Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:17:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081207.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_SRR3081207 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081207.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:17:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081207.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,828,064
Mapped reads	4,631,021 / 79.46%
Unmapped reads	1,197,043 / 20.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,502 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	428,392 / 7.35%
Duplication rate	6.83%
Clipped reads	2,465,794 / 42.31%

2.2. ACGT Content

Number/percentage of A's	84,175,525 / 28.2%
Number/percentage of C's	54,537,120 / 18.27%
Number/percentage of T's	95,628,479 / 32.03%
Number/percentage of G's	64,023,916 / 21.45%
Number/percentage of N's	166,061 / 0.06%
GC Percentage	39.71%

2.3. Coverage

Mean	0.0965

Standard Deviation	1.0847

2.4. Mapping Quality

Mean Mapping Quality	45.77

2.5. Mismatches and indels

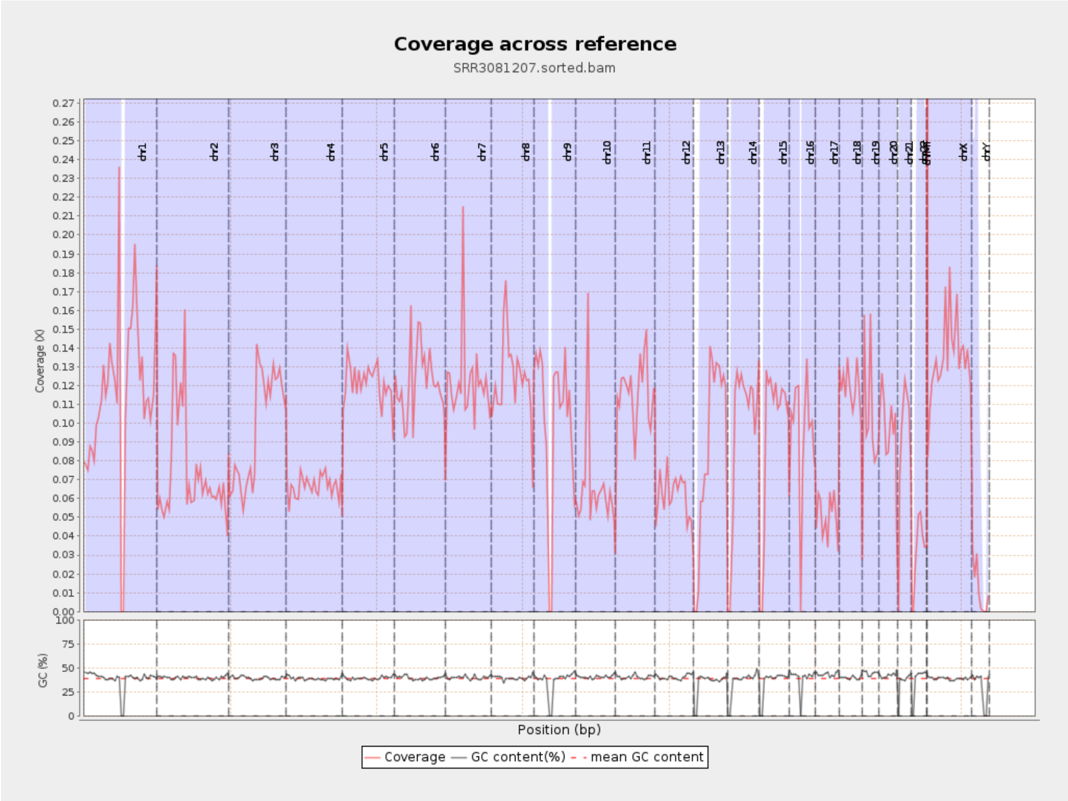
General error rate	1.04%
Mismatches	3,064,247
Insertions	22,647
Mapped reads with at least one insertion	0.49%
Deletions	67,700
Mapped reads with at least one deletion	1.45%
Homopolymer indels	46.63%

2.6. Chromosome stats

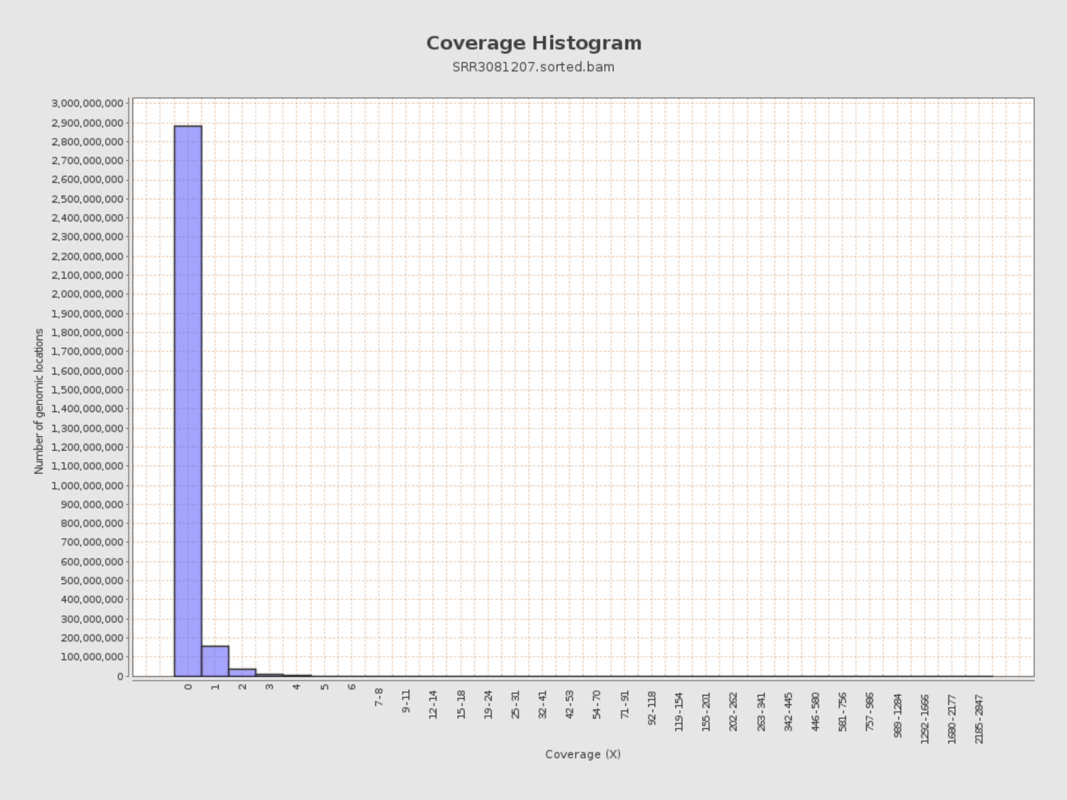
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29010740	0.1164	2.5351
chr2	243199373	18136347	0.0746	0.751
chr3	198022430	19223630	0.0971	0.4305
chr4	191154276	12790300	0.0669	0.3477
chr5	180915260	21773911	0.1204	0.4665
chr6	171115067	20939613	0.1224	0.6835
chr7	159138663	19232298	0.1209	1.486

chr8	146364022	18066958	0.1234	1.7527
chr9	141213431	14396794	0.102	0.7342
chr10	135534747	8893522	0.0656	0.9711
chr11	135006516	15586264	0.1154	0.7266
chr12	133851895	8180593	0.0611	0.3604
chr13	115169878	10192346	0.0885	0.3909
chr14	107349540	10378799	0.0967	1.2535
chr15	102531392	9627341	0.0939	0.4017
chr16	90354753	8395191	0.0929	0.4624
chr17	81195210	4132242	0.0509	0.3794
chr18	78077248	9360232	0.1199	1.2383
chr19	59128983	6166157	0.1043	1.7954
chr20	63025520	6294879	0.0999	0.437
chr21	48129895	4341612	0.0902	0.4351
chr22	51304566	1639156	0.0319	0.2259
chrMT	16571	318941	19.2469	12.1018
chrX	155270560	20854178	0.1343	0.5671
chrY	59373566	704556	0.0119	0.1827

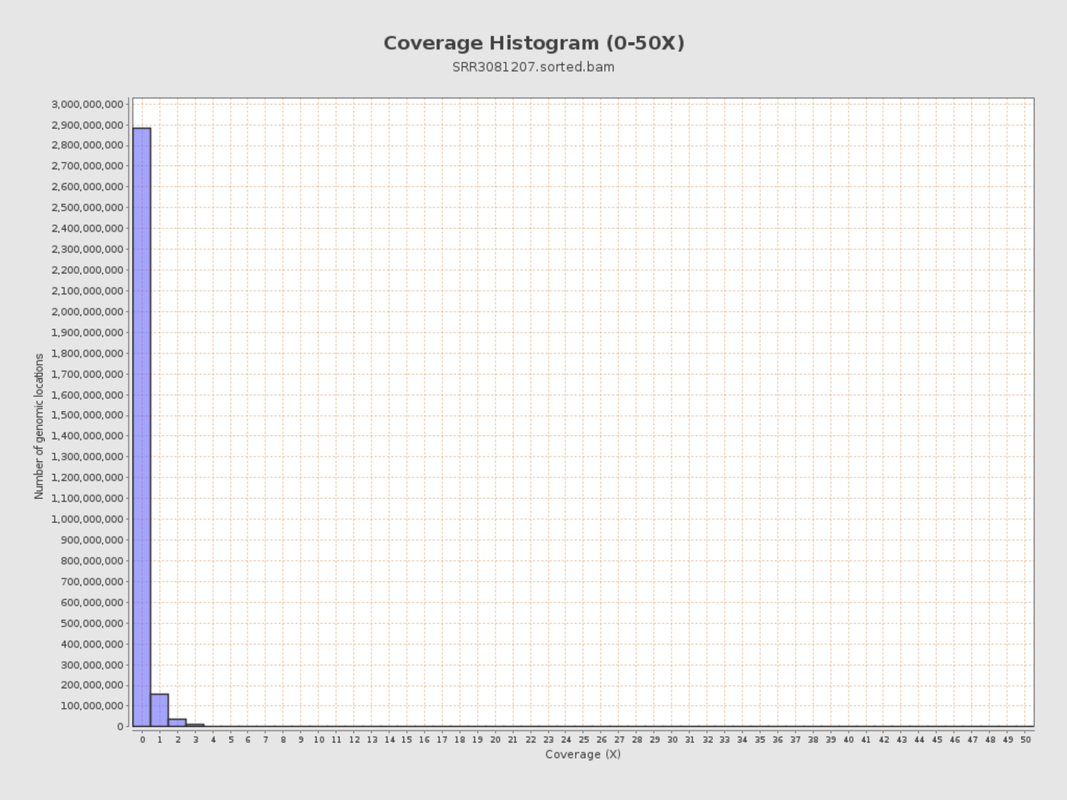
3. Results : Coverage across reference



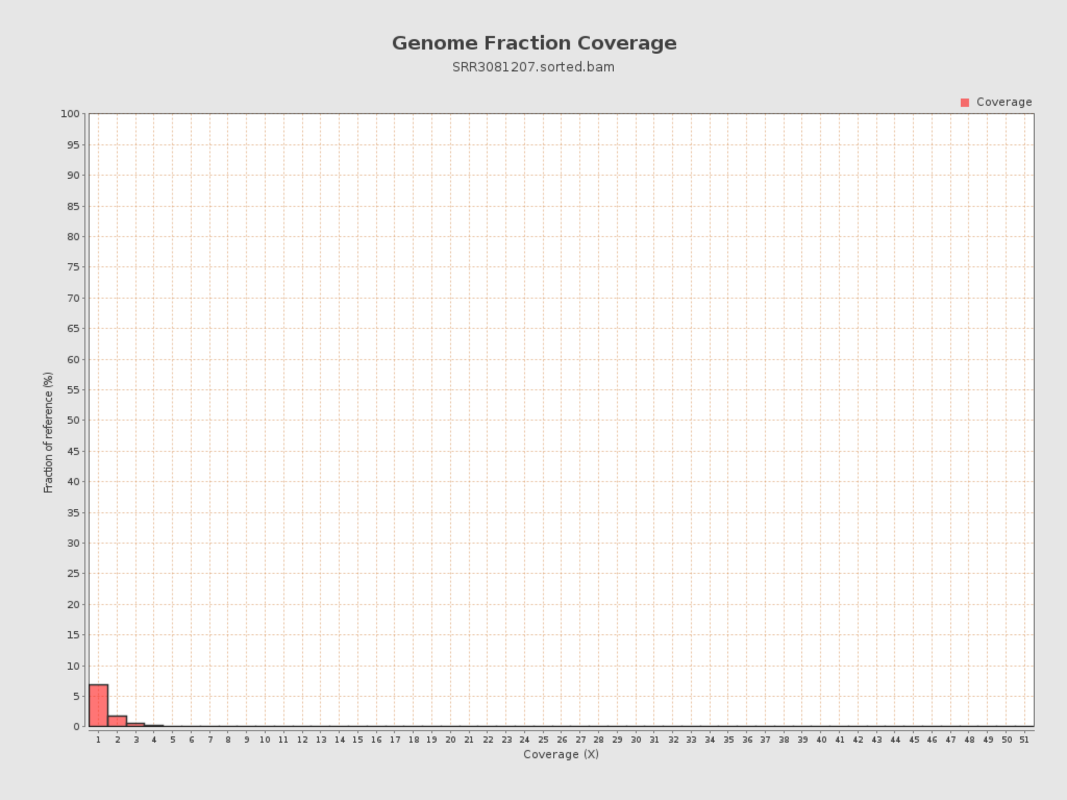
4. Results : Coverage Histogram



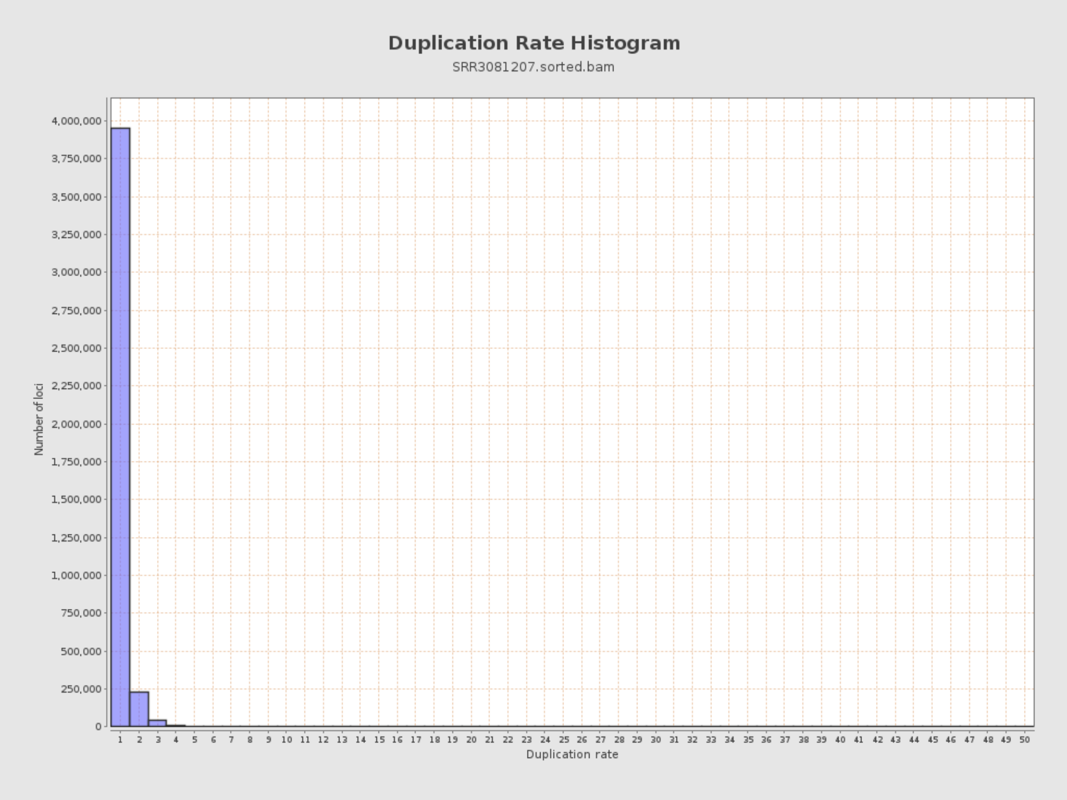
5. Results : Coverage Histogram (0-50X)



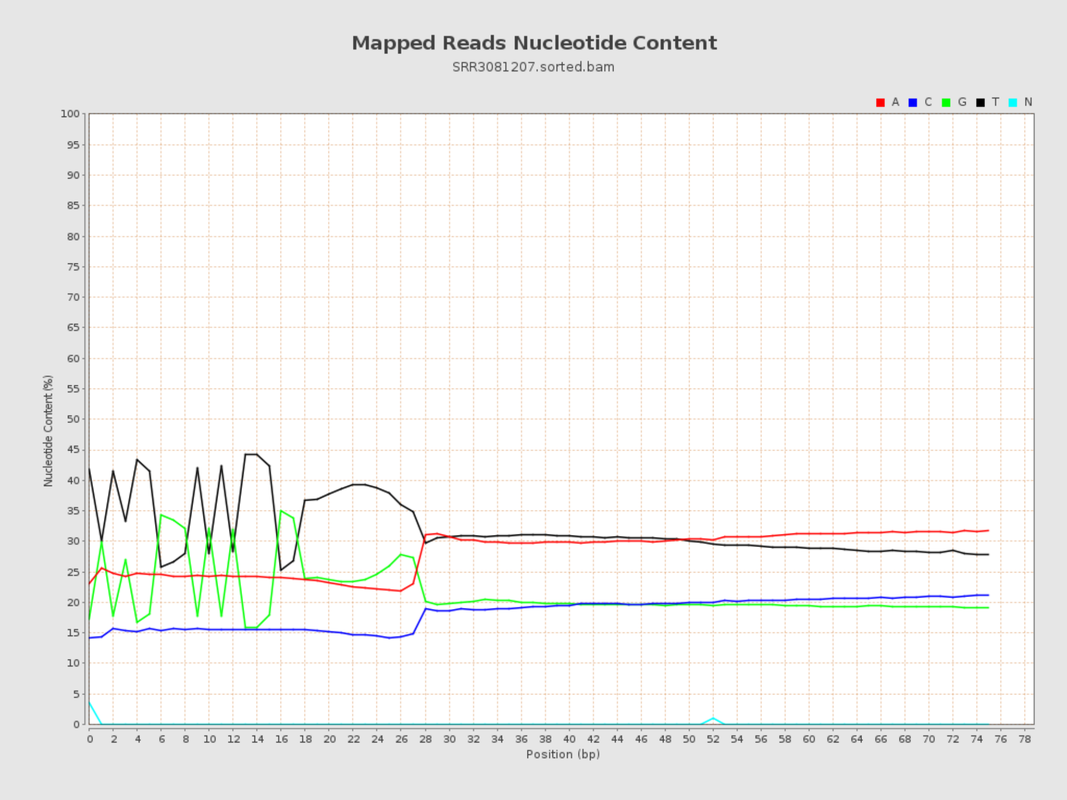
6. Results : Genome Fraction Coverage



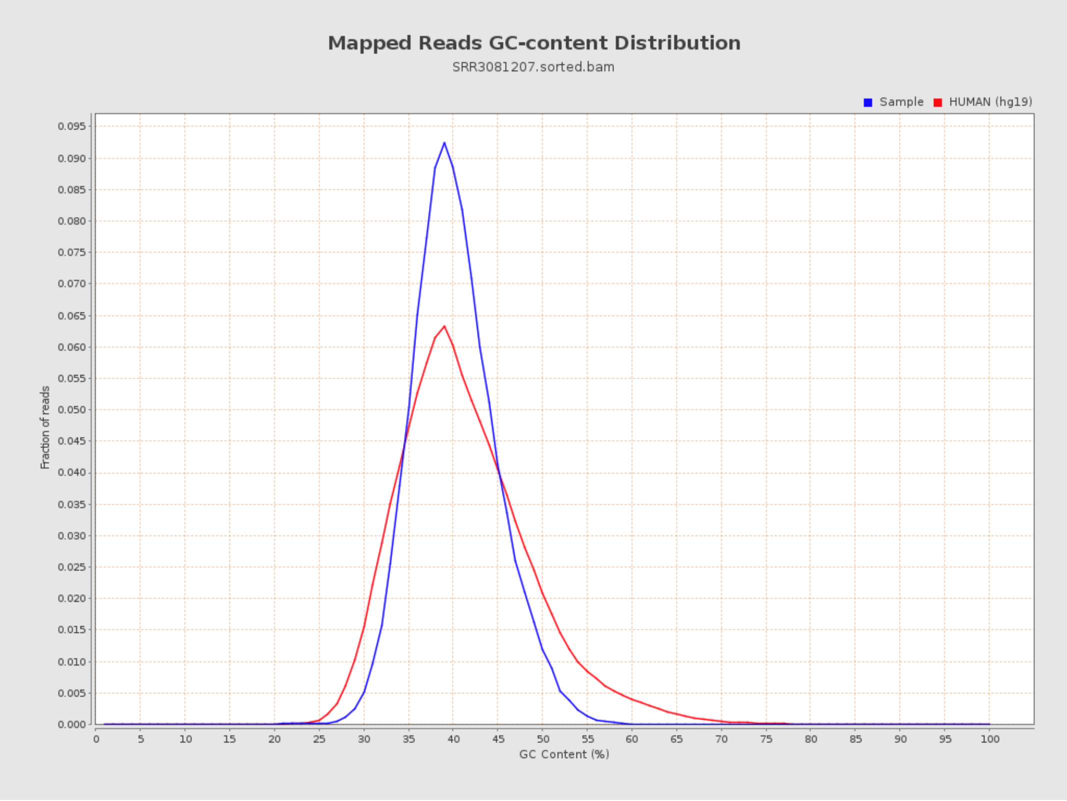
7. Results : Duplication Rate Histogram



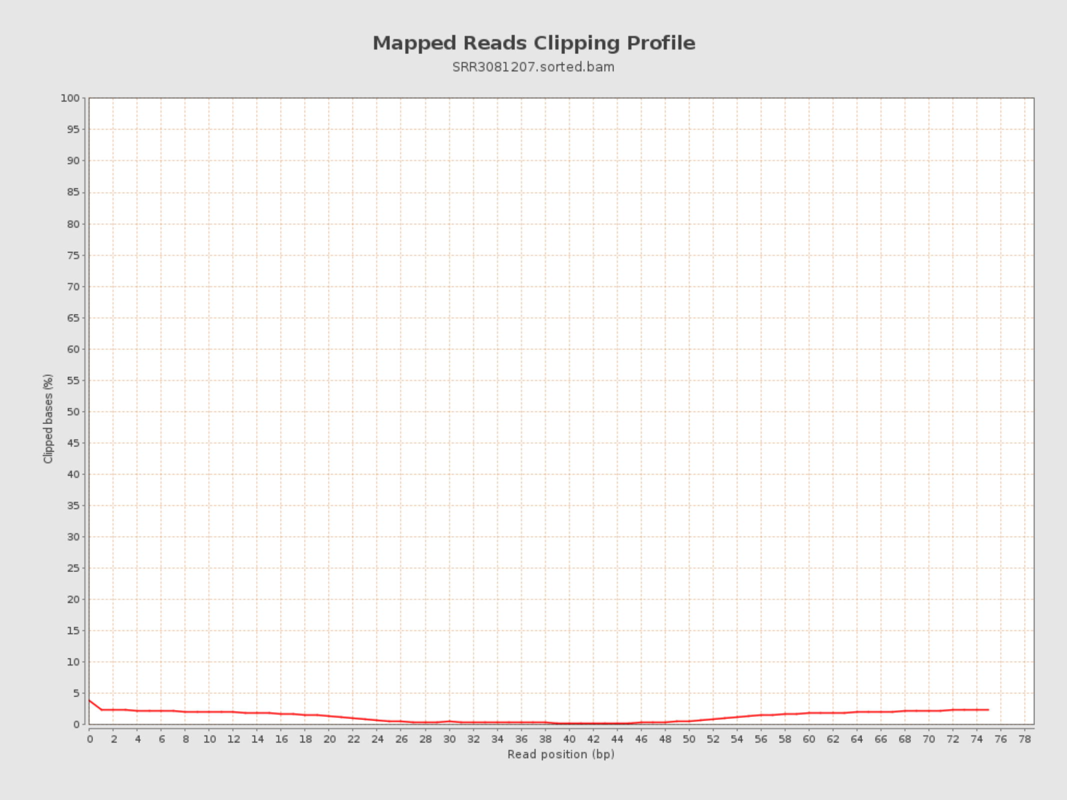
8. Results : Mapped Reads Nucleotide Content



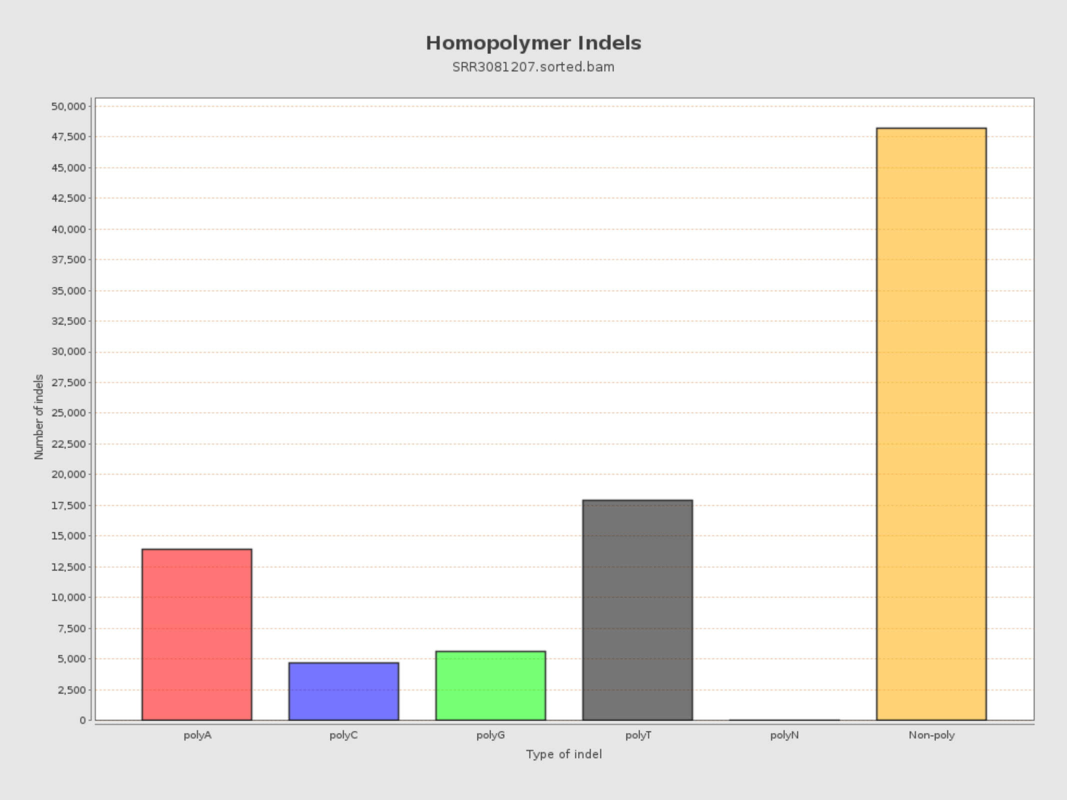
9. Results : Mapped Reads GC-content Distribution



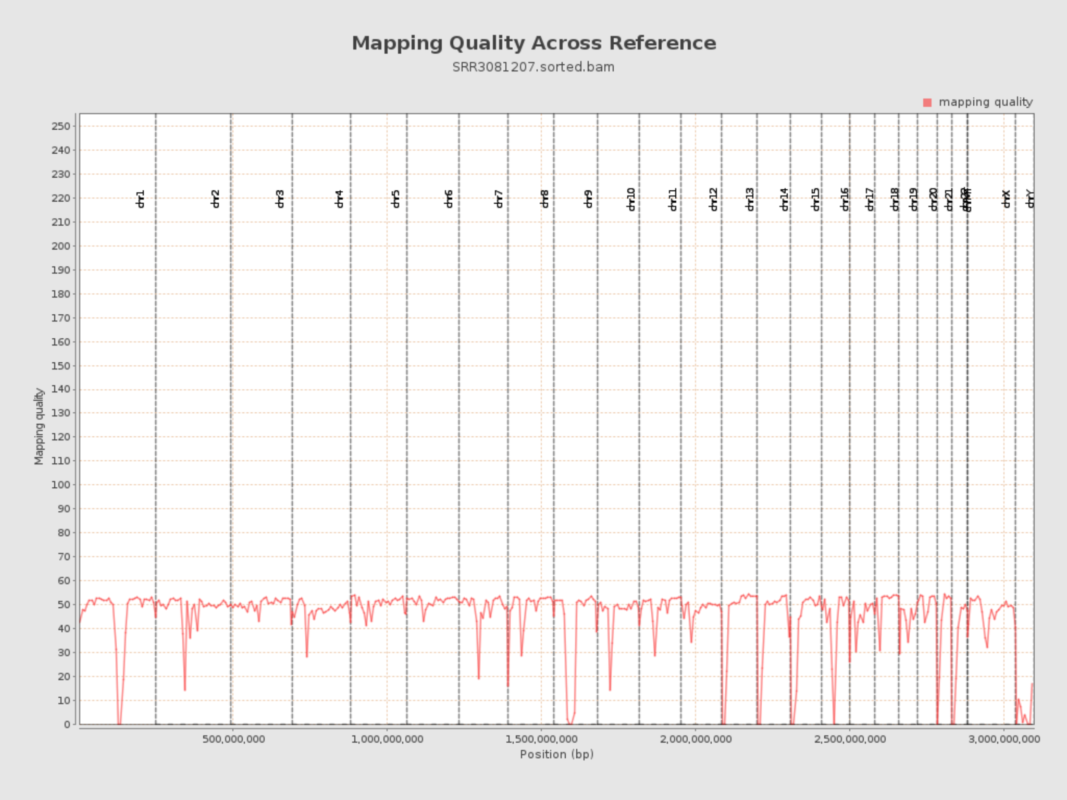
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram