

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:42:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525001.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_SRR10525001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525001.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:42:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,851,615
Mapped reads	1,685,922 / 91.05%
Unmapped reads	165,693 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,825 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	54,235 / 2.93%
Duplication rate	2.25%
Clipped reads	1,687,503 / 91.14%

2.2. ACGT Content

Number/percentage of A's	24,392,473 / 25.15%
Number/percentage of C's	17,221,416 / 17.75%
Number/percentage of T's	30,400,250 / 31.34%
Number/percentage of G's	24,986,151 / 25.76%
Number/percentage of N's	1,002 / 0%
GC Percentage	43.51%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2836
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2.4. Mapping Quality

Mean Mapping Quality	44.15
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2.5. Mismatches and indels

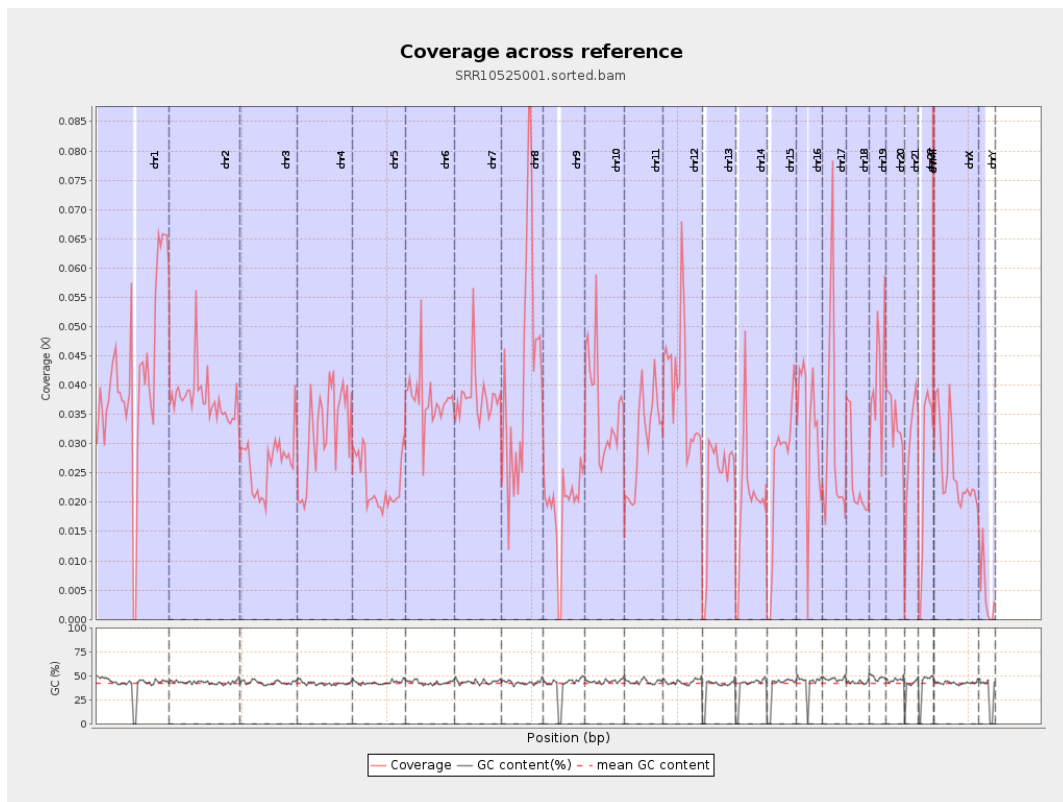
General error rate	0.5%
Mismatches	469,892
Insertions	6,227
Mapped reads with at least one insertion	0.37%
Deletions	19,463
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.22%

2.6. Chromosome stats

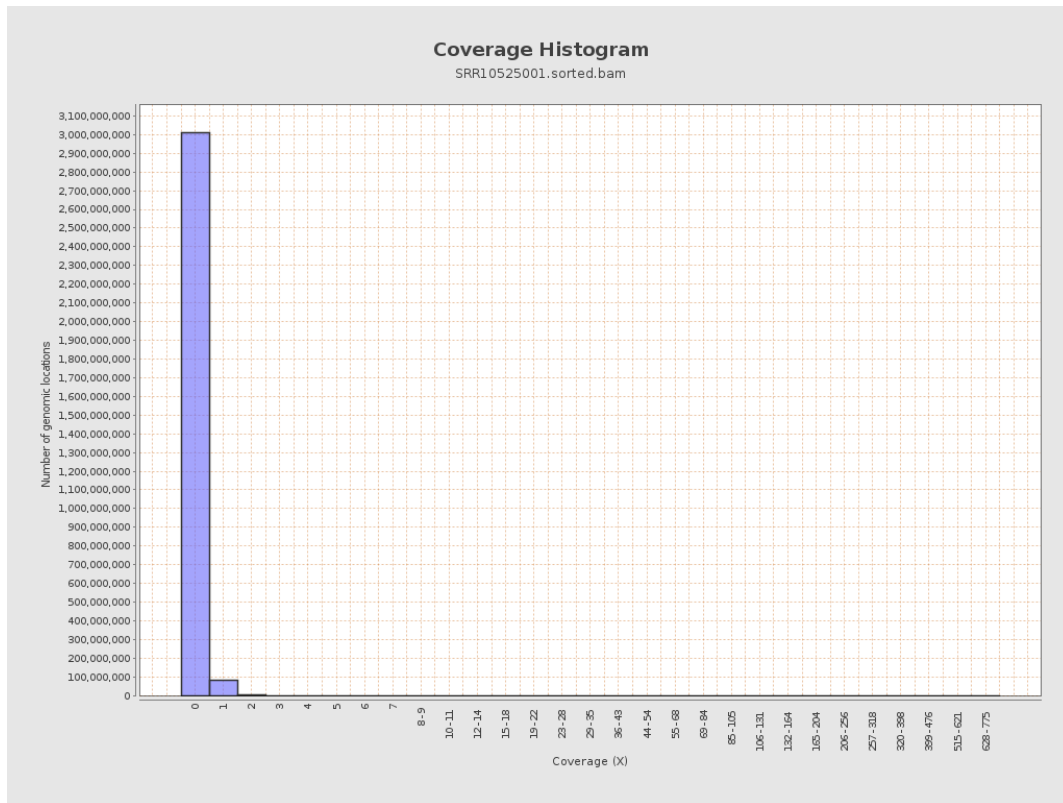
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10285767	0.0413	0.5472
chr2	243199373	9167918	0.0377	0.3242
chr3	198022430	5282859	0.0267	0.1774
chr4	191154276	6138720	0.0321	0.2117
chr5	180915260	4199548	0.0232	0.1703
chr6	171115067	6423703	0.0375	0.2844
chr7	159138663	6080200	0.0382	0.3736

chr8	146364022	6029878	0.0412	0.2798
chr9	141213431	2687816	0.019	0.2085
chr10	135534747	4894556	0.0361	0.2825
chr11	135006516	4080456	0.0302	0.2515
chr12	133851895	5211800	0.0389	0.2167
chr13	115169878	2651763	0.023	0.1646
chr14	107349540	2199033	0.0205	0.1607
chr15	102531392	2668094	0.026	0.1867
chr16	90354753	2937471	0.0325	0.2045
chr17	81195210	2559056	0.0315	0.258
chr18	78077248	1897677	0.0243	0.3532
chr19	59128983	2429684	0.0411	0.3445
chr20	63025520	2129358	0.0338	0.2003
chr21	48129895	1403524	0.0292	0.1936
chr22	51304566	1306986	0.0255	0.1712
chrMT	16571	77611	4.6835	3.3227
chrX	155270560	4013335	0.0258	0.2064
chrY	59373566	276184	0.0047	0.1202

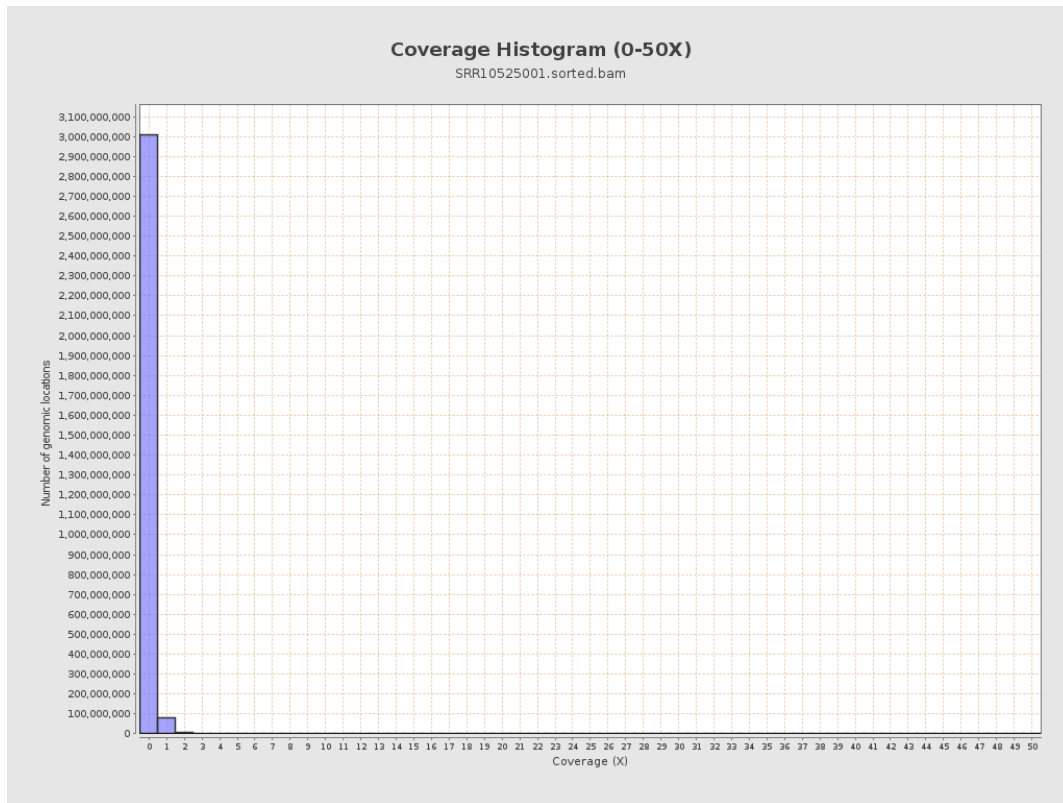
3. Results : Coverage across reference



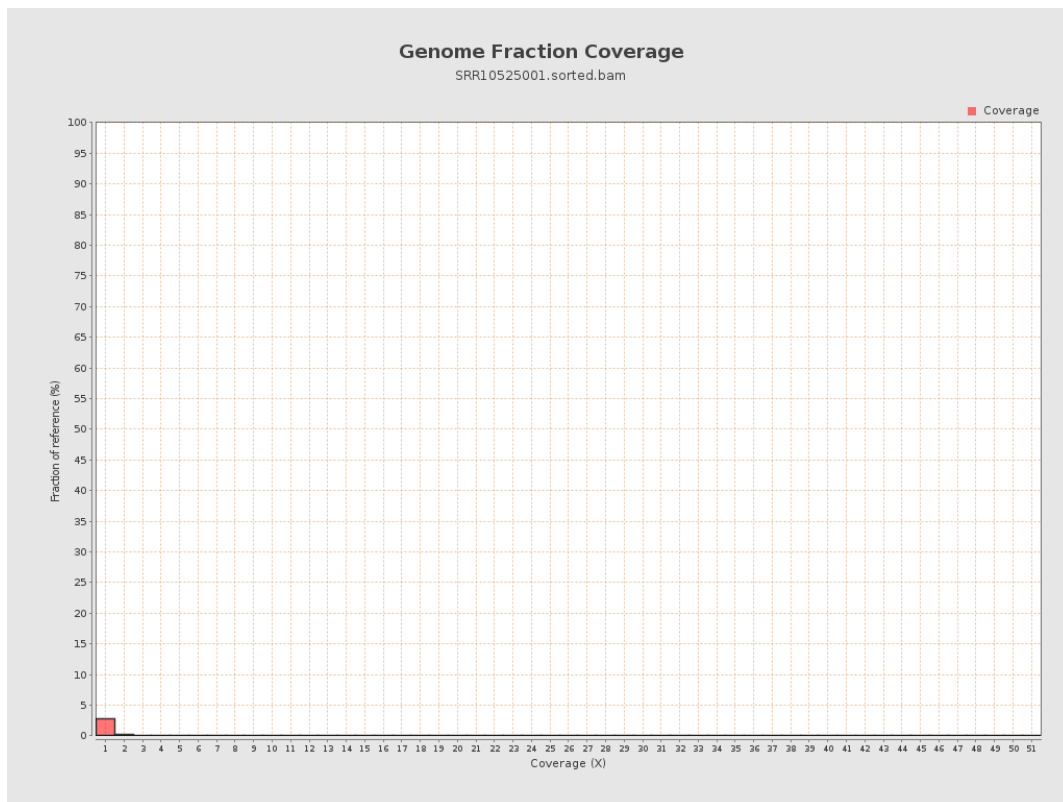
4. Results : Coverage Histogram



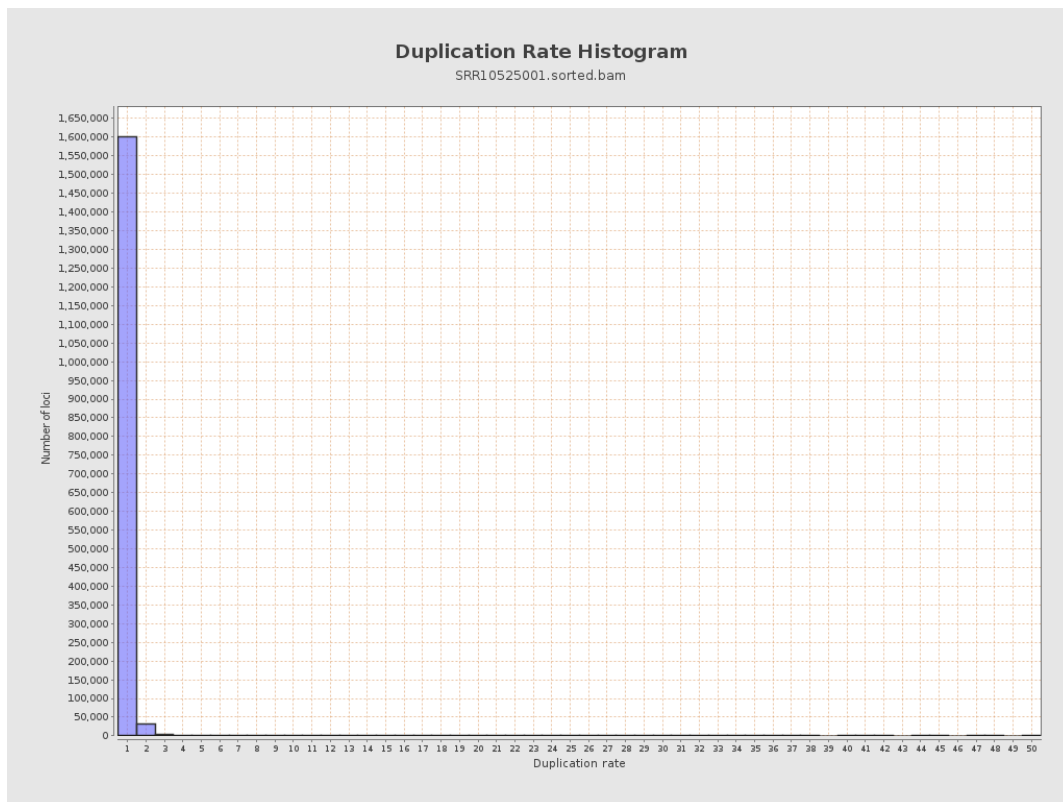
5. Results : Coverage Histogram (0-50X)



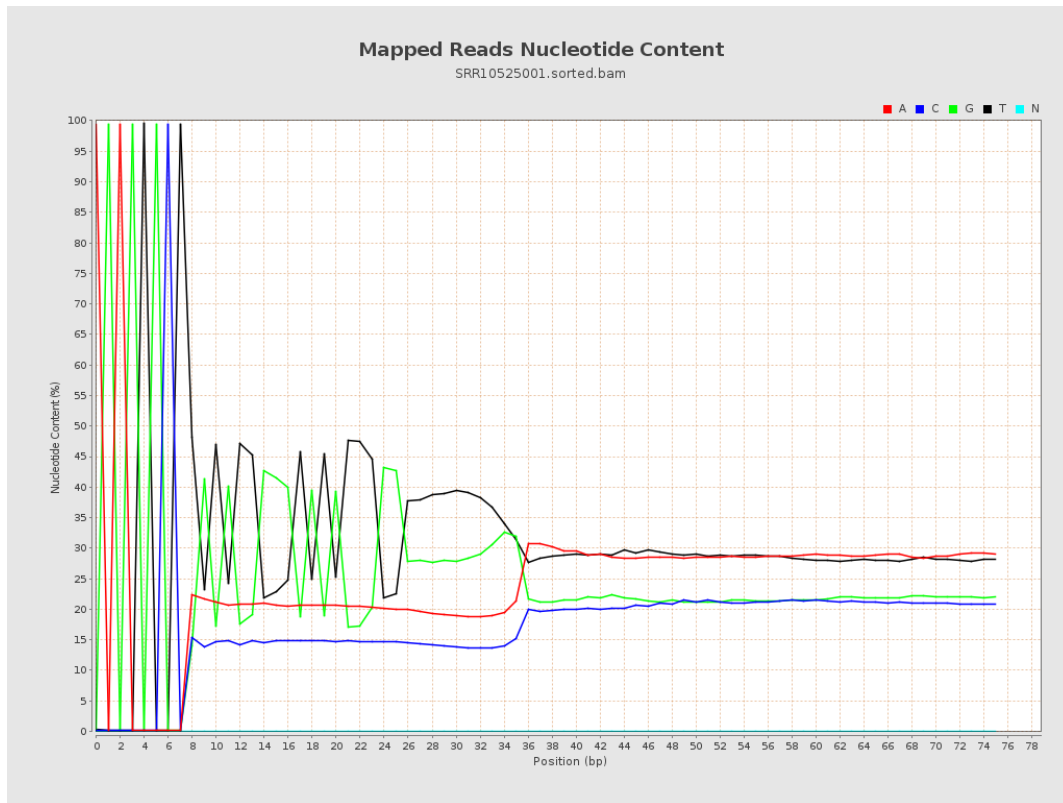
6. Results : Genome Fraction Coverage



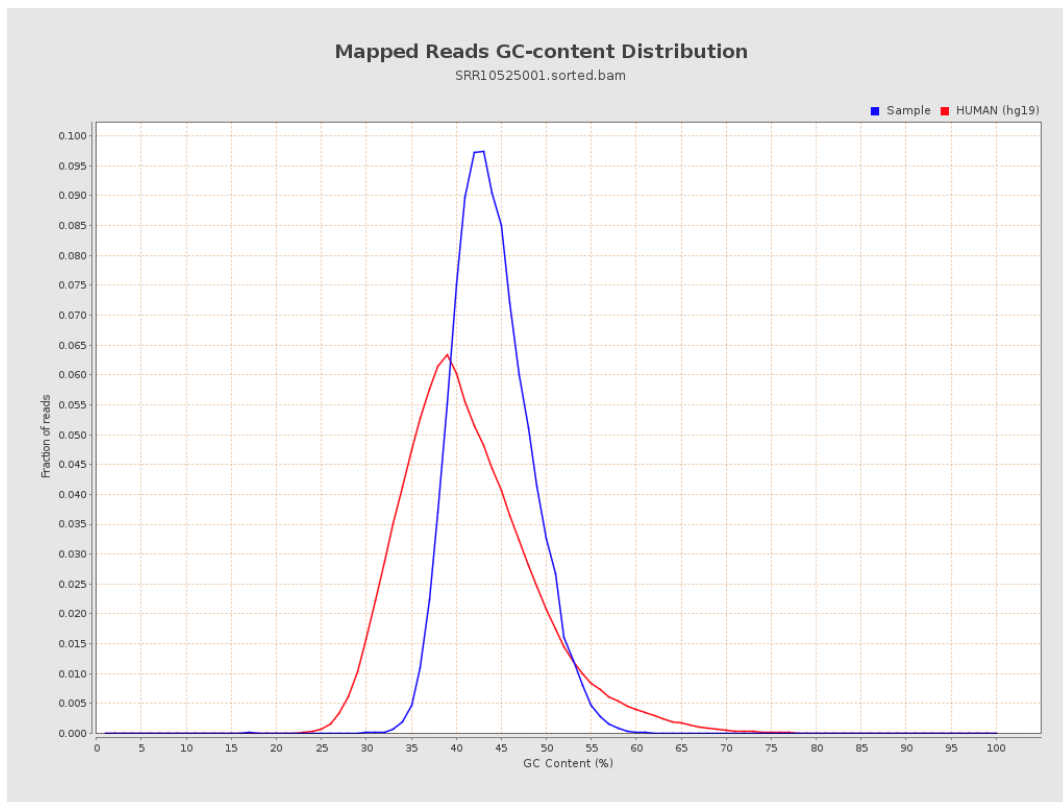
7. Results : Duplication Rate Histogram



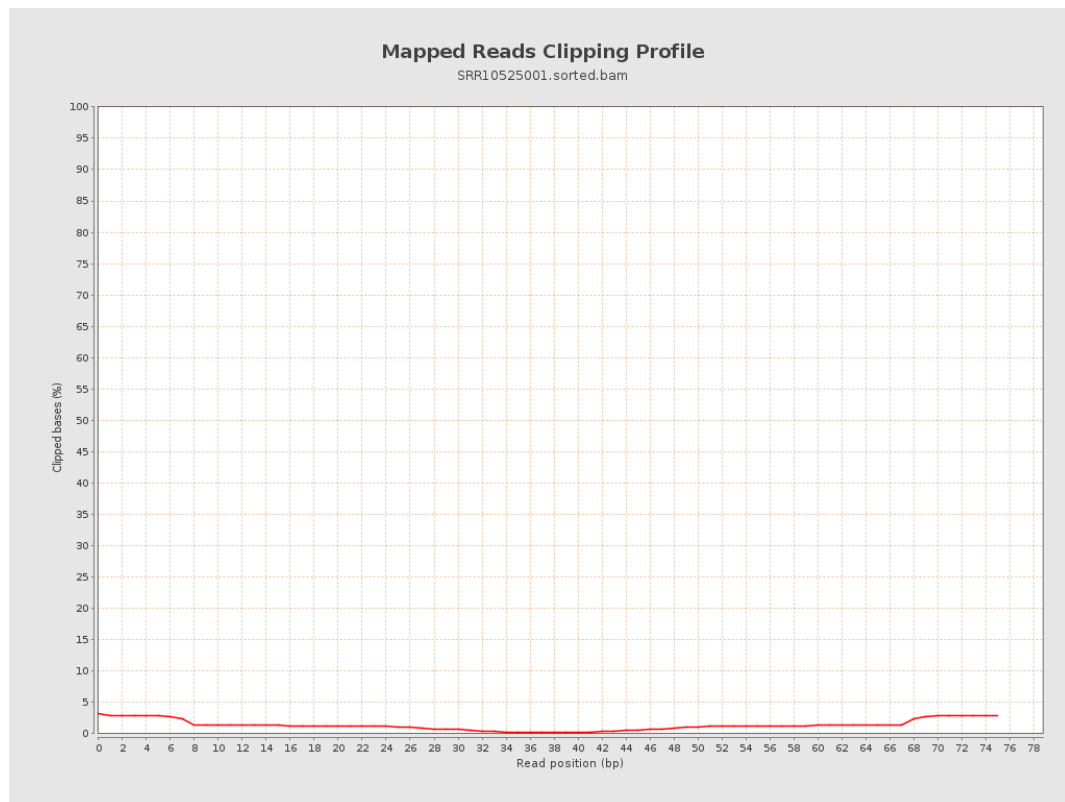
8. Results : Mapped Reads Nucleotide Content



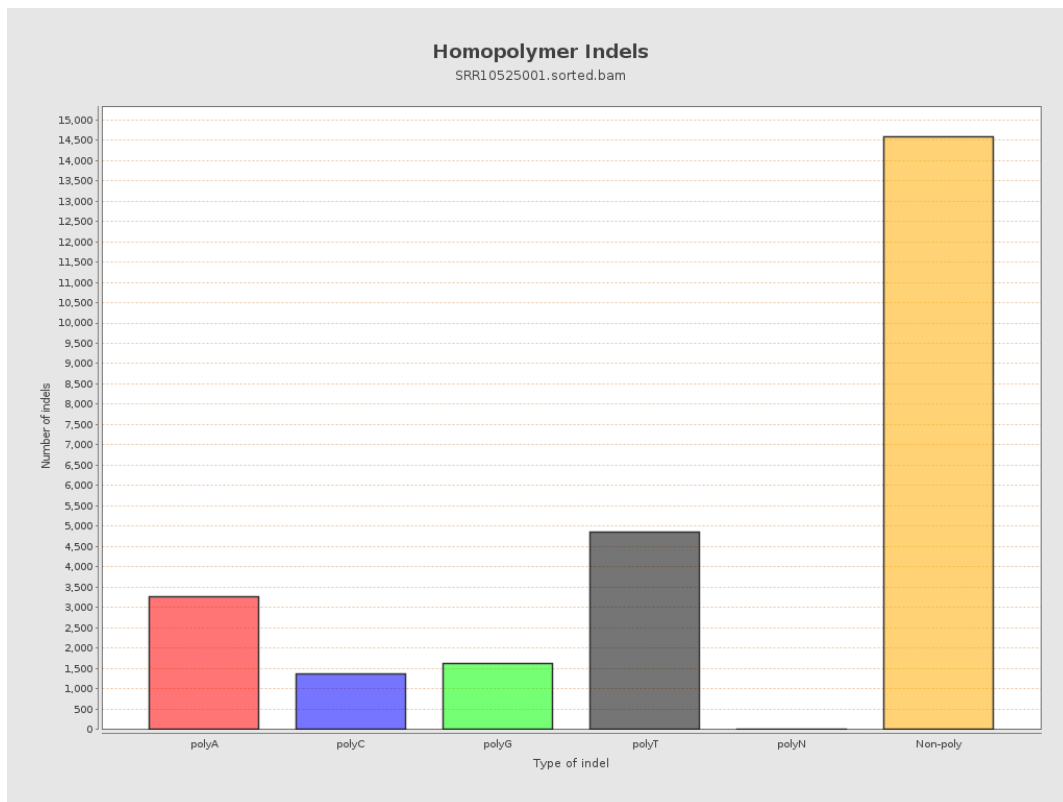
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

