Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:19:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971321.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_SRR2971321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:19:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,367,004
Mapped reads	48,566,494 / 87.72%
Unmapped reads	6,800,510 / 12.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	7,481,415 / 13.51%
Duplication rate	12.63%
Clipped reads	4,127,903 / 7.46%

2.2. ACGT Content

Number/percentage of A's	562,852,166 / 29.32%
Number/percentage of C's	398,705,729 / 20.77%
Number/percentage of T's	560,259,610 / 29.18%
Number/percentage of G's	397,878,073 / 20.73%
Number/percentage of N's	38,928 / 0%
GC Percentage	41.49%

2.3. Coverage

Mean	0.6202
Standard Deviation	7.508

2.4. Mapping Quality

Mean Mapping Quality	37.76

2.5. Mismatches and indels

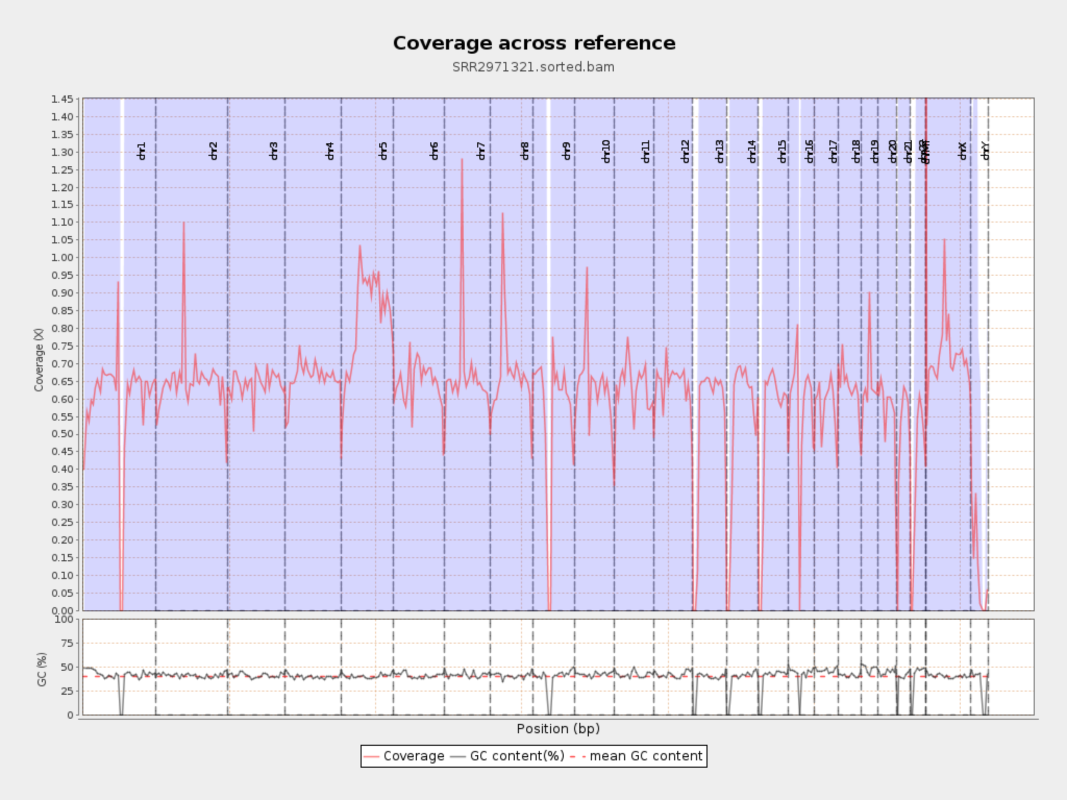
General error rate	0.33%
Mismatches	6,184,510
Insertions	69,503
Mapped reads with at least one insertion	0.14%
Deletions	161,214
Mapped reads with at least one deletion	0.33%
Homopolymer indels	39.24%

2.6. Chromosome stats

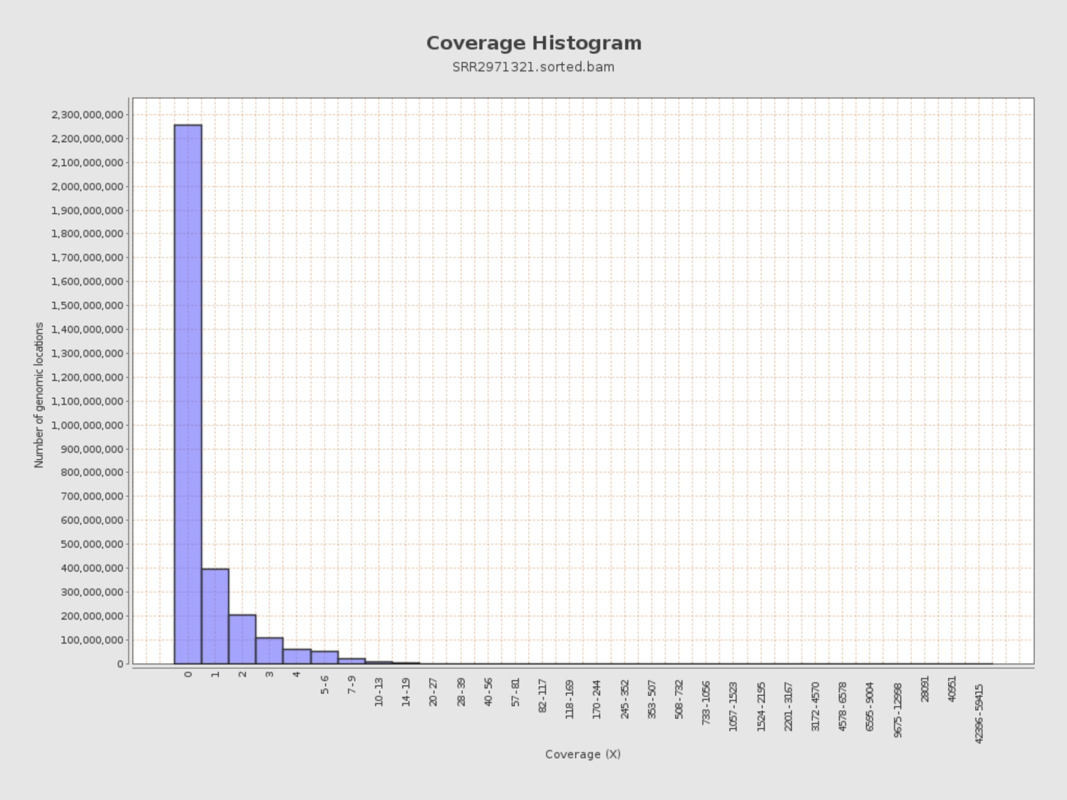
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	147496373	0.5918	8.0134
chr2	243199373	158432856	0.6515	4.4062
chr3	198022430	127682946	0.6448	1.5386
chr4	191154276	126541062	0.662	1.8253
chr5	180915260	149970524	0.829	1.9057
chr6	171115067	110738678	0.6472	2.0803
chr7	159138663	106450319	0.6689	7.0197
chr8	146364022	98803293	0.6751	28.7458

chr9	141213431	79229866	0.5611	4.5527
chr10	135534747	86570477	0.6387	3.6318
chr11	135006516	85723057	0.635	4.3313
chr12	133851895	86170011	0.6438	1.865
chr13	115169878	60819331	0.5281	1.3053
chr14	107349540	57365077	0.5344	2.6105
chr15	102531392	52683367	0.5138	1.3774
chr16	90354753	50603847	0.5601	2.1948
chr17	81195210	47762920	0.5882	1.9364
chr18	78077248	49907957	0.6392	9.291
chr19	59128983	38209698	0.6462	8.2824
chr20	63025520	36276398	0.5756	1.8131
chr21	48129895	23498900	0.4882	2.1965
chr22	51304566	19738020	0.3847	1.6314
chrMT	16571	62740	3.7861	4.4478
chrX	155270560	112127008	0.7221	3.0109
chrY	59373566	7080484	0.1193	1.3022

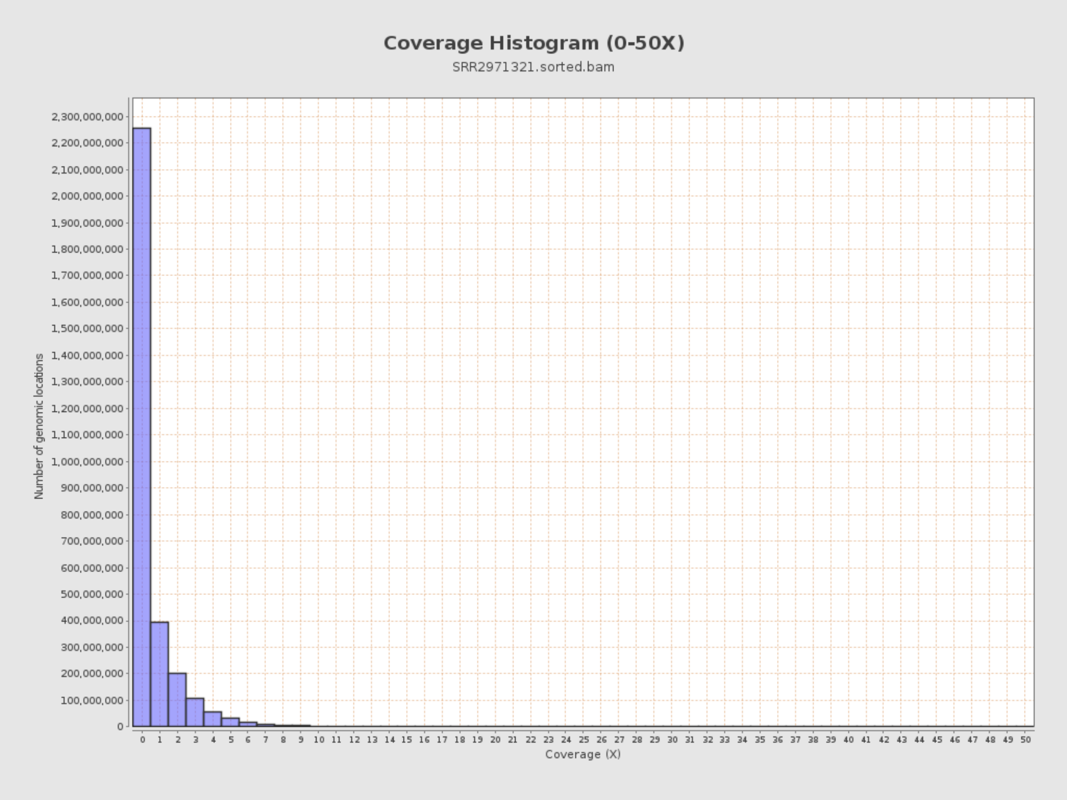
3. Results : Coverage across reference



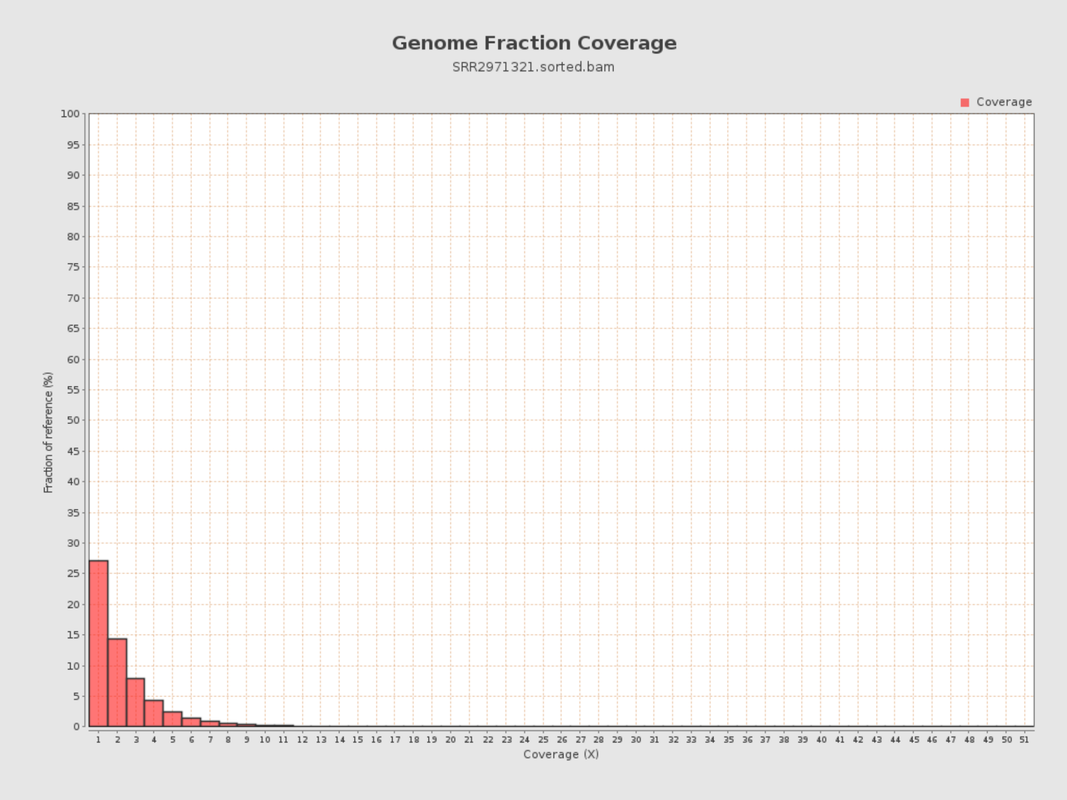
4. Results : Coverage Histogram



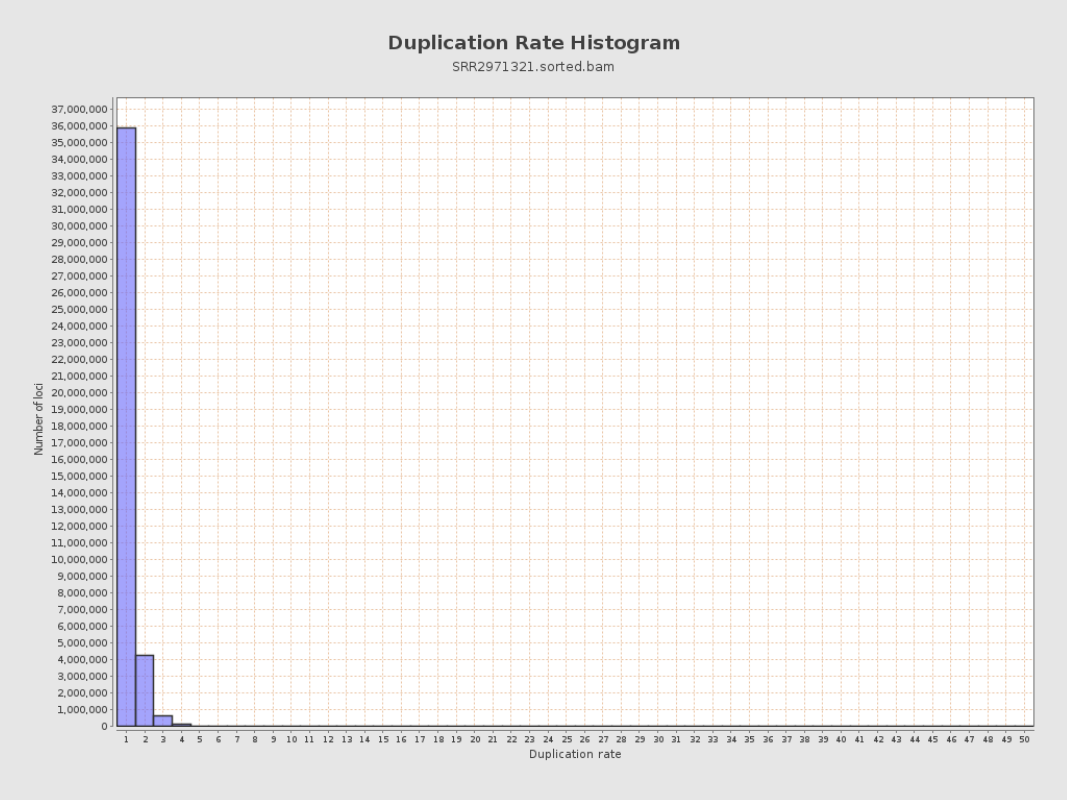
5. Results : Coverage Histogram (0-50X)



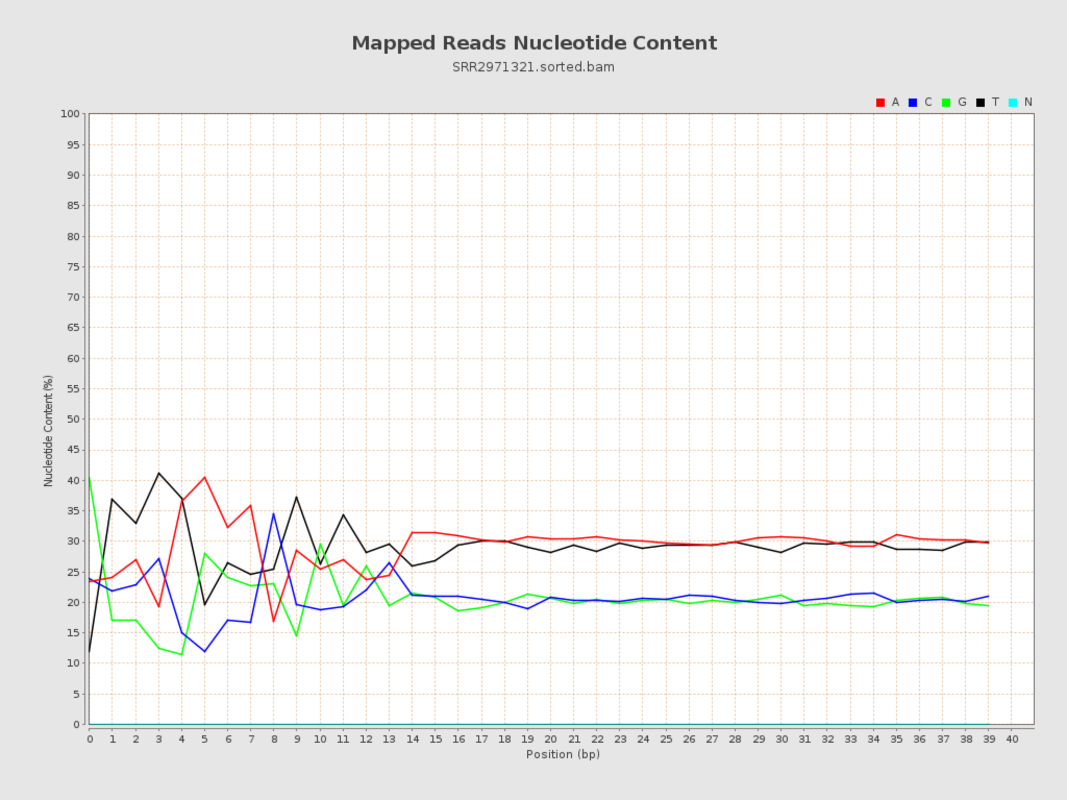
6. Results : Genome Fraction Coverage



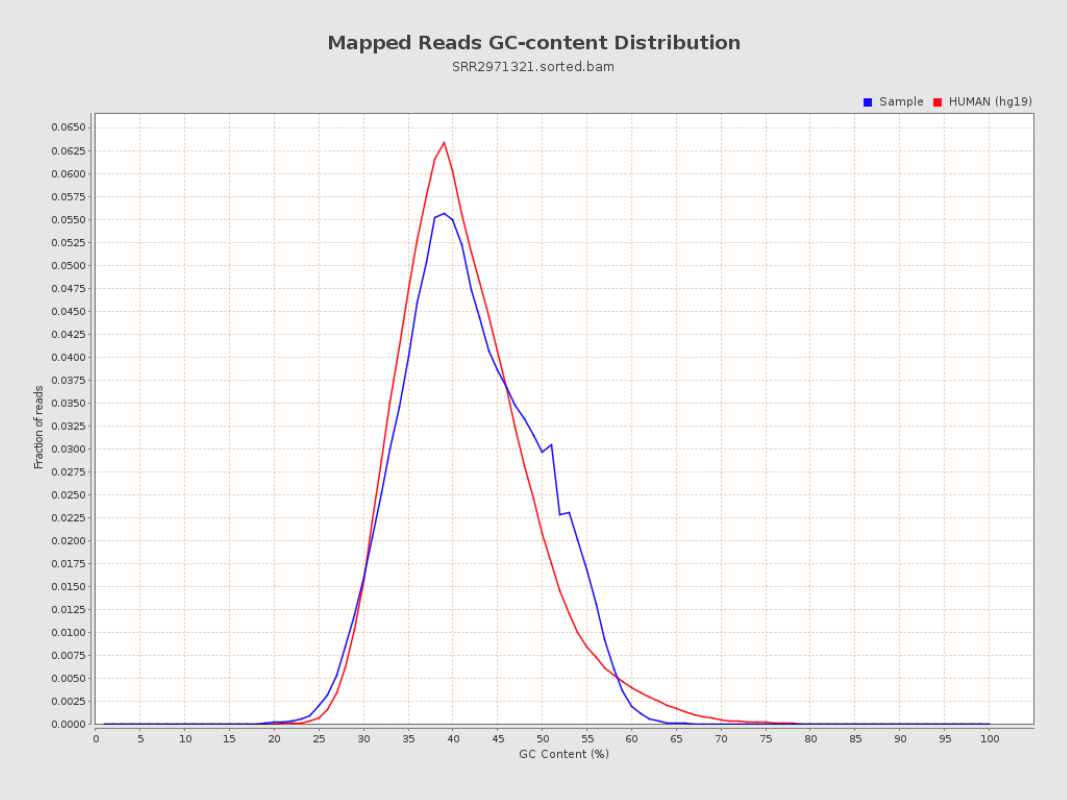
7. Results : Duplication Rate Histogram



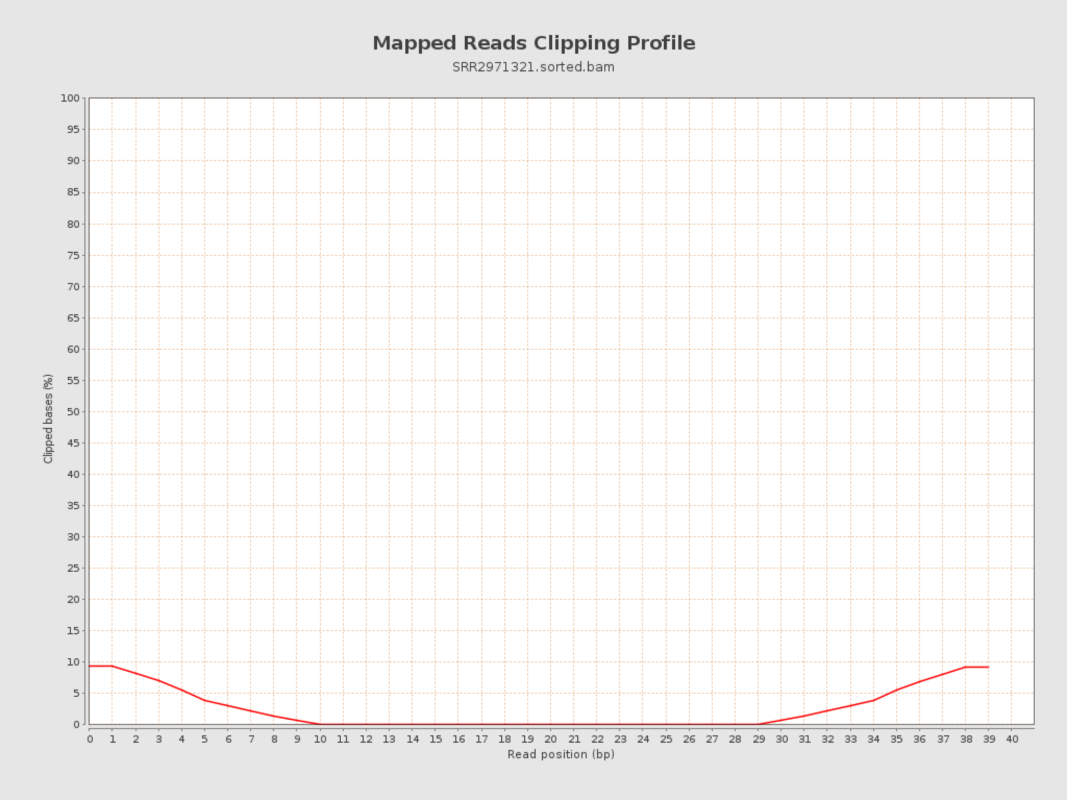
8. Results : Mapped Reads Nucleotide Content



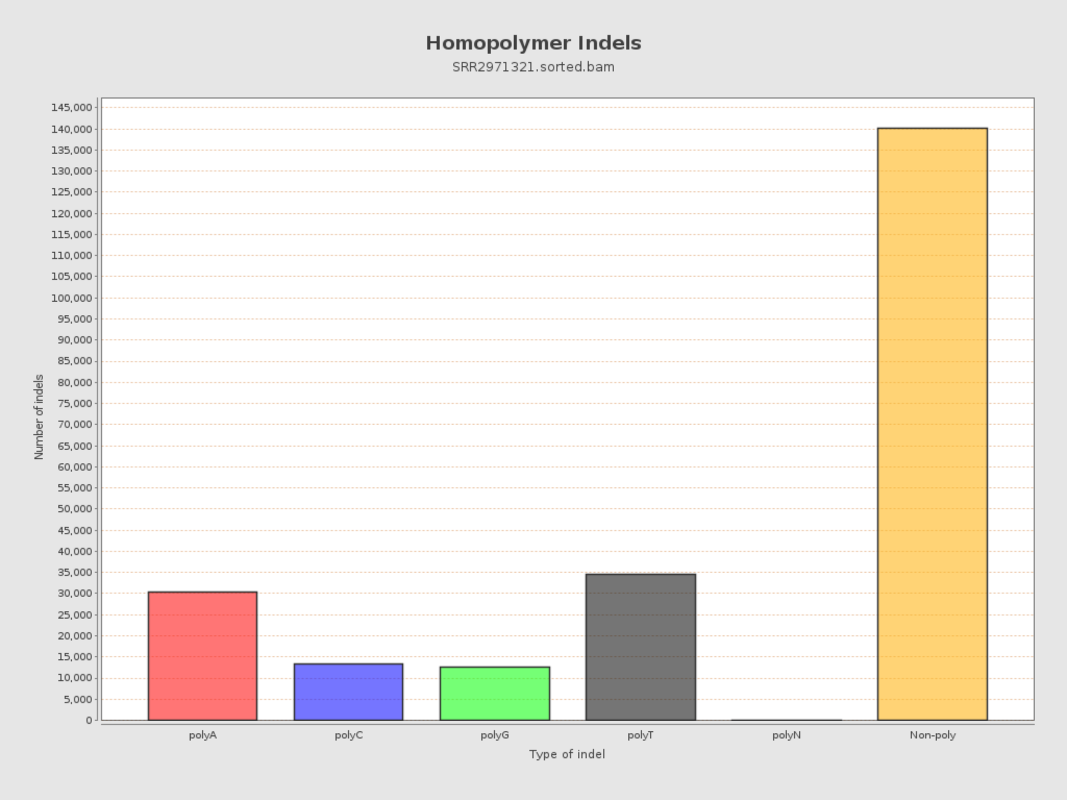
9. Results : Mapped Reads GC-content Distribution



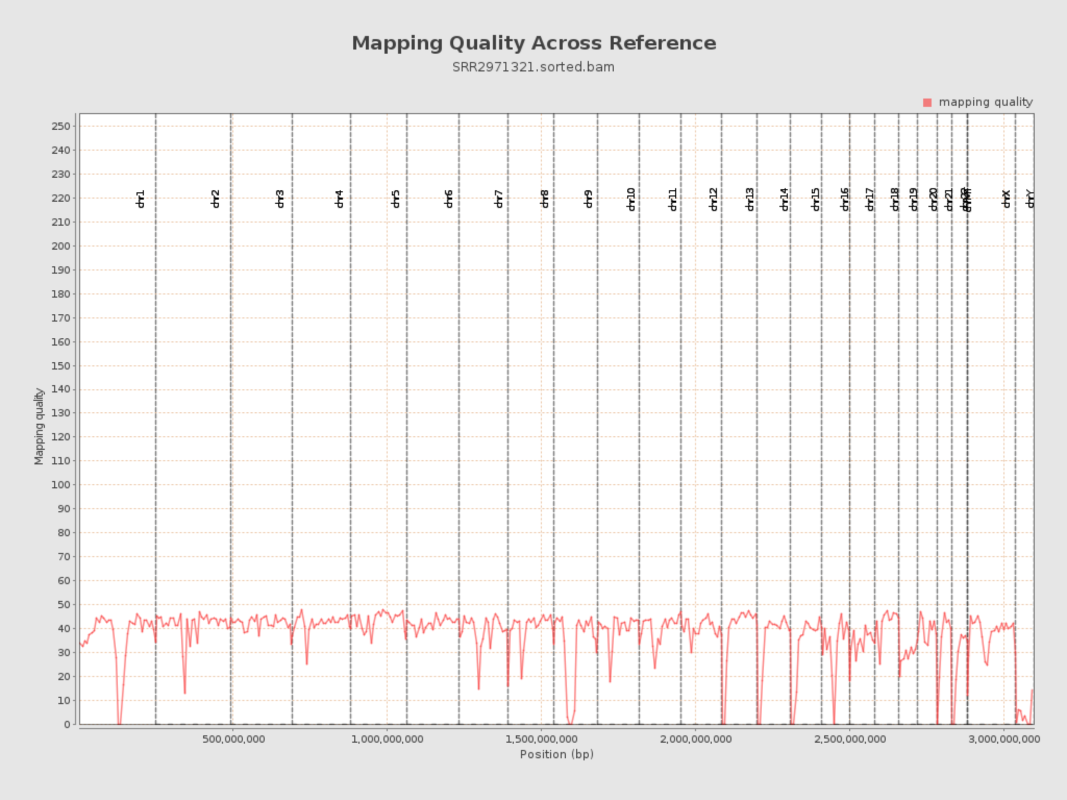
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram