

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:54:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549156.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_SRR1549156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:54:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	12,826,774
Mapped reads	10,910,398 / 85.06%
Unmapped reads	1,916,376 / 14.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	942,784 / 7.35%
Duplication rate	7.05%
Clipped reads	682,723 / 5.32%

2.2. ACGT Content

Number/percentage of A's	125,674,370 / 29.07%
Number/percentage of C's	88,825,033 / 20.55%
Number/percentage of T's	127,975,867 / 29.61%
Number/percentage of G's	89,691,748 / 20.75%
Number/percentage of N's	86,343 / 0.02%
GC Percentage	41.3%

2.3. Coverage

Mean	0.1396
Standard Deviation	1.236

2.4. Mapping Quality

Mean Mapping Quality	42.73
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2.5. Mismatches and indels

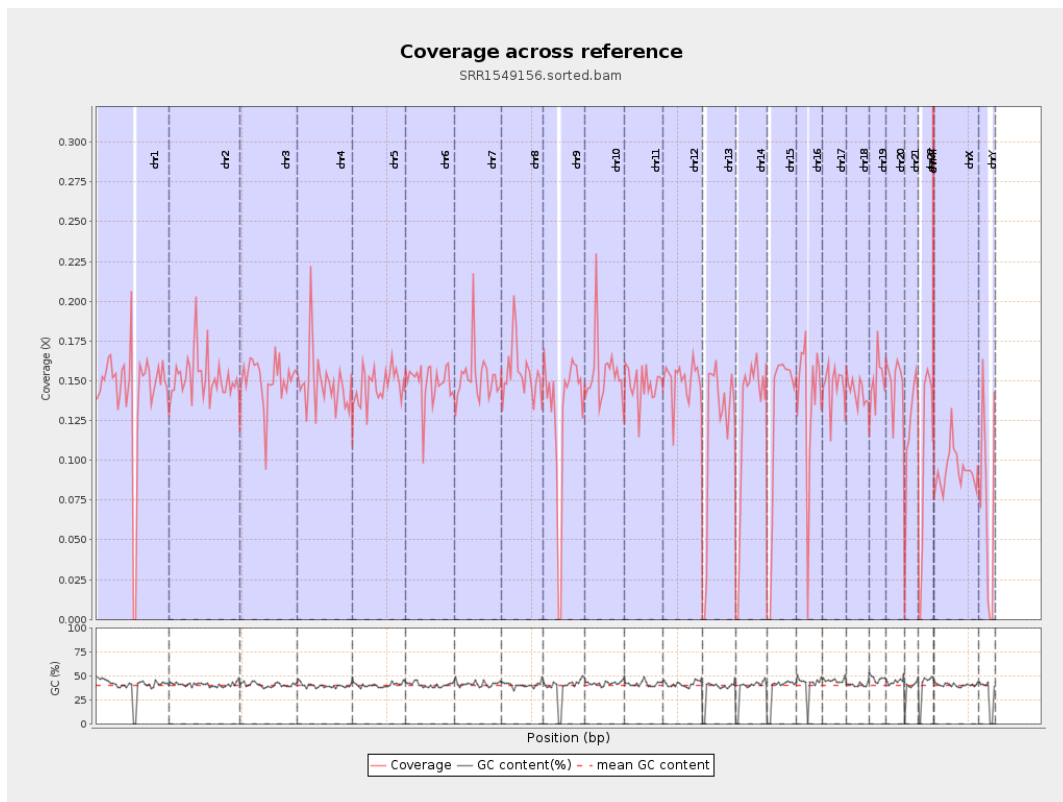
General error rate	0.33%
Mismatches	1,405,488
Insertions	11,555
Mapped reads with at least one insertion	0.11%
Deletions	35,211
Mapped reads with at least one deletion	0.32%
Homopolymer indels	45.21%

2.6. Chromosome stats

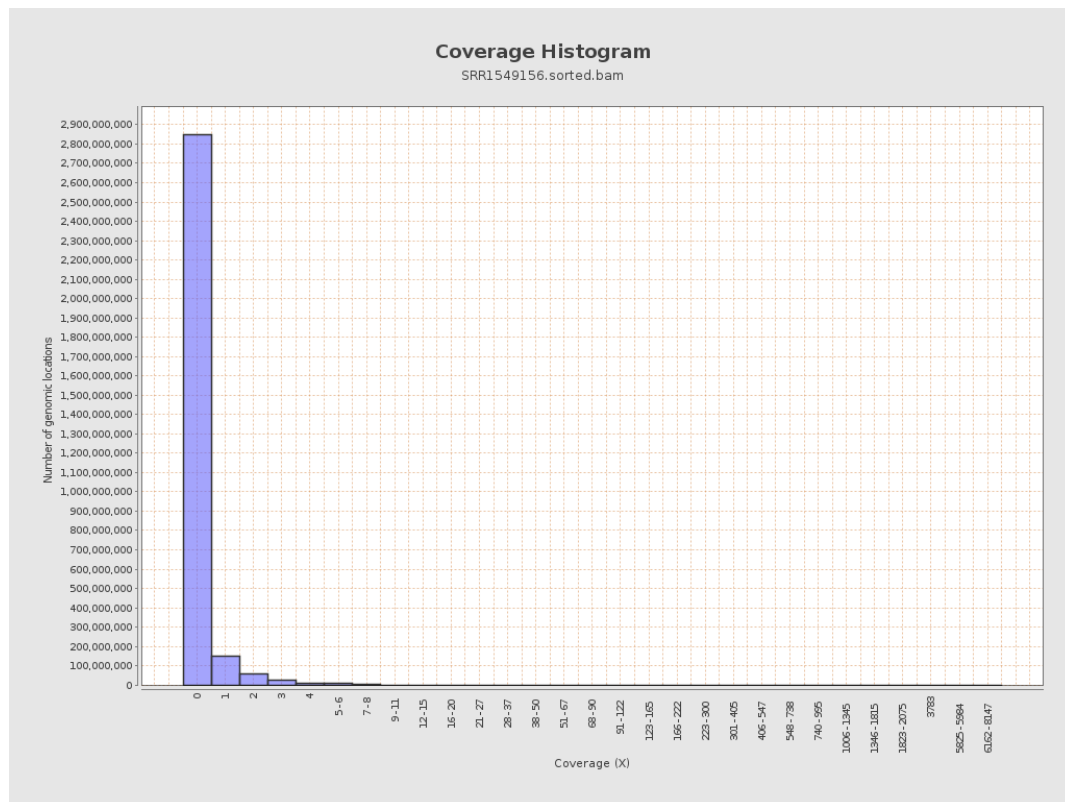
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	35565794	0.1427	1.5822
chr2	243199373	37002413	0.1521	0.8825
chr3	198022430	29775198	0.1504	0.6147
chr4	191154276	28165900	0.1473	0.7349
chr5	180915260	26573369	0.1469	0.6277
chr6	171115067	25404661	0.1485	0.644
chr7	159138663	24254134	0.1524	1.1848
chr8	146364022	22538250	0.154	4.0371

chr9	141213431	18253898	0.1293	0.754
chr10	135534747	20915028	0.1543	1
chr11	135006516	19891487	0.1473	0.8088
chr12	133851895	20100006	0.1502	0.6282
chr13	115169878	13681192	0.1188	0.5598
chr14	107349540	13387177	0.1247	0.6874
chr15	102531392	12949881	0.1263	0.551
chr16	90354753	12512864	0.1385	0.6425
chr17	81195210	11870236	0.1462	0.6549
chr18	78077248	11218924	0.1437	1.4696
chr19	59128983	8914016	0.1508	1.2744
chr20	63025520	9350027	0.1484	0.6618
chr21	48129895	5728623	0.119	0.6995
chr22	51304566	5244289	0.1022	0.5137
chrMT	16571	368882	22.2607	26.1821
chrX	155270560	14519442	0.0935	0.5724
chrY	59373566	4112200	0.0693	0.8078

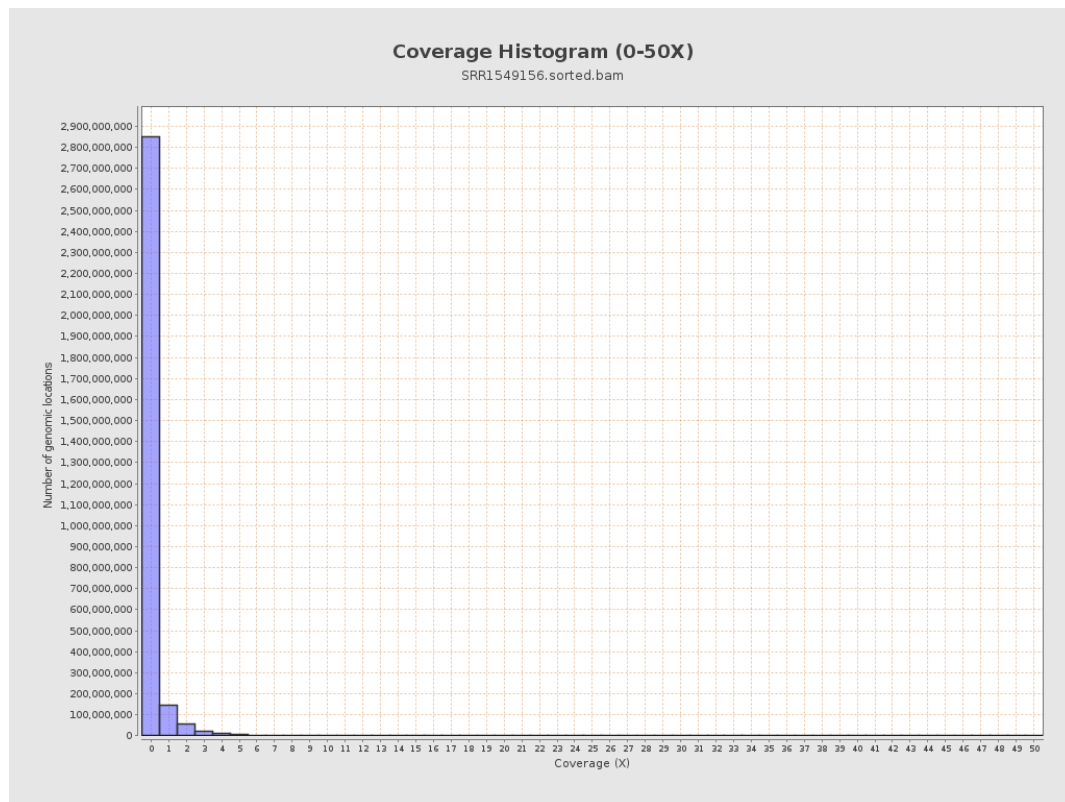
3. Results : Coverage across reference



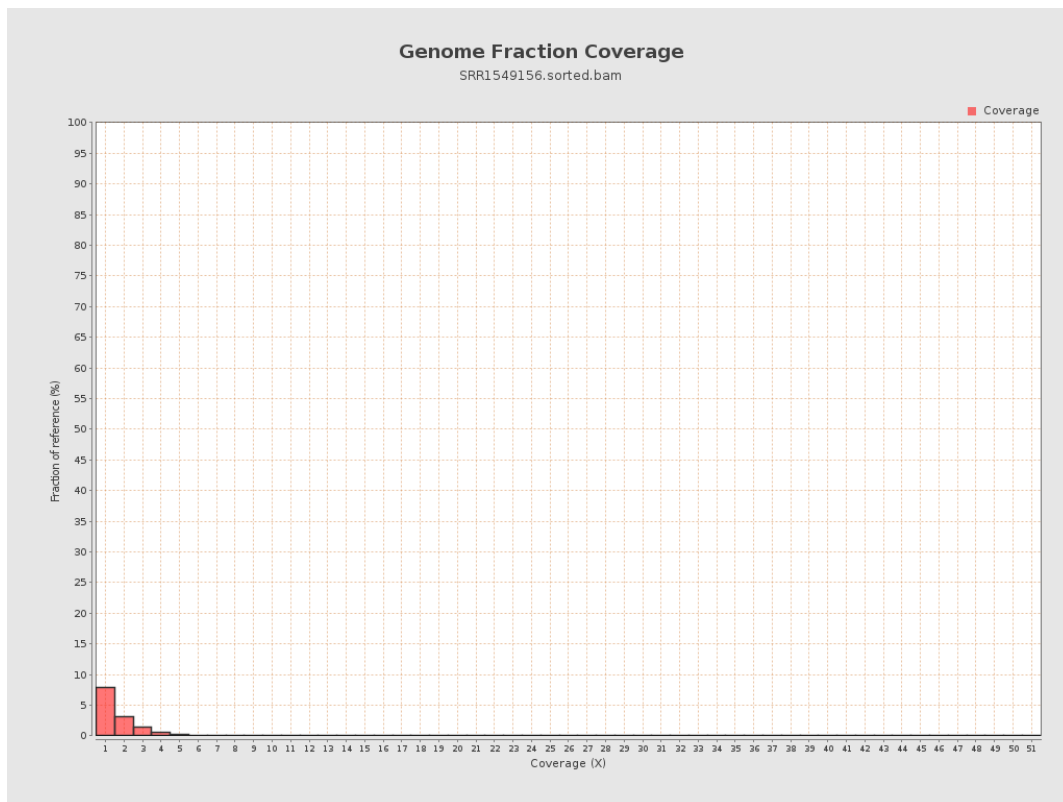
4. Results : Coverage Histogram



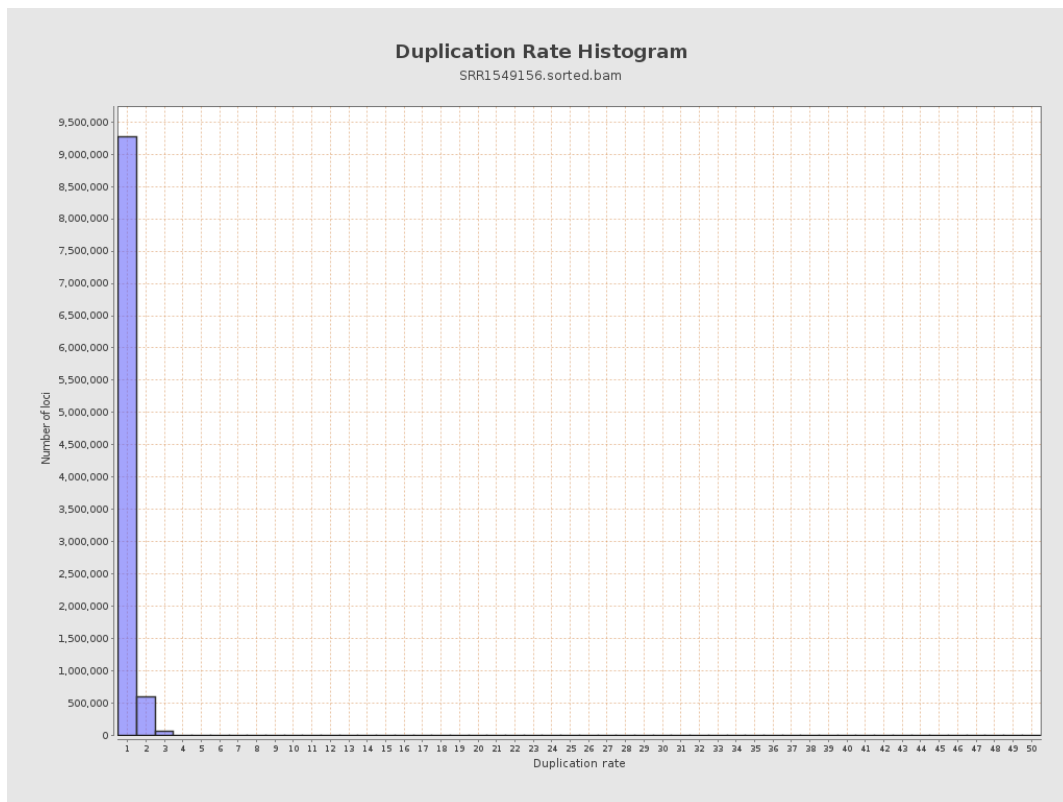
5. Results : Coverage Histogram (0-50X)



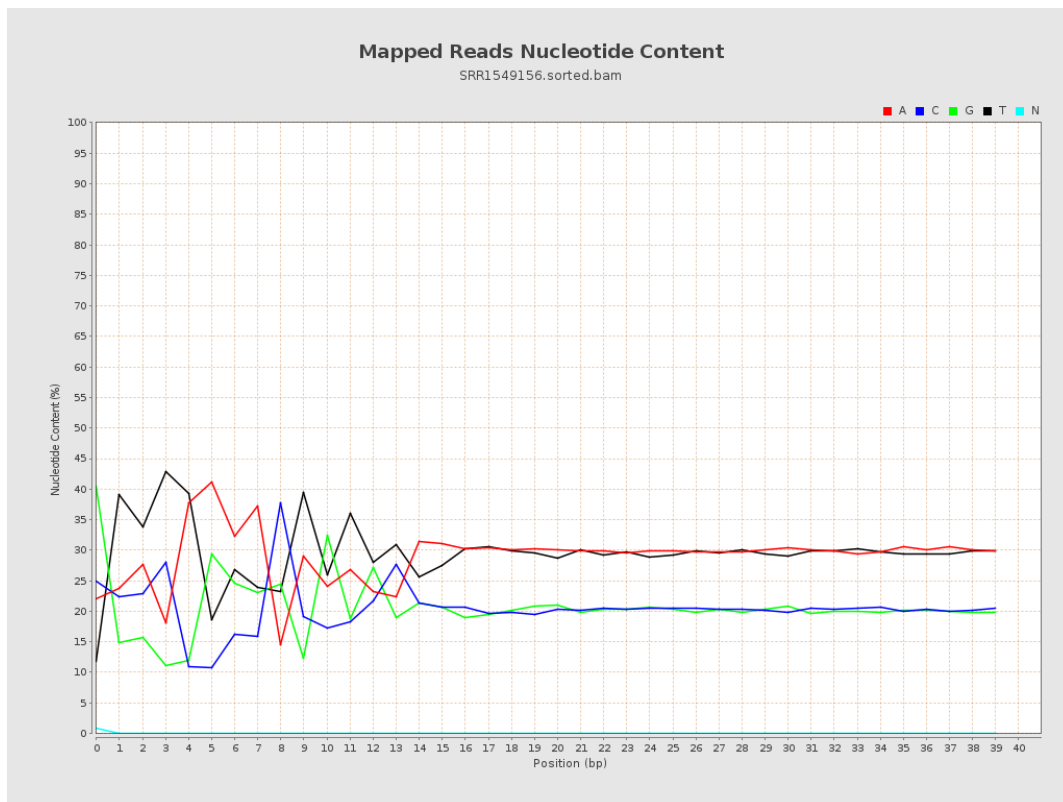
6. Results : Genome Fraction Coverage



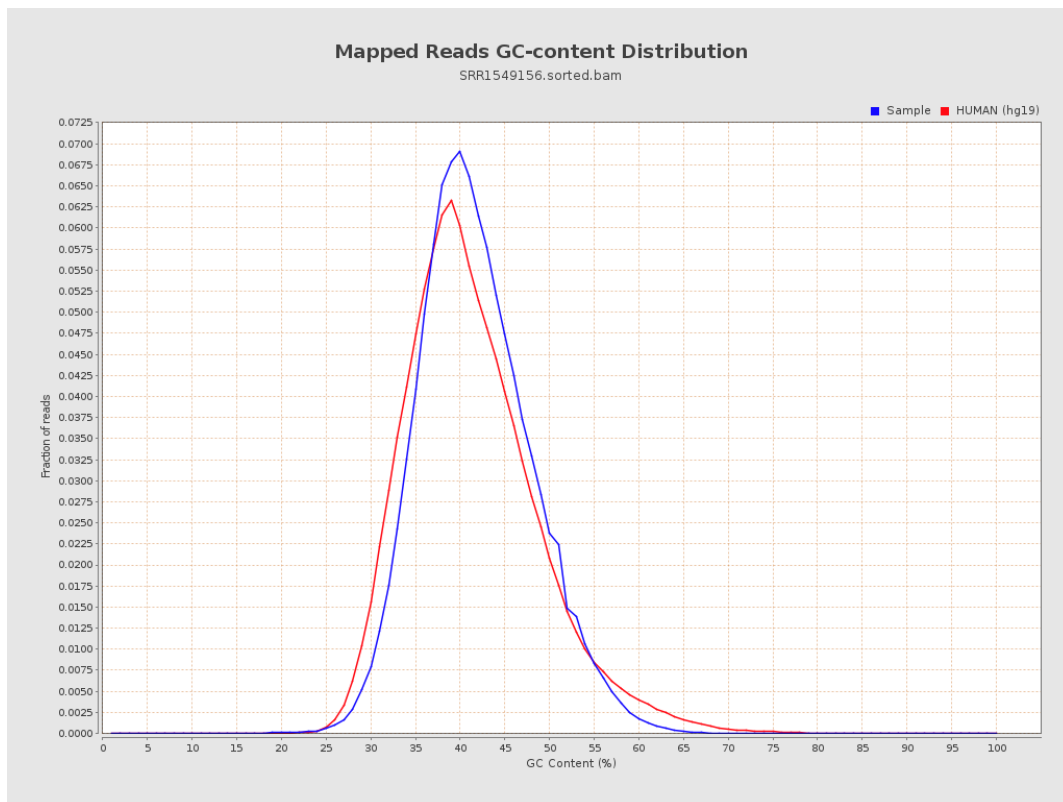
7. Results : Duplication Rate Histogram



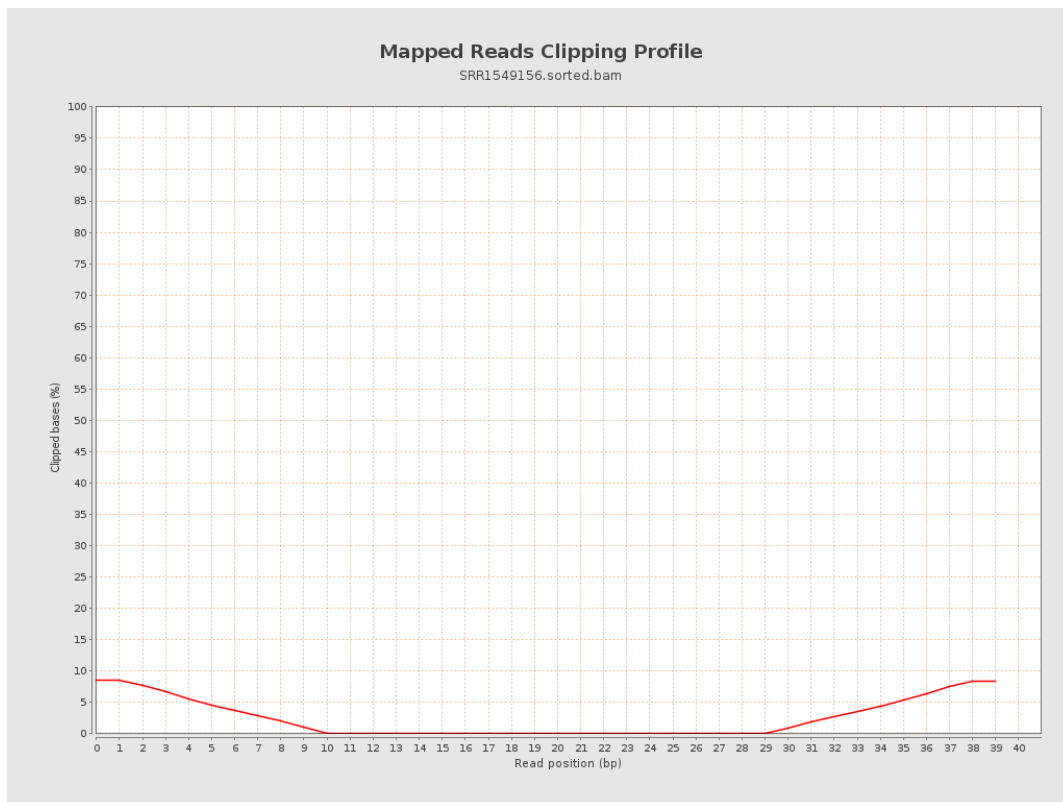
8. Results : Mapped Reads Nucleotide Content



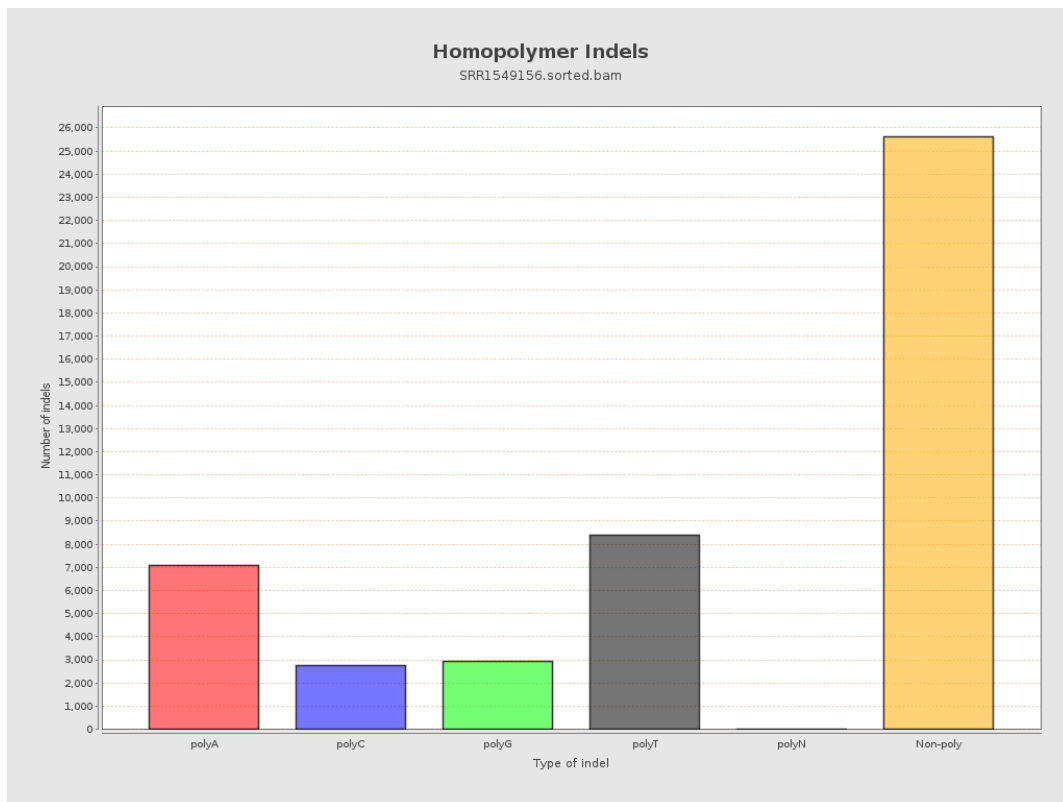
9. Results : Mapped Reads GC-content Distribution



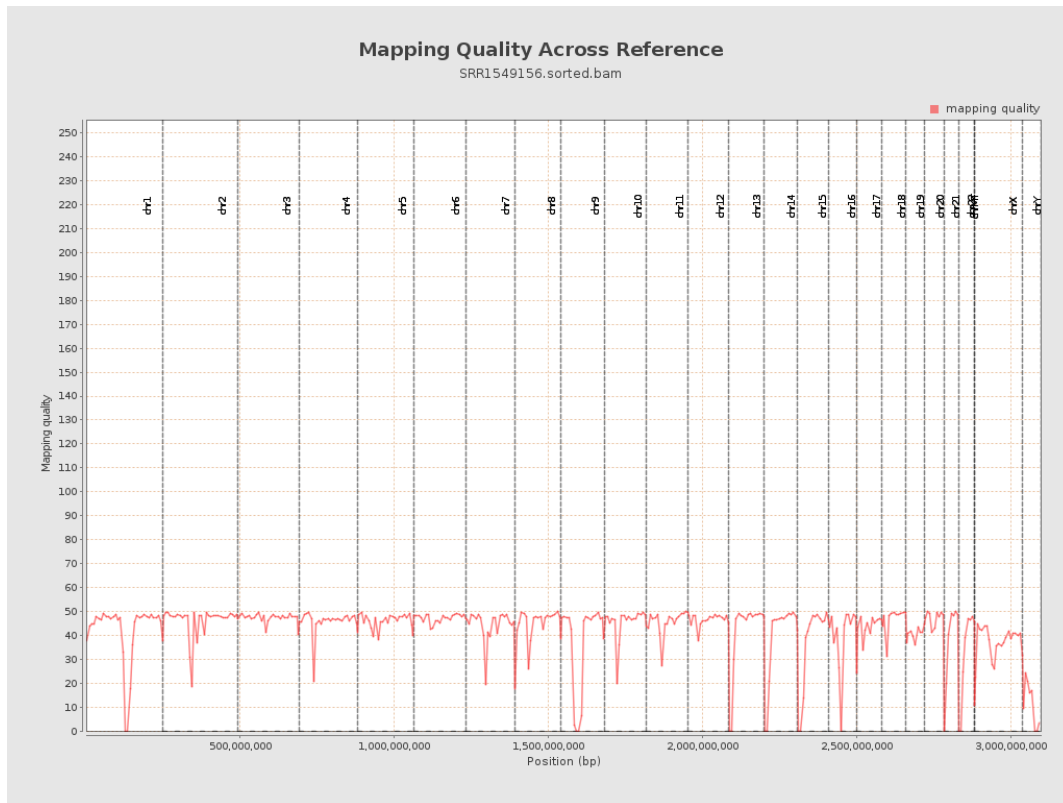
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

