Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 22:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085028.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_SRR3085028 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085028.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 22:43:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085028.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,579,793
Mapped reads	2,344,592 / 90.88%
Unmapped reads	235,201 / 9.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,131 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	77,963 / 3.02%
Duplication rate	2.62%
Clipped reads	1,071,871 / 41.55%

2.2. ACGT Content

Number/percentage of A's	44,017,899 / 28.12%
Number/percentage of C's	30,369,314 / 19.4%
Number/percentage of T's	47,750,179 / 30.5%
Number/percentage of G's	34,395,044 / 21.97%
Number/percentage of N's	7,408 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0506

Standard Deviation	0.3727

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

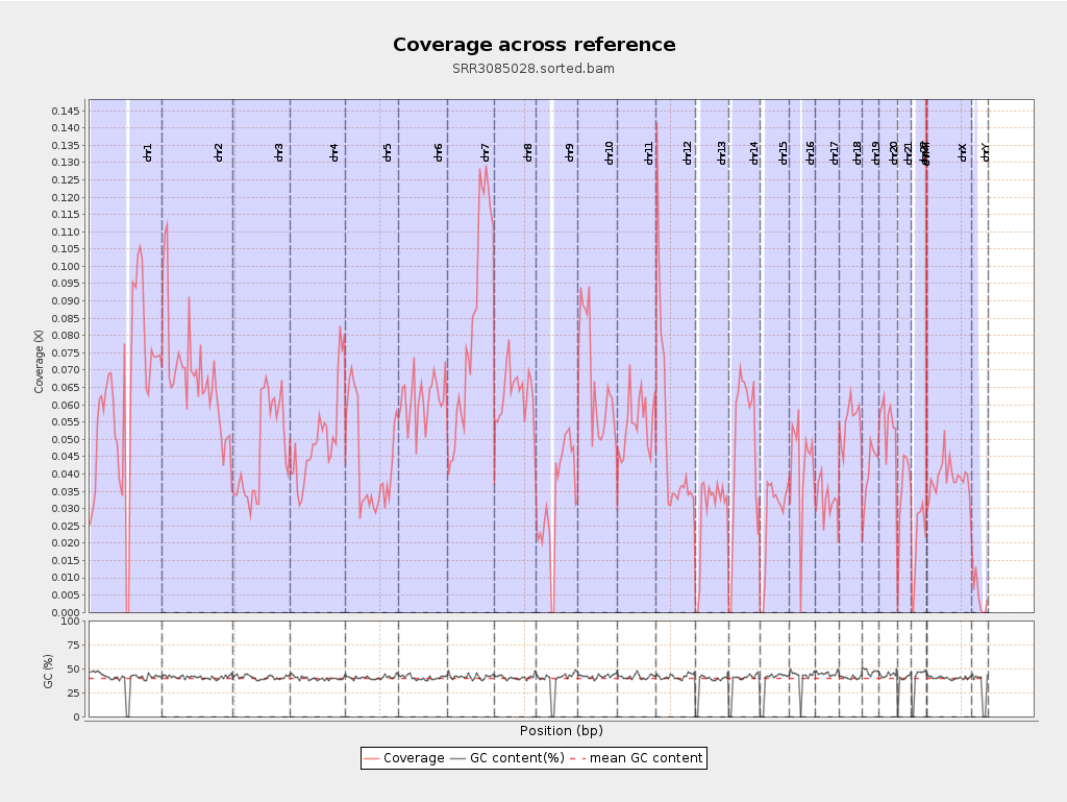
General error rate	0.86%
Mismatches	1,330,383
Insertions	10,908
Mapped reads with at least one insertion	0.46%
Deletions	32,997
Mapped reads with at least one deletion	1.39%
Homopolymer indels	46.16%

2.6. Chromosome stats

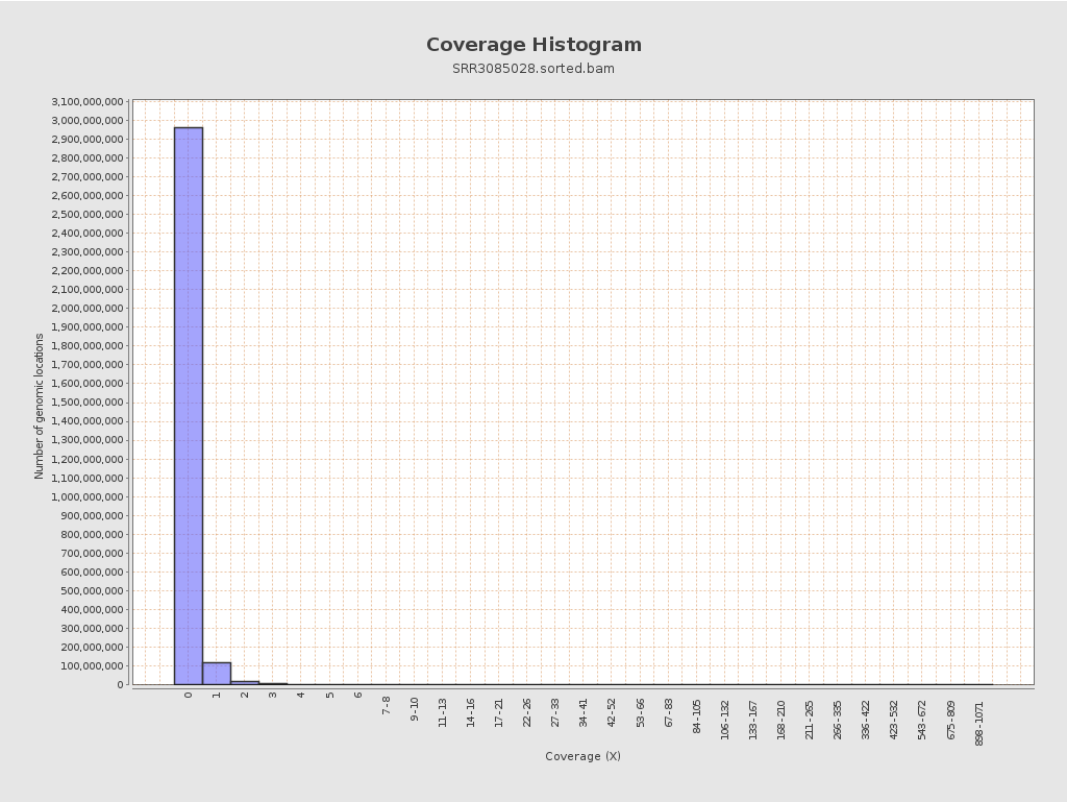
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15504447	0.0622	0.5266
chr2	243199373	16535767	0.068	0.4723
chr3	198022430	9260529	0.0468	0.2489
chr4	191154276	9618931	0.0503	0.2582
chr5	180915260	7906973	0.0437	0.2366
chr6	171115067	10498692	0.0614	0.3351
chr7	159138663	13292364	0.0835	0.4438

chr8	146364022	9223089	0.063	0.6942
chr9	141213431	4676753	0.0331	0.3012
chr10	135534747	9074780	0.067	0.4622
chr11	135006516	7363541	0.0545	0.4024
chr12	133851895	6641764	0.0496	0.2583
chr13	115169878	3277333	0.0285	0.1902
chr14	107349540	5140233	0.0479	0.2598
chr15	102531392	2824409	0.0275	0.1956
chr16	90354753	3861972	0.0427	0.2446
chr17	81195210	2597708	0.032	0.2403
chr18	78077248	4305096	0.0551	0.5304
chr19	59128983	2435477	0.0412	0.394
chr20	63025520	3405704	0.054	0.2665
chr21	48129895	1685189	0.035	0.2182
chr22	51304566	1026007	0.02	0.1572
chrMT	16571	123325	7.4422	5.2558
chrX	155270560	6022702	0.0388	0.2621
chrY	59373566	293368	0.0049	0.0933

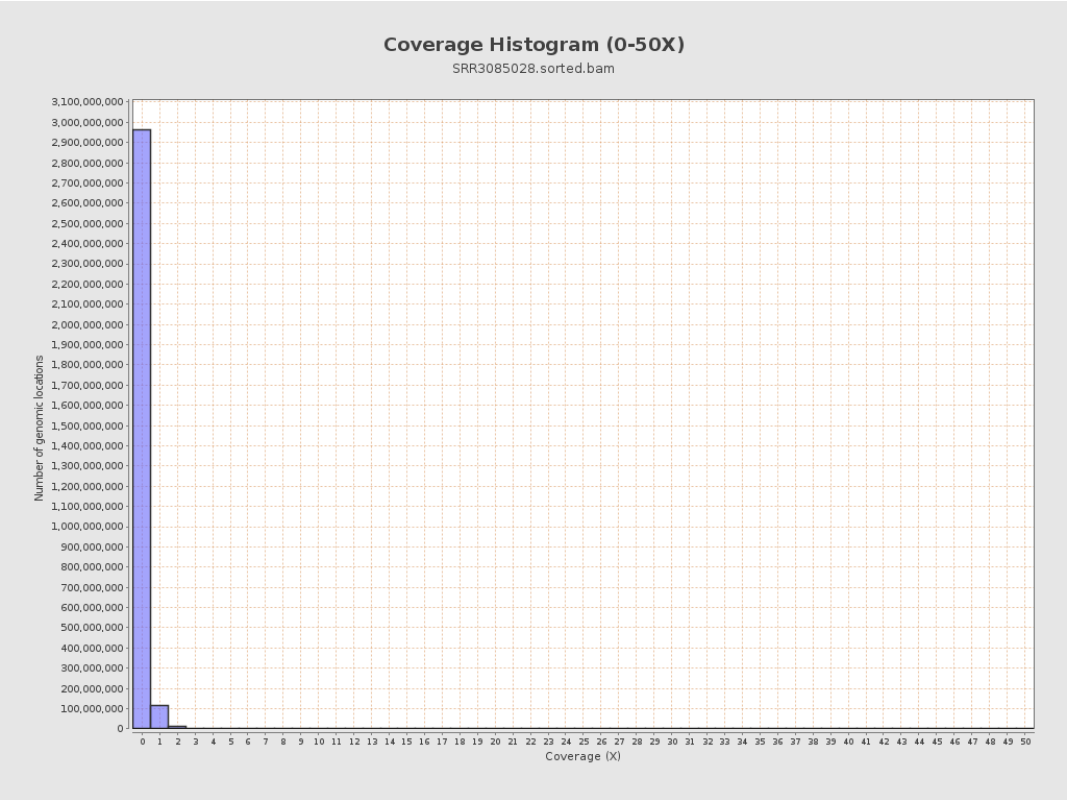
3. Results : Coverage across reference



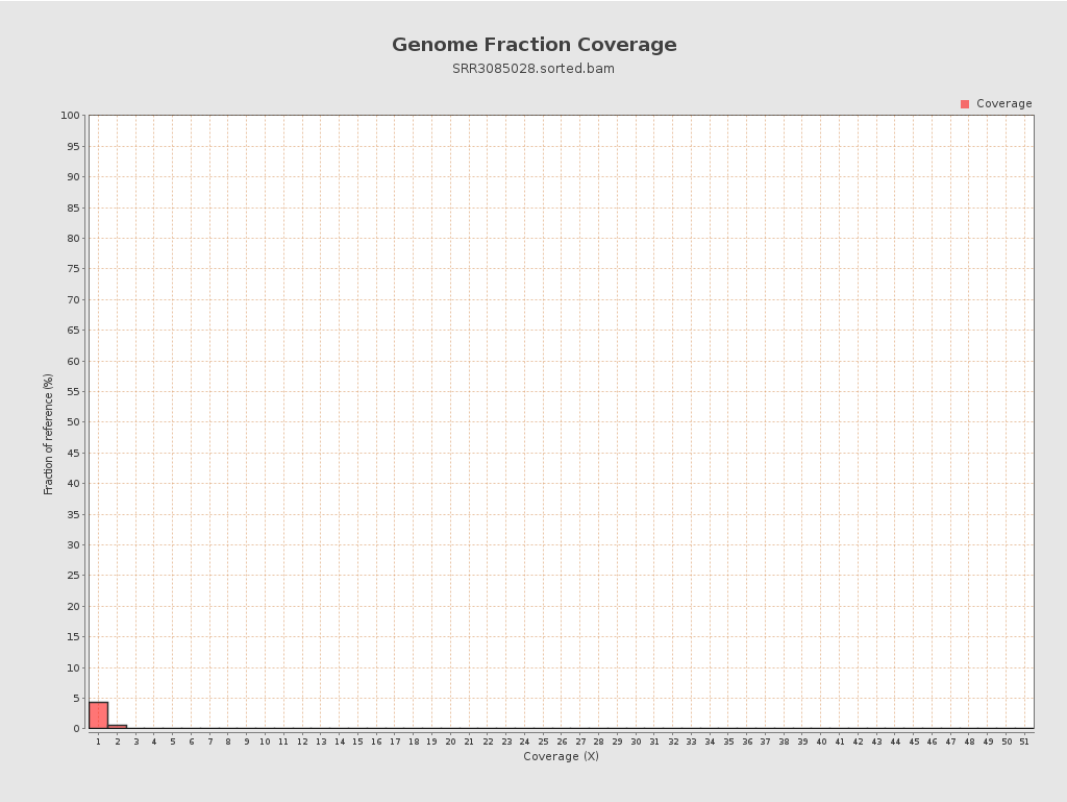
4. Results : Coverage Histogram



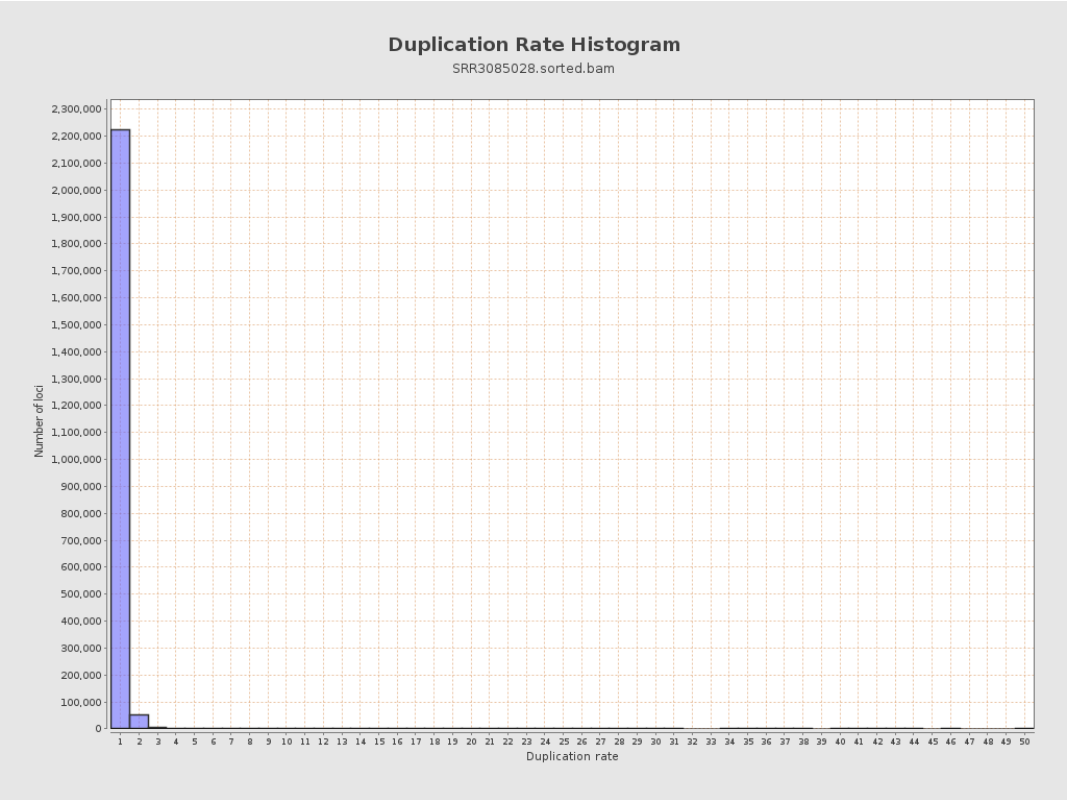
5. Results : Coverage Histogram (0-50X)



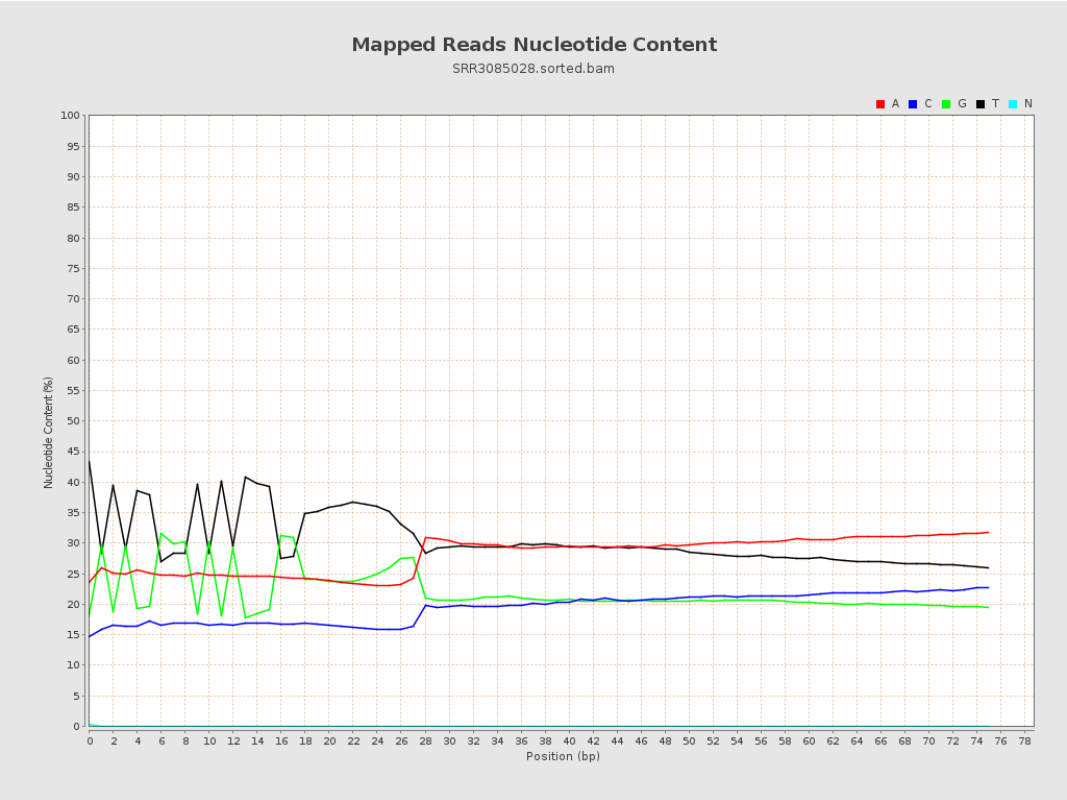
6. Results : Genome Fraction Coverage



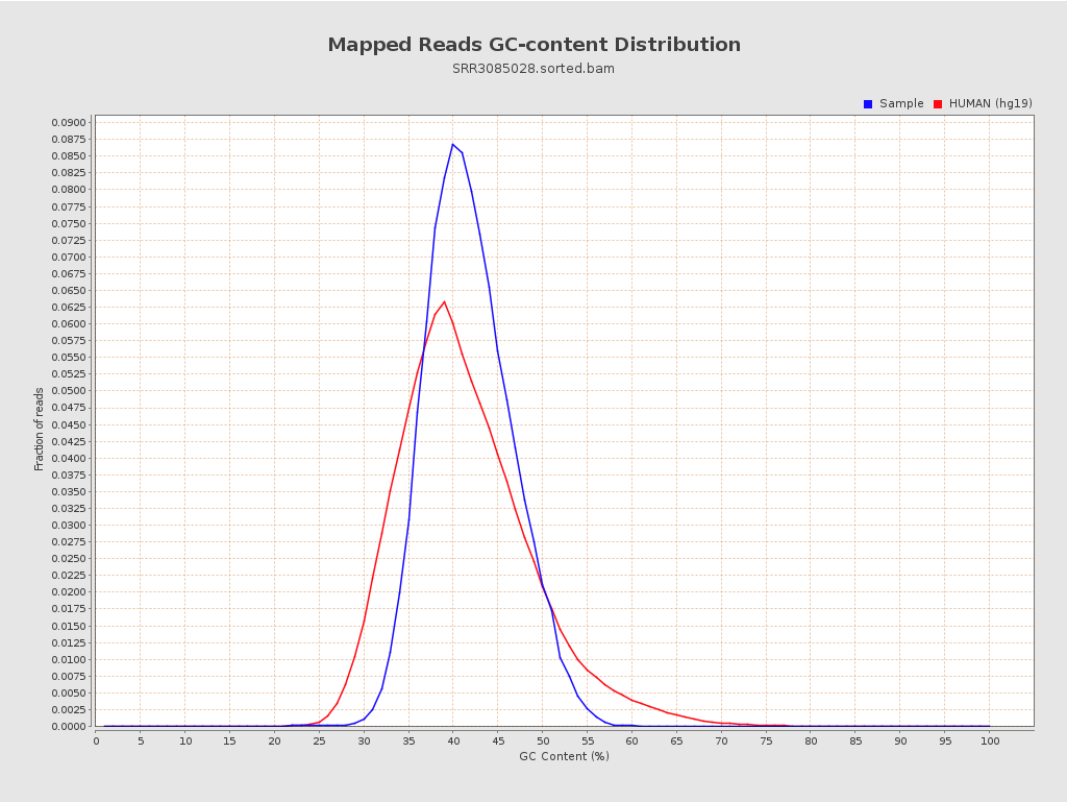
7. Results : Duplication Rate Histogram



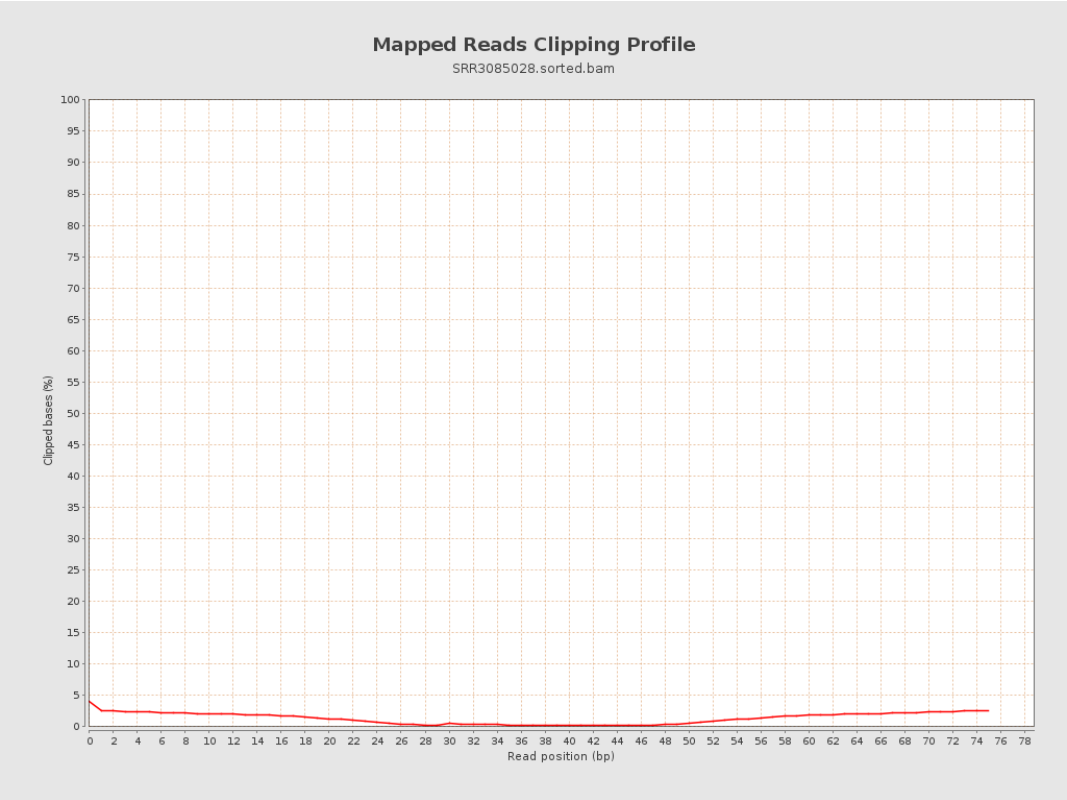
8. Results : Mapped Reads Nucleotide Content



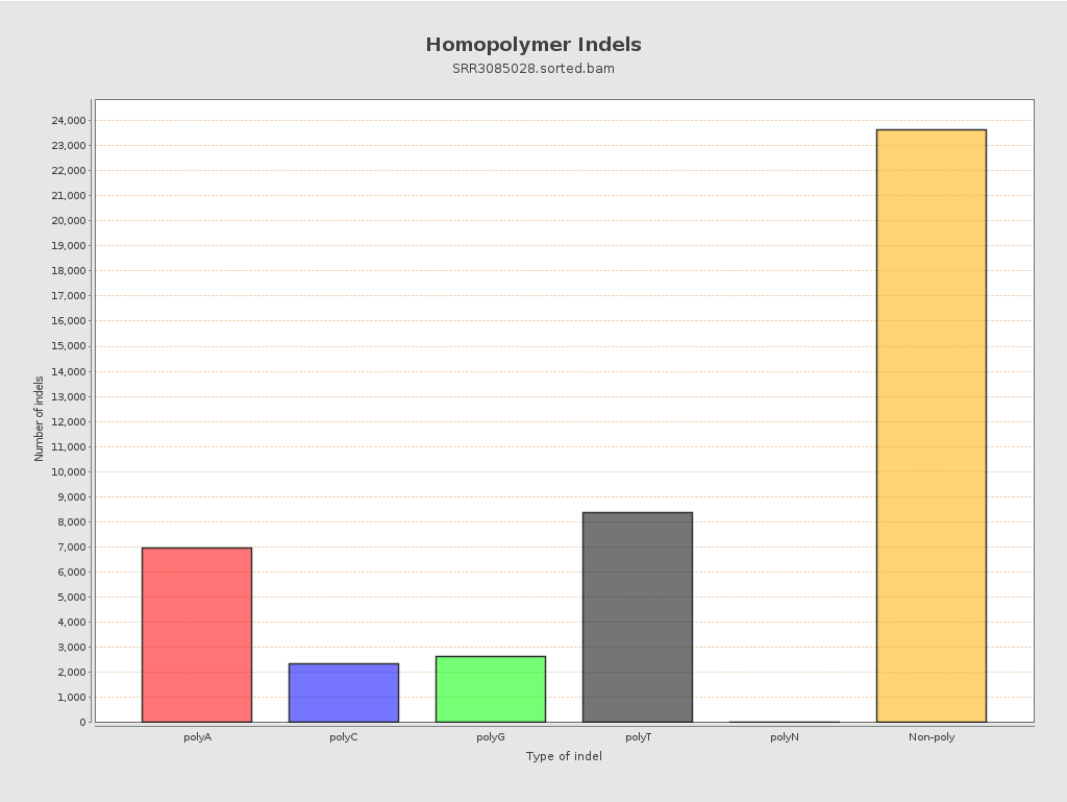
9. Results : Mapped Reads GC-content Distribution



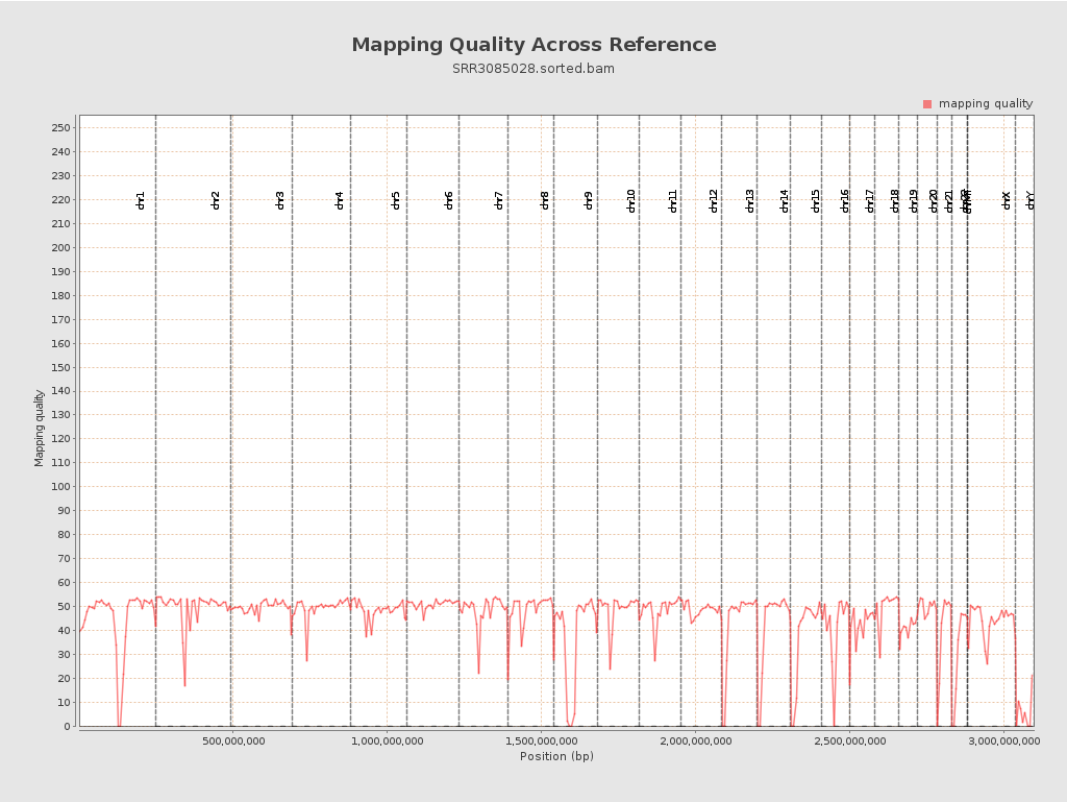
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram