

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:25:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506322.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_SRR1506322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506322.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506322.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,376,677
Mapped reads	3,104,668 / 70.94%
Unmapped reads	1,272,009 / 29.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	42,703 / 0.98%
Read min/max/mean length	30 / 94 / 94.35
Duplicated reads (estimated)	372,965 / 8.52%
Duplication rate	9.16%
Clipped reads	1,865,856 / 42.63%

2.2. ACGT Content

Number/percentage of A's	65,836,403 / 26.76%
Number/percentage of C's	47,589,970 / 19.34%
Number/percentage of T's	70,785,567 / 28.77%
Number/percentage of G's	61,793,794 / 25.11%
Number/percentage of N's	57,932 / 0.02%
GC Percentage	44.45%

2.3. Coverage

Mean	0.0795

Standard Deviation	0.58
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2.4. Mapping Quality

Mean Mapping Quality	47.66
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2.5. Mismatches and indels

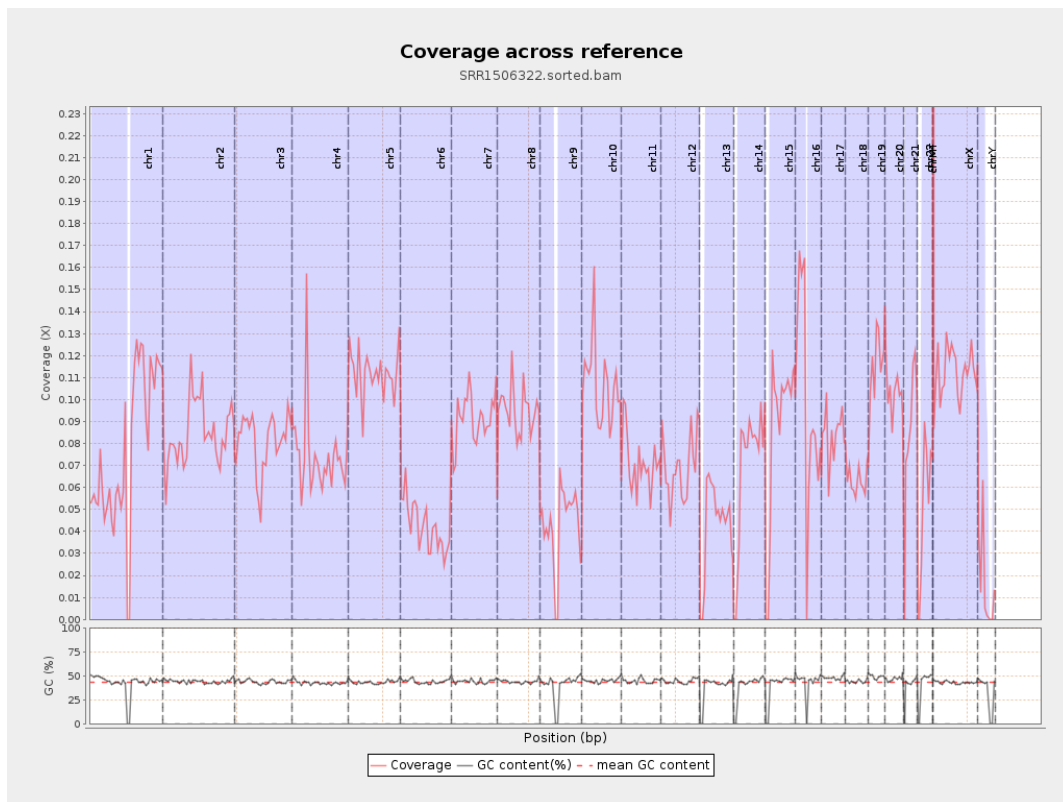
General error rate	0.7%
Mismatches	1,671,390
Insertions	19,782
Mapped reads with at least one insertion	0.62%
Deletions	49,228
Mapped reads with at least one deletion	1.55%
Homopolymer indels	42.26%

2.6. Chromosome stats

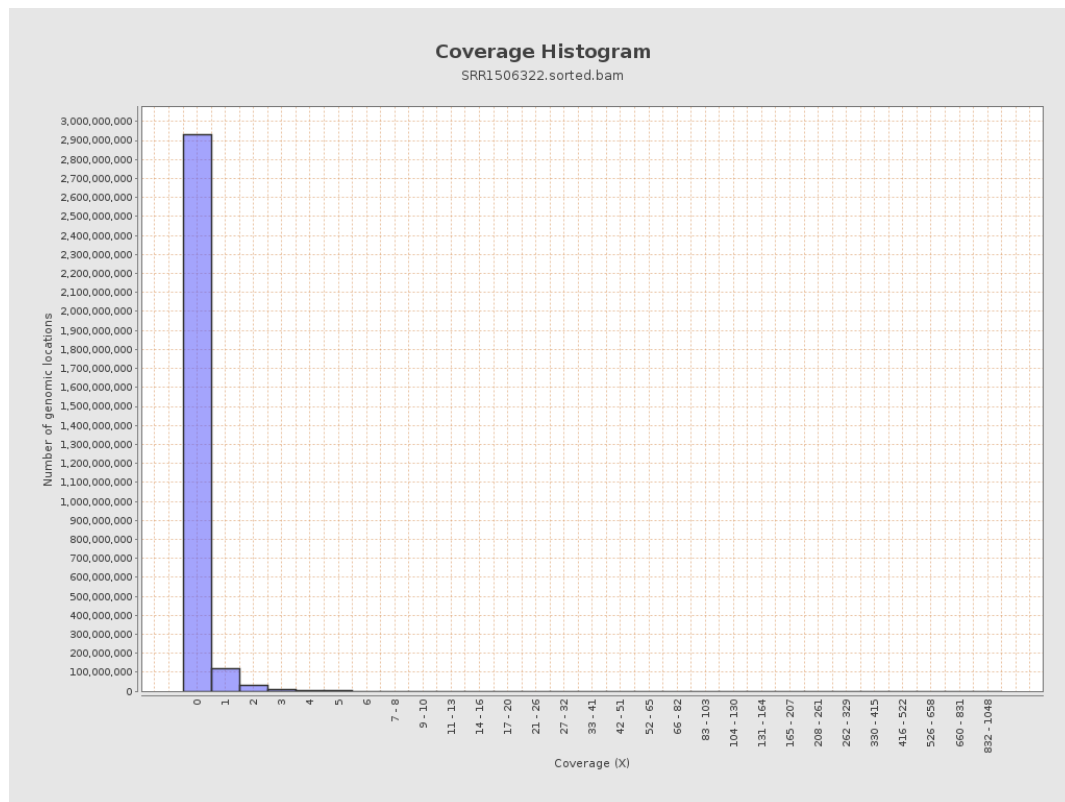
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19298932	0.0774	0.9709
chr2	243199373	20658444	0.0849	0.6443
chr3	198022430	16068972	0.0811	0.3949
chr4	191154276	14246560	0.0745	0.5361
chr5	180915260	20292794	0.1122	0.4746
chr6	171115067	7260622	0.0424	0.3006
chr7	159138663	14622030	0.0919	0.7812

chr8	146364022	13866965	0.0947	0.6133
chr9	141213431	6105827	0.0432	0.4779
chr10	135534747	14317452	0.1056	0.7099
chr11	135006516	9591744	0.071	0.4801
chr12	133851895	9321049	0.0696	0.3793
chr13	115169878	4955463	0.043	0.2824
chr14	107349540	7479704	0.0697	0.3835
chr15	102531392	8789439	0.0857	0.4184
chr16	90354753	8880578	0.0983	0.5129
chr17	81195210	6872841	0.0846	0.4877
chr18	78077248	4927301	0.0631	0.7178
chr19	59128983	6892008	0.1166	0.7693
chr20	63025520	6468968	0.1026	0.4889
chr21	48129895	4161711	0.0865	0.5153
chr22	51304566	2628235	0.0512	0.3419
chrMT	16571	44339	2.6757	2.6415
chrX	155270560	17468010	0.1125	0.5143
chrY	59373566	945950	0.0159	0.6133

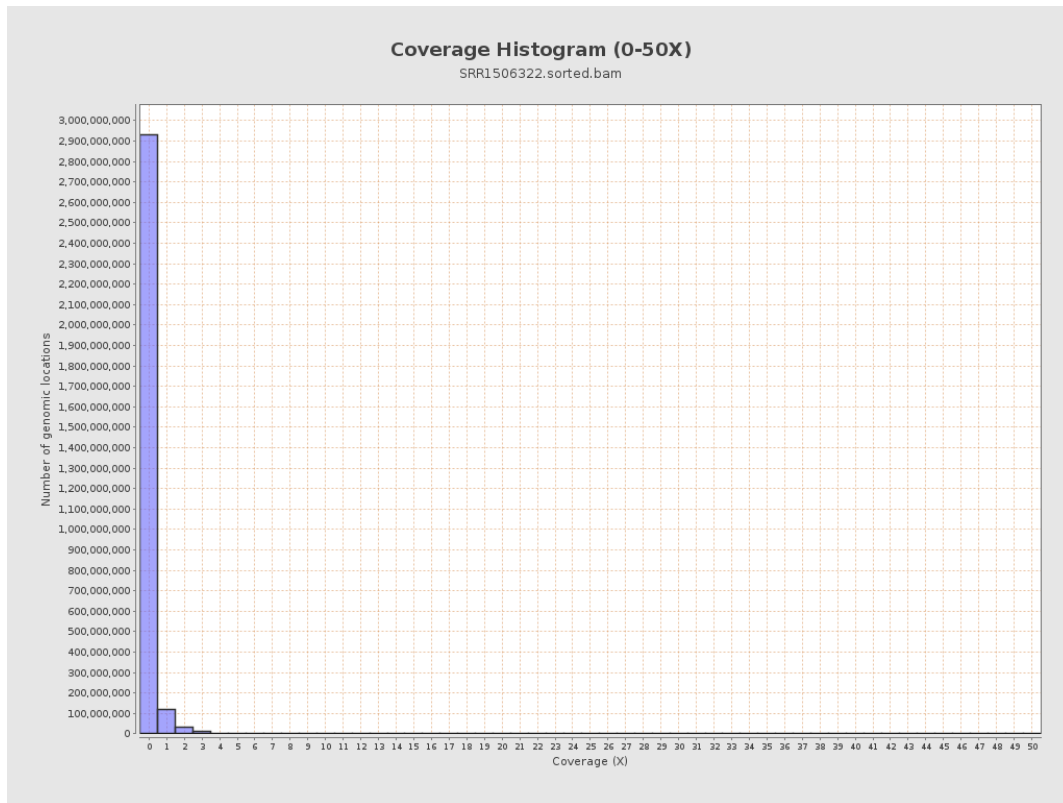
3. Results : Coverage across reference



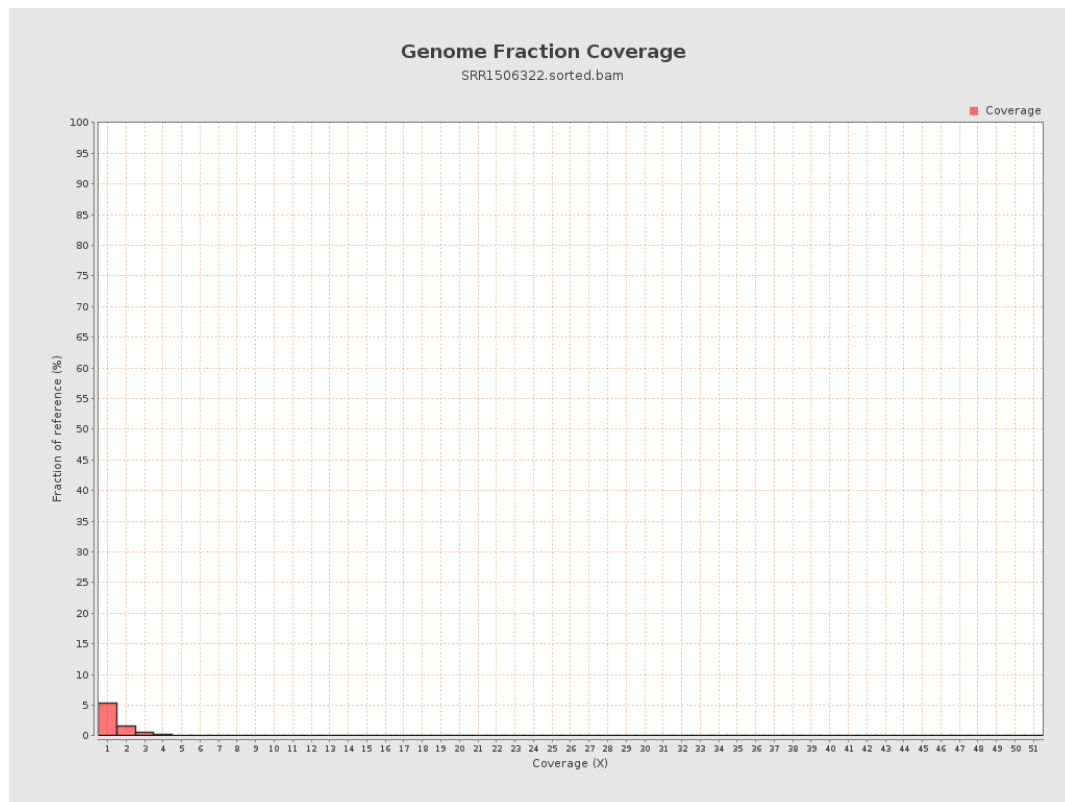
4. Results : Coverage Histogram



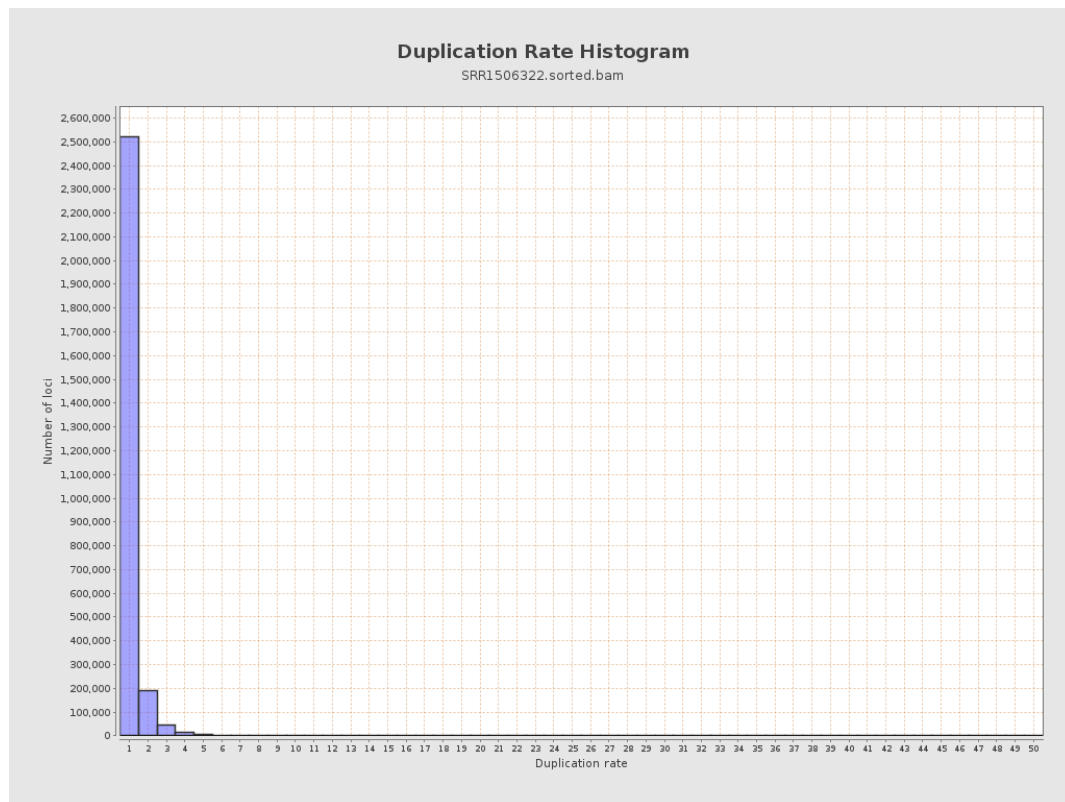
5. Results : Coverage Histogram (0-50X)



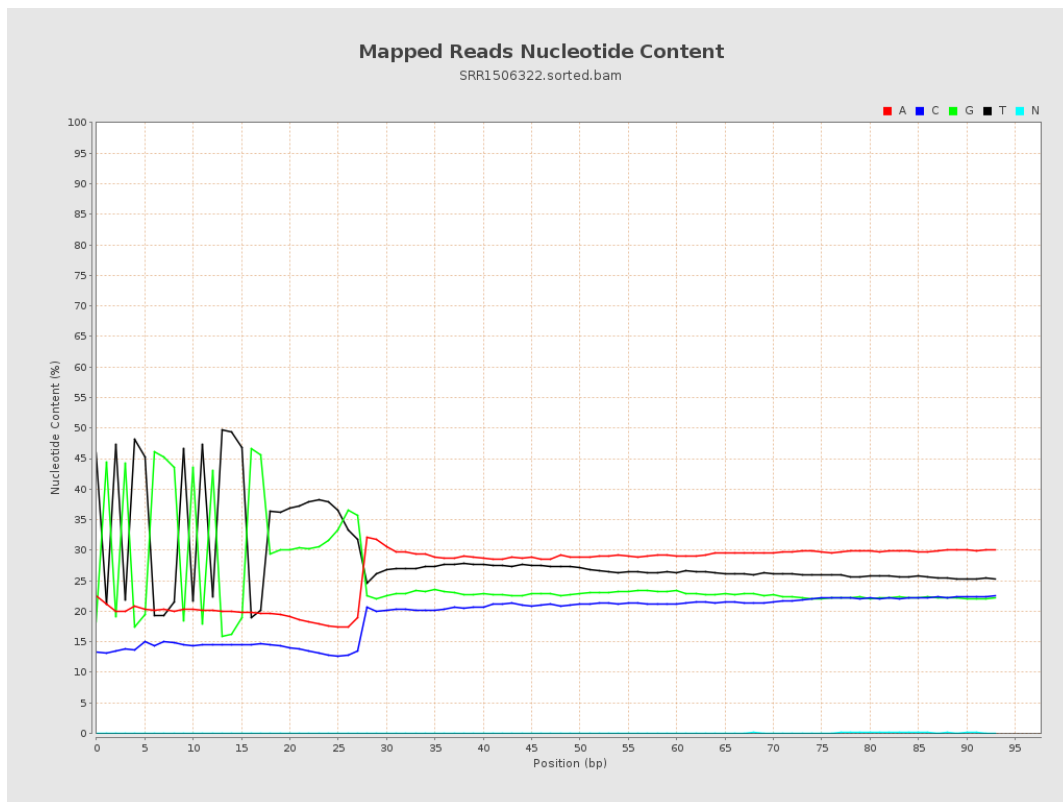
6. Results : Genome Fraction Coverage



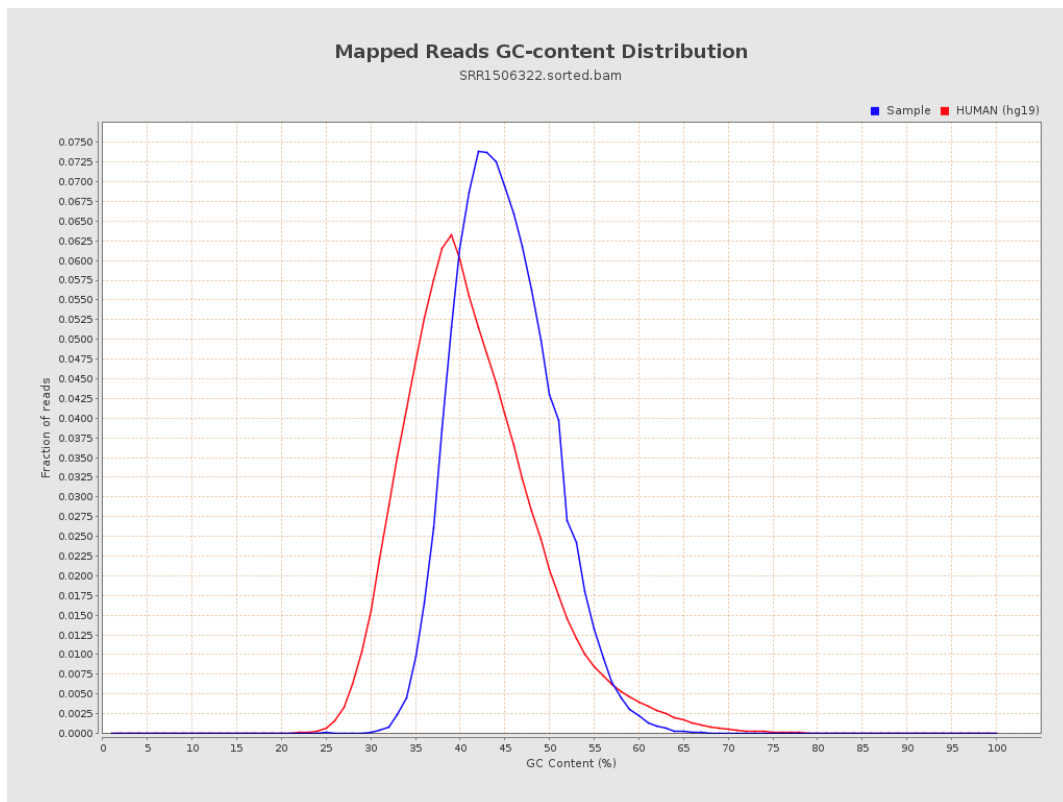
7. Results : Duplication Rate Histogram



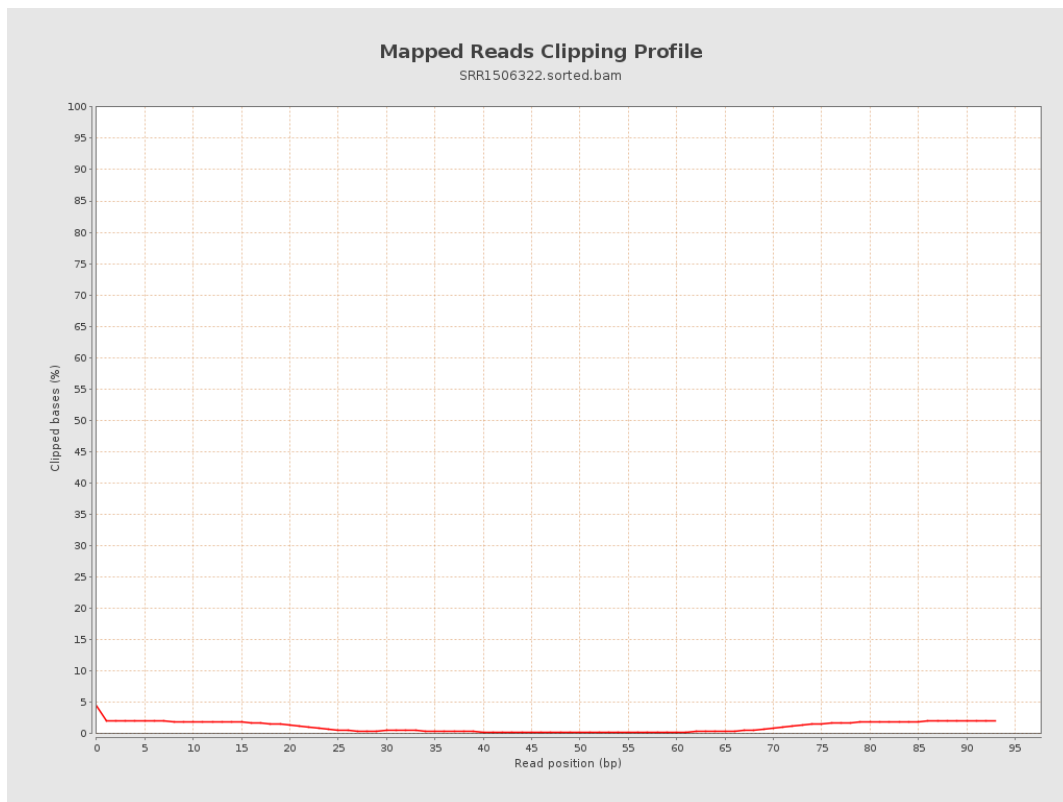
8. Results : Mapped Reads Nucleotide Content



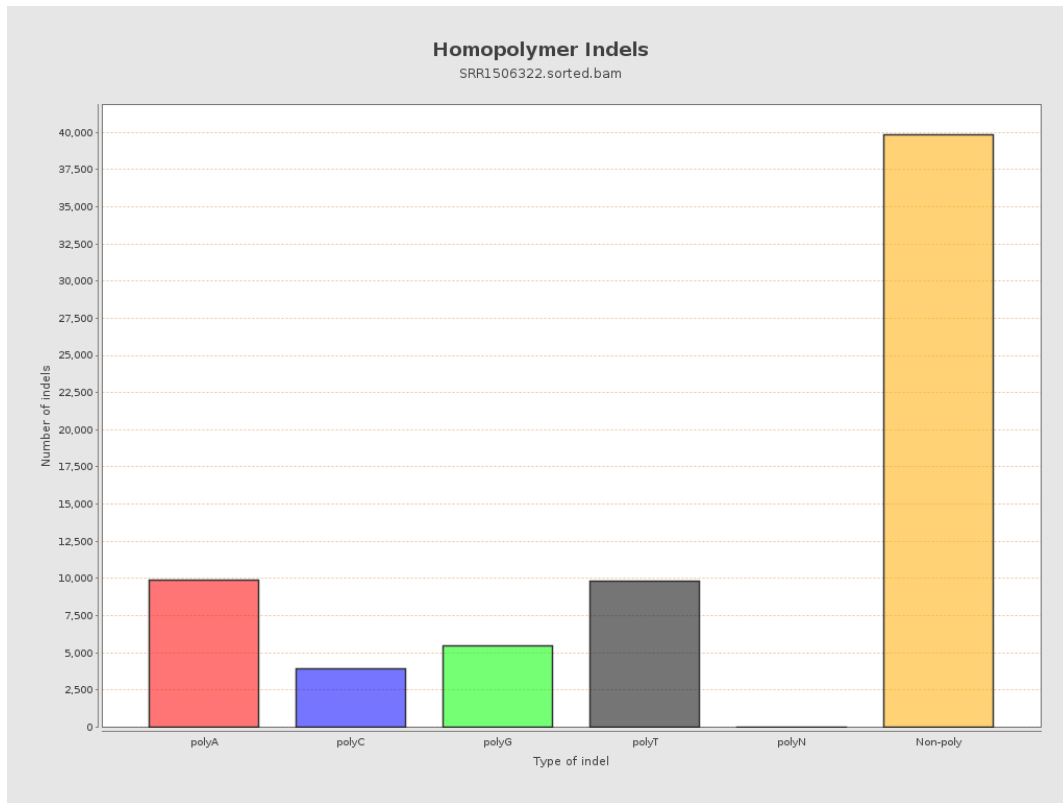
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

