Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:15:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240223.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_SRR6240223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:15:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,158,536
Mapped reads	1,764,848 / 81.76%
Unmapped reads	393,688 / 18.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,677 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	199,525 / 9.24%
Duplication rate	8.54%
Clipped reads	740,986 / 34.33%

2.2. ACGT Content

Number/percentage of A's	34,125,576 / 28.6%
Number/percentage of C's	22,471,907 / 18.84%
Number/percentage of T's	37,673,950 / 31.58%
Number/percentage of G's	25,018,772 / 20.97%
Number/percentage of N's	10,822 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.4867

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

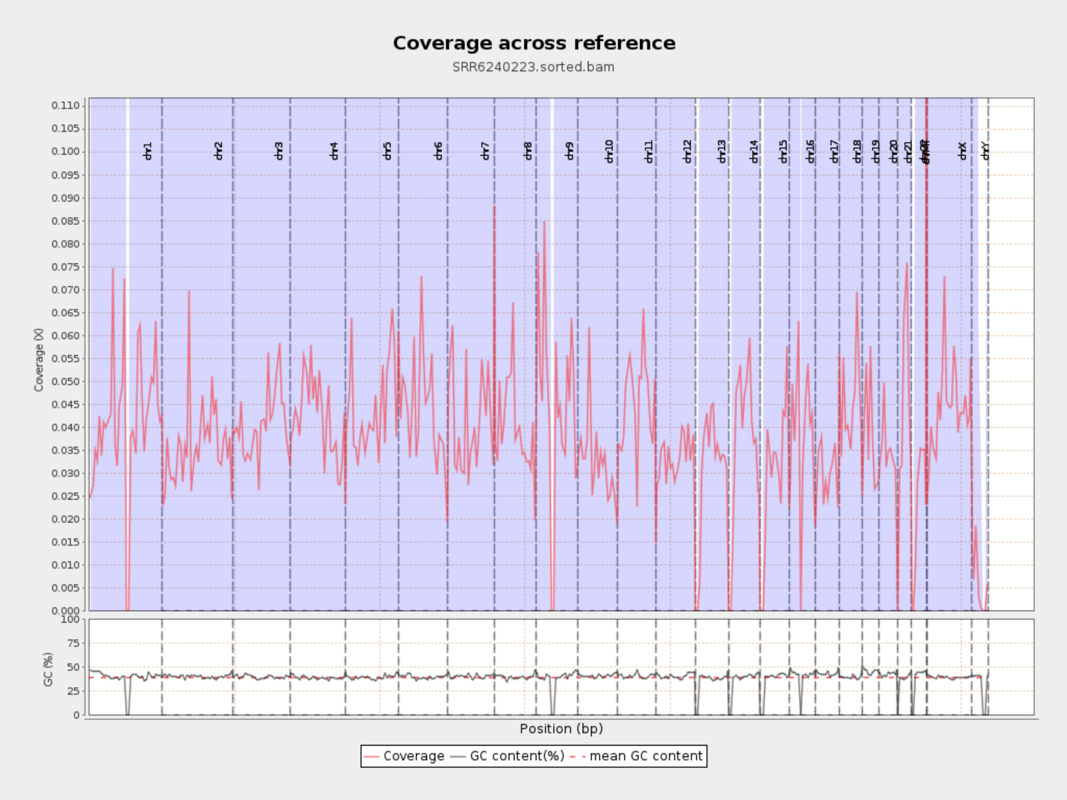
General error rate	0.78%
Mismatches	916,005
Insertions	9,248
Mapped reads with at least one insertion	0.52%
Deletions	27,606
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.56%

2.6. Chromosome stats

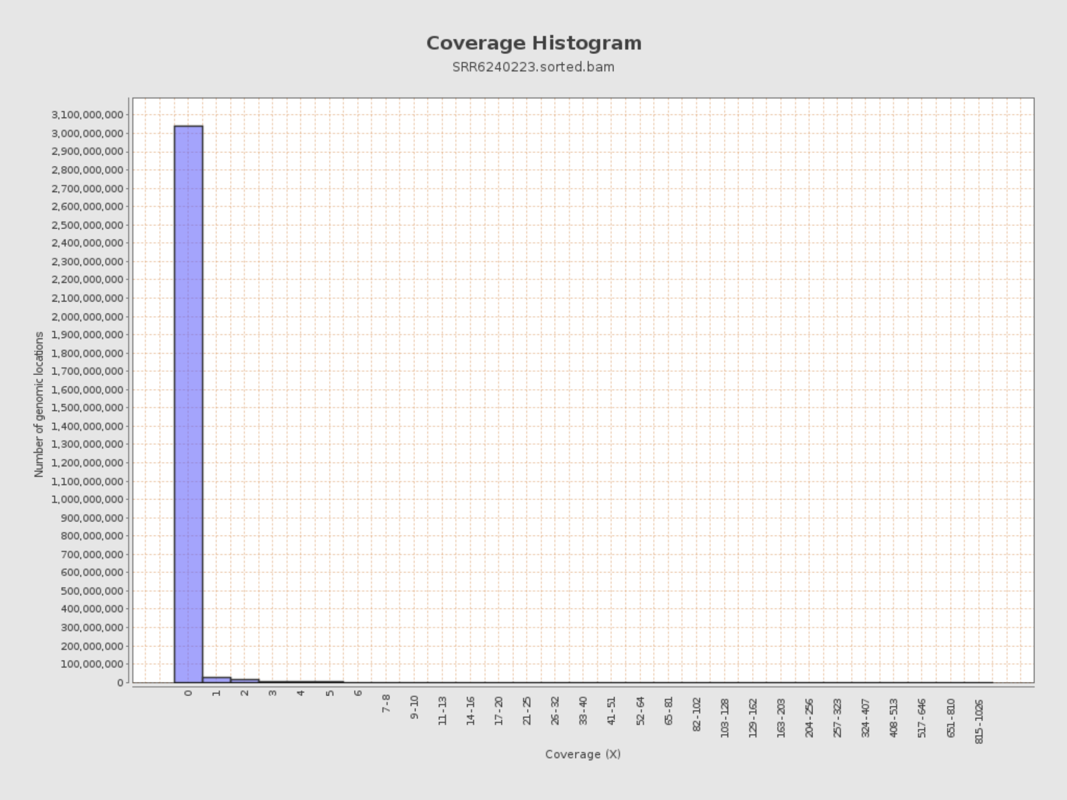
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10282862	0.0413	0.7635
chr2	243199373	8785528	0.0361	0.4764
chr3	198022430	8057715	0.0407	0.375
chr4	191154276	8033131	0.042	0.388
chr5	180915260	7920310	0.0438	0.3825
chr6	171115067	7562337	0.0442	0.4345
chr7	159138663	6595750	0.0414	0.4678

chr8	146364022	5866294	0.0401	0.7208
chr9	141213431	6418286	0.0455	0.5103
chr10	135534747	4441997	0.0328	0.4158
chr11	135006516	6103585	0.0452	0.5282
chr12	133851895	4468340	0.0334	0.3376
chr13	115169878	3460613	0.03	0.321
chr14	107349540	3933078	0.0366	0.3788
chr15	102531392	3039138	0.0296	0.3266
chr16	90354753	3523044	0.039	0.3808
chr17	81195210	2377447	0.0293	0.3424
chr18	78077248	3623406	0.0464	0.9047
chr19	59128983	2286075	0.0387	0.5867
chr20	63025520	2176123	0.0345	0.3554
chr21	48129895	2050130	0.0426	0.4135
chr22	51304566	1146884	0.0224	0.2606
chrMT	16571	8265	0.4988	1.1855
chrX	155270560	6858138	0.0442	0.4165
chrY	59373566	331864	0.0056	0.1575

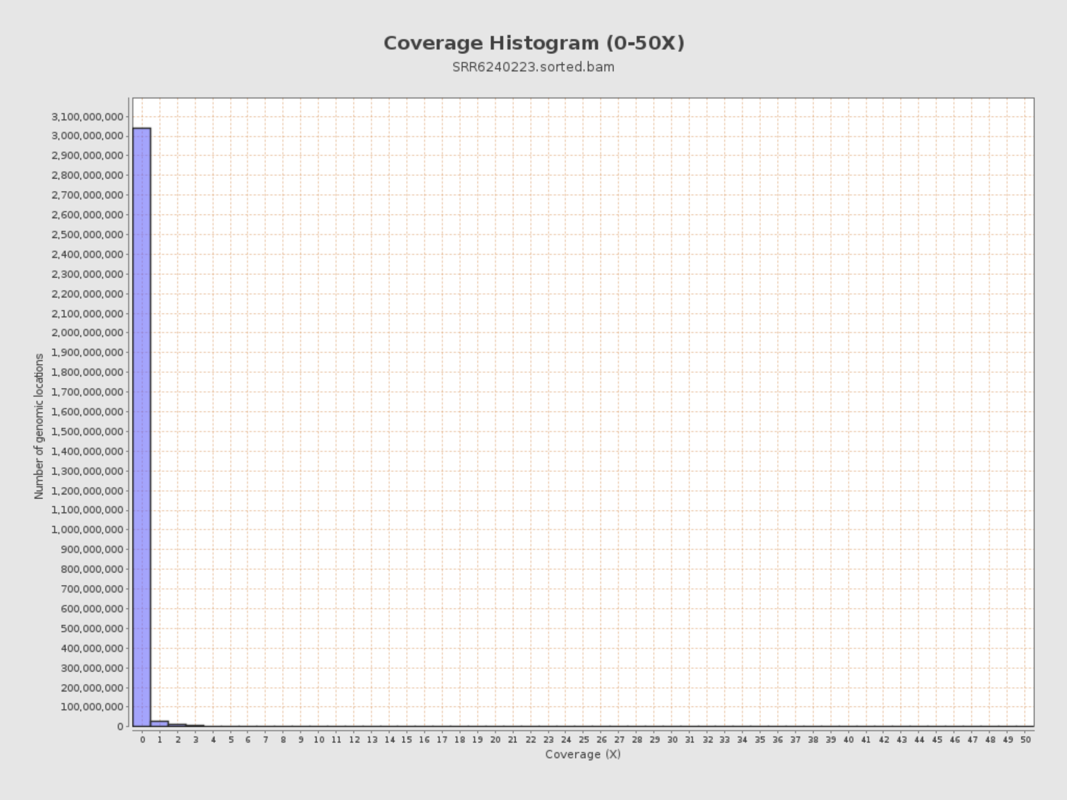
3. Results : Coverage across reference



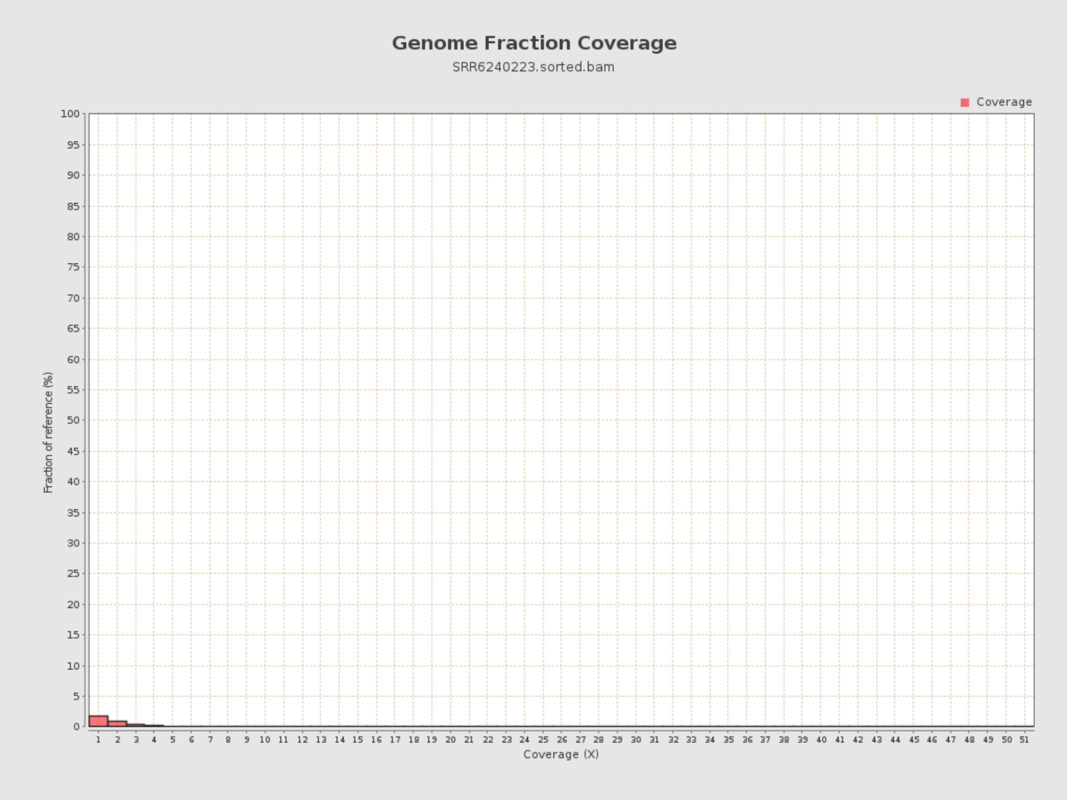
4. Results : Coverage Histogram



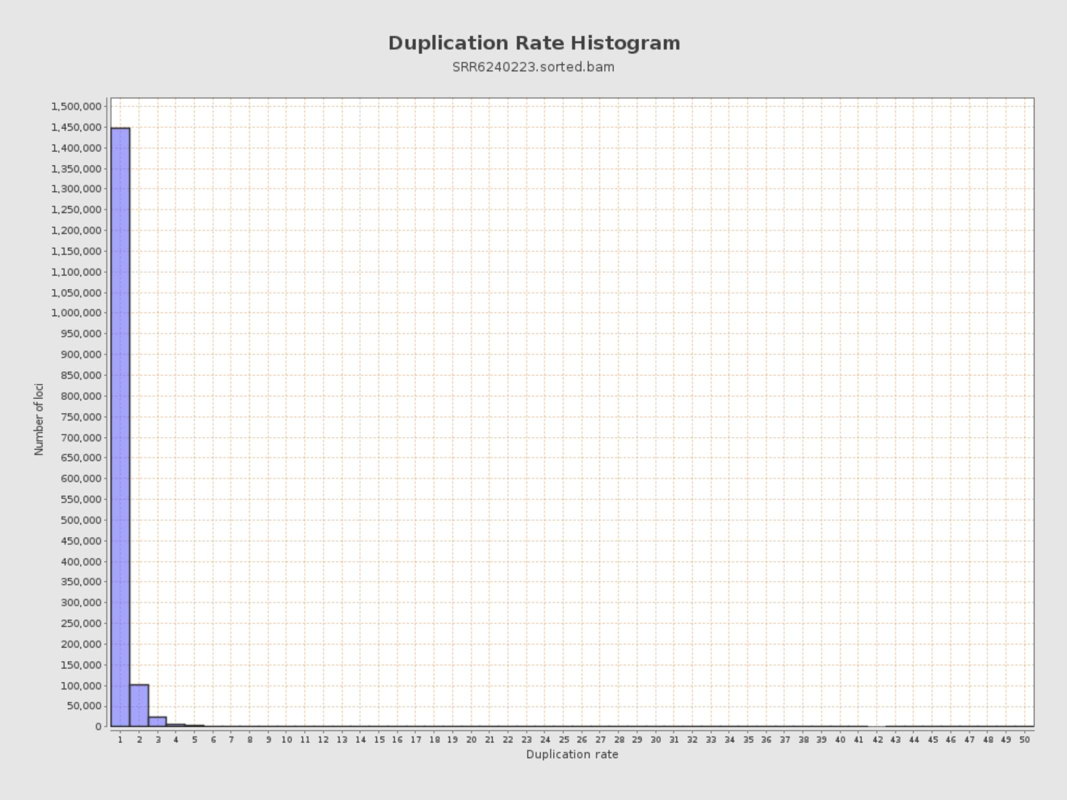
5. Results : Coverage Histogram (0-50X)



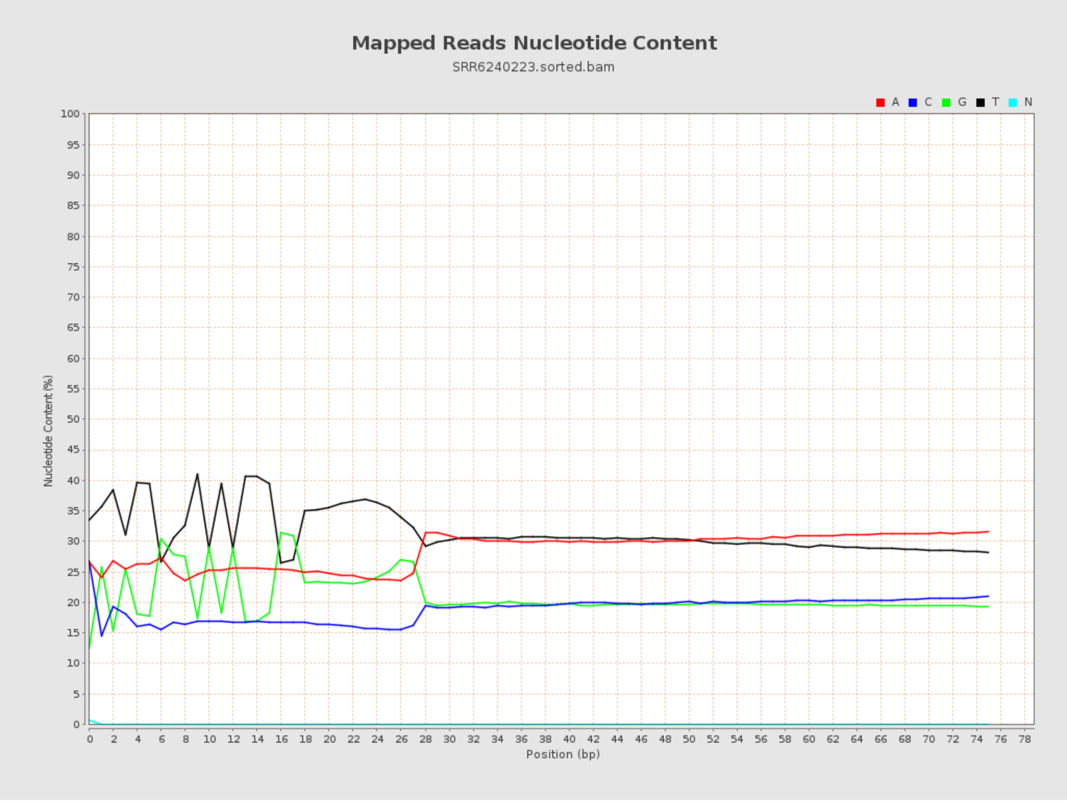
6. Results : Genome Fraction Coverage



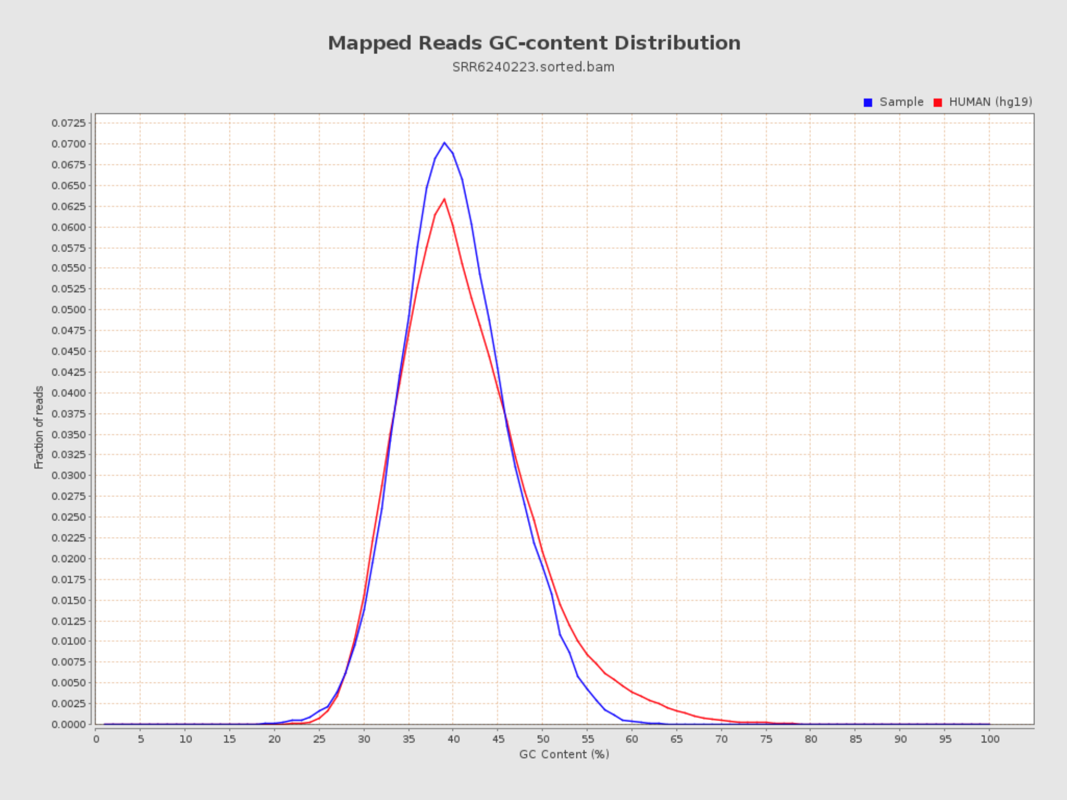
7. Results : Duplication Rate Histogram



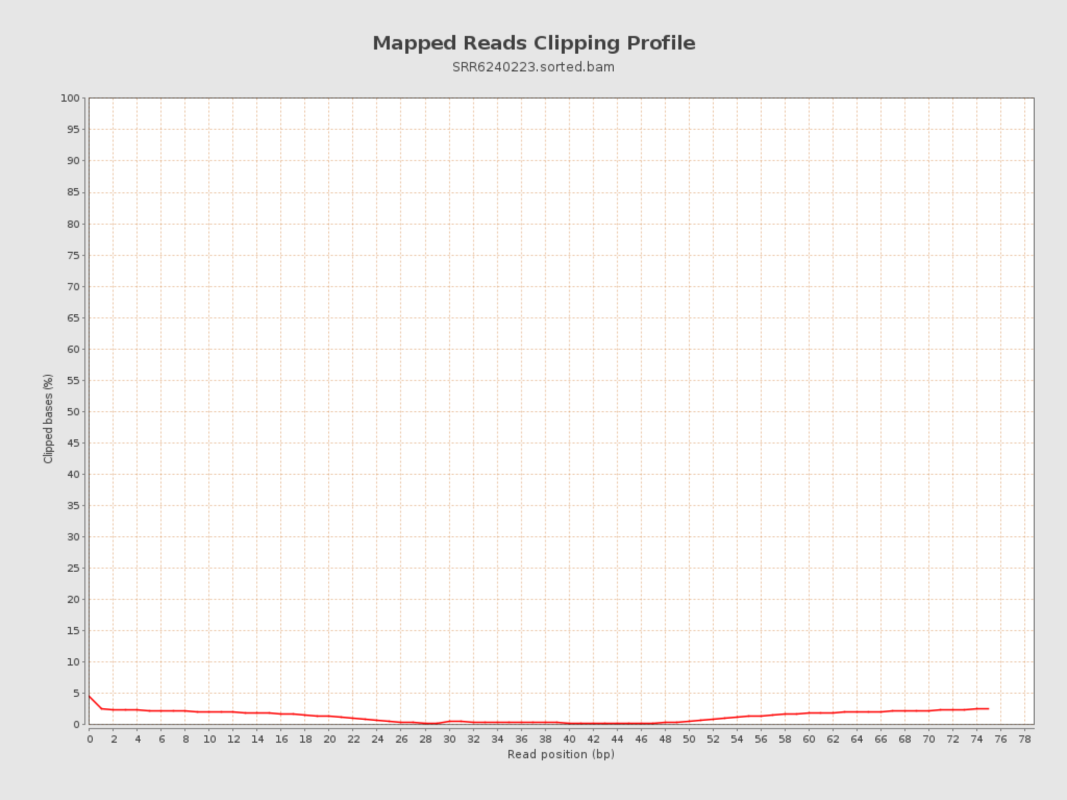
8. Results : Mapped Reads Nucleotide Content



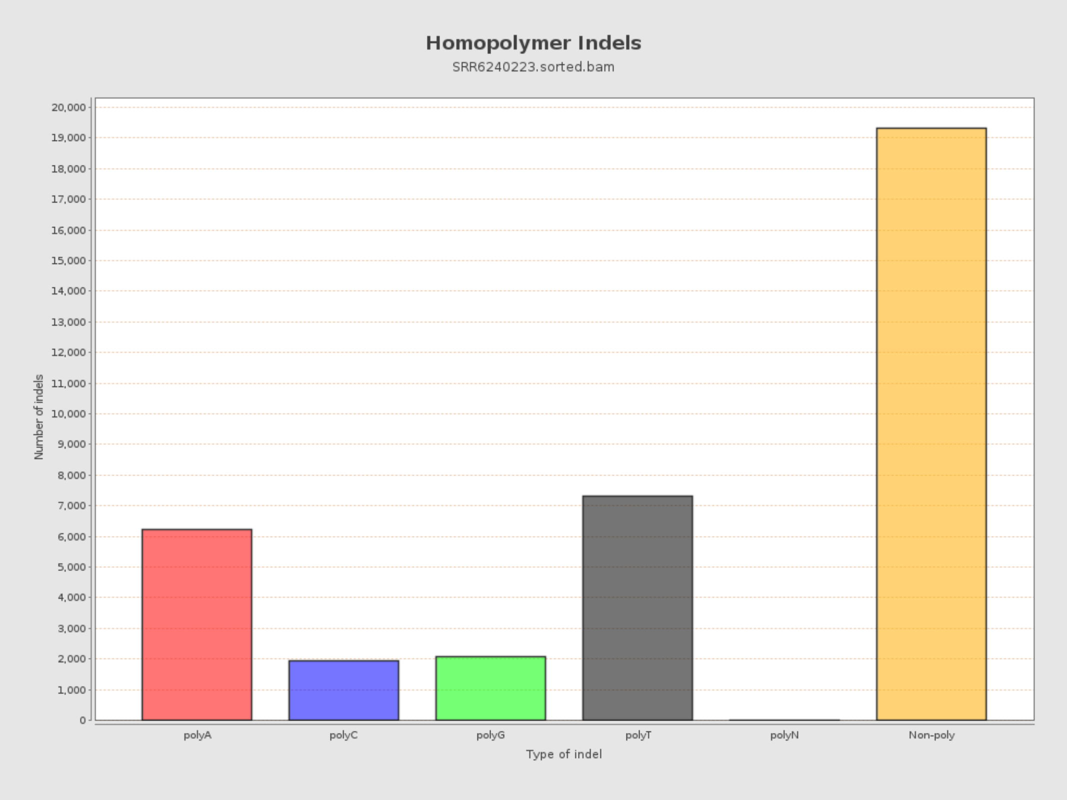
9. Results : Mapped Reads GC-content Distribution



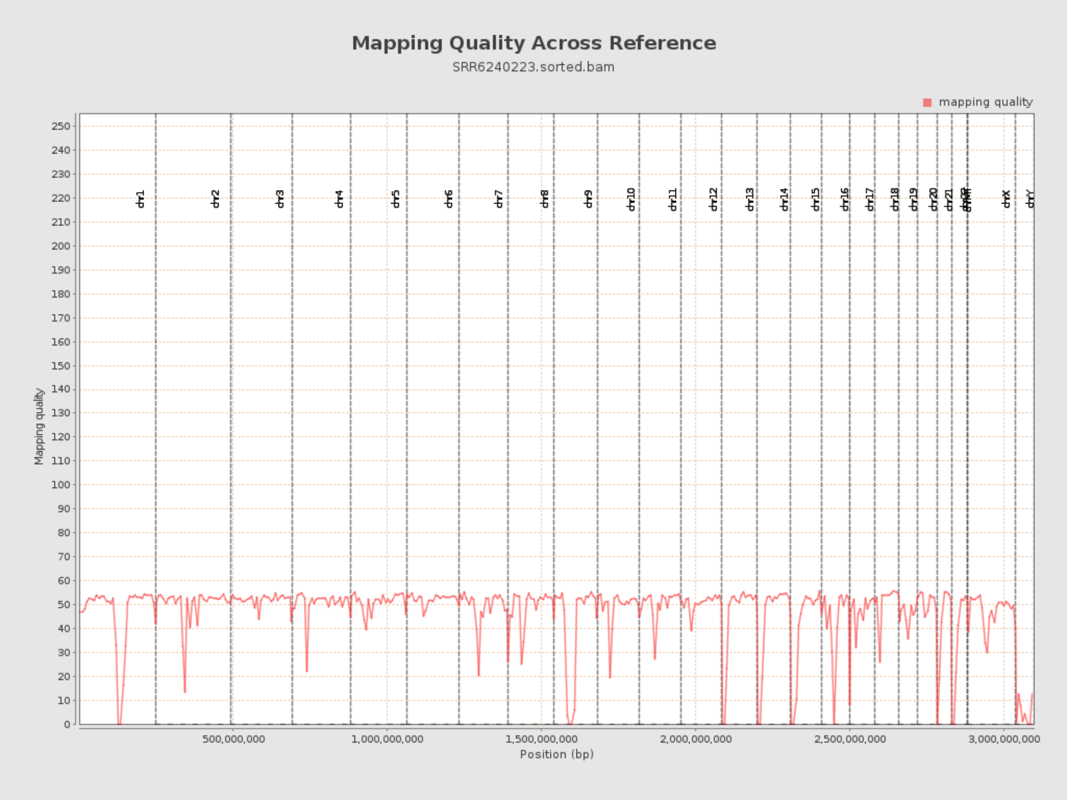
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram