Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:01:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085018.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_SRR3085018 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085018.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:01:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085018.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,507,083
Mapped reads	2,266,471 / 90.4%
Unmapped reads	240,612 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,244 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	82,081 / 3.27%
Duplication rate	2.93%
Clipped reads	1,085,083 / 43.28%

2.2. ACGT Content

Number/percentage of A's	42,429,663 / 28.26%
Number/percentage of C's	28,824,414 / 19.2%
Number/percentage of T's	46,242,809 / 30.8%
Number/percentage of G's	32,619,297 / 21.73%
Number/percentage of N's	14,791 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.3639

2.4. Mapping Quality

Mean Mapping Quality	45.39

2.5. Mismatches and indels

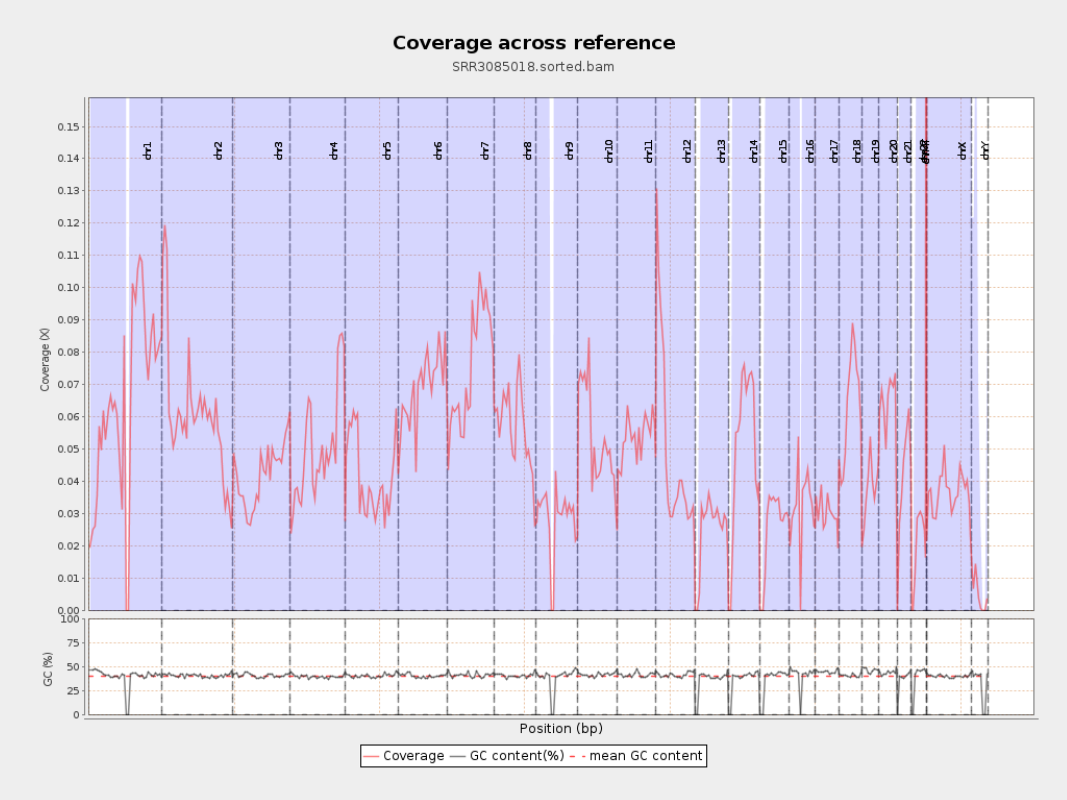
General error rate	0.89%
Mismatches	1,315,304
Insertions	10,544
Mapped reads with at least one insertion	0.46%
Deletions	31,469
Mapped reads with at least one deletion	1.37%
Homopolymer indels	46.14%

2.6. Chromosome stats

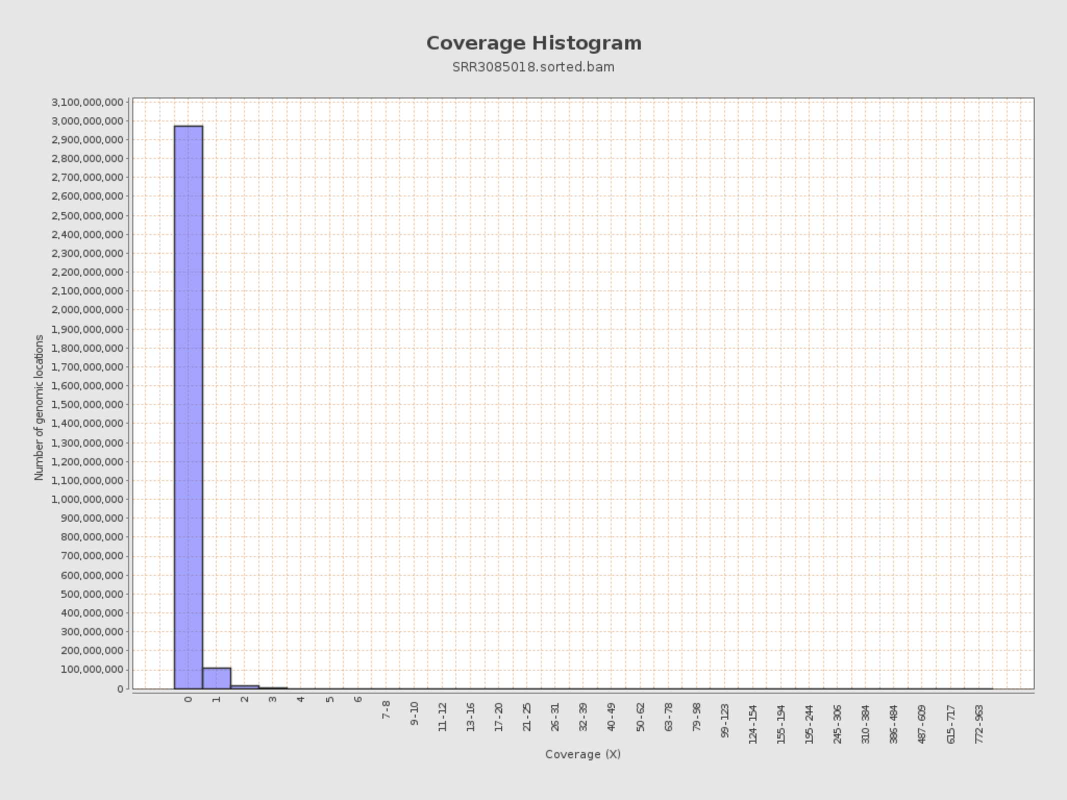
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16068392	0.0645	0.6011
chr2	243199373	14835767	0.061	0.4302
chr3	198022430	8262079	0.0417	0.2368
chr4	191154276	9632792	0.0504	0.2608
chr5	180915260	7575623	0.0419	0.2338
chr6	171115067	11705603	0.0684	0.3637
chr7	159138663	12104609	0.0761	0.3816

chr8	146364022	8286962	0.0566	0.6349
chr9	141213431	4010443	0.0284	0.2771
chr10	135534747	7346808	0.0542	0.457
chr11	135006516	7221562	0.0535	0.359
chr12	133851895	6575603	0.0491	0.2586
chr13	115169878	2860060	0.0248	0.1794
chr14	107349540	5468522	0.0509	0.265
chr15	102531392	2629478	0.0256	0.1927
chr16	90354753	2914093	0.0323	0.2174
chr17	81195210	2456396	0.0303	0.2307
chr18	78077248	5015042	0.0642	0.4735
chr19	59128983	2257036	0.0382	0.401
chr20	63025520	4040419	0.0641	0.2919
chr21	48129895	1982376	0.0412	0.2375
chr22	51304566	996746	0.0194	0.1566
chrMT	16571	12824	0.7739	1.0647
chrX	155270560	5646466	0.0364	0.2443
chrY	59373566	279053	0.0047	0.0949

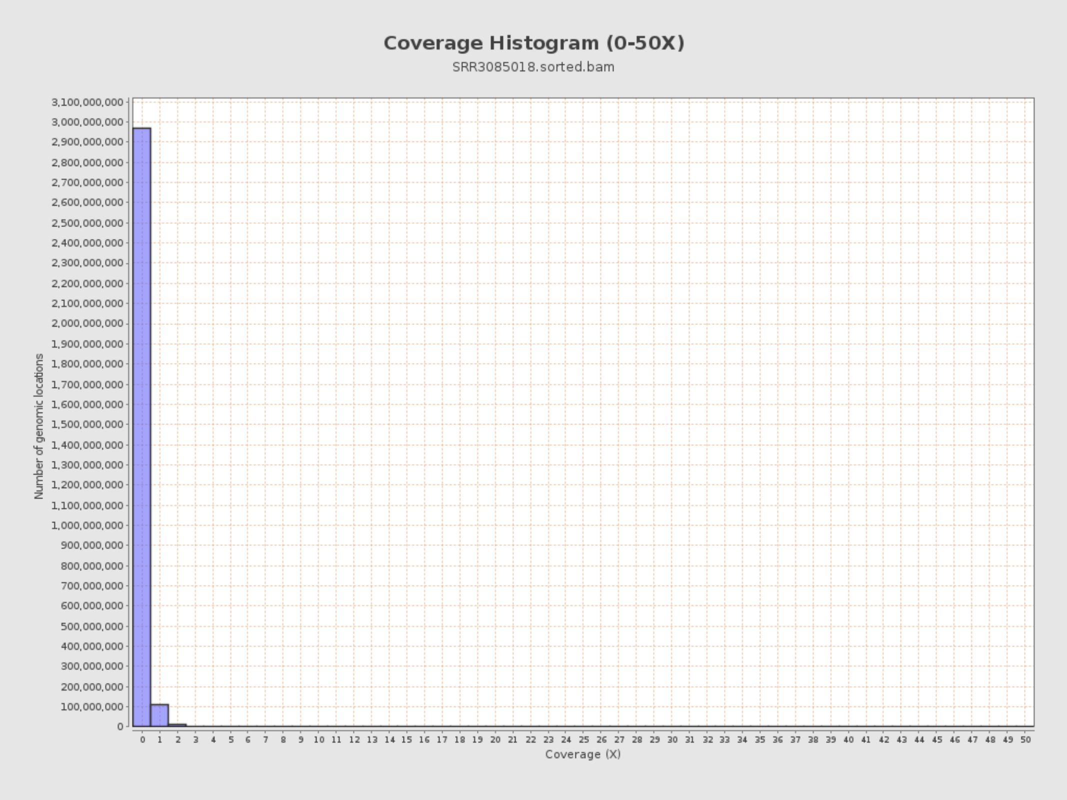
3. Results : Coverage across reference



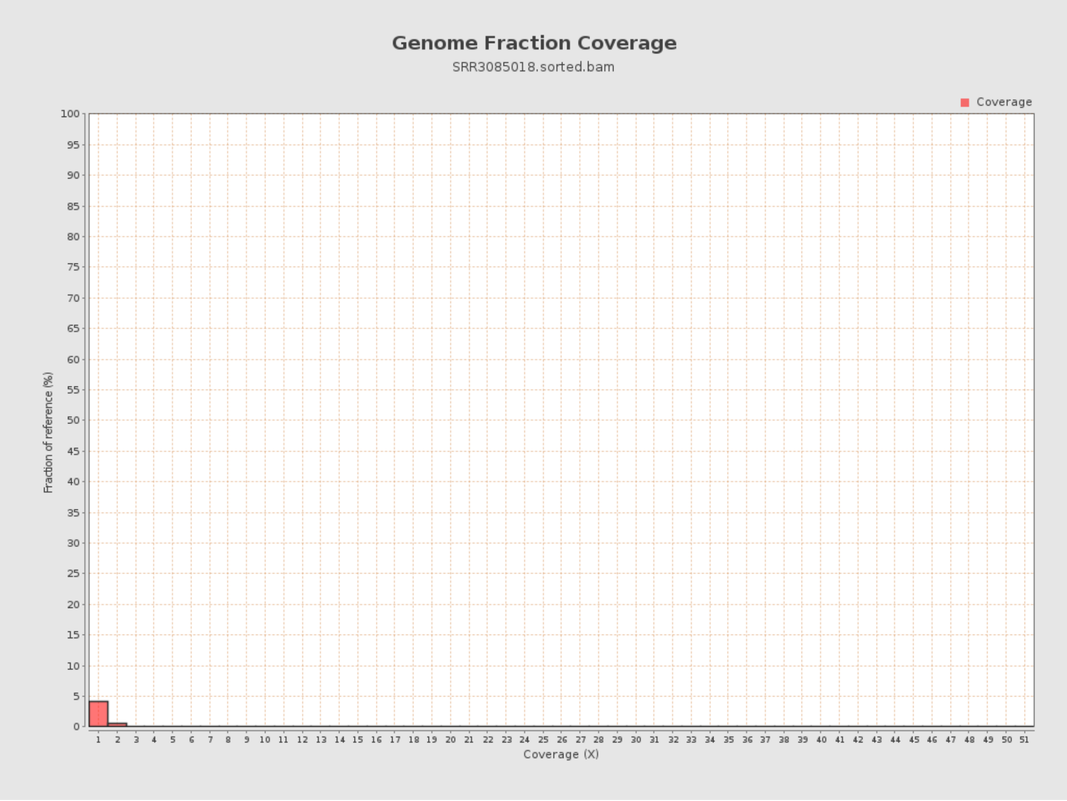
4. Results : Coverage Histogram



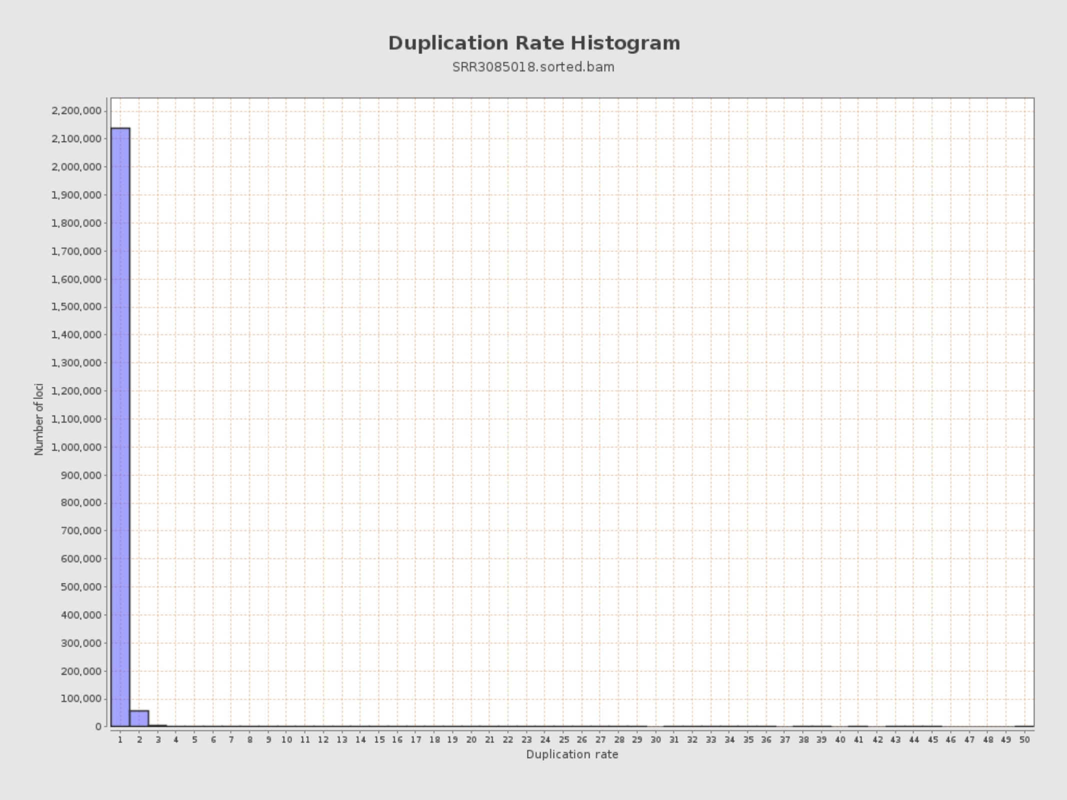
5. Results : Coverage Histogram (0-50X)



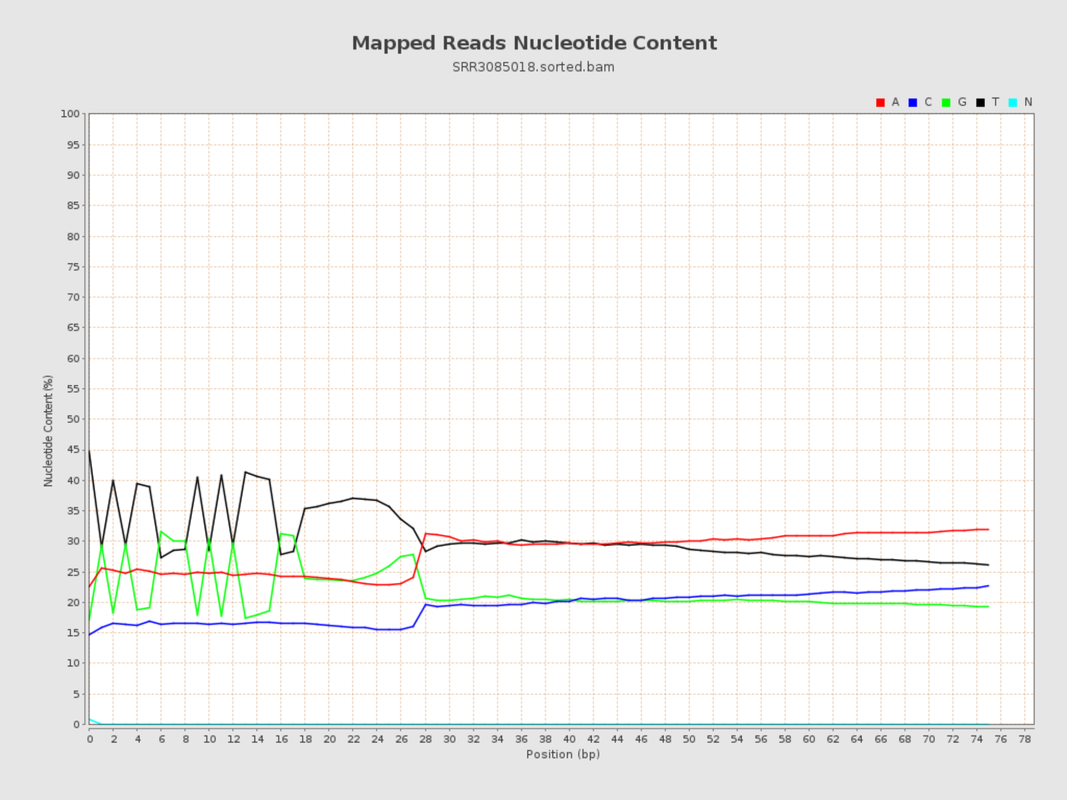
6. Results : Genome Fraction Coverage



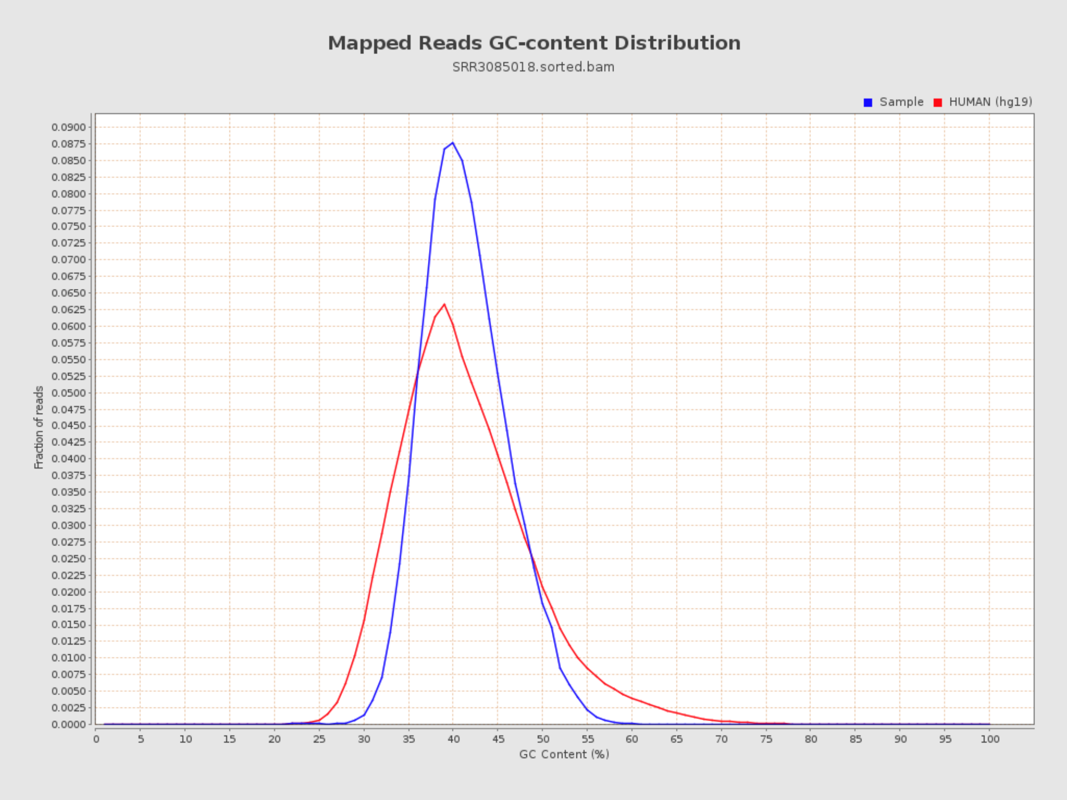
7. Results : Duplication Rate Histogram



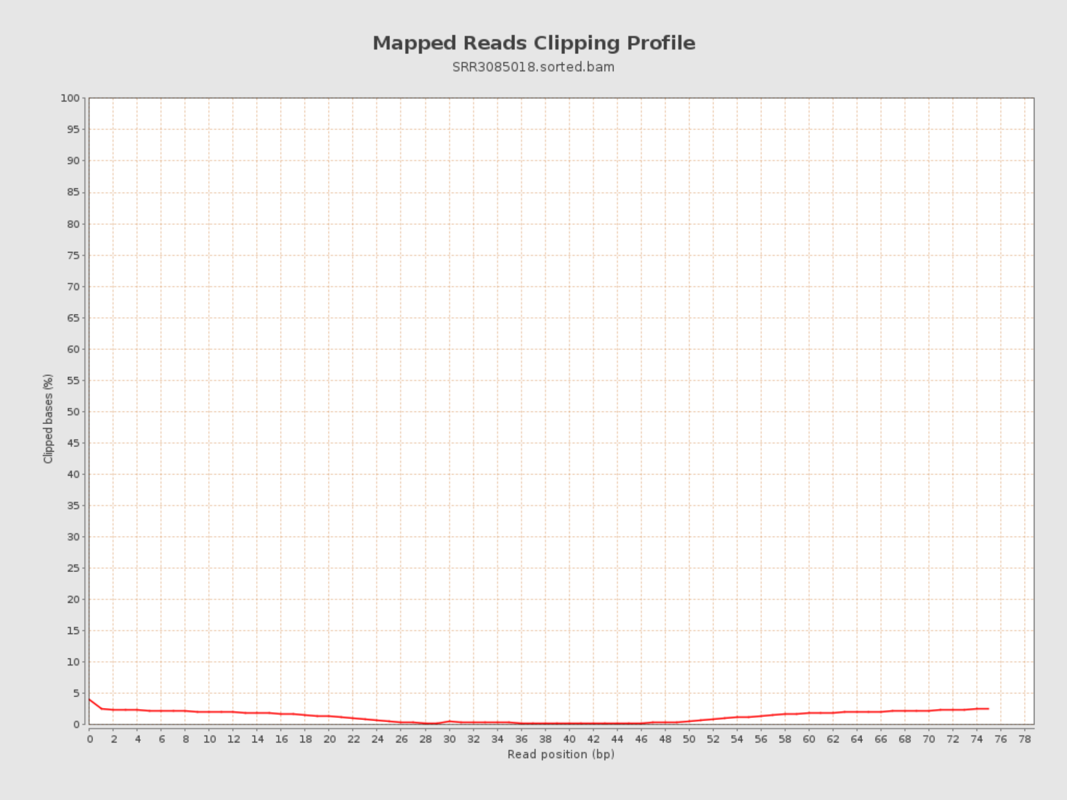
8. Results : Mapped Reads Nucleotide Content



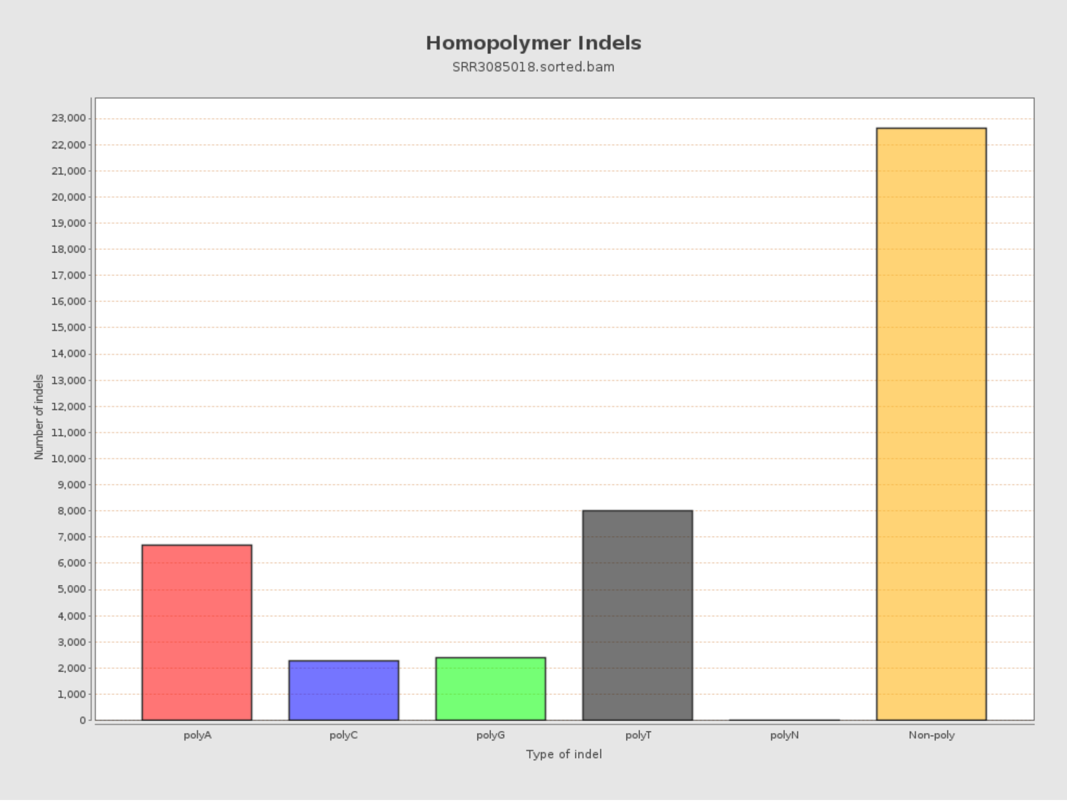
9. Results : Mapped Reads GC-content Distribution



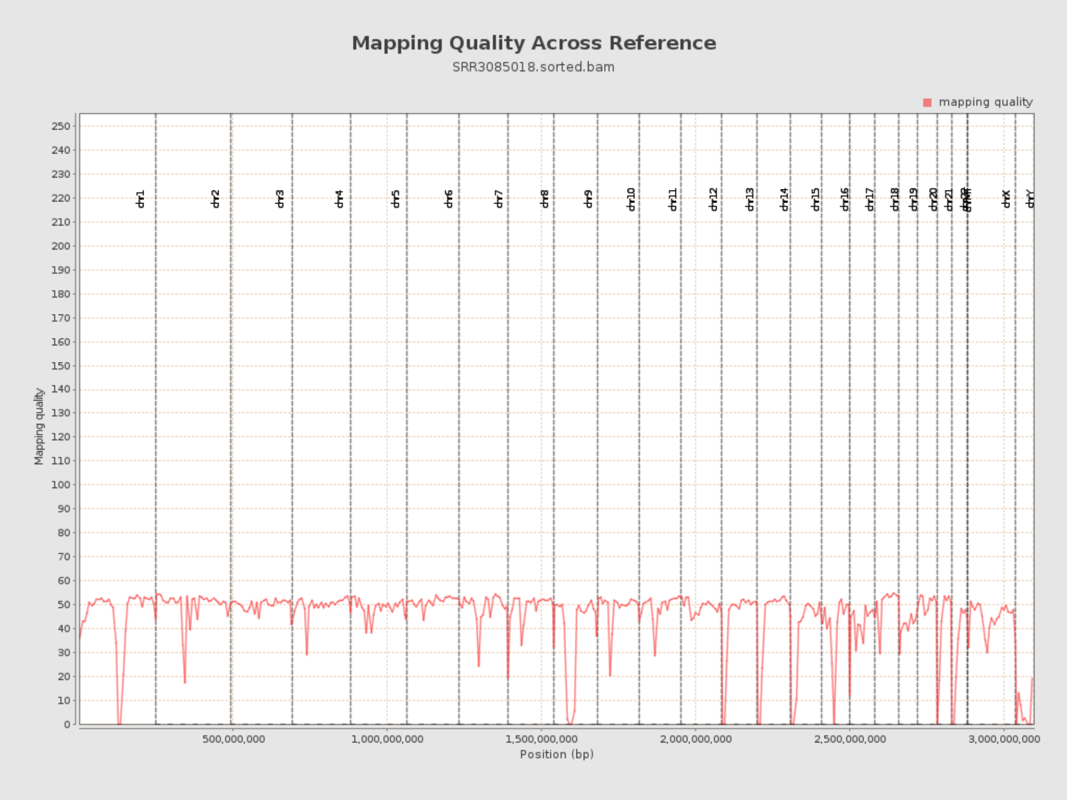
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram