Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 20:59:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084972.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_SRR3084972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084972.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 20:59:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084972.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,765,097
Mapped reads	2,513,474 / 90.9%
Unmapped reads	251,623 / 9.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,375 / 0.88%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	100,506 / 3.63%
Duplication rate	2.58%
Clipped reads	880,264 / 31.83%

2.2. ACGT Content

Number/percentage of A's	51,361,780 / 29.49%
Number/percentage of C's	32,264,910 / 18.53%
Number/percentage of T's	54,363,460 / 31.21%
Number/percentage of G's	36,145,501 / 20.75%
Number/percentage of N's	24,934 / 0.01%
GC Percentage	39.28%

2.3. Coverage

Mean	0.0563

Standard Deviation	0.6138

2.4. Mapping Quality

Mean Mapping Quality	46.57

2.5. Mismatches and indels

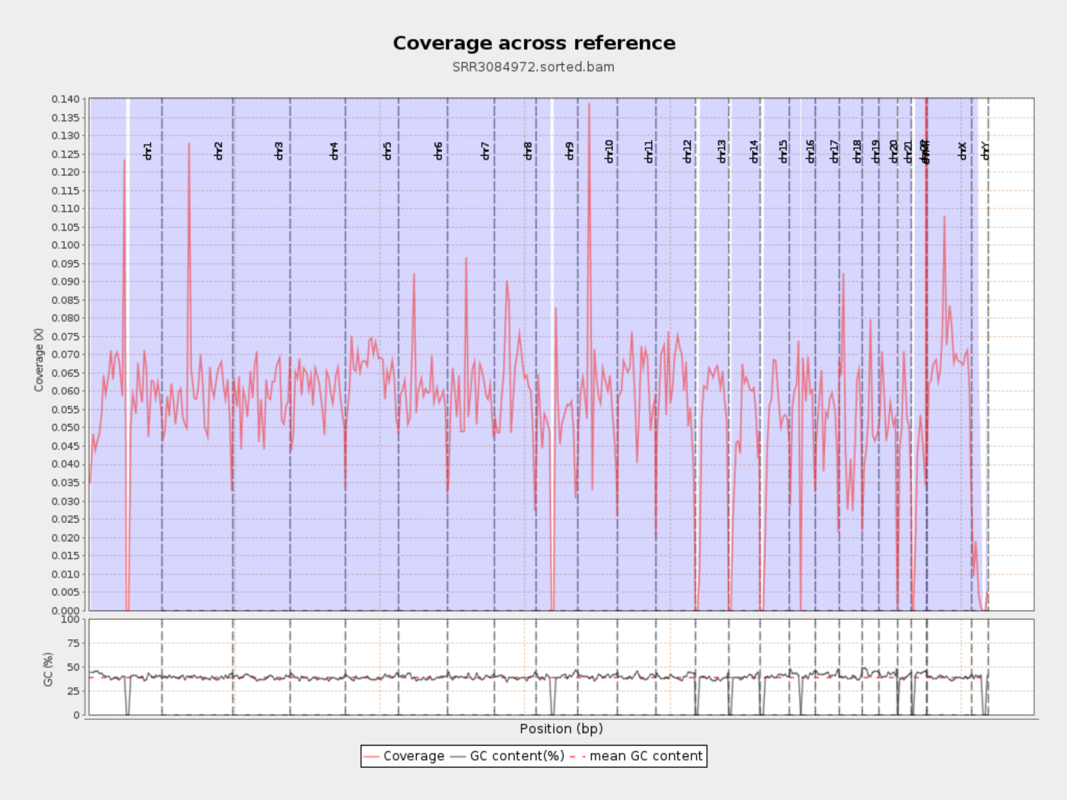
General error rate	0.89%
Mismatches	1,524,410
Insertions	15,192
Mapped reads with at least one insertion	0.6%
Deletions	42,902
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.85%

2.6. Chromosome stats

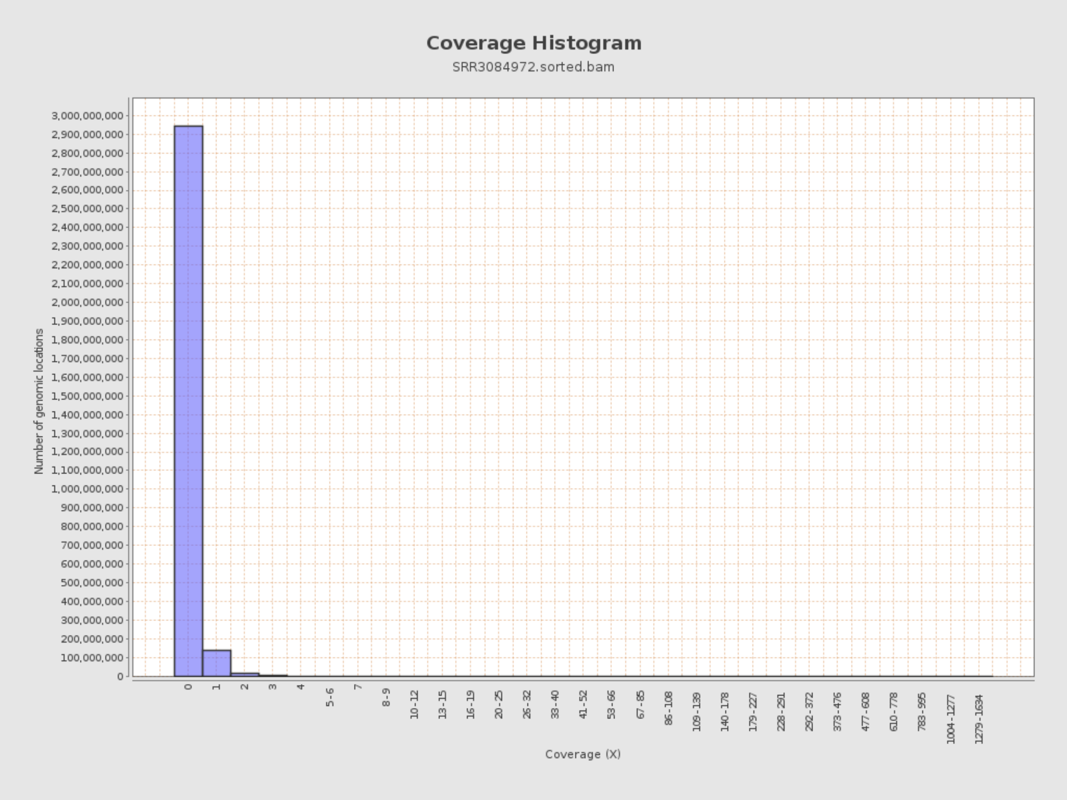
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14228207	0.0571	1.2597
chr2	243199373	14592356	0.06	0.6237
chr3	198022430	11610602	0.0586	0.3006
chr4	191154276	11469249	0.06	0.2808
chr5	180915260	11959753	0.0661	0.2892
chr6	171115067	10309753	0.0603	0.4132
chr7	159138663	9536974	0.0599	0.4977

chr8	146364022	8980083	0.0614	1.0287
chr9	141213431	6740706	0.0477	0.5392
chr10	135534747	8391494	0.0619	0.8373
chr11	135006516	8257137	0.0612	0.4897
chr12	133851895	8223031	0.0614	0.2846
chr13	115169878	5864015	0.0509	0.2454
chr14	107349540	4936193	0.046	0.276
chr15	102531392	4640618	0.0453	0.2355
chr16	90354753	4839090	0.0536	0.3763
chr17	81195210	4150111	0.0511	0.3359
chr18	78077248	4136196	0.053	1.1361
chr19	59128983	2951461	0.0499	0.9049
chr20	63025520	3362721	0.0534	0.2802
chr21	48129895	2241599	0.0466	0.2672
chr22	51304566	1597885	0.0311	0.1926
chrMT	16571	29911	1.805	1.639
chrX	155270560	10785867	0.0695	0.3732
chrY	59373566	396201	0.0067	0.1307

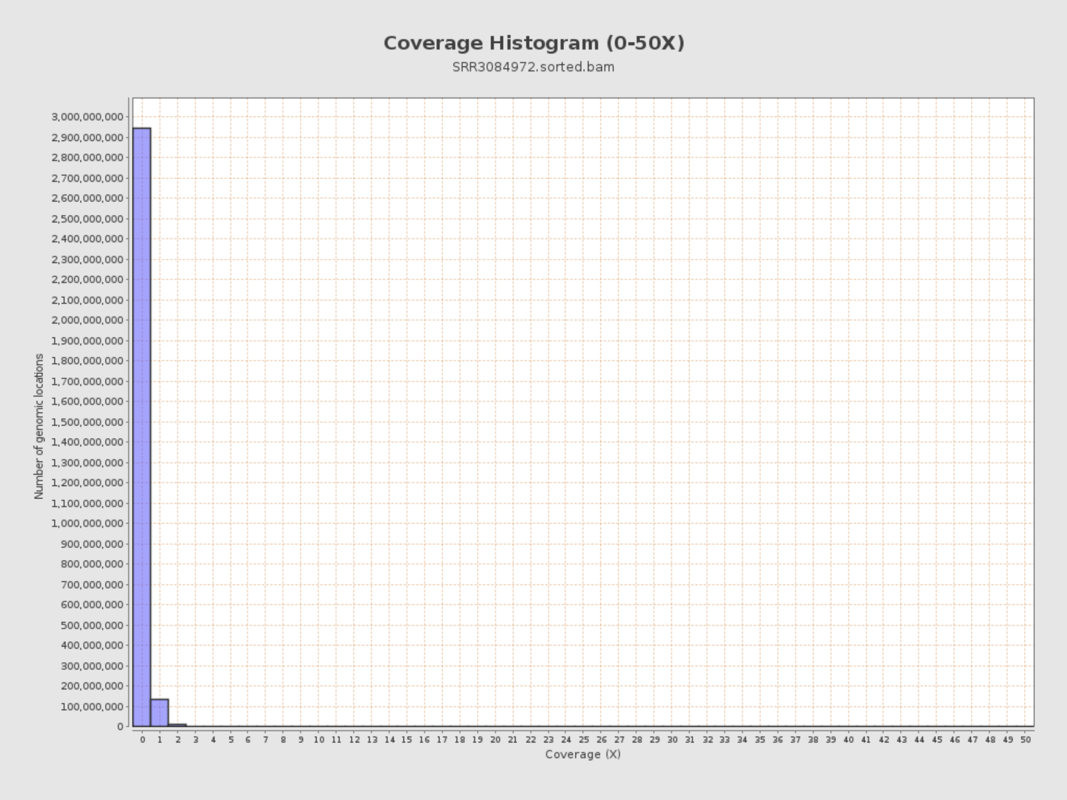
3. Results : Coverage across reference



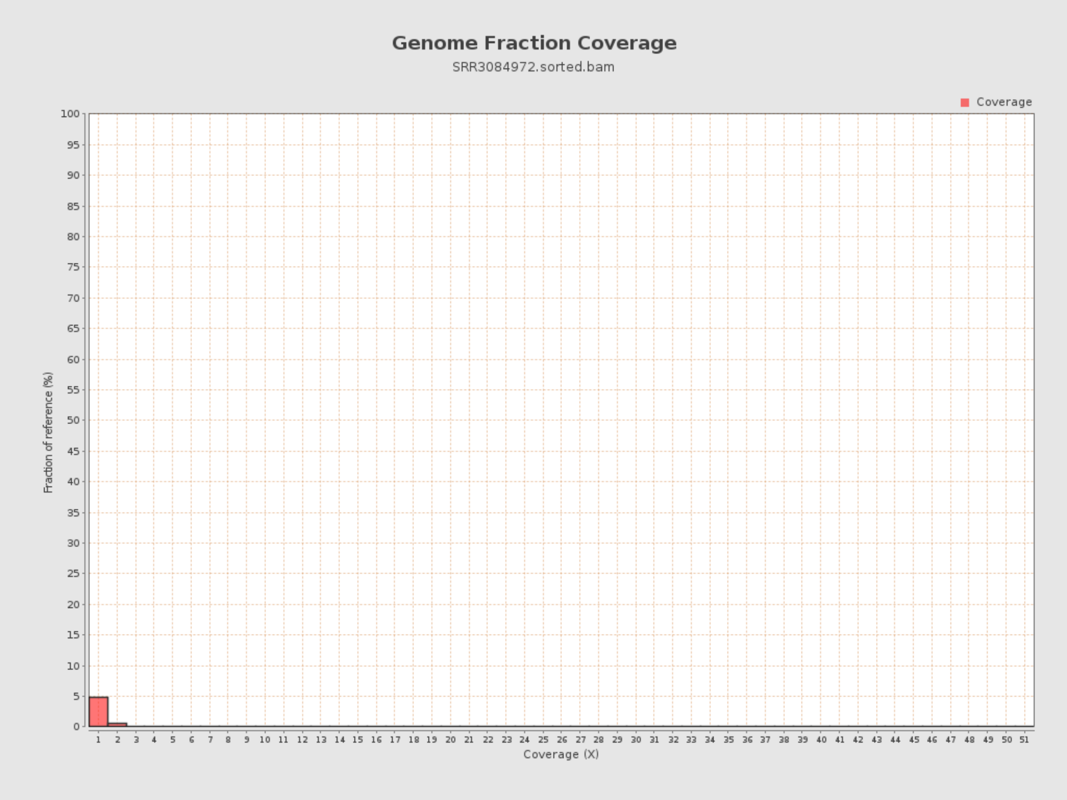
4. Results : Coverage Histogram



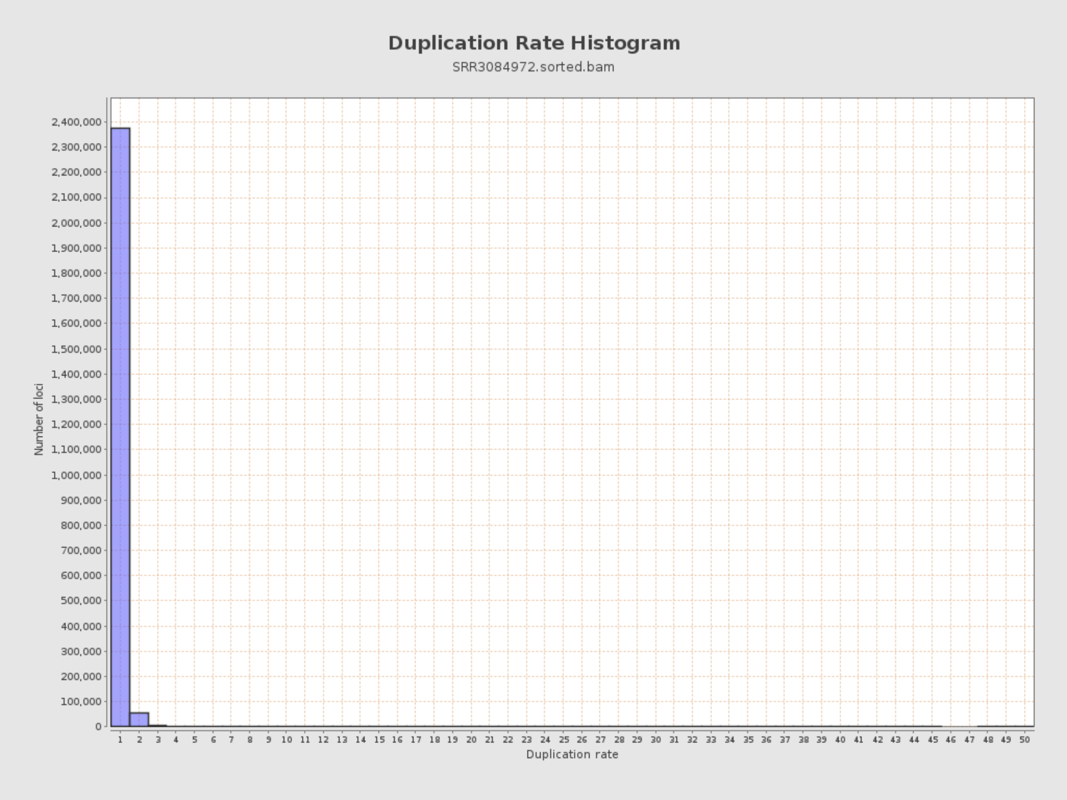
5. Results : Coverage Histogram (0-50X)



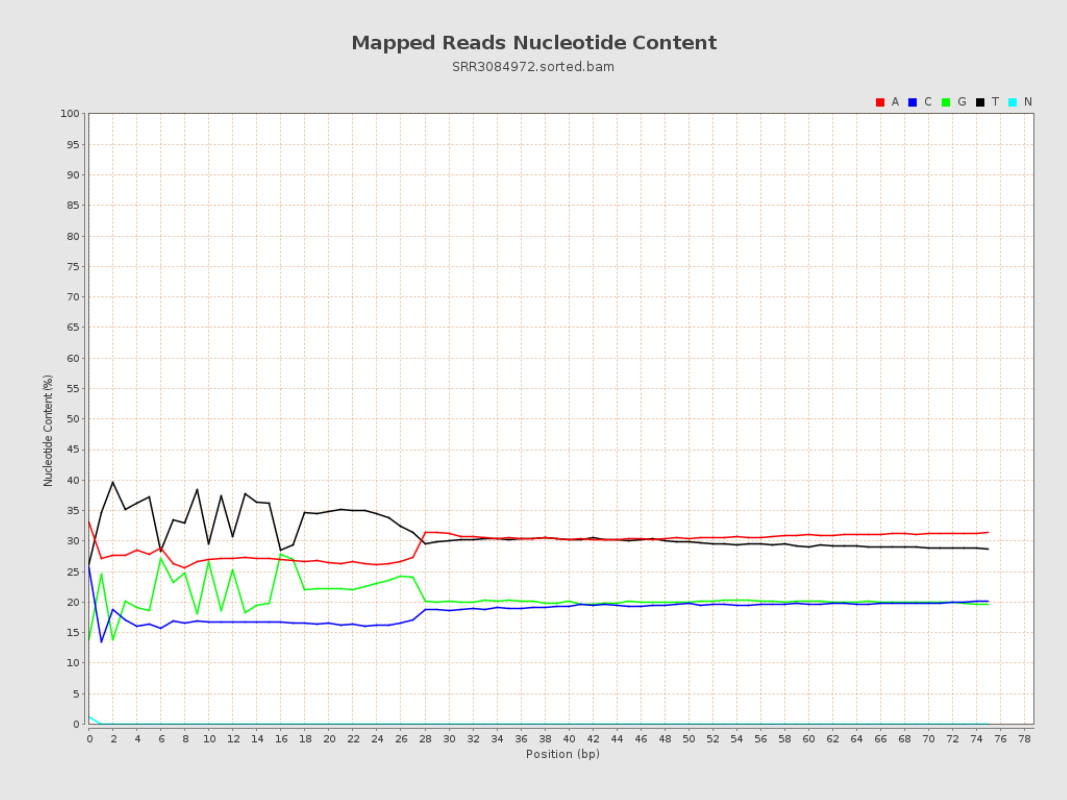
6. Results : Genome Fraction Coverage



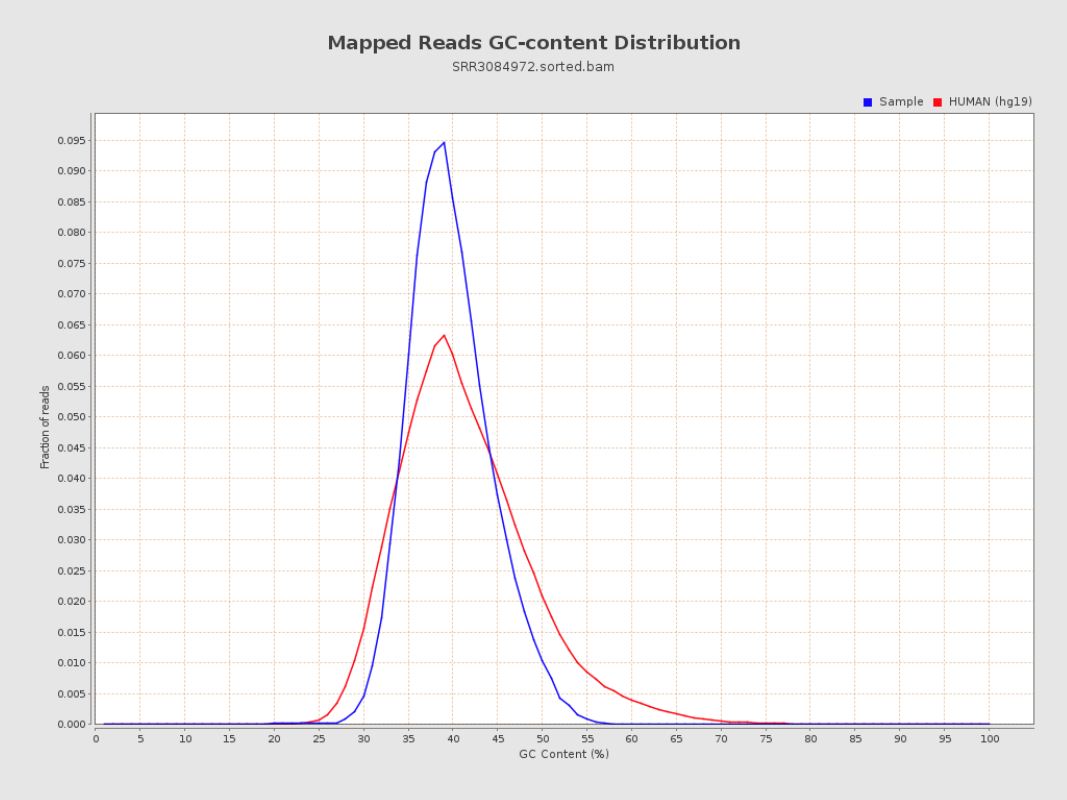
7. Results : Duplication Rate Histogram



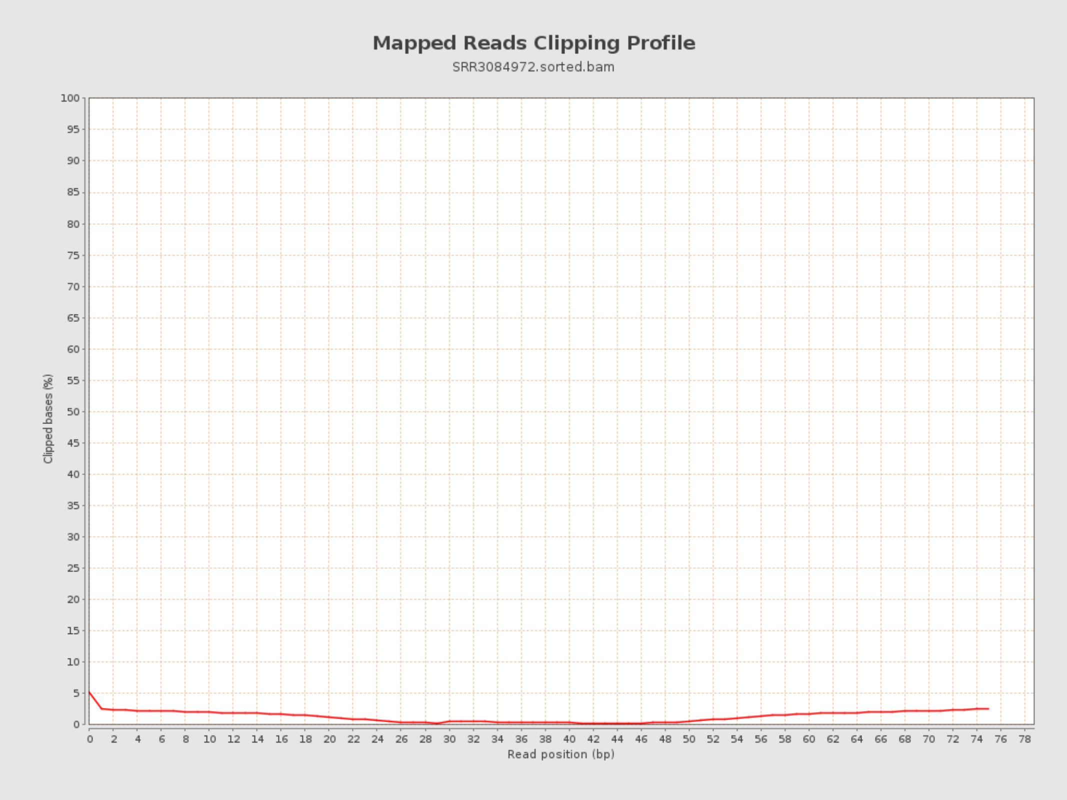
8. Results : Mapped Reads Nucleotide Content



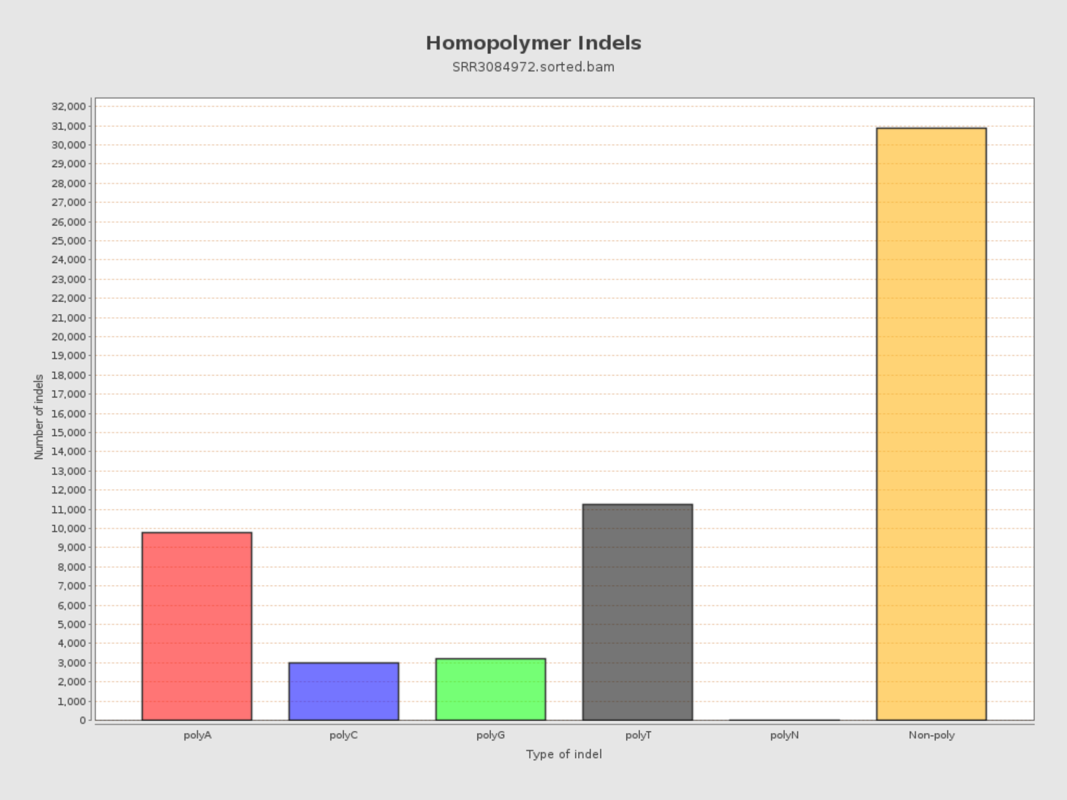
9. Results : Mapped Reads GC-content Distribution



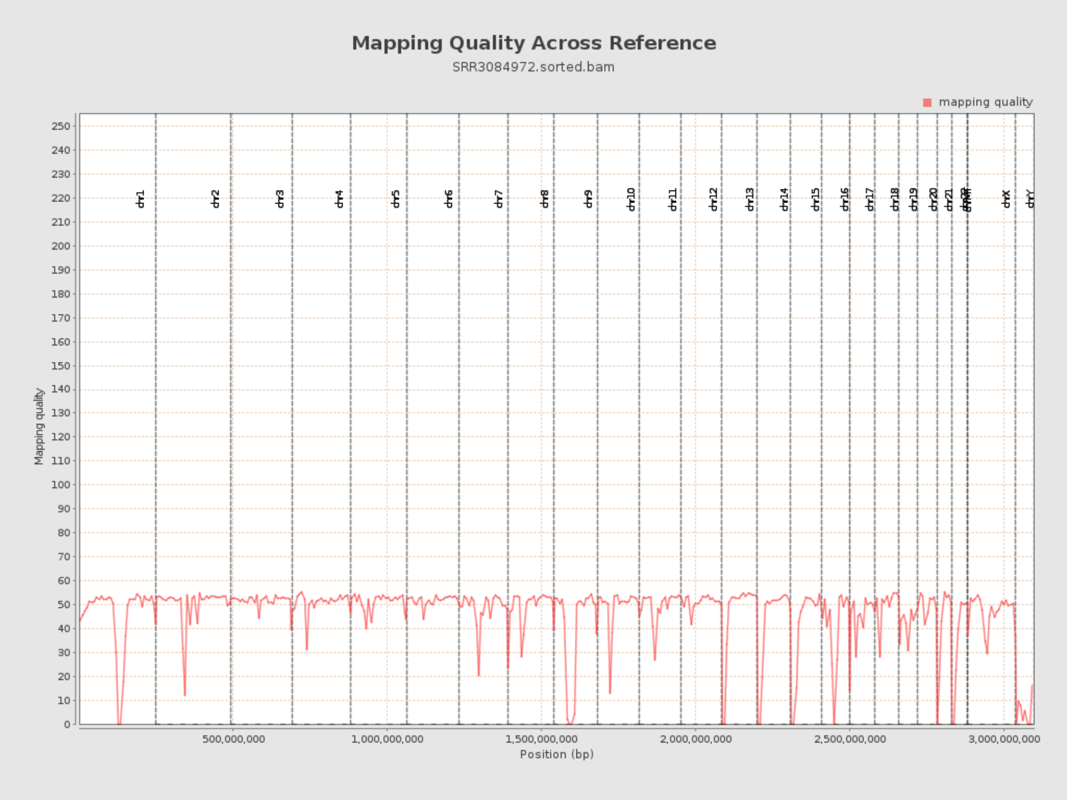
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram