Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 09:46:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081916.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_SRR3081916 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081916.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 09:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081916.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,403,868
Mapped reads	2,244,151 / 93.36%
Unmapped reads	159,717 / 6.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,430 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	77,715 / 3.23%
Duplication rate	2.78%
Clipped reads	868,359 / 36.12%

2.2. ACGT Content

Number/percentage of A's	42,704,725 / 27.91%
Number/percentage of C's	29,081,381 / 19.01%
Number/percentage of T's	47,431,918 / 31%
Number/percentage of G's	33,764,615 / 22.07%
Number/percentage of N's	1,755 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.0494

Standard Deviation	0.3596

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

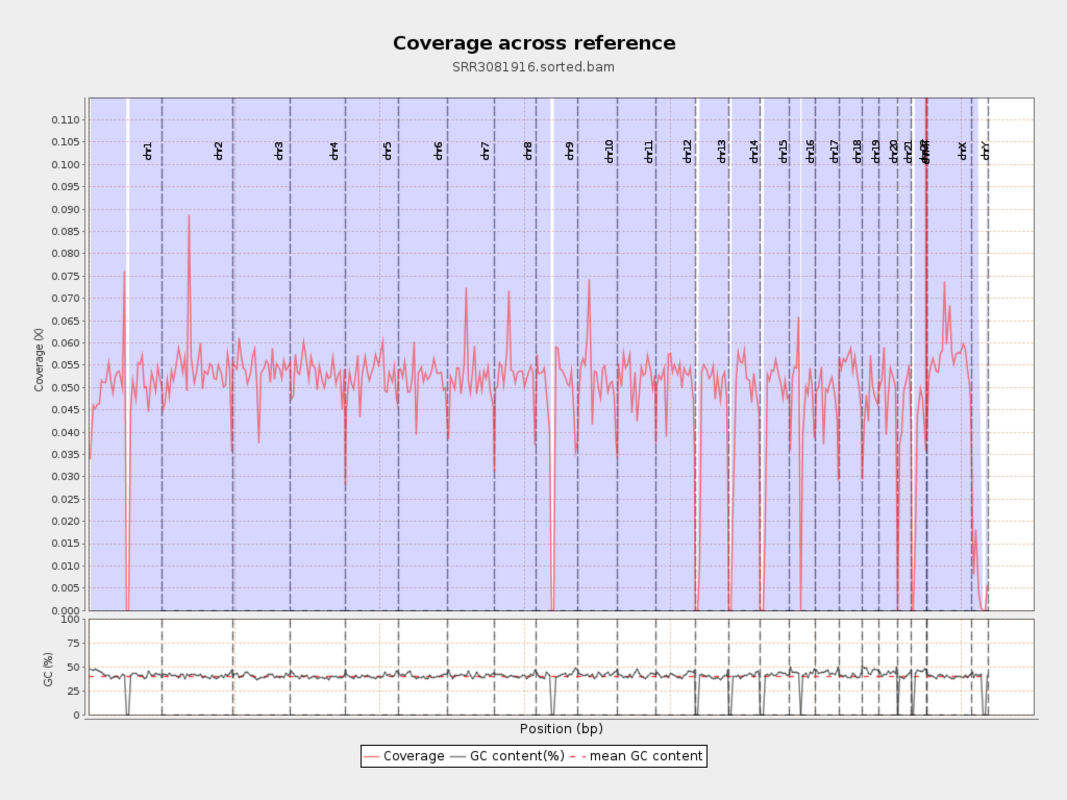
General error rate	0.85%
Mismatches	1,274,695
Insertions	11,500
Mapped reads with at least one insertion	0.51%
Deletions	33,553
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.46%

2.6. Chromosome stats

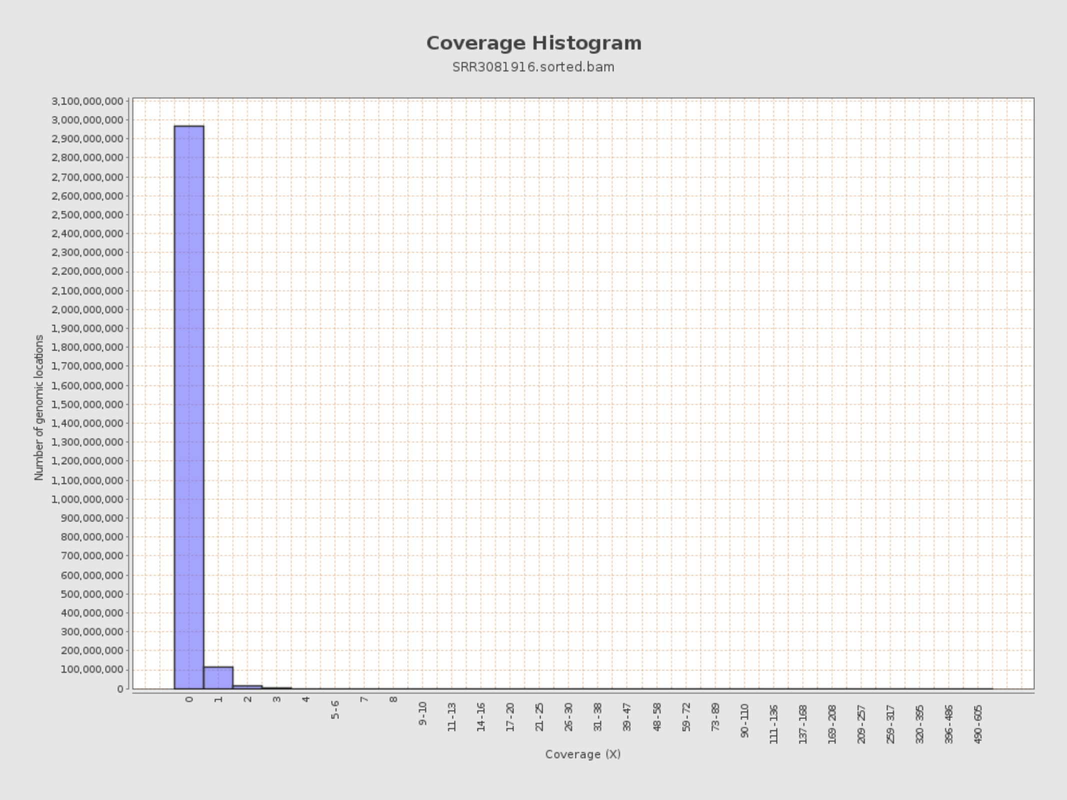
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11921797	0.0478	0.5873
chr2	243199373	13131640	0.054	0.4335
chr3	198022430	10709141	0.0541	0.2637
chr4	191154276	10147227	0.0531	0.2741
chr5	180915260	9502859	0.0525	0.2601
chr6	171115067	8921795	0.0521	0.2908
chr7	159138663	8358594	0.0525	0.4486

chr8	146364022	7795142	0.0533	0.4296
chr9	141213431	6426605	0.0455	0.3476
chr10	135534747	7137302	0.0527	0.3644
chr11	135006516	7030313	0.0521	0.3279
chr12	133851895	6977235	0.0521	0.261
chr13	115169878	4957279	0.043	0.2352
chr14	107349540	4701854	0.0438	0.2507
chr15	102531392	4308538	0.042	0.2385
chr16	90354753	4123951	0.0456	0.2667
chr17	81195210	3848716	0.0474	0.2681
chr18	78077248	4259242	0.0546	0.6108
chr19	59128983	2783405	0.0471	0.4495
chr20	63025520	3130647	0.0497	0.2567
chr21	48129895	2016127	0.0419	0.246
chr22	51304566	1602734	0.0312	0.198
chrMT	16571	30803	1.8588	1.6988
chrX	155270560	8838158	0.0569	0.2927
chrY	59373566	378233	0.0064	0.1347

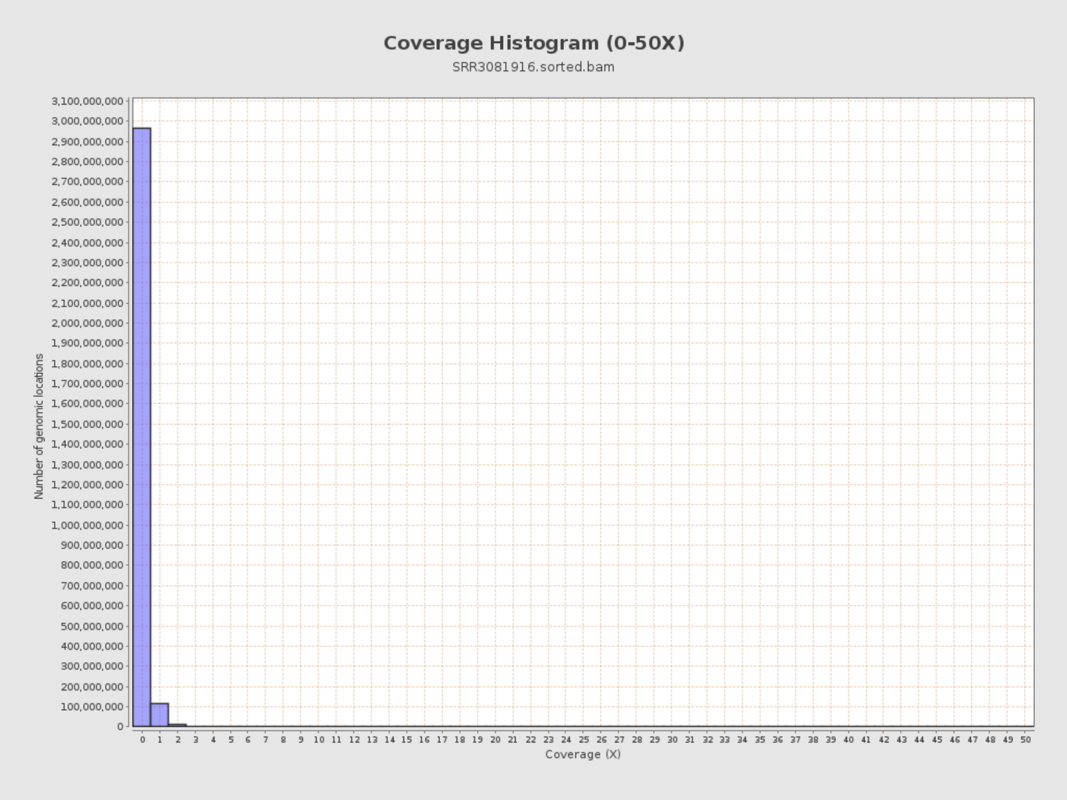
3. Results : Coverage across reference



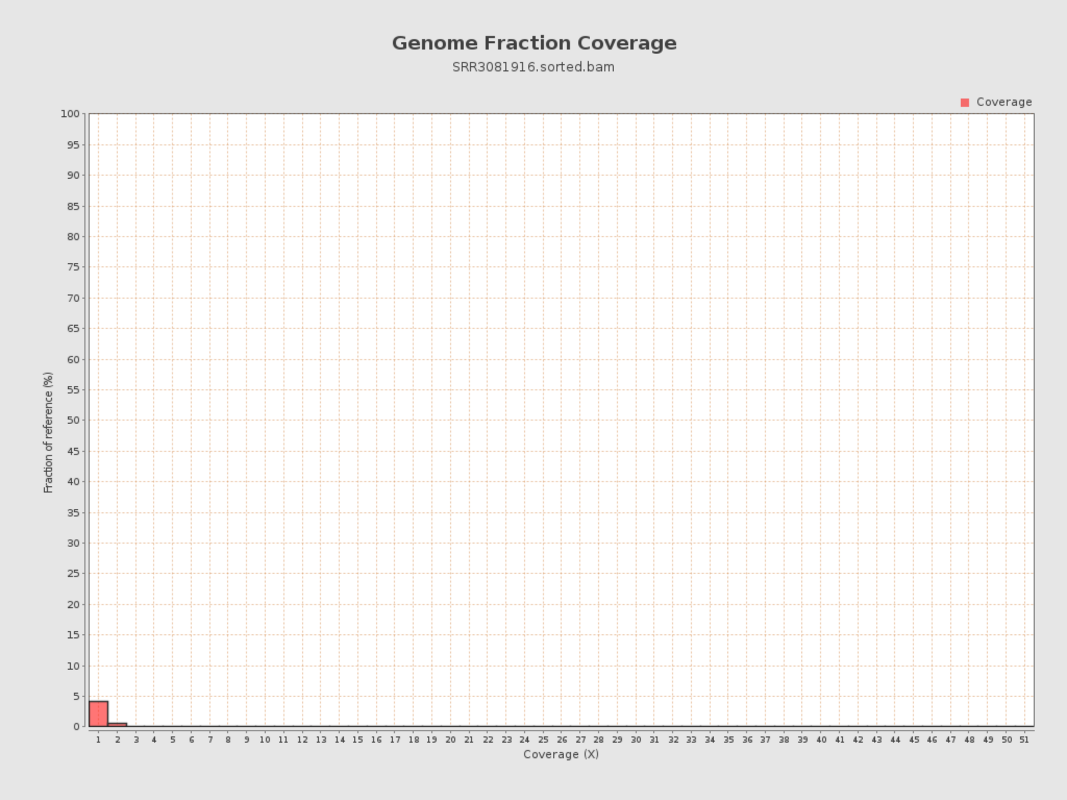
4. Results : Coverage Histogram



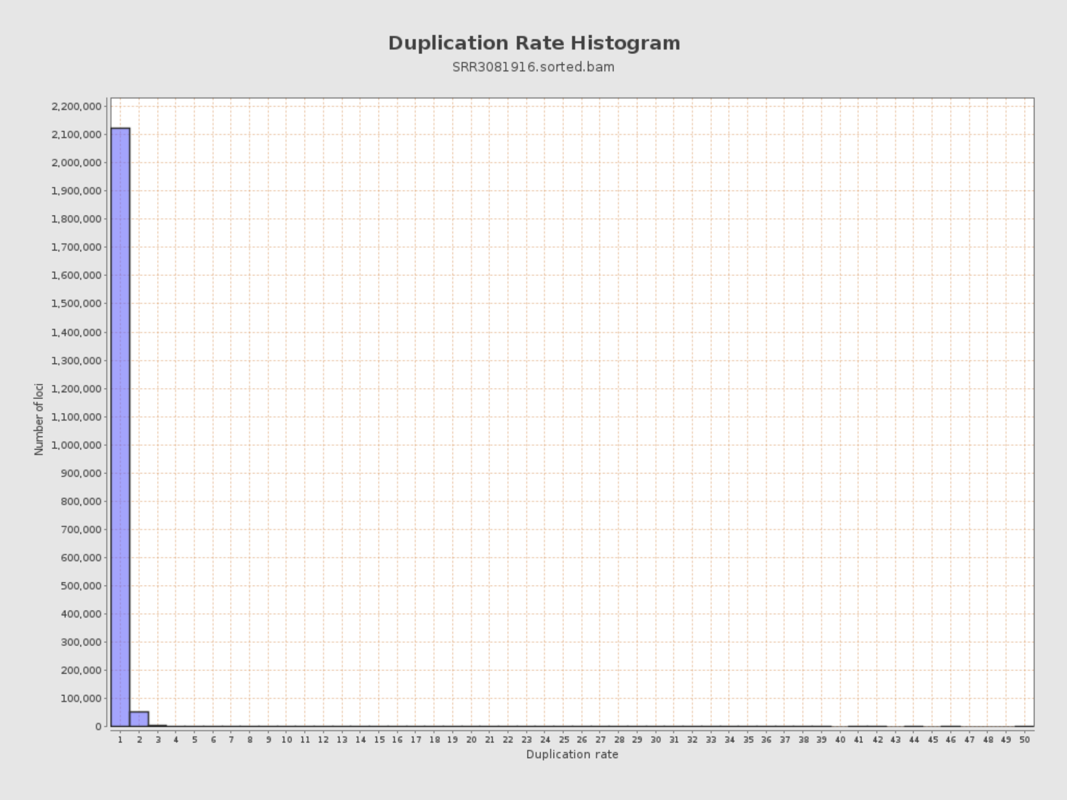
5. Results : Coverage Histogram (0-50X)



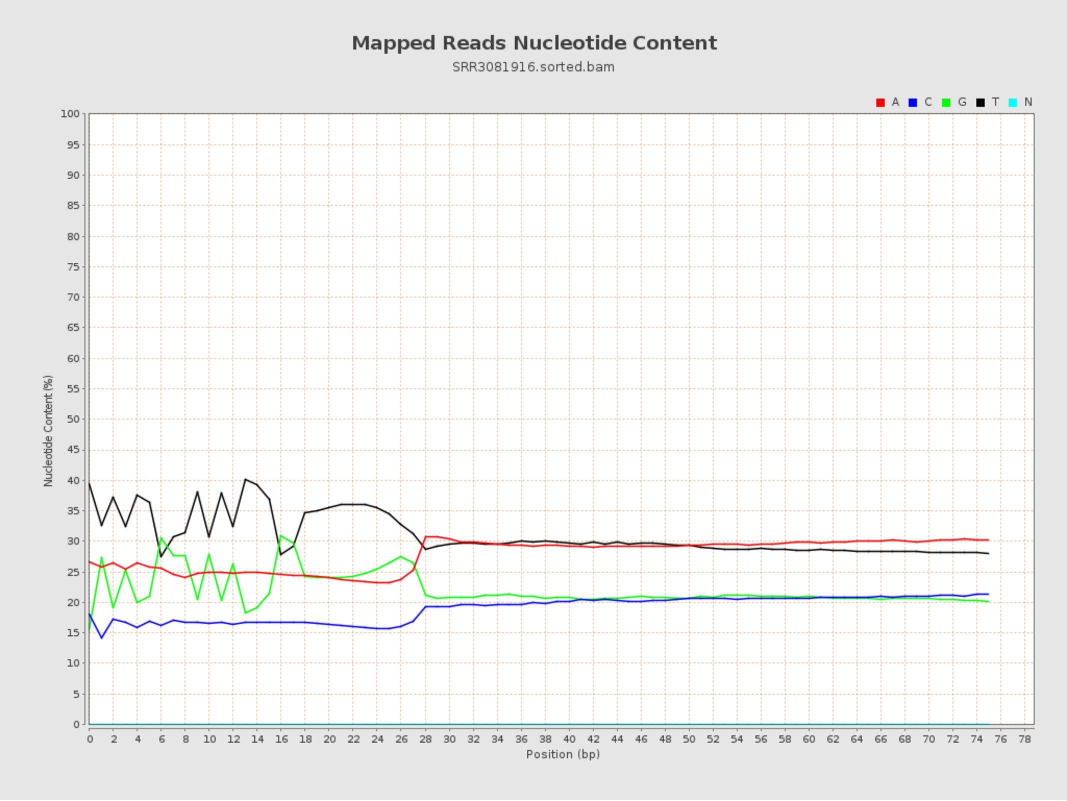
6. Results : Genome Fraction Coverage



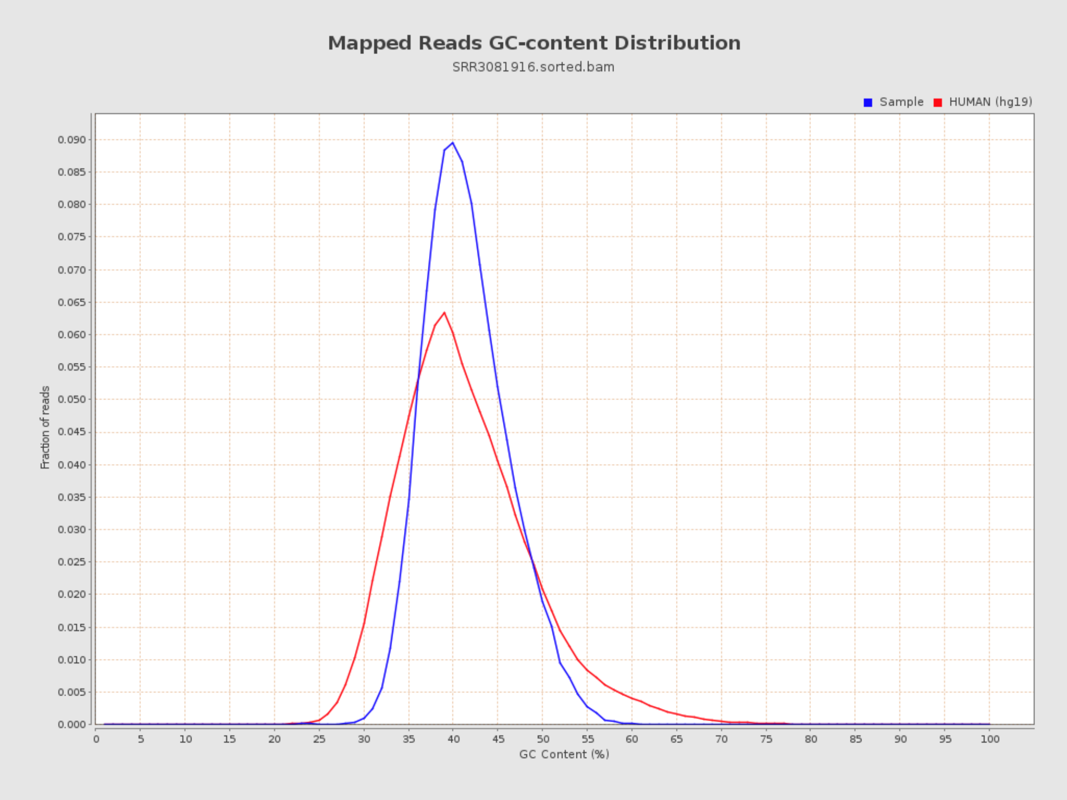
7. Results : Duplication Rate Histogram



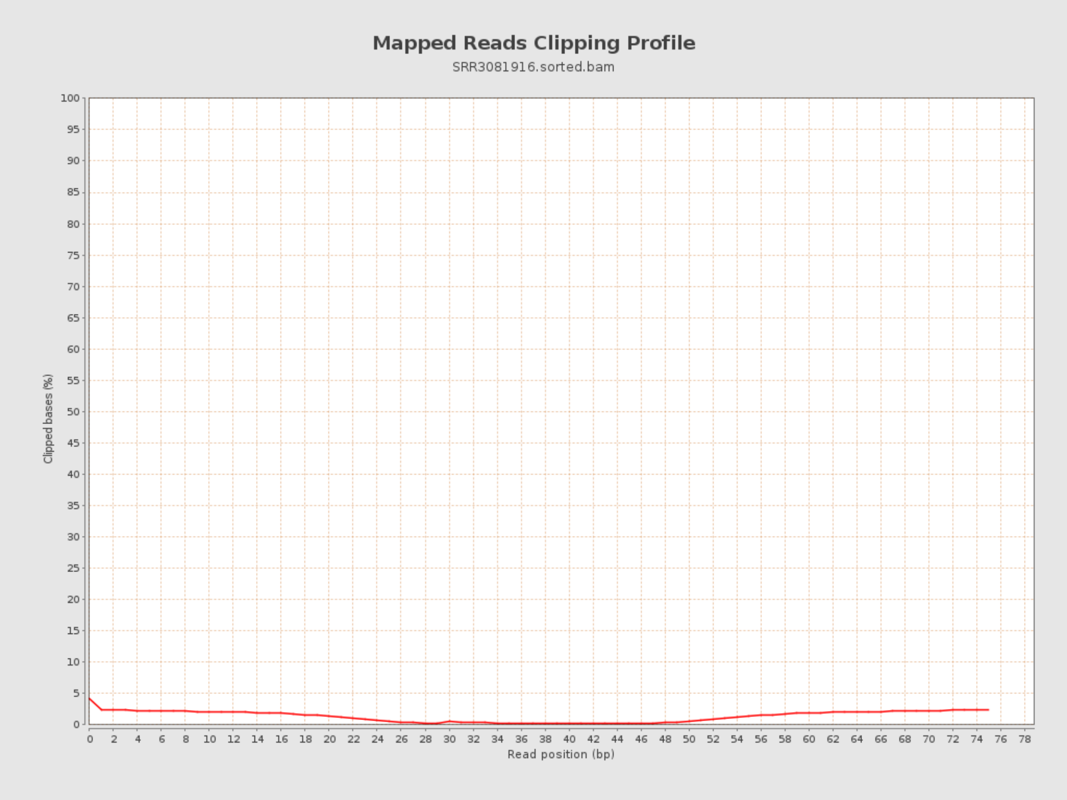
8. Results : Mapped Reads Nucleotide Content



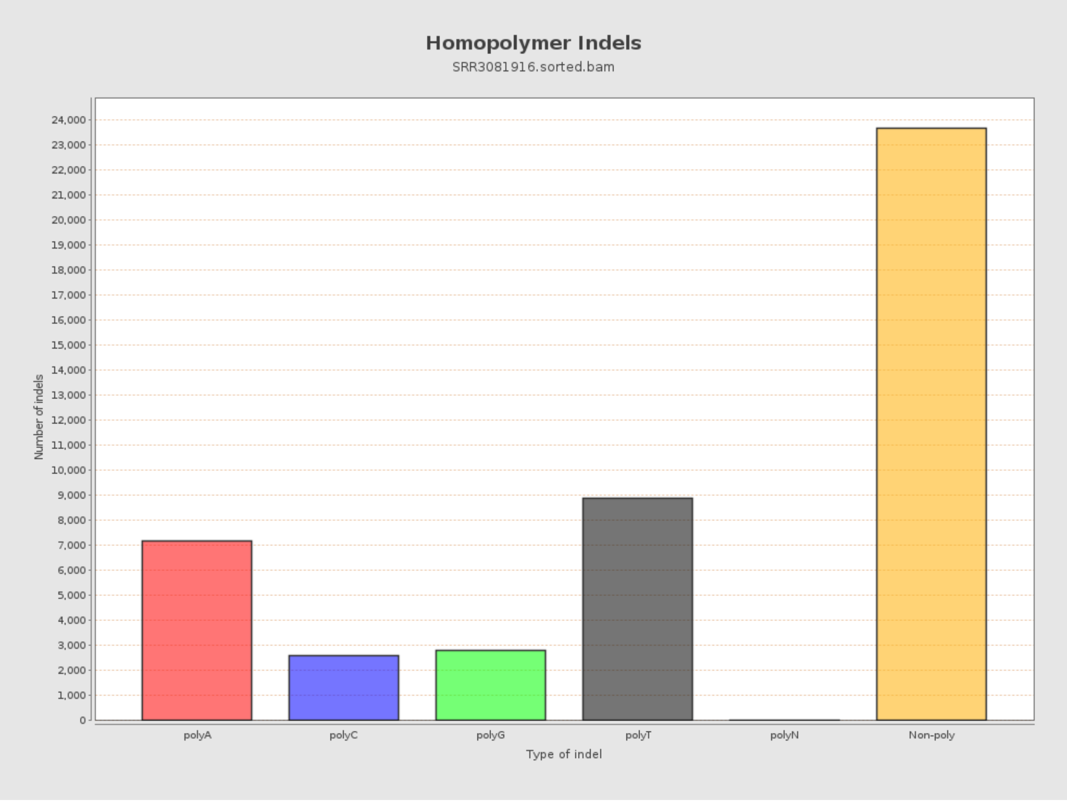
9. Results : Mapped Reads GC-content Distribution



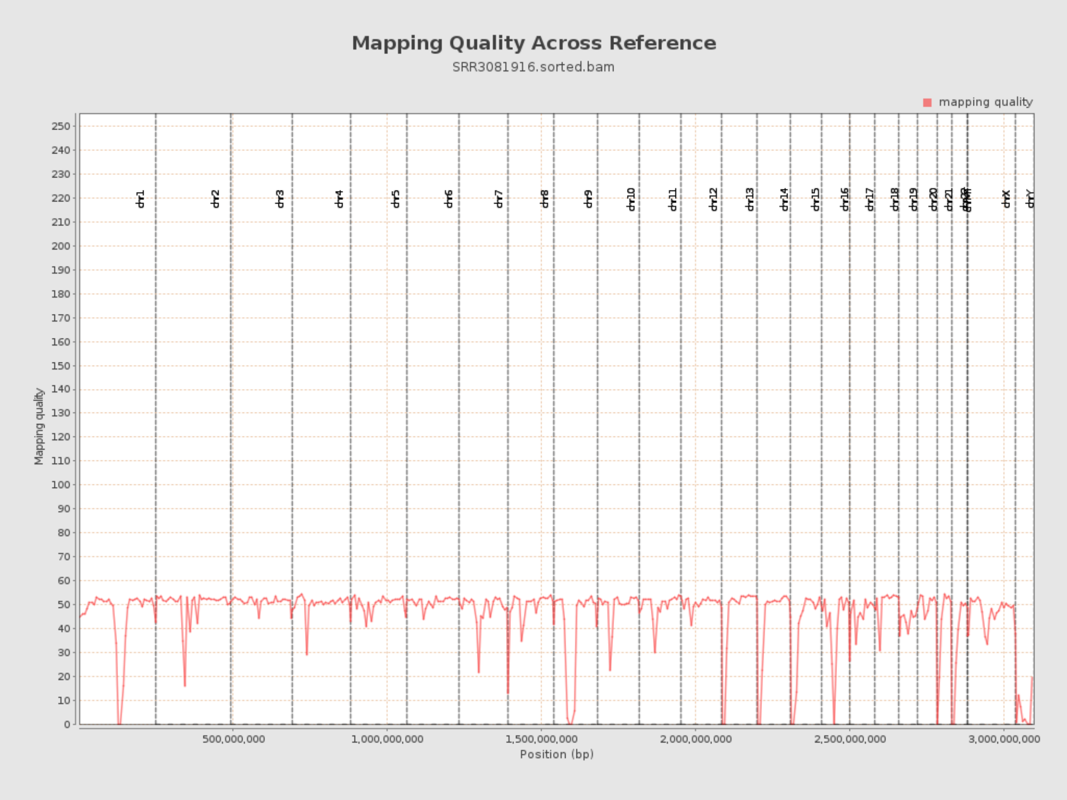
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram