Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:26:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008721.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_SRR6008721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008721.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:26:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,313,630
Mapped reads	1,620,686 / 70.05%
Unmapped reads	692,944 / 29.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,531 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	42,693 / 1.85%
Duplication rate	2.05%
Clipped reads	801,288 / 34.63%

2.2. ACGT Content

Number/percentage of A's	30,885,408 / 29.52%
Number/percentage of C's	18,369,345 / 17.56%
Number/percentage of T's	31,532,866 / 30.14%
Number/percentage of G's	23,816,061 / 22.76%
Number/percentage of N's	29,728 / 0.03%
GC Percentage	40.32%

2.3. Coverage

Mean	0.0338

Standard Deviation	0.2606

2.4. Mapping Quality

Mean Mapping Quality	46.83

2.5. Mismatches and indels

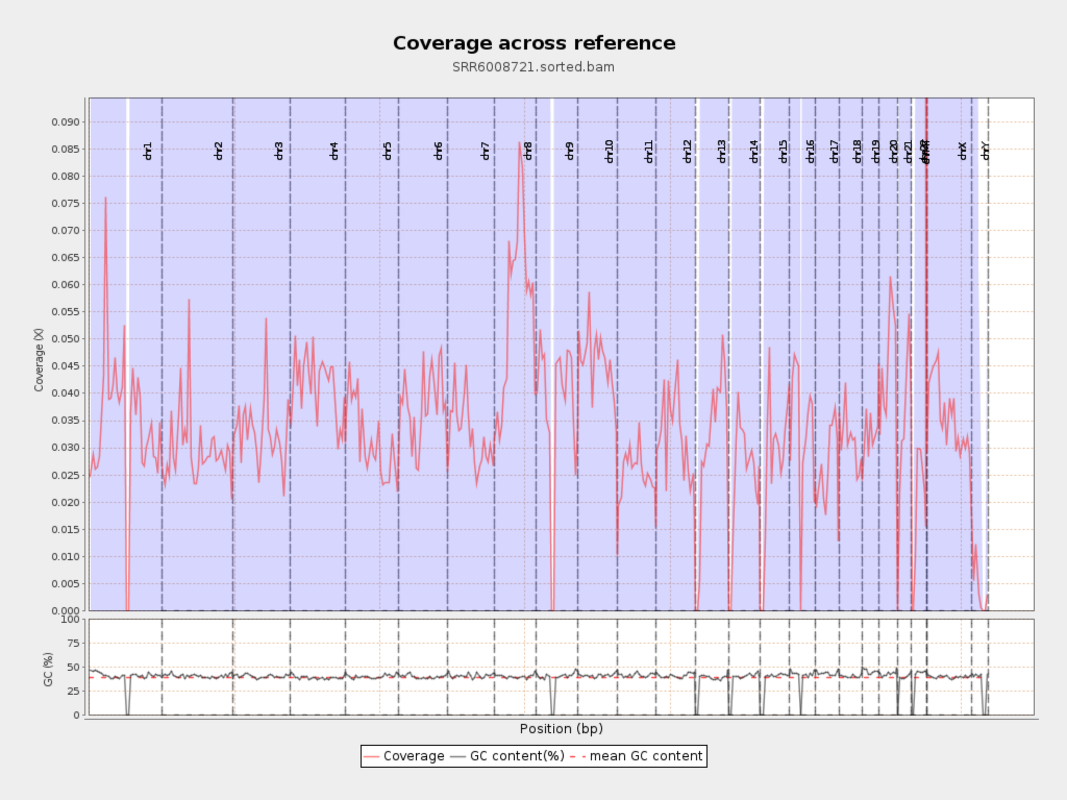
General error rate	1.02%
Mismatches	1,057,048
Insertions	8,308
Mapped reads with at least one insertion	0.51%
Deletions	35,904
Mapped reads with at least one deletion	2.19%
Homopolymer indels	47.04%

2.6. Chromosome stats

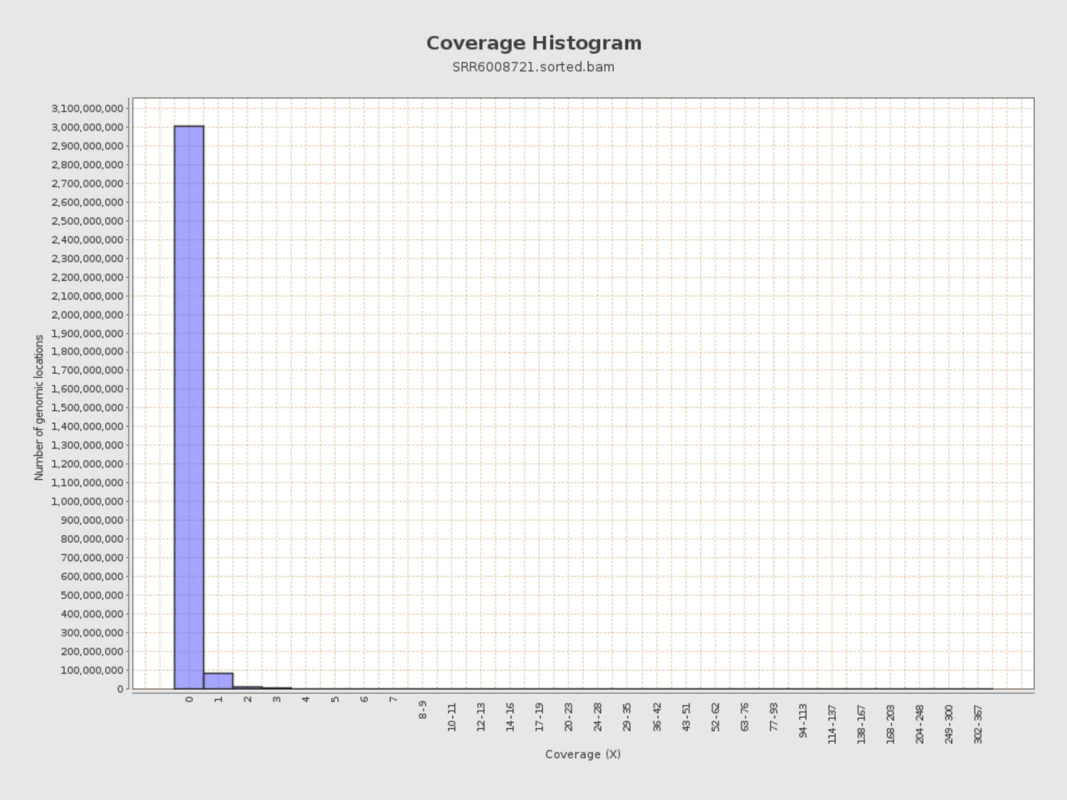
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8511087	0.0341	0.354
chr2	243199373	7274526	0.0299	0.3251
chr3	198022430	6498882	0.0328	0.2023
chr4	191154276	7932820	0.0415	0.2326
chr5	180915260	5630246	0.0311	0.1965
chr6	171115067	6466631	0.0378	0.2386
chr7	159138663	5206910	0.0327	0.2943

chr8	146364022	8182991	0.0559	0.3545
chr9	141213431	5311218	0.0376	0.2777
chr10	135534747	6258662	0.0462	0.2775
chr11	135006516	3430957	0.0254	0.219
chr12	133851895	4313489	0.0322	0.2036
chr13	115169878	3499971	0.0304	0.1942
chr14	107349540	2641118	0.0246	0.1857
chr15	102531392	2733025	0.0267	0.182
chr16	90354753	3037942	0.0336	0.2203
chr17	81195210	2122864	0.0261	0.1988
chr18	78077248	2445343	0.0313	0.4154
chr19	59128983	1930423	0.0326	0.2665
chr20	63025520	2866216	0.0455	0.2416
chr21	48129895	1631400	0.0339	0.2189
chr22	51304566	935613	0.0182	0.1484
chrMT	16571	31729	1.9147	1.9319
chrX	155270560	5549738	0.0357	0.2248
chrY	59373566	247224	0.0042	0.0988

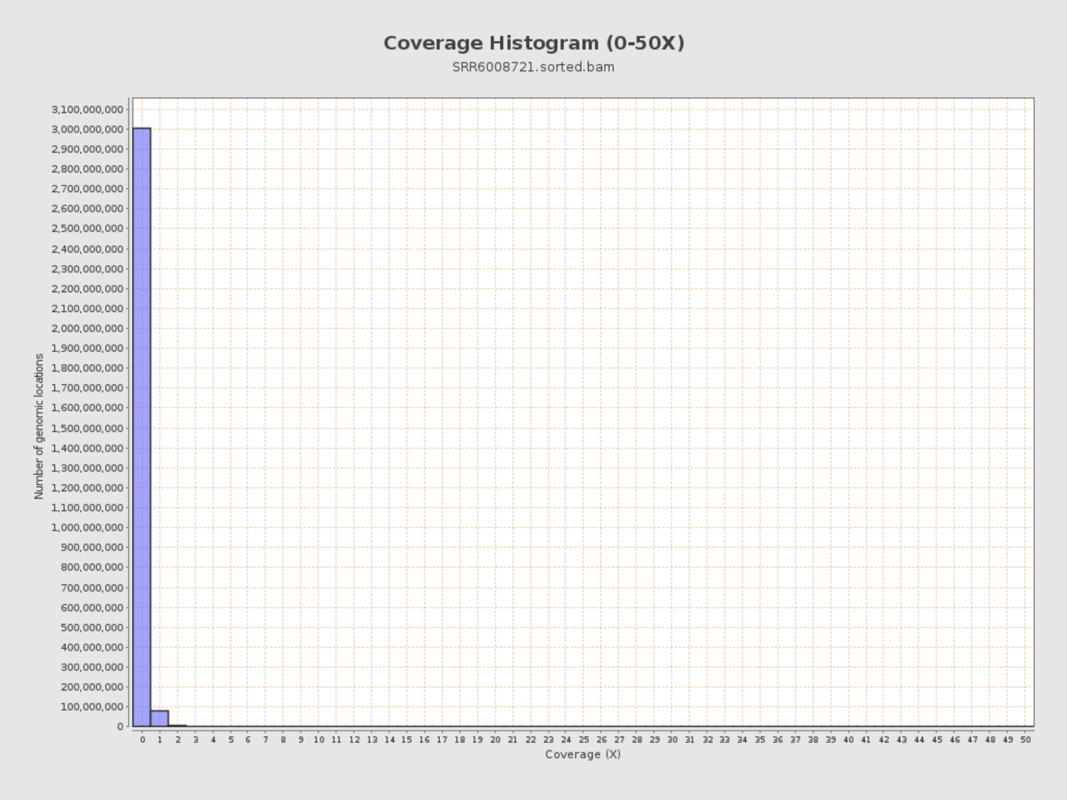
3. Results : Coverage across reference



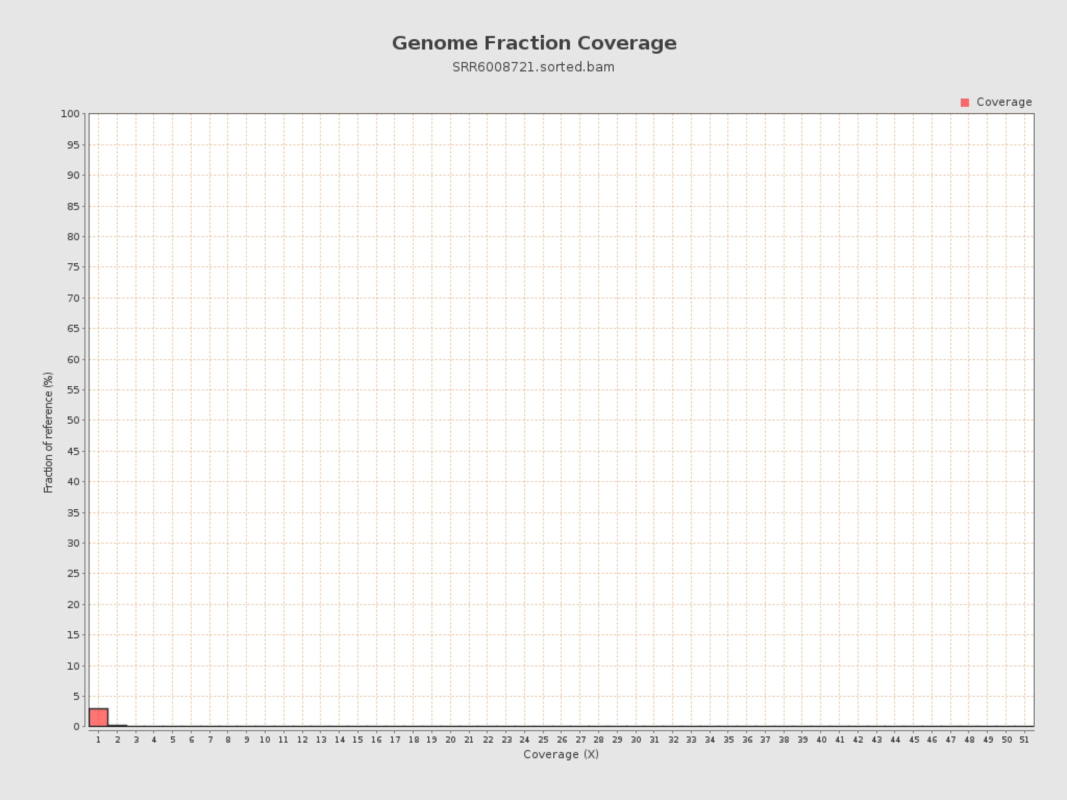
4. Results : Coverage Histogram



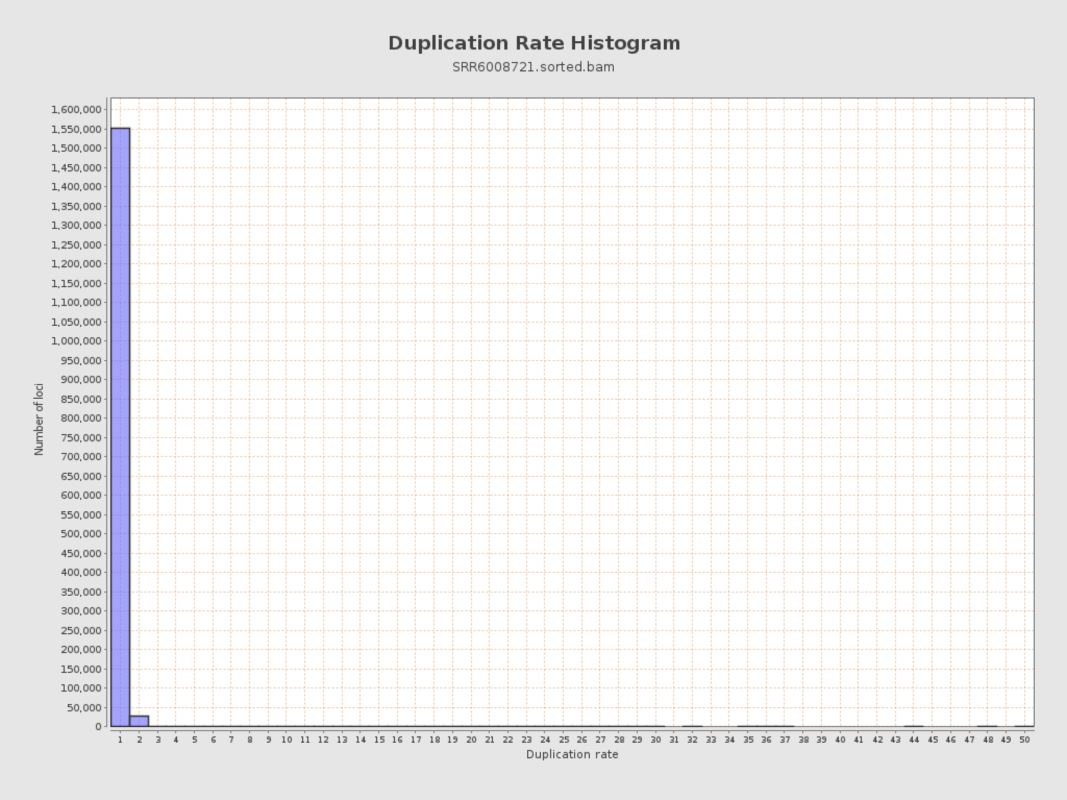
5. Results : Coverage Histogram (0-50X)



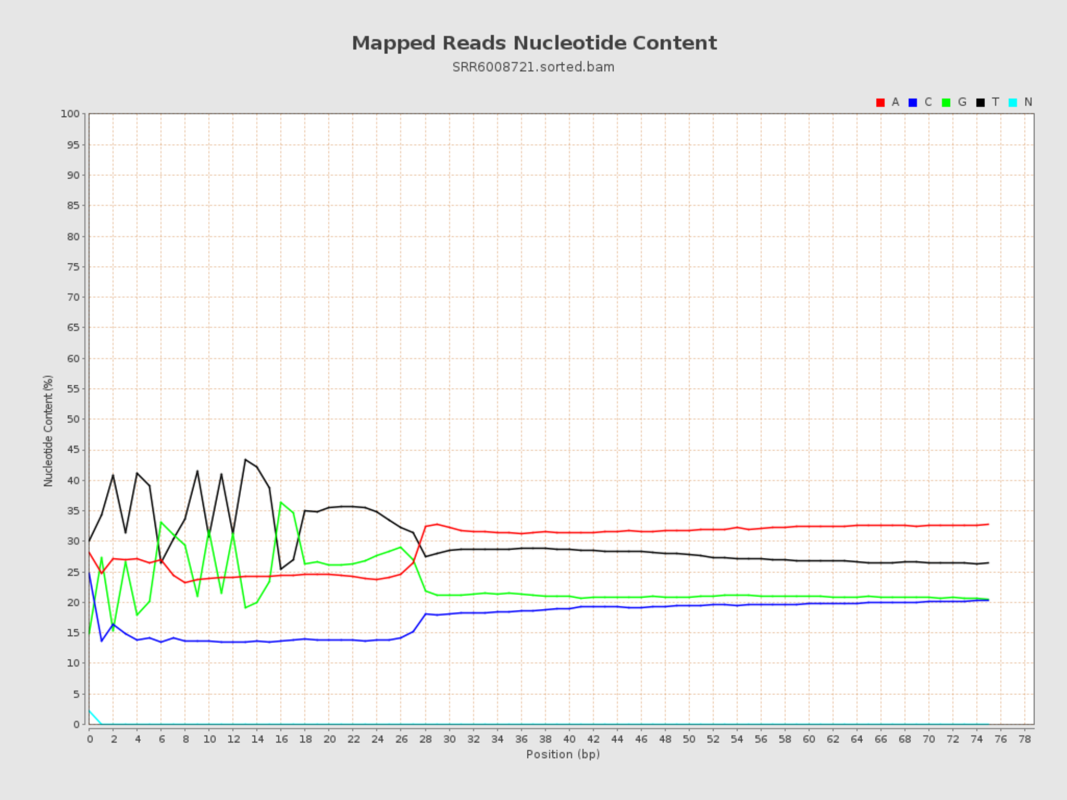
6. Results : Genome Fraction Coverage



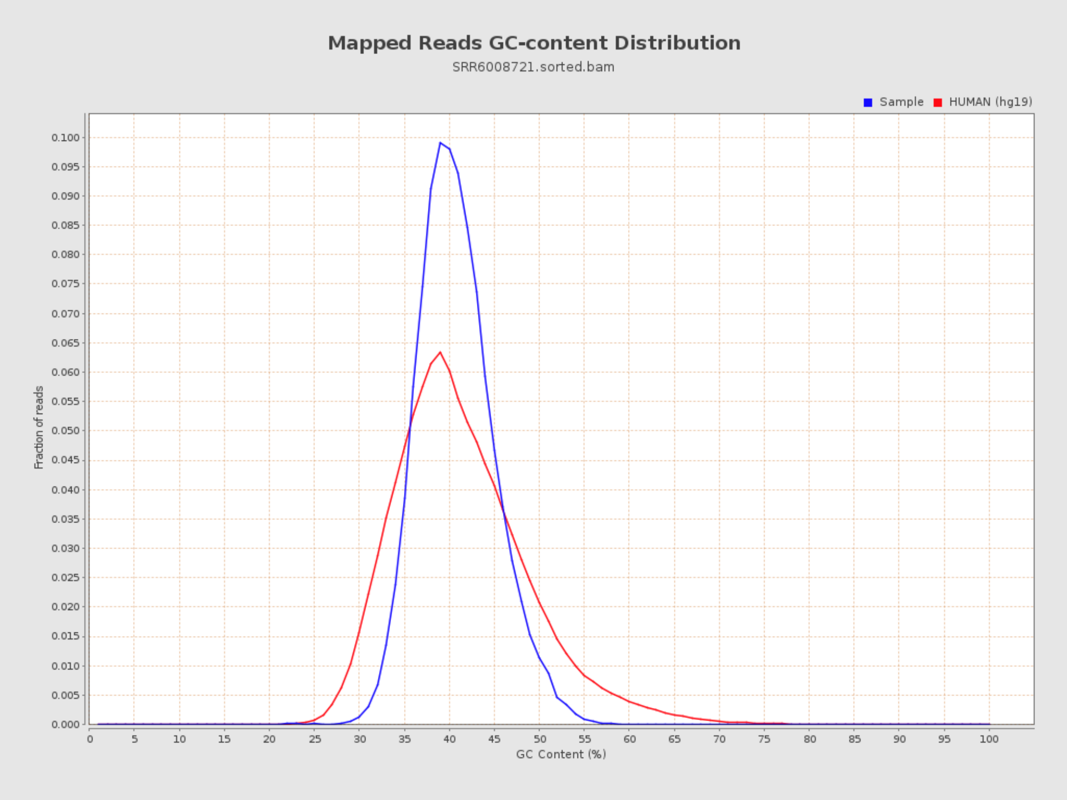
7. Results : Duplication Rate Histogram



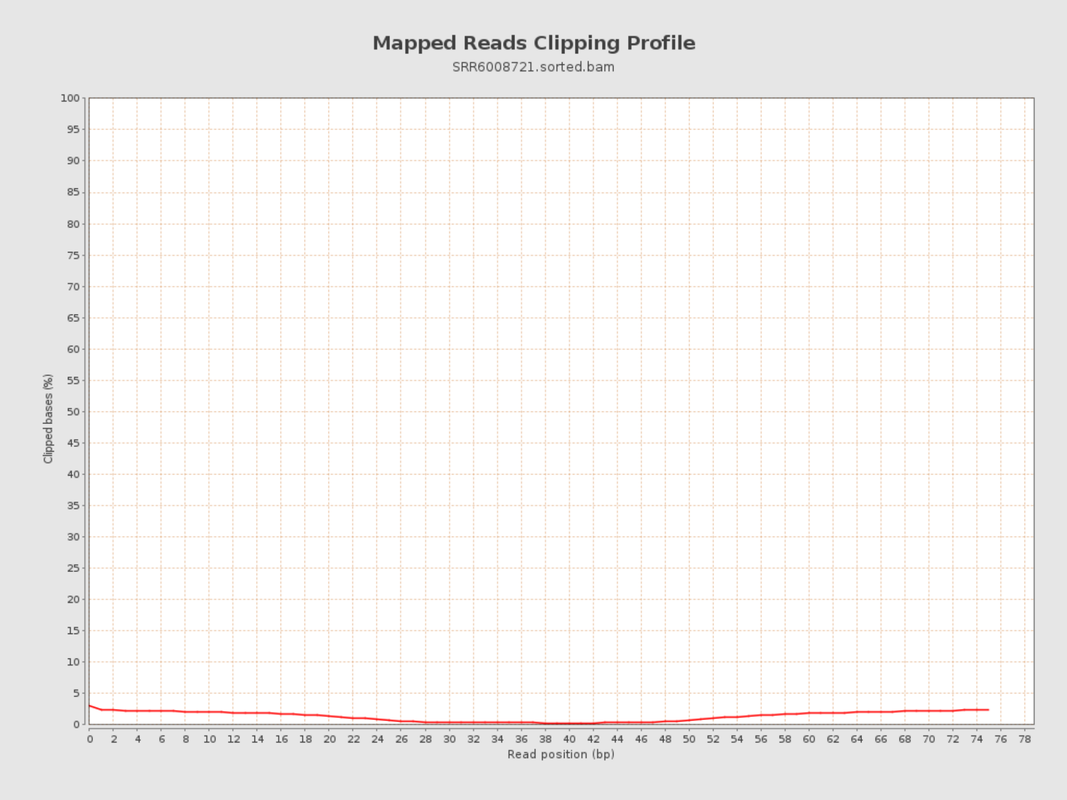
8. Results : Mapped Reads Nucleotide Content



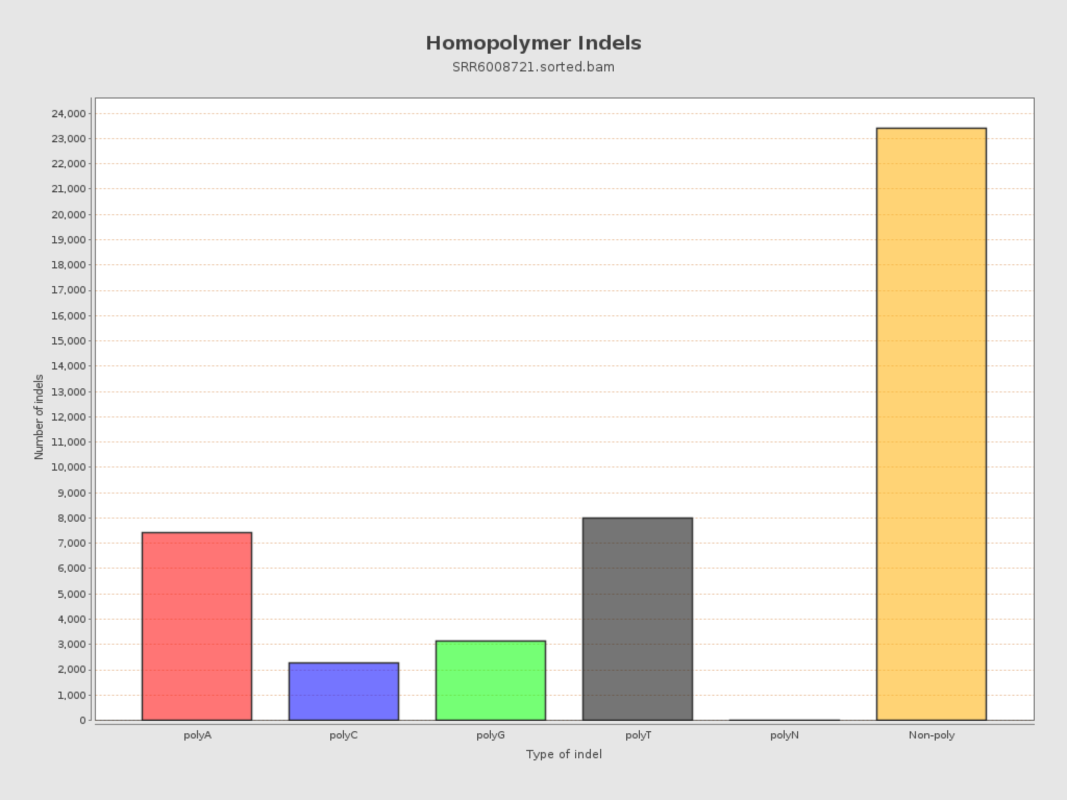
9. Results : Mapped Reads GC-content Distribution



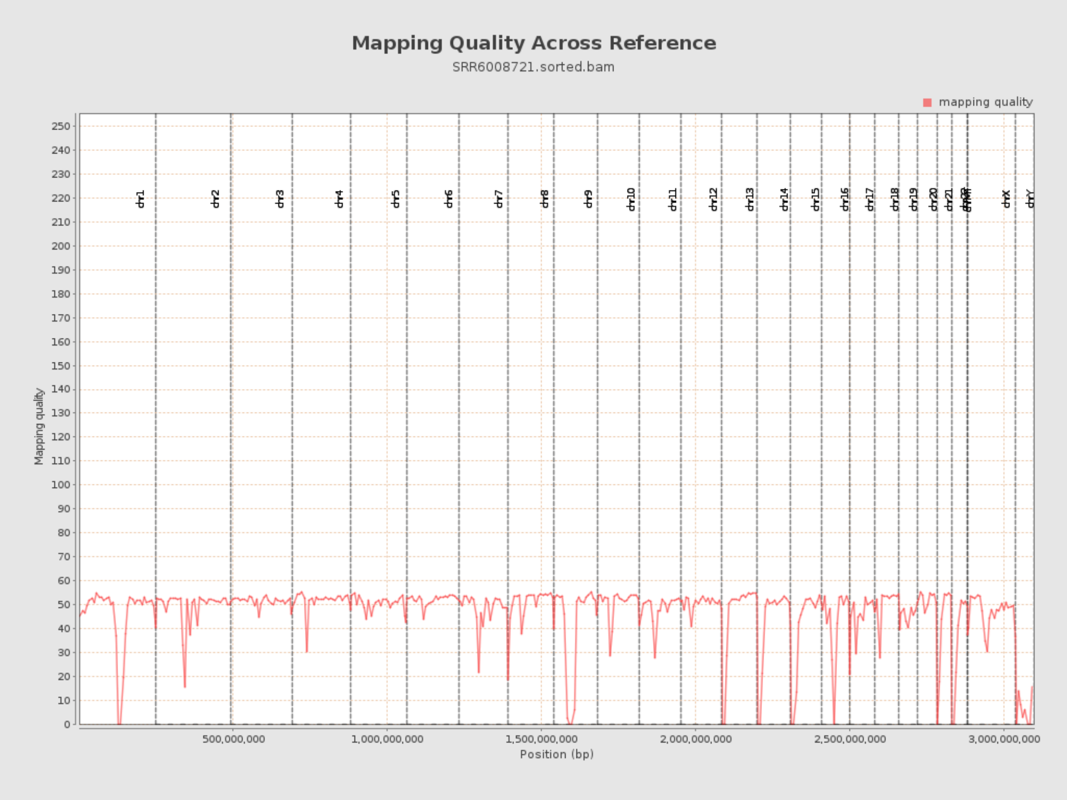
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram