

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:59:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004073.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_SRR6004073 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004073.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:59:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004073.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,062,068
Mapped reads	1,835,510 / 89.01%
Unmapped reads	226,558 / 10.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,897 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	254,013 / 12.32%
Duplication rate	9.74%
Clipped reads	821,691 / 39.85%

2.2. ACGT Content

Number/percentage of A's	34,816,507 / 28.35%
Number/percentage of C's	22,665,701 / 18.45%
Number/percentage of T's	39,076,064 / 31.81%
Number/percentage of G's	26,249,043 / 21.37%
Number/percentage of N's	21,634 / 0.02%
GC Percentage	39.82%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.5289
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2.4. Mapping Quality

Mean Mapping Quality	45.36
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2.5. Mismatches and indels

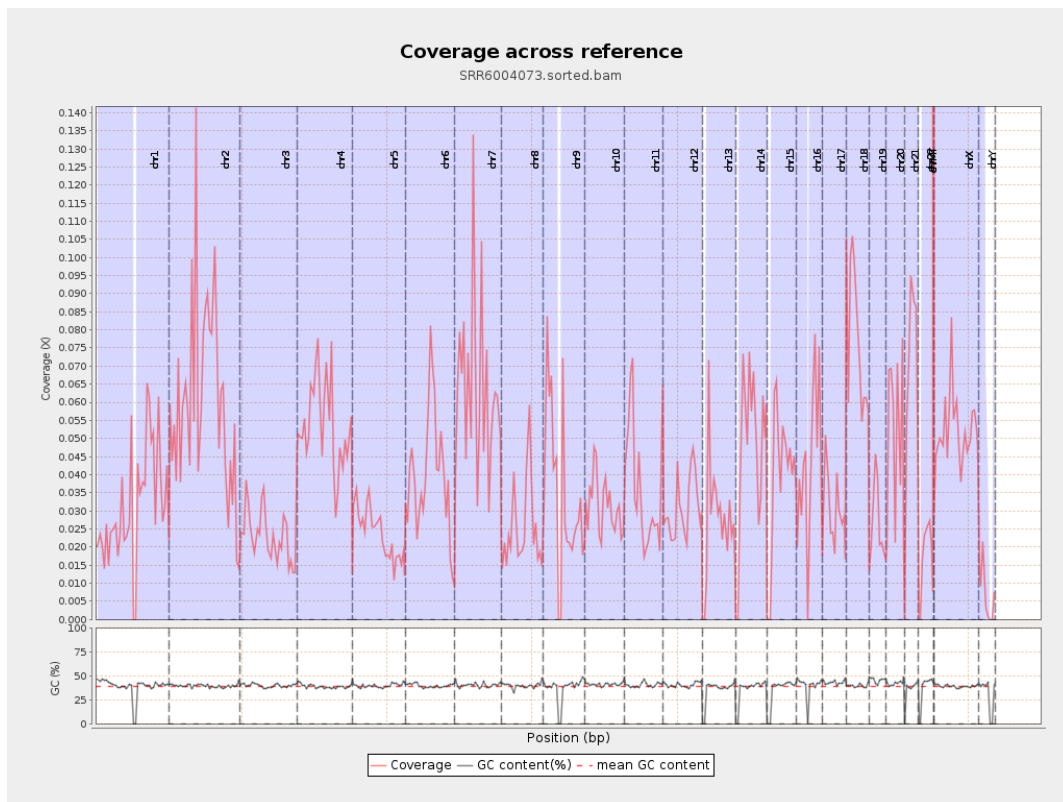
General error rate	0.91%
Mismatches	1,101,163
Insertions	9,257
Mapped reads with at least one insertion	0.5%
Deletions	25,838
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.7%

2.6. Chromosome stats

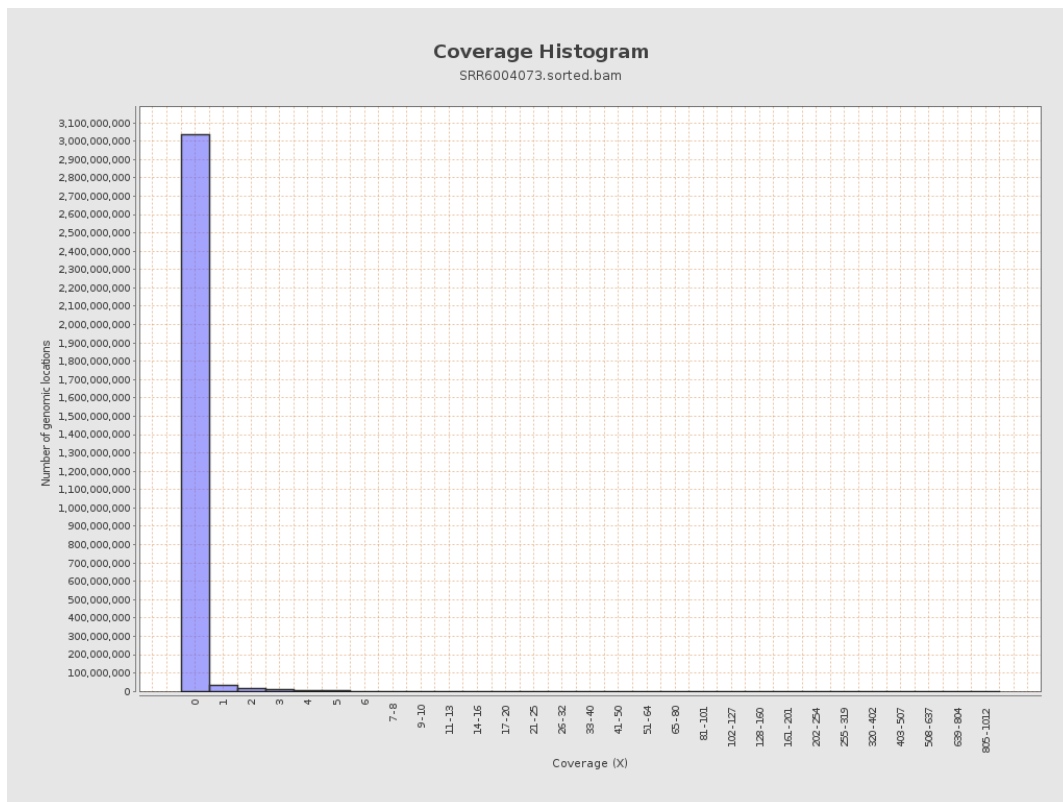
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7868706	0.0316	0.6648
chr2	243199373	14750624	0.0607	0.7245
chr3	198022430	4591968	0.0232	0.26
chr4	191154276	10272062	0.0537	0.4172
chr5	180915260	4295495	0.0237	0.2659
chr6	171115067	6788360	0.0397	0.3748
chr7	159138663	10199824	0.0641	1.0063

chr8	146364022	3660848	0.025	0.6938
chr9	141213431	4963066	0.0351	0.5229
chr10	135534747	4285832	0.0316	0.3392
chr11	135006516	4831769	0.0358	0.3947
chr12	133851895	4165161	0.0311	0.3121
chr13	115169878	3131011	0.0272	0.2938
chr14	107349540	4979636	0.0464	0.3954
chr15	102531392	4077071	0.0398	0.3455
chr16	90354753	3878795	0.0429	0.3838
chr17	81195210	2461242	0.0303	0.3391
chr18	78077248	6011125	0.077	1.0858
chr19	59128983	1613445	0.0273	0.5022
chr20	63025520	3323909	0.0527	0.4227
chr21	48129895	3245005	0.0674	0.4629
chr22	51304566	888268	0.0173	0.2168
chrMT	16571	137840	8.3181	6.4096
chrX	155270560	8062014	0.0519	0.424
chrY	59373566	390457	0.0066	0.1744

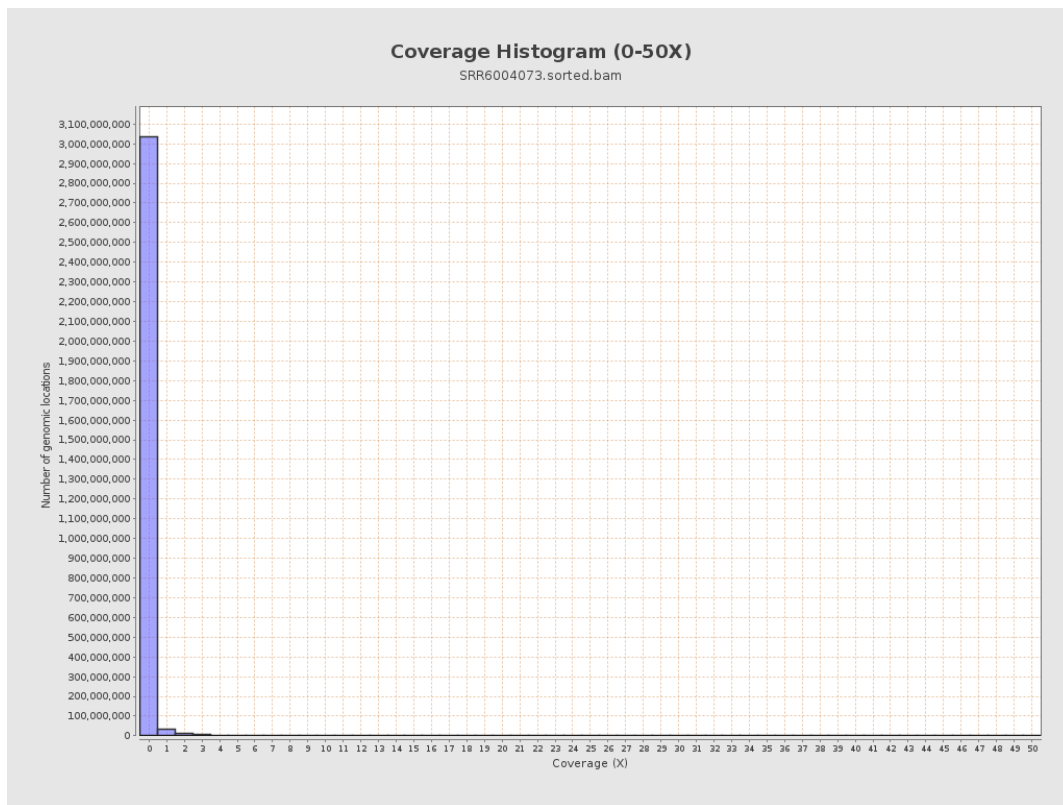
3. Results : Coverage across reference



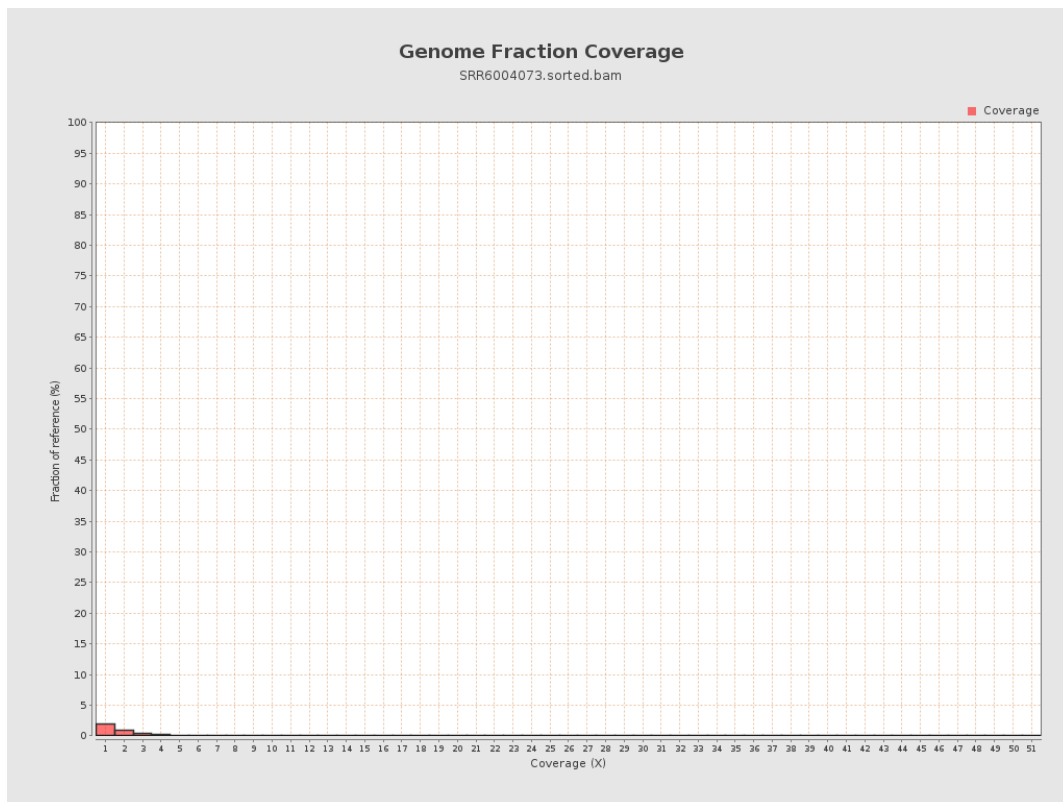
4. Results : Coverage Histogram



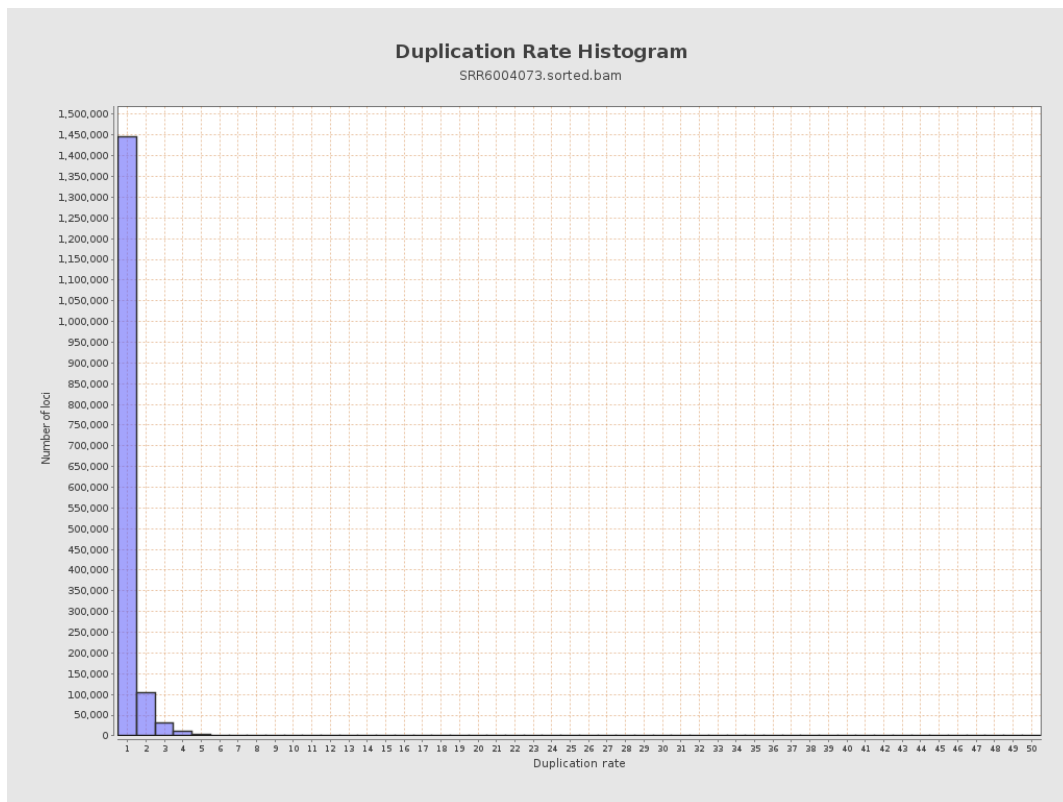
5. Results : Coverage Histogram (0-50X)



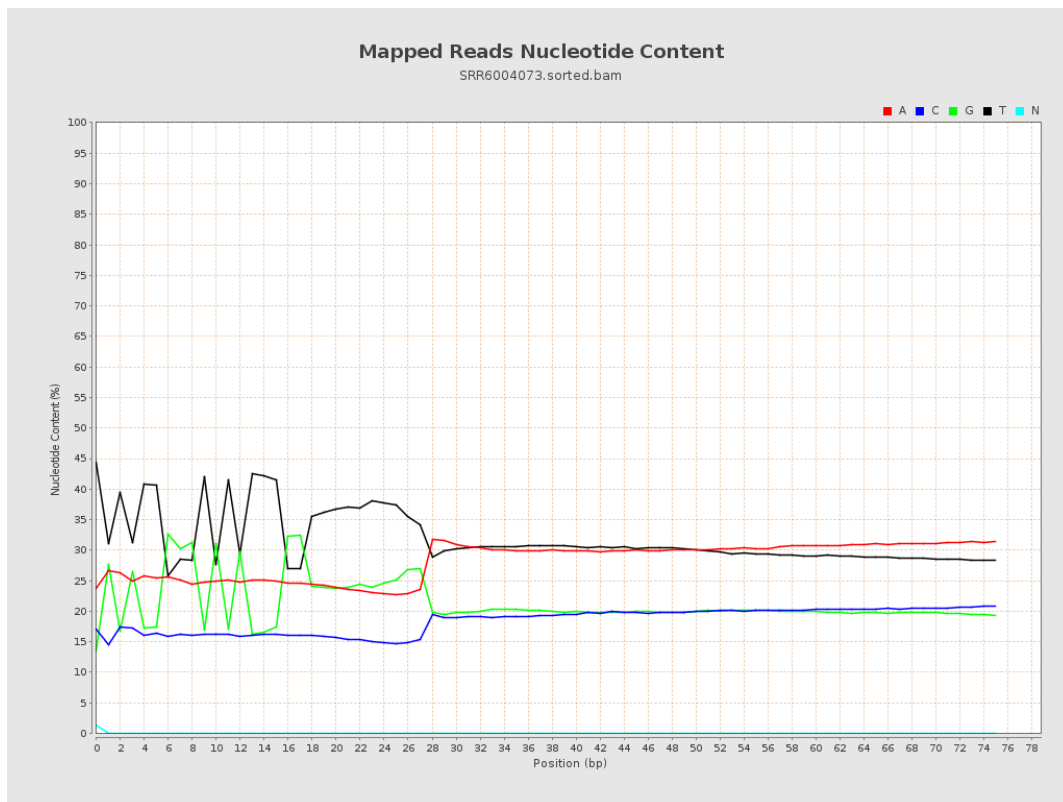
6. Results : Genome Fraction Coverage



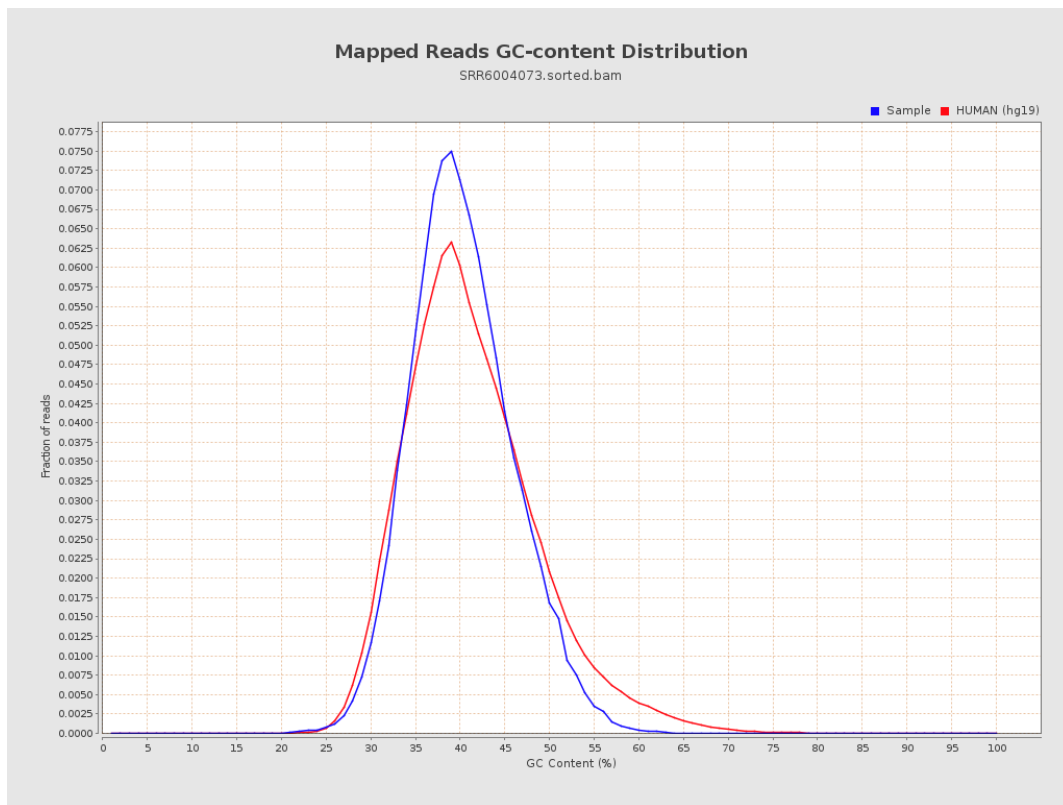
7. Results : Duplication Rate Histogram



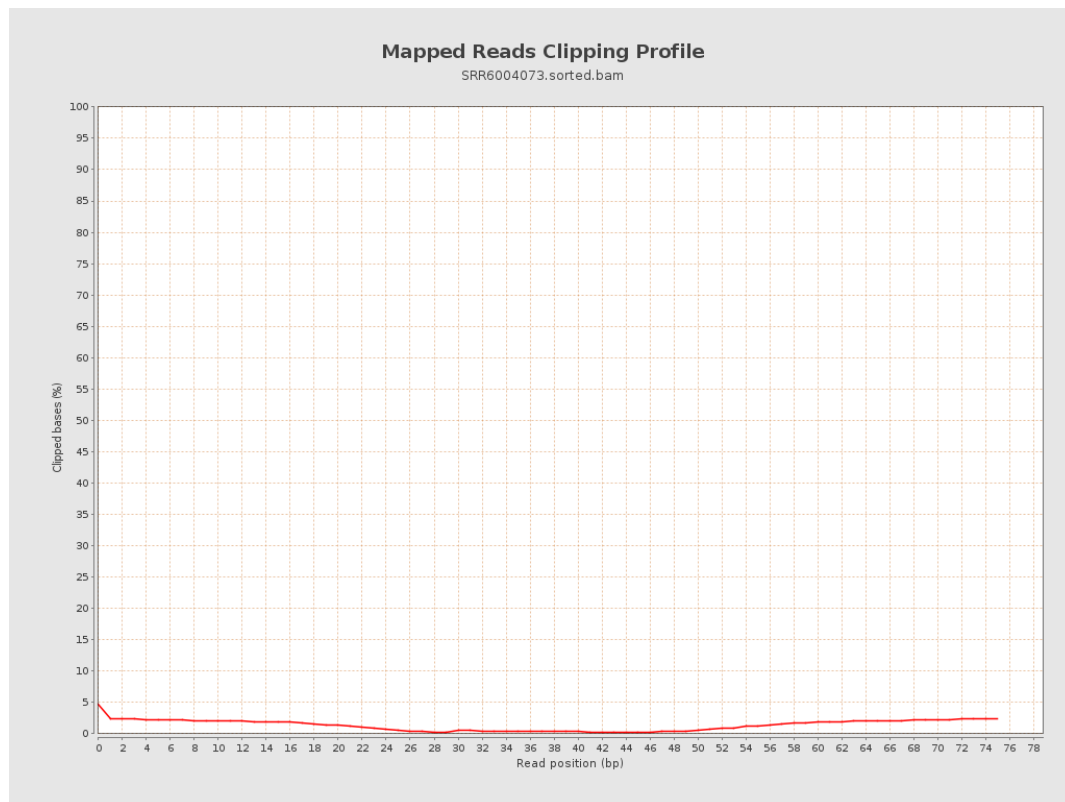
8. Results : Mapped Reads Nucleotide Content



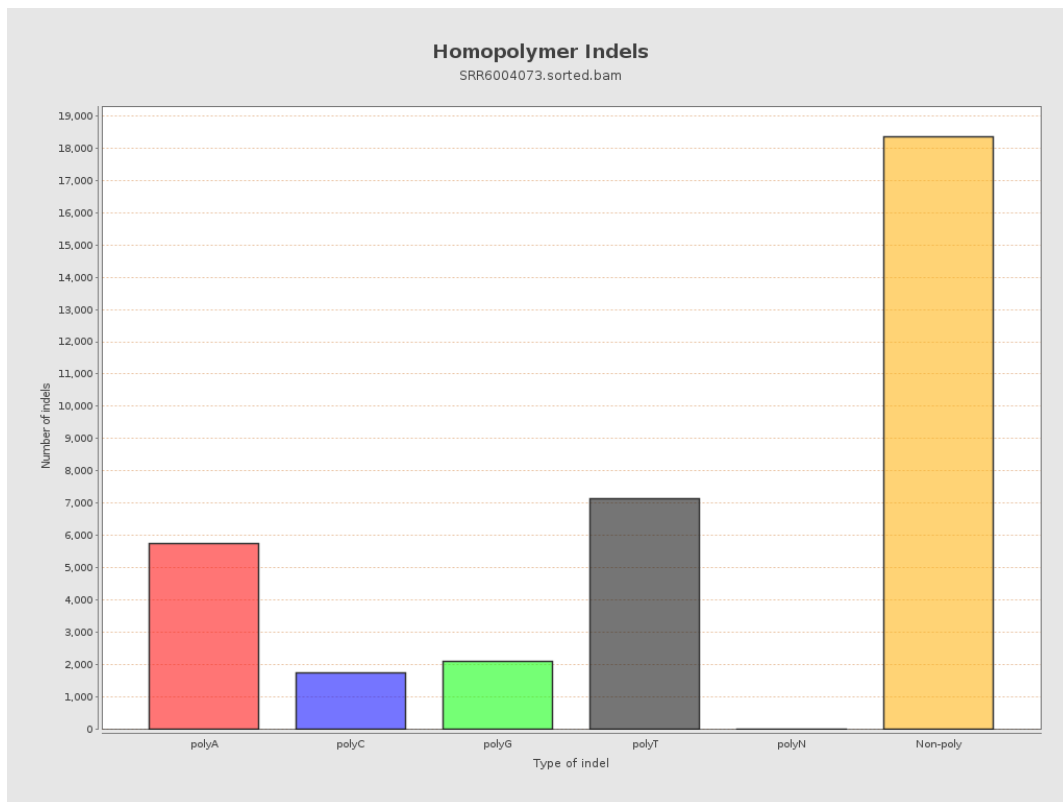
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

