

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:47:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506325.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_SRR1506325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:47:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,459,390
Mapped reads	4,496,792 / 69.62%
Unmapped reads	1,962,598 / 30.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,210 / 0.99%
Read min/max/mean length	30 / 94 / 94.36
Duplicated reads (estimated)	669,372 / 10.36%
Duplication rate	10.7%
Clipped reads	2,903,416 / 44.95%

2.2. ACGT Content

Number/percentage of A's	90,853,228 / 26.02%
Number/percentage of C's	68,458,611 / 19.6%
Number/percentage of T's	100,163,980 / 28.68%
Number/percentage of G's	89,647,076 / 25.67%
Number/percentage of N's	67,586 / 0.02%
GC Percentage	45.28%

2.3. Coverage

Mean	0.1128

Standard Deviation	0.8312
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2.4. Mapping Quality

Mean Mapping Quality	46.94
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2.5. Mismatches and indels

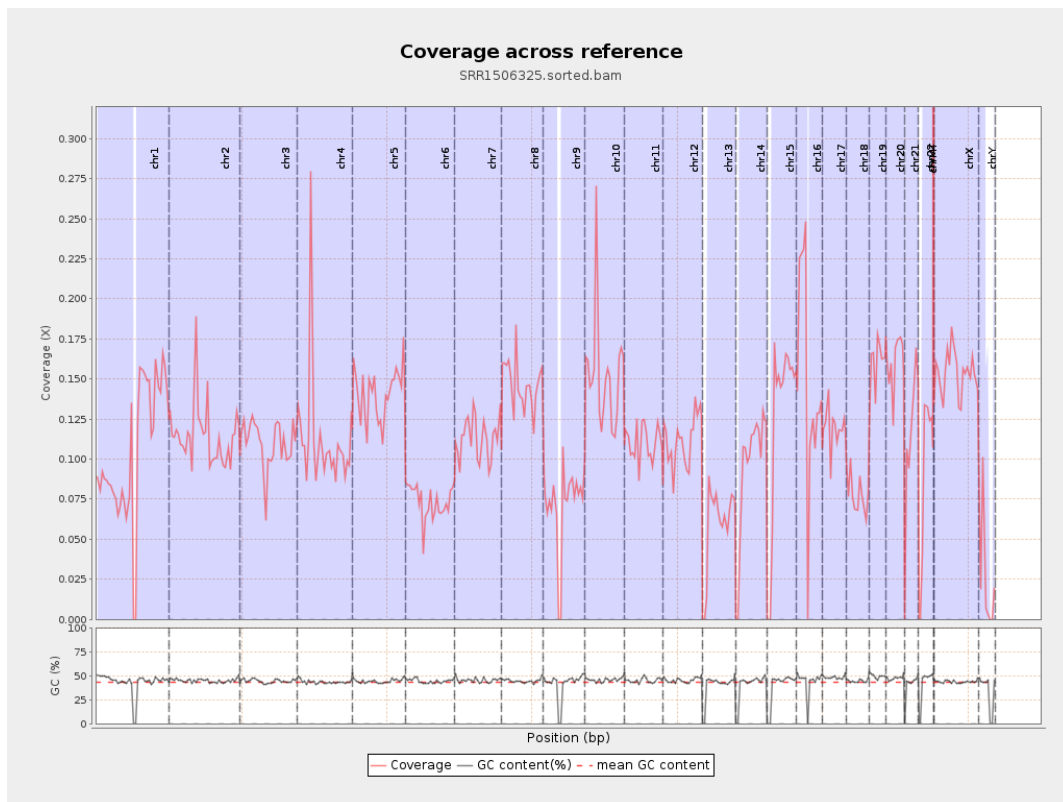
General error rate	0.78%
Mismatches	2,648,597
Insertions	29,412
Mapped reads with at least one insertion	0.64%
Deletions	68,364
Mapped reads with at least one deletion	1.49%
Homopolymer indels	40.44%

2.6. Chromosome stats

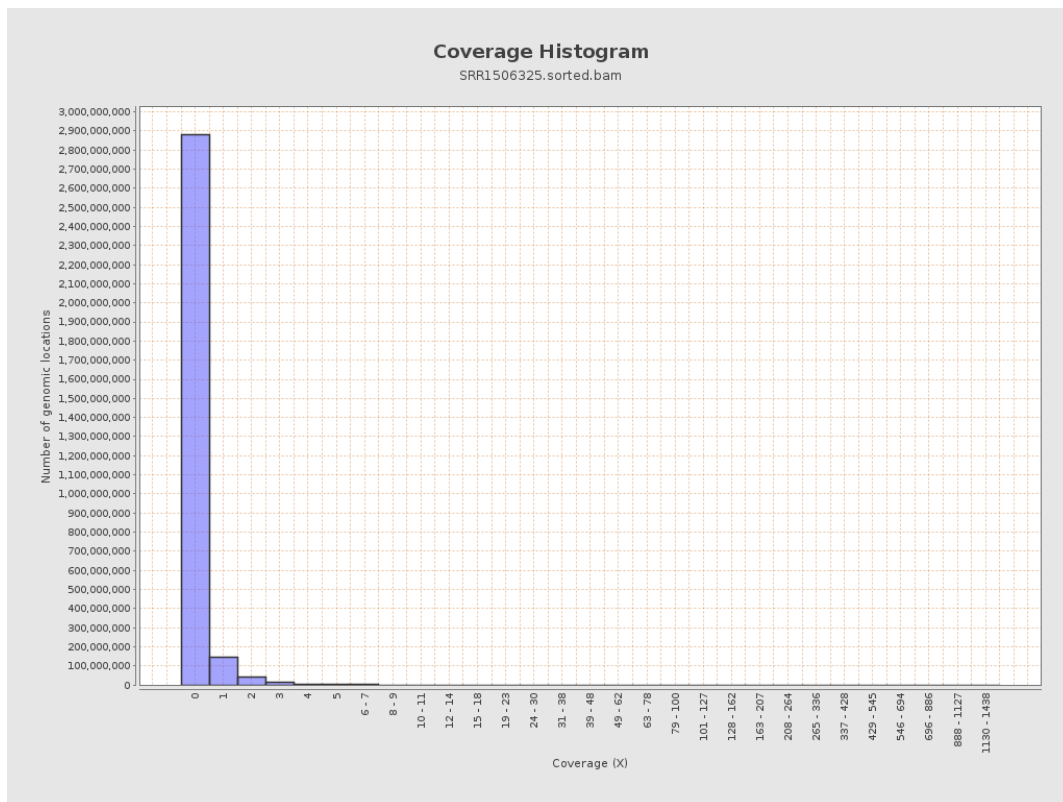
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26238443	0.1053	1.3103
chr2	243199373	27967599	0.115	0.9861
chr3	198022430	21737886	0.1098	0.5018
chr4	191154276	21252514	0.1112	0.8512
chr5	180915260	25455553	0.1407	0.586
chr6	171115067	12582576	0.0735	0.437
chr7	159138663	17954934	0.1128	0.8693

chr8	146364022	21462381	0.1466	0.9312
chr9	141213431	9951130	0.0705	0.7944
chr10	135534747	20564480	0.1517	1.1951
chr11	135006516	14840057	0.1099	0.7946
chr12	133851895	14949499	0.1117	0.5273
chr13	115169878	6796529	0.059	0.3696
chr14	107349540	10104856	0.0941	0.5385
chr15	102531392	12937558	0.1262	0.5569
chr16	90354753	13636438	0.1509	0.7651
chr17	81195210	9685970	0.1193	0.6547
chr18	78077248	6066336	0.0777	1.1722
chr19	59128983	9558164	0.1616	1.0585
chr20	63025520	10076394	0.1599	0.696
chr21	48129895	5624088	0.1169	0.7387
chr22	51304566	4530821	0.0883	0.4767
chrMT	16571	21247	1.2822	1.9552
chrX	155270560	23875110	0.1538	0.6932
chrY	59373566	1464296	0.0247	0.9452

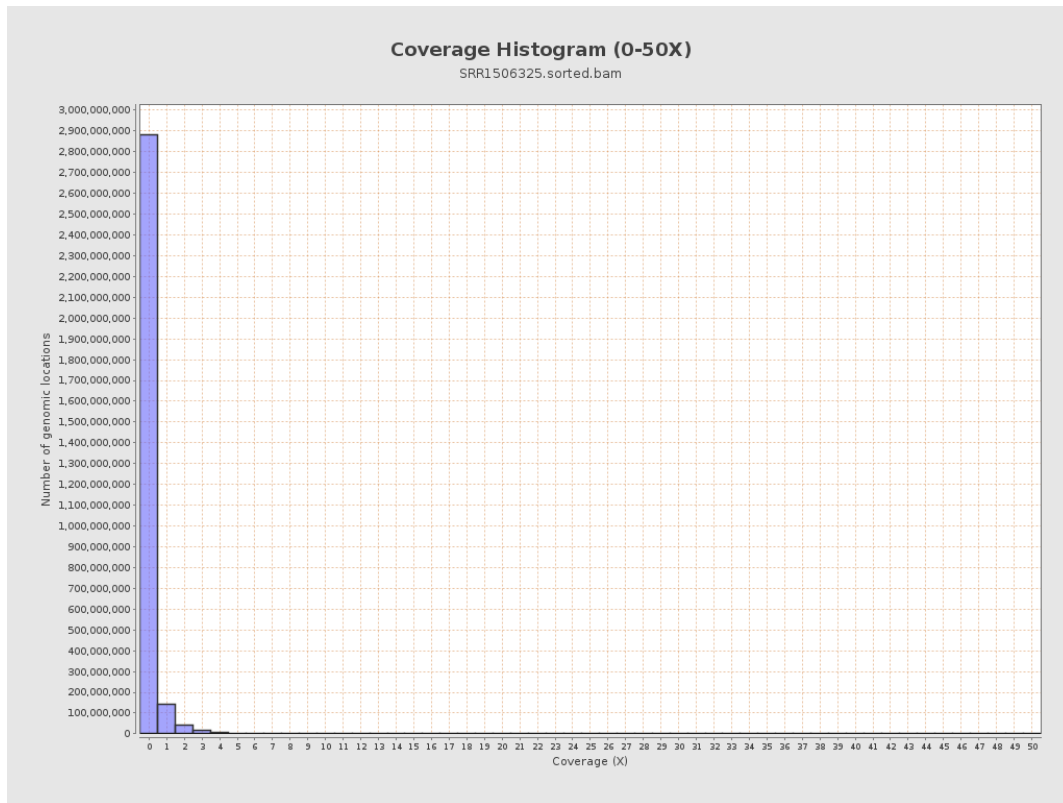
3. Results : Coverage across reference



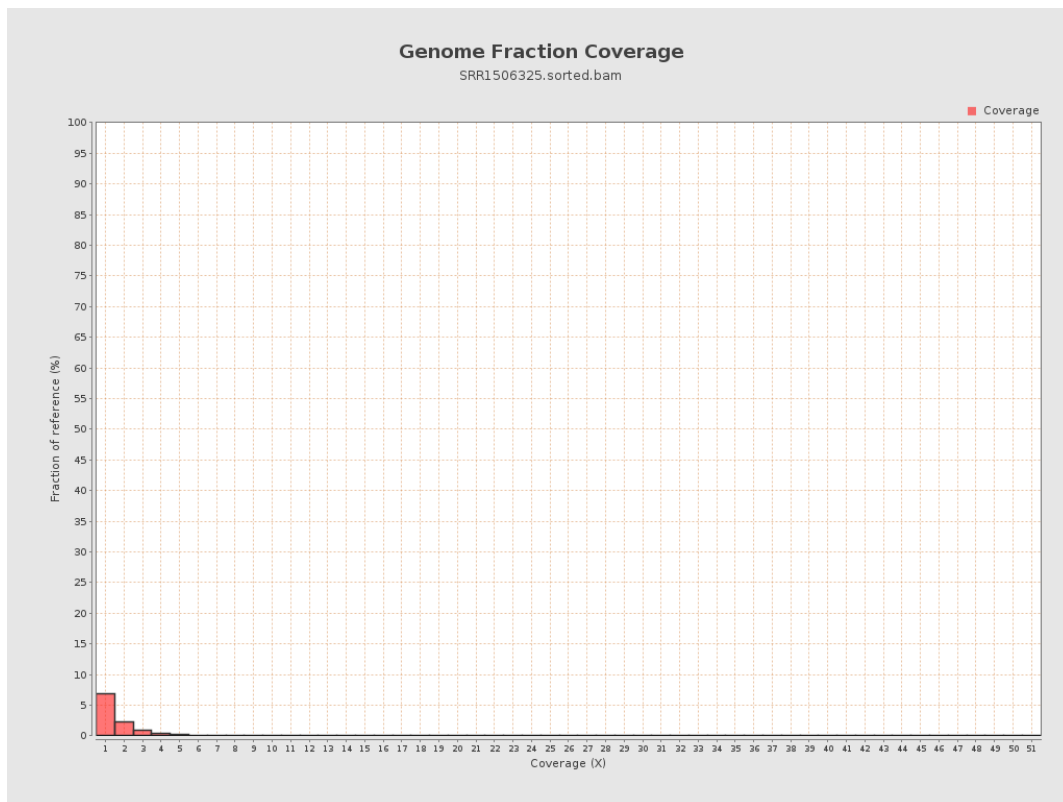
4. Results : Coverage Histogram



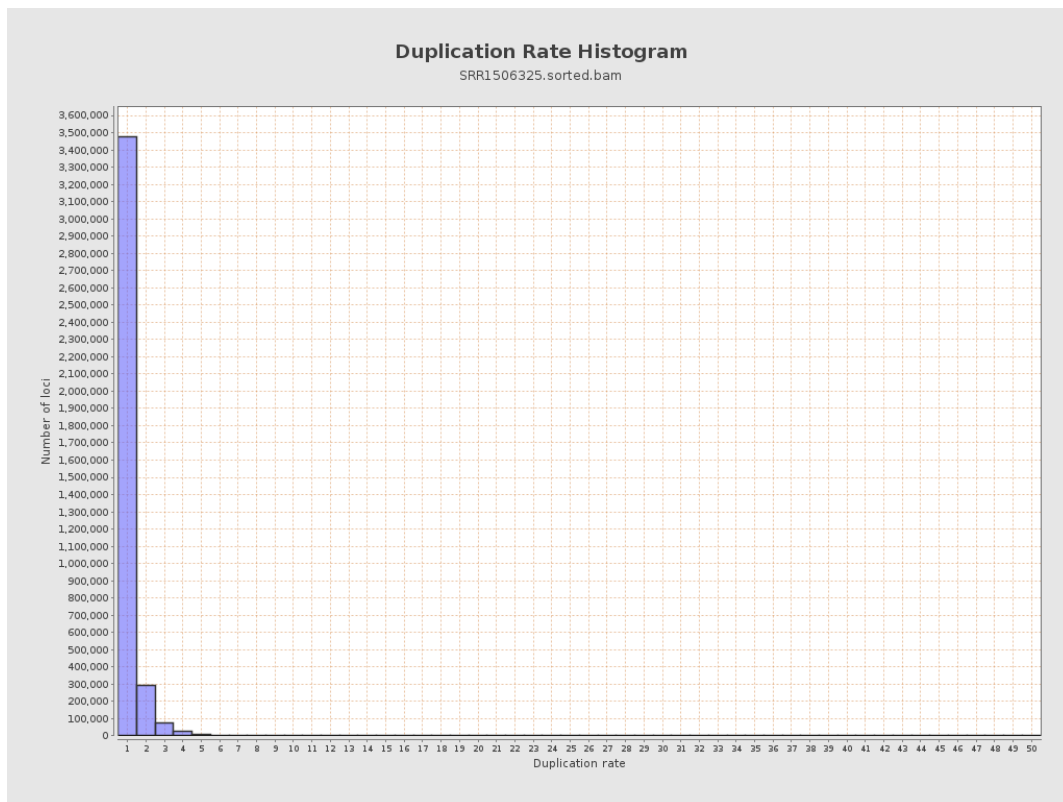
5. Results : Coverage Histogram (0-50X)



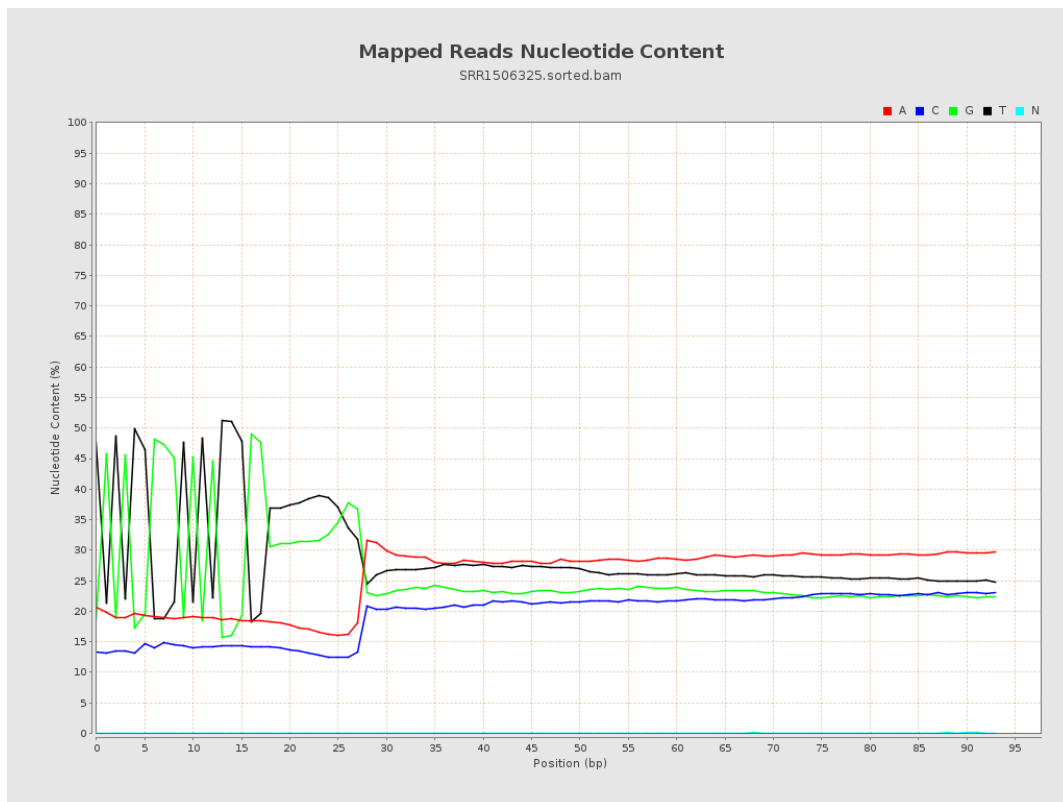
6. Results : Genome Fraction Coverage



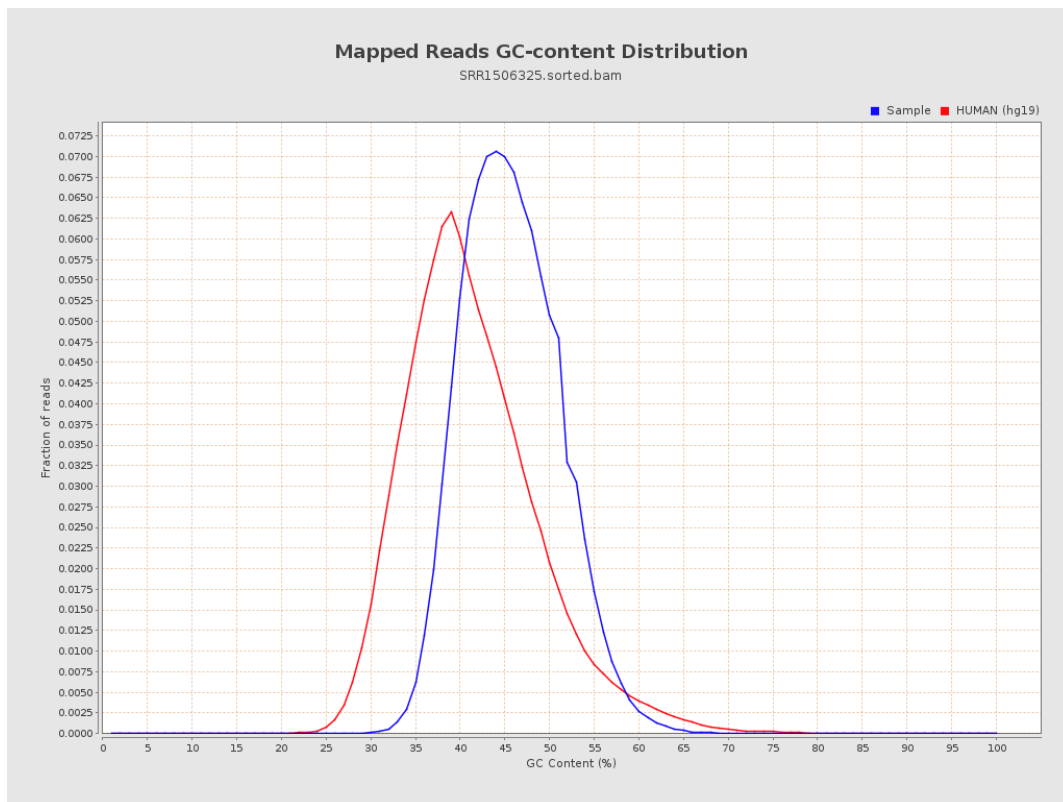
7. Results : Duplication Rate Histogram



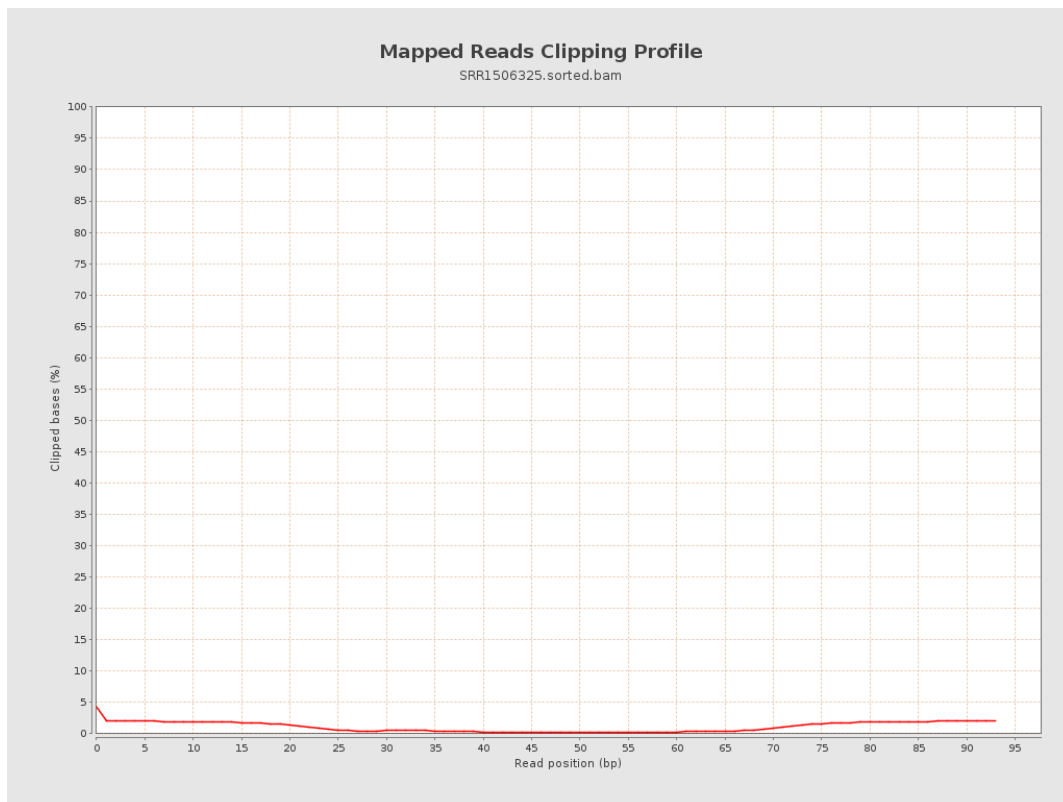
8. Results : Mapped Reads Nucleotide Content



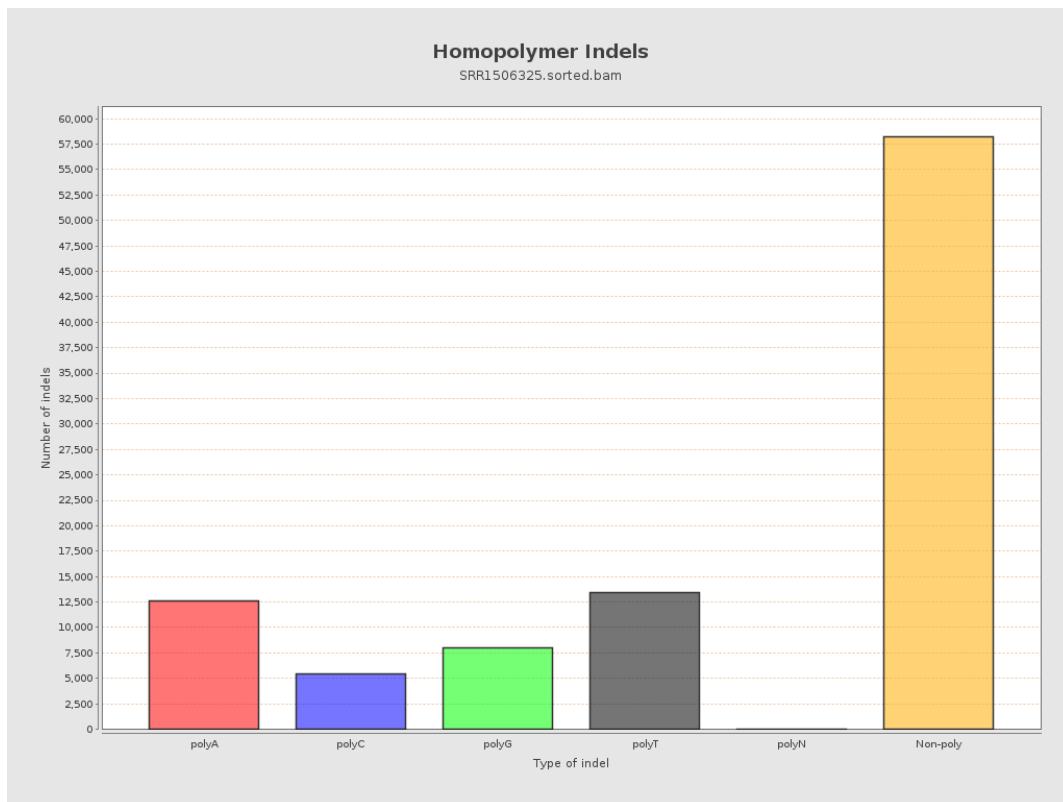
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

