Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:01:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008711.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_SRR6008711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008711.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:01:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008711.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,474,527
Mapped reads	1,153,036 / 78.2%
Unmapped reads	321,491 / 21.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,126 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	21,003 / 1.42%
Duplication rate	1.5%
Clipped reads	442,083 / 29.98%

2.2. ACGT Content

Number/percentage of A's	23,919,528 / 30.54%
Number/percentage of C's	13,469,888 / 17.2%
Number/percentage of T's	23,300,993 / 29.75%
Number/percentage of G's	17,616,132 / 22.5%
Number/percentage of N's	3,950 / 0.01%
GC Percentage	39.7%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.1982

2.4. Mapping Quality

Mean Mapping Quality	48.18

2.5. Mismatches and indels

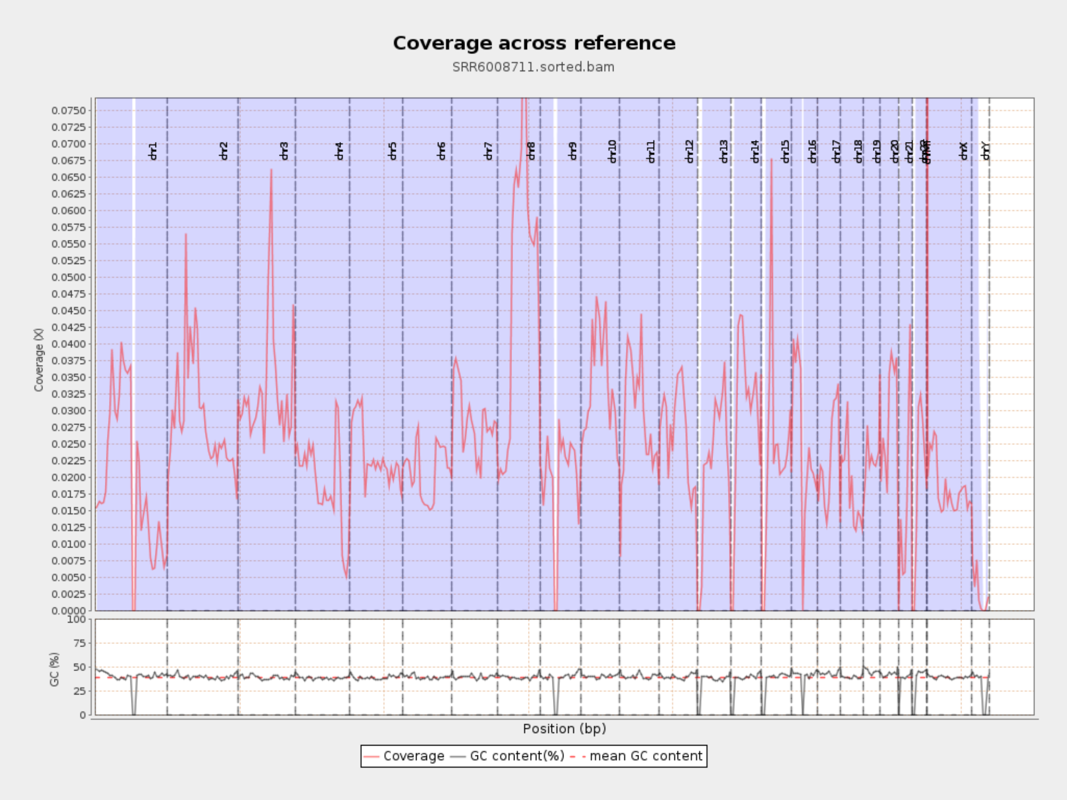
General error rate	0.86%
Mismatches	660,927
Insertions	5,733
Mapped reads with at least one insertion	0.49%
Deletions	22,707
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.53%

2.6. Chromosome stats

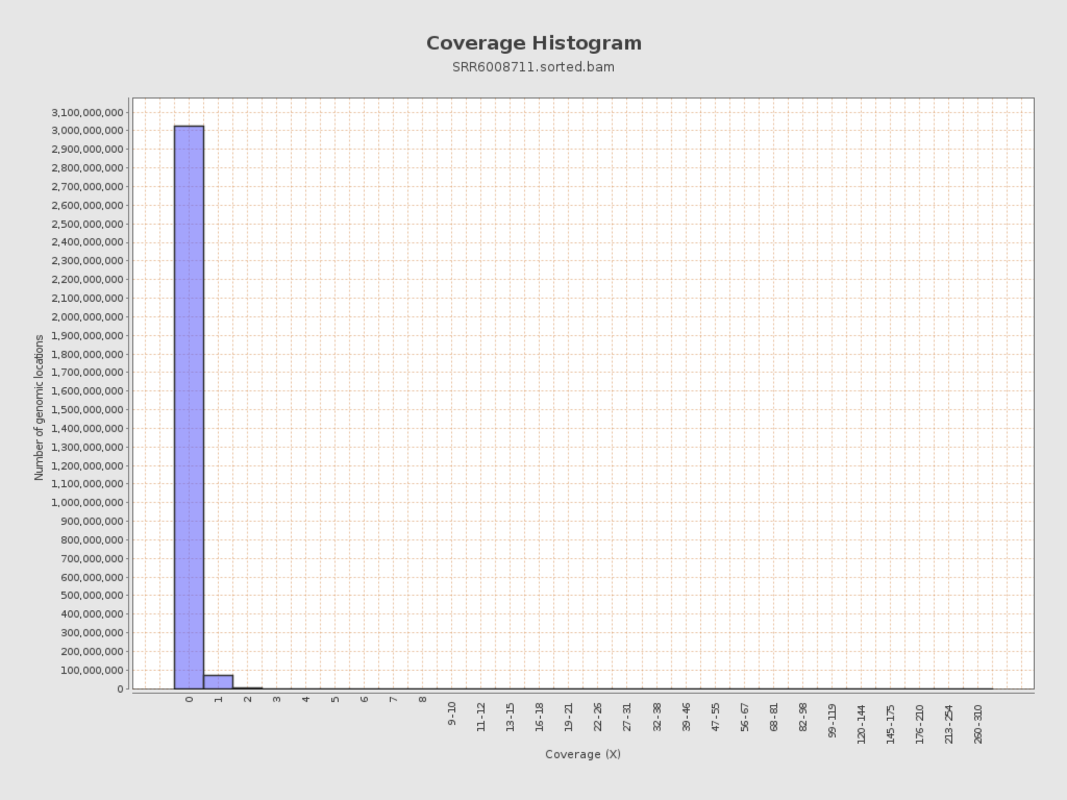
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4845778	0.0194	0.2314
chr2	243199373	7048332	0.029	0.2643
chr3	198022430	6595822	0.0333	0.1922
chr4	191154276	3627925	0.019	0.1469
chr5	180915260	4235681	0.0234	0.1603
chr6	171115067	3574882	0.0209	0.1602
chr7	159138663	4541244	0.0285	0.2109

chr8	146364022	7346434	0.0502	0.3092
chr9	141213431	2788771	0.0197	0.1693
chr10	135534747	4593699	0.0339	0.2264
chr11	135006516	3949013	0.0293	0.2069
chr12	133851895	3589308	0.0268	0.1718
chr13	115169878	2534464	0.022	0.1551
chr14	107349540	3138346	0.0292	0.1849
chr15	102531392	2417457	0.0236	0.1631
chr16	90354753	2229214	0.0247	0.176
chr17	81195210	1830052	0.0225	0.1641
chr18	78077248	1424766	0.0182	0.2446
chr19	59128983	1355414	0.0229	0.1907
chr20	63025520	1837130	0.0291	0.1805
chr21	48129895	785561	0.0163	0.1405
chr22	51304566	994779	0.0194	0.1462
chrMT	16571	16766	1.0118	1.1982
chrX	155270560	2892942	0.0186	0.1489
chrY	59373566	153217	0.0026	0.0694

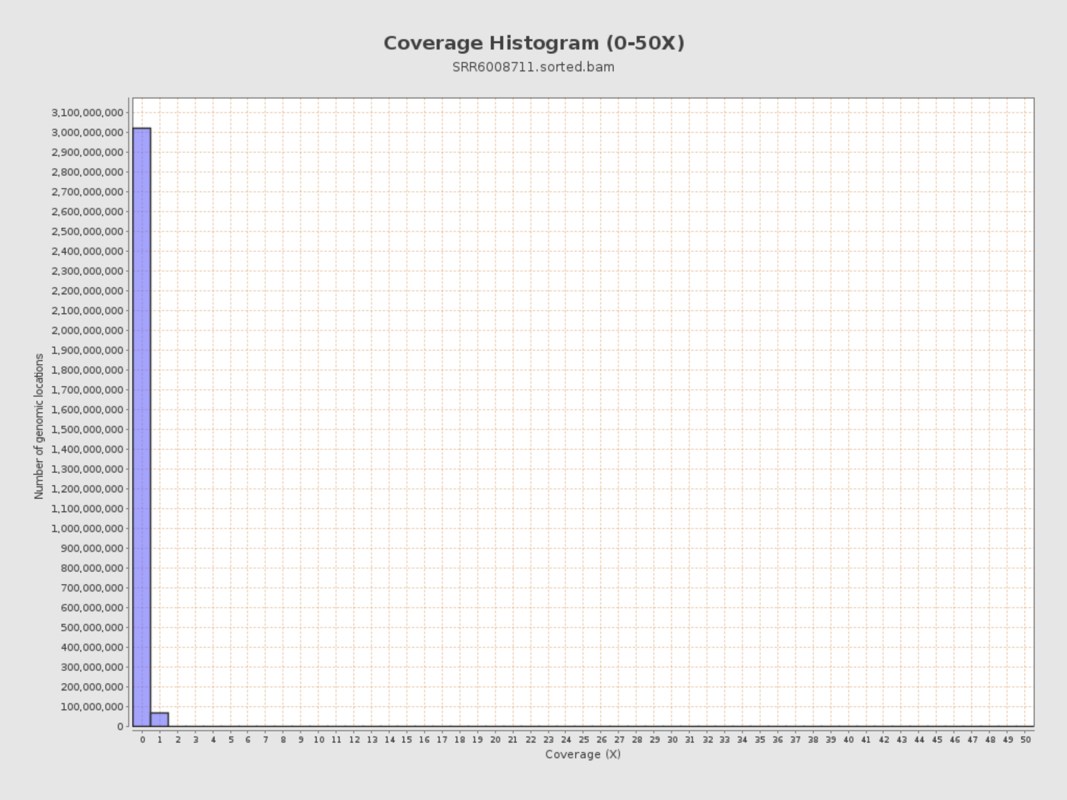
3. Results : Coverage across reference



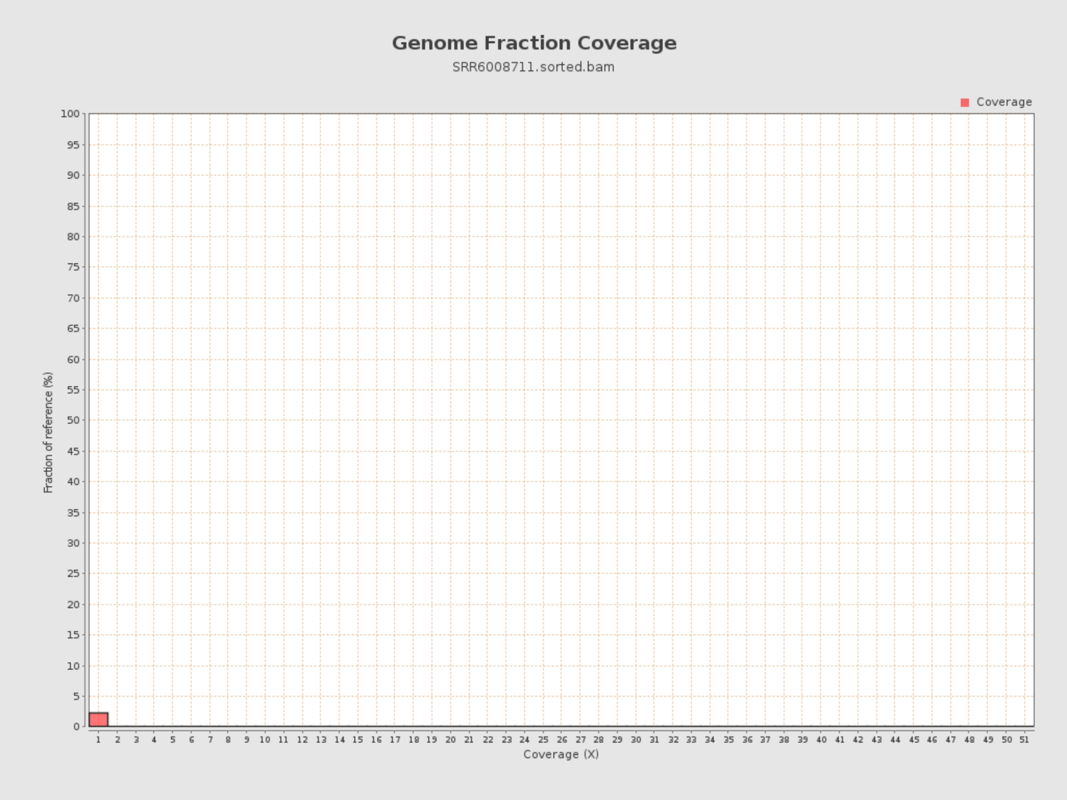
4. Results : Coverage Histogram



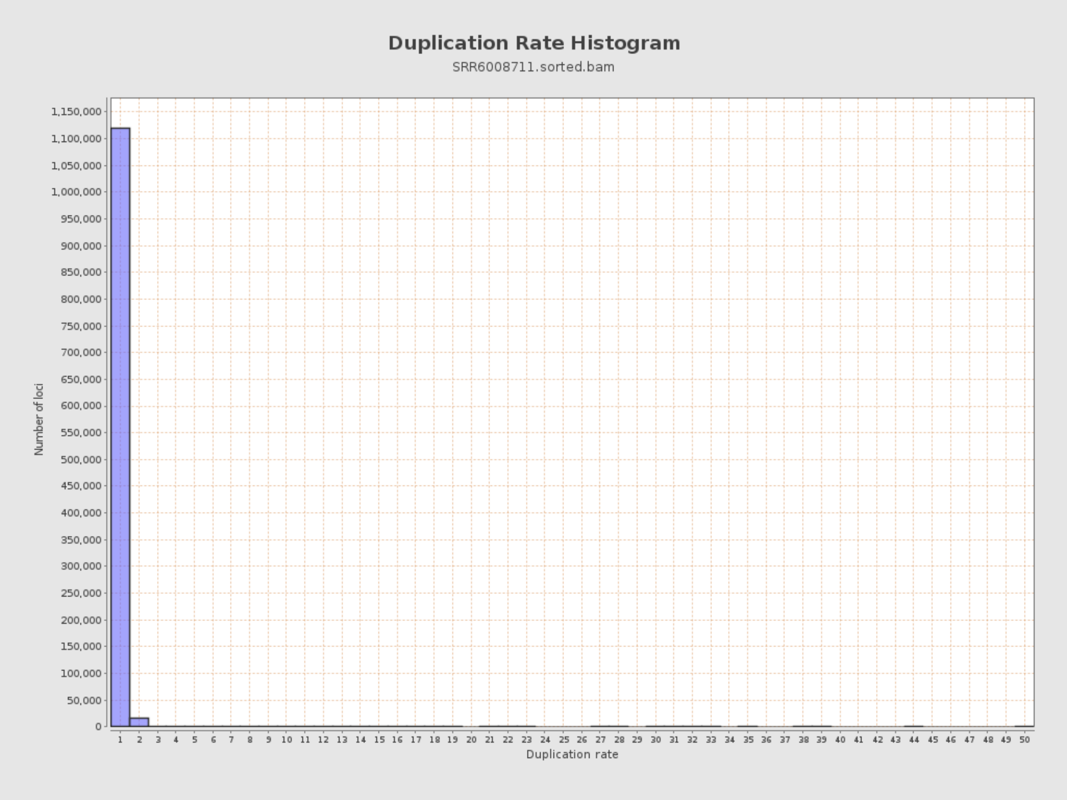
5. Results : Coverage Histogram (0-50X)



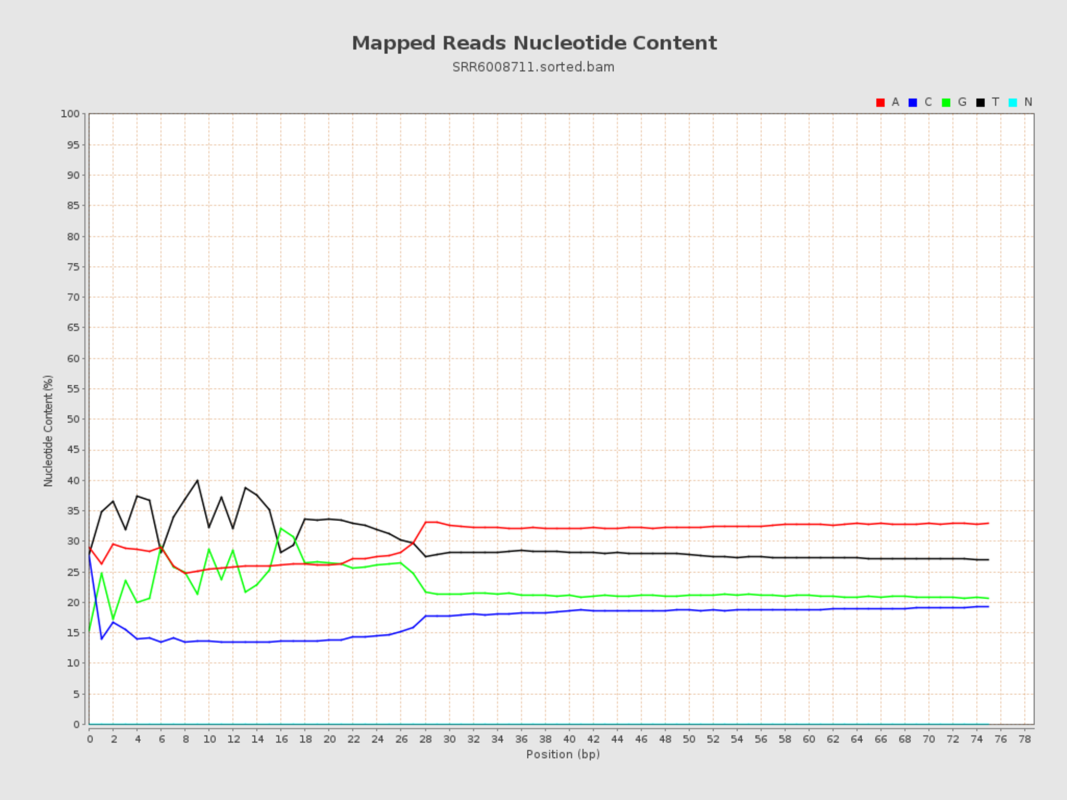
6. Results : Genome Fraction Coverage



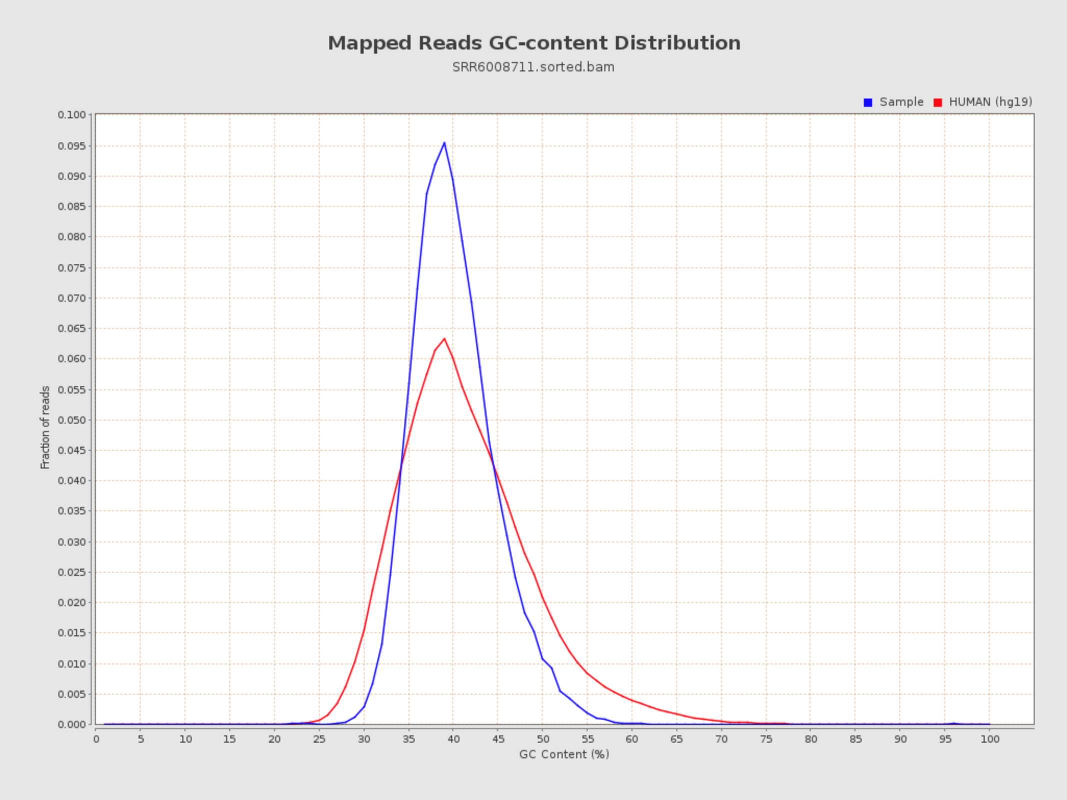
7. Results : Duplication Rate Histogram



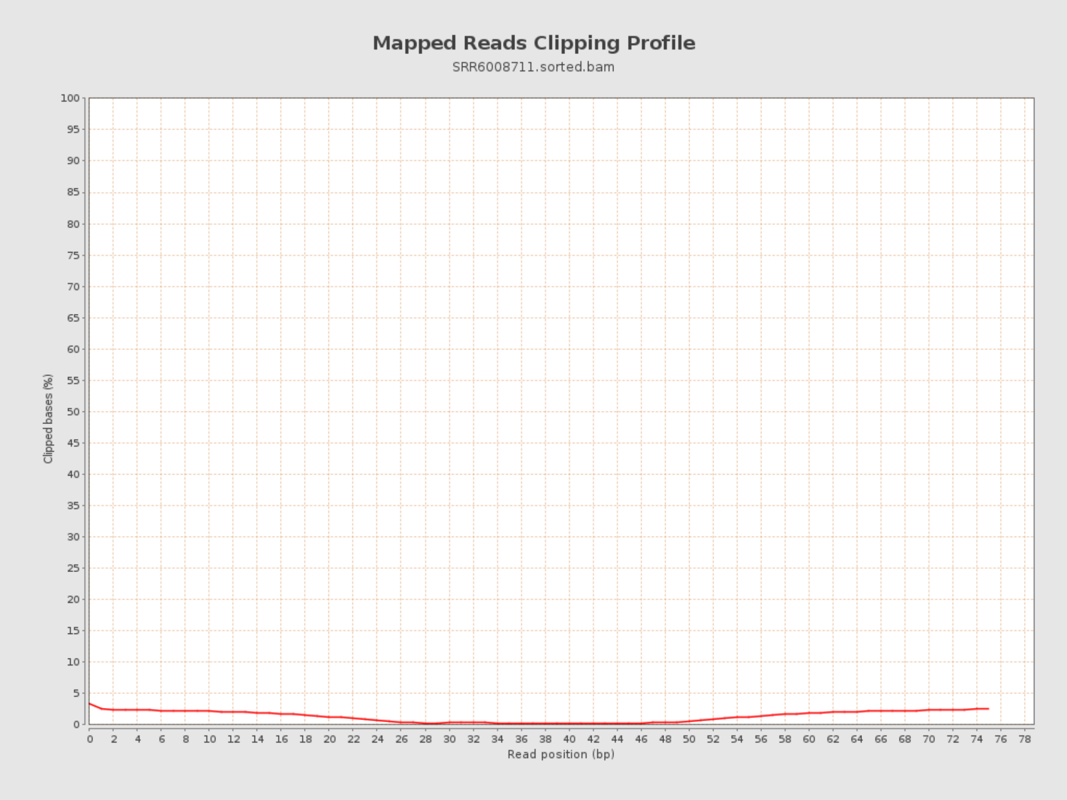
8. Results : Mapped Reads Nucleotide Content



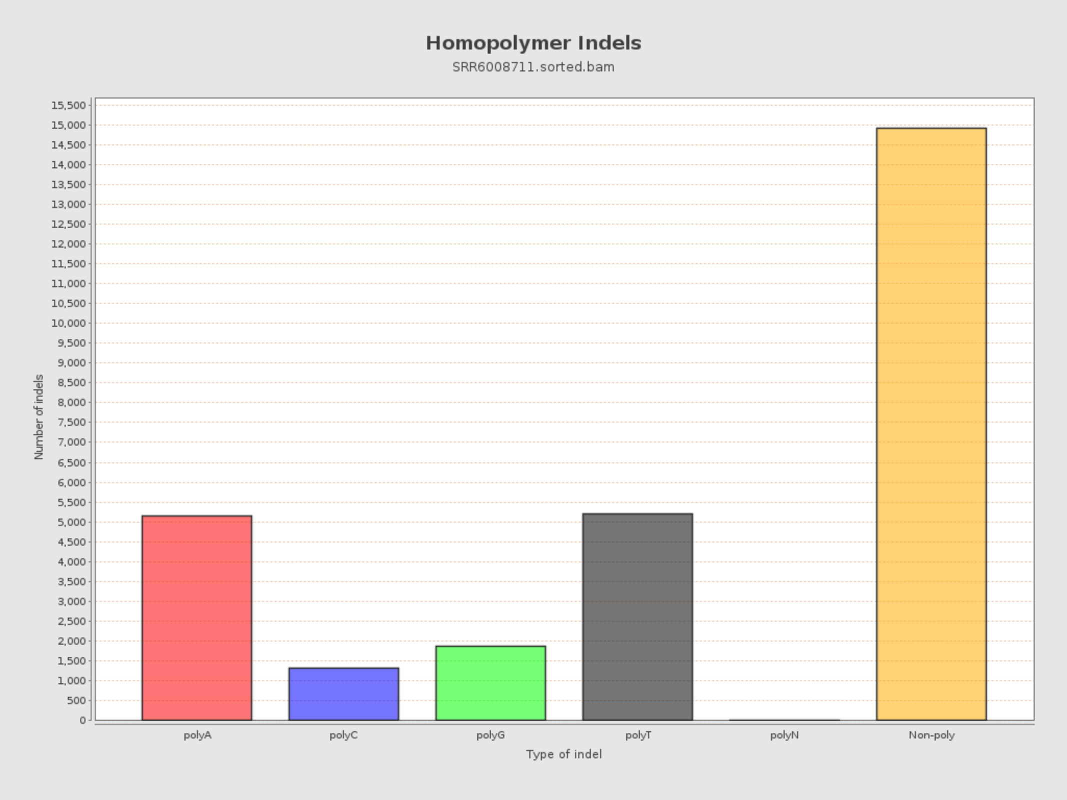
9. Results : Mapped Reads GC-content Distribution



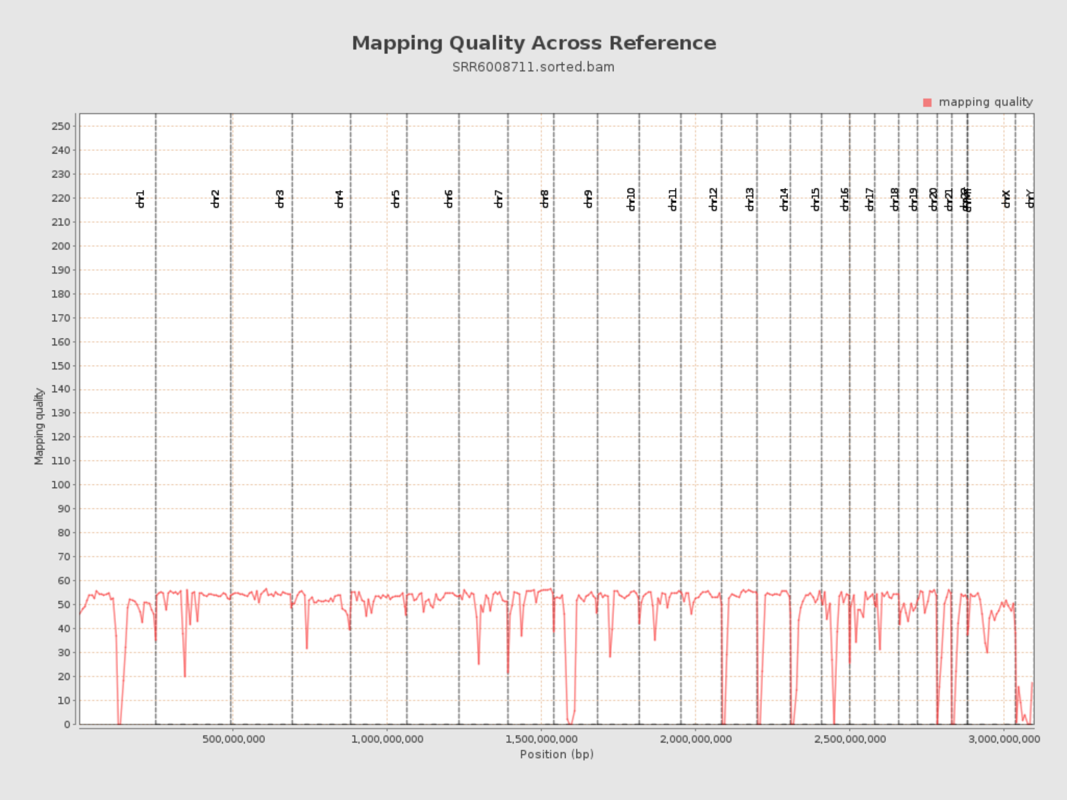
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram