Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:51:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008683.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_SRR6008683 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008683.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:51:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008683.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,920,779
Mapped reads	1,620,186 / 84.35%
Unmapped reads	300,593 / 15.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,077 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	67,040 / 3.49%
Duplication rate	2.7%
Clipped reads	992,142 / 51.65%

2.2. ACGT Content

Number/percentage of A's	25,962,785 / 25.78%
Number/percentage of C's	18,426,737 / 18.3%
Number/percentage of T's	31,460,481 / 31.24%
Number/percentage of G's	24,824,121 / 24.65%
Number/percentage of N's	41,862 / 0.04%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.3847

2.4. Mapping Quality

Mean Mapping Quality	42.2

2.5. Mismatches and indels

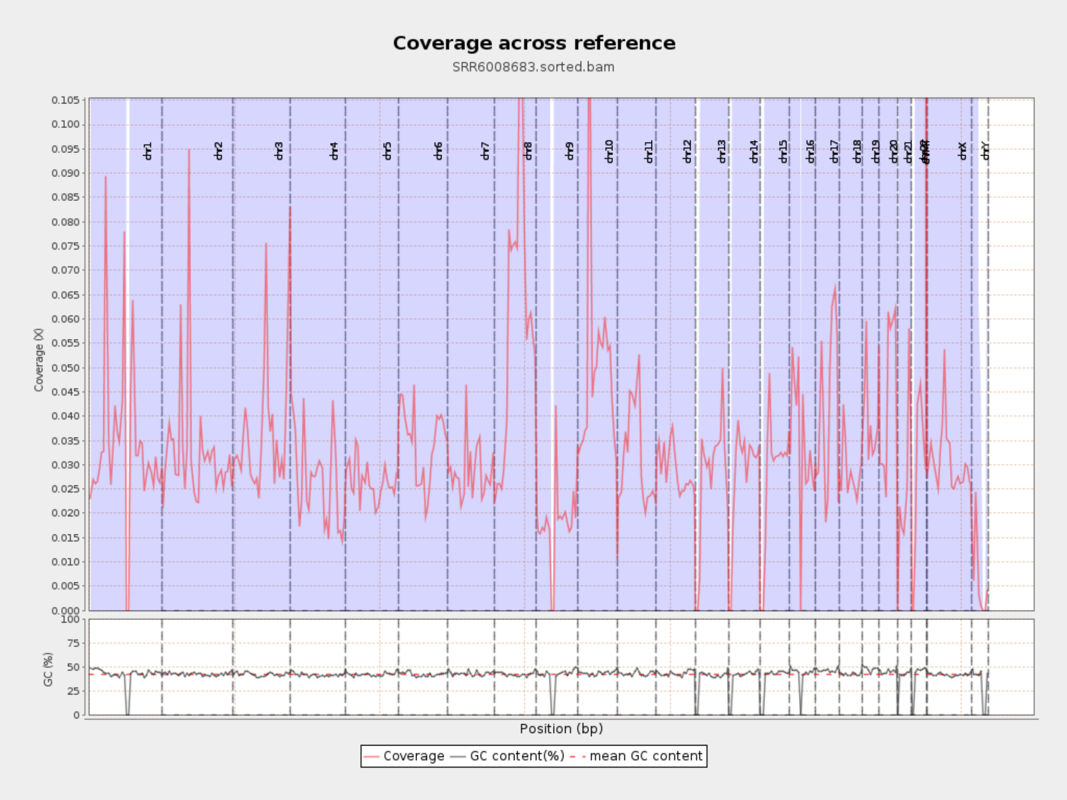
General error rate	0.87%
Mismatches	858,293
Insertions	7,307
Mapped reads with at least one insertion	0.45%
Deletions	34,600
Mapped reads with at least one deletion	2.11%
Homopolymer indels	42.33%

2.6. Chromosome stats

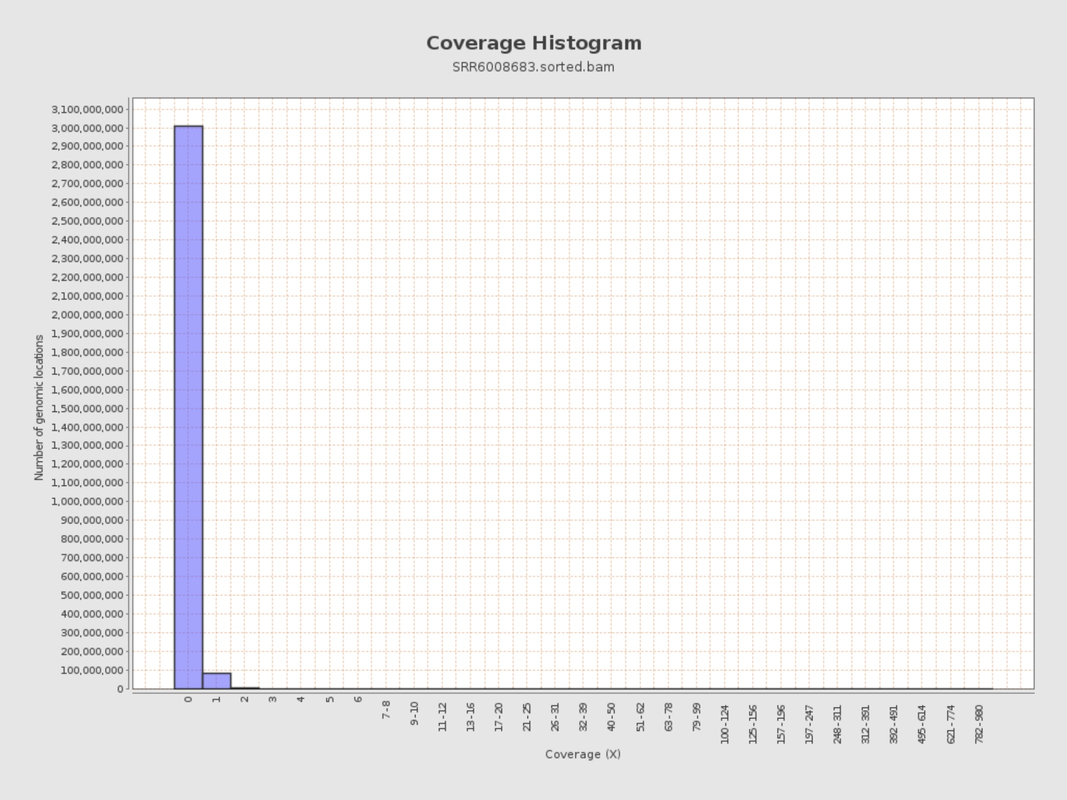
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8402886	0.0337	0.7157
chr2	243199373	8035610	0.033	0.5033
chr3	198022430	7164089	0.0362	0.2419
chr4	191154276	5087932	0.0266	0.2015
chr5	180915260	4813974	0.0266	0.1795
chr6	171115067	5876049	0.0343	0.2507
chr7	159138663	4535685	0.0285	0.3031

chr8	146364022	8690269	0.0594	0.3713
chr9	141213431	2497246	0.0177	0.3181
chr10	135534747	6859345	0.0506	0.7785
chr11	135006516	4277641	0.0317	0.3059
chr12	133851895	3902335	0.0292	0.191
chr13	115169878	3157985	0.0274	0.178
chr14	107349540	2988029	0.0278	0.1914
chr15	102531392	2831675	0.0276	0.1828
chr16	90354753	3096897	0.0343	0.2882
chr17	81195210	3383774	0.0417	0.3126
chr18	78077248	2229175	0.0286	0.5519
chr19	59128983	2346350	0.0397	0.4975
chr20	63025520	2810049	0.0446	0.2383
chr21	48129895	1219969	0.0253	0.1949
chr22	51304566	1403098	0.0273	0.1788
chrMT	16571	33067	1.9955	1.8019
chrX	155270560	4769197	0.0307	0.2406
chrY	59373566	364539	0.0061	0.2252

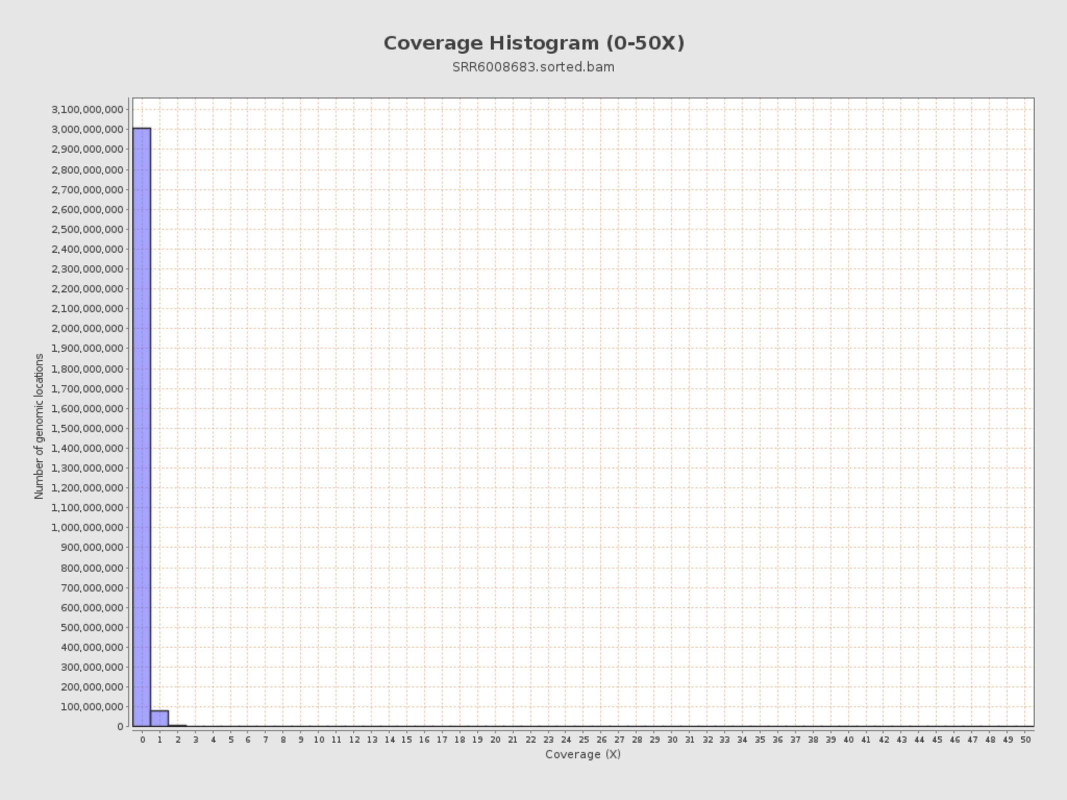
3. Results : Coverage across reference



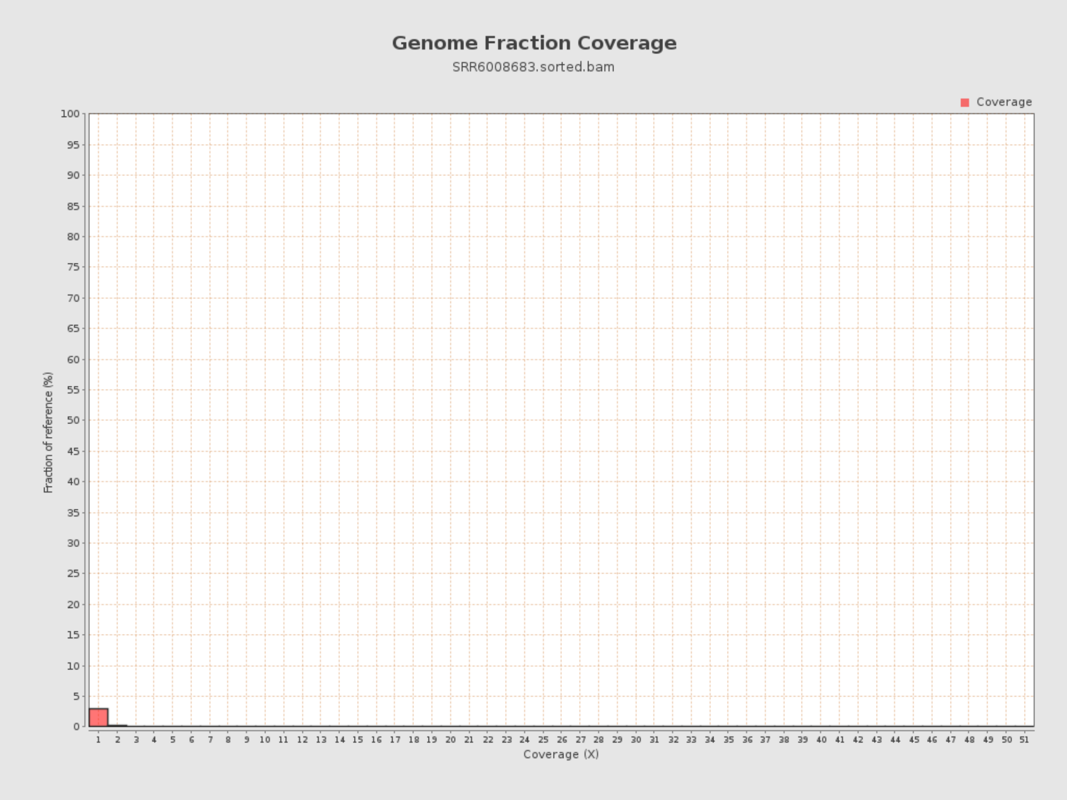
4. Results : Coverage Histogram



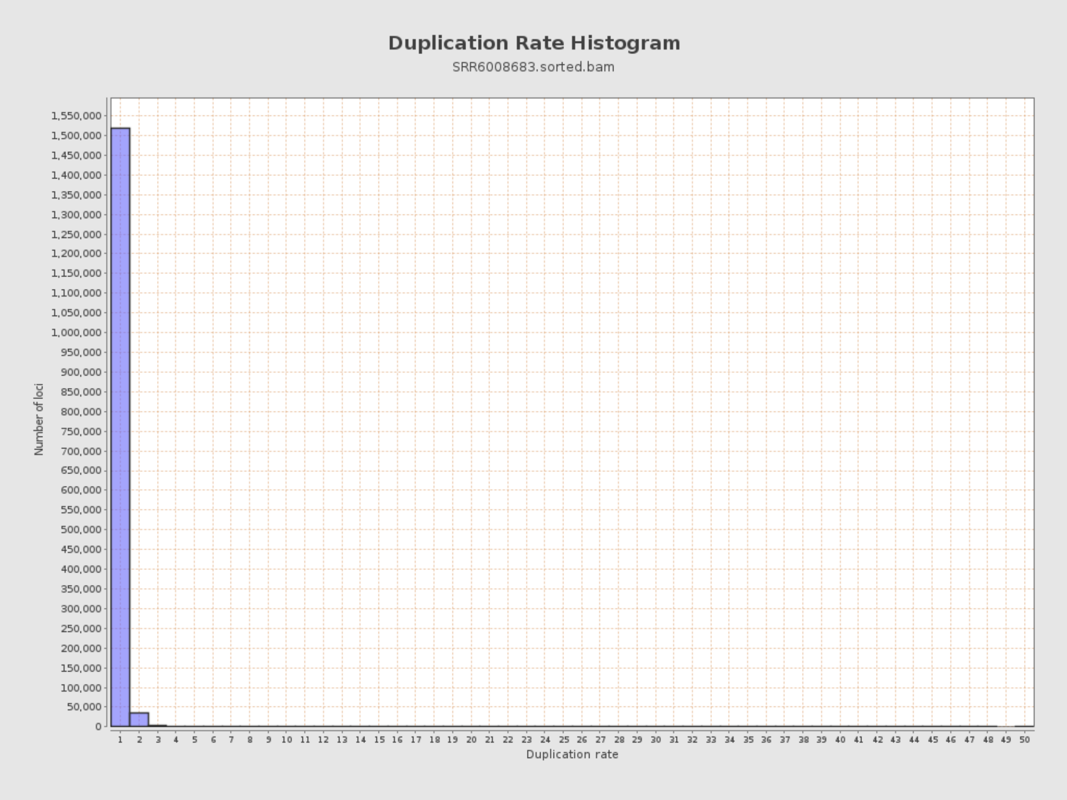
5. Results : Coverage Histogram (0-50X)



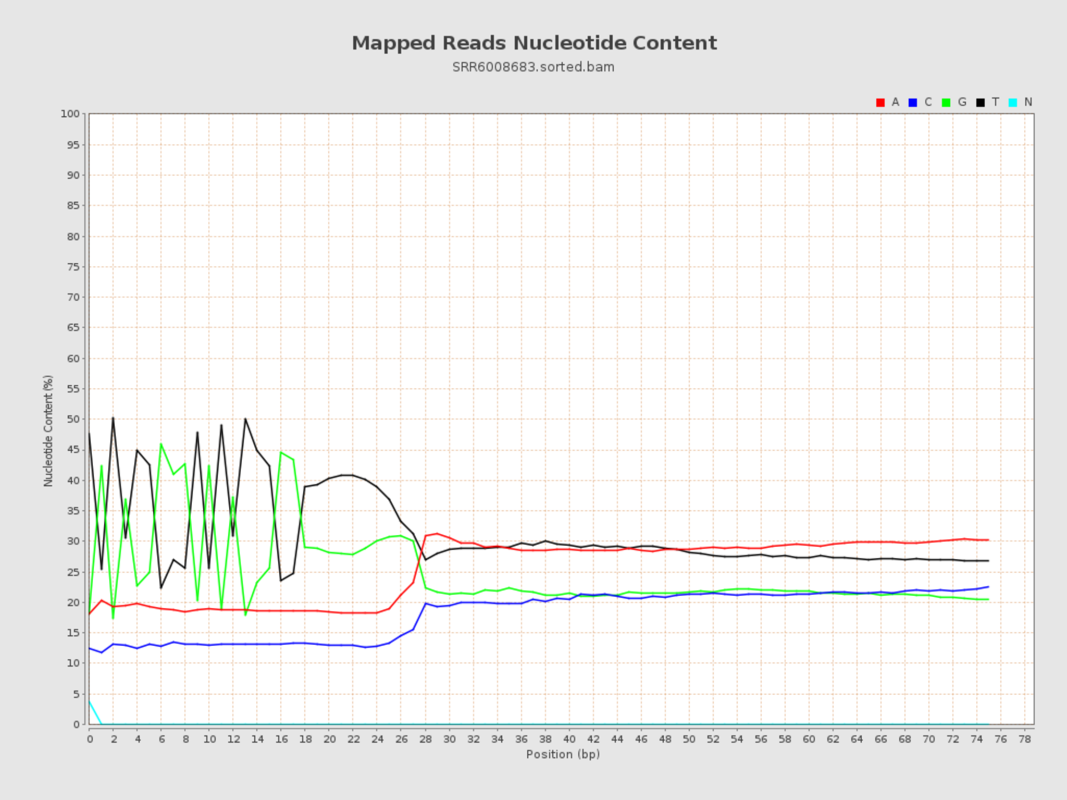
6. Results : Genome Fraction Coverage



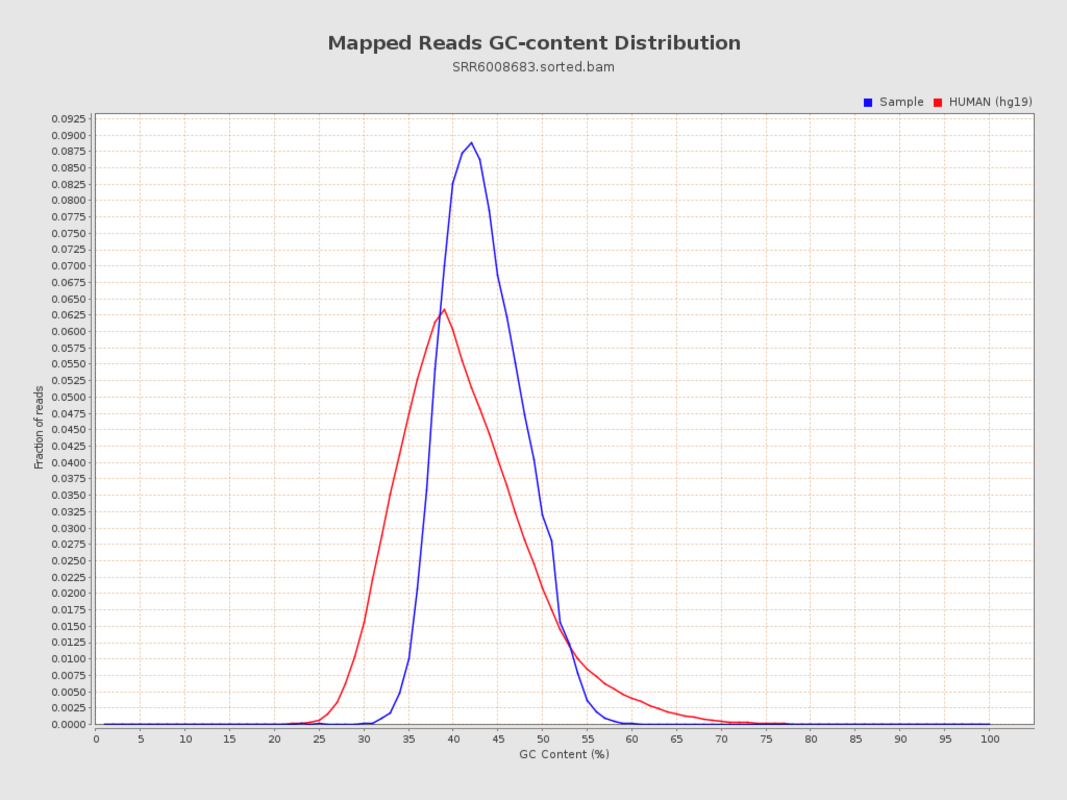
7. Results : Duplication Rate Histogram



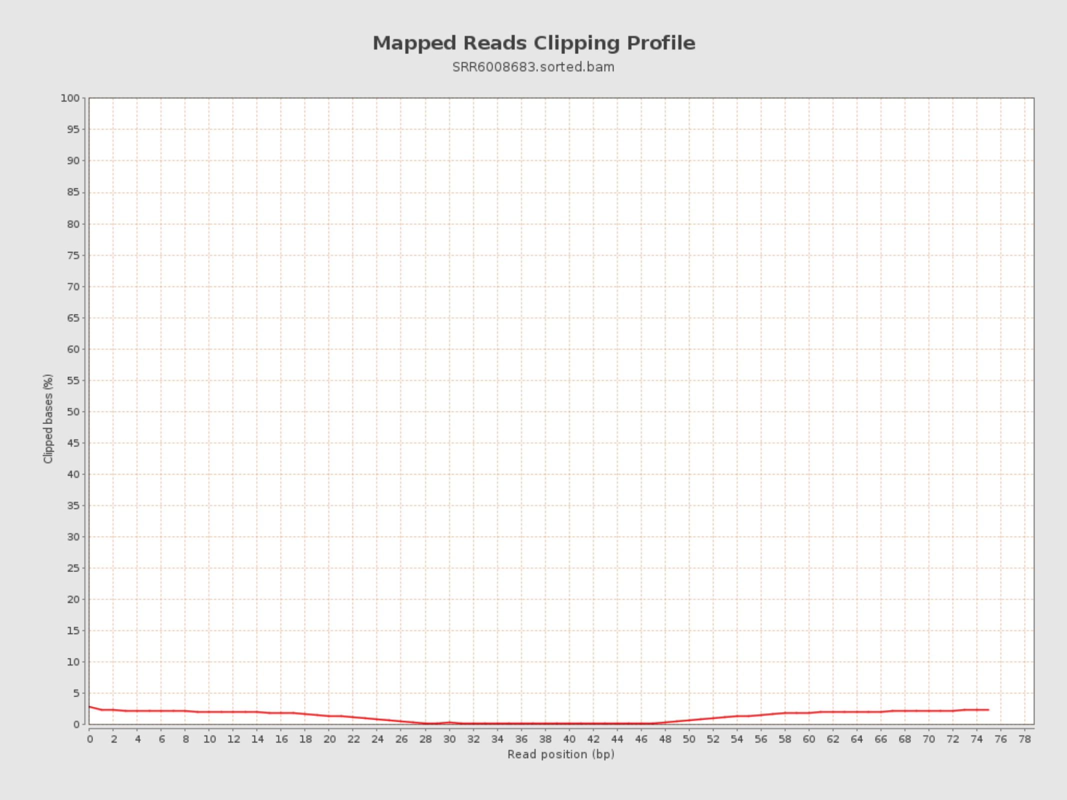
8. Results : Mapped Reads Nucleotide Content



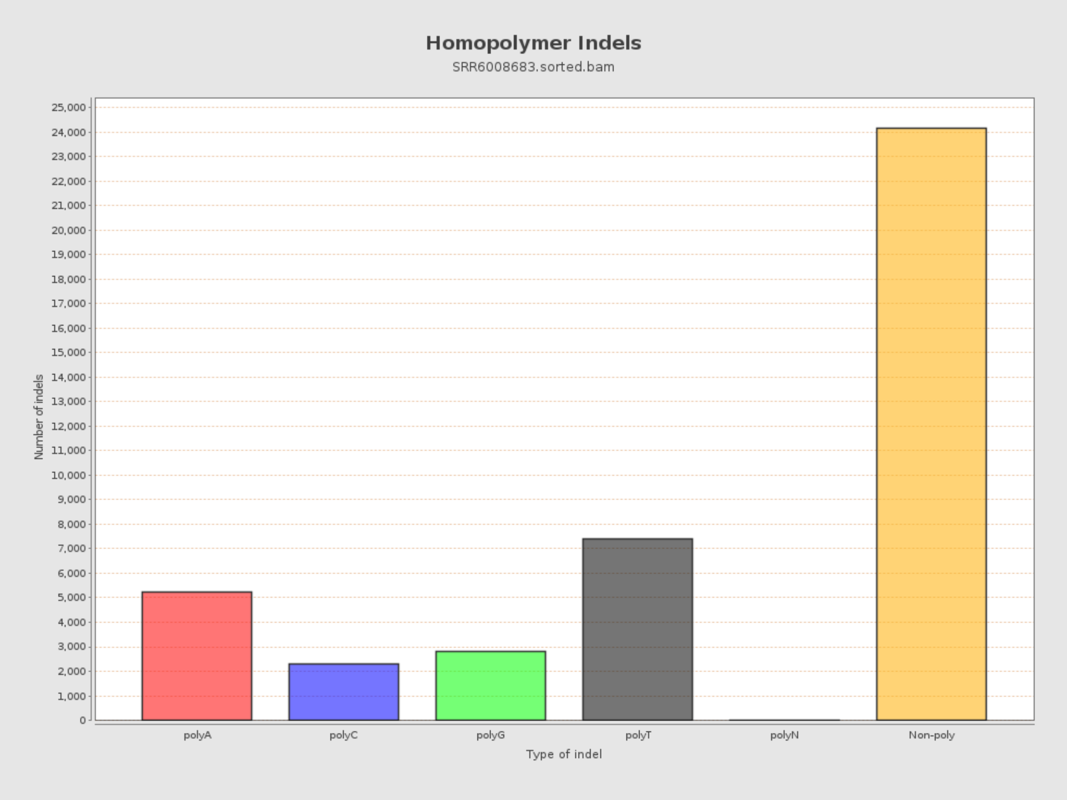
9. Results : Mapped Reads GC-content Distribution



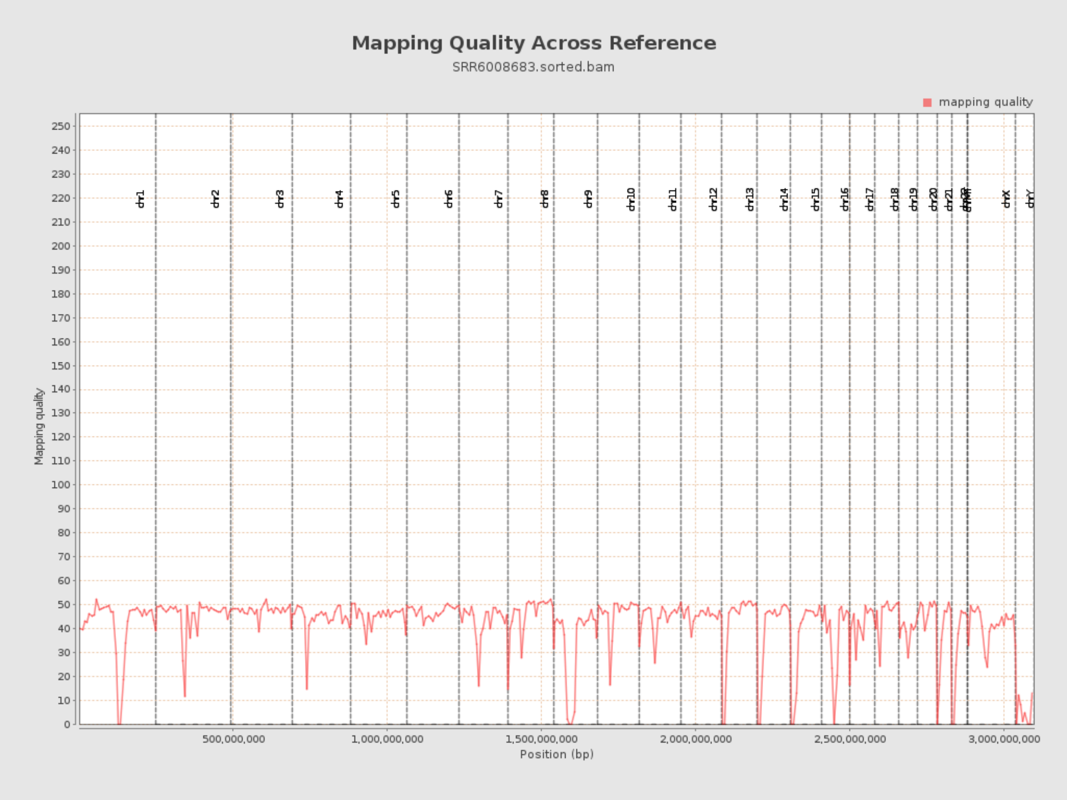
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram