Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:23:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008720.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_SRR6008720 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008720.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:23:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008720.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,491,839
Mapped reads	1,208,401 / 81%
Unmapped reads	283,438 / 19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,752 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	23,836 / 1.6%
Duplication rate	1.72%
Clipped reads	412,040 / 27.62%

2.2. ACGT Content

Number/percentage of A's	28,024,747 / 33.26%
Number/percentage of C's	14,253,167 / 16.92%
Number/percentage of T's	24,675,058 / 29.29%
Number/percentage of G's	17,297,738 / 20.53%
Number/percentage of N's	4,732 / 0.01%
GC Percentage	37.45%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.206

2.4. Mapping Quality

Mean Mapping Quality	49.48

2.5. Mismatches and indels

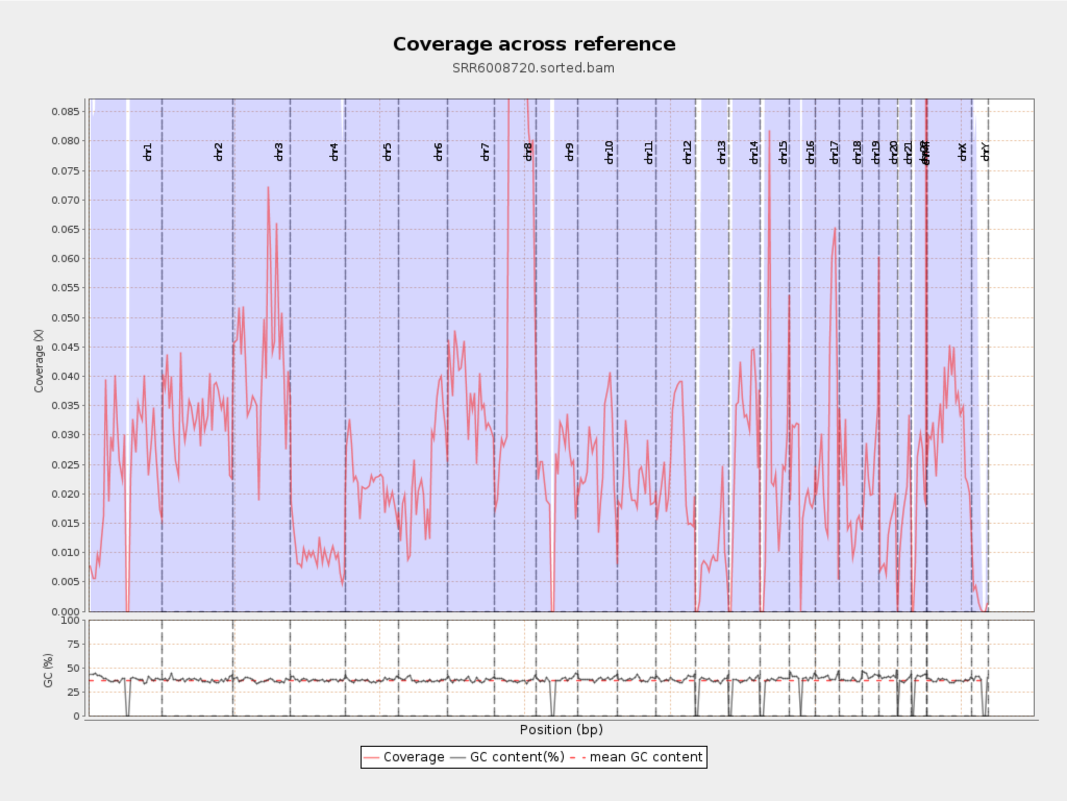
General error rate	0.85%
Mismatches	703,750
Insertions	6,414
Mapped reads with at least one insertion	0.53%
Deletions	26,306
Mapped reads with at least one deletion	2.15%
Homopolymer indels	48.35%

2.6. Chromosome stats

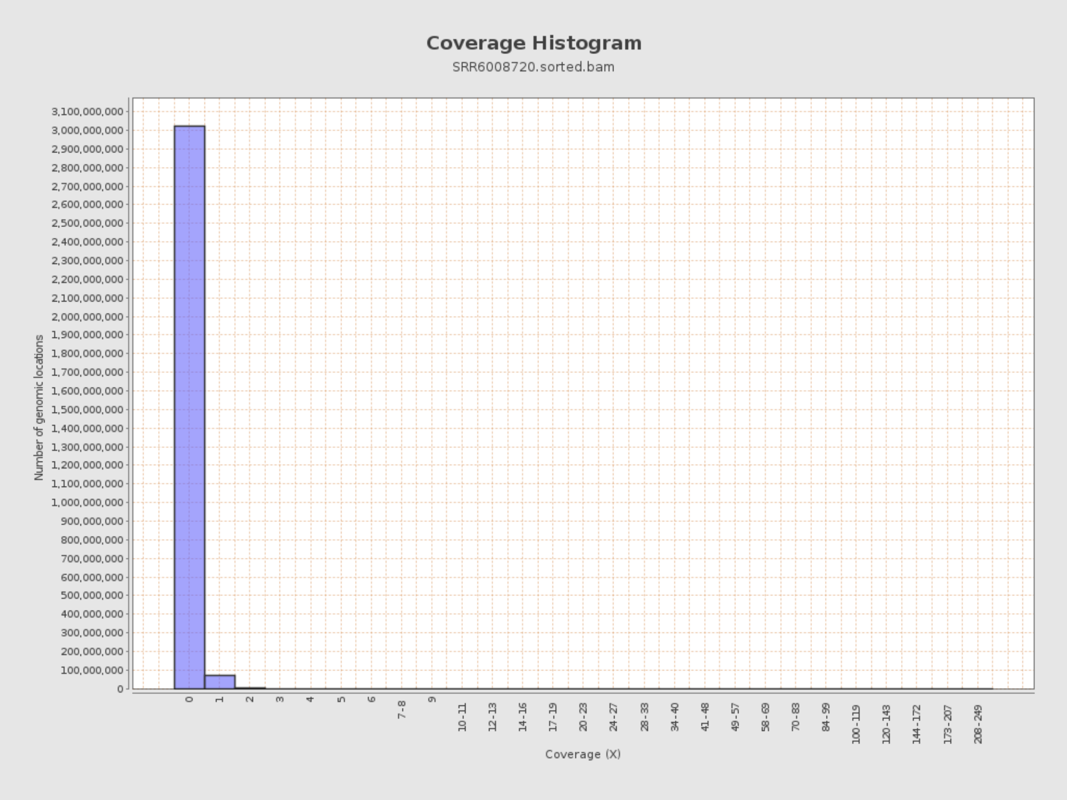
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5761661	0.0231	0.2428
chr2	243199373	8245003	0.0339	0.2659
chr3	198022430	8647137	0.0437	0.2288
chr4	191154276	1827970	0.0096	0.106
chr5	180915260	3956055	0.0219	0.1602
chr6	171115067	3873731	0.0226	0.1709
chr7	159138663	5895840	0.037	0.2566

chr8	146364022	11374862	0.0777	0.3589
chr9	141213431	3156756	0.0224	0.1687
chr10	135534747	3536237	0.0261	0.1971
chr11	135006516	2921793	0.0216	0.1754
chr12	133851895	3314238	0.0248	0.171
chr13	115169878	989020	0.0086	0.0996
chr14	107349540	3230492	0.0301	0.1914
chr15	102531392	2472302	0.0241	0.1719
chr16	90354753	1945186	0.0215	0.1631
chr17	81195210	2586409	0.0319	0.2042
chr18	78077248	1450099	0.0186	0.2352
chr19	59128983	1507211	0.0255	0.1917
chr20	63025520	739703	0.0117	0.1171
chr21	48129895	822690	0.0171	0.1453
chr22	51304566	899294	0.0175	0.1435
chrMT	16571	17667	1.0661	1.3217
chrX	155270560	4996570	0.0322	0.2033
chrY	59373566	128812	0.0022	0.0536

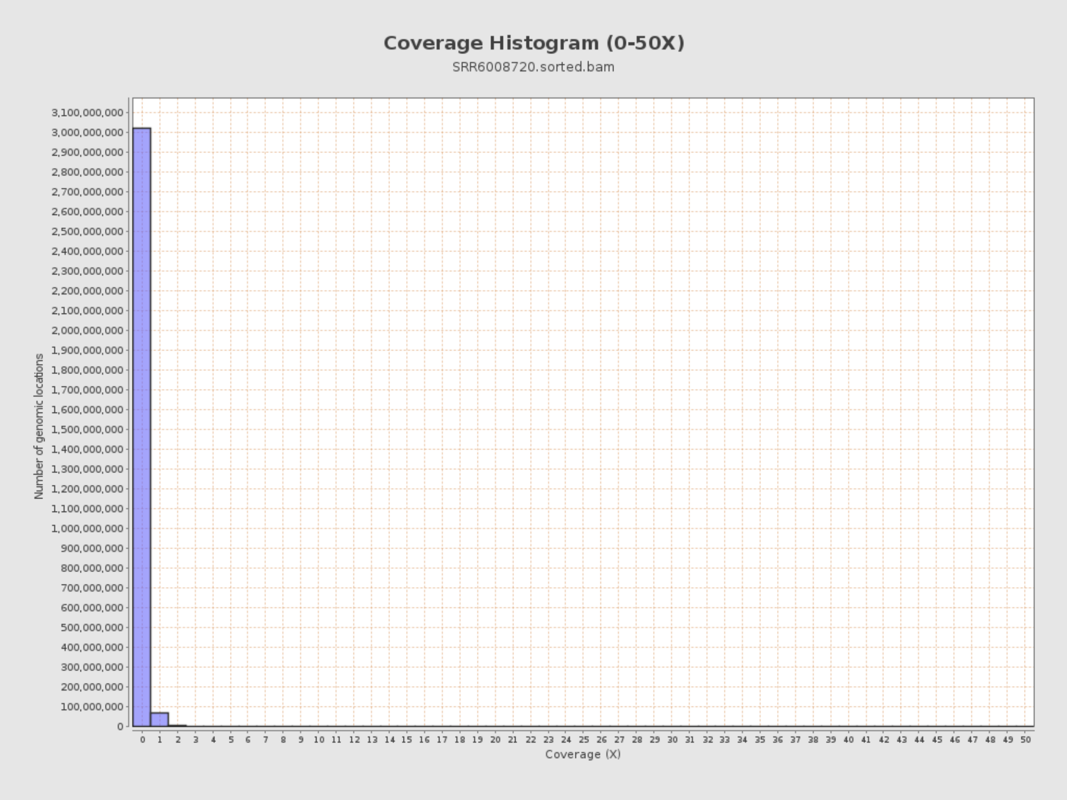
3. Results : Coverage across reference



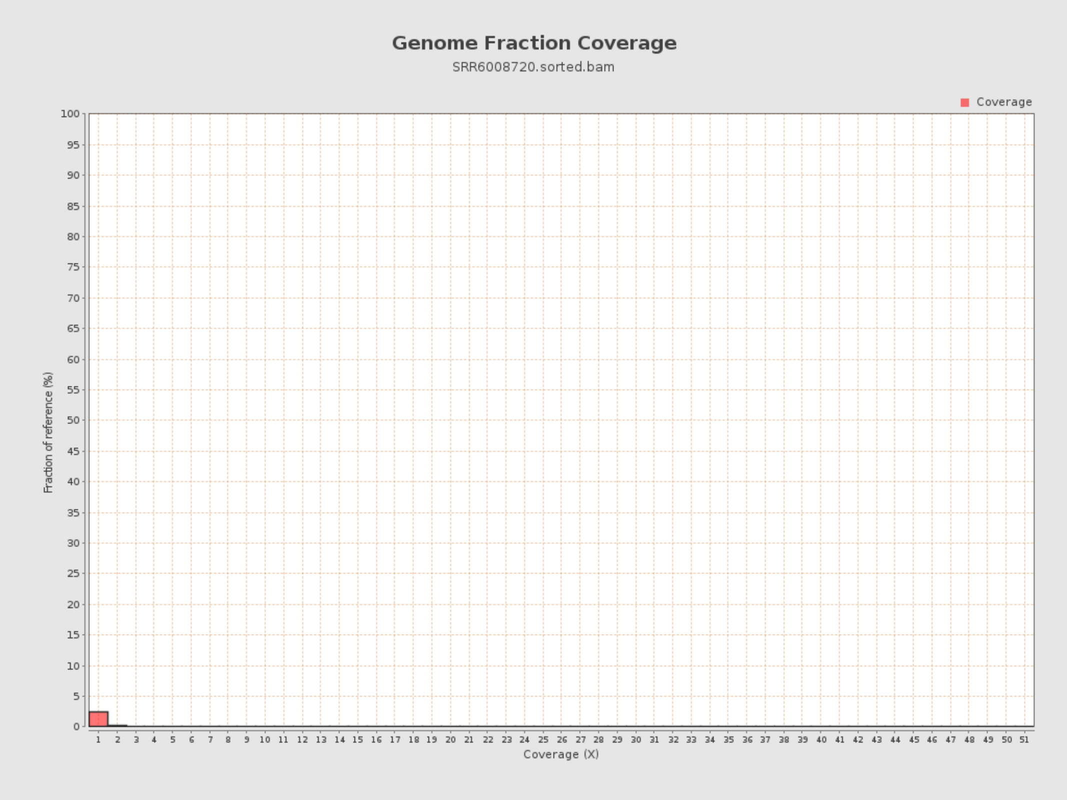
4. Results : Coverage Histogram



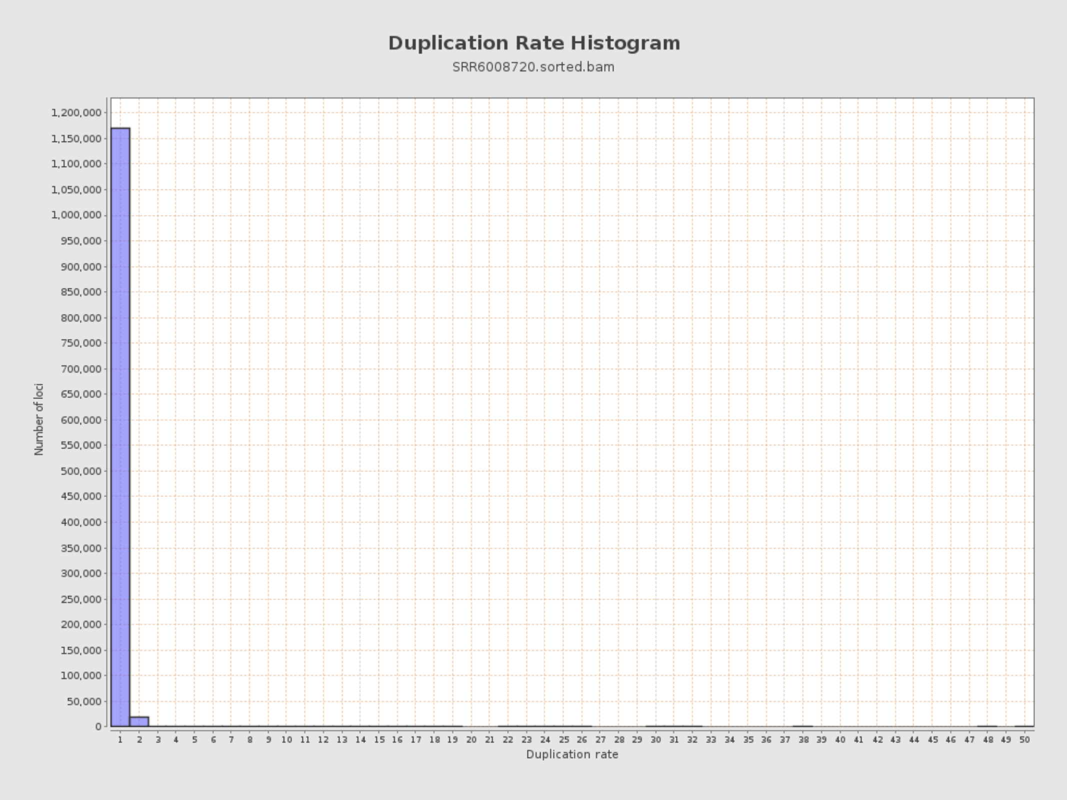
5. Results : Coverage Histogram (0-50X)



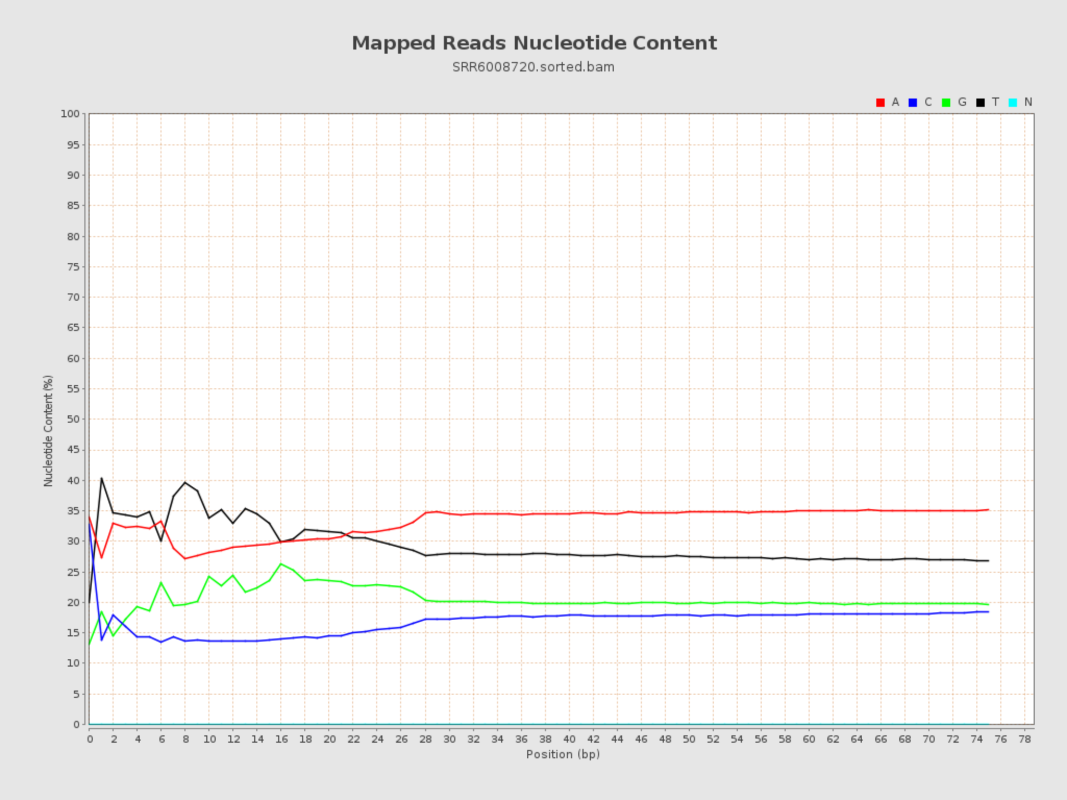
6. Results : Genome Fraction Coverage



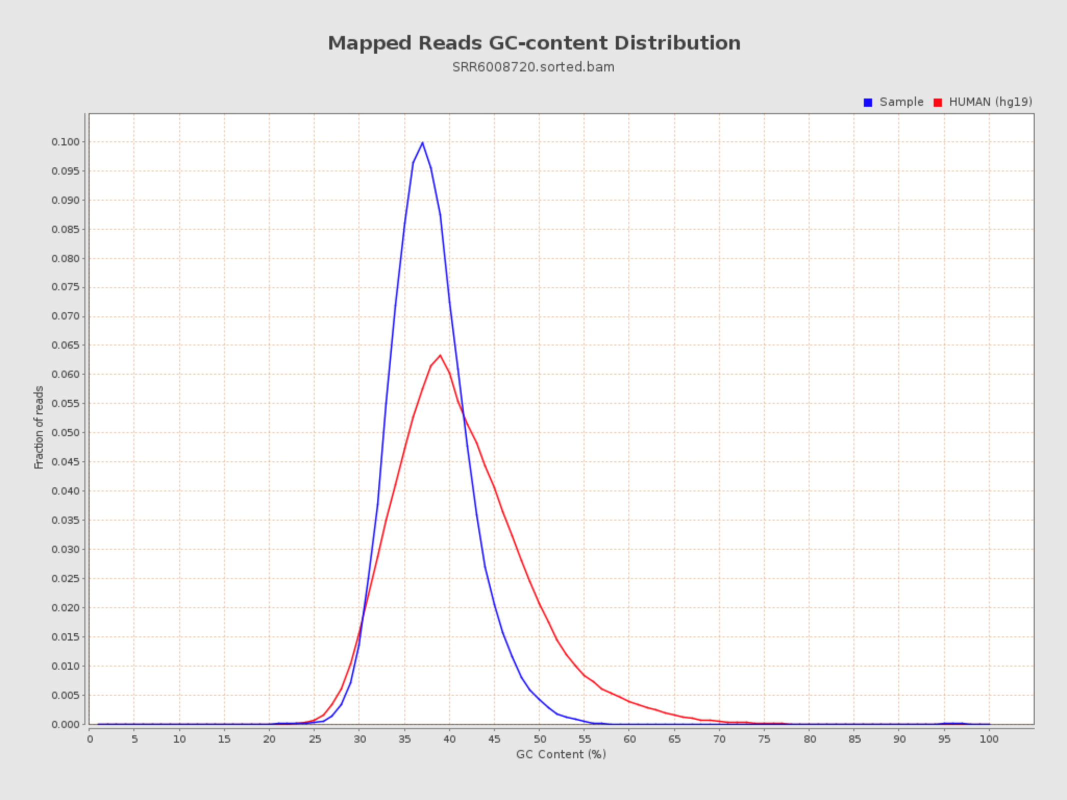
7. Results : Duplication Rate Histogram



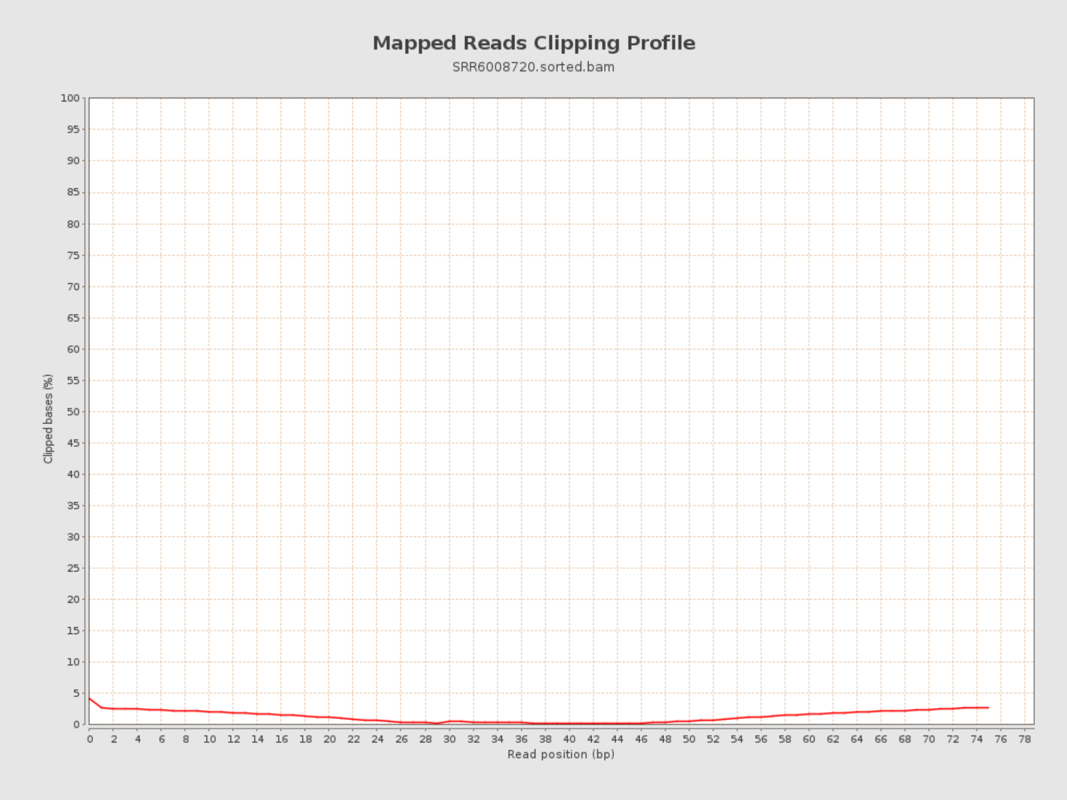
8. Results : Mapped Reads Nucleotide Content



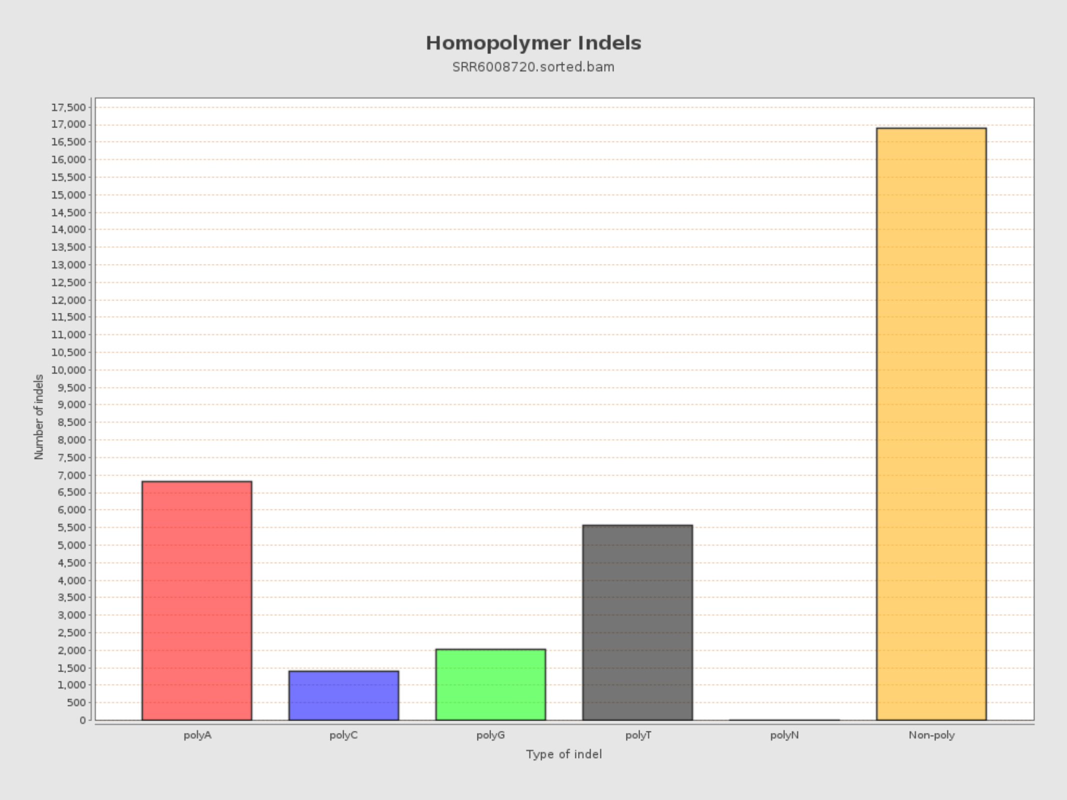
9. Results : Mapped Reads GC-content Distribution



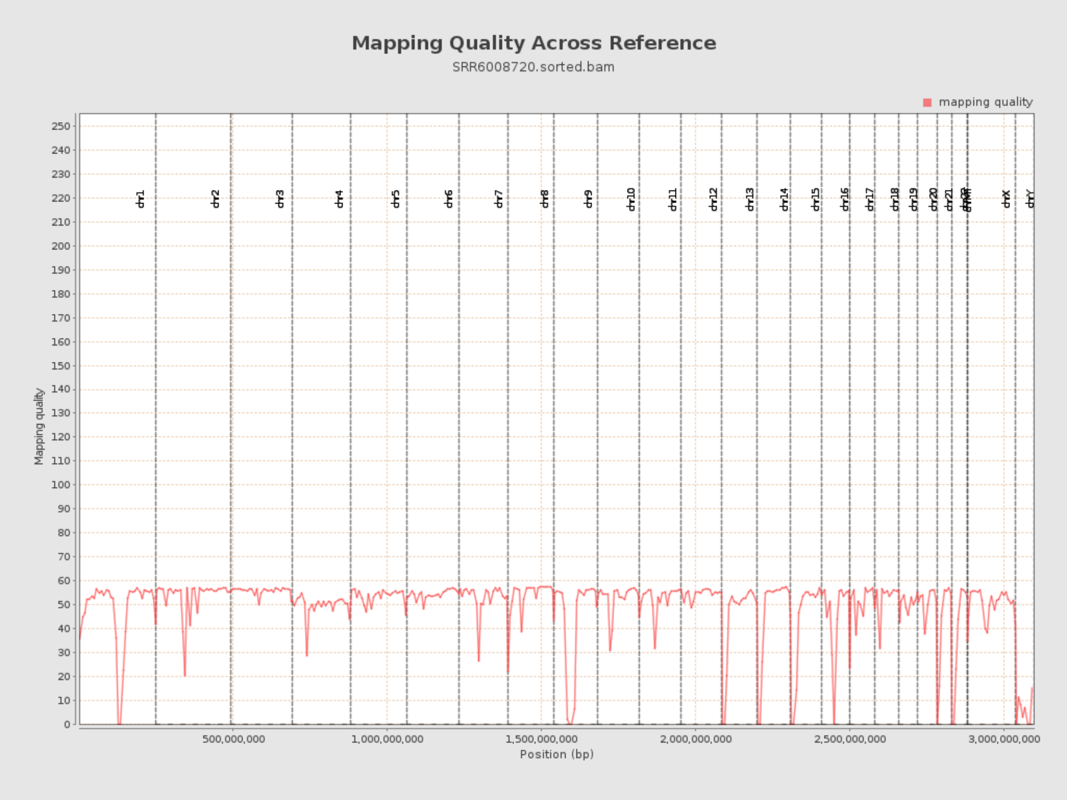
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram