Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 01:03:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717017.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_SRR9717017 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717017.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 01:03:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717017.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,374,465
Mapped reads	3,037,180 / 90%
Unmapped reads	337,285 / 10%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,077 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	122,449 / 3.63%
Duplication rate	3.07%
Clipped reads	3,041,268 / 90.13%

2.2. ACGT Content

Number/percentage of A's	45,388,083 / 26.08%
Number/percentage of C's	34,000,220 / 19.54%
Number/percentage of T's	51,505,309 / 29.6%
Number/percentage of G's	43,135,046 / 24.79%
Number/percentage of N's	3,812 / 0%
GC Percentage	44.32%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.3742

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

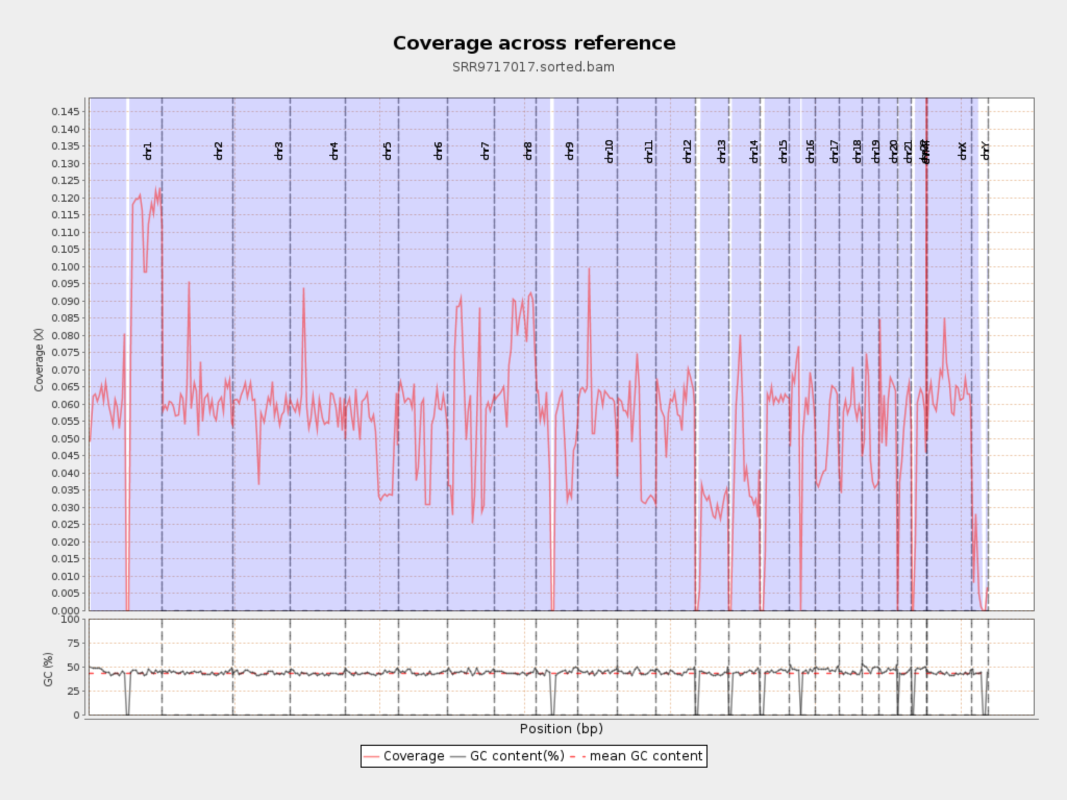
General error rate	0.5%
Mismatches	847,375
Insertions	13,119
Mapped reads with at least one insertion	0.43%
Deletions	27,191
Mapped reads with at least one deletion	0.89%
Homopolymer indels	40.11%

2.6. Chromosome stats

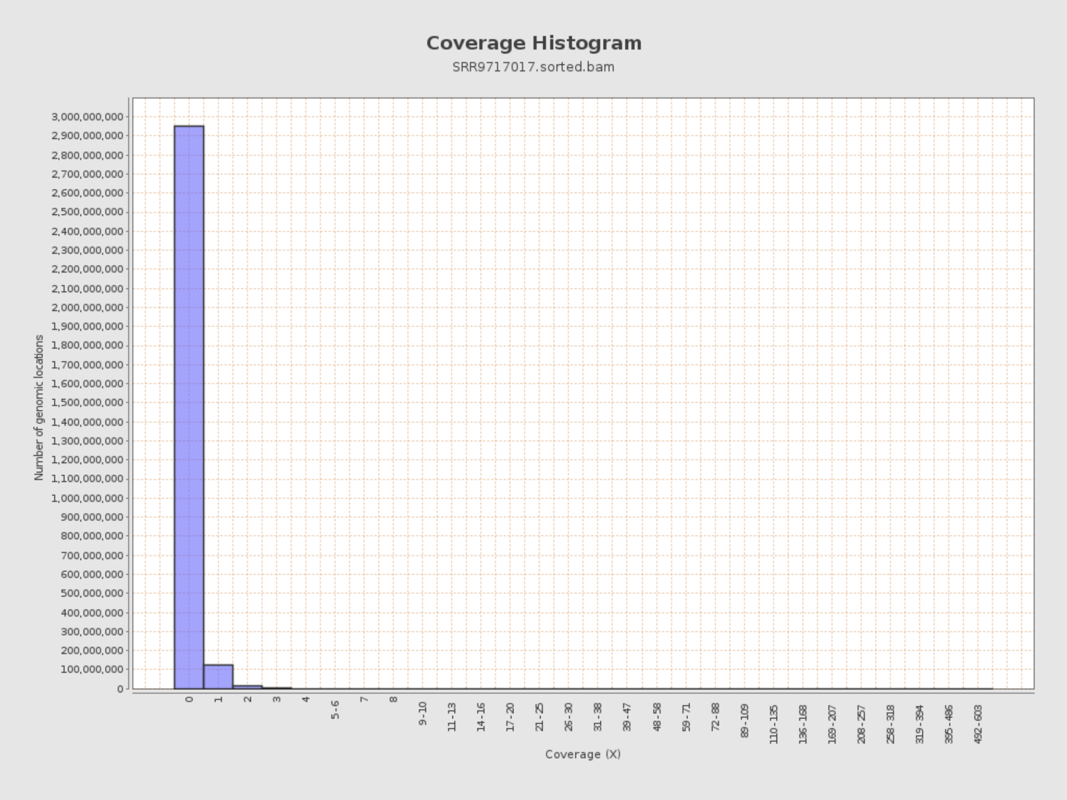
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19931935	0.08	0.5636
chr2	243199373	14974067	0.0616	0.4549
chr3	198022430	11706173	0.0591	0.2828
chr4	191154276	11375587	0.0595	0.3214
chr5	180915260	9060023	0.0501	0.2642
chr6	171115067	9383739	0.0548	0.2981
chr7	159138663	8997128	0.0565	0.3566

chr8	146364022	11268710	0.077	0.3699
chr9	141213431	6463558	0.0458	0.4013
chr10	135534747	8554722	0.0631	0.4403
chr11	135006516	6624594	0.0491	0.3775
chr12	133851895	8085384	0.0604	0.2904
chr13	115169878	3029562	0.0263	0.184
chr14	107349540	4156995	0.0387	0.2558
chr15	102531392	5109120	0.0498	0.2587
chr16	90354753	5259243	0.0582	0.3191
chr17	81195210	4031311	0.0496	0.2762
chr18	78077248	4410455	0.0565	0.737
chr19	59128983	2886795	0.0488	0.4233
chr20	63025520	3845713	0.061	0.3005
chr21	48129895	2293235	0.0476	0.2968
chr22	51304566	2146739	0.0418	0.2362
chrMT	16571	3770	0.2275	0.5087
chrX	155270560	9969238	0.0642	0.3517
chrY	59373566	510659	0.0086	0.1835

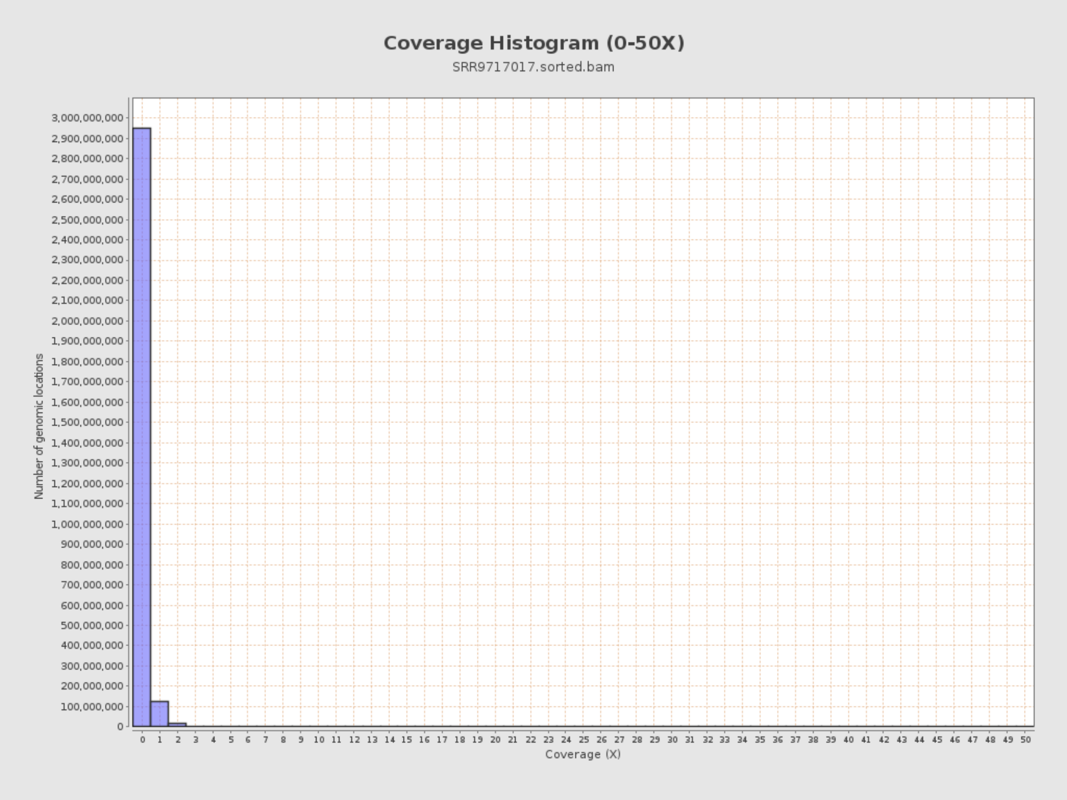
3. Results : Coverage across reference



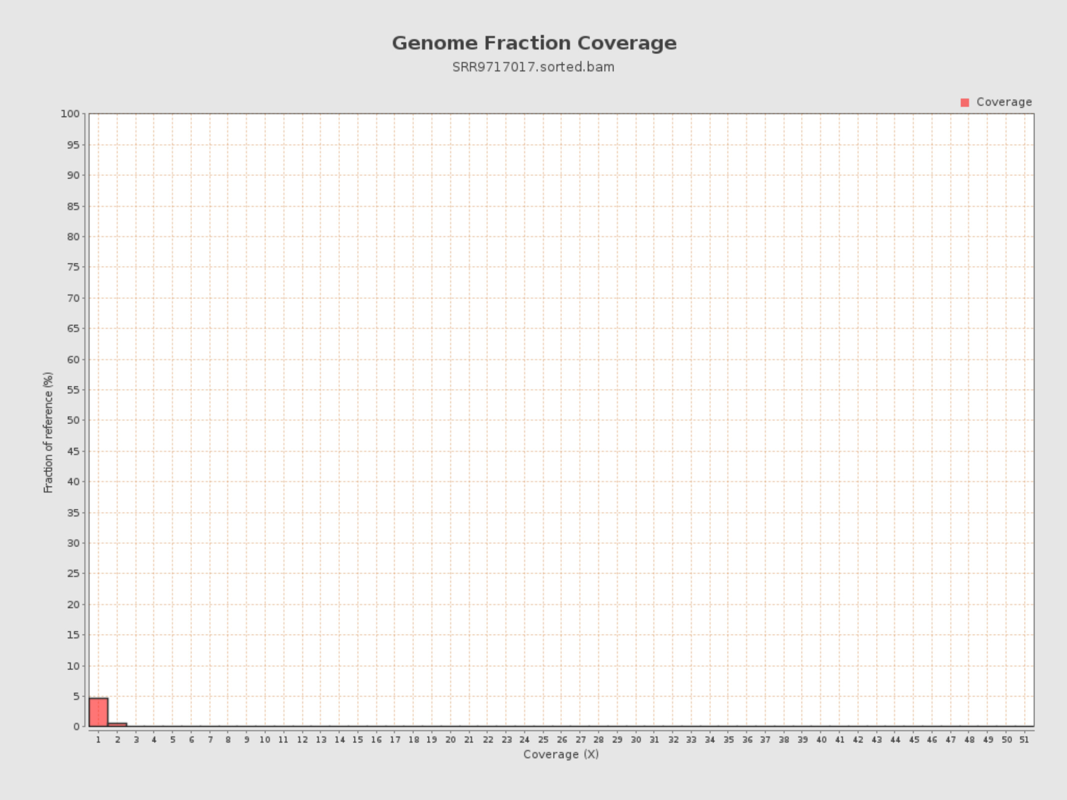
4. Results : Coverage Histogram



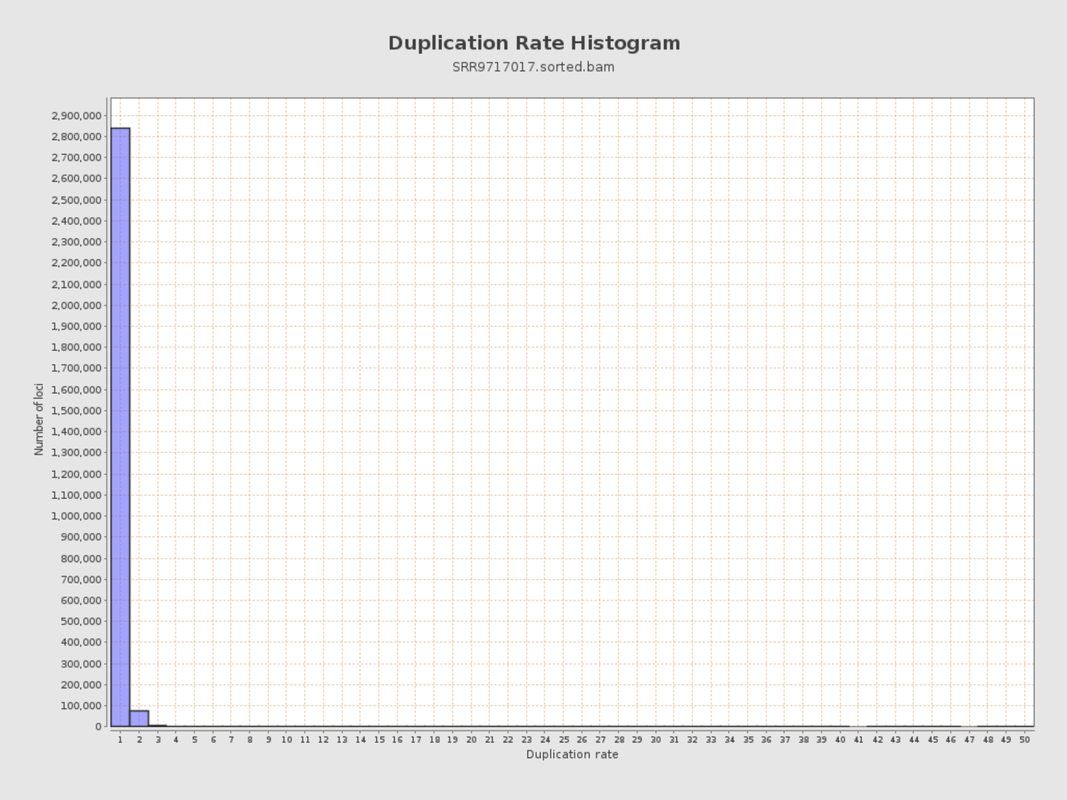
5. Results : Coverage Histogram (0-50X)



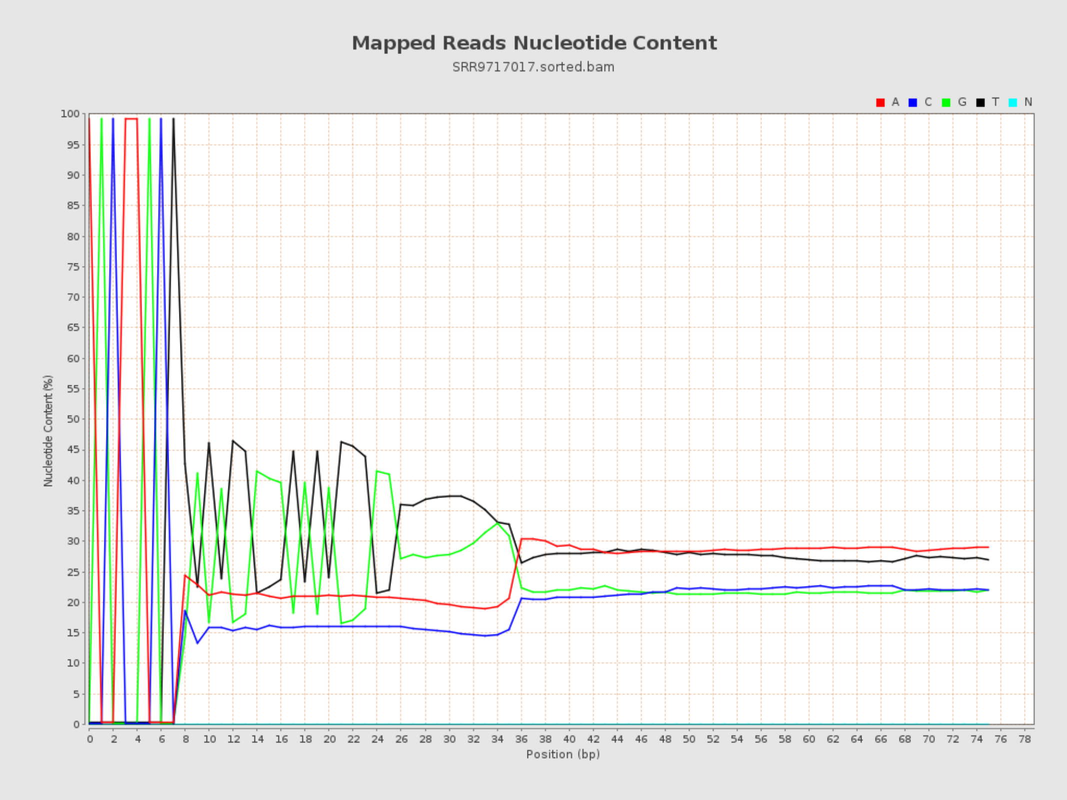
6. Results : Genome Fraction Coverage



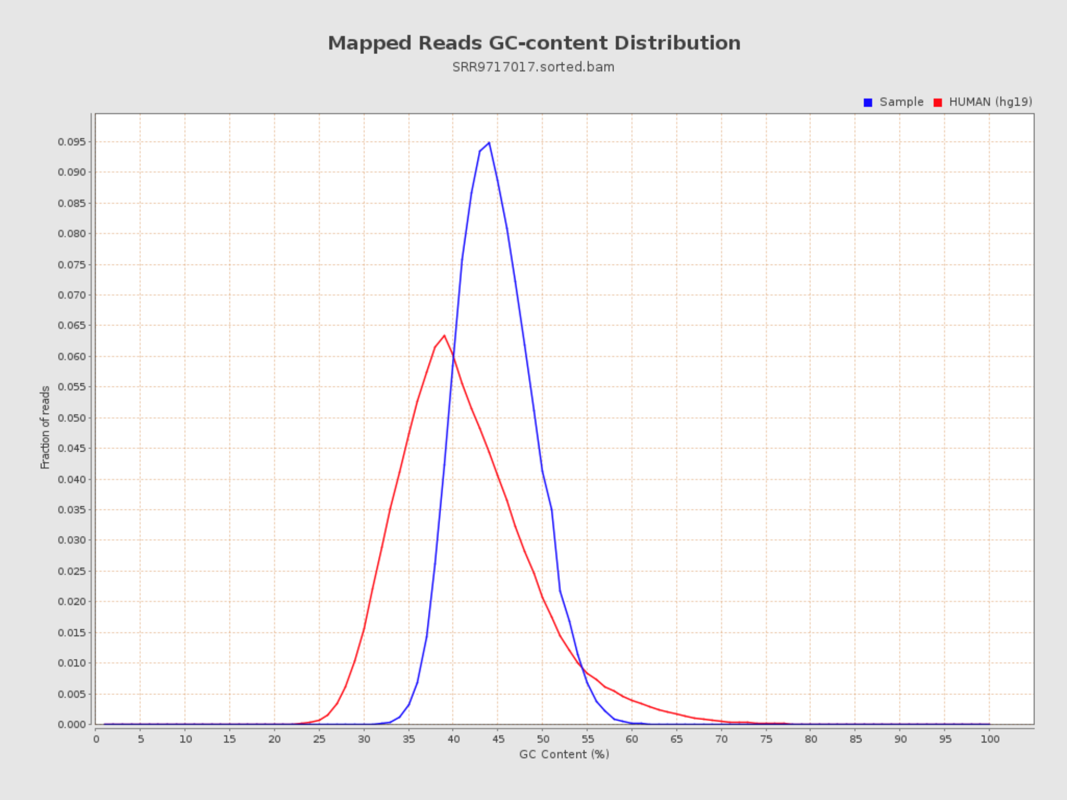
7. Results : Duplication Rate Histogram



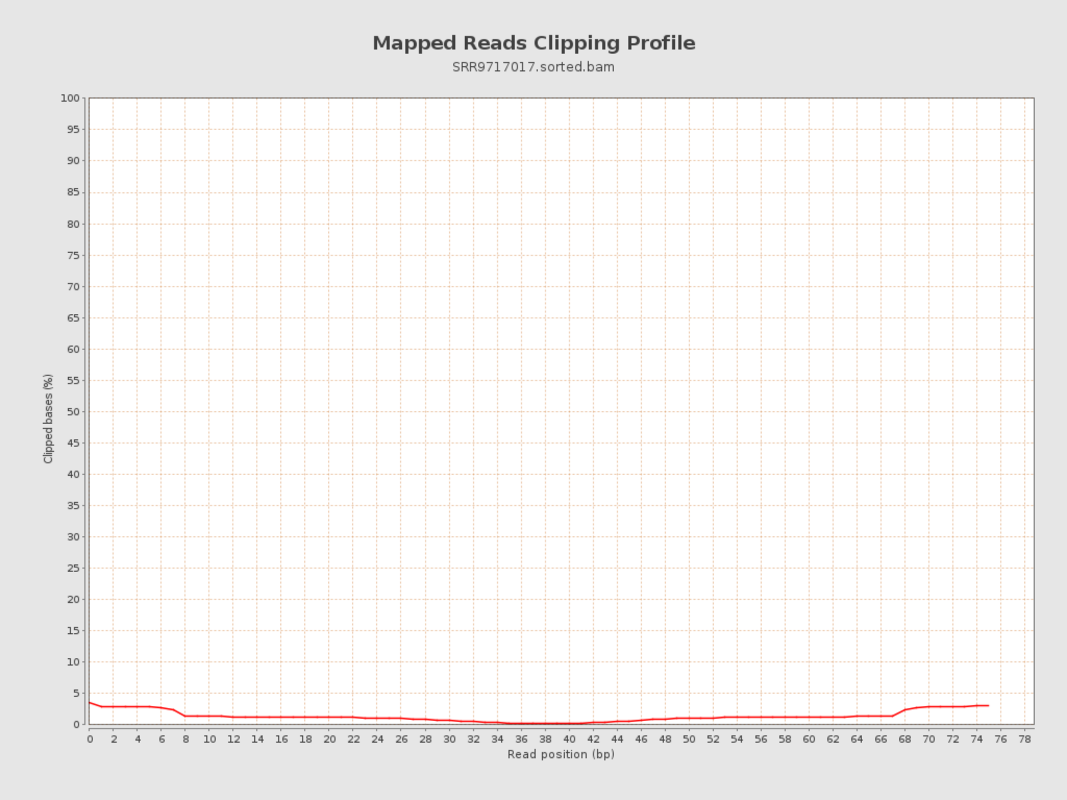
8. Results : Mapped Reads Nucleotide Content



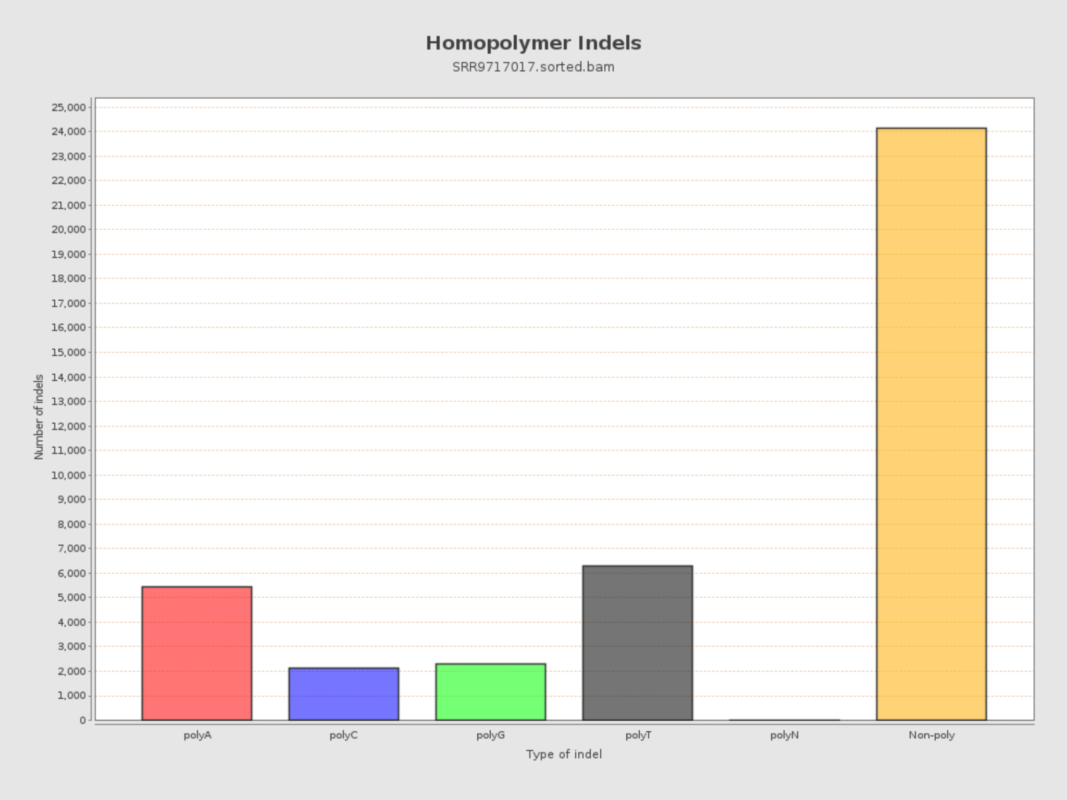
9. Results : Mapped Reads GC-content Distribution



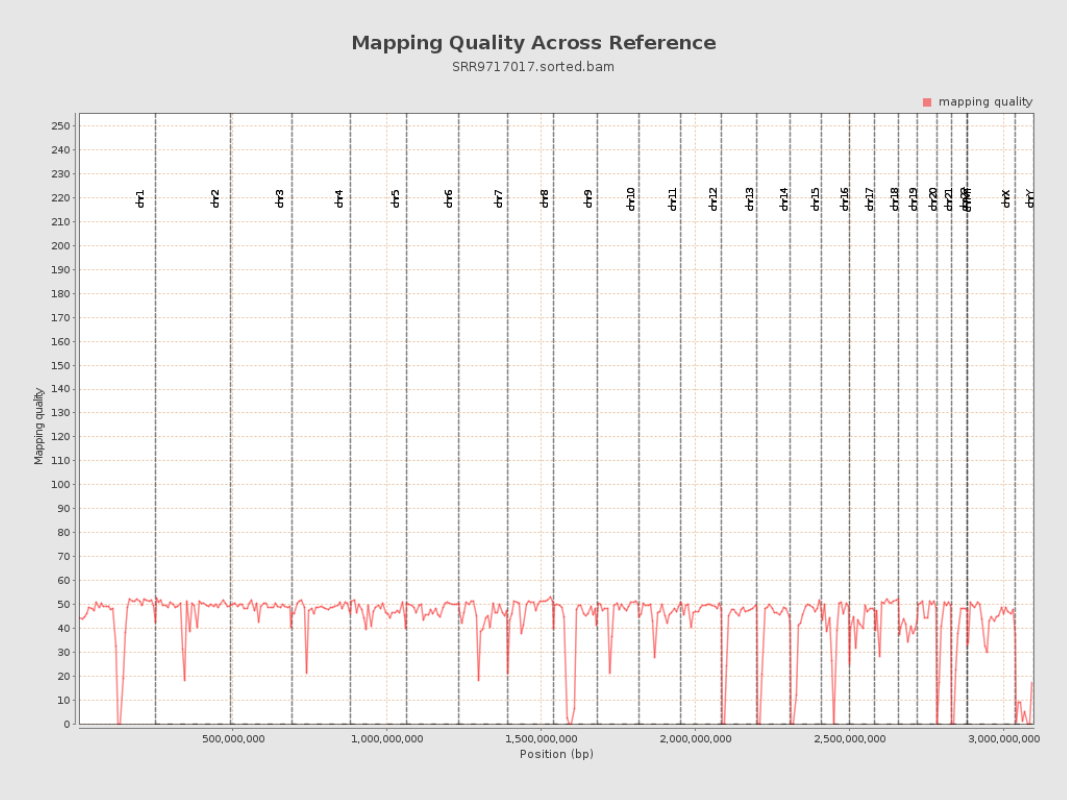
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram