

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:13:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819150.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_SRR1819150 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819150.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:13:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819150.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,104,378
Mapped reads	5,626,195 / 92.17%
Unmapped reads	478,183 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,833 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	635,308 / 10.41%
Duplication rate	8%
Clipped reads	5,644,301 / 92.46%

2.2. ACGT Content

Number/percentage of A's	84,691,696 / 25.63%
Number/percentage of C's	68,731,400 / 20.8%
Number/percentage of T's	98,687,515 / 29.87%
Number/percentage of G's	78,278,312 / 23.69%
Number/percentage of N's	5,058 / 0%
GC Percentage	44.5%

2.3. Coverage

Mean	0.1068

Standard Deviation	0.8419
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2.4. Mapping Quality

Mean Mapping Quality	44.81
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2.5. Mismatches and indels

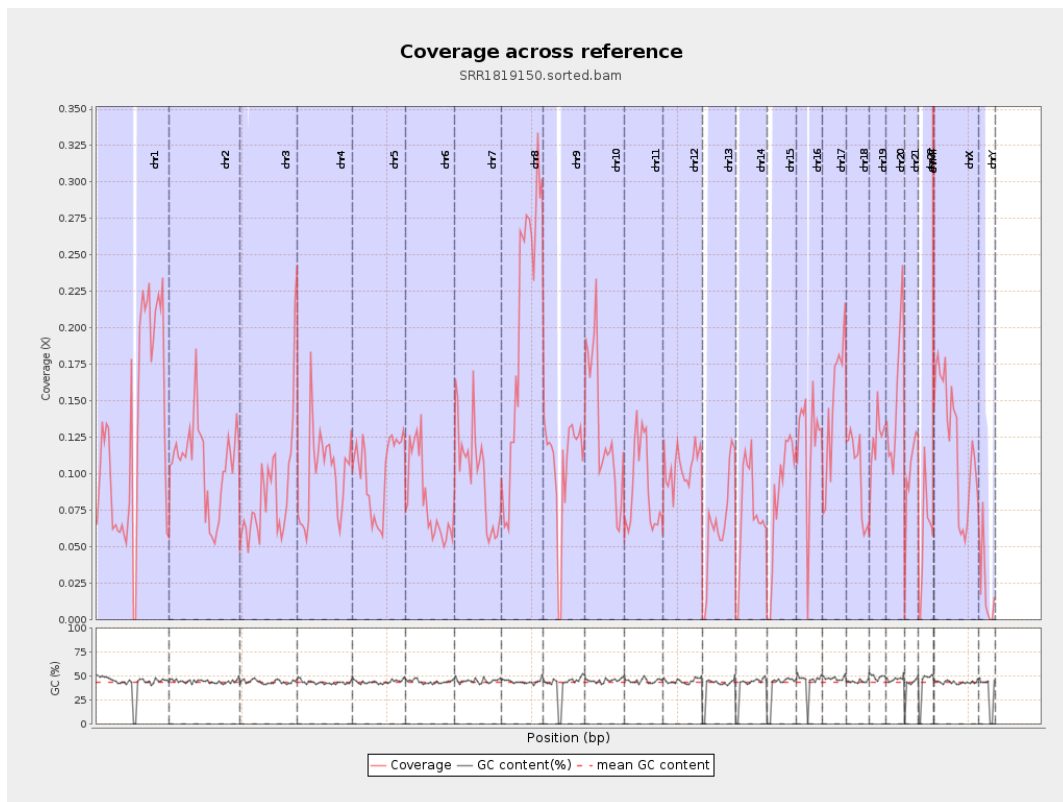
General error rate	0.51%
Mismatches	1,645,672
Insertions	20,134
Mapped reads with at least one insertion	0.36%
Deletions	56,483
Mapped reads with at least one deletion	1%
Homopolymer indels	43.9%

2.6. Chromosome stats

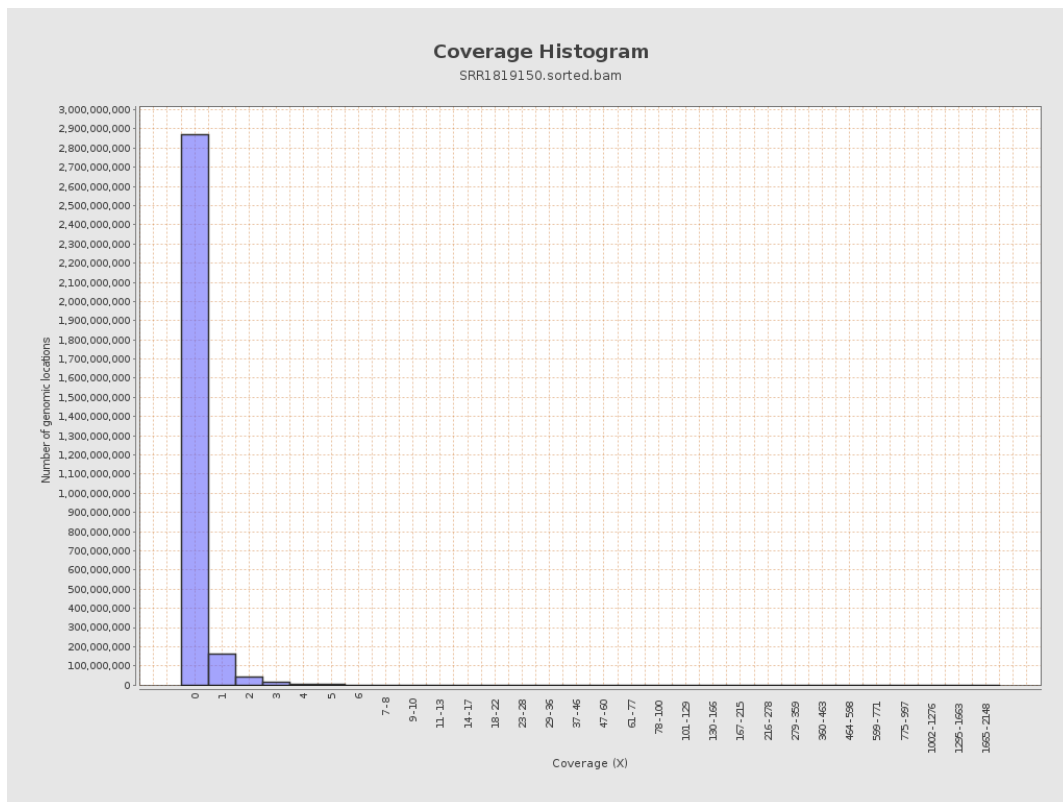
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	31976408	0.1283	1.6921
chr2	243199373	26039481	0.1071	1.0556
chr3	198022430	17205193	0.0869	0.4191
chr4	191154276	18984196	0.0993	0.6219
chr5	180915260	18281420	0.101	0.4452
chr6	171115067	13988435	0.0817	0.5747
chr7	159138663	15870793	0.0997	1.0254

chr8	146364022	29706757	0.203	0.8338
chr9	141213431	14815661	0.1049	0.6557
chr10	135534747	17659143	0.1303	0.9704
chr11	135006516	12166360	0.0901	0.6928
chr12	133851895	14081437	0.1052	0.4591
chr13	115169878	7570392	0.0657	0.3605
chr14	107349540	7809848	0.0728	0.4019
chr15	102531392	8709241	0.0849	0.4174
chr16	90354753	10937481	0.1211	0.5643
chr17	81195210	12060837	0.1485	0.6225
chr18	78077248	7836236	0.1004	1.3579
chr19	59128983	7305270	0.1235	1.1816
chr20	63025520	9661079	0.1533	0.5911
chr21	48129895	4823850	0.1002	0.5814
chr22	51304566	2859307	0.0557	0.3342
chrMT	16571	51752	3.123	2.6479
chrX	155270560	18843213	0.1214	0.5671
chrY	59373566	1245669	0.021	0.6358

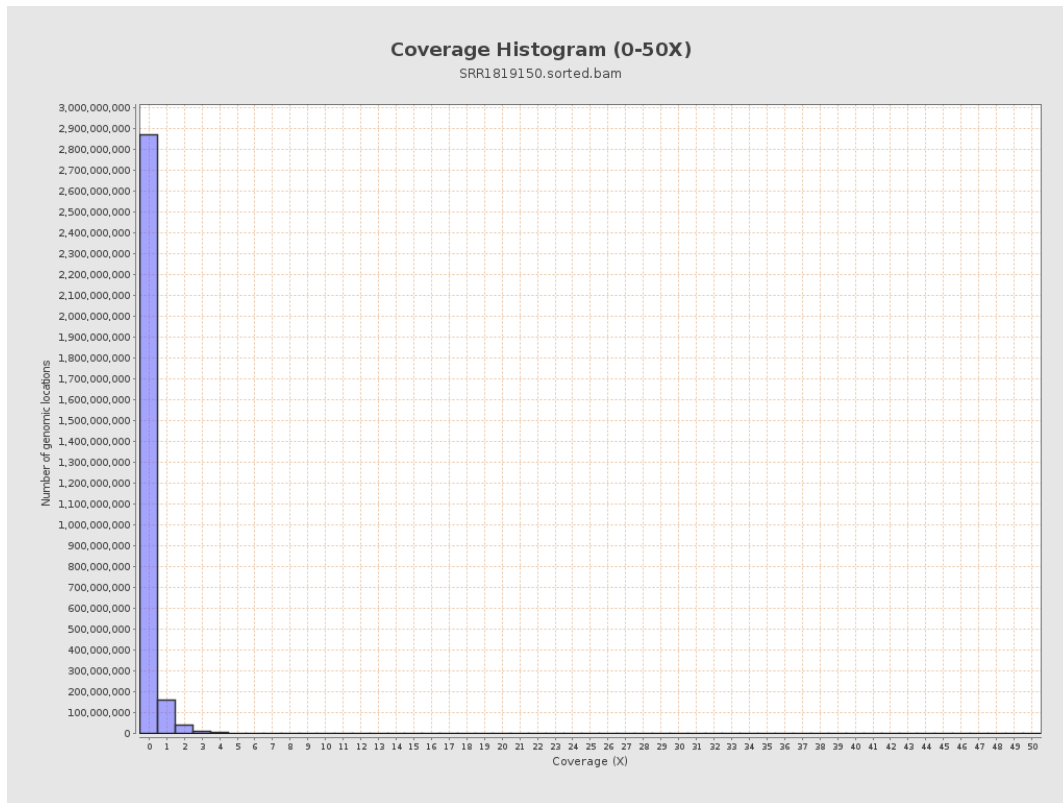
3. Results : Coverage across reference



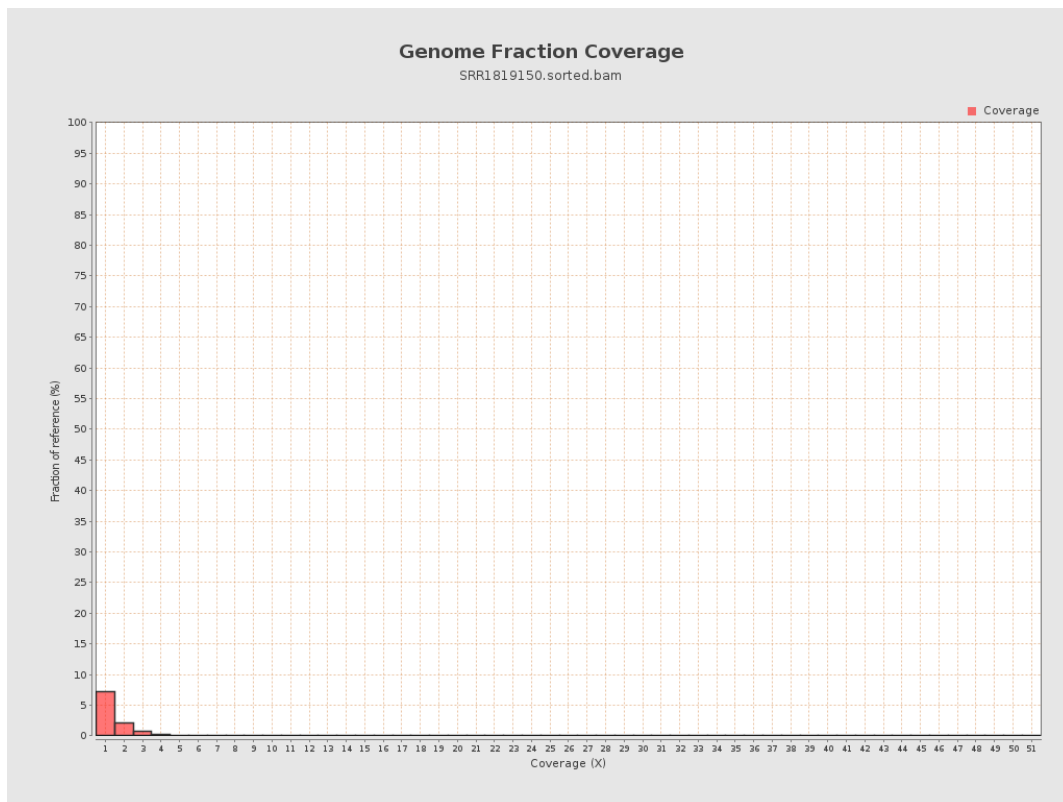
4. Results : Coverage Histogram



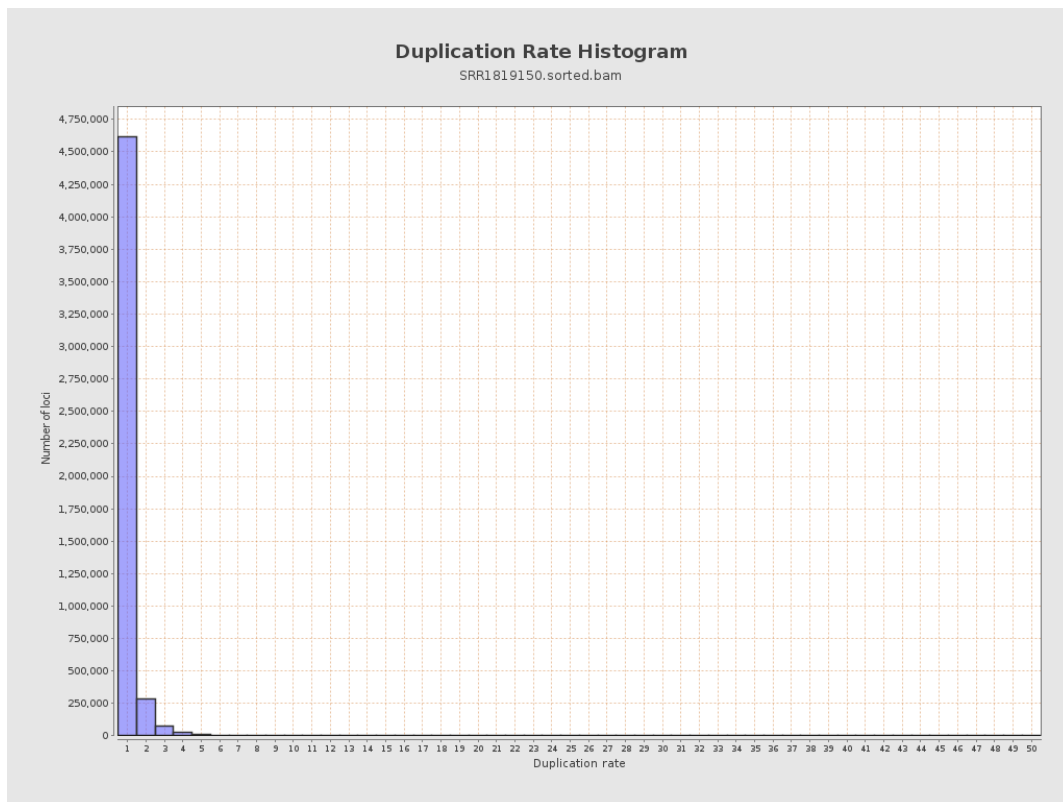
5. Results : Coverage Histogram (0-50X)



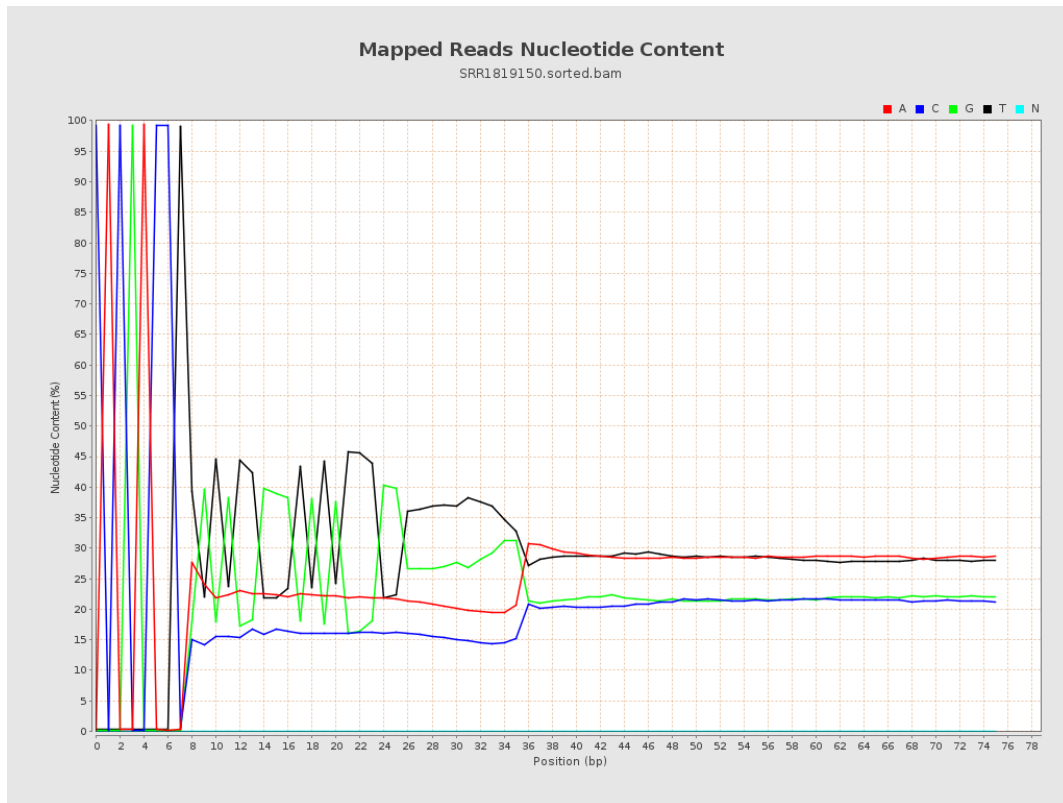
6. Results : Genome Fraction Coverage



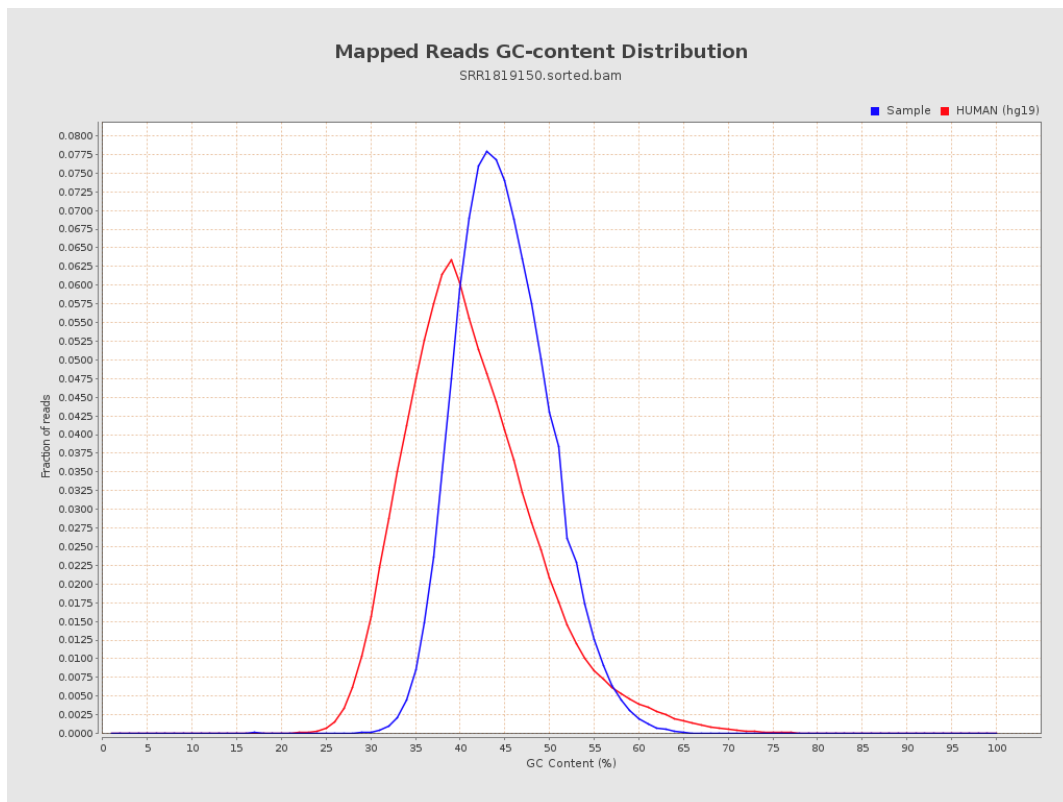
7. Results : Duplication Rate Histogram



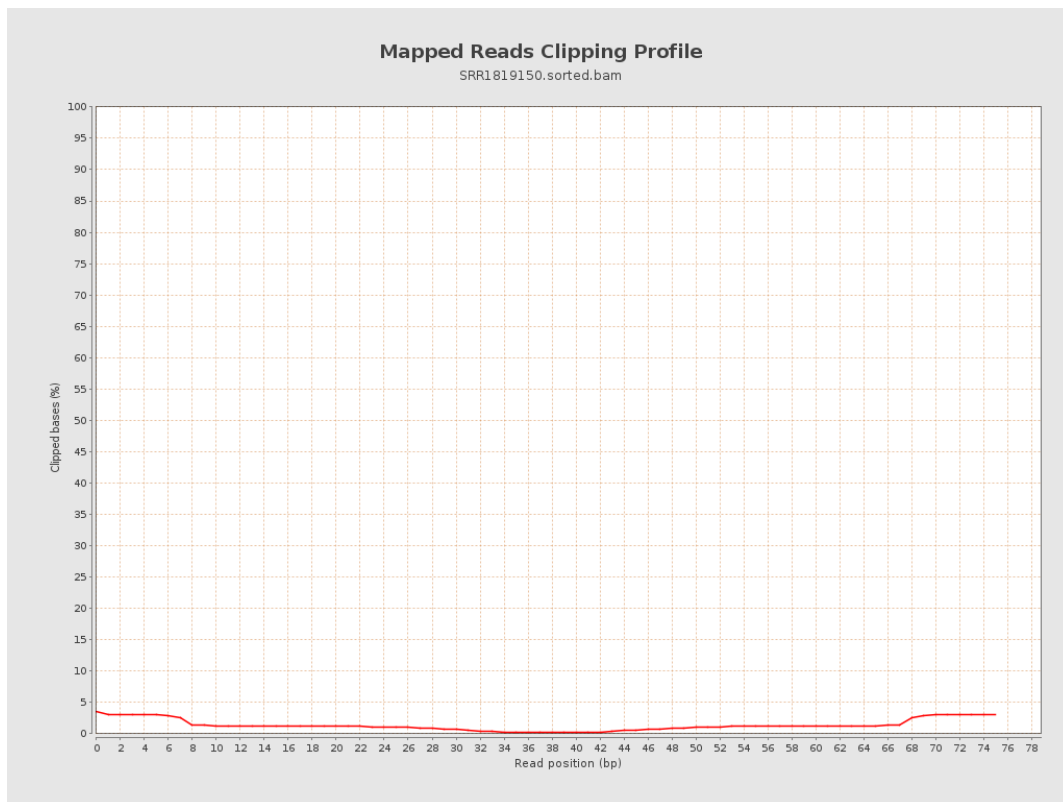
8. Results : Mapped Reads Nucleotide Content



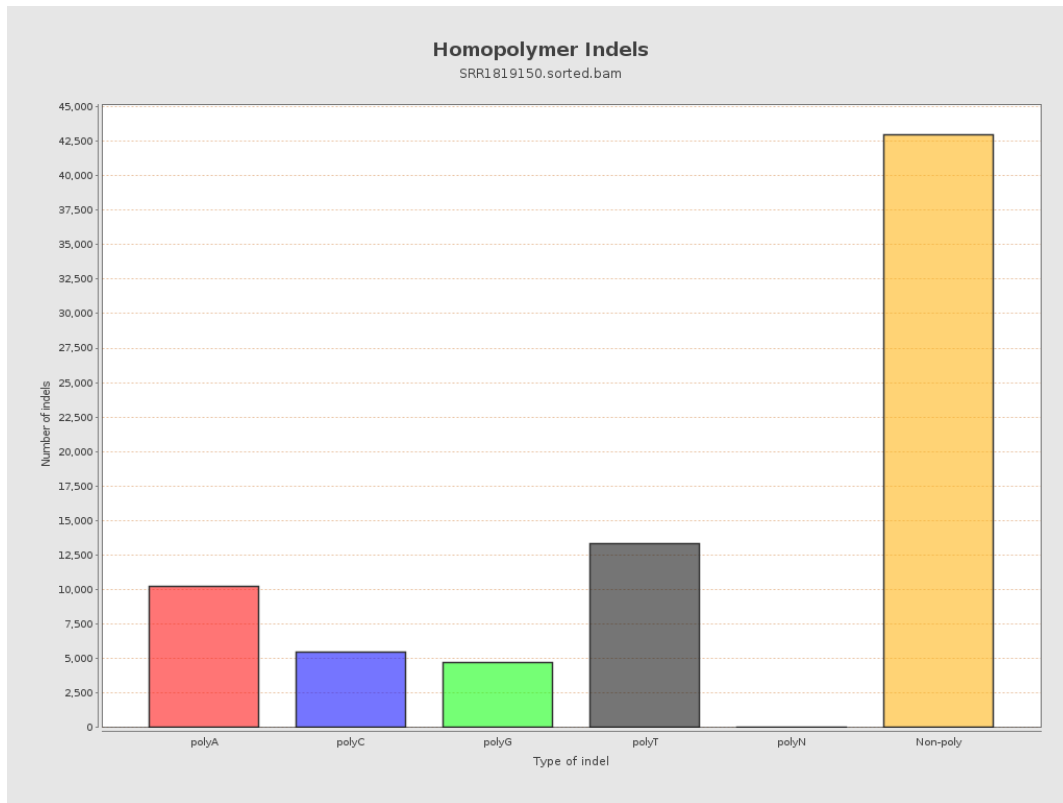
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

