Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:41:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081024.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_SRR3081024 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081024.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:41:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081024.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,601,484
Mapped reads	1,809,678 / 69.56%
Unmapped reads	791,806 / 30.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,730 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	51,959 / 2%
Duplication rate	2.29%
Clipped reads	1,052,658 / 40.46%

2.2. ACGT Content

Number/percentage of A's	31,669,611 / 28.21%
Number/percentage of C's	22,308,282 / 19.87%
Number/percentage of T's	32,578,002 / 29.02%
Number/percentage of G's	25,692,934 / 22.89%
Number/percentage of N's	1,424 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.2755

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

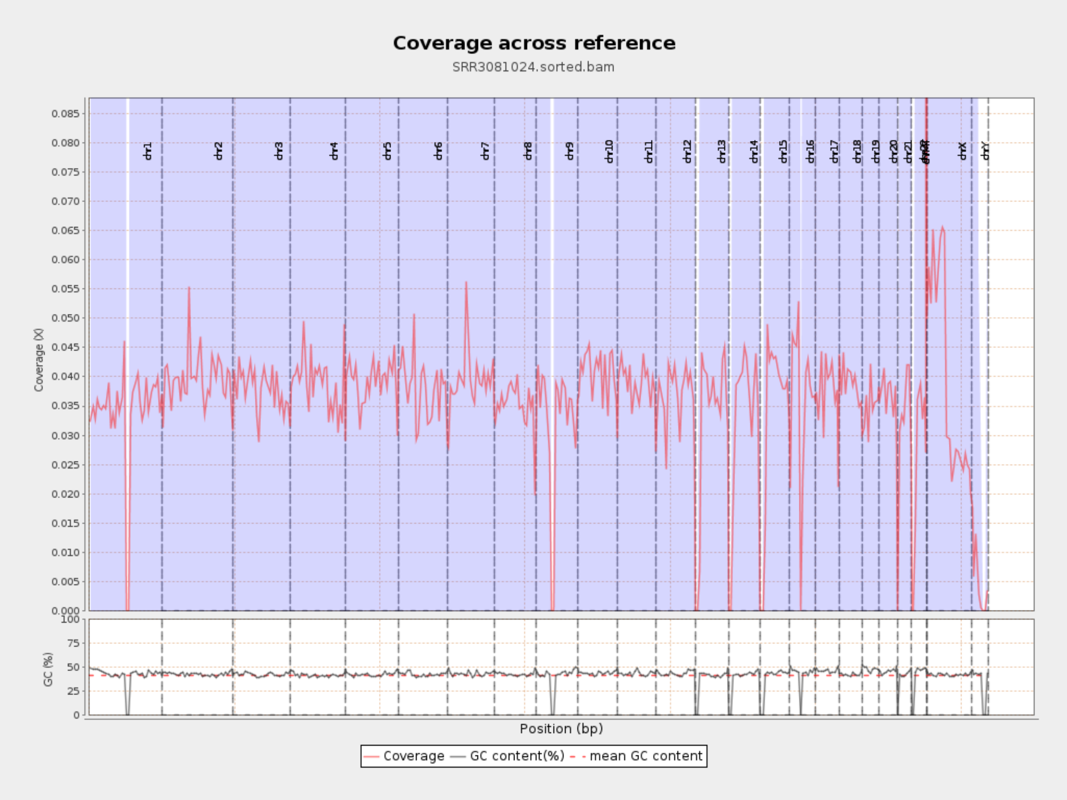
General error rate	0.77%
Mismatches	849,733
Insertions	7,246
Mapped reads with at least one insertion	0.4%
Deletions	22,236
Mapped reads with at least one deletion	1.22%
Homopolymer indels	46.68%

2.6. Chromosome stats

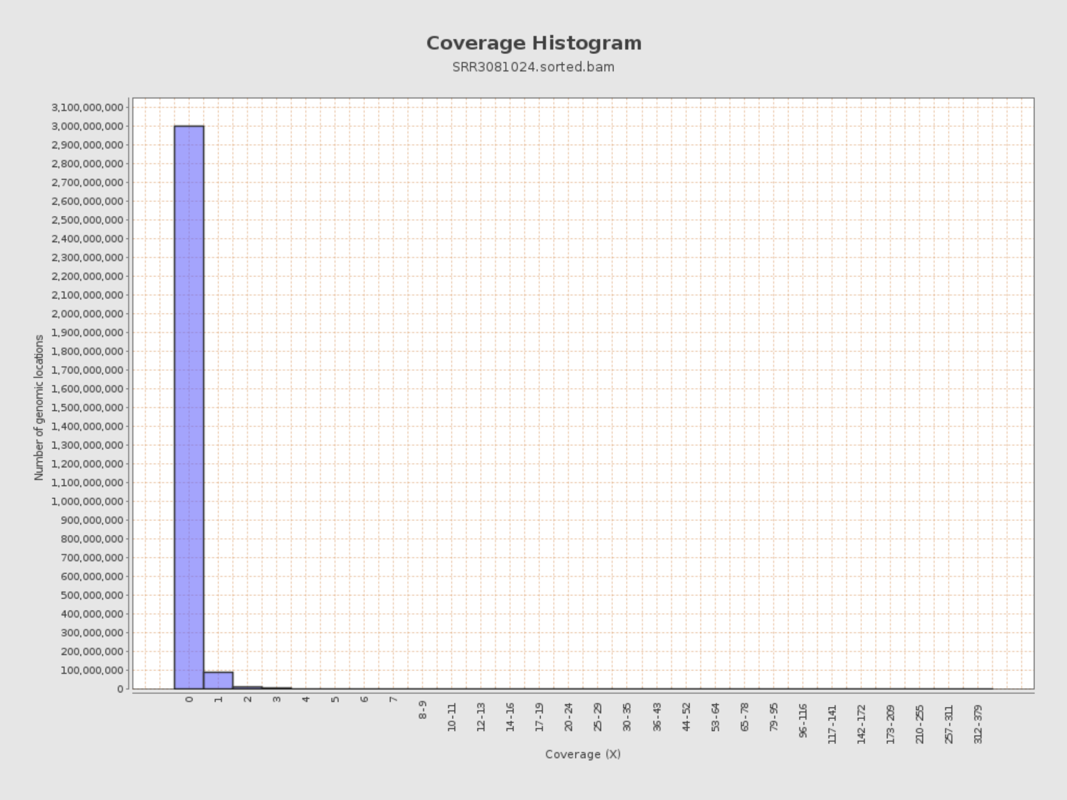
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8413386	0.0338	0.3654
chr2	243199373	9683384	0.0398	0.3235
chr3	198022430	7493148	0.0378	0.2161
chr4	191154276	7466004	0.0391	0.2282
chr5	180915260	7118202	0.0393	0.2222
chr6	171115067	6520234	0.0381	0.2549
chr7	159138663	6345495	0.0399	0.3911

chr8	146364022	5145496	0.0352	0.2602
chr9	141213431	4496243	0.0318	0.2684
chr10	135534747	5557585	0.041	0.2585
chr11	135006516	5253915	0.0389	0.2782
chr12	133851895	4952197	0.037	0.2162
chr13	115169878	3722661	0.0323	0.2005
chr14	107349540	3482743	0.0324	0.2127
chr15	102531392	3434500	0.0335	0.2141
chr16	90354753	3282767	0.0363	0.2317
chr17	81195210	3048867	0.0375	0.2371
chr18	78077248	3049475	0.0391	0.5112
chr19	59128983	2062921	0.0349	0.2936
chr20	63025520	2331926	0.037	0.2202
chr21	48129895	1533897	0.0319	0.2118
chr22	51304566	1283692	0.025	0.1759
chrMT	16571	35357	2.1337	1.8815
chrX	155270560	6285205	0.0405	0.2539
chrY	59373566	289610	0.0049	0.0983

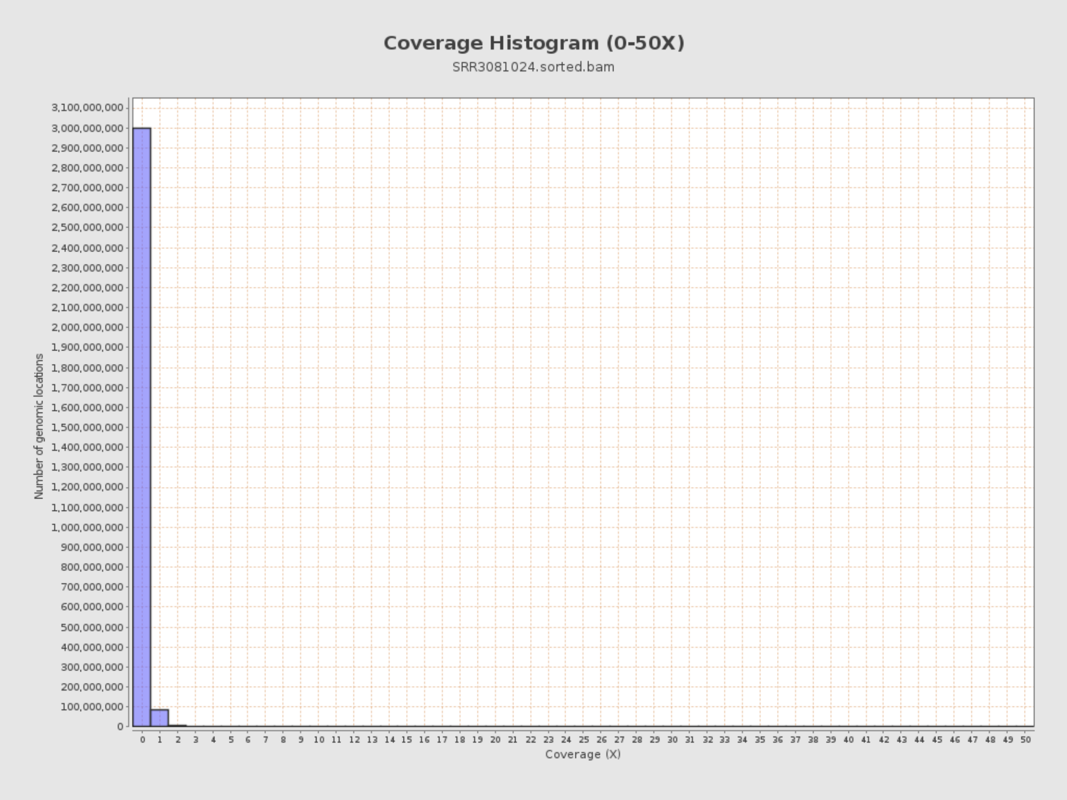
3. Results : Coverage across reference



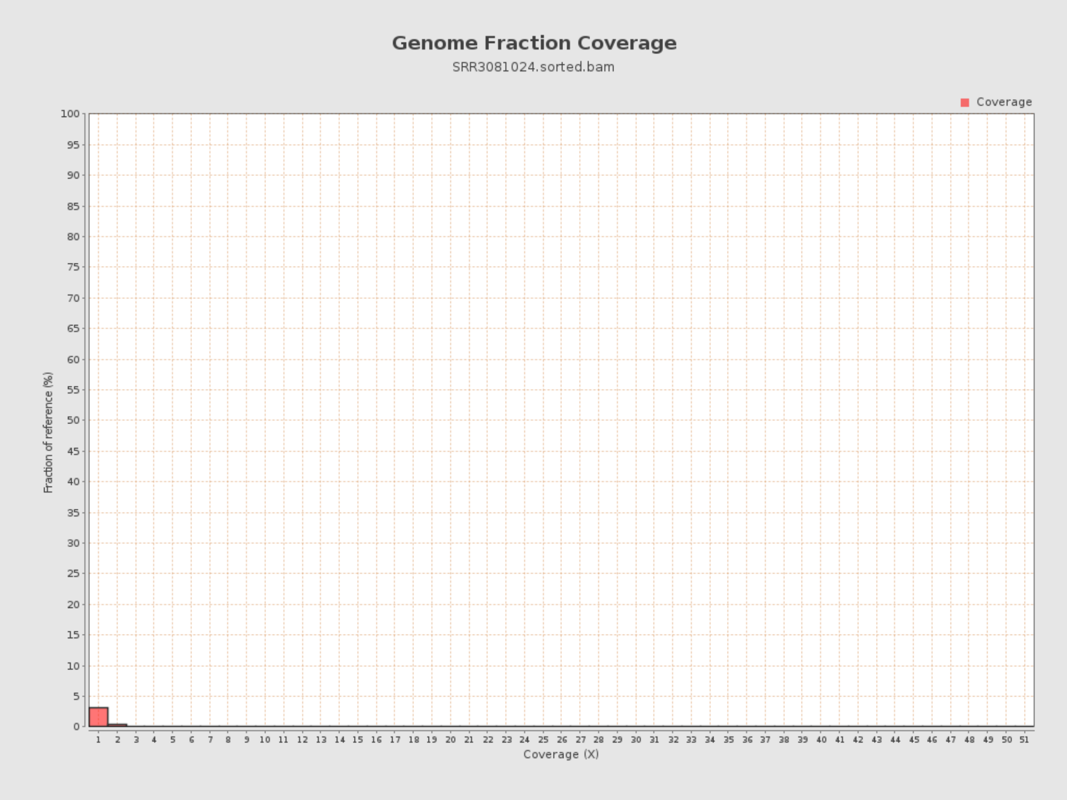
4. Results : Coverage Histogram



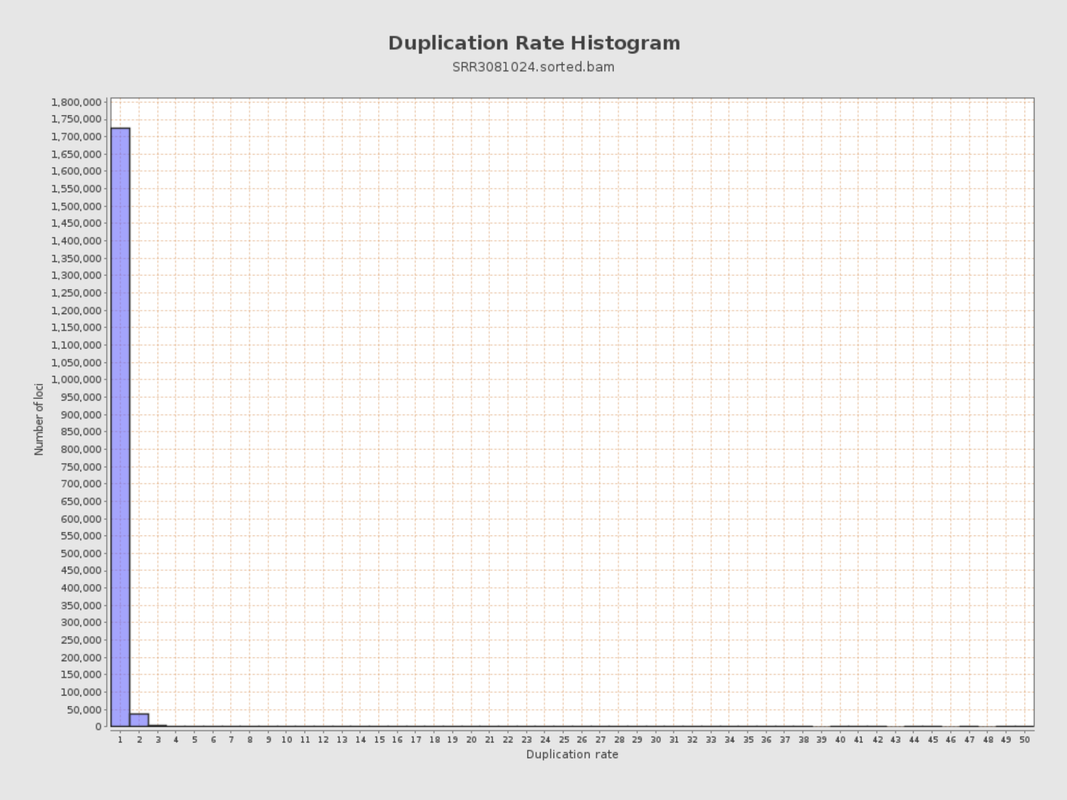
5. Results : Coverage Histogram (0-50X)



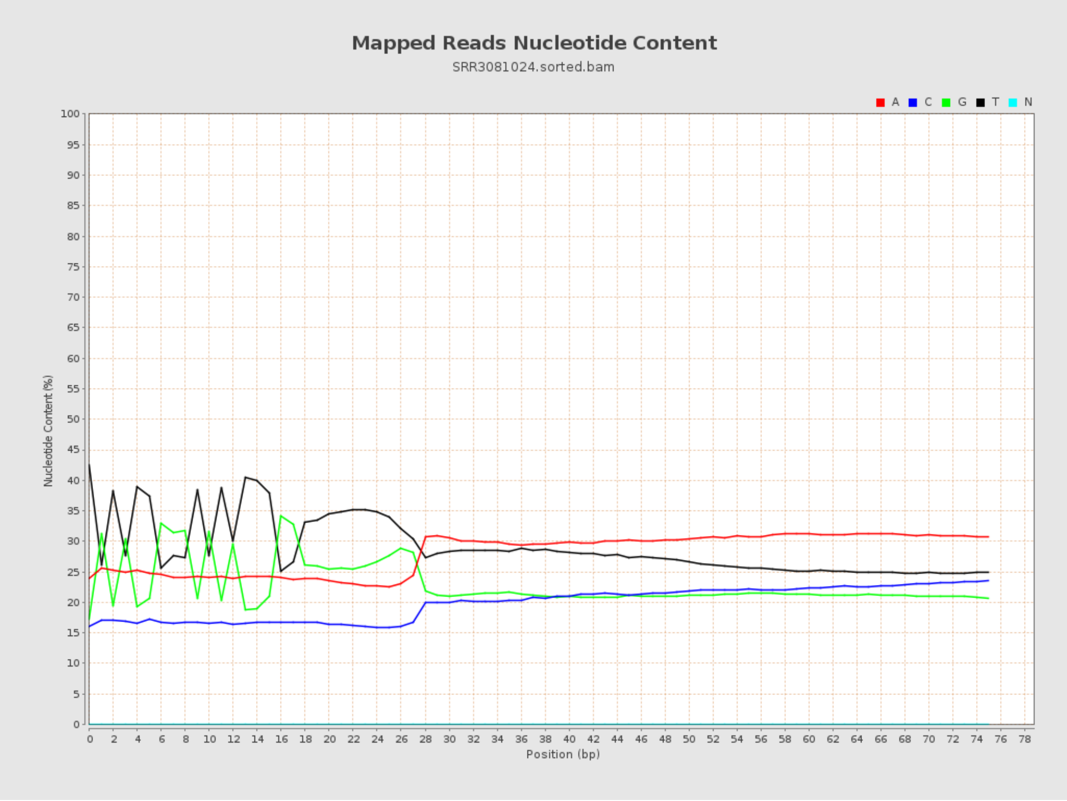
6. Results : Genome Fraction Coverage



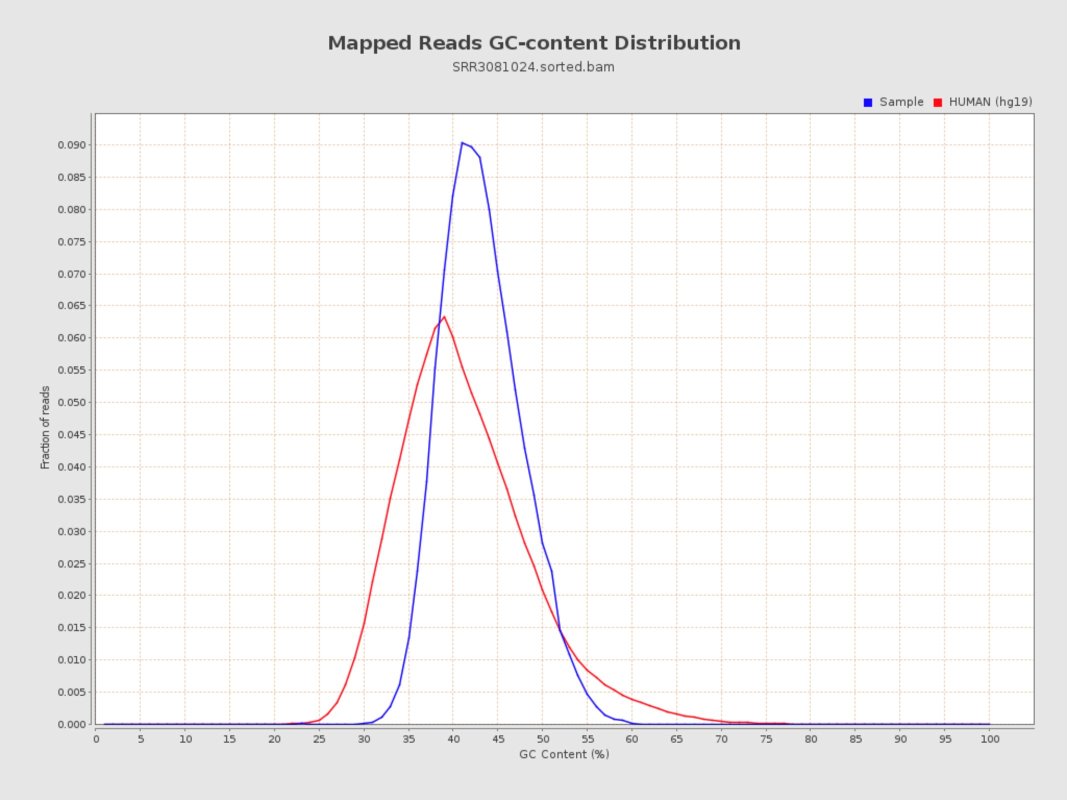
7. Results : Duplication Rate Histogram



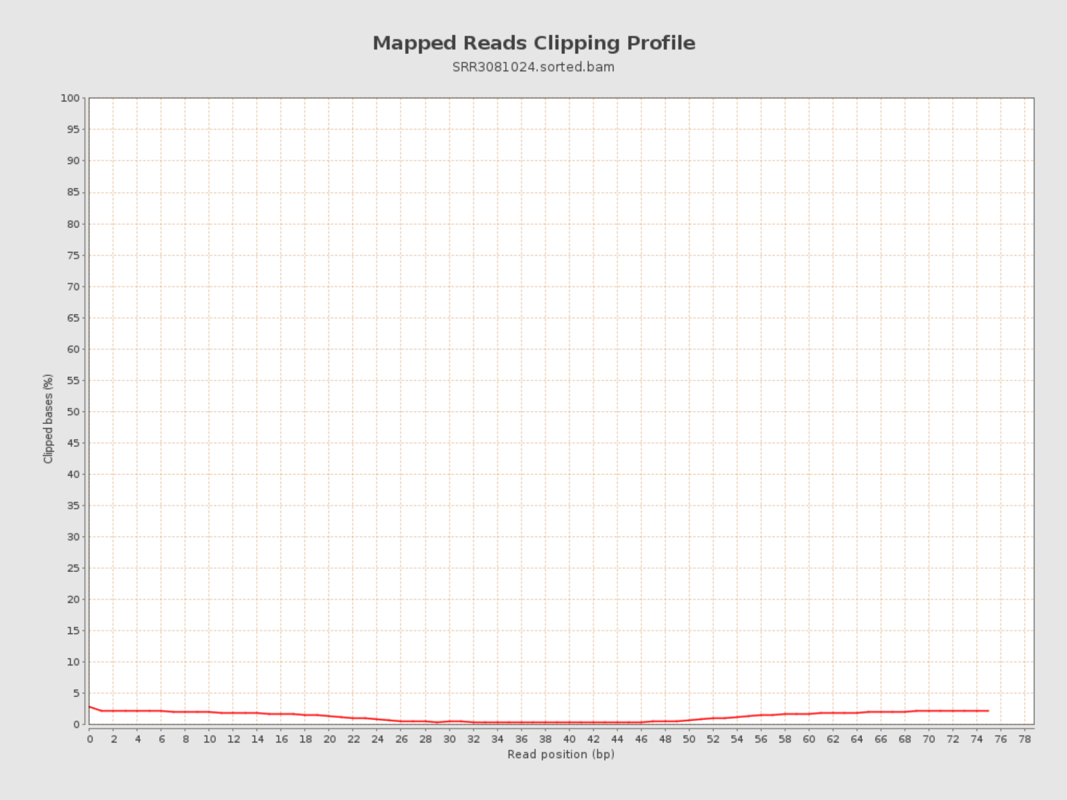
8. Results : Mapped Reads Nucleotide Content



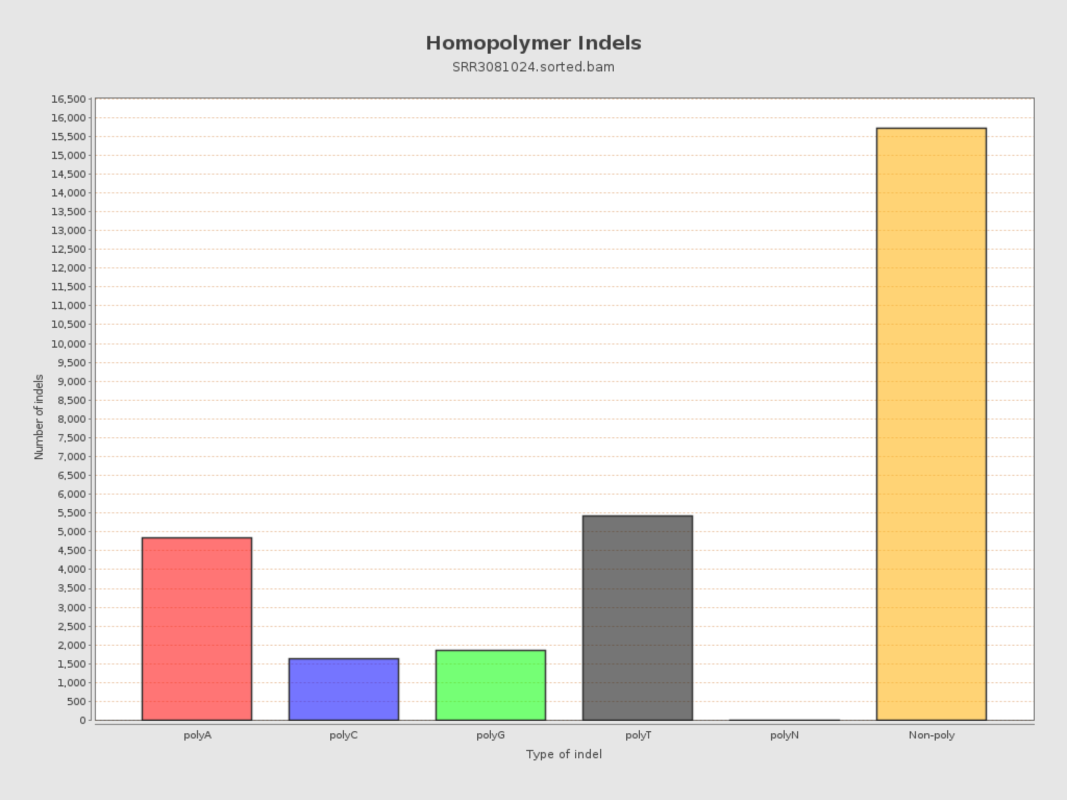
9. Results : Mapped Reads GC-content Distribution



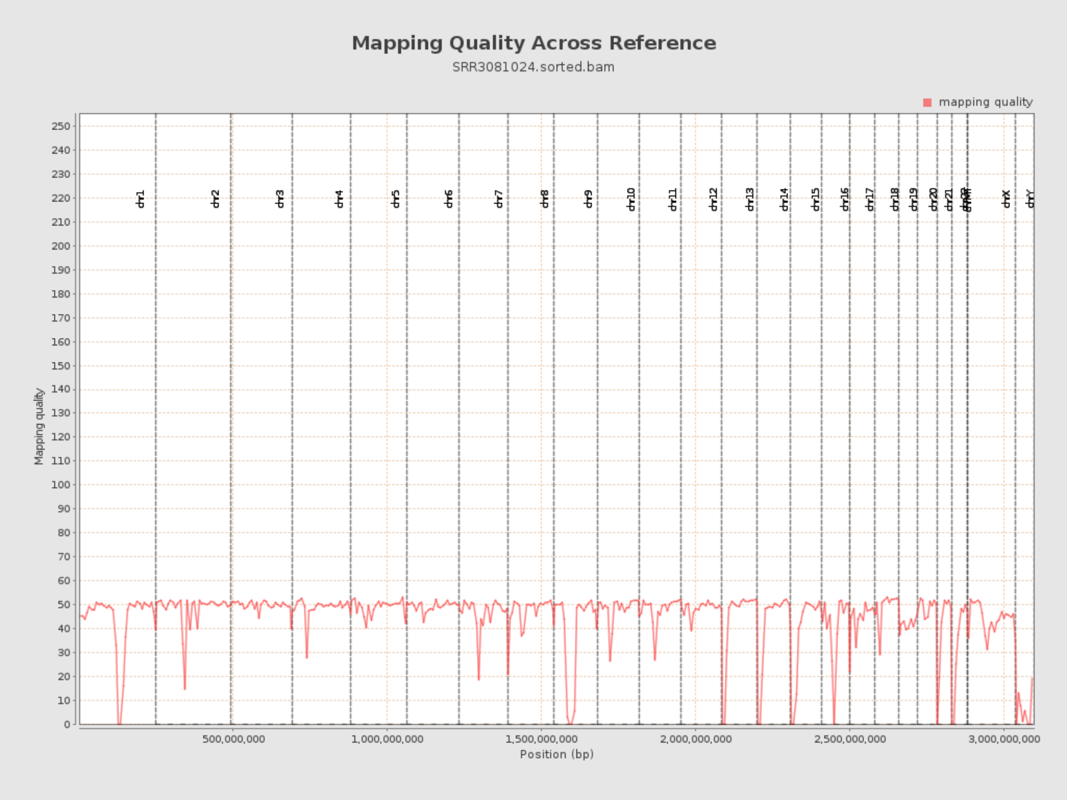
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram