

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:09:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549001.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_SRR1549001 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549001.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:09:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549001.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,821,846
Mapped reads	8,511,747 / 86.66%
Unmapped reads	1,310,099 / 13.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	755,190 / 7.69%
Duplication rate	8.23%
Clipped reads	421,417 / 4.29%

2.2. ACGT Content

Number/percentage of A's	101,731,586 / 30.1%
Number/percentage of C's	66,738,648 / 19.75%
Number/percentage of T's	101,957,298 / 30.17%
Number/percentage of G's	67,510,257 / 19.98%
Number/percentage of N's	3,405 / 0%
GC Percentage	39.73%

2.3. Coverage

Mean	0.1092
Standard Deviation	0.8588

2.4. Mapping Quality

Mean Mapping Quality	44.52
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2.5. Mismatches and indels

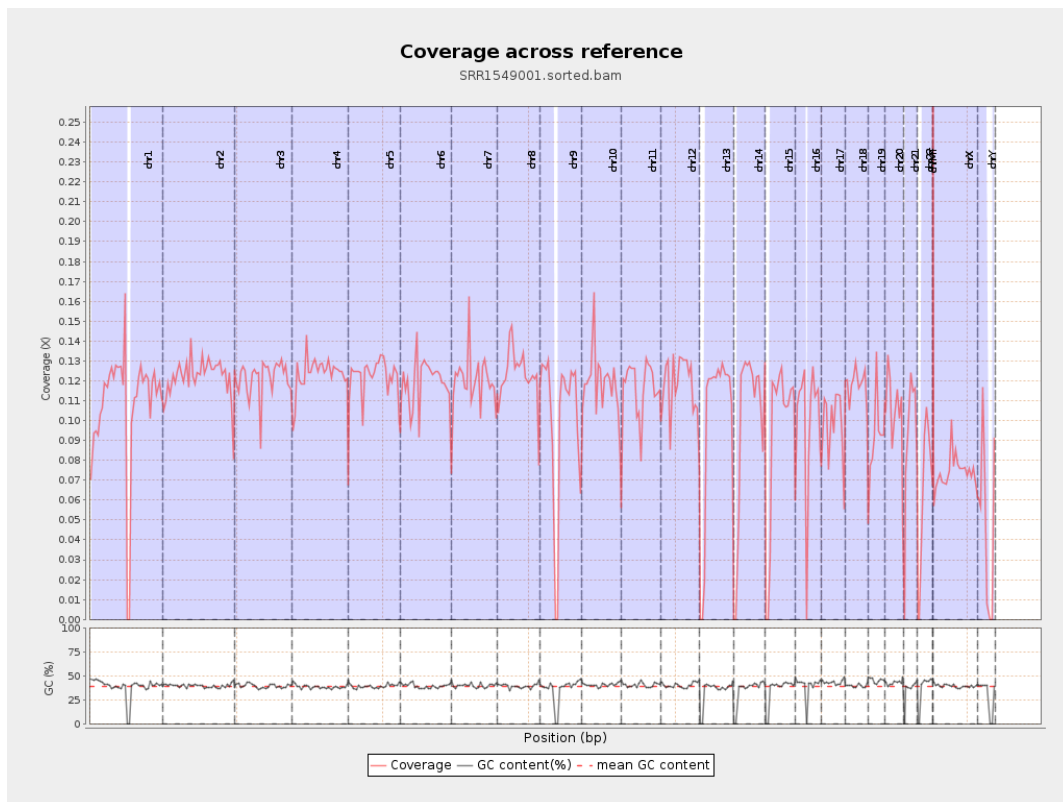
General error rate	0.29%
Mismatches	966,658
Insertions	10,439
Mapped reads with at least one insertion	0.12%
Deletions	28,940
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.75%

2.6. Chromosome stats

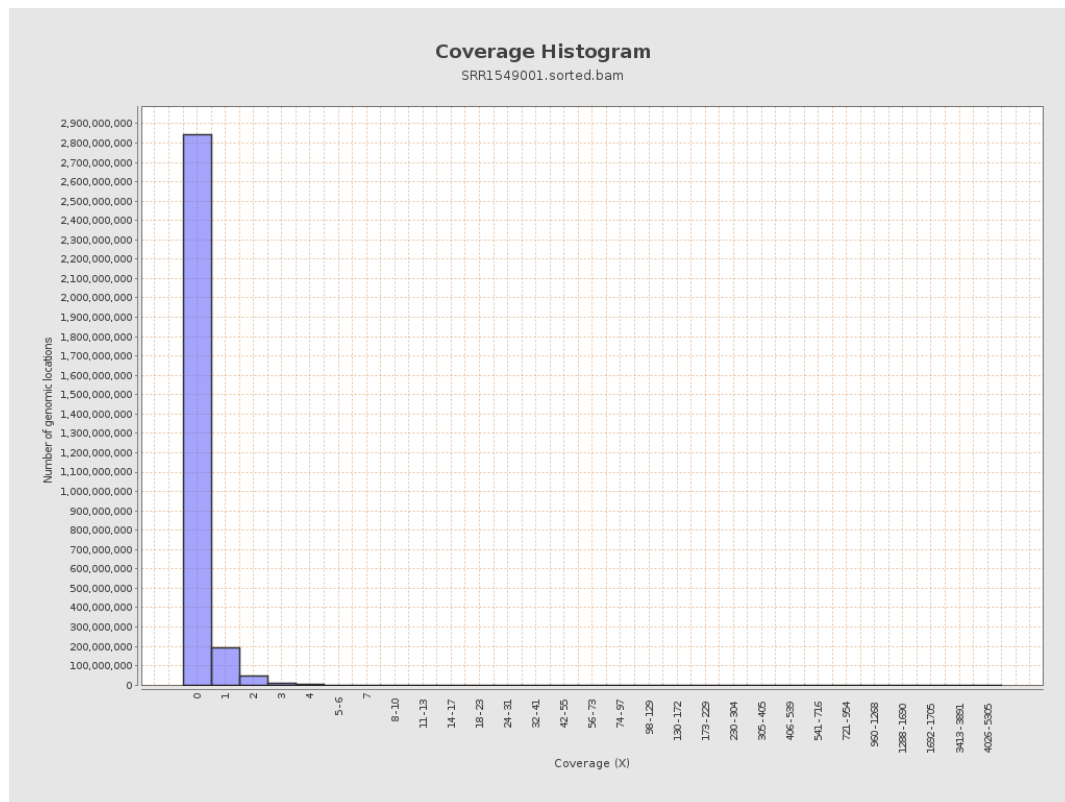
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	26932857	0.1081	1.3191
chr2	243199373	29711289	0.1222	0.5785
chr3	198022430	24048437	0.1214	0.4397
chr4	191154276	23660407	0.1238	0.4778
chr5	180915260	22005936	0.1216	0.4476
chr6	171115067	20467065	0.1196	0.5137
chr7	159138663	19018851	0.1195	0.8747
chr8	146364022	18000084	0.123	2.6282

chr9	141213431	14293005	0.1012	0.5387
chr10	135534747	16108735	0.1189	0.645
chr11	135006516	15660166	0.116	0.5483
chr12	133851895	15814332	0.1181	0.452
chr13	115169878	11550994	0.1003	0.3967
chr14	107349540	10650382	0.0992	0.487
chr15	102531392	9514435	0.0928	0.3804
chr16	90354753	8831199	0.0977	0.4296
chr17	81195210	8052080	0.0992	0.4358
chr18	78077248	9242840	0.1184	1.0551
chr19	59128983	5512095	0.0932	0.9665
chr20	63025520	6704736	0.1064	0.4377
chr21	48129895	4408159	0.0916	0.4624
chr22	51304566	3330279	0.0649	0.3539
chrMT	16571	6345	0.3829	0.765
chrX	155270560	11479468	0.0739	0.4323
chrY	59373566	2974477	0.0501	0.5109

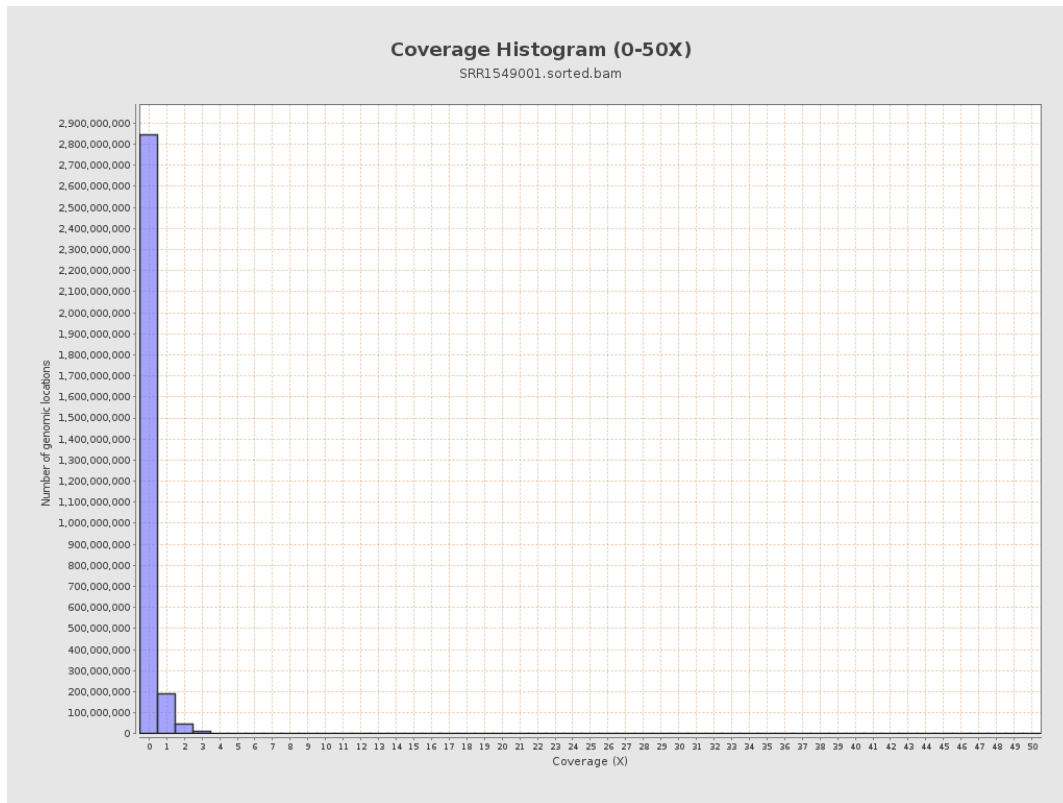
3. Results : Coverage across reference



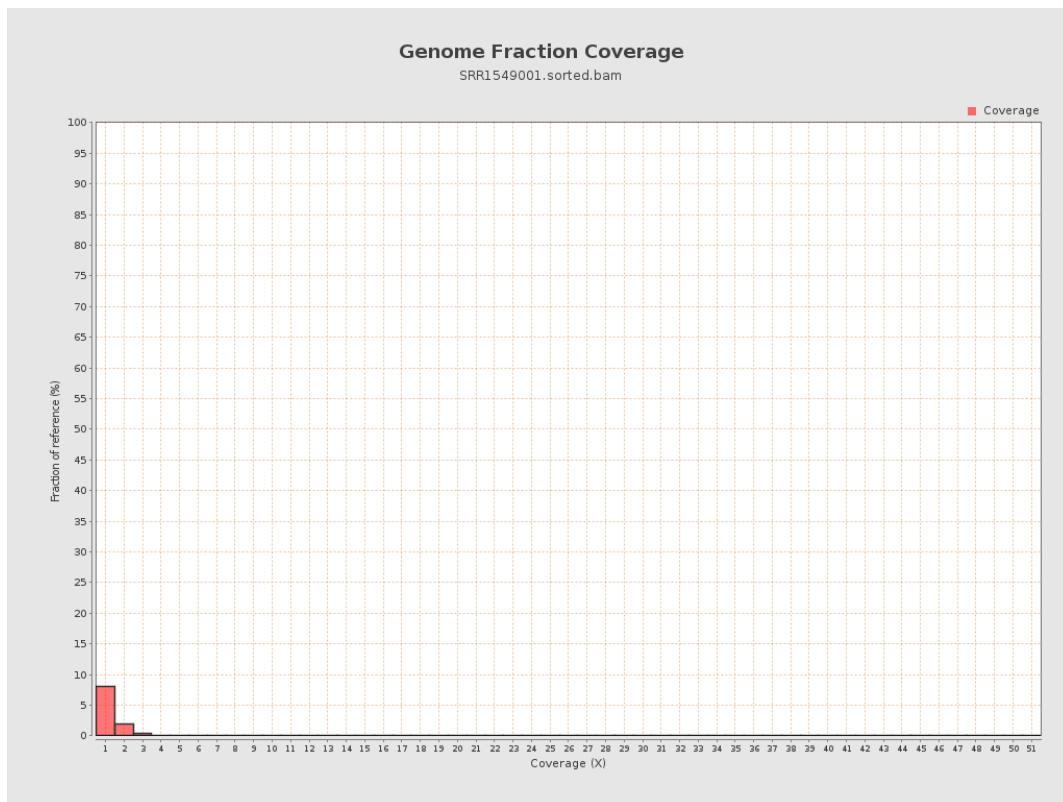
4. Results : Coverage Histogram



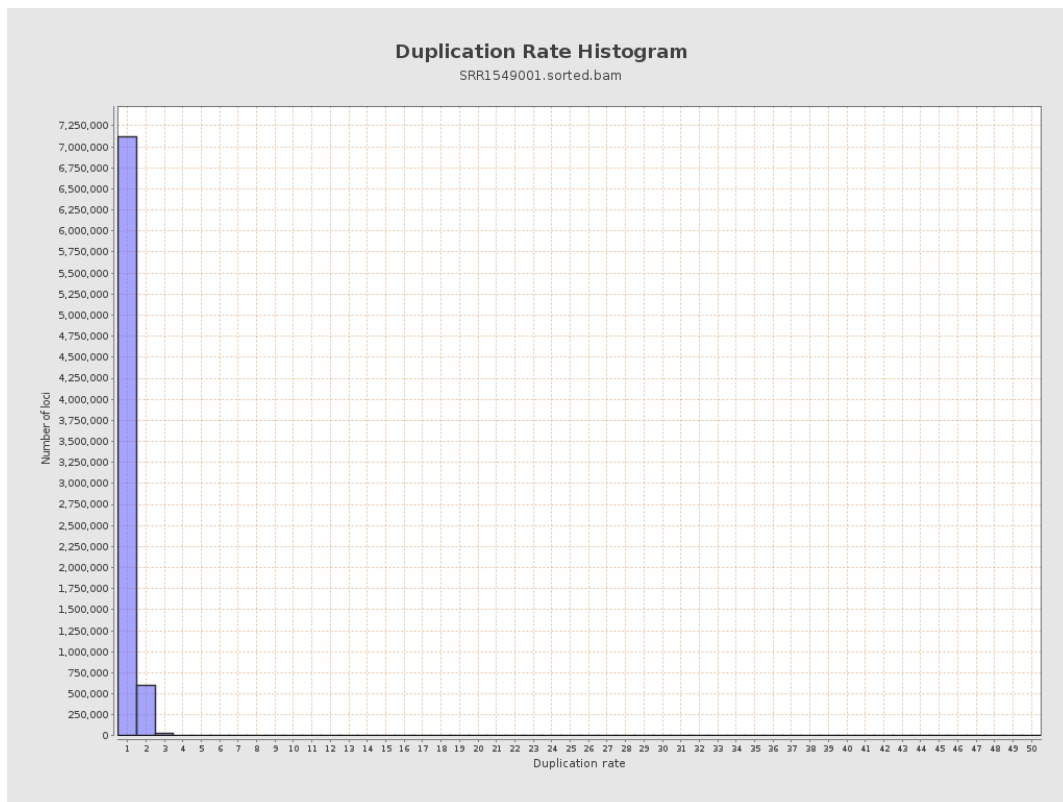
5. Results : Coverage Histogram (0-50X)



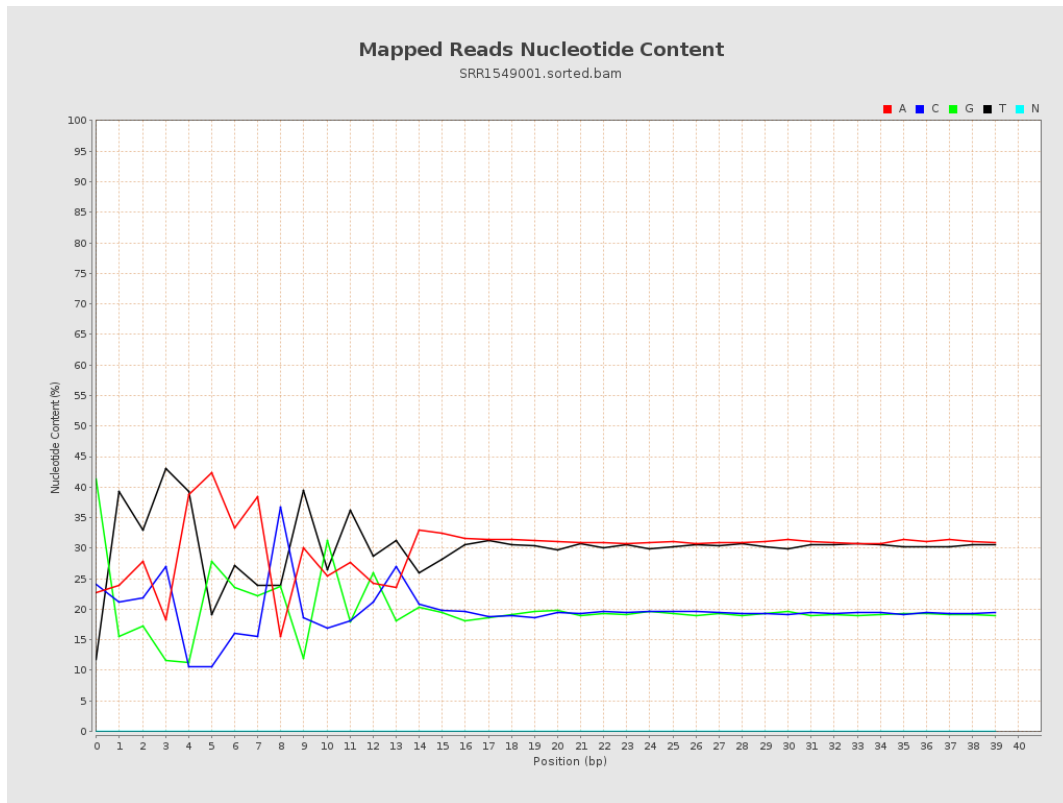
6. Results : Genome Fraction Coverage



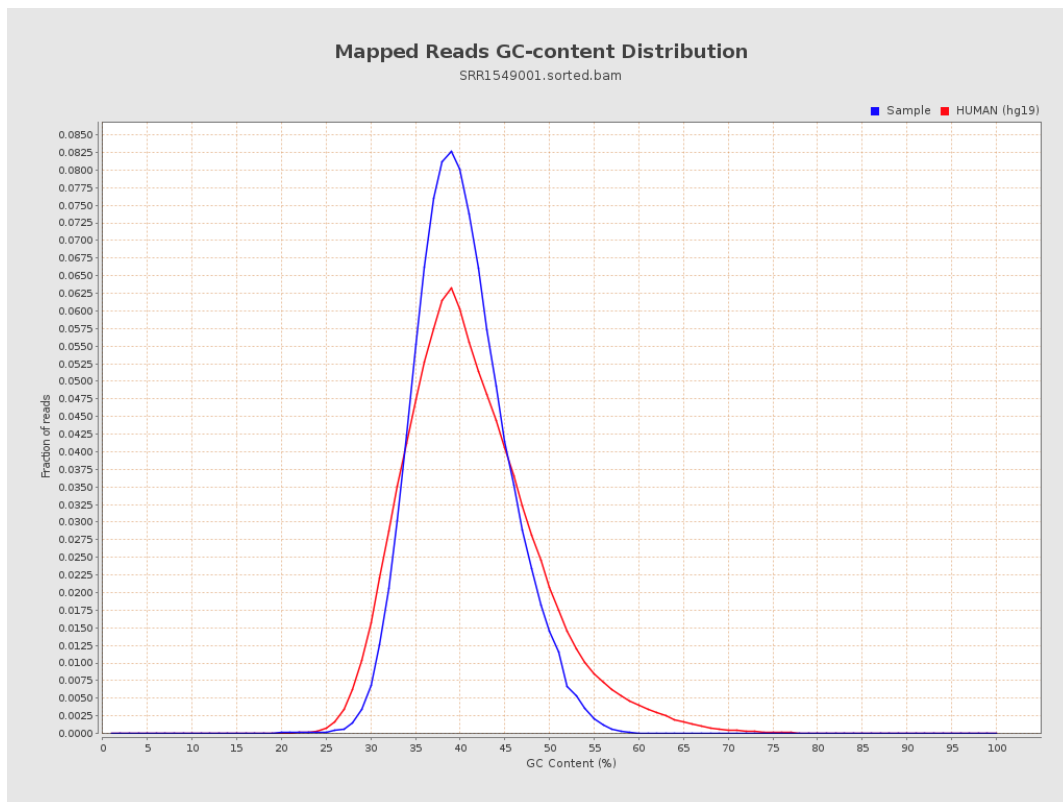
7. Results : Duplication Rate Histogram



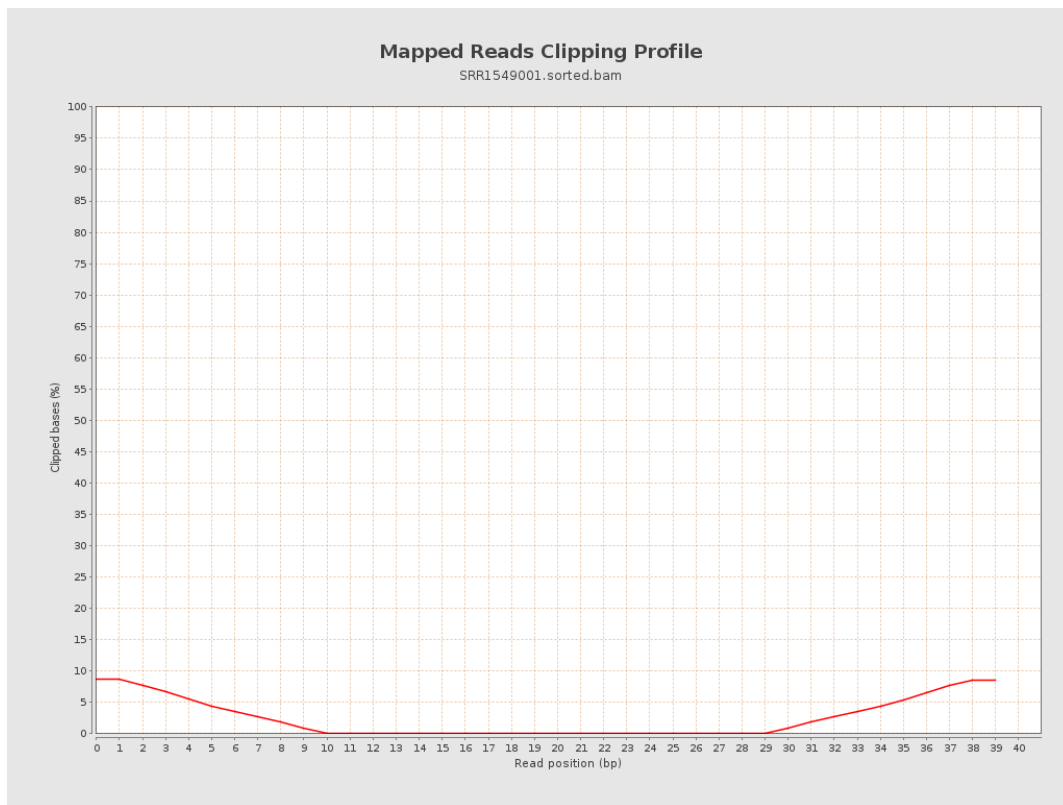
8. Results : Mapped Reads Nucleotide Content



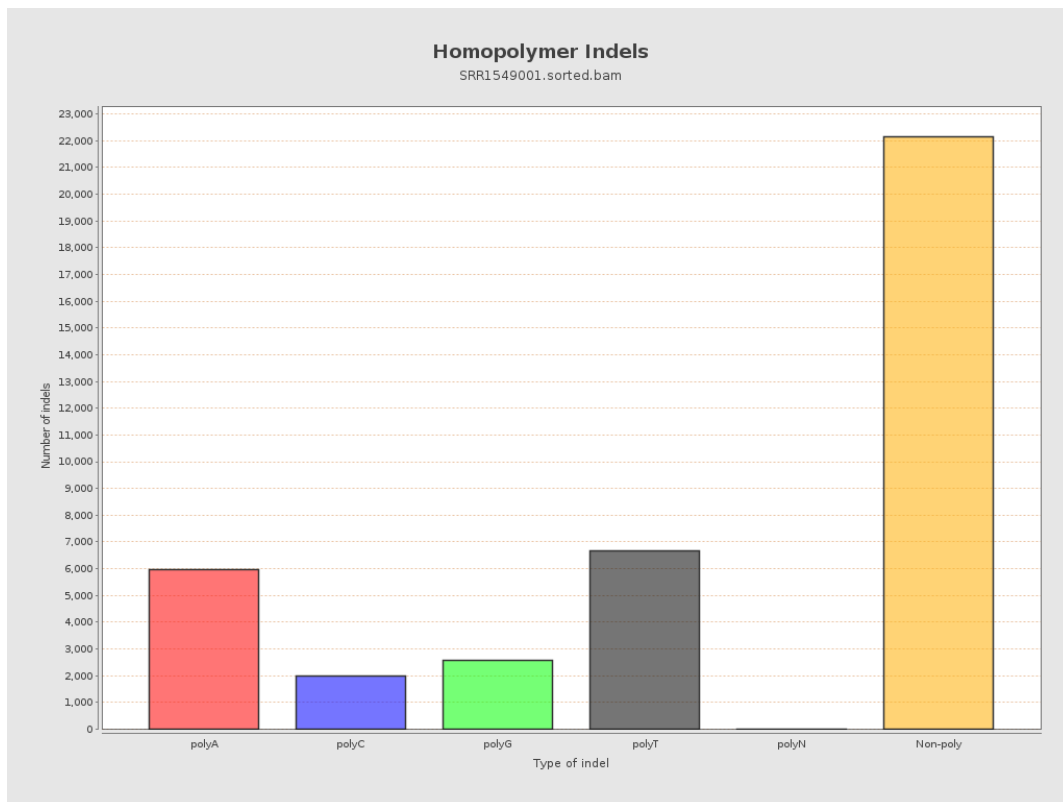
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

