Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:32:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008699.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_SRR6008699 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008699.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:32:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008699.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,774,703
Mapped reads	1,112,835 / 40.11%
Unmapped reads	1,661,868 / 59.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,717 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	81,180 / 2.93%
Duplication rate	6.01%
Clipped reads	924,526 / 33.32%

2.2. ACGT Content

Number/percentage of A's	16,779,329 / 27.8%
Number/percentage of C's	11,316,848 / 18.75%
Number/percentage of T's	18,263,002 / 30.26%
Number/percentage of G's	13,977,646 / 23.16%
Number/percentage of N's	22,181 / 0.04%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0195

Standard Deviation	0.2027

2.4. Mapping Quality

Mean Mapping Quality	42.77

2.5. Mismatches and indels

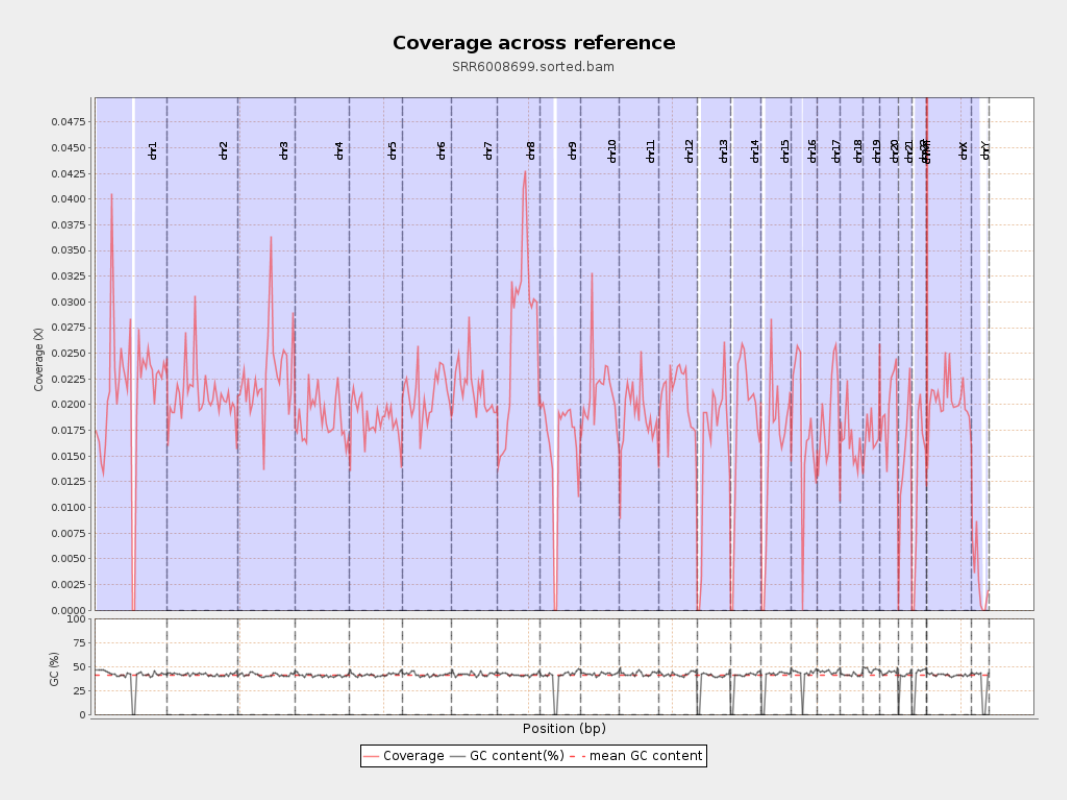
General error rate	1.03%
Mismatches	615,661
Insertions	4,288
Mapped reads with at least one insertion	0.38%
Deletions	21,087
Mapped reads with at least one deletion	1.87%
Homopolymer indels	47.01%

2.6. Chromosome stats

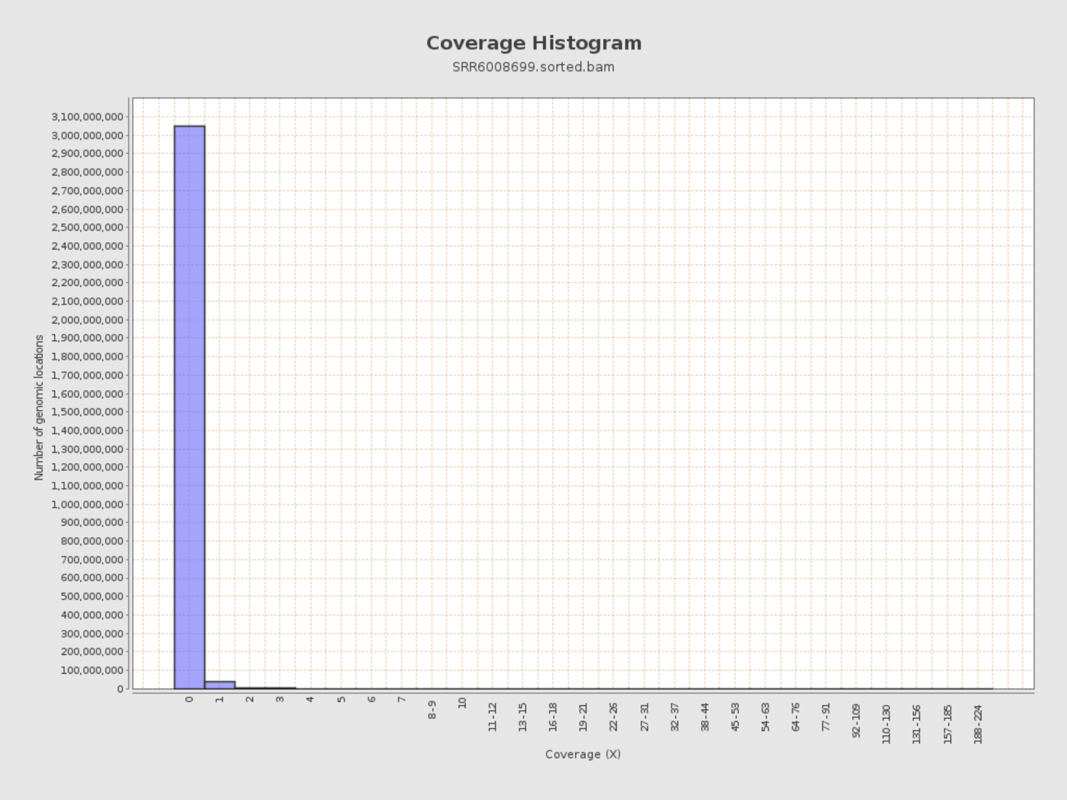
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5249759	0.0211	0.2454
chr2	243199373	5084340	0.0209	0.2231
chr3	198022430	4529225	0.0229	0.1881
chr4	191154276	3583622	0.0187	0.1712
chr5	180915260	3377643	0.0187	0.1705
chr6	171115067	3590905	0.021	0.1907
chr7	159138663	3415642	0.0215	0.2252

chr8	146364022	3958036	0.027	0.2408
chr9	141213431	2233413	0.0158	0.1724
chr10	135534747	2862974	0.0211	0.2085
chr11	135006516	2572967	0.0191	0.1881
chr12	133851895	2790038	0.0208	0.178
chr13	115169878	1860887	0.0162	0.1604
chr14	107349540	1945375	0.0181	0.1704
chr15	102531392	1615987	0.0158	0.1582
chr16	90354753	1563065	0.0173	0.1709
chr17	81195210	1534614	0.0189	0.1749
chr18	78077248	1282646	0.0164	0.2169
chr19	59128983	1019474	0.0172	0.1918
chr20	63025520	1238296	0.0196	0.1763
chr21	48129895	710607	0.0148	0.1518
chr22	51304566	643112	0.0125	0.1355
chrMT	16571	382549	23.0855	11.5937
chrX	155270560	3174515	0.0204	0.1852
chrY	59373566	171643	0.0029	0.0715

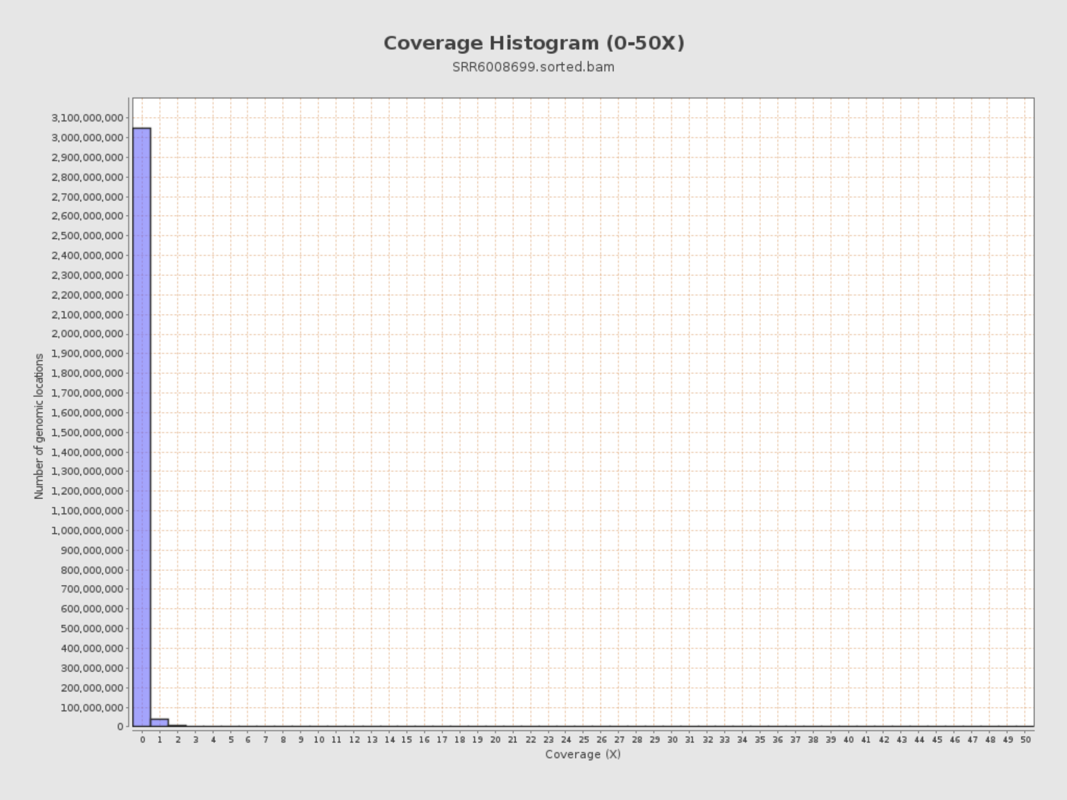
3. Results : Coverage across reference



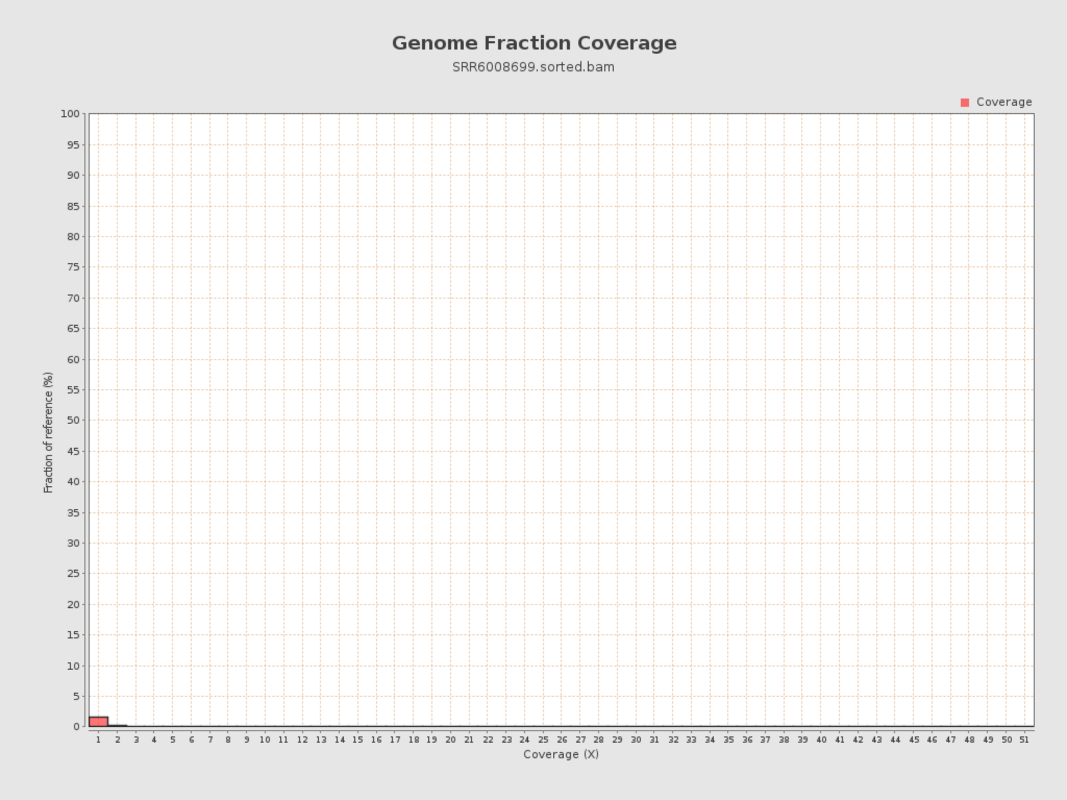
4. Results : Coverage Histogram



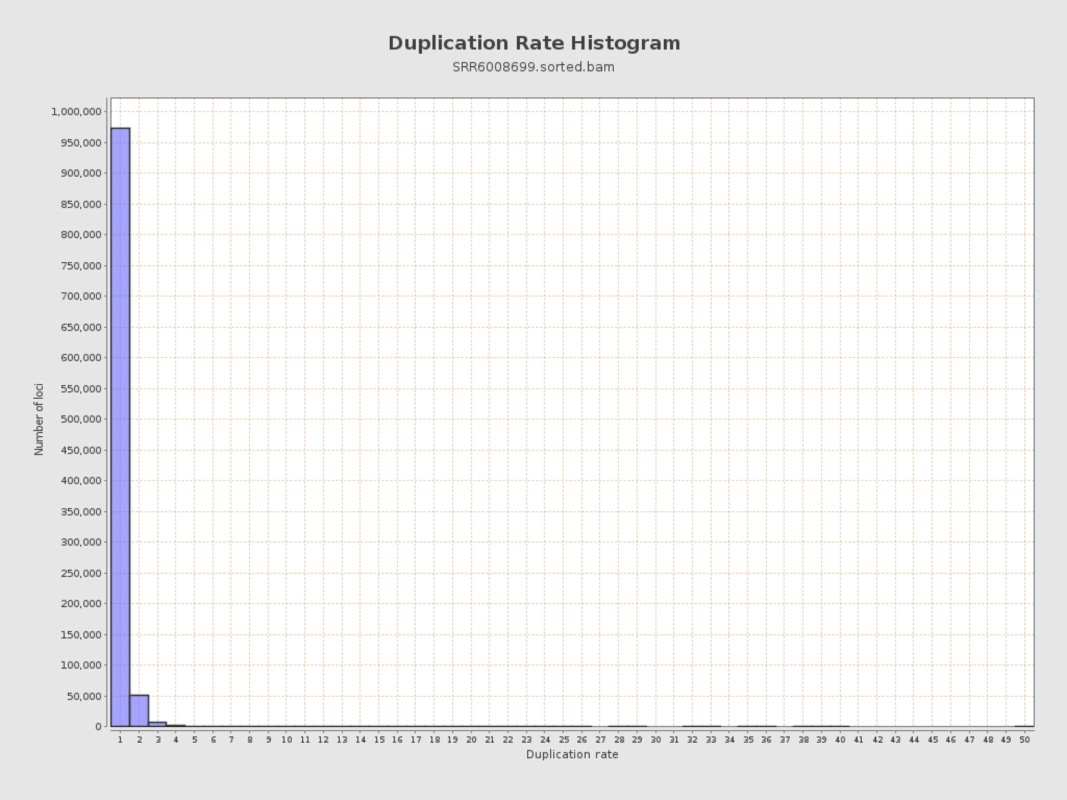
5. Results : Coverage Histogram (0-50X)



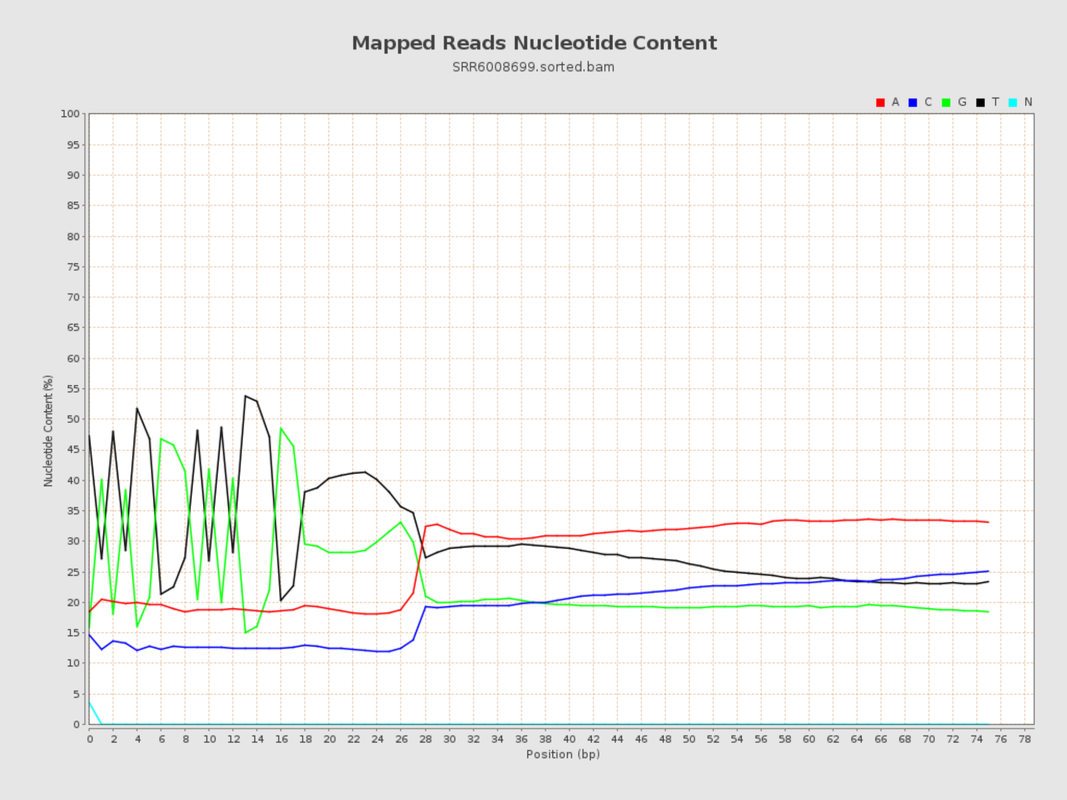
6. Results : Genome Fraction Coverage



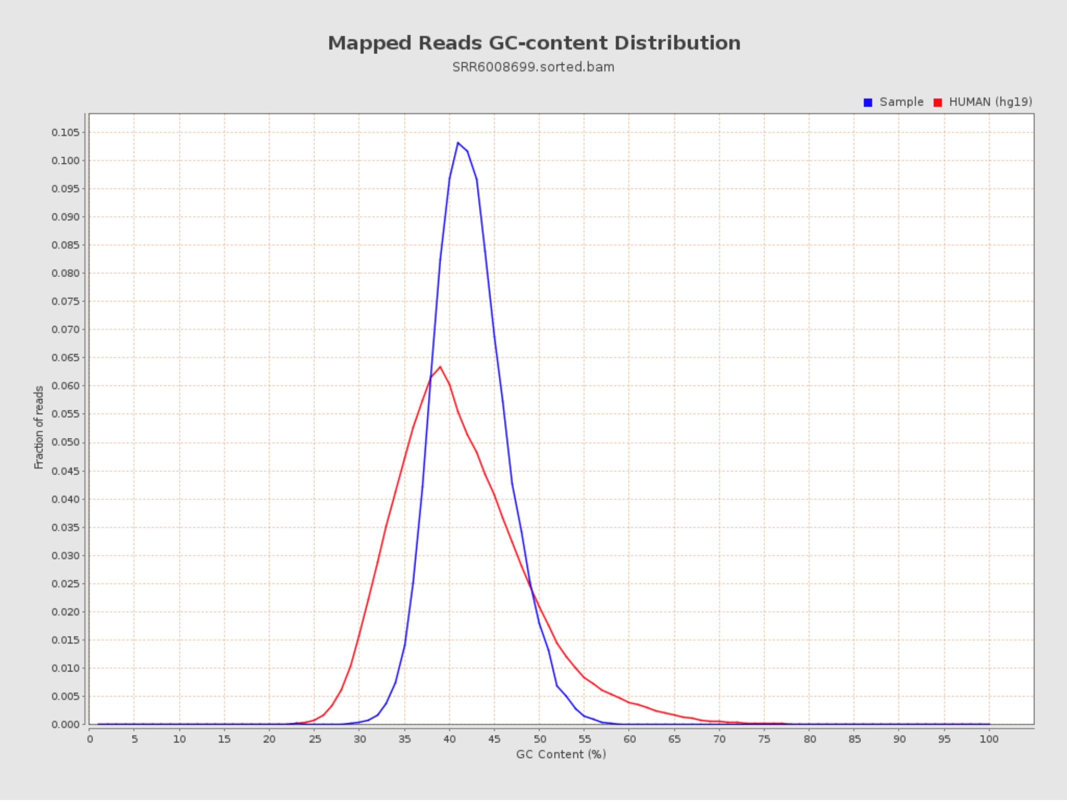
7. Results : Duplication Rate Histogram



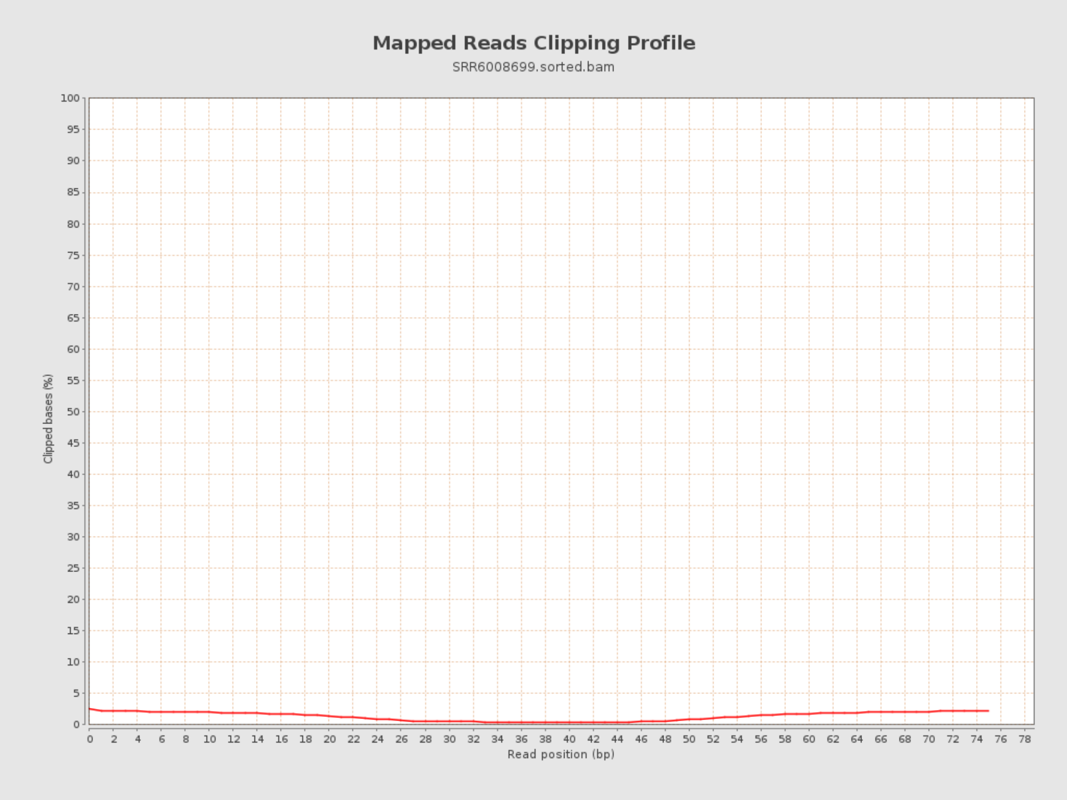
8. Results : Mapped Reads Nucleotide Content



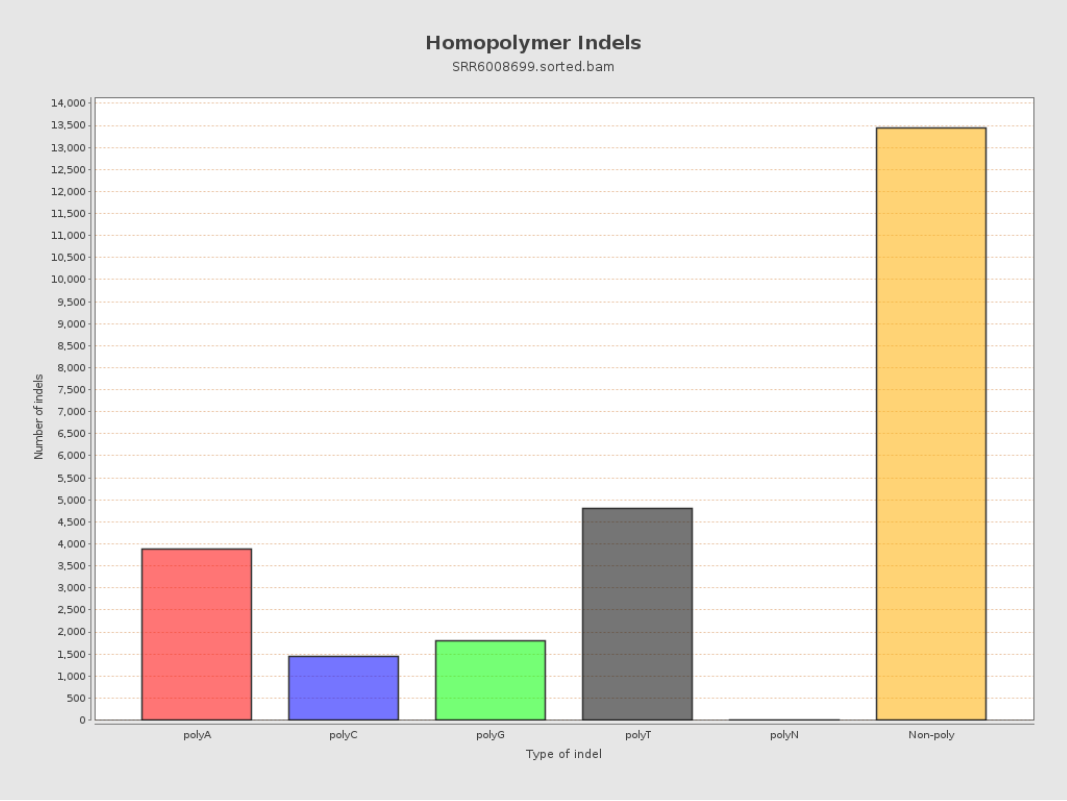
9. Results : Mapped Reads GC-content Distribution



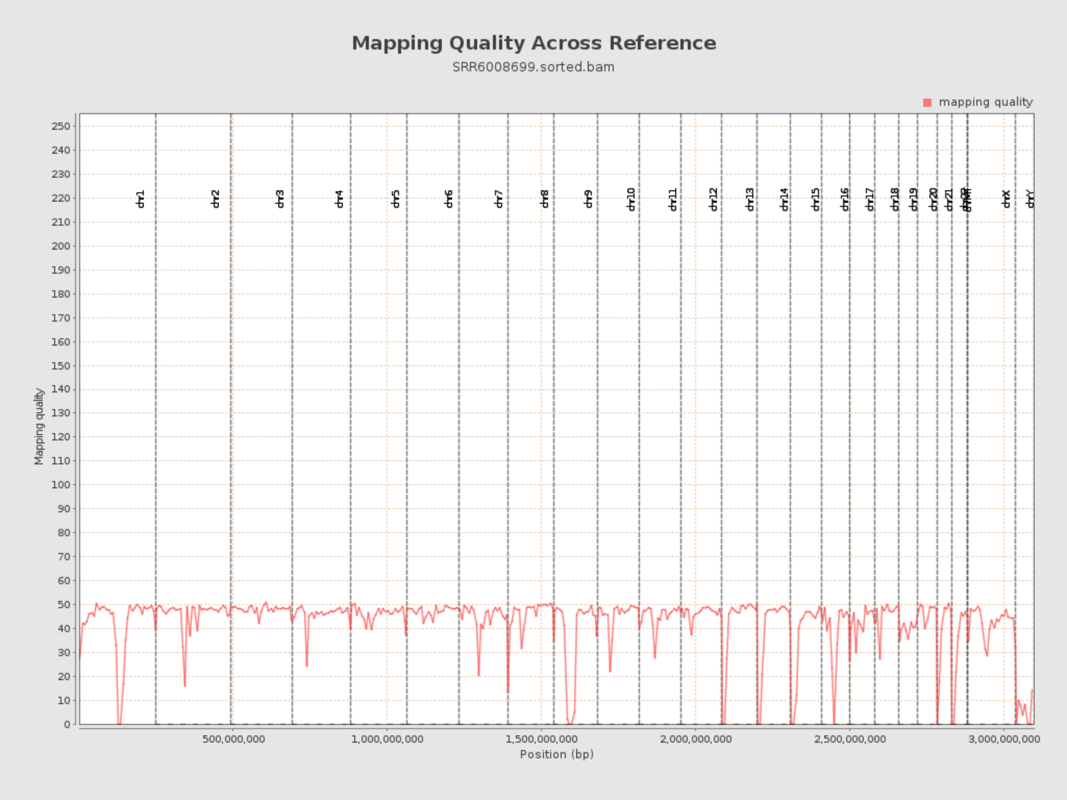
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram