Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:04:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008824.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_SRR6008824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:04:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,254,809
Mapped reads	1,562,130 / 69.28%
Unmapped reads	692,679 / 30.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,016 / 0.44%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	85,821 / 3.81%
Duplication rate	4.17%
Clipped reads	718,868 / 31.88%

2.2. ACGT Content

Number/percentage of A's	27,652,209 / 26.89%
Number/percentage of C's	20,002,154 / 19.45%
Number/percentage of T's	31,502,530 / 30.63%
Number/percentage of G's	23,532,163 / 22.88%
Number/percentage of N's	153,513 / 0.15%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0332

Standard Deviation	0.3315

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

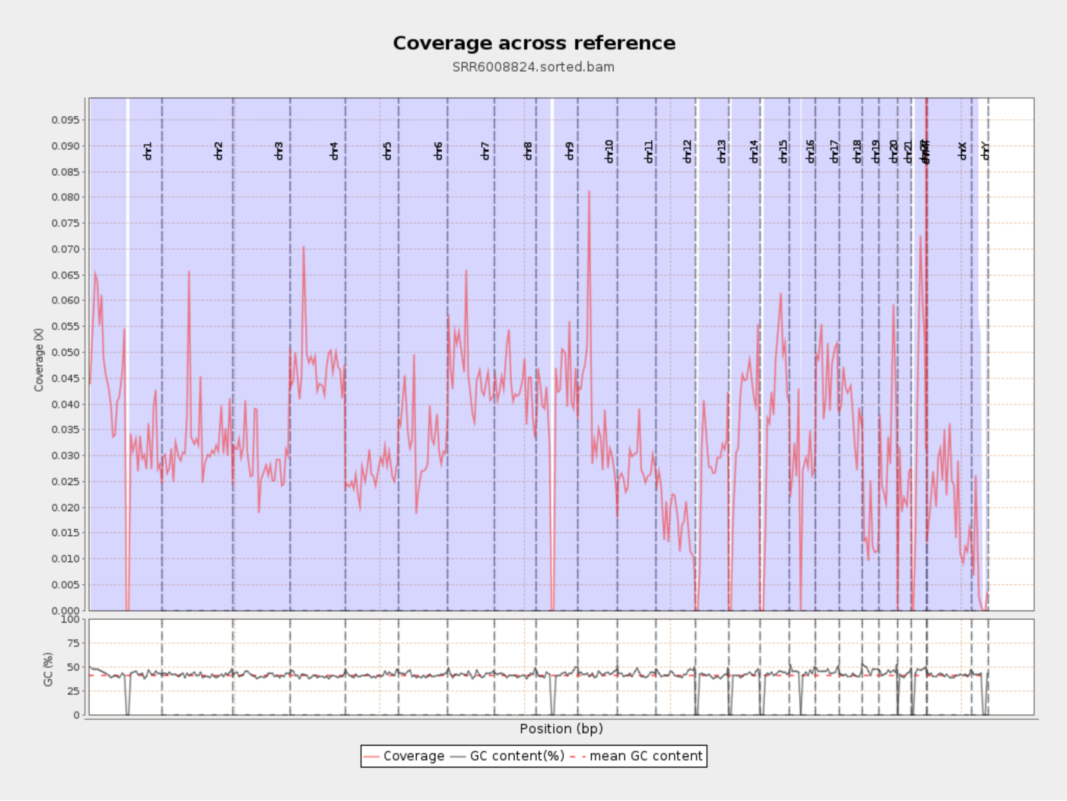
General error rate	0.88%
Mismatches	887,002
Insertions	7,887
Mapped reads with at least one insertion	0.5%
Deletions	27,898
Mapped reads with at least one deletion	1.76%
Homopolymer indels	44.98%

2.6. Chromosome stats

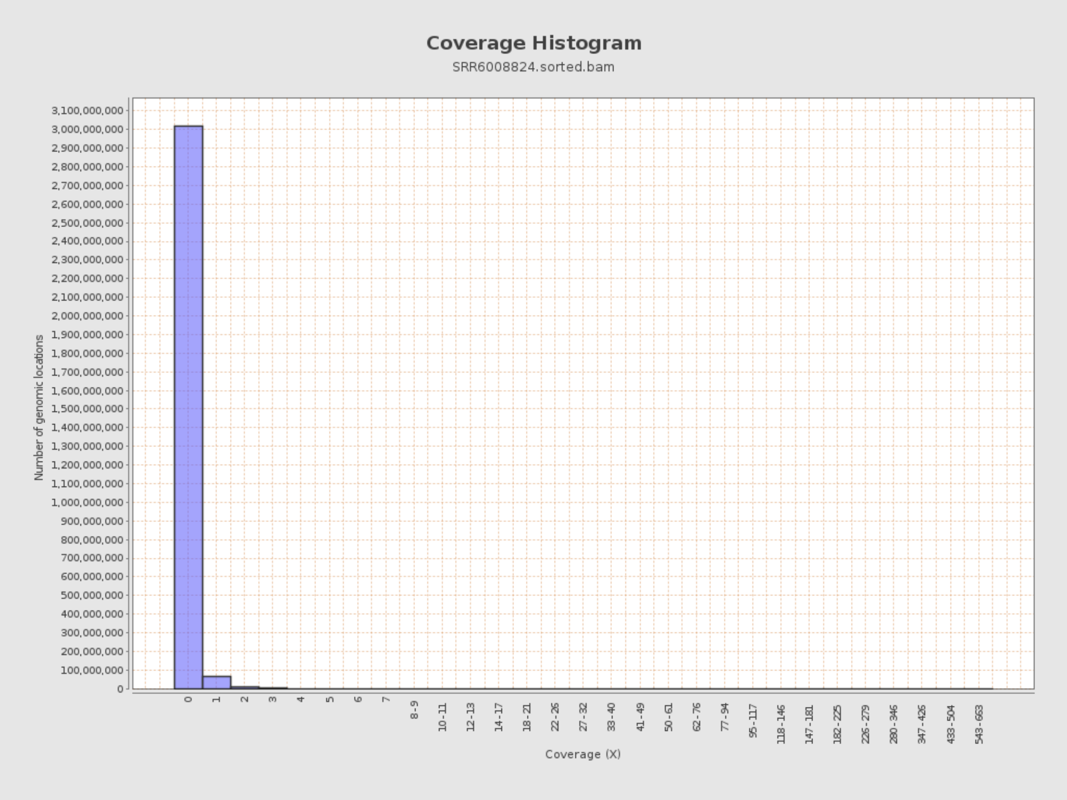
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9493771	0.0381	0.4189
chr2	243199373	7971489	0.0328	0.4039
chr3	198022430	5815540	0.0294	0.2163
chr4	191154276	9045553	0.0473	0.3103
chr5	180915260	4799143	0.0265	0.2001
chr6	171115067	5624072	0.0329	0.2523
chr7	159138663	7392217	0.0465	0.4506

chr8	146364022	6353286	0.0434	0.4728
chr9	141213431	5485334	0.0388	0.3552
chr10	135534747	5144385	0.038	0.4559
chr11	135006516	3741148	0.0277	0.2769
chr12	133851895	2413325	0.018	0.1792
chr13	115169878	2996981	0.026	0.1977
chr14	107349540	3793301	0.0353	0.2747
chr15	102531392	3810450	0.0372	0.2387
chr16	90354753	2439352	0.027	0.2909
chr17	81195210	3803507	0.0468	0.302
chr18	78077248	3041982	0.039	0.5774
chr19	59128983	897129	0.0152	0.3001
chr20	63025520	2140621	0.034	0.2402
chr21	48129895	1064957	0.0221	0.245
chr22	51304566	1905030	0.0371	0.2401
chrMT	16571	6496	0.392	0.6998
chrX	155270560	3350861	0.0216	0.2066
chrY	59373566	363431	0.0061	0.2602

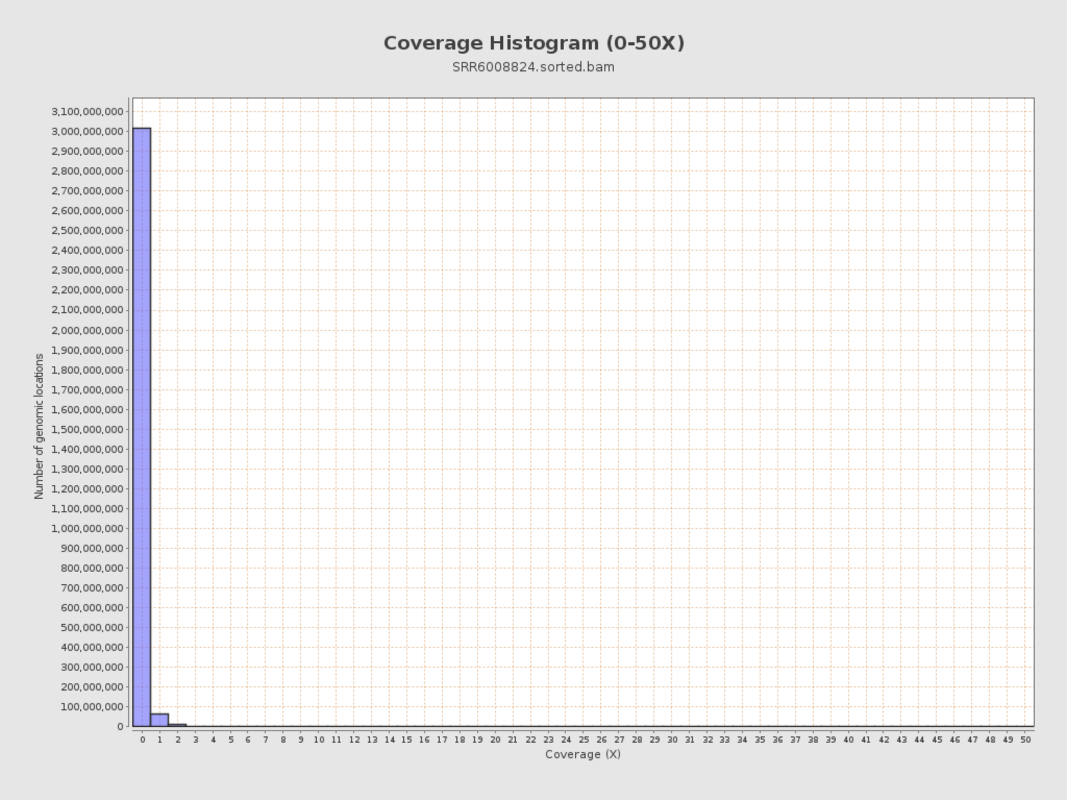
3. Results : Coverage across reference



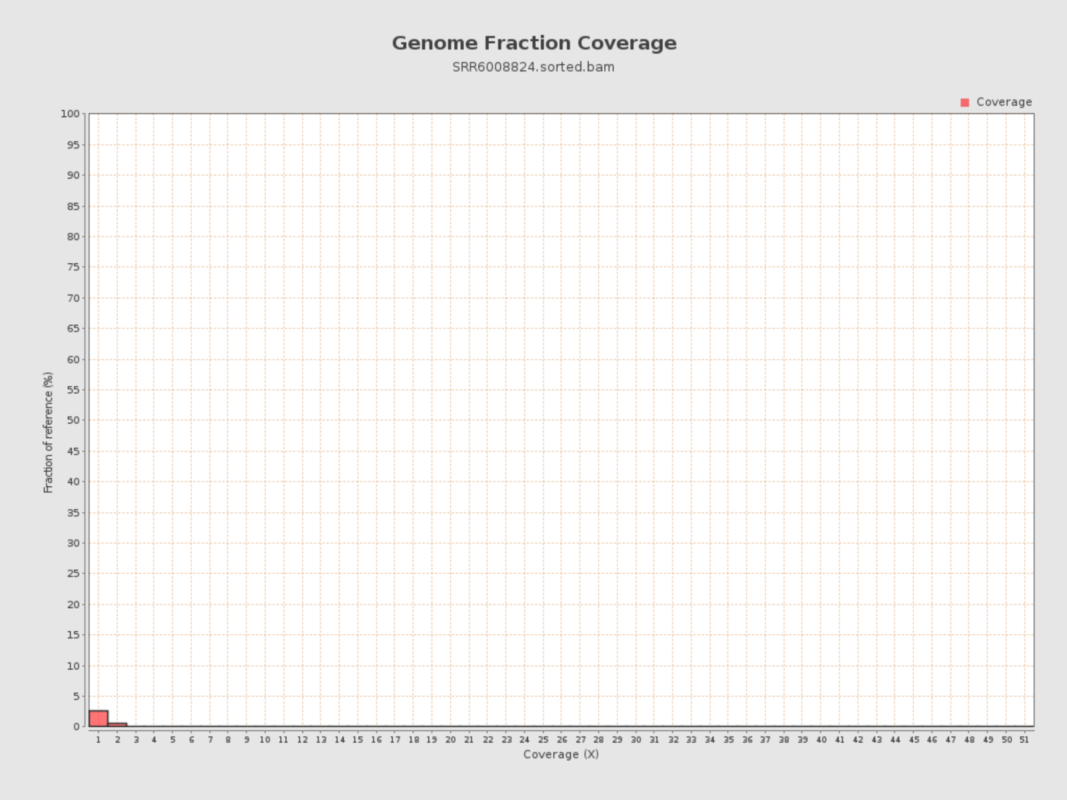
4. Results : Coverage Histogram



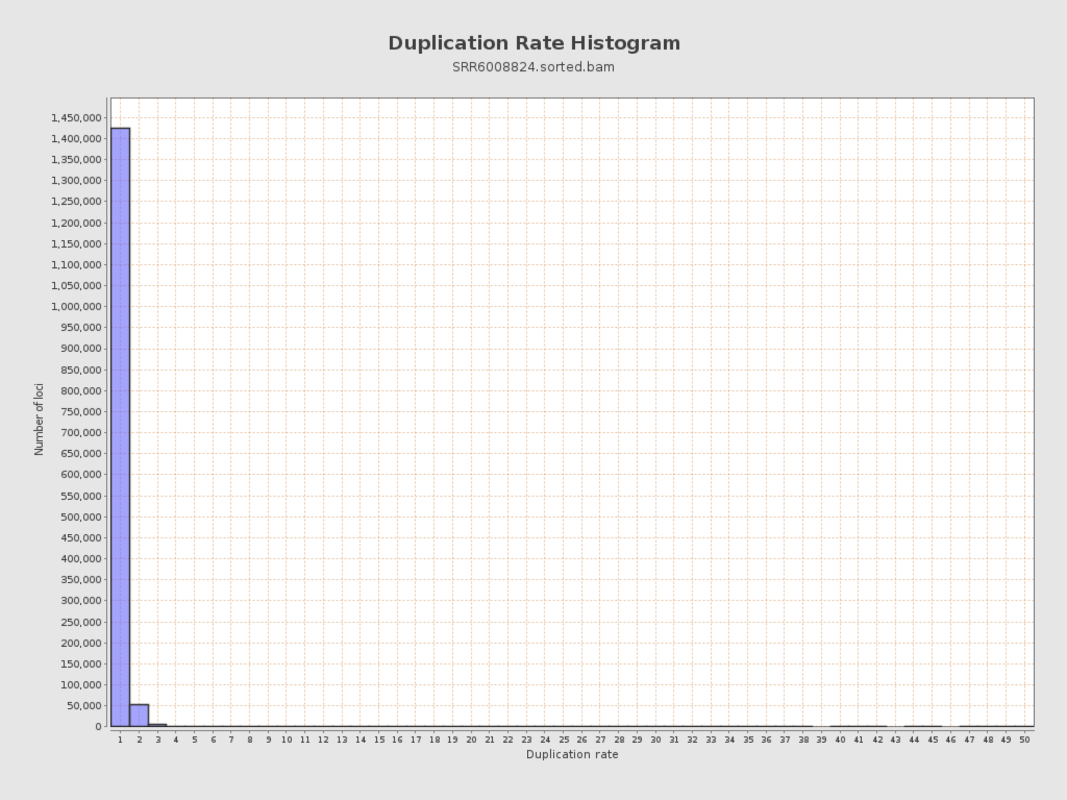
5. Results : Coverage Histogram (0-50X)



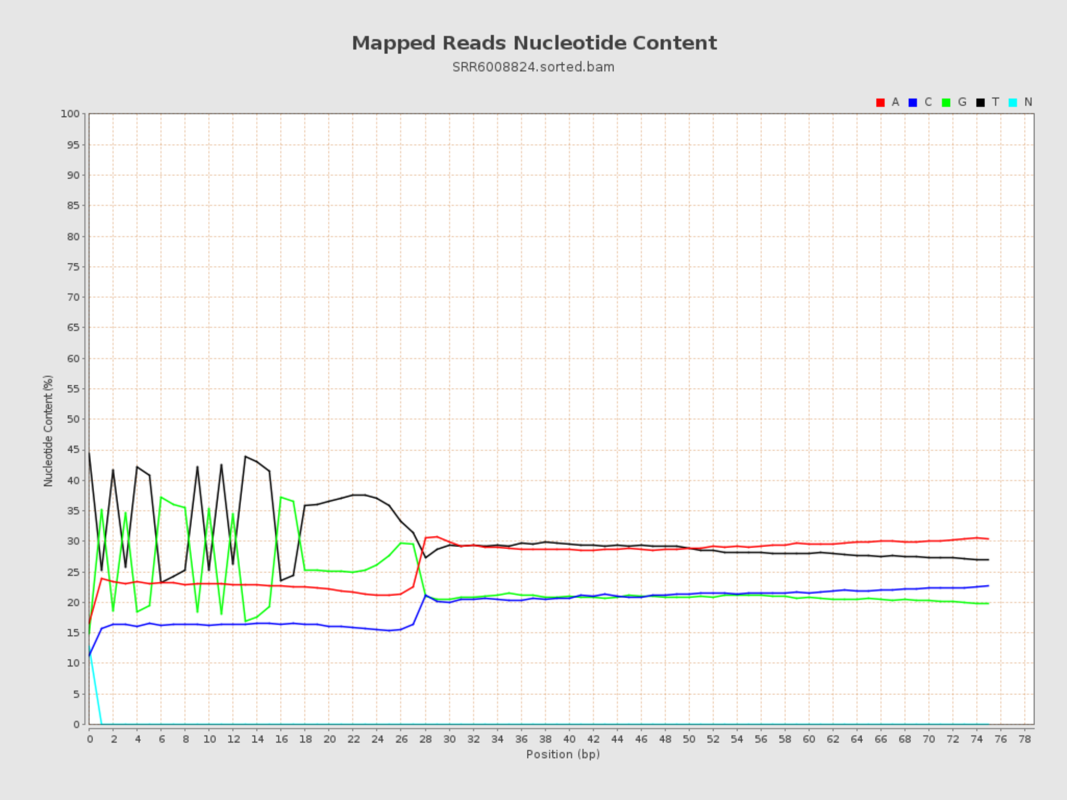
6. Results : Genome Fraction Coverage



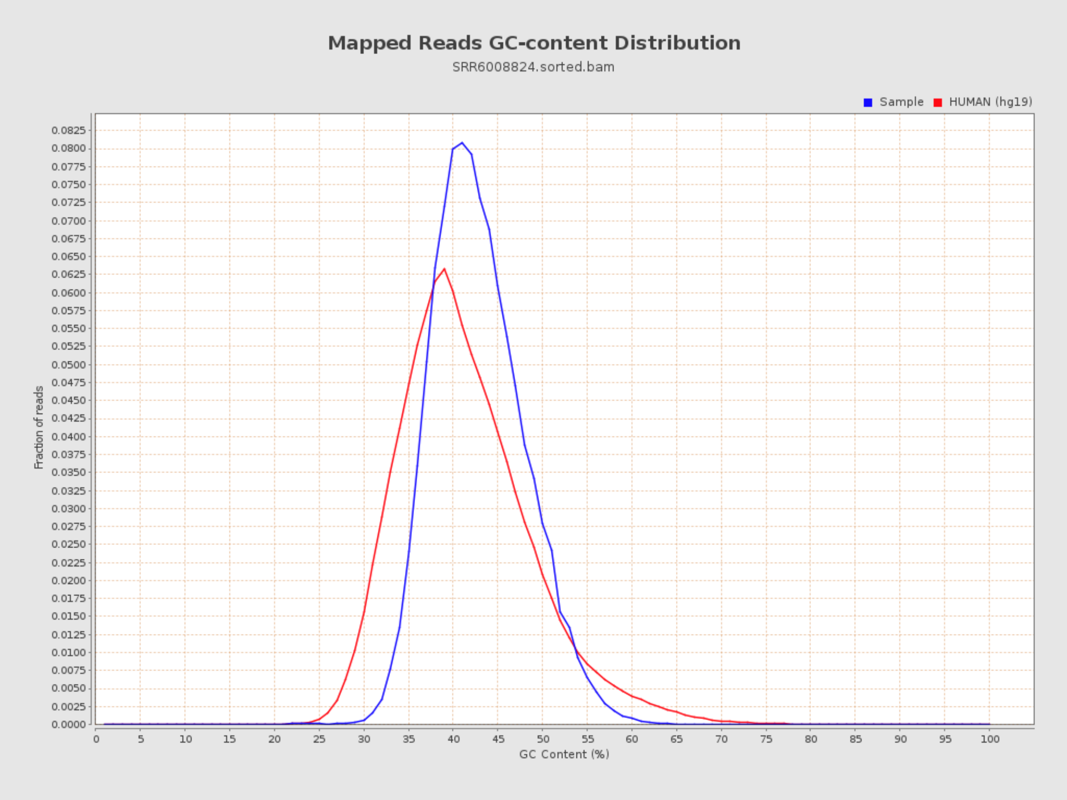
7. Results : Duplication Rate Histogram



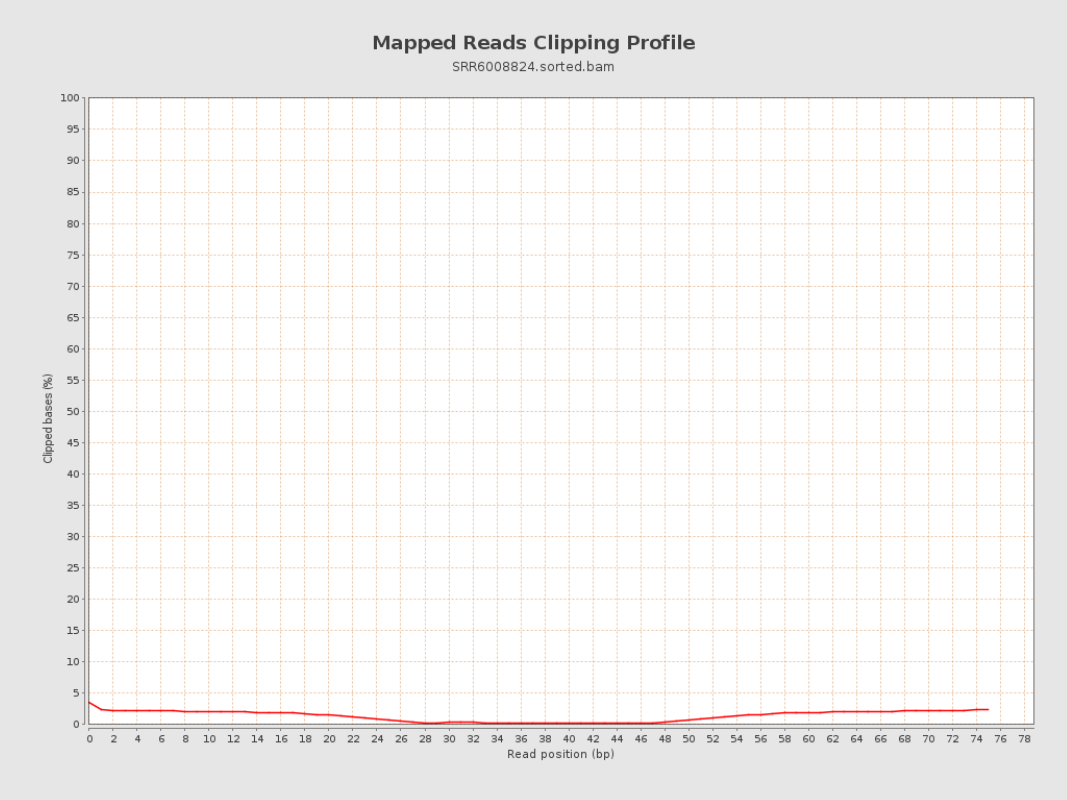
8. Results : Mapped Reads Nucleotide Content



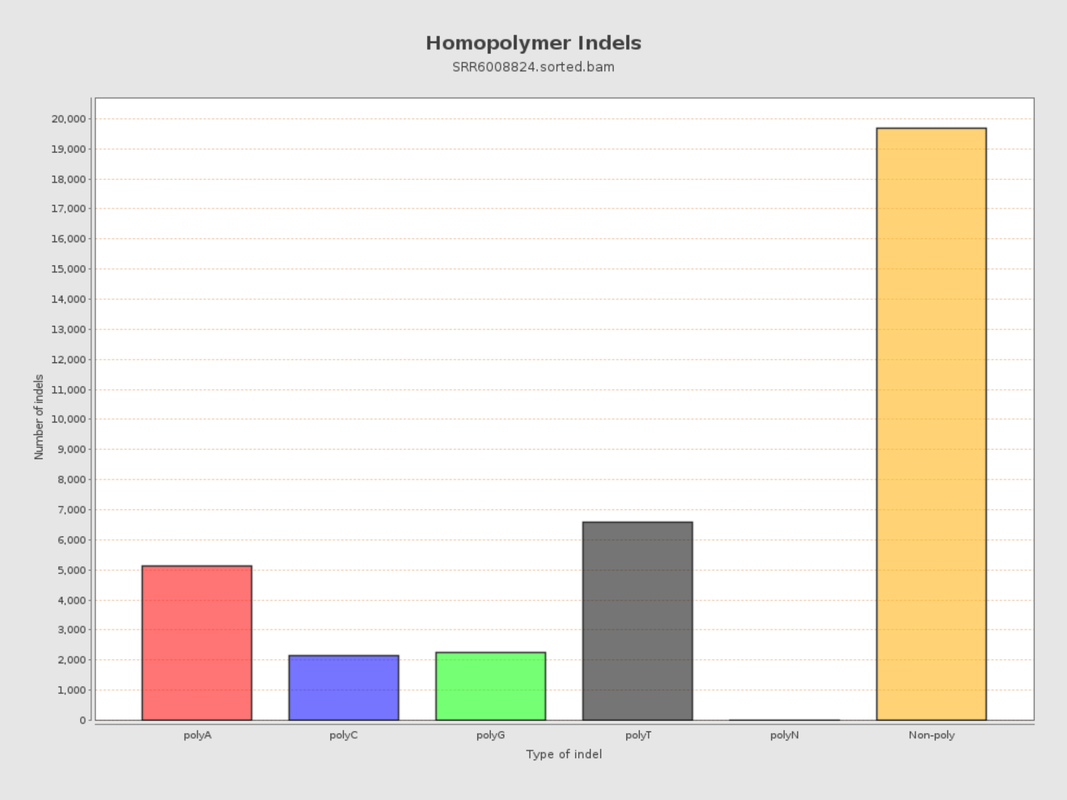
9. Results : Mapped Reads GC-content Distribution



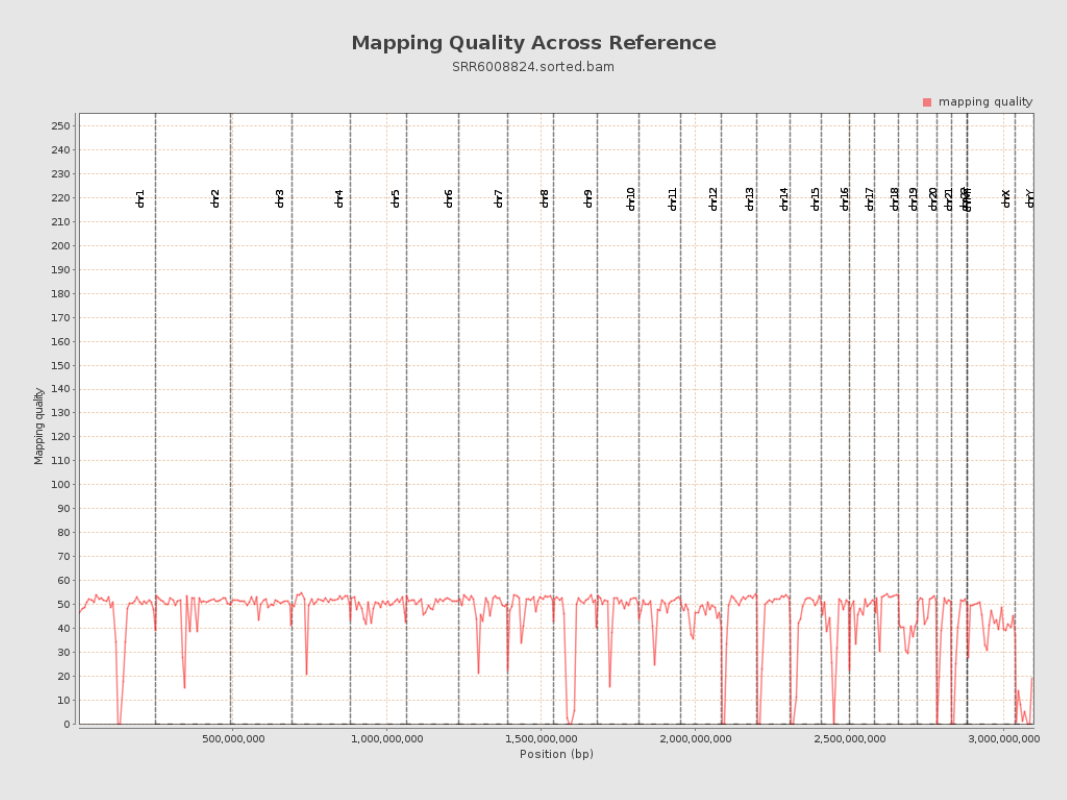
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram