Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 15:10:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084809.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_SRR3084809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 15:10:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,829,147
Mapped reads	2,579,194 / 91.17%
Unmapped reads	249,953 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,424 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	110,757 / 3.91%
Duplication rate	3.74%
Clipped reads	1,104,953 / 39.06%

2.2. ACGT Content

Number/percentage of A's	47,732,905 / 27.52%
Number/percentage of C's	32,635,044 / 18.82%
Number/percentage of T's	54,281,769 / 31.3%
Number/percentage of G's	38,742,544 / 22.34%
Number/percentage of N's	24,842 / 0.01%
GC Percentage	41.16%

2.3. Coverage

Mean	0.056

Standard Deviation	0.3318

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

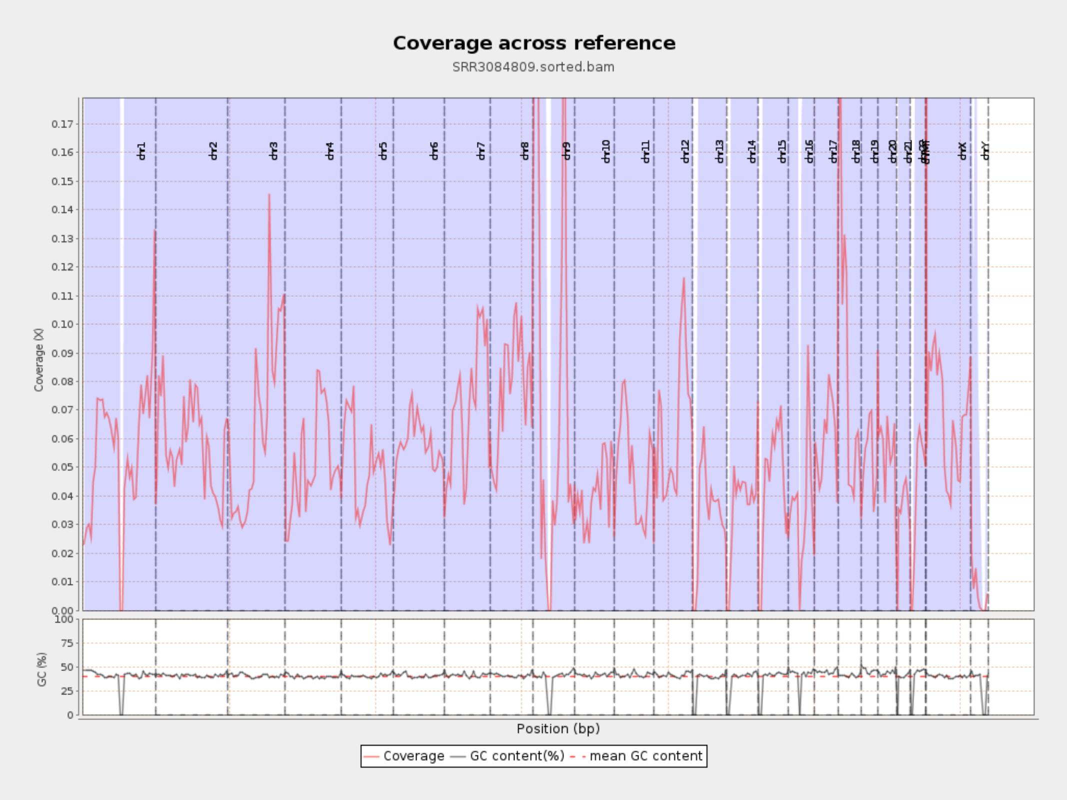
General error rate	0.78%
Mismatches	1,322,980
Insertions	13,740
Mapped reads with at least one insertion	0.53%
Deletions	40,003
Mapped reads with at least one deletion	1.53%
Homopolymer indels	48.18%

2.6. Chromosome stats

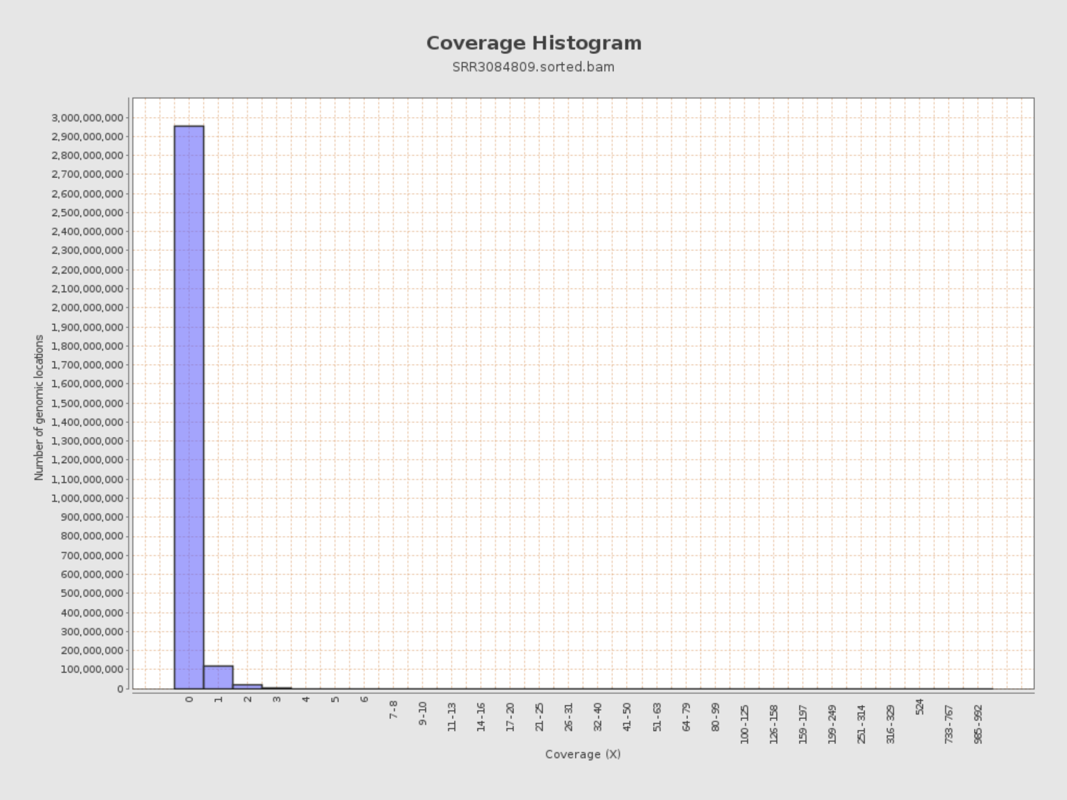
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14071267	0.0565	0.3641
chr2	243199373	14053916	0.0578	0.5261
chr3	198022430	12668335	0.064	0.2959
chr4	191154276	9857077	0.0516	0.2702
chr5	180915260	8843081	0.0489	0.2575
chr6	171115067	10028940	0.0586	0.301
chr7	159138663	11293409	0.071	0.3697

chr8	146364022	11351229	0.0776	0.3901
chr9	141213431	11512179	0.0815	0.3986
chr10	135534747	5561787	0.041	0.2494
chr11	135006516	6680708	0.0495	0.2912
chr12	133851895	8735105	0.0653	0.2996
chr13	115169878	3889289	0.0338	0.2145
chr14	107349540	3867437	0.036	0.2215
chr15	102531392	4499018	0.0439	0.2533
chr16	90354753	3179238	0.0352	0.2236
chr17	81195210	4962740	0.0611	0.2924
chr18	78077248	6981552	0.0894	0.5267
chr19	59128983	3243276	0.0549	0.3228
chr20	63025520	3547789	0.0563	0.2786
chr21	48129895	1665474	0.0346	0.2205
chr22	51304566	2072483	0.0404	0.2321
chrMT	16571	60780	3.6679	2.6561
chrX	155270560	10500569	0.0676	0.3116
chrY	59373566	356980	0.006	0.1139

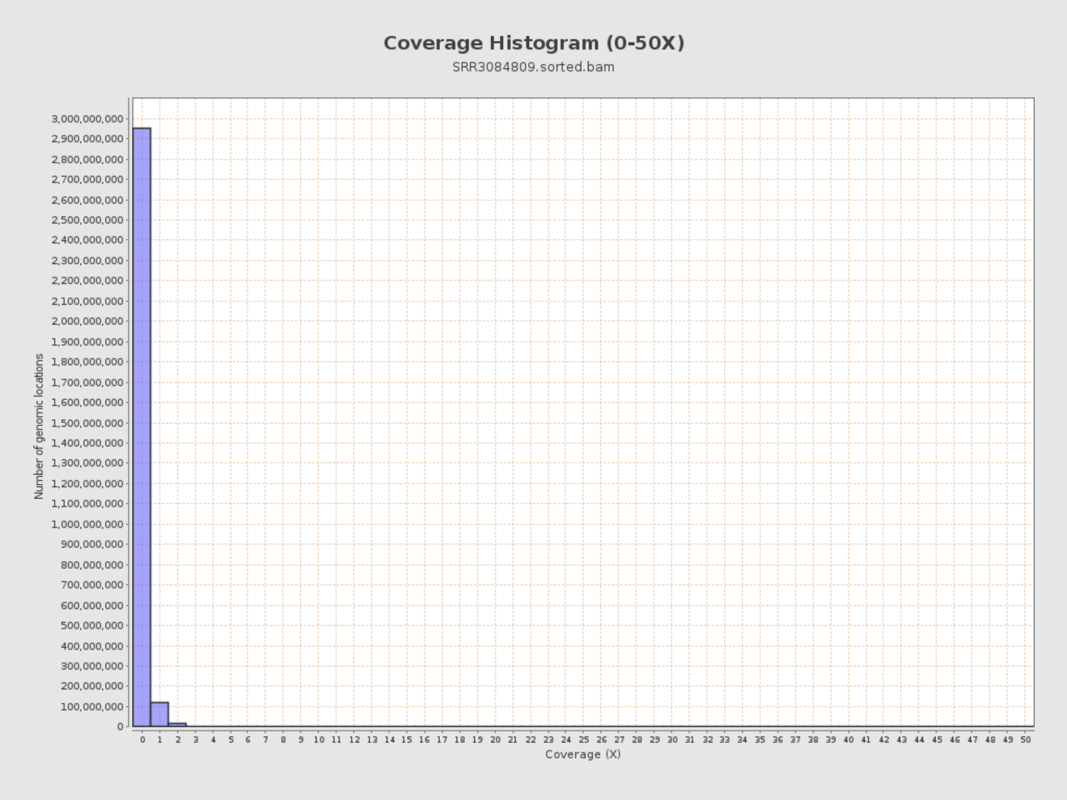
3. Results : Coverage across reference



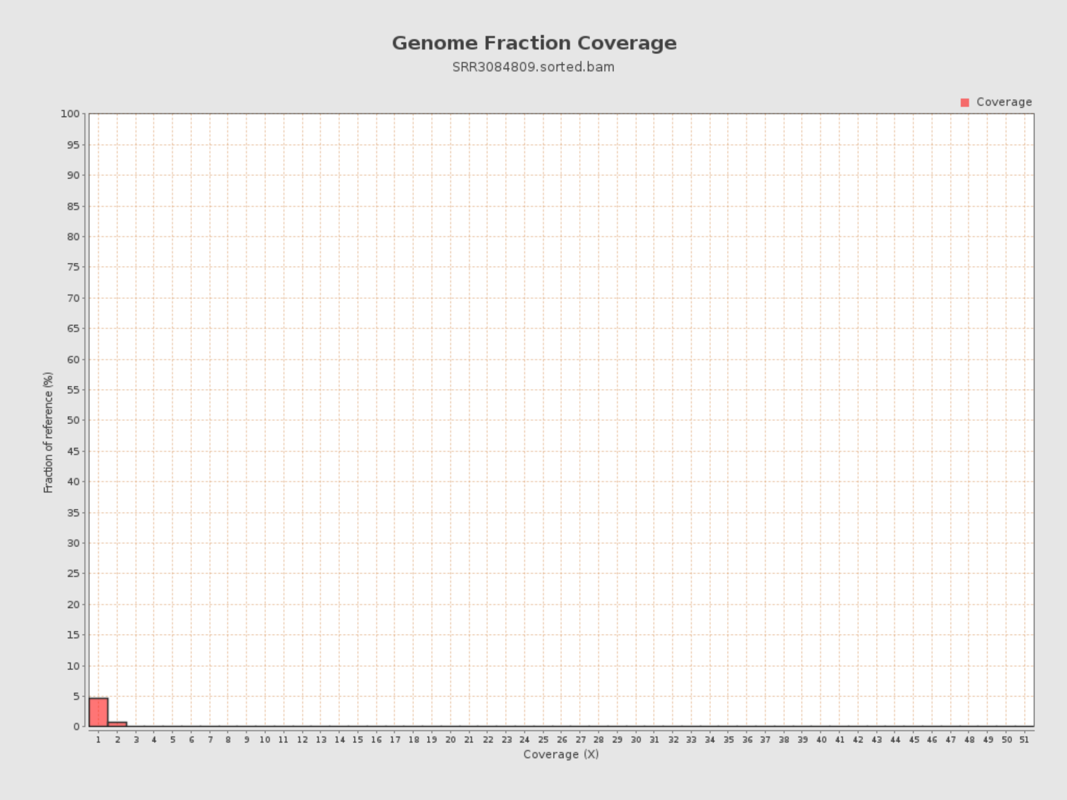
4. Results : Coverage Histogram



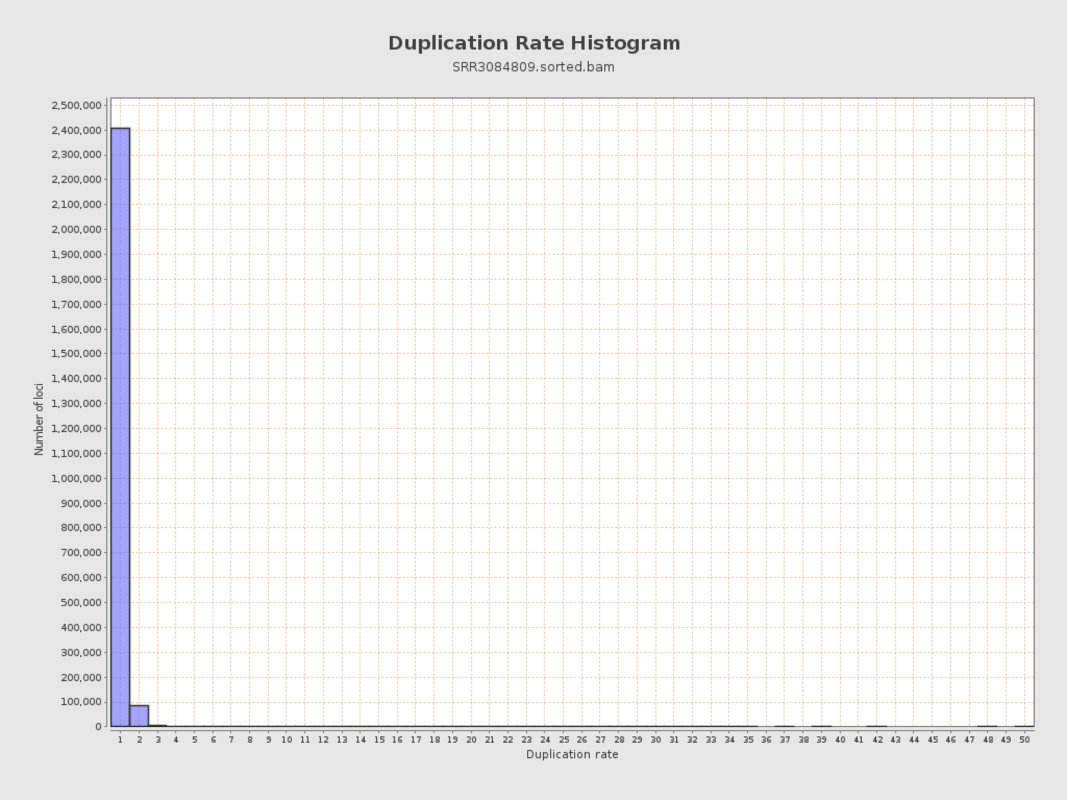
5. Results : Coverage Histogram (0-50X)



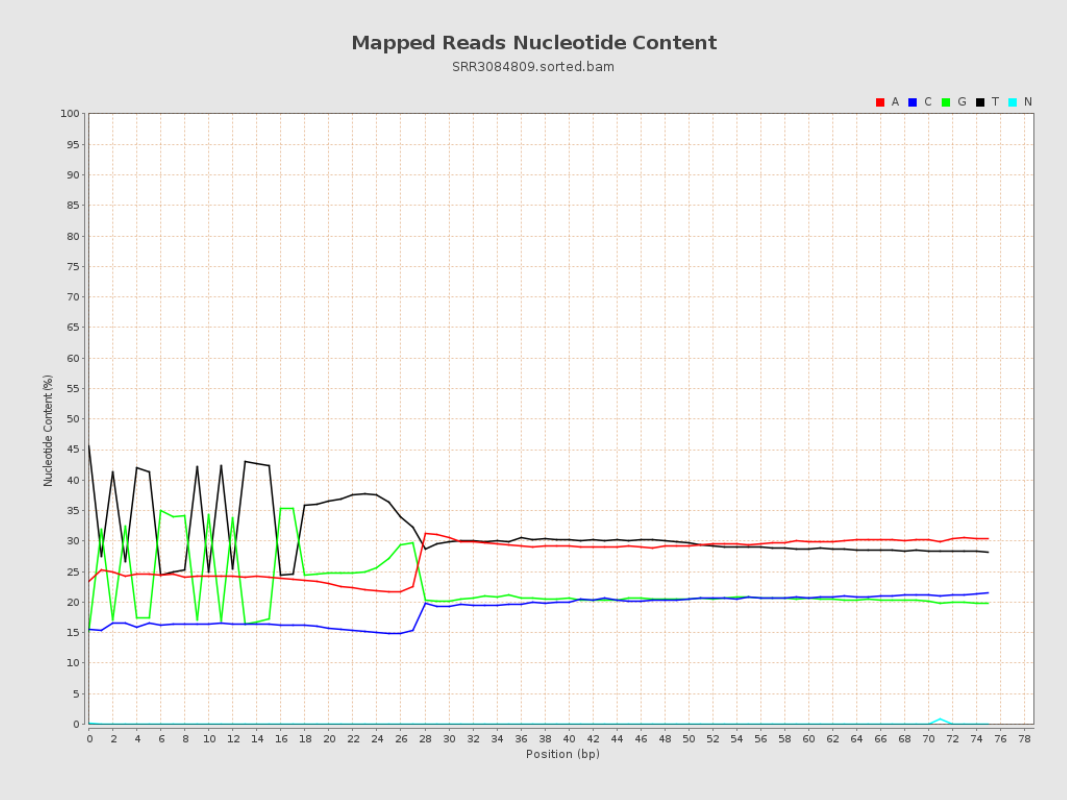
6. Results : Genome Fraction Coverage



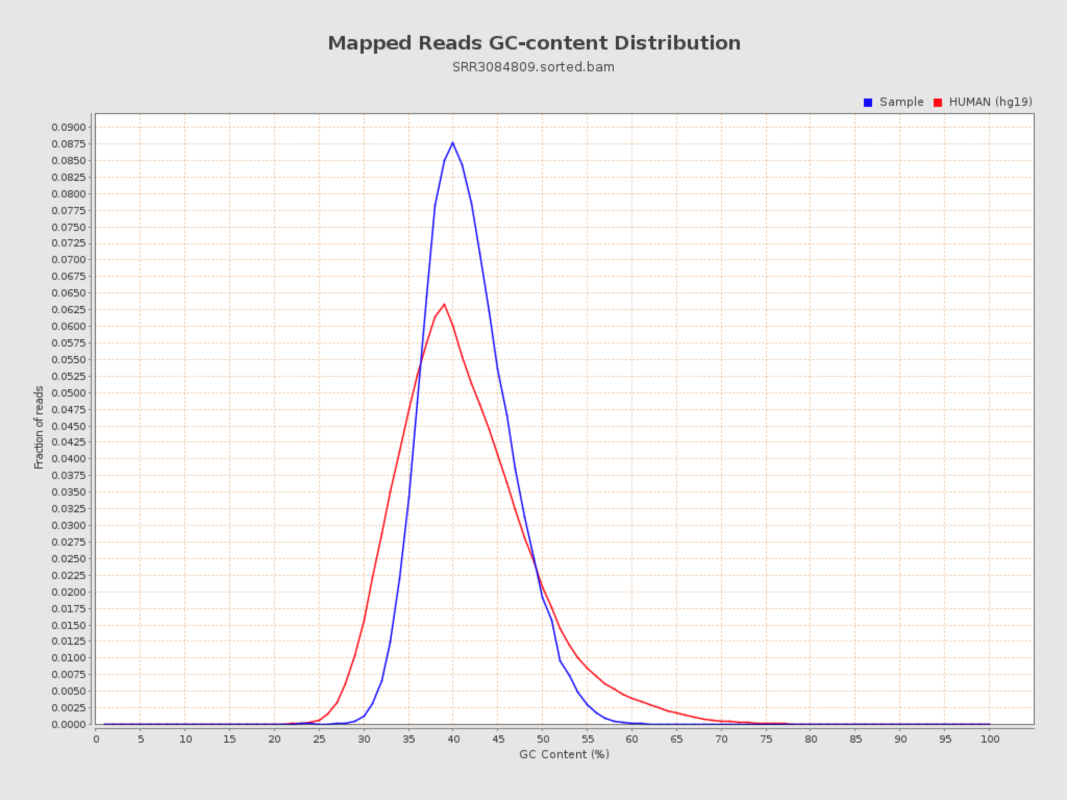
7. Results : Duplication Rate Histogram



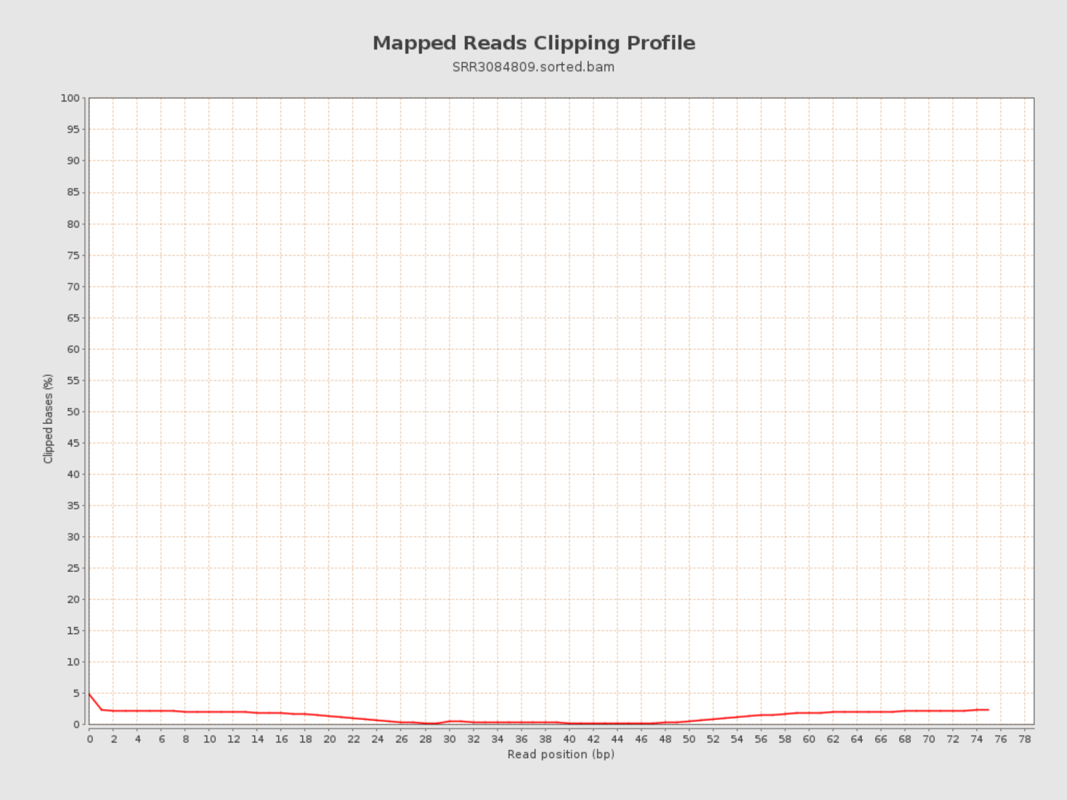
8. Results : Mapped Reads Nucleotide Content



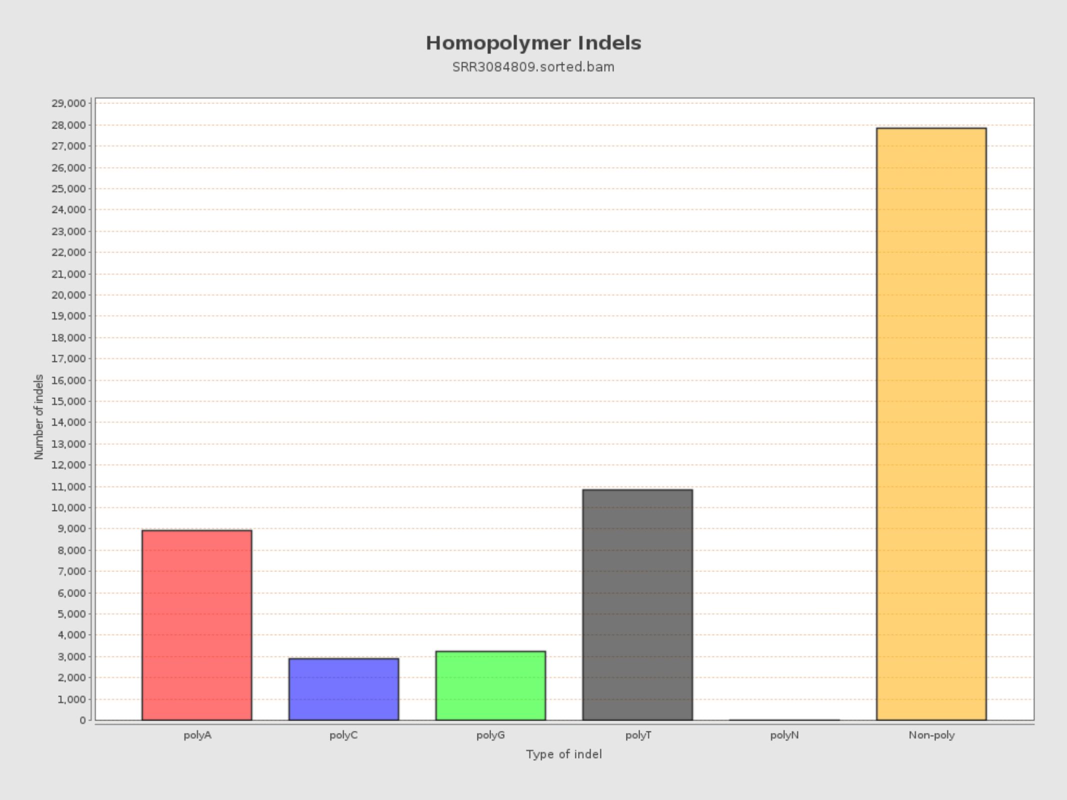
9. Results : Mapped Reads GC-content Distribution



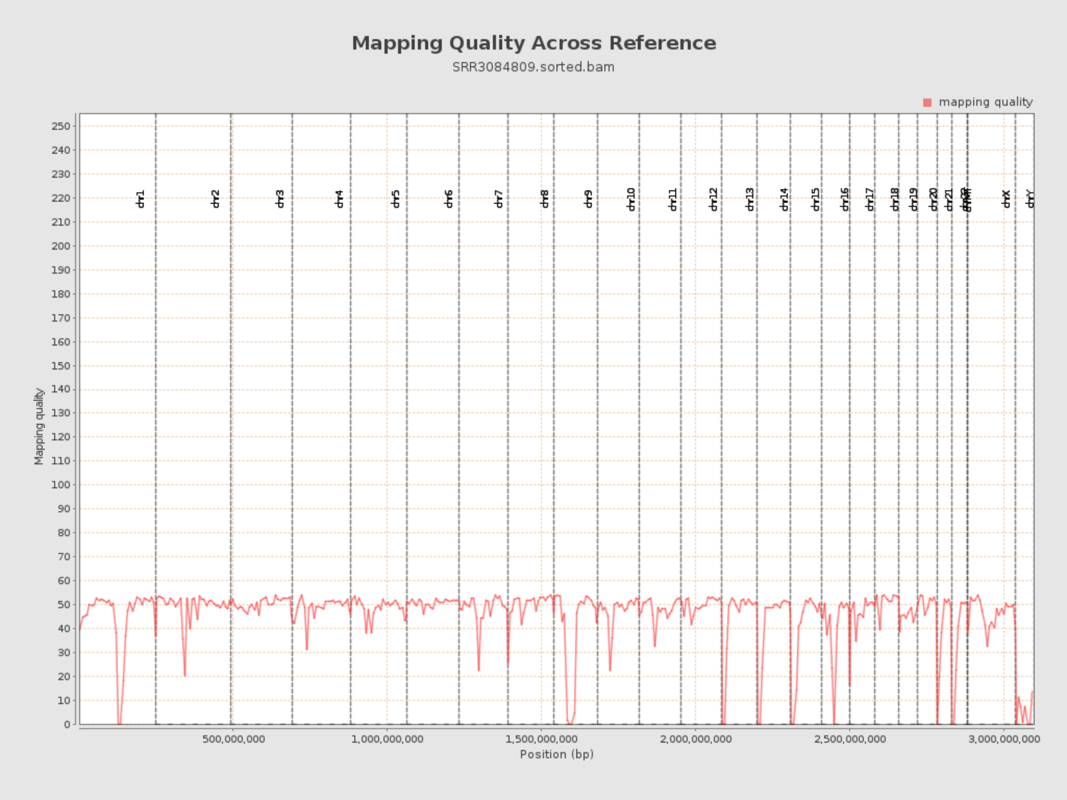
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram