Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 08:14:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472818.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_SRR3472818 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472818.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 08:14:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472818.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,000,000
Mapped reads	3,424,383 / 85.61%
Unmapped reads	575,617 / 14.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,108 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	106,724 / 2.67%
Duplication rate	2.2%
Clipped reads	1,735,336 / 43.38%

2.2. ACGT Content

Number/percentage of A's	60,000,518 / 26.92%
Number/percentage of C's	44,683,357 / 20.05%
Number/percentage of T's	66,040,476 / 29.63%
Number/percentage of G's	52,130,010 / 23.39%
Number/percentage of N's	3,898 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.072

Standard Deviation	0.4712

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

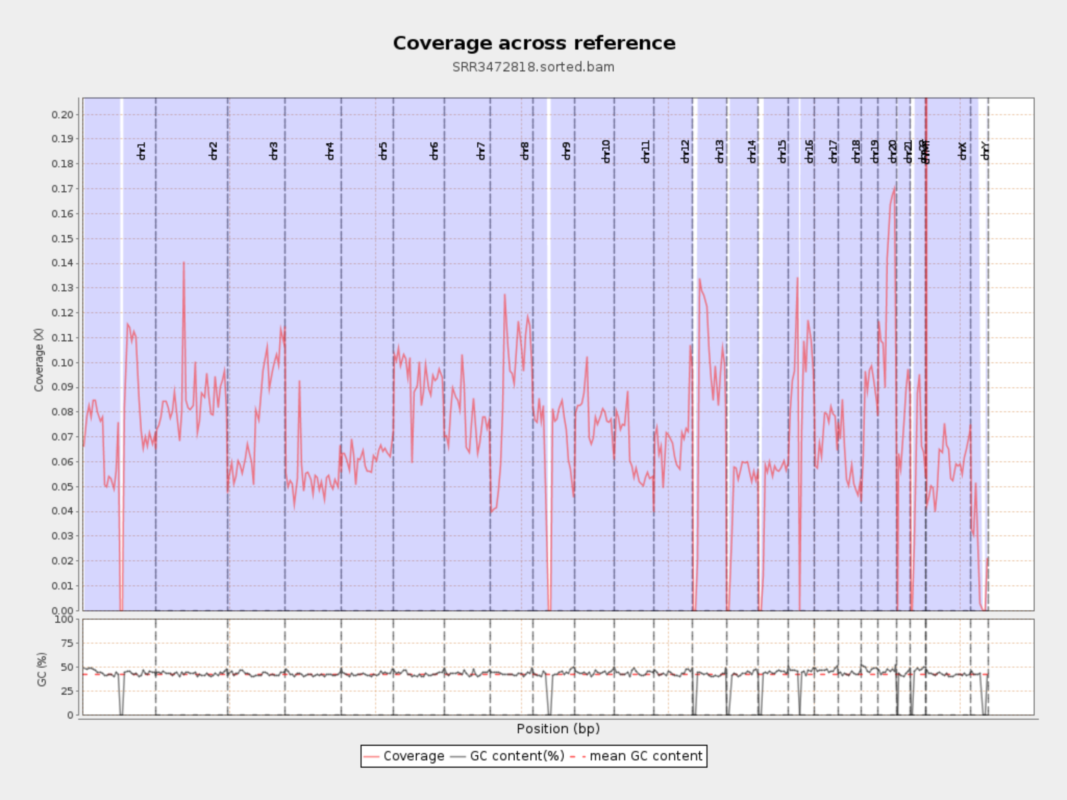
General error rate	0.85%
Mismatches	1,869,168
Insertions	17,349
Mapped reads with at least one insertion	0.5%
Deletions	50,427
Mapped reads with at least one deletion	1.46%
Homopolymer indels	45.07%

2.6. Chromosome stats

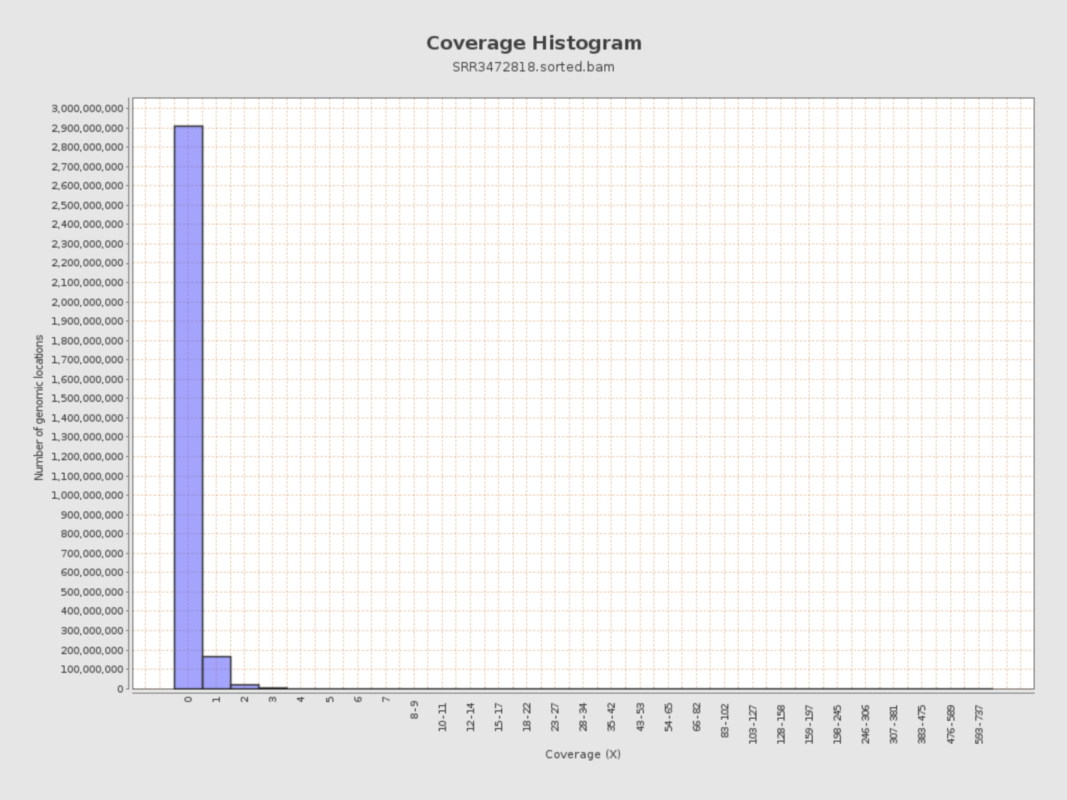
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17973036	0.0721	0.5982
chr2	243199373	20699812	0.0851	0.7099
chr3	198022430	15442794	0.078	0.3165
chr4	191154276	10279870	0.0538	0.3126
chr5	180915260	11171904	0.0618	0.2831
chr6	171115067	16023980	0.0936	0.3942
chr7	159138663	12329685	0.0775	0.5924

chr8	146364022	13037066	0.0891	0.4872
chr9	141213431	9143615	0.0648	0.5207
chr10	135534747	10674810	0.0788	0.4504
chr11	135006516	8472306	0.0628	0.5004
chr12	133851895	9321010	0.0696	0.3086
chr13	115169878	10208865	0.0886	0.3551
chr14	107349540	5096568	0.0475	0.3023
chr15	102531392	4717584	0.046	0.2662
chr16	90354753	8095647	0.0896	0.3972
chr17	81195210	5818752	0.0717	0.3534
chr18	78077248	4612044	0.0591	0.9849
chr19	59128983	5083991	0.086	0.5097
chr20	63025520	8397255	0.1332	0.4504
chr21	48129895	3377942	0.0702	0.3719
chr22	51304566	2736689	0.0533	0.2971
chrMT	16571	52235	3.1522	2.7015
chrX	155270560	8976096	0.0578	0.3334
chrY	59373566	1205090	0.0203	0.242

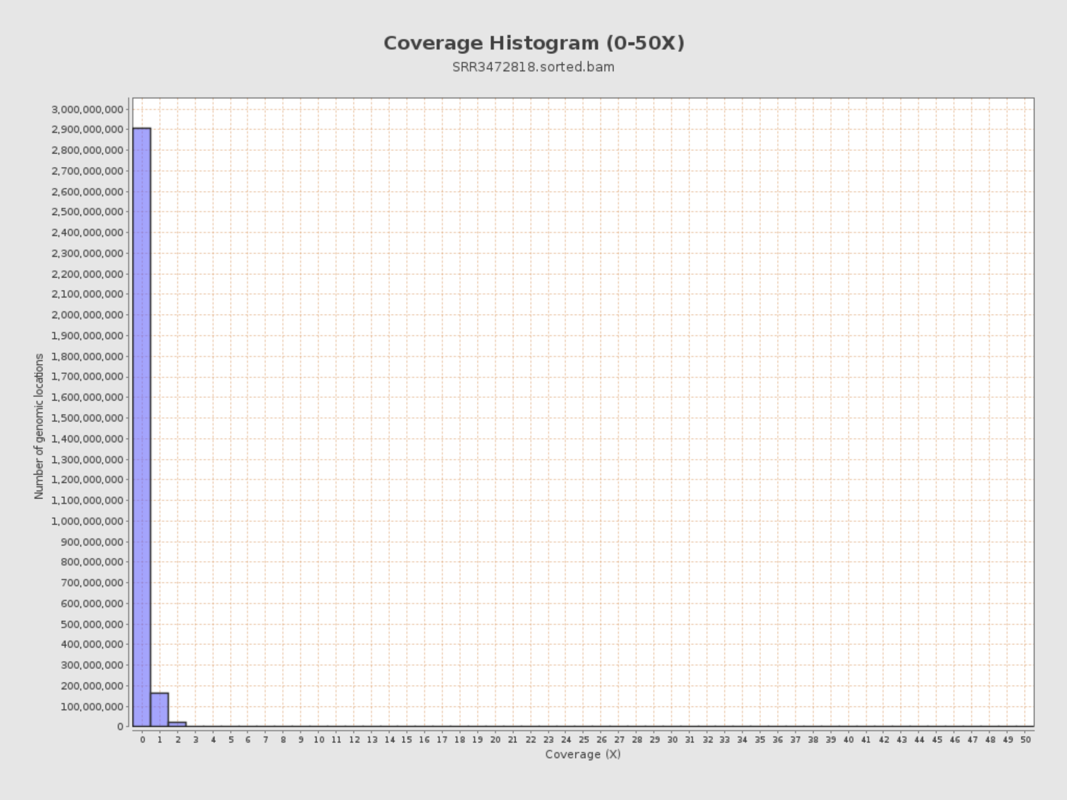
3. Results : Coverage across reference



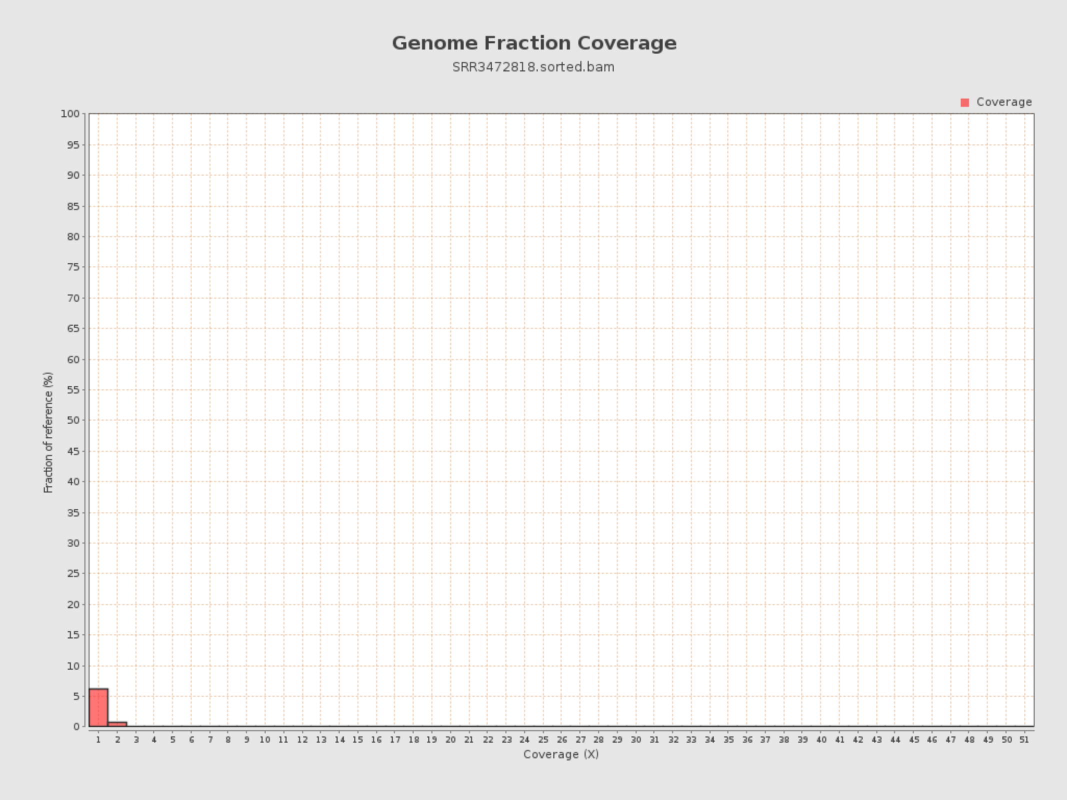
4. Results : Coverage Histogram



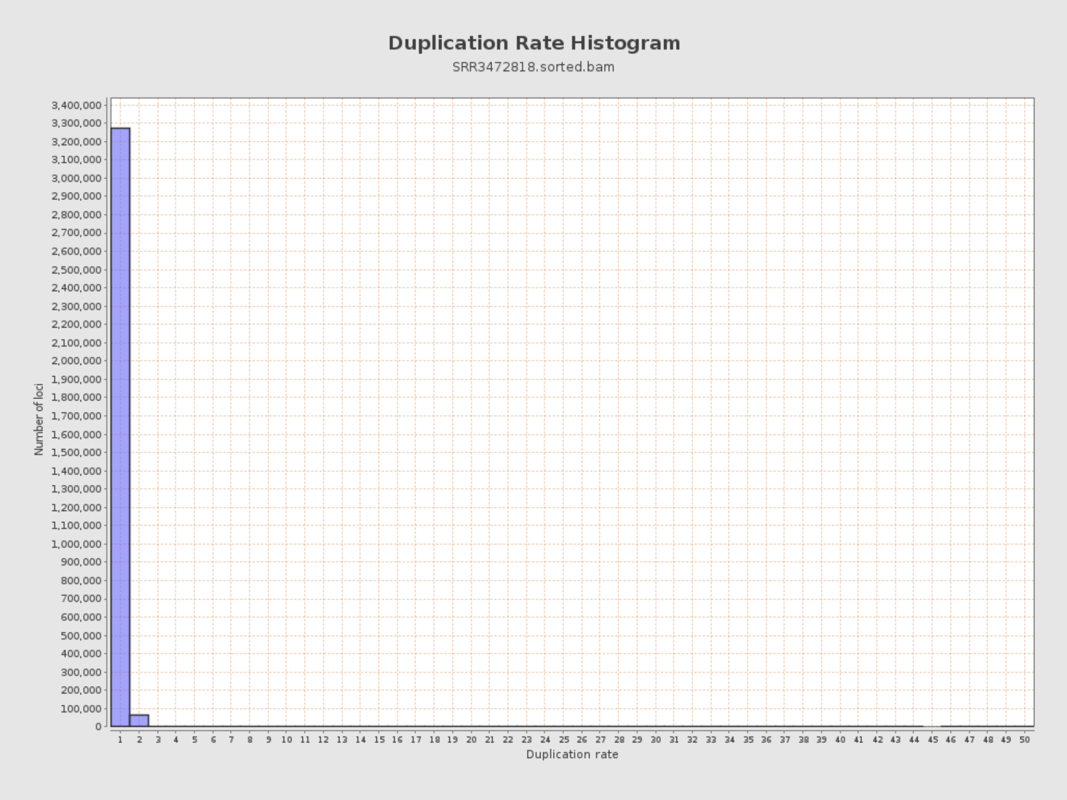
5. Results : Coverage Histogram (0-50X)



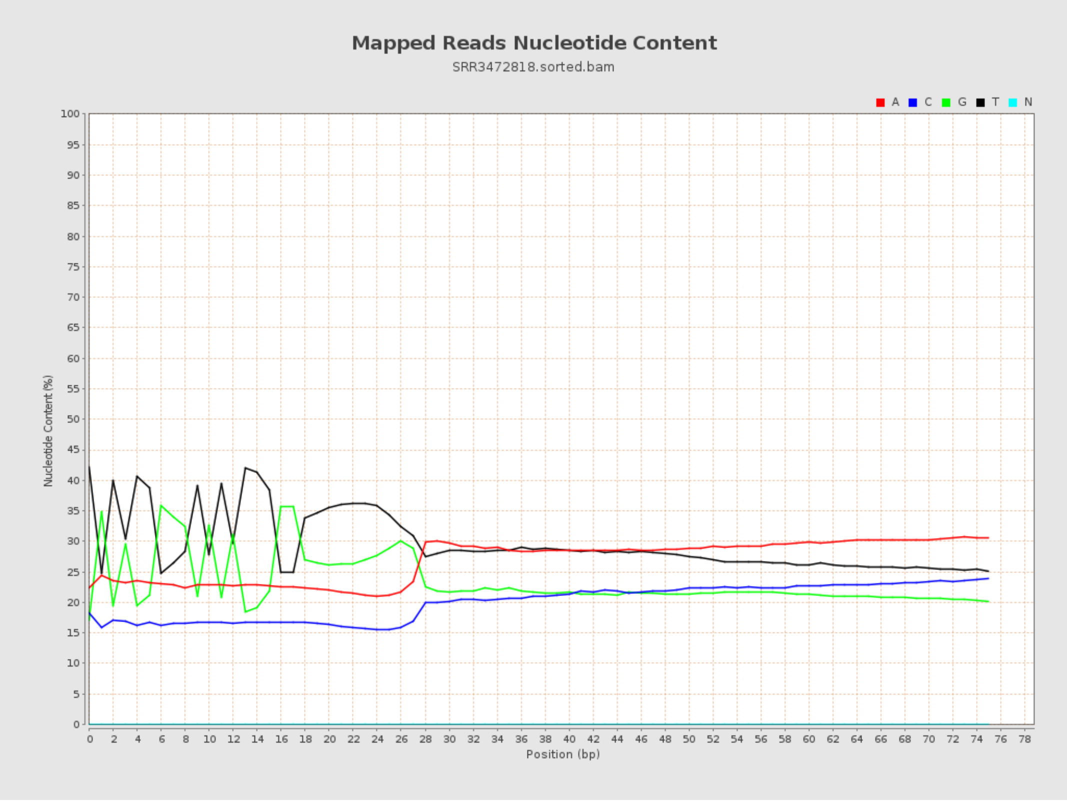
6. Results : Genome Fraction Coverage



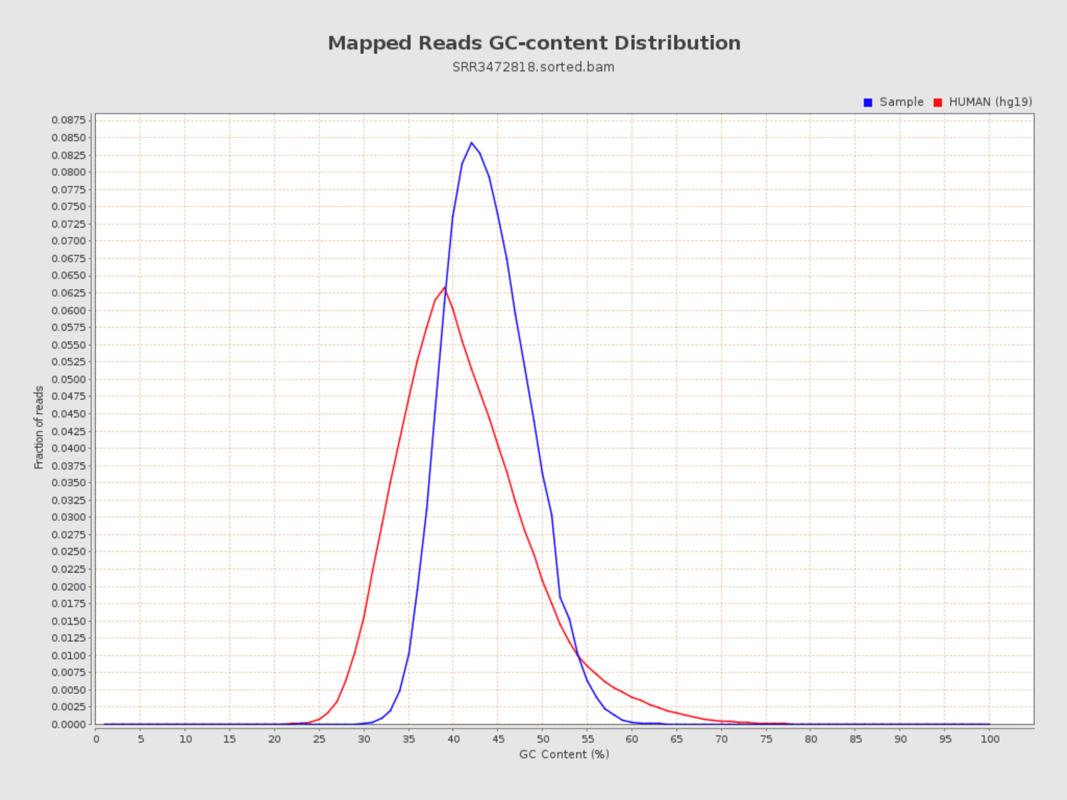
7. Results : Duplication Rate Histogram



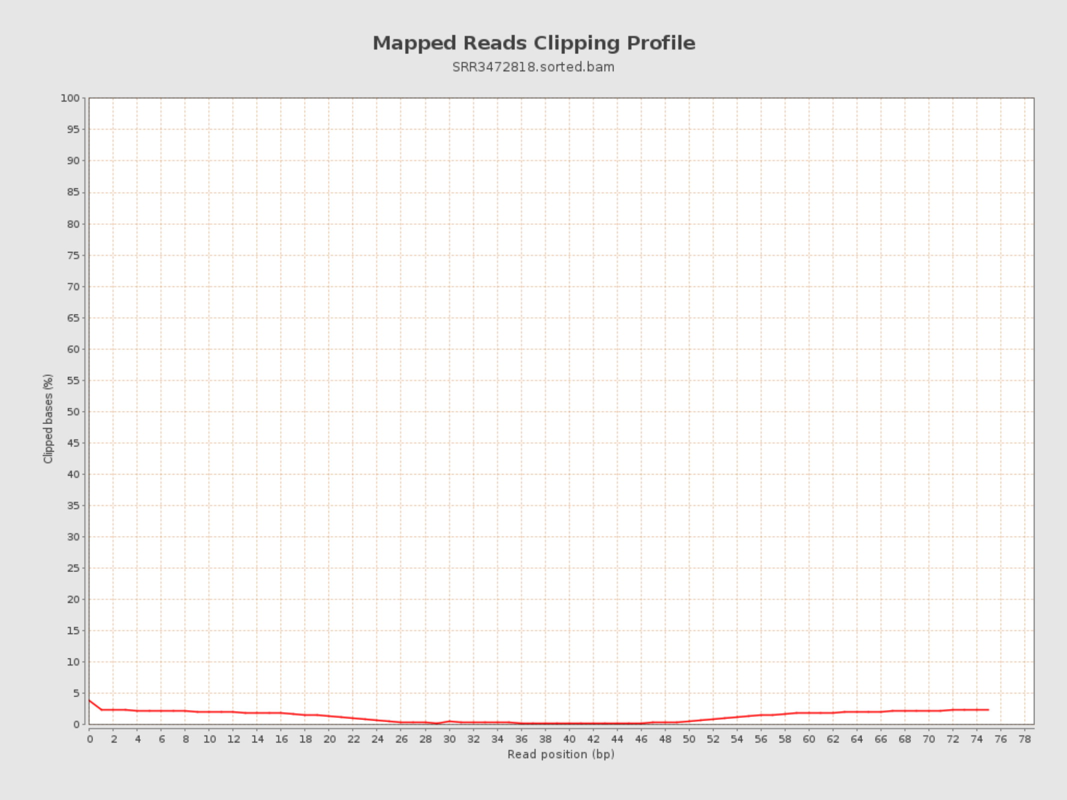
8. Results : Mapped Reads Nucleotide Content



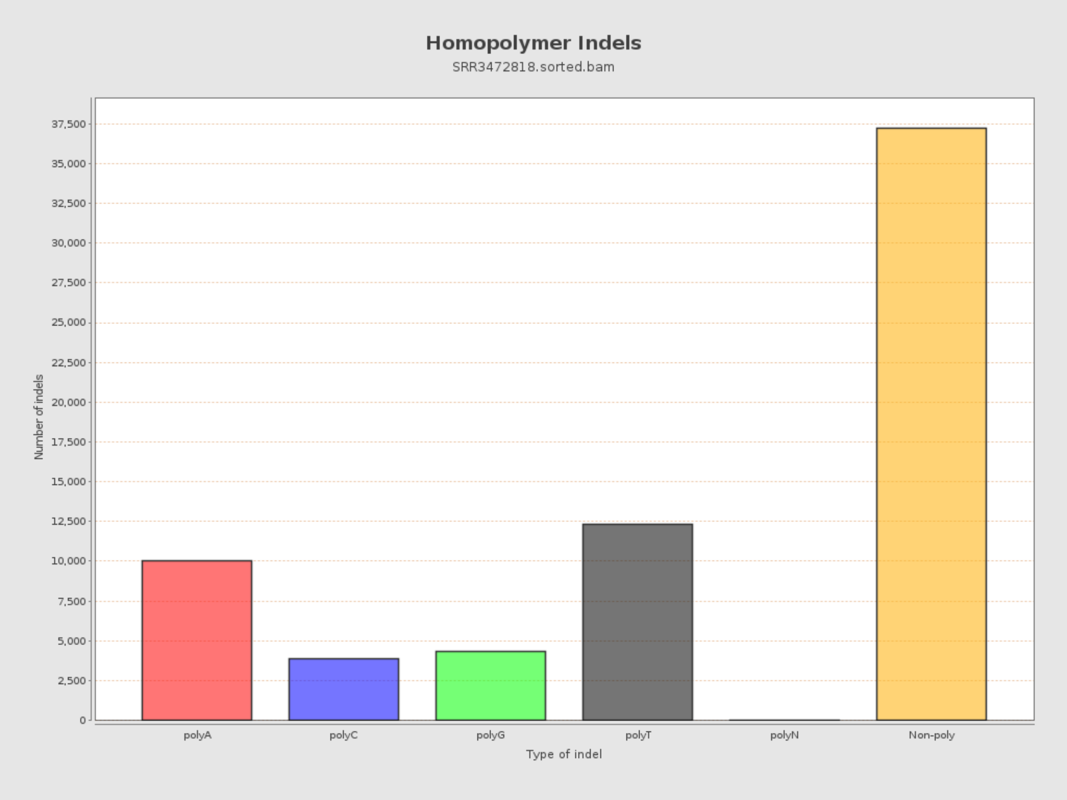
9. Results : Mapped Reads GC-content Distribution



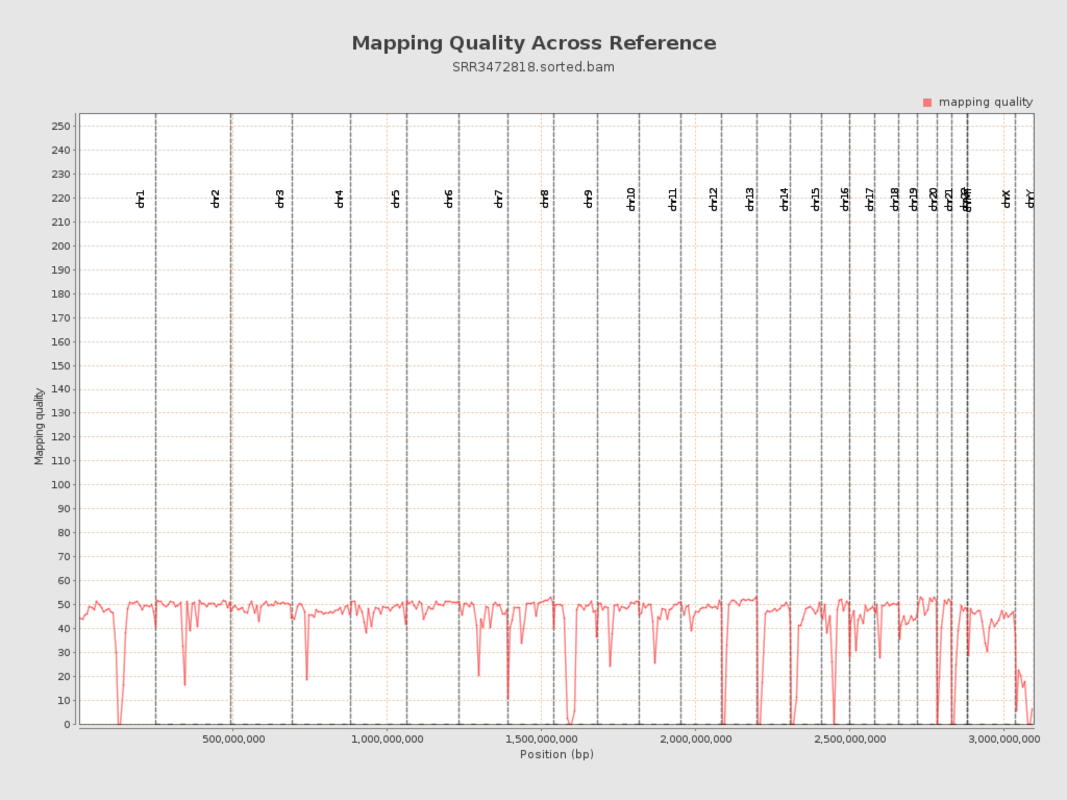
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram