

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:40:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234039.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_SRR6234039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:40:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,471,942
Mapped reads	4,132,937 / 92.42%
Unmapped reads	339,005 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,390 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	1,067,549 / 23.87%
Duplication rate	18.46%
Clipped reads	2,326,291 / 52.02%

2.2. ACGT Content

Number/percentage of A's	63,204,073 / 24.15%
Number/percentage of C's	49,816,844 / 19.03%
Number/percentage of T's	83,650,520 / 31.96%
Number/percentage of G's	65,050,066 / 24.85%
Number/percentage of N's	24,721 / 0.01%
GC Percentage	43.88%

2.3. Coverage

Mean	0.0846

Standard Deviation	1.1134
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2.4. Mapping Quality

Mean Mapping Quality	32.59
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2.5. Mismatches and indels

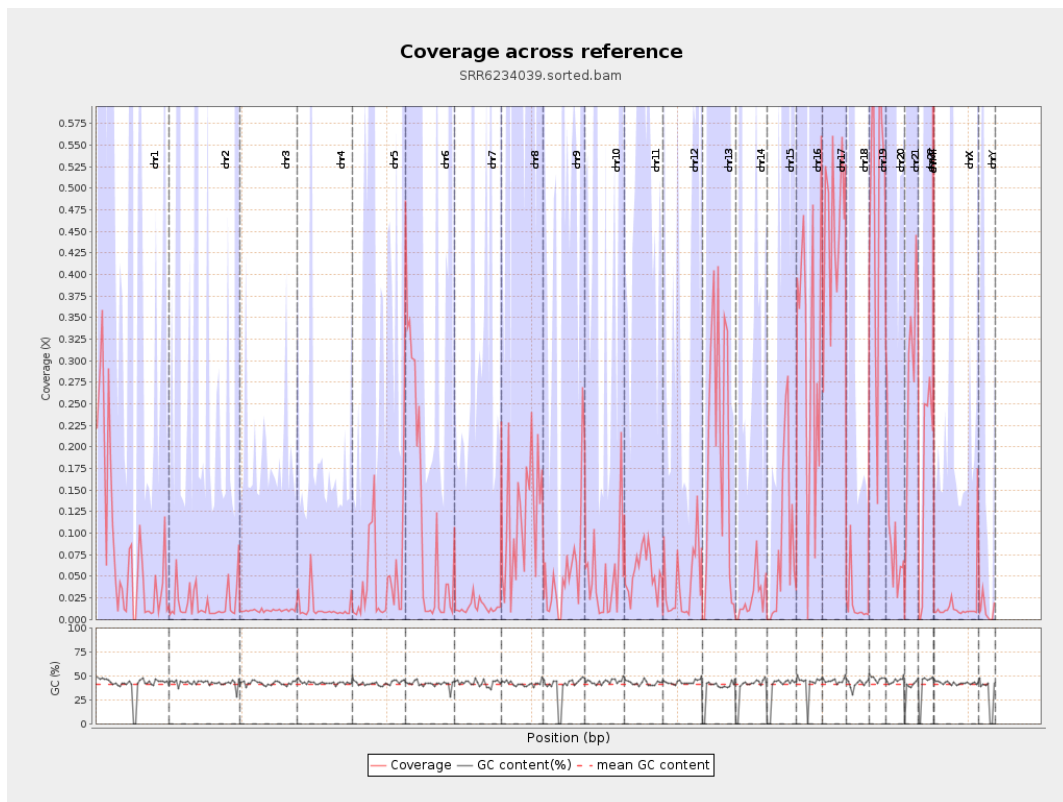
General error rate	0.58%
Mismatches	1,495,653
Insertions	17,280
Mapped reads with at least one insertion	0.41%
Deletions	64,634
Mapped reads with at least one deletion	1.55%
Homopolymer indels	42.93%

2.6. Chromosome stats

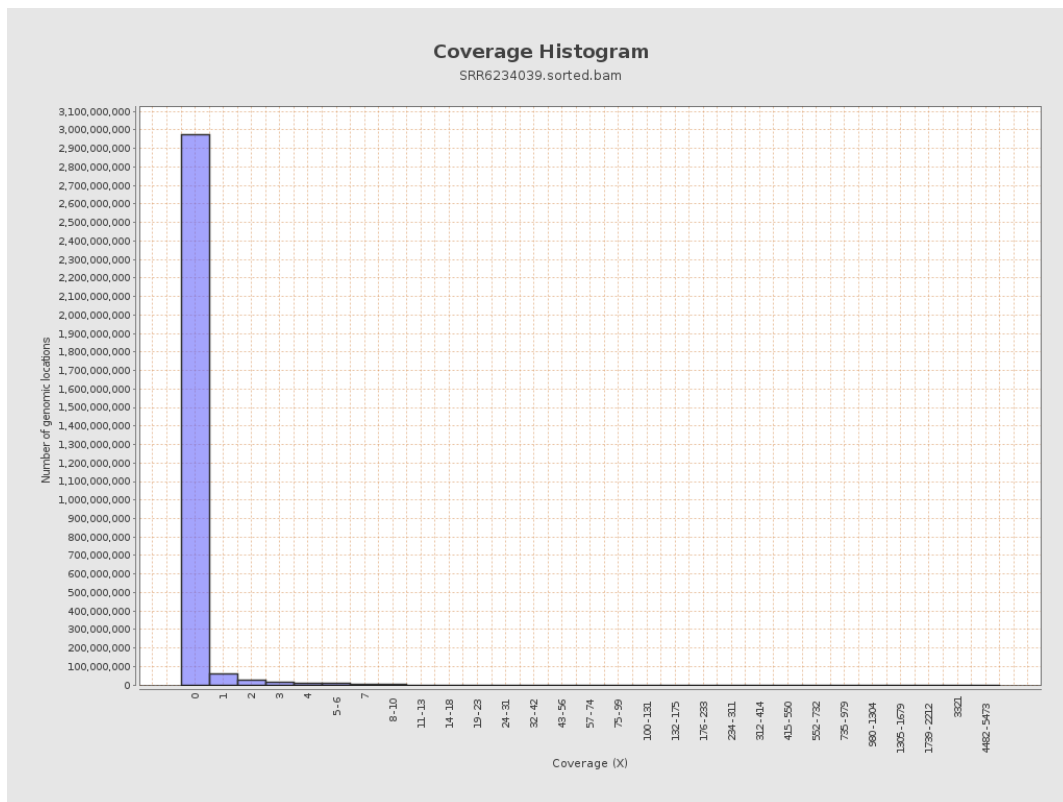
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19822827	0.0795	1.4704
chr2	243199373	4485369	0.0184	2.3883
chr3	198022430	2088031	0.0105	0.194
chr4	191154276	2422506	0.0127	0.2423
chr5	180915260	8292943	0.0458	0.4159
chr6	171115067	20174868	0.1179	0.957
chr7	159138663	2268195	0.0143	0.4274

chr8	146364022	17434743	0.1191	1.0072
chr9	141213431	7892516	0.0559	0.5198
chr10	135534747	6667556	0.0492	0.4485
chr11	135006516	7744048	0.0574	0.4904
chr12	133851895	5514718	0.0412	0.3859
chr13	115169878	20973844	0.1821	0.857
chr14	107349540	2635746	0.0246	0.5871
chr15	102531392	8502041	0.0829	0.5961
chr16	90354753	28189637	0.312	1.1753
chr17	81195210	36452917	0.449	1.6324
chr18	78077248	1483775	0.019	2.6591
chr19	59128983	28486376	0.4818	1.6889
chr20	63025520	5630430	0.0893	0.7867
chr21	48129895	13549500	0.2815	1.0158
chr22	51304566	8436752	0.1644	0.7443
chrMT	16571	60739	3.6654	3.7822
chrX	155270560	2046615	0.0132	0.4387
chrY	59373566	604324	0.0102	0.3417

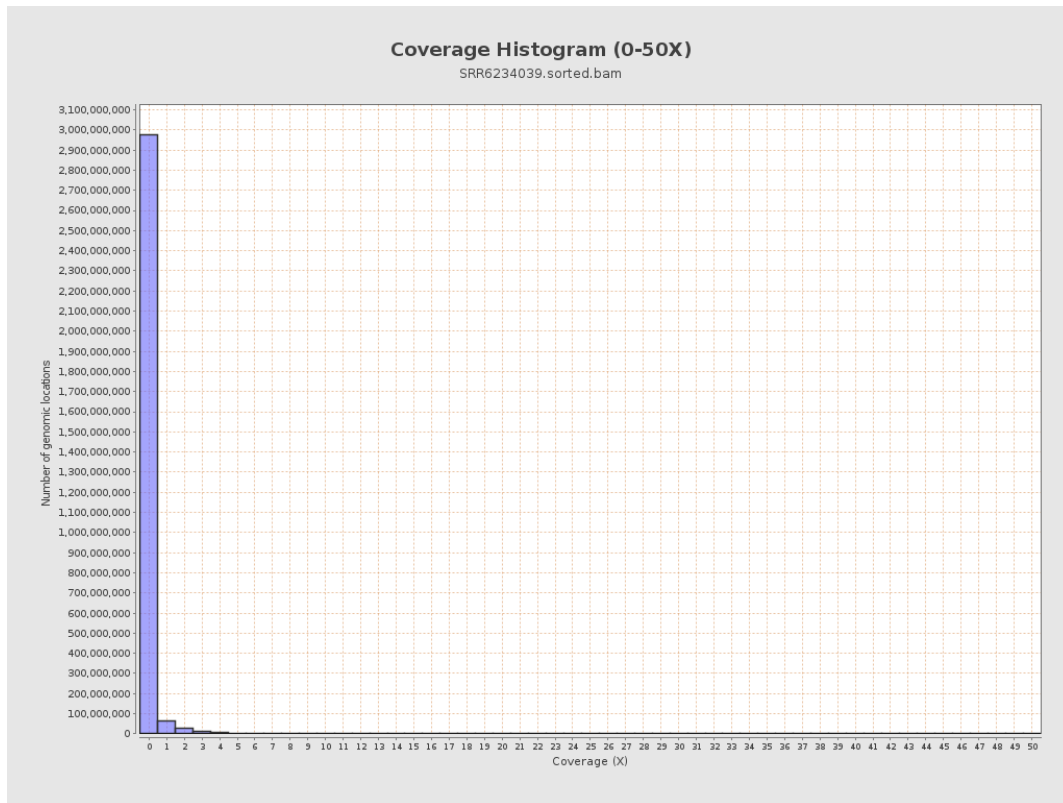
3. Results : Coverage across reference



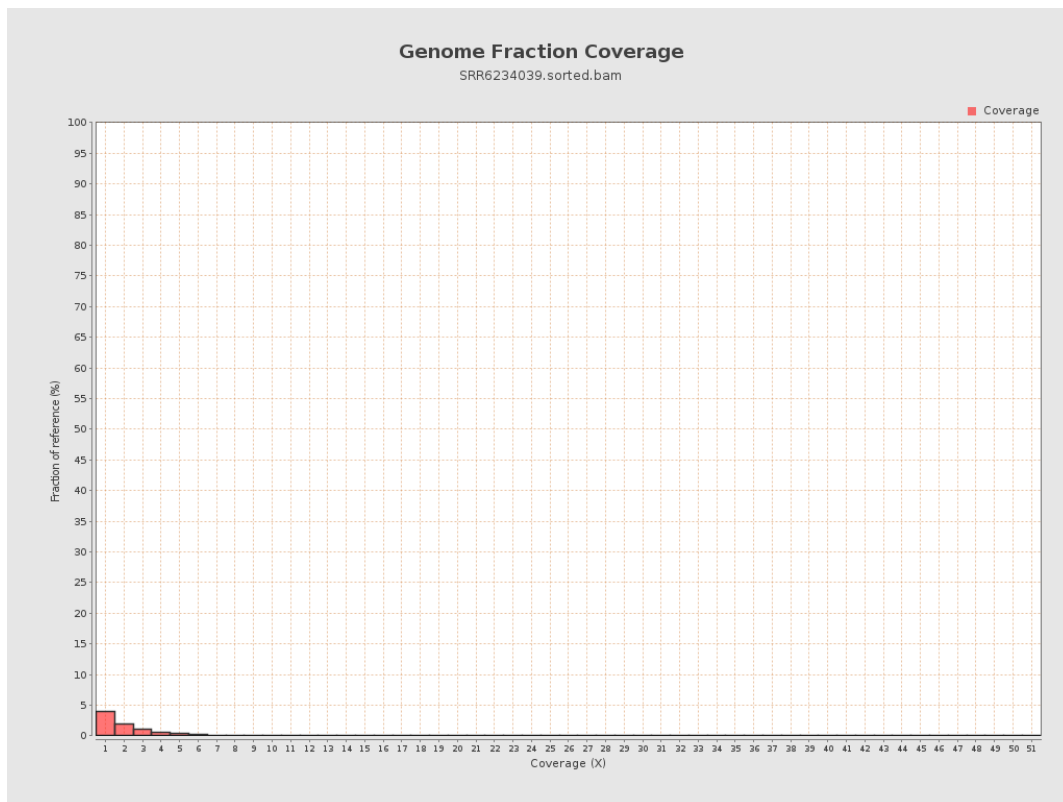
4. Results : Coverage Histogram



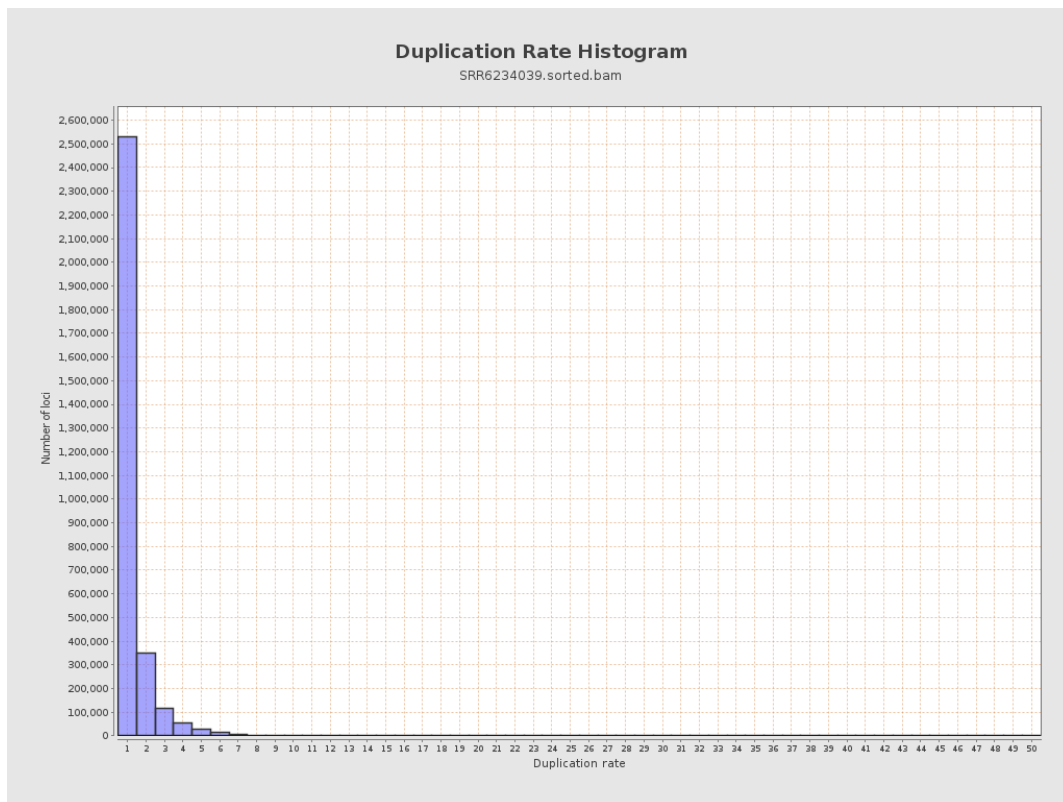
5. Results : Coverage Histogram (0-50X)



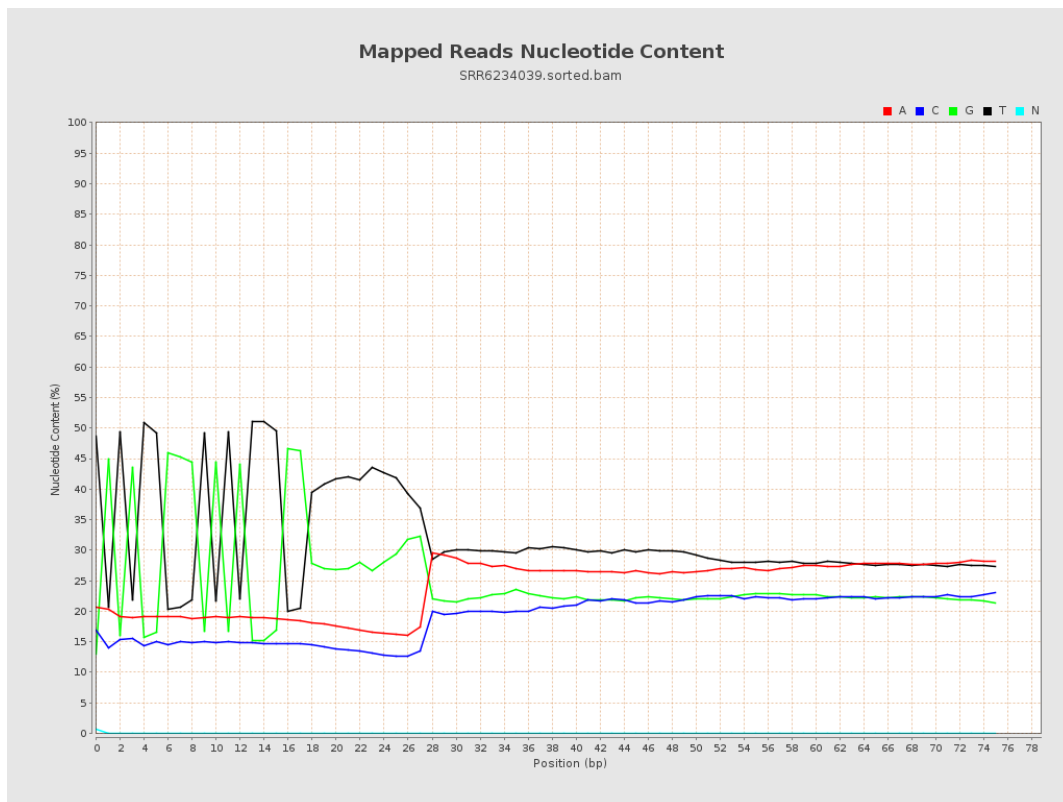
6. Results : Genome Fraction Coverage



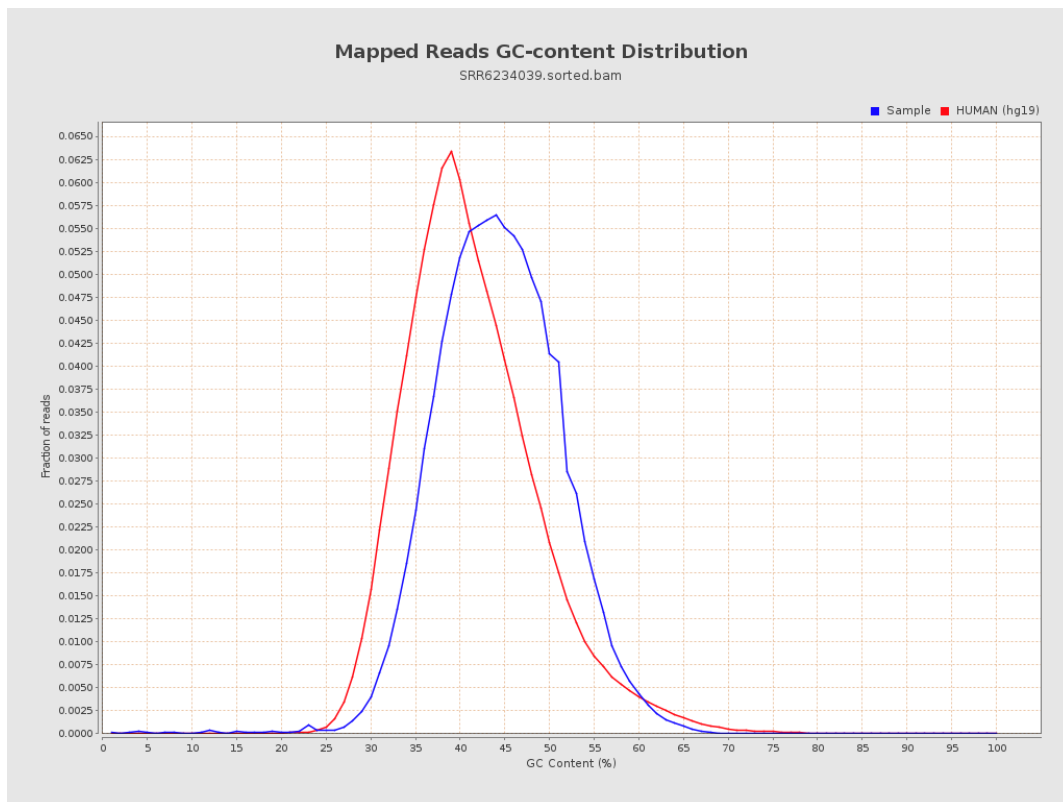
7. Results : Duplication Rate Histogram



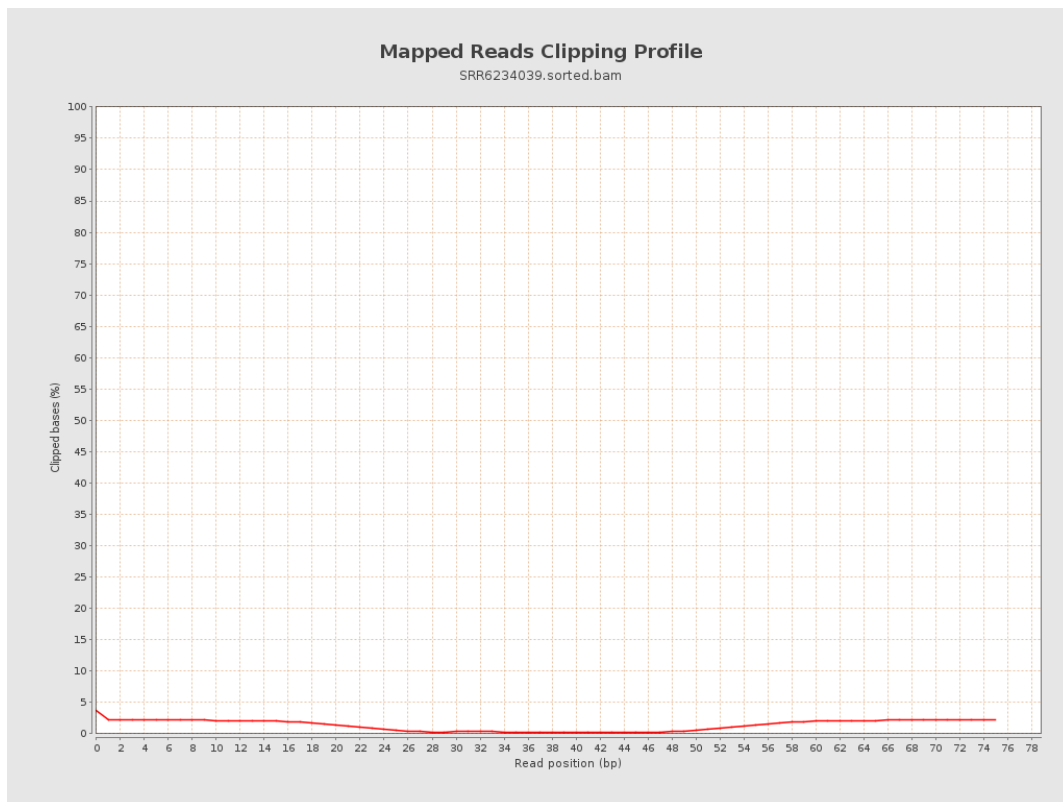
8. Results : Mapped Reads Nucleotide Content



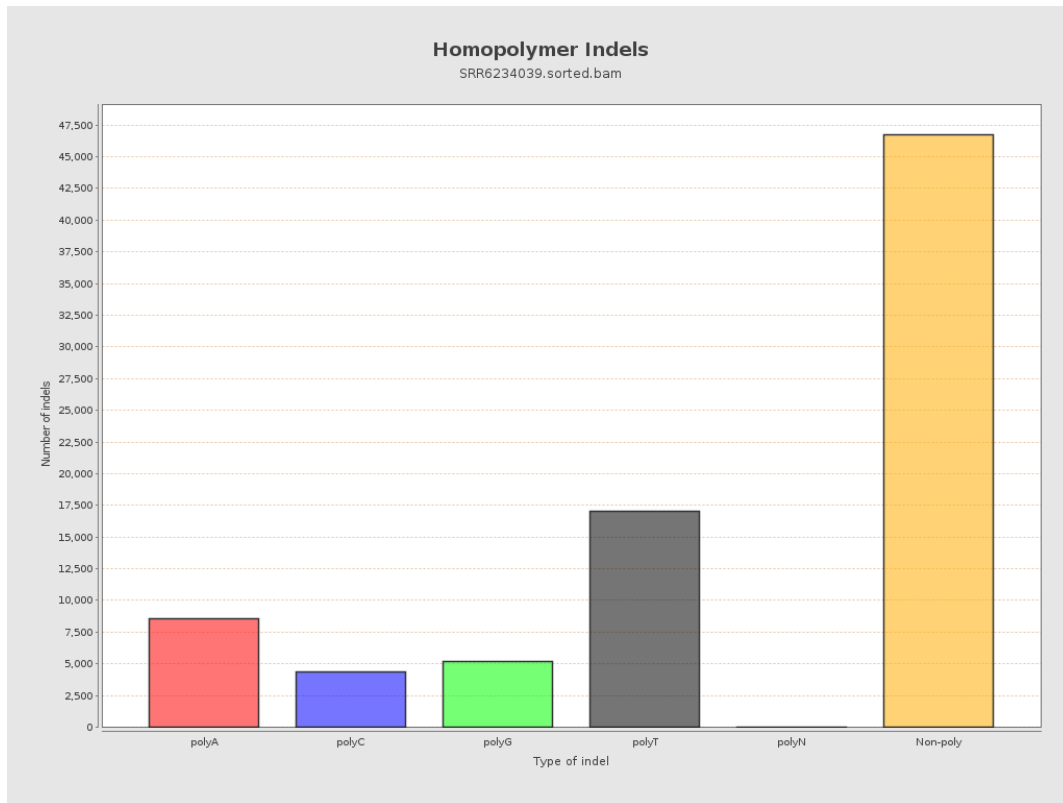
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

