Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:31:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008723.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_SRR6008723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:31:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,768,083
Mapped reads	1,275,770 / 72.16%
Unmapped reads	492,313 / 27.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,858 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	45,509 / 2.57%
Duplication rate	2.92%
Clipped reads	676,053 / 38.24%

2.2. ACGT Content

Number/percentage of A's	23,307,601 / 28.46%
Number/percentage of C's	13,734,893 / 16.77%
Number/percentage of T's	25,498,655 / 31.14%
Number/percentage of G's	19,337,888 / 23.61%
Number/percentage of N's	9,838 / 0.01%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2354

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

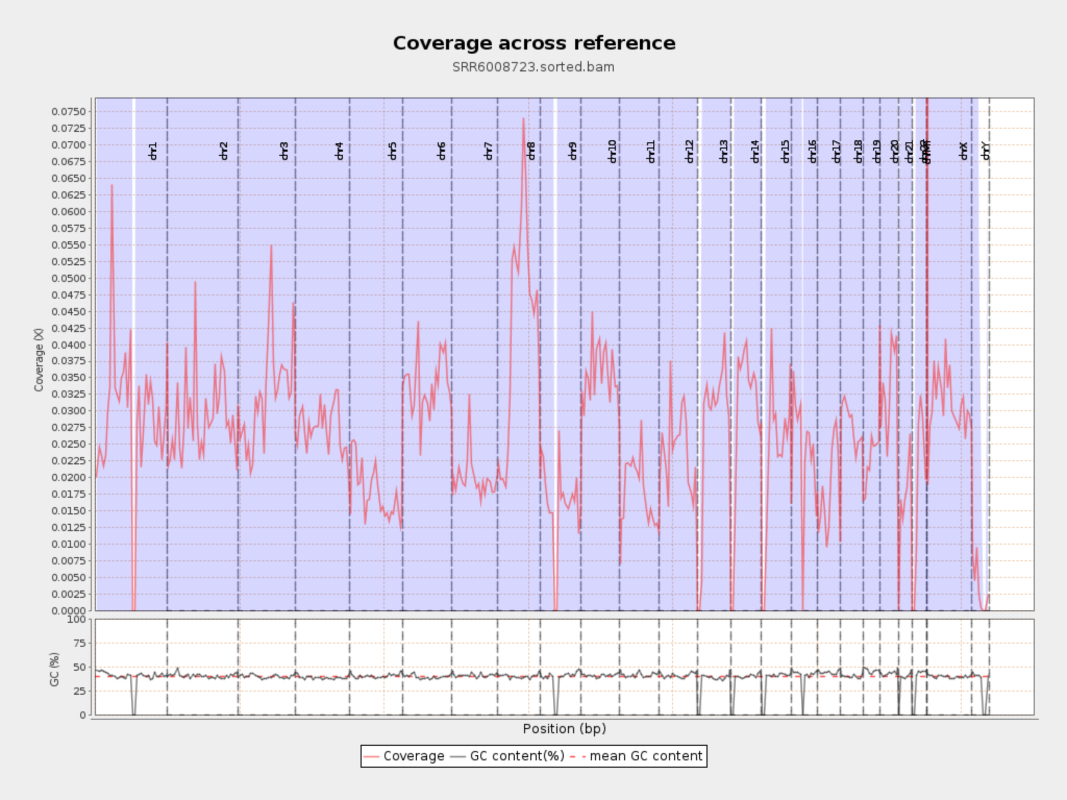
General error rate	0.95%
Mismatches	767,064
Insertions	6,560
Mapped reads with at least one insertion	0.51%
Deletions	26,341
Mapped reads with at least one deletion	2.04%
Homopolymer indels	48.4%

2.6. Chromosome stats

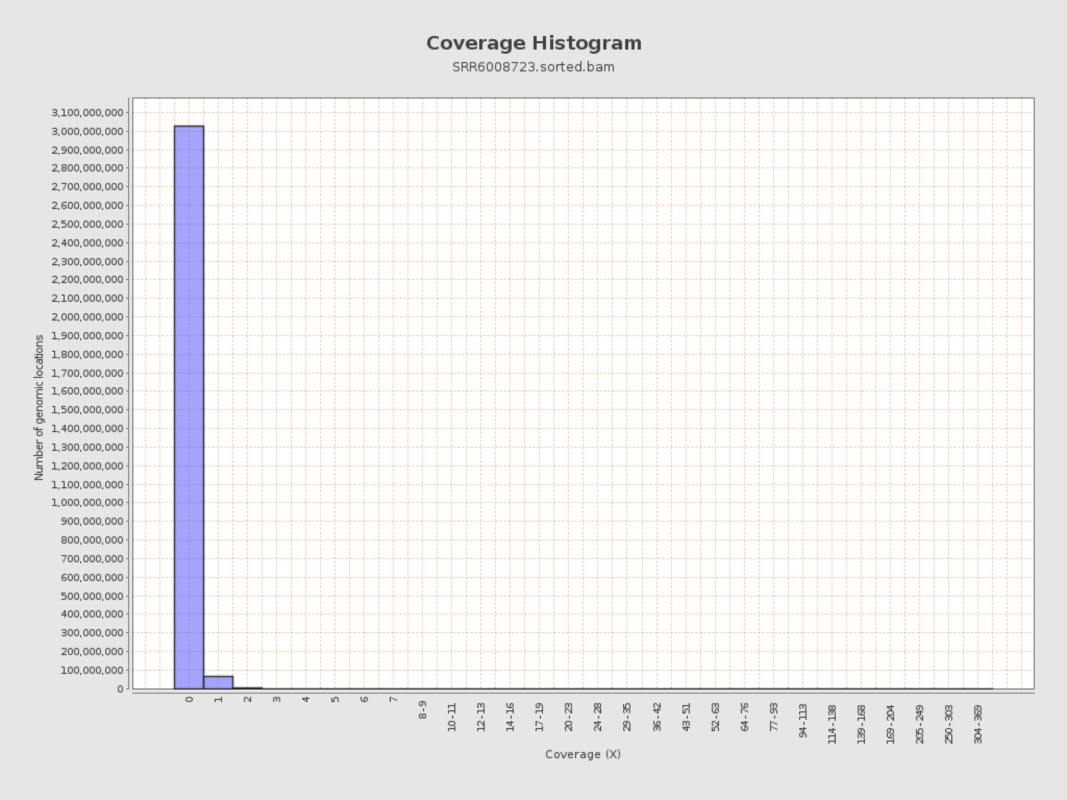
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7224967	0.029	0.3204
chr2	243199373	7032971	0.0289	0.3293
chr3	198022430	6441968	0.0325	0.2039
chr4	191154276	5238115	0.0274	0.1888
chr5	180915260	3242099	0.0179	0.1504
chr6	171115067	5807962	0.0339	0.2332
chr7	159138663	3168091	0.0199	0.2373

chr8	146364022	6356401	0.0434	0.3375
chr9	141213431	2254261	0.016	0.2054
chr10	135534747	4818695	0.0356	0.2512
chr11	135006516	2425873	0.018	0.1933
chr12	133851895	3233574	0.0242	0.176
chr13	115169878	3126493	0.0271	0.1857
chr14	107349540	3117496	0.029	0.1951
chr15	102531392	2374356	0.0232	0.172
chr16	90354753	2131968	0.0236	0.1803
chr17	81195210	1474015	0.0182	0.159
chr18	78077248	2187677	0.028	0.3599
chr19	59128983	1380411	0.0233	0.2296
chr20	63025520	2088995	0.0331	0.2096
chr21	48129895	799279	0.0166	0.1492
chr22	51304566	957587	0.0187	0.1526
chrMT	16571	26011	1.5697	1.7641
chrX	155270560	4828878	0.0311	0.21
chrY	59373566	192318	0.0032	0.0804

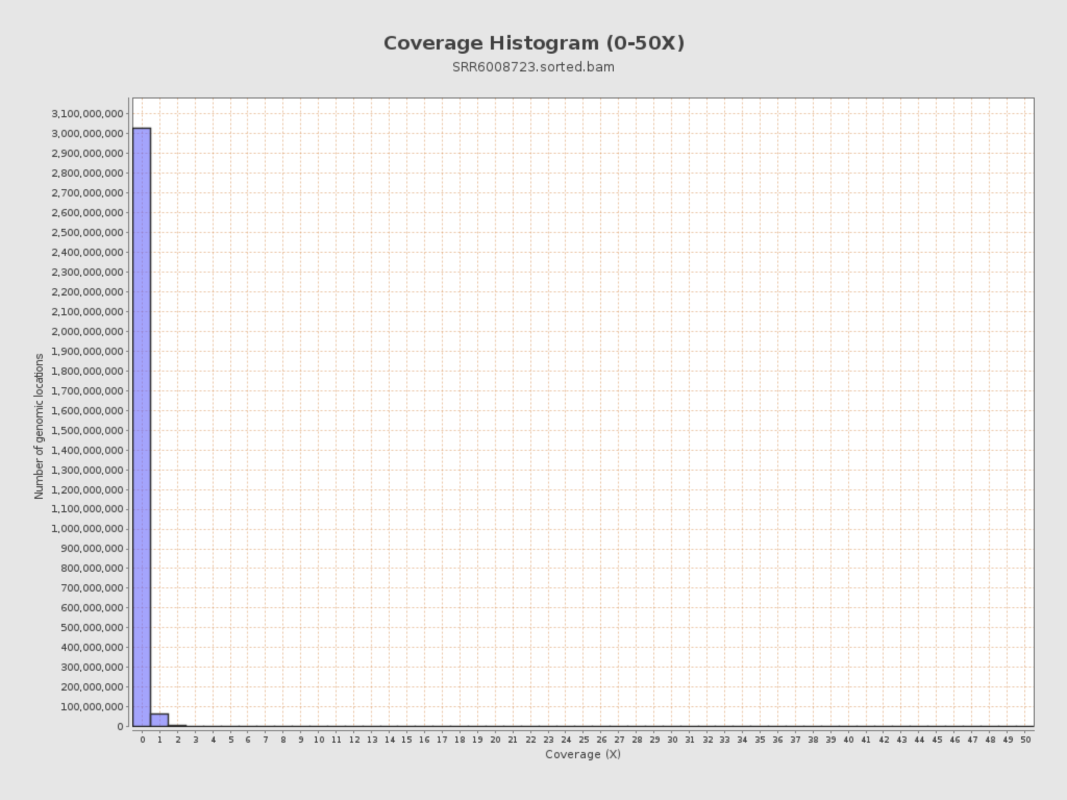
3. Results : Coverage across reference



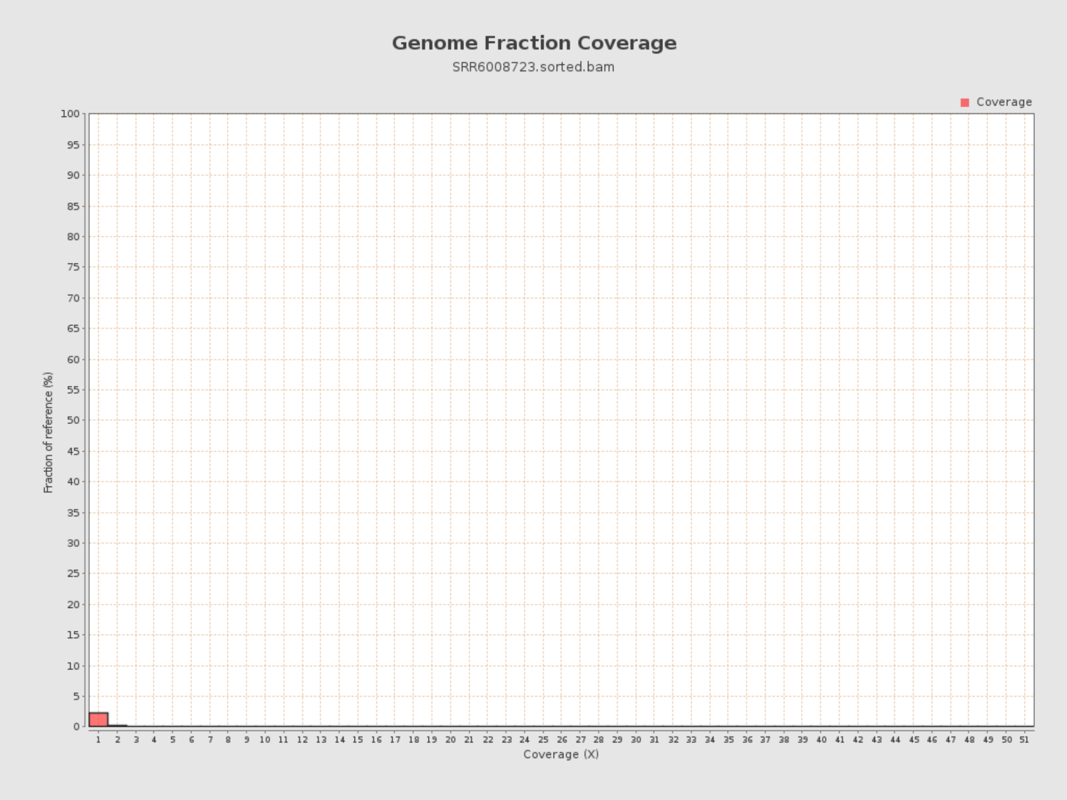
4. Results : Coverage Histogram



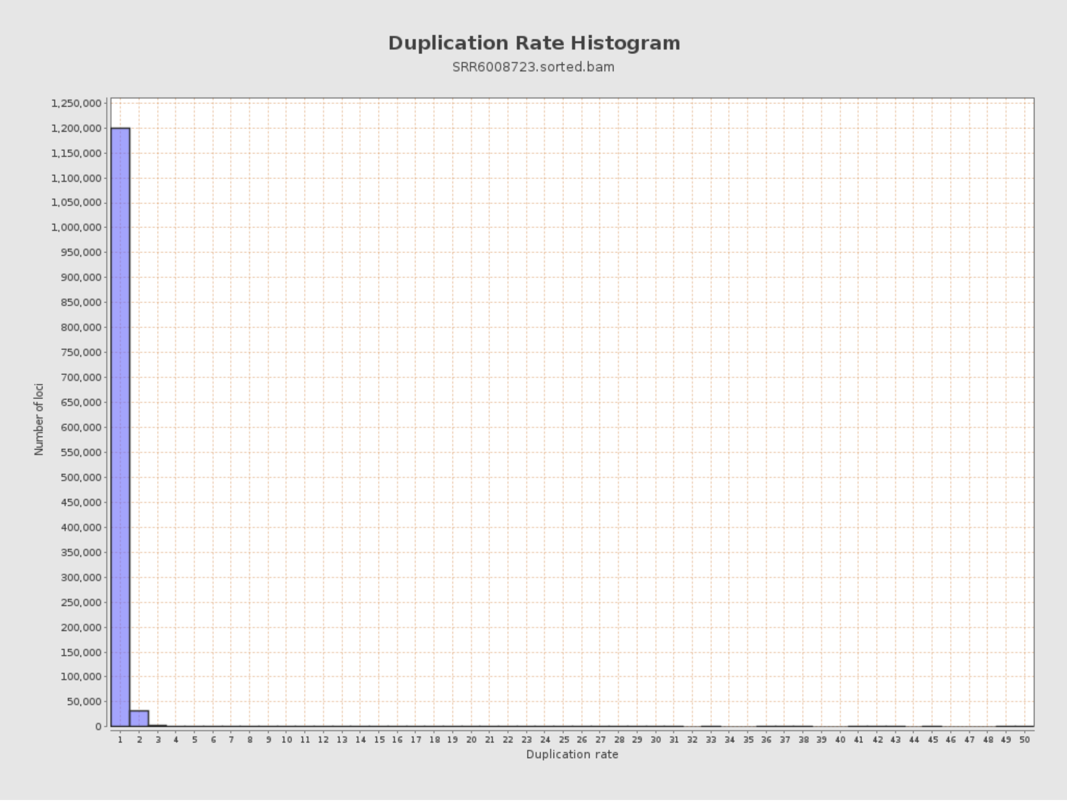
5. Results : Coverage Histogram (0-50X)



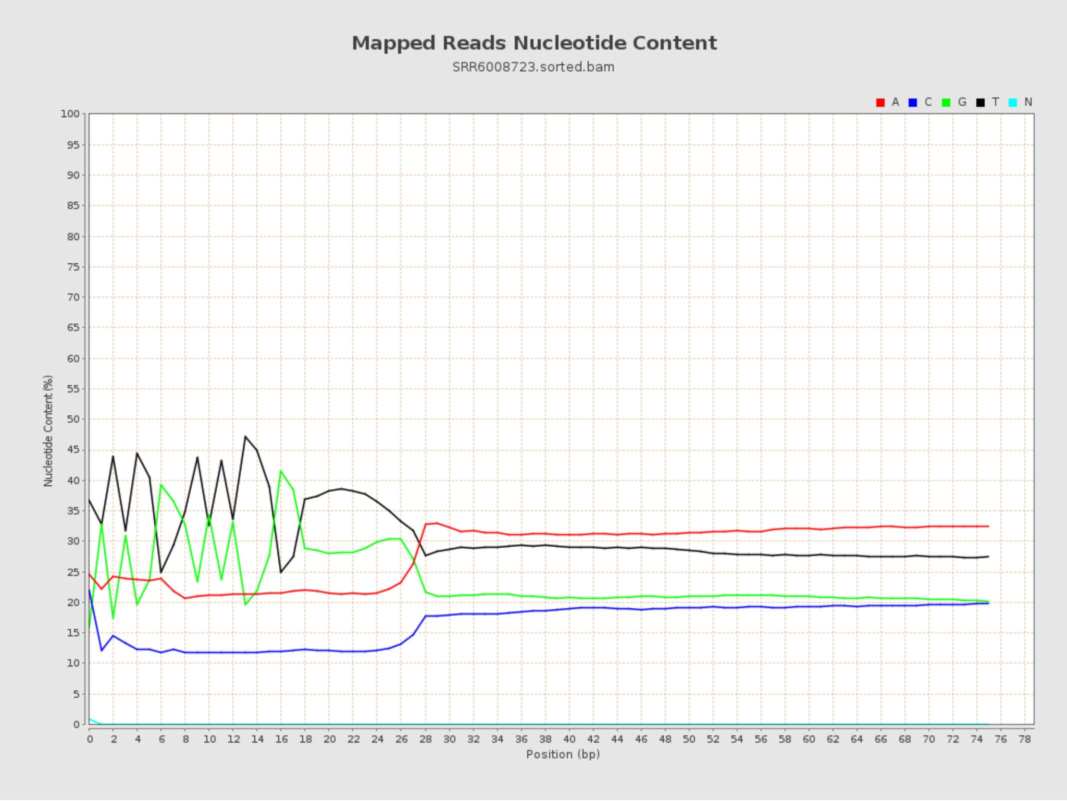
6. Results : Genome Fraction Coverage



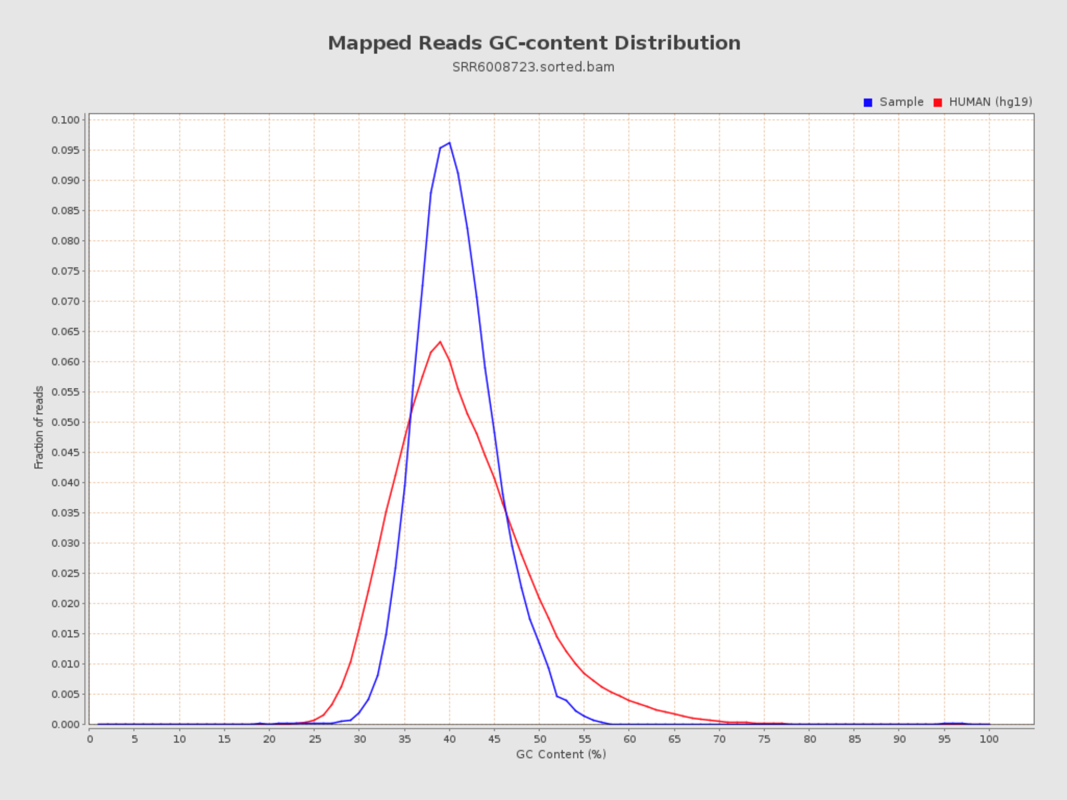
7. Results : Duplication Rate Histogram



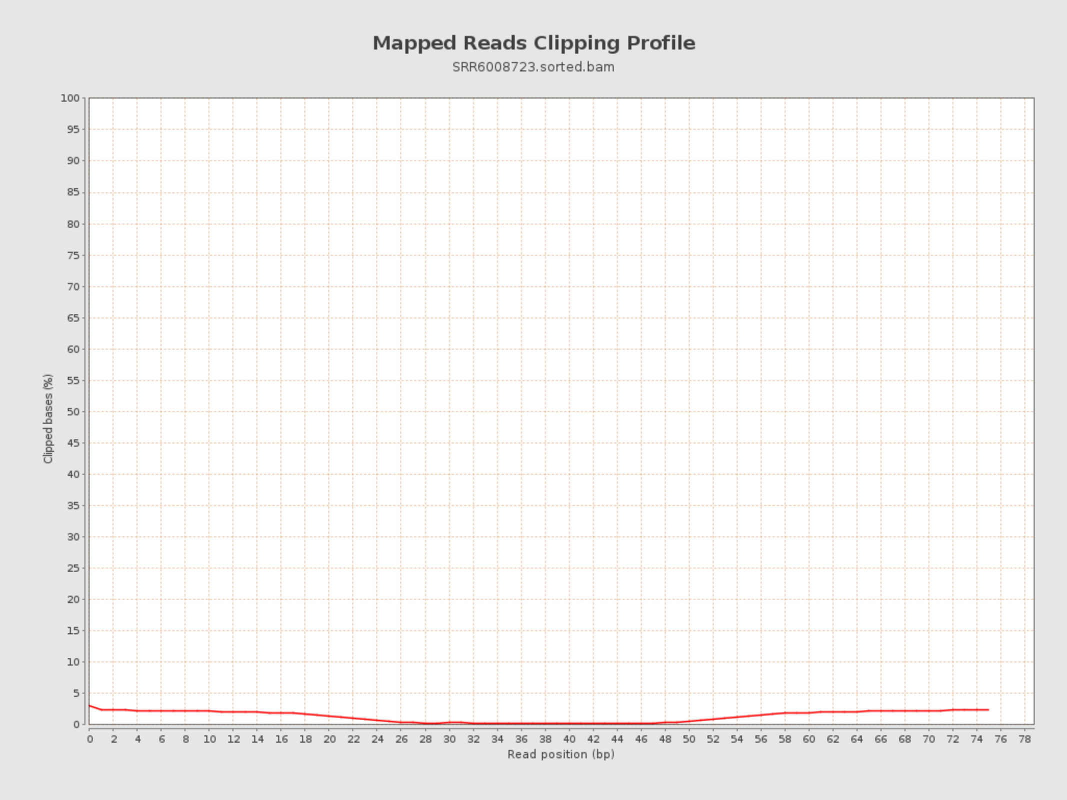
8. Results : Mapped Reads Nucleotide Content



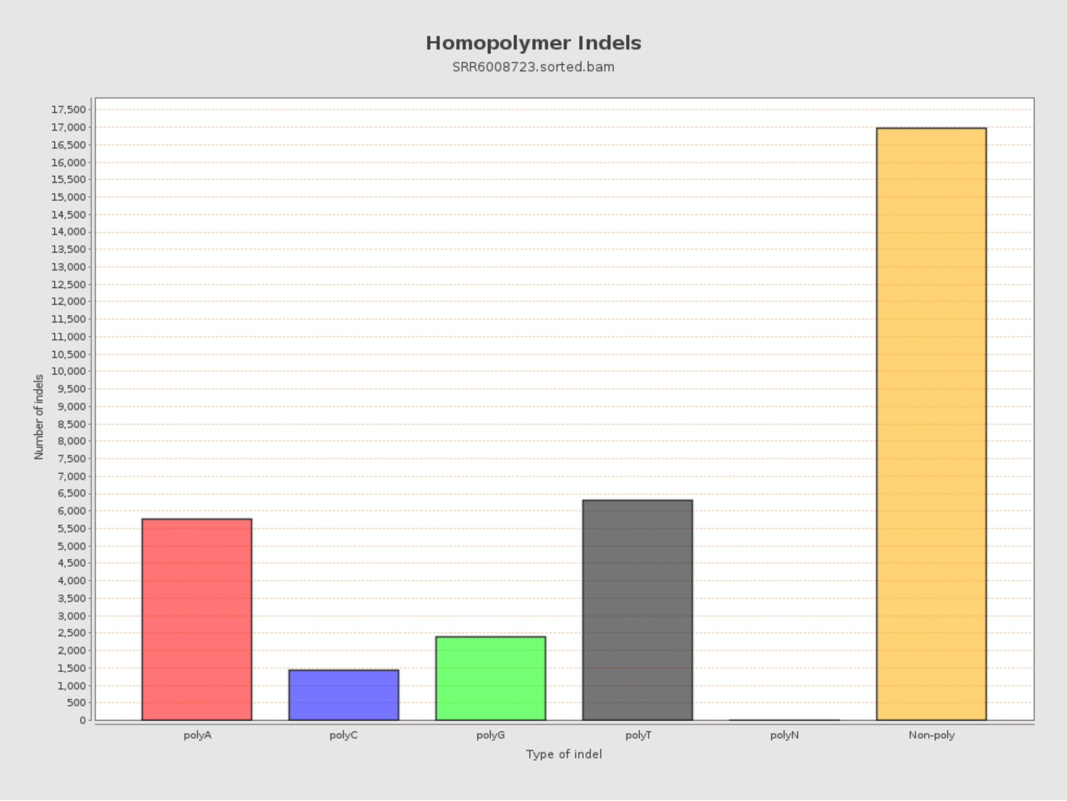
9. Results : Mapped Reads GC-content Distribution



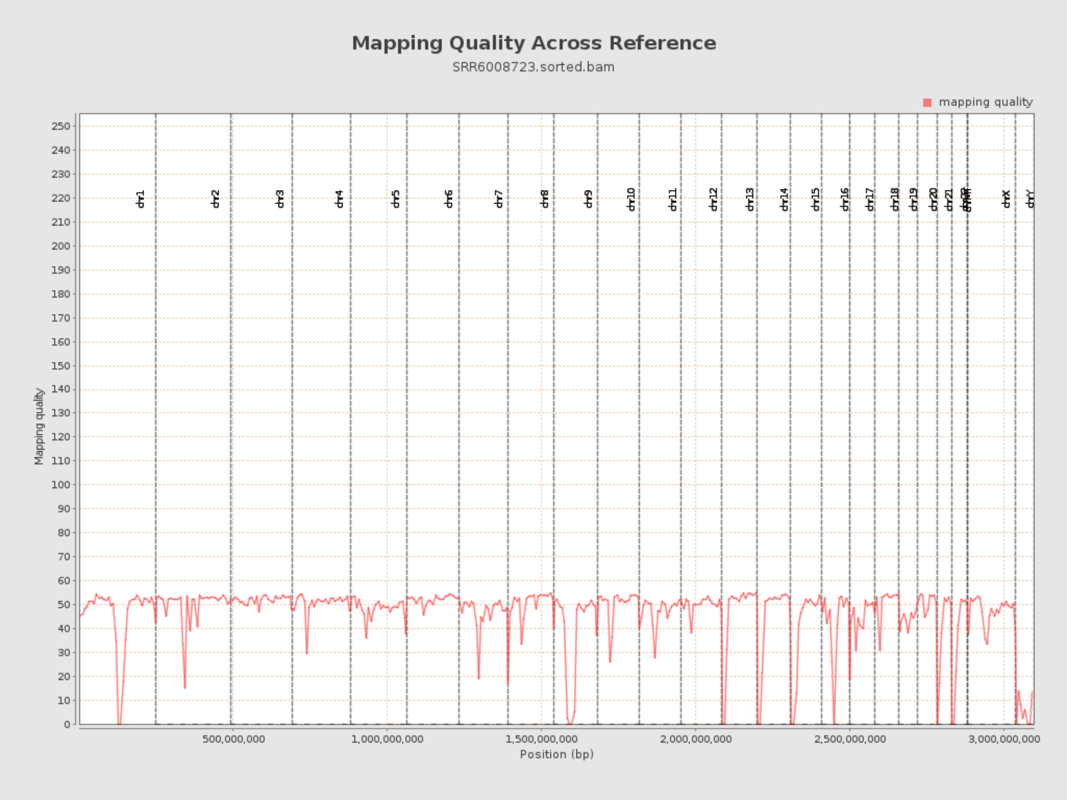
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram