Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:00:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008732.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_SRR6008732 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008732.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:00:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008732.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,656,106
Mapped reads	3,339,149 / 91.33%
Unmapped reads	316,957 / 8.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,423 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	184,984 / 5.06%
Duplication rate	4.38%
Clipped reads	1,607,290 / 43.96%

2.2. ACGT Content

Number/percentage of A's	58,962,507 / 26.87%
Number/percentage of C's	40,752,357 / 18.57%
Number/percentage of T's	68,909,598 / 31.4%
Number/percentage of G's	50,660,847 / 23.08%
Number/percentage of N's	169,172 / 0.08%
GC Percentage	41.65%

2.3. Coverage

Mean	0.0709

Standard Deviation	0.5304

2.4. Mapping Quality

Mean Mapping Quality	45.62

2.5. Mismatches and indels

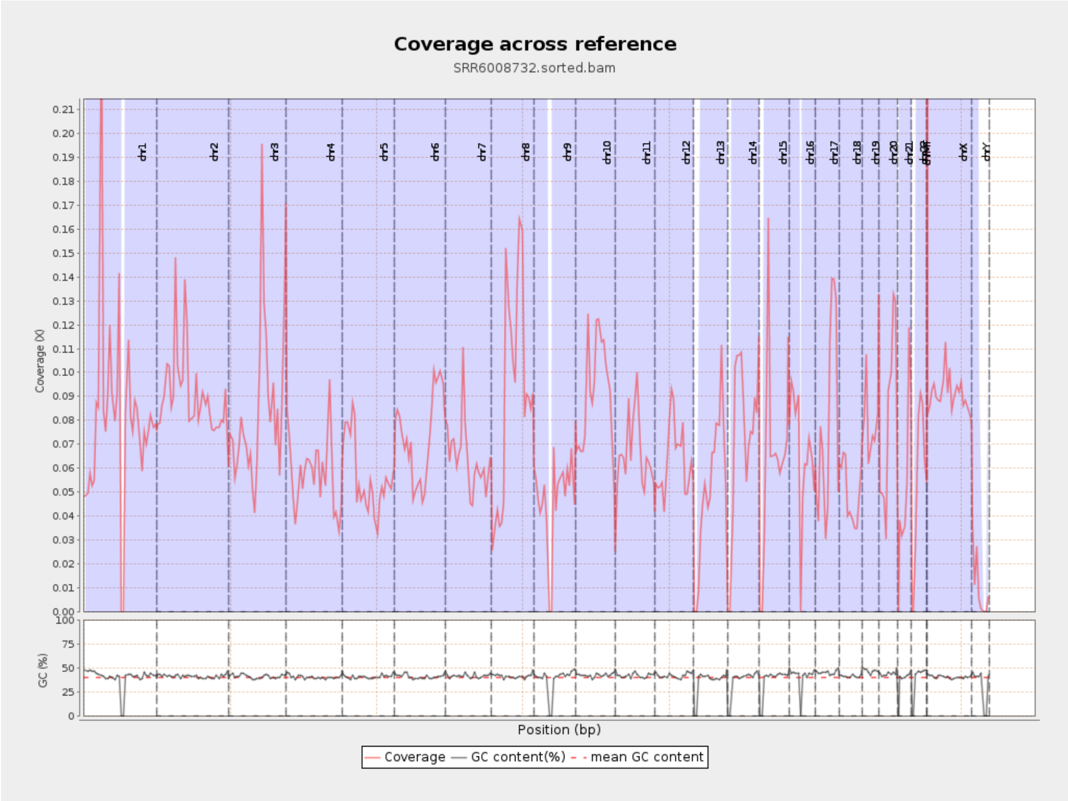
General error rate	0.84%
Mismatches	1,824,094
Insertions	16,301
Mapped reads with at least one insertion	0.48%
Deletions	71,430
Mapped reads with at least one deletion	2.11%
Homopolymer indels	46.52%

2.6. Chromosome stats

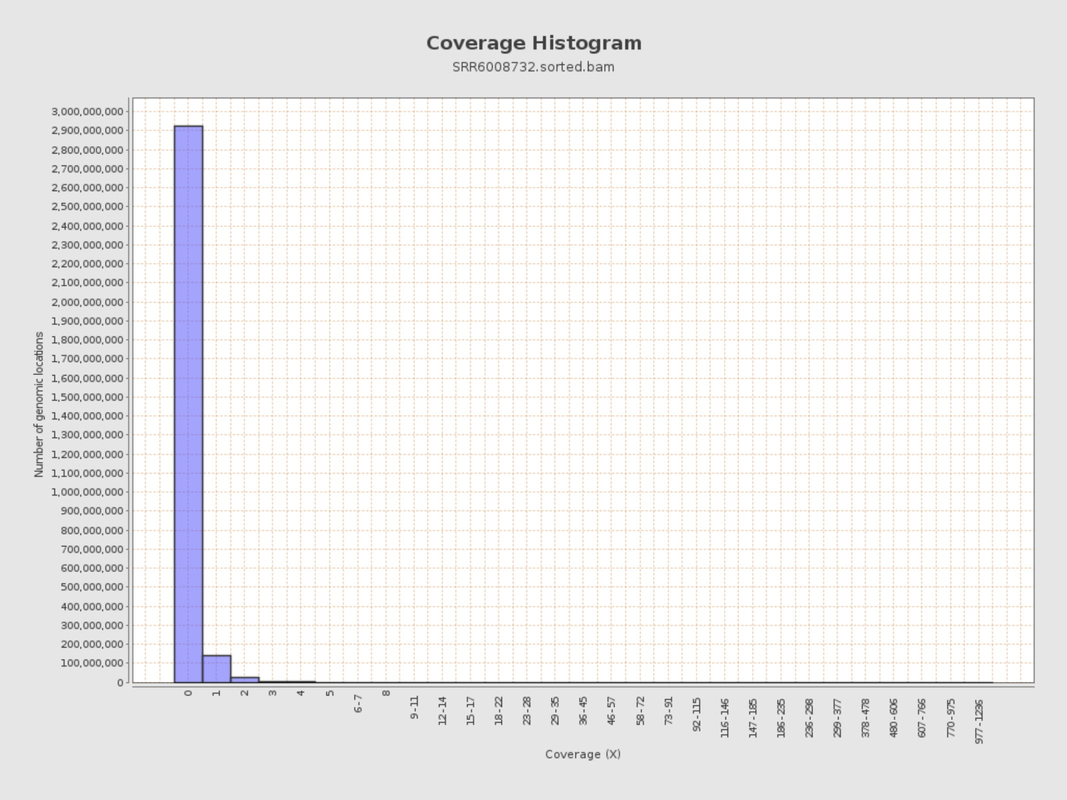
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20064409	0.0805	0.9833
chr2	243199373	22160874	0.0911	0.7228
chr3	198022430	16628026	0.084	0.3548
chr4	191154276	11173976	0.0585	0.3166
chr5	180915260	10240119	0.0566	0.2898
chr6	171115067	12507182	0.0731	0.3828
chr7	159138663	10323681	0.0649	0.7287

chr8	146364022	13258350	0.0906	0.5443
chr9	141213431	6580882	0.0466	0.4115
chr10	135534747	12426774	0.0917	0.5064
chr11	135006516	8936030	0.0662	0.5231
chr12	133851895	8522612	0.0637	0.3101
chr13	115169878	5986194	0.052	0.2752
chr14	107349540	7861354	0.0732	0.3413
chr15	102531392	6496846	0.0634	0.3242
chr16	90354753	5983426	0.0662	0.3563
chr17	81195210	6600007	0.0813	0.426
chr18	78077248	3834400	0.0491	0.7854
chr19	59128983	4708474	0.0796	0.6924
chr20	63025520	5080120	0.0806	0.3559
chr21	48129895	2602558	0.0541	0.3015
chr22	51304566	2812114	0.0548	0.2802
chrMT	16571	54538	3.2912	3.1642
chrX	155270560	14148862	0.0911	0.4149
chrY	59373566	581197	0.0098	0.2285

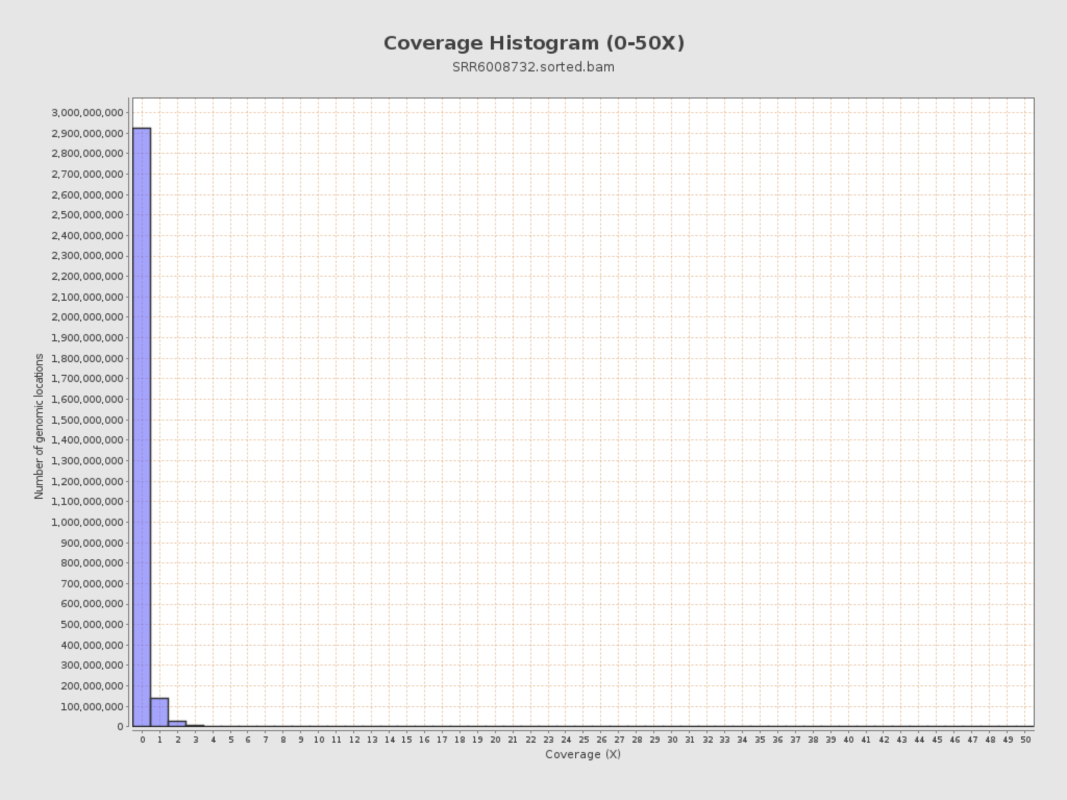
3. Results : Coverage across reference



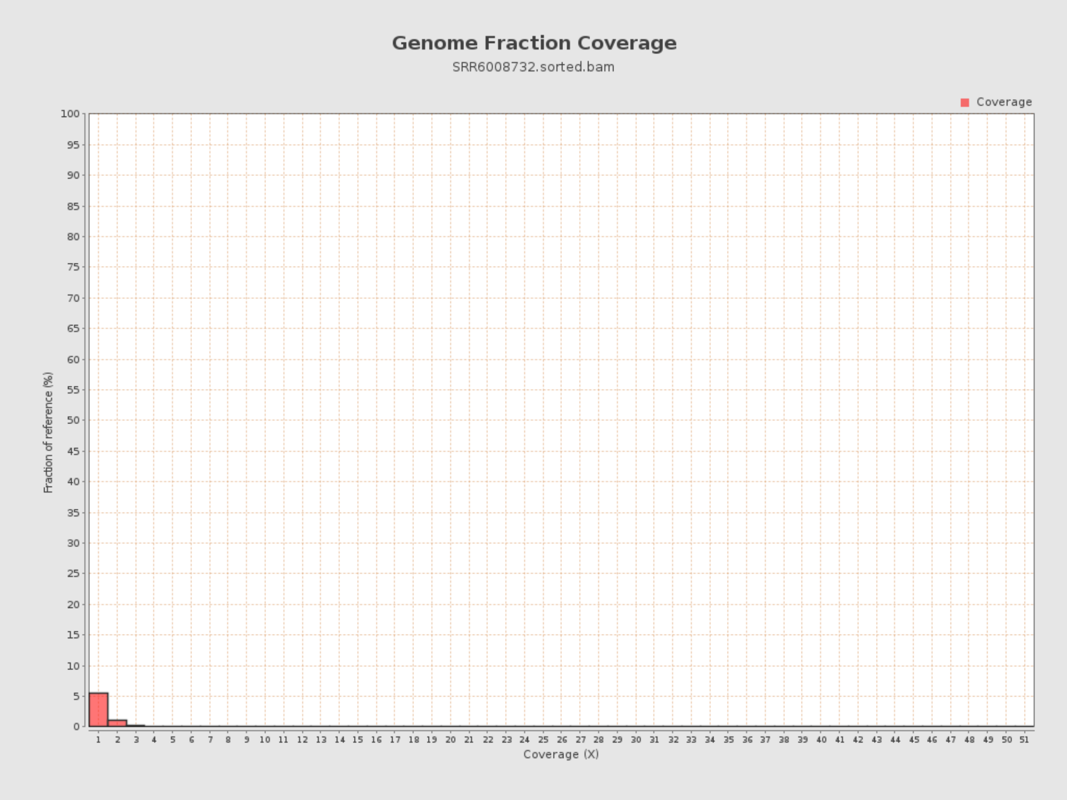
4. Results : Coverage Histogram



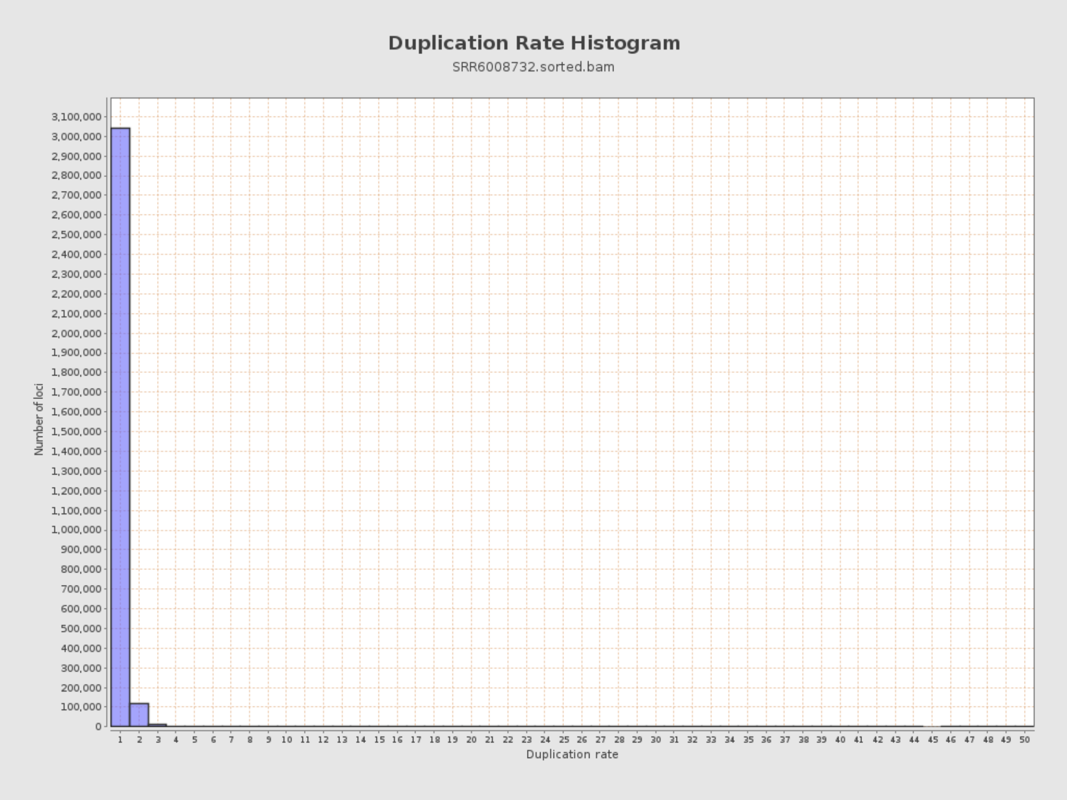
5. Results : Coverage Histogram (0-50X)



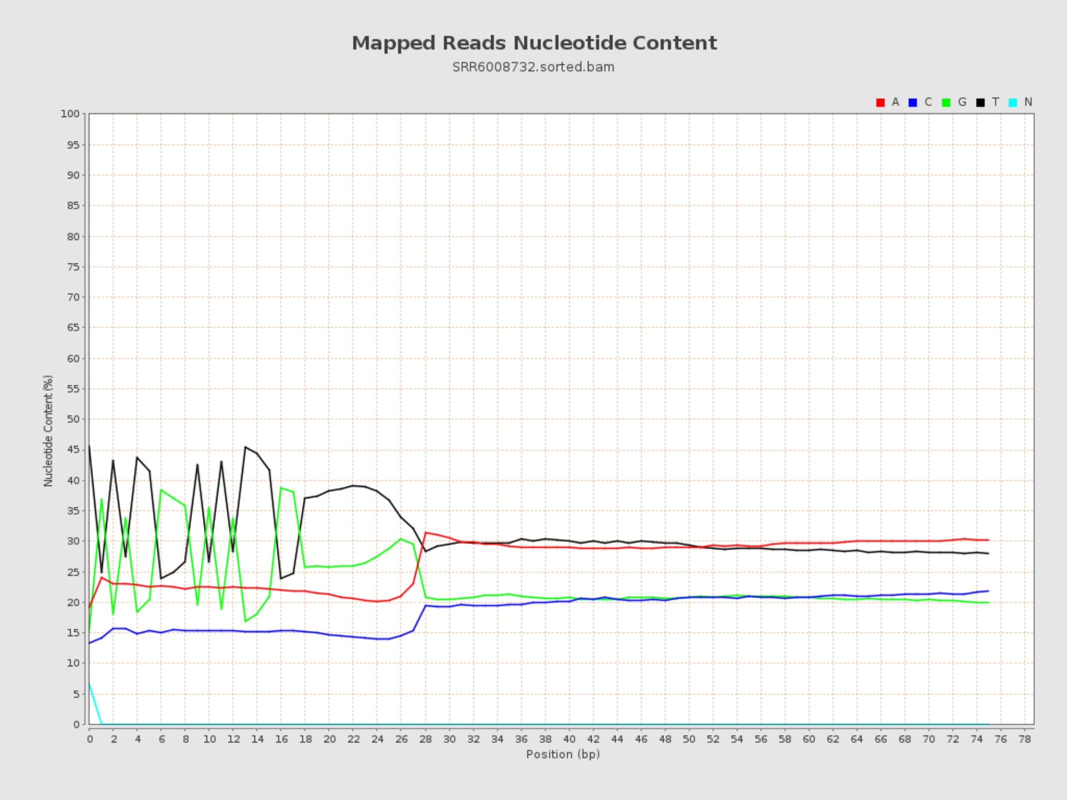
6. Results : Genome Fraction Coverage



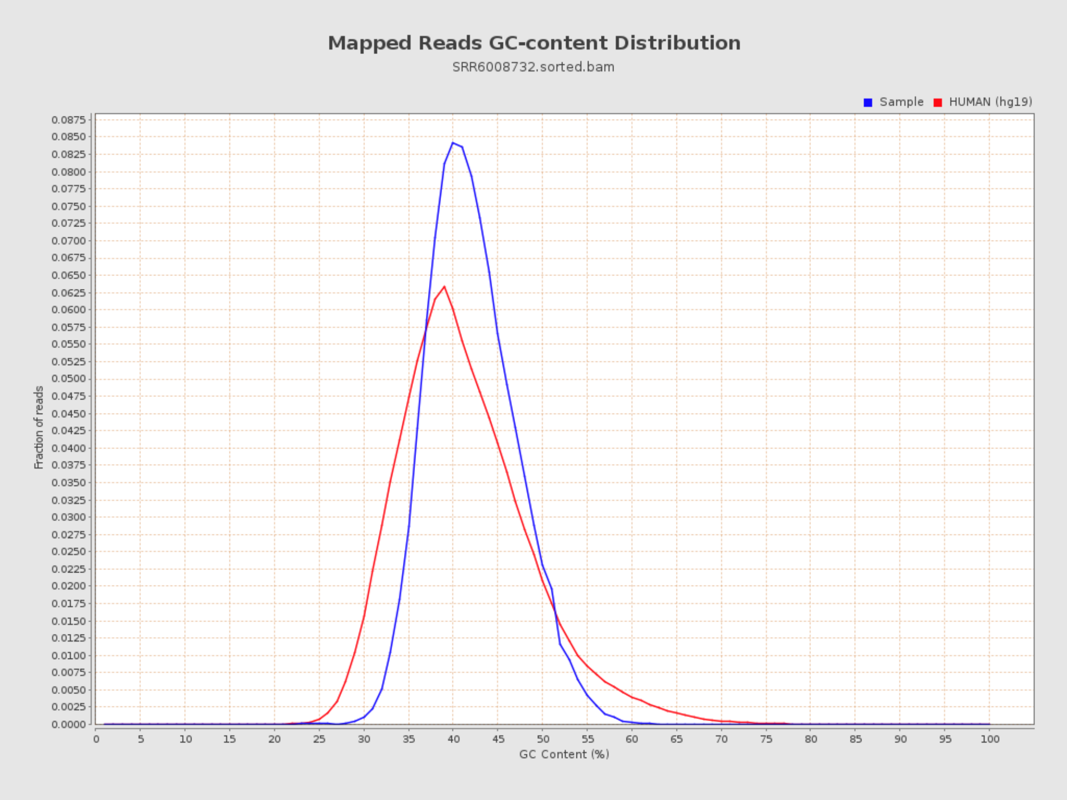
7. Results : Duplication Rate Histogram



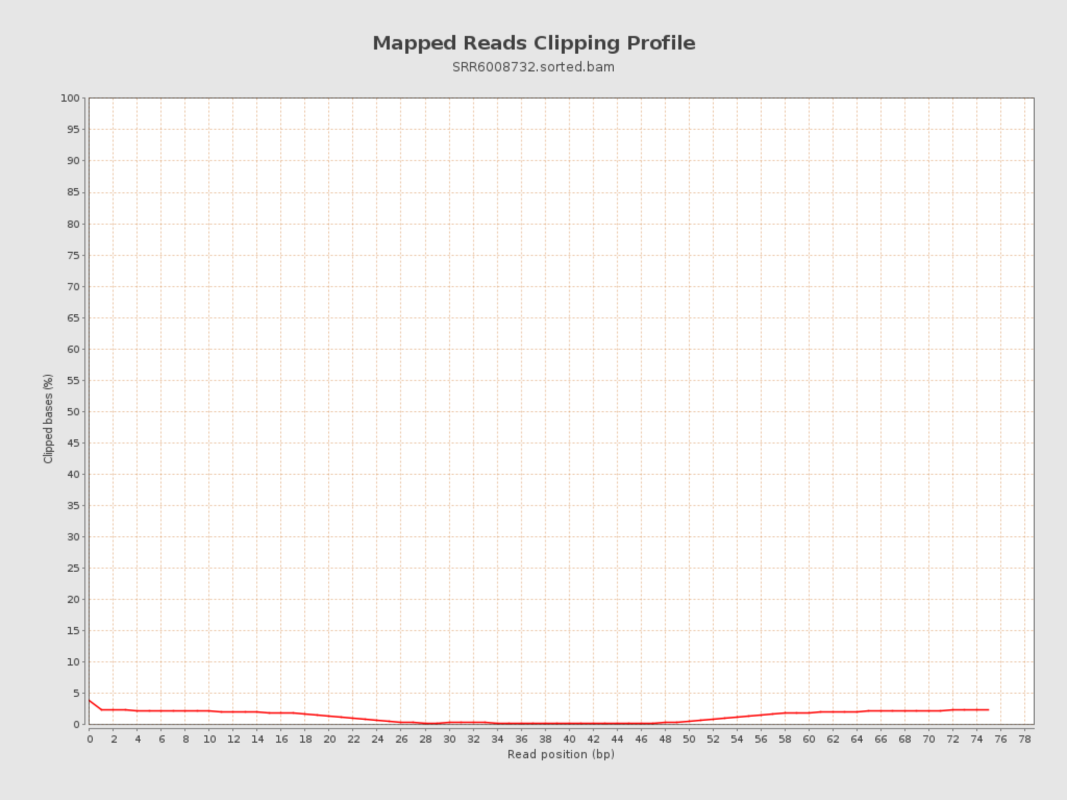
8. Results : Mapped Reads Nucleotide Content



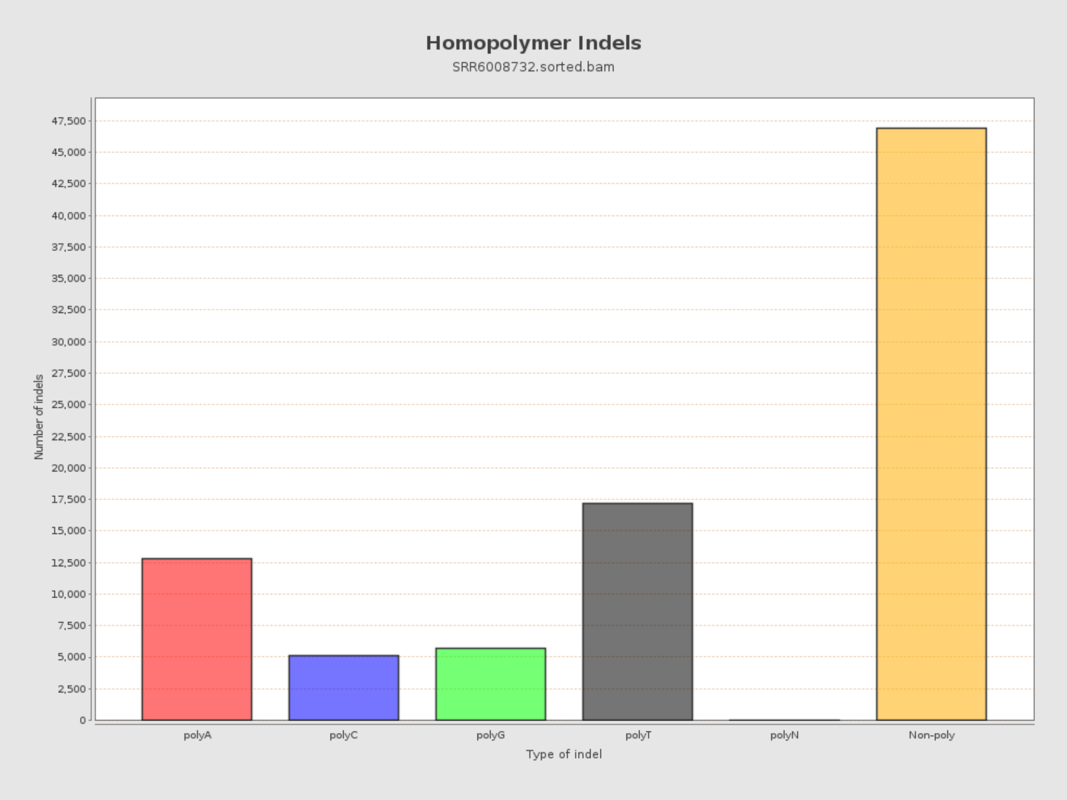
9. Results : Mapped Reads GC-content Distribution



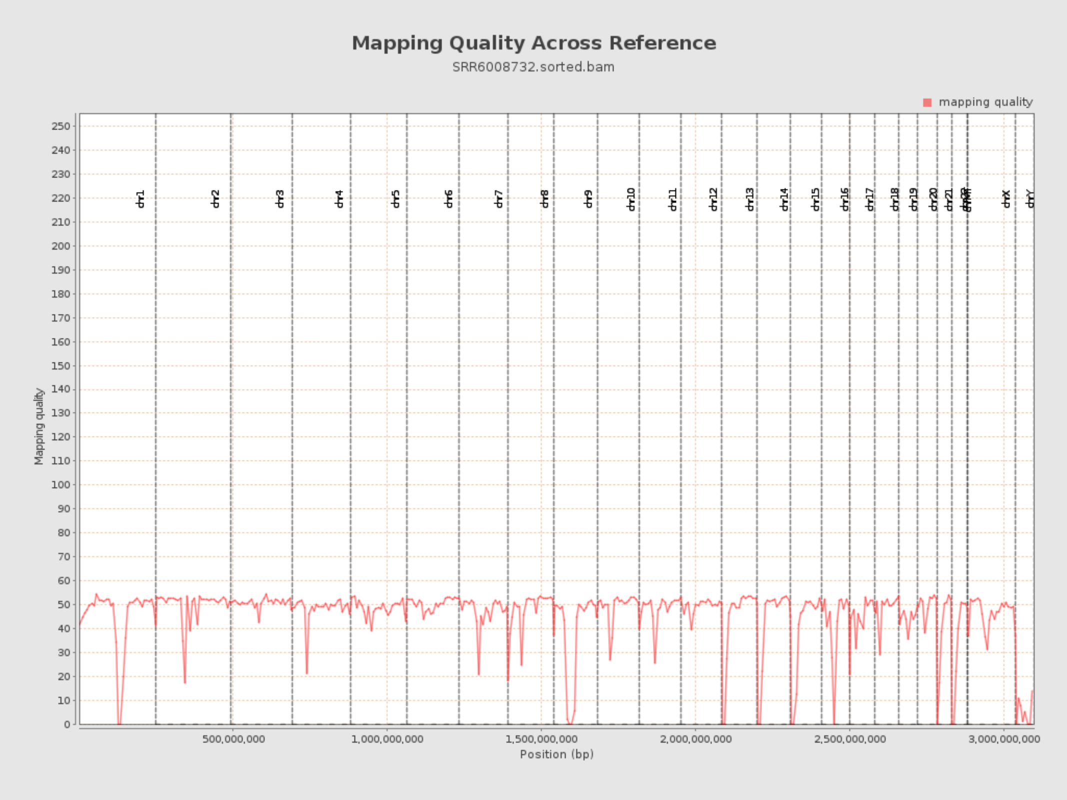
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram