Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:51:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081026.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_SRR3081026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:51:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,088,393
Mapped reads	1,432,255 / 68.58%
Unmapped reads	656,138 / 31.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,686 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	42,293 / 2.03%
Duplication rate	2.5%
Clipped reads	756,706 / 36.23%

2.2. ACGT Content

Number/percentage of A's	25,147,915 / 27.69%
Number/percentage of C's	17,737,010 / 19.53%
Number/percentage of T's	27,196,224 / 29.95%
Number/percentage of G's	20,727,238 / 22.82%
Number/percentage of N's	1,196 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.2262

2.4. Mapping Quality

Mean Mapping Quality	45.94

2.5. Mismatches and indels

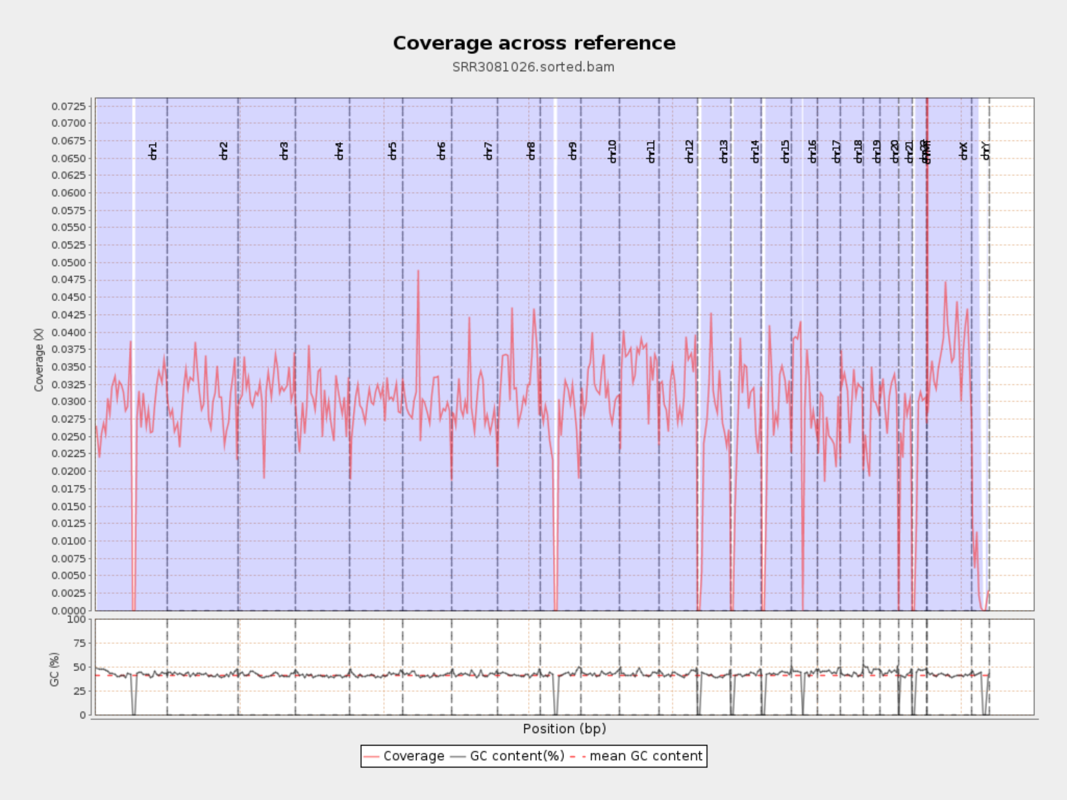
General error rate	0.69%
Mismatches	620,102
Insertions	5,815
Mapped reads with at least one insertion	0.4%
Deletions	17,413
Mapped reads with at least one deletion	1.2%
Homopolymer indels	47.43%

2.6. Chromosome stats

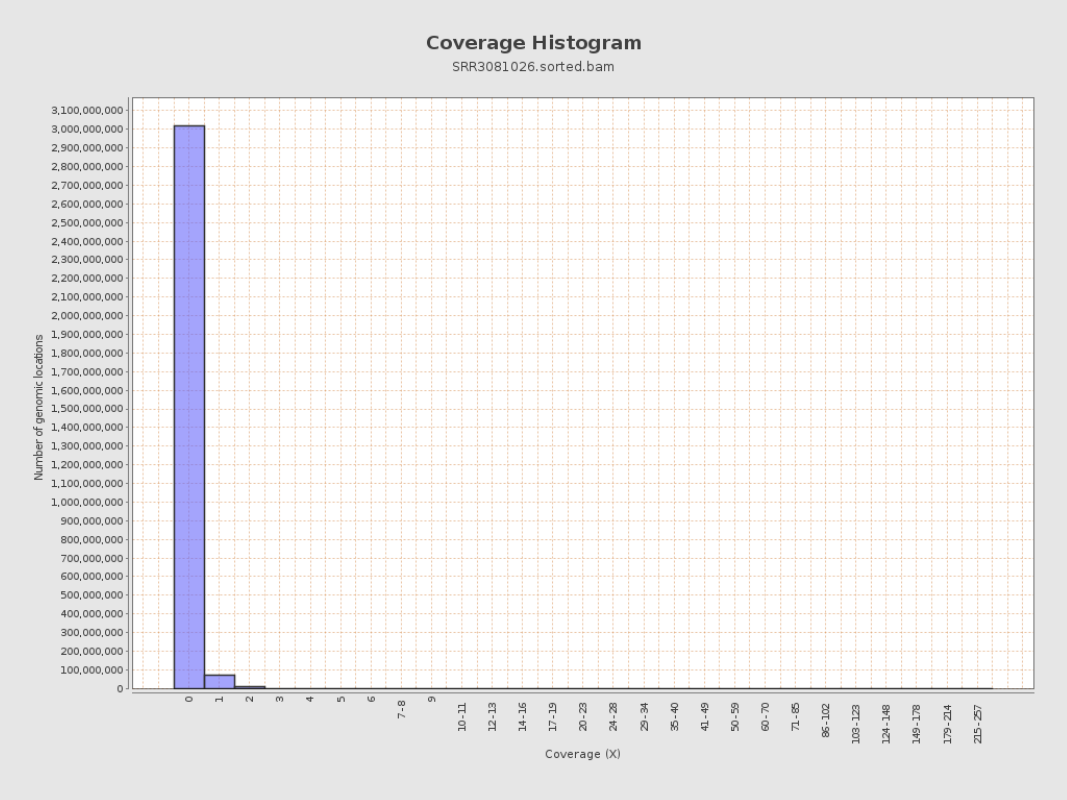
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6994429	0.0281	0.2735
chr2	243199373	7372118	0.0303	0.2454
chr3	198022430	6279589	0.0317	0.1987
chr4	191154276	5658537	0.0296	0.1982
chr5	180915260	5427789	0.03	0.193
chr6	171115067	5204887	0.0304	0.2339
chr7	159138663	4712759	0.0296	0.2738

chr8	146364022	4880464	0.0333	0.2302
chr9	141213431	3511101	0.0249	0.2189
chr10	135534747	4347533	0.0321	0.2339
chr11	135006516	4808558	0.0356	0.2483
chr12	133851895	4320204	0.0323	0.2021
chr13	115169878	2813960	0.0244	0.1747
chr14	107349540	2752886	0.0256	0.1859
chr15	102531392	2683743	0.0262	0.1841
chr16	90354753	2748611	0.0304	0.2072
chr17	81195210	2062002	0.0254	0.188
chr18	78077248	2474494	0.0317	0.3719
chr19	59128983	1591678	0.0269	0.2458
chr20	63025520	1912637	0.0303	0.1976
chr21	48129895	1166540	0.0242	0.184
chr22	51304566	1095221	0.0213	0.1642
chrMT	16571	25072	1.513	1.5457
chrX	155270560	5754726	0.0371	0.2276
chrY	59373566	240496	0.0041	0.0918

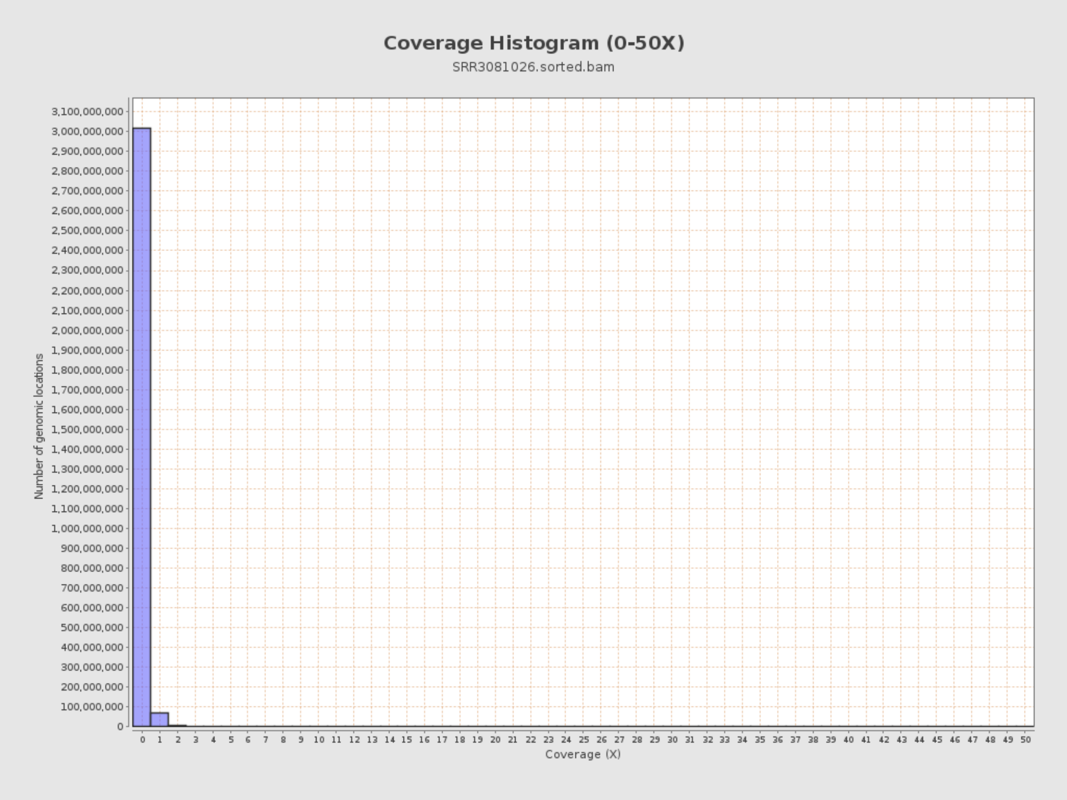
3. Results : Coverage across reference



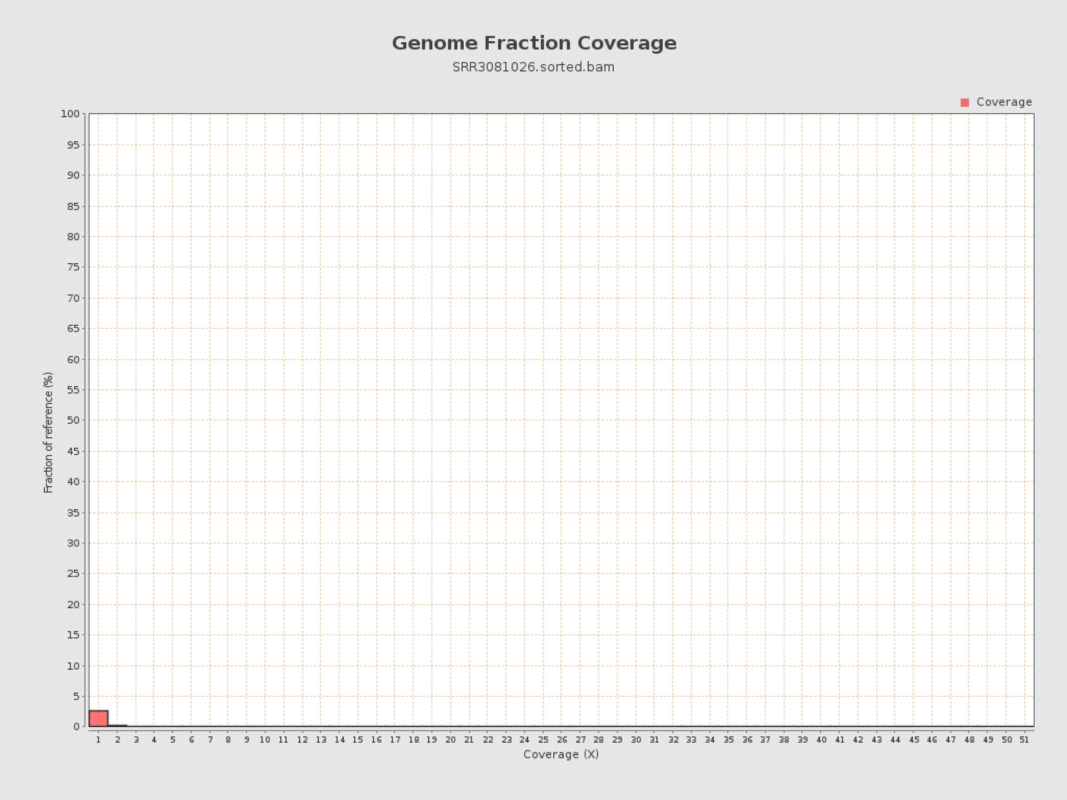
4. Results : Coverage Histogram



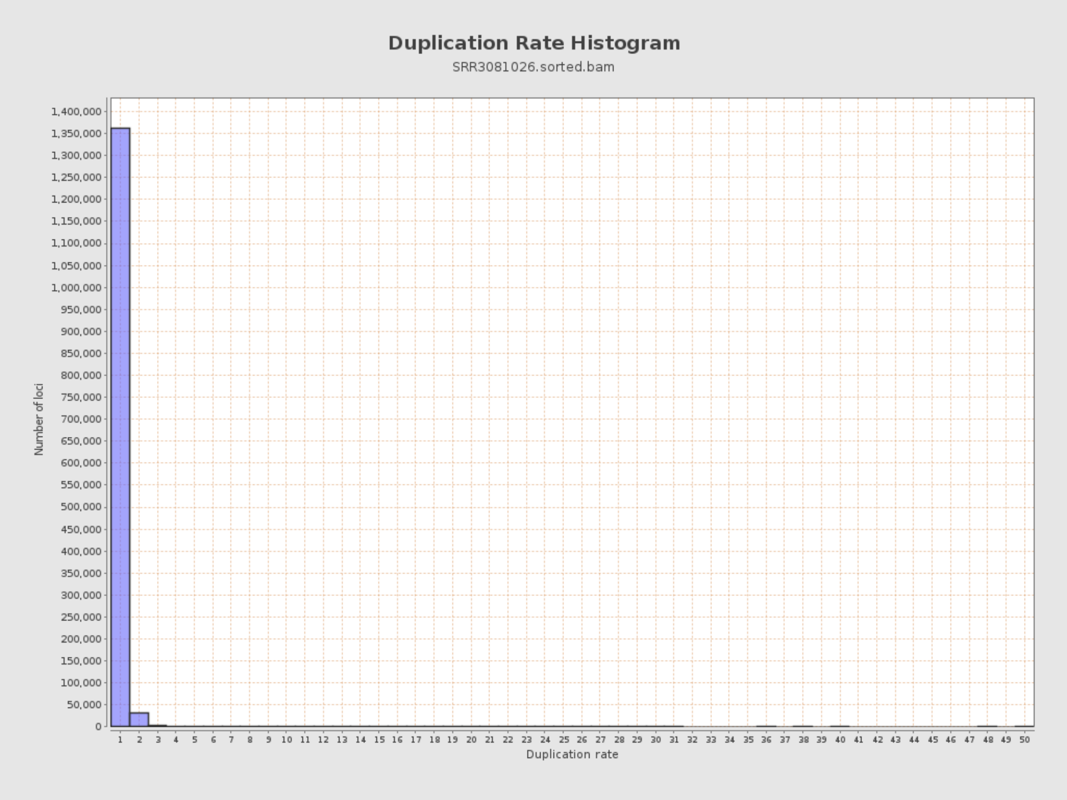
5. Results : Coverage Histogram (0-50X)



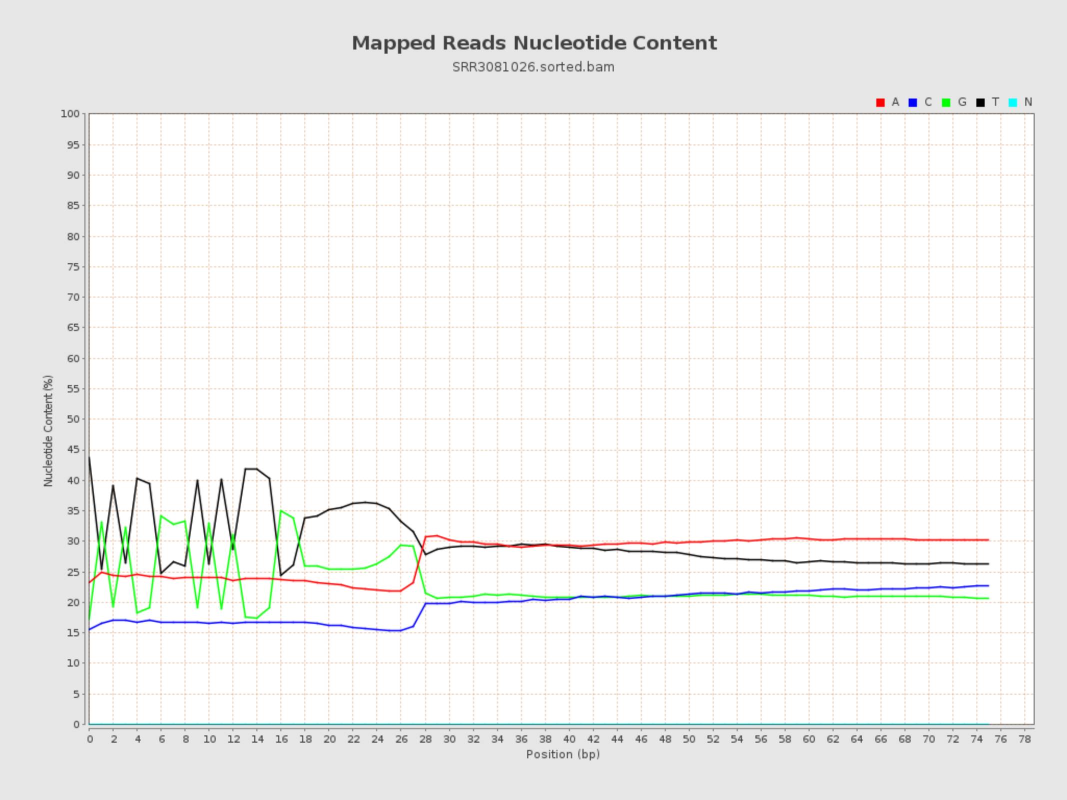
6. Results : Genome Fraction Coverage



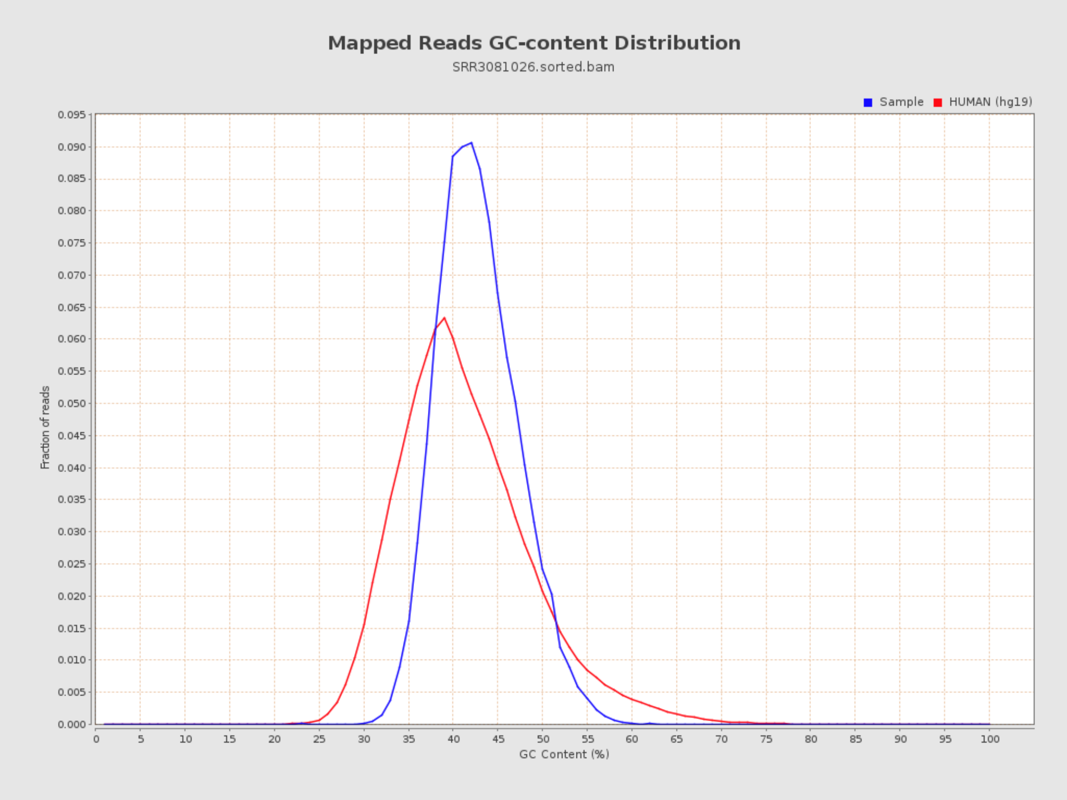
7. Results : Duplication Rate Histogram



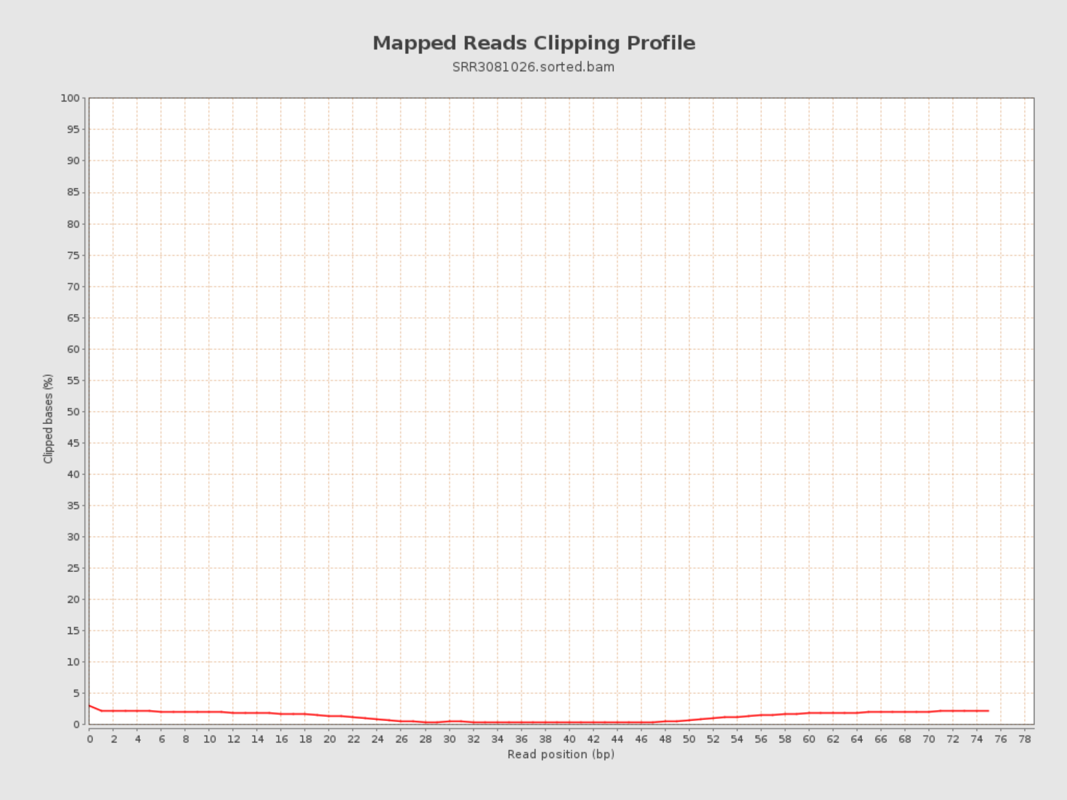
8. Results : Mapped Reads Nucleotide Content



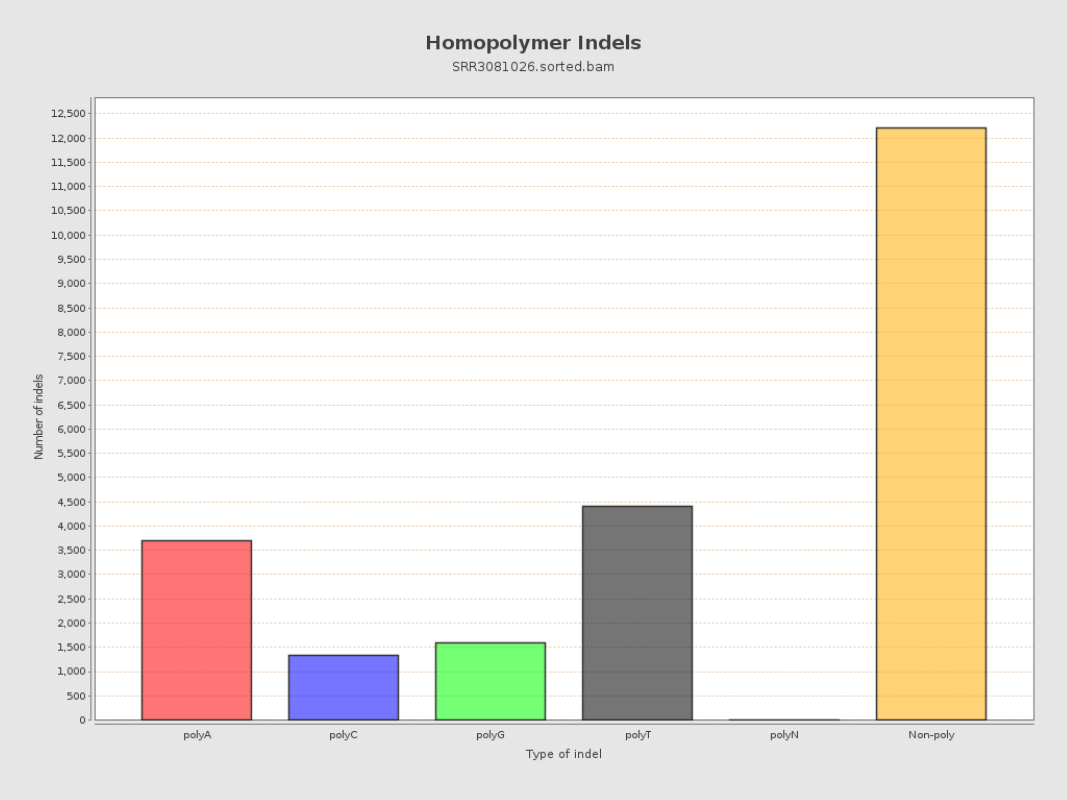
9. Results : Mapped Reads GC-content Distribution



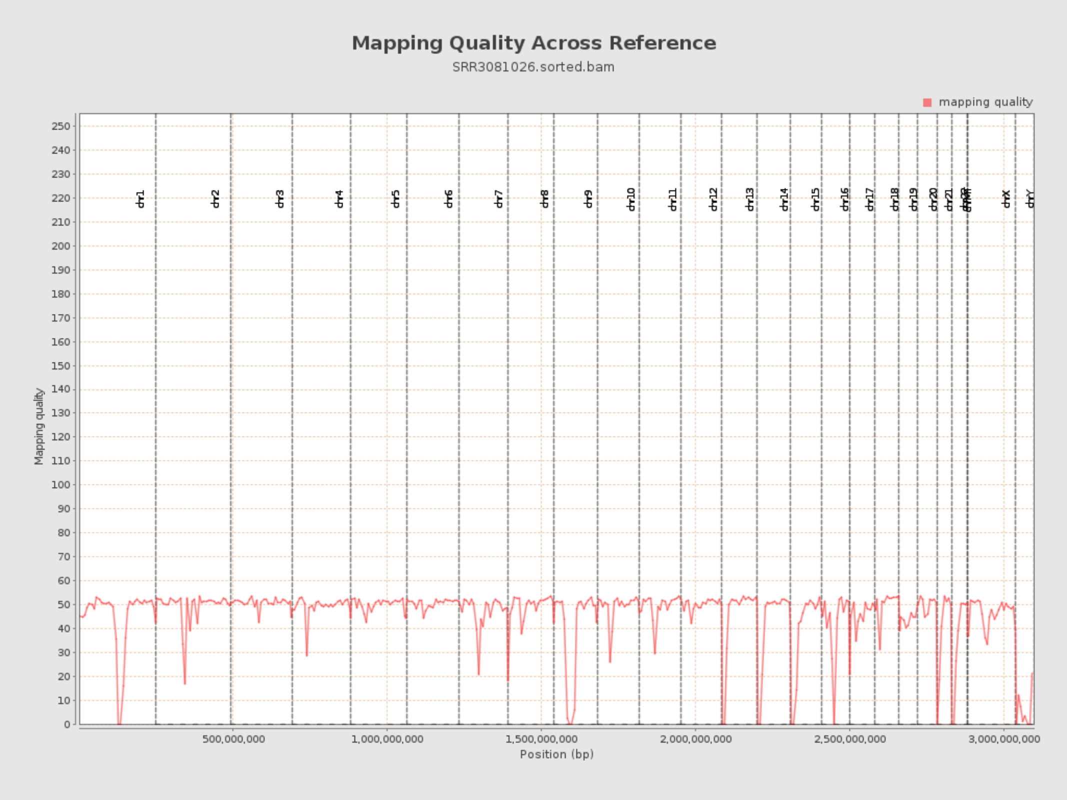
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram