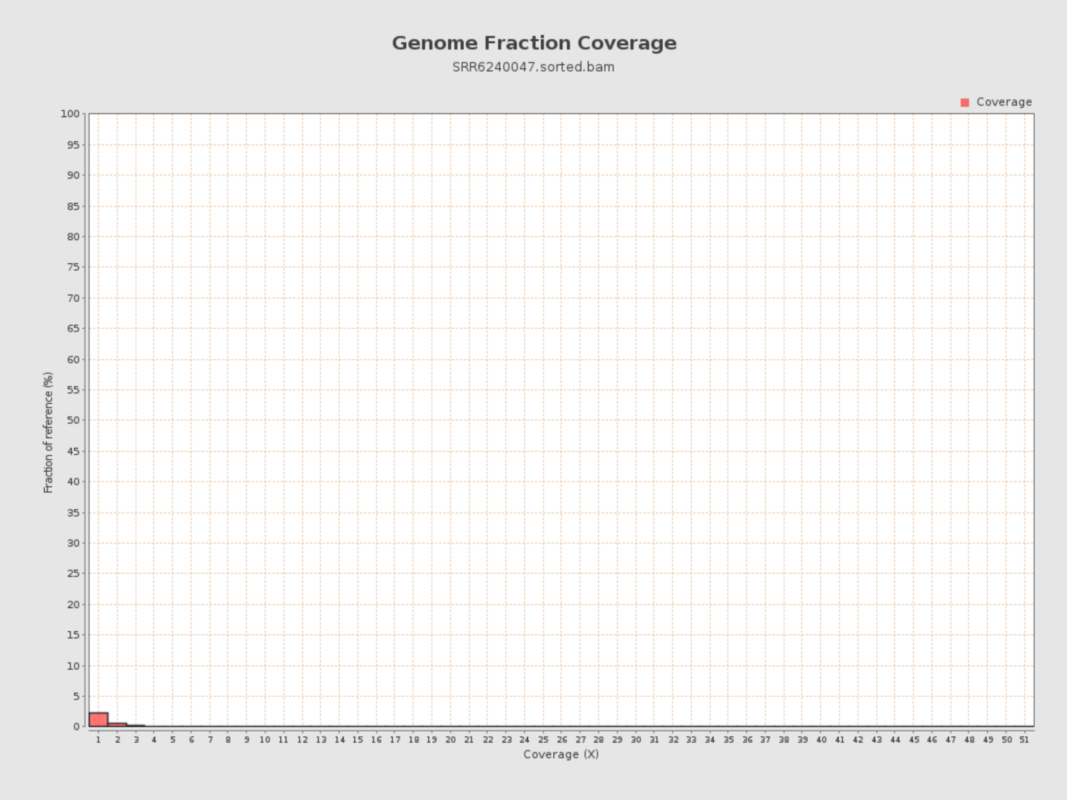
4. Results : Coverage Histogram



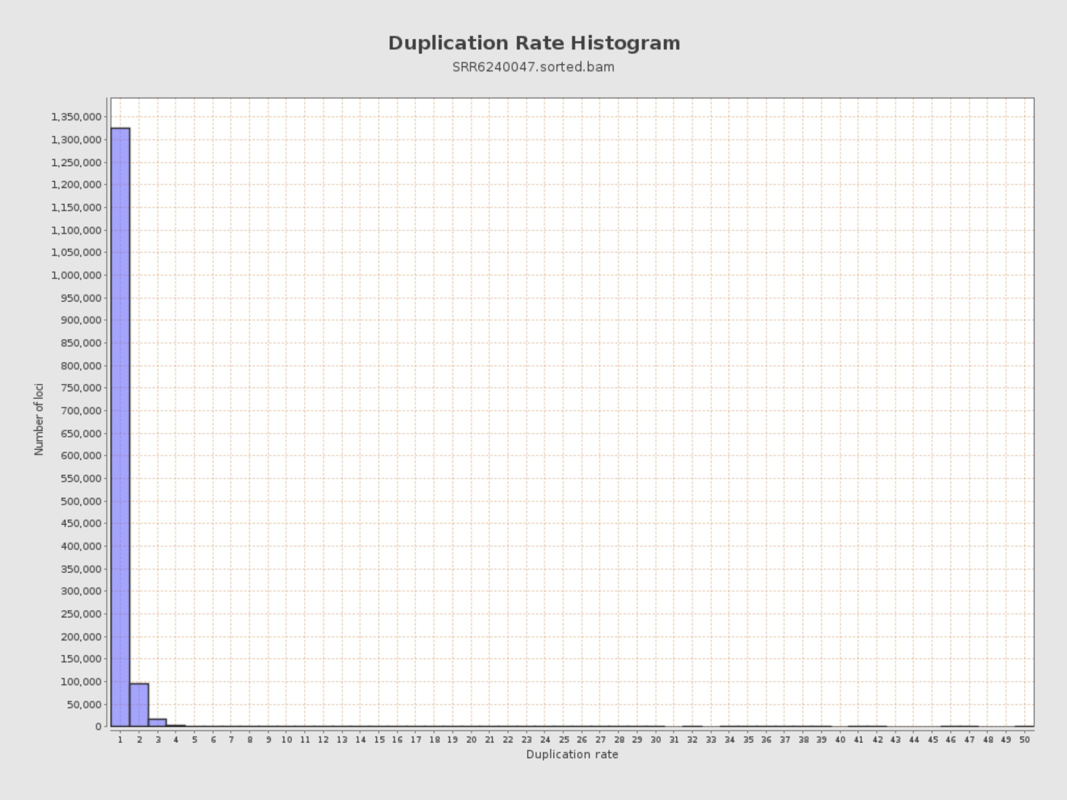
5. Results : Coverage Histogram (0-50X)



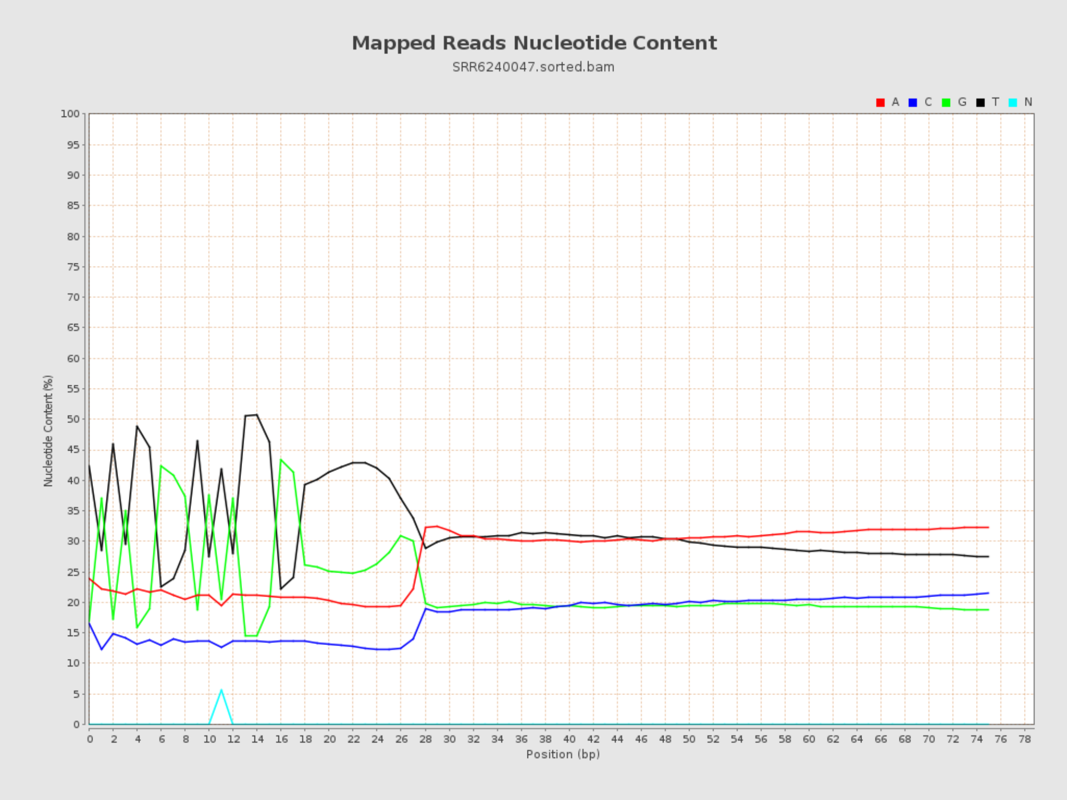
6. Results : Genome Fraction Coverage



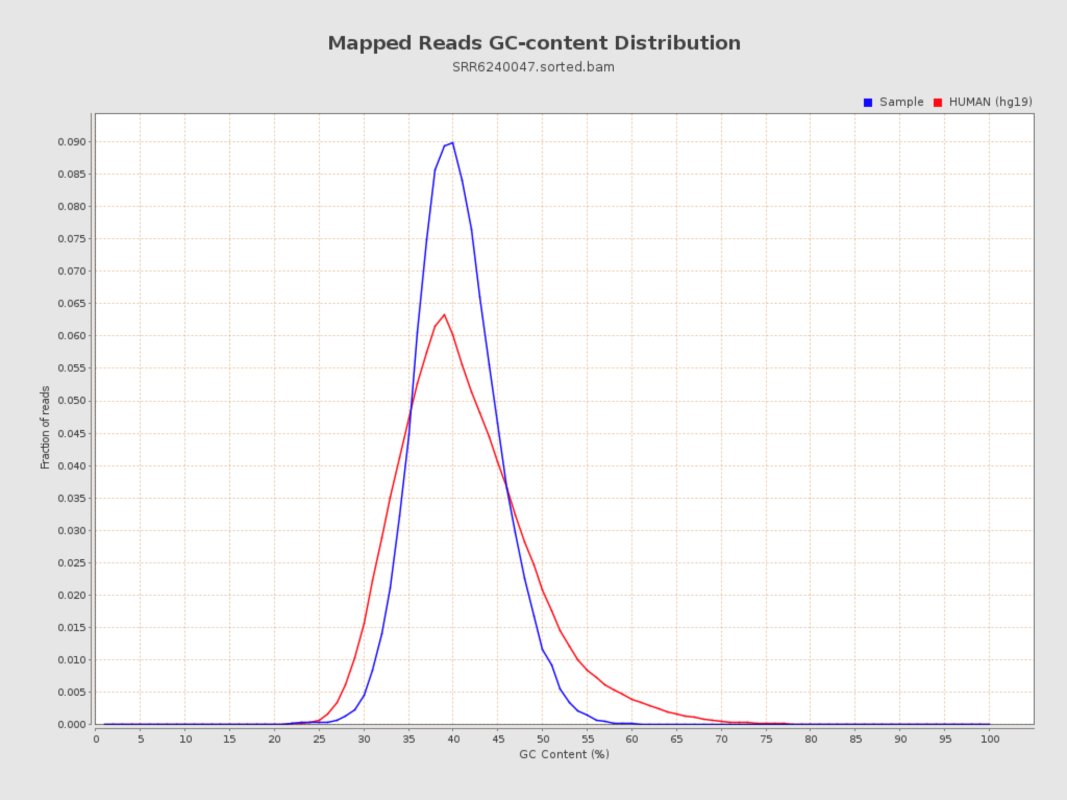
7. Results : Duplication Rate Histogram



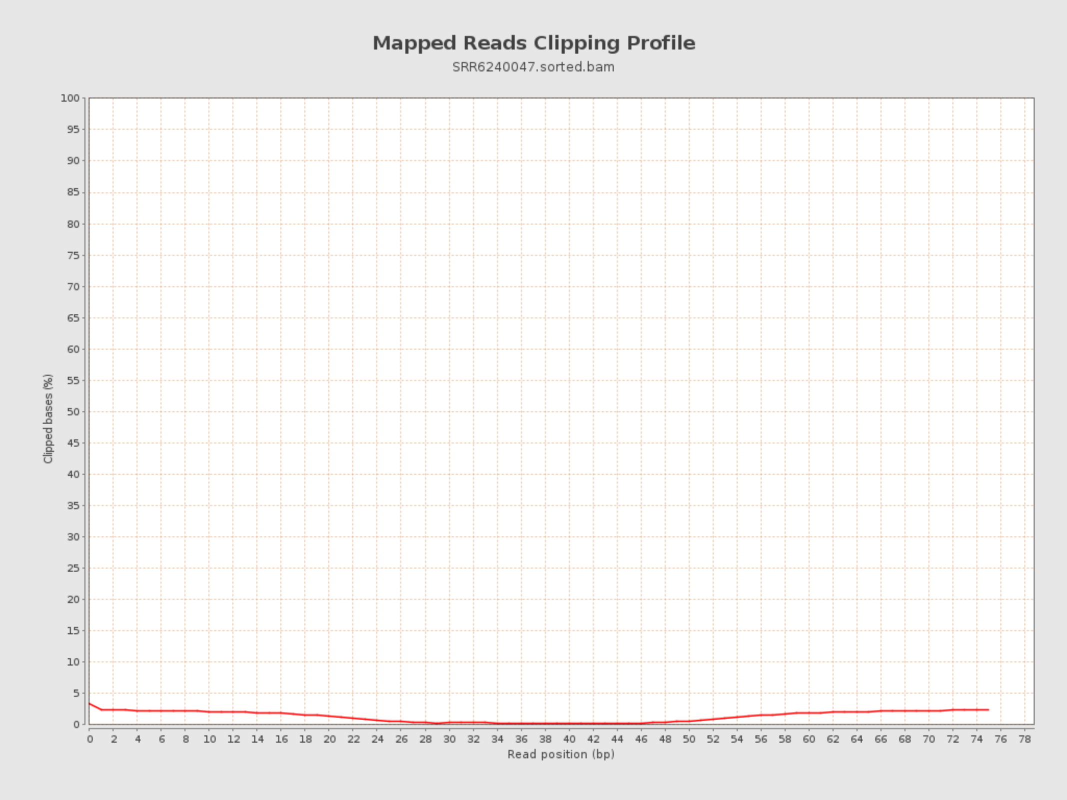
8. Results : Mapped Reads Nucleotide Content



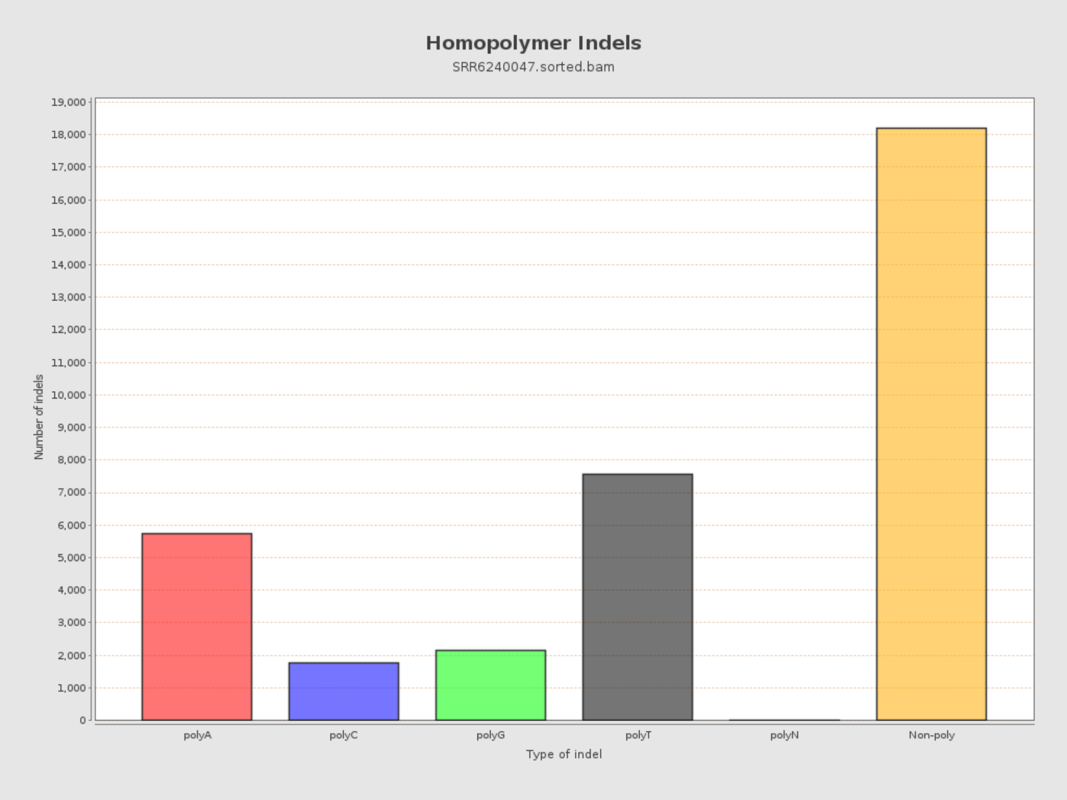
9. Results : Mapped Reads GC-content Distribution



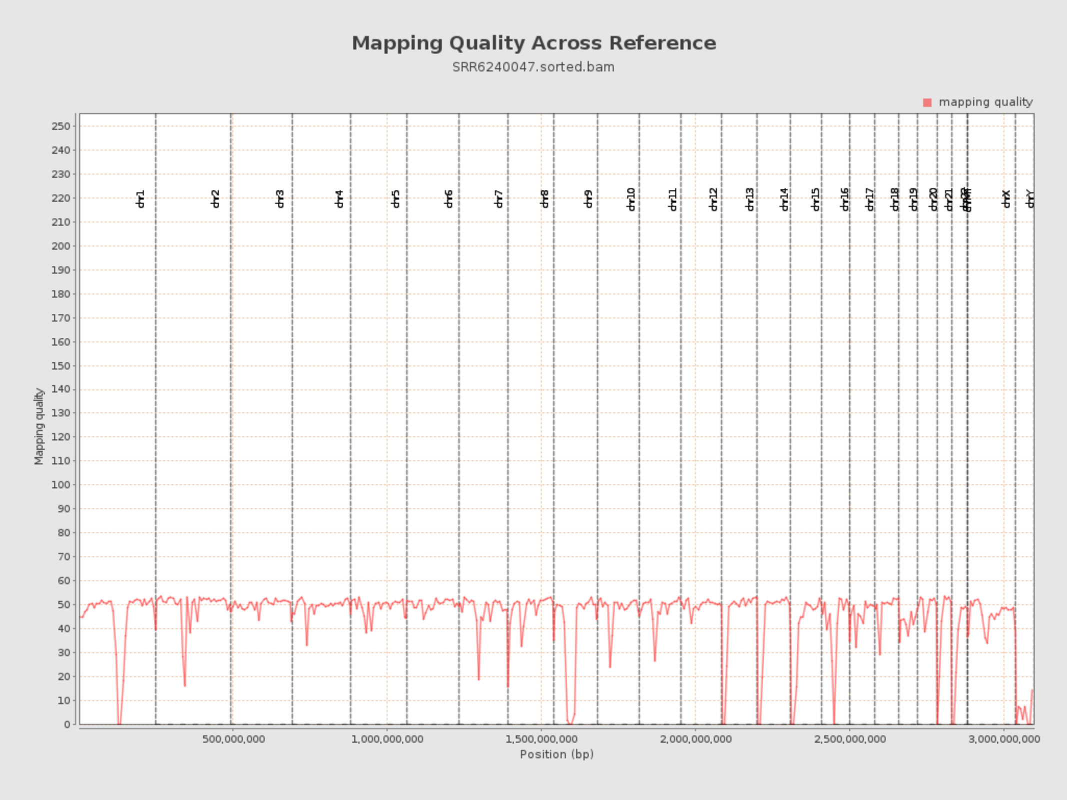
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram