Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 12:05:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549157.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_SRR1549157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 12:05:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,267,025
Mapped reads	12,523,153 / 87.78%
Unmapped reads	1,743,872 / 12.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	767,541 / 5.38%
Duplication rate	5.09%
Clipped reads	643,899 / 4.51%

2.2. ACGT Content

Number/percentage of A's	143,608,775 / 28.89%
Number/percentage of C's	103,982,546 / 20.92%
Number/percentage of T's	145,495,353 / 29.27%
Number/percentage of G's	103,889,601 / 20.9%
Number/percentage of N's	100,481 / 0.02%
GC Percentage	41.82%

2.3. Coverage

Mean	0.1606
Standard Deviation	0.8835

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Mismatches and indels

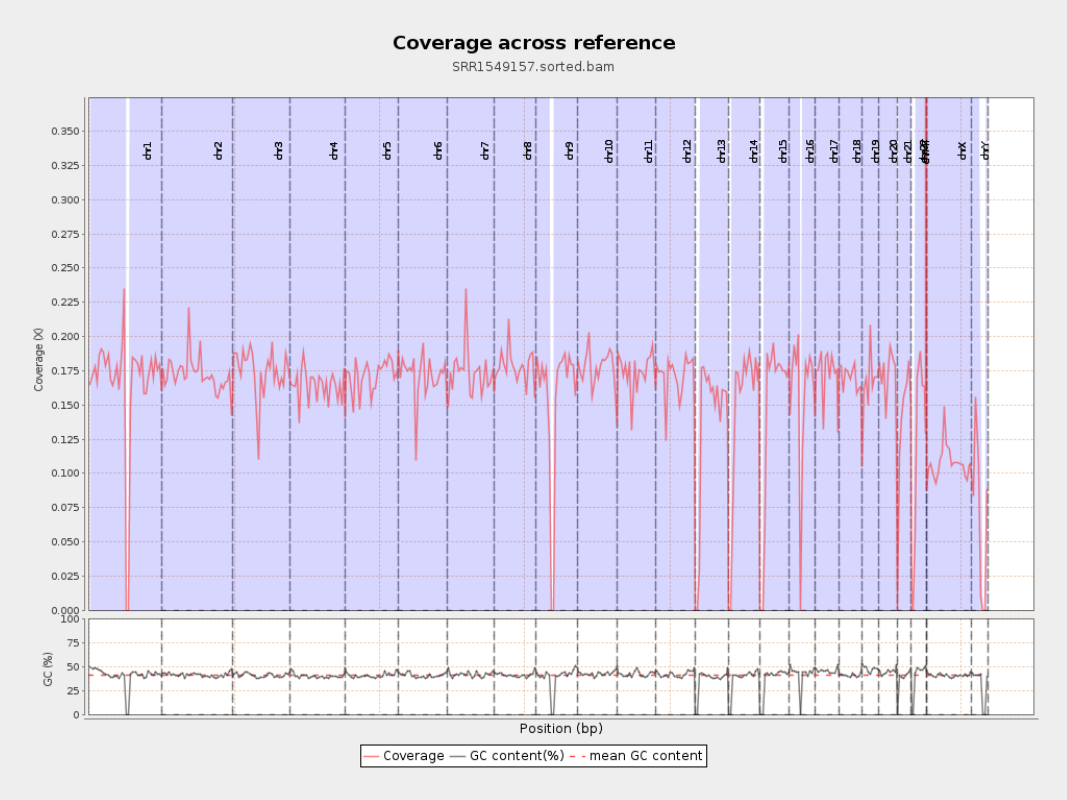
General error rate	0.31%
Mismatches	1,516,392
Insertions	12,268
Mapped reads with at least one insertion	0.1%
Deletions	37,102
Mapped reads with at least one deletion	0.3%
Homopolymer indels	45.47%

2.6. Chromosome stats

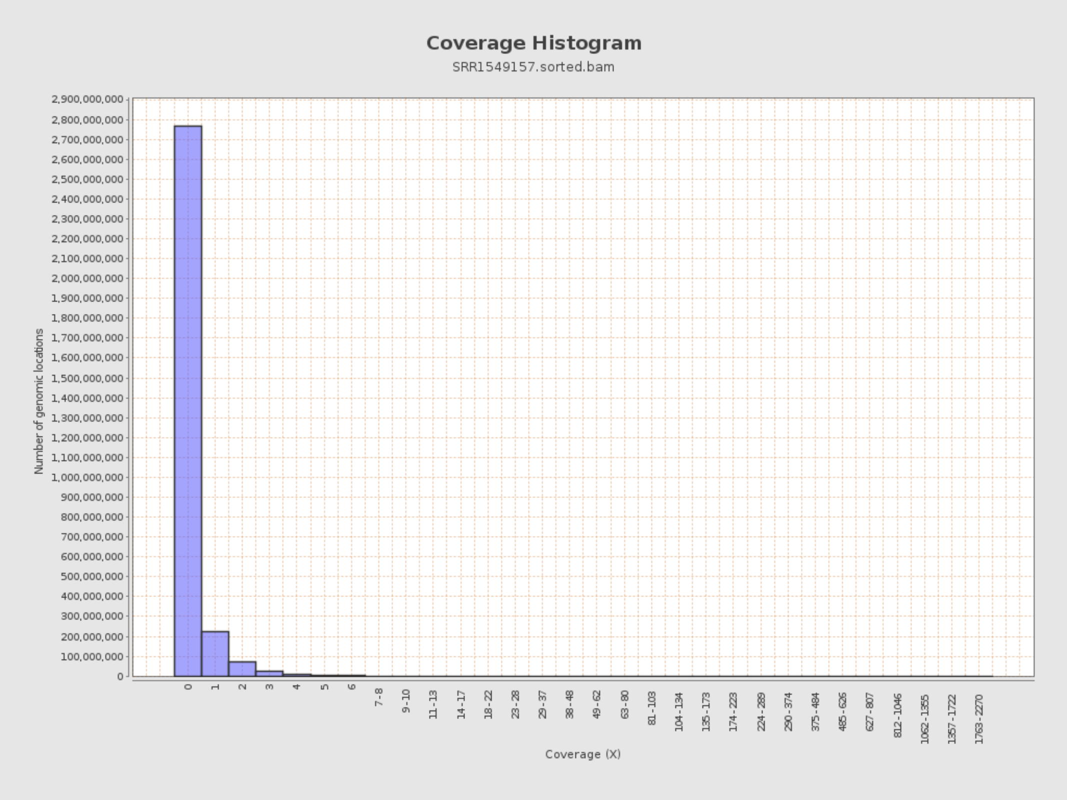
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	41422846	0.1662	1.6428
chr2	243199373	41994357	0.1727	0.8164
chr3	198022430	34459624	0.174	0.5845
chr4	191154276	31357885	0.164	0.59
chr5	180915260	30959975	0.1711	0.5882
chr6	171115067	29353065	0.1715	0.6266
chr7	159138663	27731628	0.1743	1.104
chr8	146364022	26085134	0.1782	1.3016

chr9	141213431	21607010	0.153	0.7891
chr10	135534747	24119462	0.178	0.8042
chr11	135006516	23466498	0.1738	0.7556
chr12	133851895	22883175	0.171	0.6017
chr13	115169878	15568018	0.1352	0.5079
chr14	107349540	15497376	0.1444	0.6912
chr15	102531392	14937013	0.1457	0.5282
chr16	90354753	14256126	0.1578	0.6095
chr17	81195210	14017838	0.1726	0.6252
chr18	78077248	13305725	0.1704	1.4852
chr19	59128983	9904472	0.1675	1.3213
chr20	63025520	10794430	0.1713	0.6121
chr21	48129895	6607312	0.1373	0.6051
chr22	51304566	6002485	0.117	0.5085
chrMT	16571	154457	9.3209	11.523
chrX	155270560	16709586	0.1076	0.5625
chrY	59373566	3927797	0.0662	0.5101

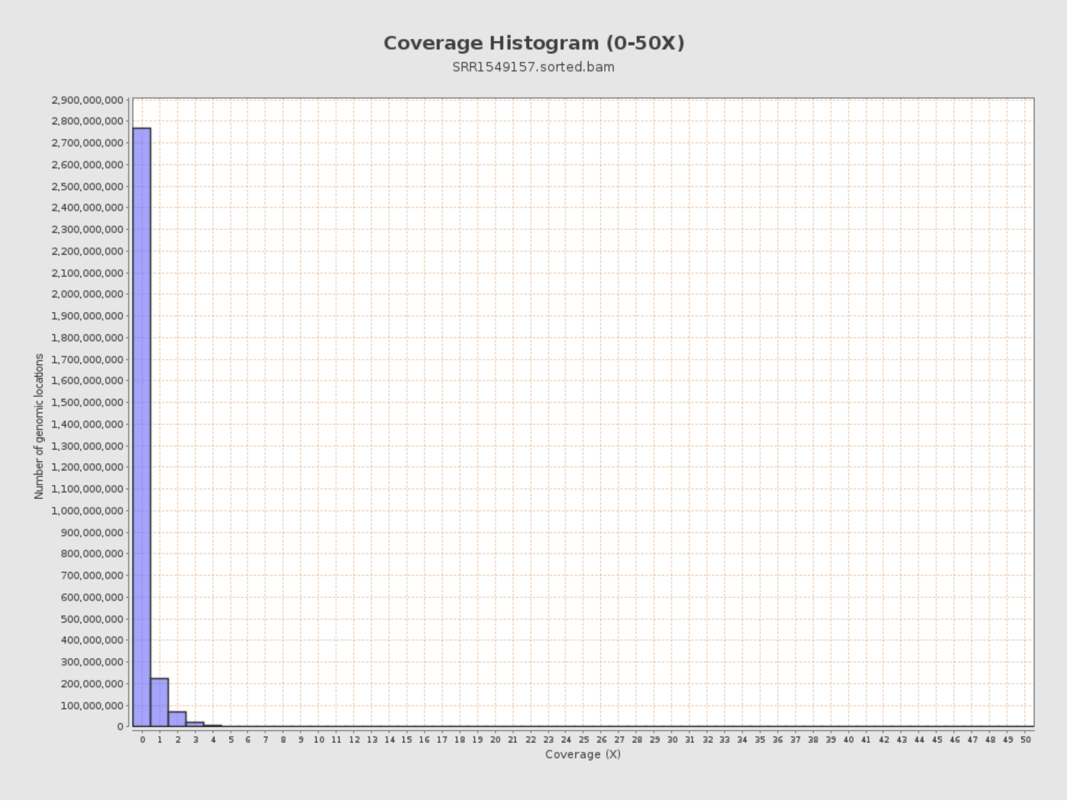
3. Results : Coverage across reference



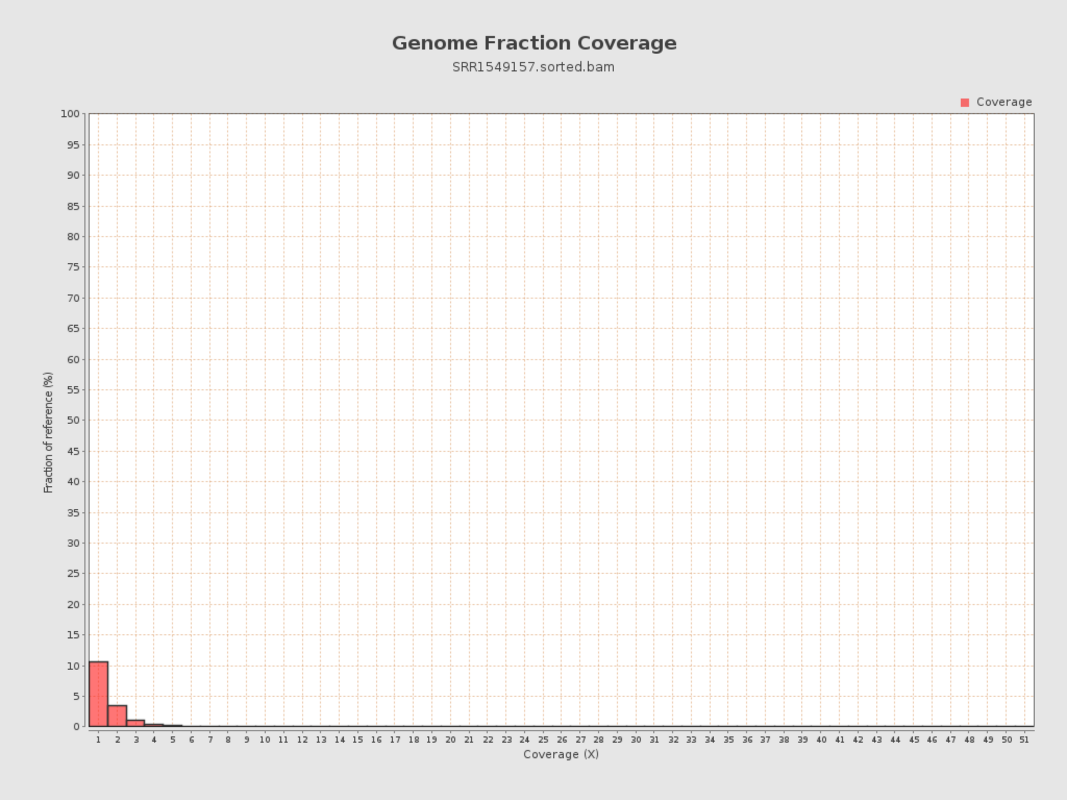
4. Results : Coverage Histogram



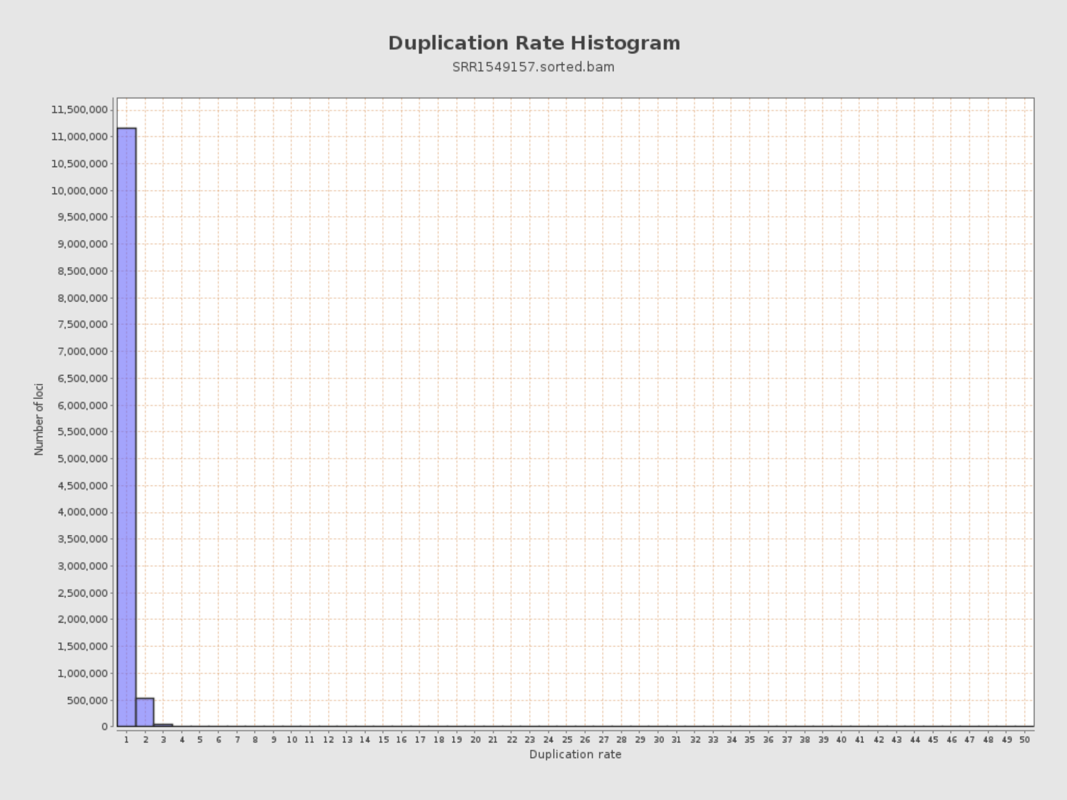
5. Results : Coverage Histogram (0-50X)



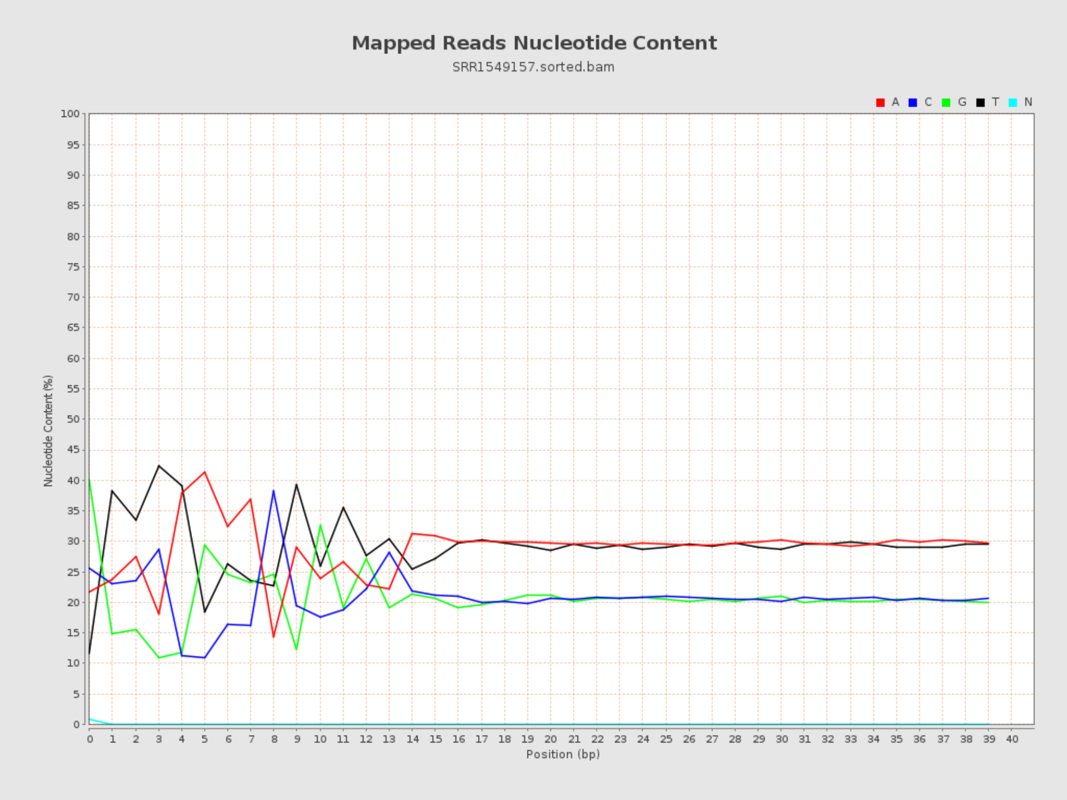
6. Results : Genome Fraction Coverage



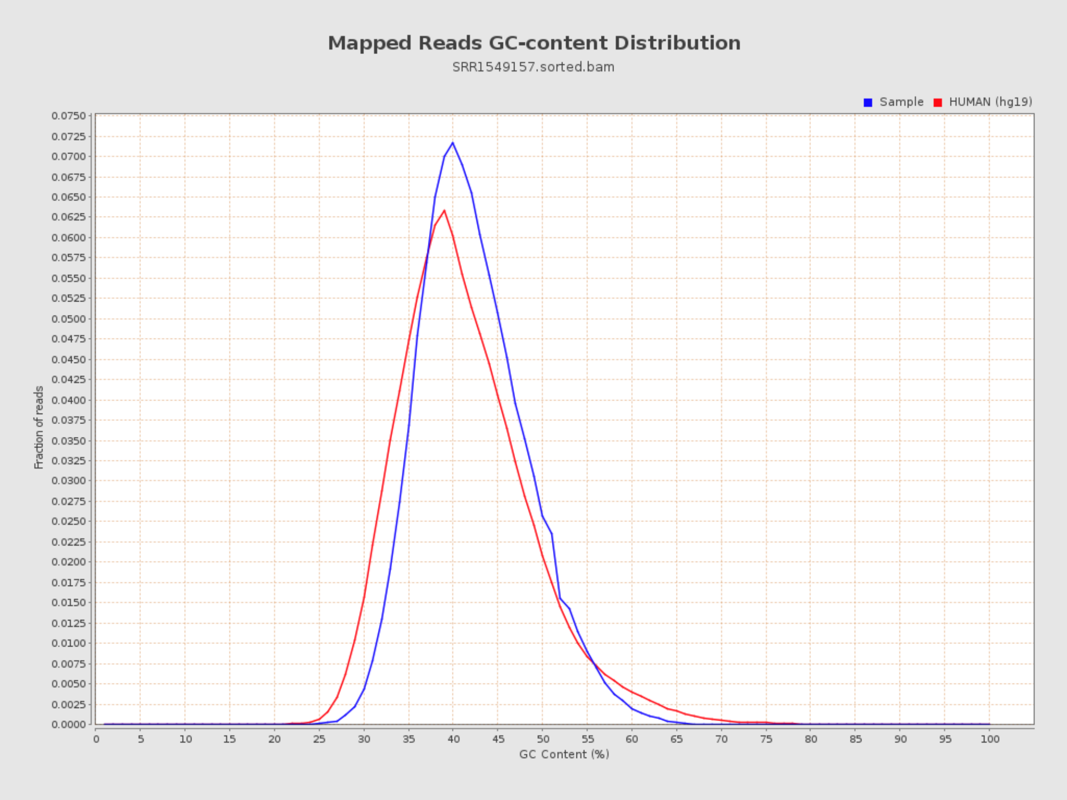
7. Results : Duplication Rate Histogram



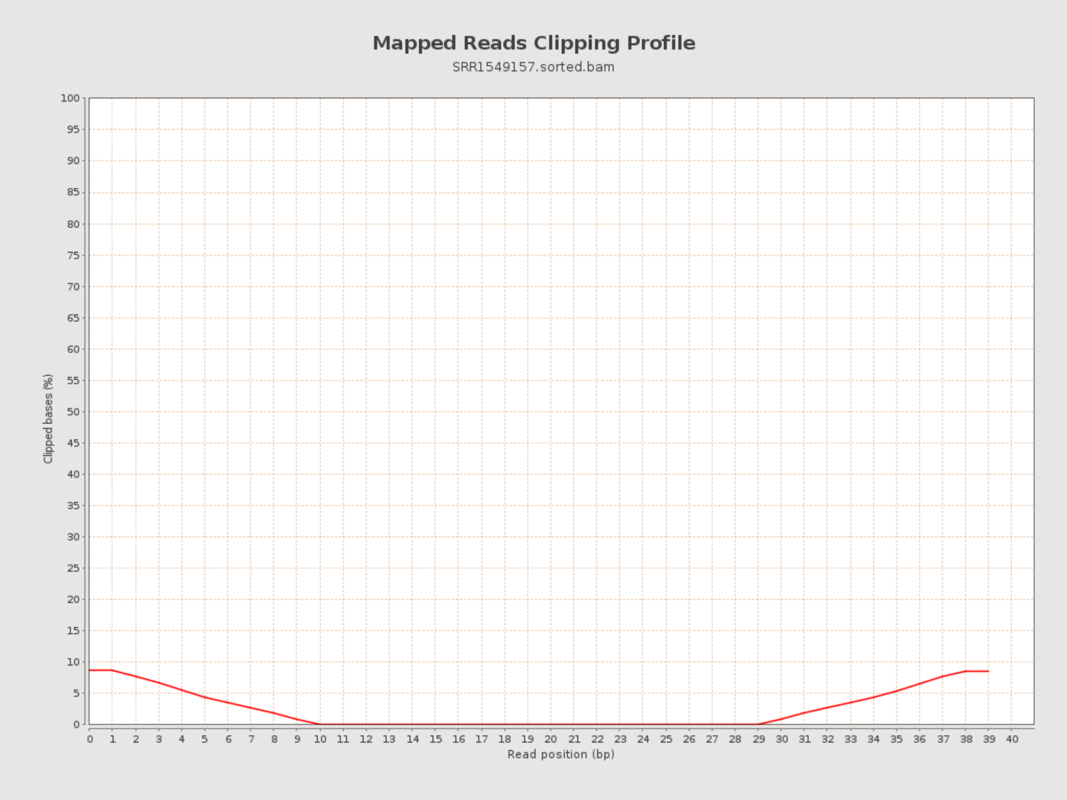
8. Results : Mapped Reads Nucleotide Content



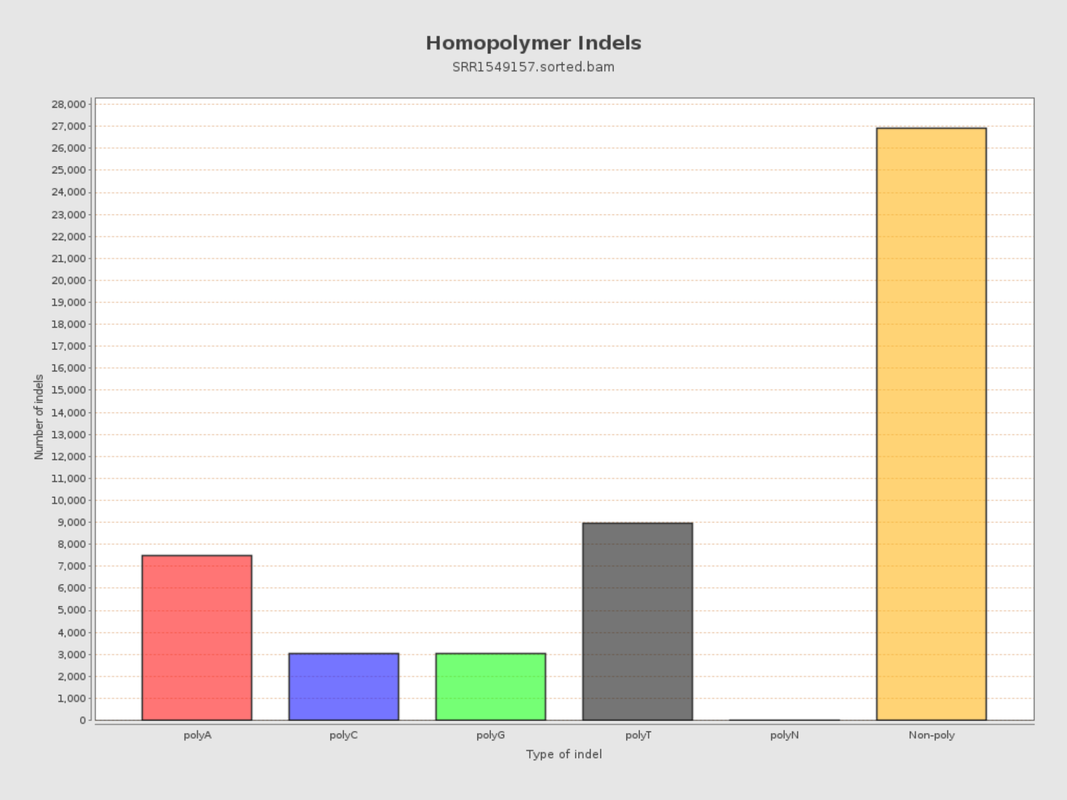
9. Results : Mapped Reads GC-content Distribution



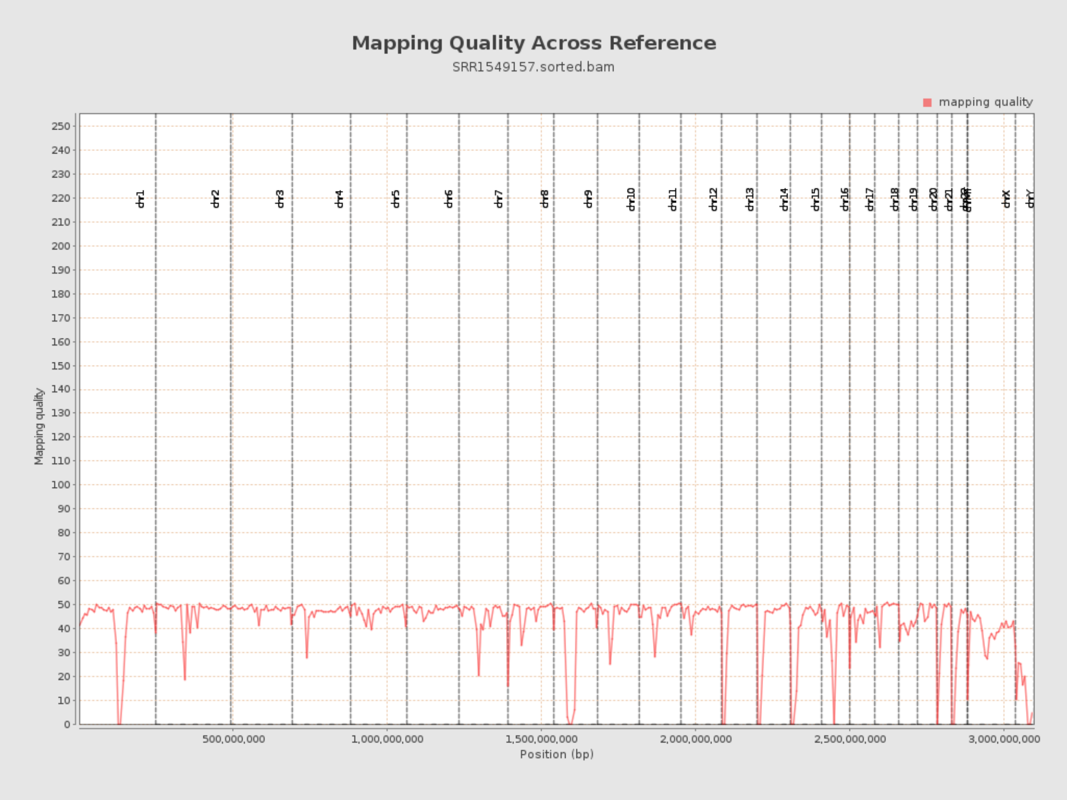
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram