Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 12:51:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084775.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_SRR3084775 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084775.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 12:51:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084775.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,595,123
Mapped reads	1,323,355 / 82.96%
Unmapped reads	271,768 / 17.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,796 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	46,876 / 2.94%
Duplication rate	2.77%
Clipped reads	545,016 / 34.17%

2.2. ACGT Content

Number/percentage of A's	24,613,635 / 27.53%
Number/percentage of C's	16,827,655 / 18.82%
Number/percentage of T's	27,989,870 / 31.31%
Number/percentage of G's	19,933,363 / 22.3%
Number/percentage of N's	32,632 / 0.04%
GC Percentage	41.12%

2.3. Coverage

Mean	0.0289

Standard Deviation	0.2685

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

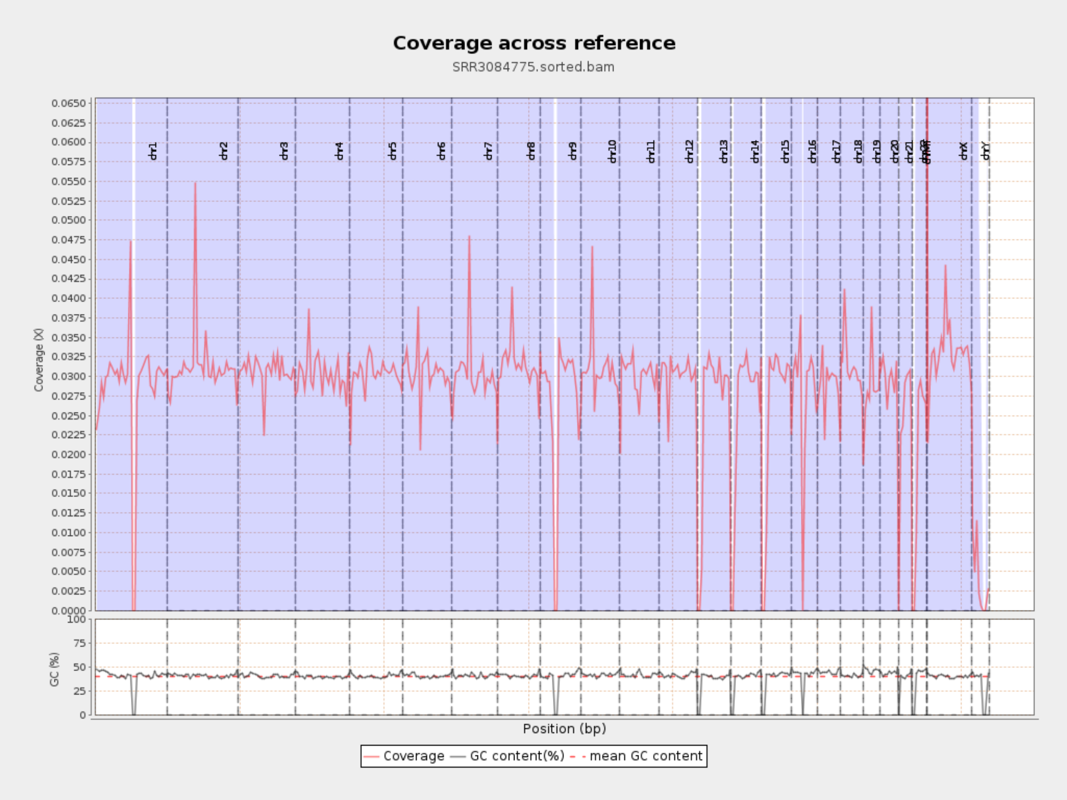
General error rate	0.91%
Mismatches	803,717
Insertions	7,004
Mapped reads with at least one insertion	0.53%
Deletions	24,615
Mapped reads with at least one deletion	1.84%
Homopolymer indels	46.86%

2.6. Chromosome stats

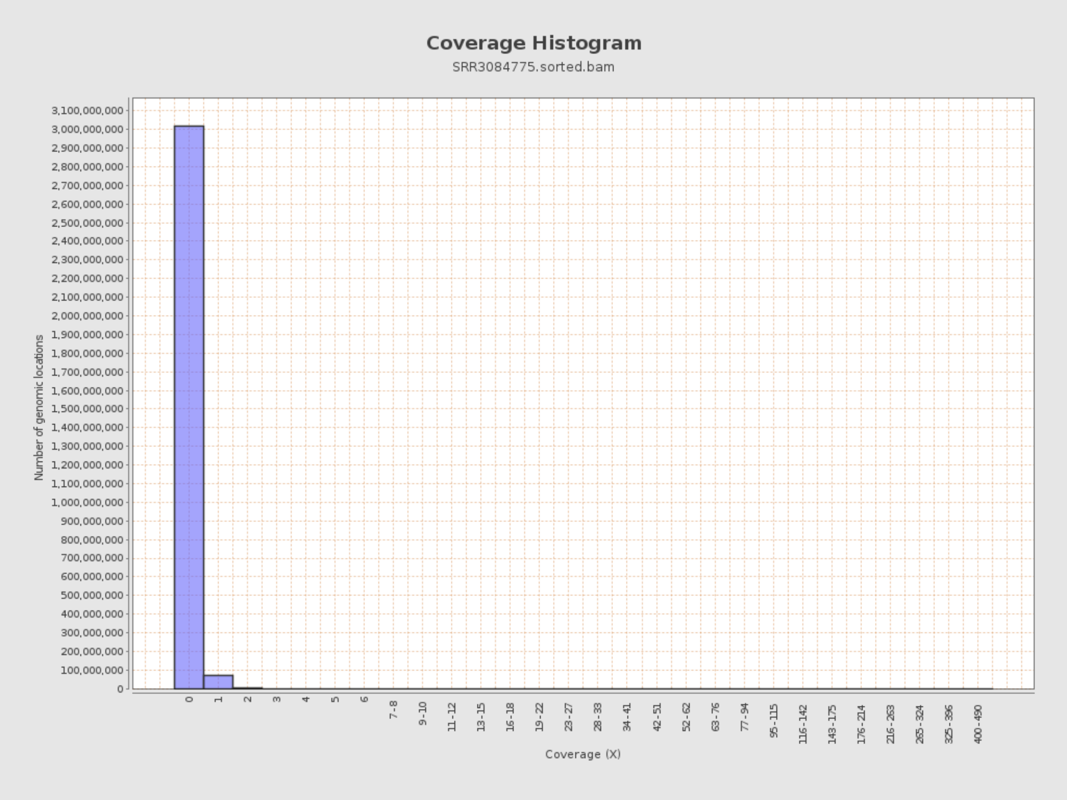
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7094842	0.0285	0.4508
chr2	243199373	7627917	0.0314	0.3163
chr3	198022430	6078294	0.0307	0.1896
chr4	191154276	5786760	0.0303	0.1986
chr5	180915260	5515477	0.0305	0.1899
chr6	171115067	5220332	0.0305	0.2181
chr7	159138663	4871439	0.0306	0.3419

chr8	146364022	4609223	0.0315	0.2871
chr9	141213431	3757437	0.0266	0.2562
chr10	135534747	4209051	0.0311	0.2613
chr11	135006516	4081272	0.0302	0.2485
chr12	133851895	4034792	0.0301	0.19
chr13	115169878	2910812	0.0253	0.1726
chr14	107349540	2713614	0.0253	0.1833
chr15	102531392	2582728	0.0252	0.1756
chr16	90354753	2460093	0.0272	0.1948
chr17	81195210	2337633	0.0288	0.2102
chr18	78077248	2455410	0.0314	0.5006
chr19	59128983	1701678	0.0288	0.335
chr20	63025520	1858593	0.0295	0.198
chr21	48129895	1181374	0.0245	0.1773
chr22	51304566	986589	0.0192	0.1485
chrMT	16571	3904	0.2356	0.5415
chrX	155270560	5132451	0.0331	0.2169
chrY	59373566	225565	0.0038	0.0969

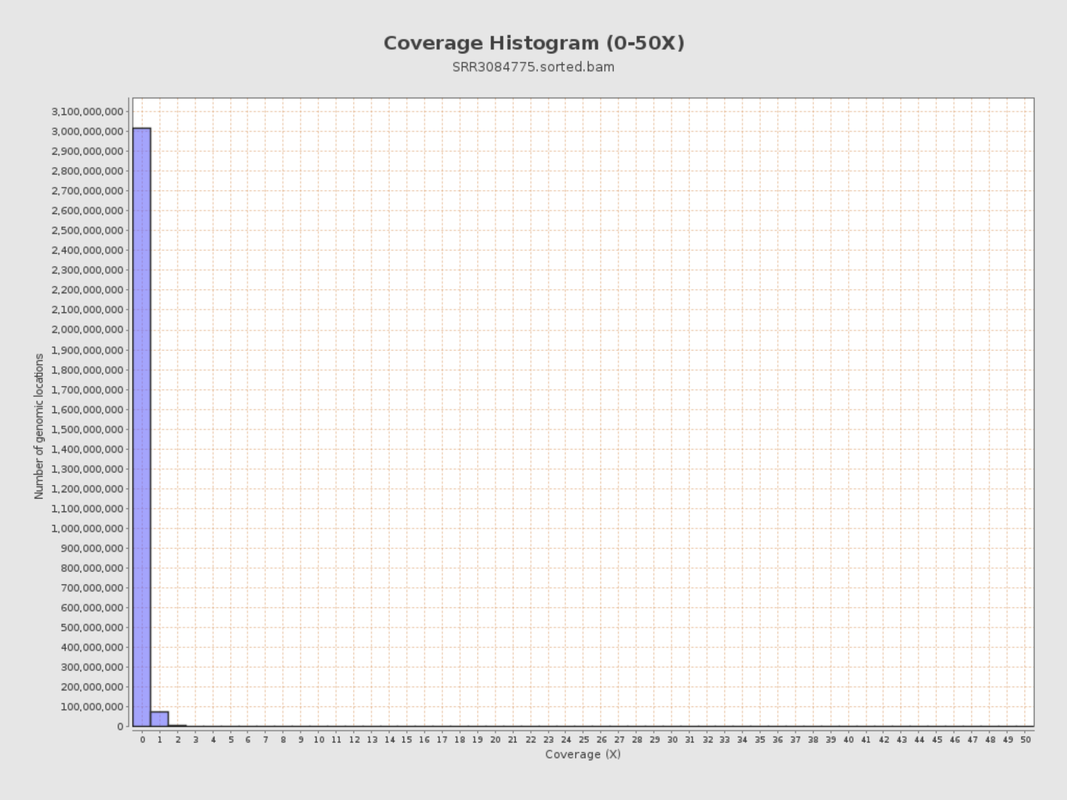
3. Results : Coverage across reference



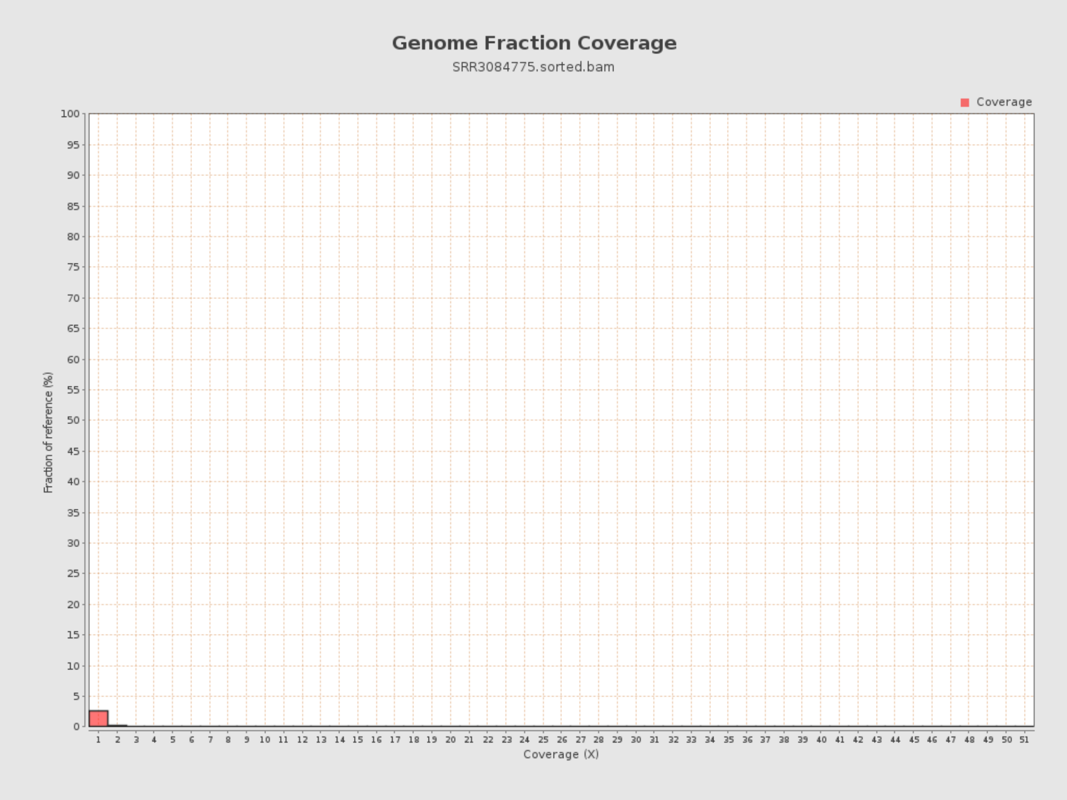
4. Results : Coverage Histogram



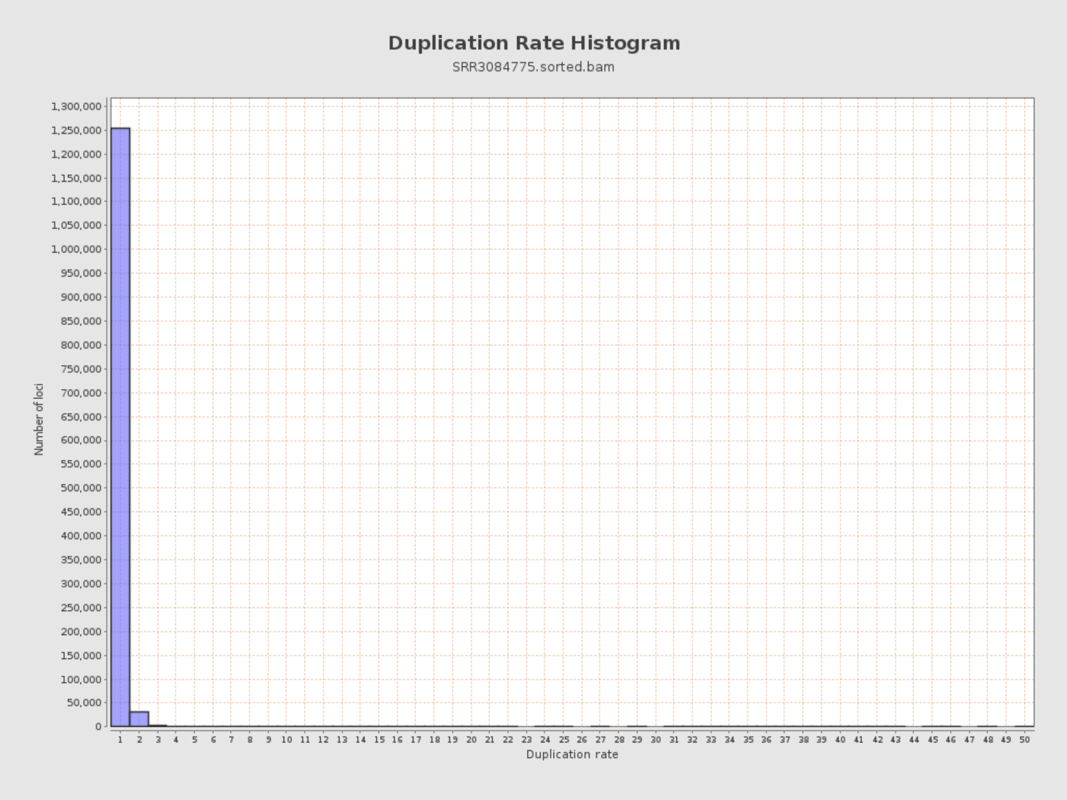
5. Results : Coverage Histogram (0-50X)



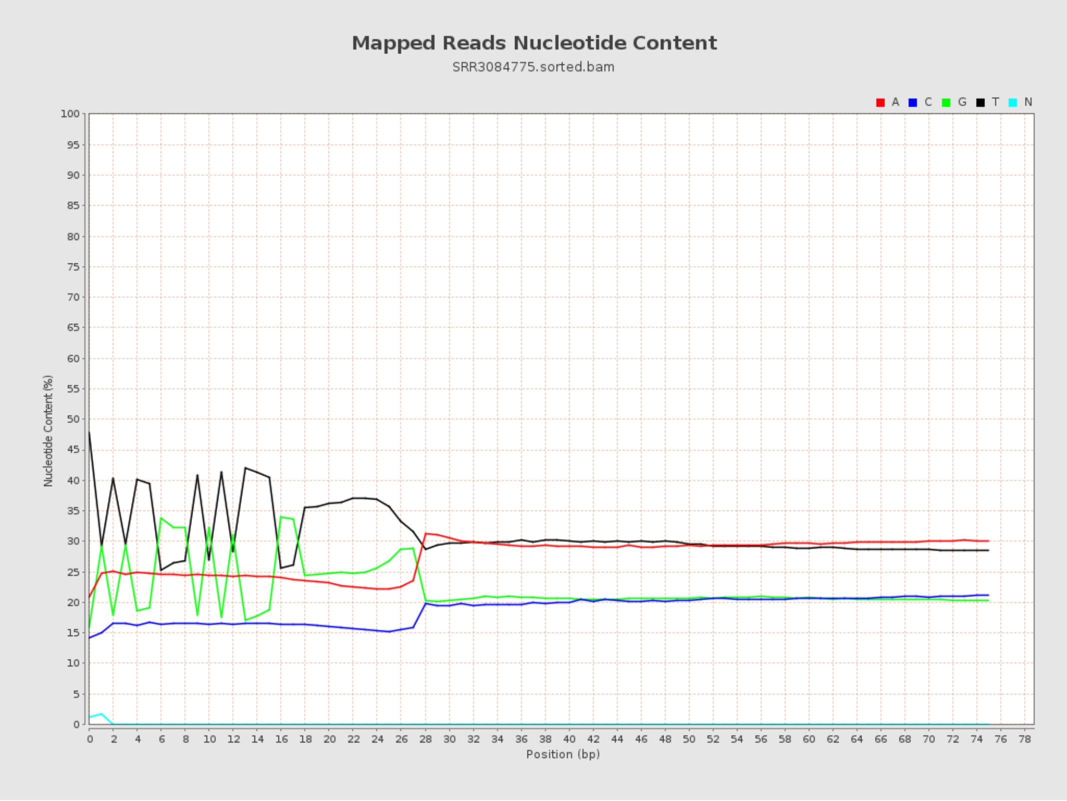
6. Results : Genome Fraction Coverage



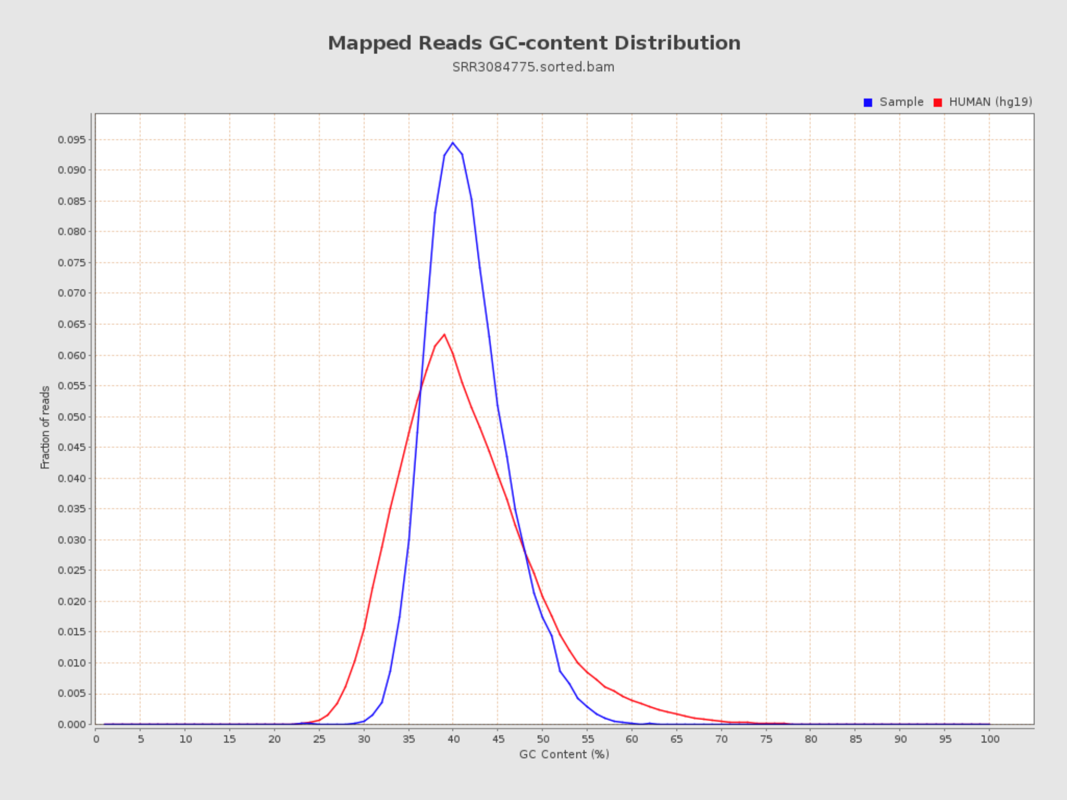
7. Results : Duplication Rate Histogram



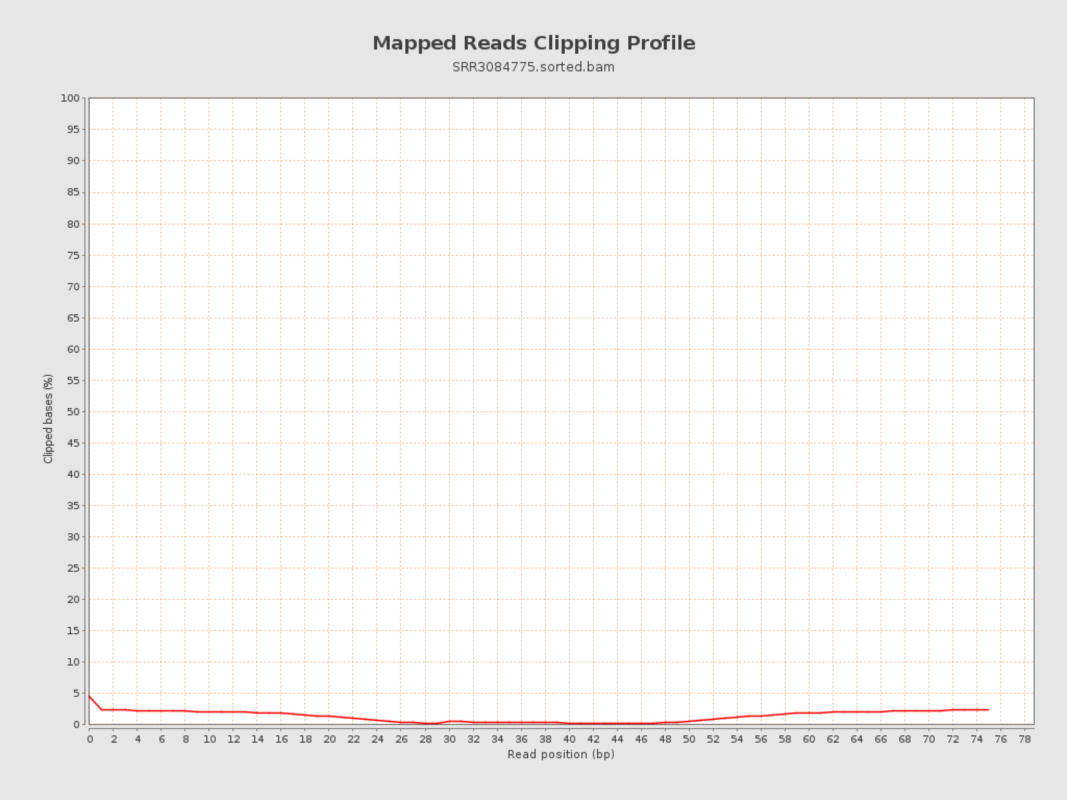
8. Results : Mapped Reads Nucleotide Content



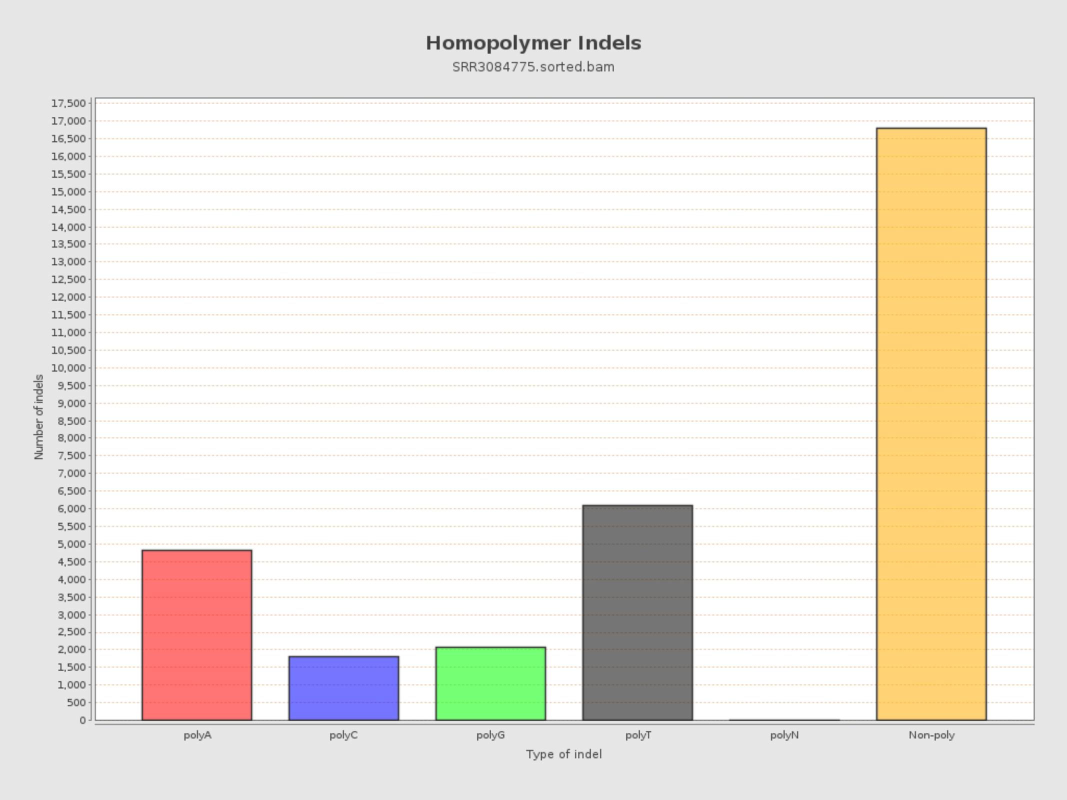
9. Results : Mapped Reads GC-content Distribution



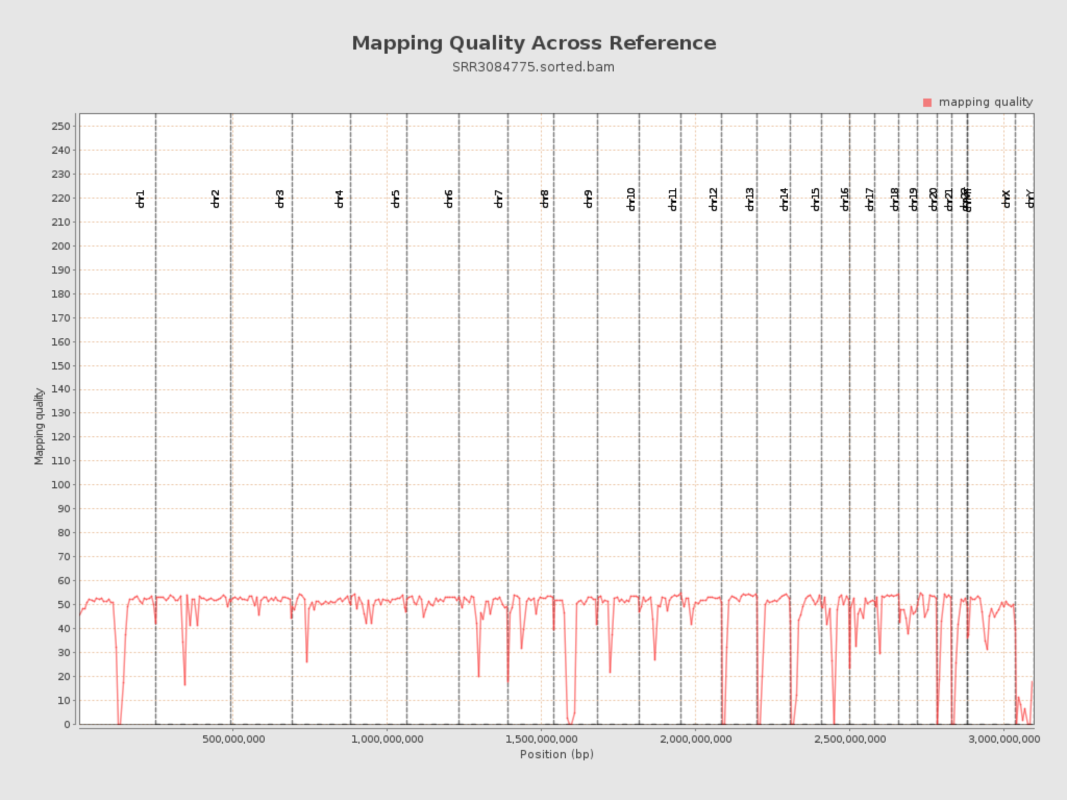
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram