Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:34:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008677.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_SRR6008677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008677.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:34:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,615,515
Mapped reads	1,406,341 / 87.05%
Unmapped reads	209,174 / 12.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,721 / 0.48%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	60,728 / 3.76%
Duplication rate	3.56%
Clipped reads	733,780 / 45.42%

2.2. ACGT Content

Number/percentage of A's	24,809,767 / 27.42%
Number/percentage of C's	16,426,106 / 18.15%
Number/percentage of T's	28,868,341 / 31.91%
Number/percentage of G's	20,354,908 / 22.5%
Number/percentage of N's	21,348 / 0.02%
GC Percentage	40.65%

2.3. Coverage

Mean	0.0292

Standard Deviation	0.2751

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

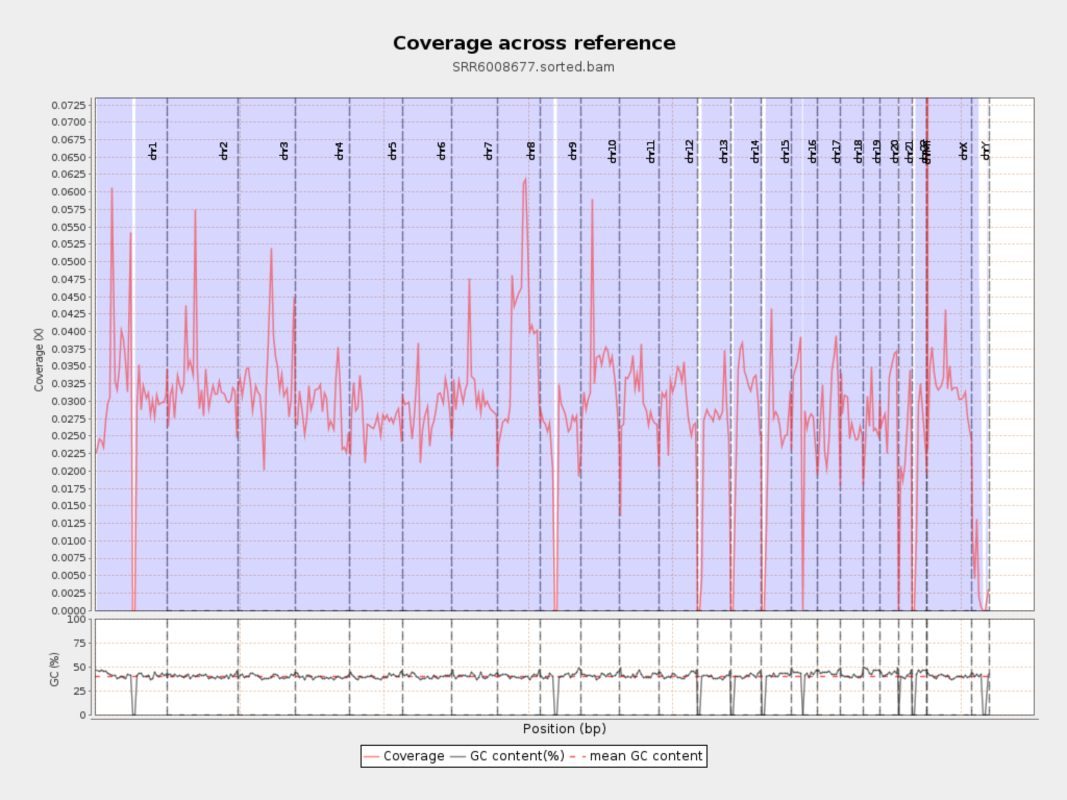
General error rate	0.81%
Mismatches	720,958
Insertions	5,849
Mapped reads with at least one insertion	0.41%
Deletions	31,380
Mapped reads with at least one deletion	2.2%
Homopolymer indels	44.77%

2.6. Chromosome stats

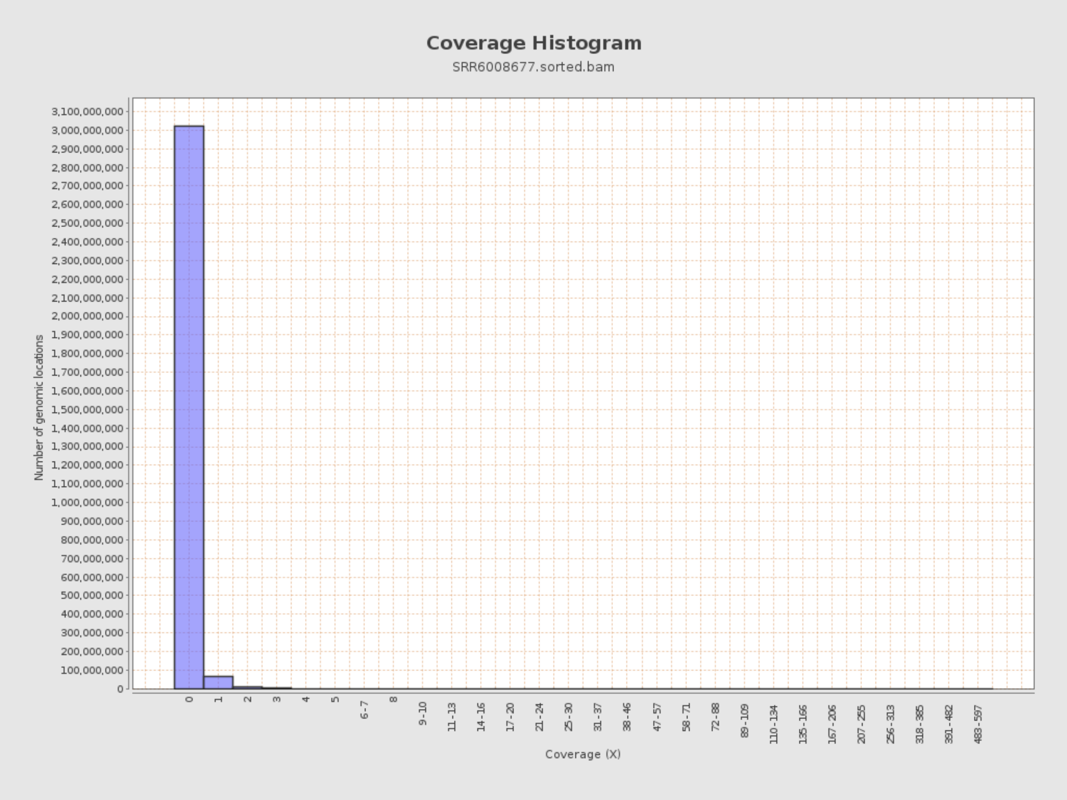
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7542260	0.0303	0.5054
chr2	243199373	7918004	0.0326	0.3001
chr3	198022430	6591073	0.0333	0.2124
chr4	191154276	5513536	0.0288	0.2014
chr5	180915260	5004869	0.0277	0.1919
chr6	171115067	4943767	0.0289	0.2164
chr7	159138663	4975377	0.0313	0.2941

chr8	146364022	5816784	0.0397	0.2989
chr9	141213431	3360732	0.0238	0.2328
chr10	135534747	4679416	0.0345	0.312
chr11	135006516	4080228	0.0302	0.2434
chr12	133851895	4015660	0.03	0.2013
chr13	115169878	2719007	0.0236	0.1771
chr14	107349540	2963322	0.0276	0.1965
chr15	102531392	2414959	0.0236	0.1765
chr16	90354753	2468762	0.0273	0.2139
chr17	81195210	2326468	0.0287	0.2125
chr18	78077248	2117107	0.0271	0.3539
chr19	59128983	1607243	0.0272	0.3428
chr20	63025520	1921225	0.0305	0.2026
chr21	48129895	1057303	0.022	0.1801
chr22	51304566	996728	0.0194	0.1582
chrMT	16571	292064	17.625	9.4802
chrX	155270560	4976160	0.032	0.2234
chrY	59373566	233106	0.0039	0.1214

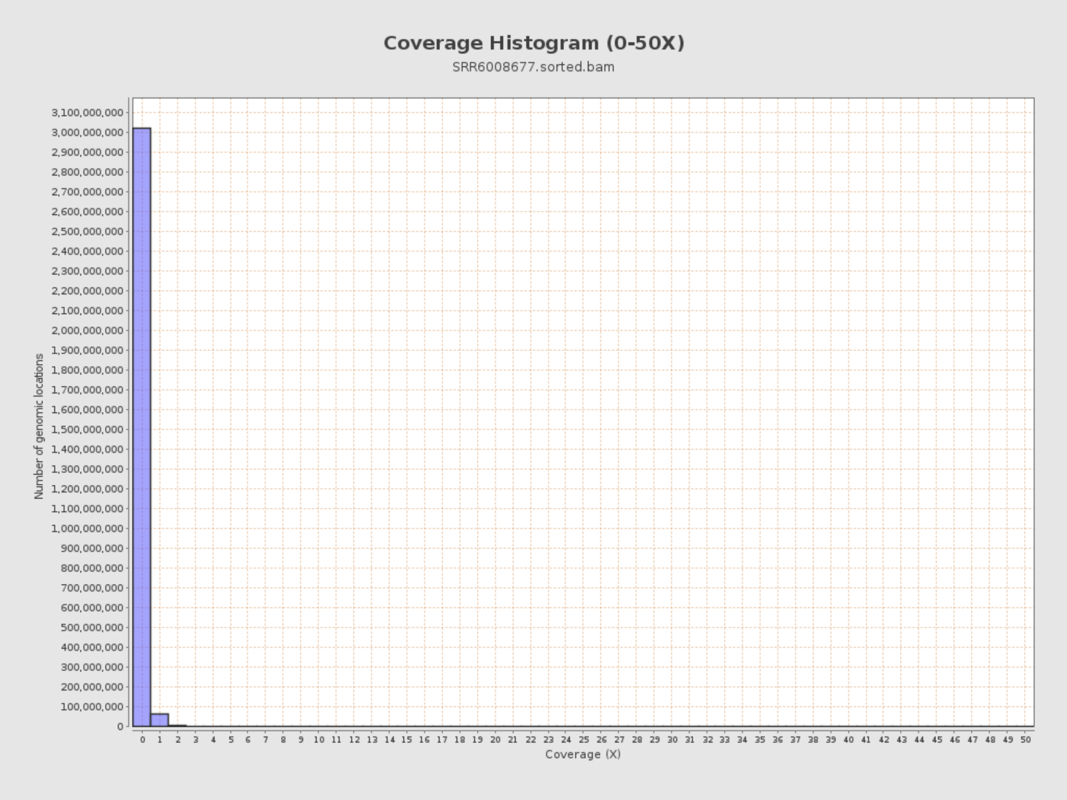
3. Results : Coverage across reference



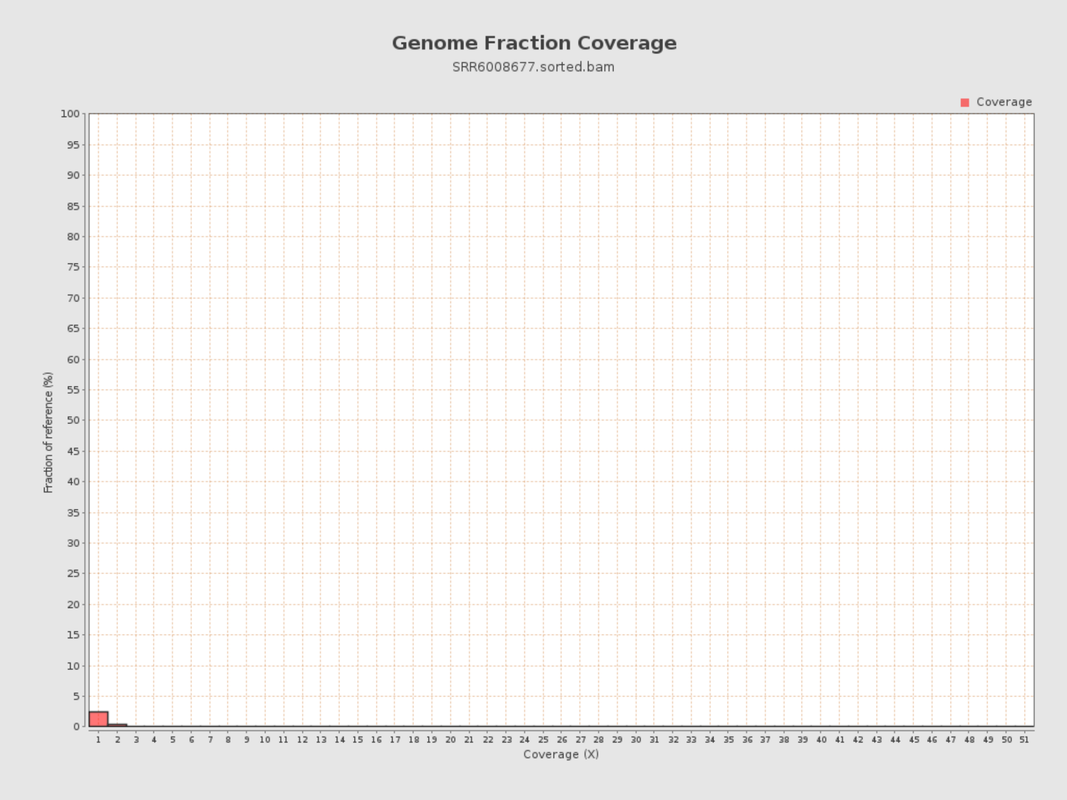
4. Results : Coverage Histogram



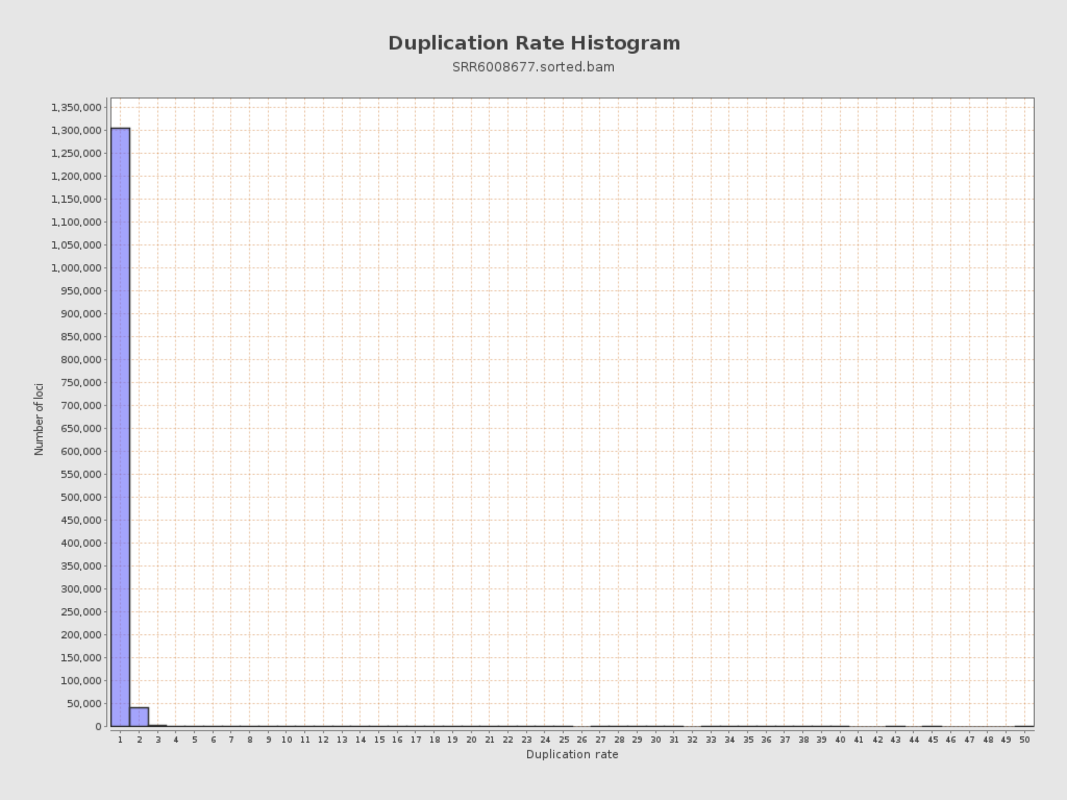
5. Results : Coverage Histogram (0-50X)



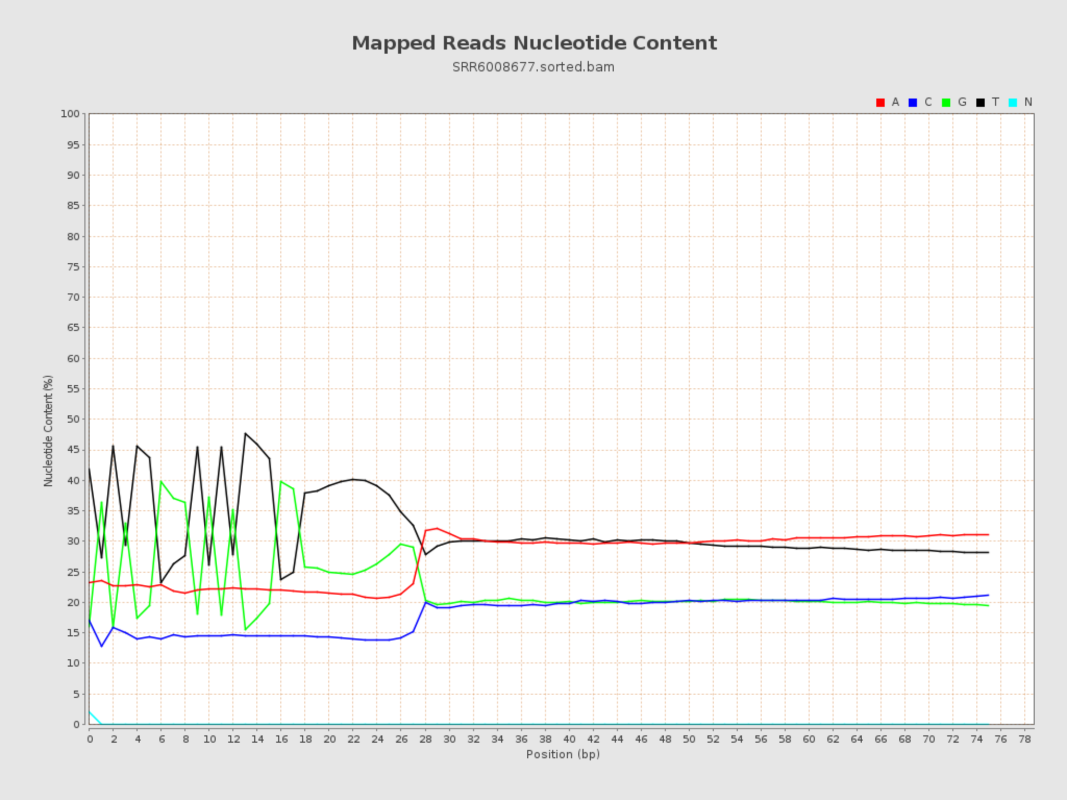
6. Results : Genome Fraction Coverage



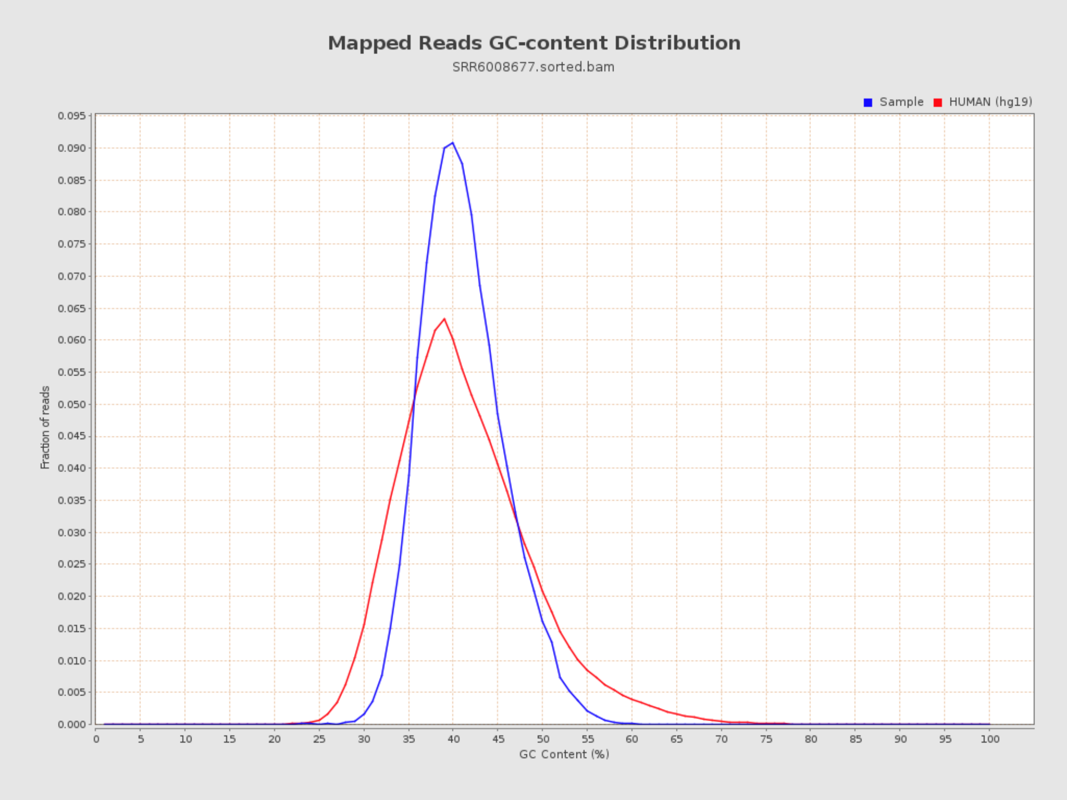
7. Results : Duplication Rate Histogram



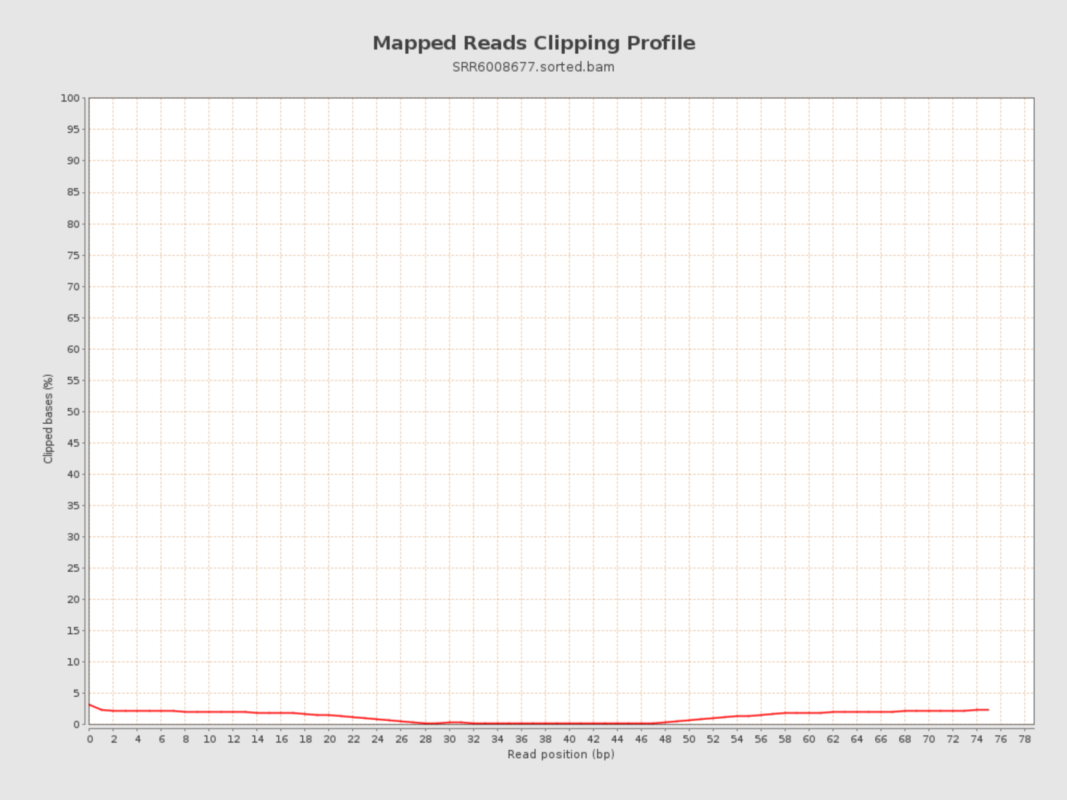
8. Results : Mapped Reads Nucleotide Content



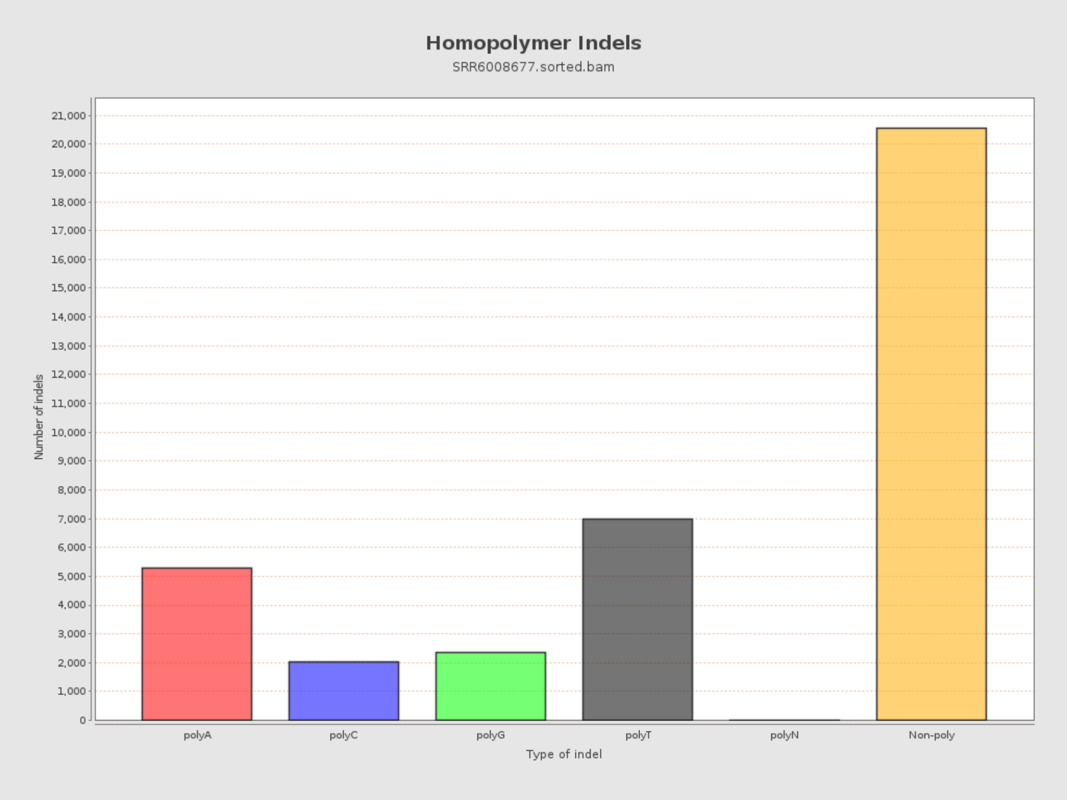
9. Results : Mapped Reads GC-content Distribution



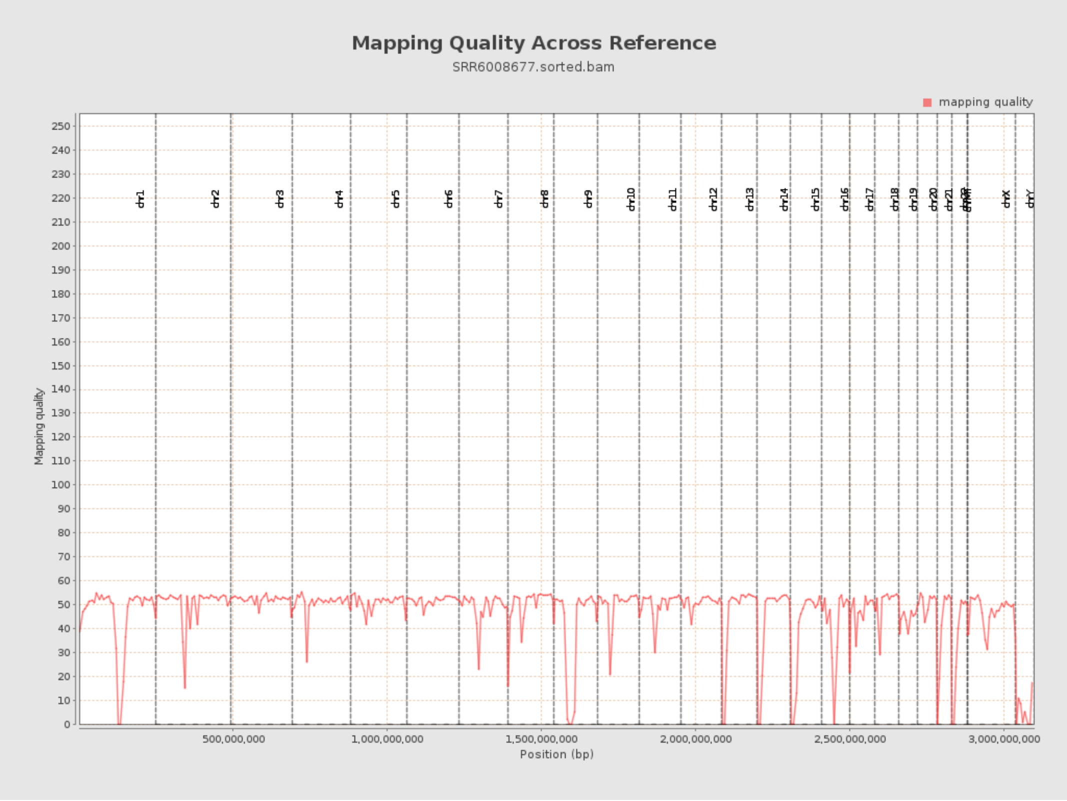
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram