Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:16:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472807.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_SRR3472807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472807.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:16:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,140,082
Mapped reads	1,576,857 / 73.68%
Unmapped reads	563,225 / 26.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,363 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	117,867 / 5.51%
Duplication rate	5.22%
Clipped reads	1,000,698 / 46.76%

2.2. ACGT Content

Number/percentage of A's	26,278,037 / 26.89%
Number/percentage of C's	19,613,374 / 20.07%
Number/percentage of T's	28,645,479 / 29.31%
Number/percentage of G's	23,198,867 / 23.74%
Number/percentage of N's	1,807 / 0%
GC Percentage	43.8%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3056

2.4. Mapping Quality

Mean Mapping Quality	42.29

2.5. Mismatches and indels

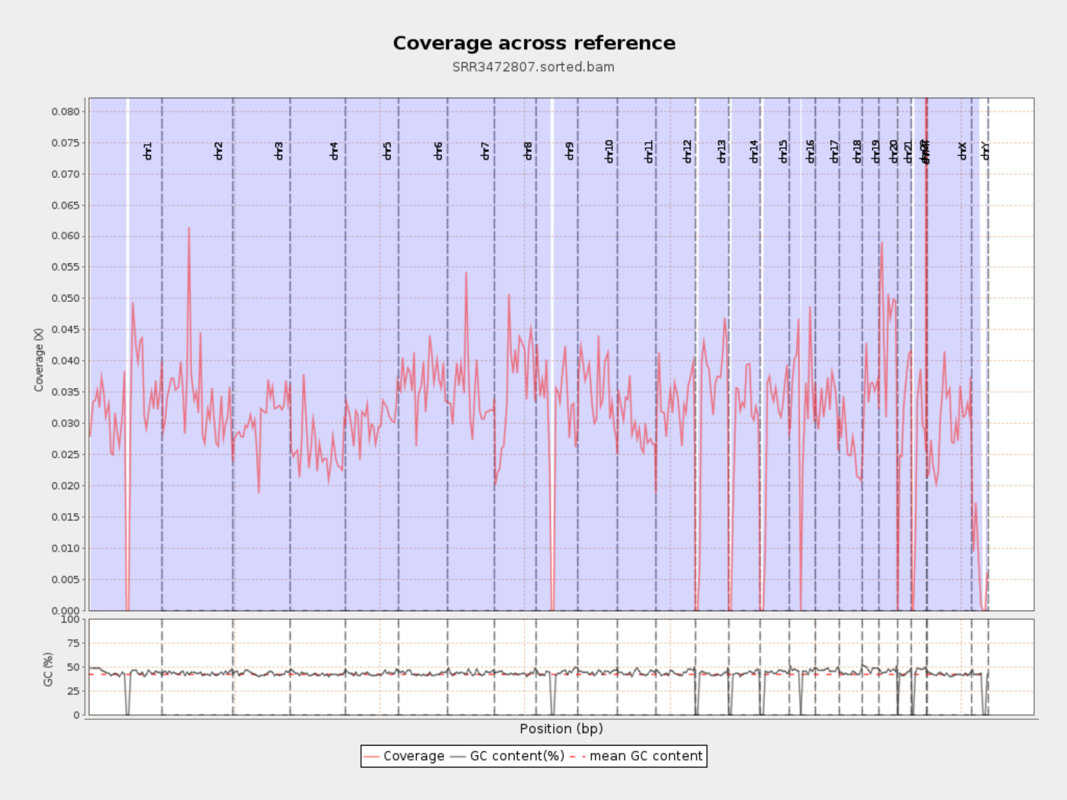
General error rate	0.94%
Mismatches	904,221
Insertions	7,729
Mapped reads with at least one insertion	0.49%
Deletions	26,447
Mapped reads with at least one deletion	1.66%
Homopolymer indels	45.19%

2.6. Chromosome stats

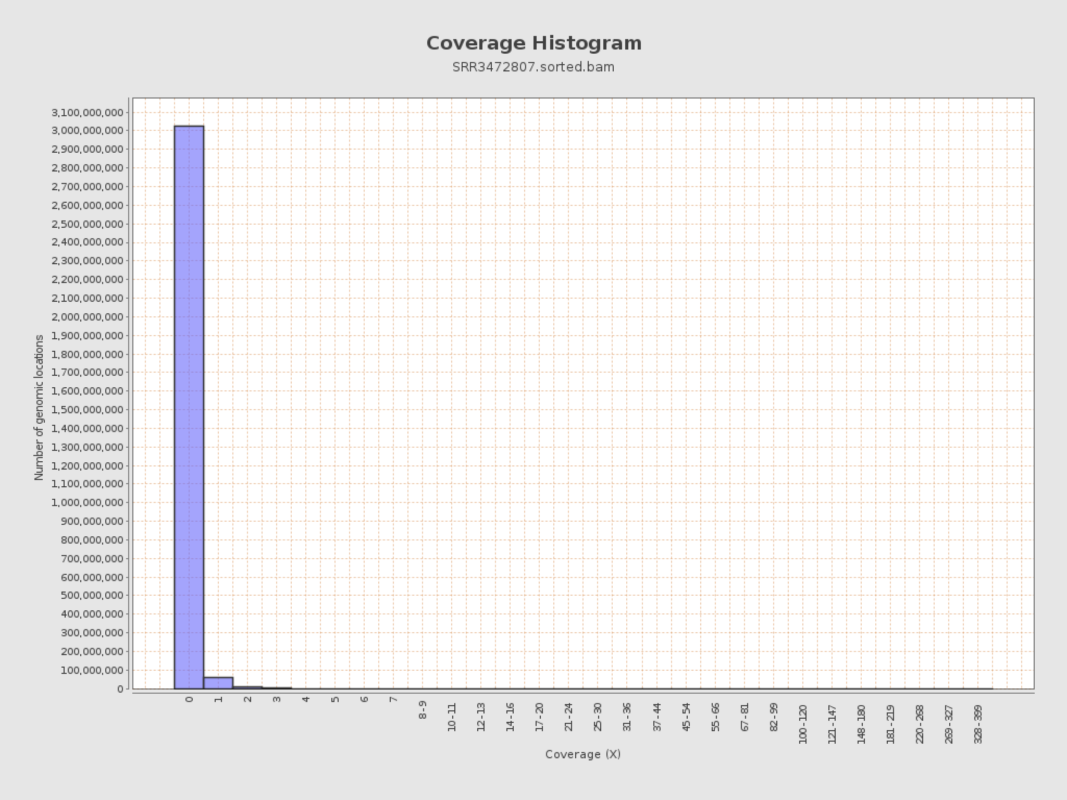
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7968458	0.032	0.3605
chr2	243199373	8262932	0.034	0.3605
chr3	198022430	6091147	0.0308	0.2461
chr4	191154276	4907017	0.0257	0.244
chr5	180915260	5529613	0.0306	0.2459
chr6	171115067	6322054	0.0369	0.2857
chr7	159138663	5535514	0.0348	0.4201

chr8	146364022	5285272	0.0361	0.2992
chr9	141213431	4303221	0.0305	0.308
chr10	135534747	4844838	0.0357	0.2994
chr11	135006516	4014758	0.0297	0.3214
chr12	133851895	4477501	0.0335	0.281
chr13	115169878	3752801	0.0326	0.2538
chr14	107349540	3044326	0.0284	0.2745
chr15	102531392	2872143	0.028	0.2807
chr16	90354753	3025940	0.0335	0.2747
chr17	81195210	2700458	0.0333	0.2844
chr18	78077248	2053412	0.0263	0.4629
chr19	59128983	2109334	0.0357	0.3231
chr20	63025520	2955859	0.0469	0.3195
chr21	48129895	1460501	0.0303	0.2608
chr22	51304566	1153812	0.0225	0.2196
chrMT	16571	130669	7.8854	6.2824
chrX	155270560	4600637	0.0296	0.2655
chrY	59373566	383254	0.0065	0.1238

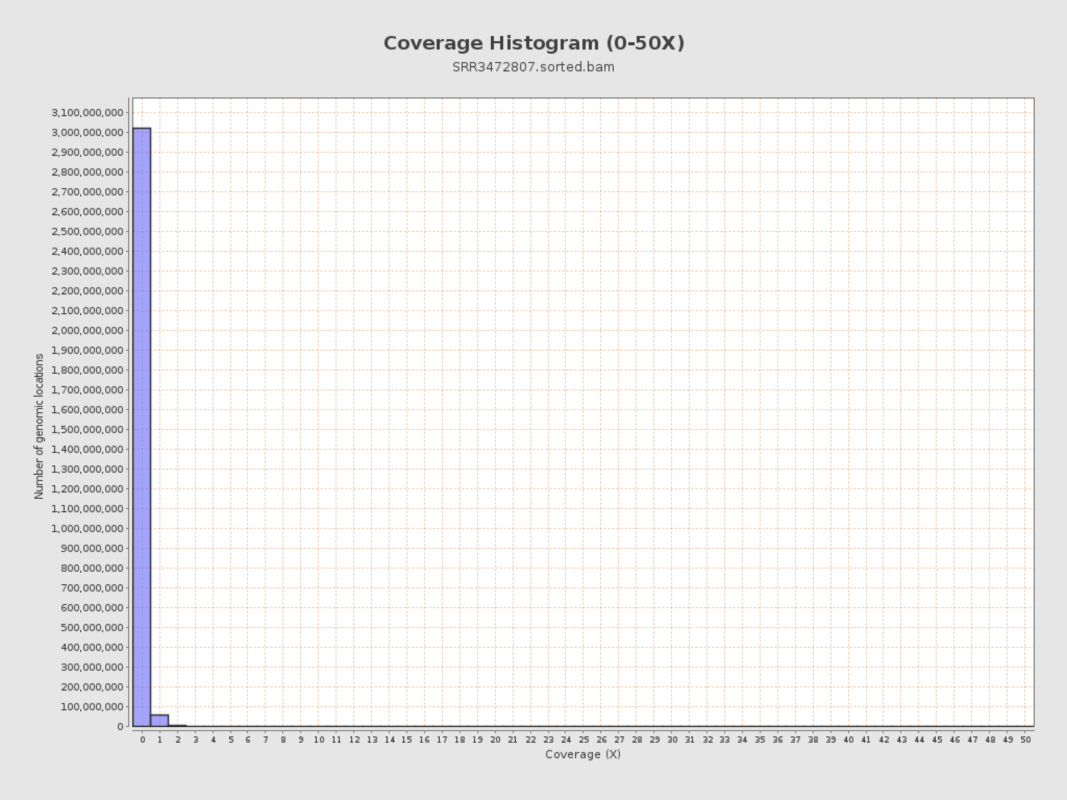
3. Results : Coverage across reference



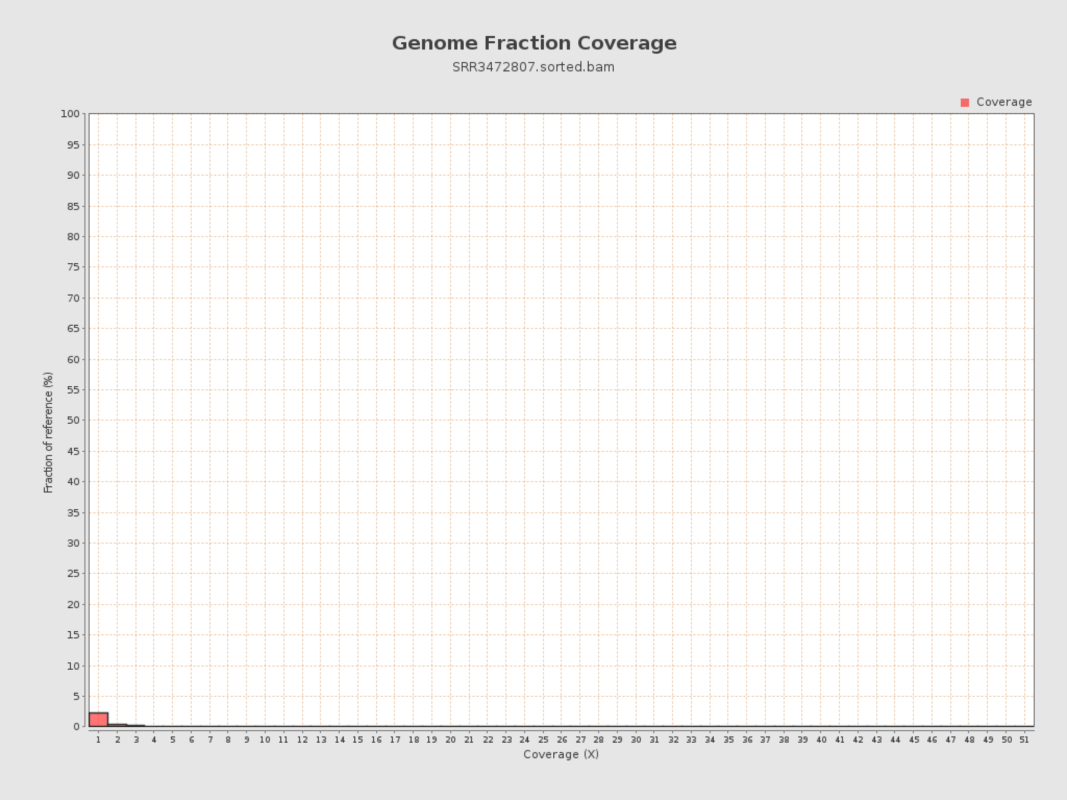
4. Results : Coverage Histogram



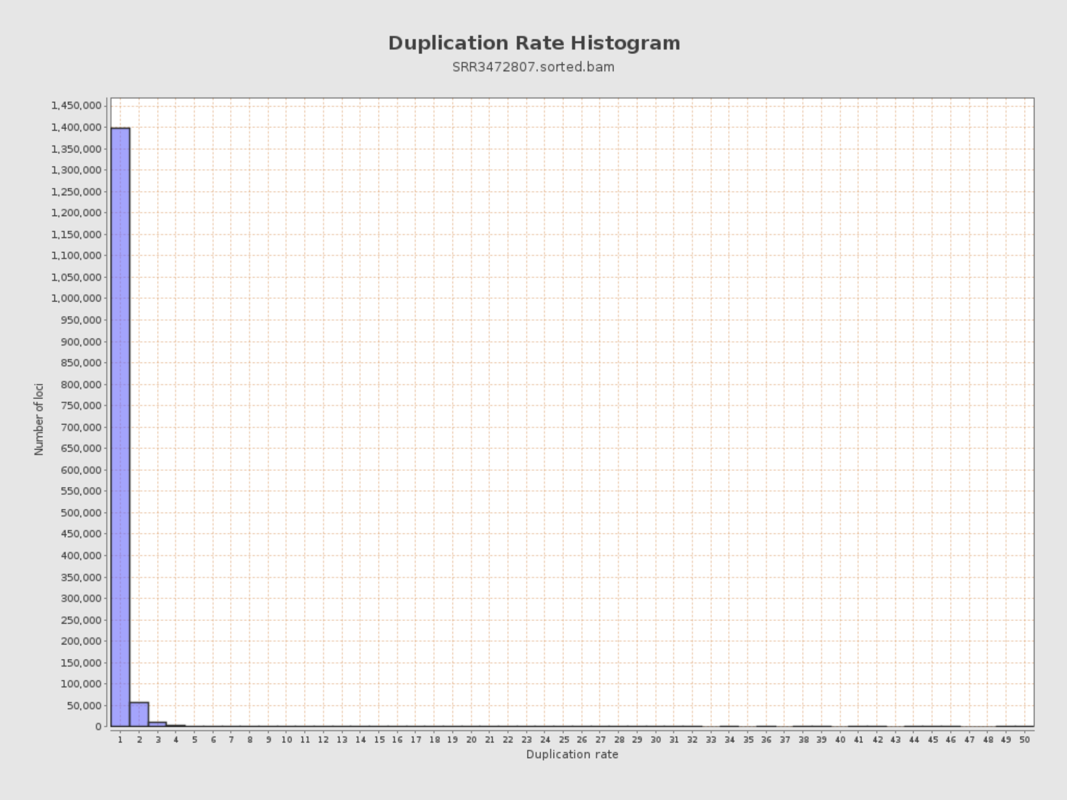
5. Results : Coverage Histogram (0-50X)



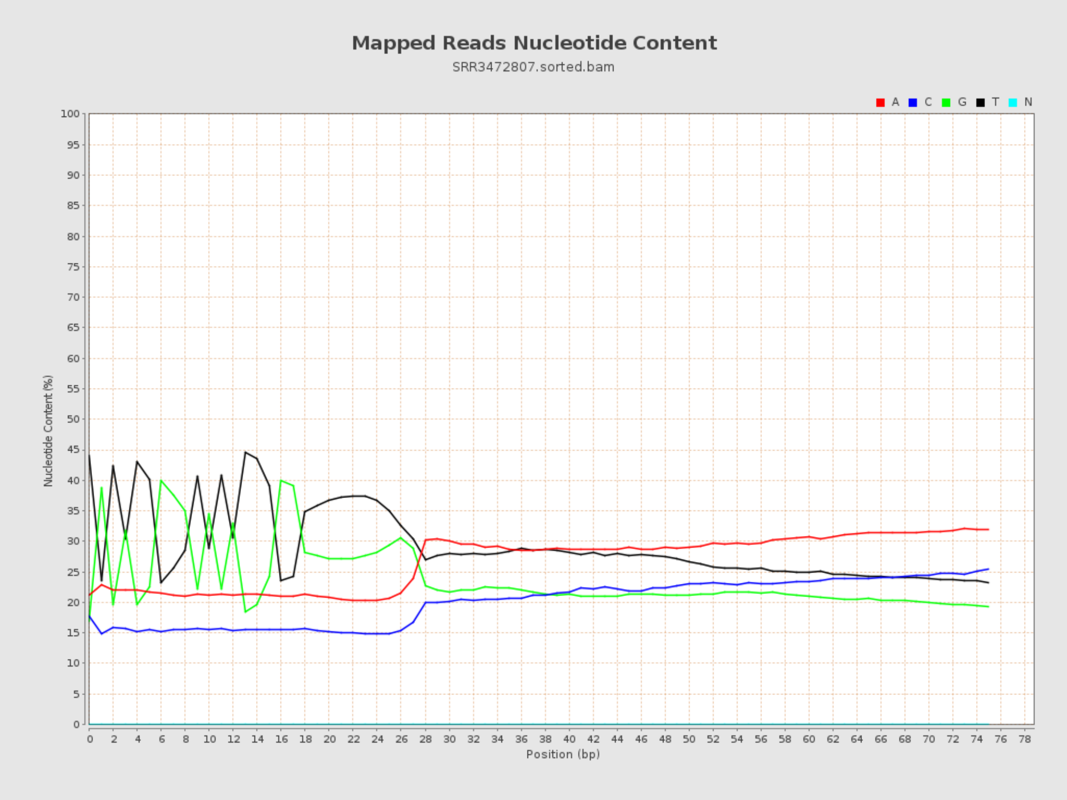
6. Results : Genome Fraction Coverage



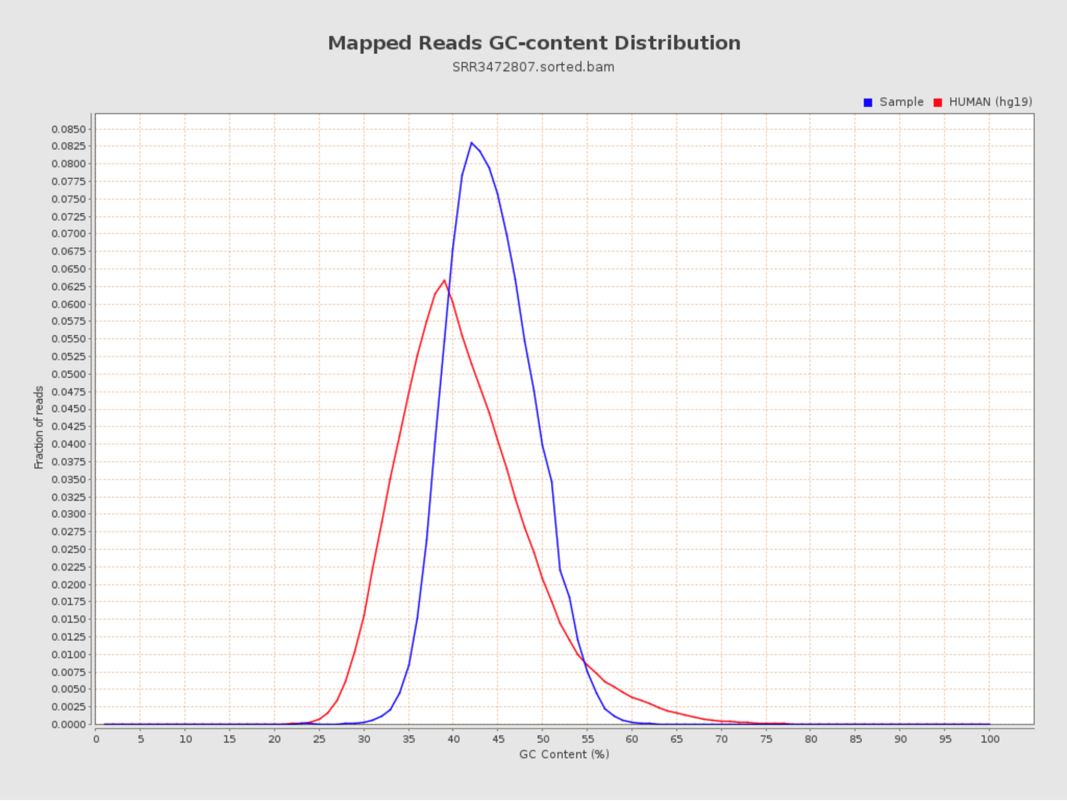
7. Results : Duplication Rate Histogram



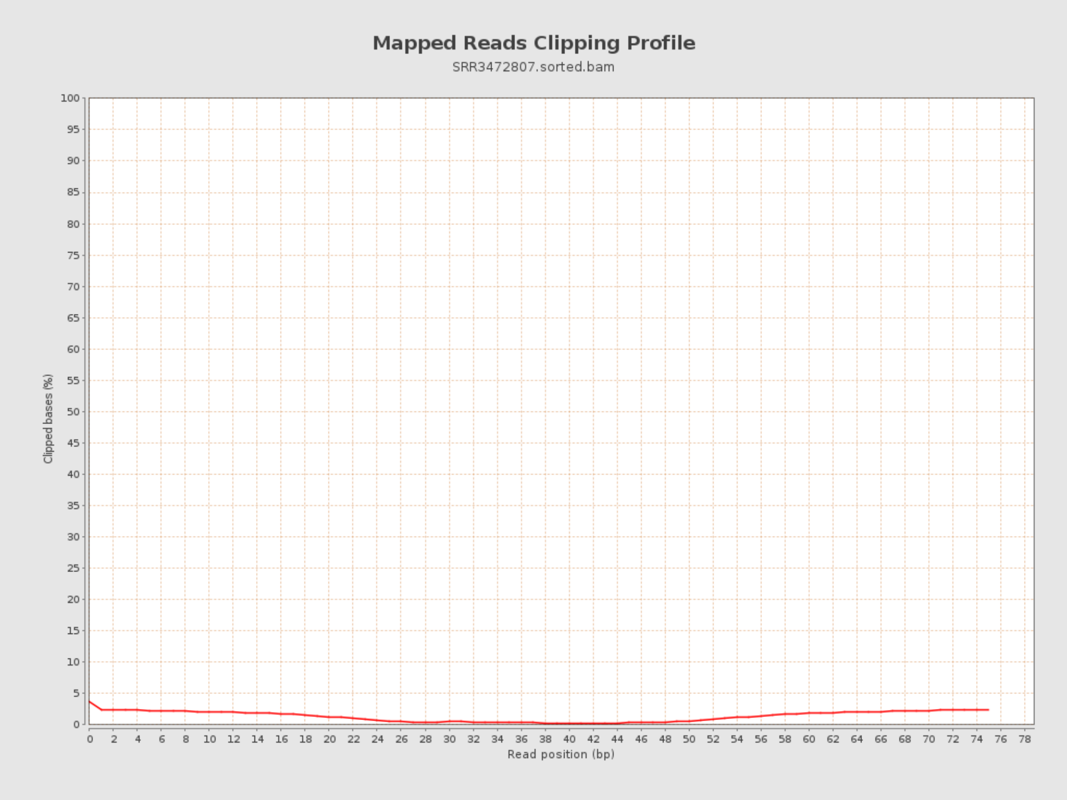
8. Results : Mapped Reads Nucleotide Content



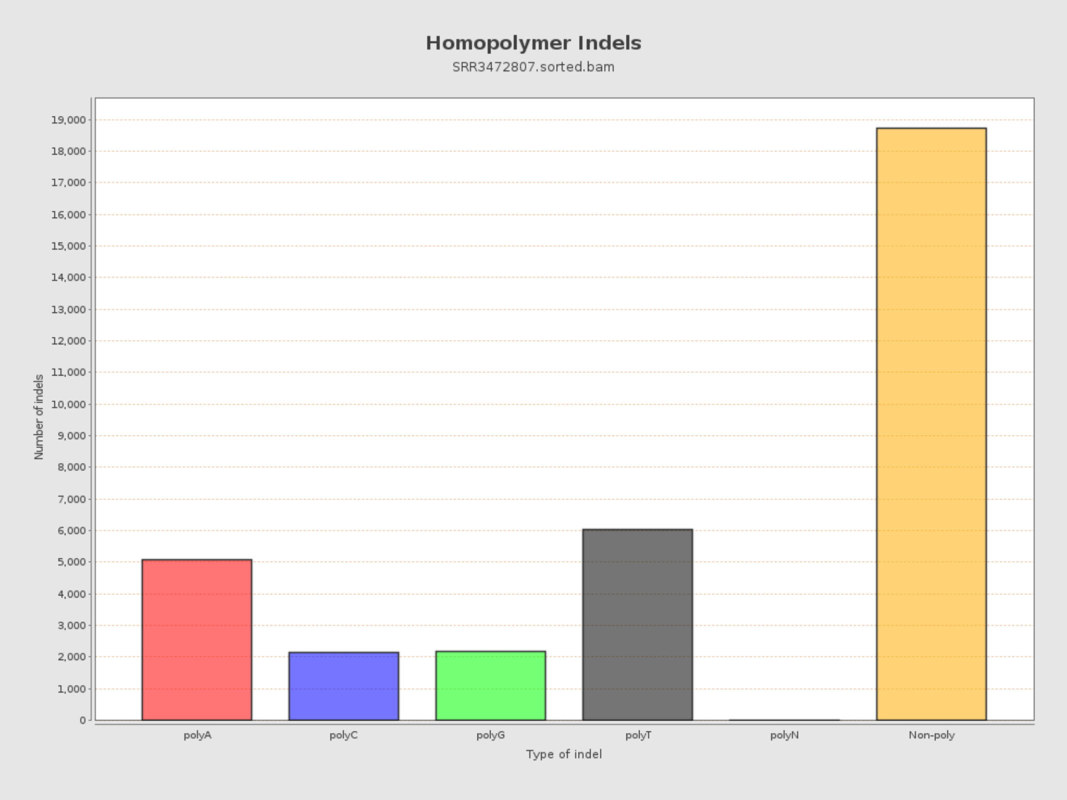
9. Results : Mapped Reads GC-content Distribution



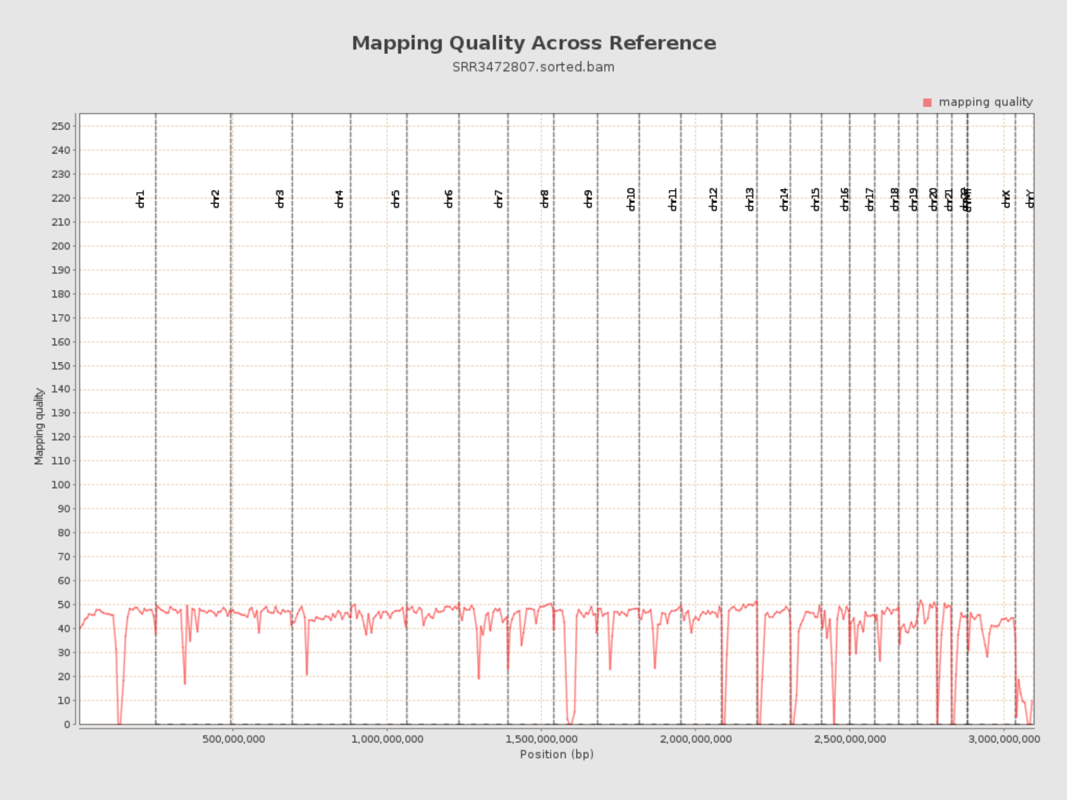
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram