

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:23:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004061.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_SRR6004061 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004061.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:23:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004061.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,936,427
Mapped reads	2,457,044 / 83.67%
Unmapped reads	479,383 / 16.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,239 / 0.62%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	145,302 / 4.95%
Duplication rate	4.72%
Clipped reads	1,261,685 / 42.97%

2.2. ACGT Content

Number/percentage of A's	43,401,164 / 27.17%
Number/percentage of C's	30,685,141 / 19.21%
Number/percentage of T's	48,901,199 / 30.61%
Number/percentage of G's	36,726,010 / 22.99%
Number/percentage of N's	32,312 / 0.02%
GC Percentage	42.2%

2.3. Coverage

Mean	0.0516

Standard Deviation	0.4498
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2.4. Mapping Quality

Mean Mapping Quality	42.17
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2.5. Mismatches and indels

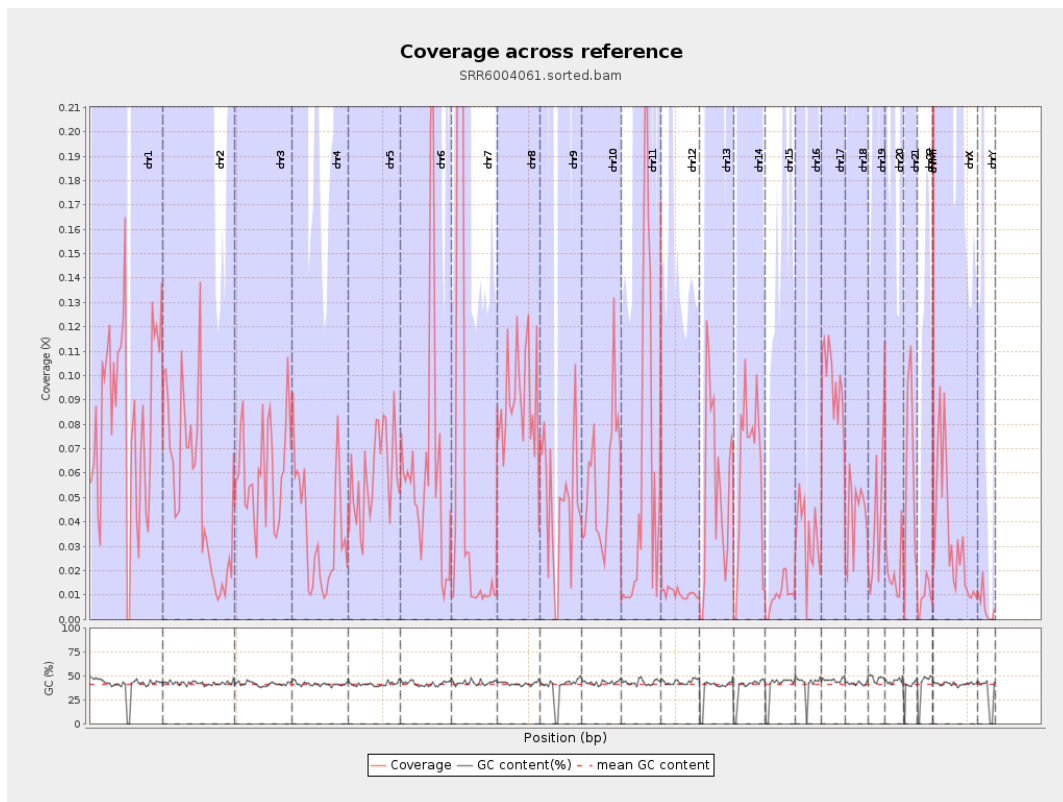
General error rate	0.83%
Mismatches	1,300,595
Insertions	11,690
Mapped reads with at least one insertion	0.47%
Deletions	40,441
Mapped reads with at least one deletion	1.63%
Homopolymer indels	46.33%

2.6. Chromosome stats

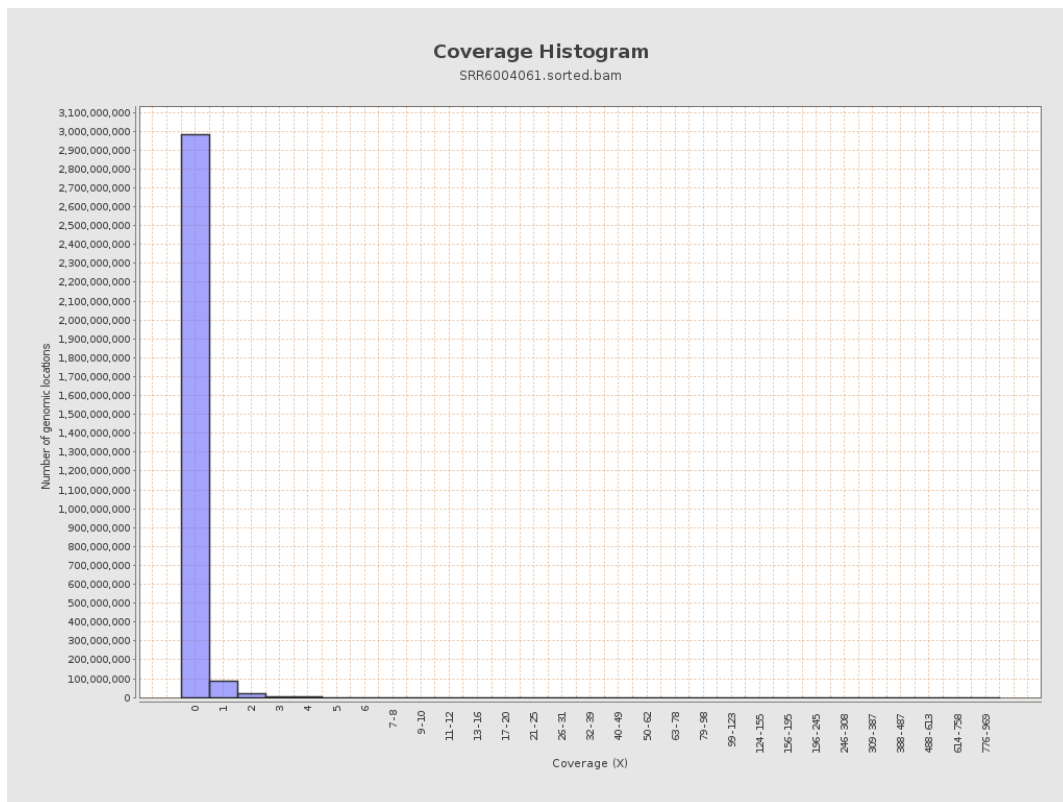
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	20534141	0.0824	0.9131
chr2	243199373	12541765	0.0516	0.513
chr3	198022430	12068611	0.0609	0.3177
chr4	191154276	6779191	0.0355	0.2637
chr5	180915260	10627832	0.0587	0.3139
chr6	171115067	10927728	0.0639	0.3974
chr7	159138663	8544758	0.0537	0.3486

chr8	146364022	13032234	0.089	0.5053
chr9	141213431	6799203	0.0481	0.4149
chr10	135534747	7732487	0.0571	0.4547
chr11	135006516	7751623	0.0574	0.3606
chr12	133851895	1426635	0.0107	0.154
chr13	115169878	6348724	0.0551	0.3089
chr14	107349540	6665354	0.0621	0.3743
chr15	102531392	1003206	0.0098	0.1476
chr16	90354753	3009730	0.0333	0.2899
chr17	81195210	7994370	0.0985	0.4671
chr18	78077248	3390999	0.0434	0.7509
chr19	59128983	2449610	0.0414	0.6469
chr20	63025520	1299578	0.0206	0.2133
chr21	48129895	2771300	0.0576	0.342
chr22	51304566	501584	0.0098	0.1206
chrMT	16571	46208	2.7885	2.546
chrX	155270560	5234469	0.0337	0.2793
chrY	59373566	331848	0.0056	0.1463

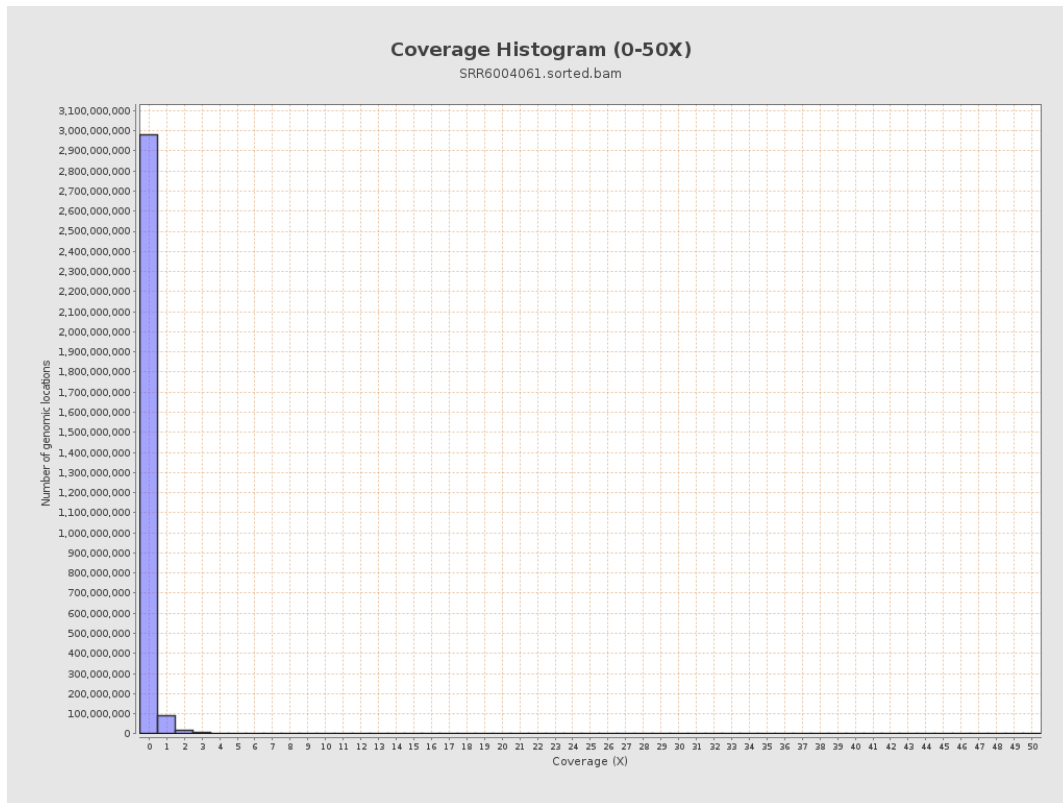
3. Results : Coverage across reference



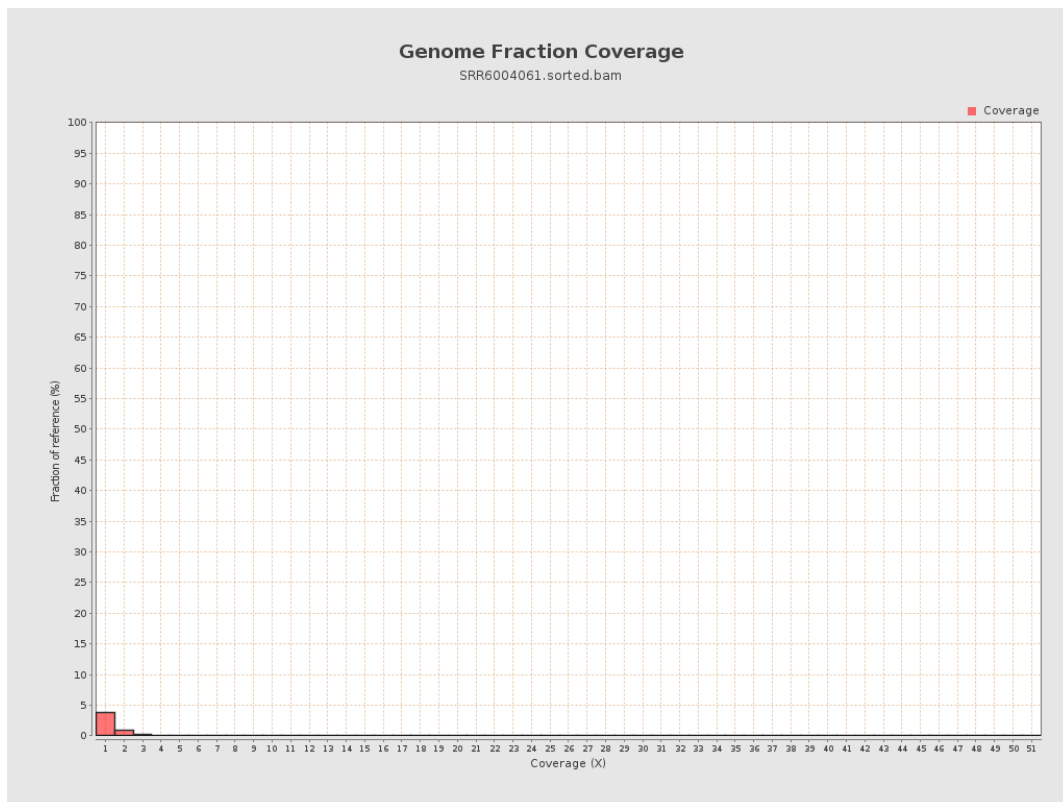
4. Results : Coverage Histogram



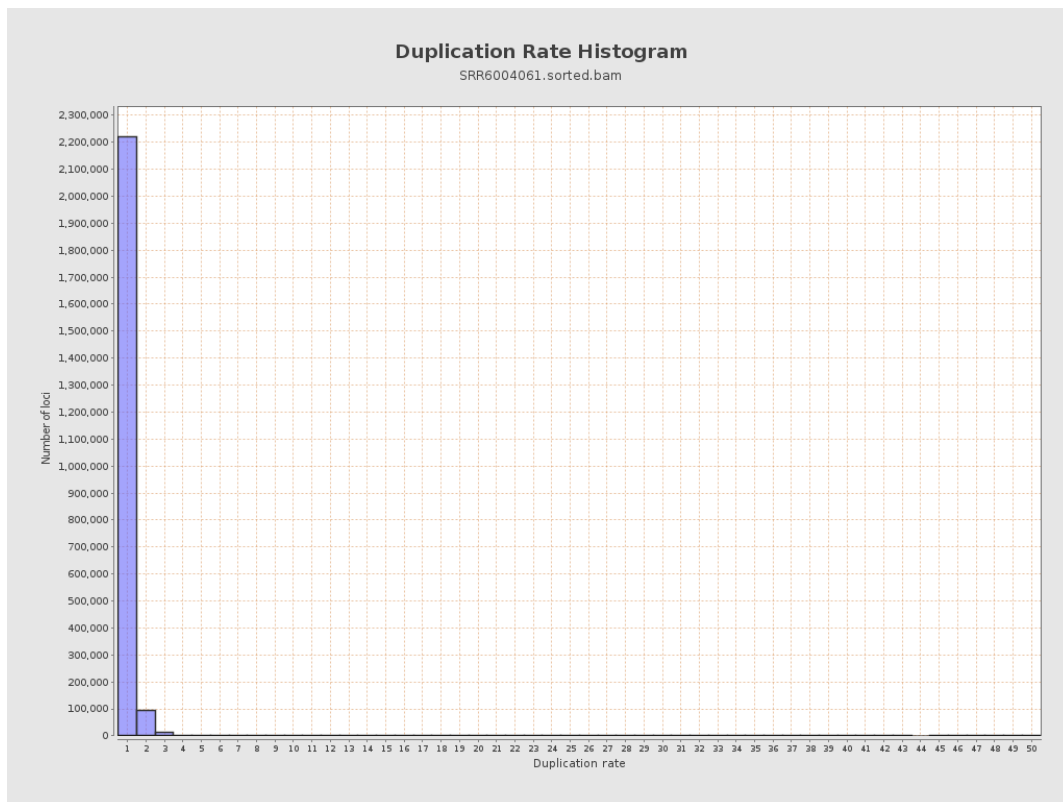
5. Results : Coverage Histogram (0-50X)



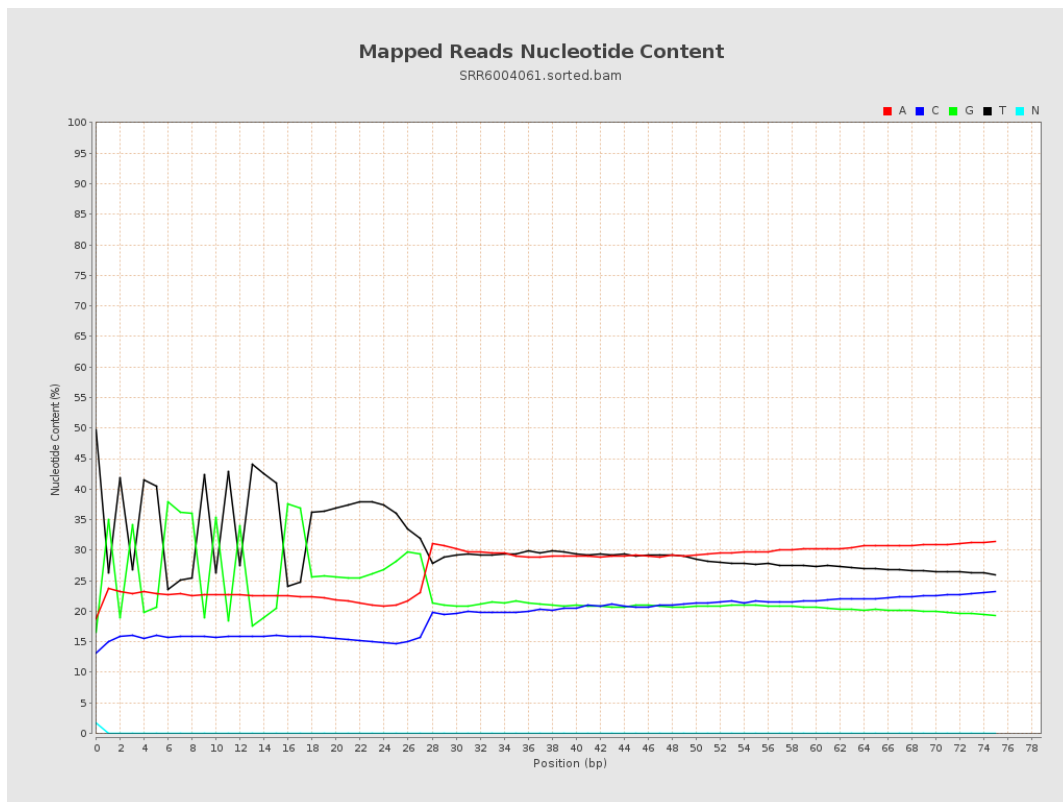
6. Results : Genome Fraction Coverage



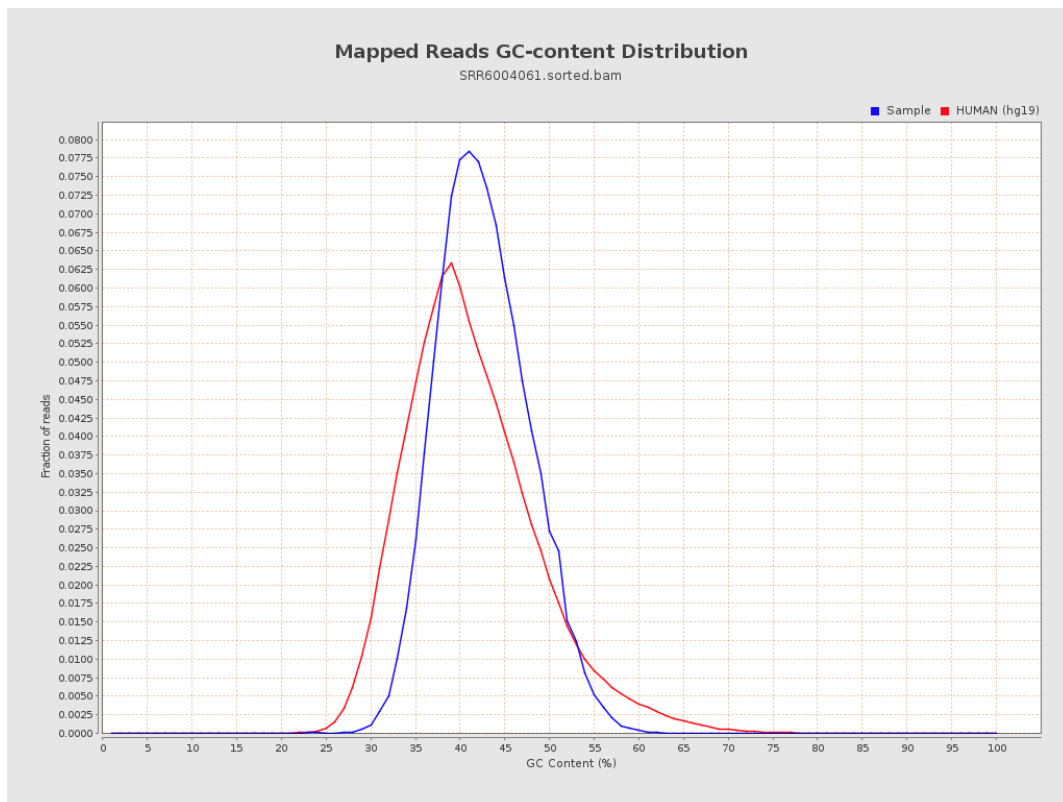
7. Results : Duplication Rate Histogram



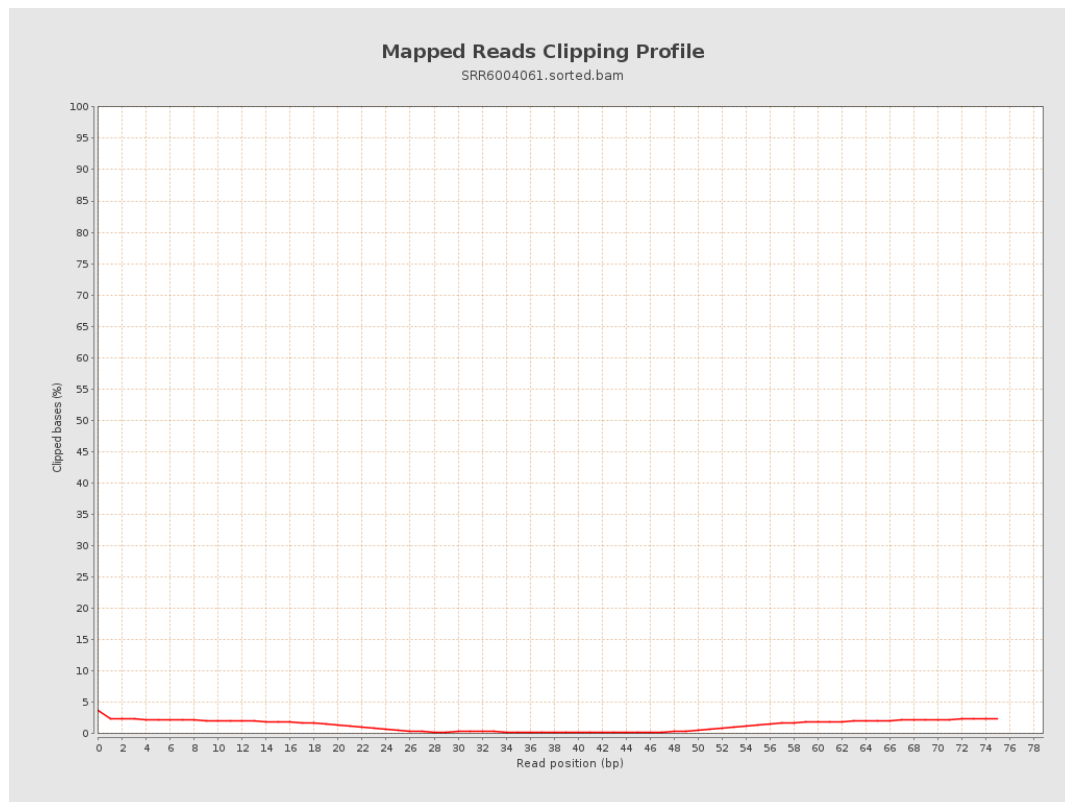
8. Results : Mapped Reads Nucleotide Content



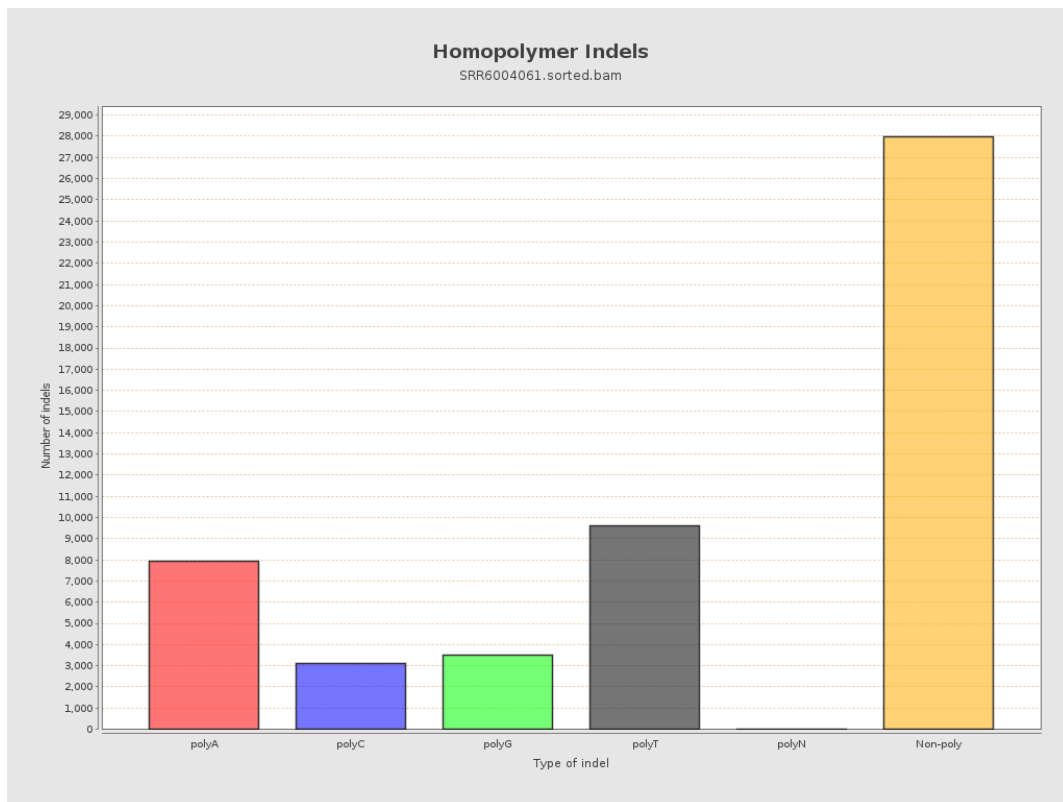
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

