Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:19:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008694.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_SRR6008694 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008694.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:19:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008694.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,281,743
Mapped reads	1,928,613 / 84.52%
Unmapped reads	353,130 / 15.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,330 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	97,010 / 4.25%
Duplication rate	3.69%
Clipped reads	1,142,869 / 50.09%

2.2. ACGT Content

Number/percentage of A's	32,002,867 / 26.3%
Number/percentage of C's	22,699,121 / 18.65%
Number/percentage of T's	37,698,124 / 30.98%
Number/percentage of G's	29,251,418 / 24.04%
Number/percentage of N's	29,245 / 0.02%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0393

Standard Deviation	0.3547

2.4. Mapping Quality

Mean Mapping Quality	43.66

2.5. Mismatches and indels

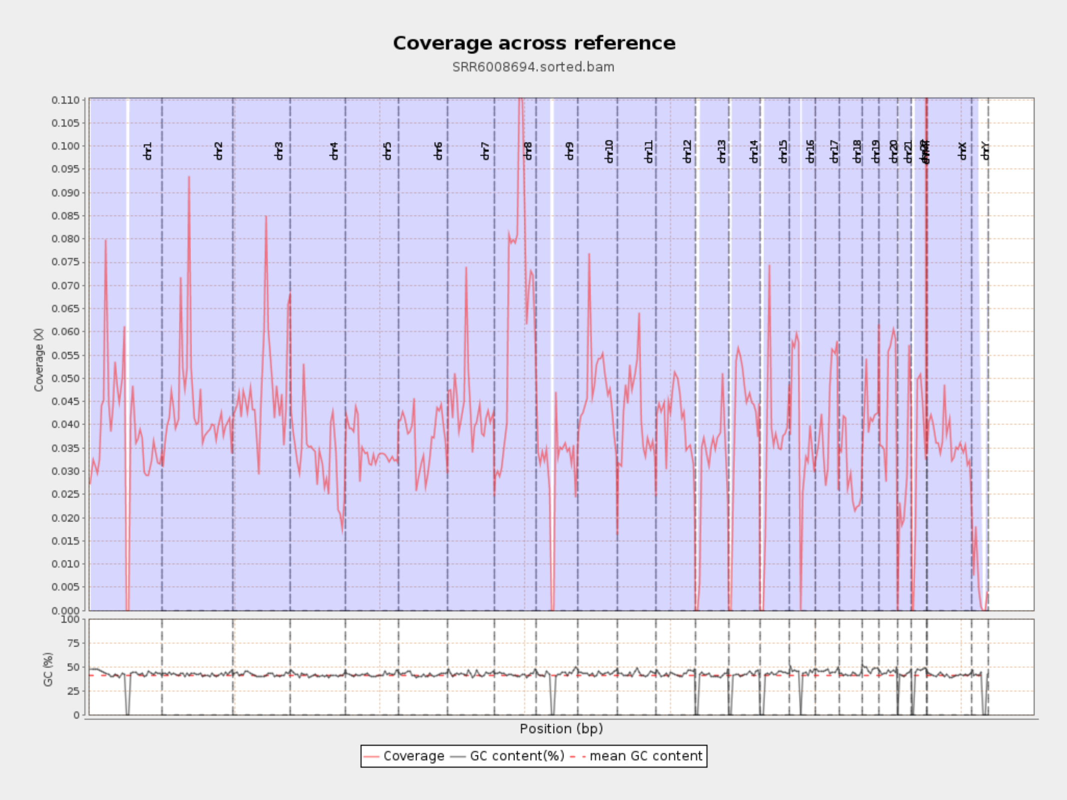
General error rate	1.02%
Mismatches	1,222,621
Insertions	10,797
Mapped reads with at least one insertion	0.56%
Deletions	50,640
Mapped reads with at least one deletion	2.59%
Homopolymer indels	48.99%

2.6. Chromosome stats

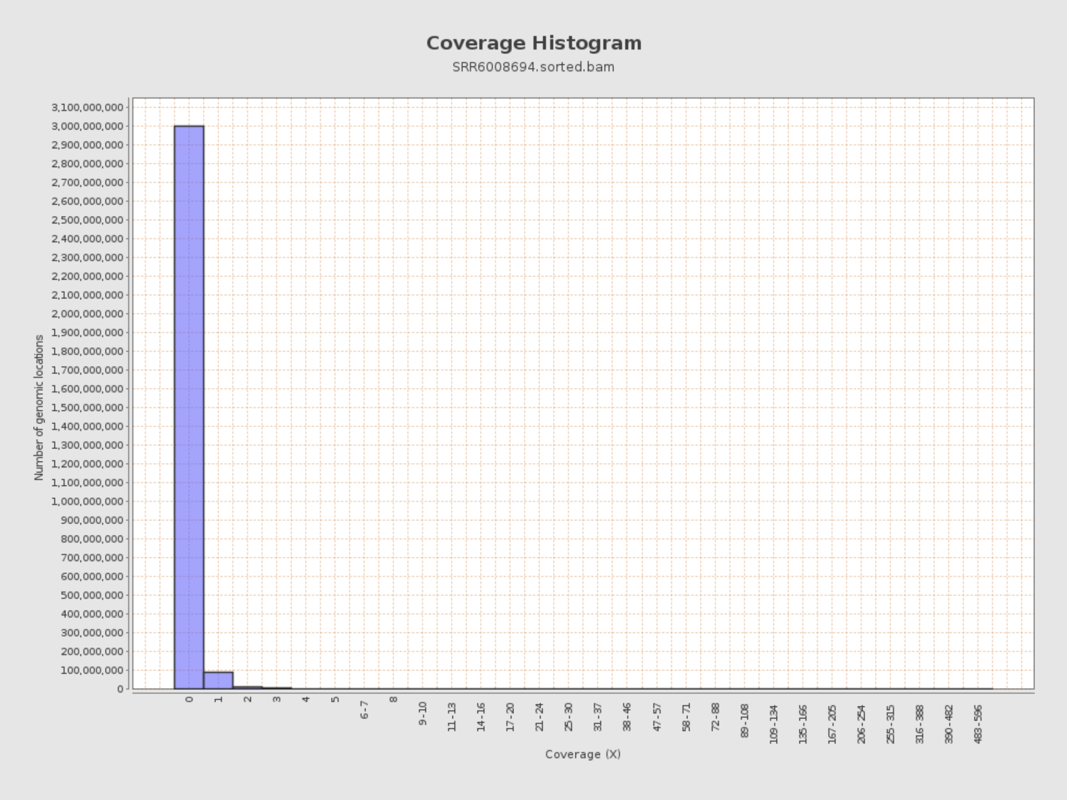
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9345592	0.0375	0.433
chr2	243199373	10710799	0.044	0.493
chr3	198022430	9430277	0.0476	0.2675
chr4	191154276	6216610	0.0325	0.2376
chr5	180915260	6302315	0.0348	0.2248
chr6	171115067	6335659	0.037	0.2683
chr7	159138663	7032802	0.0442	0.5957

chr8	146364022	9543160	0.0652	0.3796
chr9	141213431	4252184	0.0301	0.3623
chr10	135534747	6529577	0.0482	0.3727
chr11	135006516	5623275	0.0417	0.4777
chr12	133851895	5535365	0.0414	0.252
chr13	115169878	3490602	0.0303	0.2137
chr14	107349540	4298151	0.04	0.2558
chr15	102531392	3493042	0.0341	0.2297
chr16	90354753	3500477	0.0387	0.2639
chr17	81195210	3346489	0.0412	0.3083
chr18	78077248	2282969	0.0292	0.523
chr19	59128983	2563275	0.0434	0.3569
chr20	63025520	2861524	0.0454	0.2665
chr21	48129895	1356348	0.0282	0.2221
chr22	51304566	1596341	0.0311	0.2097
chrMT	16571	104416	6.3011	5.4836
chrX	155270560	5658658	0.0364	0.2613
chrY	59373566	353046	0.0059	0.1431

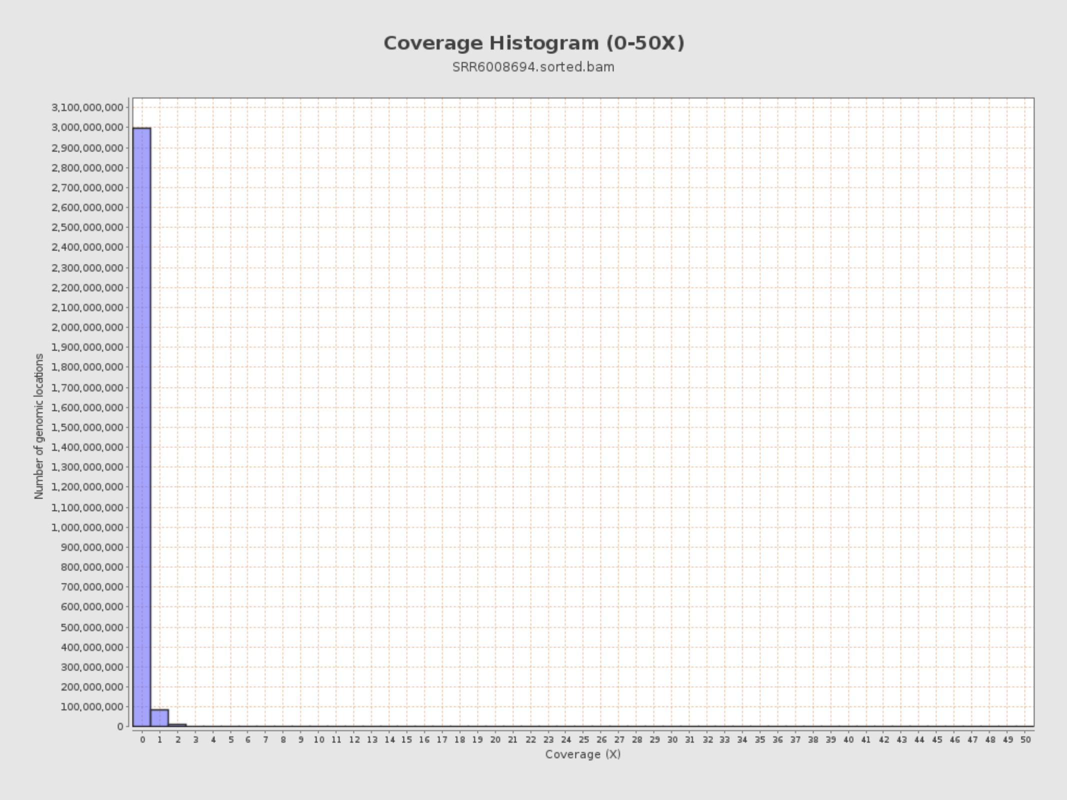
3. Results : Coverage across reference



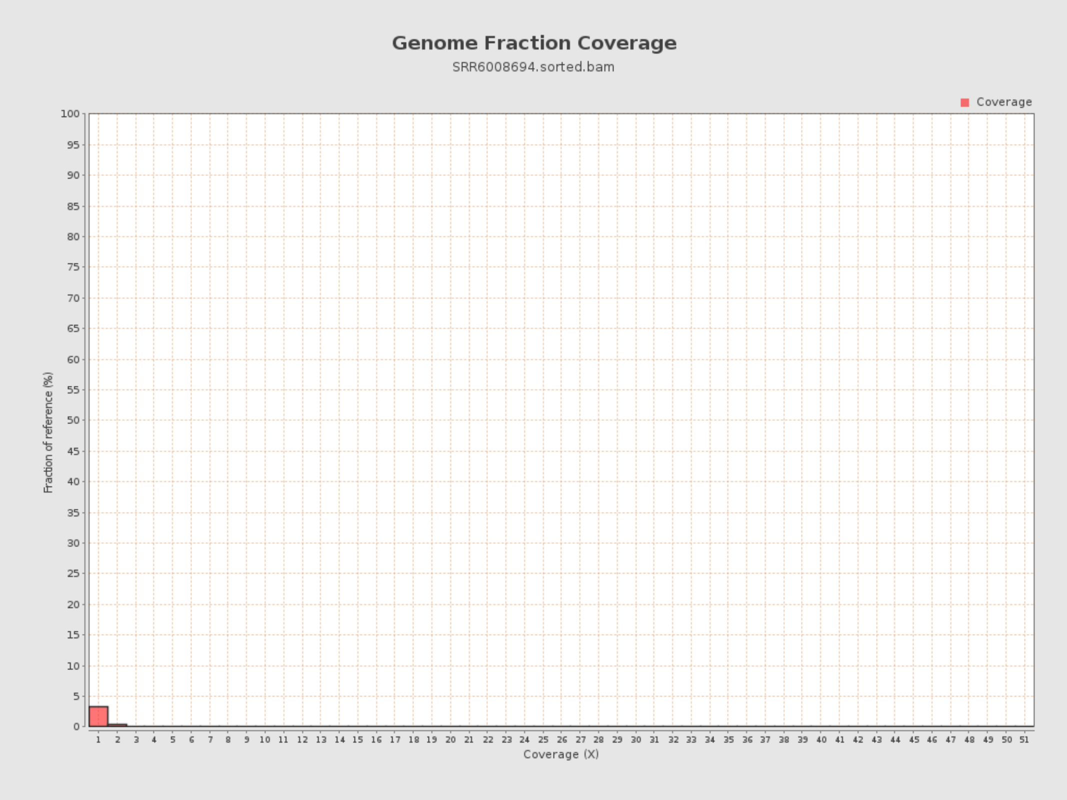
4. Results : Coverage Histogram



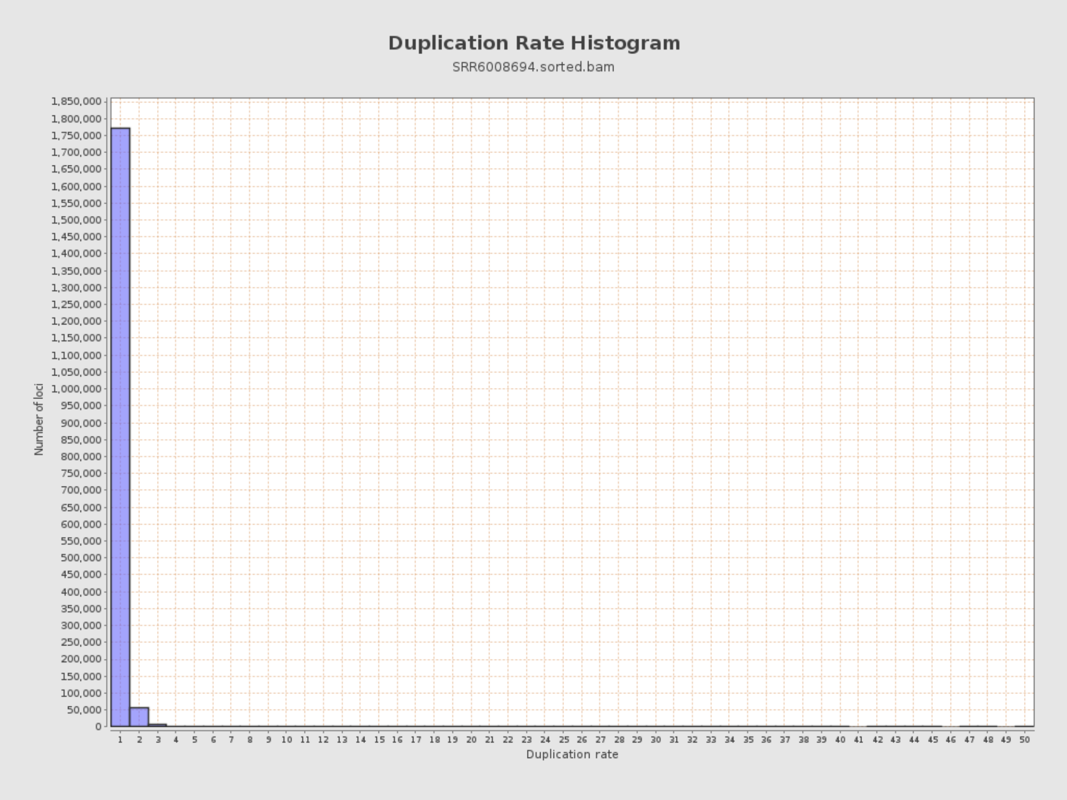
5. Results : Coverage Histogram (0-50X)



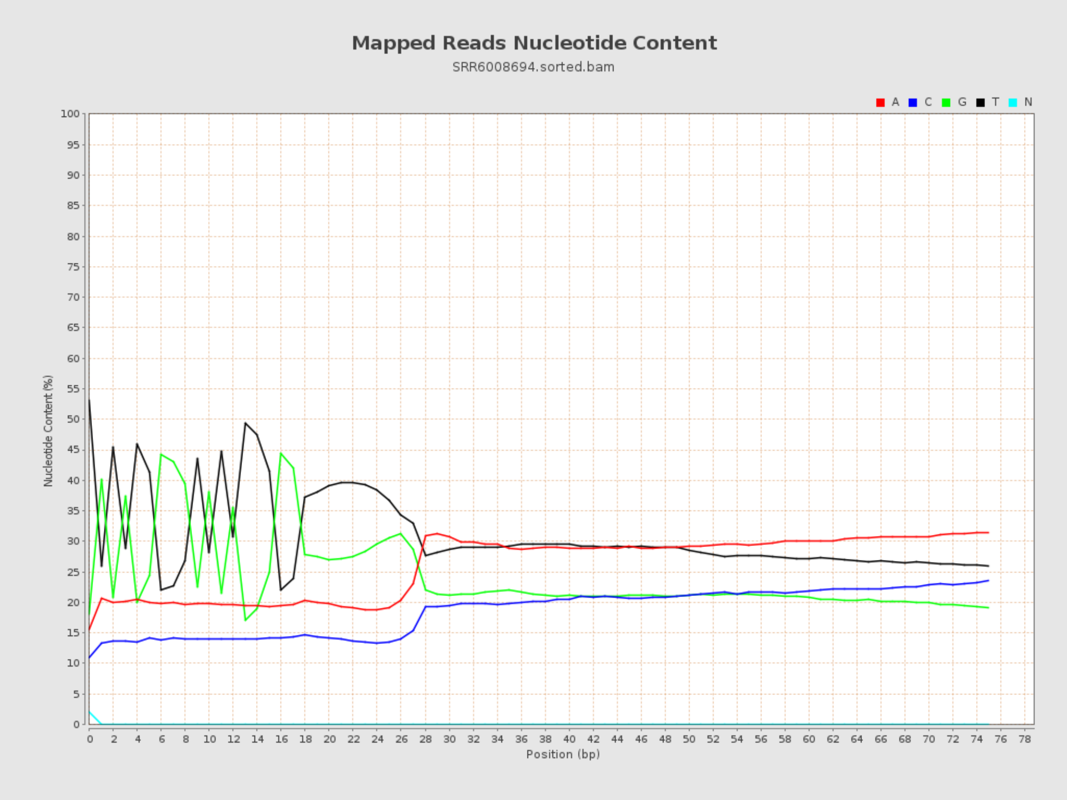
6. Results : Genome Fraction Coverage



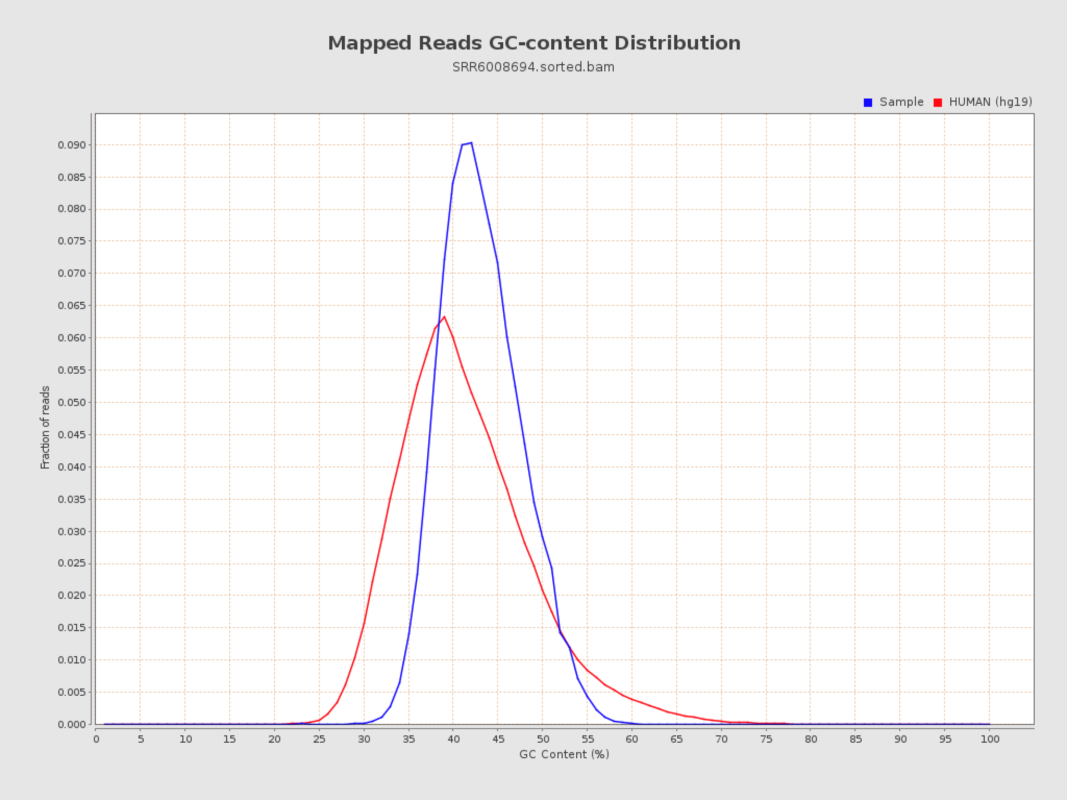
7. Results : Duplication Rate Histogram



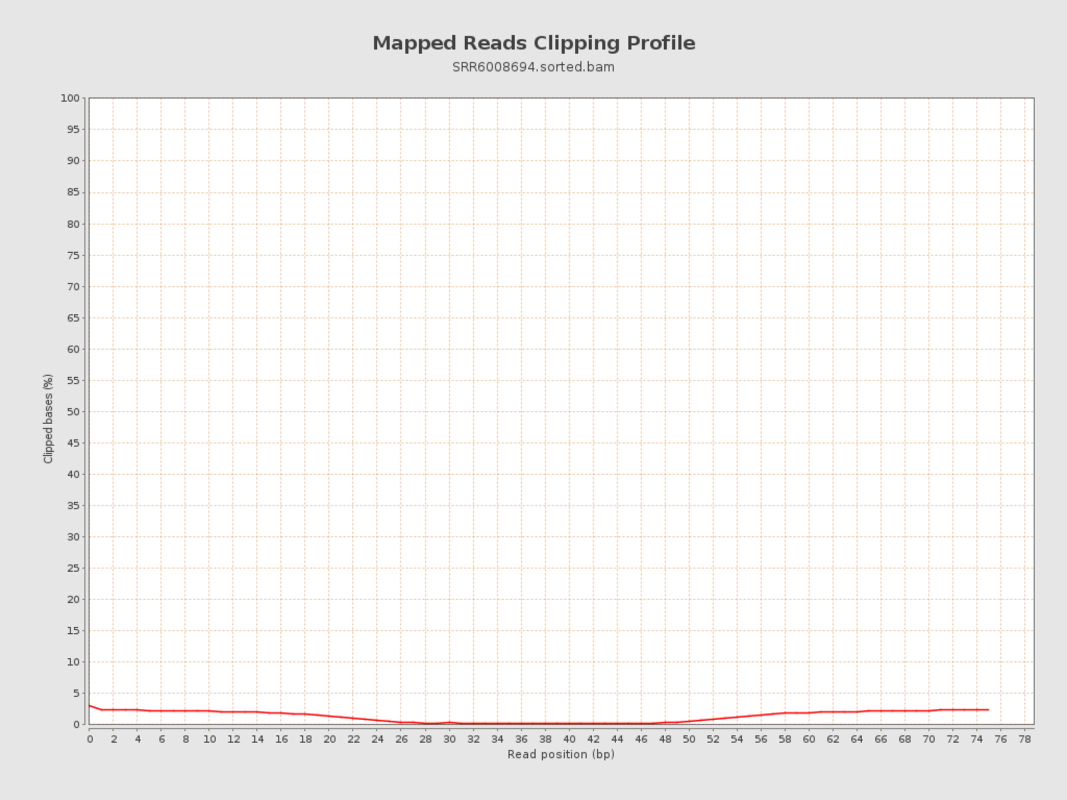
8. Results : Mapped Reads Nucleotide Content



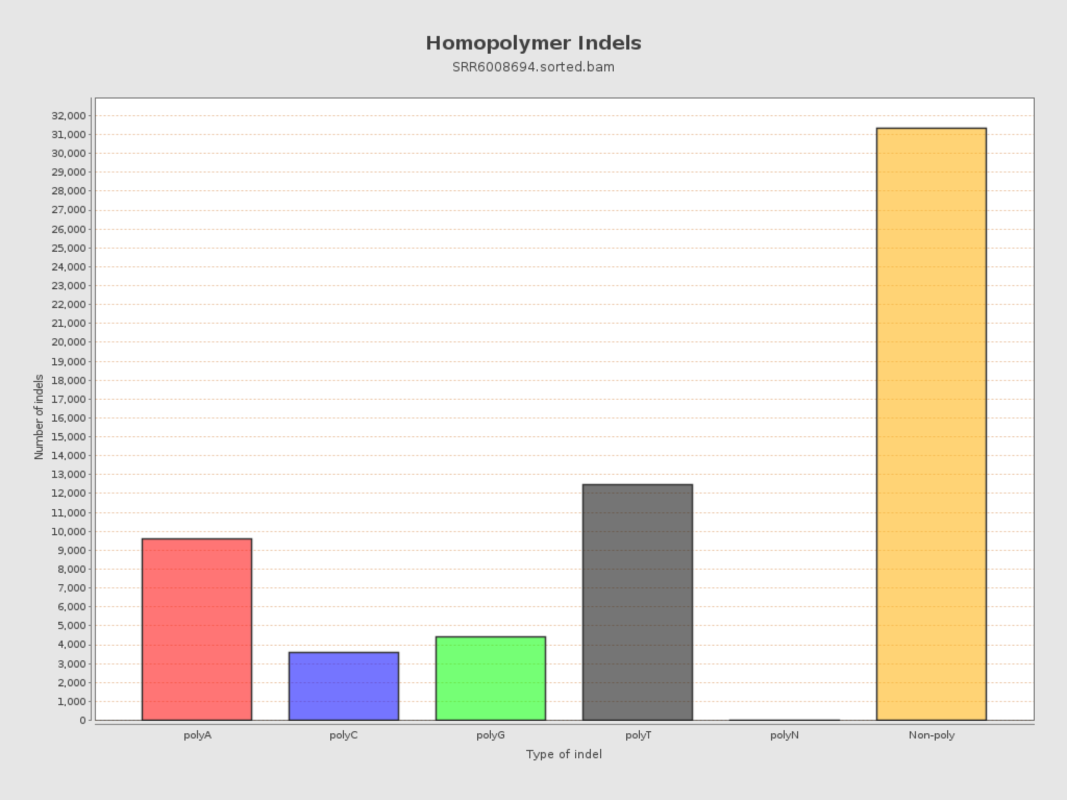
9. Results : Mapped Reads GC-content Distribution



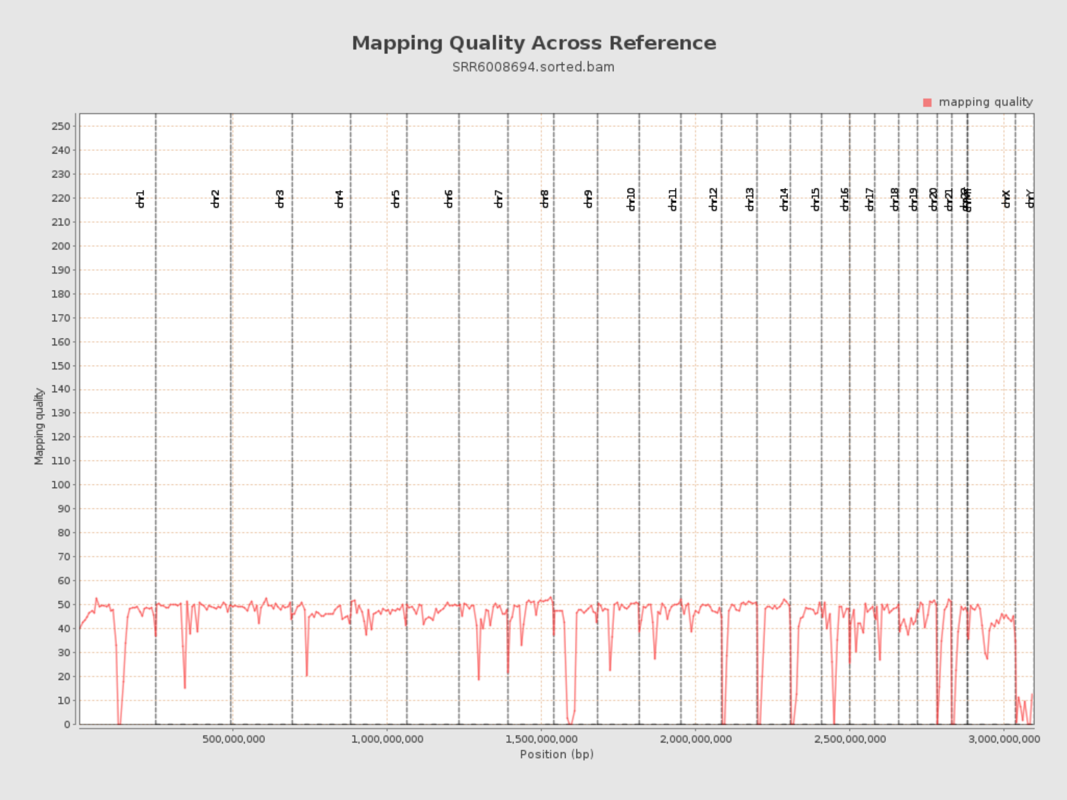
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram