Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:50:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549041.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_SRR1549041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:50:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,045,929
Mapped reads	9,300,884 / 84.2%
Unmapped reads	1,745,045 / 15.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	692,179 / 6.27%
Duplication rate	6.17%
Clipped reads	651,267 / 5.9%

2.2. ACGT Content

Number/percentage of A's	104,816,073 / 28.46%
Number/percentage of C's	77,027,837 / 20.91%
Number/percentage of T's	107,640,559 / 29.23%
Number/percentage of G's	78,817,948 / 21.4%
Number/percentage of N's	333 / 0%
GC Percentage	42.31%

2.3. Coverage

Mean	0.119
Standard Deviation	0.845

2.4. Mapping Quality

Mean Mapping Quality	42.07

2.5. Mismatches and indels

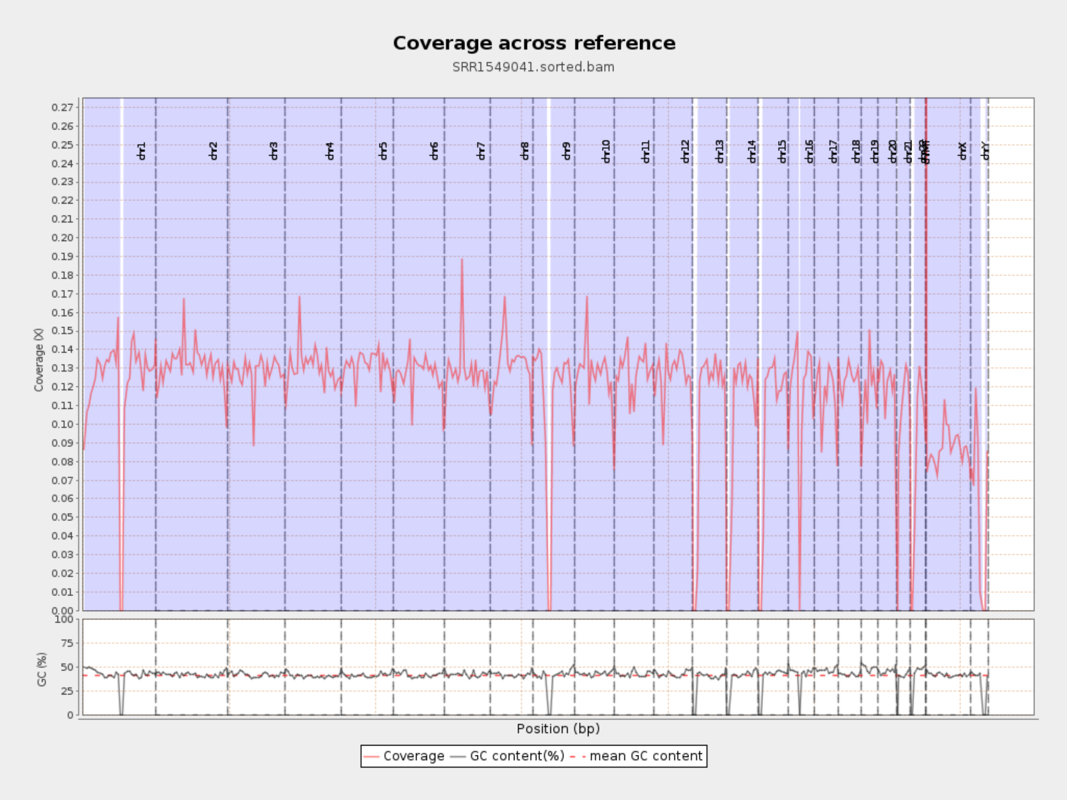
General error rate	0.26%
Mismatches	932,764
Insertions	10,238
Mapped reads with at least one insertion	0.11%
Deletions	25,540
Mapped reads with at least one deletion	0.27%
Homopolymer indels	41.93%

2.6. Chromosome stats

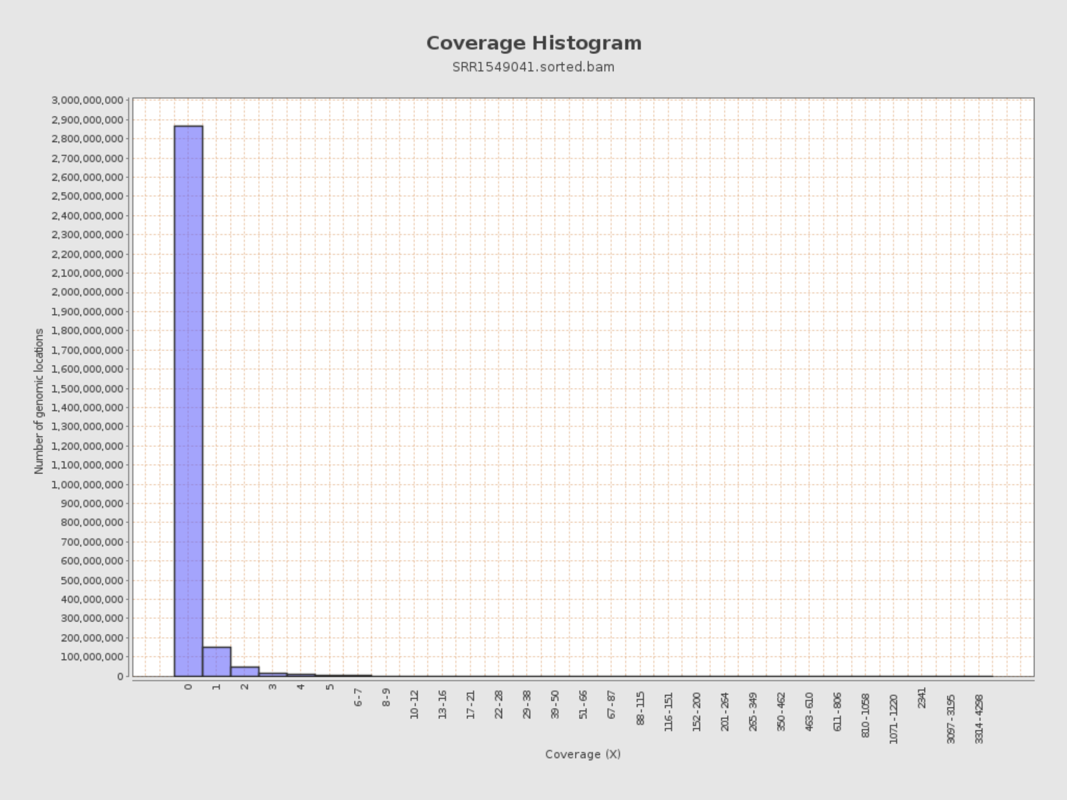
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	30031308	0.1205	1.073
chr2	243199373	32070667	0.1319	0.7773
chr3	198022430	25304321	0.1278	0.5444
chr4	191154276	25091874	0.1313	0.5943
chr5	180915260	23717915	0.1311	0.558
chr6	171115067	21802393	0.1274	0.5839
chr7	159138663	20437930	0.1284	1.0337
chr8	146364022	19235492	0.1314	2.1895

chr9	141213431	15624449	0.1106	0.7322
chr10	135534747	17372957	0.1282	0.7059
chr11	135006516	17235458	0.1277	0.6547
chr12	133851895	16934643	0.1265	0.5502
chr13	115169878	12227611	0.1062	0.5014
chr14	107349540	11068229	0.1031	0.5483
chr15	102531392	10302399	0.1005	0.4822
chr16	90354753	10219192	0.1131	0.5637
chr17	81195210	9484817	0.1168	0.5471
chr18	78077248	9711496	0.1244	1.1964
chr19	59128983	6965396	0.1178	0.9771
chr20	63025520	7625685	0.121	0.5555
chr21	48129895	4900400	0.1018	0.6116
chr22	51304566	4163482	0.0812	0.6213
chrMT	16571	24207	1.4608	4.3655
chrX	155270560	13488027	0.0869	0.5168
chrY	59373566	3295723	0.0555	0.5201

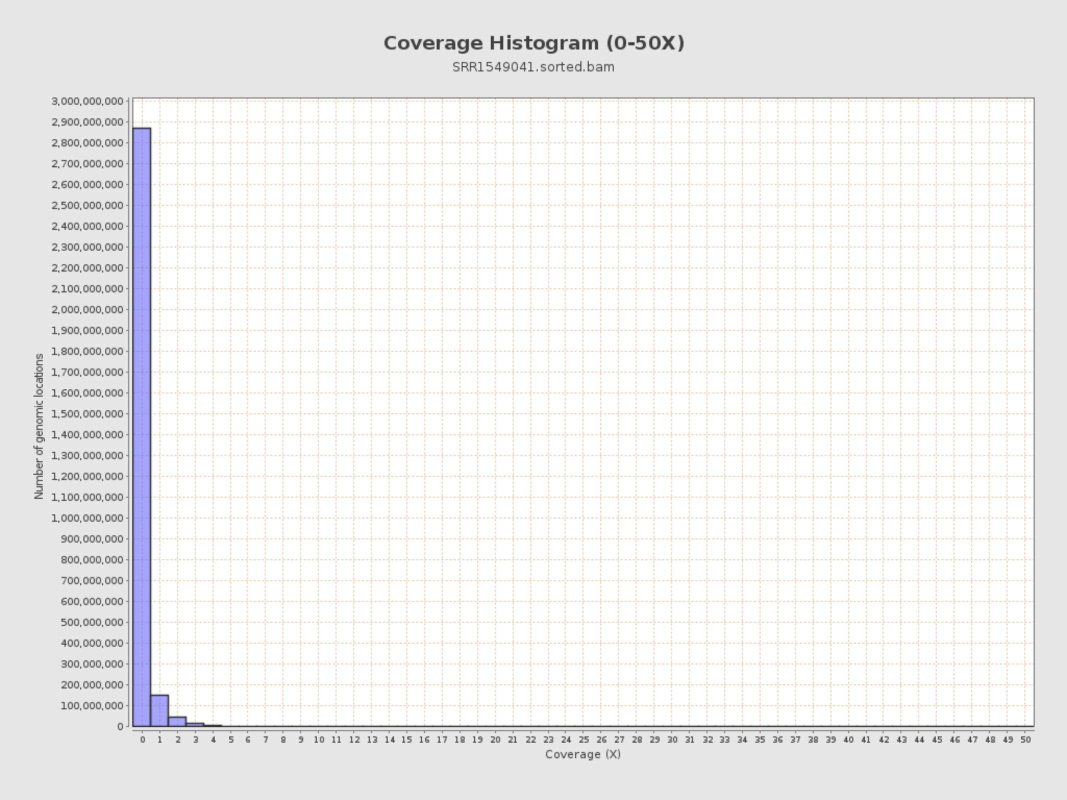
3. Results : Coverage across reference



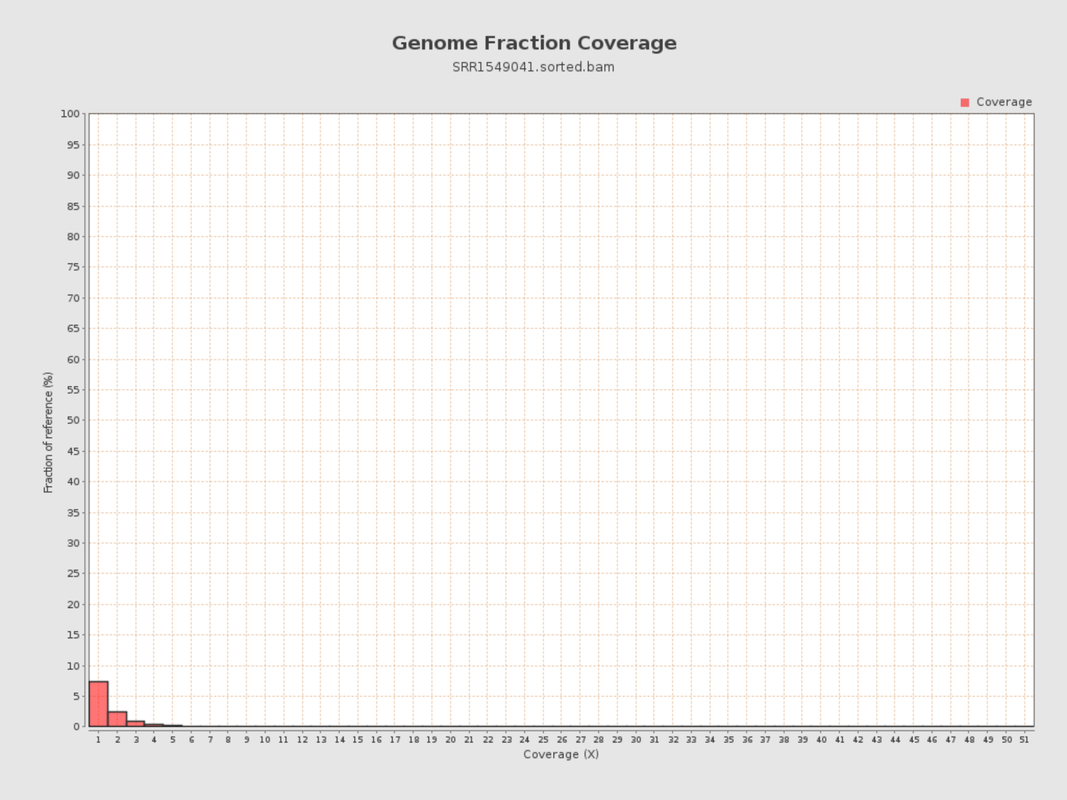
4. Results : Coverage Histogram



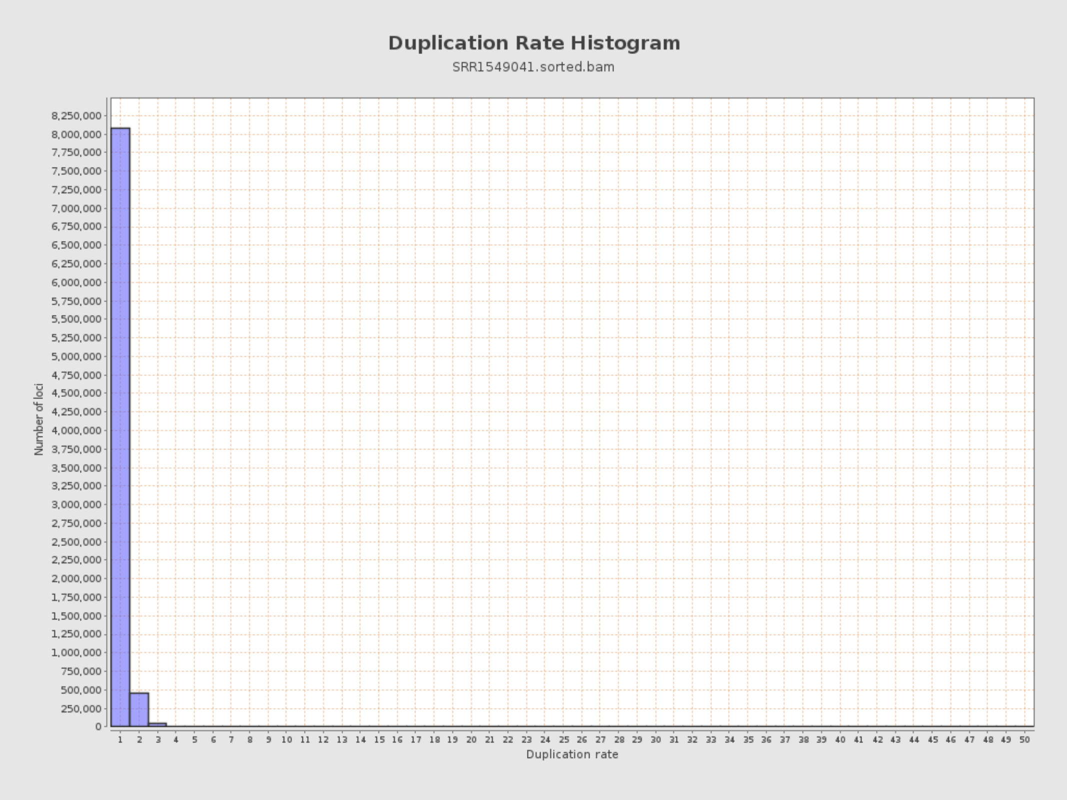
5. Results : Coverage Histogram (0-50X)



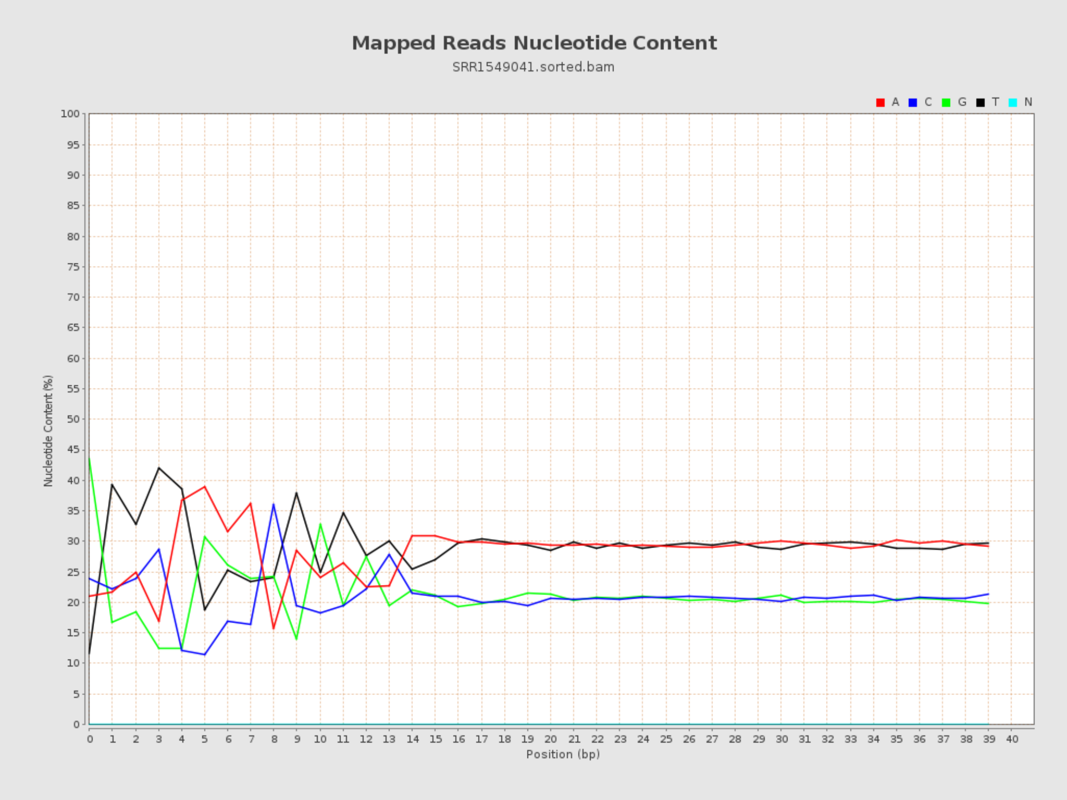
6. Results : Genome Fraction Coverage



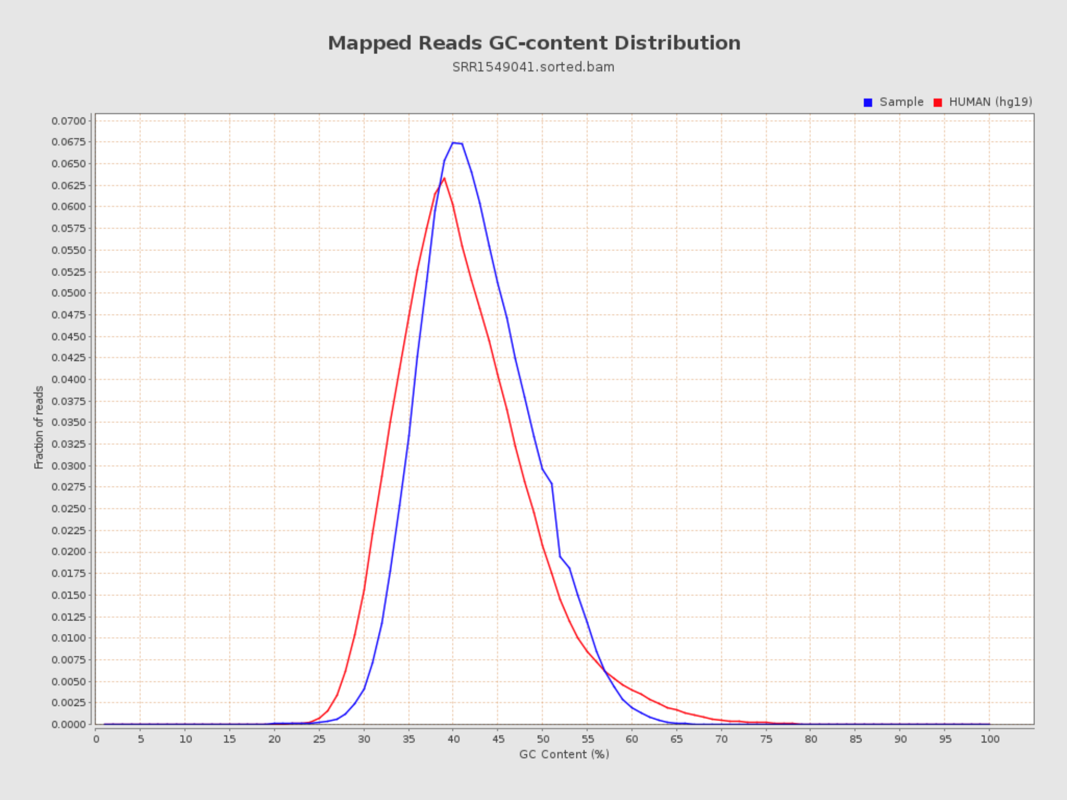
7. Results : Duplication Rate Histogram



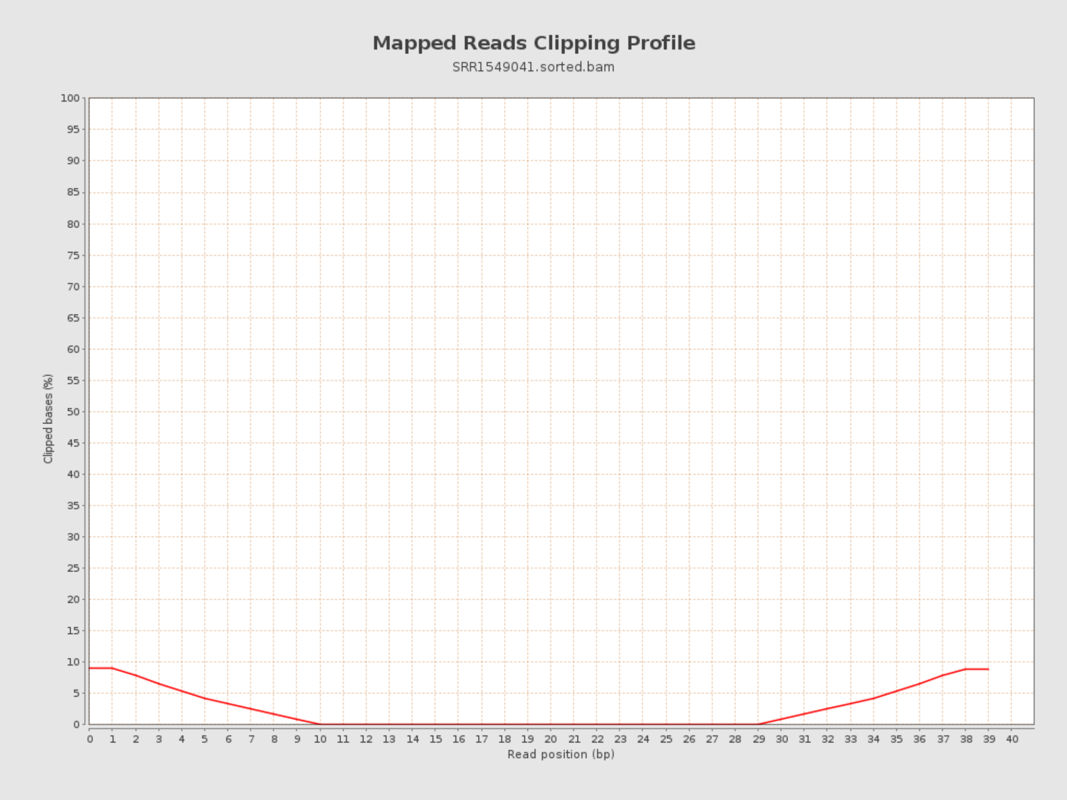
8. Results : Mapped Reads Nucleotide Content



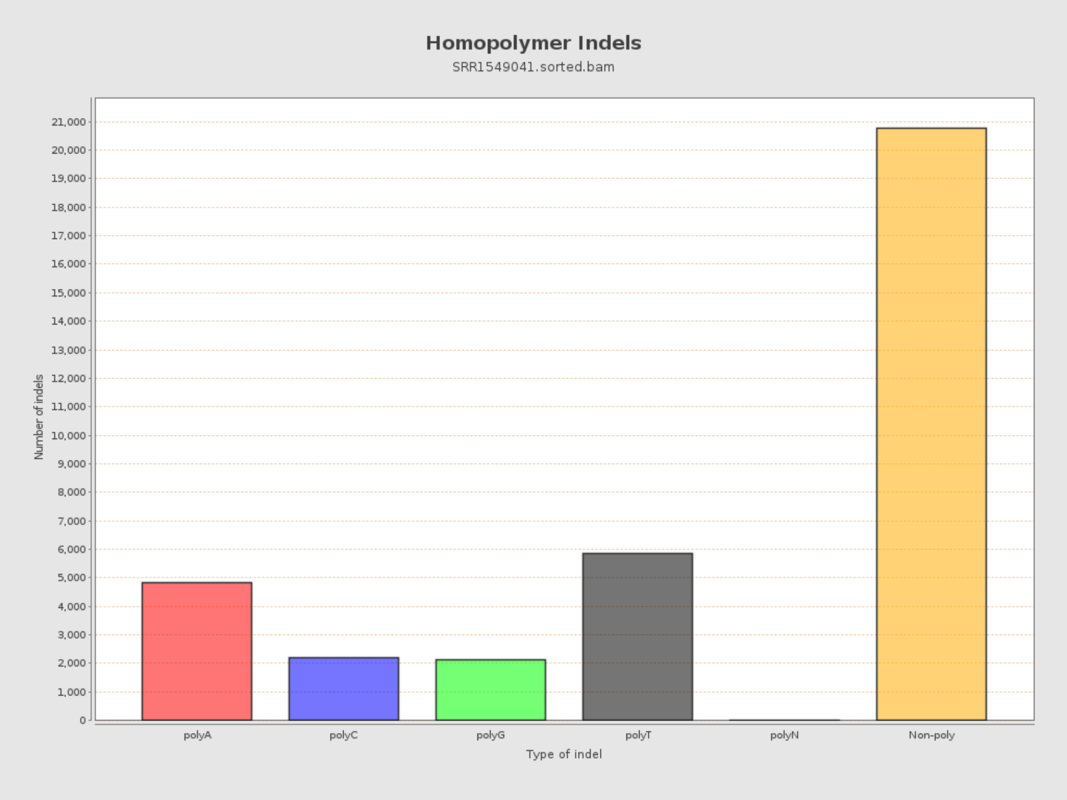
9. Results : Mapped Reads GC-content Distribution



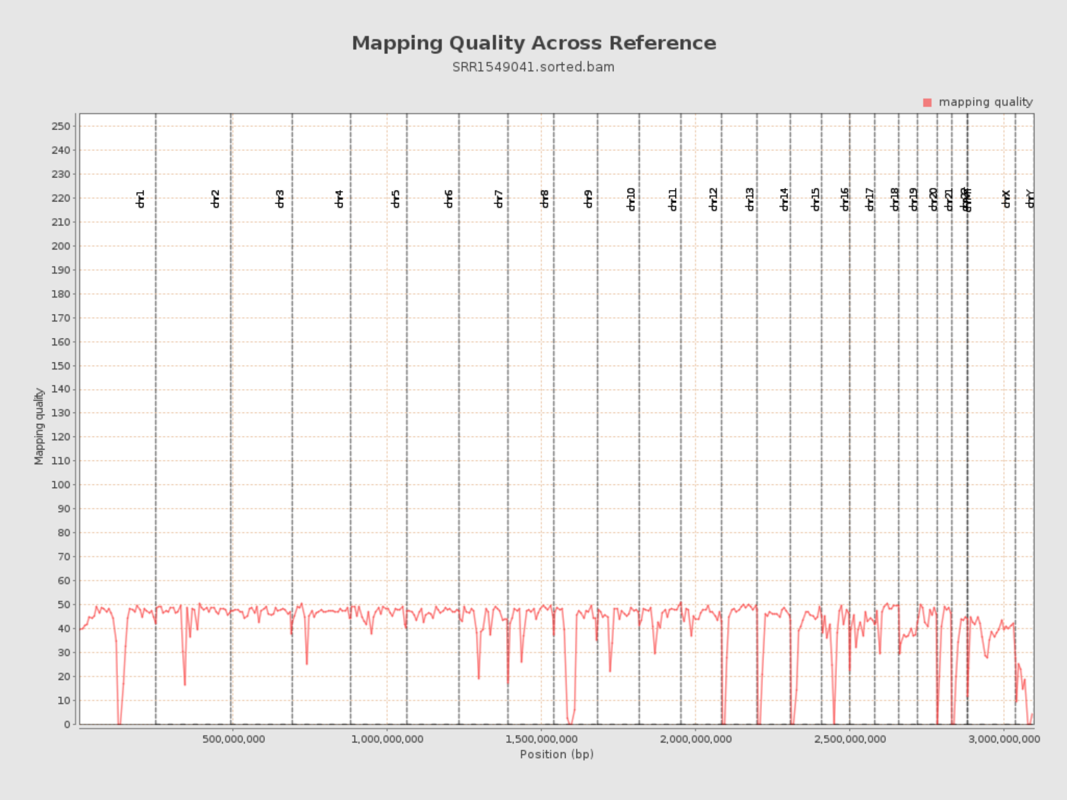
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram