Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:37:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008725.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_SRR6008725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008725.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:37:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,194,993
Mapped reads	2,892,844 / 90.54%
Unmapped reads	302,149 / 9.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,220 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	160,732 / 5.03%
Duplication rate	4.44%
Clipped reads	1,543,864 / 48.32%

2.2. ACGT Content

Number/percentage of A's	49,213,913 / 26.36%
Number/percentage of C's	34,770,530 / 18.63%
Number/percentage of T's	58,497,409 / 31.34%
Number/percentage of G's	44,064,002 / 23.6%
Number/percentage of N's	133,600 / 0.07%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0603

Standard Deviation	0.461

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

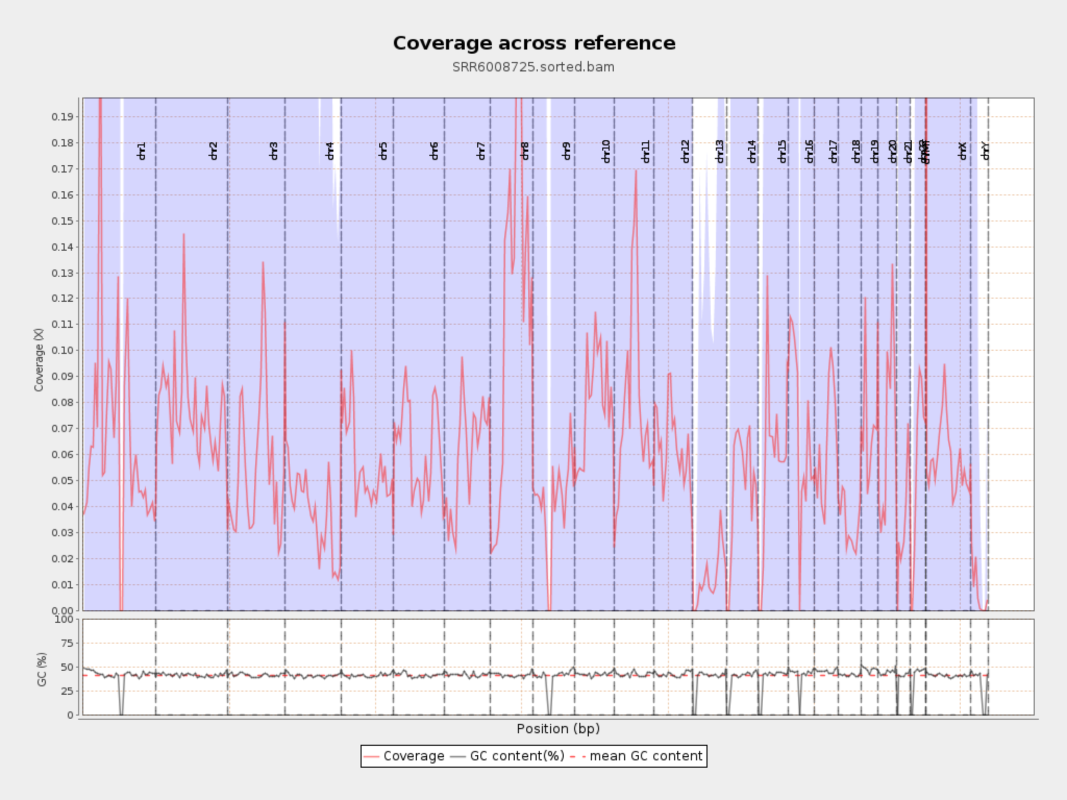
General error rate	0.82%
Mismatches	1,514,908
Insertions	13,808
Mapped reads with at least one insertion	0.47%
Deletions	56,393
Mapped reads with at least one deletion	1.93%
Homopolymer indels	46.1%

2.6. Chromosome stats

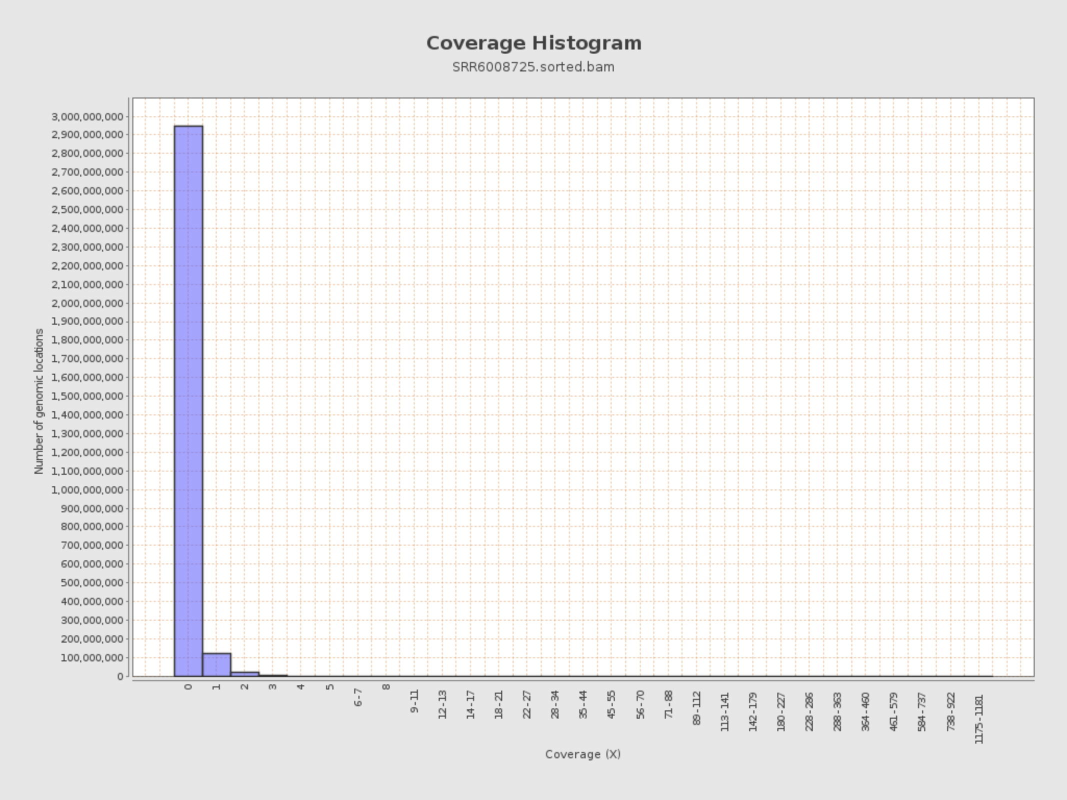
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16271523	0.0653	0.8037
chr2	243199373	18975493	0.078	0.7062
chr3	198022430	11040380	0.0558	0.2881
chr4	191154276	7241969	0.0379	0.2537
chr5	180915260	10138978	0.056	0.2865
chr6	171115067	10780939	0.063	0.3695
chr7	159138663	9690528	0.0609	0.5447

chr8	146364022	16939032	0.1157	0.5552
chr9	141213431	5874668	0.0416	0.3757
chr10	135534747	10863827	0.0802	0.4593
chr11	135006516	10749493	0.0796	0.4969
chr12	133851895	8608502	0.0643	0.3097
chr13	115169878	1501323	0.013	0.1395
chr14	107349540	5264025	0.049	0.2749
chr15	102531392	5738154	0.056	0.2968
chr16	90354753	6216954	0.0688	0.3505
chr17	81195210	5398641	0.0665	0.371
chr18	78077248	2582254	0.0331	0.5336
chr19	59128983	4177993	0.0707	0.5828
chr20	63025520	4456819	0.0707	0.3291
chr21	48129895	1656708	0.0344	0.2375
chr22	51304566	2861517	0.0558	0.2855
chrMT	16571	203435	12.2766	8.7146
chrX	155270560	9107434	0.0587	0.3333
chrY	59373566	432003	0.0073	0.1627

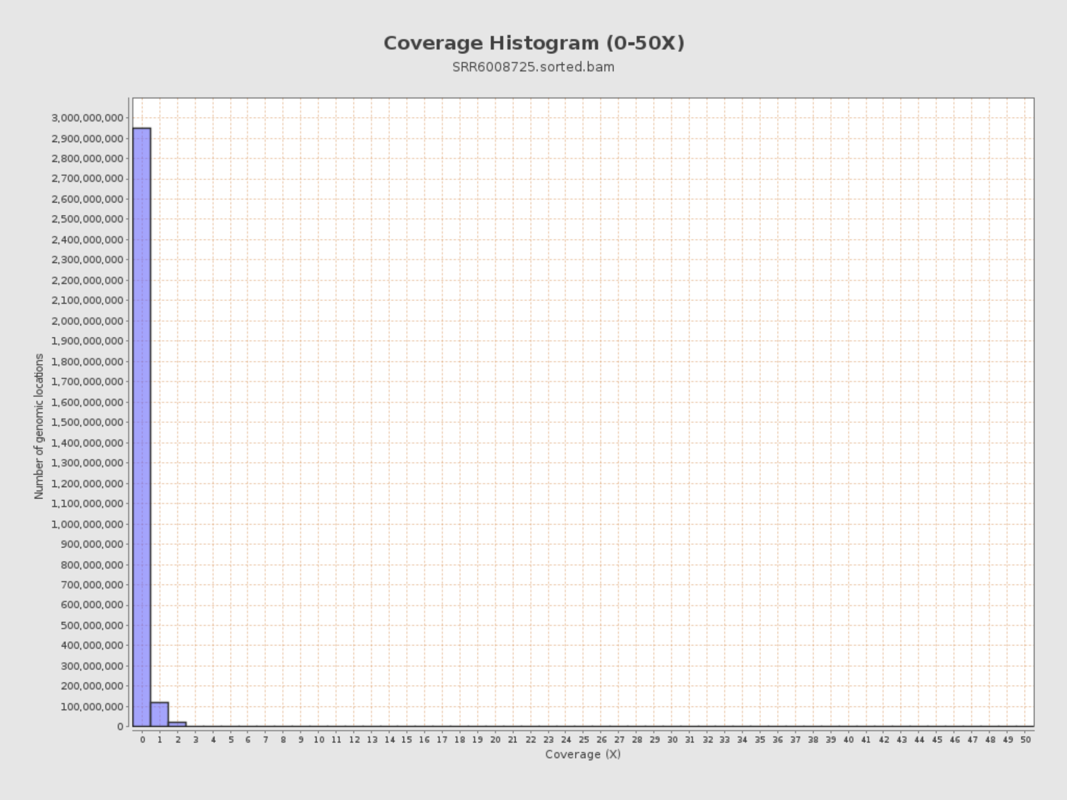
3. Results : Coverage across reference



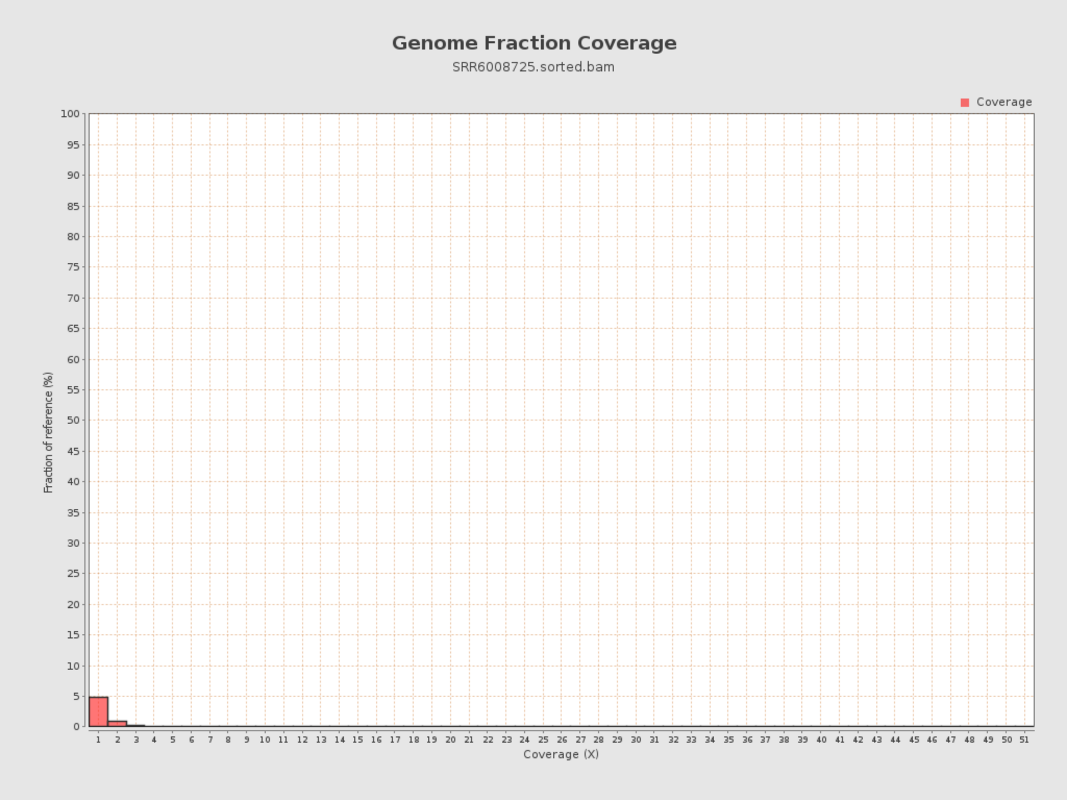
4. Results : Coverage Histogram



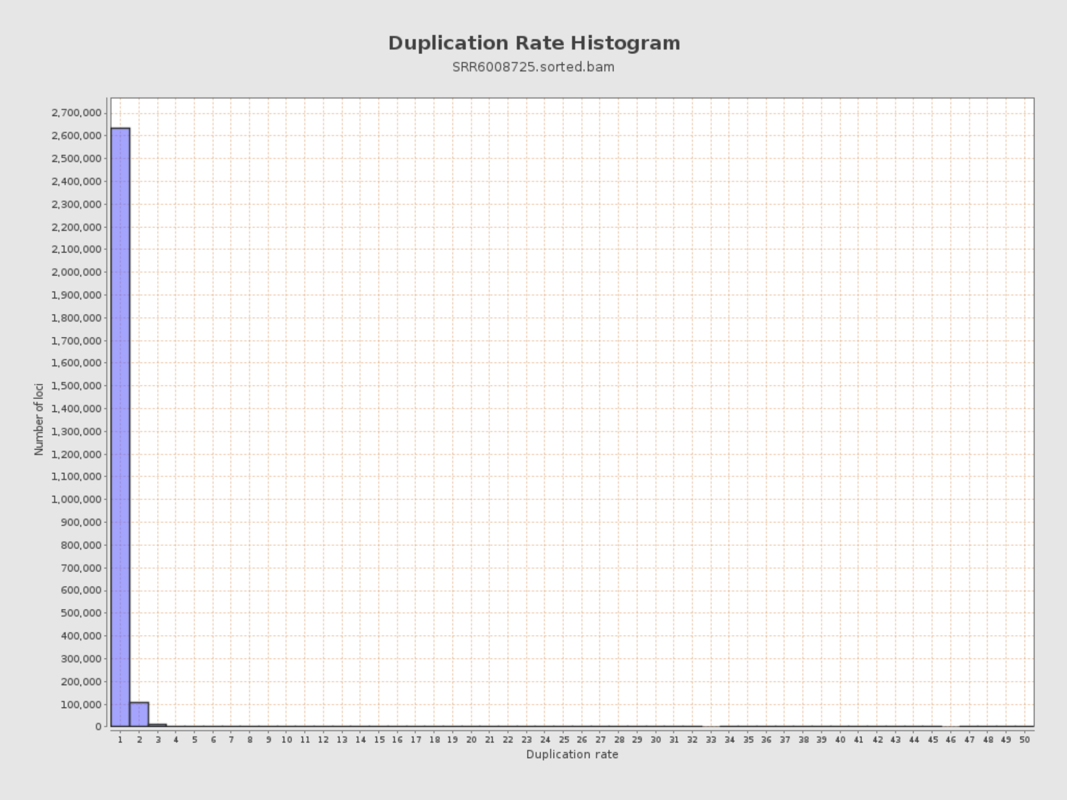
5. Results : Coverage Histogram (0-50X)



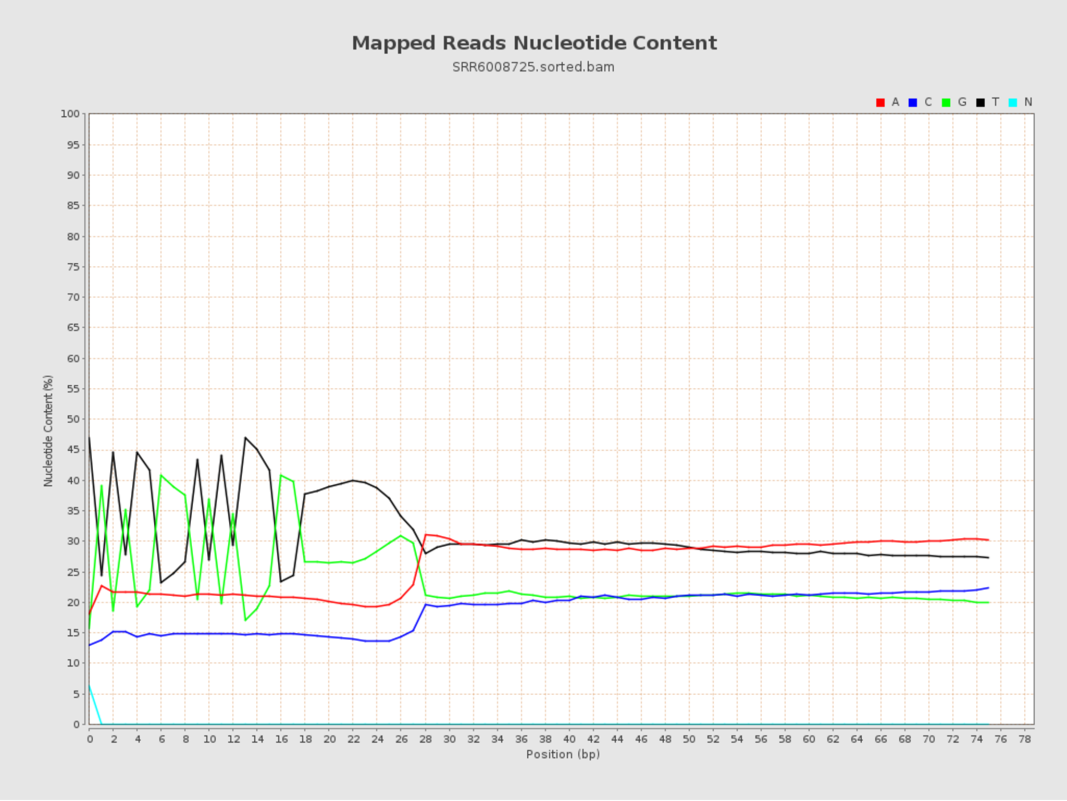
6. Results : Genome Fraction Coverage



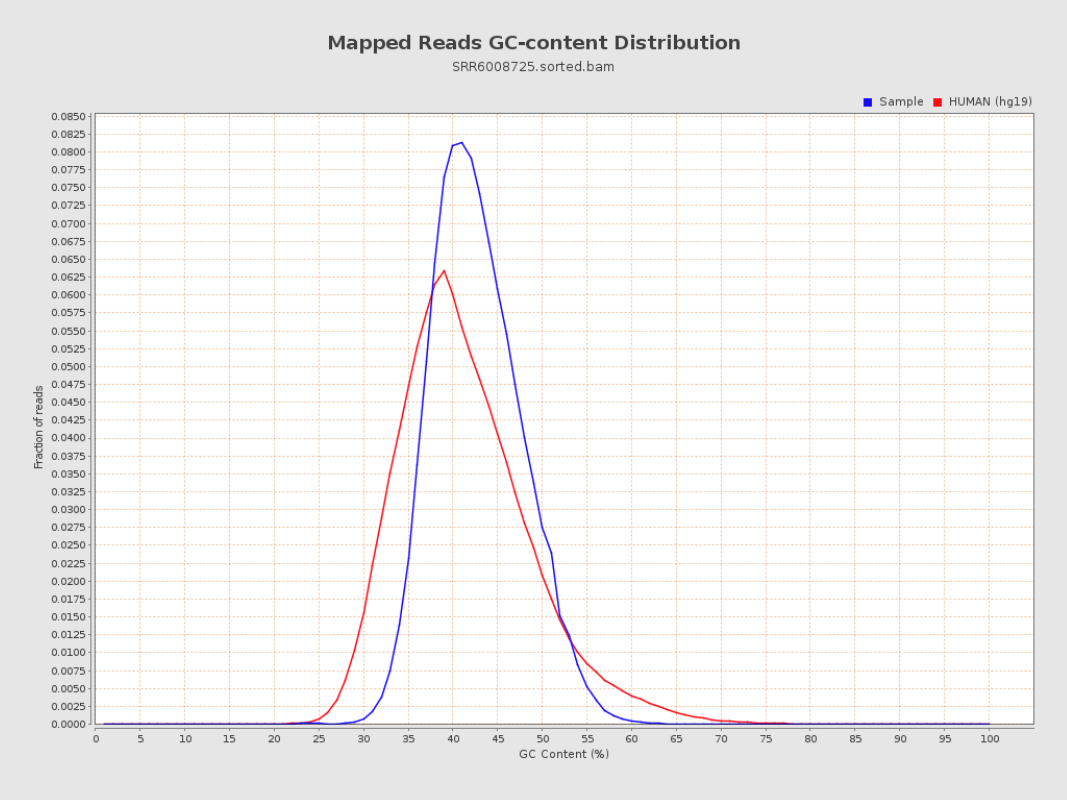
7. Results : Duplication Rate Histogram



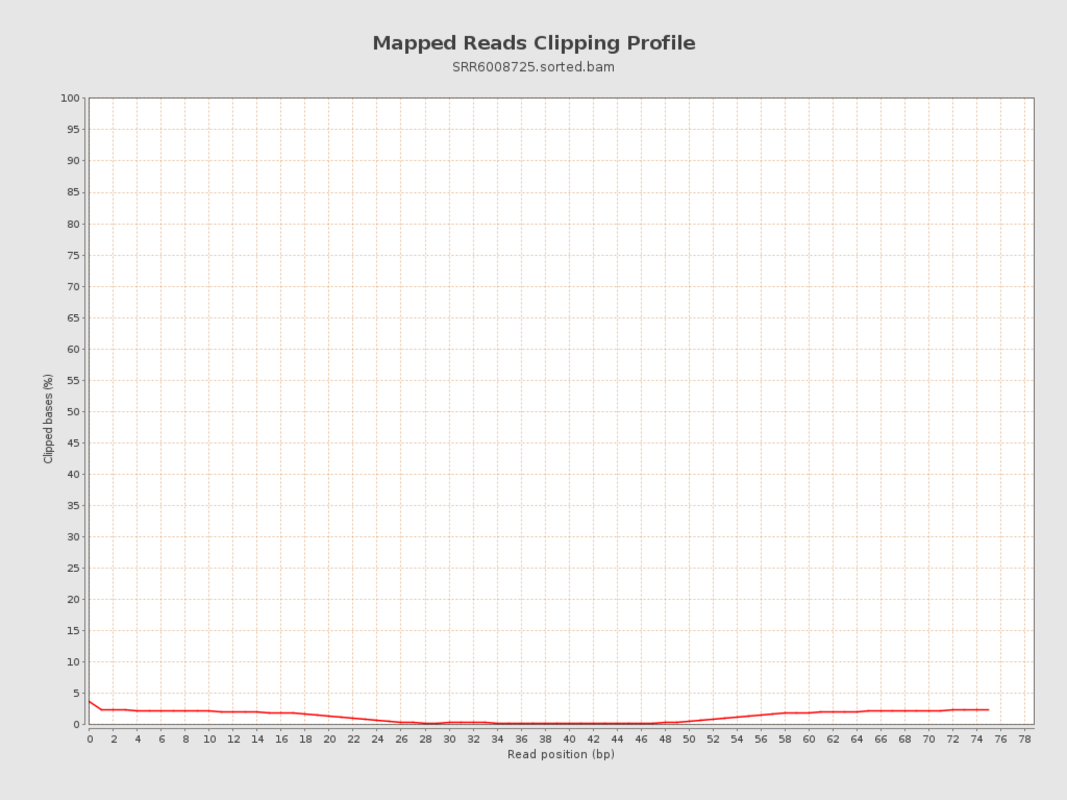
8. Results : Mapped Reads Nucleotide Content



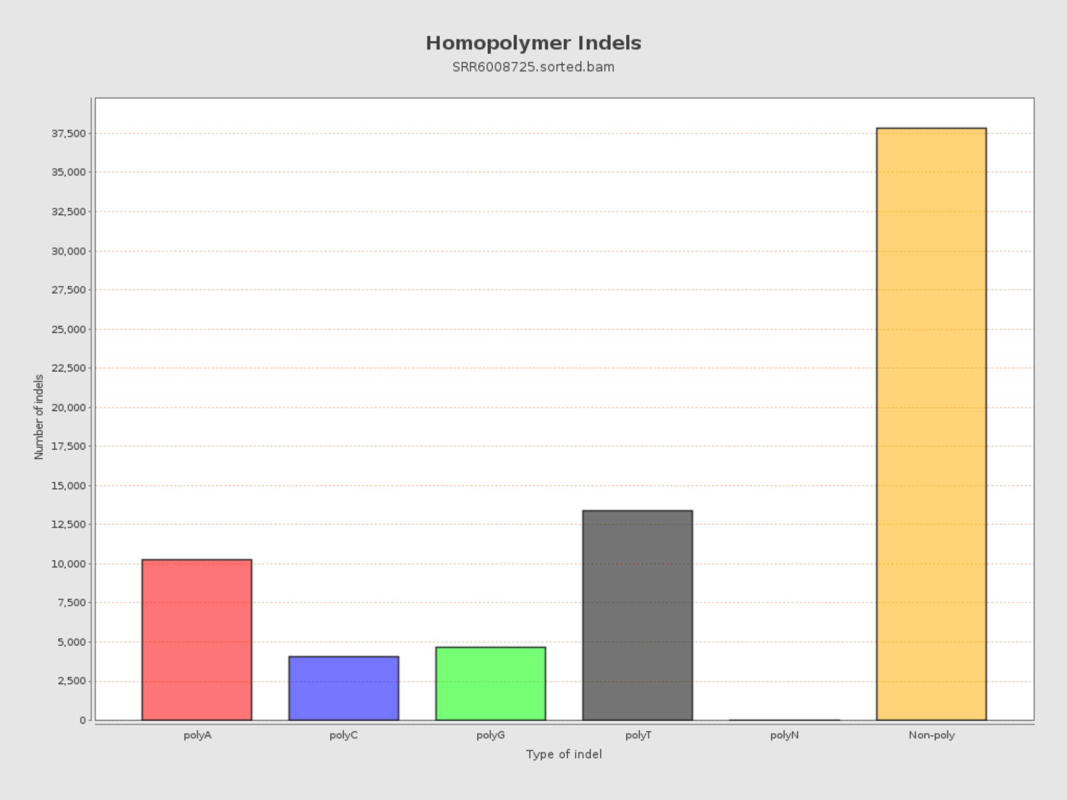
9. Results : Mapped Reads GC-content Distribution



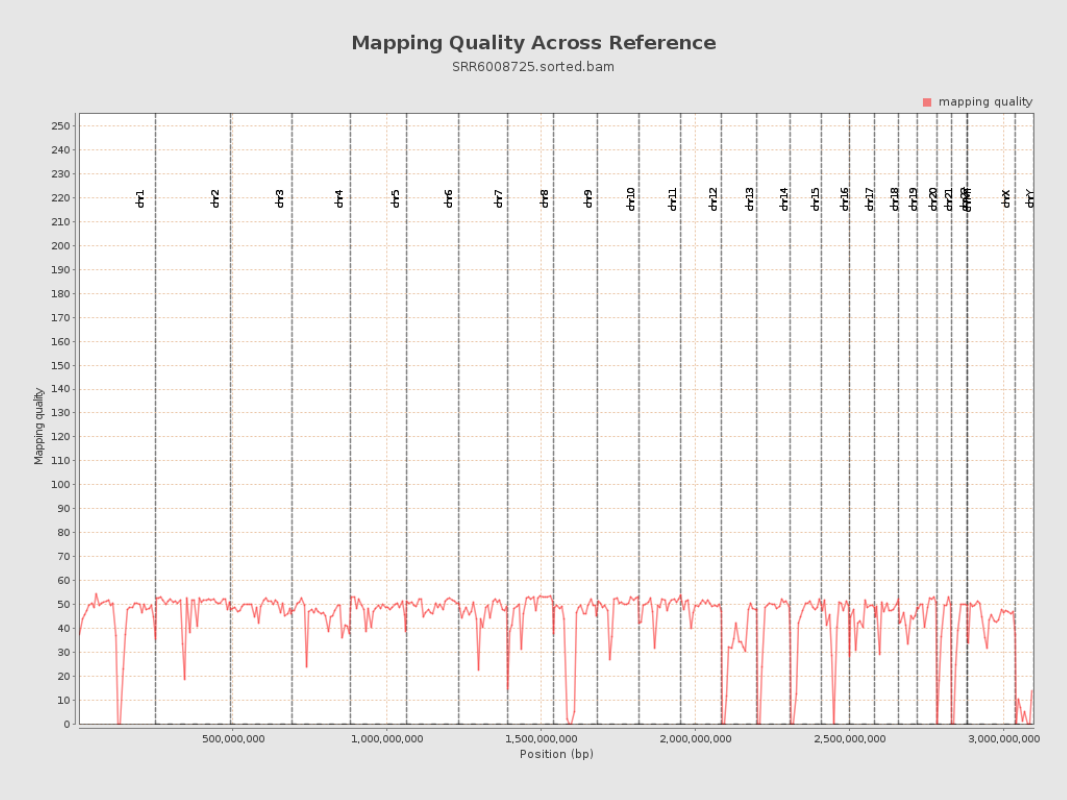
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram