Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:54:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008663.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_SRR6008663 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008663.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:54:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008663.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,806,472
Mapped reads	1,445,491 / 80.02%
Unmapped reads	360,981 / 19.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,733 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	232,042 / 12.85%
Duplication rate	11.46%
Clipped reads	725,160 / 40.14%

2.2. ACGT Content

Number/percentage of A's	24,494,743 / 26.13%
Number/percentage of C's	17,837,203 / 19.03%
Number/percentage of T's	29,002,813 / 30.94%
Number/percentage of G's	22,356,456 / 23.85%
Number/percentage of N's	61,203 / 0.07%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0303

Standard Deviation	0.3425

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

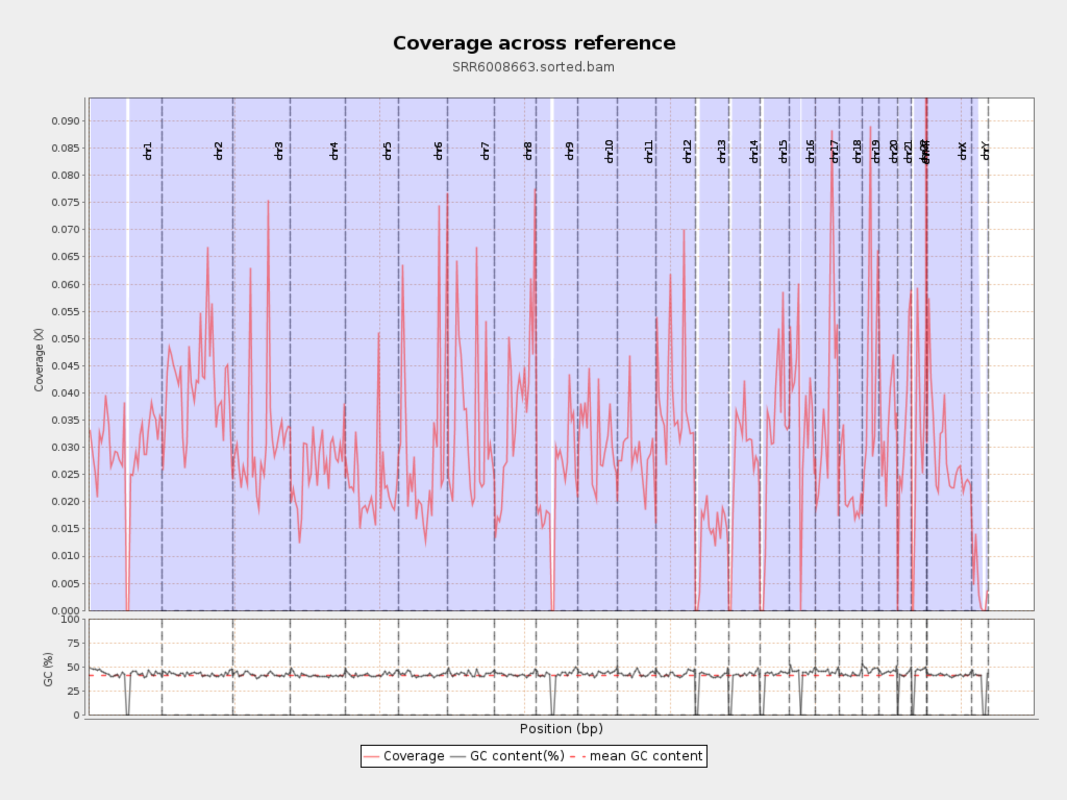
General error rate	0.82%
Mismatches	760,529
Insertions	6,464
Mapped reads with at least one insertion	0.44%
Deletions	24,504
Mapped reads with at least one deletion	1.67%
Homopolymer indels	48.61%

2.6. Chromosome stats

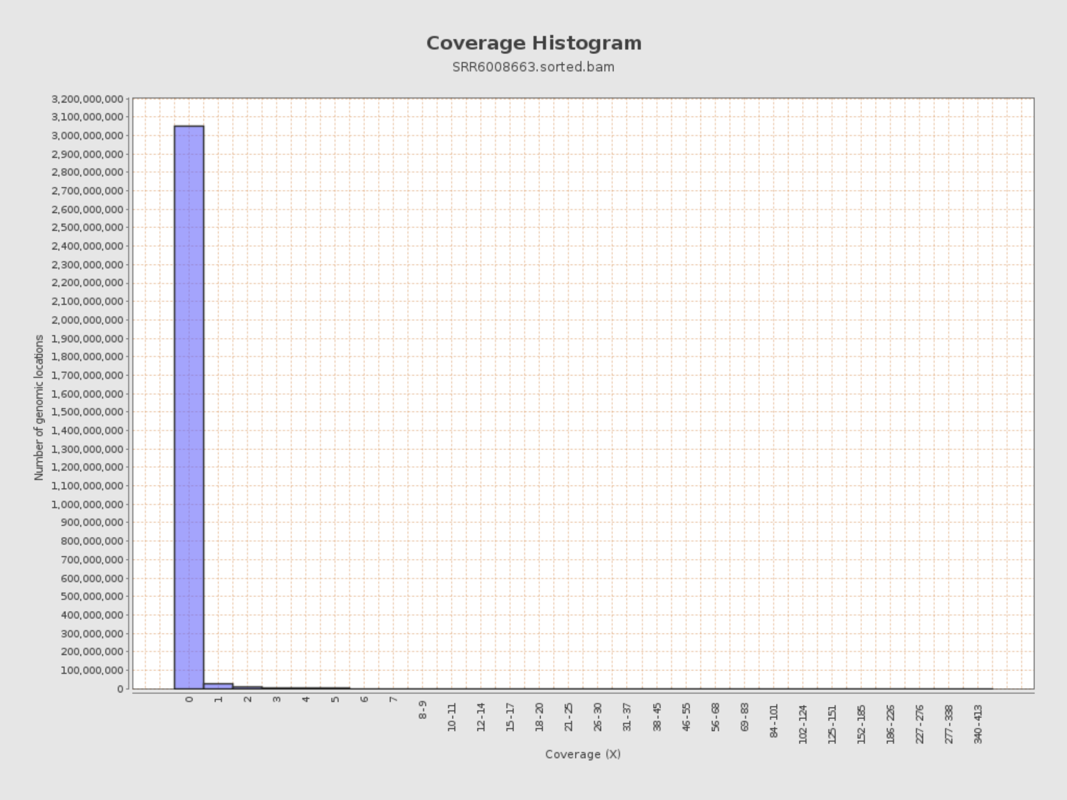
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7192853	0.0289	0.4499
chr2	243199373	10131253	0.0417	0.3969
chr3	198022430	6214641	0.0314	0.309
chr4	191154276	5018001	0.0263	0.2886
chr5	180915260	4131840	0.0228	0.2584
chr6	171115067	5106868	0.0298	0.3065
chr7	159138663	5345019	0.0336	0.3946

chr8	146364022	5392805	0.0368	0.3529
chr9	141213431	3213986	0.0228	0.3039
chr10	135534747	4256303	0.0314	0.3539
chr11	135006516	3851395	0.0285	0.3463
chr12	133851895	5280925	0.0395	0.3545
chr13	115169878	1566870	0.0136	0.1971
chr14	107349540	2918896	0.0272	0.2945
chr15	102531392	3181575	0.031	0.3225
chr16	90354753	3282362	0.0363	0.3502
chr17	81195210	3215515	0.0396	0.3589
chr18	78077248	1724826	0.0221	0.4588
chr19	59128983	2694916	0.0456	0.4273
chr20	63025520	2150948	0.0341	0.3335
chr21	48129895	1614904	0.0336	0.3312
chr22	51304566	1475418	0.0288	0.2886
chrMT	16571	69396	4.1878	3.9391
chrX	155270560	4506410	0.029	0.3023
chrY	59373566	258788	0.0044	0.1132

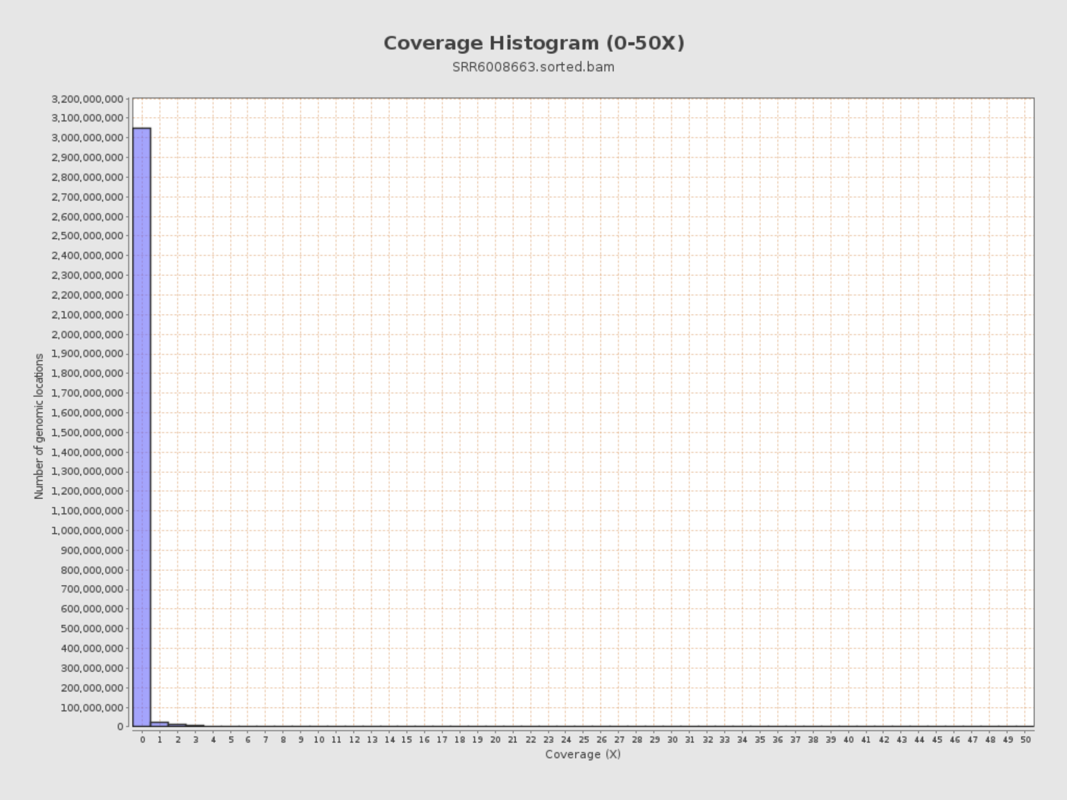
3. Results : Coverage across reference



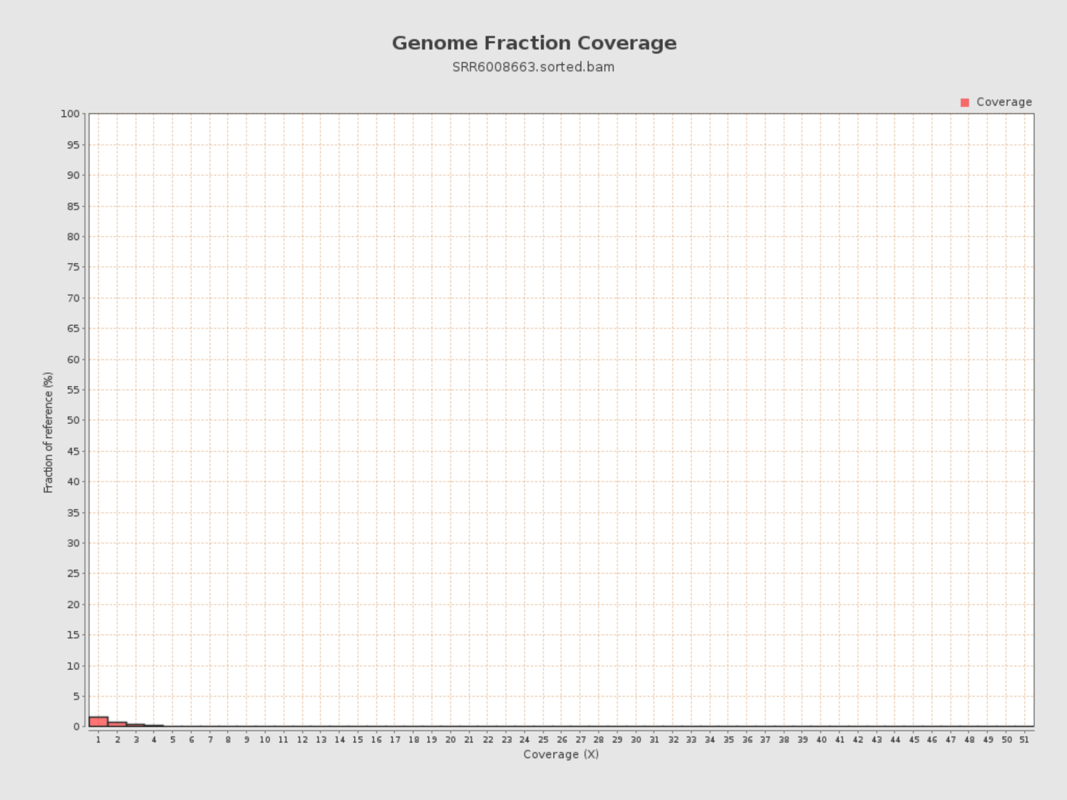
4. Results : Coverage Histogram



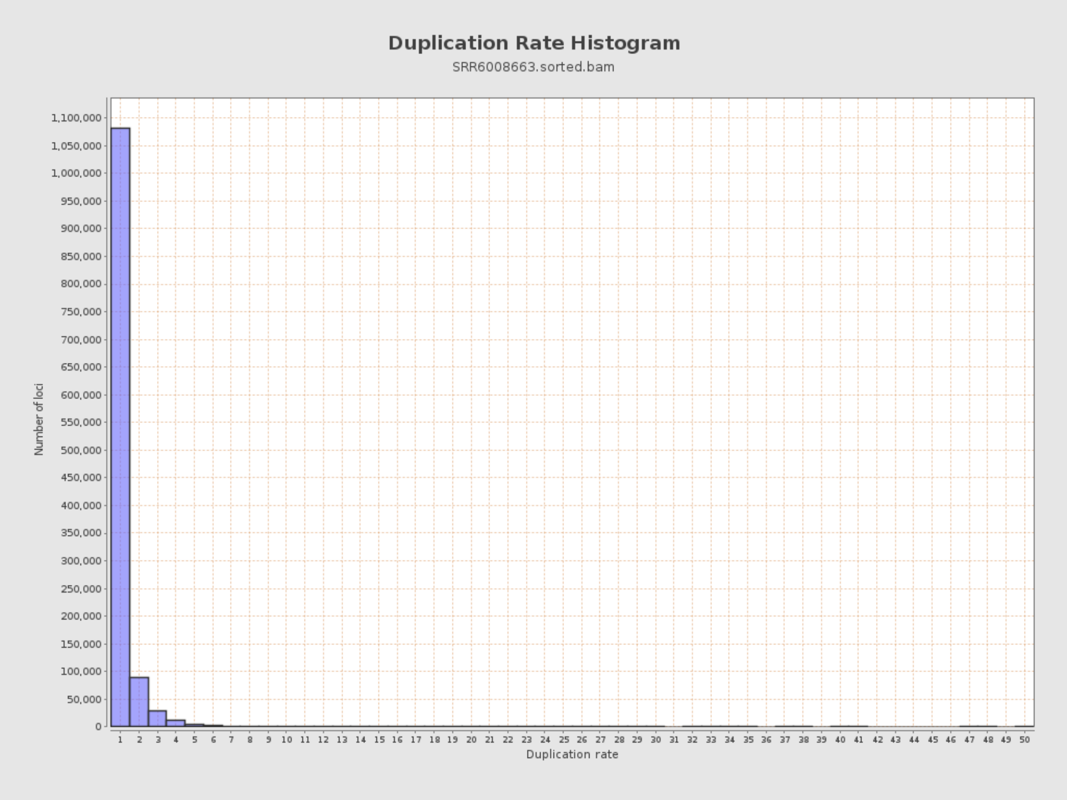
5. Results : Coverage Histogram (0-50X)



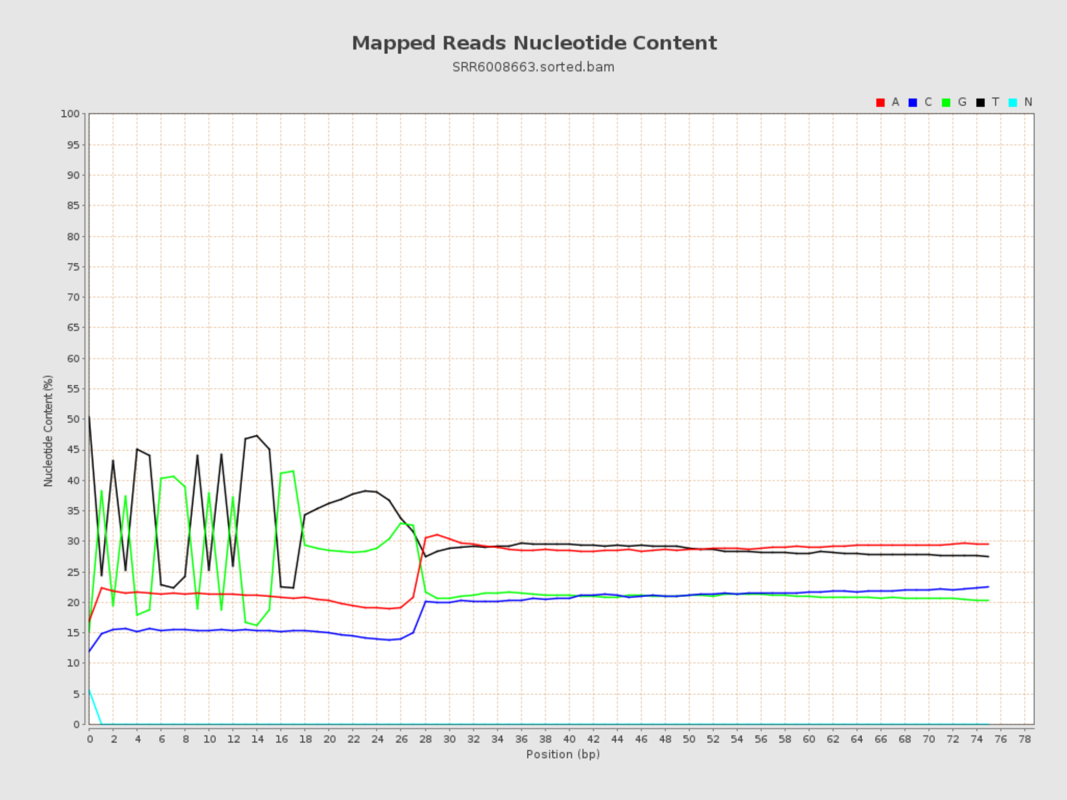
6. Results : Genome Fraction Coverage



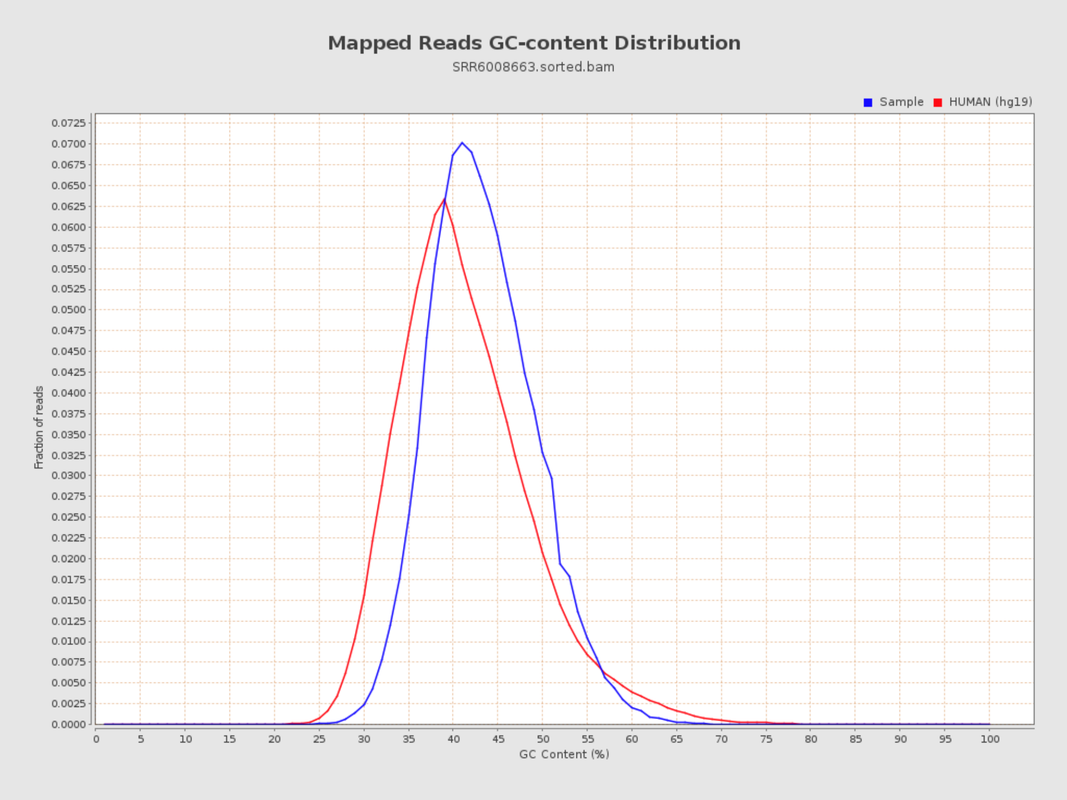
7. Results : Duplication Rate Histogram



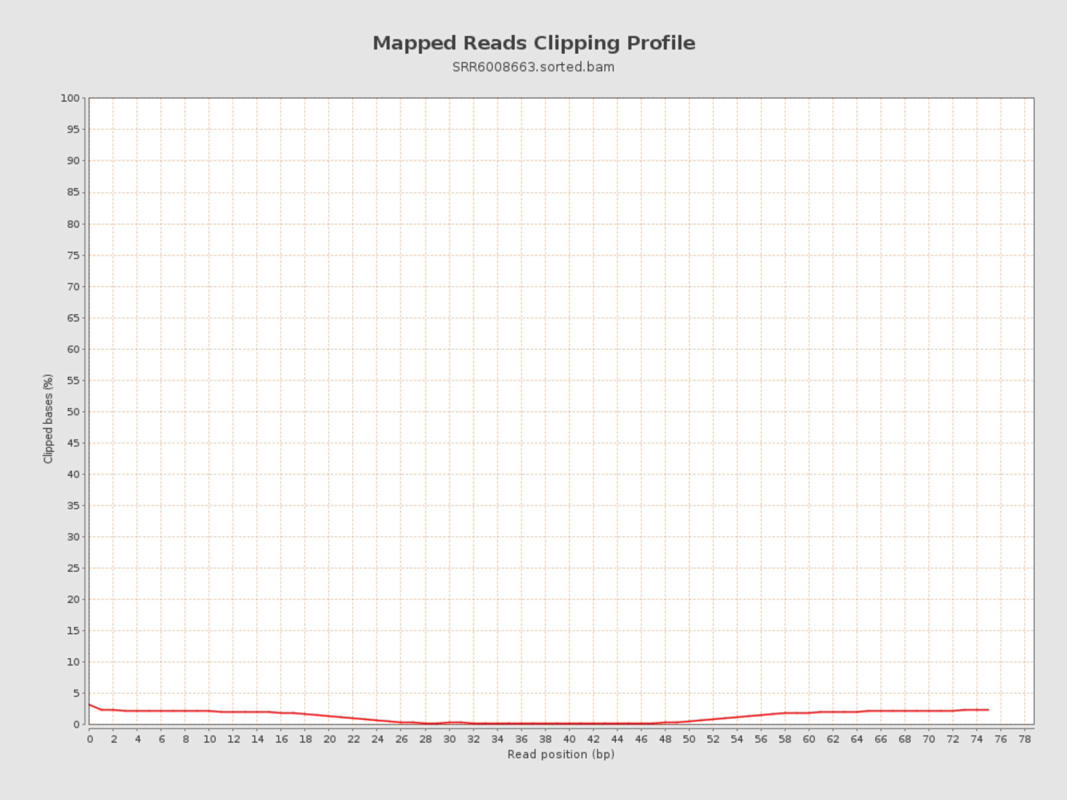
8. Results : Mapped Reads Nucleotide Content



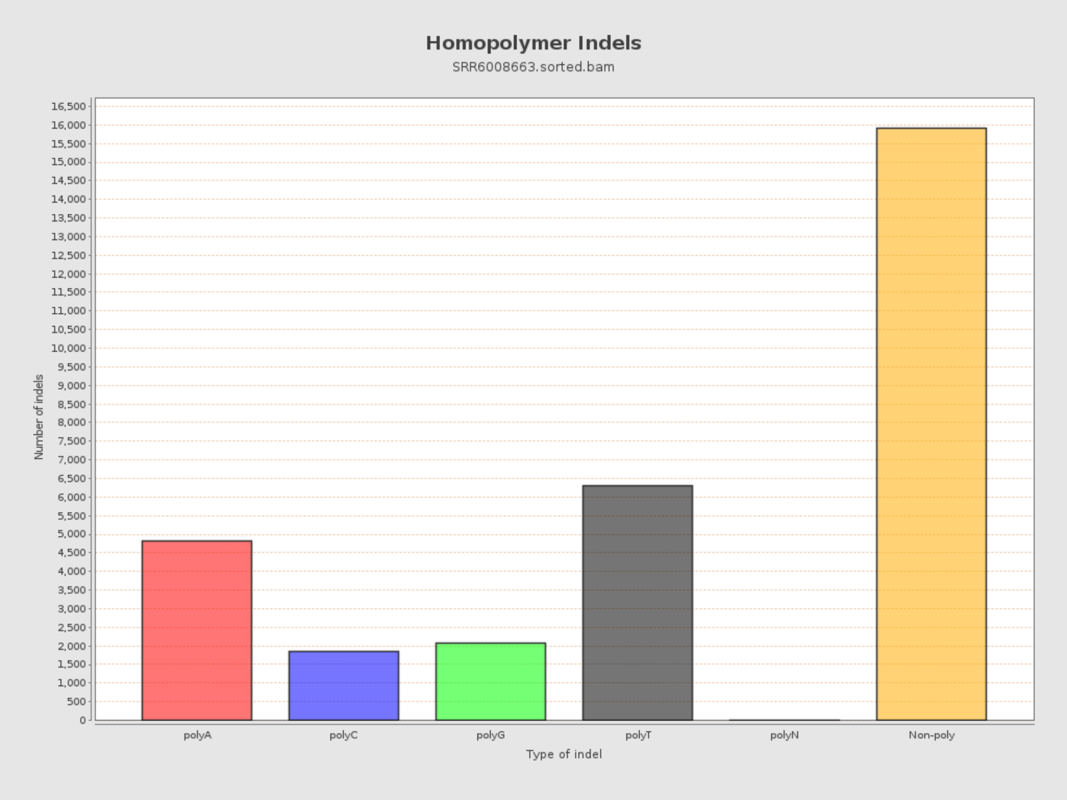
9. Results : Mapped Reads GC-content Distribution



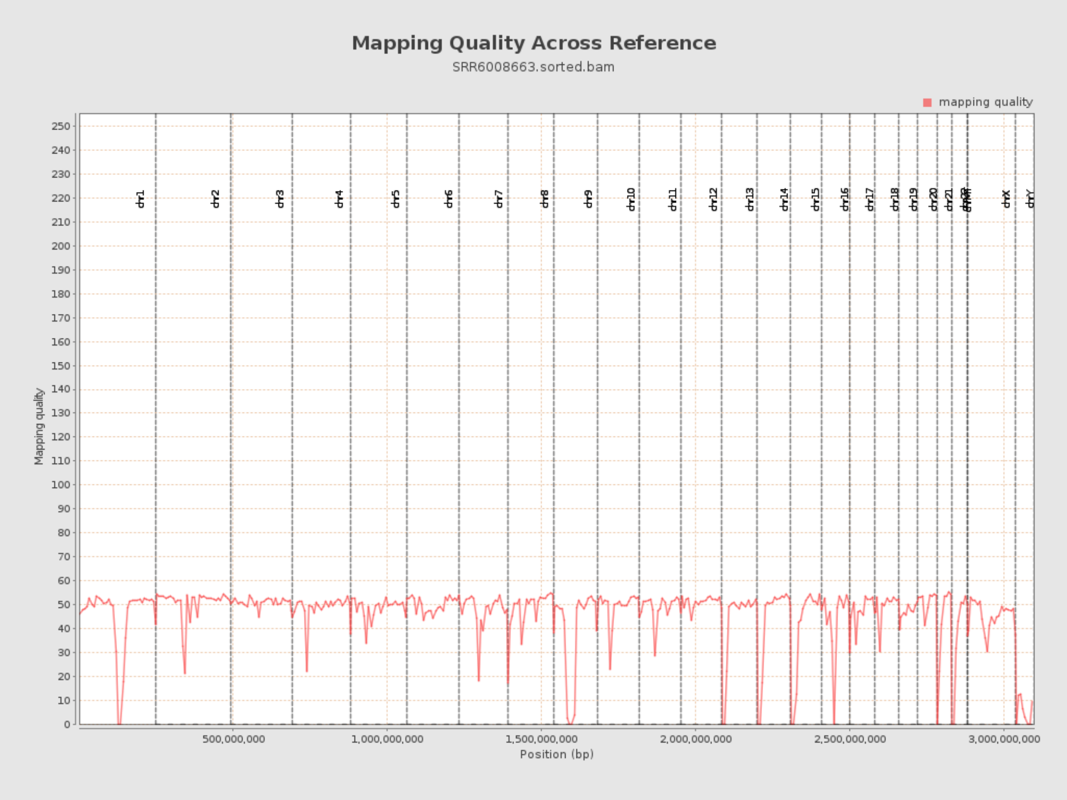
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram