Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 07:56:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472815.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_SRR3472815 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472815.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 07:56:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472815.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,749,167
Mapped reads	1,336,037 / 76.38%
Unmapped reads	413,130 / 23.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,647 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	57,601 / 3.29%
Duplication rate	3.22%
Clipped reads	804,057 / 45.97%

2.2. ACGT Content

Number/percentage of A's	22,277,993 / 26.54%
Number/percentage of C's	16,996,493 / 20.25%
Number/percentage of T's	24,546,662 / 29.24%
Number/percentage of G's	20,116,906 / 23.97%
Number/percentage of N's	1,641 / 0%
GC Percentage	44.21%

2.3. Coverage

Mean	0.0271

Standard Deviation	0.24

2.4. Mapping Quality

Mean Mapping Quality	42.26

2.5. Mismatches and indels

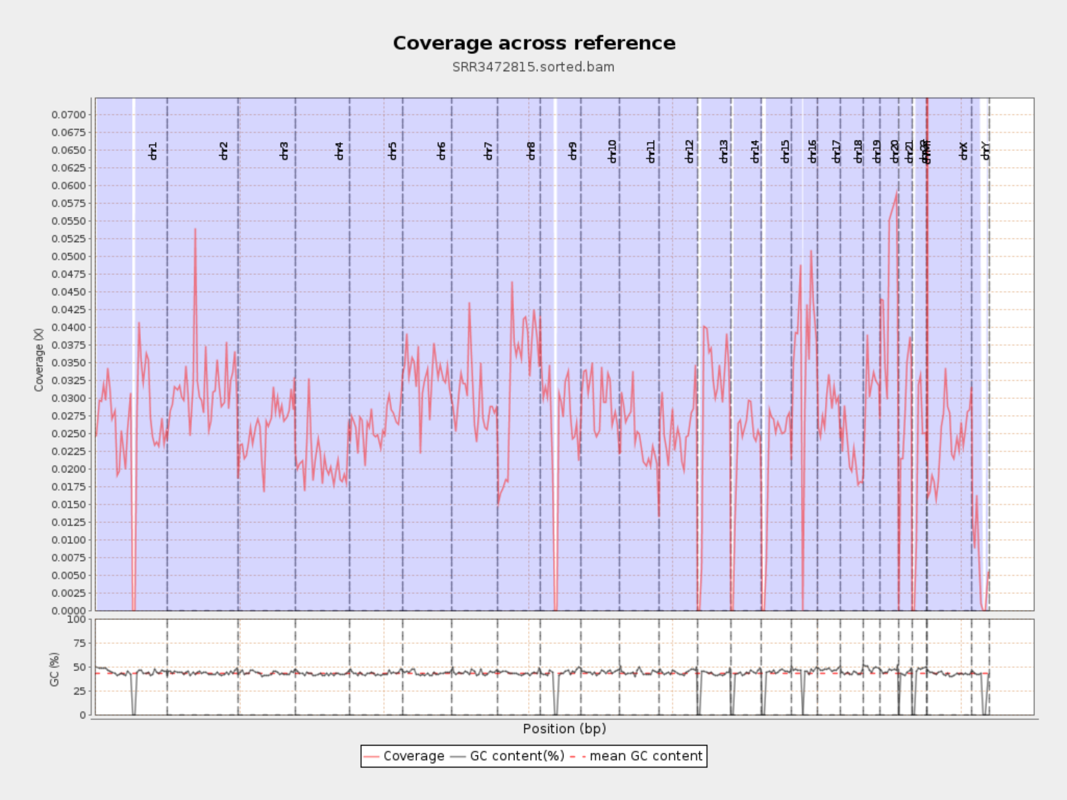
General error rate	0.92%
Mismatches	762,453
Insertions	6,689
Mapped reads with at least one insertion	0.49%
Deletions	20,607
Mapped reads with at least one deletion	1.52%
Homopolymer indels	44.91%

2.6. Chromosome stats

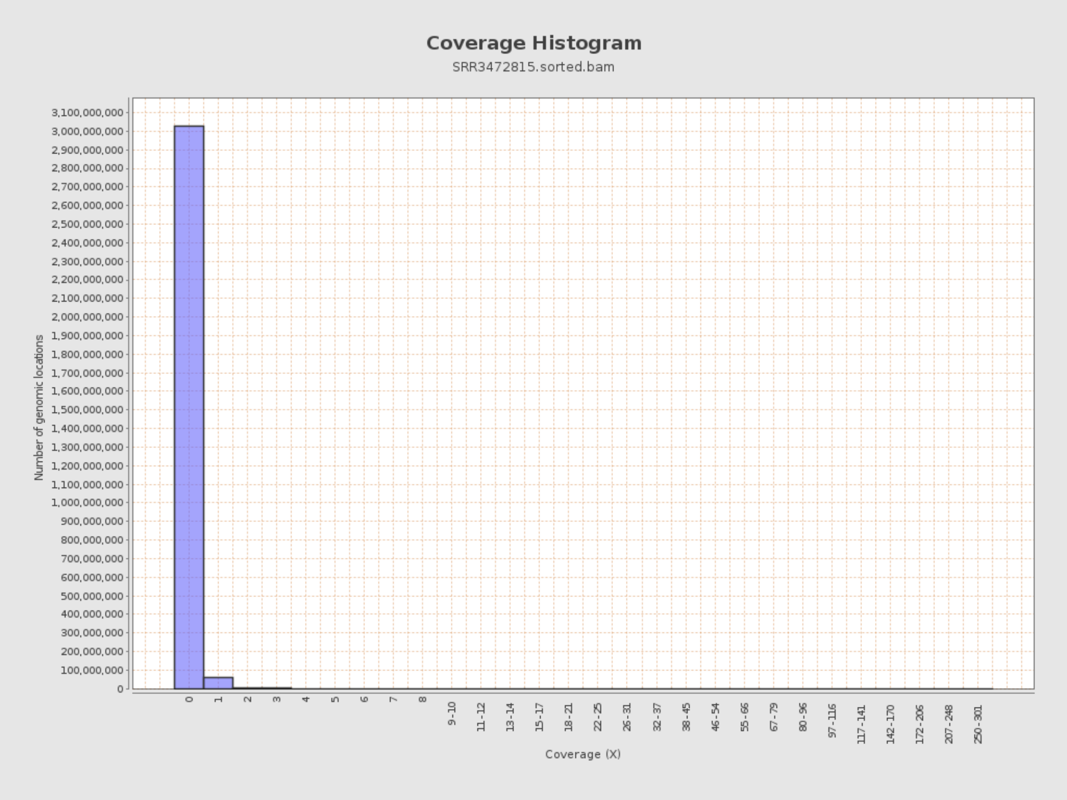
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6494484	0.0261	0.2703
chr2	243199373	7677675	0.0316	0.3191
chr3	198022430	5116165	0.0258	0.1916
chr4	191154276	4010115	0.021	0.1836
chr5	180915260	4746786	0.0262	0.1927
chr6	171115067	5664325	0.0331	0.2292
chr7	159138663	4739198	0.0298	0.3067

chr8	146364022	4765862	0.0326	0.2501
chr9	141213431	3608021	0.0256	0.251
chr10	135534747	4039543	0.0298	0.2361
chr11	135006516	3331948	0.0247	0.2491
chr12	133851895	3415666	0.0255	0.1989
chr13	115169878	3341166	0.029	0.2013
chr14	107349540	2344609	0.0218	0.1992
chr15	102531392	2183257	0.0213	0.1935
chr16	90354753	3222971	0.0357	0.2339
chr17	81195210	2312287	0.0285	0.2147
chr18	78077248	1682620	0.0216	0.3676
chr19	59128983	1863515	0.0315	0.2561
chr20	63025520	2985733	0.0474	0.2633
chr21	48129895	1287899	0.0268	0.2068
chr22	51304566	1006348	0.0196	0.1735
chrMT	16571	84502	5.0994	4.2111
chrX	155270560	3685108	0.0237	0.2027
chrY	59373566	367299	0.0062	0.1064

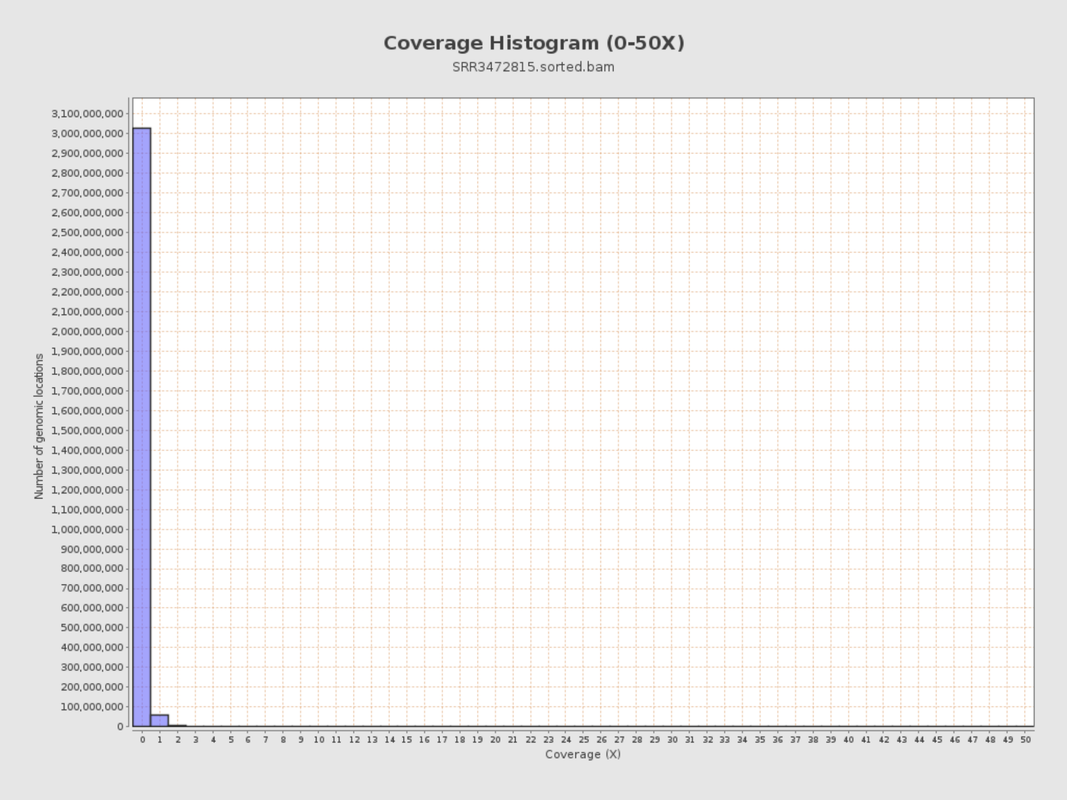
3. Results : Coverage across reference



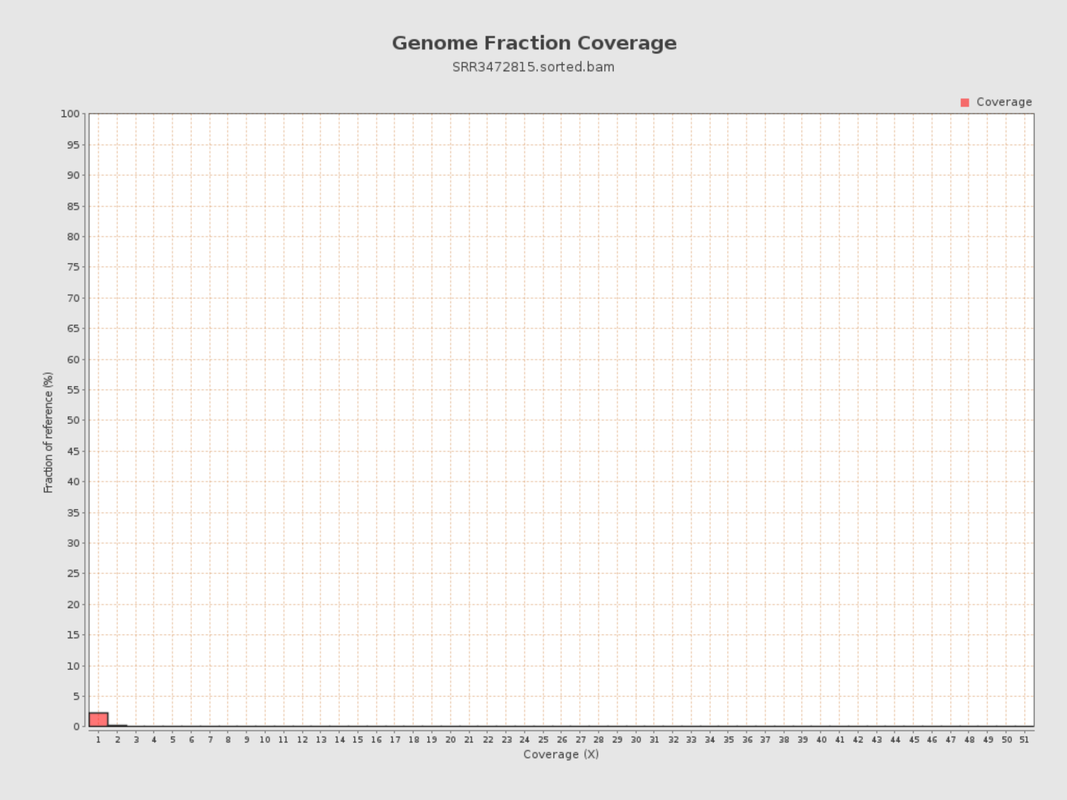
4. Results : Coverage Histogram



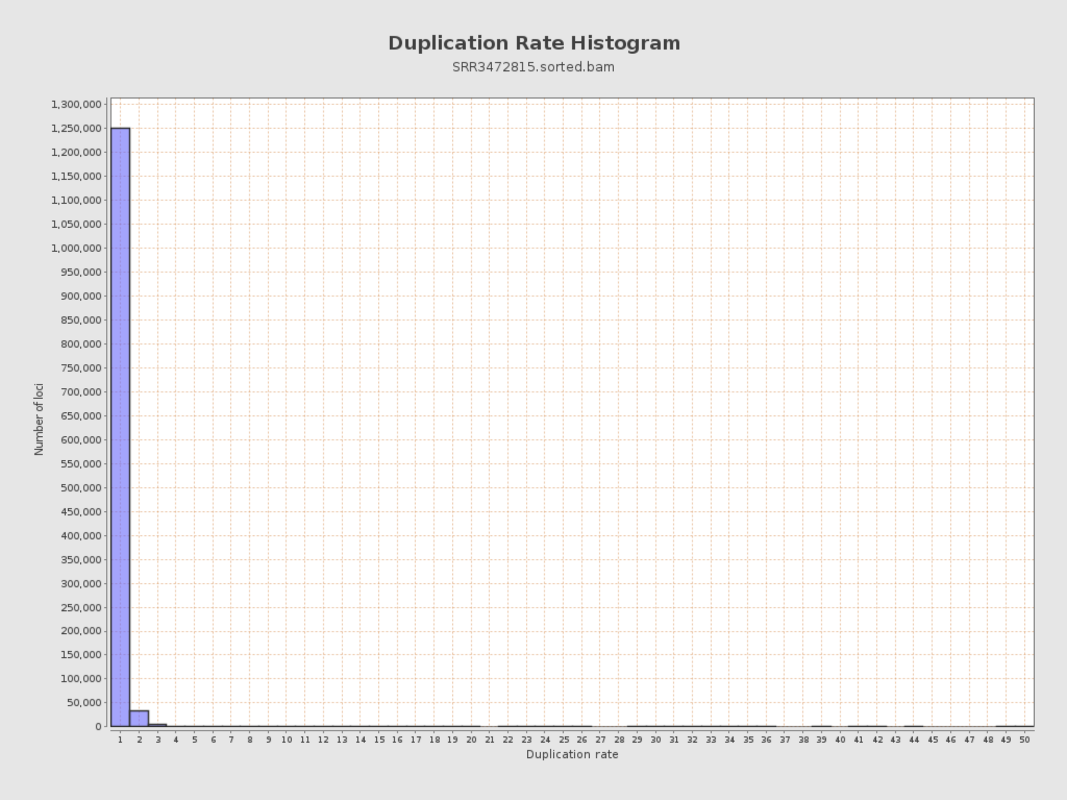
5. Results : Coverage Histogram (0-50X)



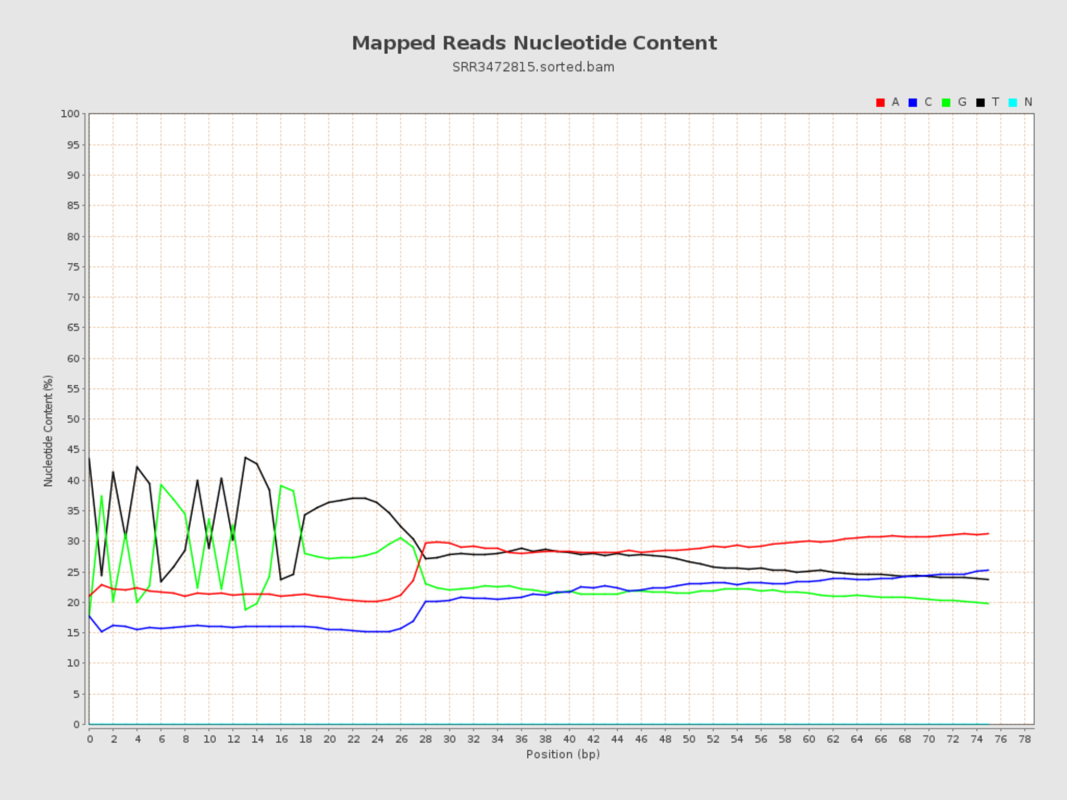
6. Results : Genome Fraction Coverage



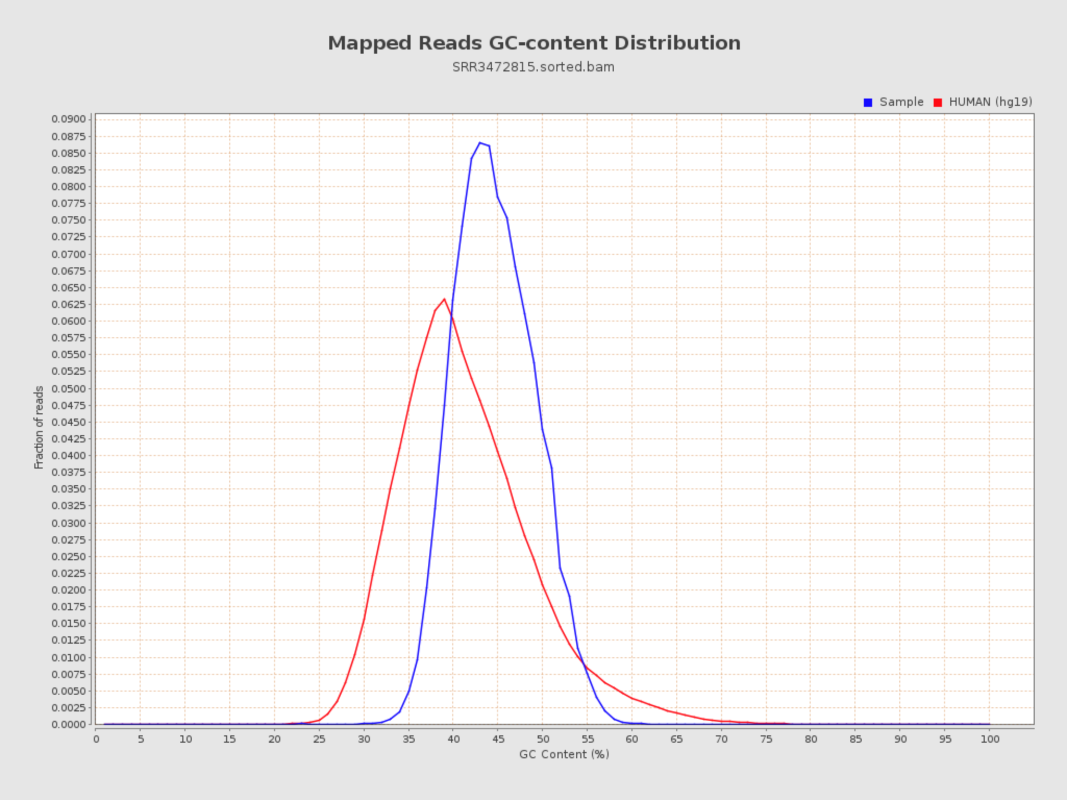
7. Results : Duplication Rate Histogram



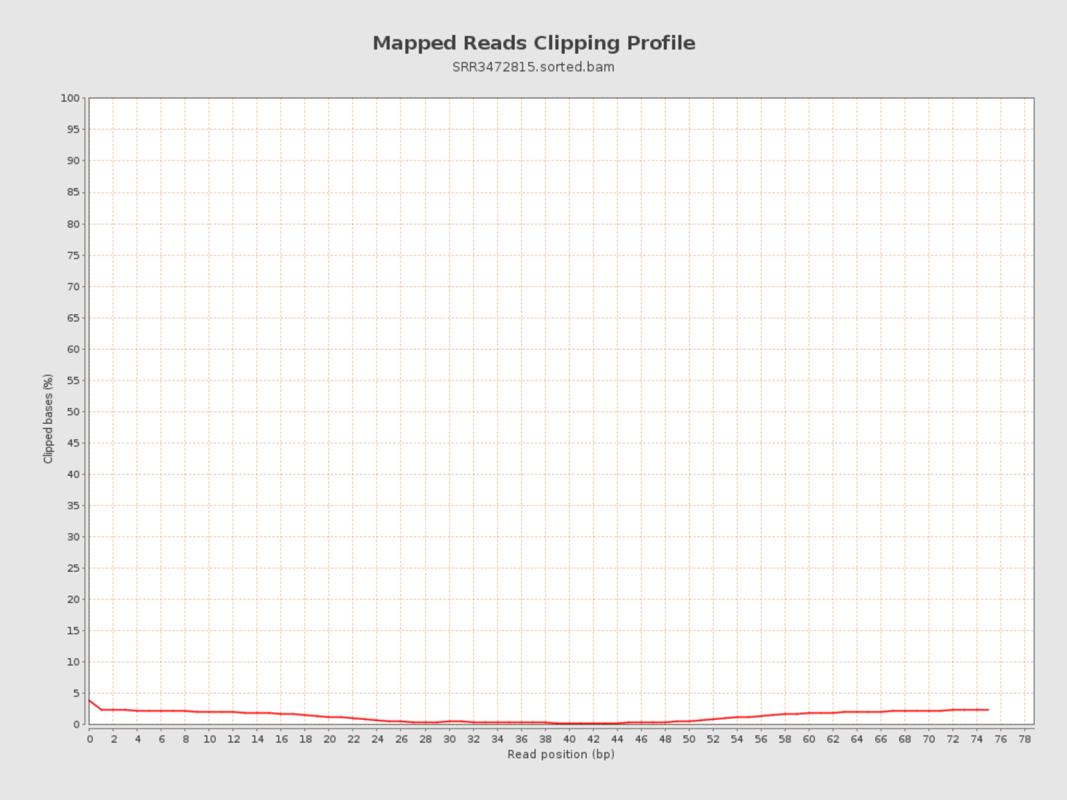
8. Results : Mapped Reads Nucleotide Content



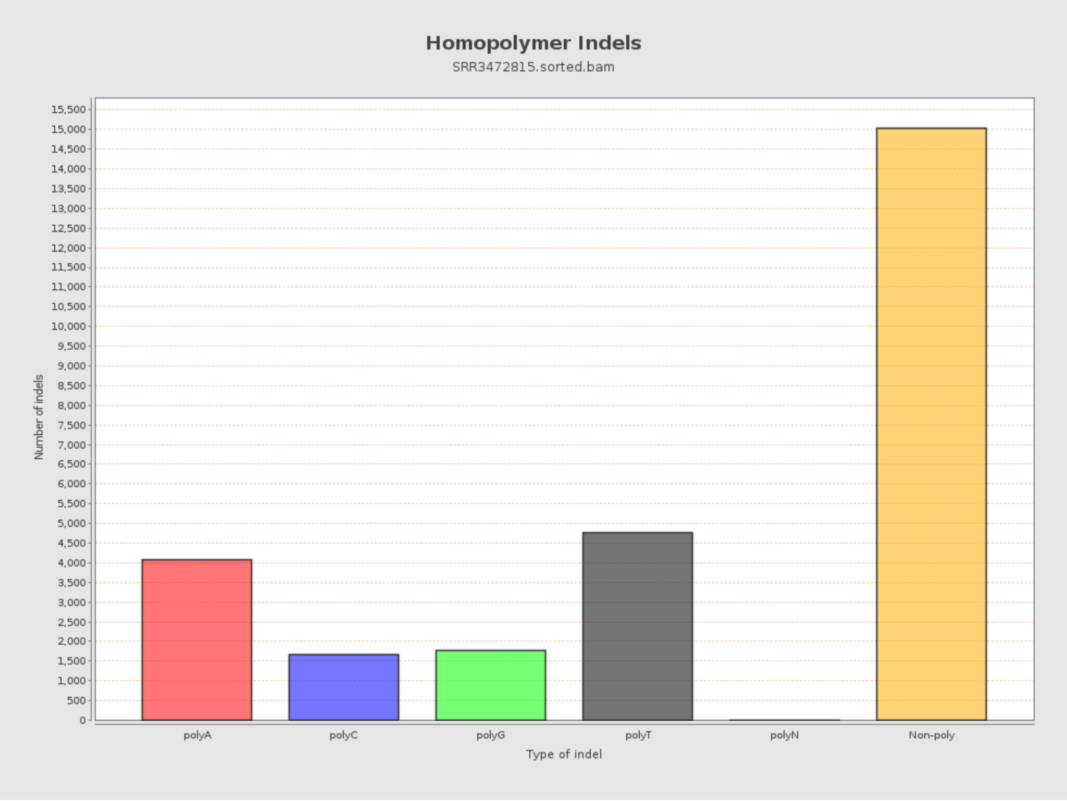
9. Results : Mapped Reads GC-content Distribution



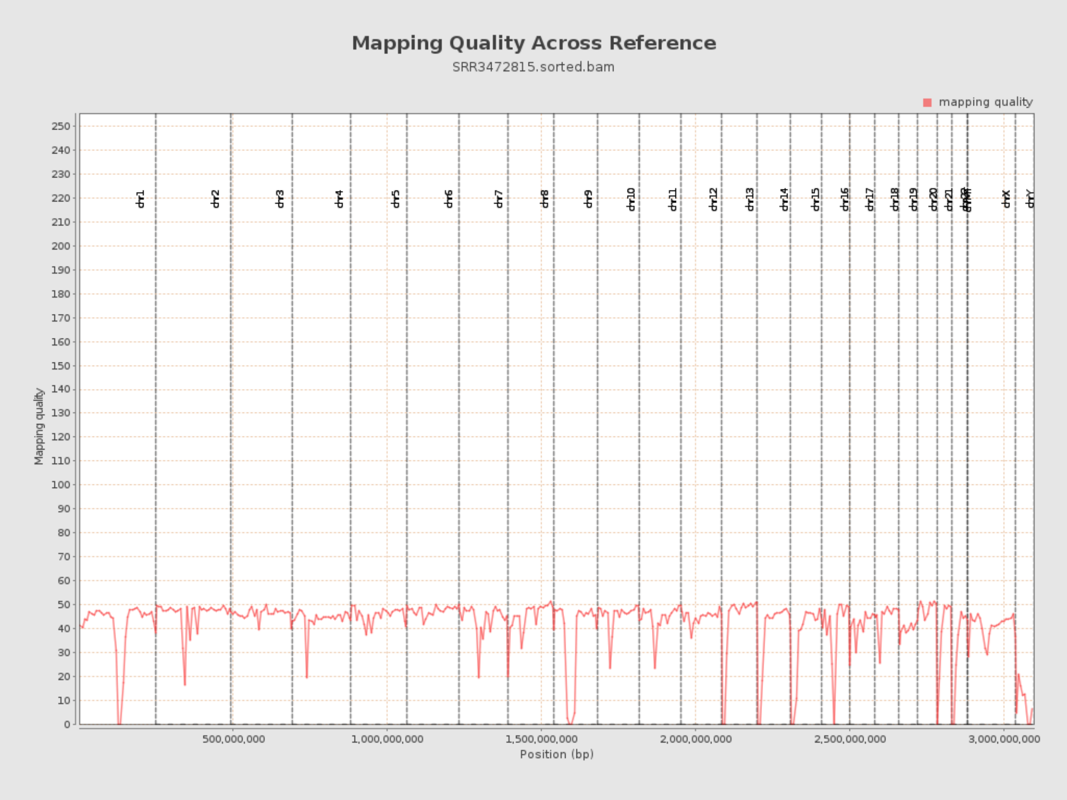
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram