

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:26:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549071.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_SRR1549071 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549071.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:26:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549071.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,309,583
Mapped reads	8,064,626 / 86.63%
Unmapped reads	1,244,957 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	290,349 / 3.12%
Duplication rate	2.31%
Clipped reads	405,179 / 4.35%

2.2. ACGT Content

Number/percentage of A's	95,033,579 / 29.68%
Number/percentage of C's	64,867,019 / 20.26%
Number/percentage of T's	95,294,902 / 29.76%
Number/percentage of G's	64,975,799 / 20.29%
Number/percentage of N's	5,844 / 0%
GC Percentage	40.55%

2.3. Coverage

Mean	0.1034
Standard Deviation	0.9773

2.4. Mapping Quality

Mean Mapping Quality	42.9
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2.5. Mismatches and indels

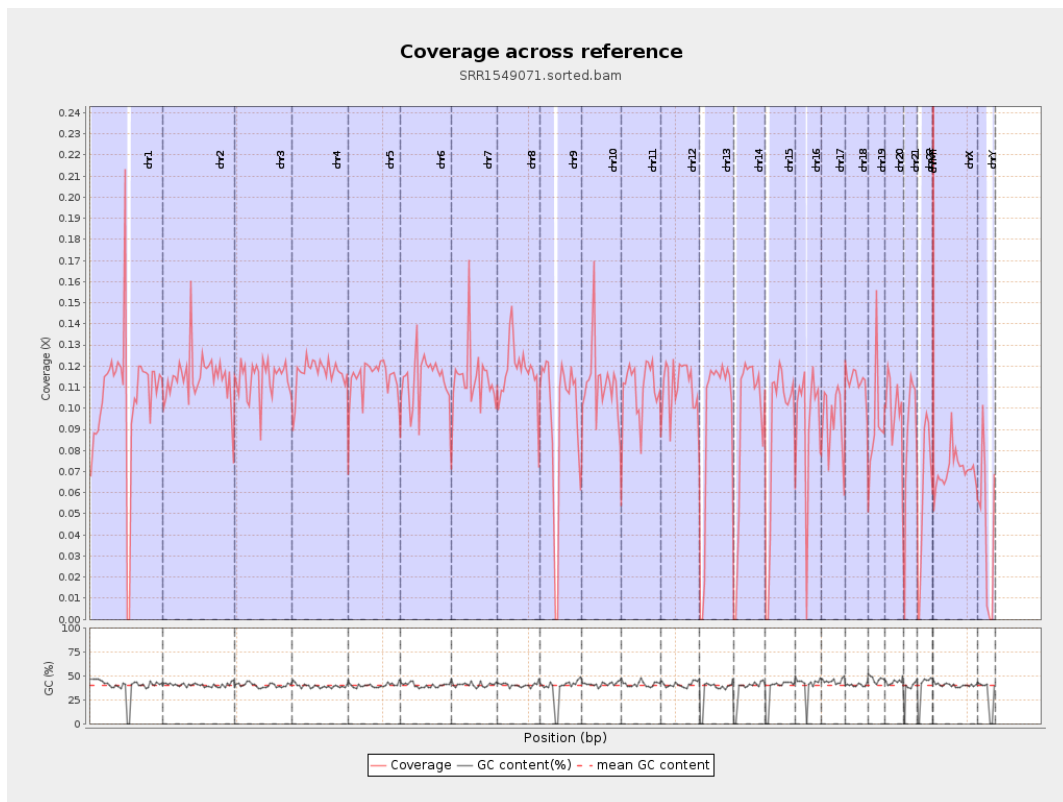
General error rate	0.32%
Mismatches	1,015,956
Insertions	8,298
Mapped reads with at least one insertion	0.1%
Deletions	25,497
Mapped reads with at least one deletion	0.32%
Homopolymer indels	44.34%

2.6. Chromosome stats

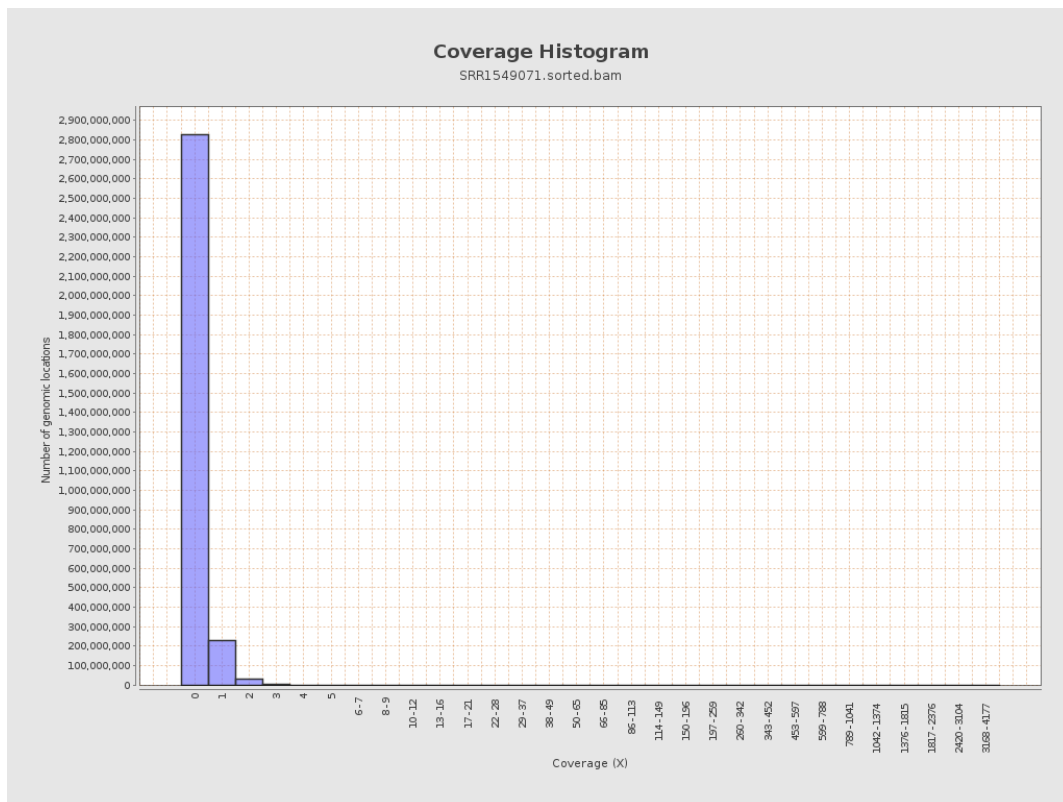
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26168193	0.105	2.3242
chr2	243199373	27834507	0.1145	0.6195
chr3	198022430	22604865	0.1142	0.3888
chr4	191154276	22341700	0.1169	0.4114
chr5	180915260	20672031	0.1143	0.3954
chr6	171115067	19491765	0.1139	0.4728
chr7	159138663	18072770	0.1136	0.8805
chr8	146364022	17141519	0.1171	2.0898

chr9	141213431	13534875	0.0958	0.6041
chr10	135534747	15093823	0.1114	0.7255
chr11	135006516	14794618	0.1096	0.5593
chr12	133851895	14776578	0.1104	0.4092
chr13	115169878	10919975	0.0948	0.3455
chr14	107349540	9983362	0.093	0.4185
chr15	102531392	9095983	0.0887	0.3367
chr16	90354753	8402247	0.093	0.4202
chr17	81195210	7720477	0.0951	0.4067
chr18	78077248	8825222	0.113	1.2027
chr19	59128983	5523313	0.0934	1.8092
chr20	63025520	6322871	0.1003	0.3767
chr21	48129895	4169002	0.0866	0.4093
chr22	51304566	3124851	0.0609	0.3296
chrMT	16571	19607	1.1832	1.5606
chrX	155270560	10944990	0.0705	0.4105
chrY	59373566	2630276	0.0443	0.3813

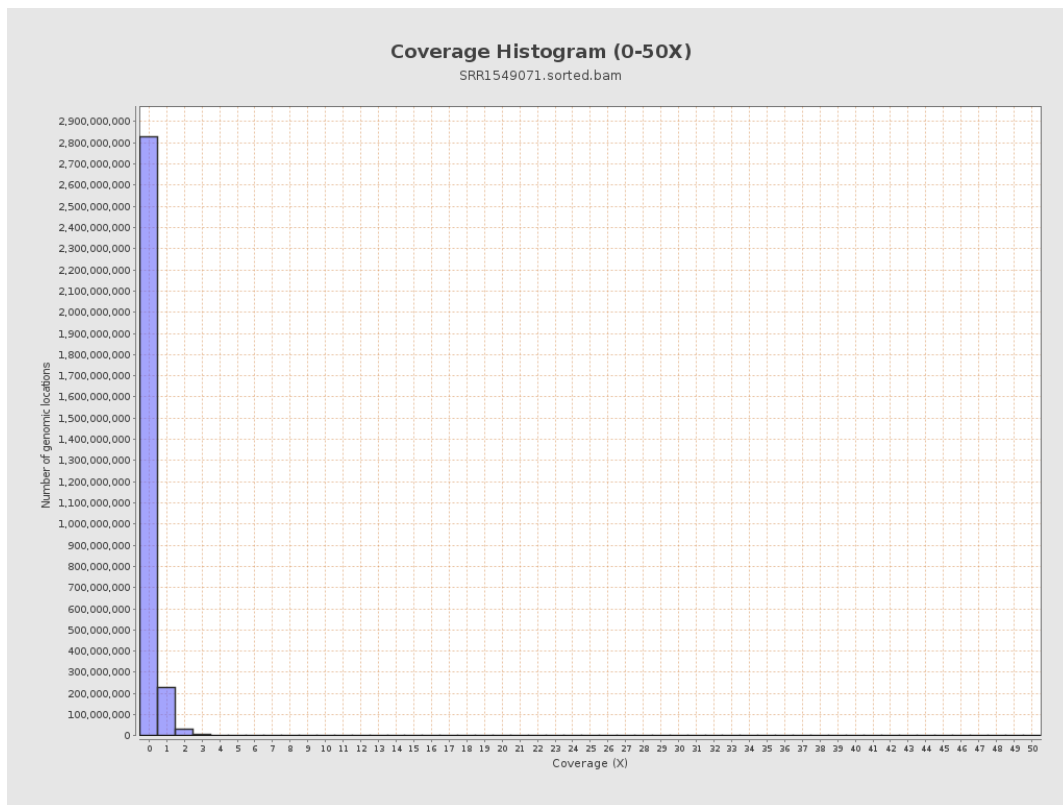
3. Results : Coverage across reference



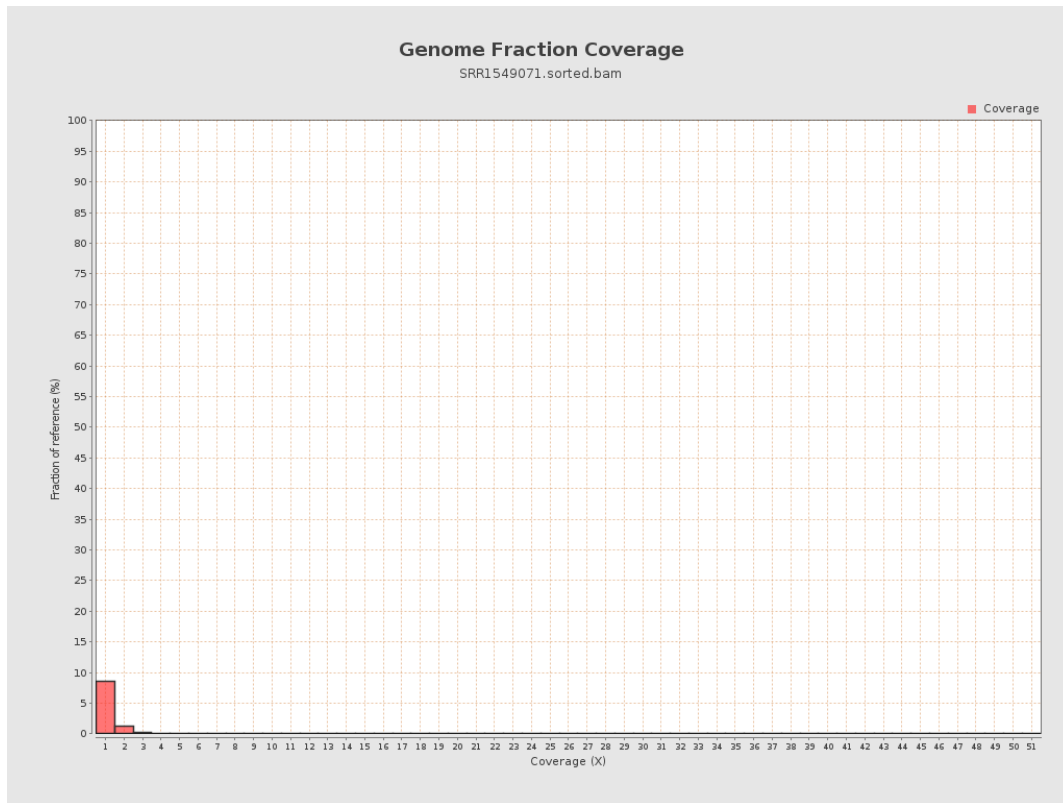
4. Results : Coverage Histogram



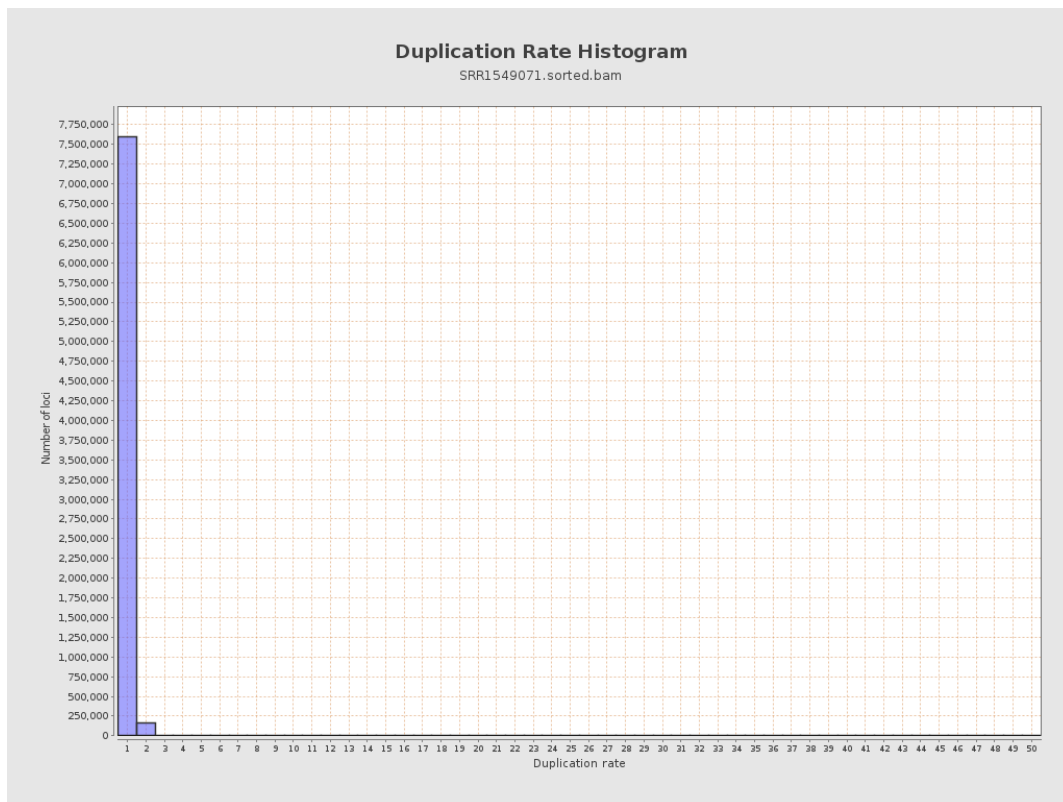
5. Results : Coverage Histogram (0-50X)



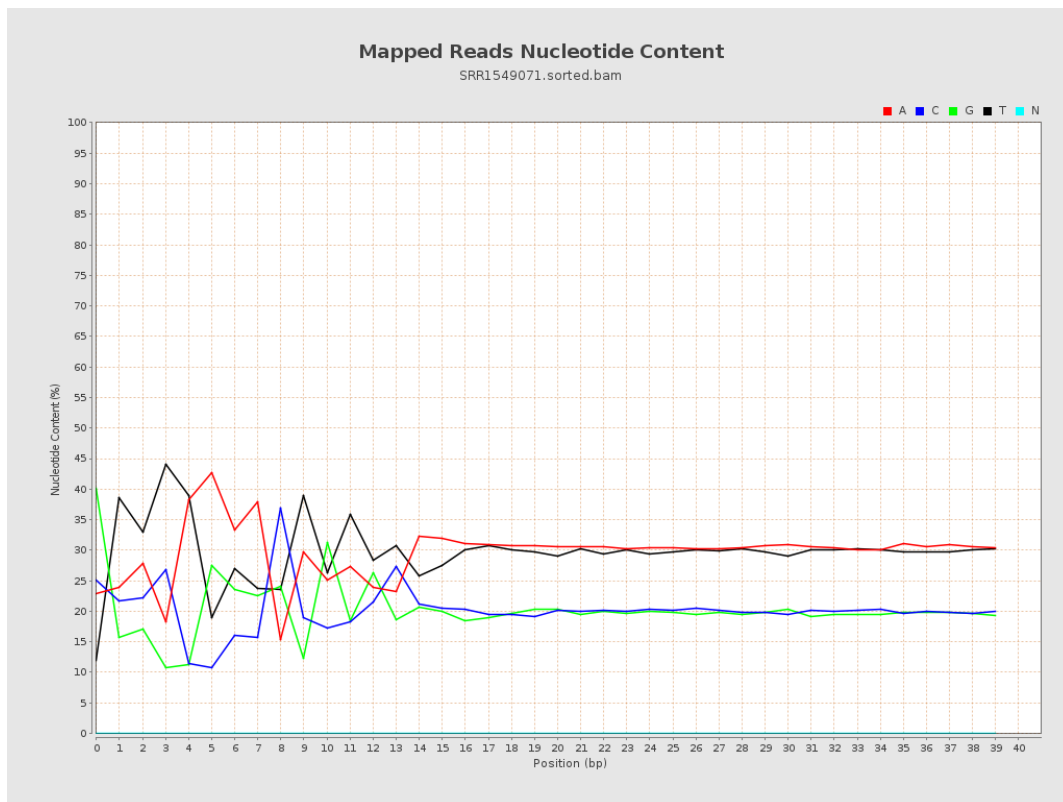
6. Results : Genome Fraction Coverage



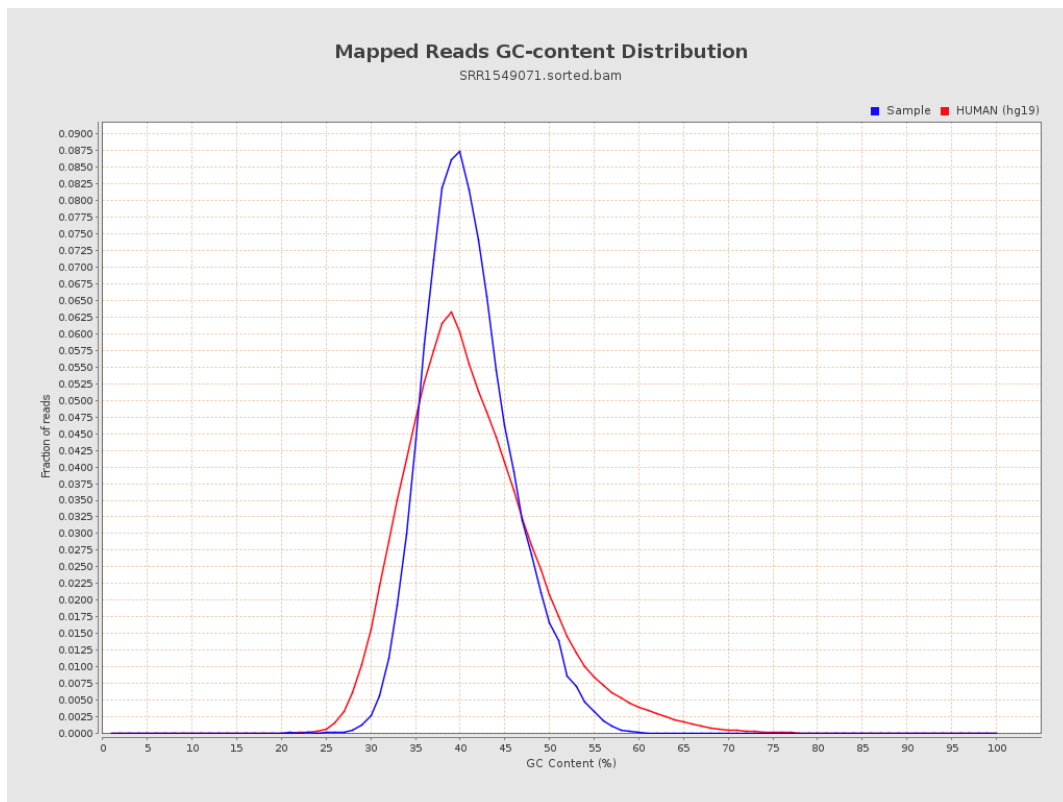
7. Results : Duplication Rate Histogram



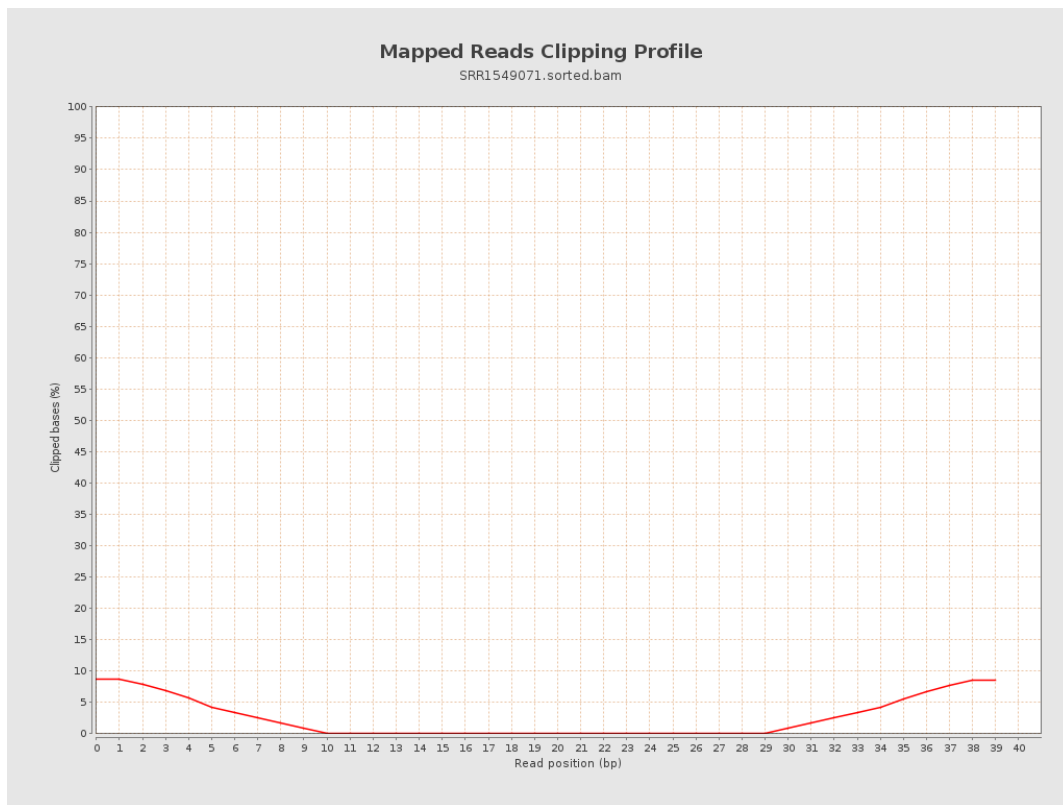
8. Results : Mapped Reads Nucleotide Content



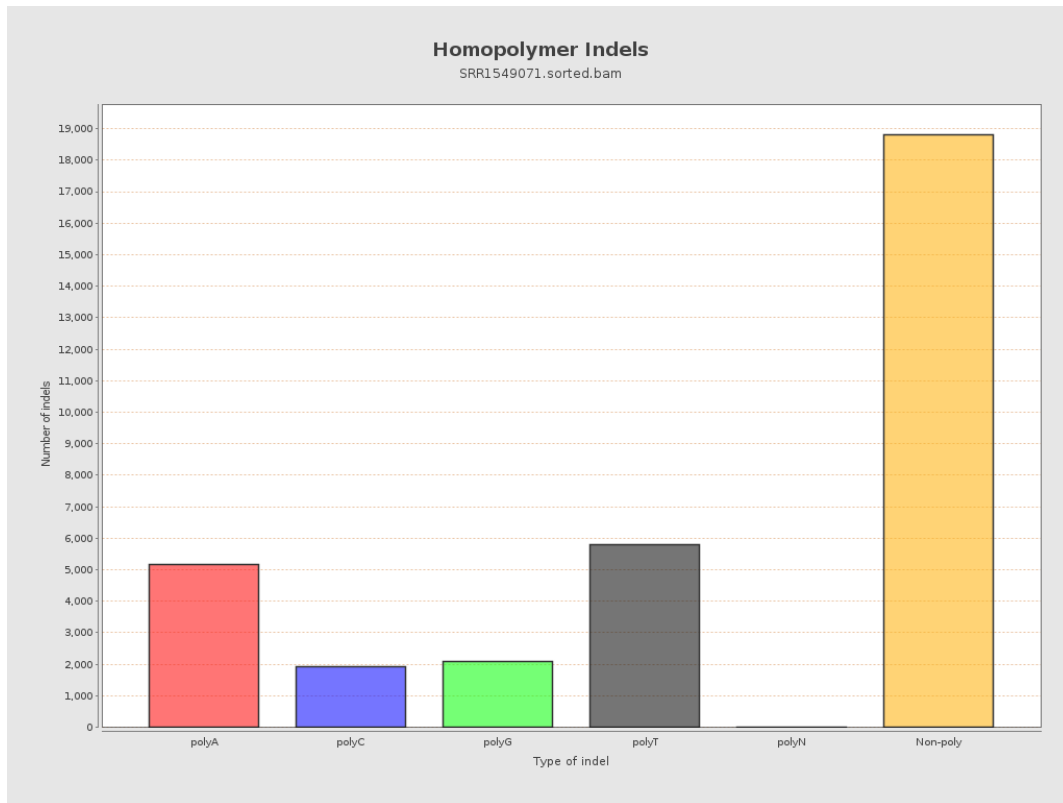
9. Results : Mapped Reads GC-content Distribution



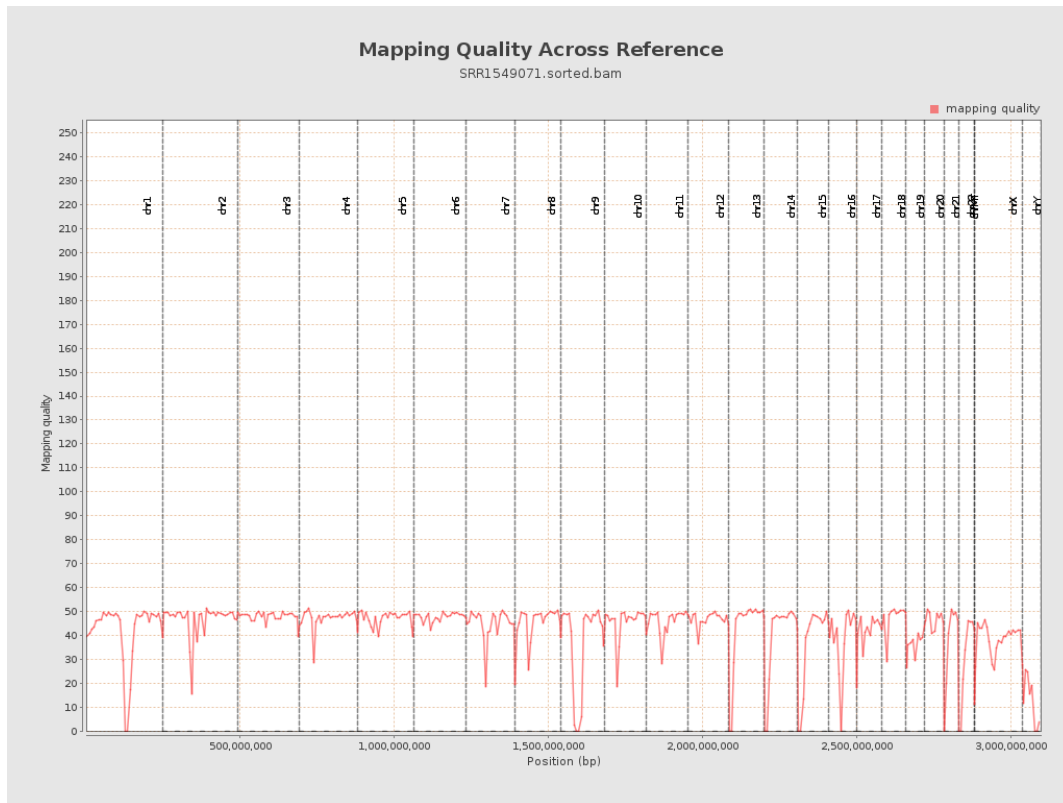
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

