Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:48:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081177.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_SRR3081177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:48:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,817,408
Mapped reads	2,523,506 / 89.57%
Unmapped reads	293,902 / 10.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,842 / 0.95%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	124,551 / 4.42%
Duplication rate	3.78%
Clipped reads	1,117,266 / 39.66%

2.2. ACGT Content

Number/percentage of A's	47,244,213 / 27.95%
Number/percentage of C's	31,059,739 / 18.37%
Number/percentage of T's	53,753,236 / 31.8%
Number/percentage of G's	36,940,134 / 21.85%
Number/percentage of N's	50,313 / 0.03%
GC Percentage	40.23%

2.3. Coverage

Mean	0.0546

Standard Deviation	0.4792

2.4. Mapping Quality

Mean Mapping Quality	46.73

2.5. Mismatches and indels

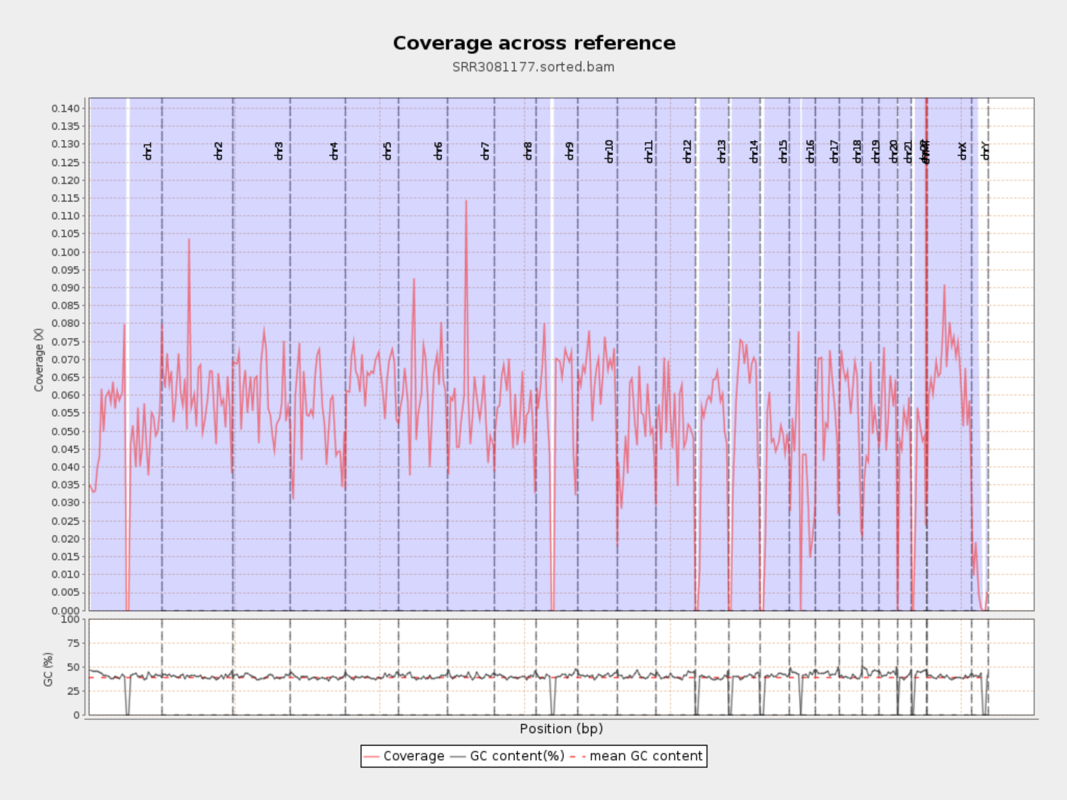
General error rate	0.84%
Mismatches	1,401,944
Insertions	13,349
Mapped reads with at least one insertion	0.52%
Deletions	39,123
Mapped reads with at least one deletion	1.54%
Homopolymer indels	47.15%

2.6. Chromosome stats

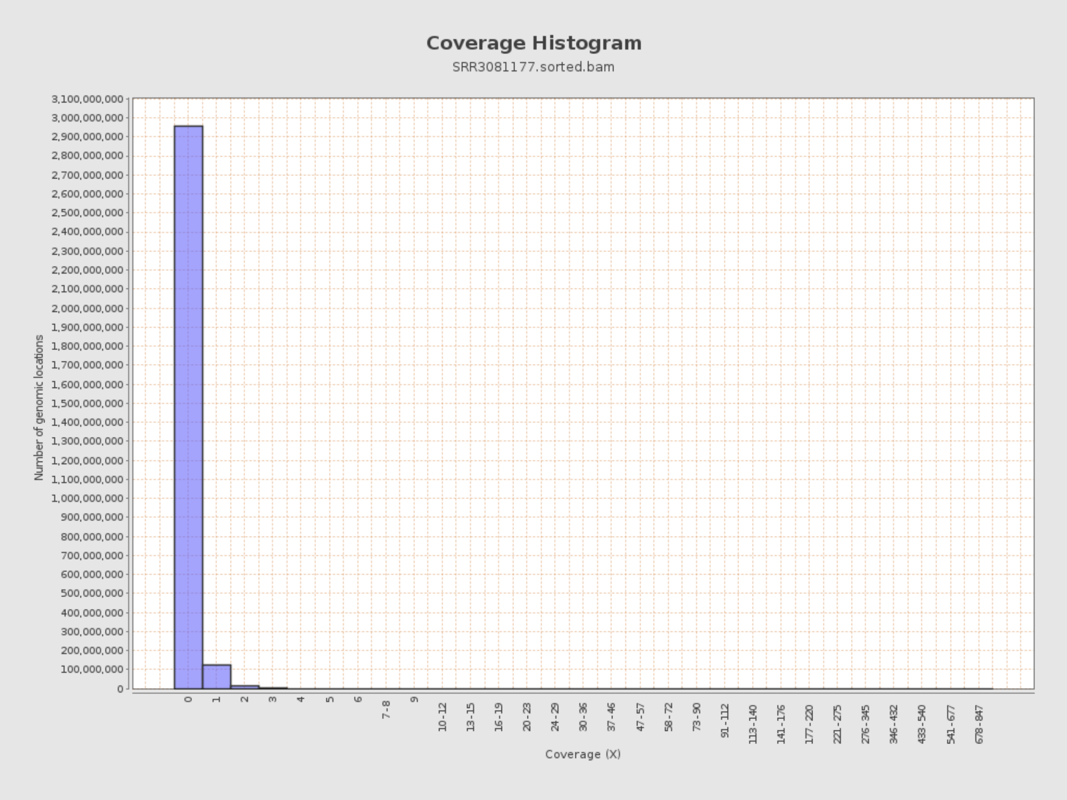
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12057114	0.0484	0.7829
chr2	243199373	14844617	0.061	0.5397
chr3	198022430	12011131	0.0607	0.2809
chr4	191154276	10315305	0.054	0.2793
chr5	180915260	11802966	0.0652	0.2941
chr6	171115067	10609053	0.062	0.358
chr7	159138663	9047374	0.0569	0.8424

chr8	146364022	8153373	0.0557	0.5771
chr9	141213431	7891457	0.0559	0.4713
chr10	135534747	9024687	0.0666	0.3937
chr11	135006516	6647729	0.0492	0.4724
chr12	133851895	7068183	0.0528	0.2731
chr13	115169878	5543803	0.0481	0.2511
chr14	107349540	5967128	0.0556	0.3065
chr15	102531392	4119090	0.0402	0.2399
chr16	90354753	3332528	0.0369	0.2689
chr17	81195210	4612292	0.0568	0.3668
chr18	78077248	4726316	0.0605	0.933
chr19	59128983	2820638	0.0477	0.6085
chr20	63025520	3652594	0.058	0.2853
chr21	48129895	2179278	0.0453	0.2677
chr22	51304566	1801791	0.0351	0.2124
chrMT	16571	197681	11.9293	6.7364
chrX	155270560	10295165	0.0663	0.3498
chrY	59373566	389215	0.0066	0.1326

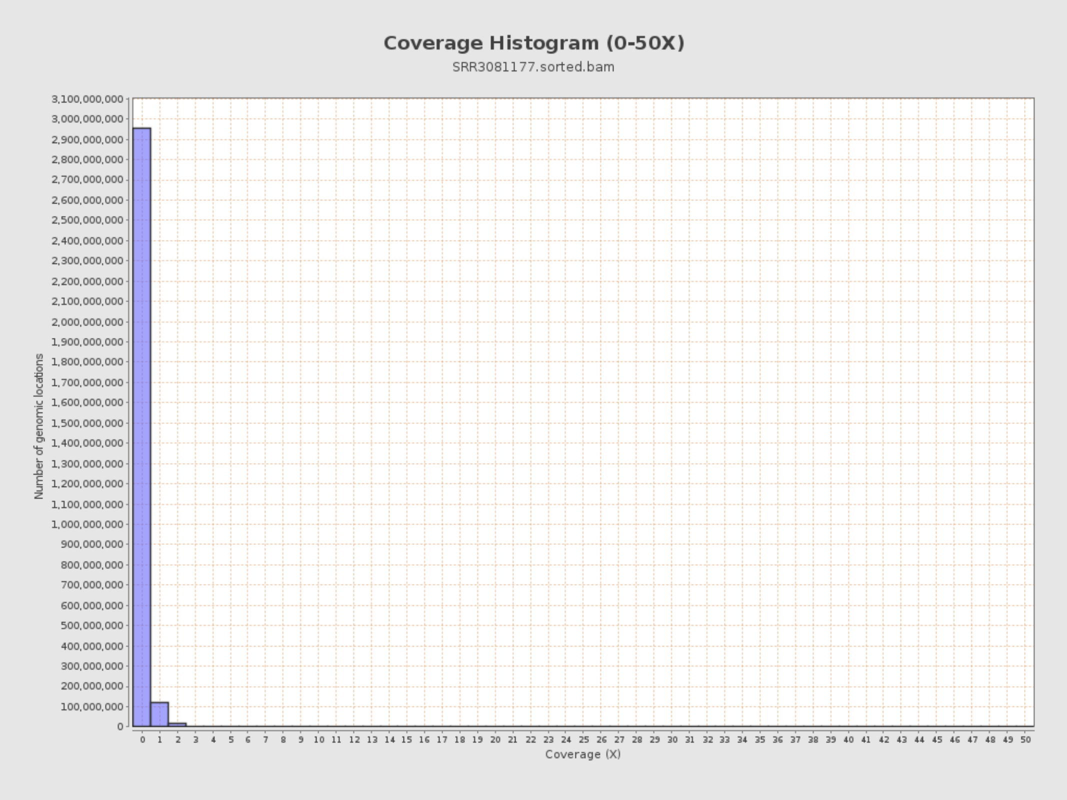
3. Results : Coverage across reference



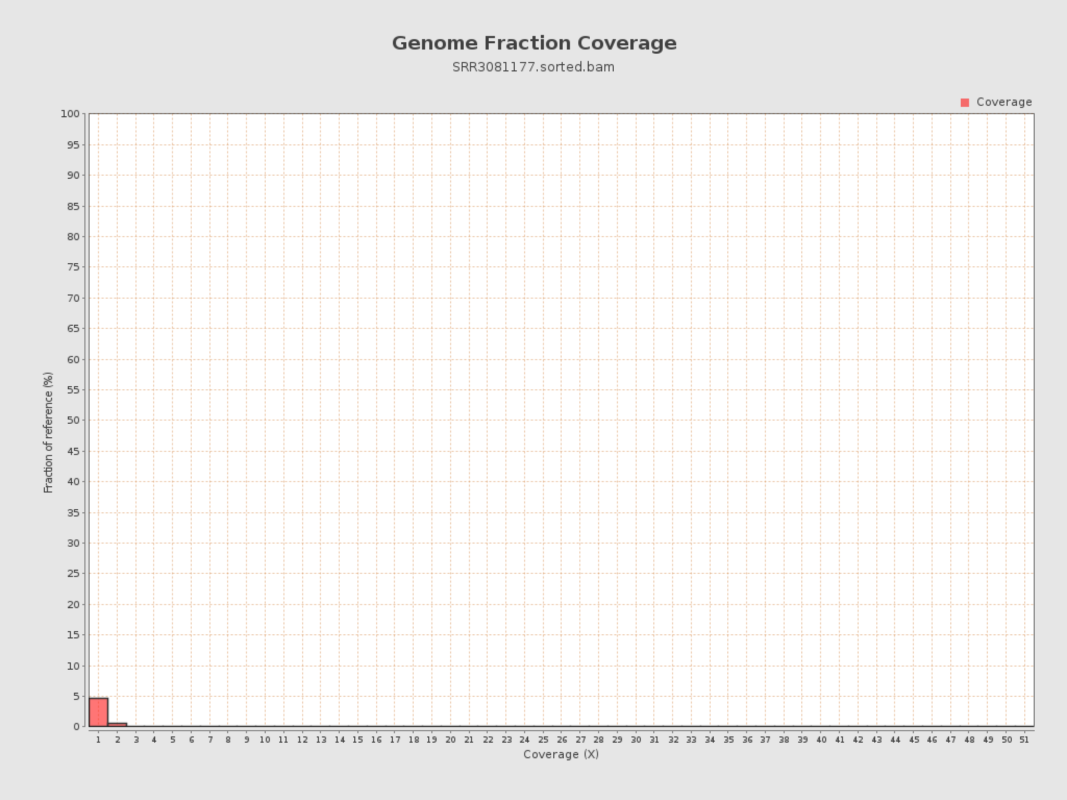
4. Results : Coverage Histogram



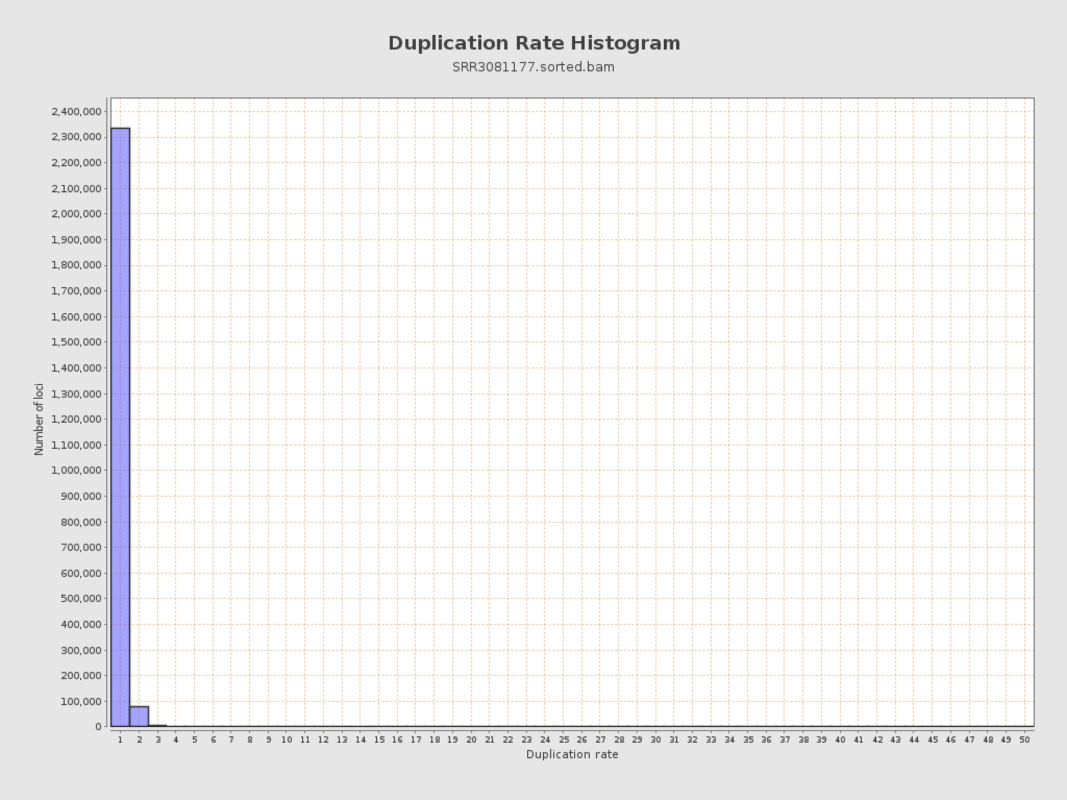
5. Results : Coverage Histogram (0-50X)



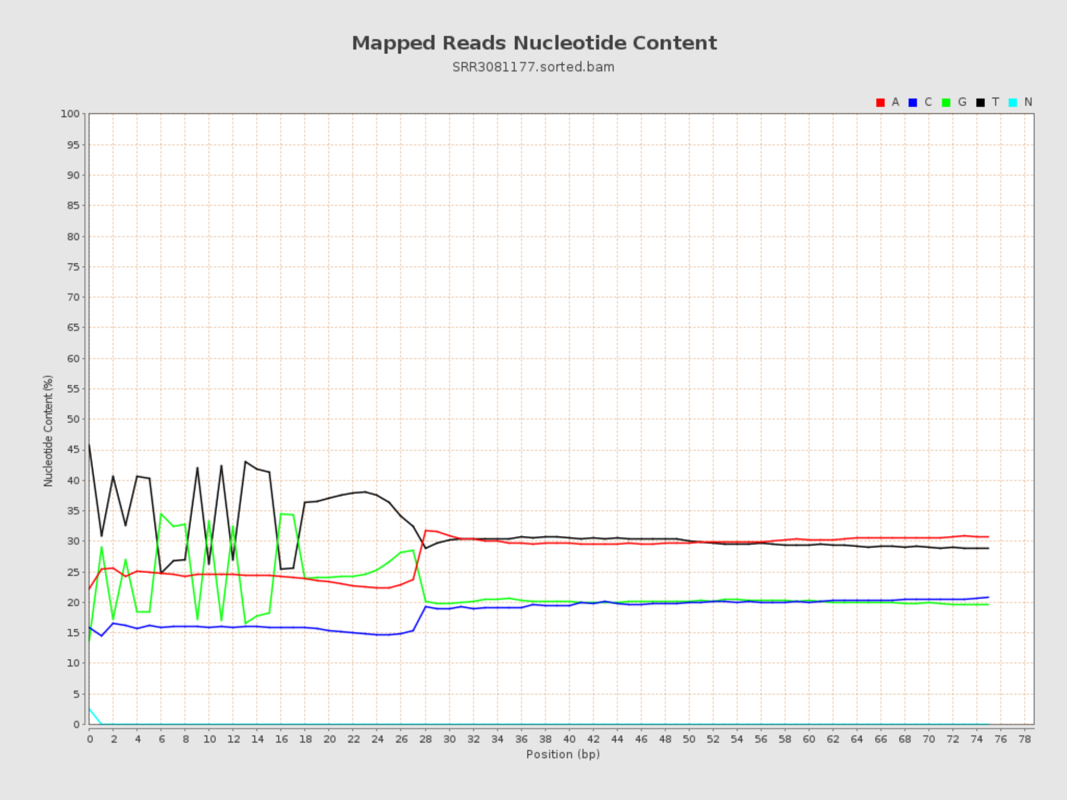
6. Results : Genome Fraction Coverage



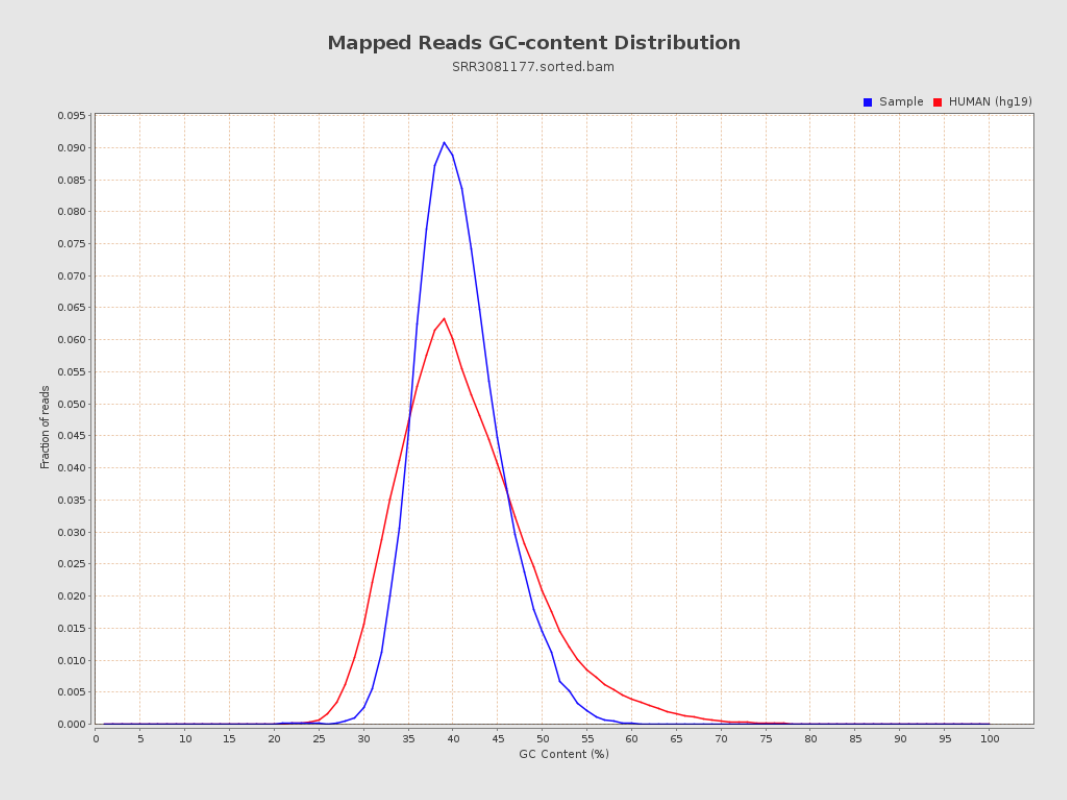
7. Results : Duplication Rate Histogram



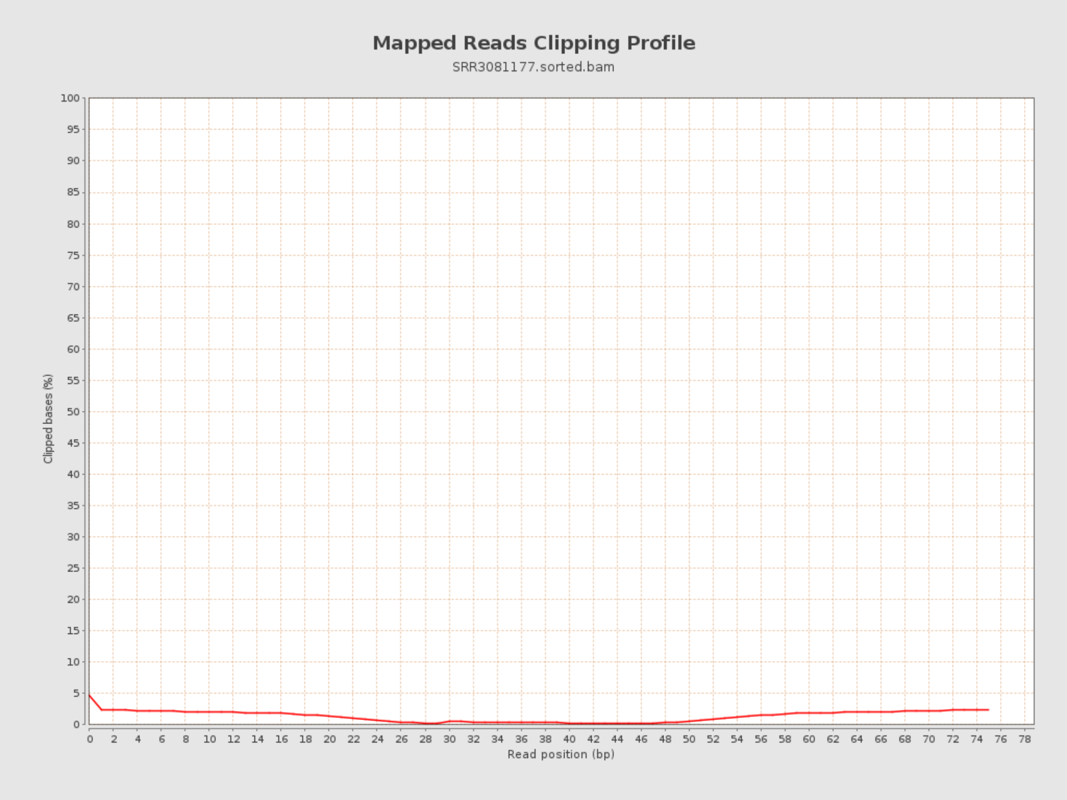
8. Results : Mapped Reads Nucleotide Content



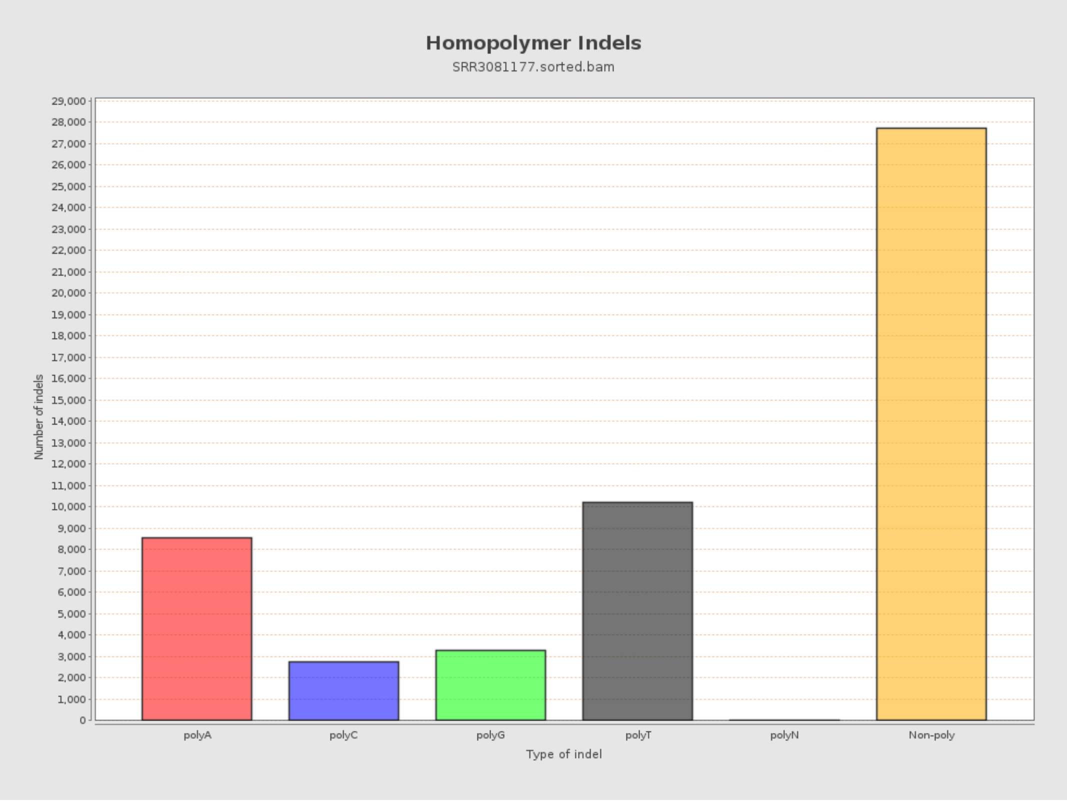
9. Results : Mapped Reads GC-content Distribution



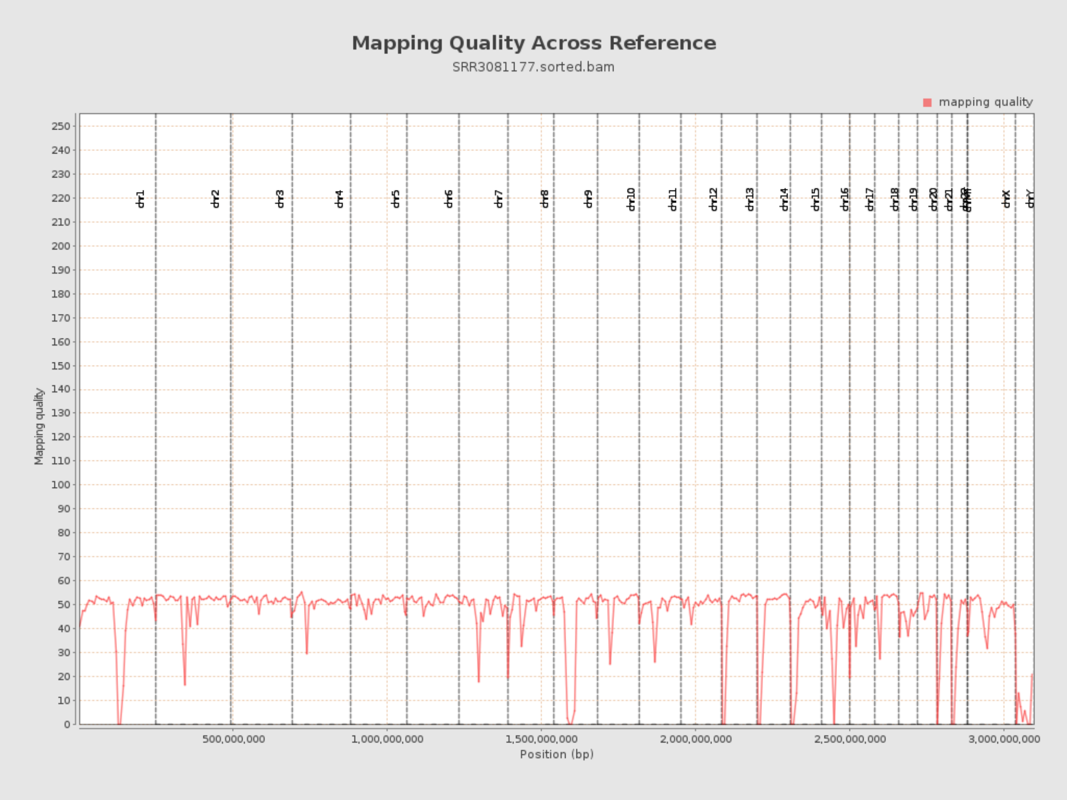
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram