Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 14:03:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080673.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_SRR3080673 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080673.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 14:03:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080673.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,512,233
Mapped reads	1,352,089 / 89.41%
Unmapped reads	160,144 / 10.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,594 / 1.03%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	58,989 / 3.9%
Duplication rate	3.76%
Clipped reads	662,759 / 43.83%

2.2. ACGT Content

Number/percentage of A's	23,959,576 / 26.99%
Number/percentage of C's	16,345,181 / 18.41%
Number/percentage of T's	28,145,954 / 31.7%
Number/percentage of G's	20,319,654 / 22.89%
Number/percentage of N's	4,143 / 0%
GC Percentage	41.3%

2.3. Coverage

Mean	0.0287

Standard Deviation	0.2476

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

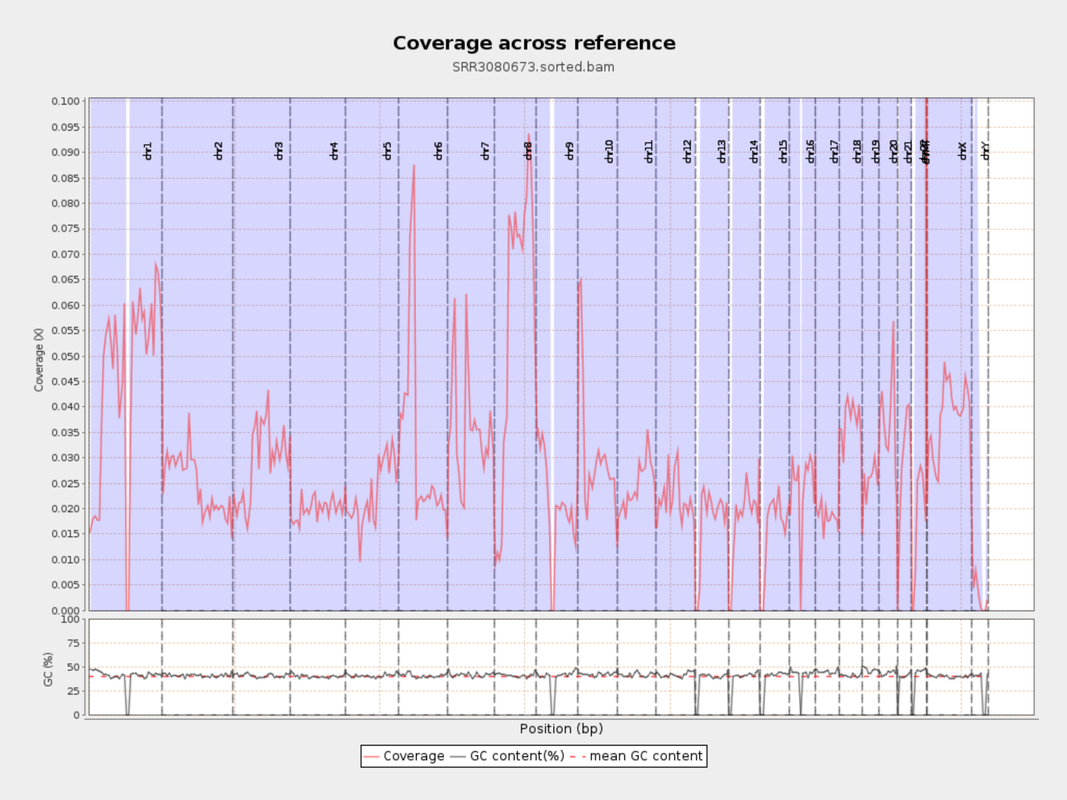
General error rate	0.71%
Mismatches	622,760
Insertions	6,537
Mapped reads with at least one insertion	0.48%
Deletions	20,588
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.33%

2.6. Chromosome stats

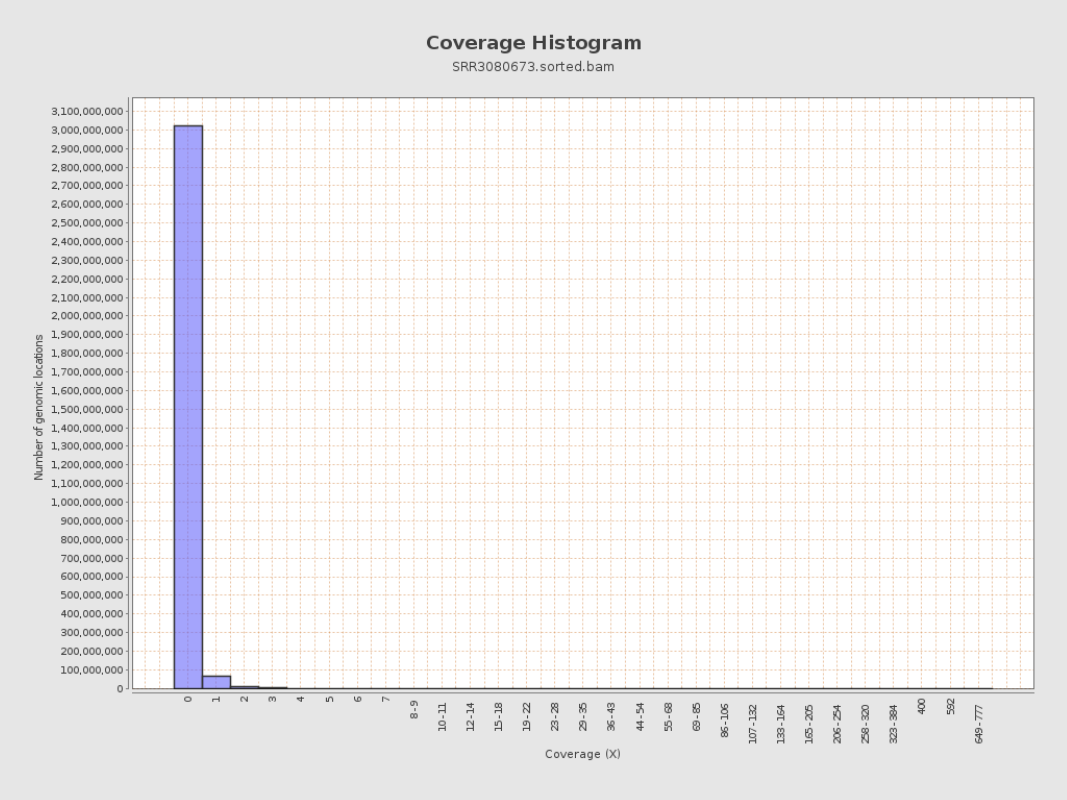
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11227133	0.045	0.3172
chr2	243199373	6003064	0.0247	0.3674
chr3	198022430	5794382	0.0293	0.1927
chr4	191154276	3820158	0.02	0.1638
chr5	180915260	4186338	0.0231	0.1716
chr6	171115067	5668008	0.0331	0.2574
chr7	159138663	5802401	0.0365	0.4614

chr8	146364022	8515779	0.0582	0.2979
chr9	141213431	2892237	0.0205	0.1784
chr10	135534747	4266461	0.0315	0.2097
chr11	135006516	3288550	0.0244	0.1848
chr12	133851895	2911595	0.0218	0.1675
chr13	115169878	1995492	0.0173	0.1501
chr14	107349540	1851100	0.0172	0.1503
chr15	102531392	1626783	0.0159	0.1496
chr16	90354753	2182972	0.0242	0.1779
chr17	81195210	1495133	0.0184	0.1558
chr18	78077248	2935924	0.0376	0.2723
chr19	59128983	1516144	0.0256	0.2099
chr20	63025520	2355765	0.0374	0.2221
chr21	48129895	1372943	0.0285	0.1934
chr22	51304566	879058	0.0171	0.1464
chrMT	16571	142811	8.6181	5.5733
chrX	155270560	5891908	0.0379	0.2275
chrY	59373566	185428	0.0031	0.0679

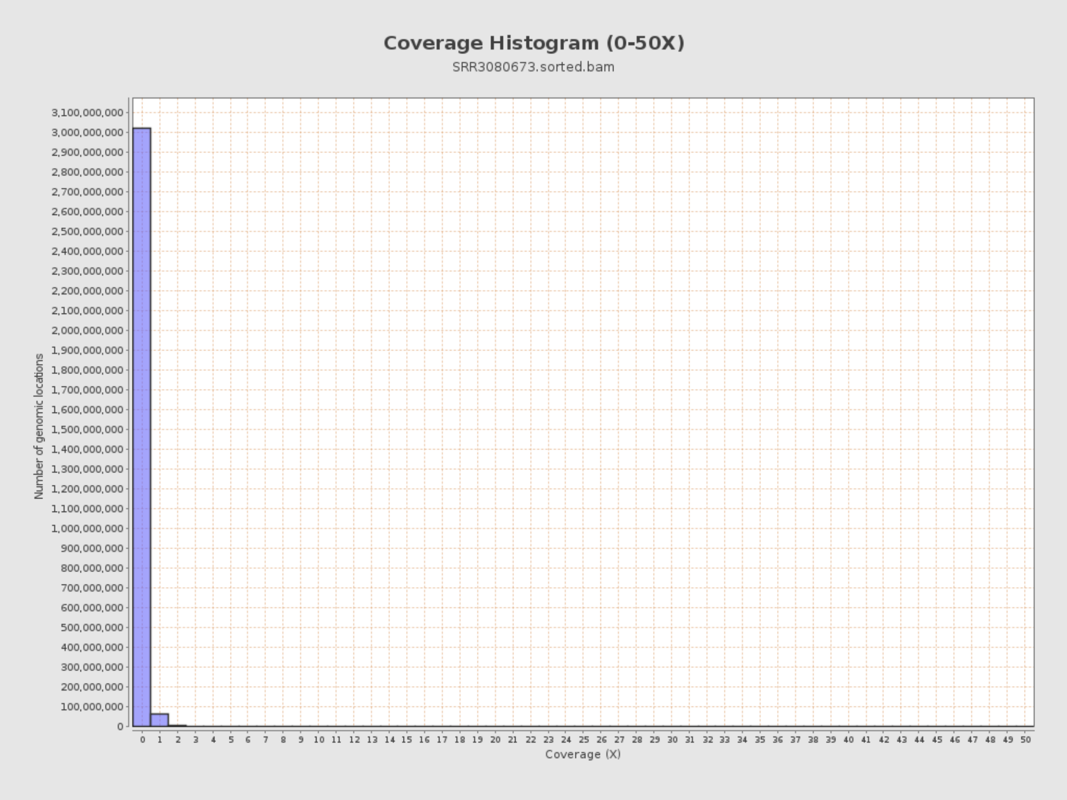
3. Results : Coverage across reference



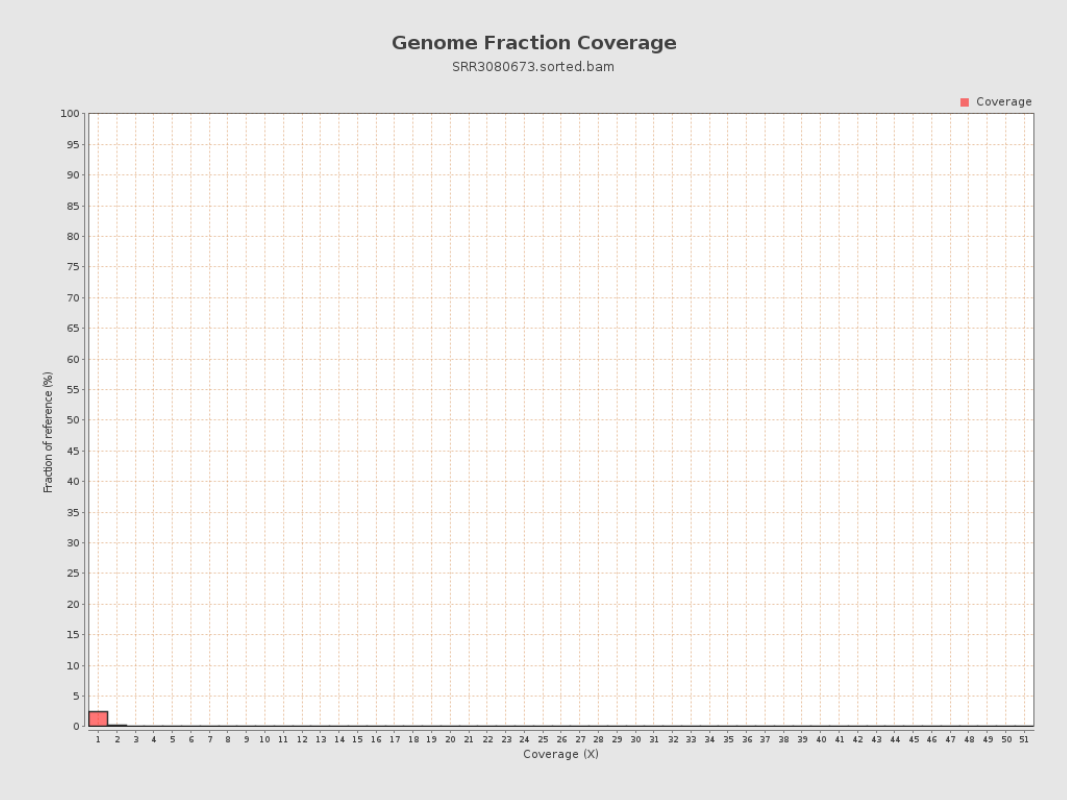
4. Results : Coverage Histogram



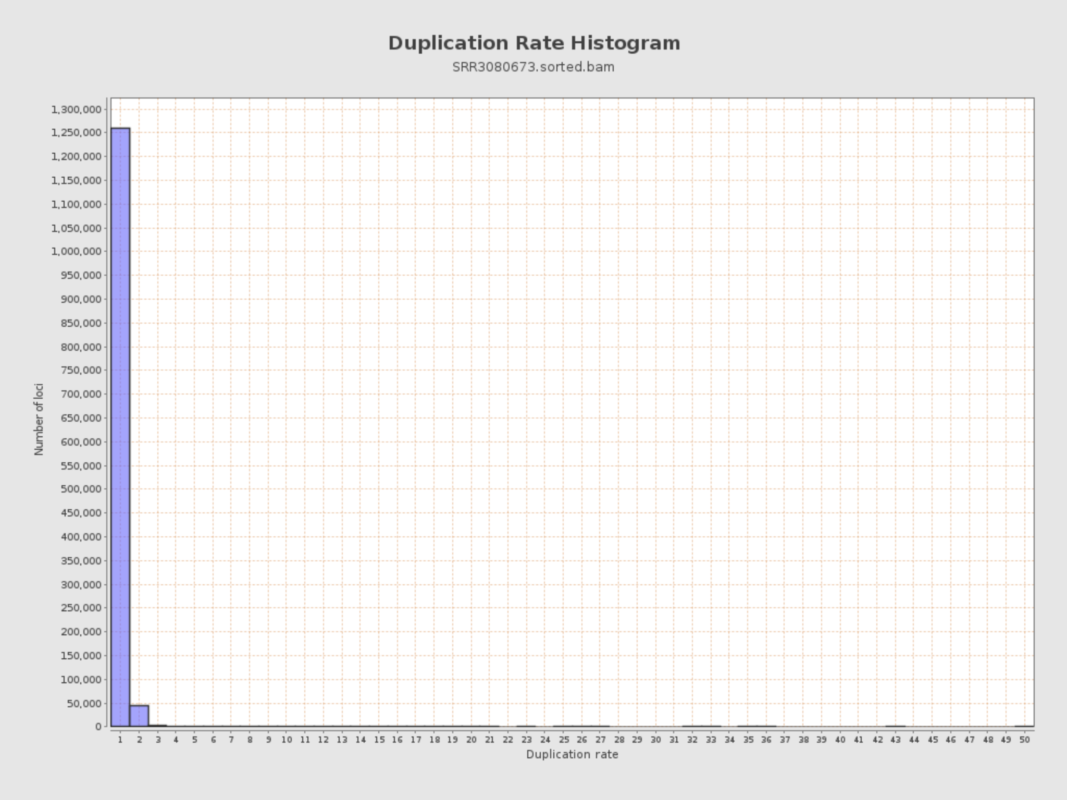
5. Results : Coverage Histogram (0-50X)



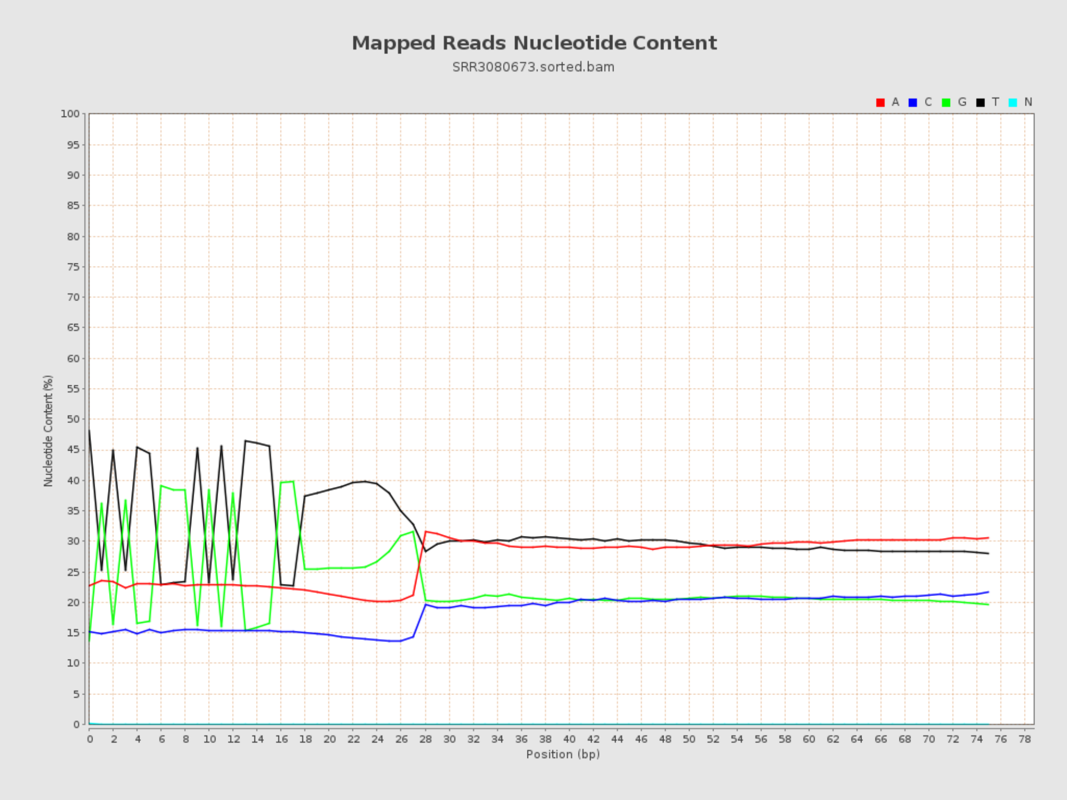
6. Results : Genome Fraction Coverage



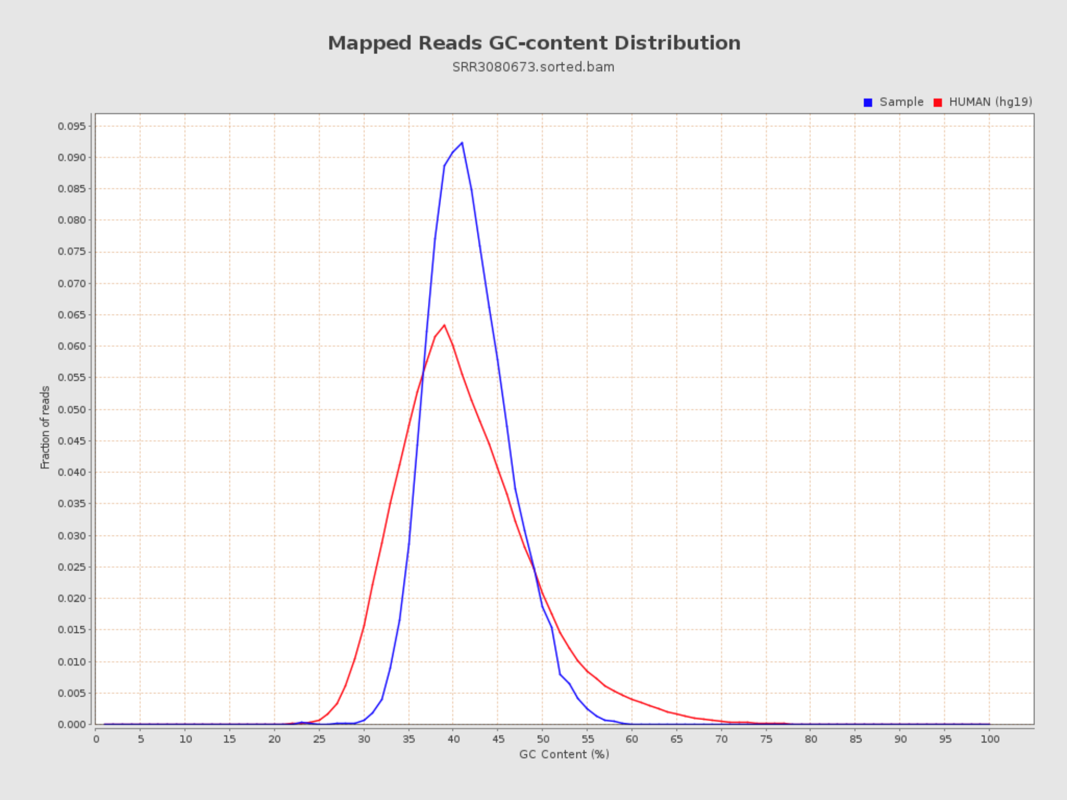
7. Results : Duplication Rate Histogram



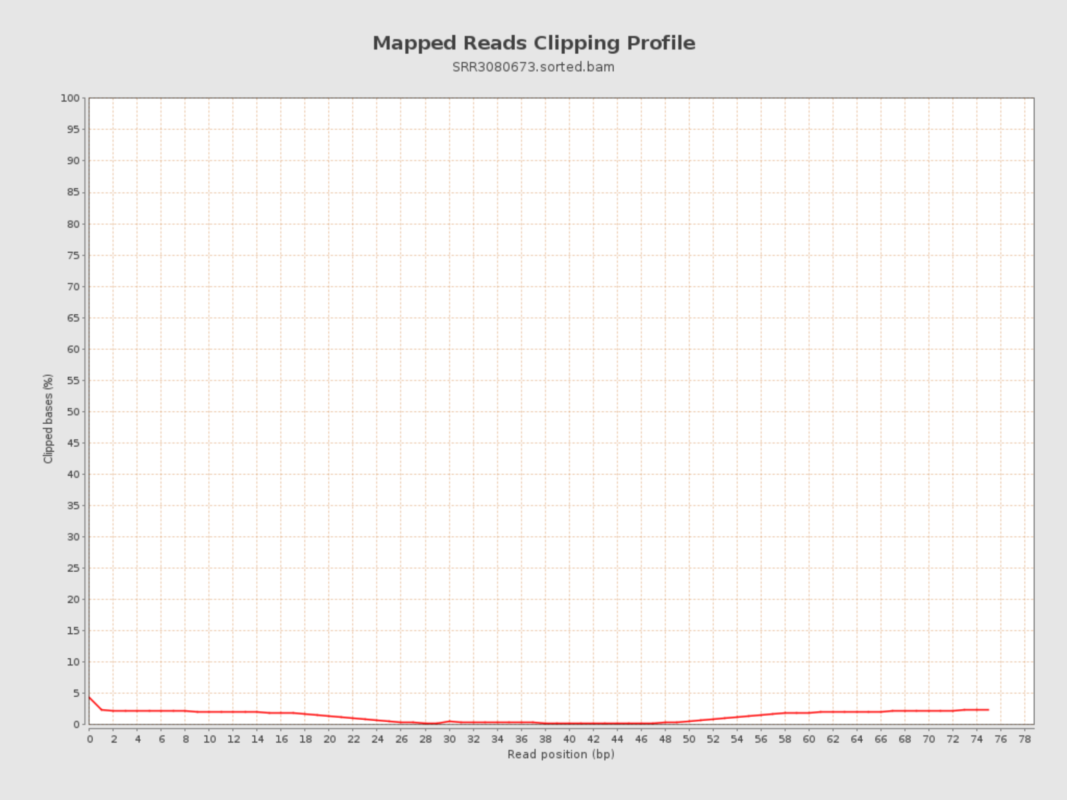
8. Results : Mapped Reads Nucleotide Content



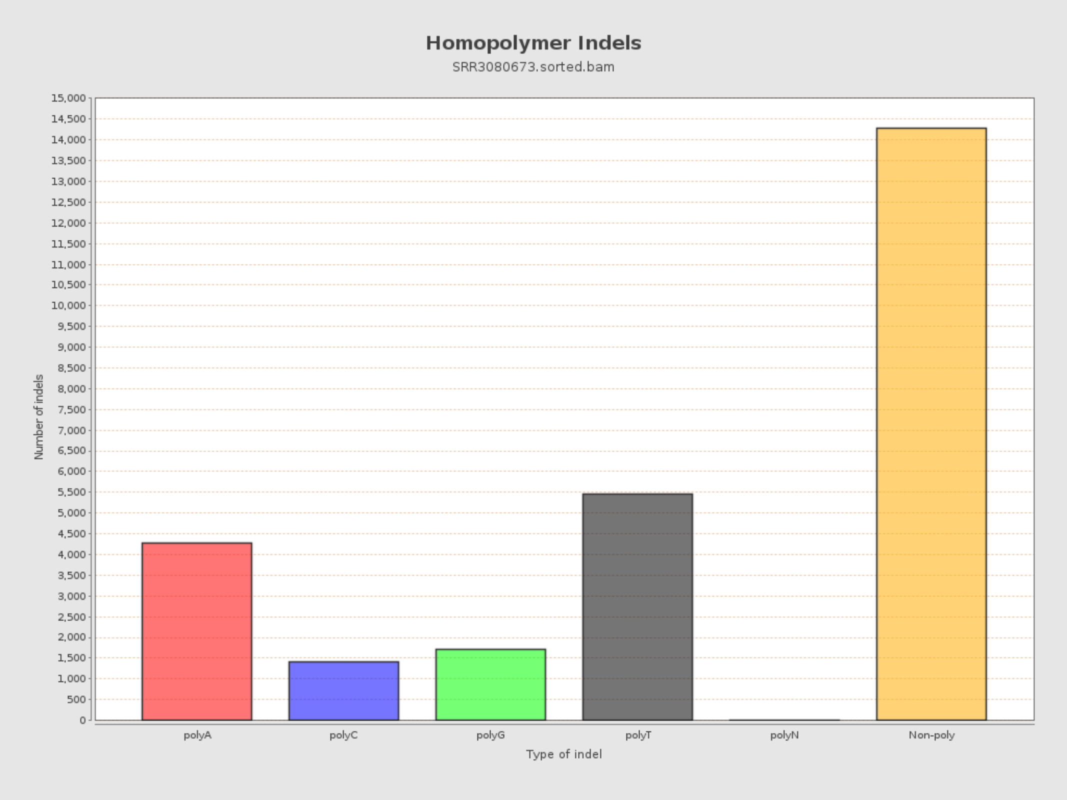
9. Results : Mapped Reads GC-content Distribution



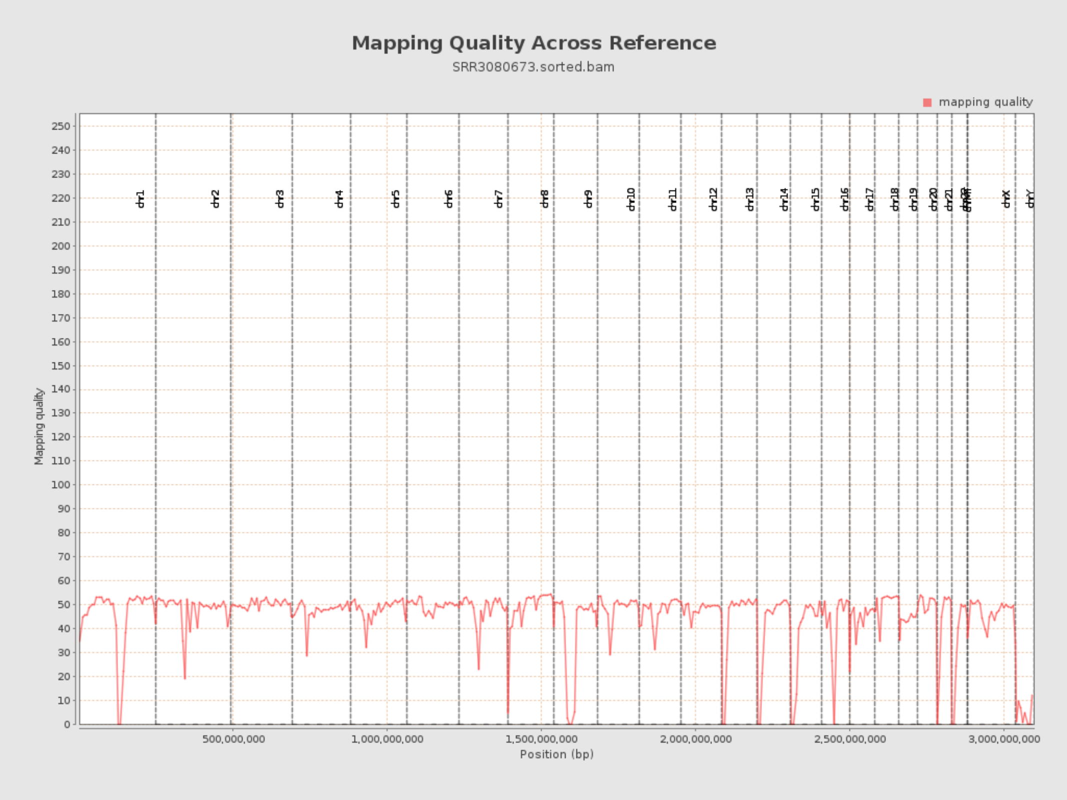
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram