

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:35:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549072.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_SRR1549072 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549072.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:35:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549072.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,492,901
Mapped reads	8,993,696 / 85.71%
Unmapped reads	1,499,205 / 14.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	422,585 / 4.03%
Duplication rate	2.61%
Clipped reads	527,652 / 5.03%

2.2. ACGT Content

Number/percentage of A's	105,087,027 / 29.47%
Number/percentage of C's	72,892,565 / 20.44%
Number/percentage of T's	105,576,730 / 29.61%
Number/percentage of G's	73,046,979 / 20.48%
Number/percentage of N's	6,437 / 0%
GC Percentage	40.92%

2.3. Coverage

Mean	0.1152
Standard Deviation	1.3621

2.4. Mapping Quality

Mean Mapping Quality	41.45
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2.5. Mismatches and indels

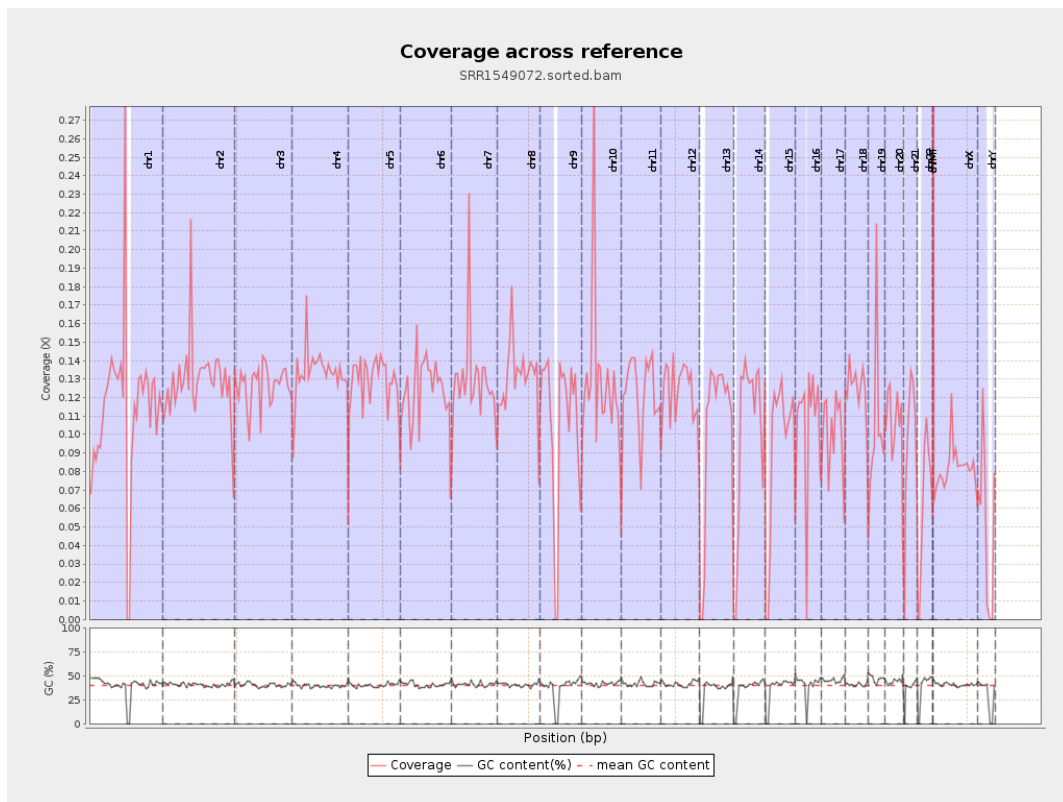
General error rate	0.34%
Mismatches	1,209,620
Insertions	9,985
Mapped reads with at least one insertion	0.11%
Deletions	26,472
Mapped reads with at least one deletion	0.29%
Homopolymer indels	42.7%

2.6. Chromosome stats

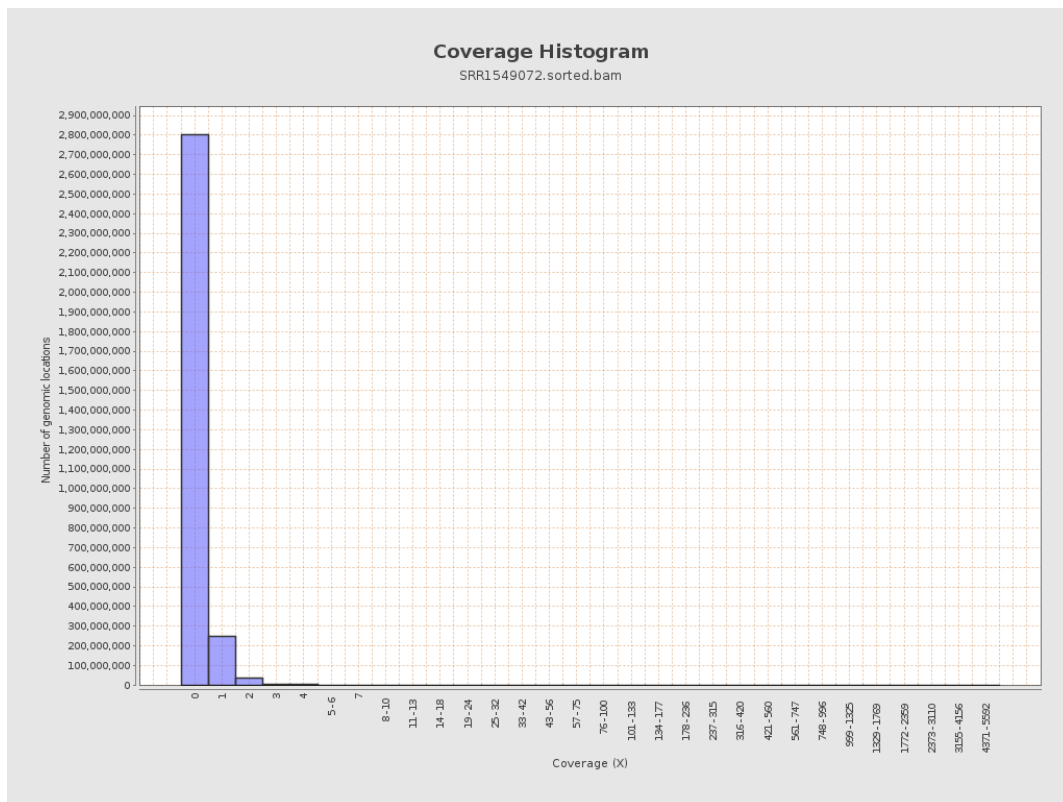
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28485365	0.1143	3.6235
chr2	243199373	31355275	0.1289	0.9163
chr3	198022430	25107570	0.1268	0.4318
chr4	191154276	25548288	0.1337	0.4951
chr5	180915260	23236887	0.1284	0.4513
chr6	171115067	21304252	0.1245	0.5696
chr7	159138663	20488729	0.1287	1.3027
chr8	146364022	19193882	0.1311	1.509

chr9	141213431	15106953	0.107	0.8899
chr10	135534747	17485933	0.129	1.3292
chr11	135006516	16490745	0.1221	0.7894
chr12	133851895	16507702	0.1233	0.4908
chr13	115169878	11855365	0.1029	0.3608
chr14	107349540	10992201	0.1024	0.5131
chr15	102531392	9482330	0.0925	0.3486
chr16	90354753	9293773	0.1029	0.6319
chr17	81195210	8259342	0.1017	0.4714
chr18	78077248	9859379	0.1263	1.9783
chr19	59128983	6220214	0.1052	2.9426
chr20	63025520	6729173	0.1068	0.4286
chr21	48129895	4550928	0.0946	0.5115
chr22	51304566	3280452	0.0639	0.363
chrMT	16571	31144	1.8794	2.2684
chrX	155270560	12660110	0.0815	0.5484
chrY	59373566	3116600	0.0525	0.4704

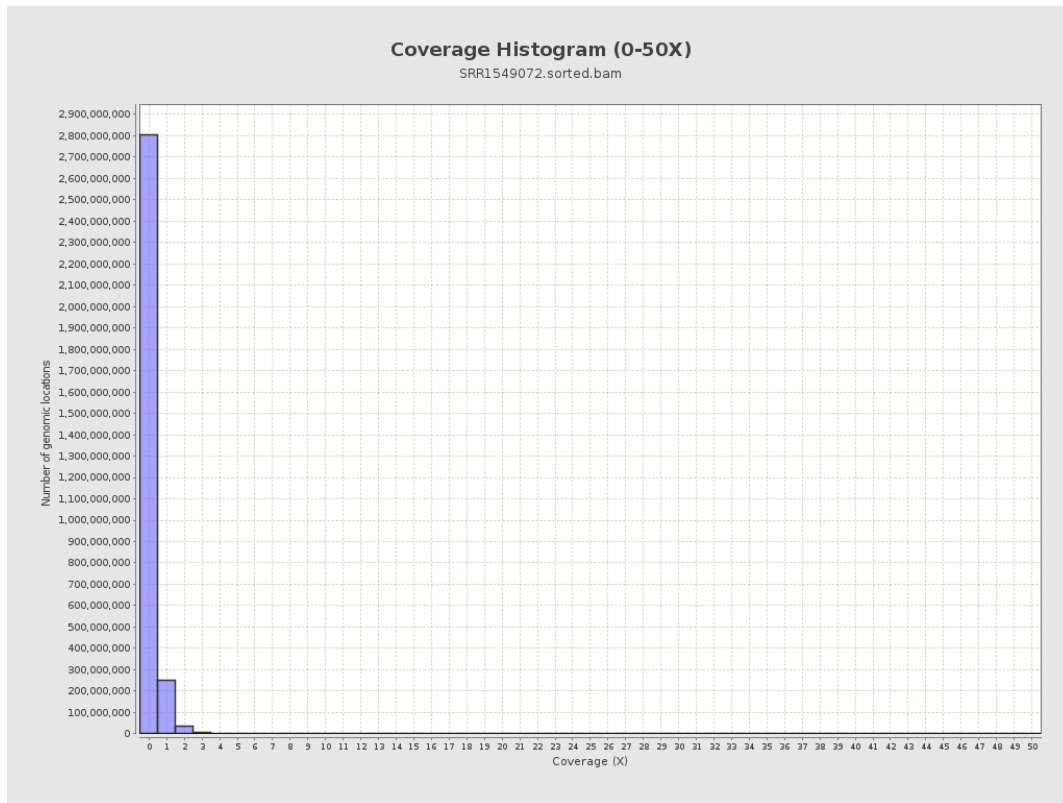
3. Results : Coverage across reference



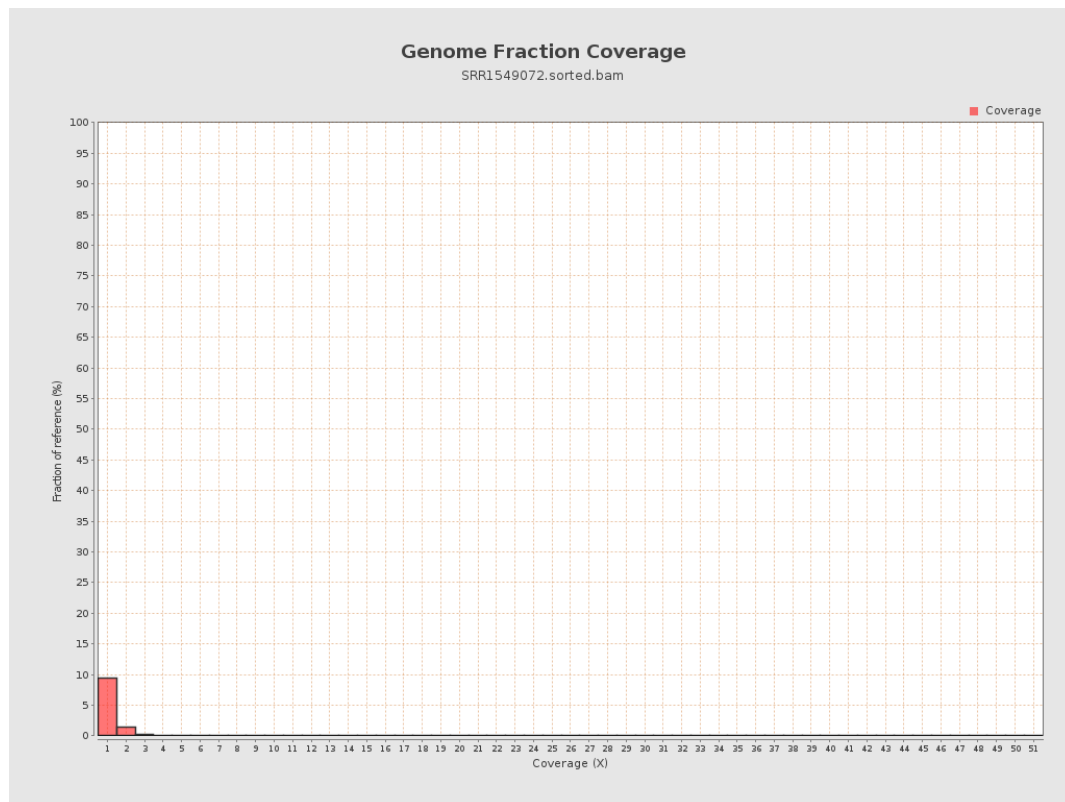
4. Results : Coverage Histogram



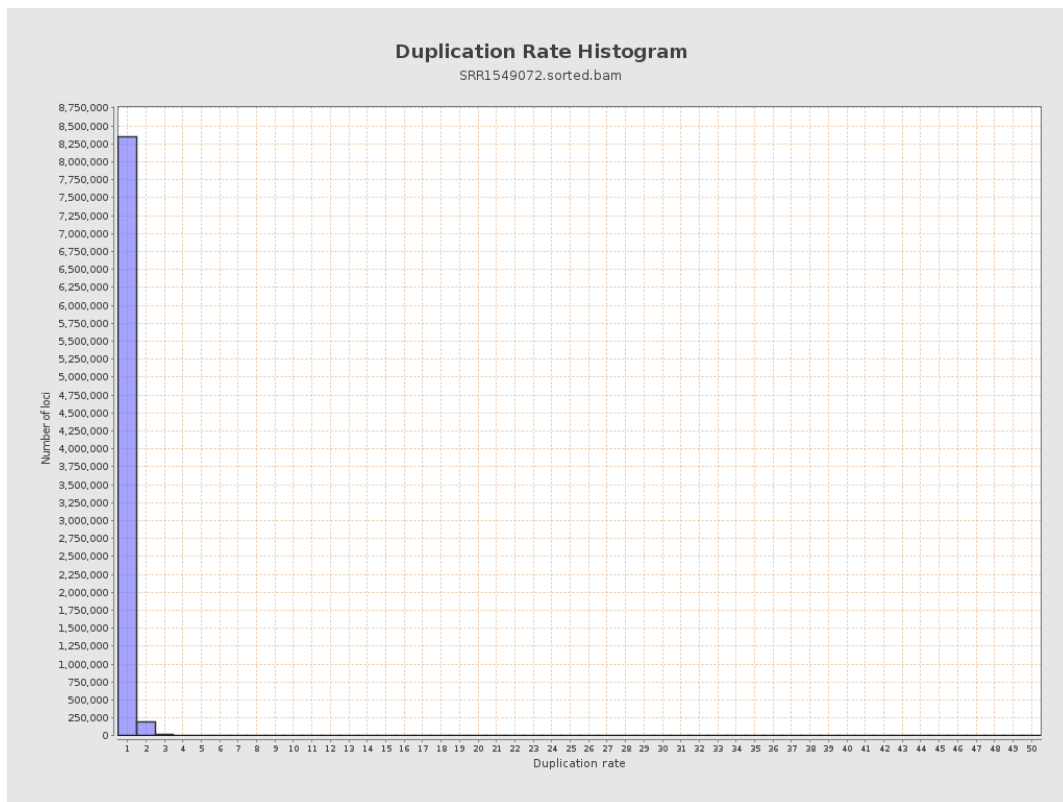
5. Results : Coverage Histogram (0-50X)



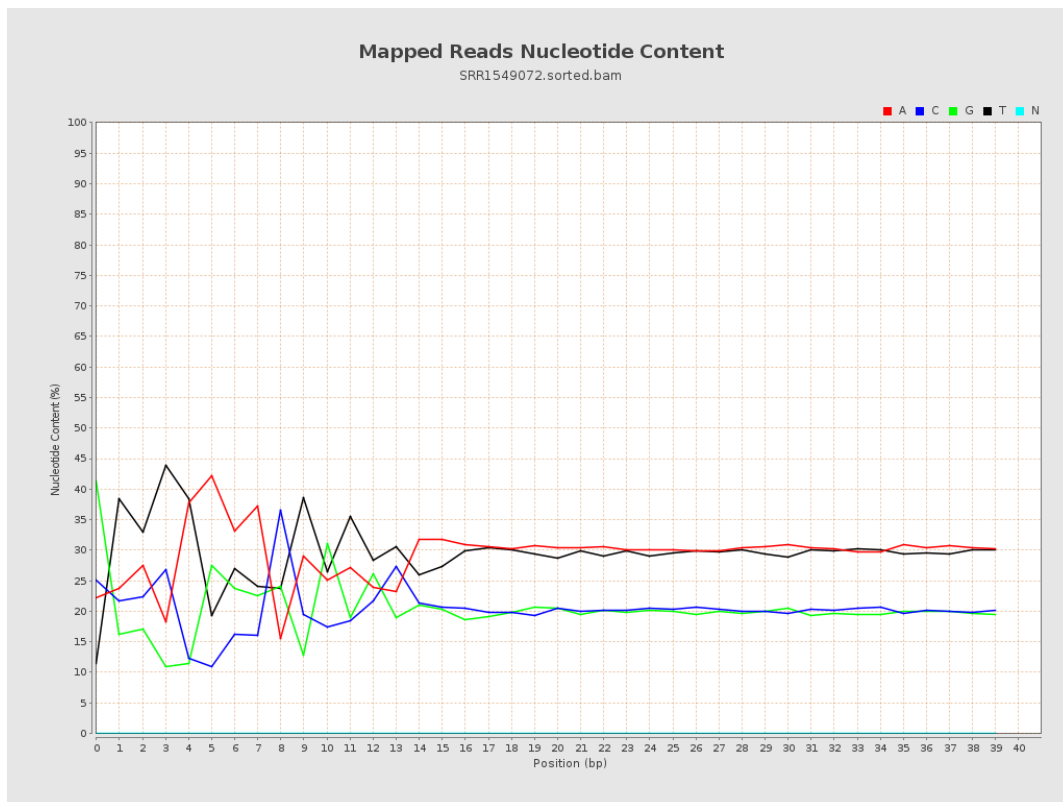
6. Results : Genome Fraction Coverage



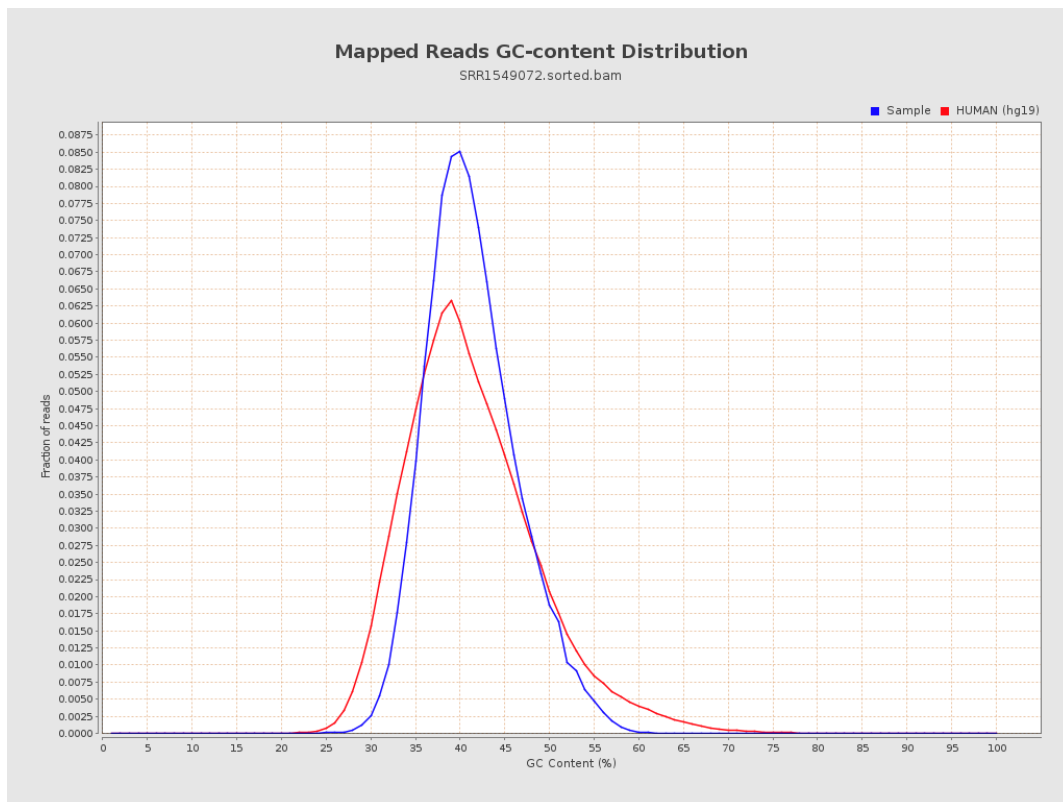
7. Results : Duplication Rate Histogram



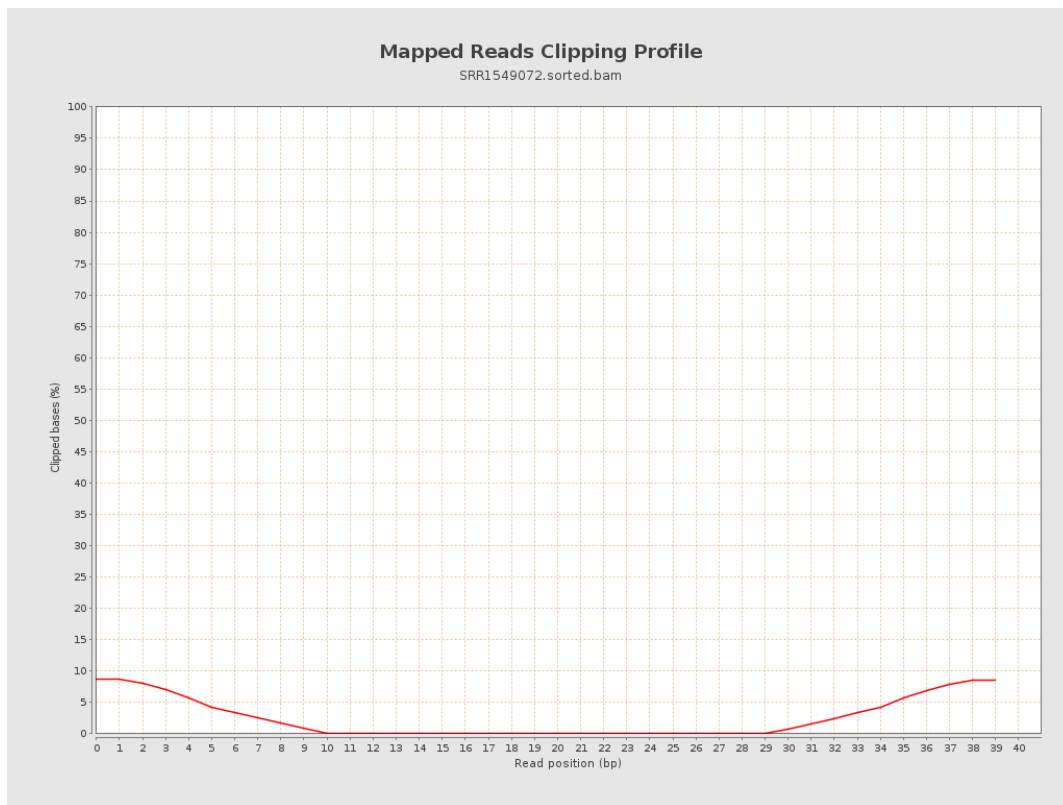
8. Results : Mapped Reads Nucleotide Content



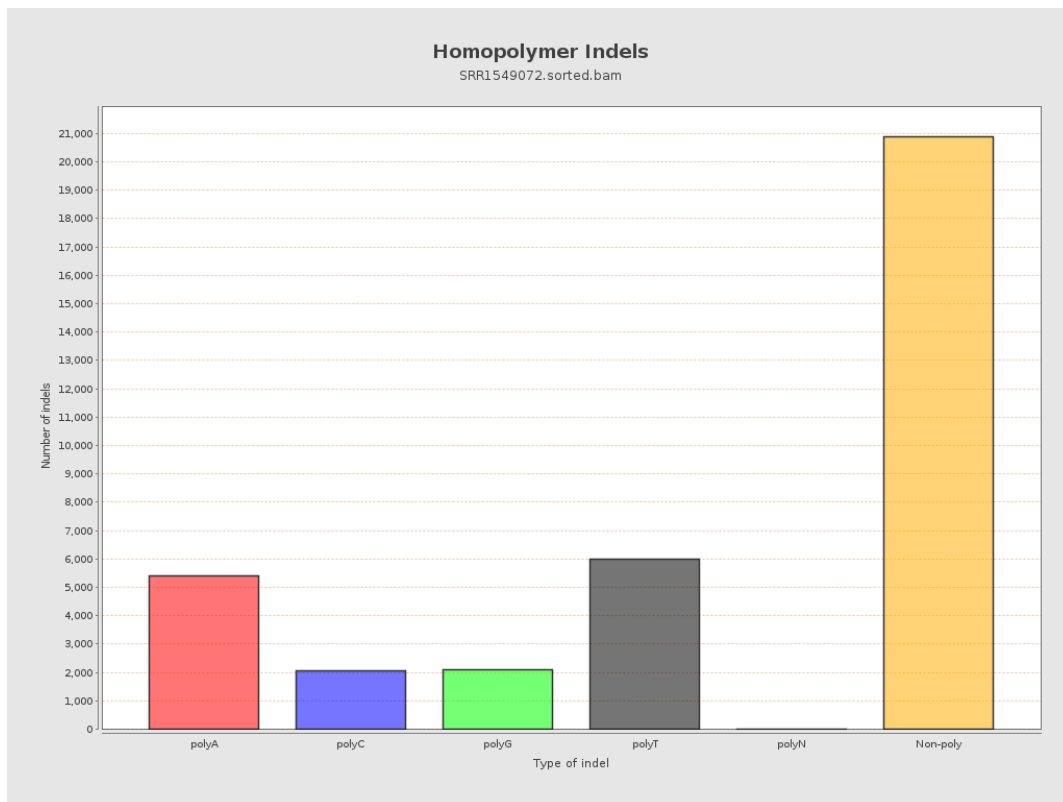
9. Results : Mapped Reads GC-content Distribution



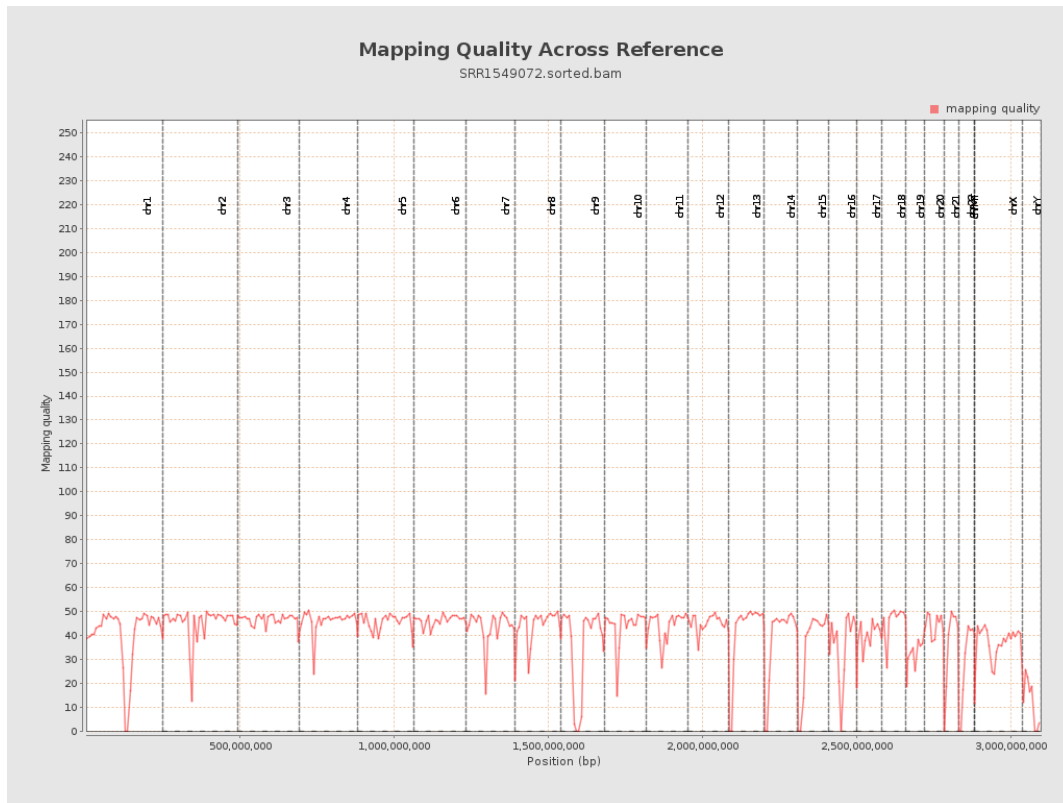
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

