Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:24:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971277.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_SRR2971277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971277.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:24:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,953,542
Mapped reads	8,667,412 / 72.51%
Unmapped reads	3,286,130 / 27.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	466,240 / 3.9%
Duplication rate	4.64%
Clipped reads	662,787 / 5.54%

2.2. ACGT Content

Number/percentage of A's	98,667,184 / 28.8%
Number/percentage of C's	70,750,729 / 20.65%
Number/percentage of T's	100,670,306 / 29.38%
Number/percentage of G's	72,500,379 / 21.16%
Number/percentage of N's	2,844 / 0%
GC Percentage	41.81%

2.3. Coverage

Mean	0.1107
Standard Deviation	0.7318

2.4. Mapping Quality

Mean Mapping Quality	43.33

2.5. Mismatches and indels

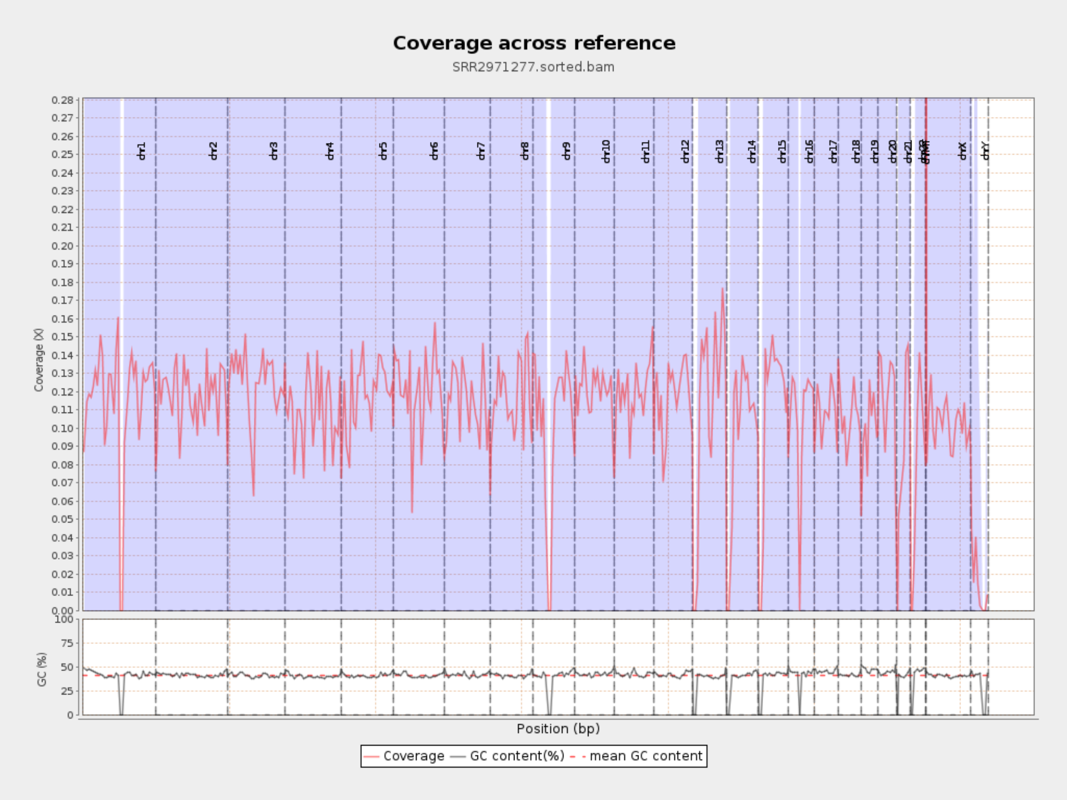
General error rate	0.28%
Mismatches	935,413
Insertions	10,326
Mapped reads with at least one insertion	0.12%
Deletions	25,643
Mapped reads with at least one deletion	0.3%
Homopolymer indels	41.85%

2.6. Chromosome stats

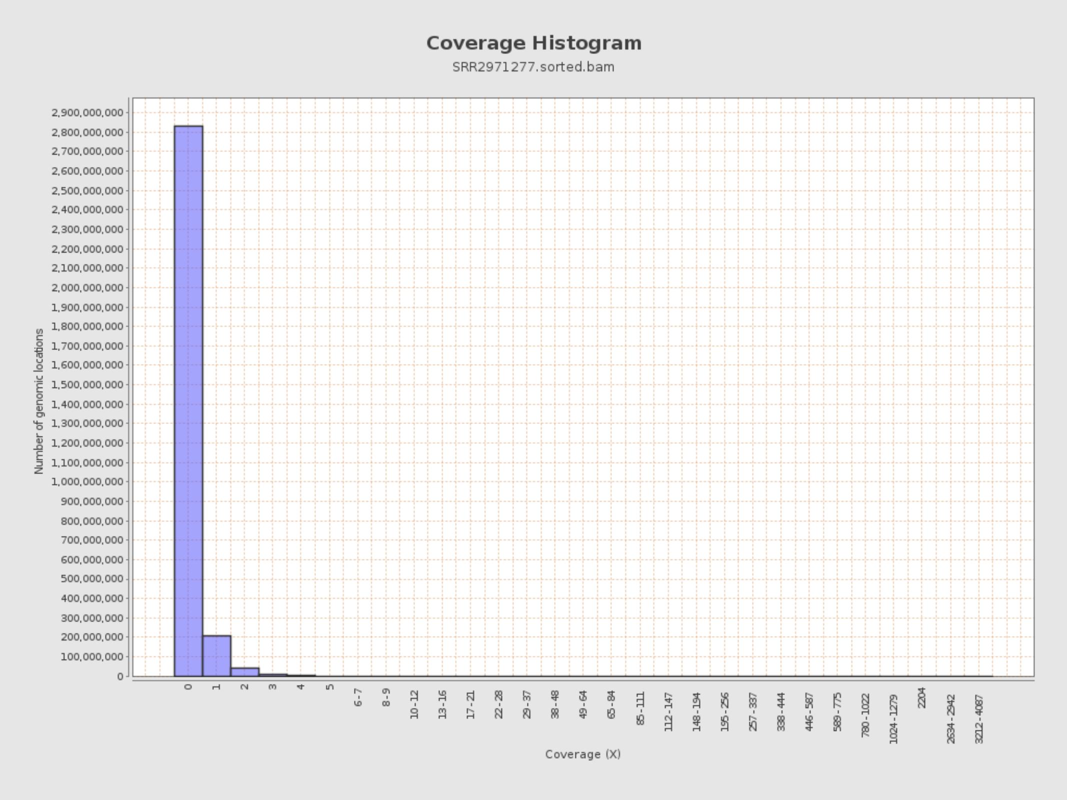
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28700192	0.1151	1.1125
chr2	243199373	28891949	0.1188	0.5534
chr3	198022430	24416084	0.1233	0.436
chr4	191154276	20893361	0.1093	0.4209
chr5	180915260	21462801	0.1186	0.4299
chr6	171115067	20617961	0.1205	0.5426
chr7	159138663	18216089	0.1145	0.8132
chr8	146364022	17129520	0.117	2.0165

chr9	141213431	14257294	0.101	0.5321
chr10	135534747	16468254	0.1215	0.5506
chr11	135006516	16126053	0.1194	0.6114
chr12	133851895	15898216	0.1188	0.4373
chr13	115169878	12883437	0.1119	0.4143
chr14	107349540	10426492	0.0971	0.427
chr15	102531392	10960745	0.1069	0.401
chr16	90354753	9391211	0.1039	0.4116
chr17	81195210	8919489	0.1099	0.4386
chr18	78077248	8313307	0.1065	0.8526
chr19	59128983	5896471	0.0997	0.9839
chr20	63025520	7606556	0.1207	0.4361
chr21	48129895	4269645	0.0887	0.4052
chr22	51304566	4021184	0.0784	0.3448
chrMT	16571	23734	1.4323	1.7976
chrX	155270560	15973018	0.1029	0.4511
chrY	59373566	861114	0.0145	0.2145

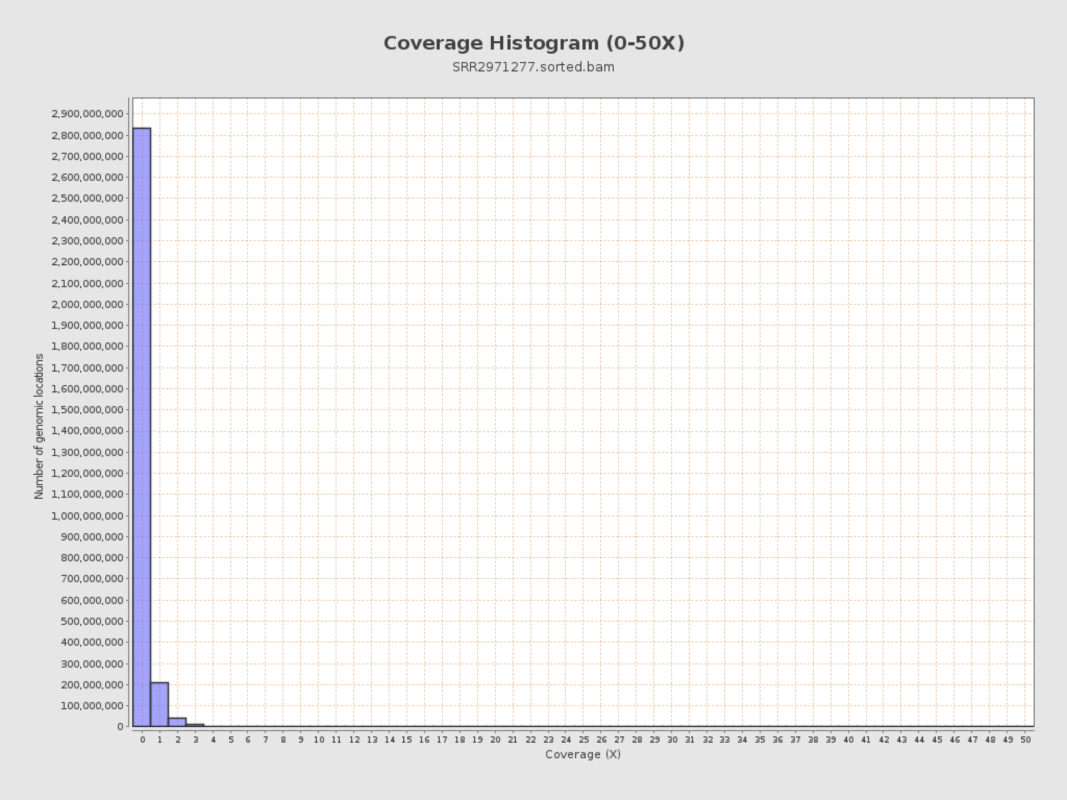
3. Results : Coverage across reference



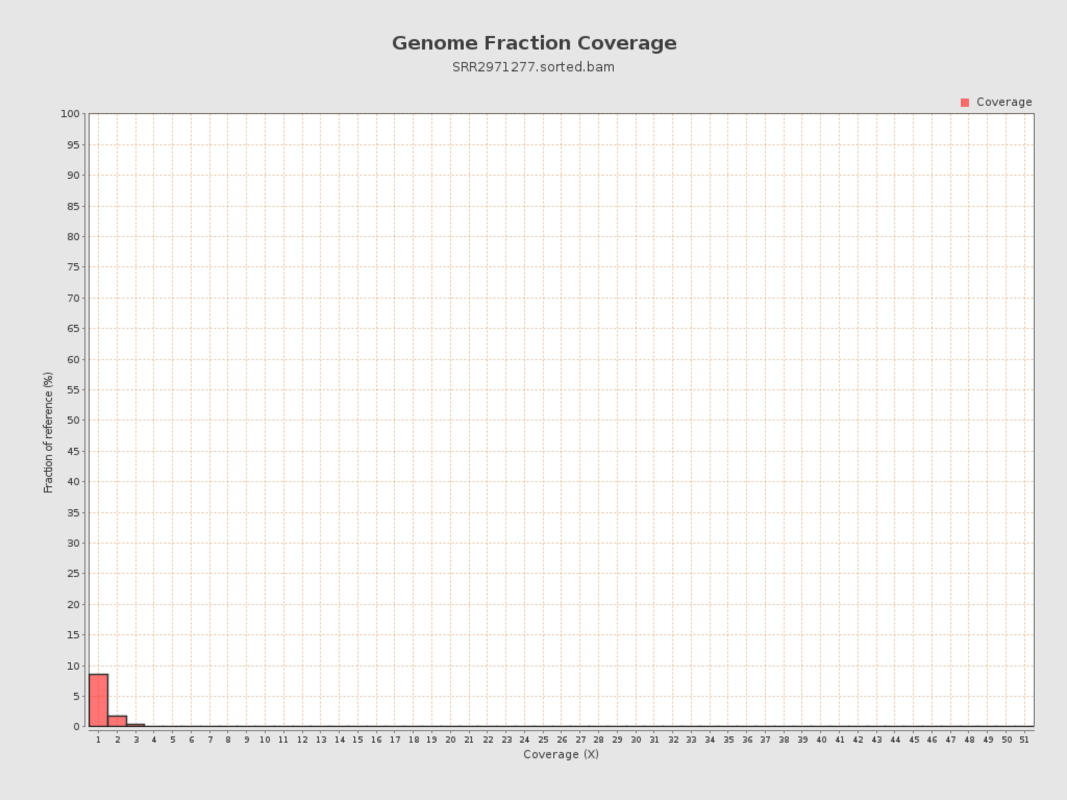
4. Results : Coverage Histogram



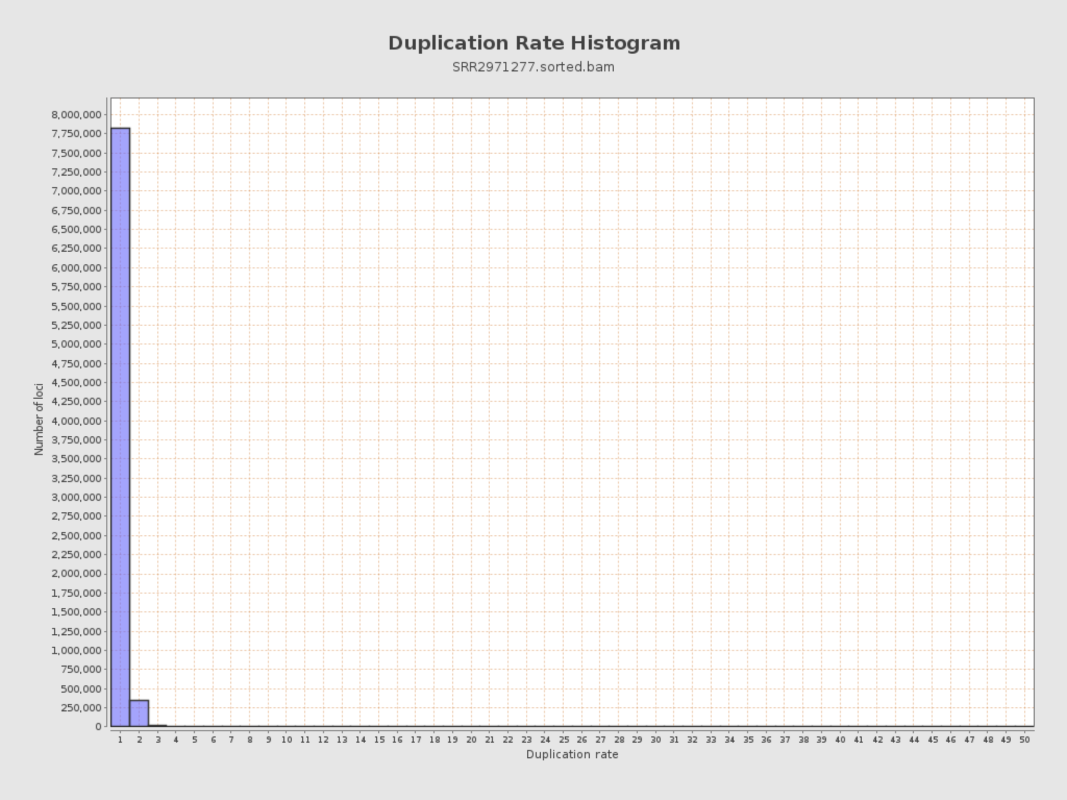
5. Results : Coverage Histogram (0-50X)



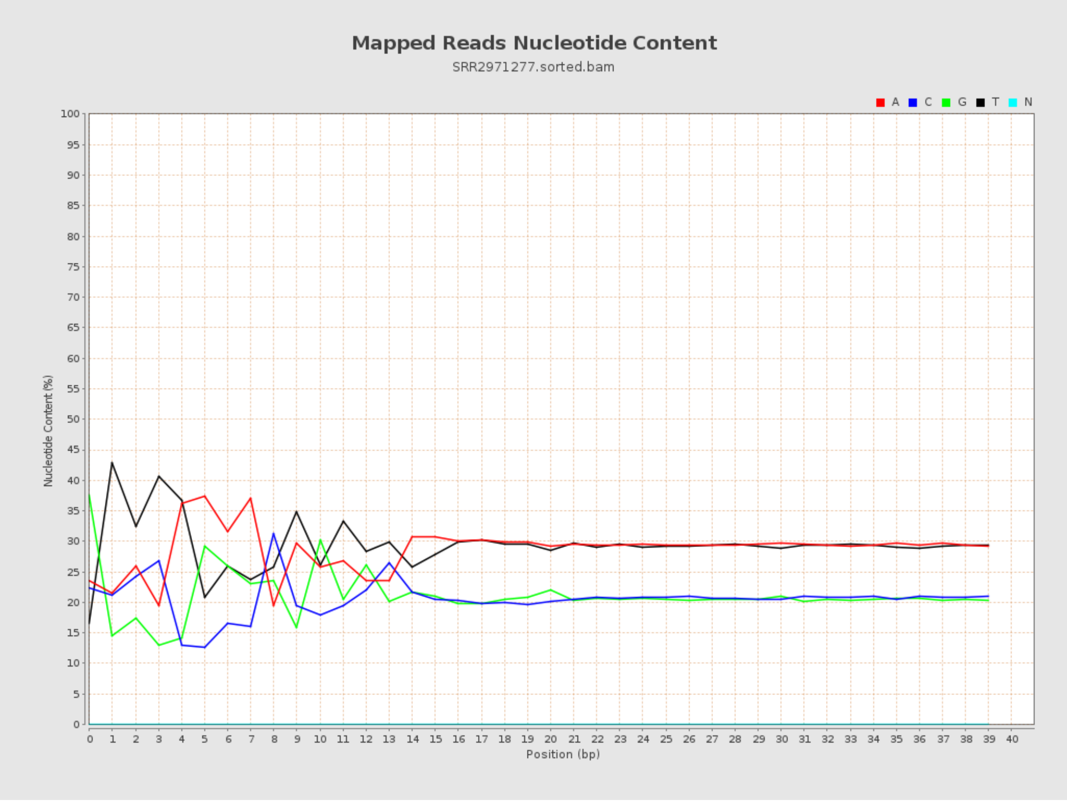
6. Results : Genome Fraction Coverage



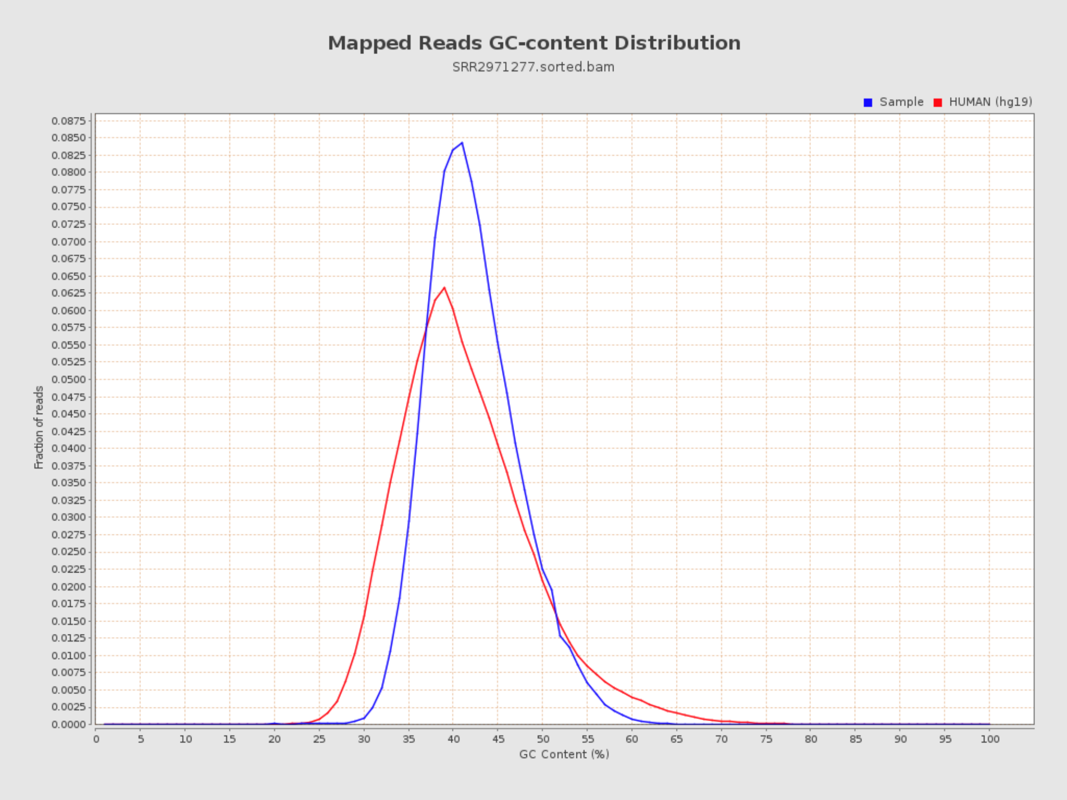
7. Results : Duplication Rate Histogram



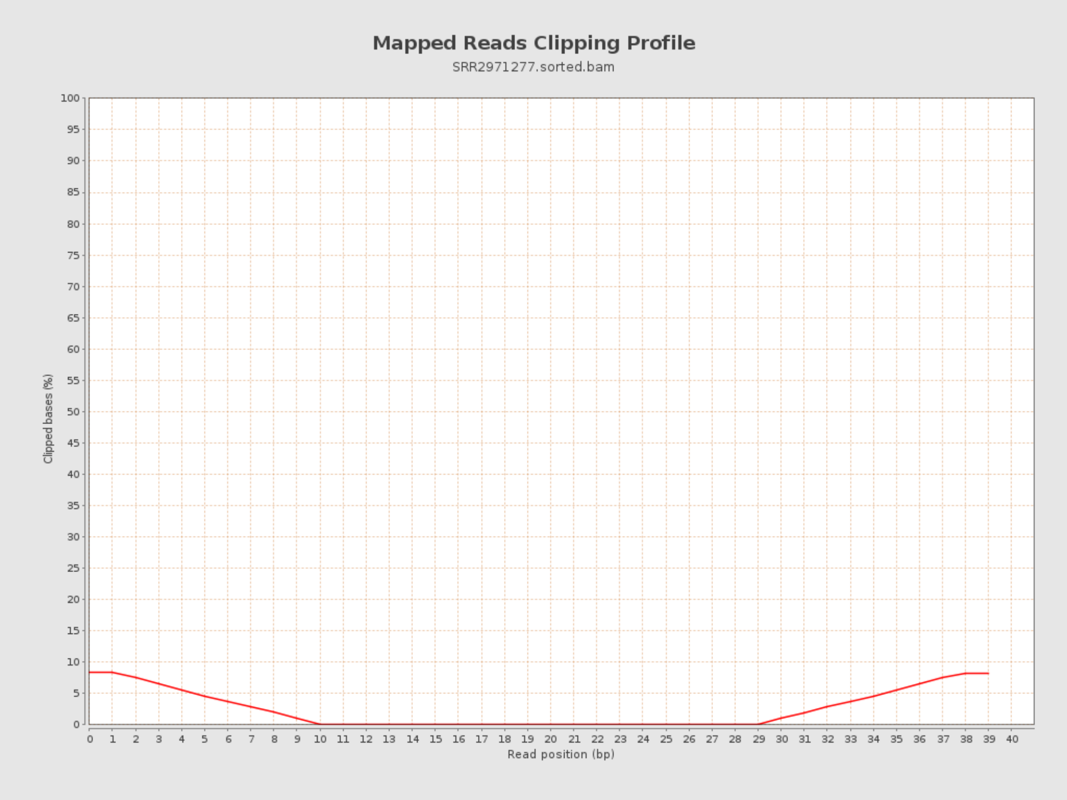
8. Results : Mapped Reads Nucleotide Content



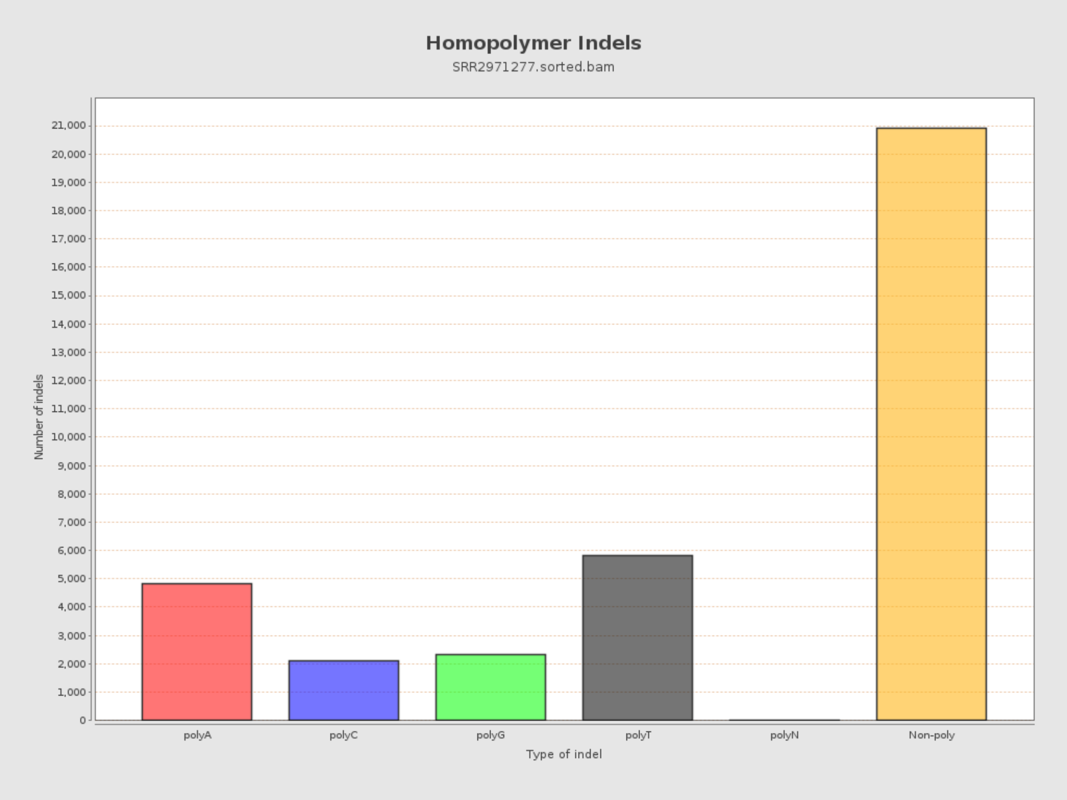
9. Results : Mapped Reads GC-content Distribution



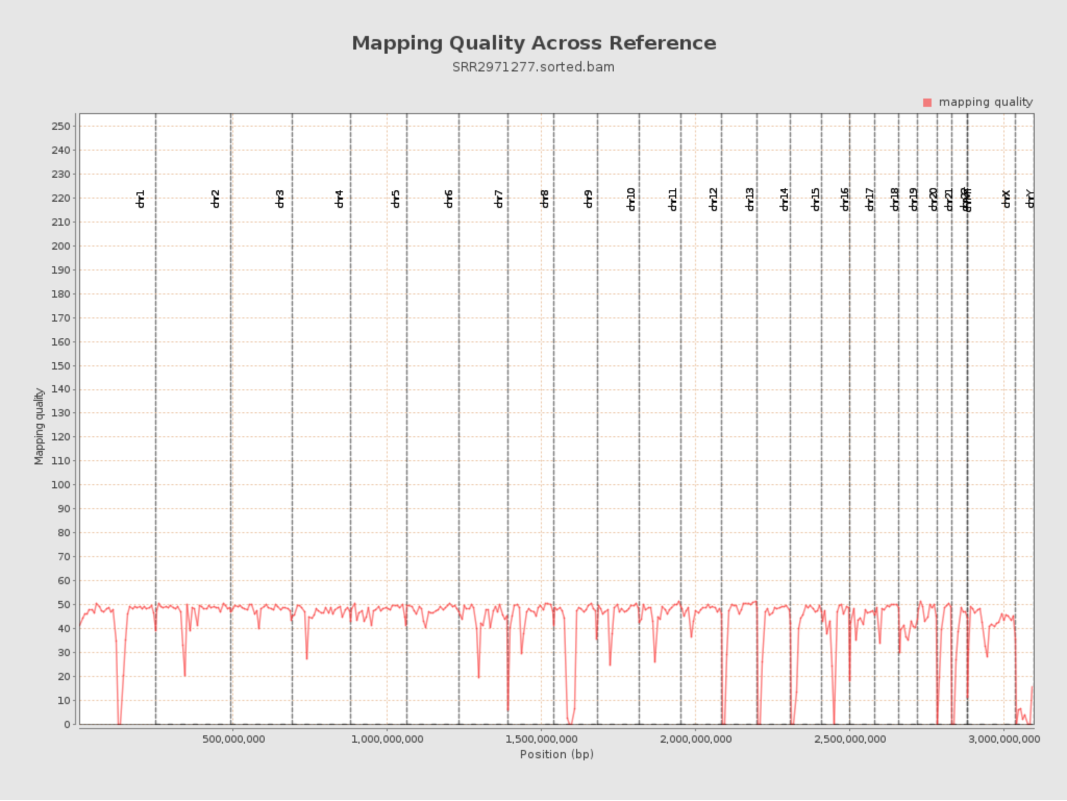
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram