

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 11:33:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234037.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_SRR6234037 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234037.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 11:33:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234037.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,435,542
Mapped reads	1,009,282 / 70.31%
Unmapped reads	426,260 / 29.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,315 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	43,329 / 3.02%
Duplication rate	3.61%
Clipped reads	460,383 / 32.07%

2.2. ACGT Content

Number/percentage of A's	18,992,659 / 28.51%
Number/percentage of C's	11,772,655 / 17.67%
Number/percentage of T's	21,761,467 / 32.67%
Number/percentage of G's	14,075,508 / 21.13%
Number/percentage of N's	11,957 / 0.02%
GC Percentage	38.8%

2.3. Coverage

Mean	0.0215

Standard Deviation	0.2216
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2.4. Mapping Quality

Mean Mapping Quality	46.4
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2.5. Mismatches and indels

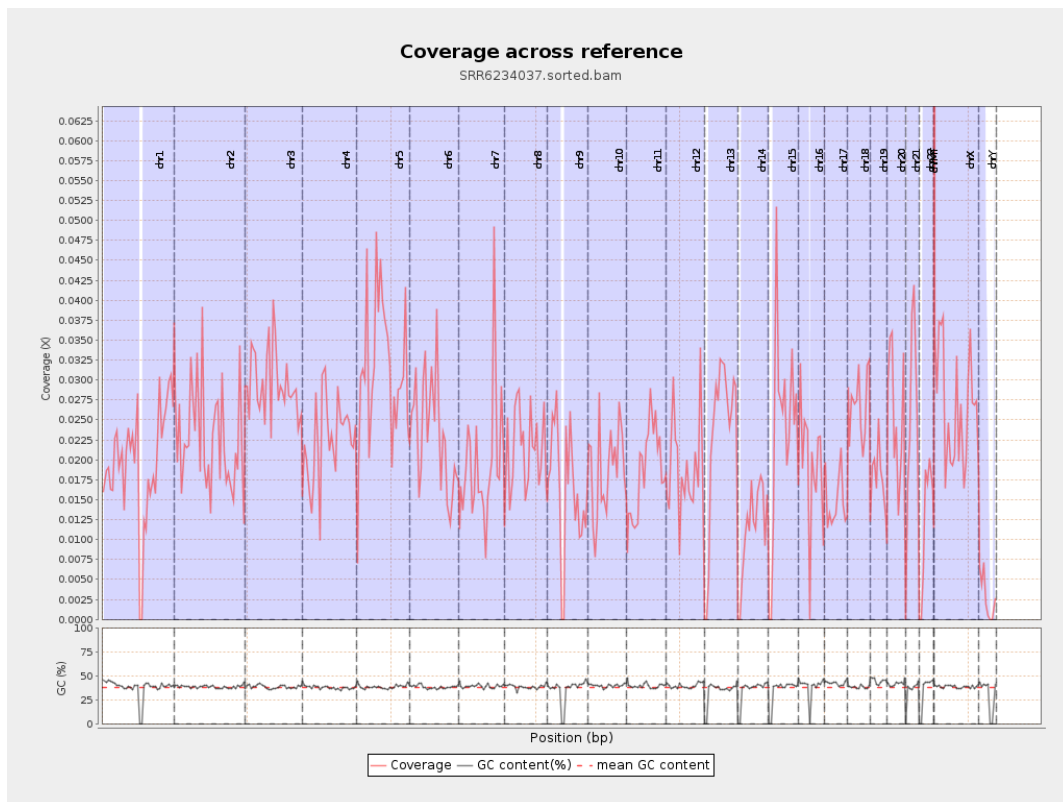
General error rate	0.84%
Mismatches	547,923
Insertions	5,210
Mapped reads with at least one insertion	0.51%
Deletions	24,757
Mapped reads with at least one deletion	2.41%
Homopolymer indels	44.1%

2.6. Chromosome stats

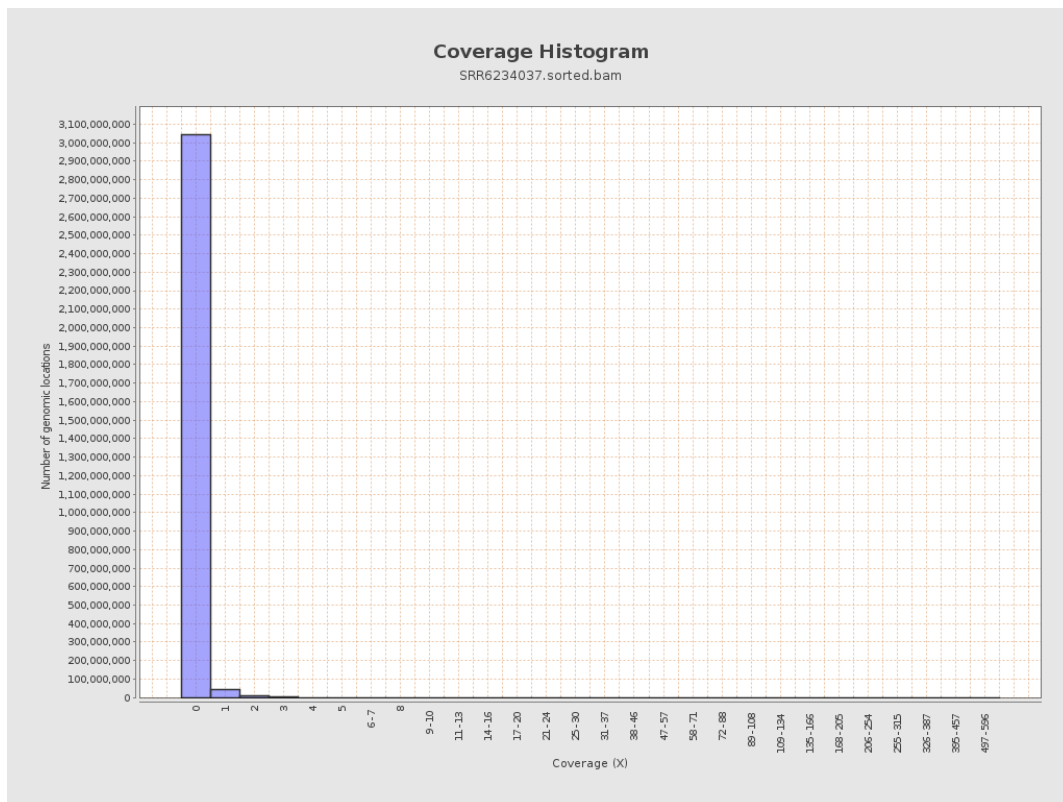
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4918959	0.0197	0.2929
chr2	243199373	5502668	0.0226	0.2393
chr3	198022430	5857820	0.0296	0.203
chr4	191154276	4275076	0.0224	0.1788
chr5	180915260	5788199	0.032	0.2117
chr6	171115067	3994520	0.0233	0.1976
chr7	159138663	3078574	0.0193	0.2024

chr8	146364022	3162280	0.0216	0.4099
chr9	141213431	2298826	0.0163	0.1886
chr10	135534747	2513266	0.0185	0.1991
chr11	135006516	2528678	0.0187	0.1794
chr12	133851895	2534264	0.0189	0.1634
chr13	115169878	2696473	0.0234	0.1815
chr14	107349540	1223025	0.0114	0.1325
chr15	102531392	2424078	0.0236	0.183
chr16	90354753	1707365	0.0189	0.1768
chr17	81195210	1197009	0.0147	0.1453
chr18	78077248	2085801	0.0267	0.3614
chr19	59128983	1057043	0.0179	0.2072
chr20	63025520	1637405	0.026	0.1958
chr21	48129895	1203818	0.025	0.1909
chr22	51304566	631802	0.0123	0.1296
chrMT	16571	14424	0.8704	1.1357
chrX	155270560	4163473	0.0268	0.2018
chrY	59373566	162736	0.0027	0.0702

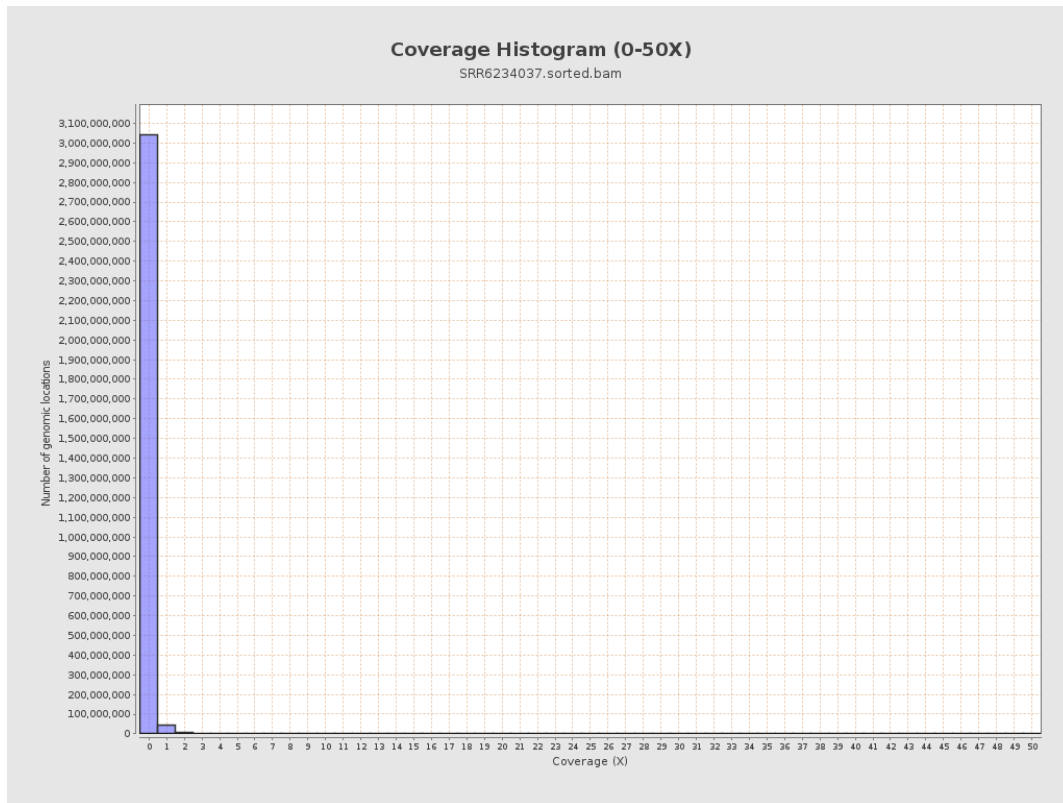
3. Results : Coverage across reference



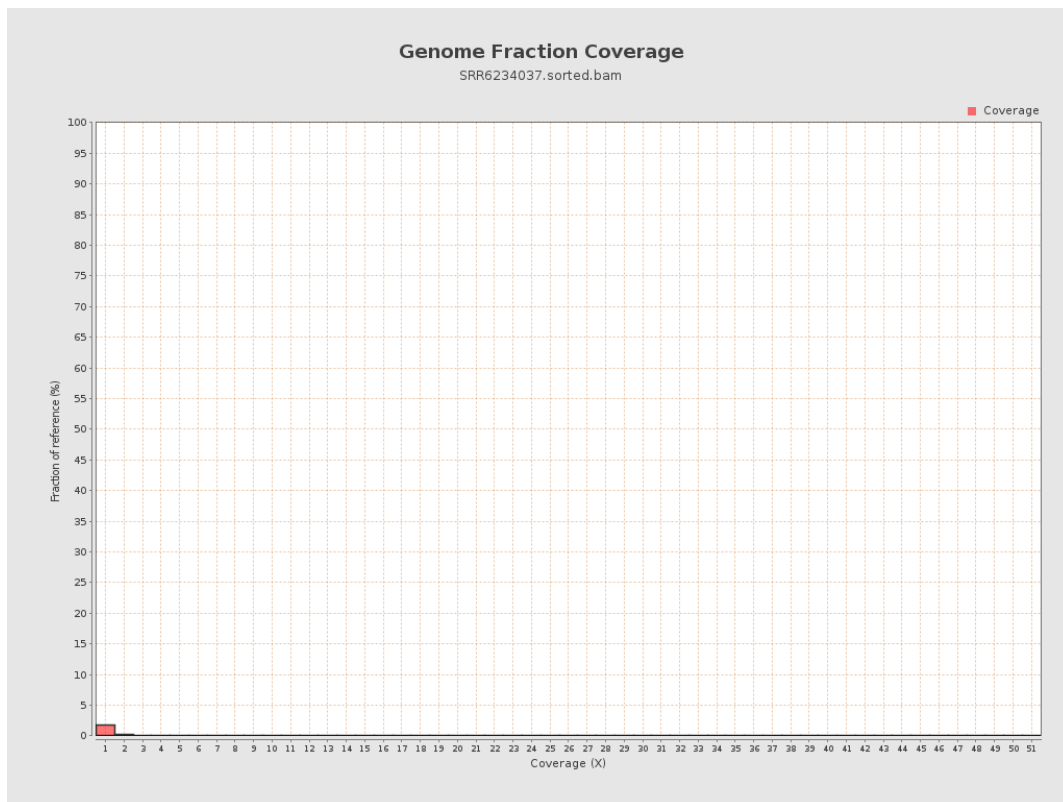
4. Results : Coverage Histogram



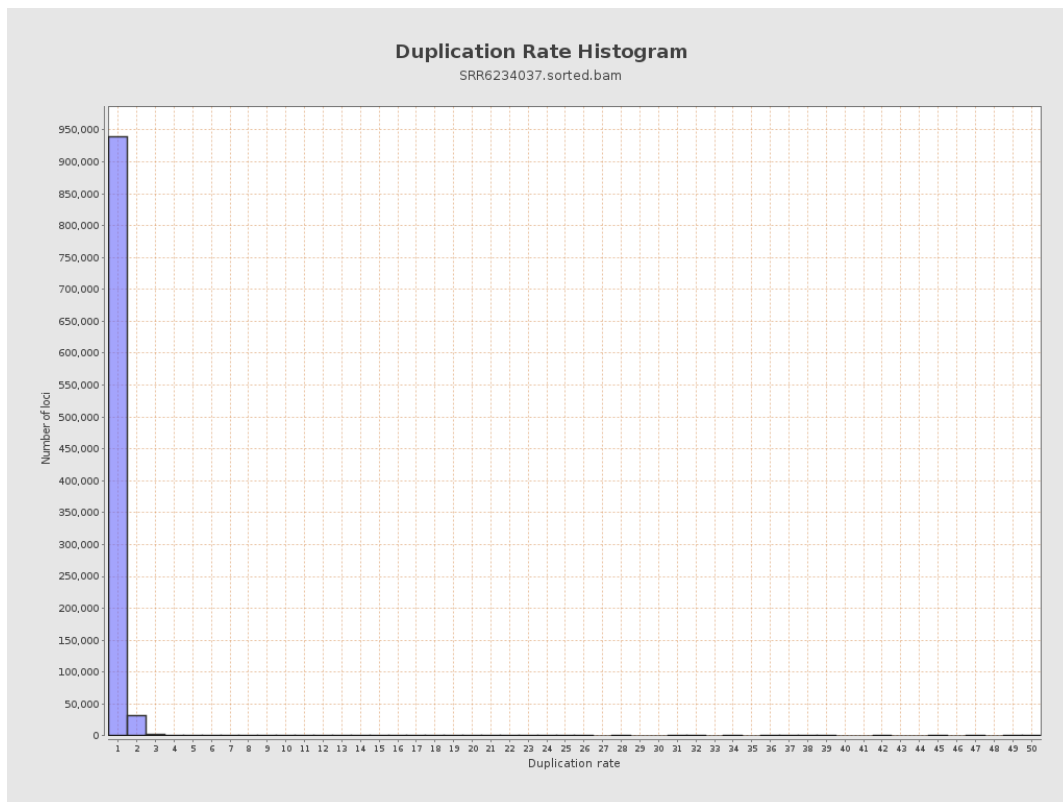
5. Results : Coverage Histogram (0-50X)



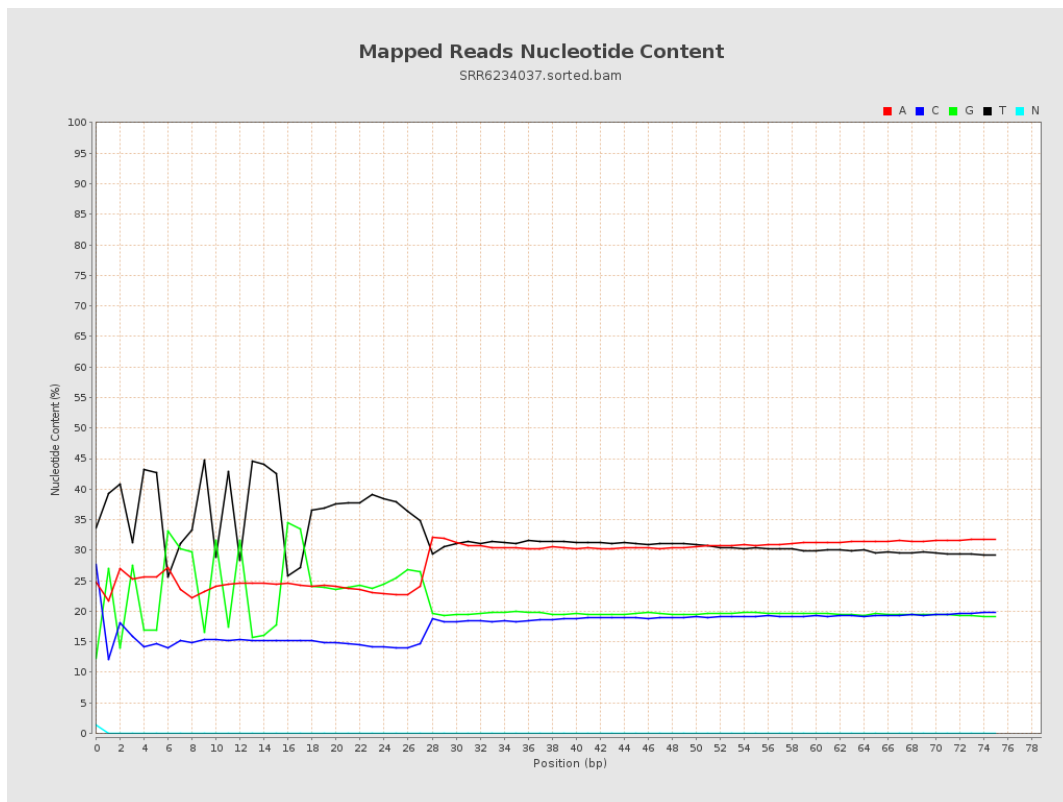
6. Results : Genome Fraction Coverage



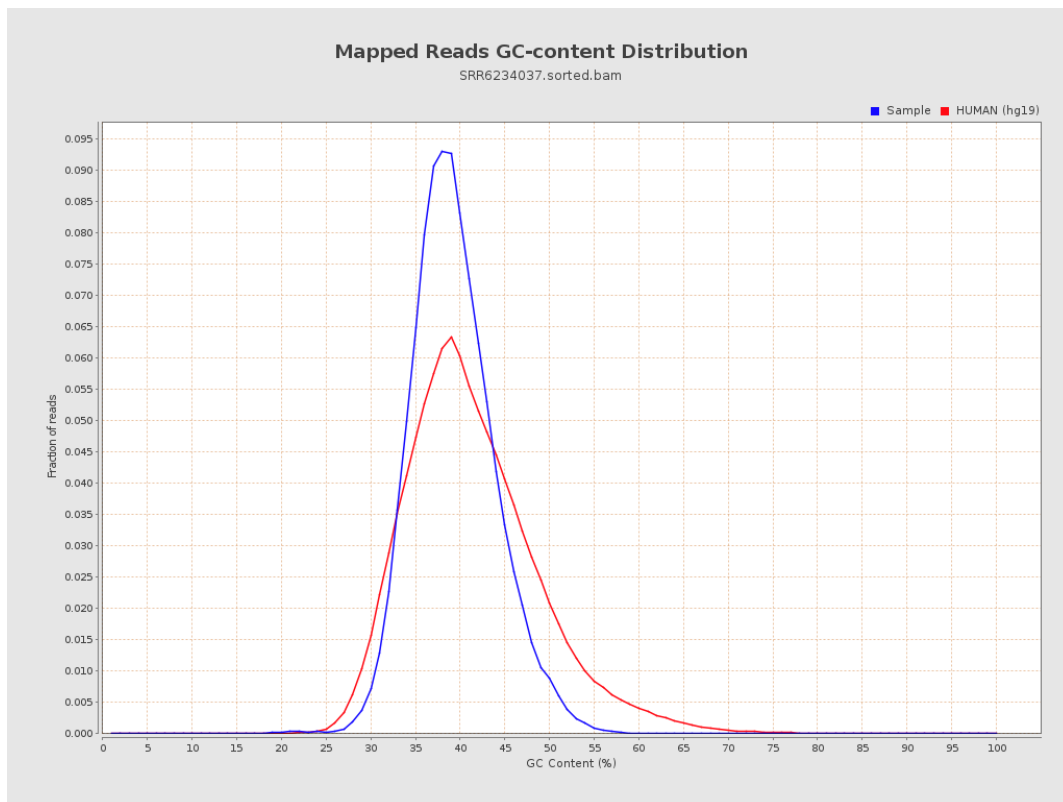
7. Results : Duplication Rate Histogram



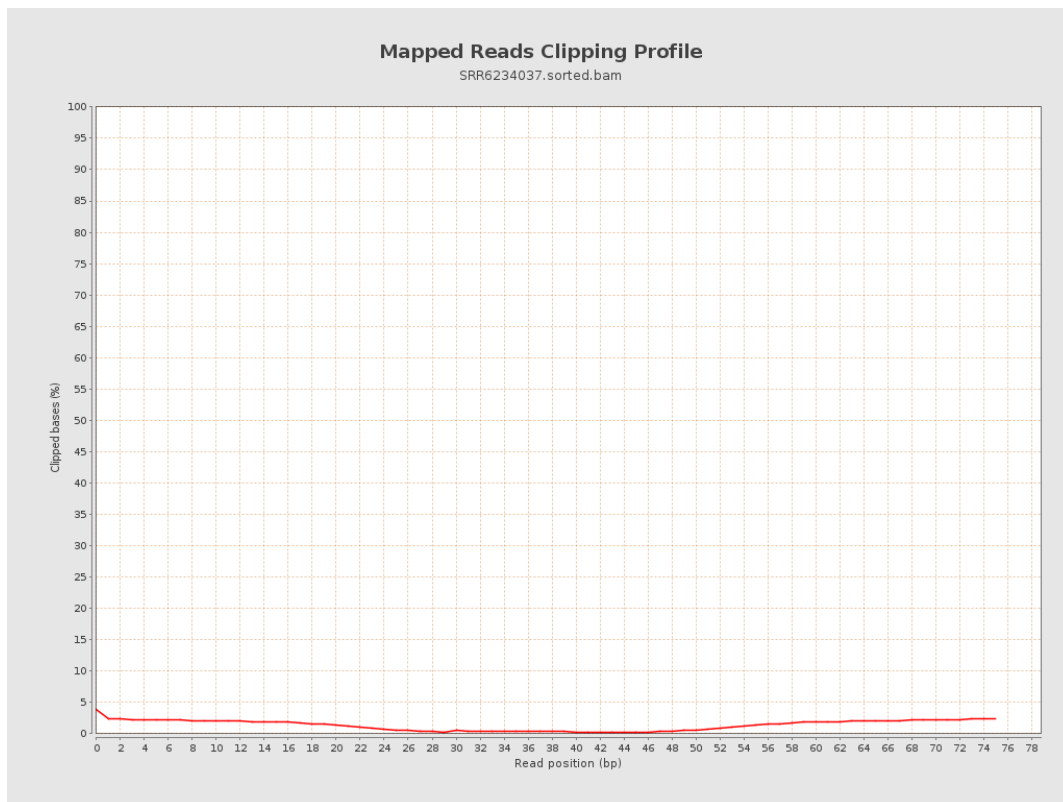
8. Results : Mapped Reads Nucleotide Content



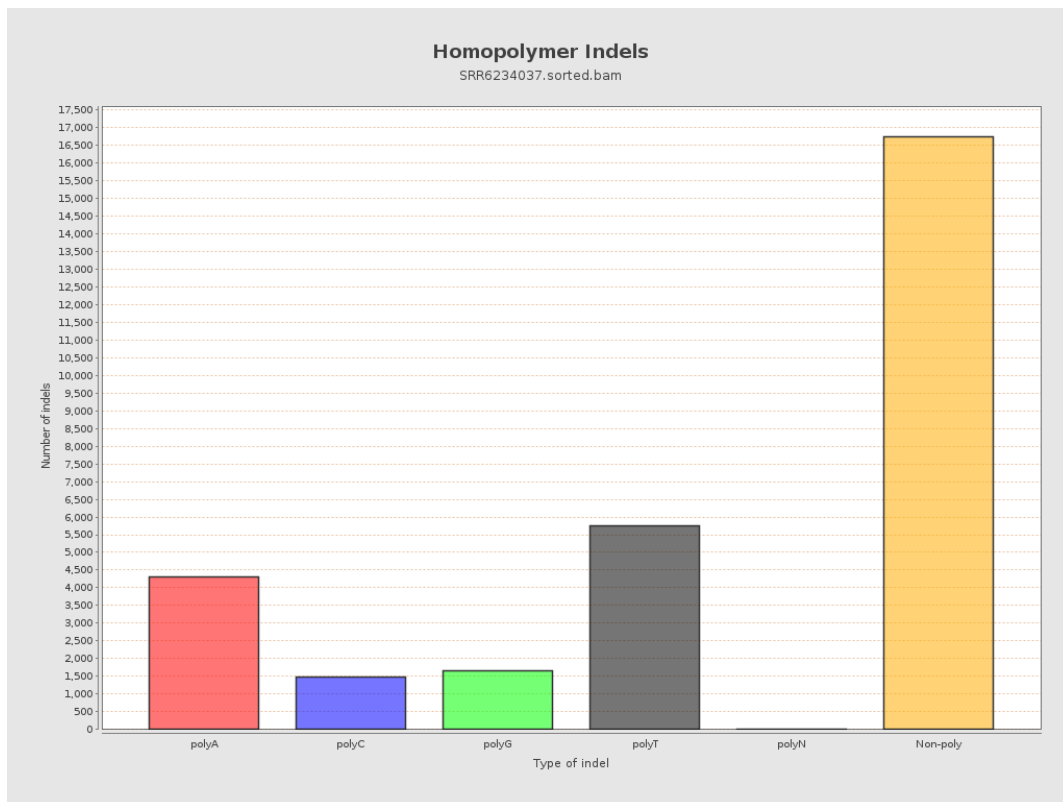
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

