Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 23:27:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085041.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_SRR3085041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 23:27:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,925,390
Mapped reads	1,686,842 / 87.61%
Unmapped reads	238,548 / 12.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,004 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	45,694 / 2.37%
Duplication rate	2.03%
Clipped reads	610,074 / 31.69%

2.2. ACGT Content

Number/percentage of A's	34,324,716 / 29.57%
Number/percentage of C's	21,274,239 / 18.32%
Number/percentage of T's	36,495,800 / 31.44%
Number/percentage of G's	23,991,143 / 20.66%
Number/percentage of N's	13,214 / 0.01%
GC Percentage	38.99%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3512

2.4. Mapping Quality

Mean Mapping Quality	46.75

2.5. Mismatches and indels

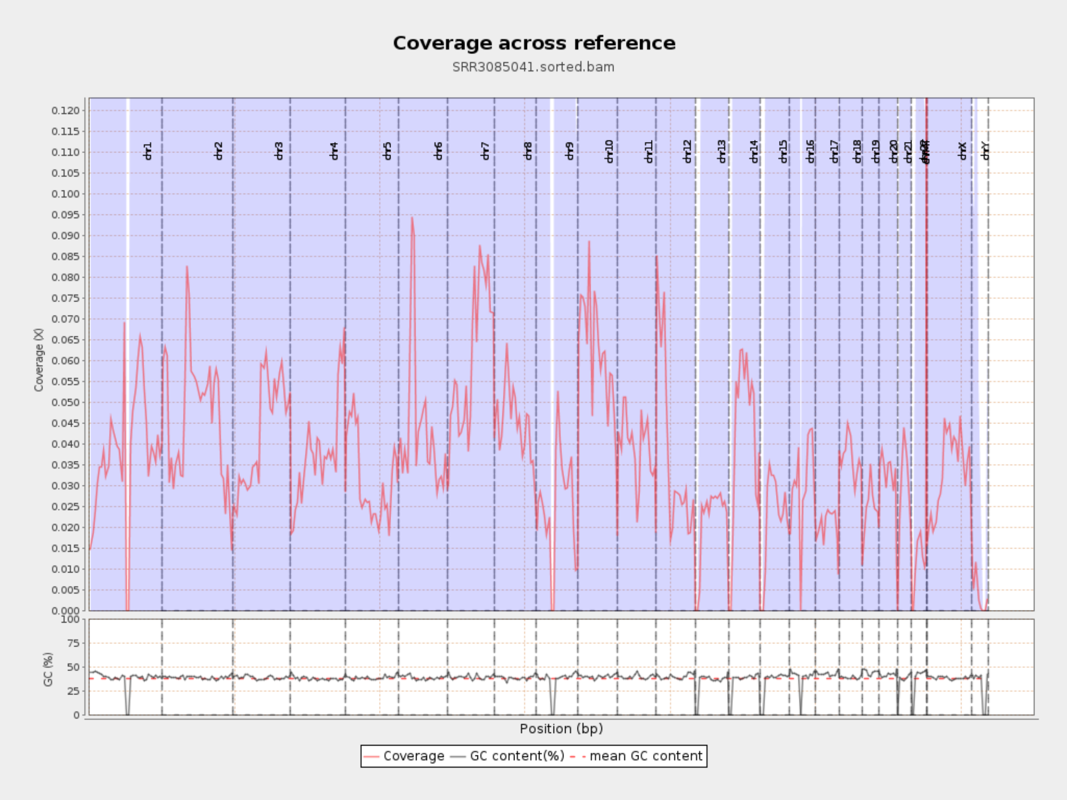
General error rate	0.91%
Mismatches	1,040,242
Insertions	8,936
Mapped reads with at least one insertion	0.53%
Deletions	26,177
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.87%

2.6. Chromosome stats

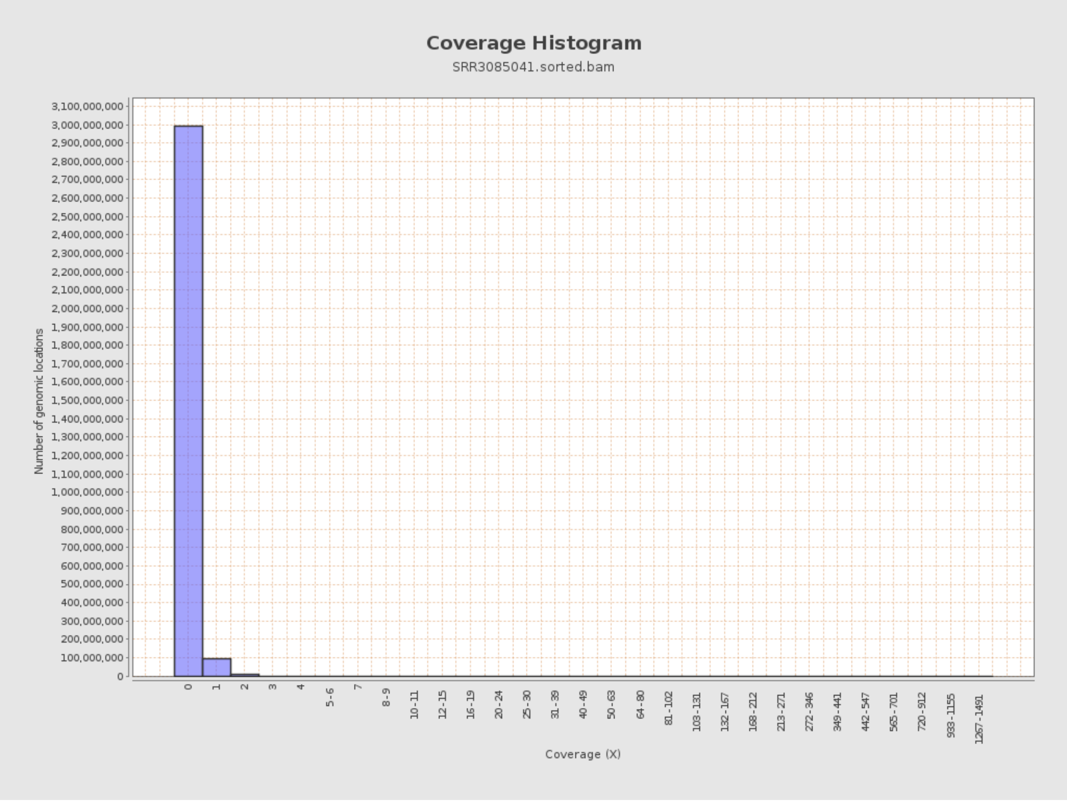
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9552799	0.0383	0.5056
chr2	243199373	11427767	0.047	0.343
chr3	198022430	8454027	0.0427	0.2332
chr4	191154276	7284776	0.0381	0.2178
chr5	180915260	5714567	0.0316	0.195
chr6	171115067	7492825	0.0438	0.2856
chr7	159138663	9792105	0.0615	0.3219

chr8	146364022	6614609	0.0452	0.9157
chr9	141213431	3655413	0.0259	0.2656
chr10	135534747	8535586	0.063	0.4552
chr11	135006516	5269817	0.039	0.3139
chr12	133851895	5017096	0.0375	0.2151
chr13	115169878	2456951	0.0213	0.1589
chr14	107349540	4496974	0.0419	0.2309
chr15	102531392	2281905	0.0223	0.1635
chr16	90354753	2750316	0.0304	0.2026
chr17	81195210	1644803	0.0203	0.1788
chr18	78077248	2854883	0.0366	0.4369
chr19	59128983	1469279	0.0248	0.3264
chr20	63025520	2068242	0.0328	0.1999
chr21	48129895	1357090	0.0282	0.1906
chr22	51304566	556307	0.0108	0.1119
chrMT	16571	3972	0.2397	0.513
chrX	155270560	5176443	0.0333	0.2188
chrY	59373566	215885	0.0036	0.0821

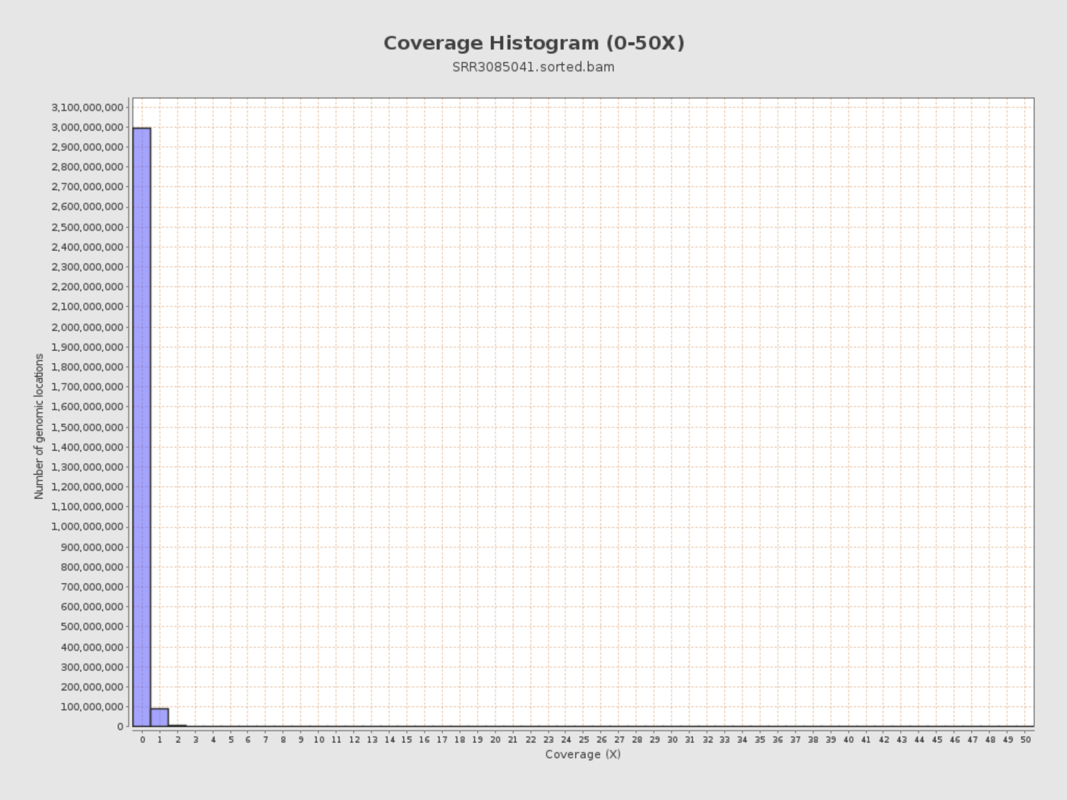
3. Results : Coverage across reference



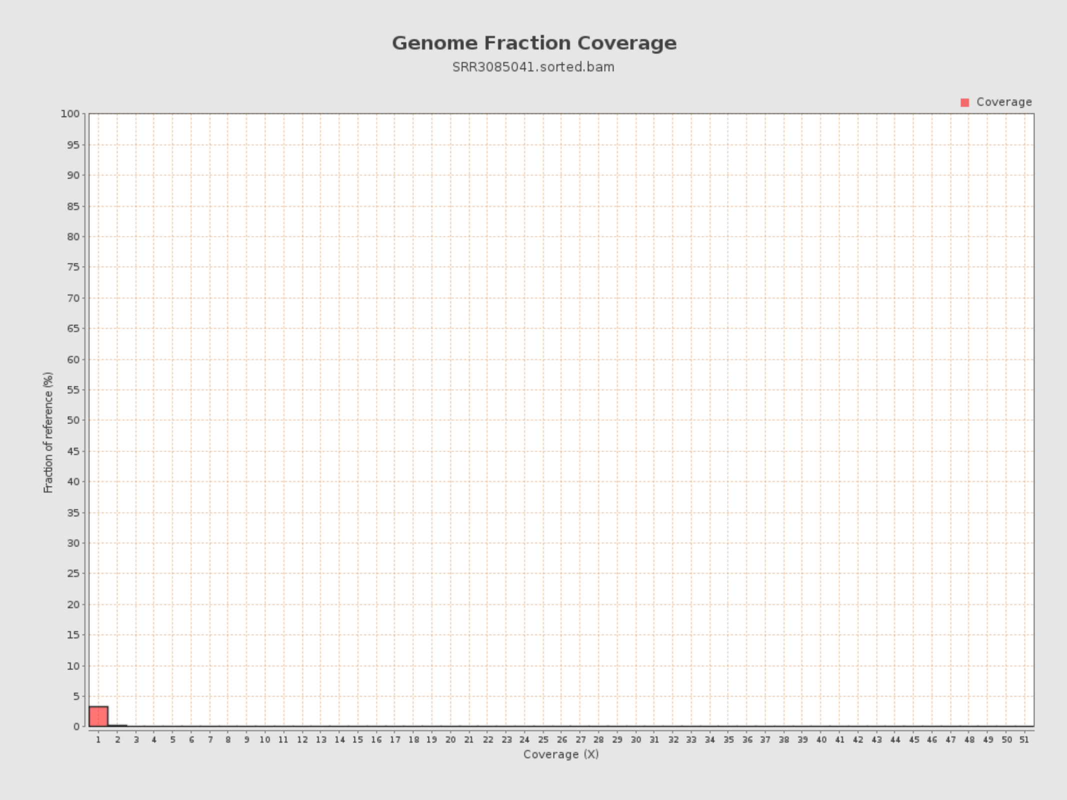
4. Results : Coverage Histogram



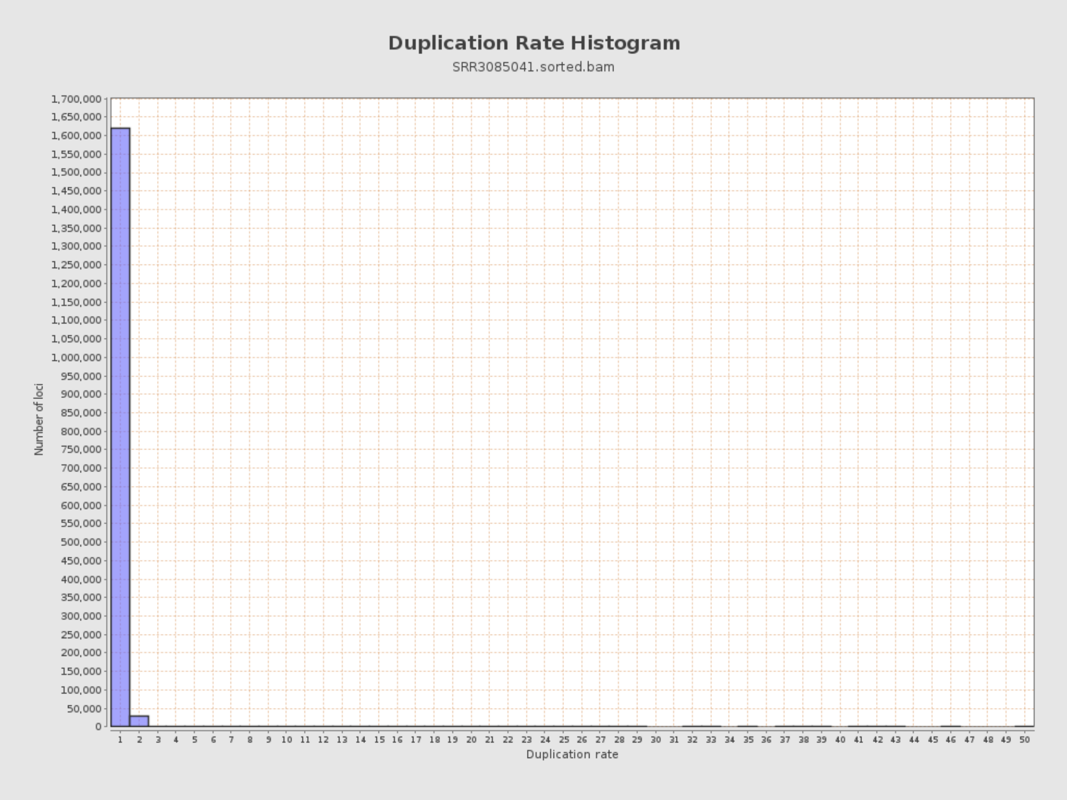
5. Results : Coverage Histogram (0-50X)



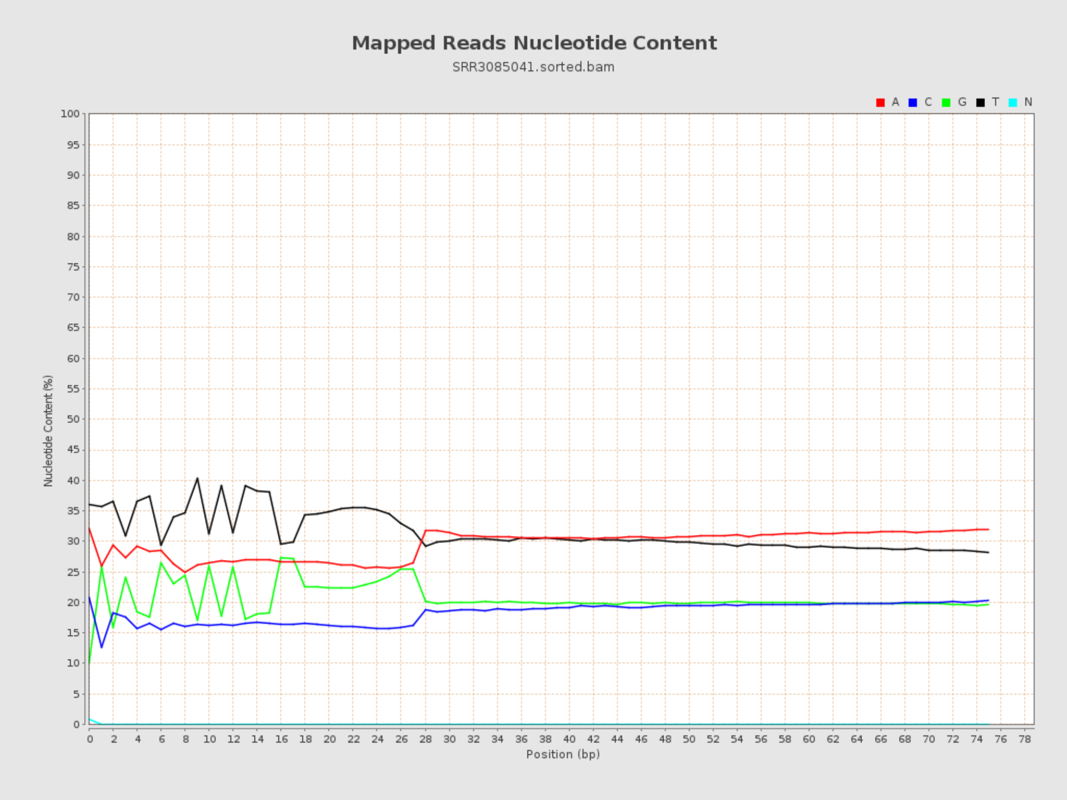
6. Results : Genome Fraction Coverage



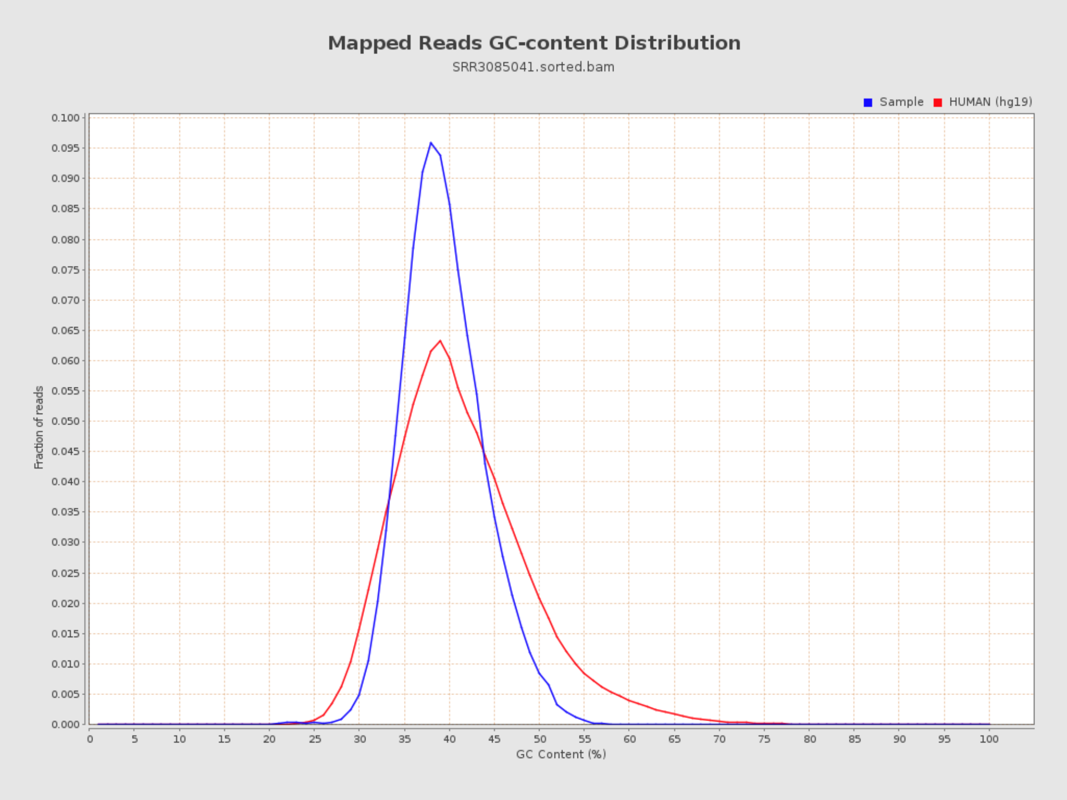
7. Results : Duplication Rate Histogram



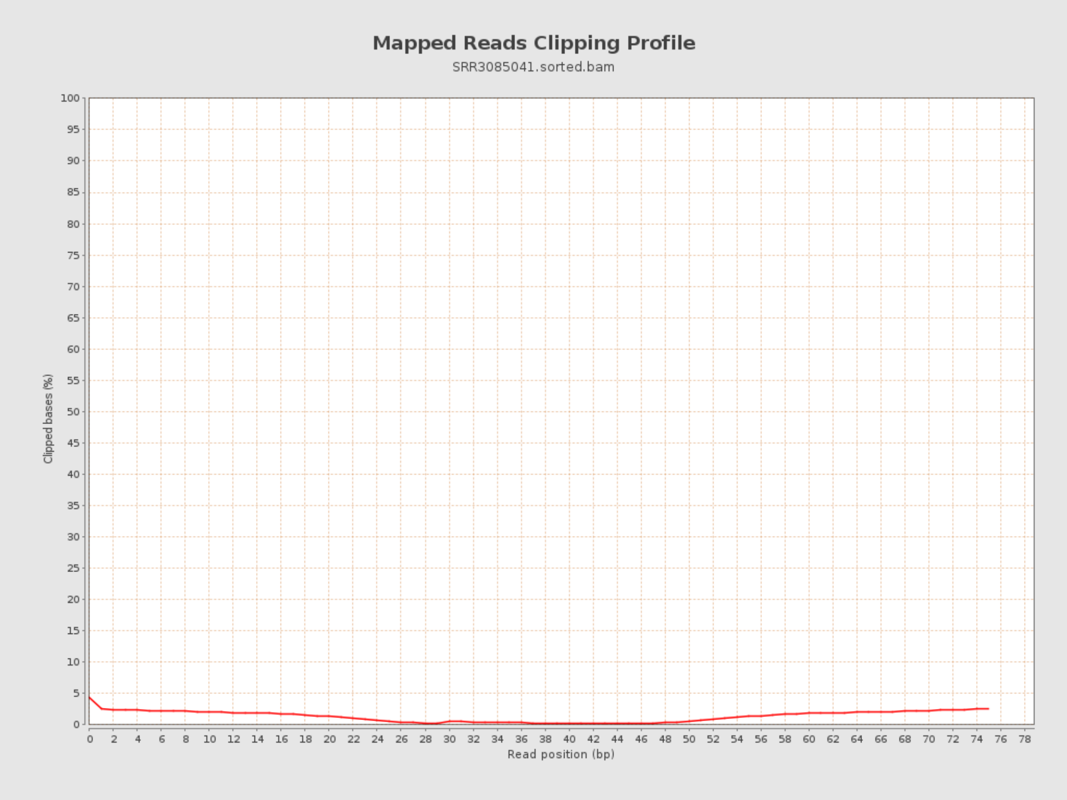
8. Results : Mapped Reads Nucleotide Content



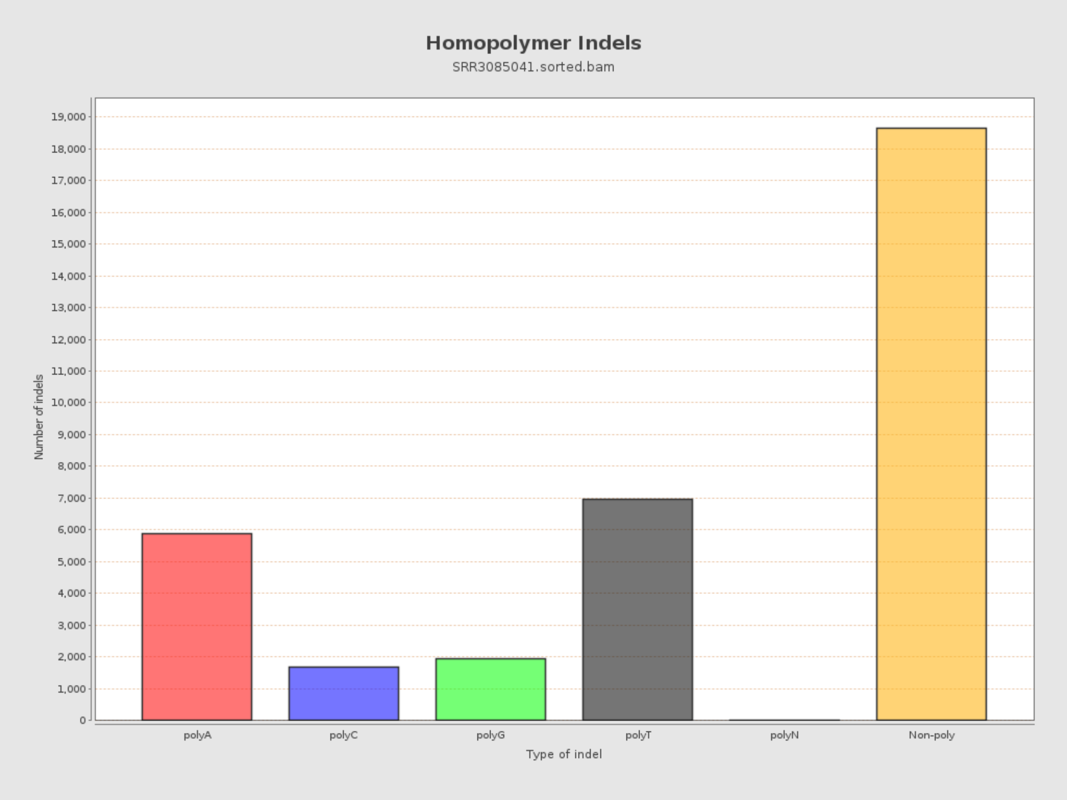
9. Results : Mapped Reads GC-content Distribution



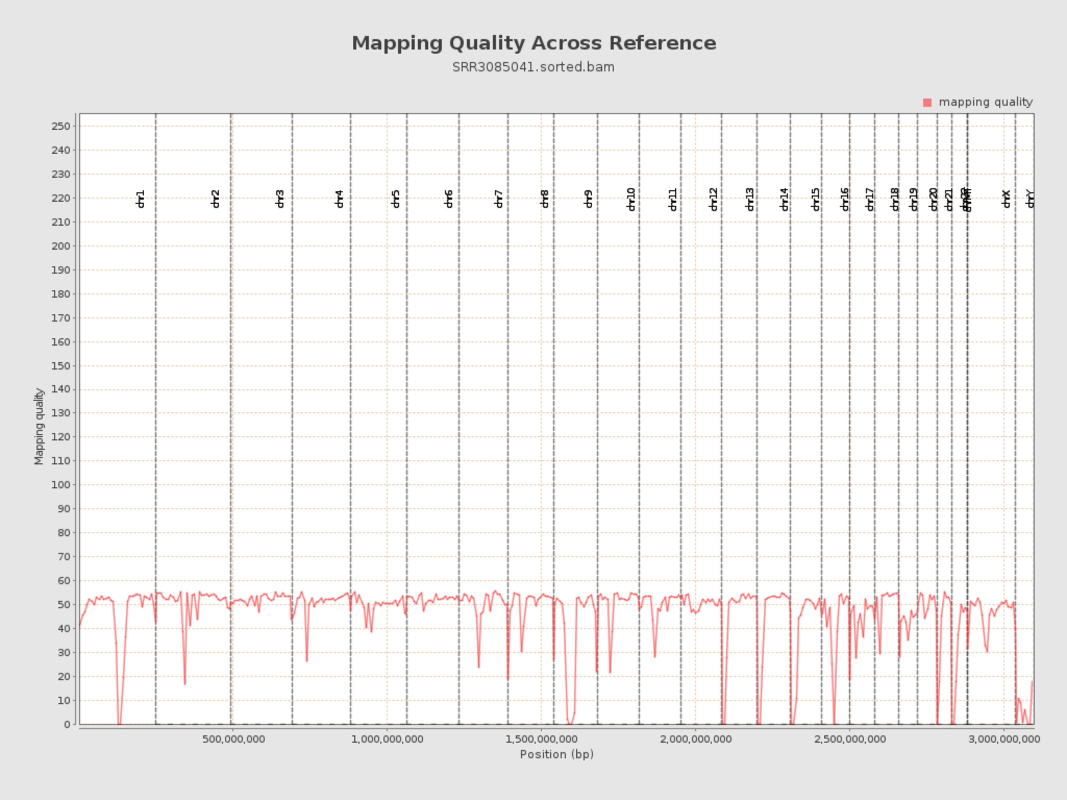
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram