Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:22:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084260.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_SRR3084260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:22:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,233,923
Mapped reads	1,841,020 / 82.41%
Unmapped reads	392,903 / 17.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,953 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	63,408 / 2.84%
Duplication rate	2.85%
Clipped reads	1,049,774 / 46.99%

2.2. ACGT Content

Number/percentage of A's	33,518,784 / 28.76%
Number/percentage of C's	21,886,829 / 18.78%
Number/percentage of T's	35,664,453 / 30.6%
Number/percentage of G's	25,480,229 / 21.86%
Number/percentage of N's	1,227 / 0%
GC Percentage	40.64%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.2779

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

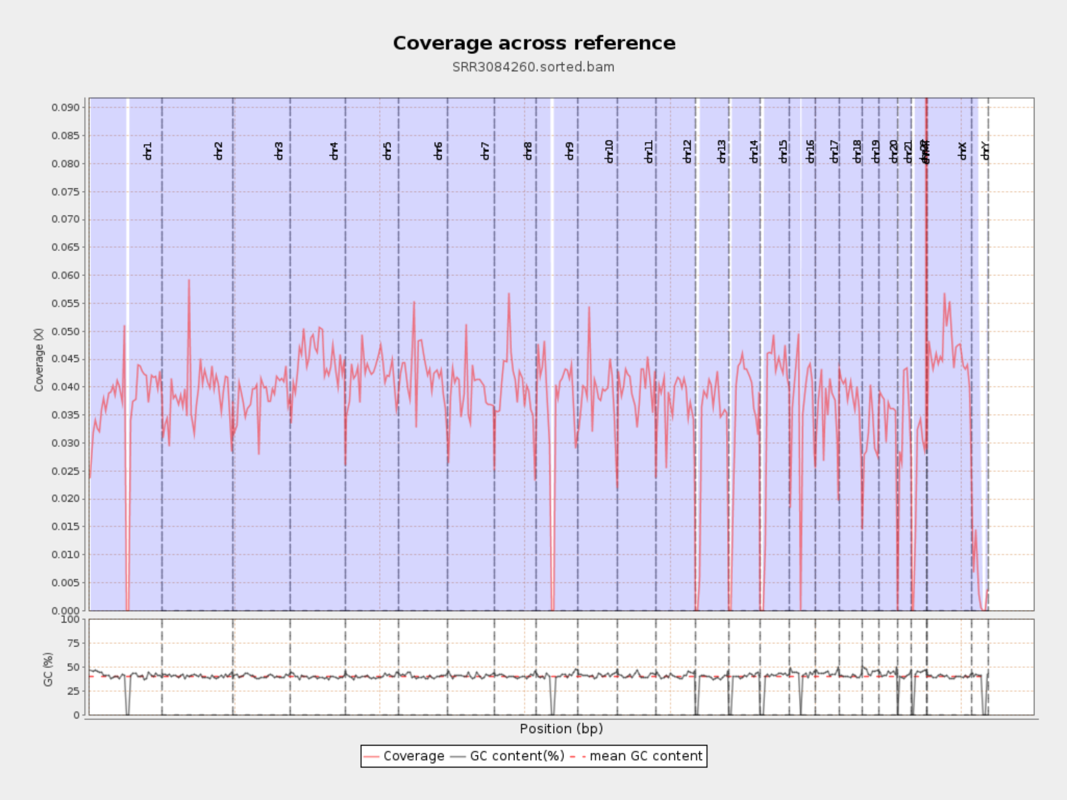
General error rate	0.84%
Mismatches	966,048
Insertions	8,680
Mapped reads with at least one insertion	0.47%
Deletions	24,326
Mapped reads with at least one deletion	1.31%
Homopolymer indels	46.6%

2.6. Chromosome stats

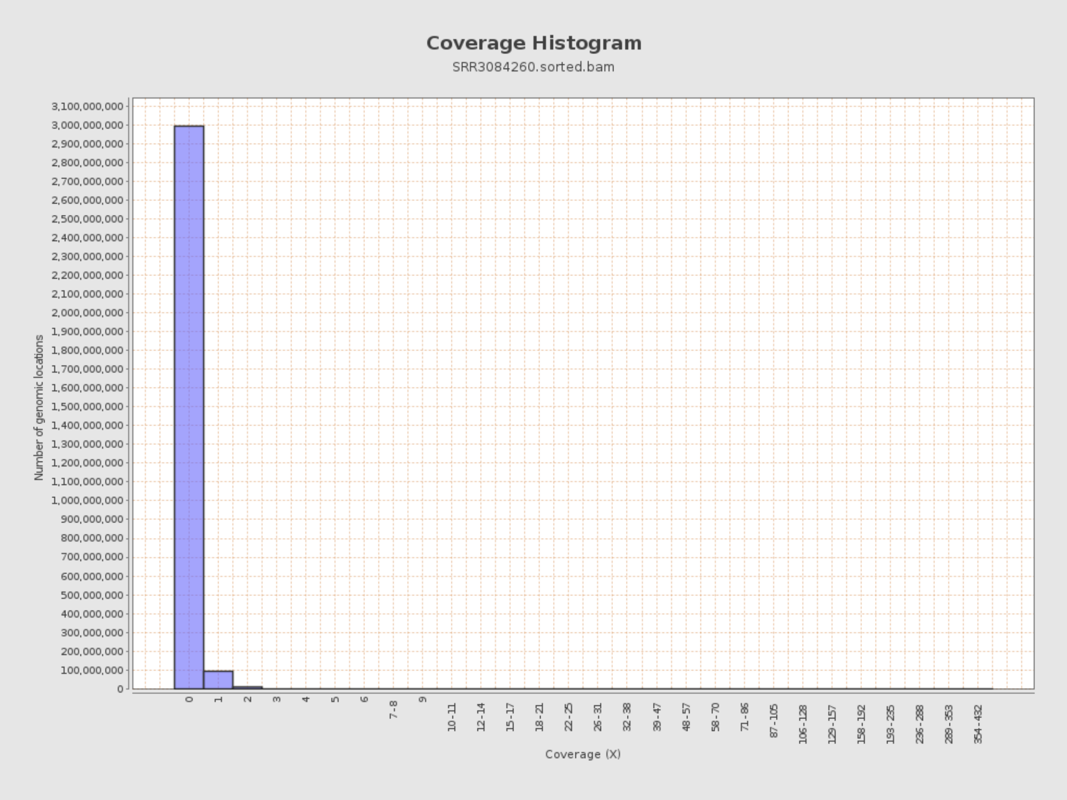
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9044623	0.0363	0.4105
chr2	243199373	9415876	0.0387	0.3258
chr3	198022430	7589369	0.0383	0.215
chr4	191154276	8543902	0.0447	0.2373
chr5	180915260	7632849	0.0422	0.2257
chr6	171115067	7265323	0.0425	0.261
chr7	159138663	6271535	0.0394	0.3262

chr8	146364022	5836733	0.0399	0.3154
chr9	141213431	5098508	0.0361	0.2643
chr10	135534747	5291998	0.039	0.2861
chr11	135006516	5369872	0.0398	0.2556
chr12	133851895	5012182	0.0374	0.2149
chr13	115169878	3609368	0.0313	0.1953
chr14	107349540	3628830	0.0338	0.2111
chr15	102531392	3694784	0.036	0.2124
chr16	90354753	3229769	0.0357	0.2271
chr17	81195210	2878000	0.0354	0.2293
chr18	78077248	3014106	0.0386	0.4609
chr19	59128983	1828905	0.0309	0.3343
chr20	63025520	2231465	0.0354	0.2124
chr21	48129895	1509412	0.0314	0.2032
chr22	51304566	1135115	0.0221	0.1631
chrMT	16571	59331	3.5804	2.6419
chrX	155270560	7108982	0.0458	0.2514
chrY	59373566	288804	0.0049	0.1019

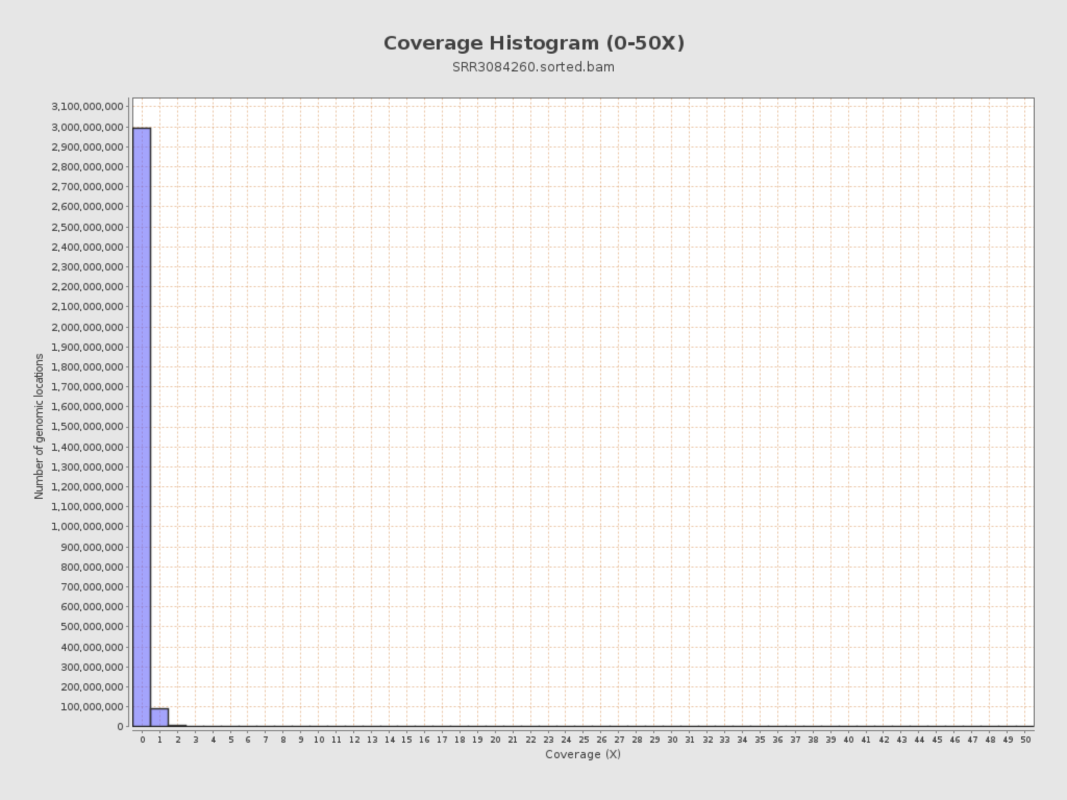
3. Results : Coverage across reference



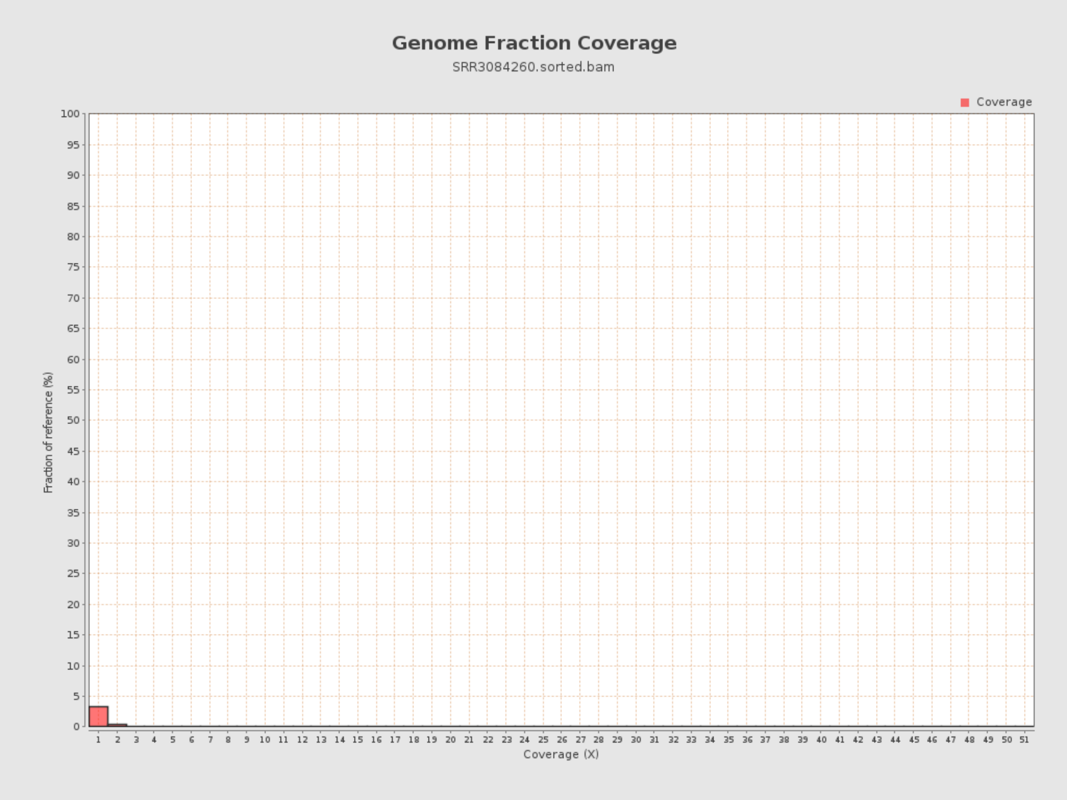
4. Results : Coverage Histogram



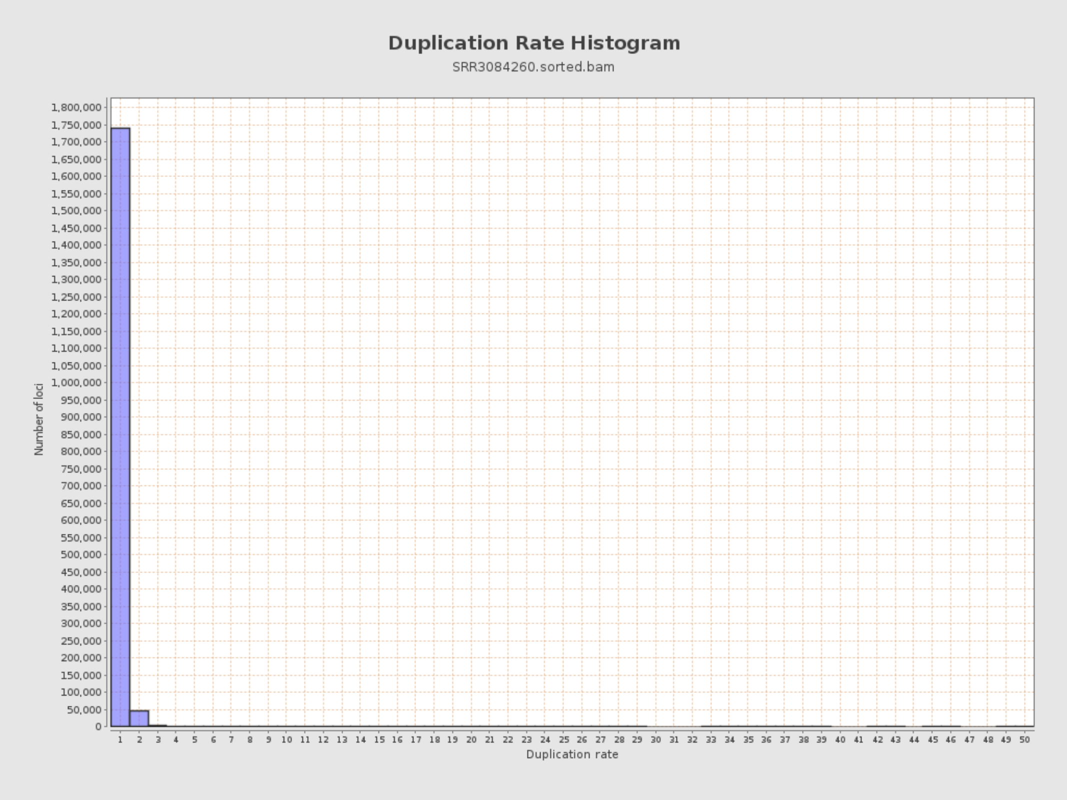
5. Results : Coverage Histogram (0-50X)



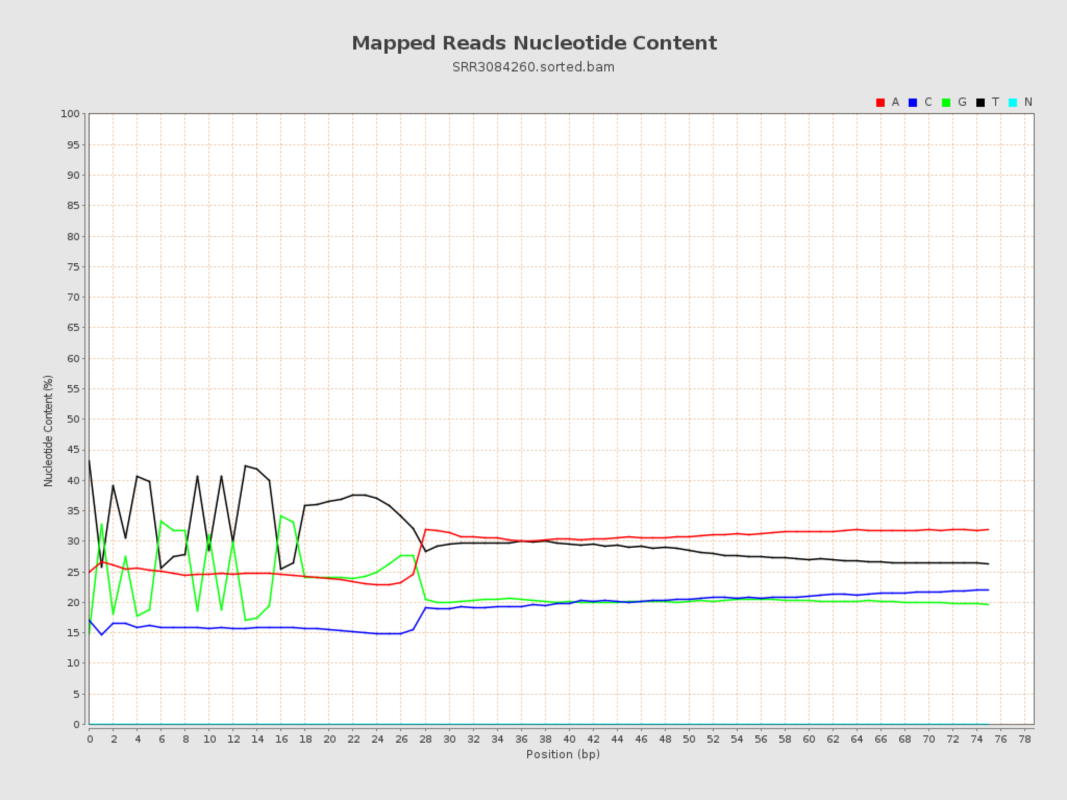
6. Results : Genome Fraction Coverage



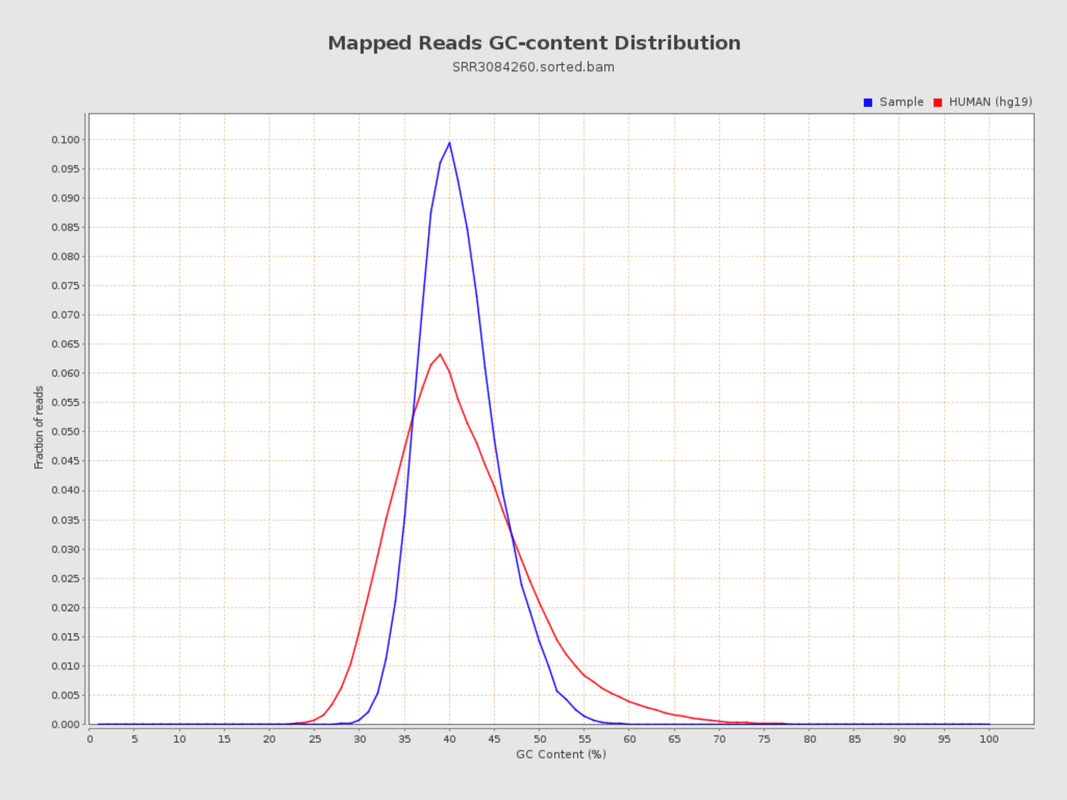
7. Results : Duplication Rate Histogram



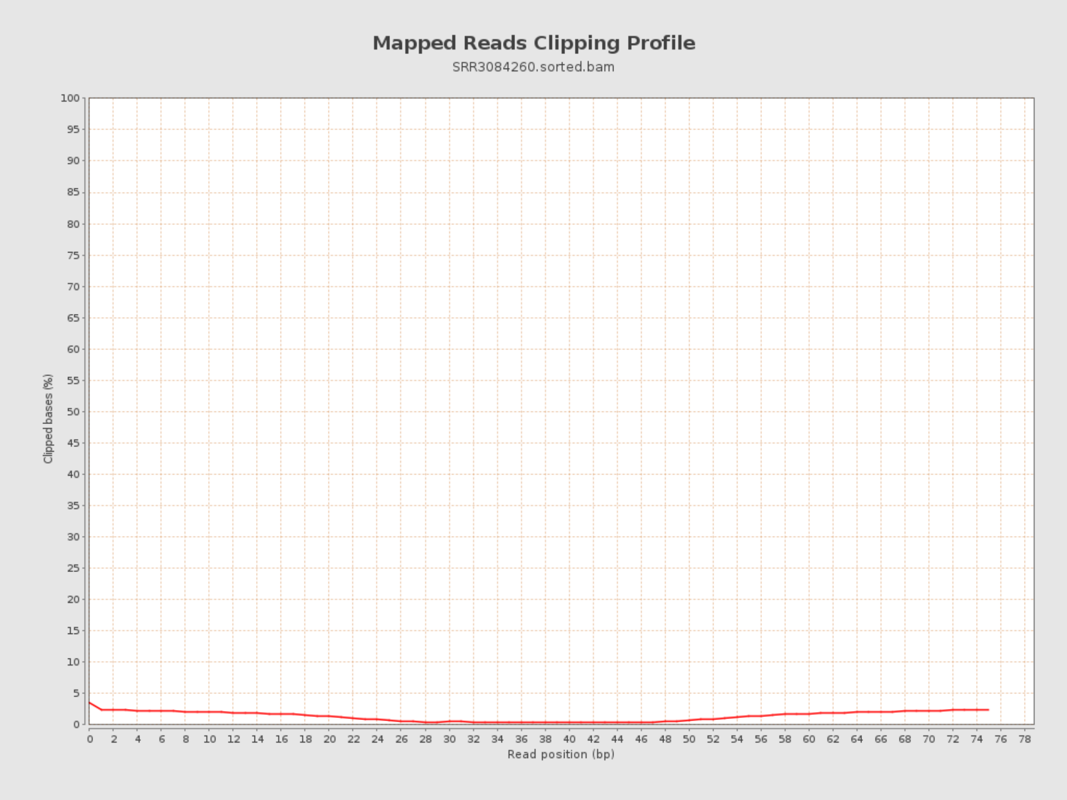
8. Results : Mapped Reads Nucleotide Content



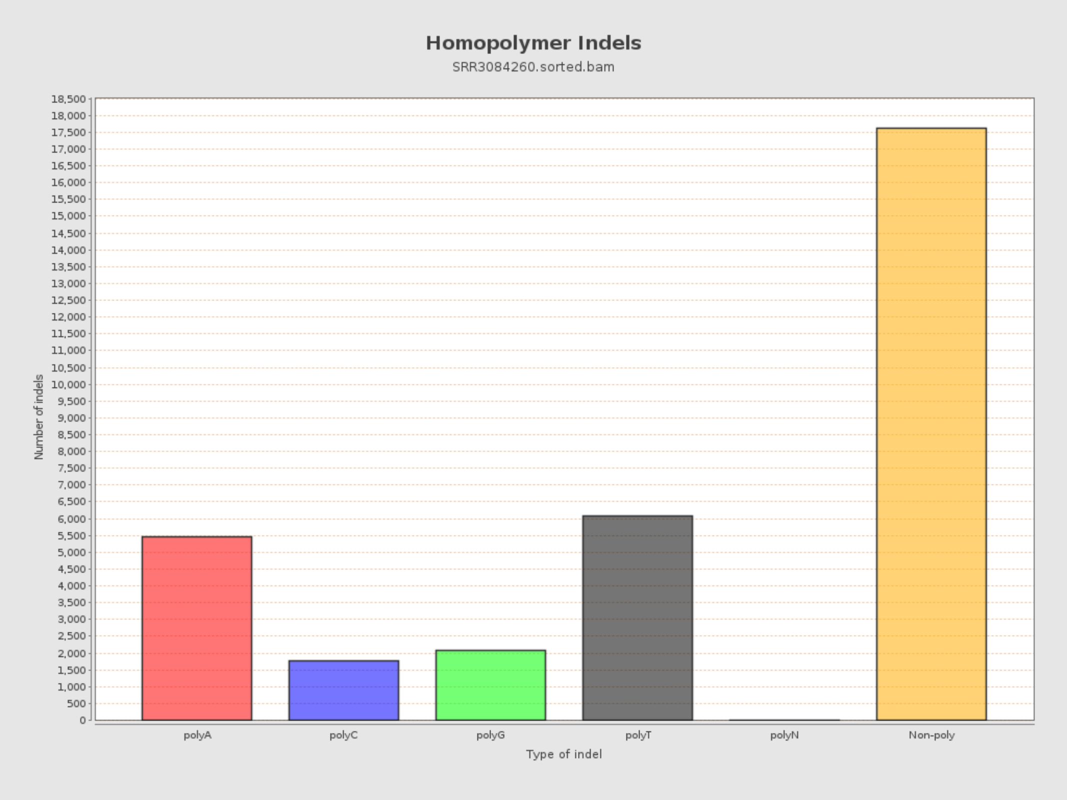
9. Results : Mapped Reads GC-content Distribution



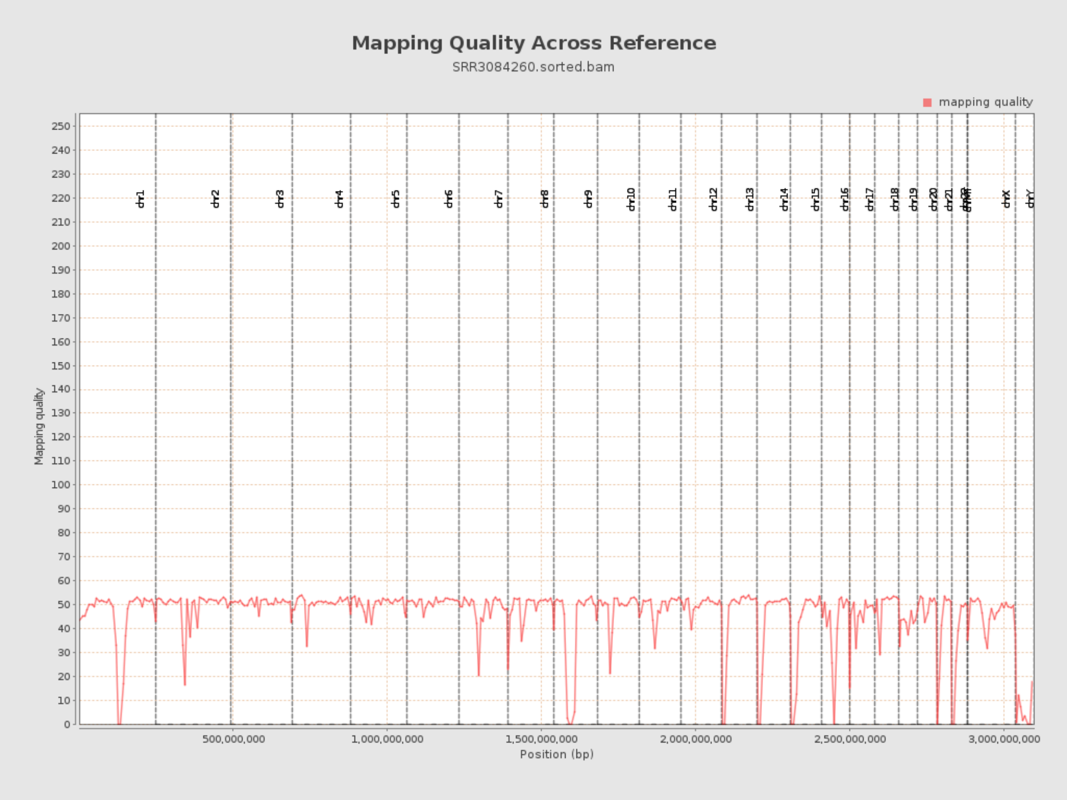
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram