Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:08:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080693.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_SRR3080693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080693.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:08:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,767,848
Mapped reads	2,471,762 / 89.3%
Unmapped reads	296,086 / 10.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,556 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	129,869 / 4.69%
Duplication rate	4.06%
Clipped reads	706,569 / 25.53%

2.2. ACGT Content

Number/percentage of A's	52,600,650 / 30.1%
Number/percentage of C's	32,463,993 / 18.58%
Number/percentage of T's	54,456,972 / 31.16%
Number/percentage of G's	35,245,279 / 20.17%
Number/percentage of N's	2,551 / 0%
GC Percentage	38.74%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.6205

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Mismatches and indels

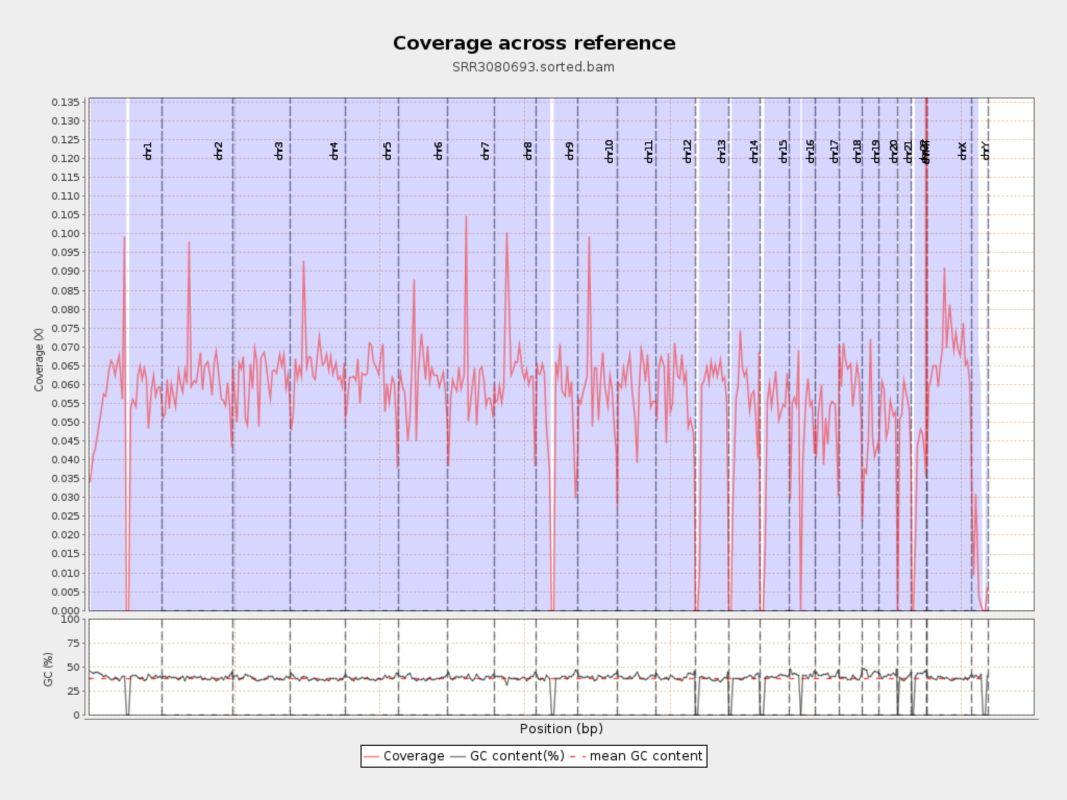
General error rate	0.84%
Mismatches	1,442,361
Insertions	14,285
Mapped reads with at least one insertion	0.57%
Deletions	37,457
Mapped reads with at least one deletion	1.5%
Homopolymer indels	47.4%

2.6. Chromosome stats

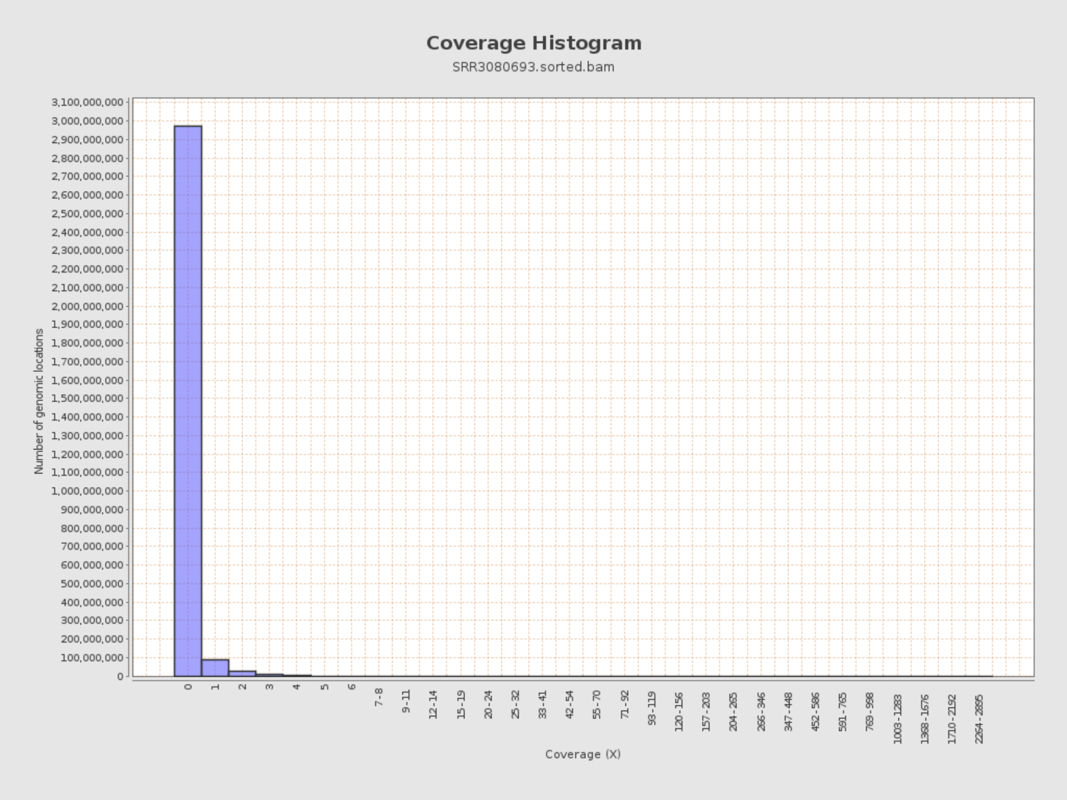
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13654466	0.0548	0.9487
chr2	243199373	14804345	0.0609	0.4794
chr3	198022430	12256770	0.0619	0.3338
chr4	191154276	12399704	0.0649	0.3798
chr5	180915260	11130950	0.0615	0.3343
chr6	171115067	10572316	0.0618	0.3832
chr7	159138663	9547594	0.06	0.7863

chr8	146364022	9330629	0.0637	1.777
chr9	141213431	7169367	0.0508	0.4414
chr10	135534747	8143873	0.0601	0.4942
chr11	135006516	7971936	0.059	0.4037
chr12	133851895	7825006	0.0585	0.329
chr13	115169878	5925348	0.0514	0.3039
chr14	107349540	5256944	0.049	0.3256
chr15	102531392	4681937	0.0457	0.282
chr16	90354753	4368958	0.0484	0.3255
chr17	81195210	3924409	0.0483	0.3325
chr18	78077248	4887687	0.0626	0.7674
chr19	59128983	2654820	0.0449	0.6187
chr20	63025520	3286874	0.0522	0.3129
chr21	48129895	2313850	0.0481	0.3238
chr22	51304566	1602956	0.0312	0.23
chrMT	16571	142783	8.6164	6.0987
chrX	155270560	10489031	0.0676	0.3715
chrY	59373566	495007	0.0083	0.2711

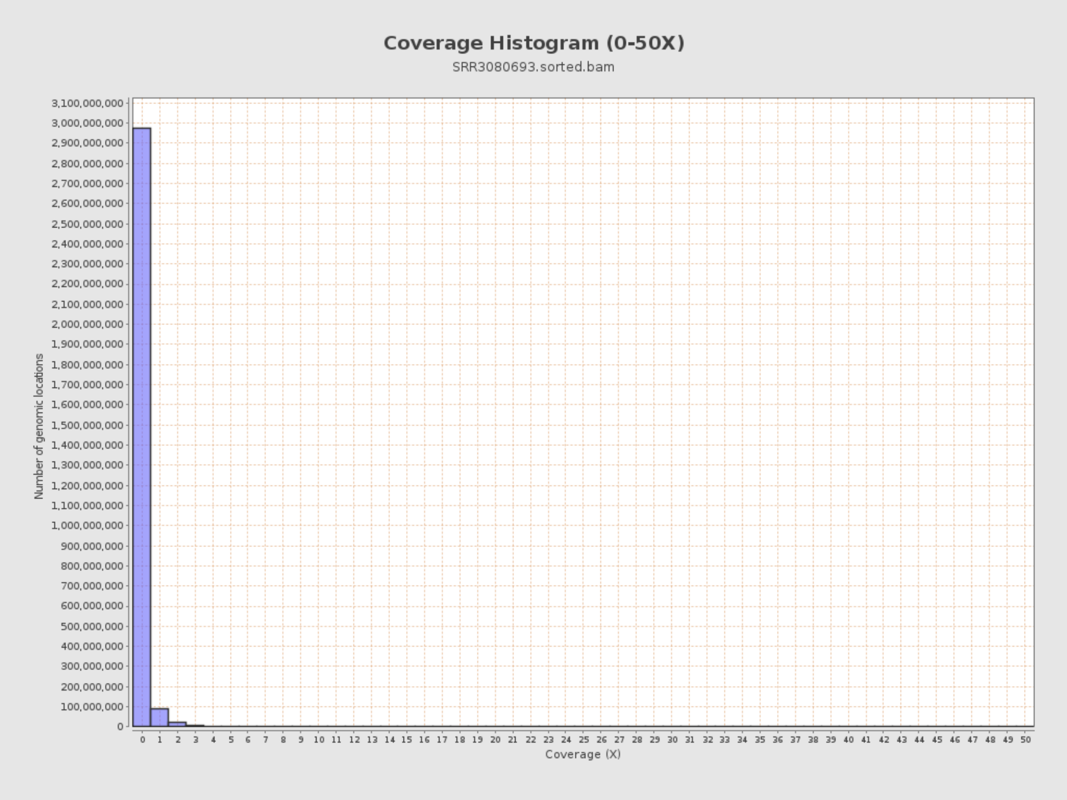
3. Results : Coverage across reference



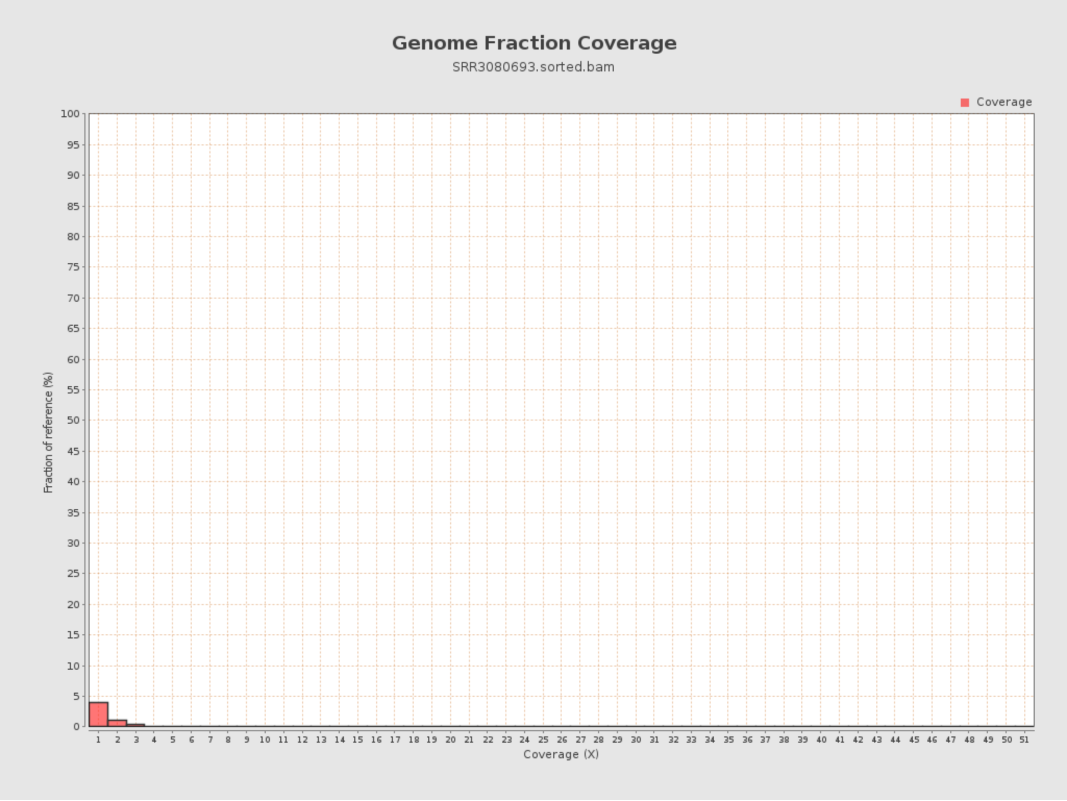
4. Results : Coverage Histogram



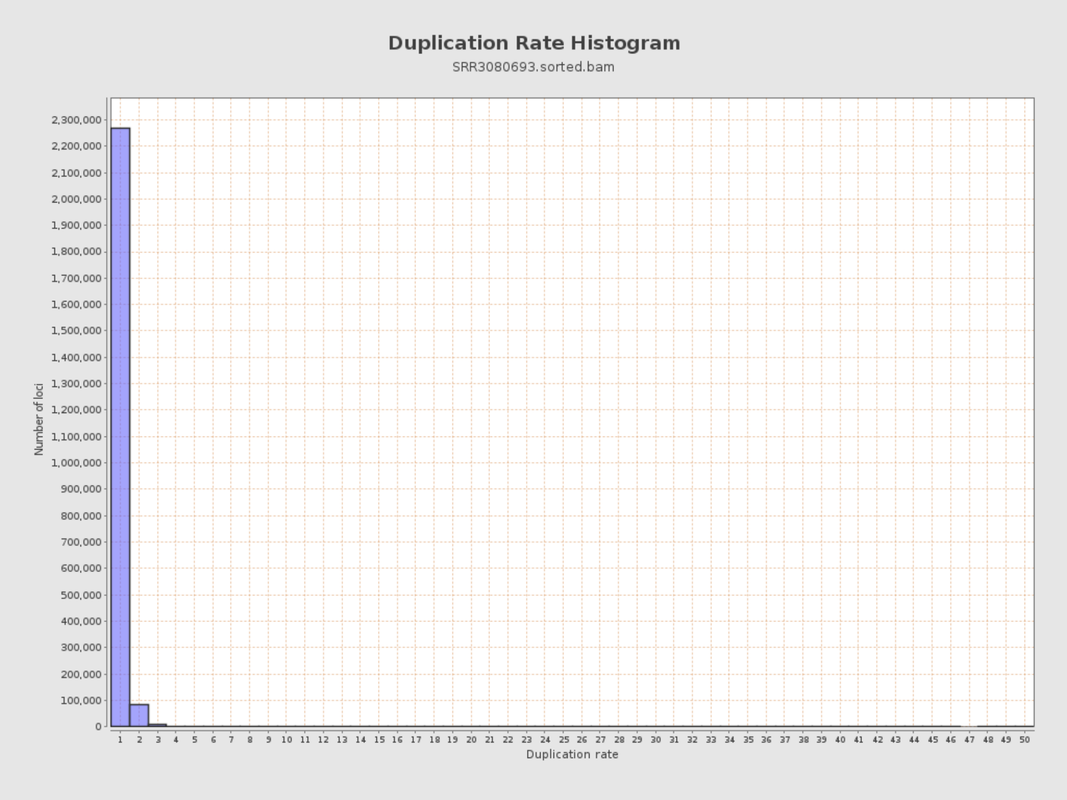
5. Results : Coverage Histogram (0-50X)



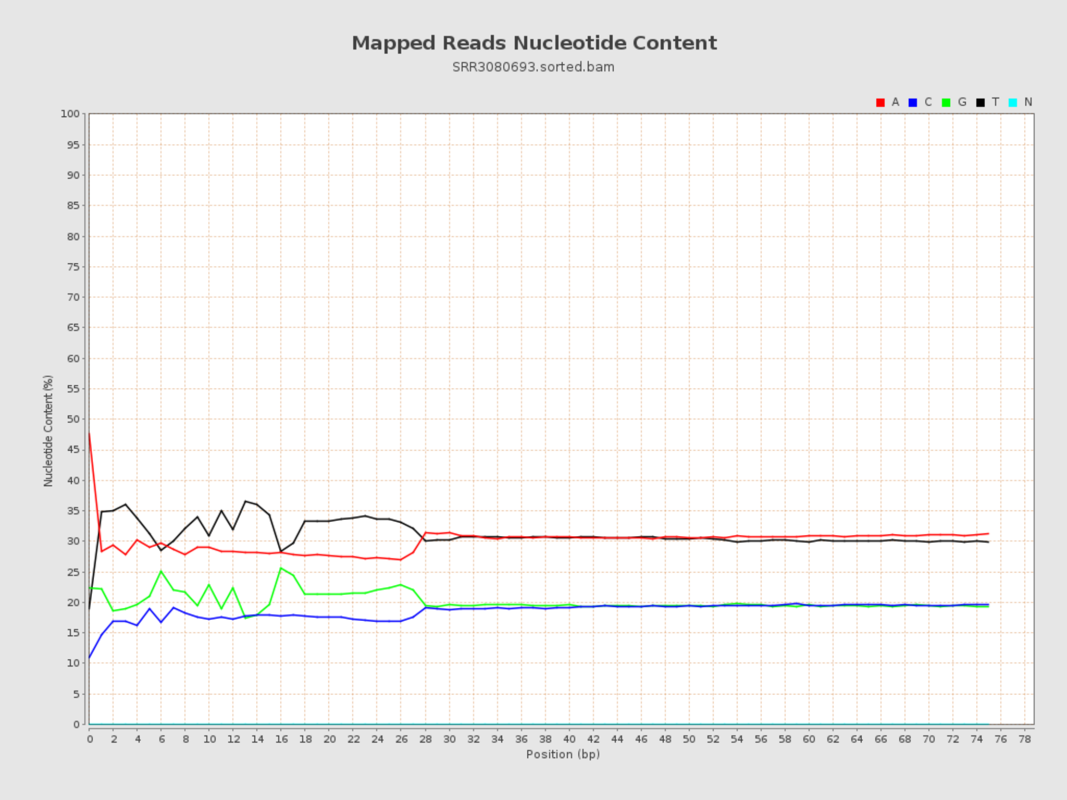
6. Results : Genome Fraction Coverage



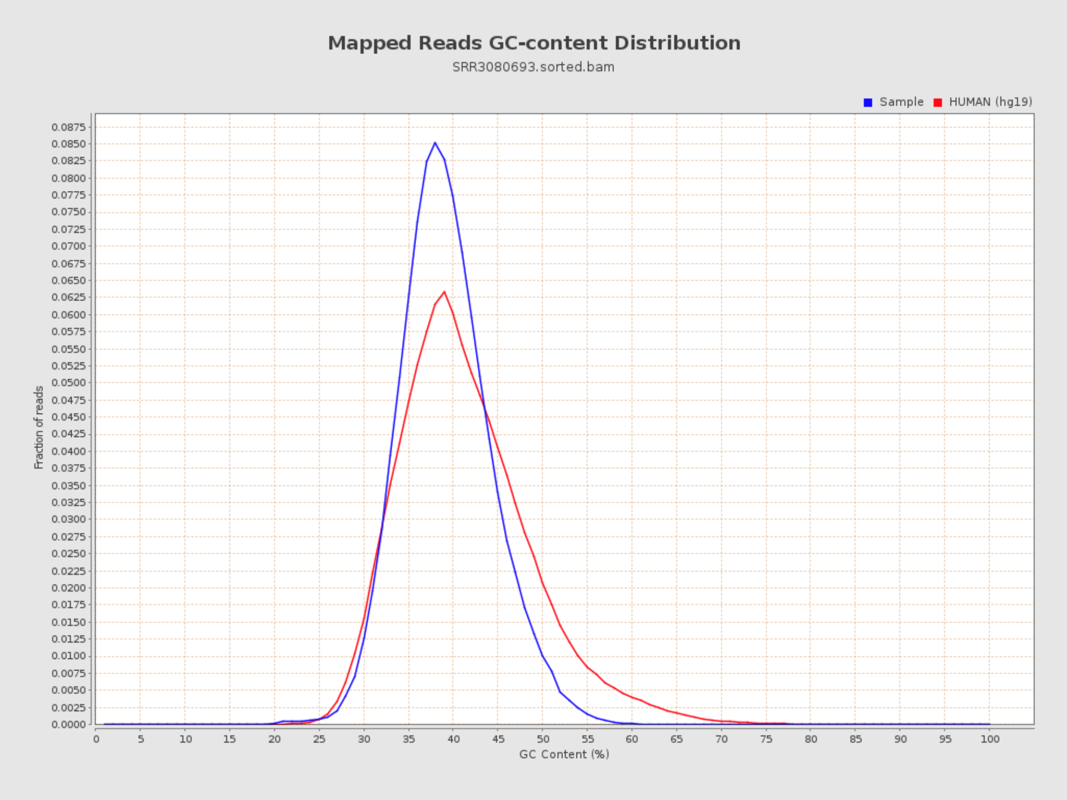
7. Results : Duplication Rate Histogram



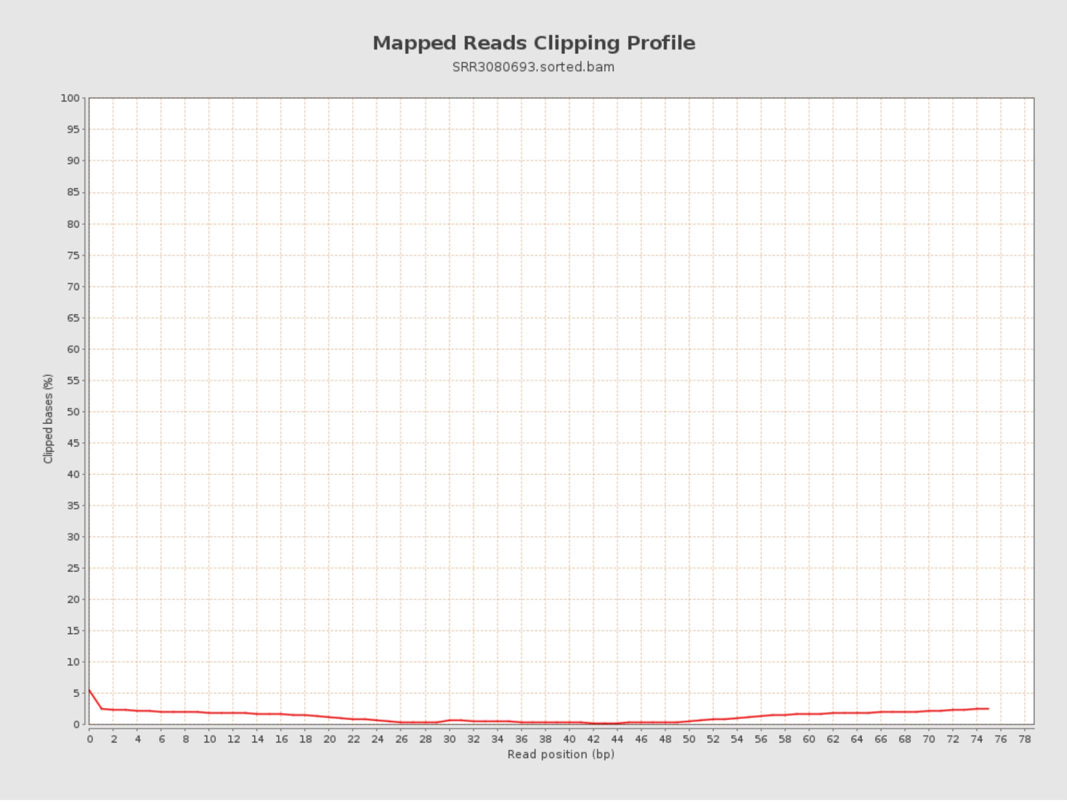
8. Results : Mapped Reads Nucleotide Content



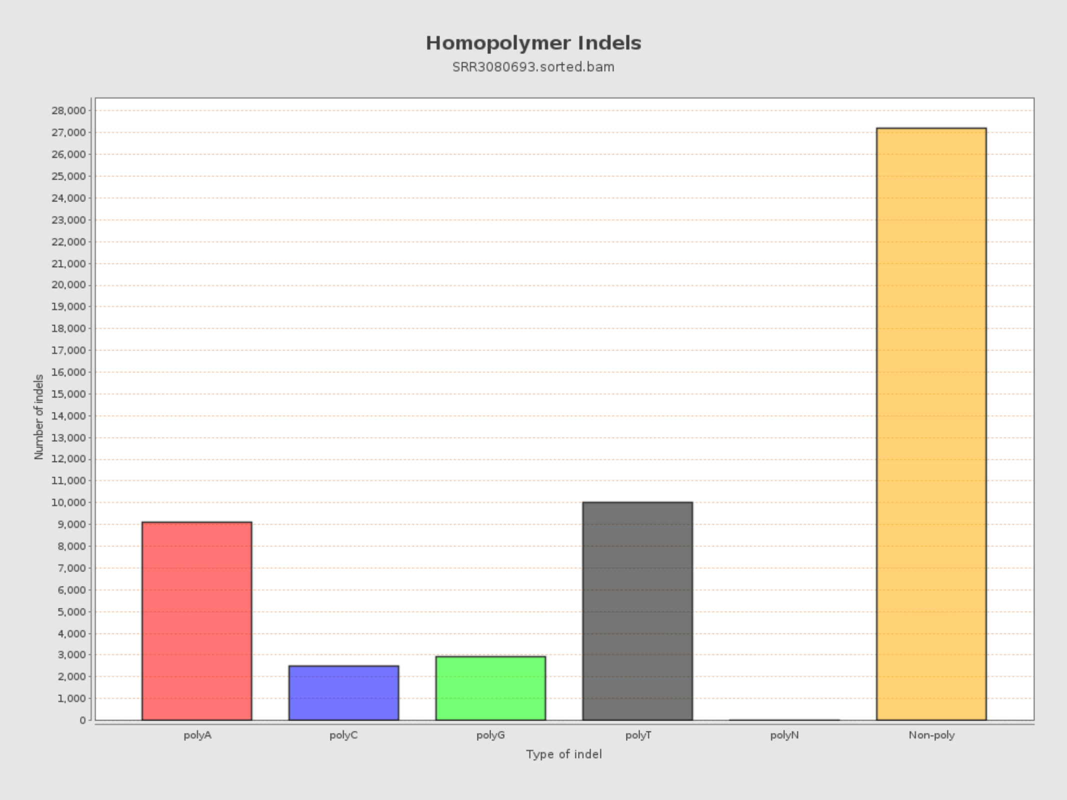
9. Results : Mapped Reads GC-content Distribution



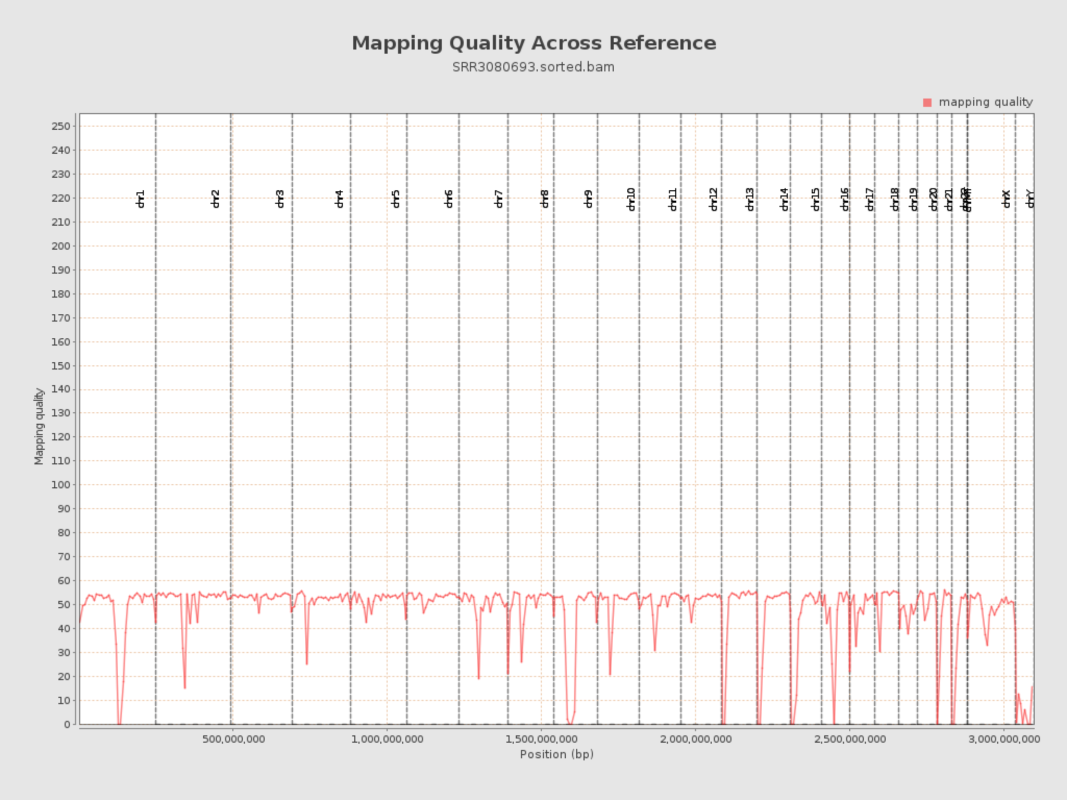
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram