Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:05:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008776.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_SRR6008776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008776.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:05:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,434,916
Mapped reads	344,521 / 24.01%
Unmapped reads	1,090,395 / 75.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,173 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,208 / 1.9%
Duplication rate	6.35%
Clipped reads	156,279 / 10.89%

2.2. ACGT Content

Number/percentage of A's	6,243,276 / 27.34%
Number/percentage of C's	4,279,169 / 18.74%
Number/percentage of T's	7,194,647 / 31.5%
Number/percentage of G's	5,085,518 / 22.27%
Number/percentage of N's	35,529 / 0.16%
GC Percentage	41%

2.3. Coverage

Mean	0.0074

Standard Deviation	0.1356

2.4. Mapping Quality

Mean Mapping Quality	43.19

2.5. Mismatches and indels

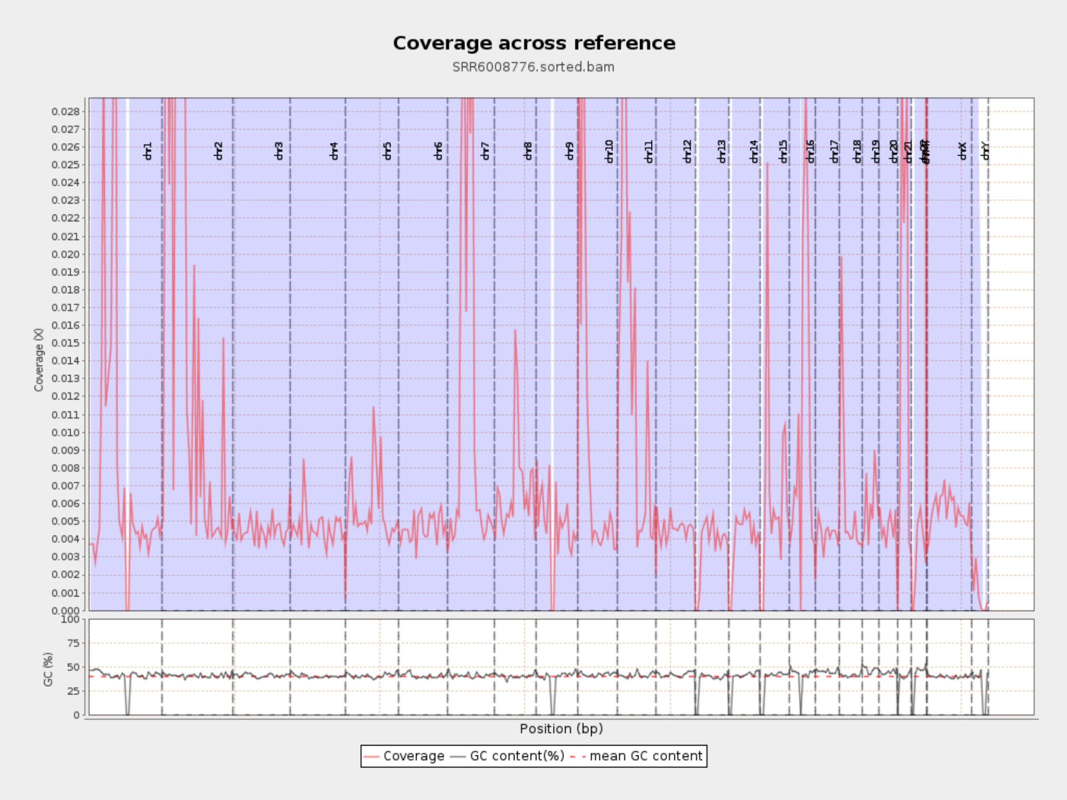
General error rate	0.88%
Mismatches	198,238
Insertions	1,612
Mapped reads with at least one insertion	0.46%
Deletions	6,140
Mapped reads with at least one deletion	1.77%
Homopolymer indels	45.34%

2.6. Chromosome stats

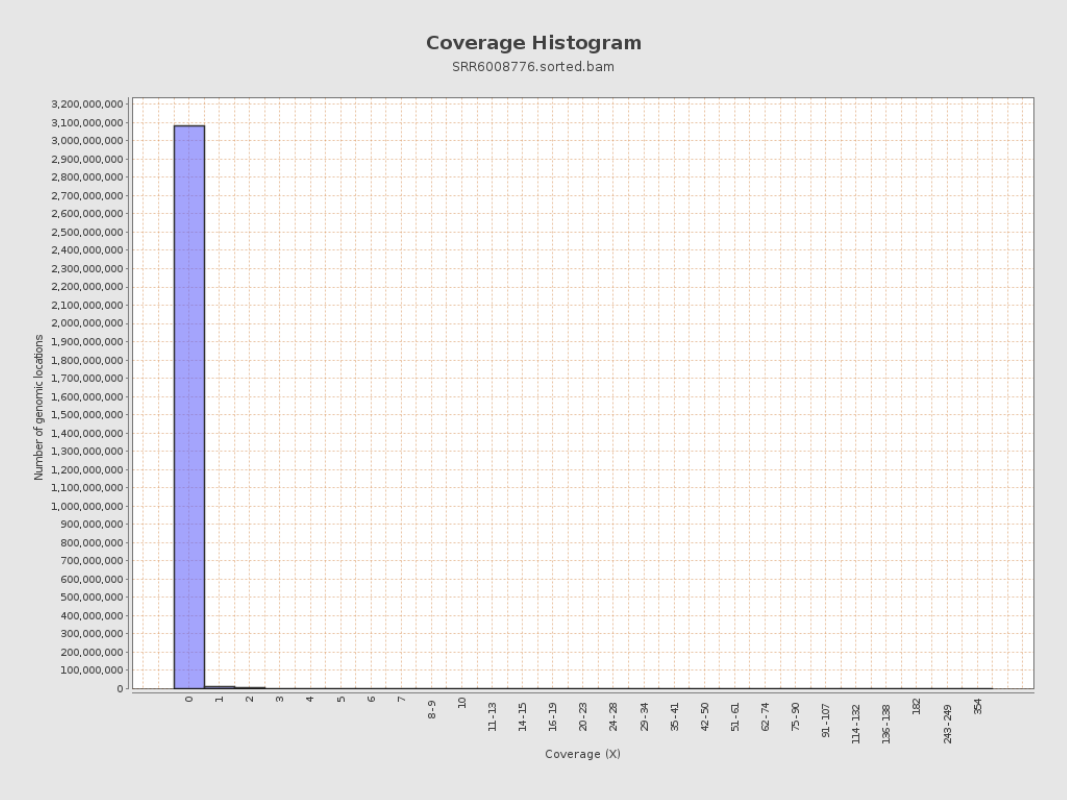
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2122685	0.0085	0.1428
chr2	243199373	3910123	0.0161	0.2294
chr3	198022430	889472	0.0045	0.0924
chr4	191154276	885478	0.0046	0.0957
chr5	180915260	1042385	0.0058	0.1078
chr6	171115067	791371	0.0046	0.1016
chr7	159138663	1926181	0.0121	0.1996

chr8	146364022	1010605	0.0069	0.1407
chr9	141213431	647576	0.0046	0.1021
chr10	135534747	1409655	0.0104	0.1501
chr11	135006516	1796327	0.0133	0.1726
chr12	133851895	618426	0.0046	0.0971
chr13	115169878	420456	0.0037	0.0834
chr14	107349540	428467	0.004	0.0888
chr15	102531392	694082	0.0068	0.1178
chr16	90354753	921927	0.0102	0.1463
chr17	81195210	344581	0.0042	0.0902
chr18	78077248	513310	0.0066	0.1524
chr19	59128983	344285	0.0058	0.1159
chr20	63025520	293205	0.0047	0.1
chr21	48129895	737808	0.0153	0.1775
chr22	51304566	162300	0.0032	0.0767
chrMT	16571	20355	1.2284	1.8187
chrX	155270560	865459	0.0056	0.1071
chrY	59373566	52110	0.0009	0.0367

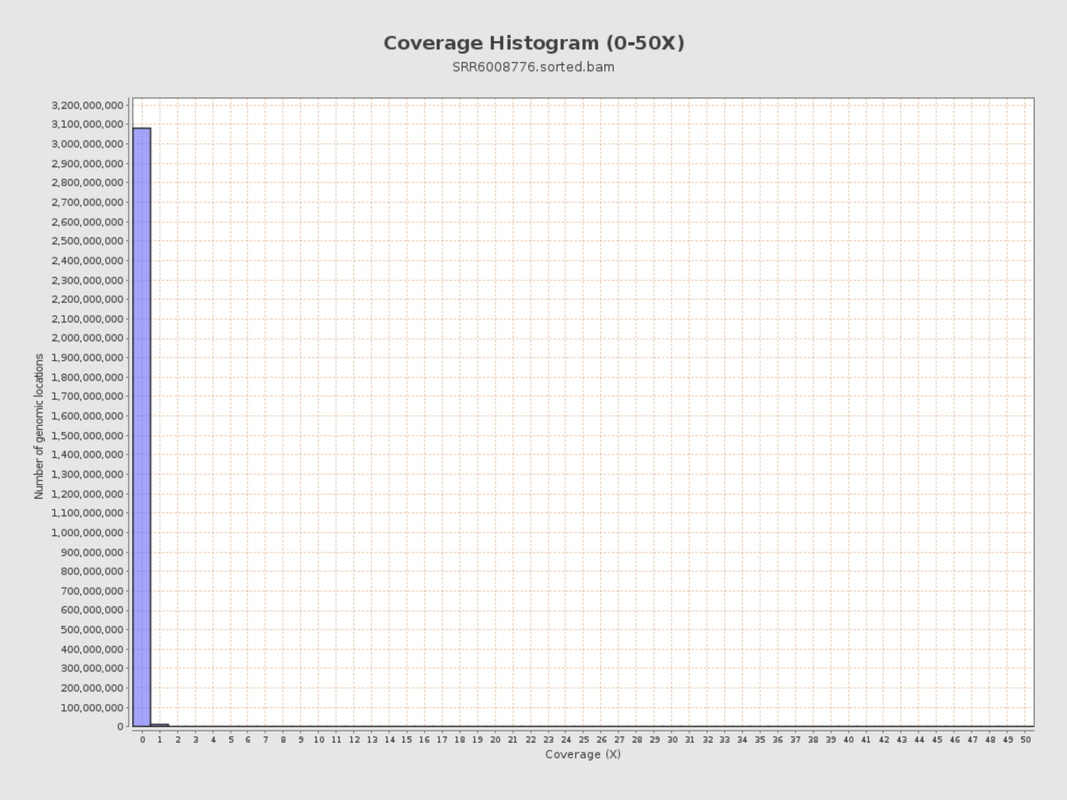
3. Results : Coverage across reference



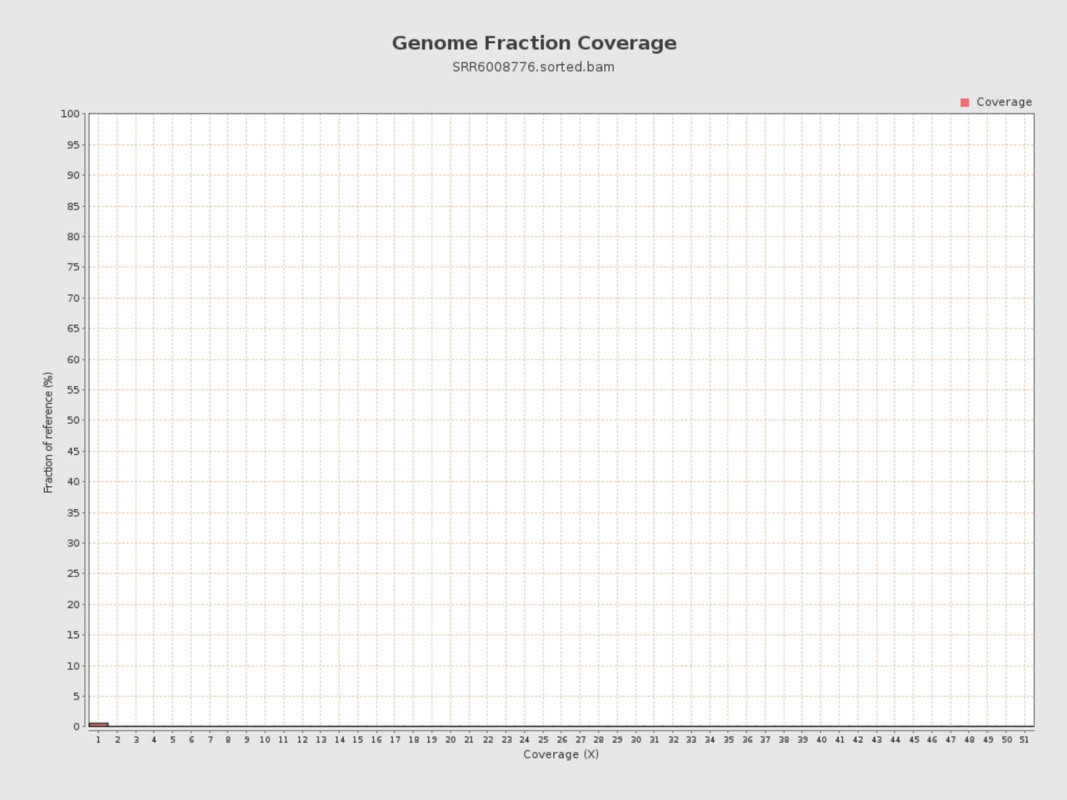
4. Results : Coverage Histogram



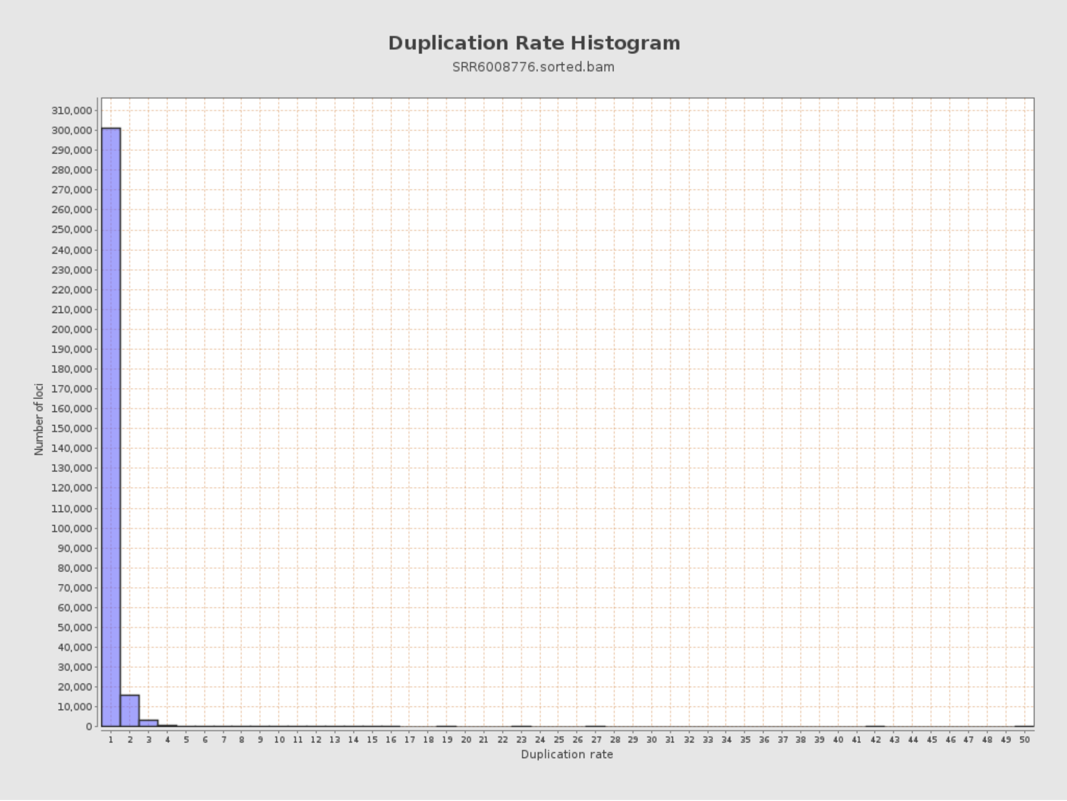
5. Results : Coverage Histogram (0-50X)



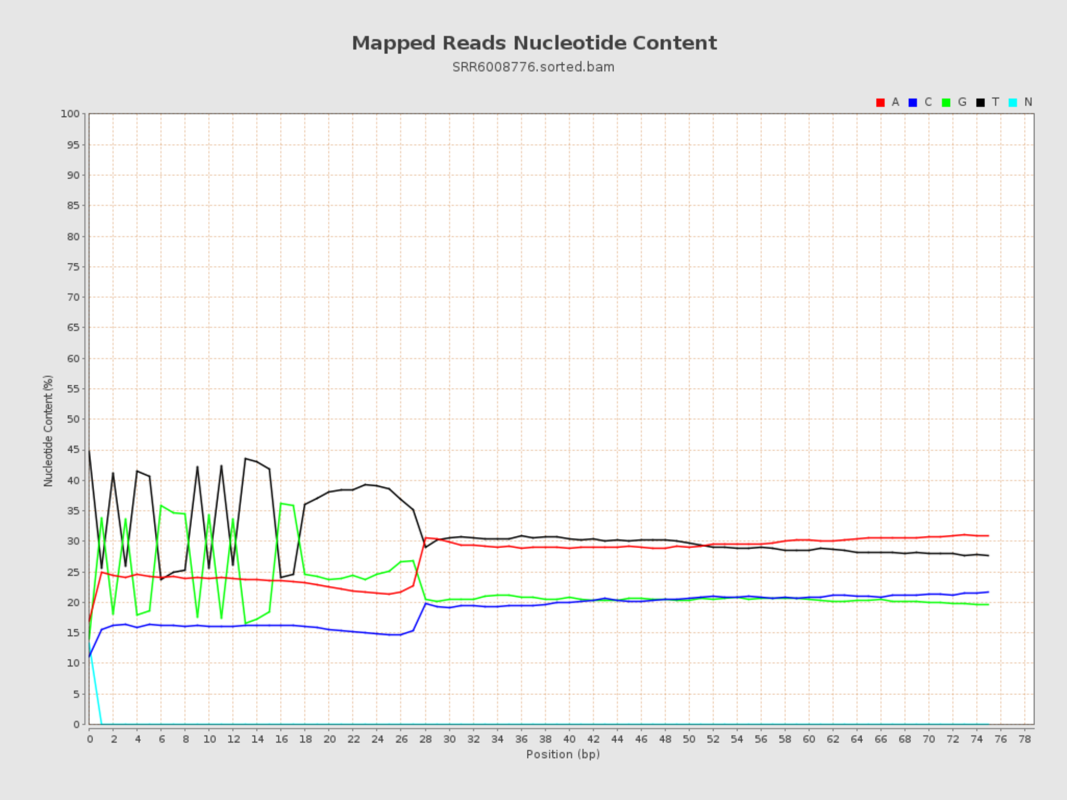
6. Results : Genome Fraction Coverage



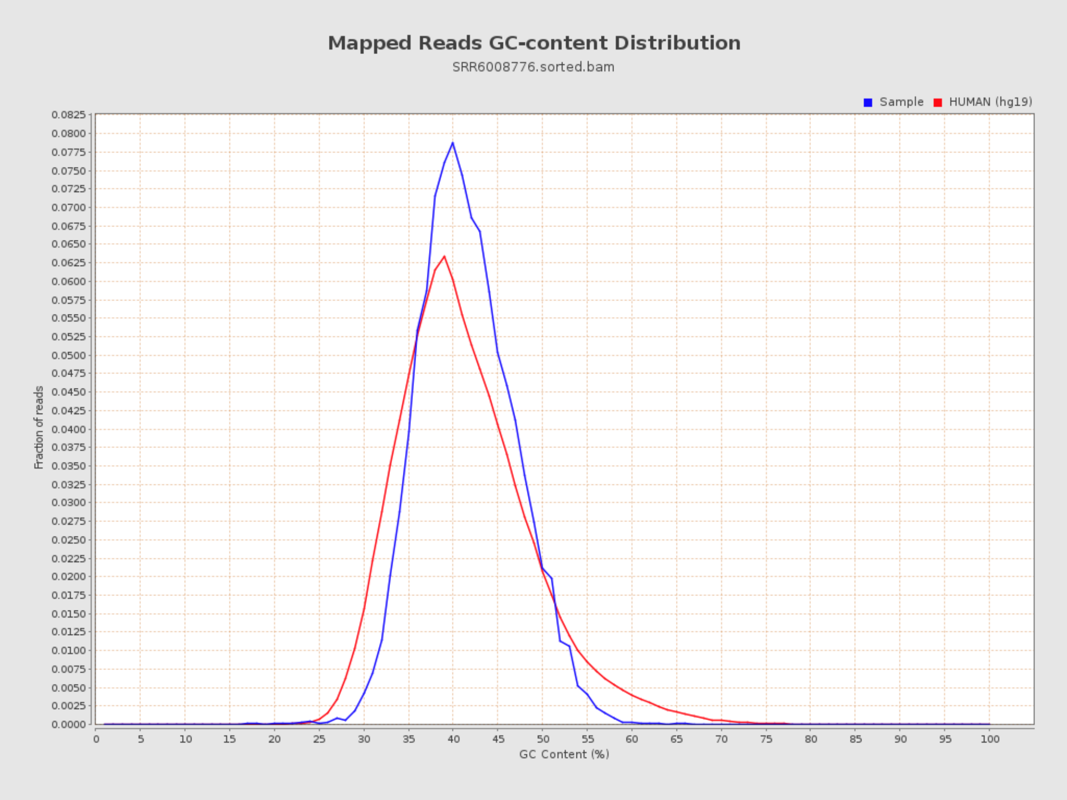
7. Results : Duplication Rate Histogram



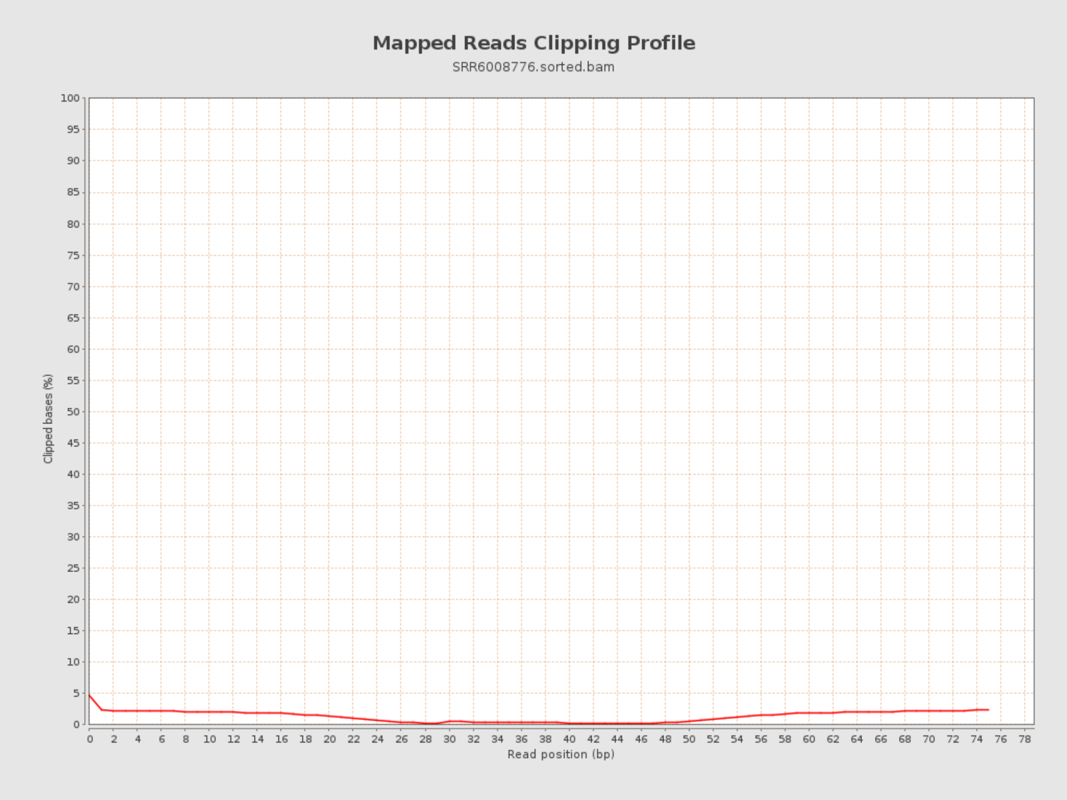
8. Results : Mapped Reads Nucleotide Content



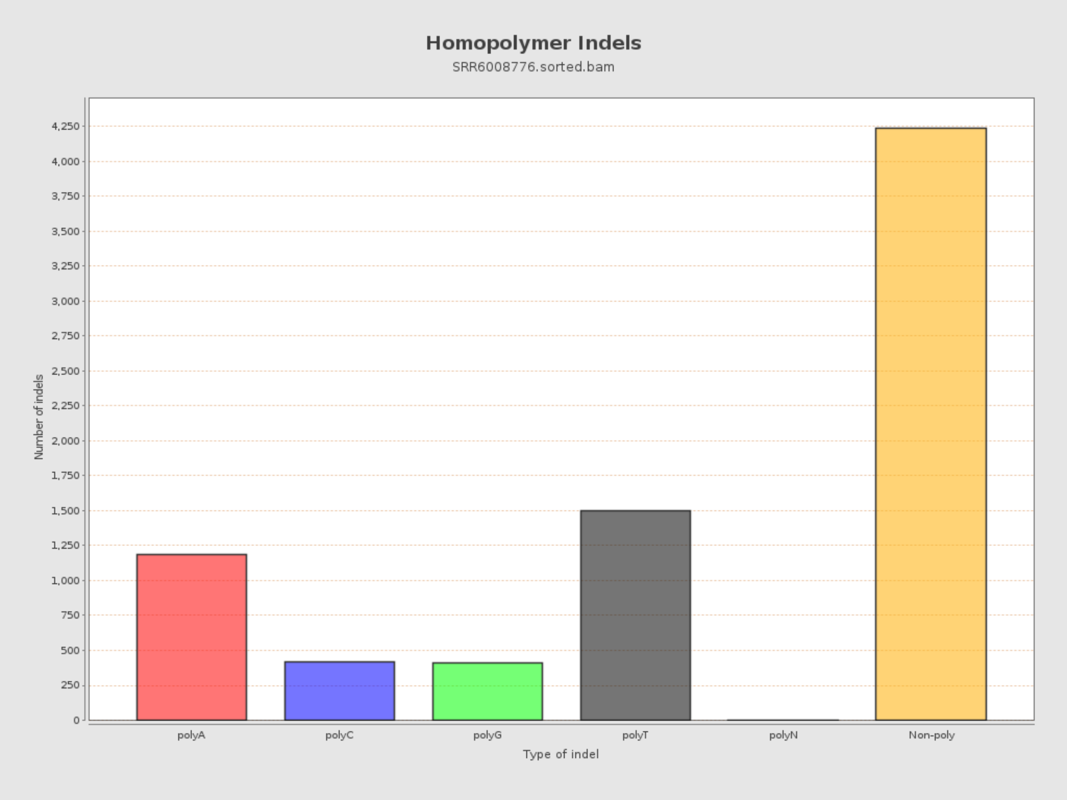
9. Results : Mapped Reads GC-content Distribution



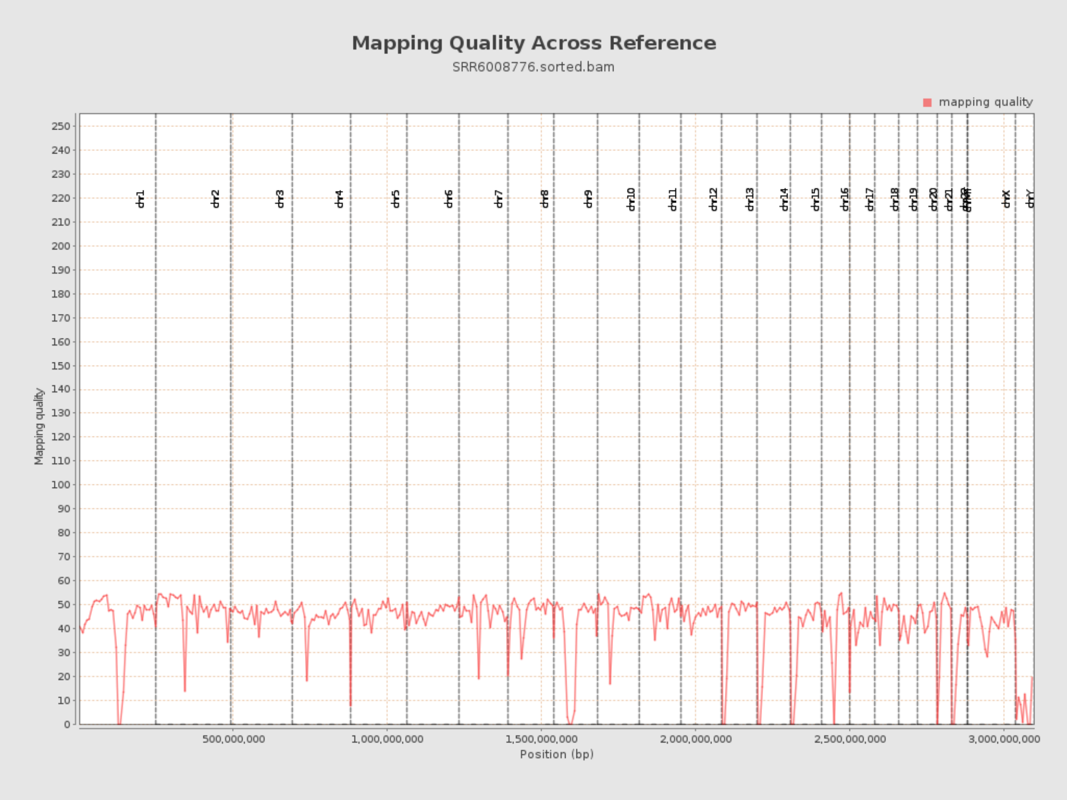
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram