

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:47:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717001.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_SRR9717001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717001.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:47:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,761,646
Mapped reads	2,535,957 / 91.83%
Unmapped reads	225,689 / 8.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,154 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	113,642 / 4.12%
Duplication rate	3.22%
Clipped reads	2,543,451 / 92.1%

2.2. ACGT Content

Number/percentage of A's	36,347,409 / 24.71%
Number/percentage of C's	27,526,495 / 18.71%
Number/percentage of T's	46,766,632 / 31.8%
Number/percentage of G's	36,441,319 / 24.78%
Number/percentage of N's	2,168 / 0%
GC Percentage	43.49%

2.3. Coverage

Mean	0.0475

Standard Deviation	0.4352
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2.4. Mapping Quality

Mean Mapping Quality	44.65
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2.5. Mismatches and indels

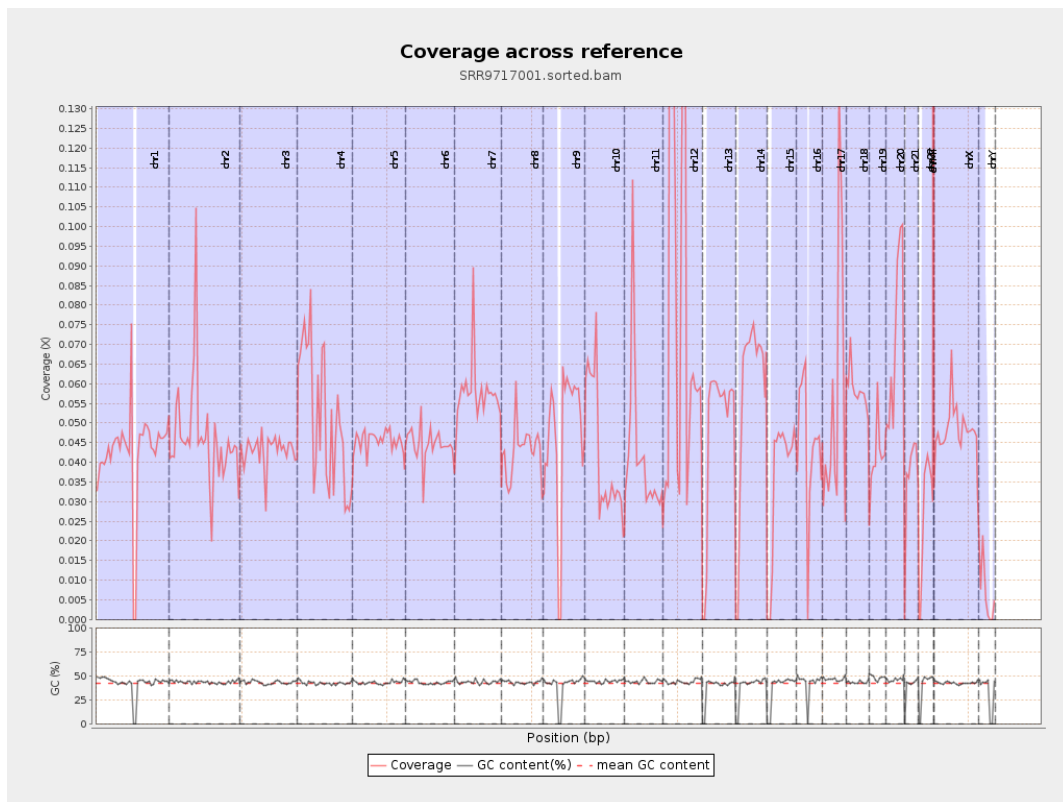
General error rate	0.53%
Mismatches	765,053
Insertions	8,962
Mapped reads with at least one insertion	0.35%
Deletions	24,587
Mapped reads with at least one deletion	0.96%
Homopolymer indels	42.82%

2.6. Chromosome stats

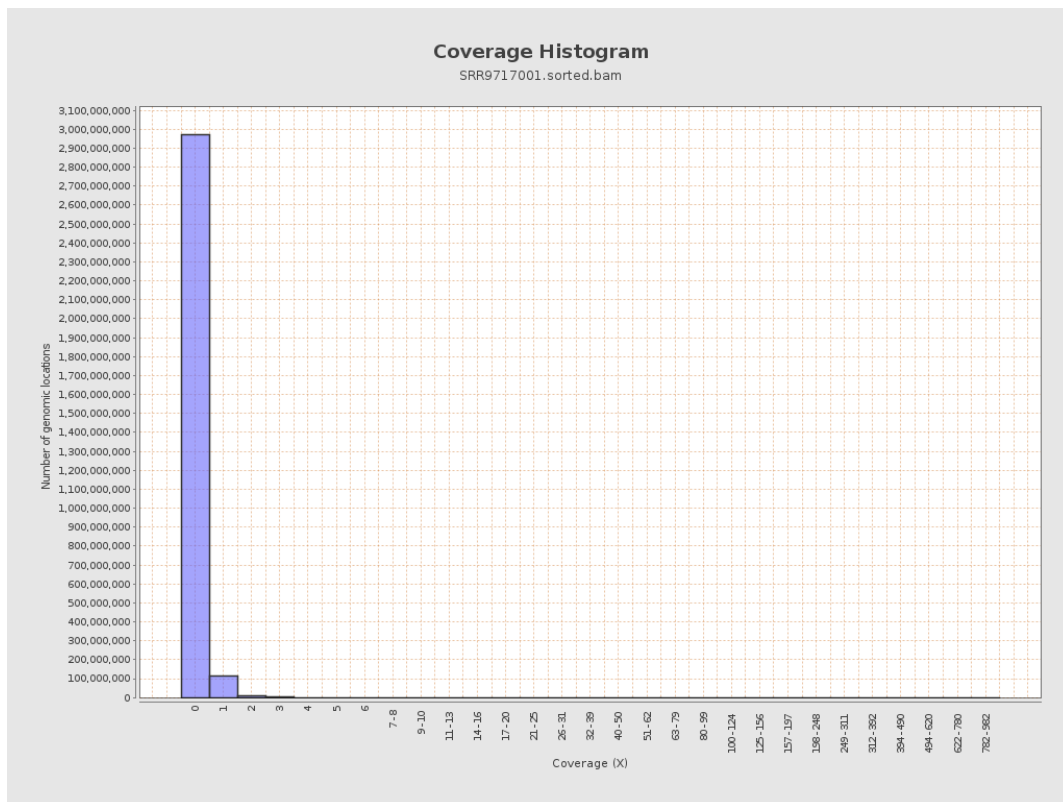
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10589926	0.0425	0.7986
chr2	243199373	11315383	0.0465	0.4907
chr3	198022430	8513290	0.043	0.2309
chr4	191154276	9838955	0.0515	0.2842
chr5	180915260	8223385	0.0455	0.2443
chr6	171115067	7623483	0.0446	0.2746
chr7	159138663	9231606	0.058	0.5933

chr8	146364022	6283894	0.0429	0.4197
chr9	141213431	6693185	0.0474	0.4648
chr10	135534747	5699735	0.0421	0.4008
chr11	135006516	5666616	0.042	0.3602
chr12	133851895	10994267	0.0821	0.3765
chr13	115169878	5523666	0.048	0.2432
chr14	107349540	6181235	0.0576	0.3119
chr15	102531392	3733339	0.0364	0.2142
chr16	90354753	4058086	0.0449	0.2775
chr17	81195210	4350438	0.0536	0.2738
chr18	78077248	4587185	0.0588	0.9003
chr19	59128983	2497029	0.0422	0.6081
chr20	63025520	4492846	0.0713	0.3142
chr21	48129895	1748818	0.0363	0.2543
chr22	51304566	1375663	0.0268	0.1803
chrMT	16571	15200	0.9173	1.1333
chrX	155270560	7496297	0.0483	0.3168
chrY	59373566	391237	0.0066	0.1498

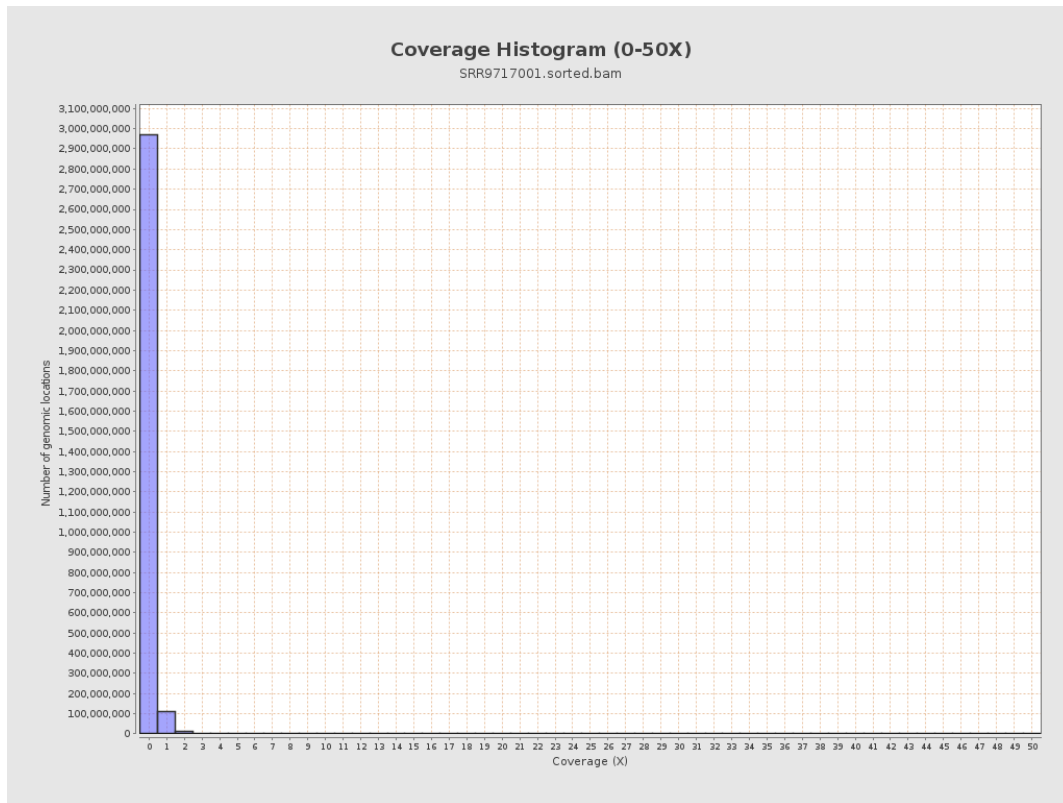
3. Results : Coverage across reference



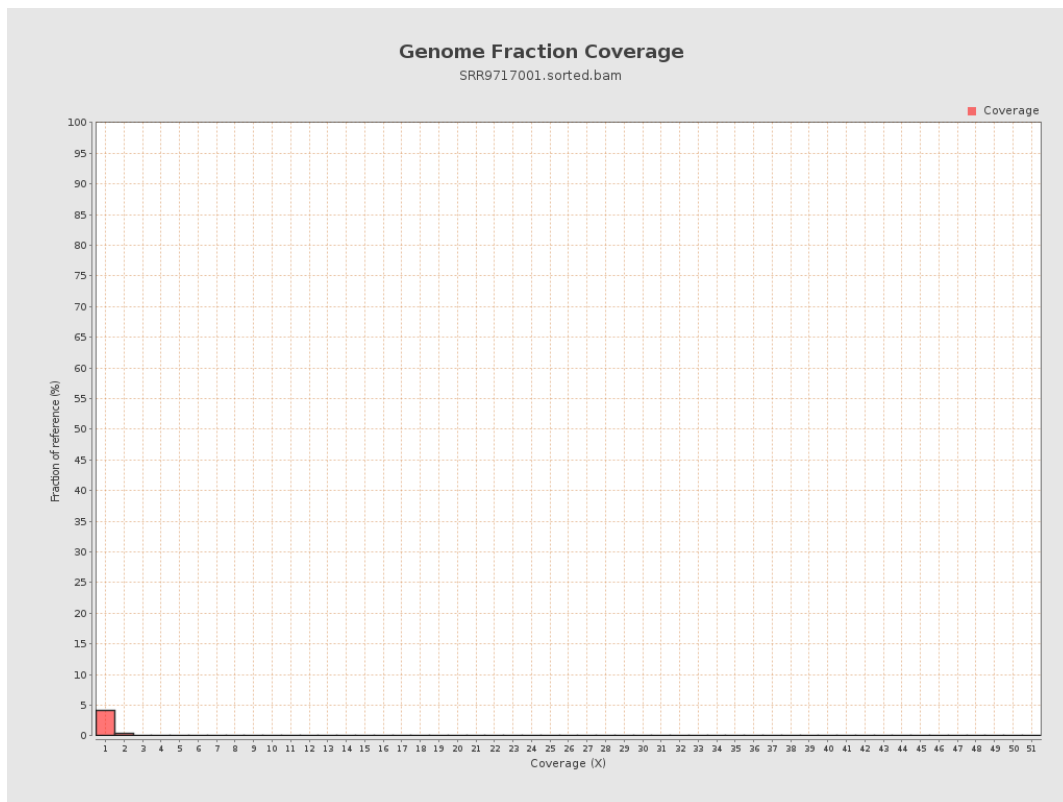
4. Results : Coverage Histogram



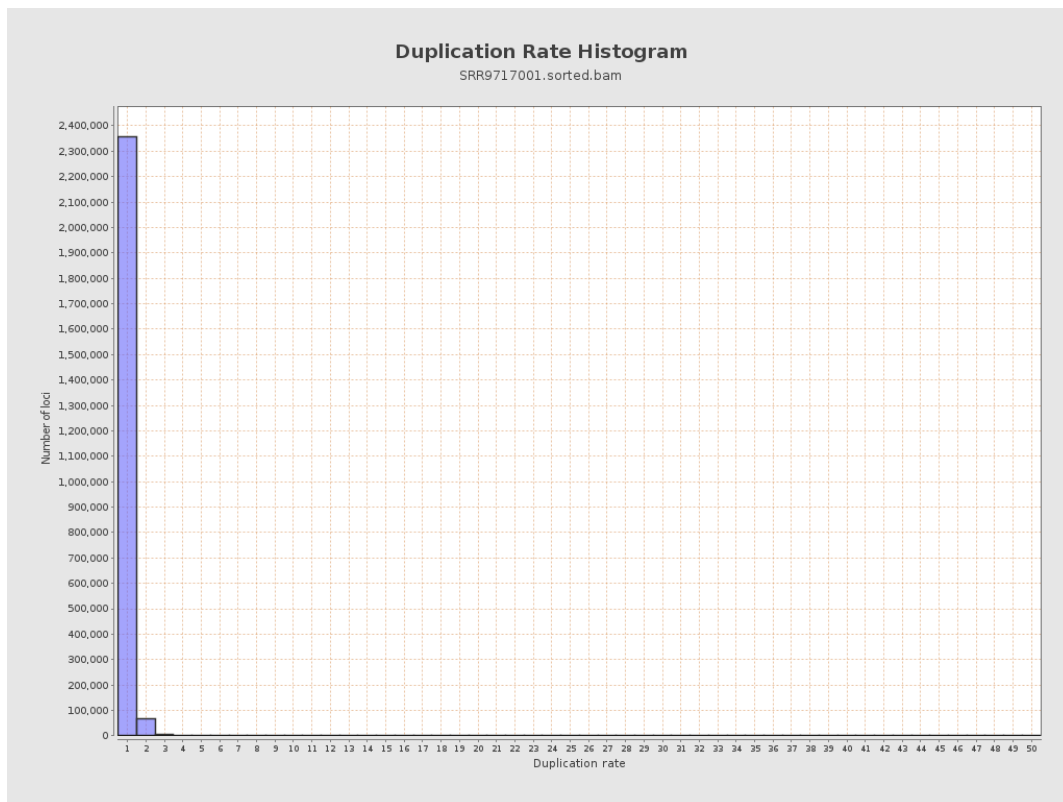
5. Results : Coverage Histogram (0-50X)



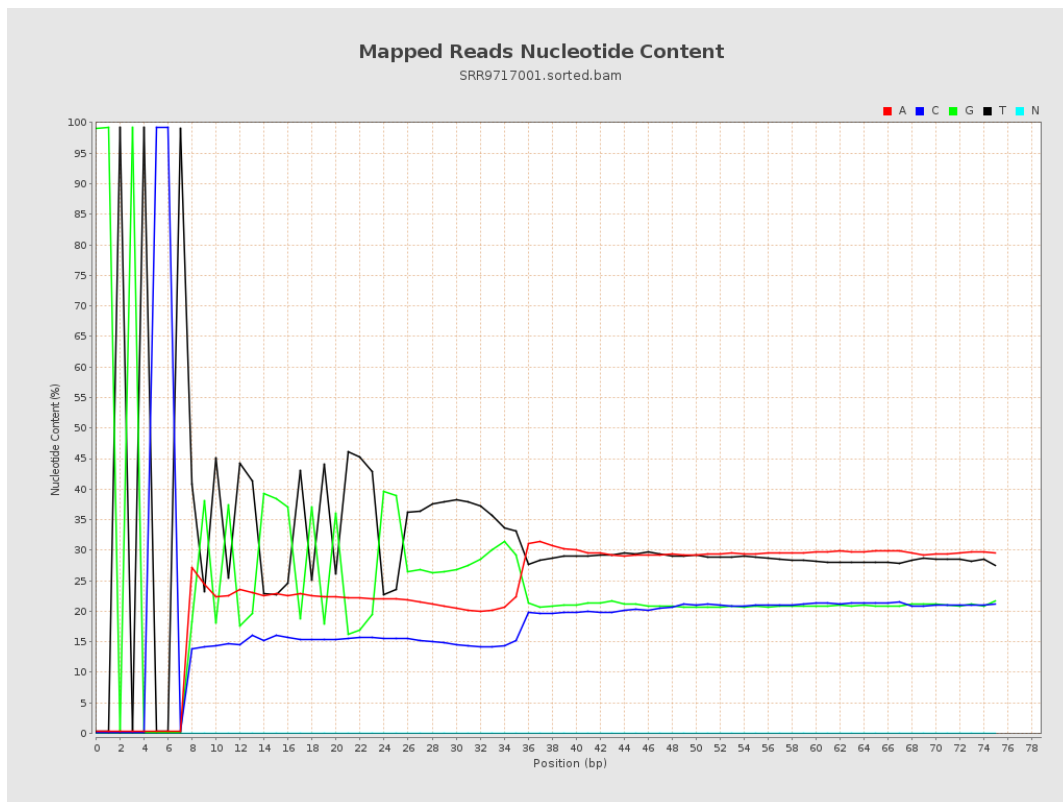
6. Results : Genome Fraction Coverage



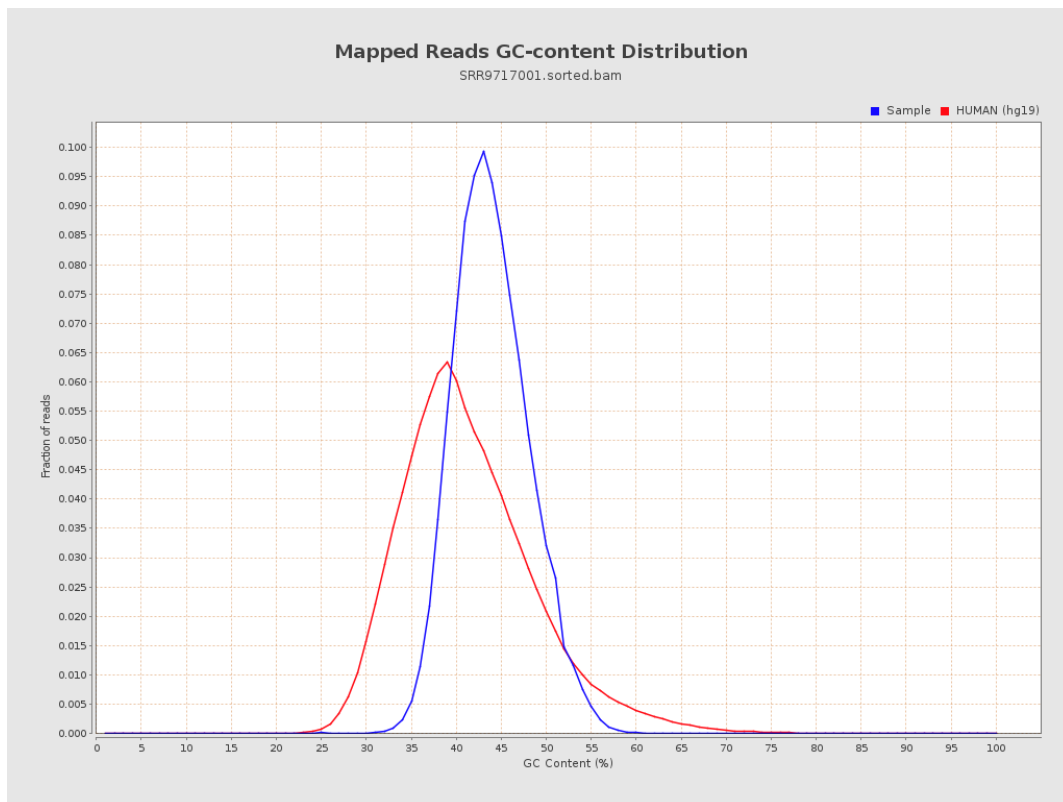
7. Results : Duplication Rate Histogram



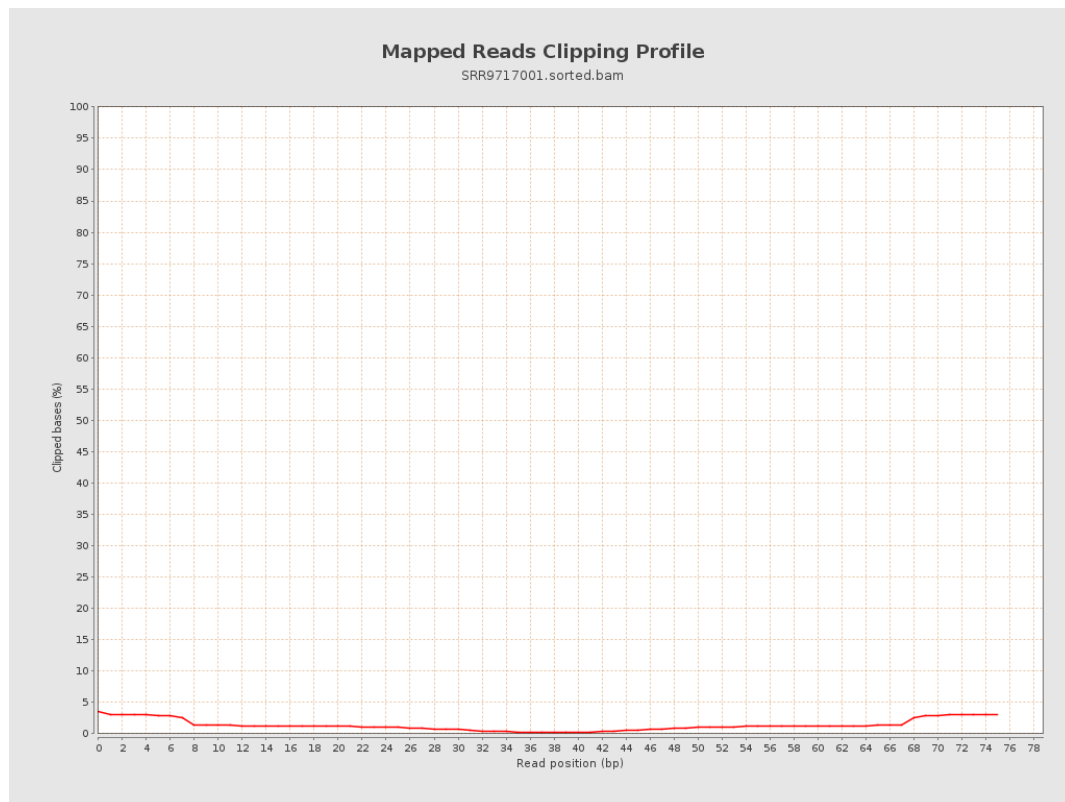
8. Results : Mapped Reads Nucleotide Content



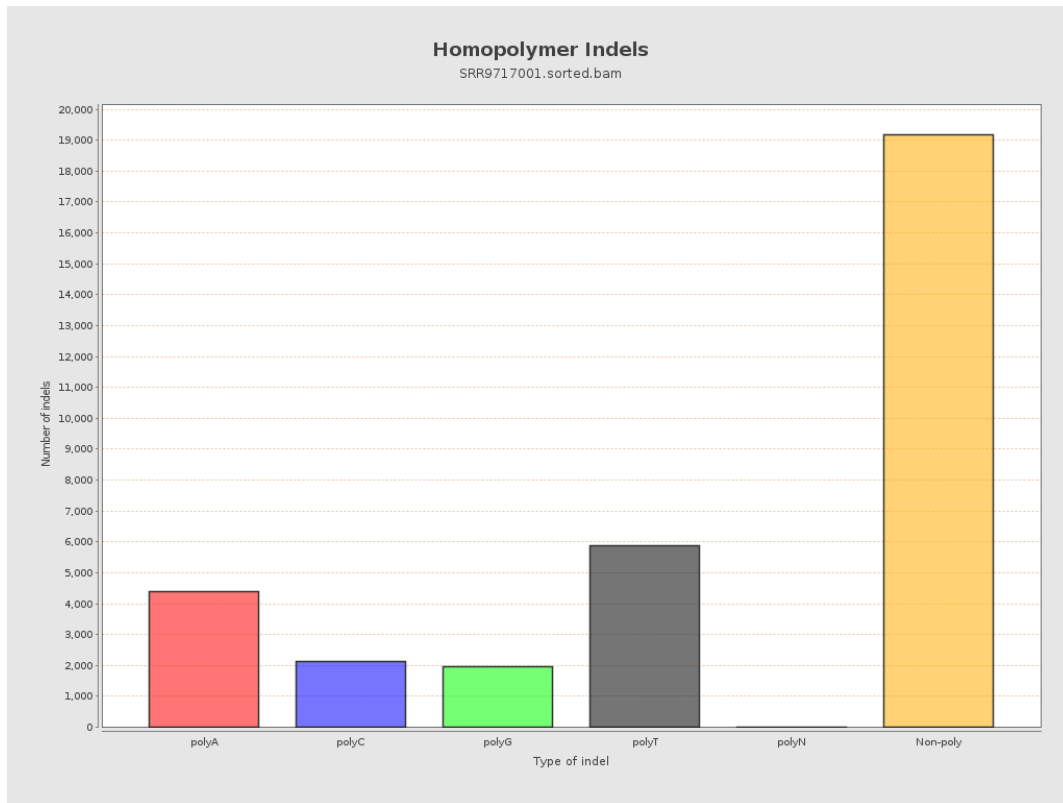
9. Results : Mapped Reads GC-content Distribution



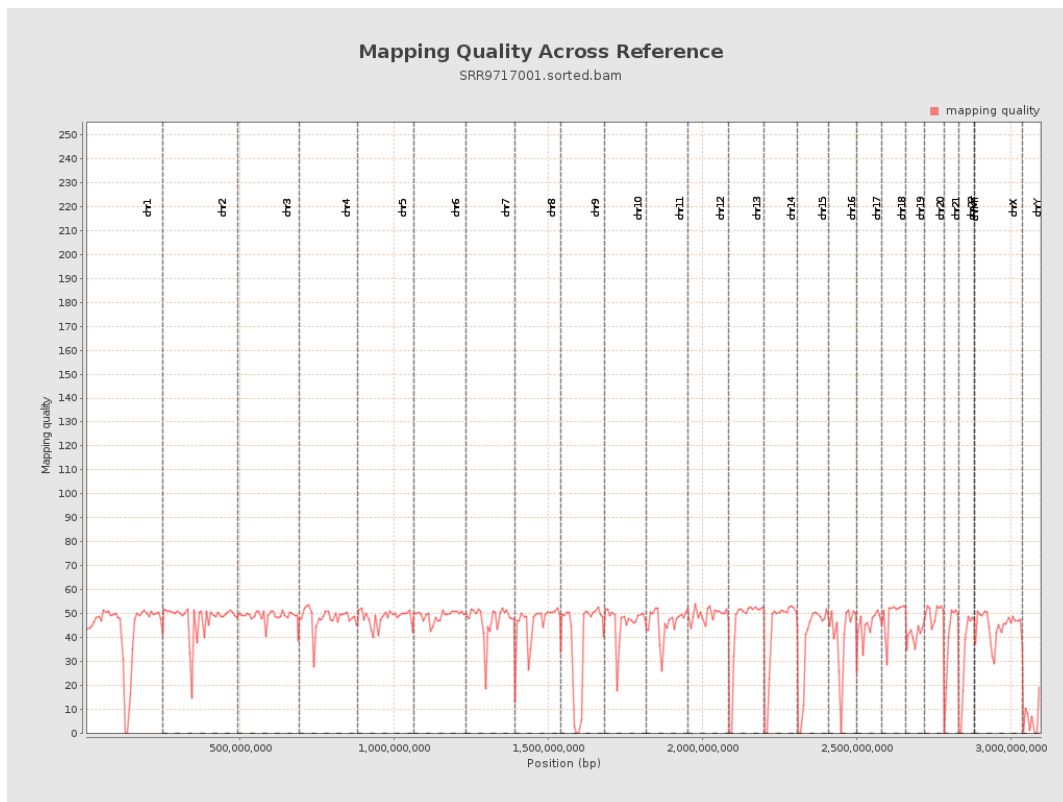
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

