

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 03:28:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717062.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_SRR9717062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 03:28:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	966,604
Mapped reads	756,965 / 78.31%
Unmapped reads	209,639 / 21.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,641 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	13,885 / 1.44%
Duplication rate	1.29%
Clipped reads	758,296 / 78.45%

2.2. ACGT Content

Number/percentage of A's	9,776,743 / 23.41%
Number/percentage of C's	8,180,935 / 19.59%
Number/percentage of T's	13,008,425 / 31.14%
Number/percentage of G's	10,802,661 / 25.86%
Number/percentage of N's	1,215 / 0%
GC Percentage	45.45%

2.3. Coverage

Mean	0.0135

Standard Deviation	0.1403
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2.4. Mapping Quality

Mean Mapping Quality	39.32
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2.5. Mismatches and indels

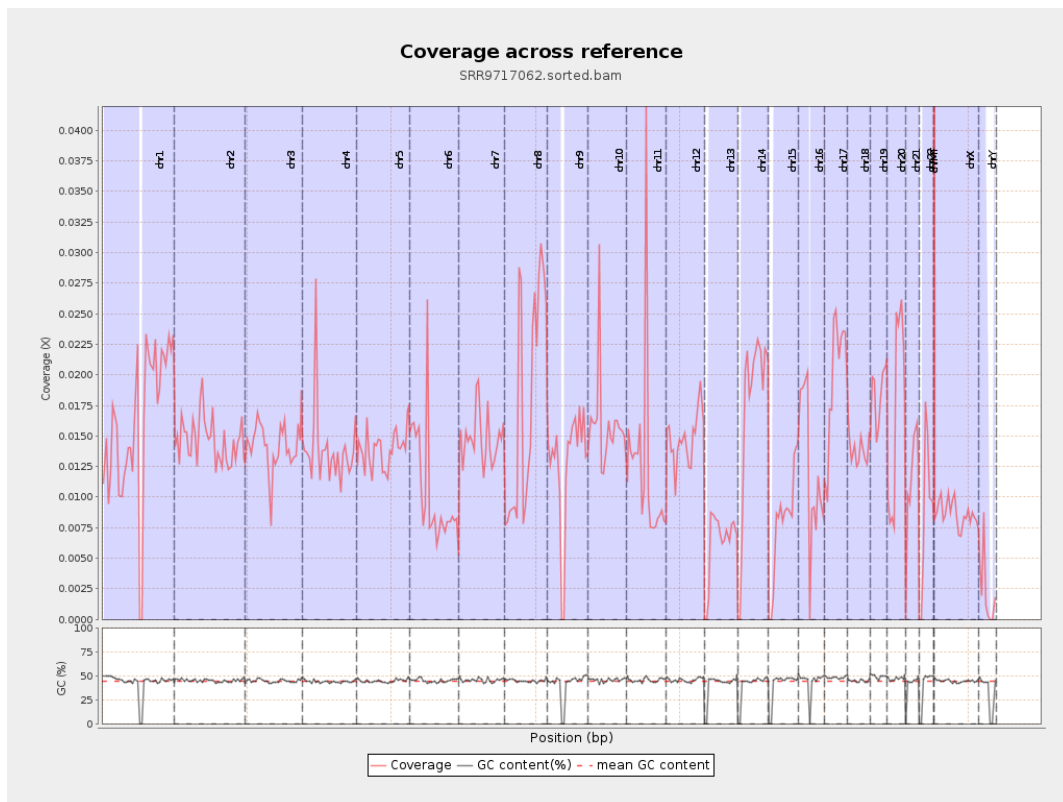
General error rate	0.55%
Mismatches	222,917
Insertions	3,017
Mapped reads with at least one insertion	0.4%
Deletions	6,860
Mapped reads with at least one deletion	0.9%
Homopolymer indels	35.17%

2.6. Chromosome stats

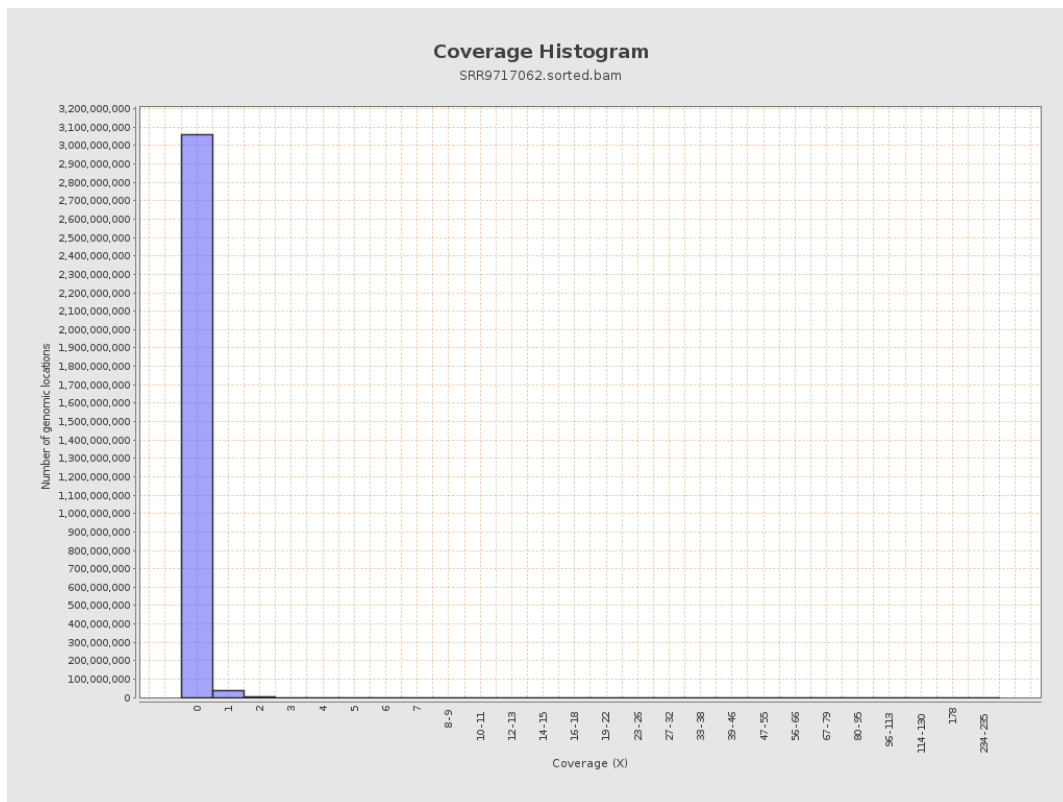
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4032733	0.0162	0.1687
chr2	243199373	3567914	0.0147	0.1724
chr3	198022430	2803380	0.0142	0.1304
chr4	191154276	2662226	0.0139	0.1393
chr5	180915260	2529569	0.014	0.1265
chr6	171115067	1781019	0.0104	0.1104
chr7	159138663	2358247	0.0148	0.1542

chr8	146364022	2592780	0.0177	0.1493
chr9	141213431	1805128	0.0128	0.1277
chr10	135534747	2158023	0.0159	0.1875
chr11	135006516	1693825	0.0125	0.1392
chr12	133851895	1982104	0.0148	0.1301
chr13	115169878	722130	0.0063	0.0839
chr14	107349540	1857202	0.0173	0.1429
chr15	102531392	808413	0.0079	0.0957
chr16	90354753	1105493	0.0122	0.1238
chr17	81195210	1596666	0.0197	0.1545
chr18	78077248	1080924	0.0138	0.1545
chr19	59128983	1082664	0.0183	0.1696
chr20	63025520	1054782	0.0167	0.1439
chr21	48129895	554817	0.0115	0.1206
chr22	51304566	466908	0.0091	0.106
chrMT	16571	2925	0.1765	0.4425
chrX	155270560	1348716	0.0087	0.1059
chrY	59373566	132887	0.0022	0.0775

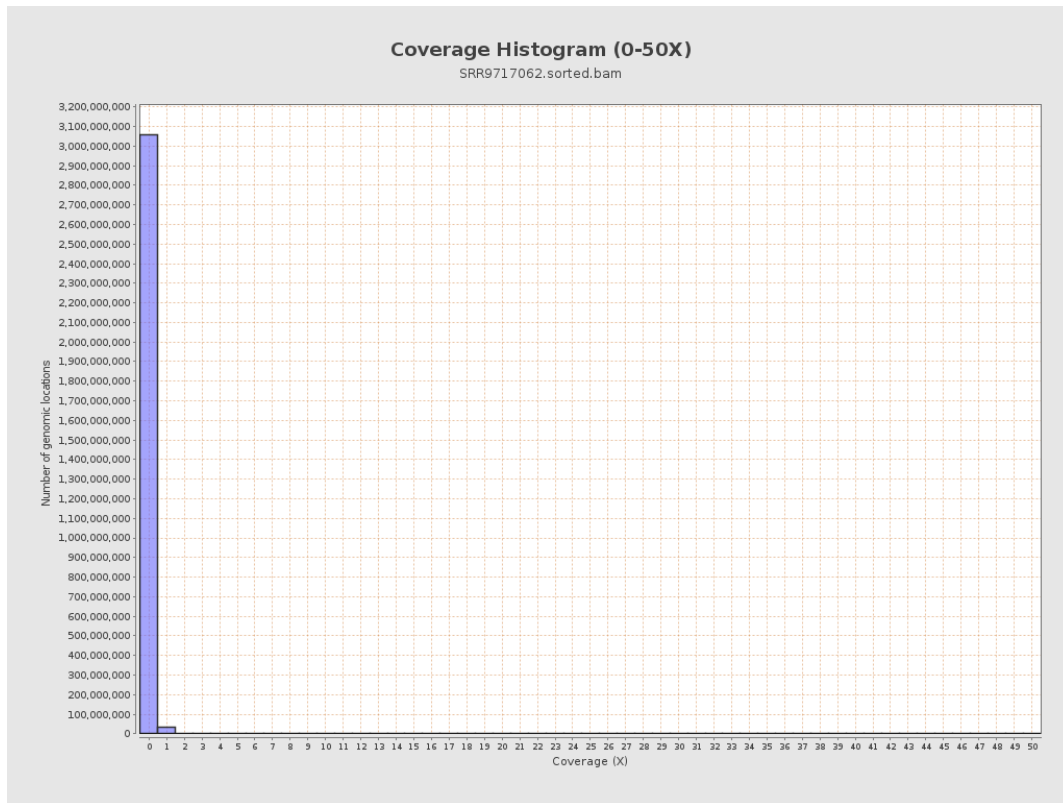
3. Results : Coverage across reference



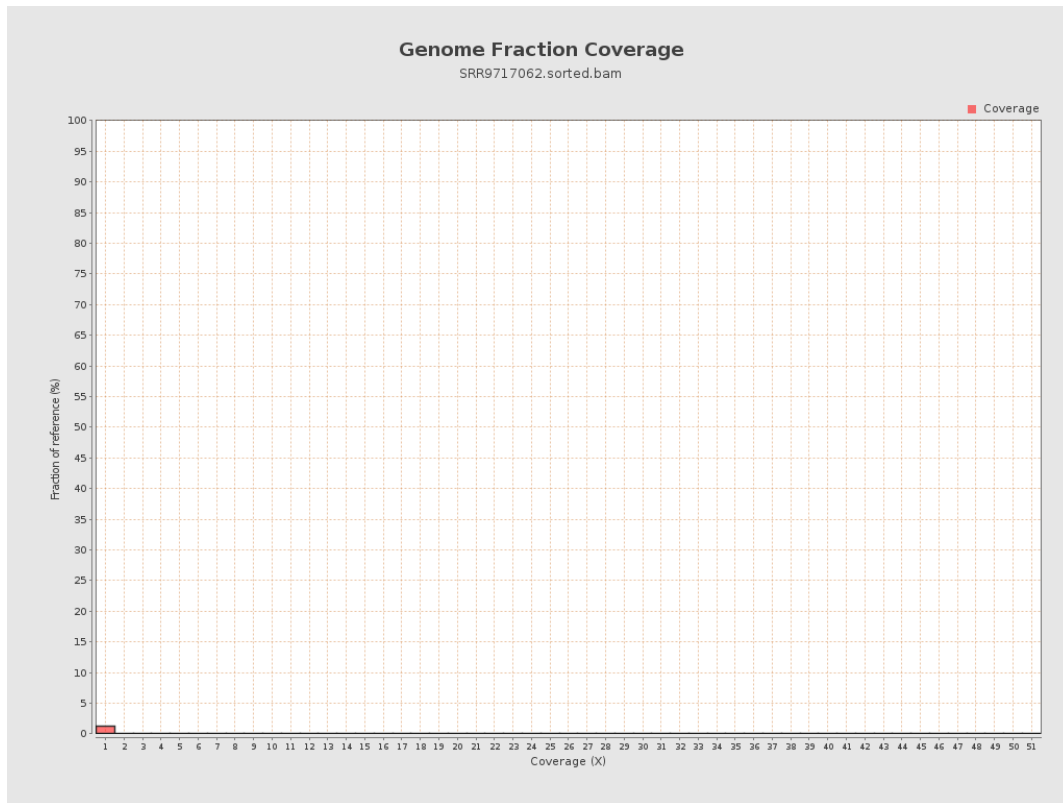
4. Results : Coverage Histogram



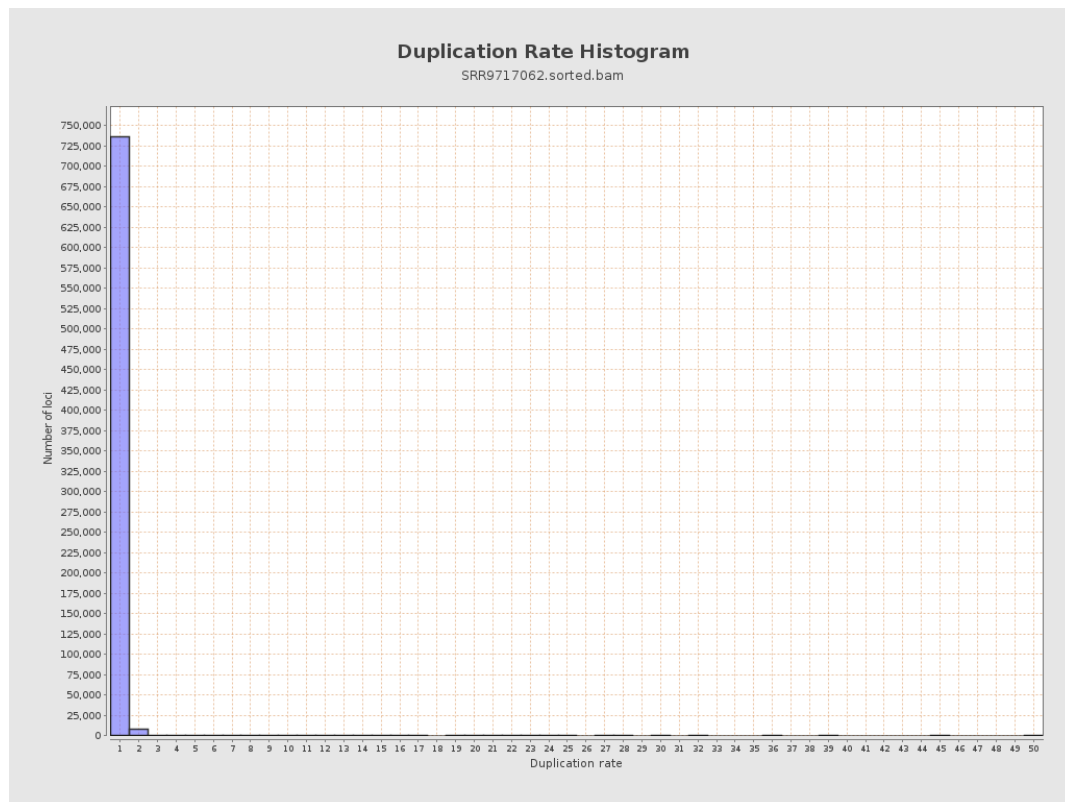
5. Results : Coverage Histogram (0-50X)



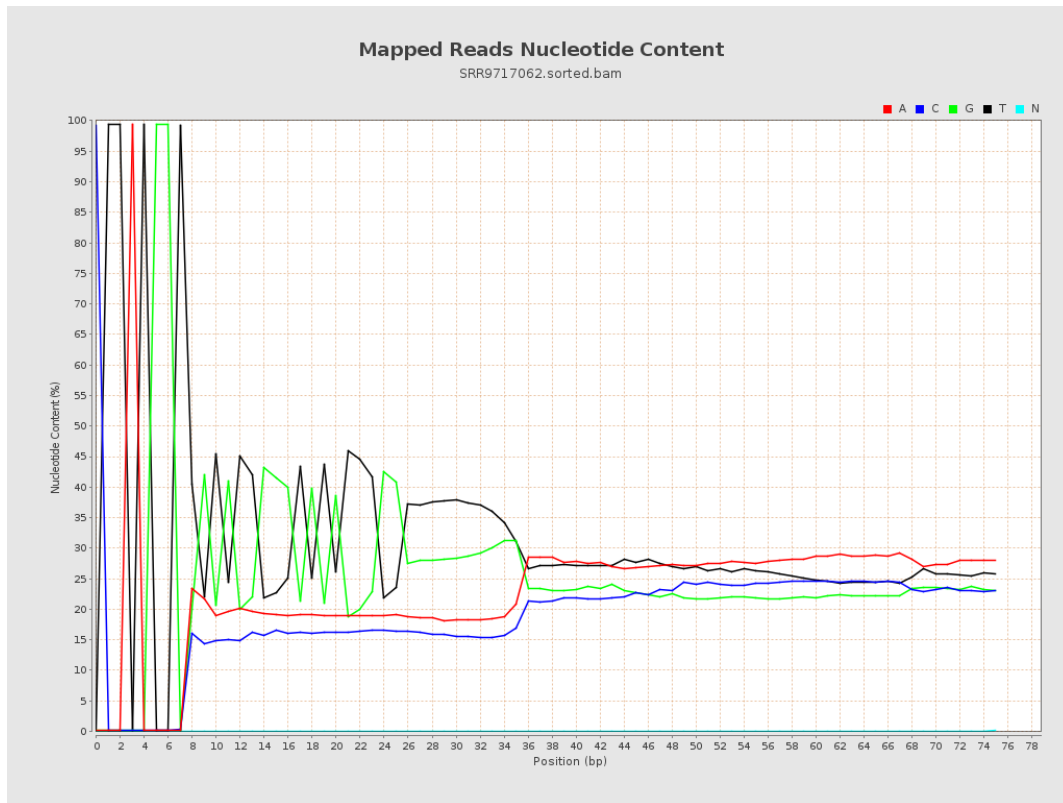
6. Results : Genome Fraction Coverage



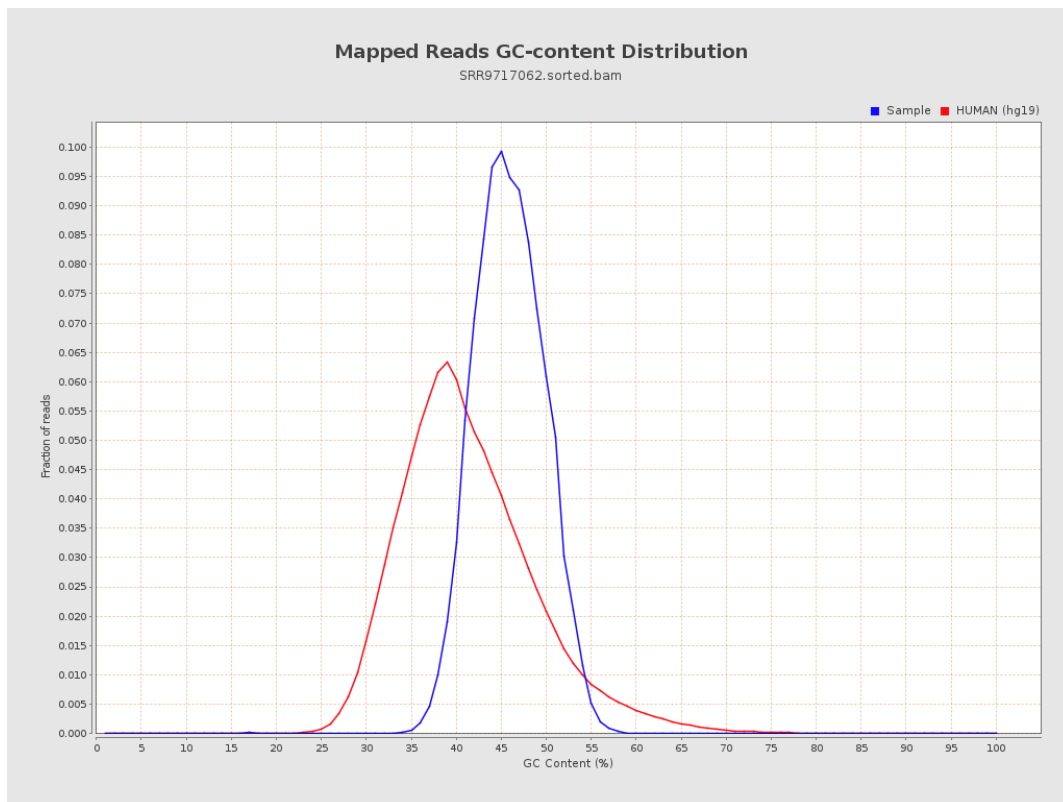
7. Results : Duplication Rate Histogram



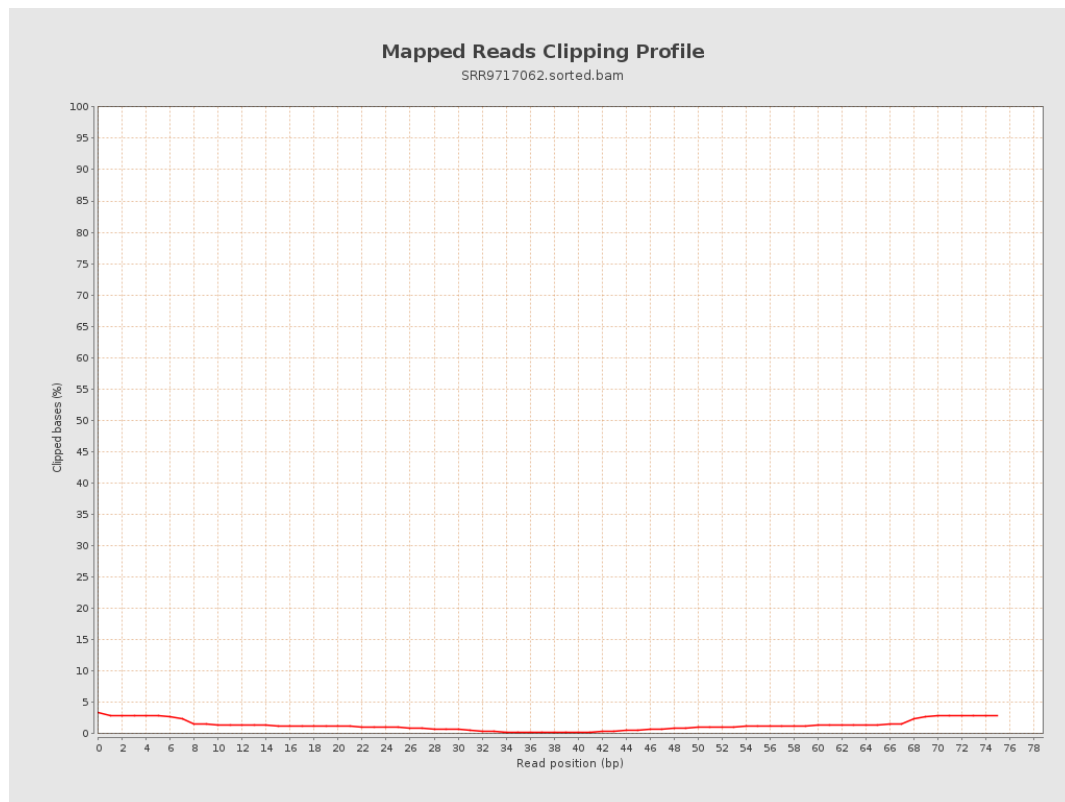
8. Results : Mapped Reads Nucleotide Content



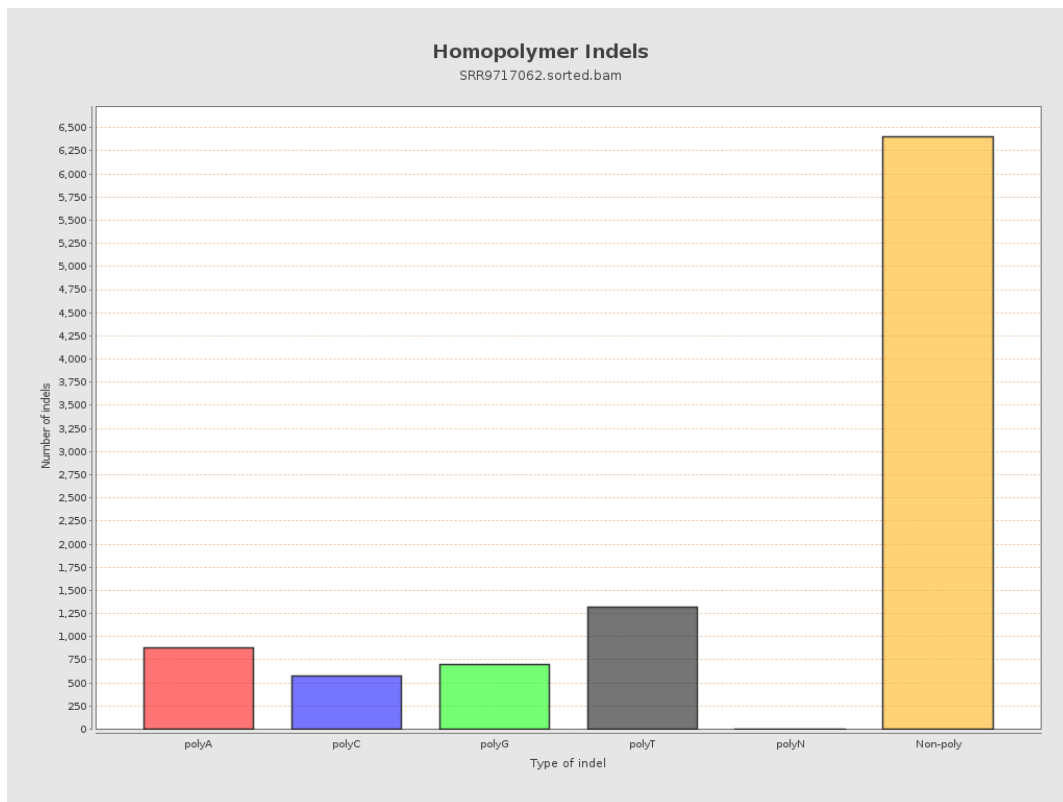
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

