Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:23:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971289.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_SRR2971289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:23:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,069,122
Mapped reads	7,597,359 / 83.77%
Unmapped reads	1,471,763 / 16.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	426,550 / 4.7%
Duplication rate	4.28%
Clipped reads	722,872 / 7.97%

2.2. ACGT Content

Number/percentage of A's	88,041,627 / 29.39%
Number/percentage of C's	60,060,546 / 20.05%
Number/percentage of T's	90,079,957 / 30.07%
Number/percentage of G's	61,401,102 / 20.49%
Number/percentage of N's	17,620 / 0.01%
GC Percentage	40.54%

2.3. Coverage

Mean	0.0968
Standard Deviation	0.8463

2.4. Mapping Quality

Mean Mapping Quality	41.19

2.5. Mismatches and indels

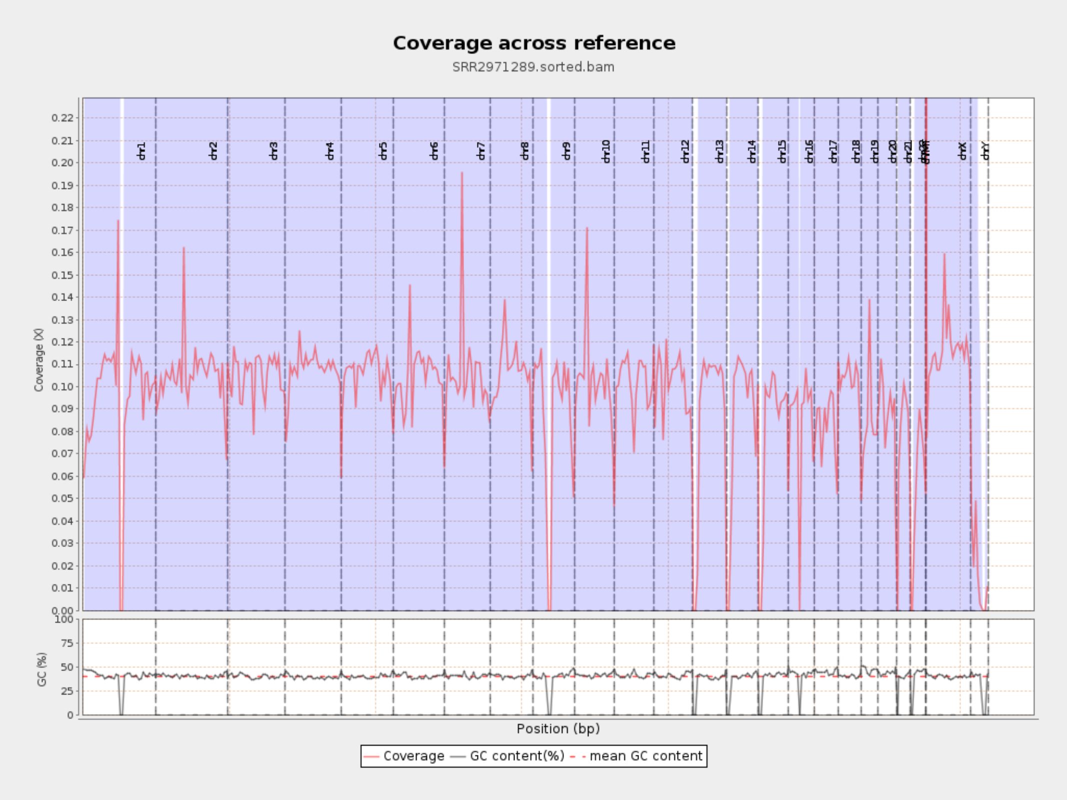
General error rate	0.3%
Mismatches	875,905
Insertions	10,177
Mapped reads with at least one insertion	0.13%
Deletions	24,770
Mapped reads with at least one deletion	0.33%
Homopolymer indels	40.91%

2.6. Chromosome stats

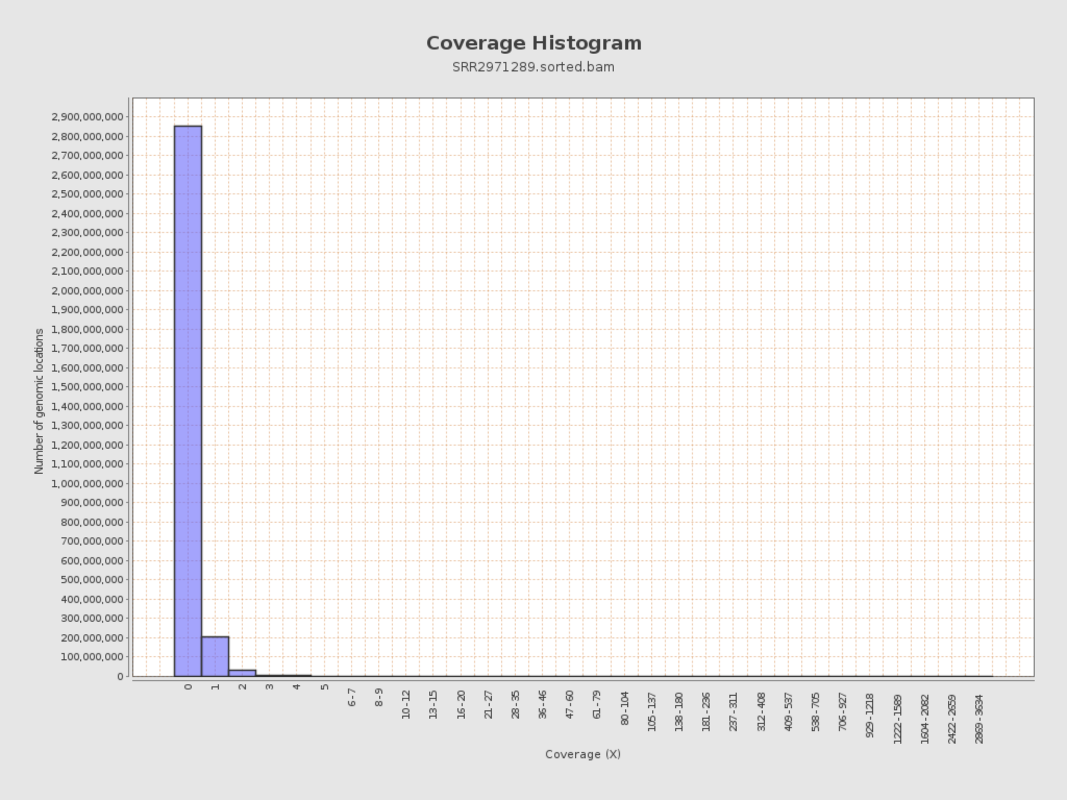
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23811774	0.0955	1.6344
chr2	243199373	25684113	0.1056	0.6505
chr3	198022430	20870916	0.1054	0.3862
chr4	191154276	20655915	0.1081	0.4141
chr5	180915260	19113160	0.1056	0.396
chr6	171115067	17978366	0.1051	0.5569
chr7	159138663	16797574	0.1056	1.1951
chr8	146364022	15574662	0.1064	1.8194

chr9	141213431	12312528	0.0872	0.636
chr10	135534747	14021517	0.1035	0.7093
chr11	135006516	13637477	0.101	0.559
chr12	133851895	13496548	0.1008	0.4009
chr13	115169878	9993532	0.0868	0.3421
chr14	107349540	9188878	0.0856	0.4819
chr15	102531392	7991545	0.0779	0.3281
chr16	90354753	7469761	0.0827	0.4285
chr17	81195210	6787778	0.0836	0.385
chr18	78077248	8099344	0.1037	1.2343
chr19	59128983	5052231	0.0854	1.5219
chr20	63025520	5693359	0.0903	0.3867
chr21	48129895	3619029	0.0752	0.4033
chr22	51304566	2796160	0.0545	0.275
chrMT	16571	24024	1.4498	1.7141
chrX	155270560	17973930	0.1158	0.5385
chrY	59373566	987549	0.0166	0.2307

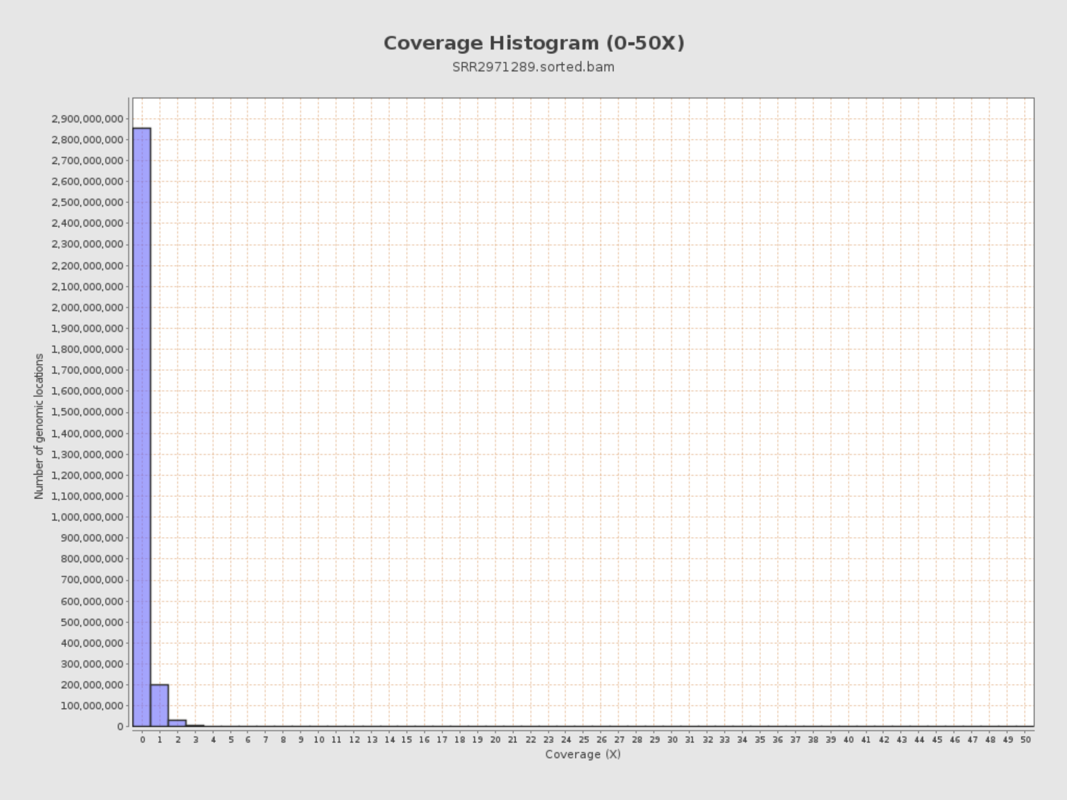
3. Results : Coverage across reference



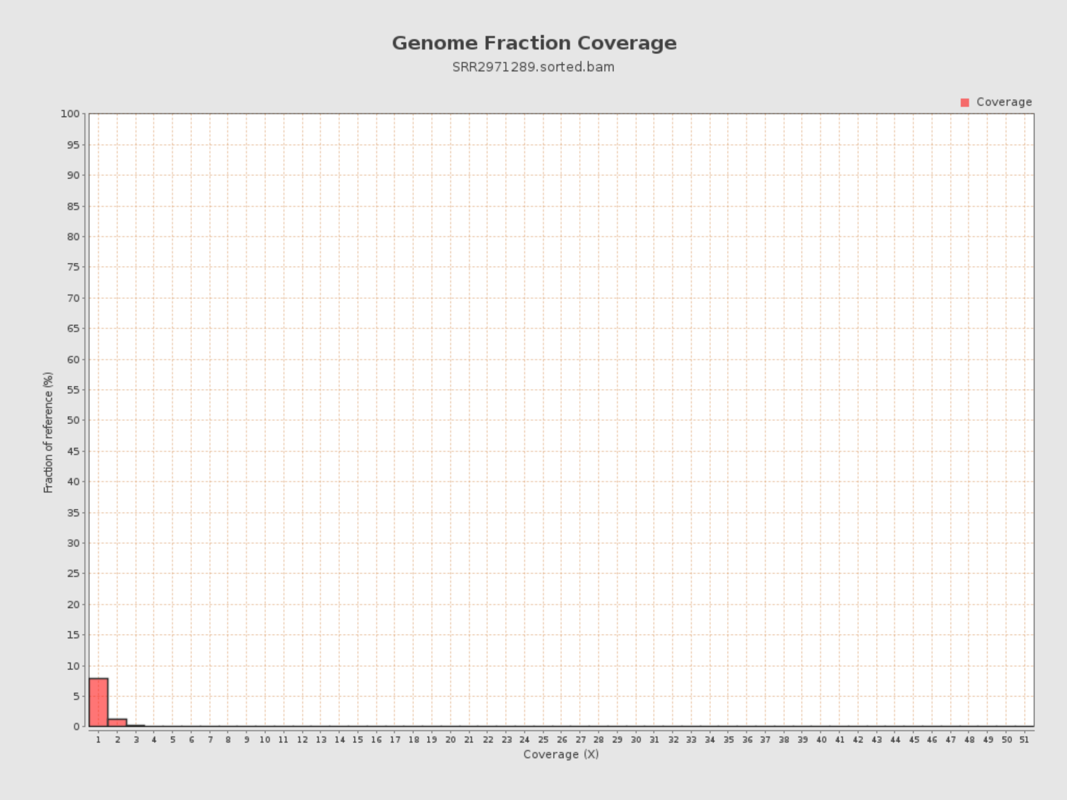
4. Results : Coverage Histogram



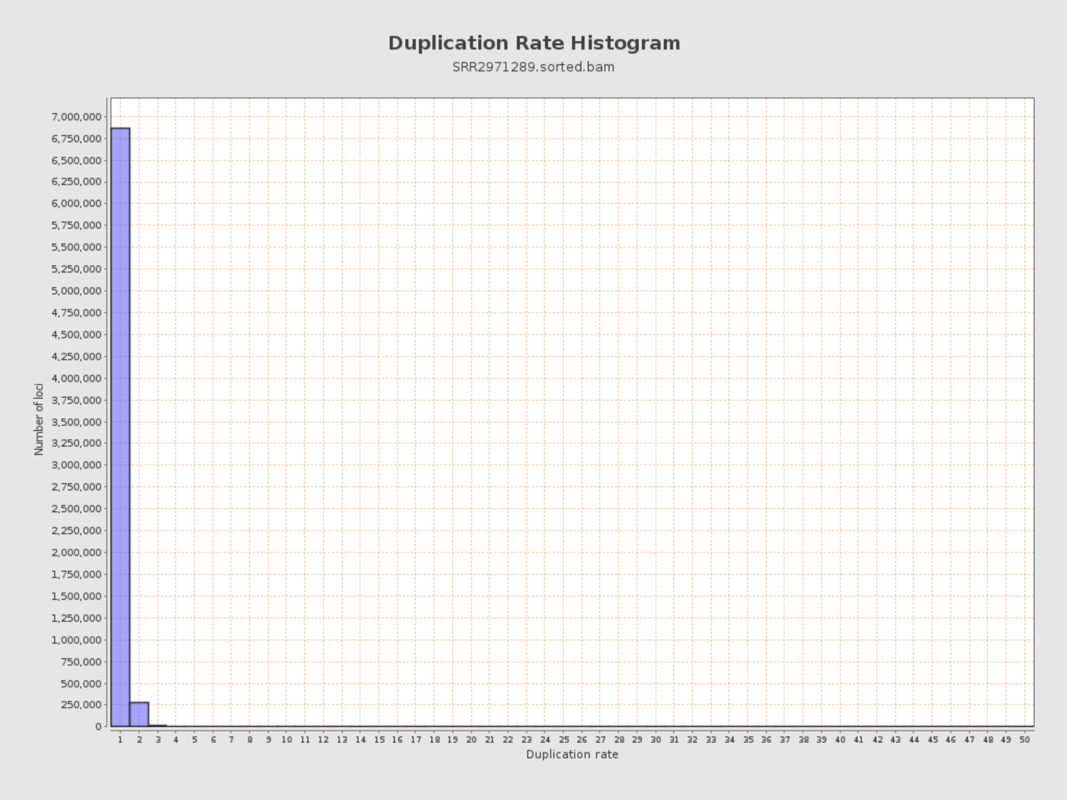
5. Results : Coverage Histogram (0-50X)



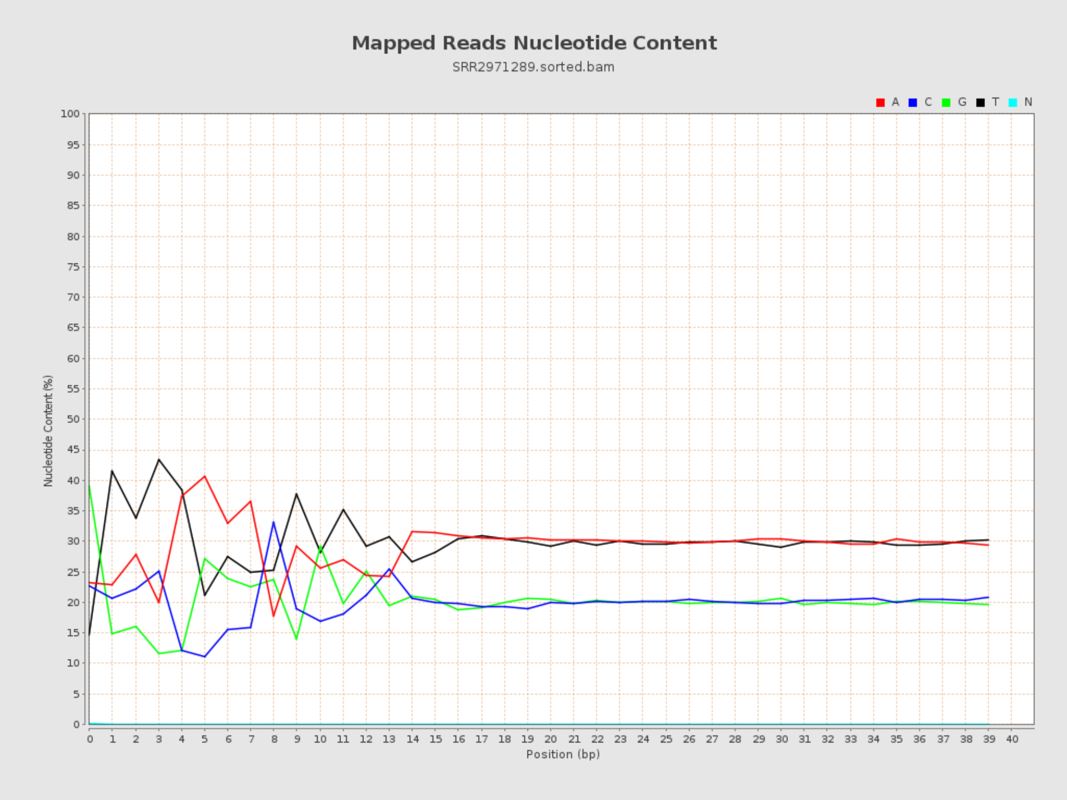
6. Results : Genome Fraction Coverage



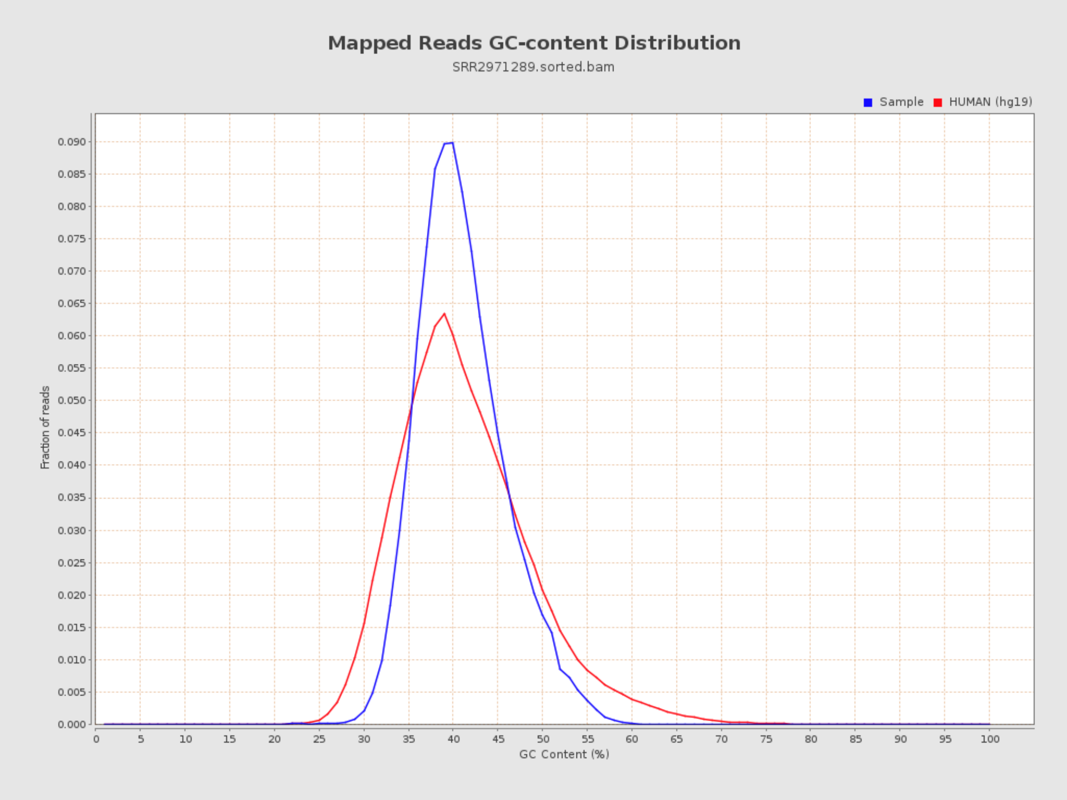
7. Results : Duplication Rate Histogram



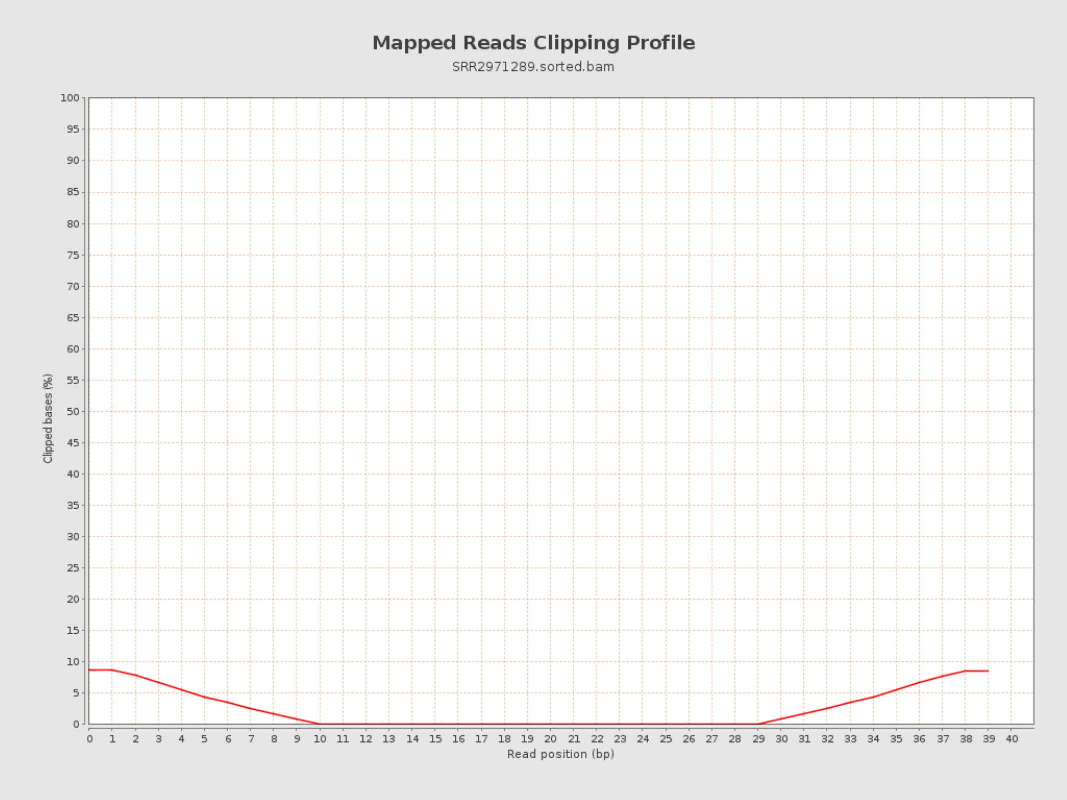
8. Results : Mapped Reads Nucleotide Content



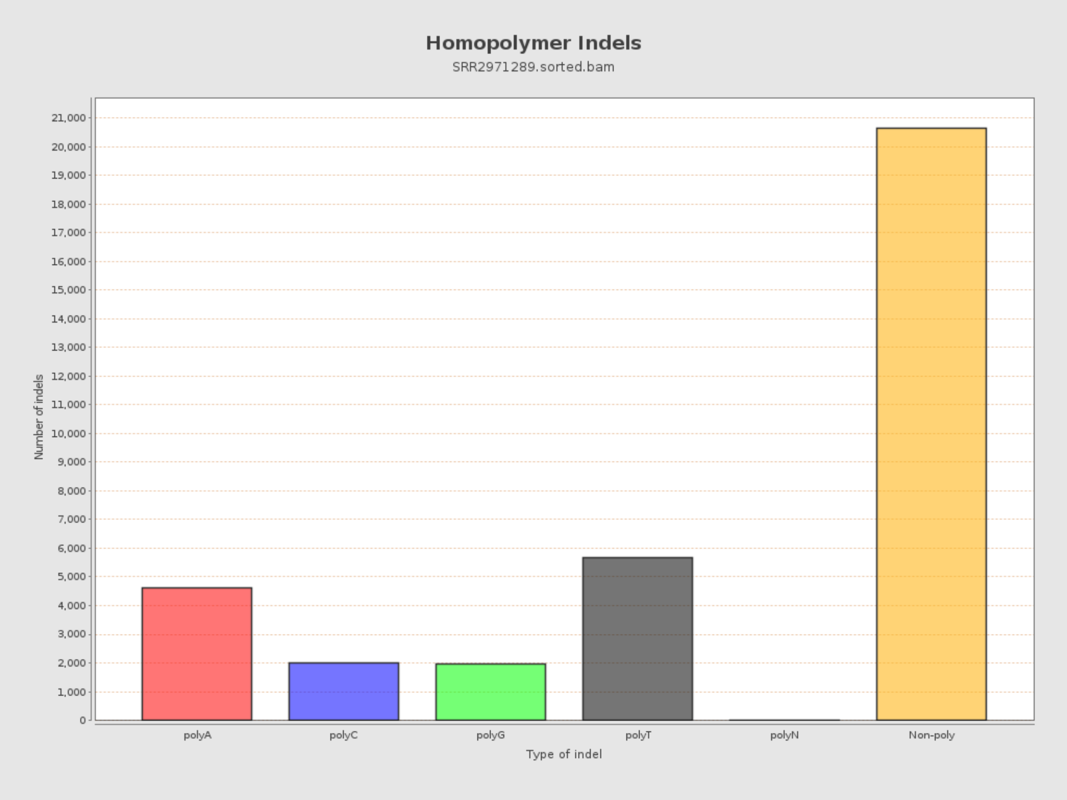
9. Results : Mapped Reads GC-content Distribution



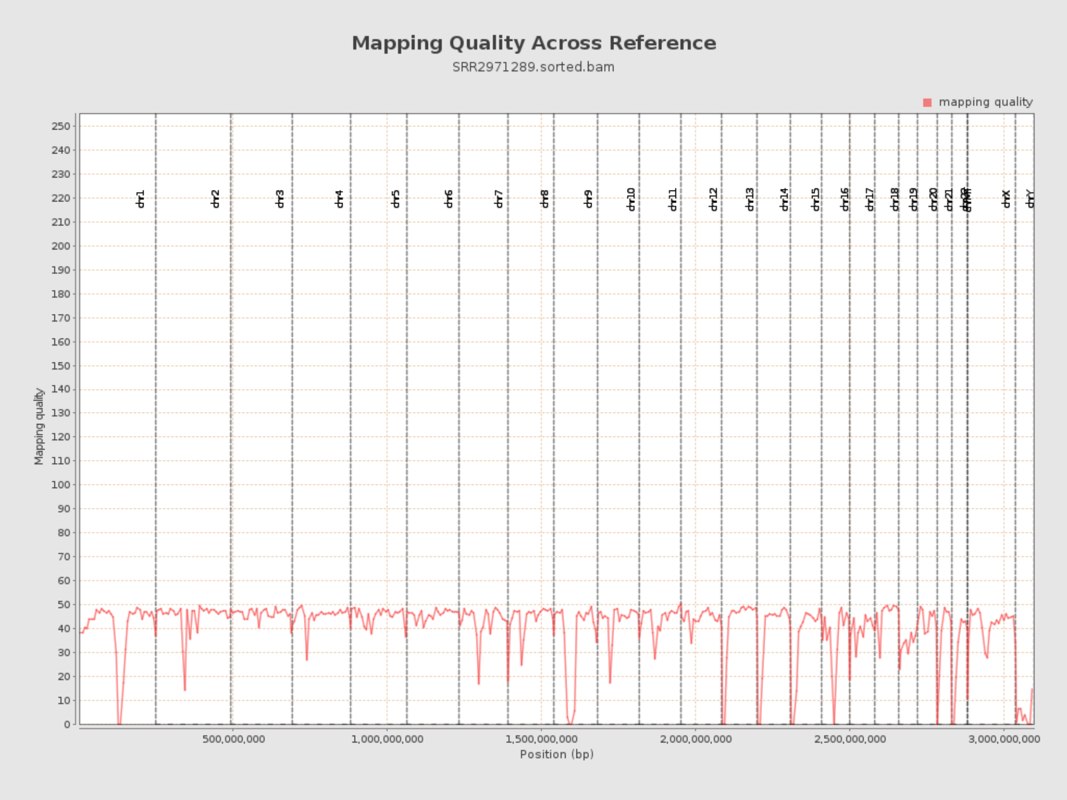
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram