Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 21:21:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085003.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_SRR3085003 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085003.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 21:21:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3085003.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,596,917
Mapped reads	2,425,954 / 93.42%
Unmapped reads	170,963 / 6.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,542 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	95,773 / 3.69%
Duplication rate	2.88%
Clipped reads	775,726 / 29.87%

2.2. ACGT Content

Number/percentage of A's	50,202,270 / 29.58%
Number/percentage of C's	31,576,560 / 18.6%
Number/percentage of T's	53,723,950 / 31.65%
Number/percentage of G's	34,205,171 / 20.15%
Number/percentage of N's	25,009 / 0.01%
GC Percentage	38.76%

2.3. Coverage

Mean	0.0549

Standard Deviation	0.5268

2.4. Mapping Quality

Mean Mapping Quality	47.99

2.5. Mismatches and indels

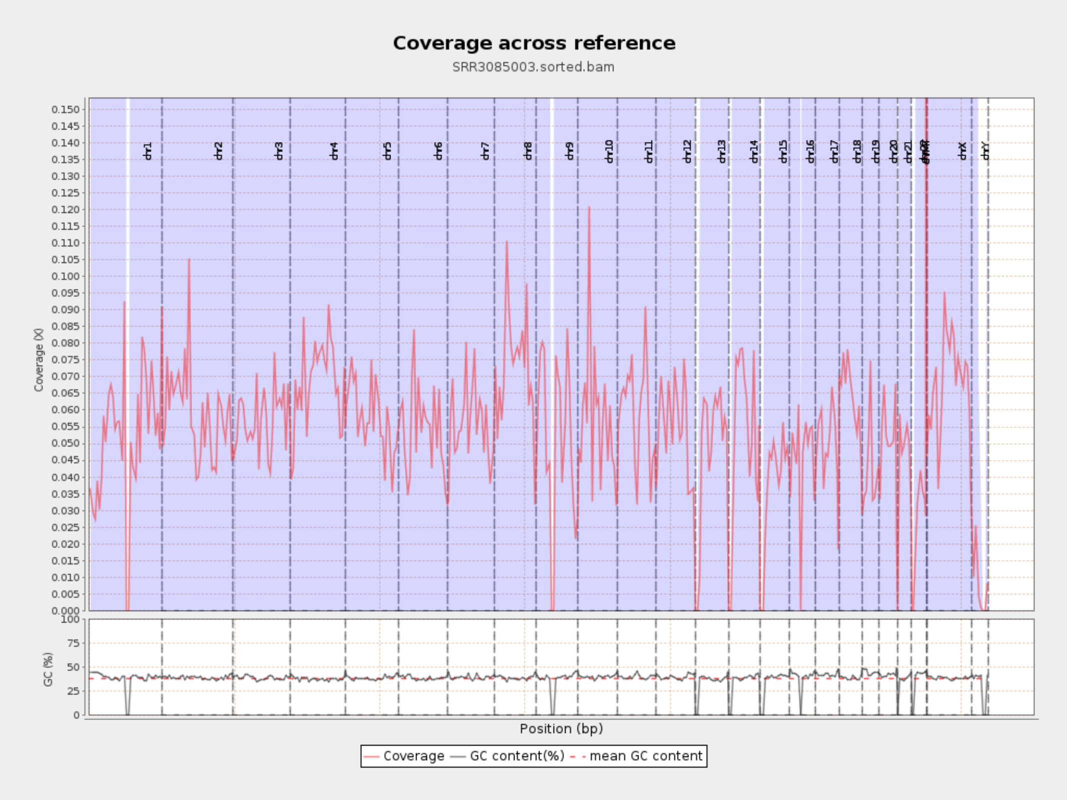
General error rate	0.84%
Mismatches	1,395,951
Insertions	14,192
Mapped reads with at least one insertion	0.58%
Deletions	41,023
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.78%

2.6. Chromosome stats

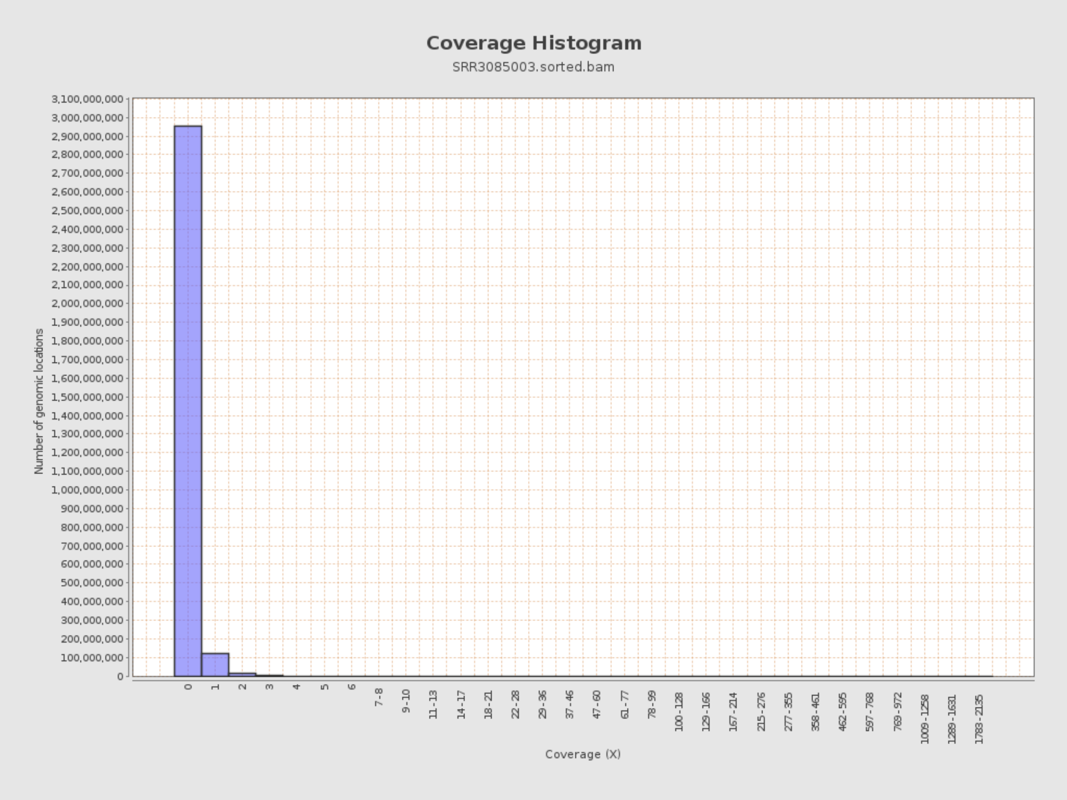
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12809108	0.0514	0.8675
chr2	243199373	14355229	0.059	0.4973
chr3	198022430	11307848	0.0571	0.2929
chr4	191154276	13103796	0.0686	0.32
chr5	180915260	10464346	0.0578	0.2812
chr6	171115067	9324462	0.0545	0.3481
chr7	159138663	9003437	0.0566	0.3886

chr8	146364022	10660502	0.0728	1.3071
chr9	141213431	7377832	0.0522	0.4842
chr10	135534747	7797870	0.0575	0.6232
chr11	135006516	8021574	0.0594	0.4086
chr12	133851895	7292418	0.0545	0.2767
chr13	115169878	5401822	0.0469	0.2467
chr14	107349540	5537930	0.0516	0.2918
chr15	102531392	3831605	0.0374	0.2213
chr16	90354753	4074839	0.0451	0.3189
chr17	81195210	4006623	0.0493	0.3025
chr18	78077248	5061970	0.0648	0.8933
chr19	59128983	2526658	0.0427	0.5303
chr20	63025520	3294762	0.0523	0.2738
chr21	48129895	2169060	0.0451	0.2821
chr22	51304566	1296839	0.0253	0.1798
chrMT	16571	21358	1.2889	1.3881
chrX	155270560	10587740	0.0682	0.3403
chrY	59373566	470424	0.0079	0.1747

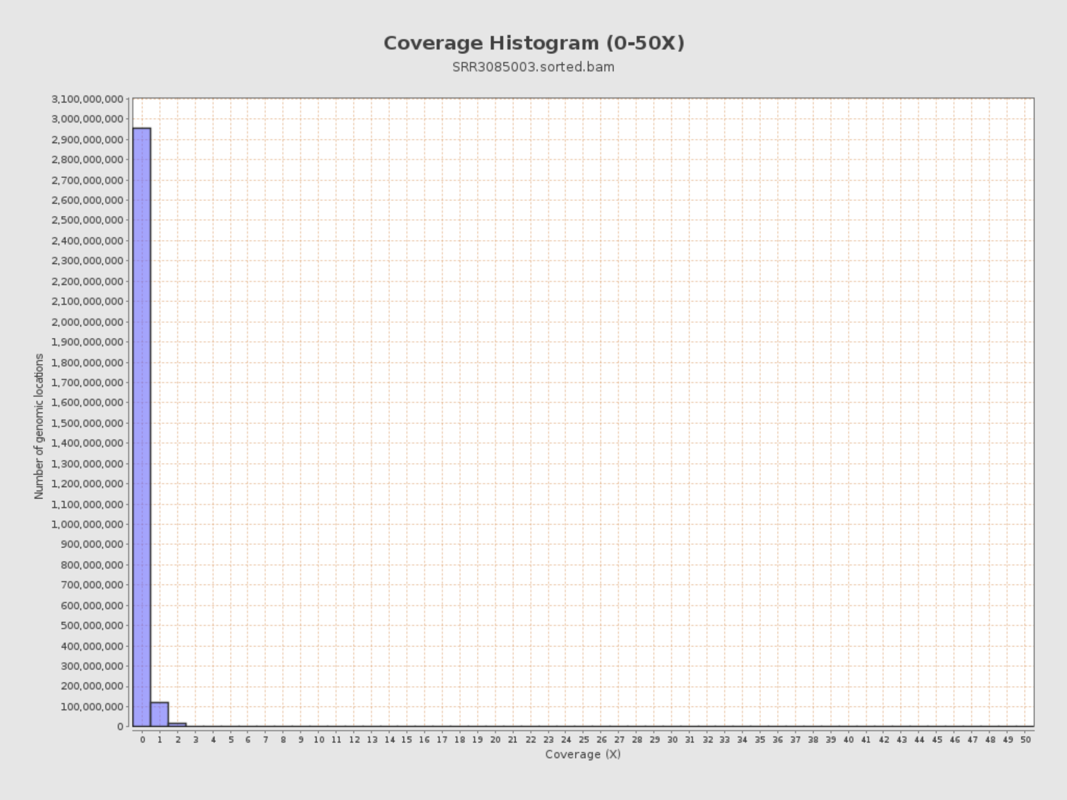
3. Results : Coverage across reference



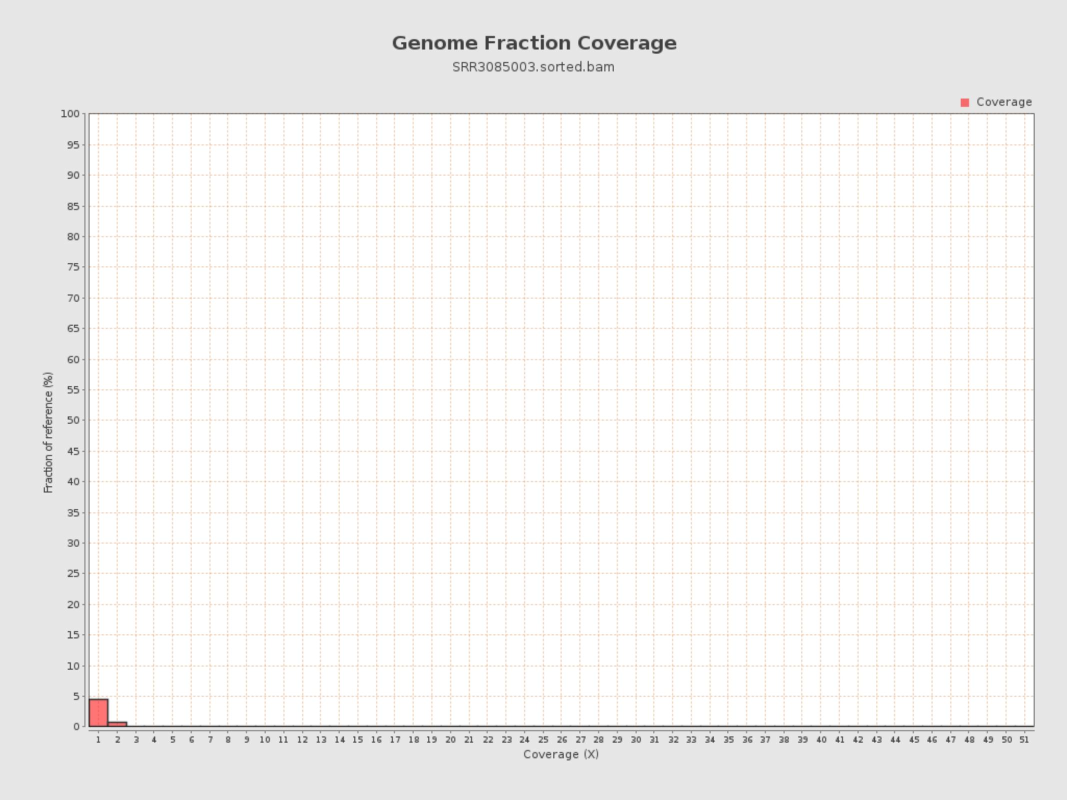
4. Results : Coverage Histogram



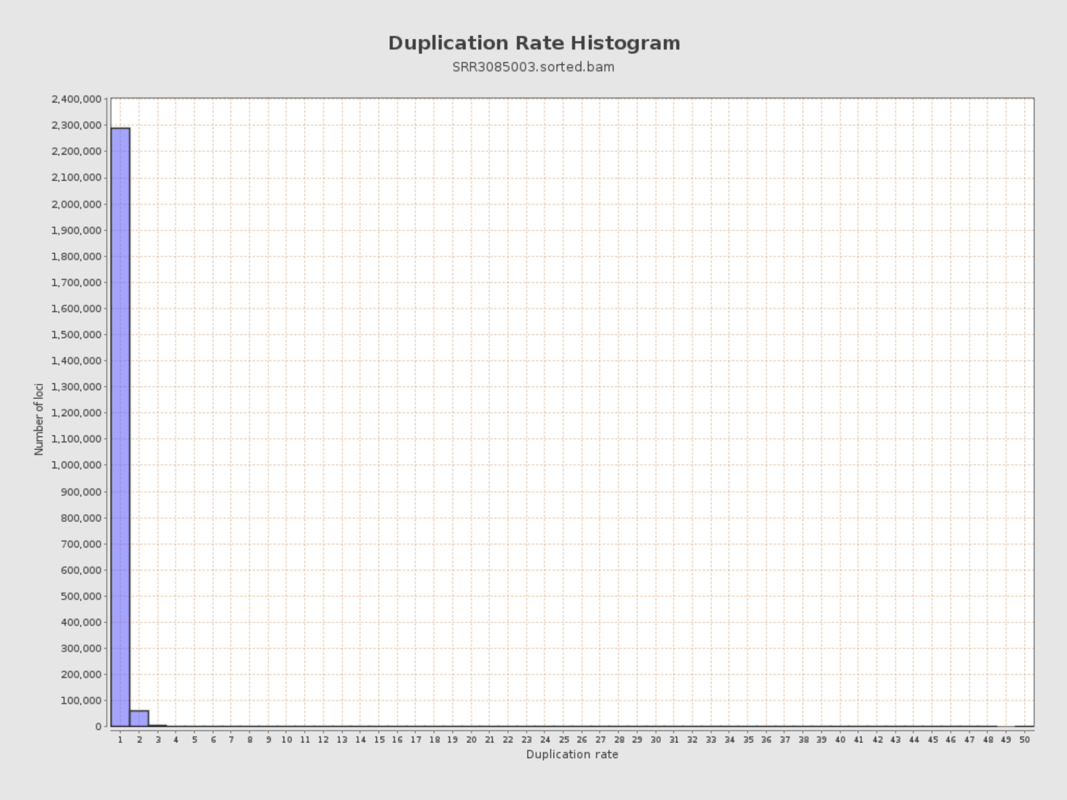
5. Results : Coverage Histogram (0-50X)



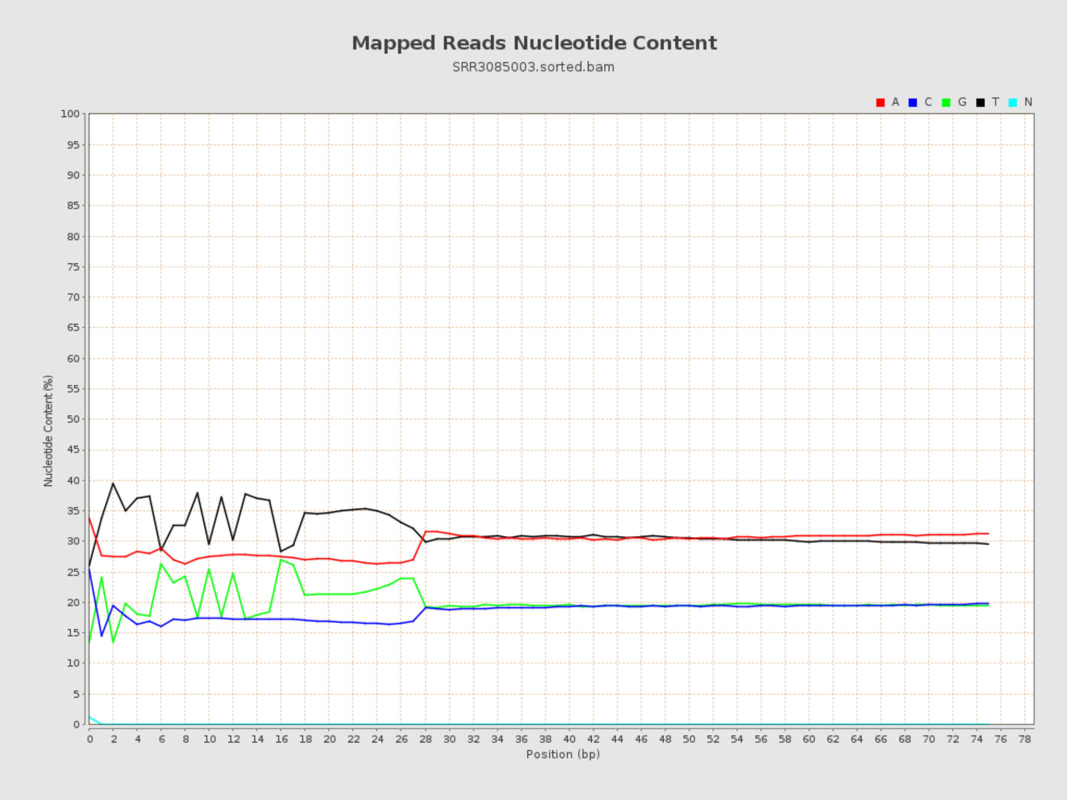
6. Results : Genome Fraction Coverage



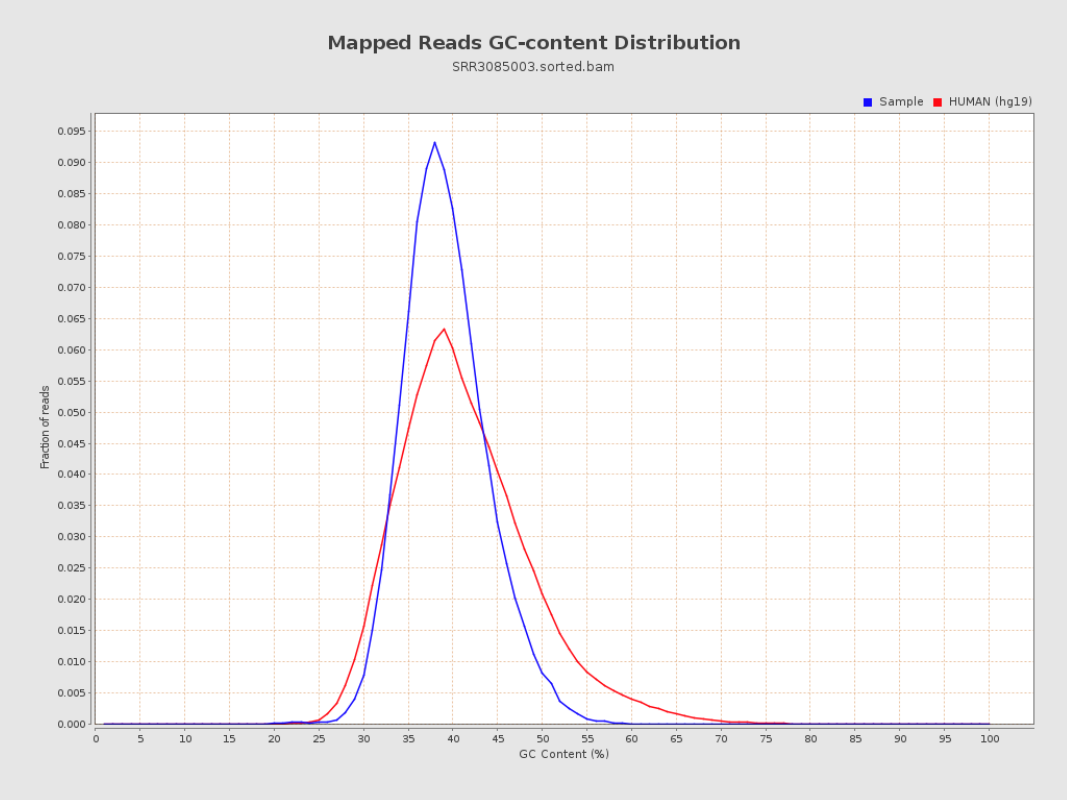
7. Results : Duplication Rate Histogram



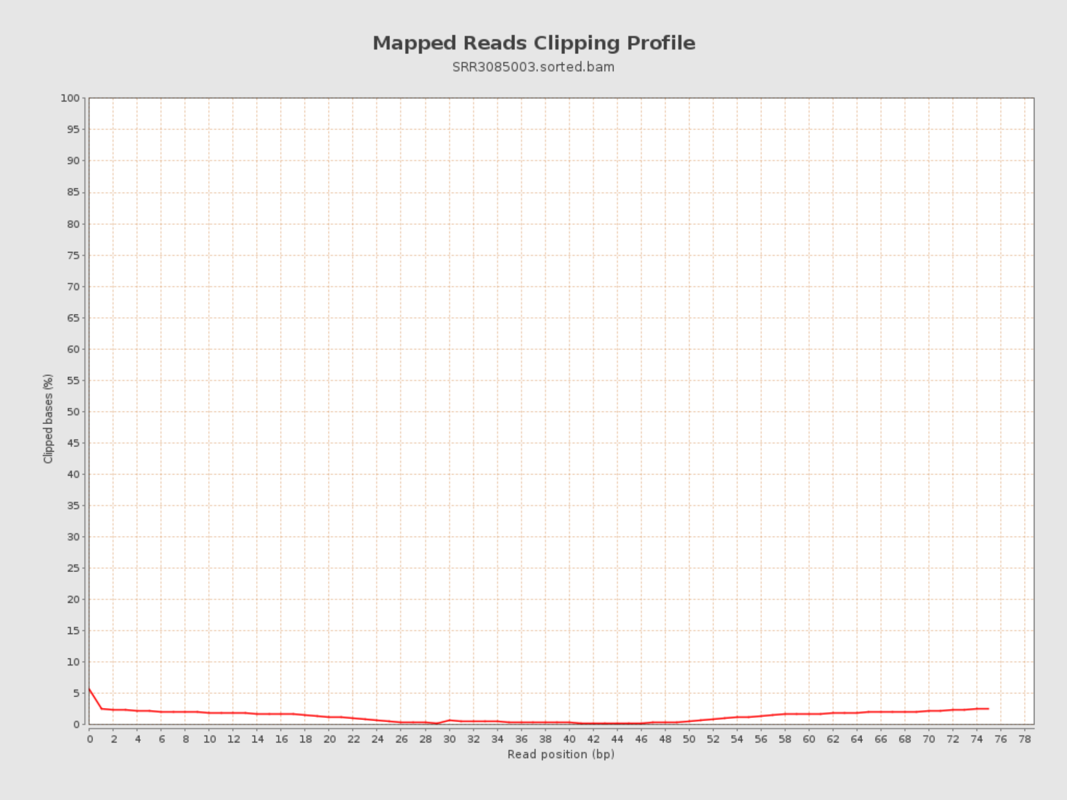
8. Results : Mapped Reads Nucleotide Content



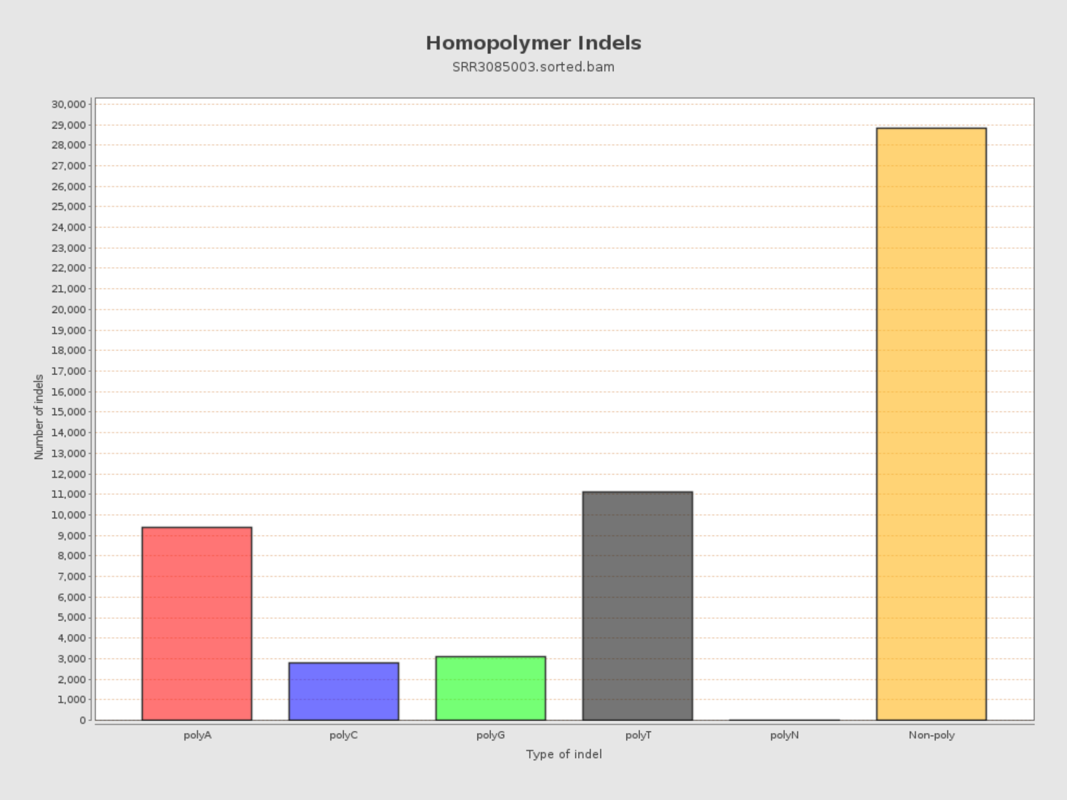
9. Results : Mapped Reads GC-content Distribution



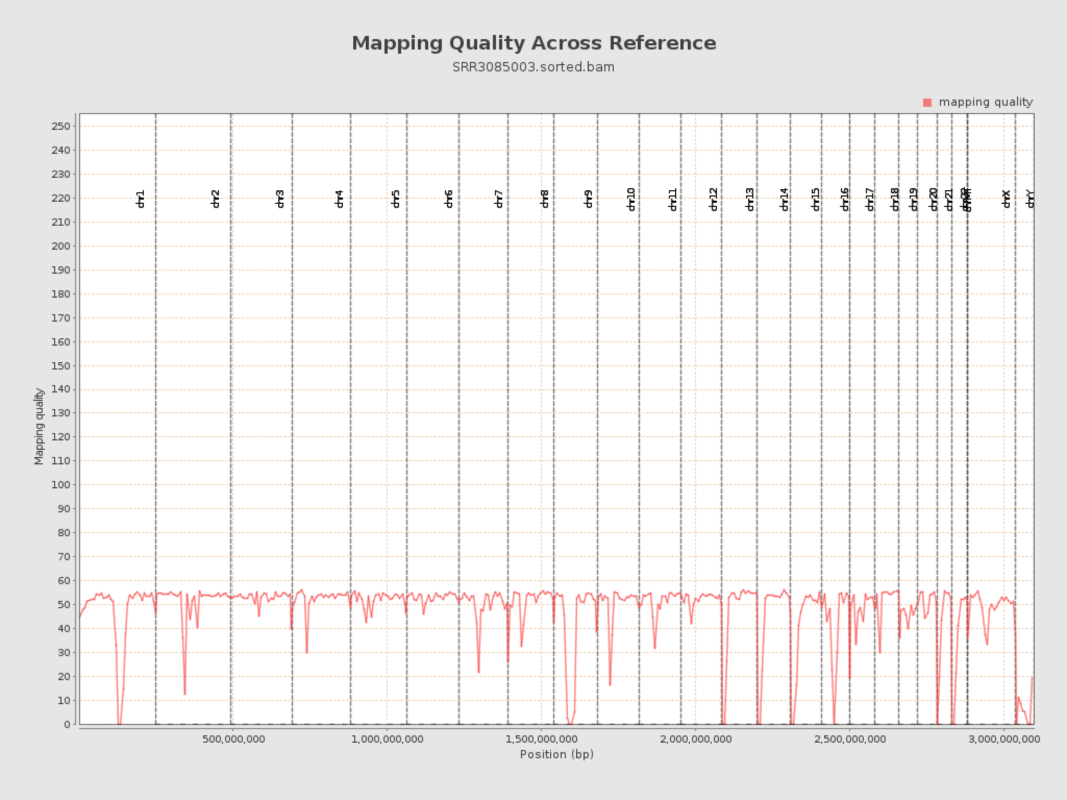
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram