Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:08:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971282.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_SRR2971282 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971282.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:08:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971282.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,131,660
Mapped reads	10,202,431 / 72.2%
Unmapped reads	3,929,229 / 27.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	1,072,311 / 7.59%
Duplication rate	9.13%
Clipped reads	880,270 / 6.23%

2.2. ACGT Content

Number/percentage of A's	114,665,604 / 28.48%
Number/percentage of C's	84,337,639 / 20.94%
Number/percentage of T's	116,820,710 / 29.01%
Number/percentage of G's	86,856,882 / 21.57%
Number/percentage of N's	3,475 / 0%
GC Percentage	42.51%

2.3. Coverage

Mean	0.1301
Standard Deviation	1.6096

2.4. Mapping Quality

Mean Mapping Quality	43.21

2.5. Mismatches and indels

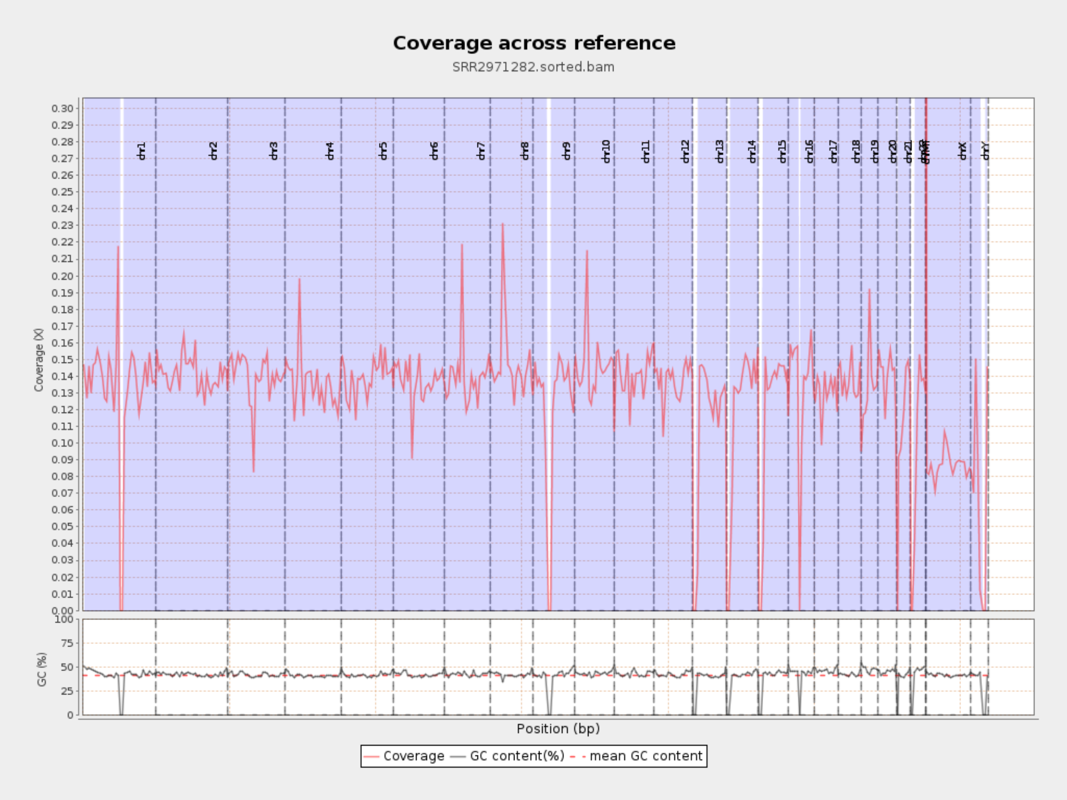
General error rate	0.27%
Mismatches	1,087,611
Insertions	13,168
Mapped reads with at least one insertion	0.13%
Deletions	31,727
Mapped reads with at least one deletion	0.31%
Homopolymer indels	39.87%

2.6. Chromosome stats

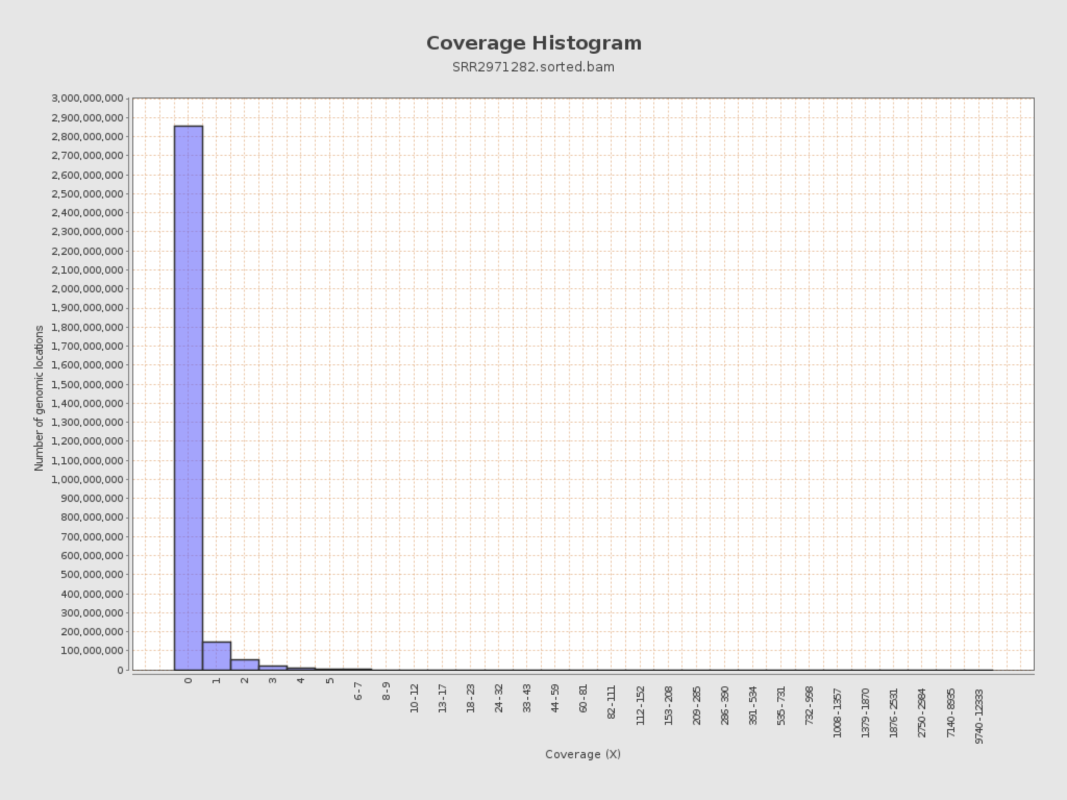
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33081031	0.1327	2.166
chr2	243199373	34431604	0.1416	0.7319
chr3	198022430	27656923	0.1397	0.5704
chr4	191154276	26085037	0.1365	0.6551
chr5	180915260	25189550	0.1392	0.587
chr6	171115067	23423016	0.1369	0.6119
chr7	159138663	22404591	0.1408	1.3924
chr8	146364022	21710014	0.1483	6.011

chr9	141213431	16941840	0.12	0.6626
chr10	135534747	19728229	0.1456	0.9572
chr11	135006516	18963739	0.1405	0.6991
chr12	133851895	18456934	0.1379	0.5873
chr13	115169878	12600818	0.1094	0.5036
chr14	107349540	12540791	0.1168	0.5629
chr15	102531392	11695067	0.1141	0.5131
chr16	90354753	11822542	0.1308	0.5895
chr17	81195210	10586860	0.1304	0.5738
chr18	78077248	10708503	0.1372	1.1243
chr19	59128983	7997929	0.1353	1.7095
chr20	63025520	8935864	0.1418	0.6138
chr21	48129895	5339344	0.1109	0.6174
chr22	51304566	4804598	0.0936	0.5253
chrMT	16571	36968	2.2309	3.0814
chrX	155270560	13535921	0.0872	0.4946
chrY	59373566	4047238	0.0682	0.7959

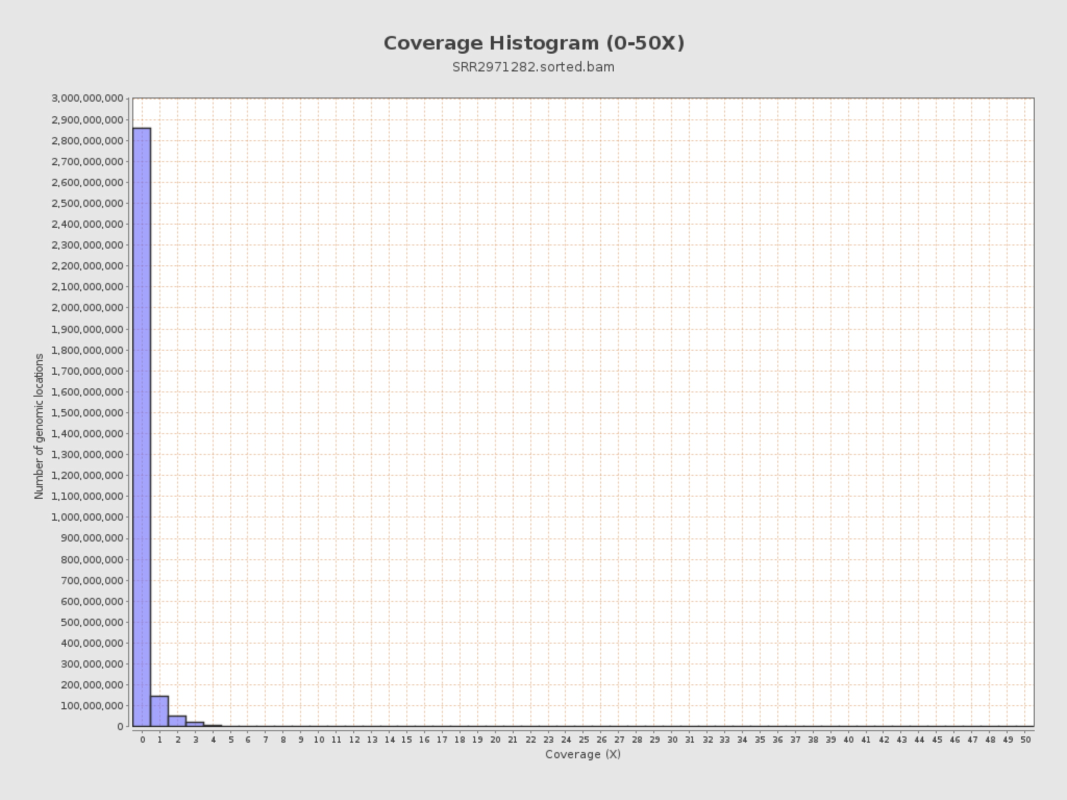
3. Results : Coverage across reference



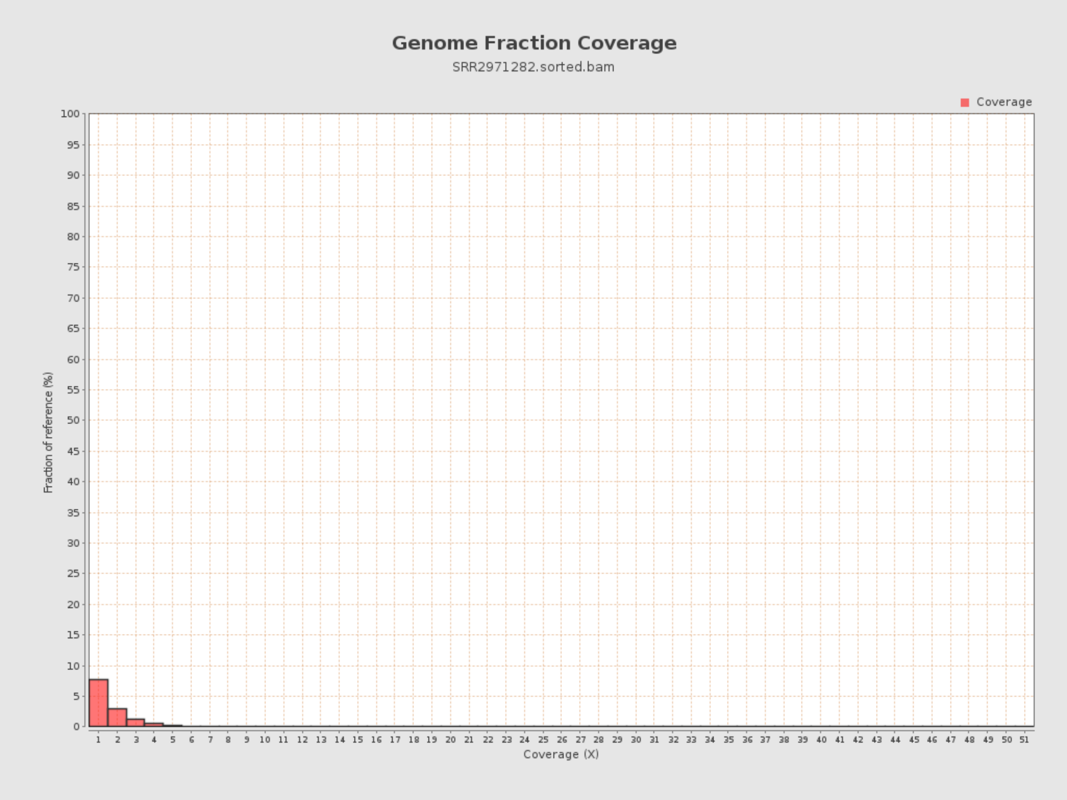
4. Results : Coverage Histogram



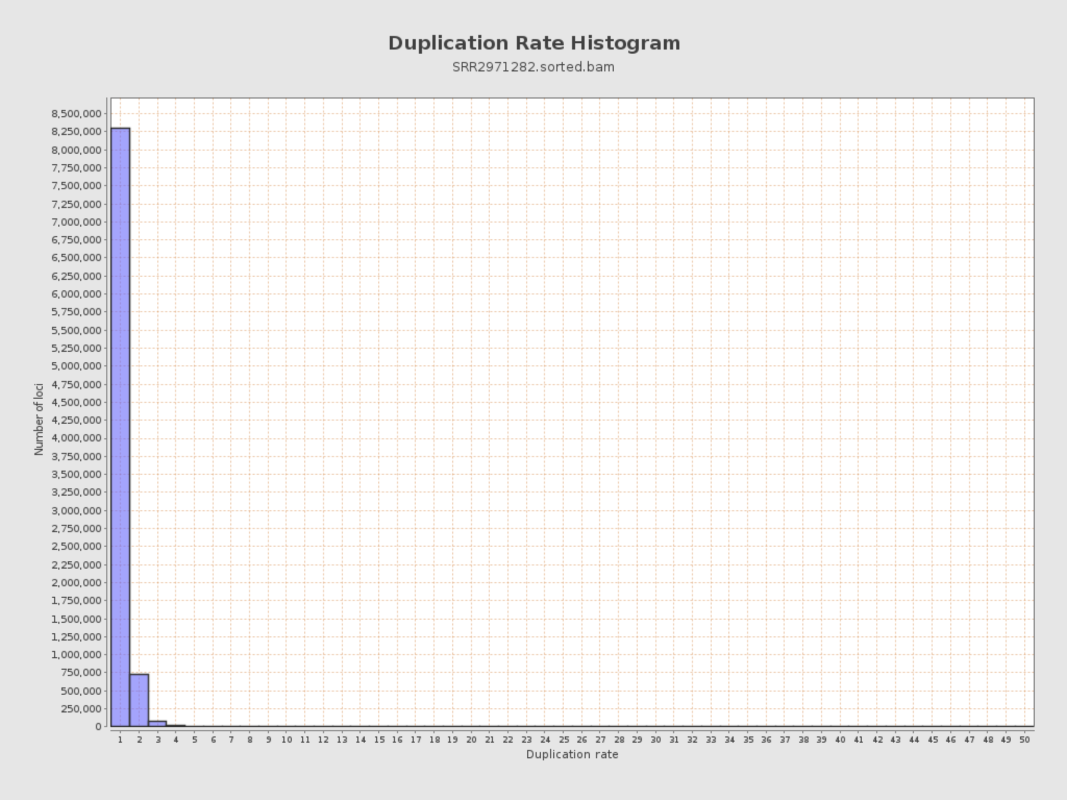
5. Results : Coverage Histogram (0-50X)



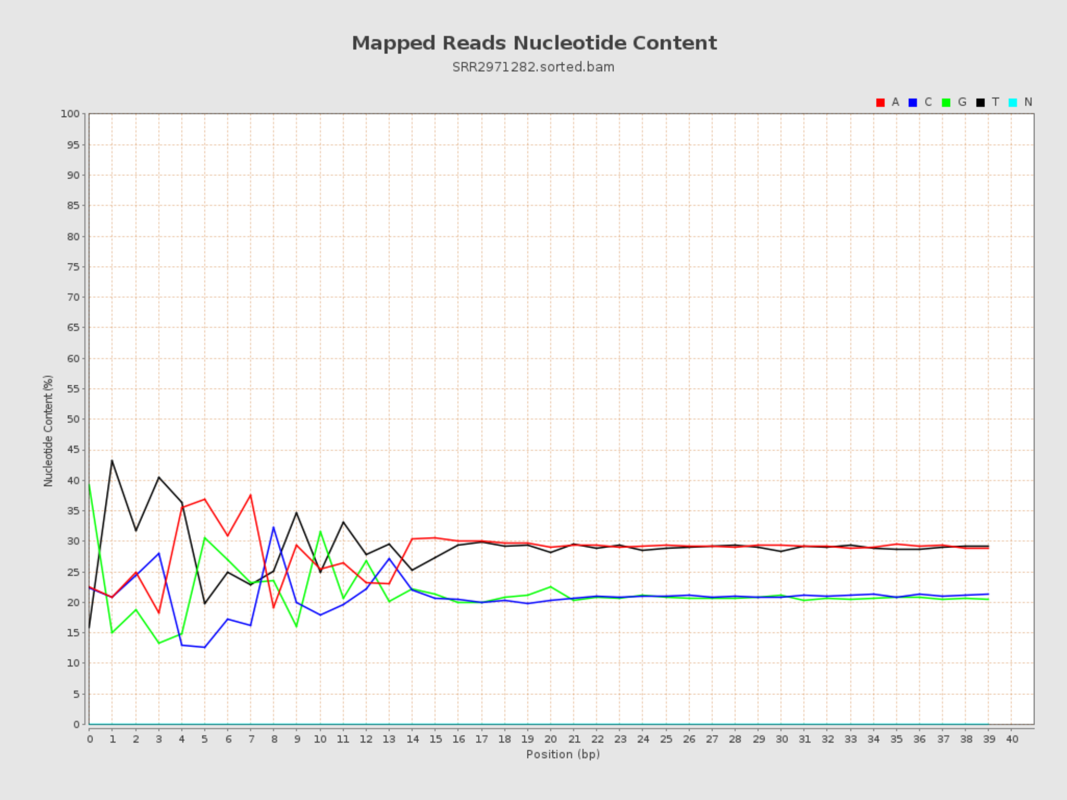
6. Results : Genome Fraction Coverage



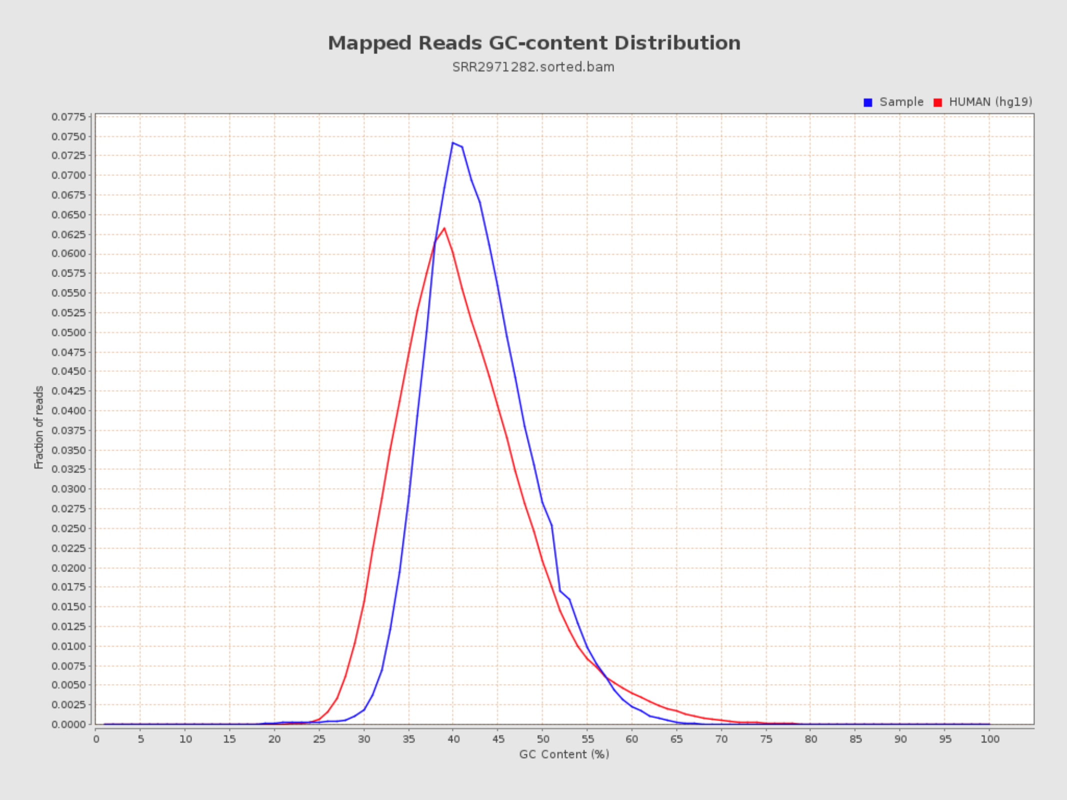
7. Results : Duplication Rate Histogram



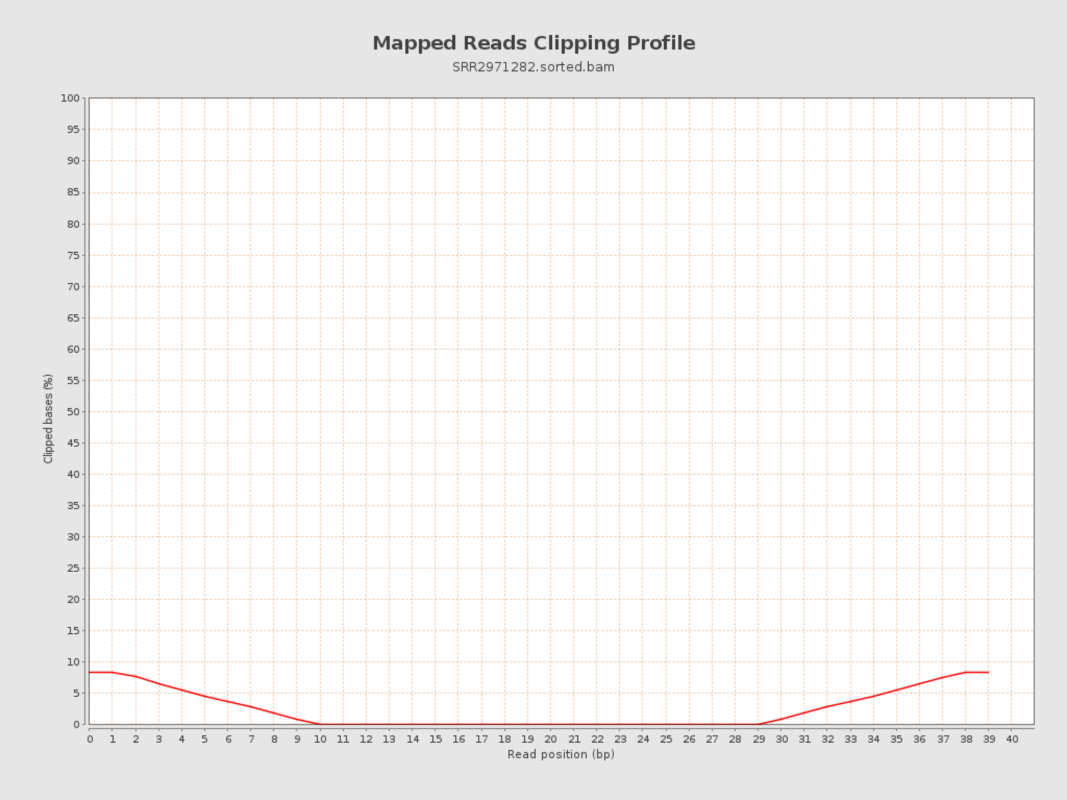
8. Results : Mapped Reads Nucleotide Content



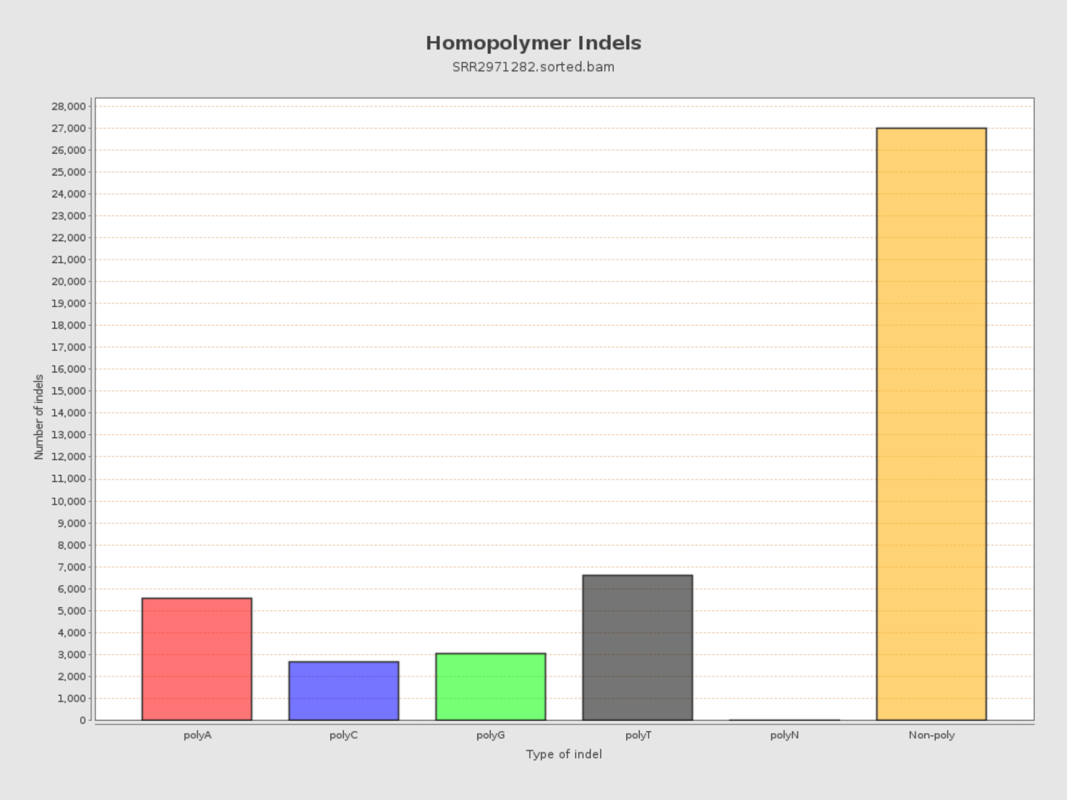
9. Results : Mapped Reads GC-content Distribution



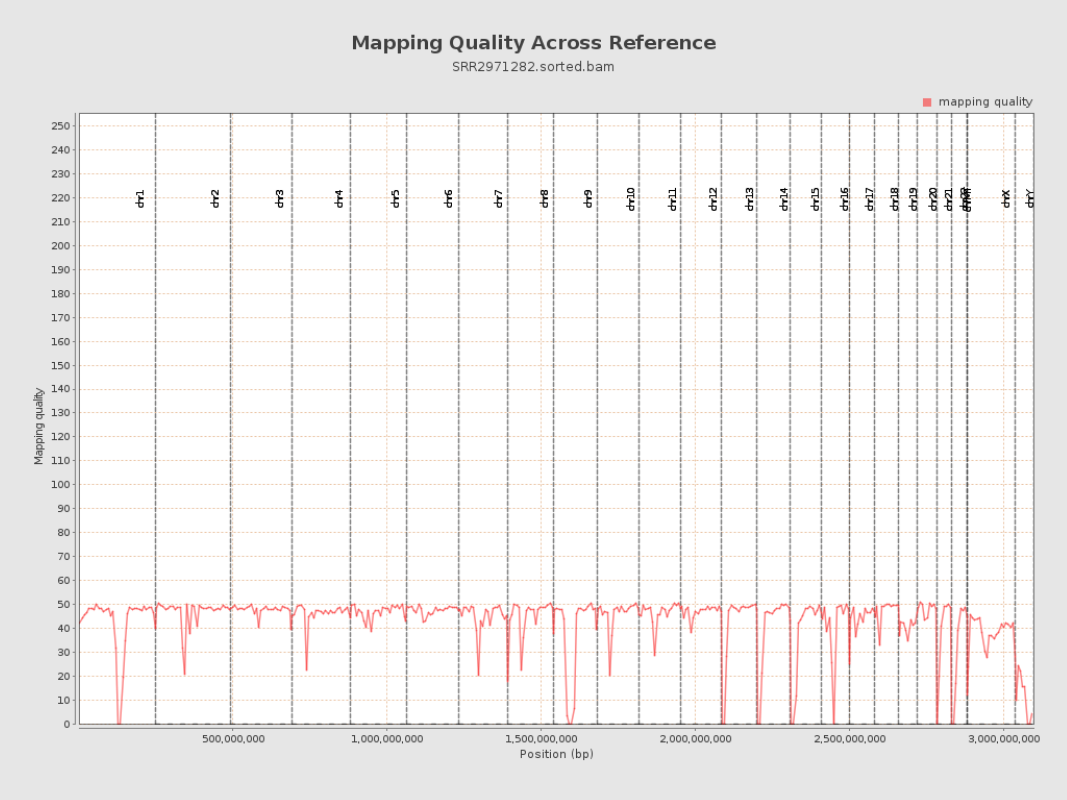
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram