Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:47:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008682.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_SRR6008682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008682.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:47:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,300,433
Mapped reads	1,991,418 / 86.57%
Unmapped reads	309,015 / 13.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,097 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	86,991 / 3.78%
Duplication rate	3.38%
Clipped reads	1,076,643 / 46.8%

2.2. ACGT Content

Number/percentage of A's	34,125,665 / 26.68%
Number/percentage of C's	24,318,747 / 19.02%
Number/percentage of T's	39,568,016 / 30.94%
Number/percentage of G's	29,837,192 / 23.33%
Number/percentage of N's	41,409 / 0.03%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0413

Standard Deviation	0.3816

2.4. Mapping Quality

Mean Mapping Quality	44.95

2.5. Mismatches and indels

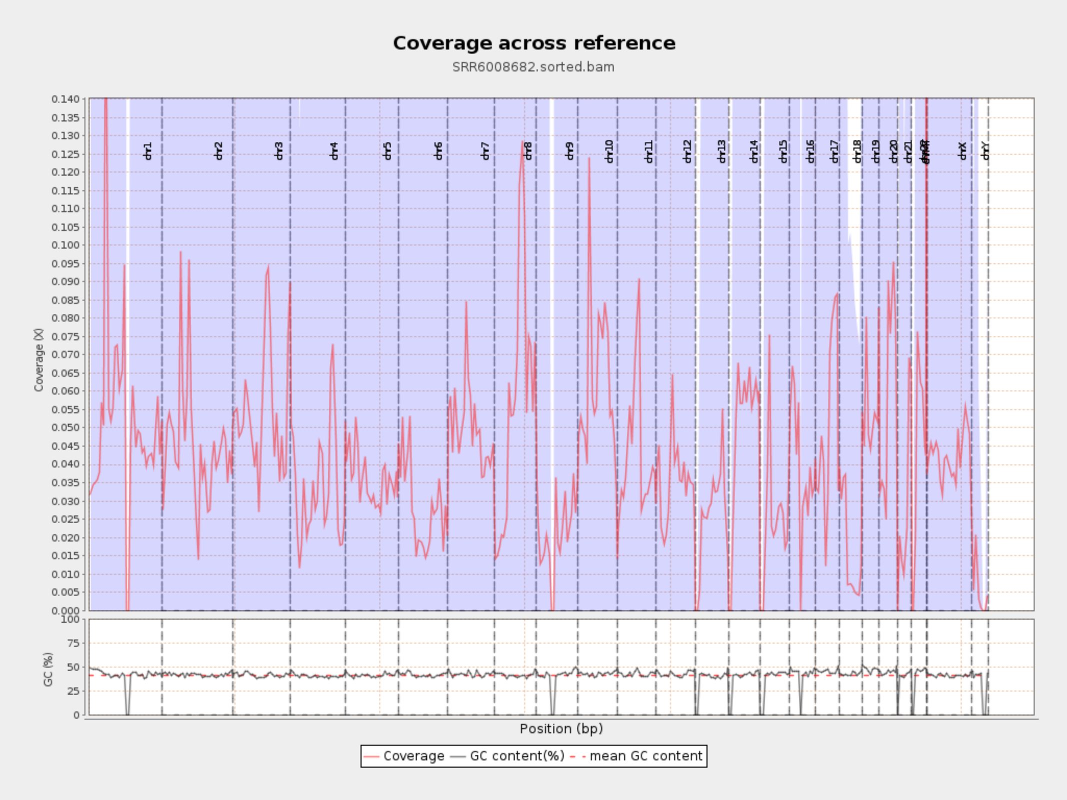
General error rate	0.87%
Mismatches	1,101,776
Insertions	7,800
Mapped reads with at least one insertion	0.39%
Deletions	51,868
Mapped reads with at least one deletion	2.56%
Homopolymer indels	41.52%

2.6. Chromosome stats

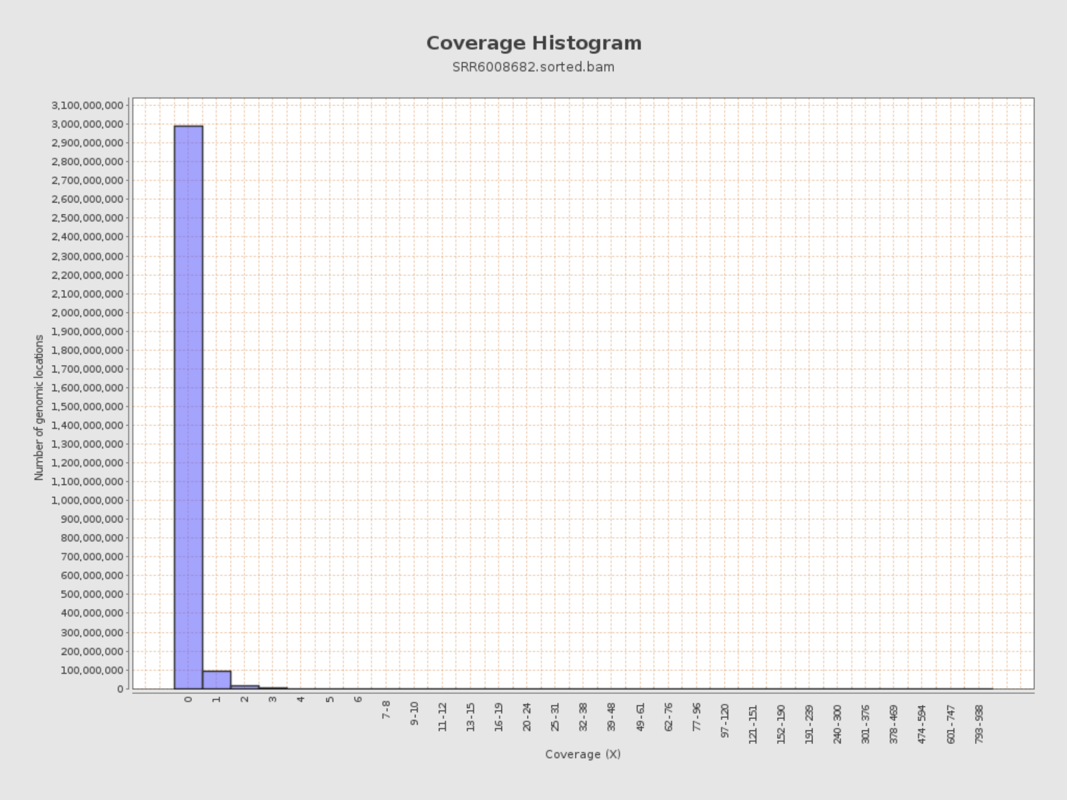
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12800619	0.0514	0.7361
chr2	243199373	11028628	0.0453	0.4086
chr3	198022430	10768174	0.0544	0.2868
chr4	191154276	6275465	0.0328	0.2173
chr5	180915260	6498437	0.0359	0.2165
chr6	171115067	4867426	0.0284	0.2028
chr7	159138663	8047125	0.0506	0.4933

chr8	146364022	8403848	0.0574	0.3665
chr9	141213431	2849015	0.0202	0.2465
chr10	135534747	8476925	0.0625	0.711
chr11	135006516	5834465	0.0432	0.3281
chr12	133851895	4825727	0.0361	0.2172
chr13	115169878	3029558	0.0263	0.1822
chr14	107349540	5332121	0.0497	0.2569
chr15	102531392	2584681	0.0252	0.1835
chr16	90354753	3549815	0.0393	0.2542
chr17	81195210	4146816	0.0511	0.3082
chr18	78077248	1269632	0.0163	0.4039
chr19	59128983	3215942	0.0544	0.4985
chr20	63025520	3723321	0.0591	0.2821
chr21	48129895	1368309	0.0284	0.2038
chr22	51304566	2131140	0.0415	0.2335
chrMT	16571	7209	0.435	0.8151
chrX	155270560	6606266	0.0425	0.2571
chrY	59373566	341822	0.0058	0.1878

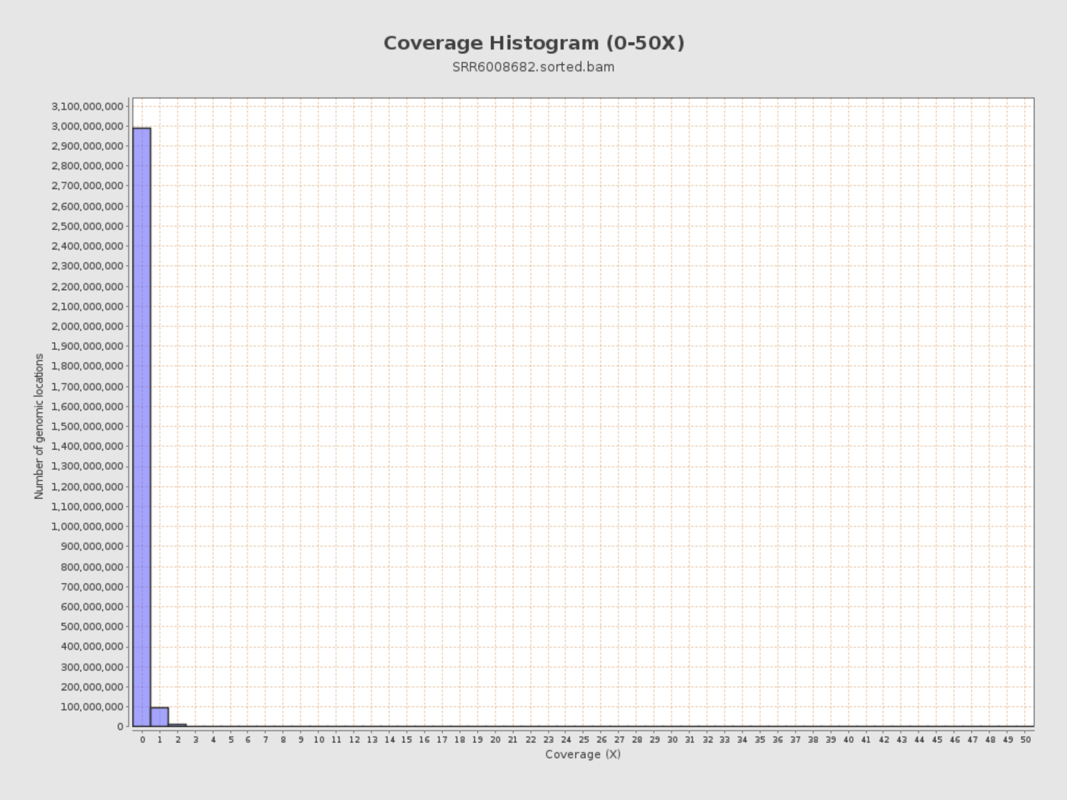
3. Results : Coverage across reference



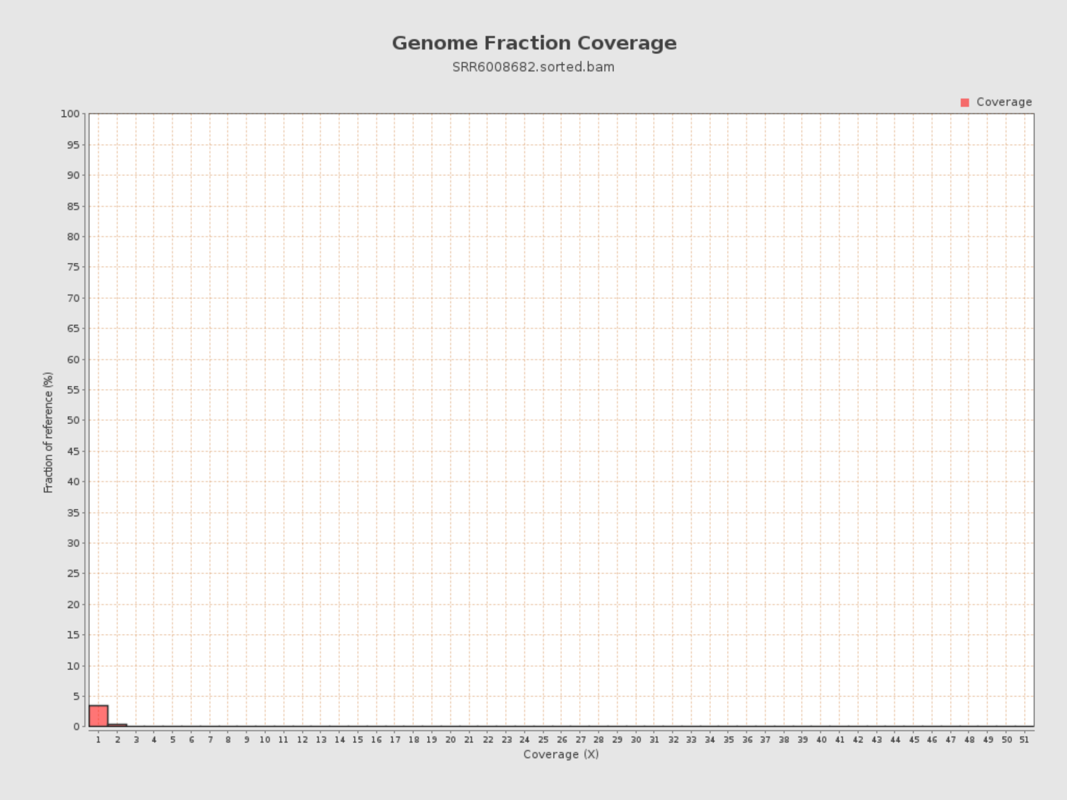
4. Results : Coverage Histogram



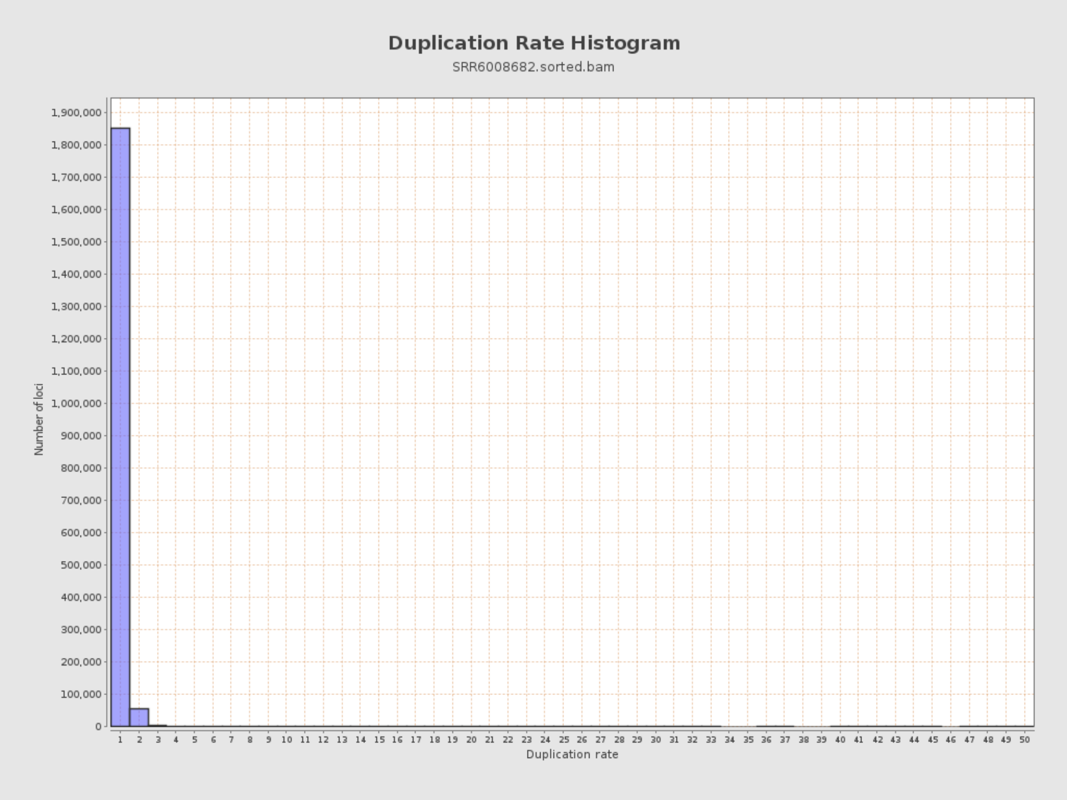
5. Results : Coverage Histogram (0-50X)



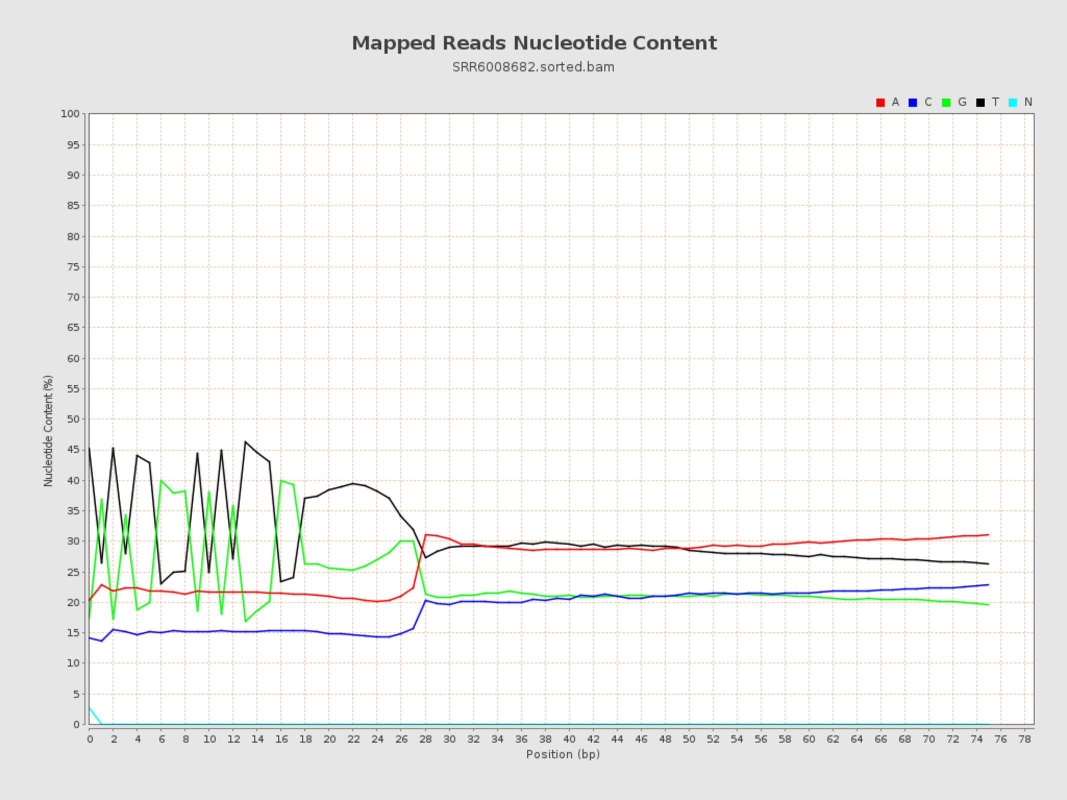
6. Results : Genome Fraction Coverage



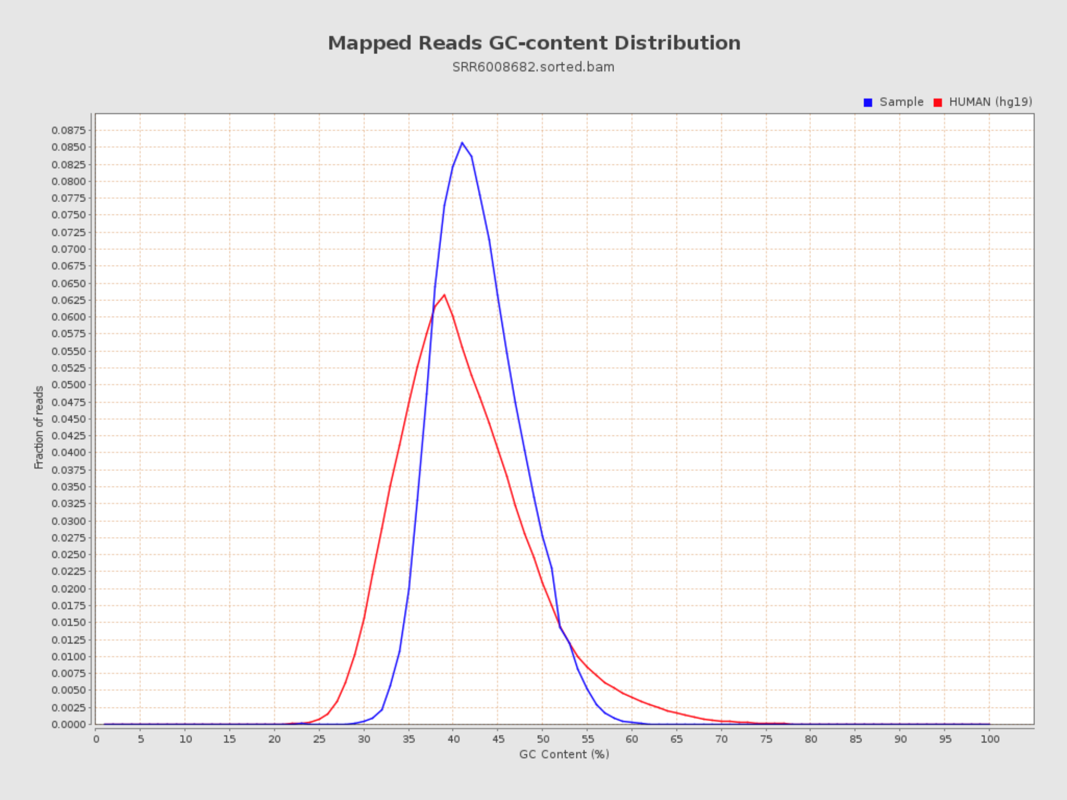
7. Results : Duplication Rate Histogram



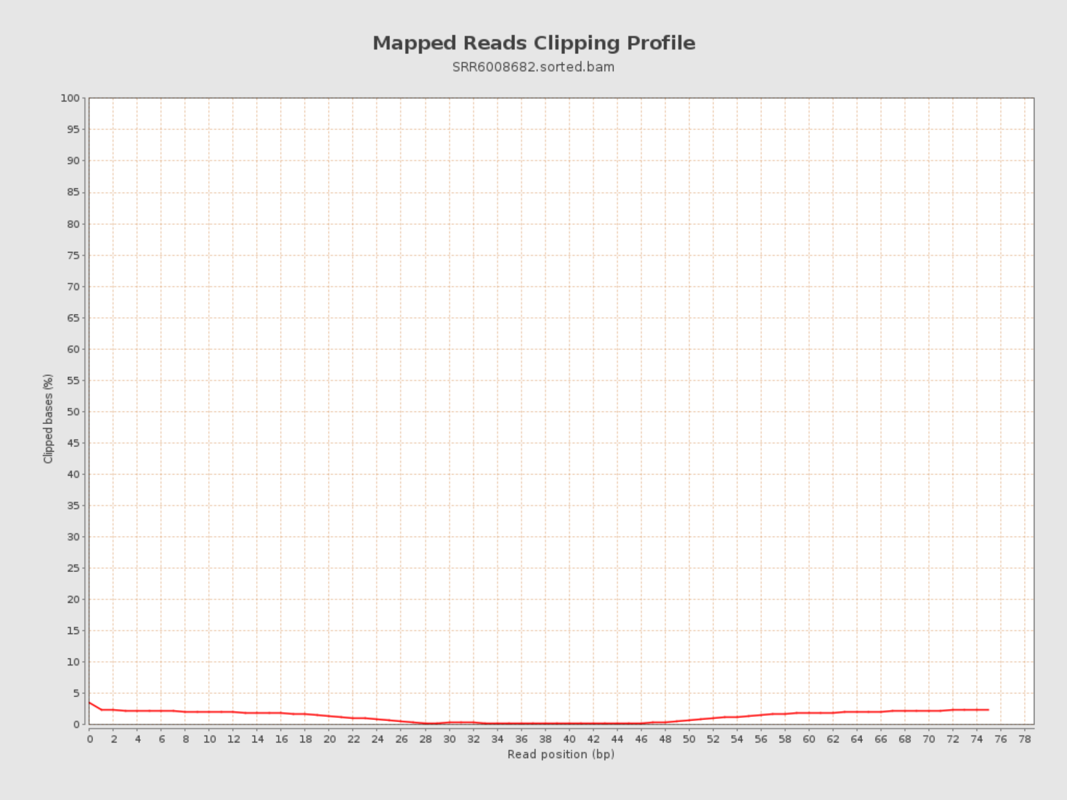
8. Results : Mapped Reads Nucleotide Content



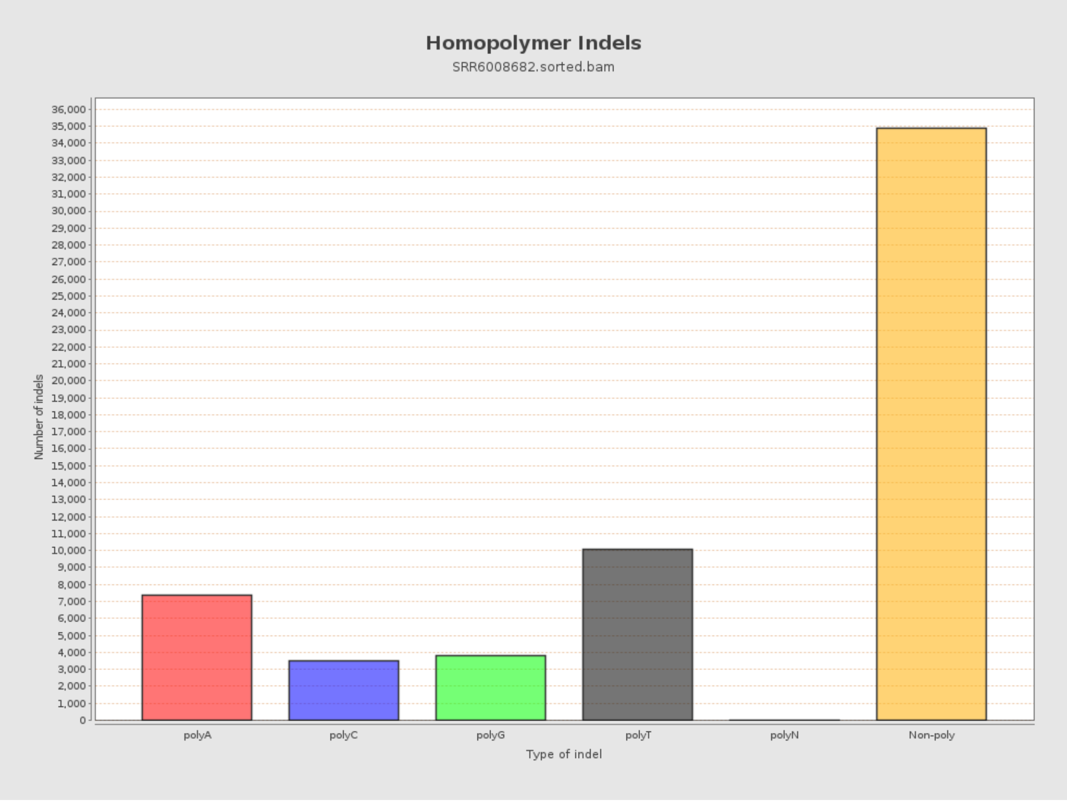
9. Results : Mapped Reads GC-content Distribution



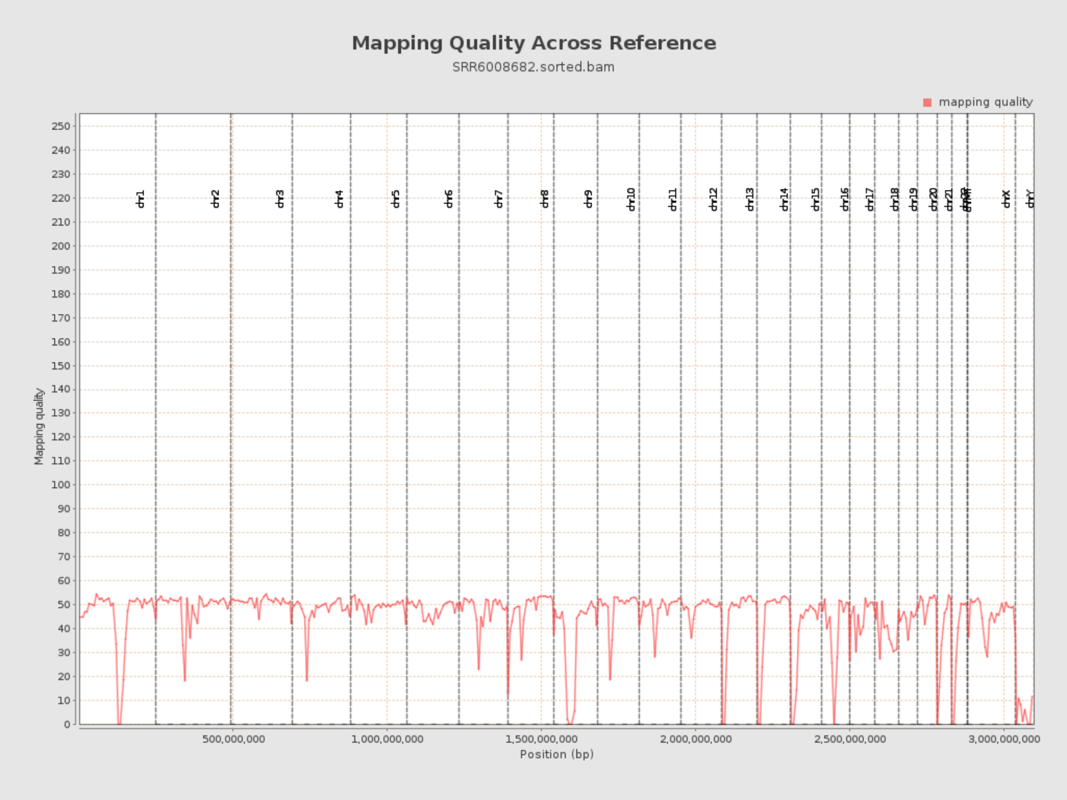
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram