

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:48:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525201.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_SRR10525201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:48:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,630,143
Mapped reads	2,406,077 / 91.48%
Unmapped reads	224,066 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,812 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	113,164 / 4.3%
Duplication rate	3.42%
Clipped reads	2,407,758 / 91.54%

2.2. ACGT Content

Number/percentage of A's	35,504,167 / 25.52%
Number/percentage of C's	26,577,386 / 19.11%
Number/percentage of T's	43,967,816 / 31.61%
Number/percentage of G's	33,052,149 / 23.76%
Number/percentage of N's	3,204 / 0%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0449

Standard Deviation	0.4101
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2.4. Mapping Quality

Mean Mapping Quality	44.71
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2.5. Mismatches and indels

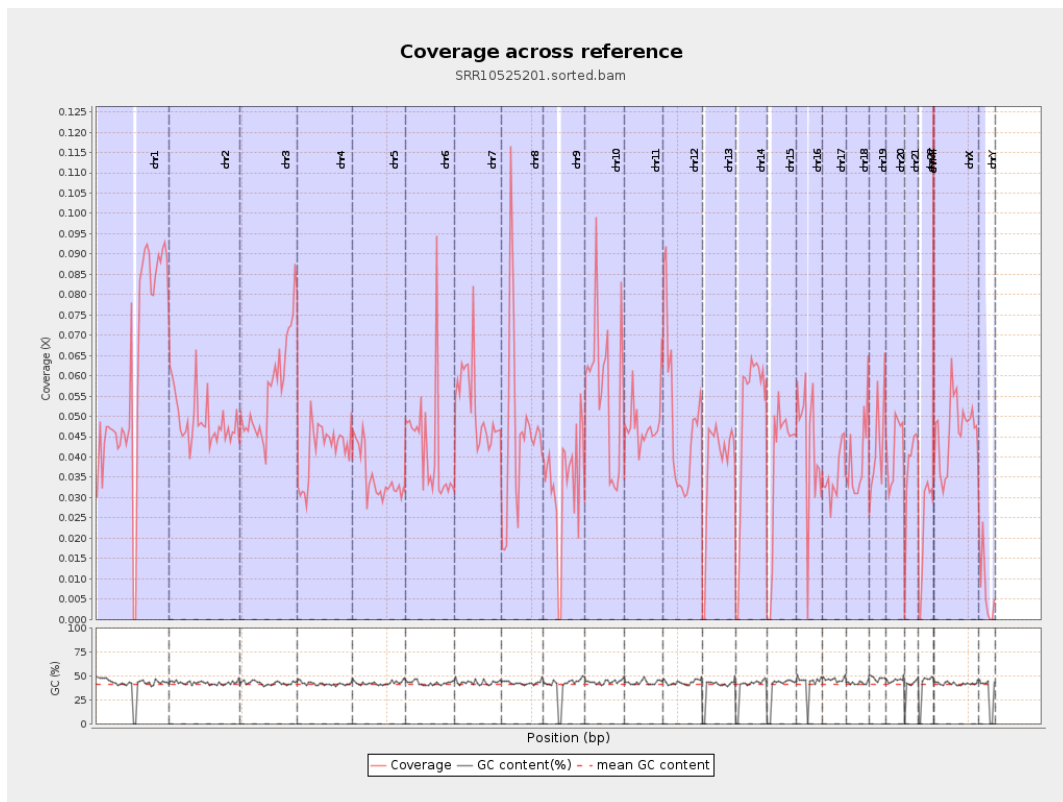
General error rate	0.53%
Mismatches	721,144
Insertions	9,188
Mapped reads with at least one insertion	0.38%
Deletions	28,348
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.63%

2.6. Chromosome stats

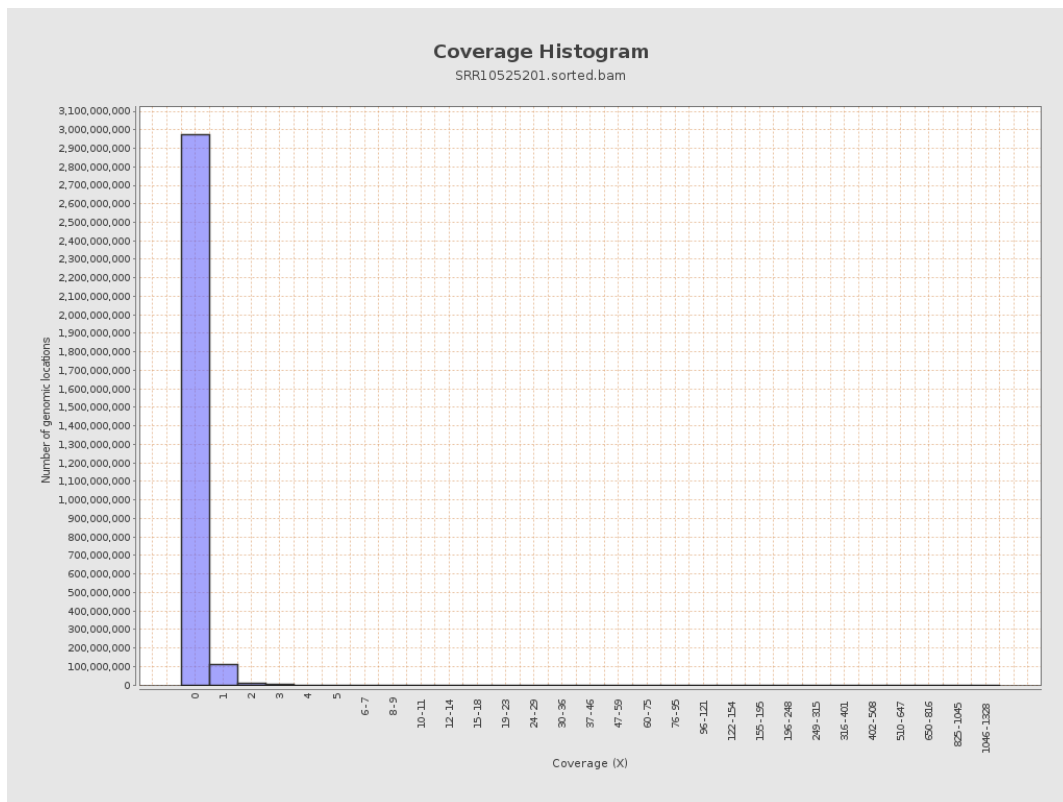
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15072216	0.0605	0.7901
chr2	243199373	11916868	0.049	0.5897
chr3	198022430	11183763	0.0565	0.2721
chr4	191154276	7991776	0.0418	0.2528
chr5	180915260	6351472	0.0351	0.2117
chr6	171115067	7196175	0.0421	0.2729
chr7	159138663	8334403	0.0524	0.605

chr8	146364022	6565105	0.0449	0.3655
chr9	141213431	4683105	0.0332	0.2816
chr10	135534747	7696735	0.0568	0.4377
chr11	135006516	6525851	0.0483	0.3432
chr12	133851895	6446736	0.0482	0.2514
chr13	115169878	4380149	0.038	0.2208
chr14	107349540	5356541	0.0499	0.2629
chr15	102531392	3912889	0.0382	0.2287
chr16	90354753	3815699	0.0422	0.2673
chr17	81195210	2864429	0.0353	0.2213
chr18	78077248	3068439	0.0393	0.5789
chr19	59128983	2563531	0.0434	0.5262
chr20	63025520	2628436	0.0417	0.2352
chr21	48129895	1794202	0.0373	0.2402
chr22	51304566	1152875	0.0225	0.1677
chrMT	16571	4563	0.2754	0.5849
chrX	155270560	7222515	0.0465	0.2753
chrY	59373566	421482	0.0071	0.1956

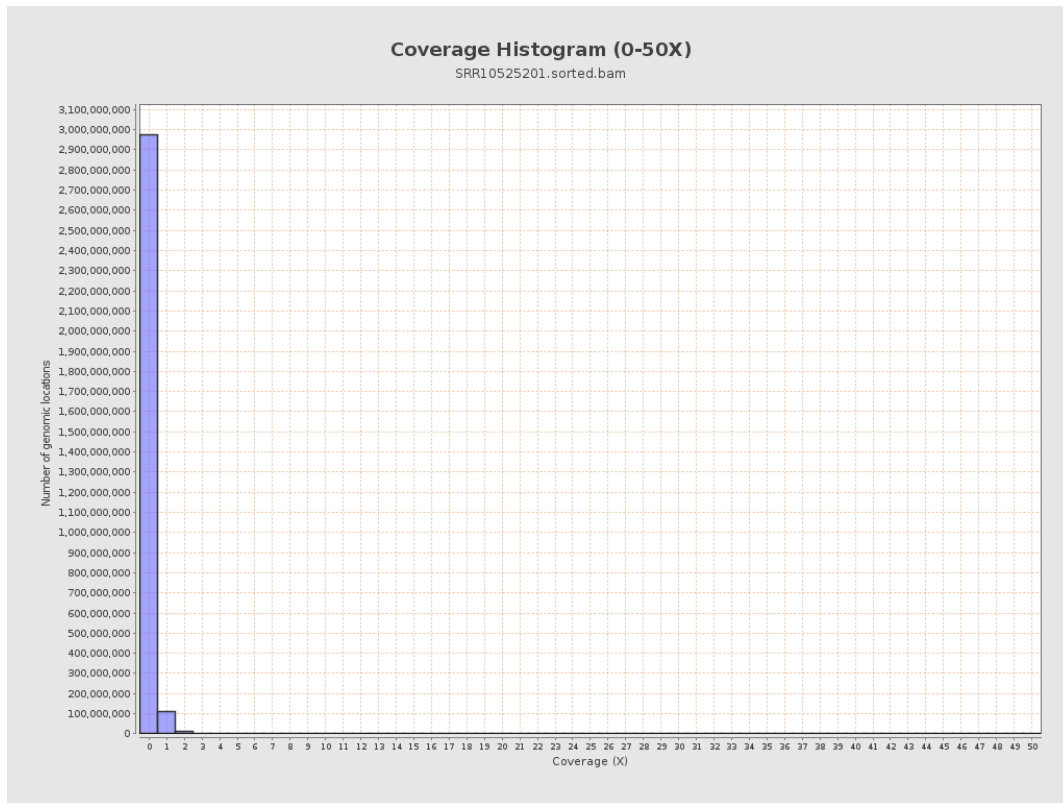
3. Results : Coverage across reference



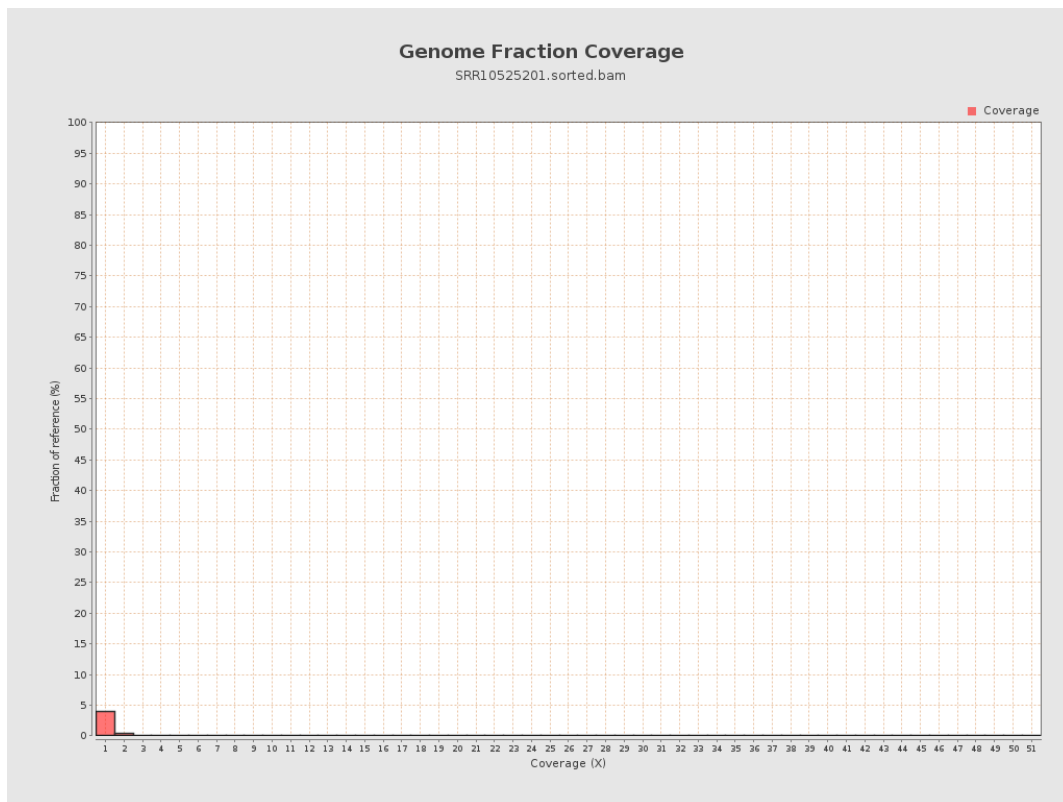
4. Results : Coverage Histogram



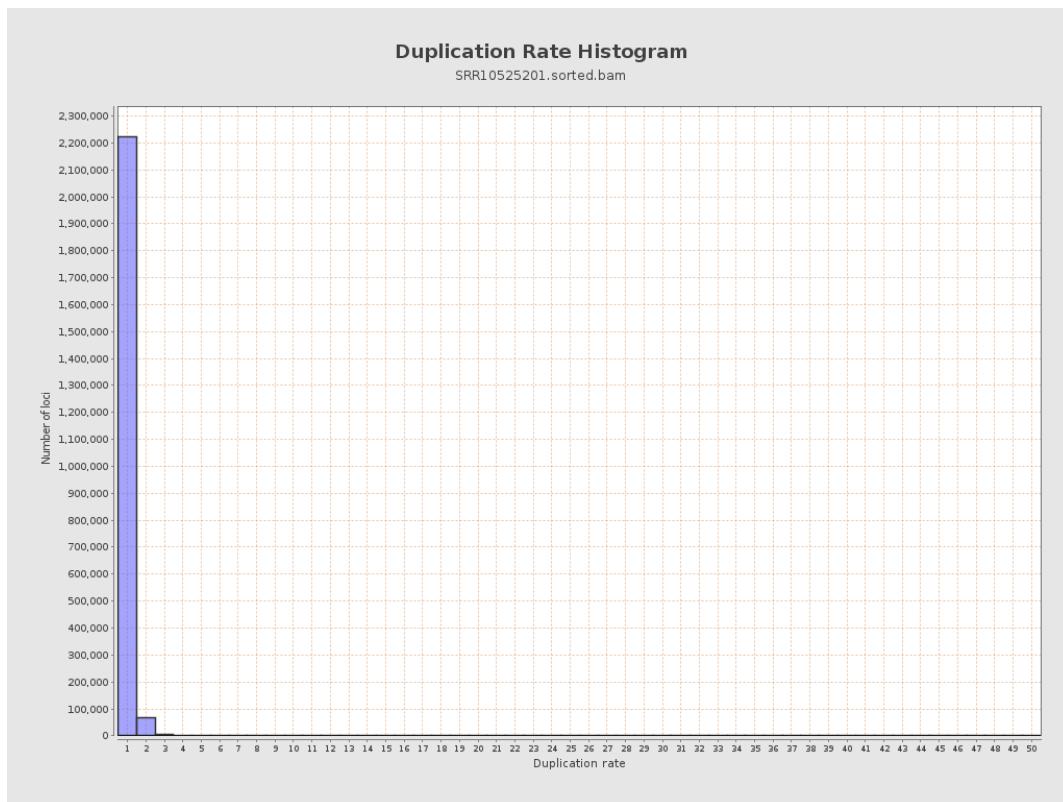
5. Results : Coverage Histogram (0-50X)



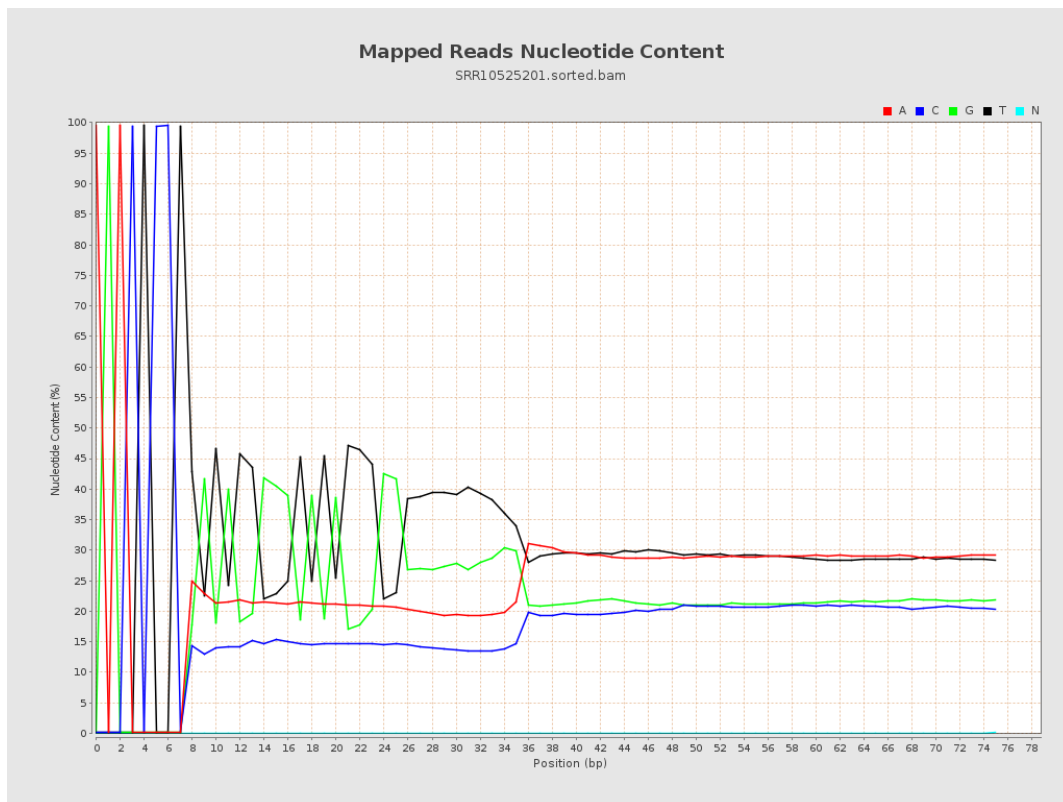
6. Results : Genome Fraction Coverage



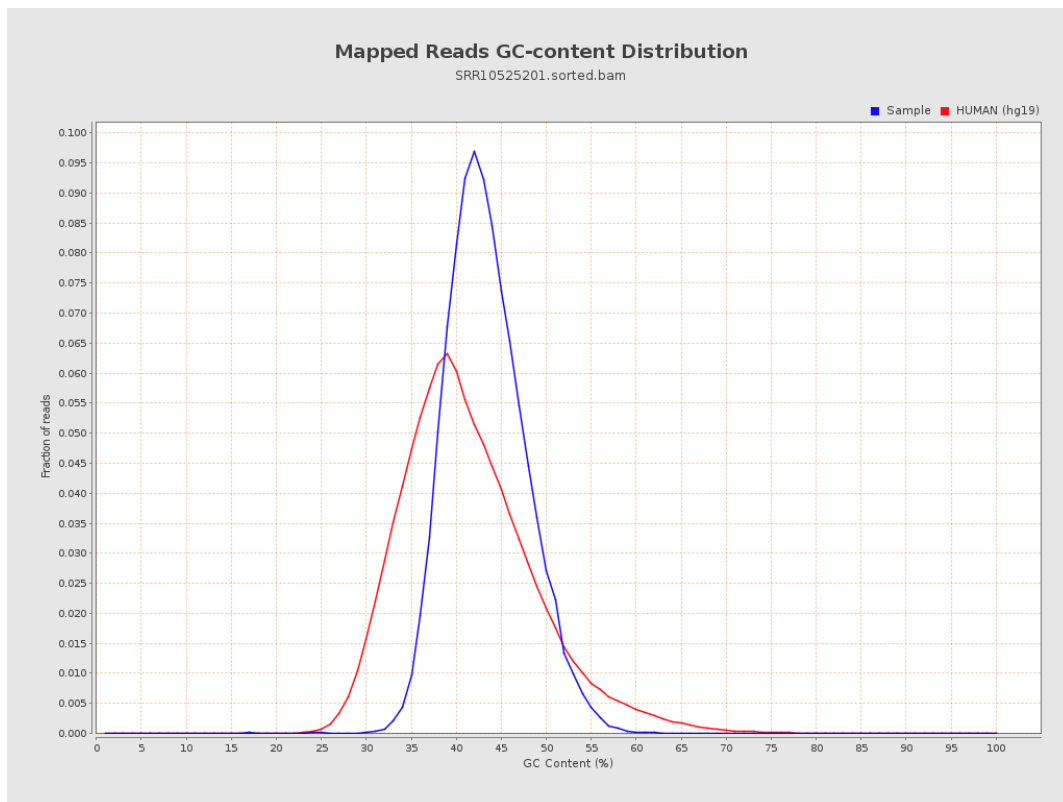
7. Results : Duplication Rate Histogram



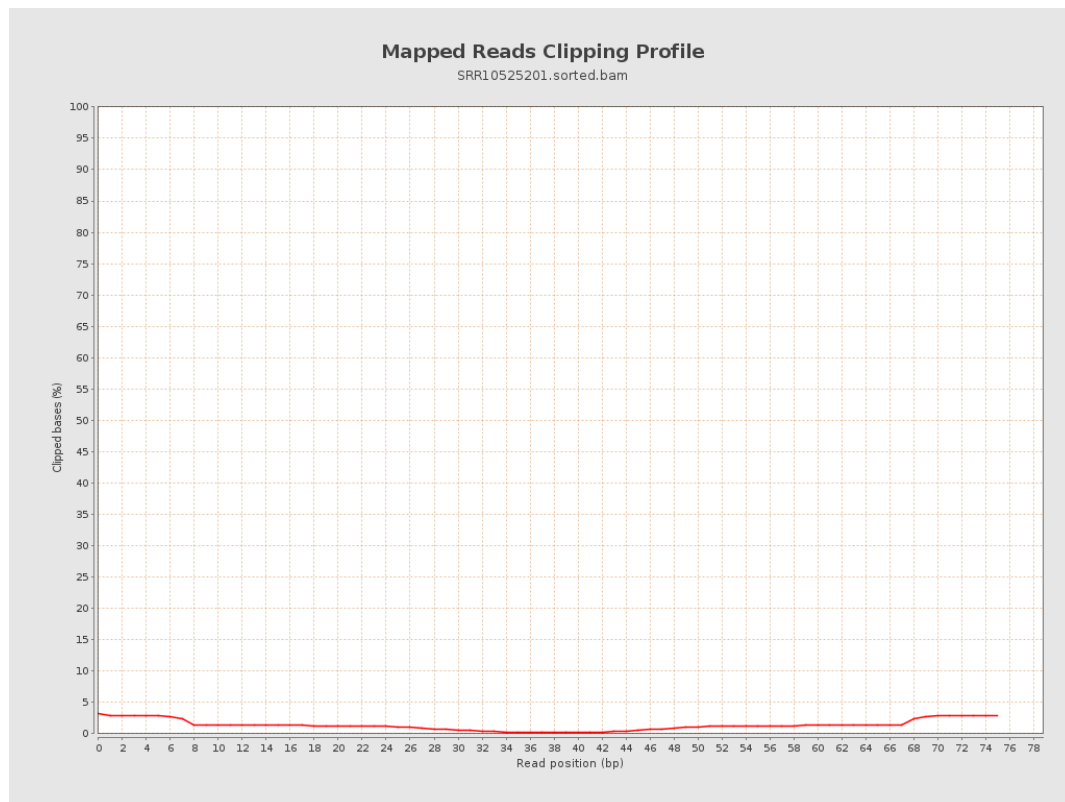
8. Results : Mapped Reads Nucleotide Content



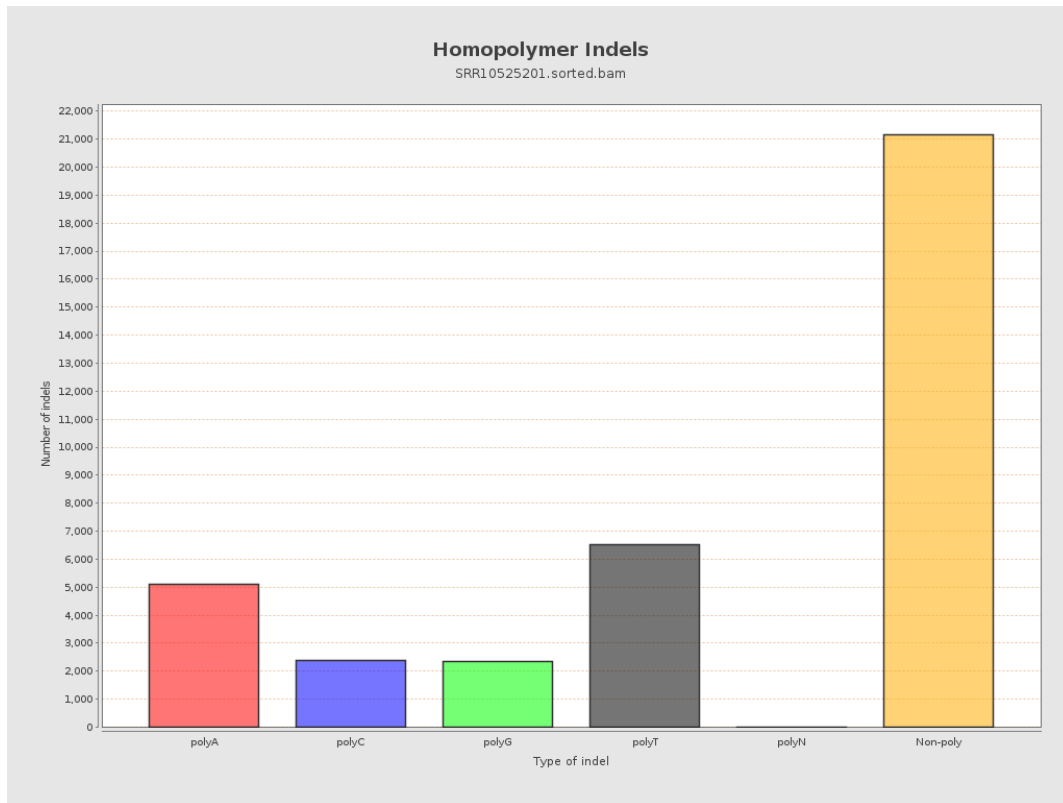
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

