Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:34:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971312.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_SRR2971312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:34:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,363,302
Mapped reads	9,517,305 / 91.84%
Unmapped reads	845,997 / 8.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,258 / 0.01%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	821,658 / 7.93%
Duplication rate	7%
Clipped reads	1,858,122 / 17.93%

2.2. ACGT Content

Number/percentage of A's	129,836,274 / 28.35%
Number/percentage of C's	96,337,314 / 21.04%
Number/percentage of T's	132,408,406 / 28.91%
Number/percentage of G's	99,375,450 / 21.7%
Number/percentage of N's	25,520 / 0.01%
GC Percentage	42.73%

2.3. Coverage

Mean	0.148

Standard Deviation	1.1987

2.4. Mapping Quality

Mean Mapping Quality	37.99

2.5. Mismatches and indels

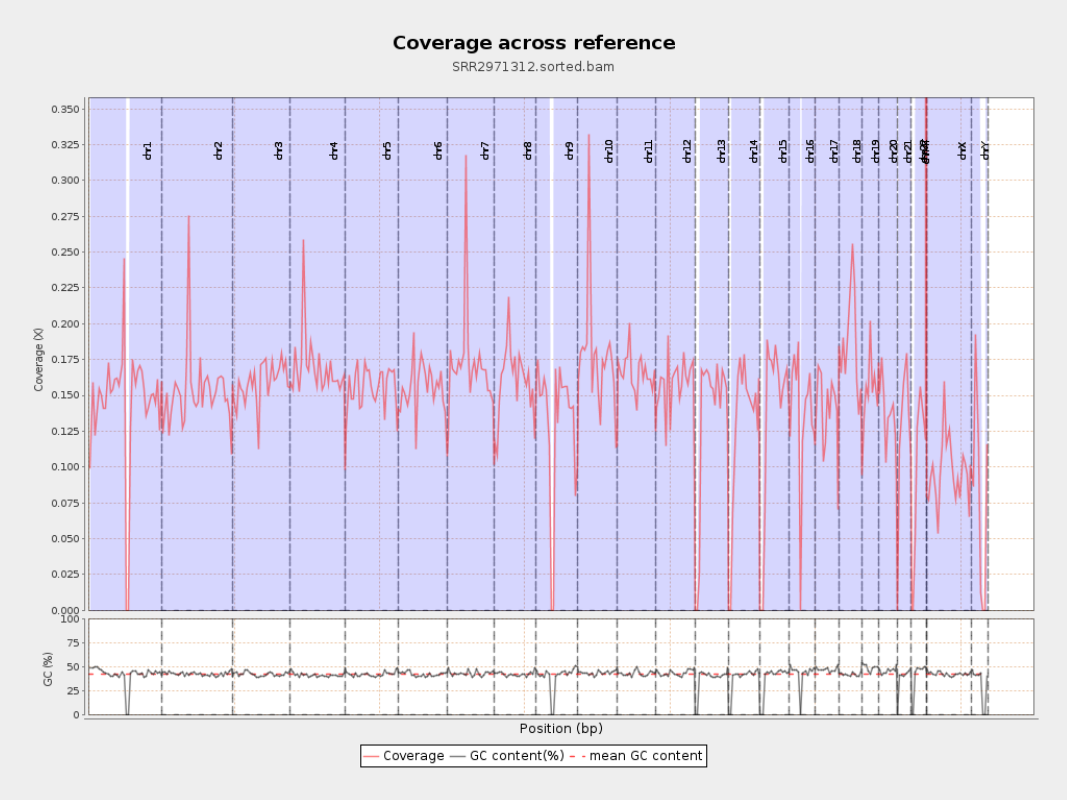
General error rate	0.49%
Mismatches	2,201,868
Insertions	28,444
Mapped reads with at least one insertion	0.3%
Deletions	66,247
Mapped reads with at least one deletion	0.69%
Homopolymer indels	41.68%

2.6. Chromosome stats

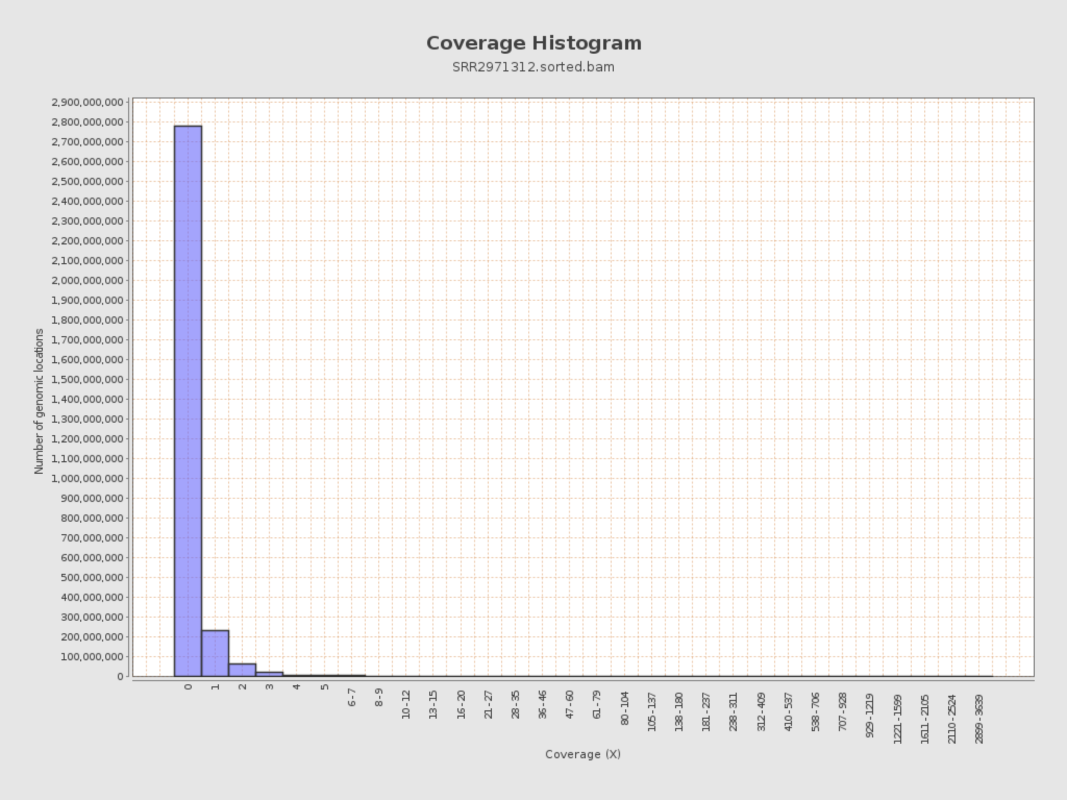
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	35944608	0.1442	2.1288
chr2	243199373	37065682	0.1524	1.1227
chr3	198022430	31454019	0.1588	0.5518
chr4	191154276	32311848	0.169	0.7645
chr5	180915260	28213974	0.156	0.5413
chr6	171115067	26570437	0.1553	0.6056
chr7	159138663	27595306	0.1734	1.9982

chr8	146364022	23322244	0.1593	1.9664
chr9	141213431	18430715	0.1305	1.0471
chr10	135534747	24147390	0.1782	1.3893
chr11	135006516	22305635	0.1652	0.9833
chr12	133851895	21050168	0.1573	0.5749
chr13	115169878	15293531	0.1328	0.4837
chr14	107349540	13609508	0.1268	0.6804
chr15	102531392	13989747	0.1364	0.4993
chr16	90354753	12468944	0.138	0.6615
chr17	81195210	11312797	0.1393	0.6791
chr18	78077248	14698282	0.1883	2.3261
chr19	59128983	9149557	0.1547	1.7565
chr20	63025520	8642471	0.1371	0.5617
chr21	48129895	6135120	0.1275	0.7333
chr22	51304566	4897370	0.0955	0.5304
chrMT	16571	82843	4.9993	4.2041
chrX	155270560	14881681	0.0958	0.5777
chrY	59373566	4505578	0.0759	0.7504

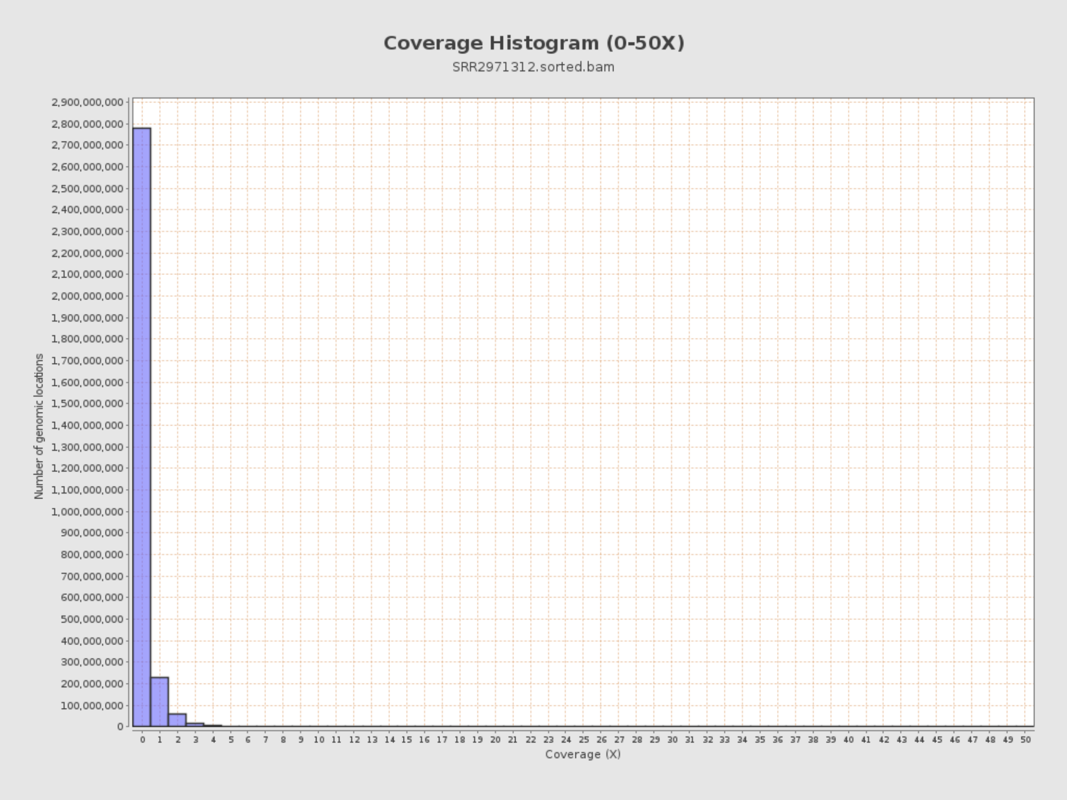
3. Results : Coverage across reference



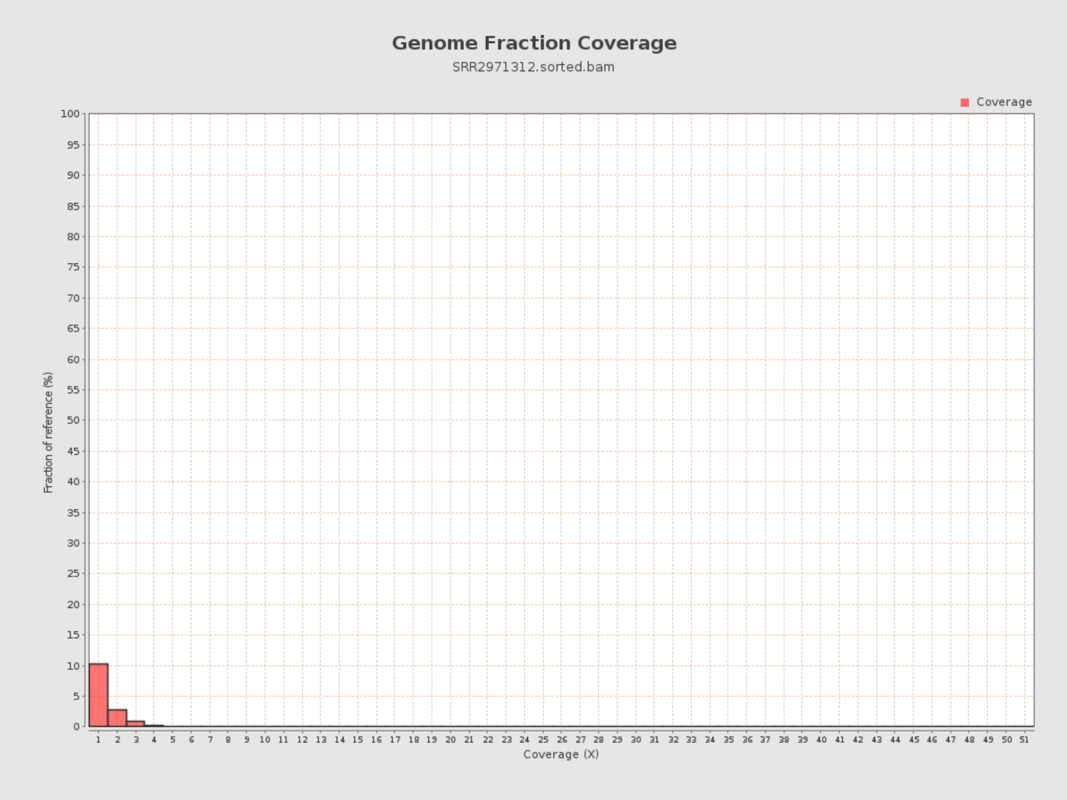
4. Results : Coverage Histogram



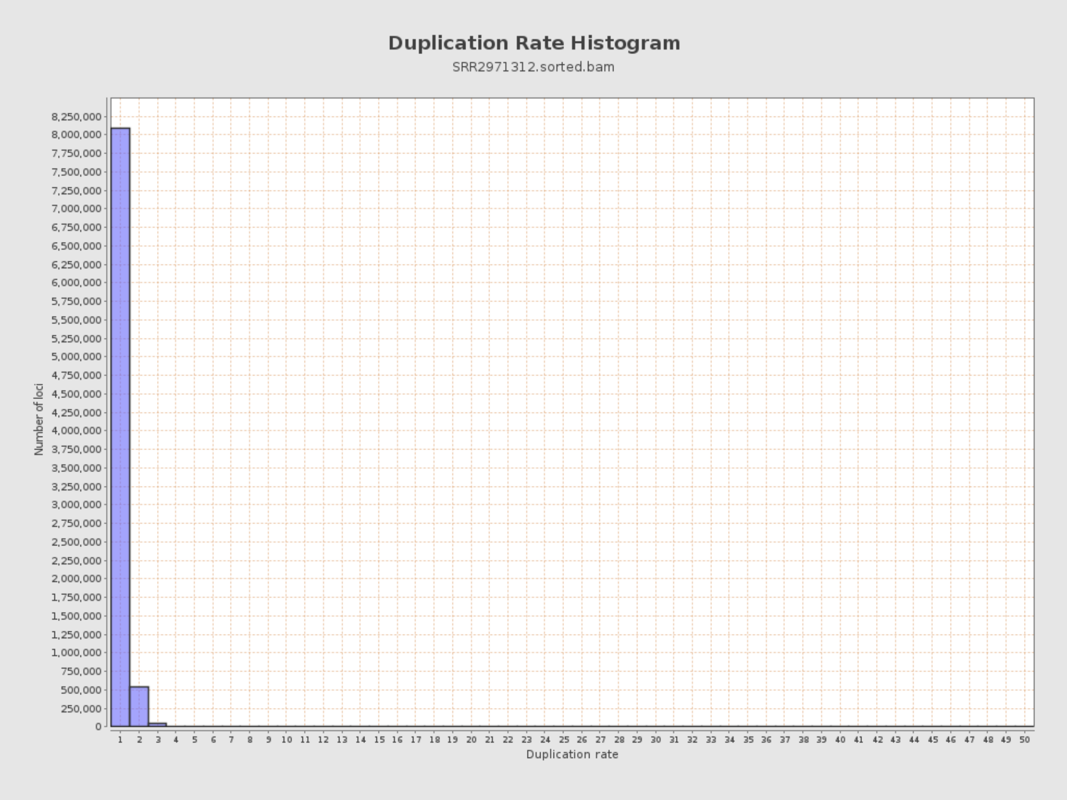
5. Results : Coverage Histogram (0-50X)



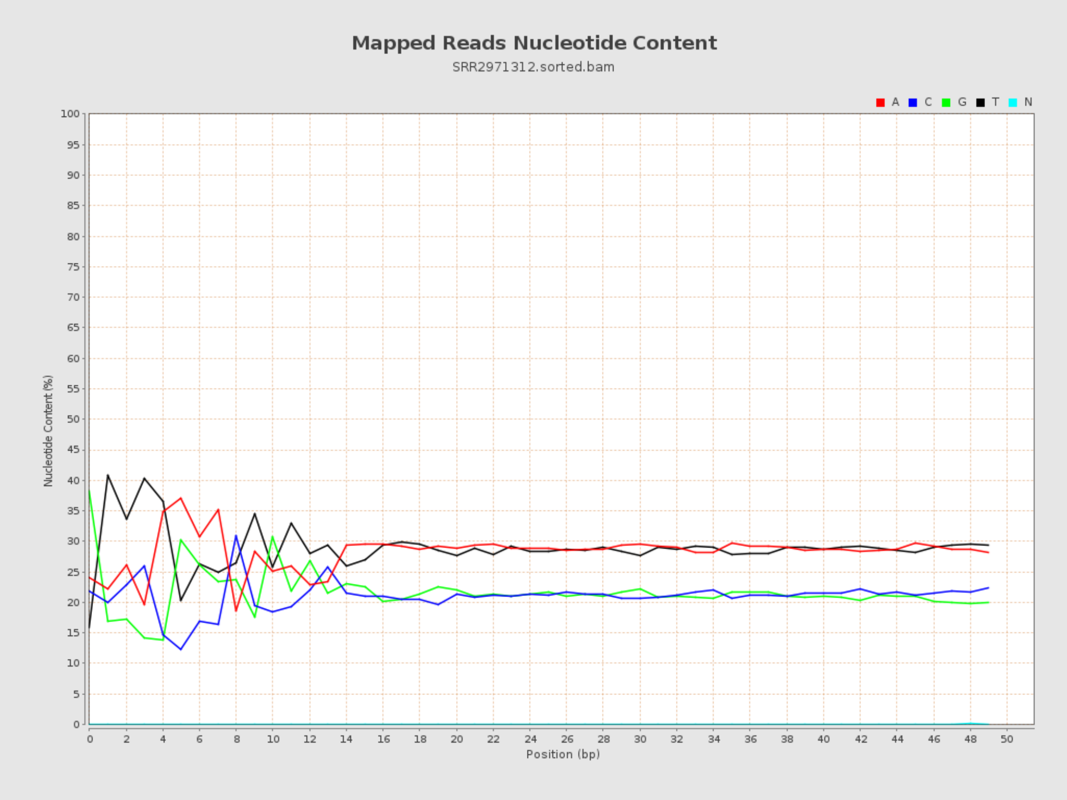
6. Results : Genome Fraction Coverage



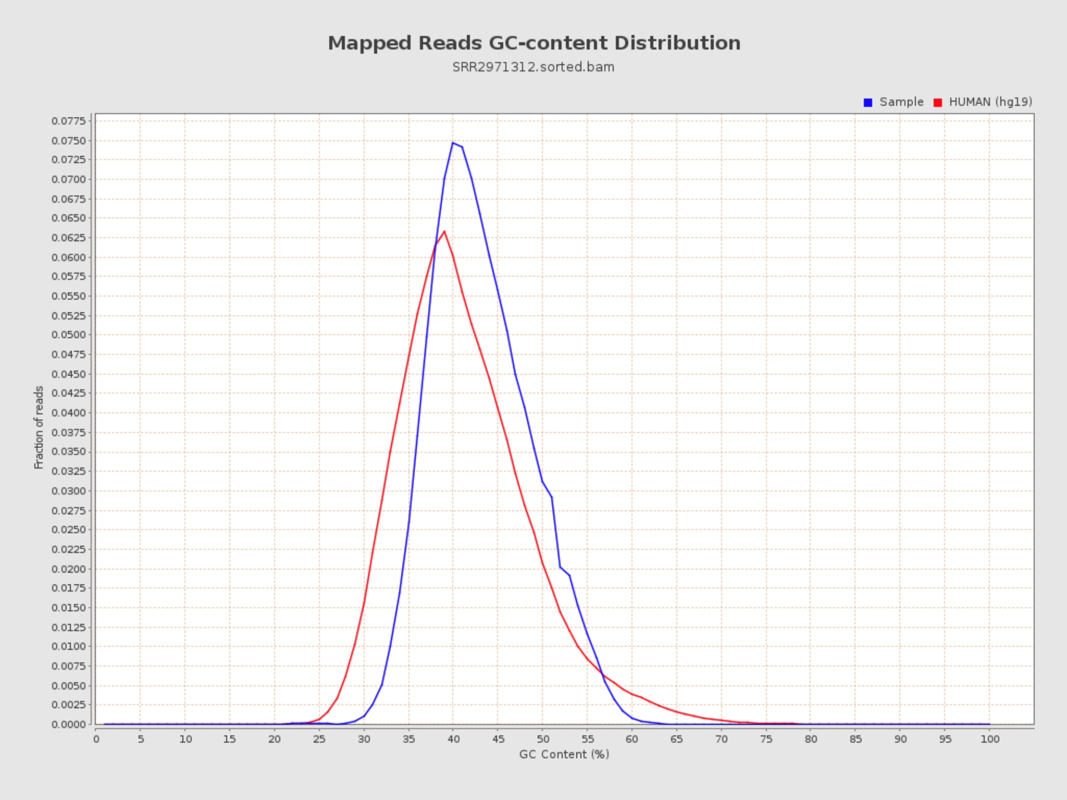
7. Results : Duplication Rate Histogram



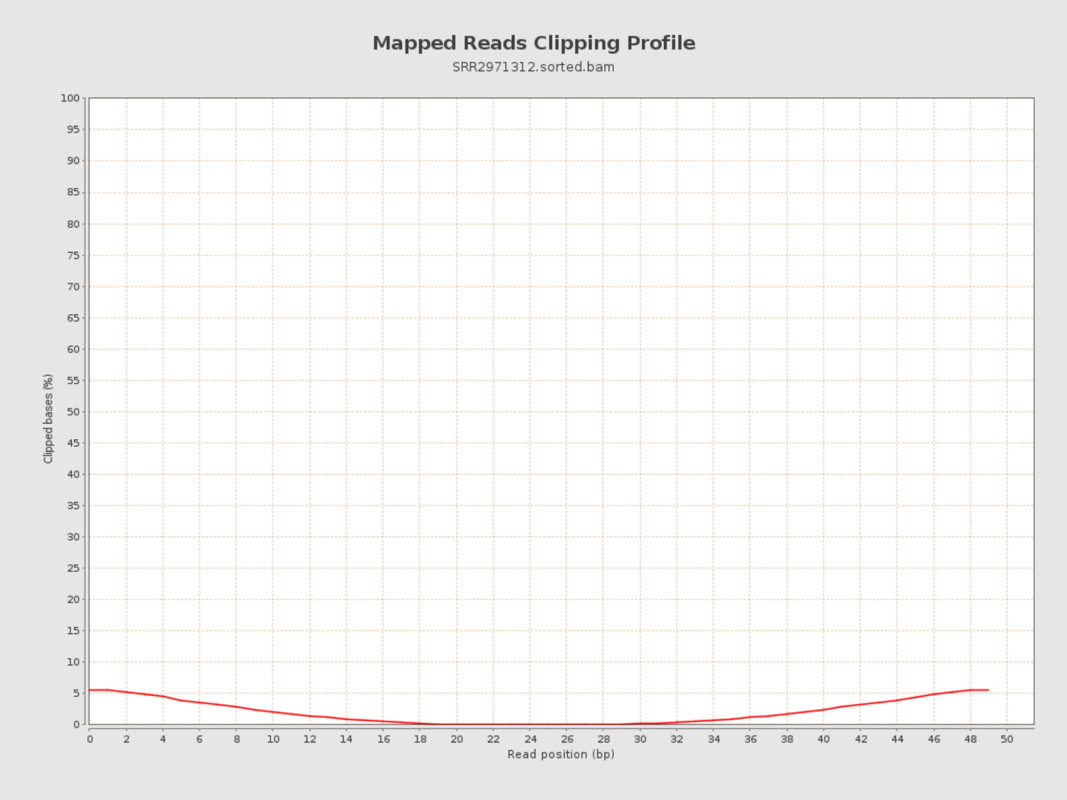
8. Results : Mapped Reads Nucleotide Content



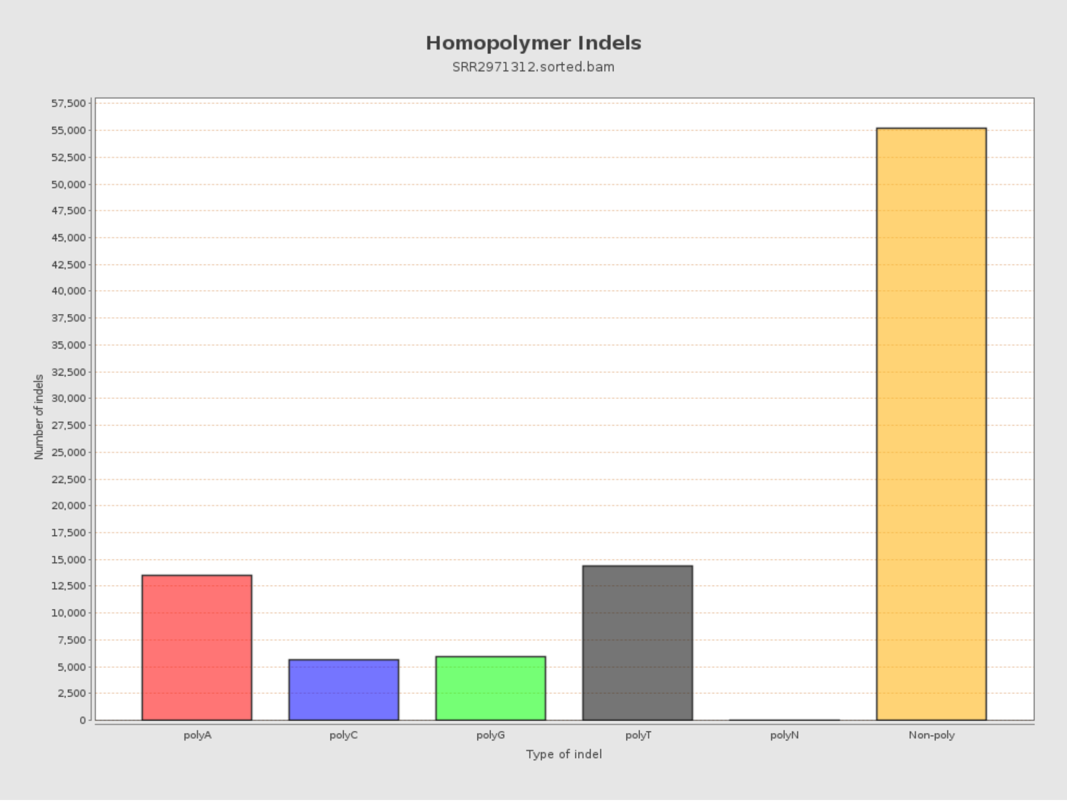
9. Results : Mapped Reads GC-content Distribution



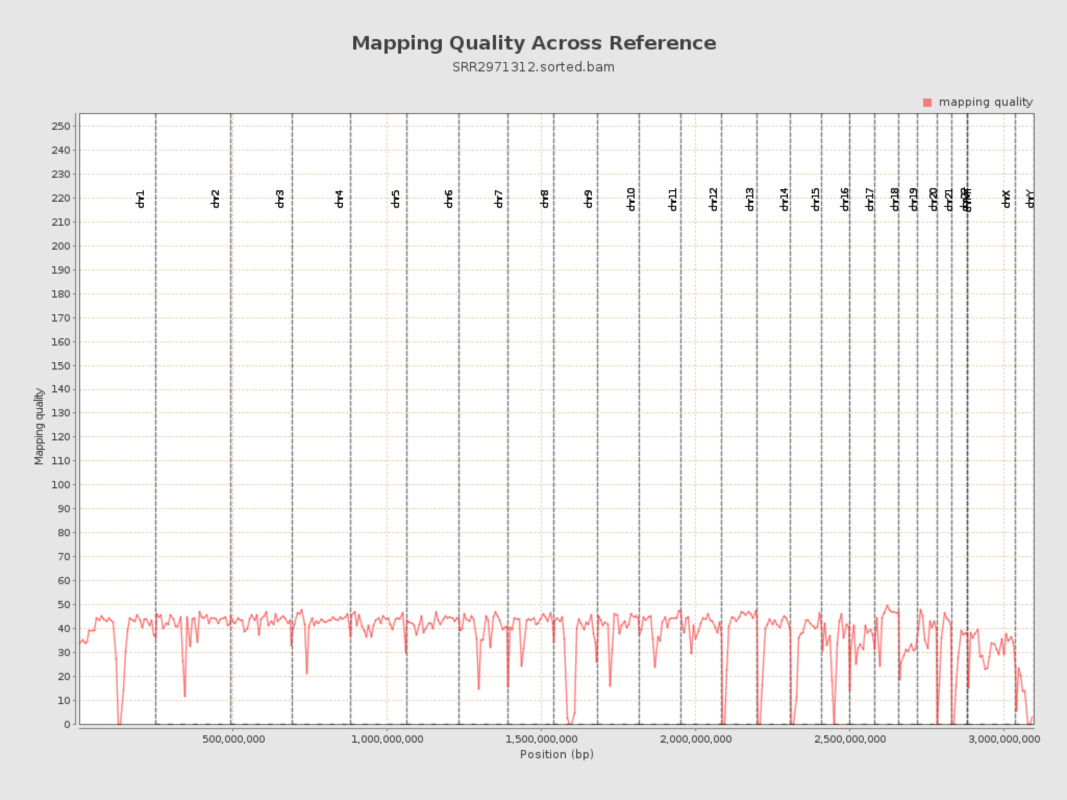
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram