Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:21:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008719.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_SRR6008719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:21:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,618,530
Mapped reads	1,172,870 / 72.47%
Unmapped reads	445,660 / 27.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,654 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	20,614 / 1.27%
Duplication rate	1.4%
Clipped reads	375,124 / 23.18%

2.2. ACGT Content

Number/percentage of A's	25,777,594 / 31.62%
Number/percentage of C's	14,159,958 / 17.37%
Number/percentage of T's	24,301,662 / 29.81%
Number/percentage of G's	17,271,016 / 21.19%
Number/percentage of N's	13,238 / 0.02%
GC Percentage	38.55%

2.3. Coverage

Mean	0.0263

Standard Deviation	0.2073

2.4. Mapping Quality

Mean Mapping Quality	48.98

2.5. Mismatches and indels

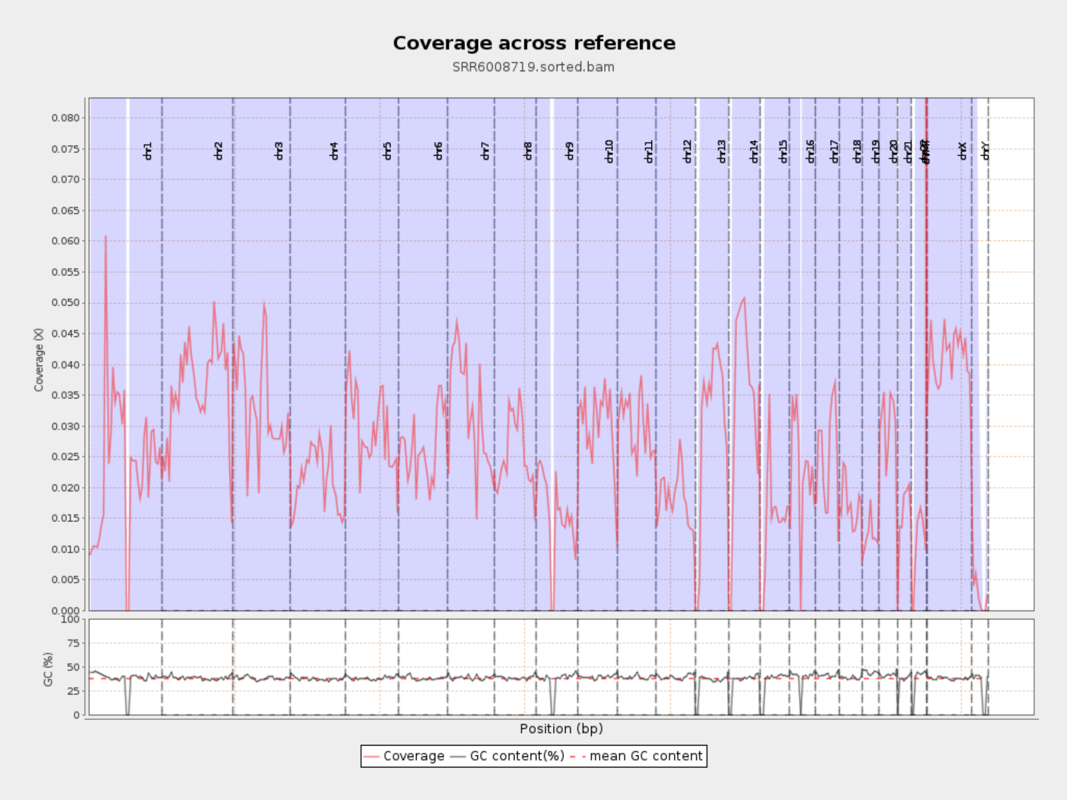
General error rate	0.93%
Mismatches	751,722
Insertions	6,027
Mapped reads with at least one insertion	0.51%
Deletions	23,309
Mapped reads with at least one deletion	1.96%
Homopolymer indels	48.51%

2.6. Chromosome stats

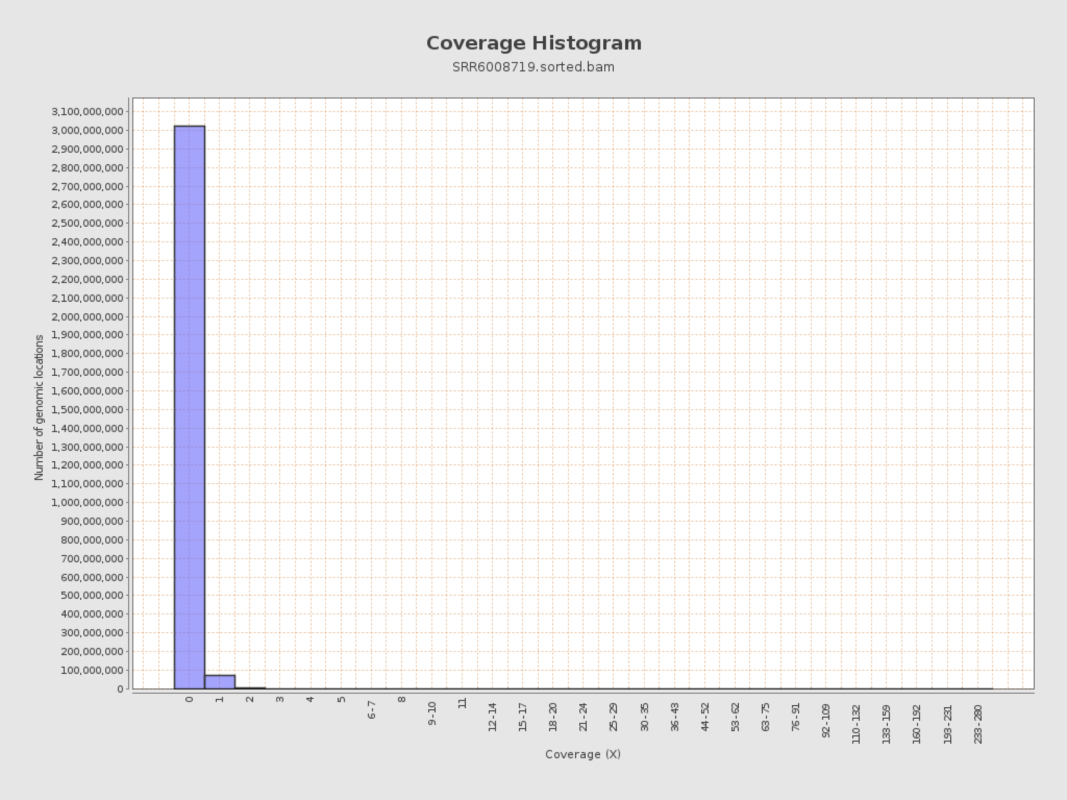
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5835120	0.0234	0.2556
chr2	243199373	8853018	0.0364	0.2707
chr3	198022430	6611112	0.0334	0.1941
chr4	191154276	4061557	0.0212	0.1544
chr5	180915260	5353226	0.0296	0.1816
chr6	171115067	4542089	0.0265	0.1835
chr7	159138663	5221825	0.0328	0.282

chr8	146364022	3724336	0.0254	0.2427
chr9	141213431	2181532	0.0154	0.1631
chr10	135534747	4155866	0.0307	0.2023
chr11	135006516	4026892	0.0298	0.222
chr12	133851895	2432215	0.0182	0.1429
chr13	115169878	3472931	0.0302	0.1845
chr14	107349540	3657311	0.0341	0.2012
chr15	102531392	1506742	0.0147	0.1289
chr16	90354753	2067312	0.0229	0.1675
chr17	81195210	2020618	0.0249	0.1818
chr18	78077248	1349014	0.0173	0.283
chr19	59128983	733377	0.0124	0.1639
chr20	63025520	1892263	0.03	0.1847
chr21	48129895	736348	0.0153	0.1346
chr22	51304566	532606	0.0104	0.1074
chrMT	16571	27399	1.6534	1.7513
chrX	155270560	6392543	0.0412	0.2273
chrY	59373566	172832	0.0029	0.0634

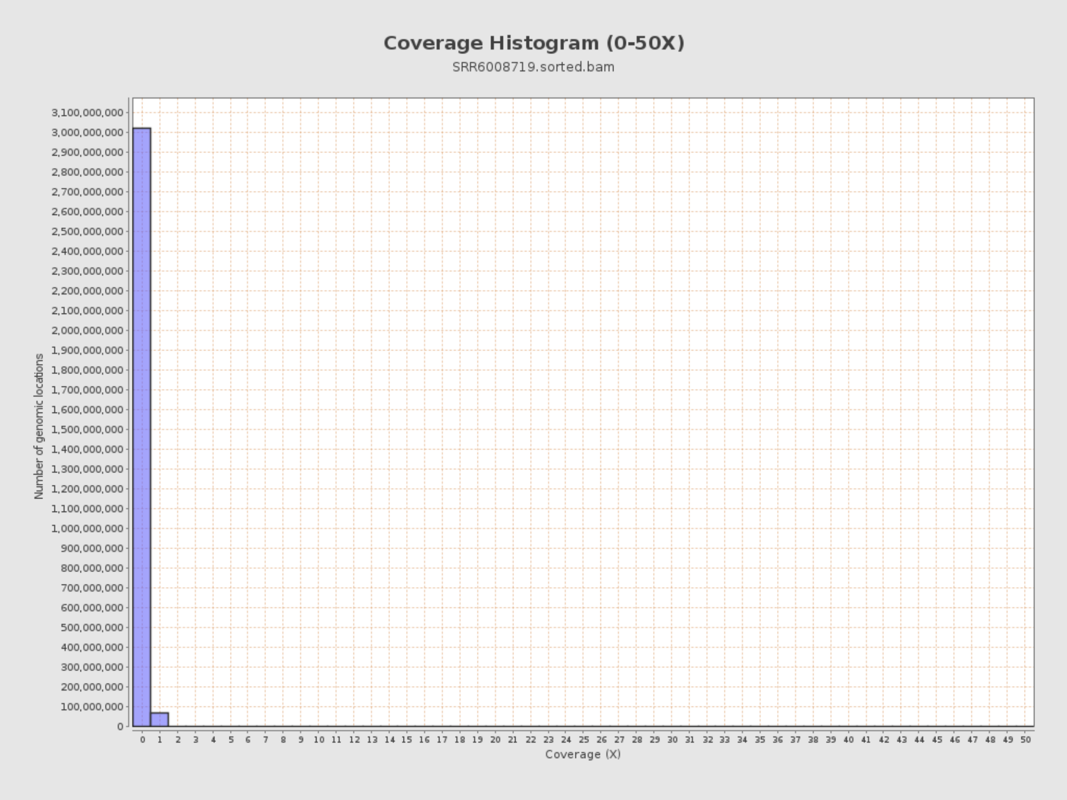
3. Results : Coverage across reference



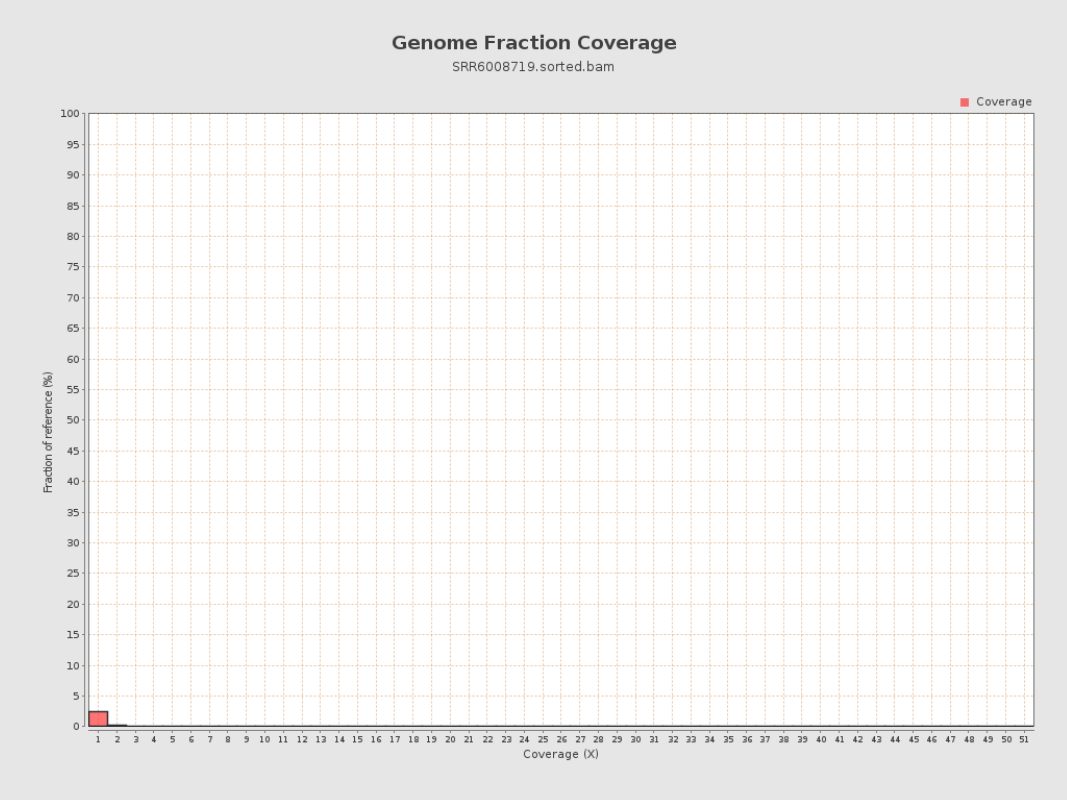
4. Results : Coverage Histogram



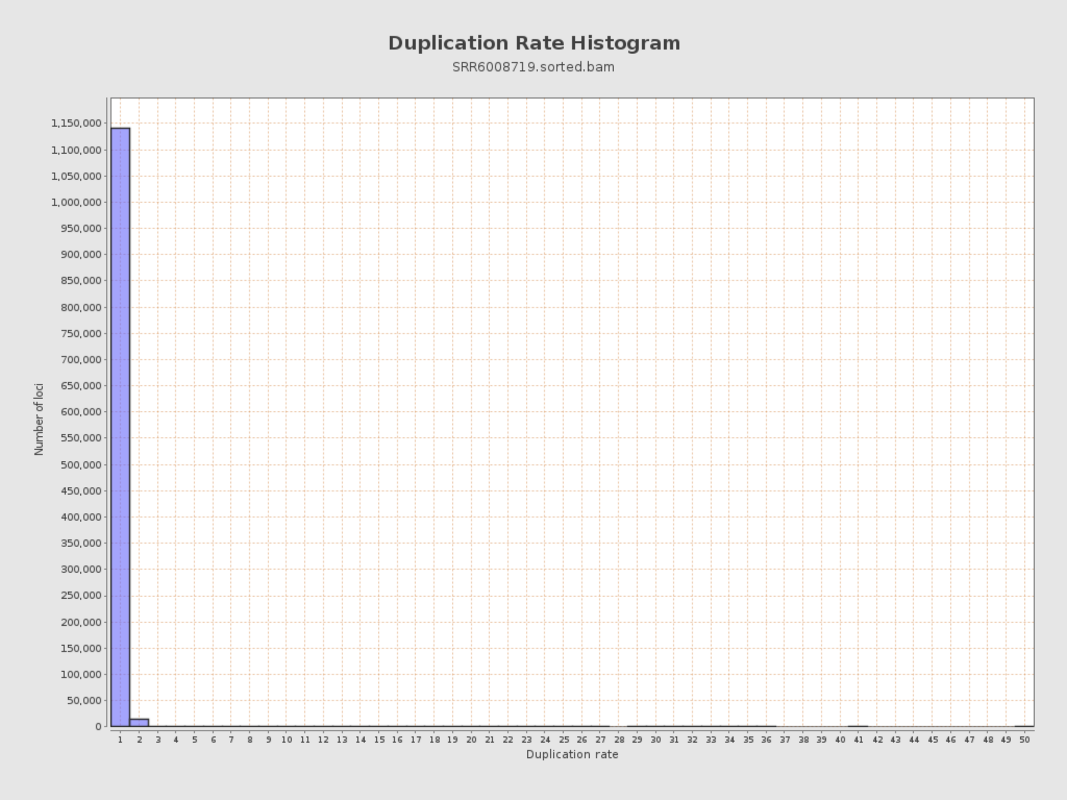
5. Results : Coverage Histogram (0-50X)



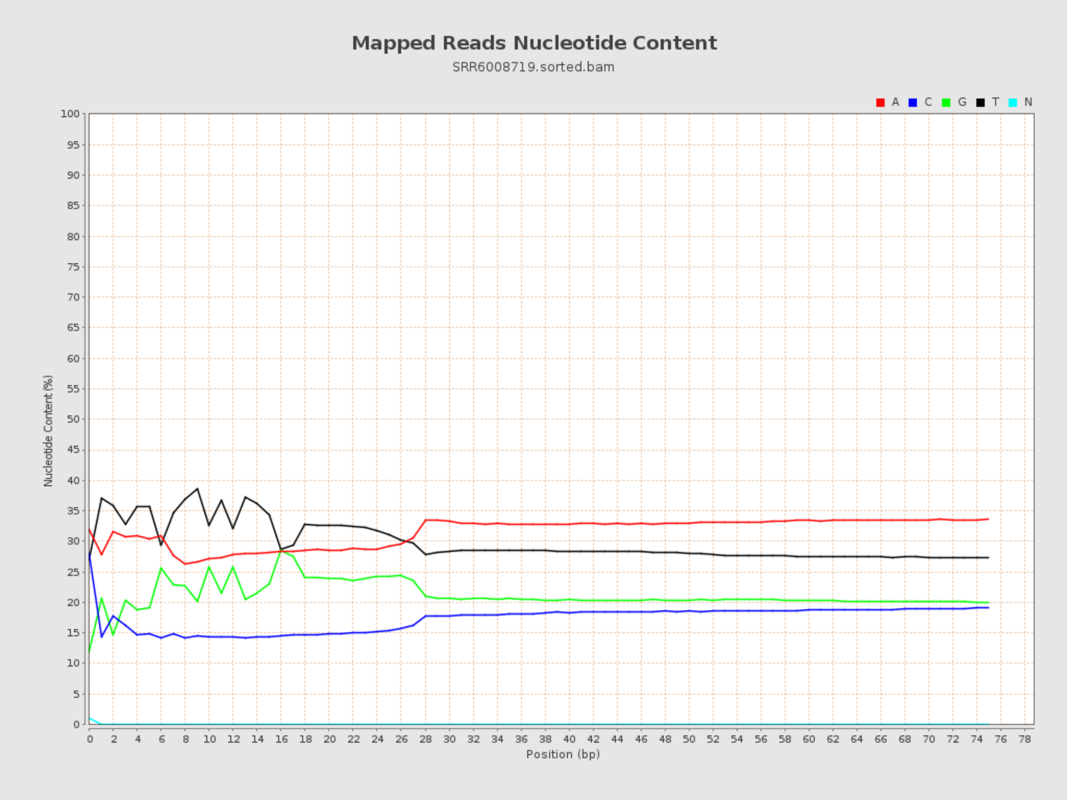
6. Results : Genome Fraction Coverage



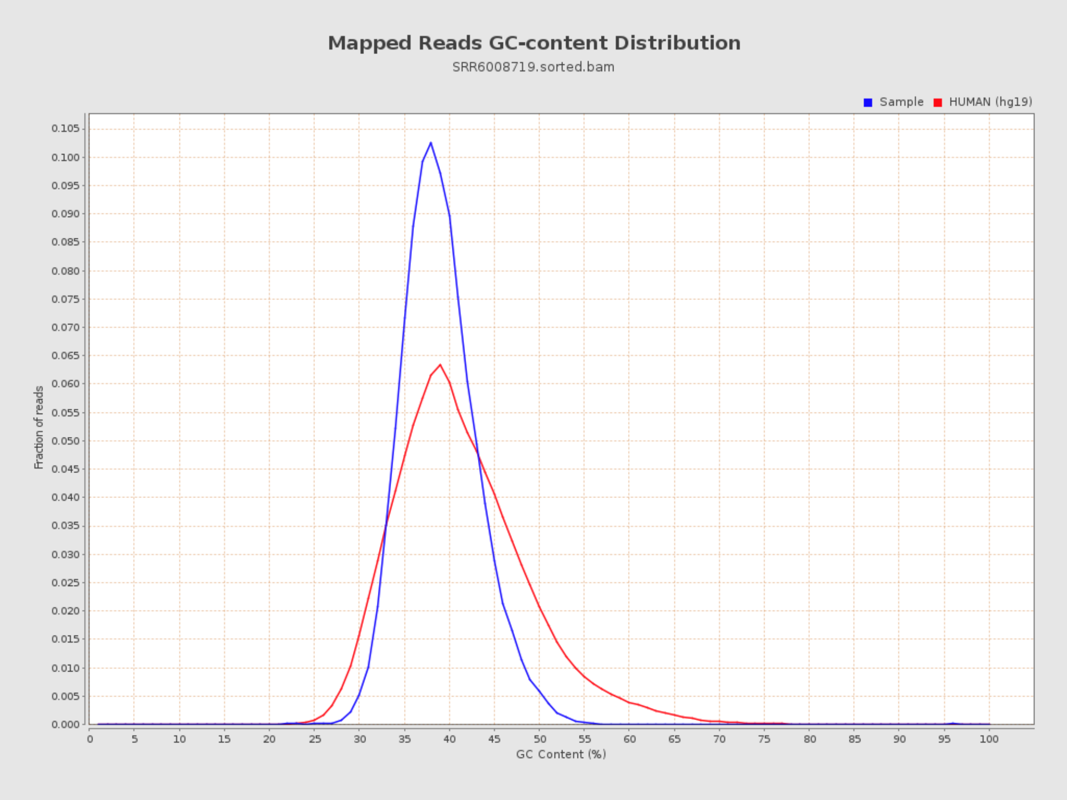
7. Results : Duplication Rate Histogram



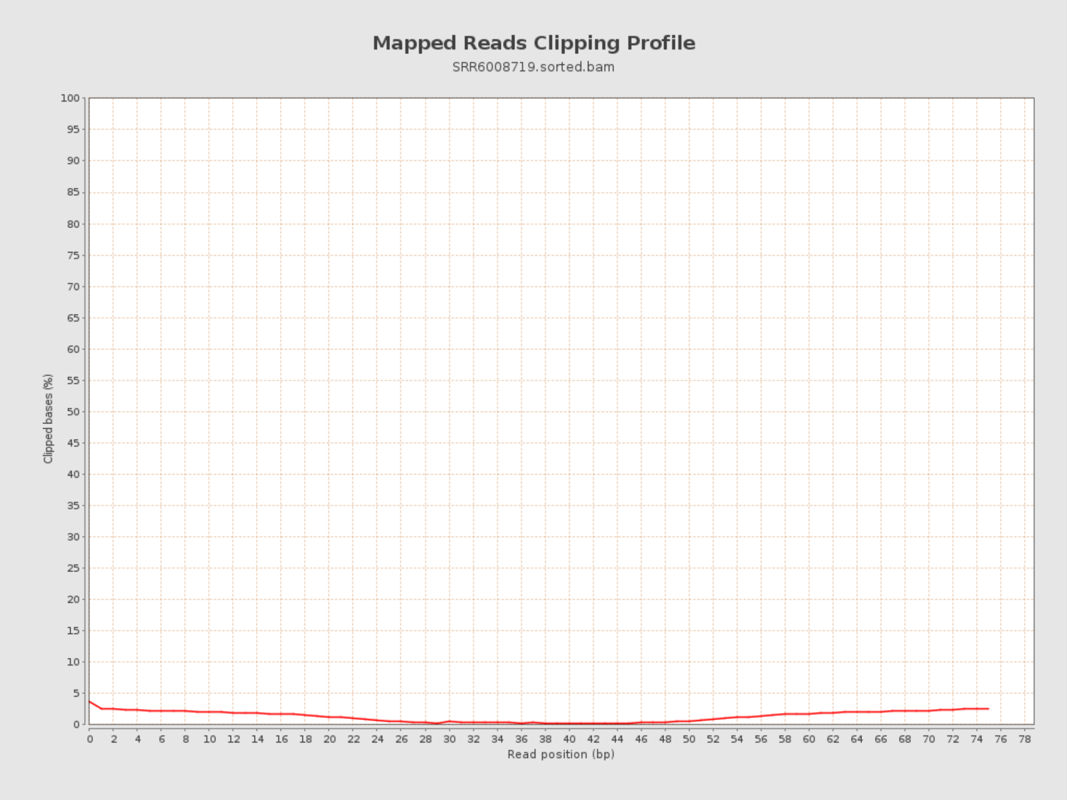
8. Results : Mapped Reads Nucleotide Content



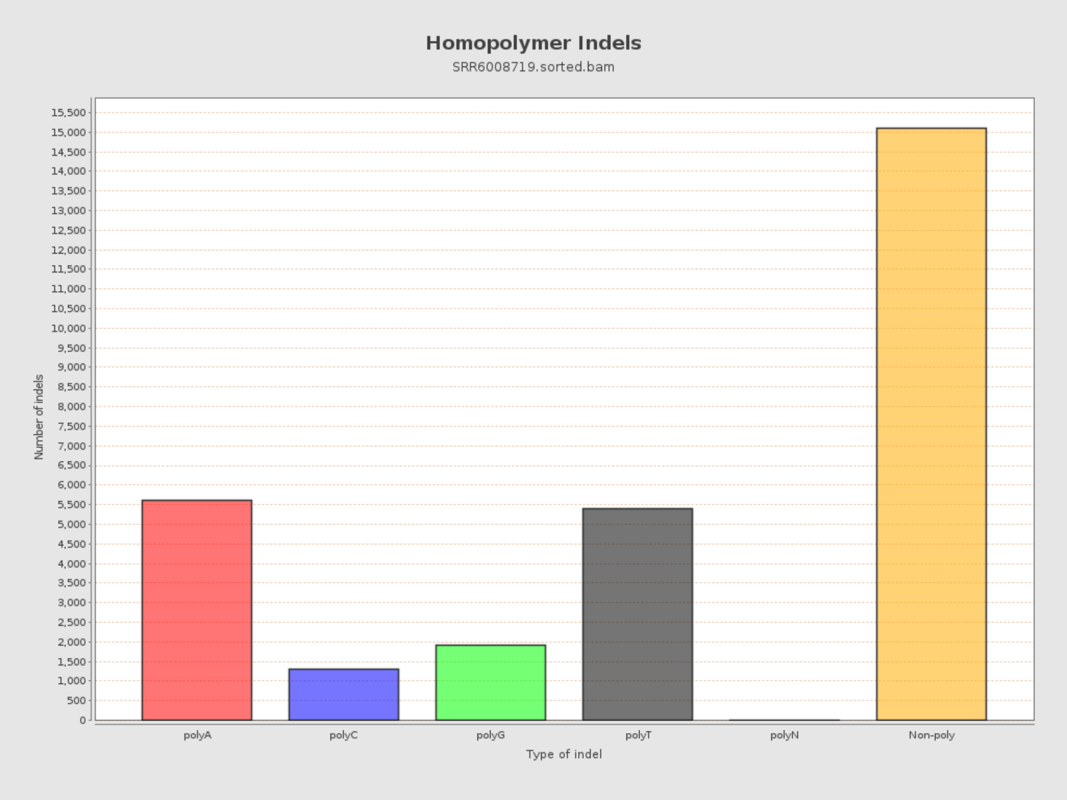
9. Results : Mapped Reads GC-content Distribution



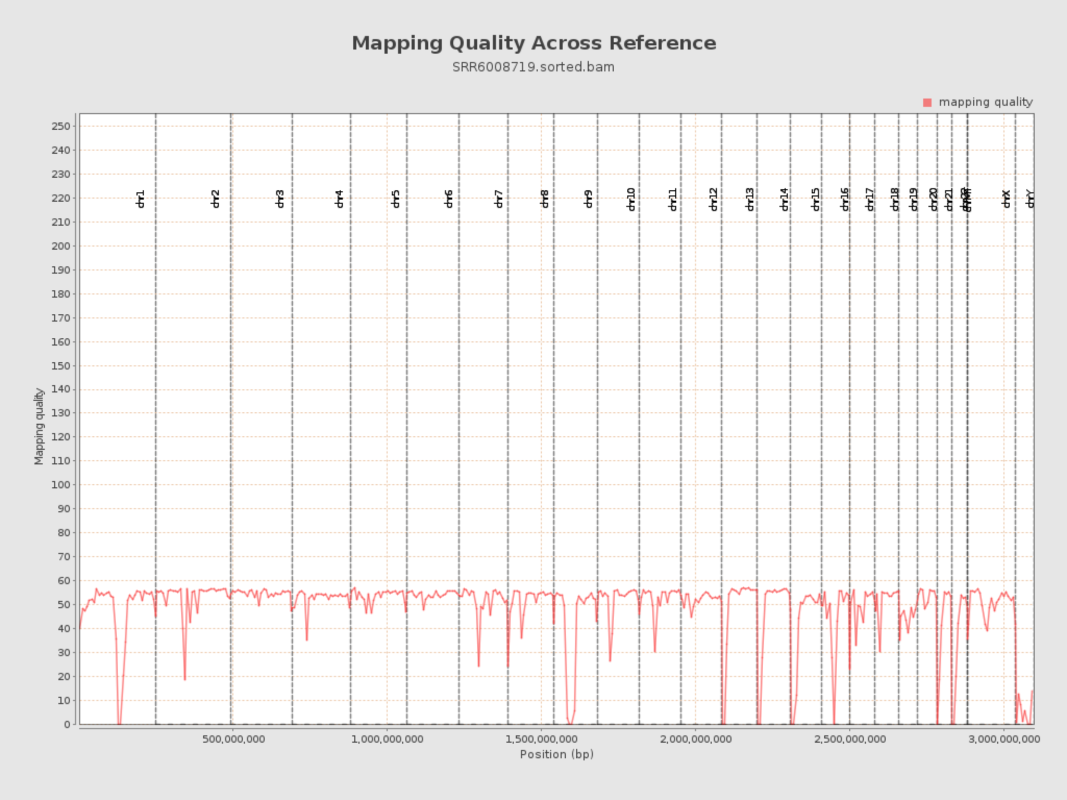
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram