Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:34:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013283.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_SRR6013283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013283.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:34:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,782,969
Mapped reads	2,466,104 / 88.61%
Unmapped reads	316,865 / 11.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,639 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	92,723 / 3.33%
Duplication rate	2.68%
Clipped reads	1,369,944 / 49.23%

2.2. ACGT Content

Number/percentage of A's	42,230,250 / 26.8%
Number/percentage of C's	29,917,072 / 18.99%
Number/percentage of T's	48,073,077 / 30.51%
Number/percentage of G's	37,324,815 / 23.69%
Number/percentage of N's	17,146 / 0.01%
GC Percentage	42.68%

2.3. Coverage

Mean	0.0509

Standard Deviation	0.447

2.4. Mapping Quality

Mean Mapping Quality	43.59

2.5. Mismatches and indels

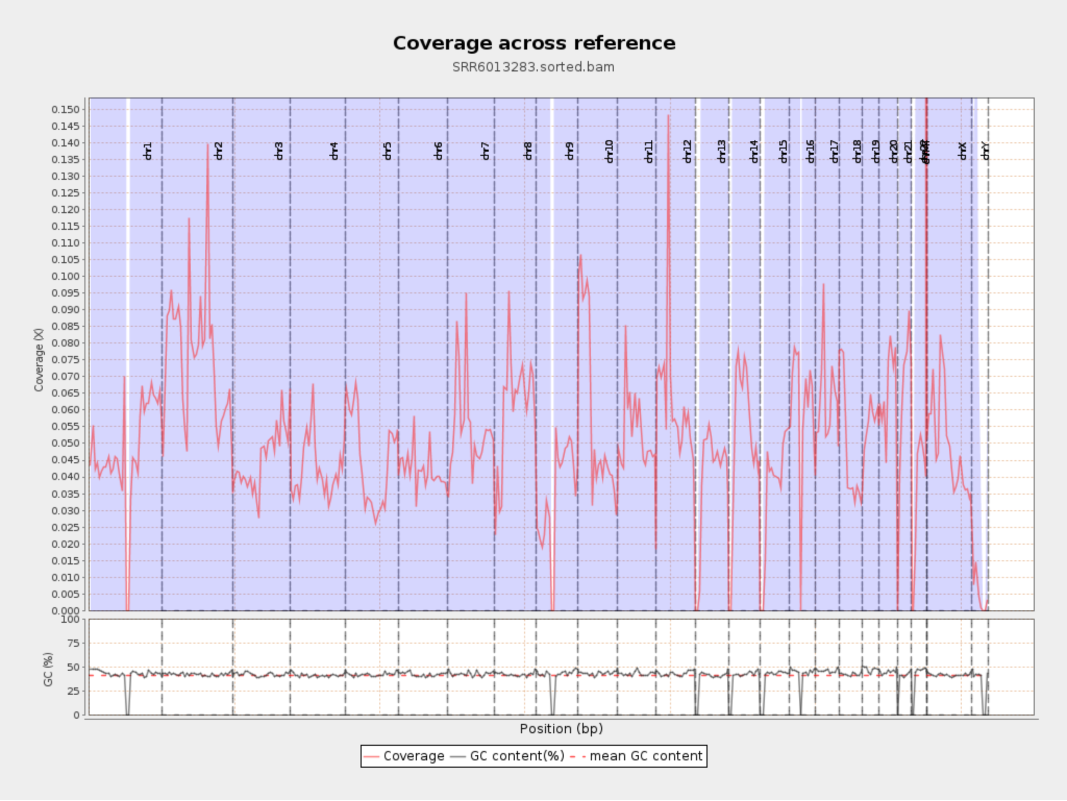
General error rate	0.81%
Mismatches	1,264,783
Insertions	11,006
Mapped reads with at least one insertion	0.44%
Deletions	44,860
Mapped reads with at least one deletion	1.8%
Homopolymer indels	45.89%

2.6. Chromosome stats

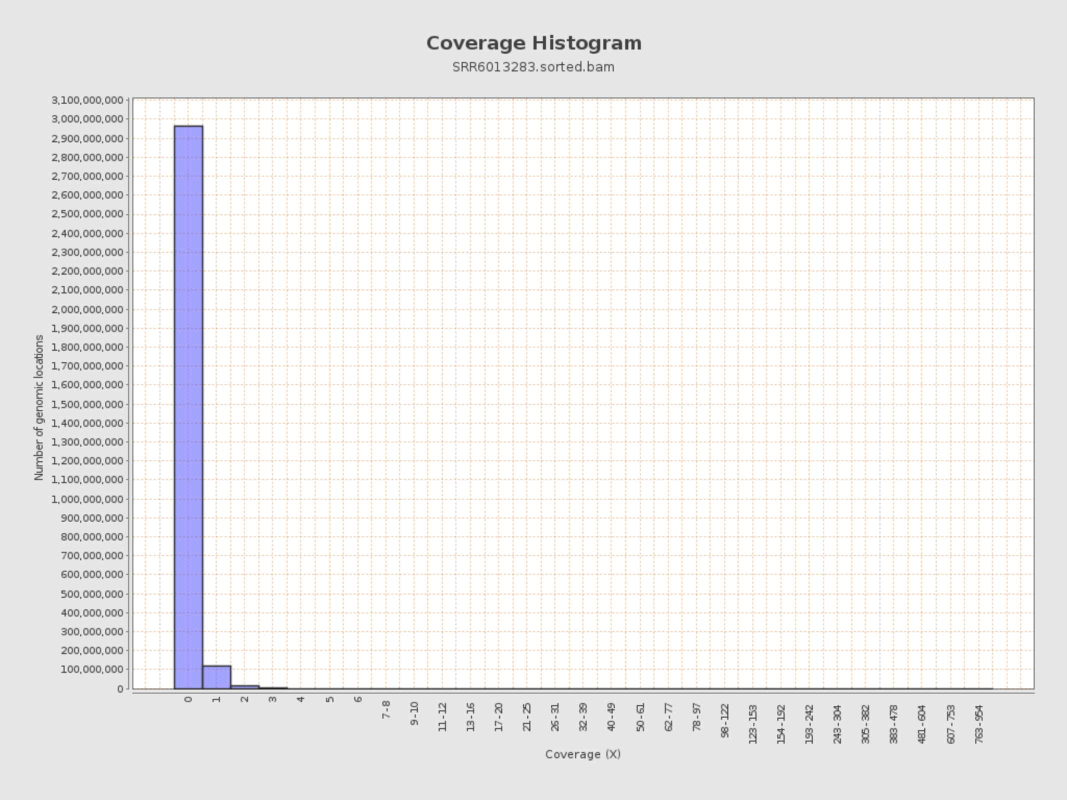
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11846870	0.0475	0.7596
chr2	243199373	18534830	0.0762	0.652
chr3	198022430	8944930	0.0452	0.2415
chr4	191154276	8111355	0.0424	0.244
chr5	180915260	8098104	0.0448	0.2454
chr6	171115067	7194388	0.042	0.3161
chr7	159138663	8840692	0.0556	0.7356

chr8	146364022	8899512	0.0608	0.4326
chr9	141213431	4811126	0.0341	0.3861
chr10	135534747	8108577	0.0598	0.4496
chr11	135006516	7169752	0.0531	0.3834
chr12	133851895	8536916	0.0638	0.2956
chr13	115169878	4520167	0.0392	0.2229
chr14	107349540	5512043	0.0513	0.2764
chr15	102531392	3731271	0.0364	0.2307
chr16	90354753	5508141	0.061	0.3081
chr17	81195210	5124028	0.0631	0.3657
chr18	78077248	3749165	0.048	0.6813
chr19	59128983	3308310	0.056	0.6095
chr20	63025520	4152319	0.0659	0.2994
chr21	48129895	3007010	0.0625	0.3006
chr22	51304566	1716561	0.0335	0.2075
chrMT	16571	62736	3.7859	2.8566
chrX	155270560	7810253	0.0503	0.3209
chrY	59373566	340915	0.0057	0.1098

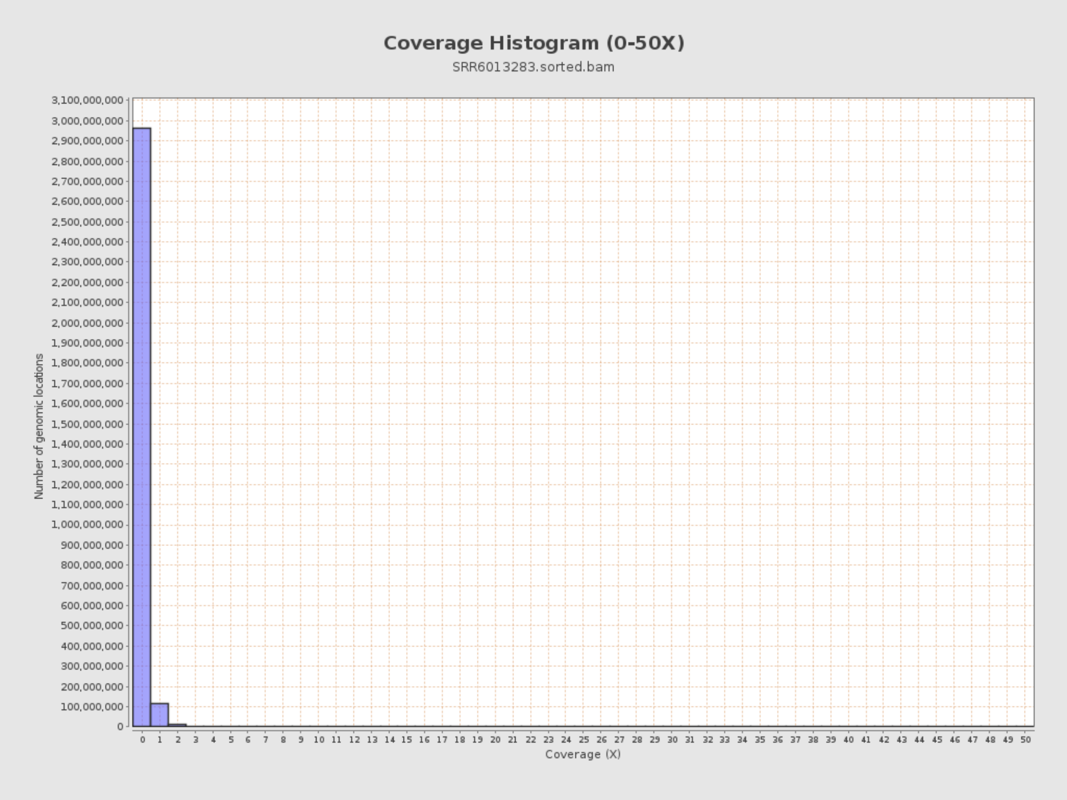
3. Results : Coverage across reference



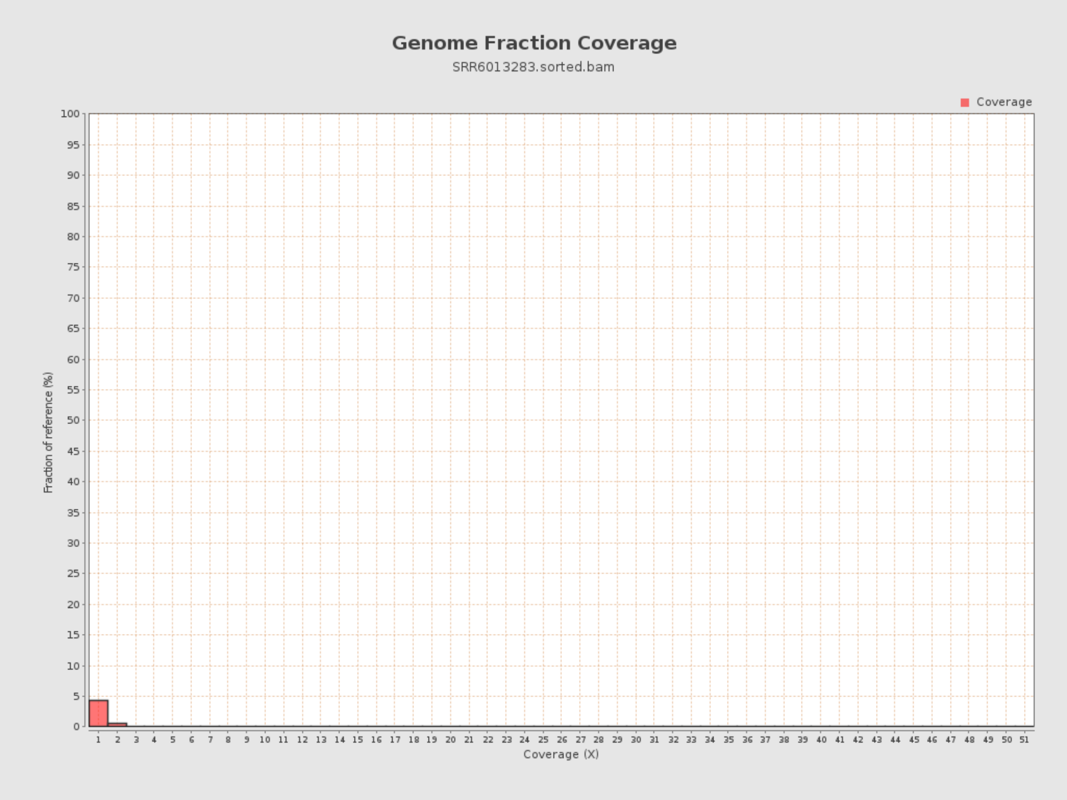
4. Results : Coverage Histogram



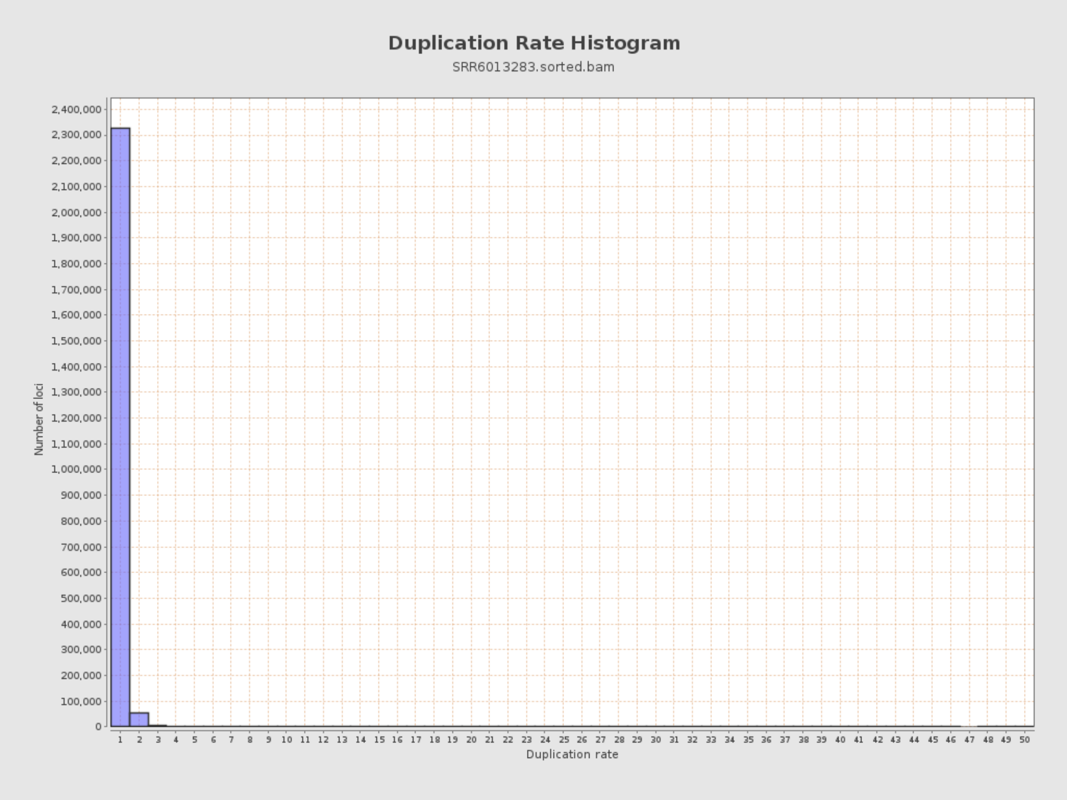
5. Results : Coverage Histogram (0-50X)



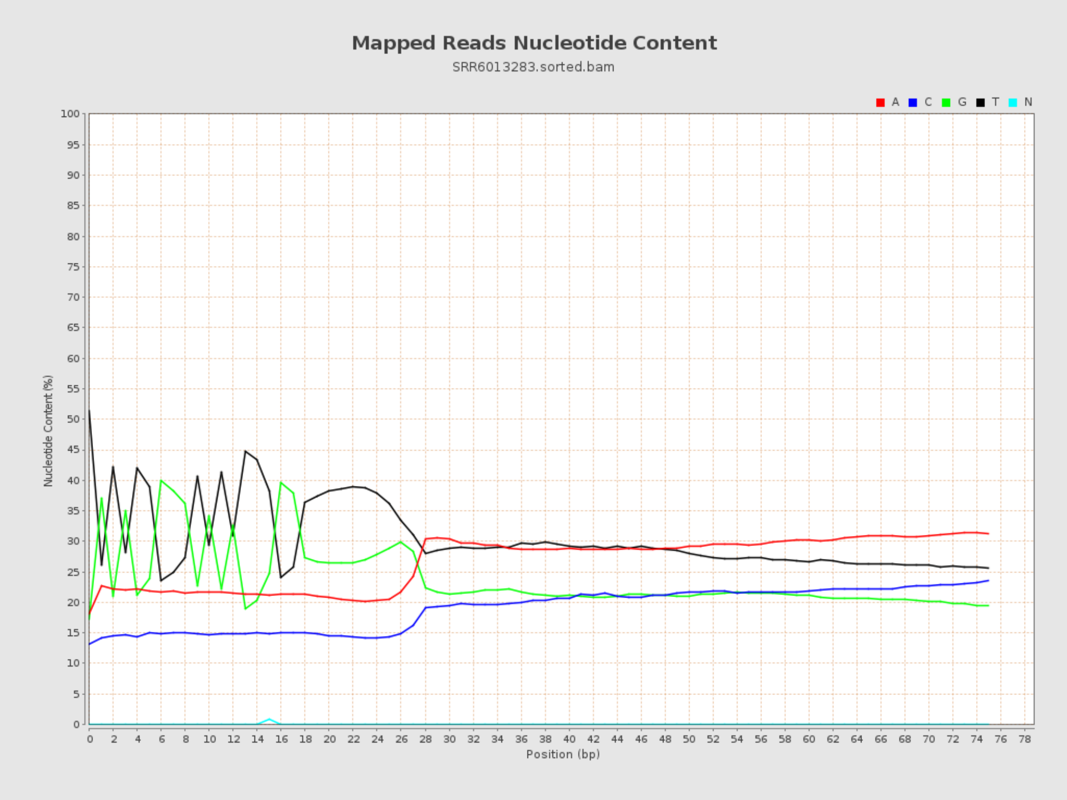
6. Results : Genome Fraction Coverage



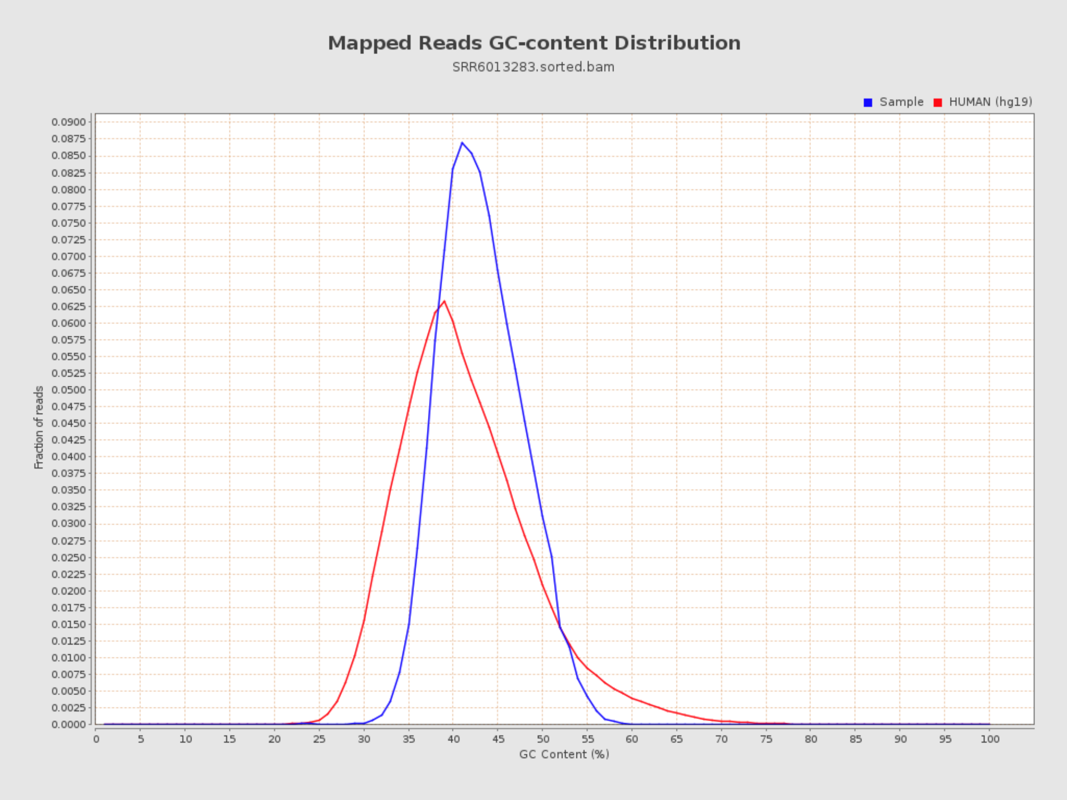
7. Results : Duplication Rate Histogram



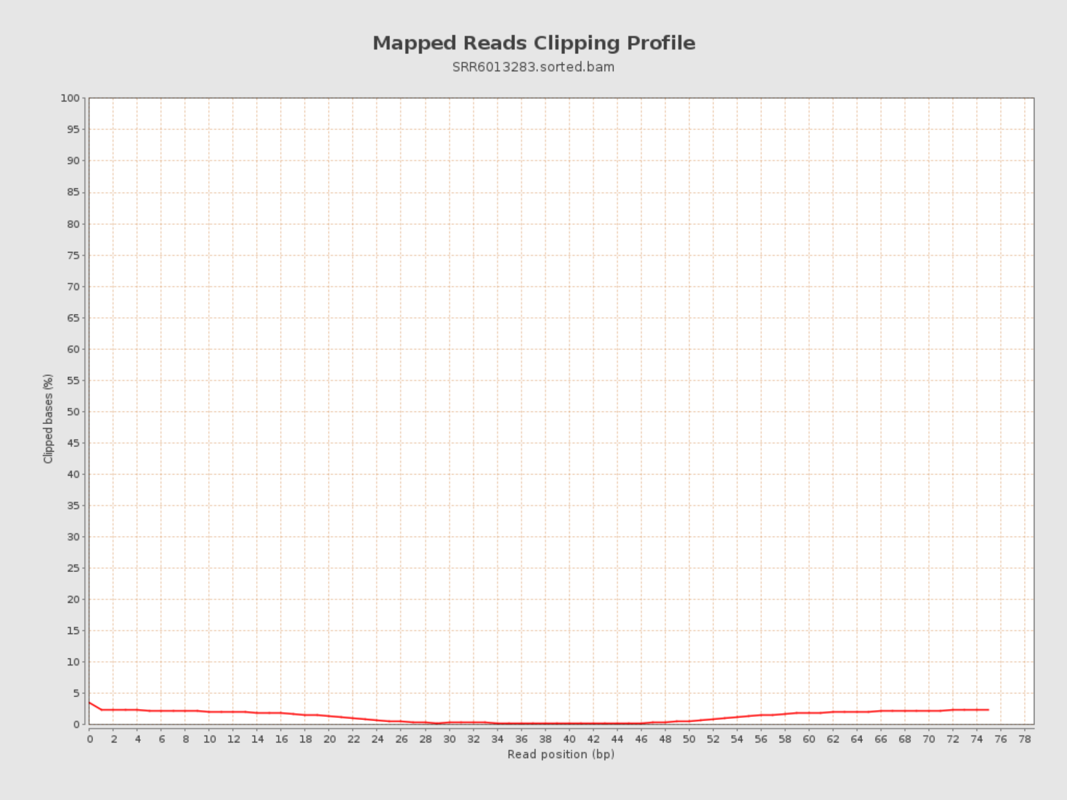
8. Results : Mapped Reads Nucleotide Content



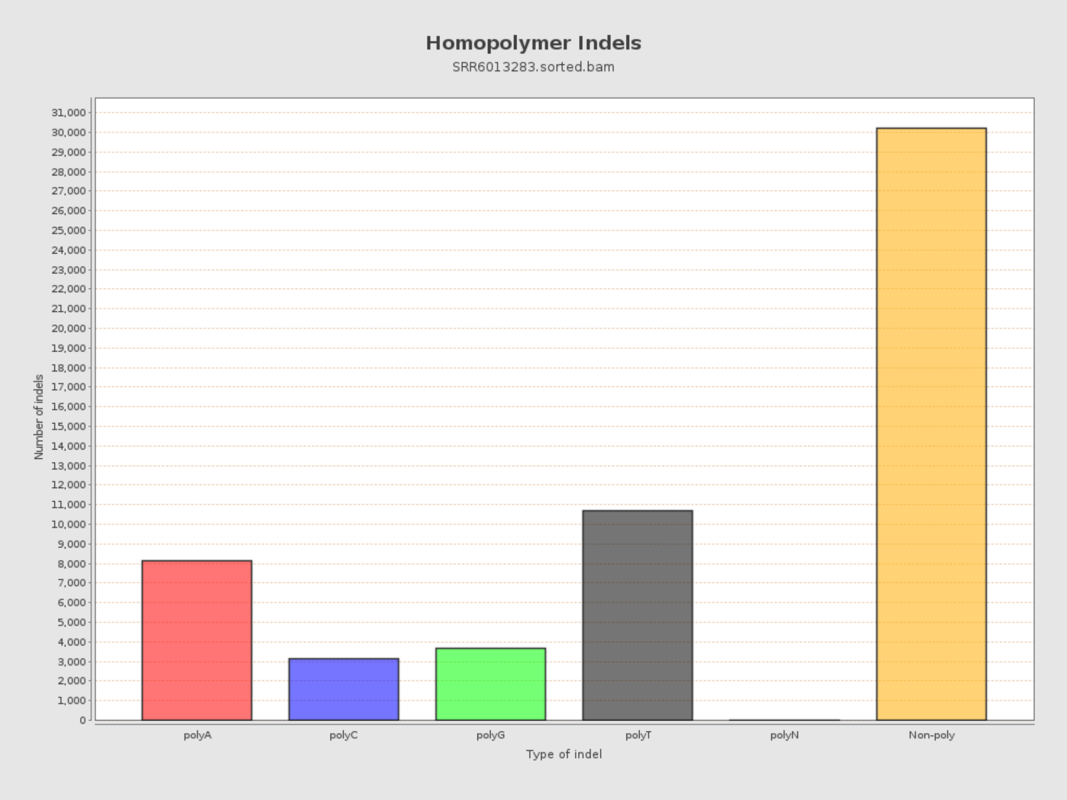
9. Results : Mapped Reads GC-content Distribution



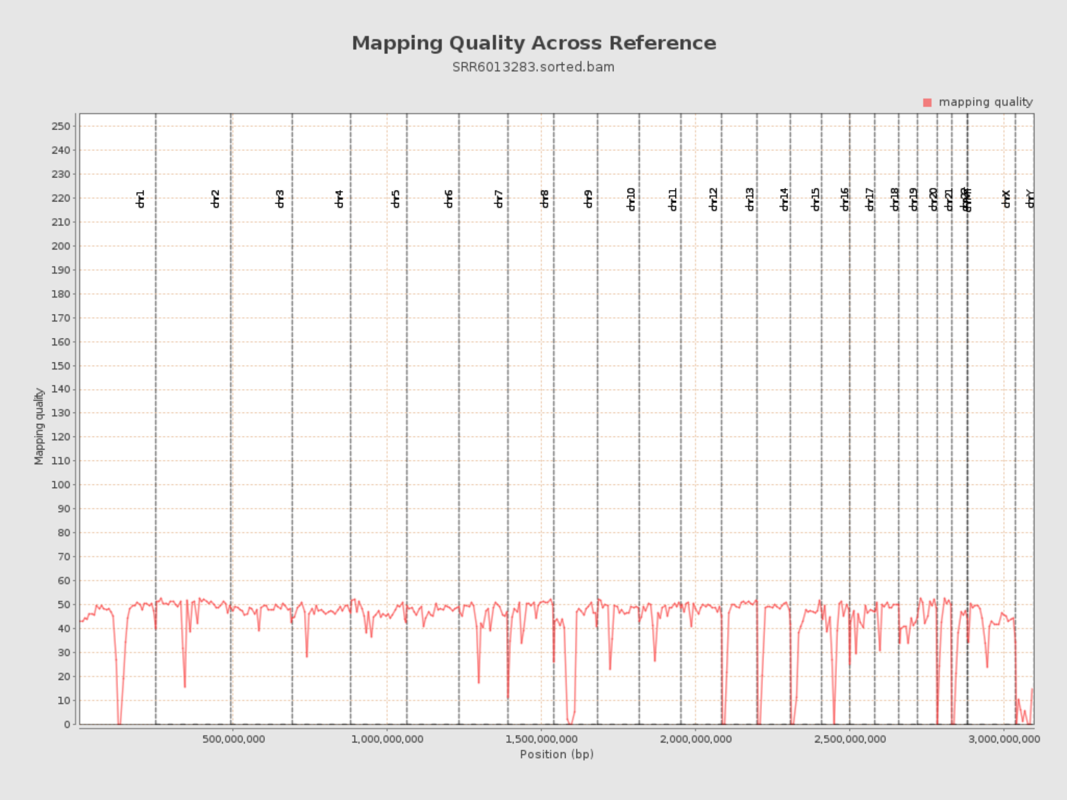
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram