Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:59:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080613.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_SRR3080613 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080613.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:59:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080613.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,372,430
Mapped reads	2,857,752 / 84.74%
Unmapped reads	514,678 / 15.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,490 / 0.67%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	147,232 / 4.37%
Duplication rate	4.35%
Clipped reads	1,297,779 / 38.48%

2.2. ACGT Content

Number/percentage of A's	52,884,593 / 27.68%
Number/percentage of C's	34,237,093 / 17.92%
Number/percentage of T's	61,792,803 / 32.35%
Number/percentage of G's	41,963,462 / 21.97%
Number/percentage of N's	160,187 / 0.08%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0617

Standard Deviation	0.4055

2.4. Mapping Quality

Mean Mapping Quality	47.59

2.5. Mismatches and indels

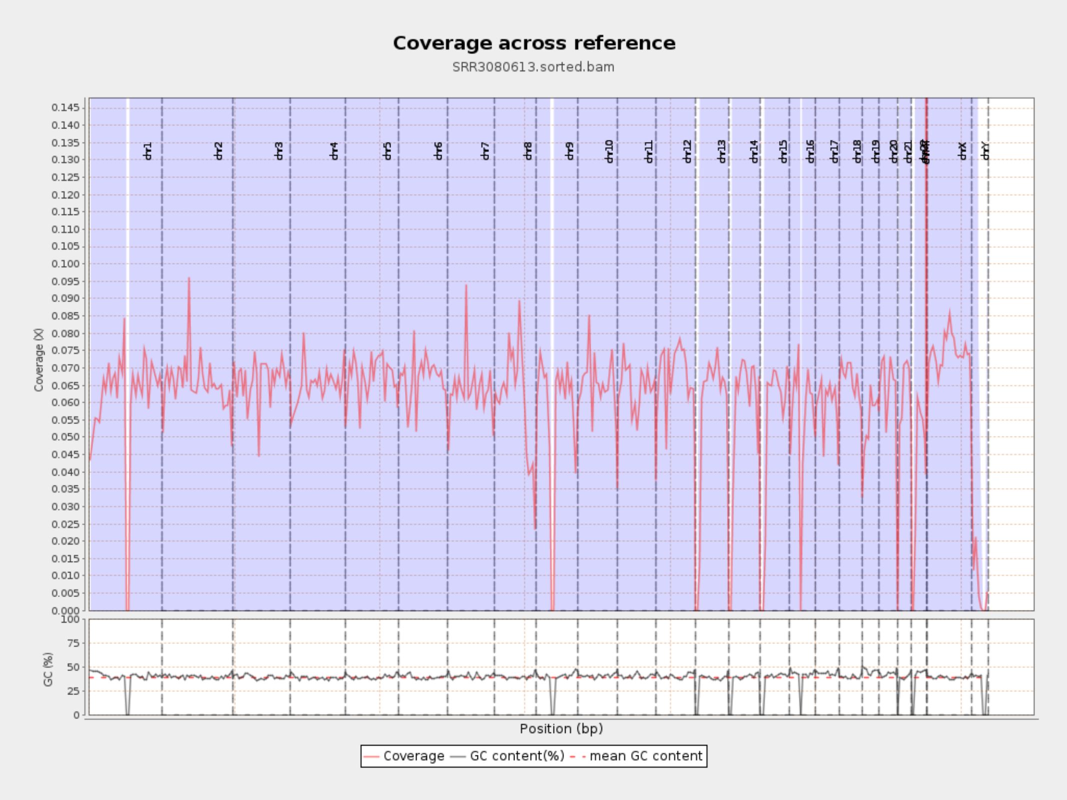
General error rate	0.92%
Mismatches	1,723,291
Insertions	15,554
Mapped reads with at least one insertion	0.54%
Deletions	46,212
Mapped reads with at least one deletion	1.6%
Homopolymer indels	48.52%

2.6. Chromosome stats

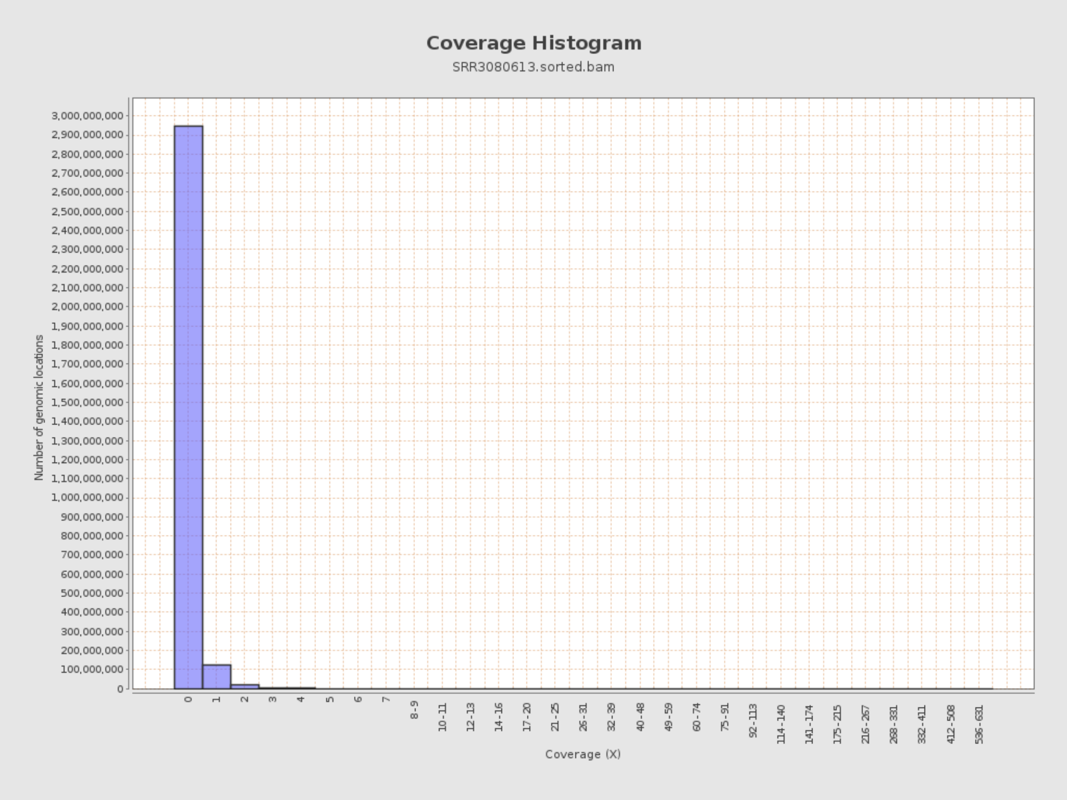
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15111894	0.0606	0.5379
chr2	243199373	16036902	0.0659	0.445
chr3	198022430	13208628	0.0667	0.3156
chr4	191154276	12418673	0.065	0.3225
chr5	180915260	12238726	0.0676	0.3161
chr6	171115067	11440840	0.0669	0.3746
chr7	159138663	10223009	0.0642	0.6461

chr8	146364022	8883388	0.0607	0.511
chr9	141213431	7987558	0.0566	0.3795
chr10	135534747	8969995	0.0662	0.4093
chr11	135006516	8667167	0.0642	0.3729
chr12	133851895	9135562	0.0683	0.3204
chr13	115169878	6429029	0.0558	0.2876
chr14	107349540	5916212	0.0551	0.3033
chr15	102531392	5360127	0.0523	0.2768
chr16	90354753	5039713	0.0558	0.318
chr17	81195210	4818870	0.0593	0.3289
chr18	78077248	5217719	0.0668	0.6637
chr19	59128983	3236371	0.0547	0.4573
chr20	63025520	4072706	0.0646	0.3167
chr21	48129895	2756264	0.0573	0.3105
chr22	51304566	1986612	0.0387	0.2377
chrMT	16571	26212	1.5818	2.5071
chrX	155270560	11472238	0.0739	0.3522
chrY	59373566	460190	0.0078	0.1532

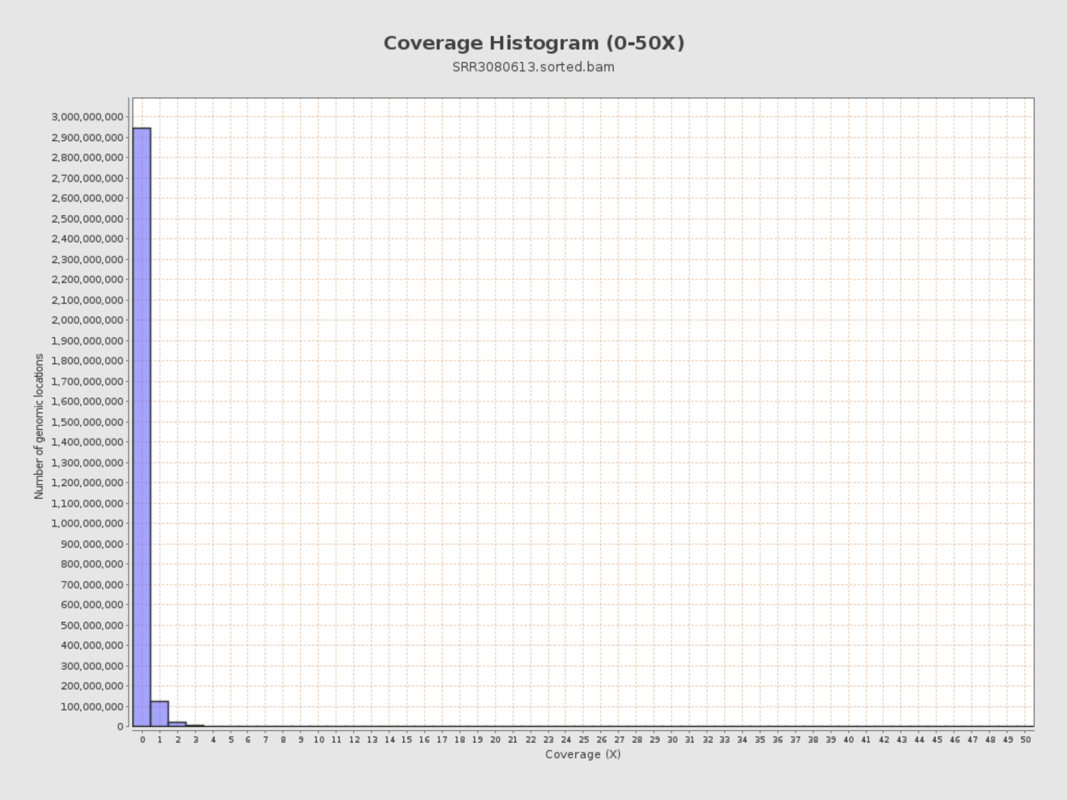
3. Results : Coverage across reference



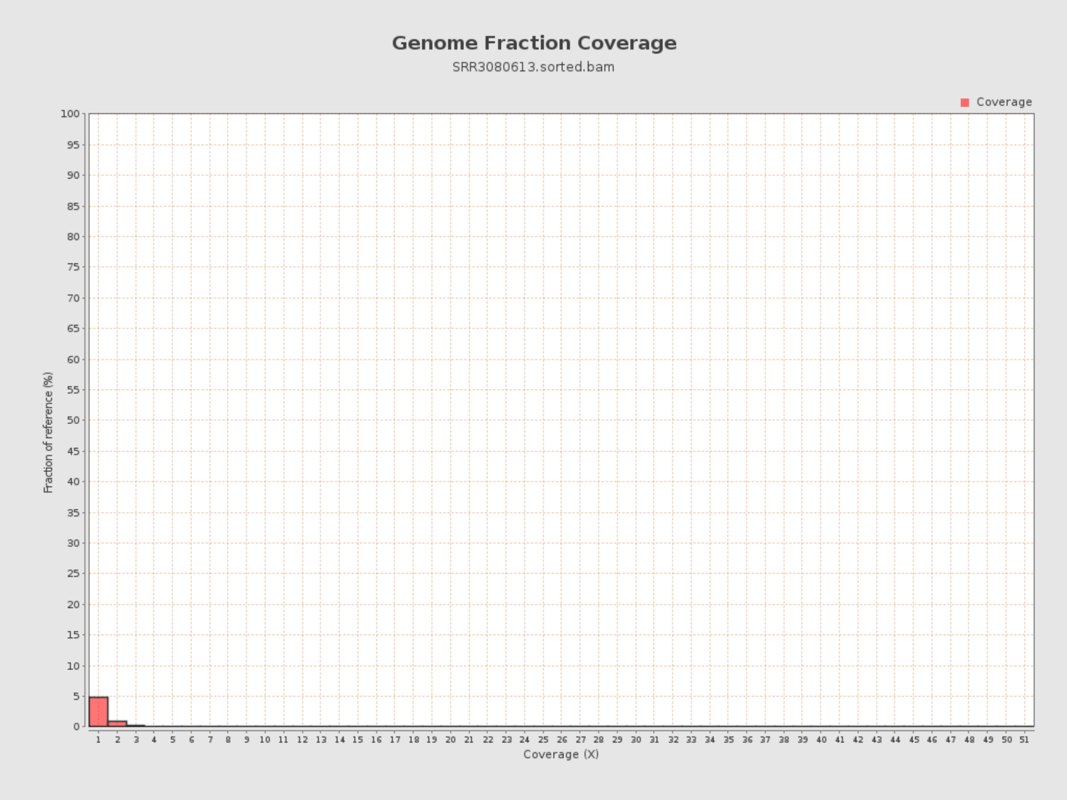
4. Results : Coverage Histogram



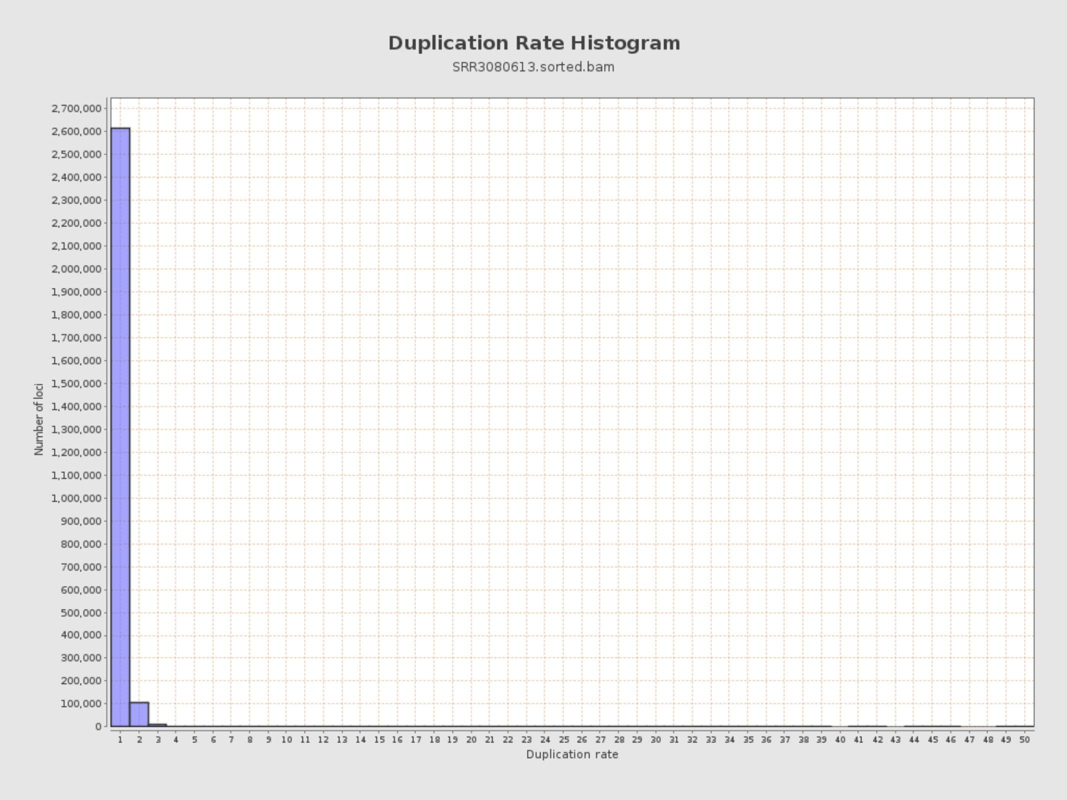
5. Results : Coverage Histogram (0-50X)



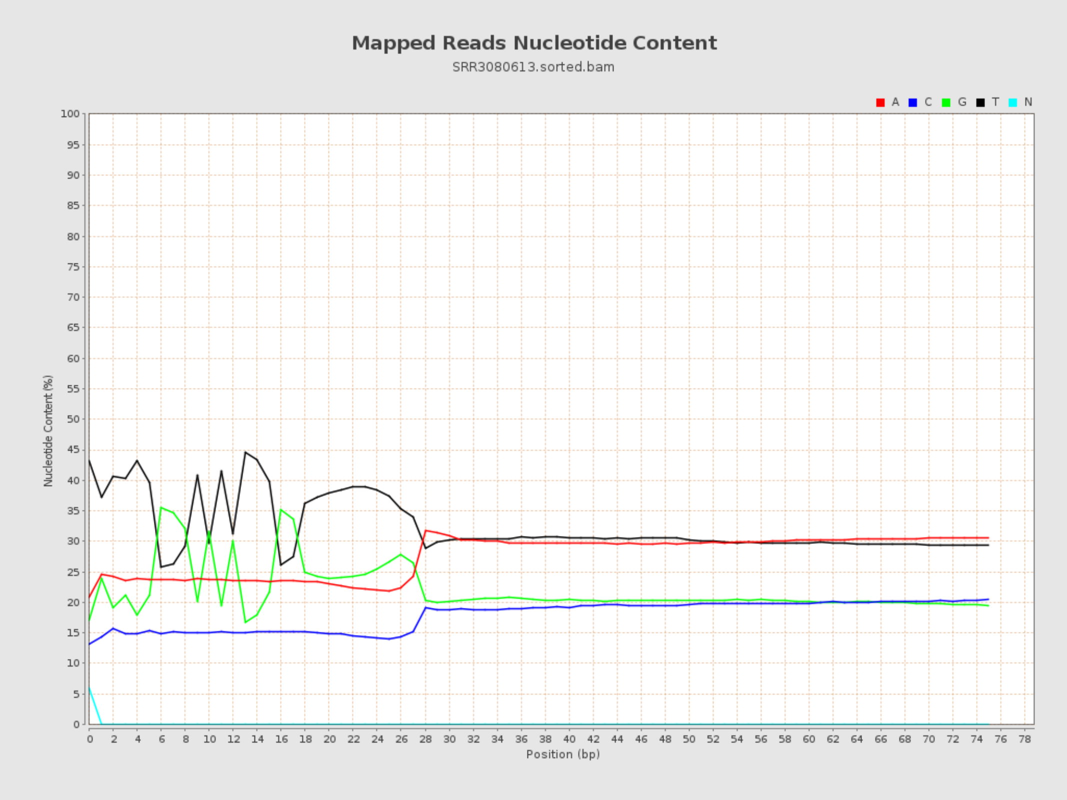
6. Results : Genome Fraction Coverage



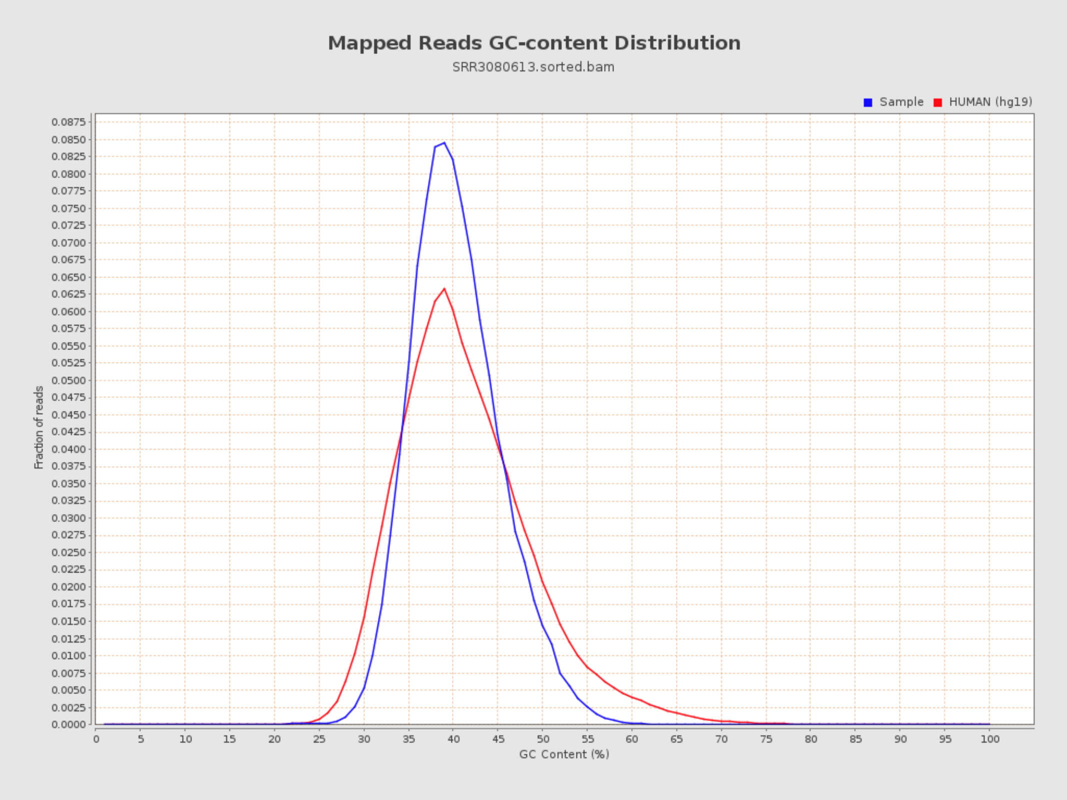
7. Results : Duplication Rate Histogram



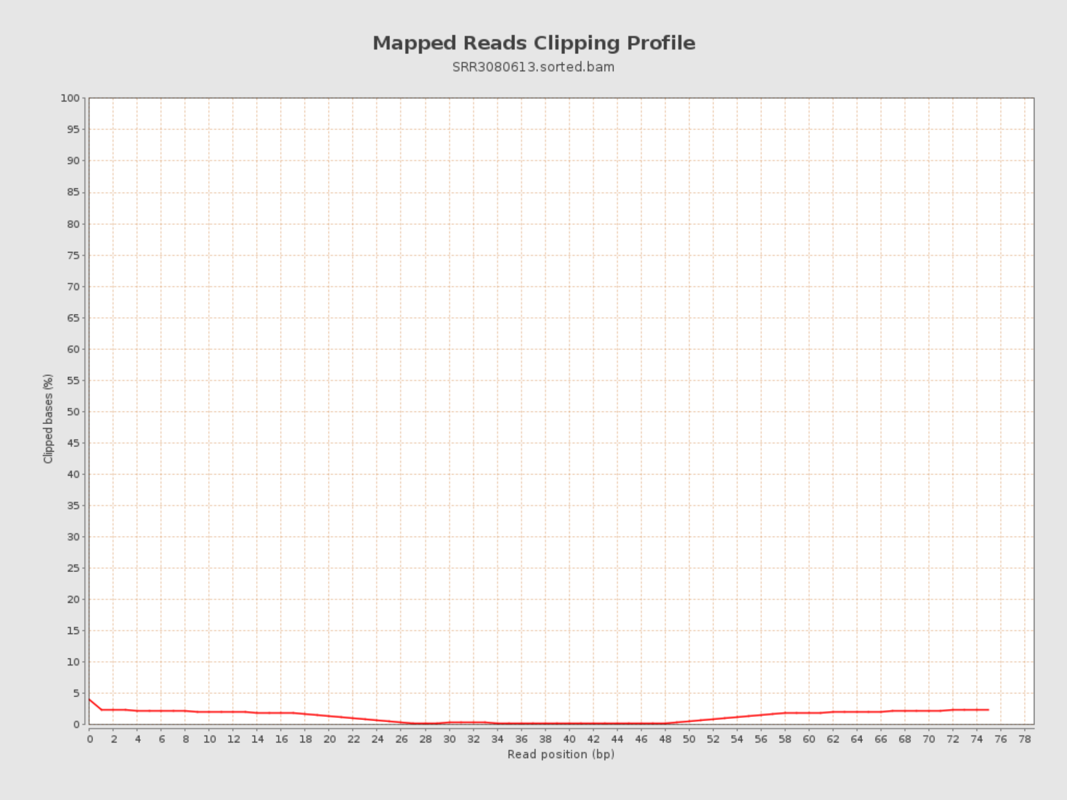
8. Results : Mapped Reads Nucleotide Content



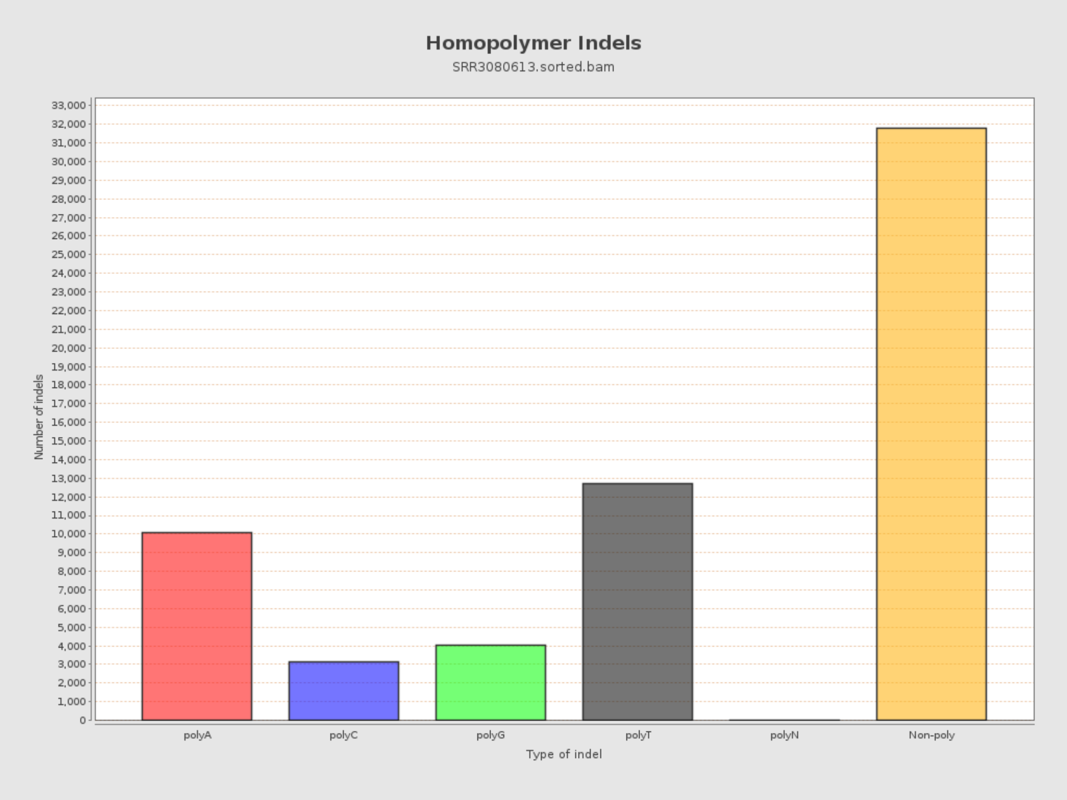
9. Results : Mapped Reads GC-content Distribution



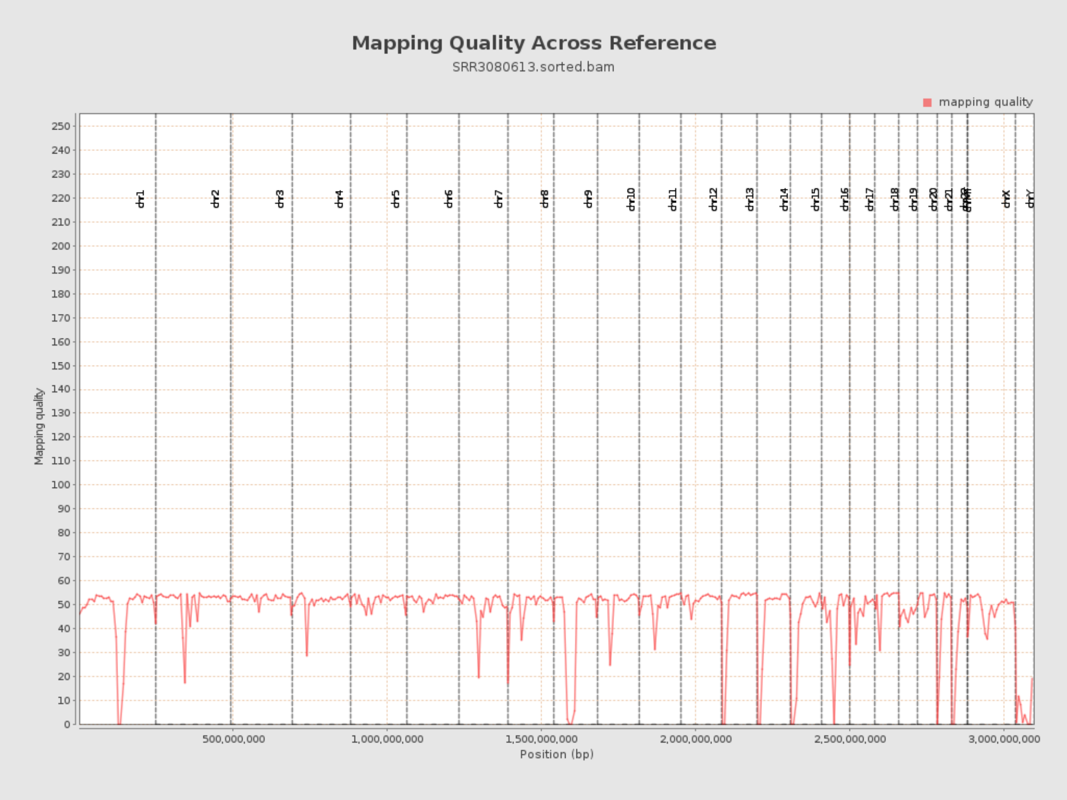
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram