Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:17:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971283.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_SRR2971283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971283.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:17:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,487,541
Mapped reads	7,949,877 / 83.79%
Unmapped reads	1,537,664 / 16.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	422,821 / 4.46%
Duplication rate	4.29%
Clipped reads	676,844 / 7.13%

2.2. ACGT Content

Number/percentage of A's	91,127,929 / 29.04%
Number/percentage of C's	63,460,853 / 20.22%
Number/percentage of T's	93,644,555 / 29.84%
Number/percentage of G's	65,589,427 / 20.9%
Number/percentage of N's	2,383 / 0%
GC Percentage	41.12%

2.3. Coverage

Mean	0.1014
Standard Deviation	0.7559

2.4. Mapping Quality

Mean Mapping Quality	42.61

2.5. Mismatches and indels

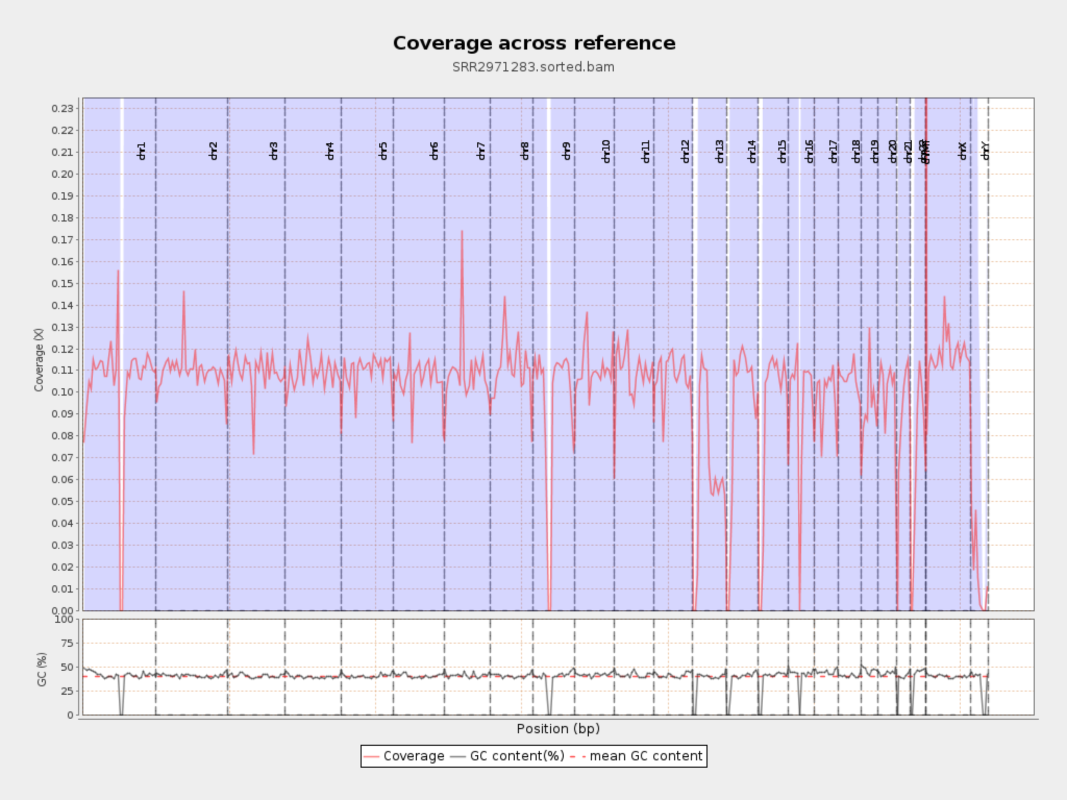
General error rate	0.28%
Mismatches	874,065
Insertions	10,343
Mapped reads with at least one insertion	0.13%
Deletions	25,229
Mapped reads with at least one deletion	0.32%
Homopolymer indels	42.13%

2.6. Chromosome stats

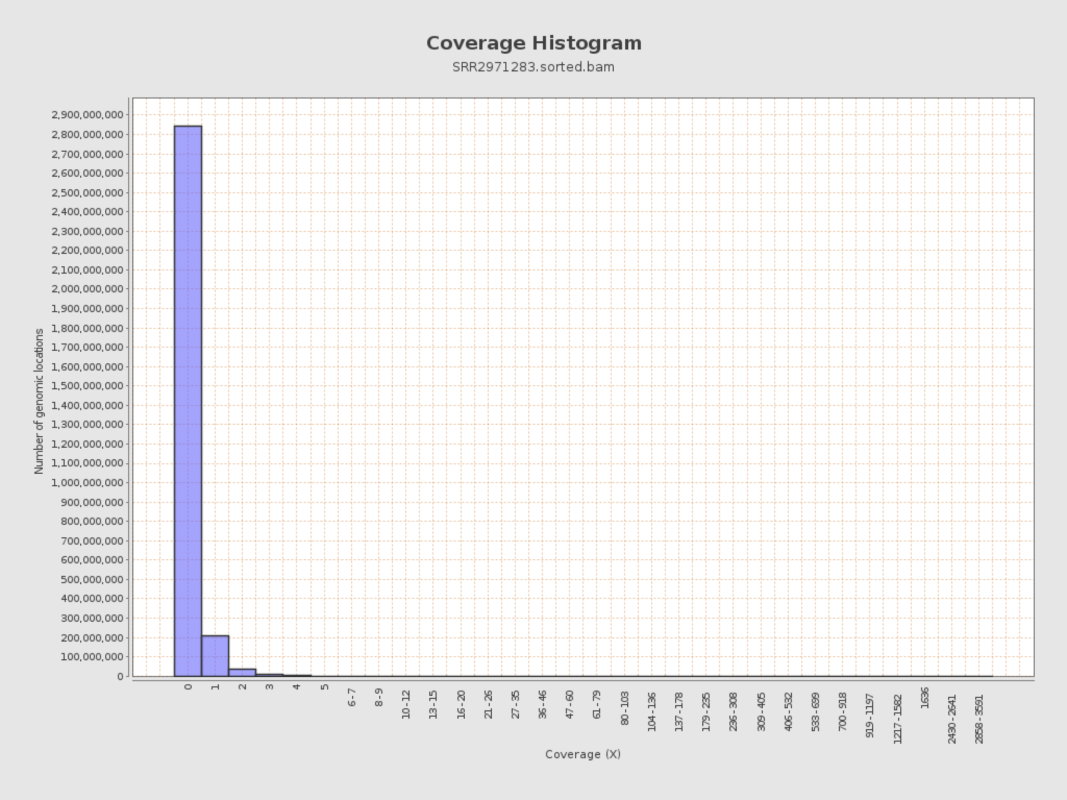
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25771306	0.1034	1.2598
chr2	243199373	26797554	0.1102	0.5976
chr3	198022430	21656039	0.1094	0.3979
chr4	191154276	20853857	0.1091	0.4175
chr5	180915260	19790445	0.1094	0.408
chr6	171115067	18298879	0.1069	0.4336
chr7	159138663	17407646	0.1094	1.0479
chr8	146364022	16306436	0.1114	1.794

chr9	141213431	13398200	0.0949	0.6109
chr10	135534747	14955207	0.1103	0.5749
chr11	135006516	14761566	0.1093	0.6318
chr12	133851895	14486037	0.1082	0.4158
chr13	115169878	7188007	0.0624	0.292
chr14	107349540	9799258	0.0913	0.484
chr15	102531392	8992977	0.0877	0.3504
chr16	90354753	8404731	0.093	0.4027
chr17	81195210	7982120	0.0983	0.4263
chr18	78077248	8333129	0.1067	1.2251
chr19	59128983	5556216	0.094	1.1248
chr20	63025520	6440353	0.1022	0.4068
chr21	48129895	4096544	0.0851	0.4053
chr22	51304566	3505988	0.0683	0.3096
chrMT	16571	26038	1.5713	2.0088
chrX	155270560	18093484	0.1165	0.5269
chrY	59373566	955352	0.0161	0.2185

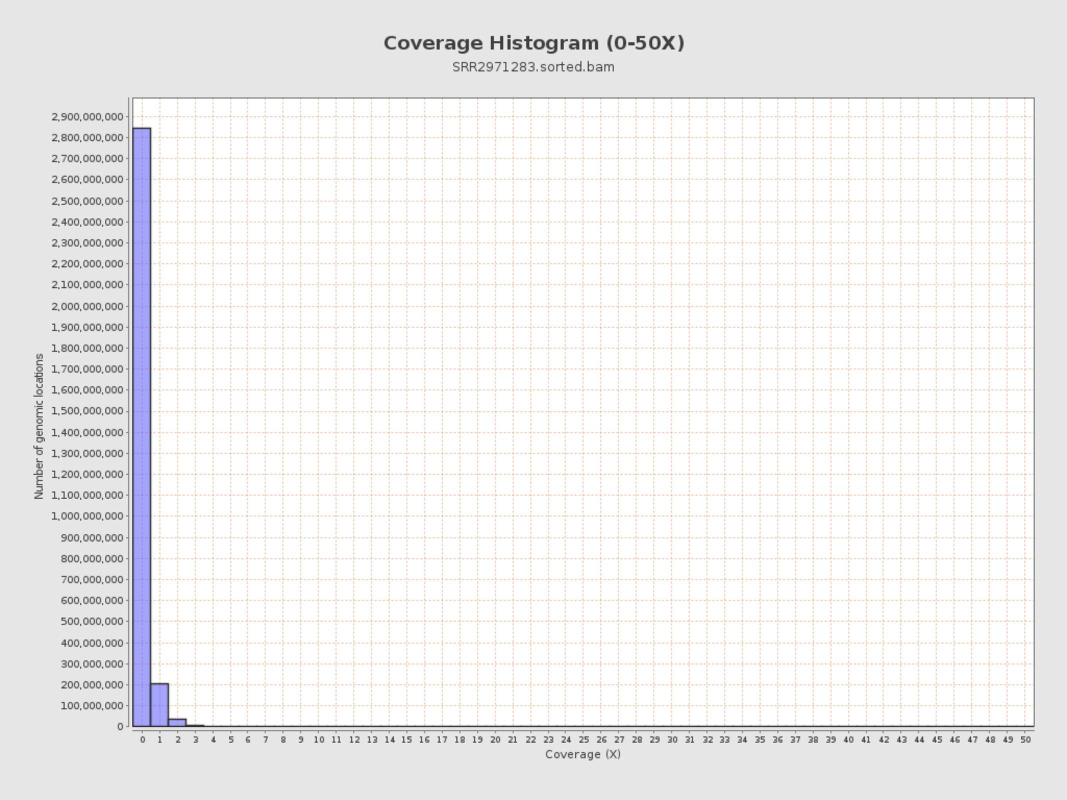
3. Results : Coverage across reference



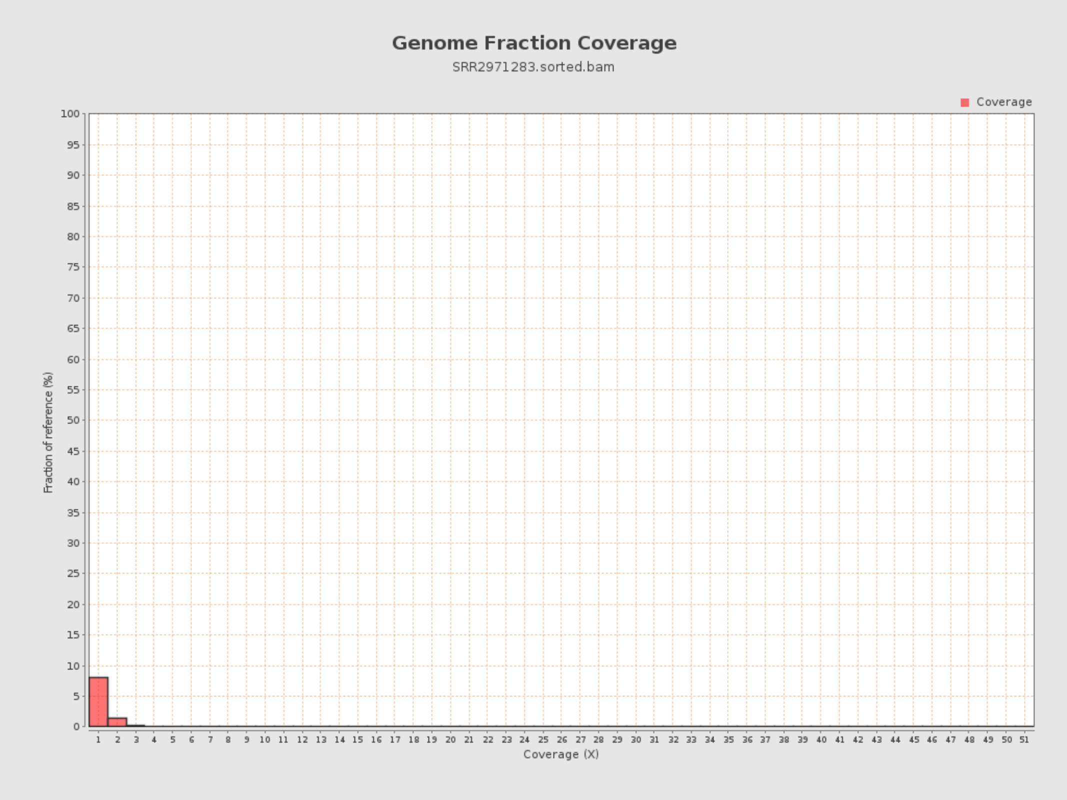
4. Results : Coverage Histogram



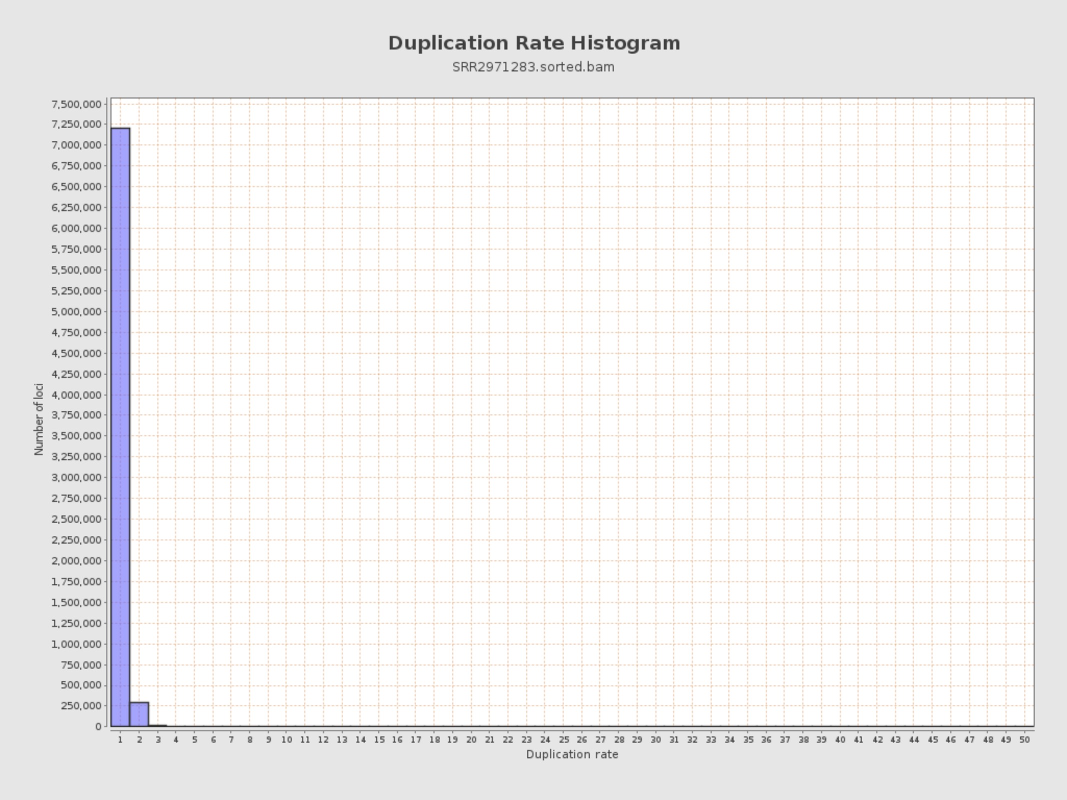
5. Results : Coverage Histogram (0-50X)



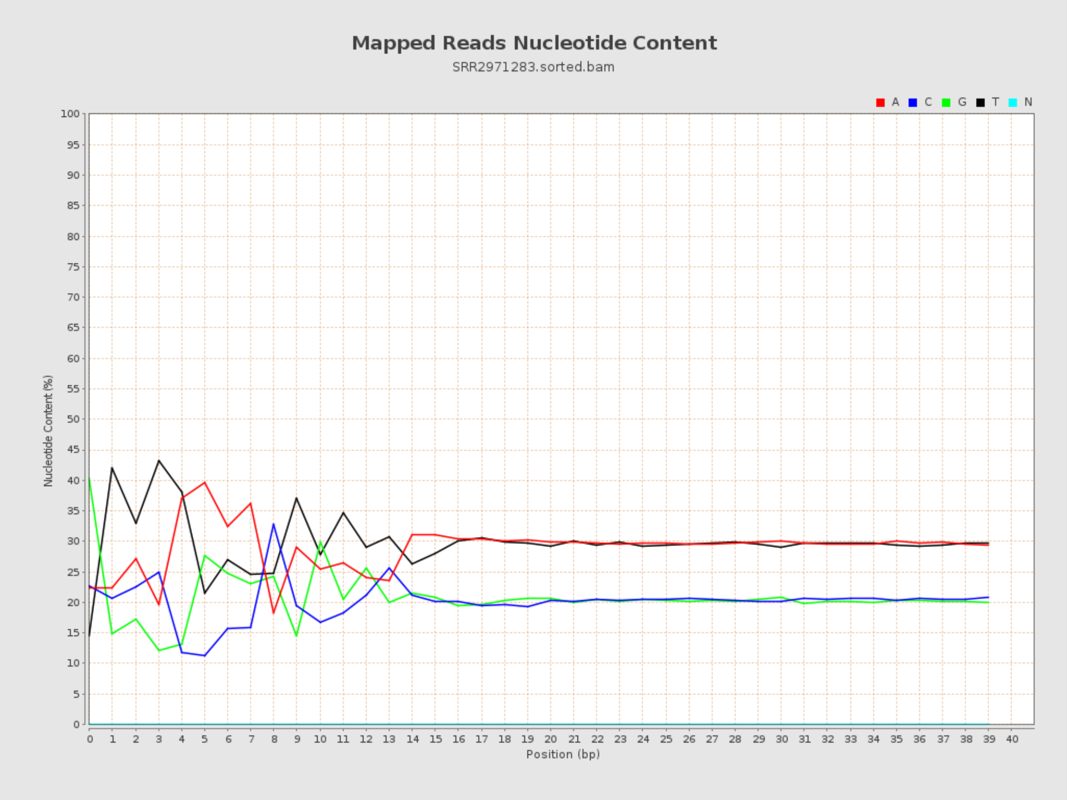
6. Results : Genome Fraction Coverage



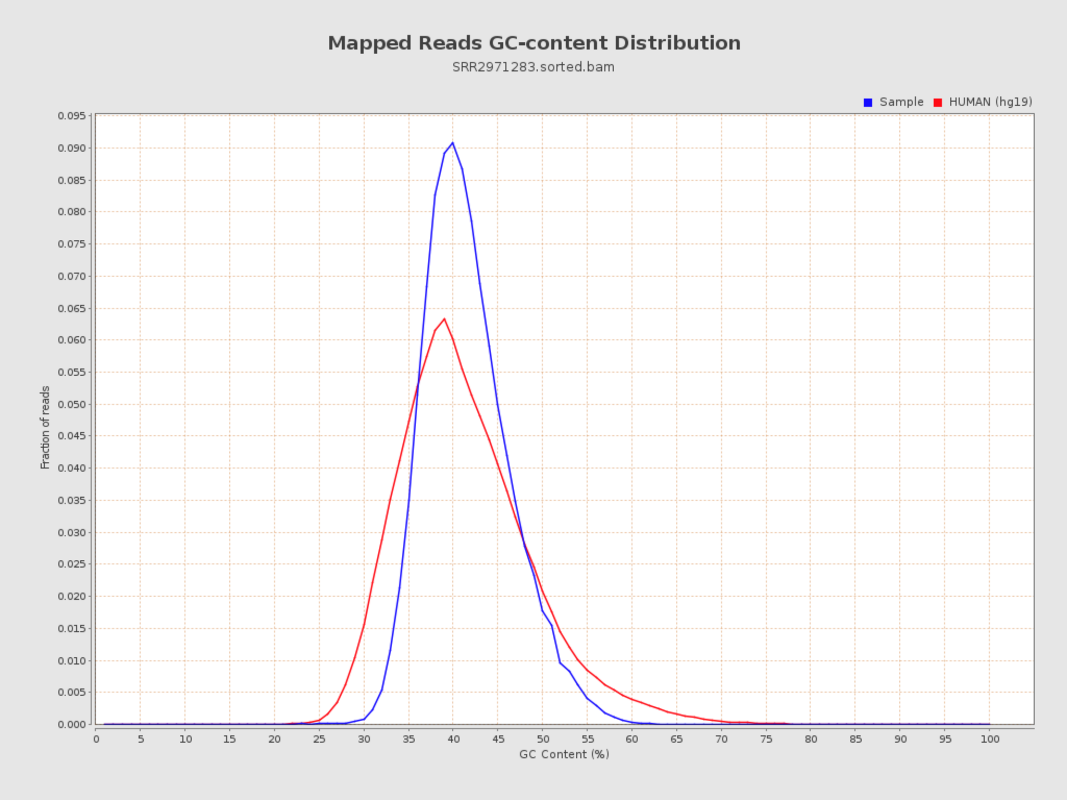
7. Results : Duplication Rate Histogram



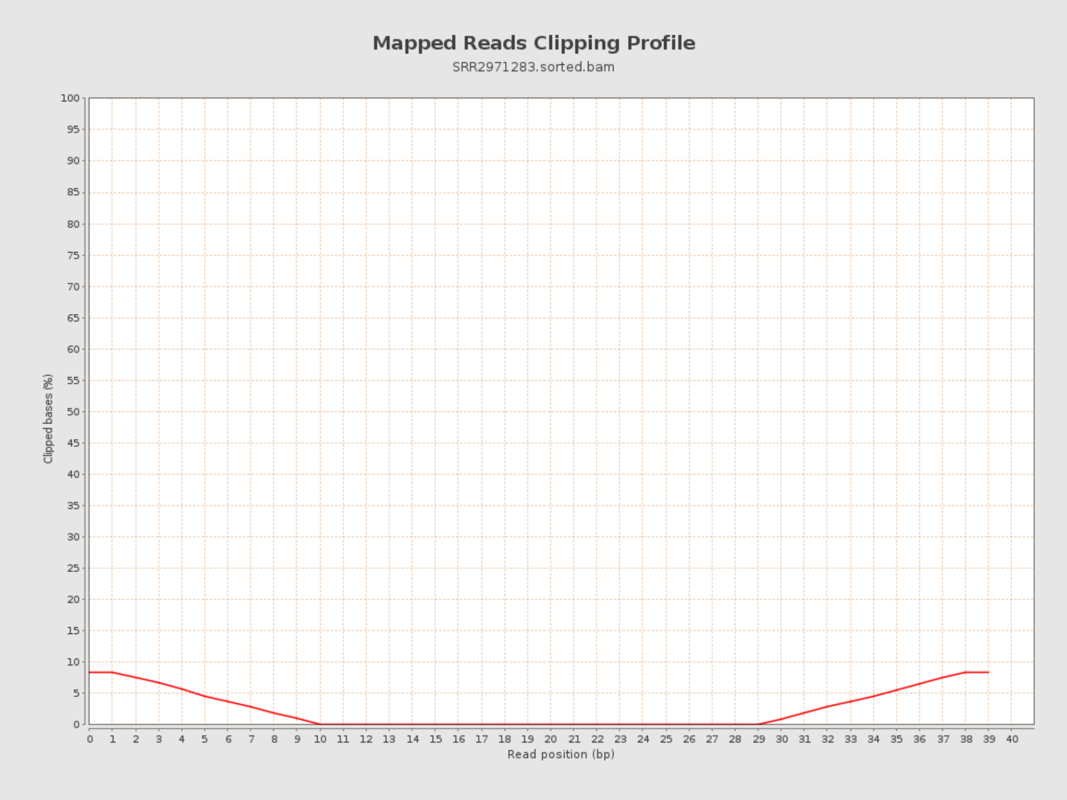
8. Results : Mapped Reads Nucleotide Content



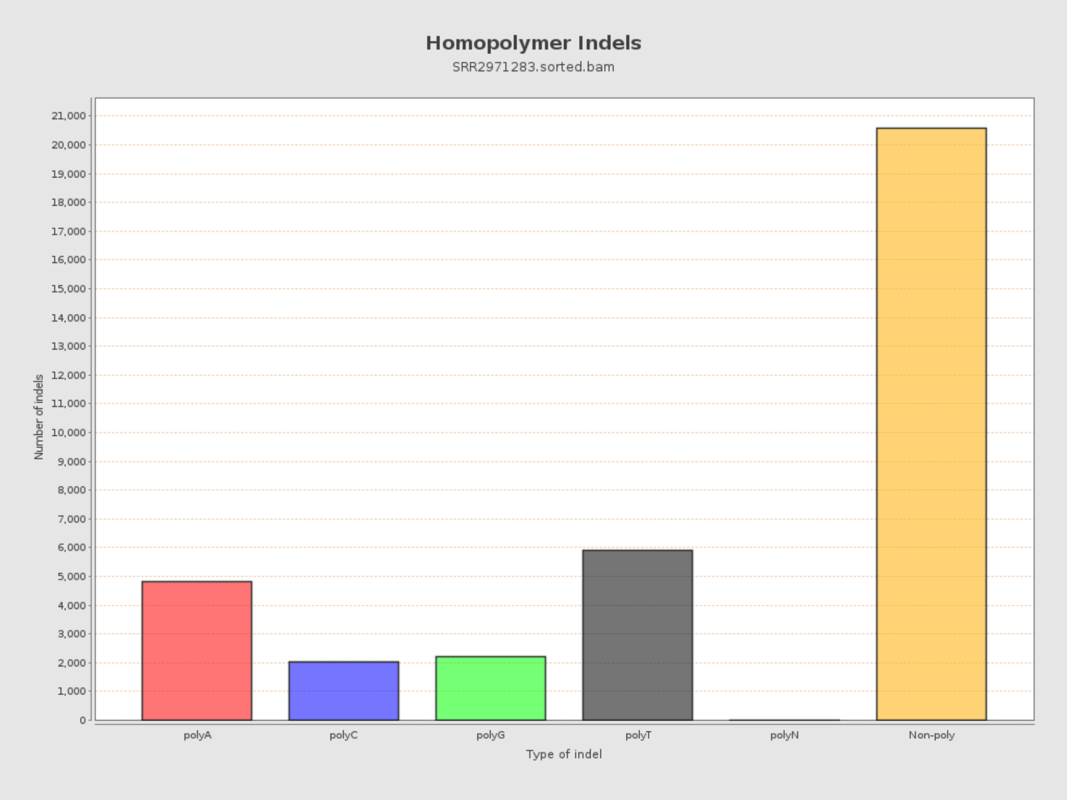
9. Results : Mapped Reads GC-content Distribution



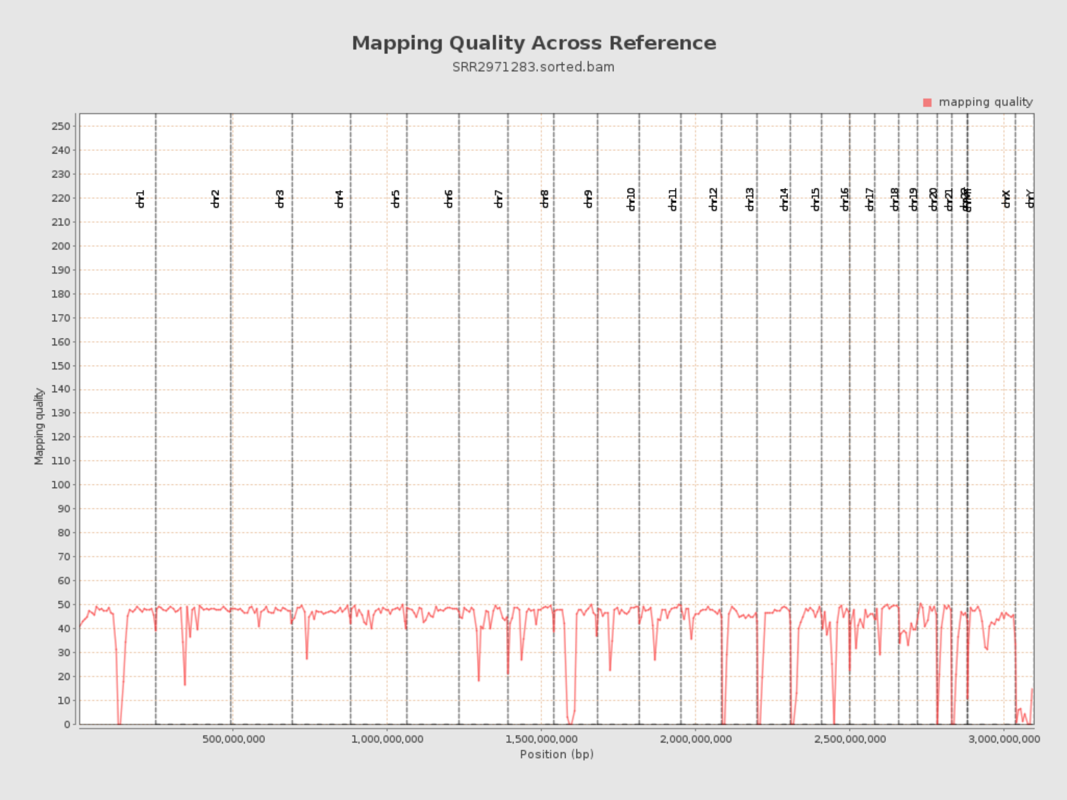
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram