Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:33:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080782.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_SRR3080782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080782.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:33:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080782.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,313,236
Mapped reads	2,972,557 / 89.72%
Unmapped reads	340,679 / 10.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,208 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	150,512 / 4.54%
Duplication rate	4.14%
Clipped reads	1,463,494 / 44.17%

2.2. ACGT Content

Number/percentage of A's	56,535,661 / 28.74%
Number/percentage of C's	38,347,319 / 19.5%
Number/percentage of T's	59,562,939 / 30.28%
Number/percentage of G's	42,247,606 / 21.48%
Number/percentage of N's	4,197 / 0%
GC Percentage	40.97%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.4602

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

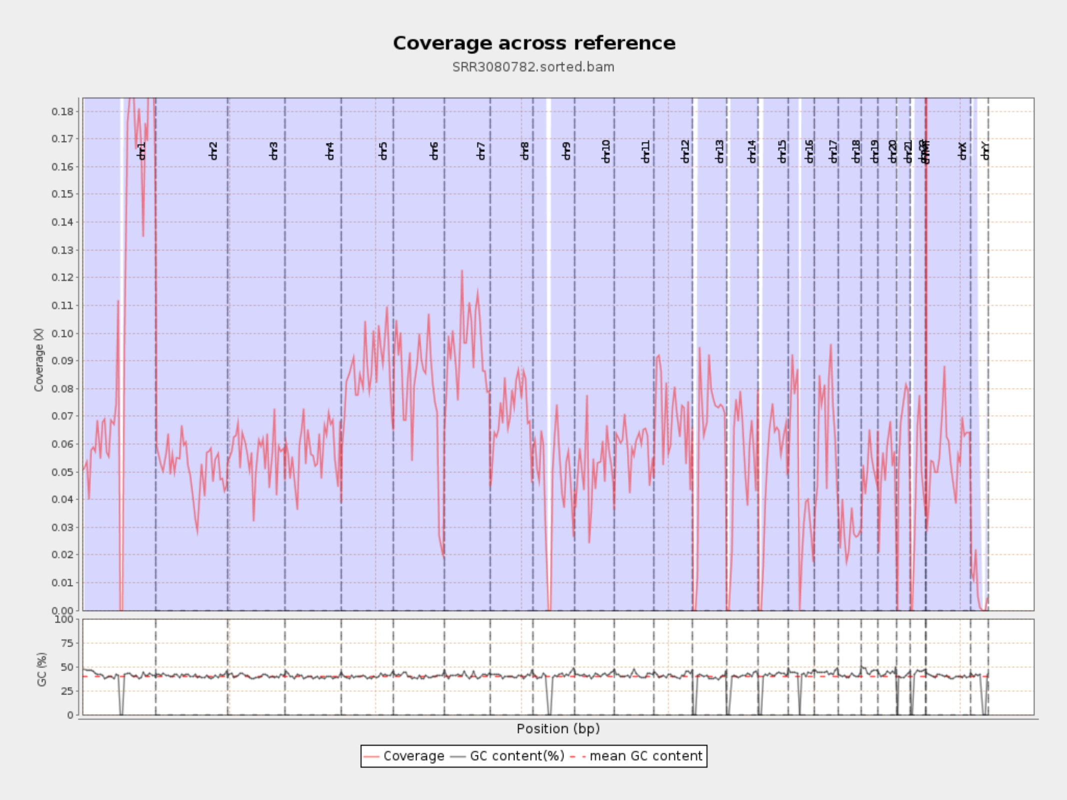
General error rate	0.76%
Mismatches	1,474,582
Insertions	14,793
Mapped reads with at least one insertion	0.49%
Deletions	42,640
Mapped reads with at least one deletion	1.42%
Homopolymer indels	47.36%

2.6. Chromosome stats

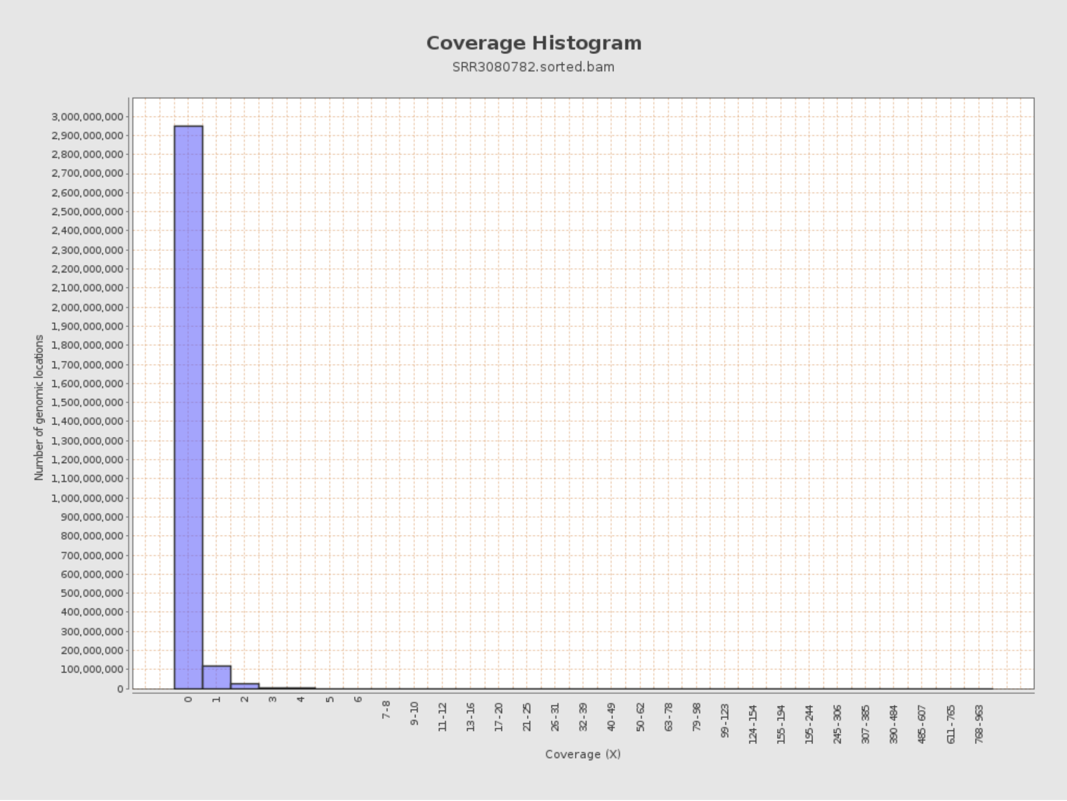
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26845654	0.1077	0.9151
chr2	243199373	12481796	0.0513	0.4527
chr3	198022430	11174385	0.0564	0.2987
chr4	191154276	11096531	0.0581	0.313
chr5	180915260	15511107	0.0857	0.3691
chr6	171115067	13508391	0.0789	0.4222
chr7	159138663	15008328	0.0943	0.6777

chr8	146364022	10429324	0.0713	0.5699
chr9	141213431	6498628	0.046	0.3226
chr10	135534747	6895768	0.0509	0.3673
chr11	135006516	7962345	0.059	0.3337
chr12	133851895	9378124	0.0701	0.3369
chr13	115169878	7298087	0.0634	0.3192
chr14	107349540	5452998	0.0508	0.2951
chr15	102531392	5037838	0.0491	0.2834
chr16	90354753	4130962	0.0457	0.2832
chr17	81195210	5435731	0.0669	0.3632
chr18	78077248	2168704	0.0278	0.5372
chr19	59128983	3019700	0.0511	0.5812
chr20	63025520	3229673	0.0512	0.2926
chr21	48129895	2955301	0.0614	0.3221
chr22	51304566	2066725	0.0403	0.2506
chrMT	16571	33701	2.0337	1.9243
chrX	155270560	8733352	0.0562	0.3186
chrY	59373566	412966	0.007	0.1397

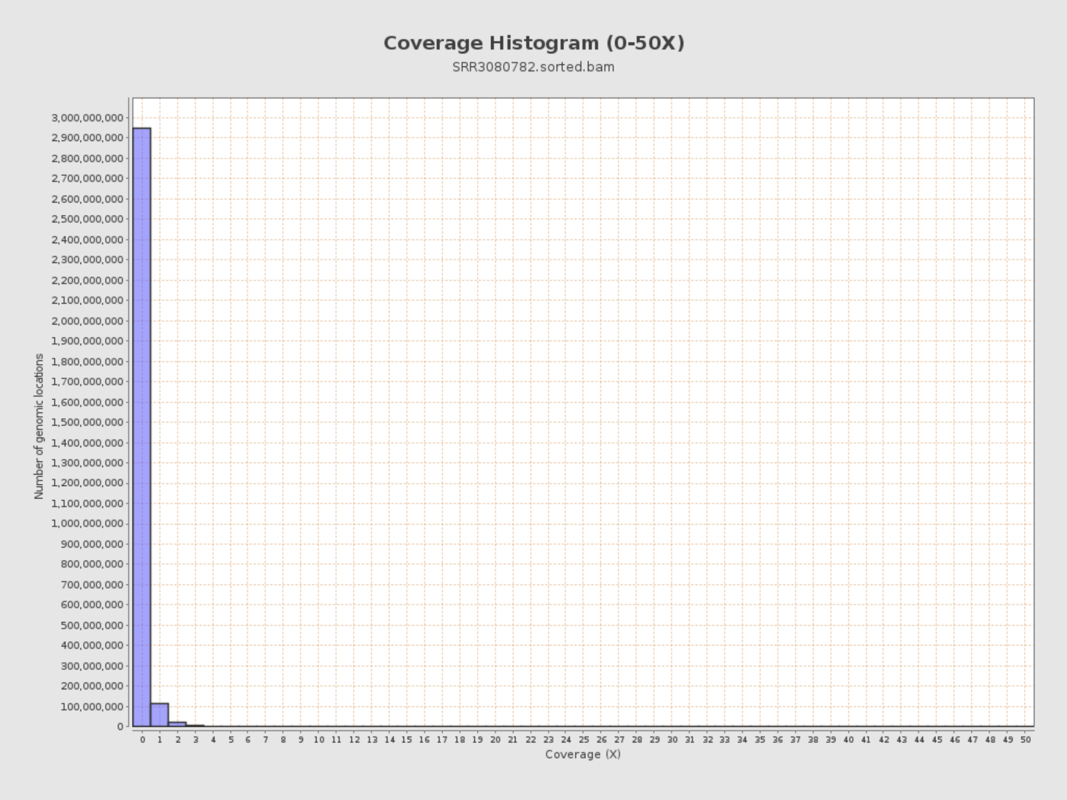
3. Results : Coverage across reference



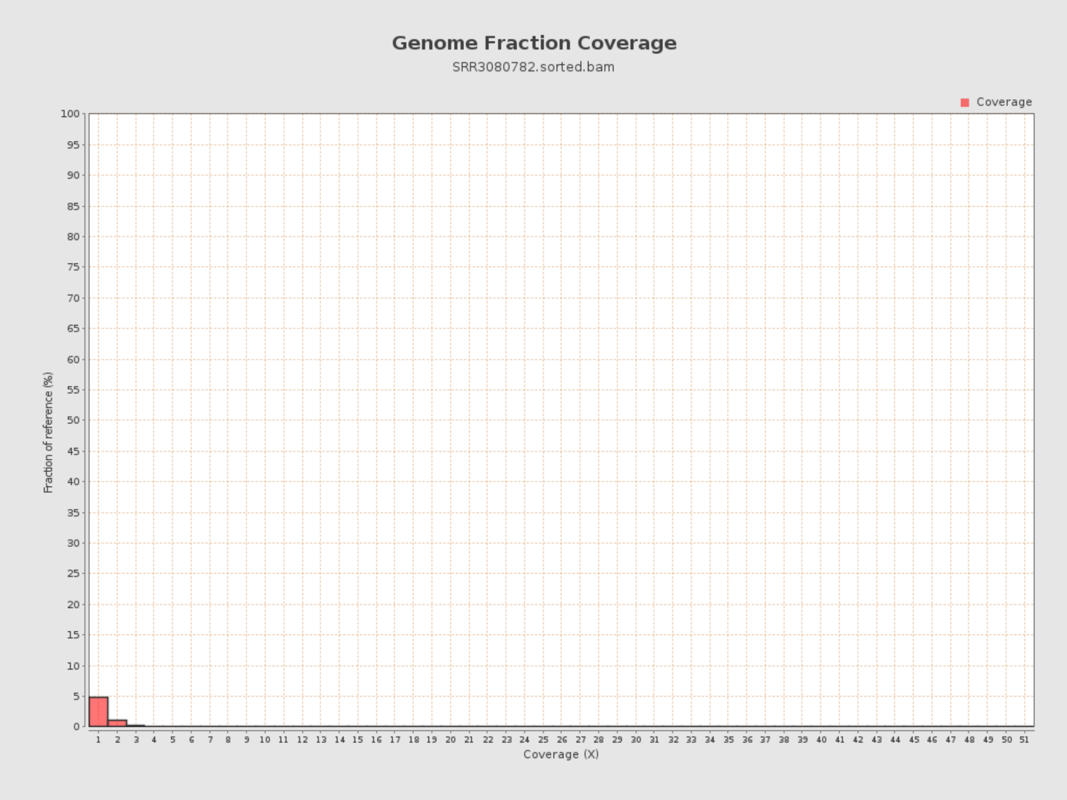
4. Results : Coverage Histogram



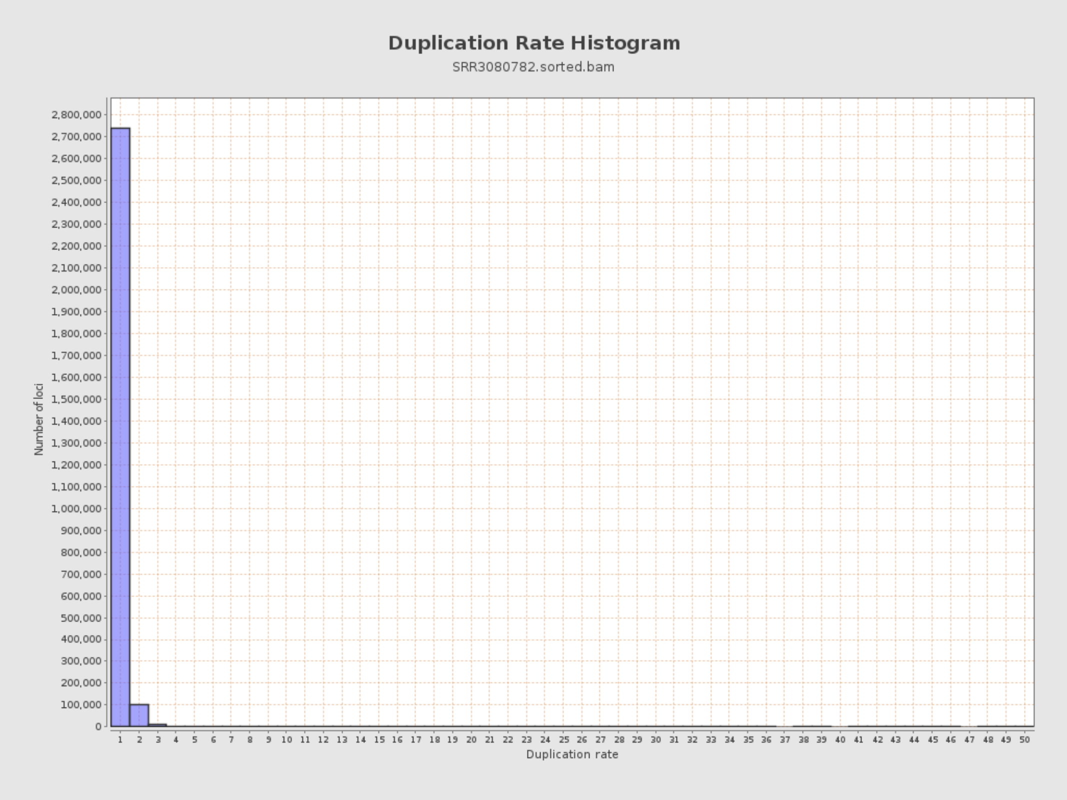
5. Results : Coverage Histogram (0-50X)



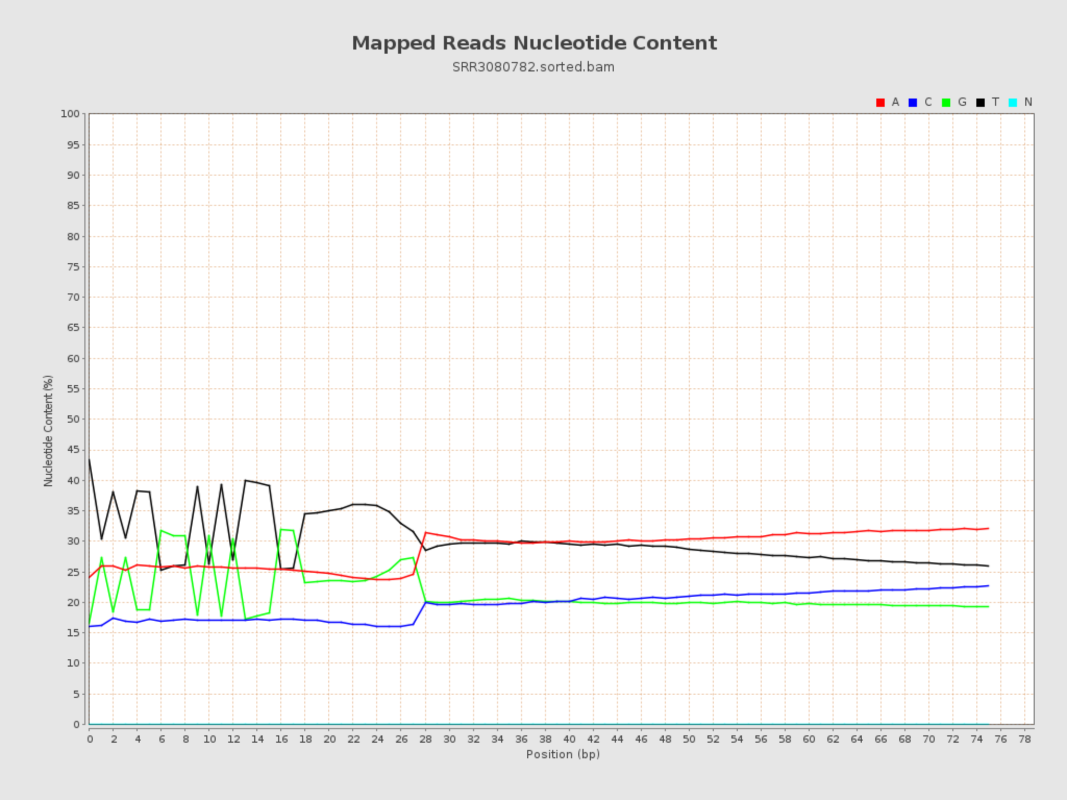
6. Results : Genome Fraction Coverage



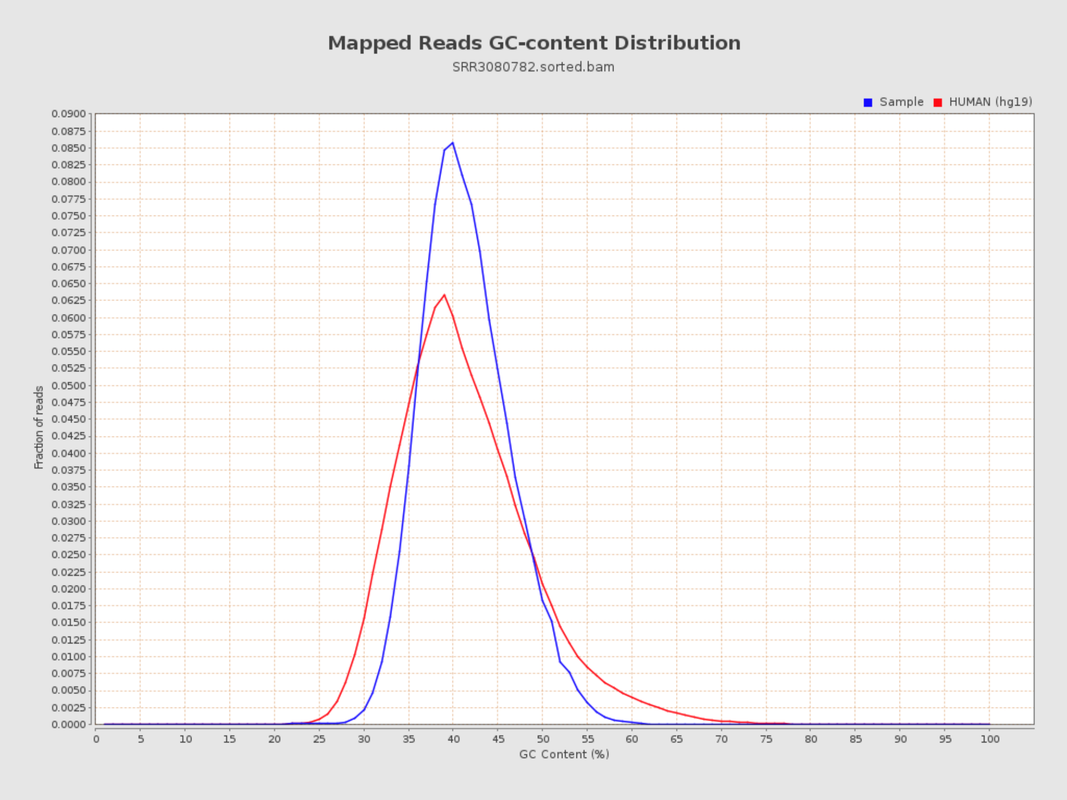
7. Results : Duplication Rate Histogram



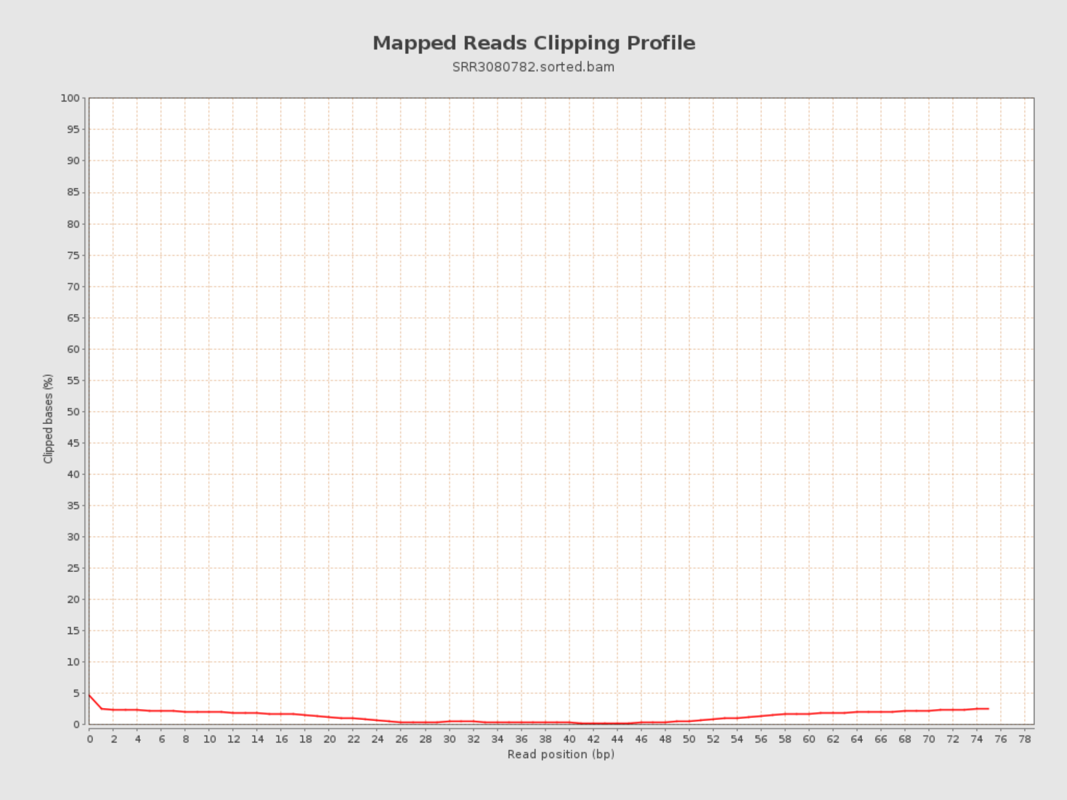
8. Results : Mapped Reads Nucleotide Content



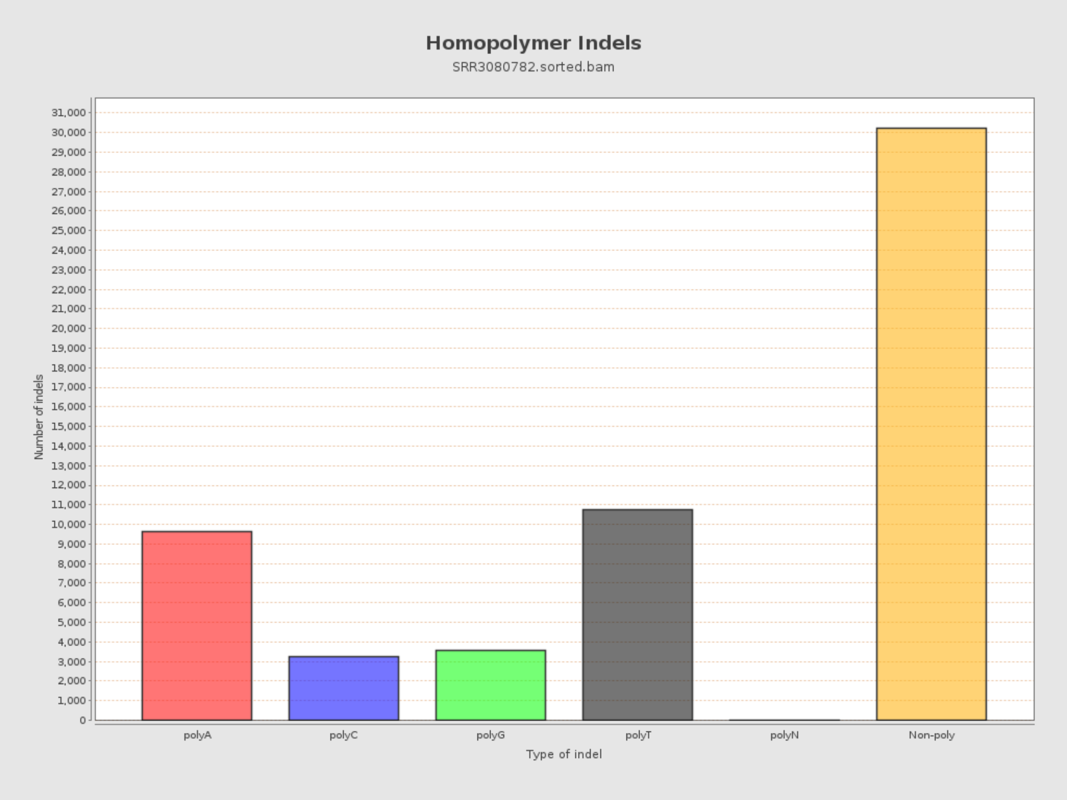
9. Results : Mapped Reads GC-content Distribution



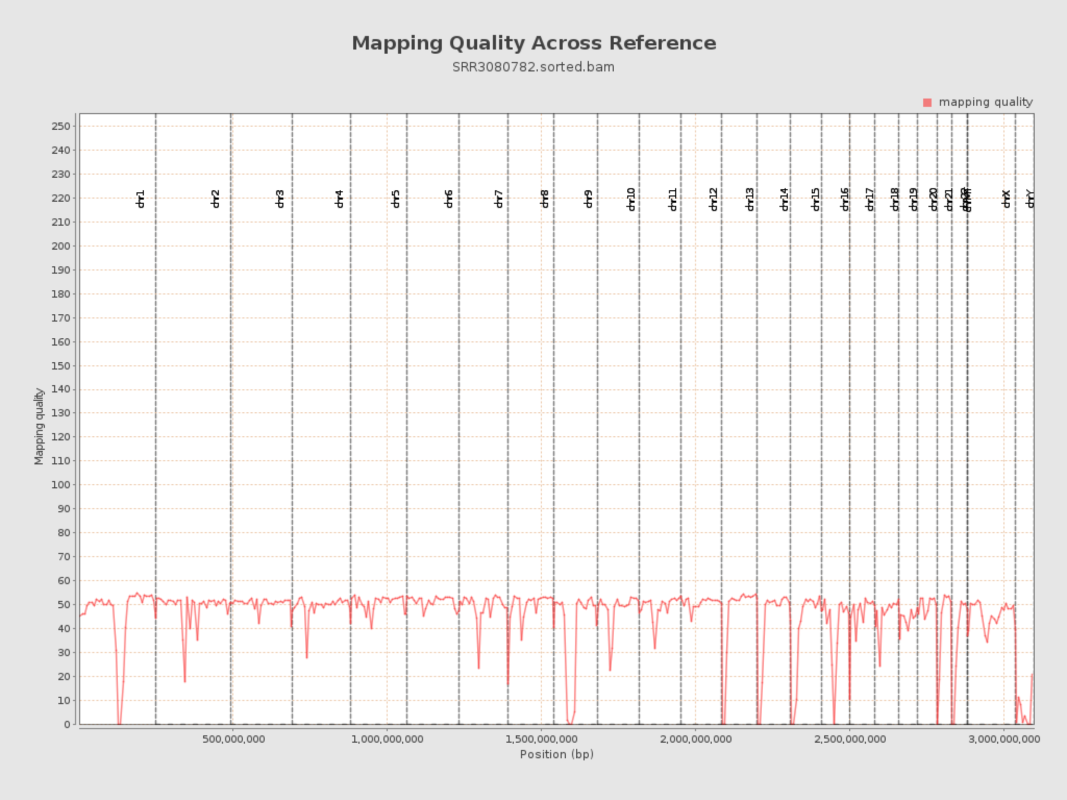
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram