Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:40:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240041.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_SRR6240041 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240041.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:40:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240041.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,798,191
Mapped reads	1,523,529 / 84.73%
Unmapped reads	274,662 / 15.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,421 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	173,322 / 9.64%
Duplication rate	9.01%
Clipped reads	828,448 / 46.07%

2.2. ACGT Content

Number/percentage of A's	27,379,053 / 27.99%
Number/percentage of C's	17,641,337 / 18.03%
Number/percentage of T's	31,420,469 / 32.12%
Number/percentage of G's	21,321,386 / 21.79%
Number/percentage of N's	67,844 / 0.07%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0316

Standard Deviation	0.3744

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

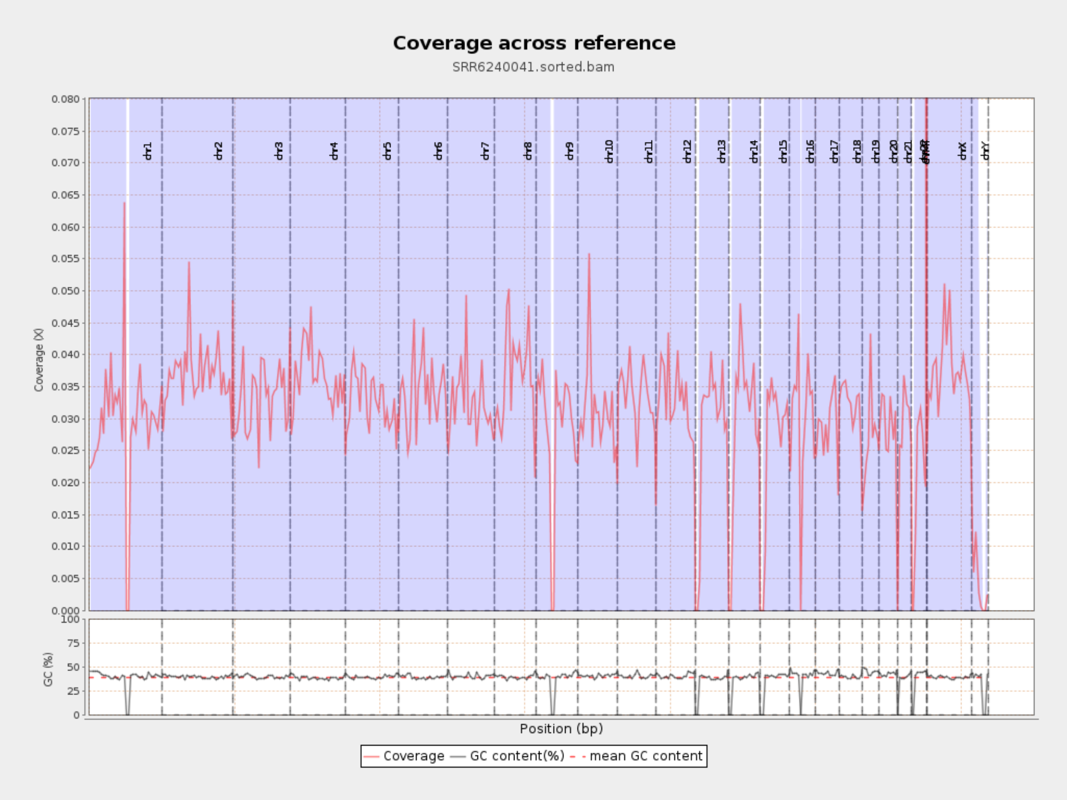
General error rate	0.86%
Mismatches	829,342
Insertions	6,813
Mapped reads with at least one insertion	0.44%
Deletions	20,598
Mapped reads with at least one deletion	1.34%
Homopolymer indels	47.57%

2.6. Chromosome stats

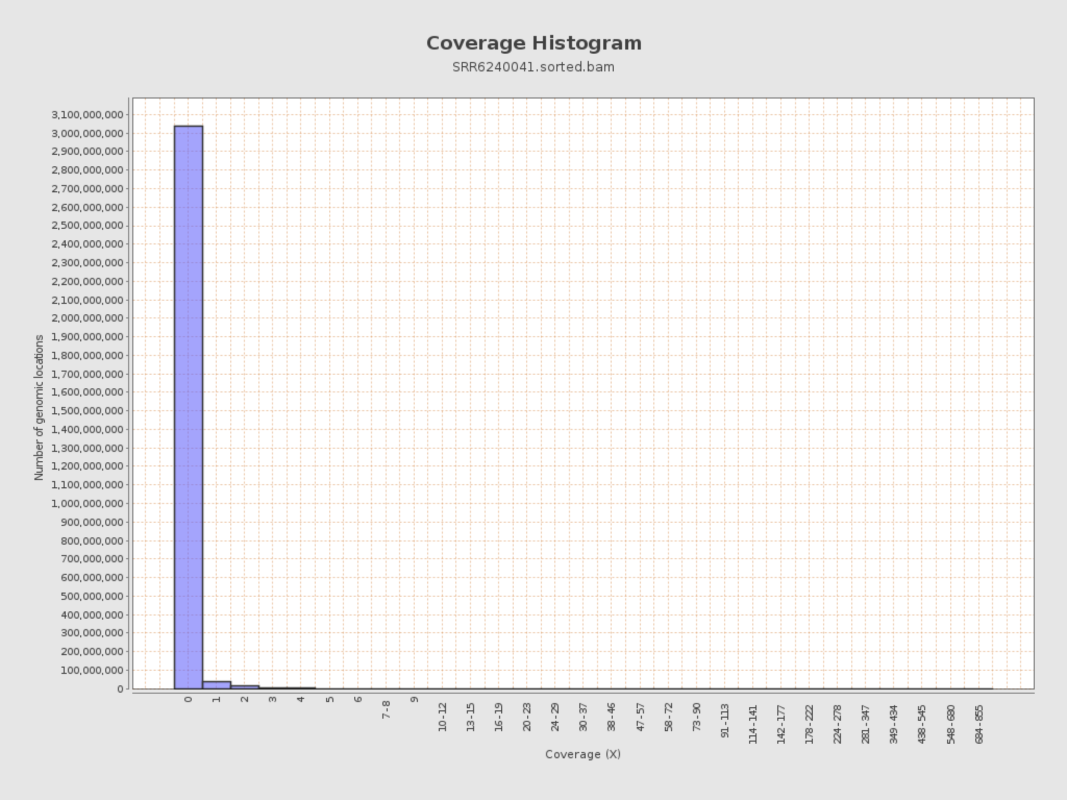
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7352438	0.0295	0.7004
chr2	243199373	9016899	0.0371	0.3848
chr3	198022430	6574954	0.0332	0.2724
chr4	191154276	6993494	0.0366	0.29
chr5	180915260	5947307	0.0329	0.2708
chr6	171115067	5866730	0.0343	0.3124
chr7	159138663	5213364	0.0328	0.395

chr8	146364022	5355022	0.0366	0.5793
chr9	141213431	4040123	0.0286	0.305
chr10	135534747	4250842	0.0314	0.3326
chr11	135006516	4515459	0.0334	0.31
chr12	133851895	4402490	0.0329	0.2716
chr13	115169878	3177428	0.0276	0.2494
chr14	107349540	3175546	0.0296	0.2627
chr15	102531392	2616081	0.0255	0.2406
chr16	90354753	2722666	0.0301	0.264
chr17	81195210	2308924	0.0284	0.2648
chr18	78077248	2544991	0.0326	0.5089
chr19	59128983	1604211	0.0271	0.4691
chr20	63025520	1826110	0.029	0.2594
chr21	48129895	1306829	0.0272	0.2503
chr22	51304566	965237	0.0188	0.1973
chrMT	16571	32619	1.9684	2.2552
chrX	155270560	5816001	0.0375	0.3021
chrY	59373566	239671	0.004	0.1001

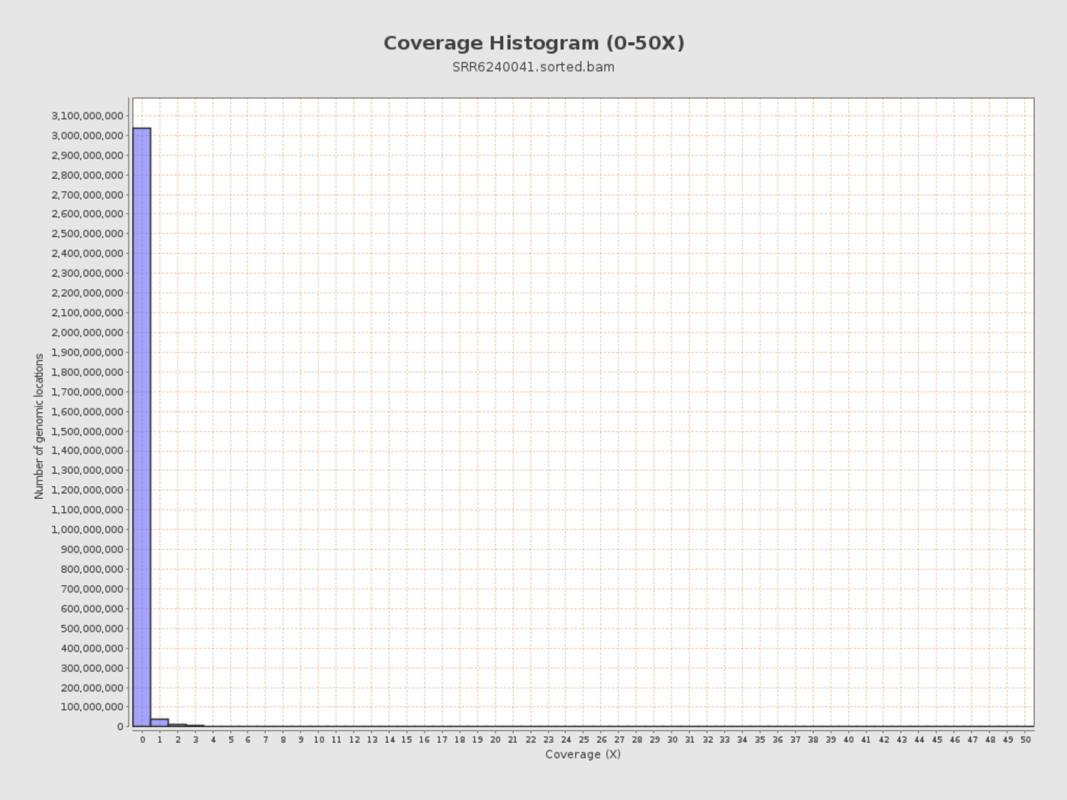
3. Results : Coverage across reference



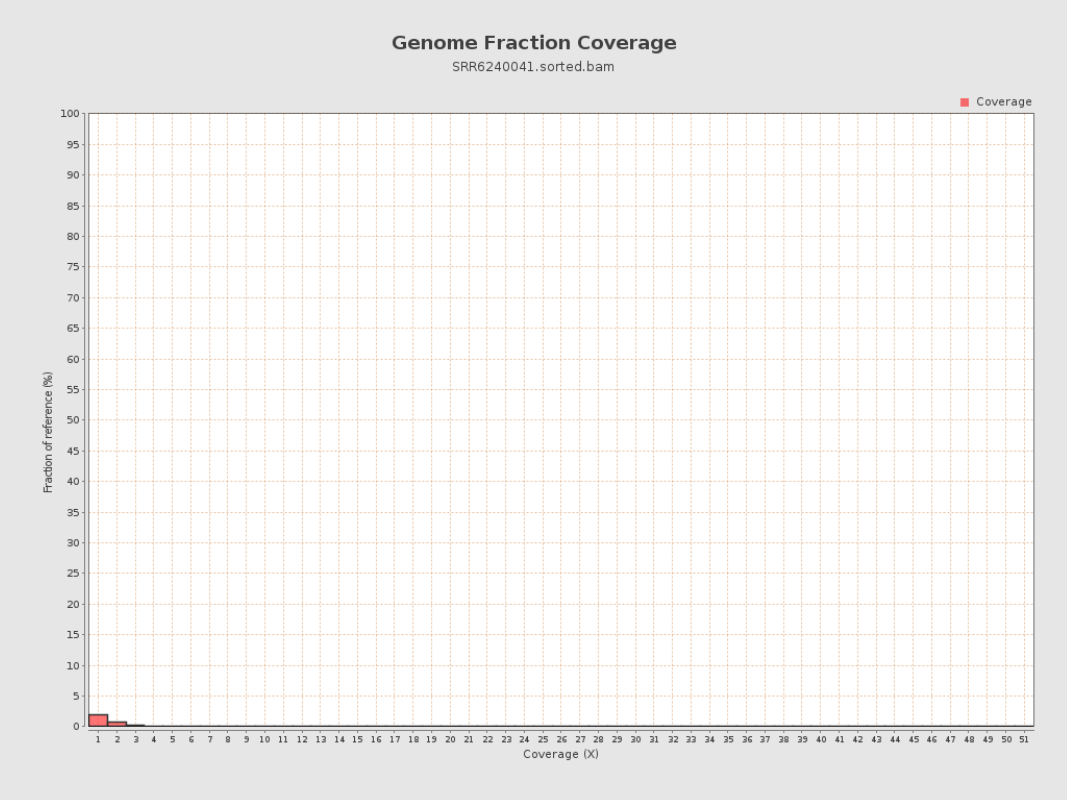
4. Results : Coverage Histogram



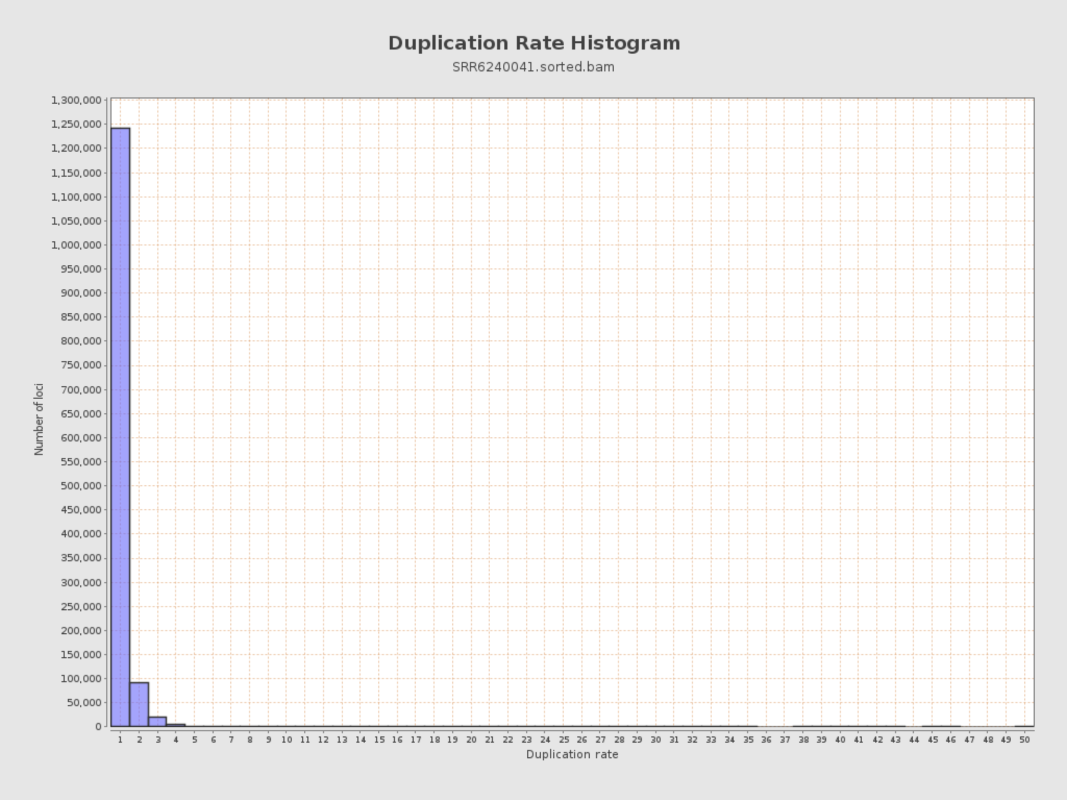
5. Results : Coverage Histogram (0-50X)



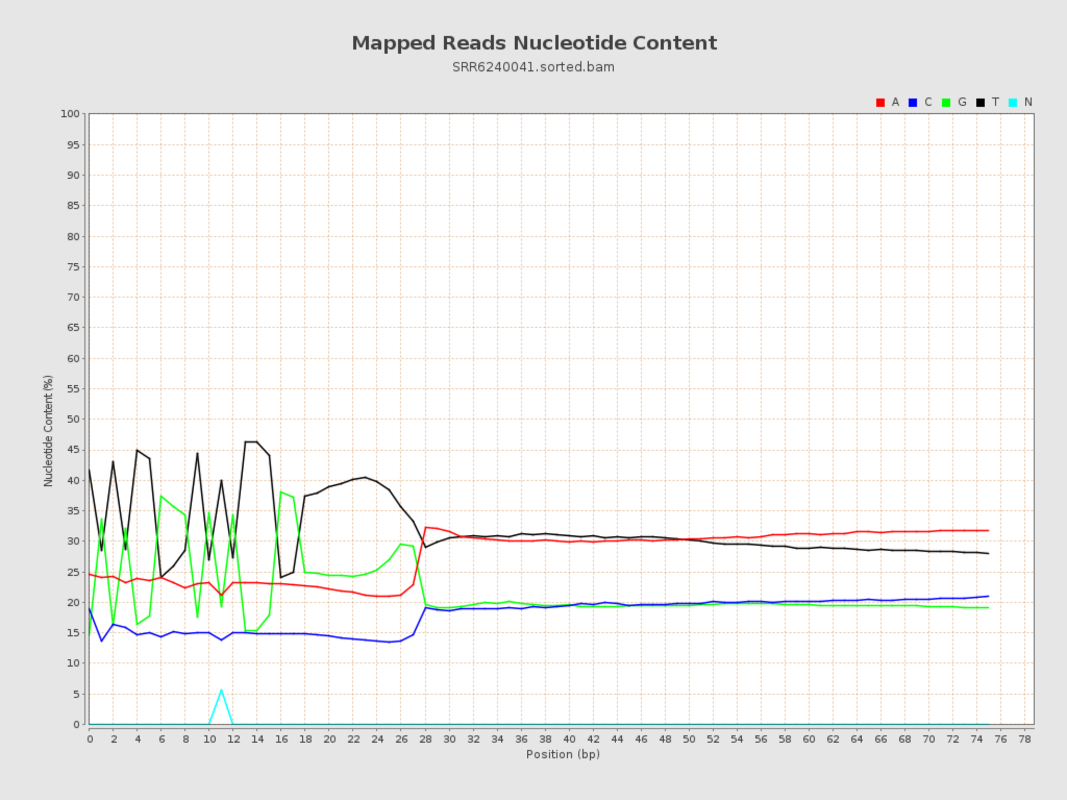
6. Results : Genome Fraction Coverage



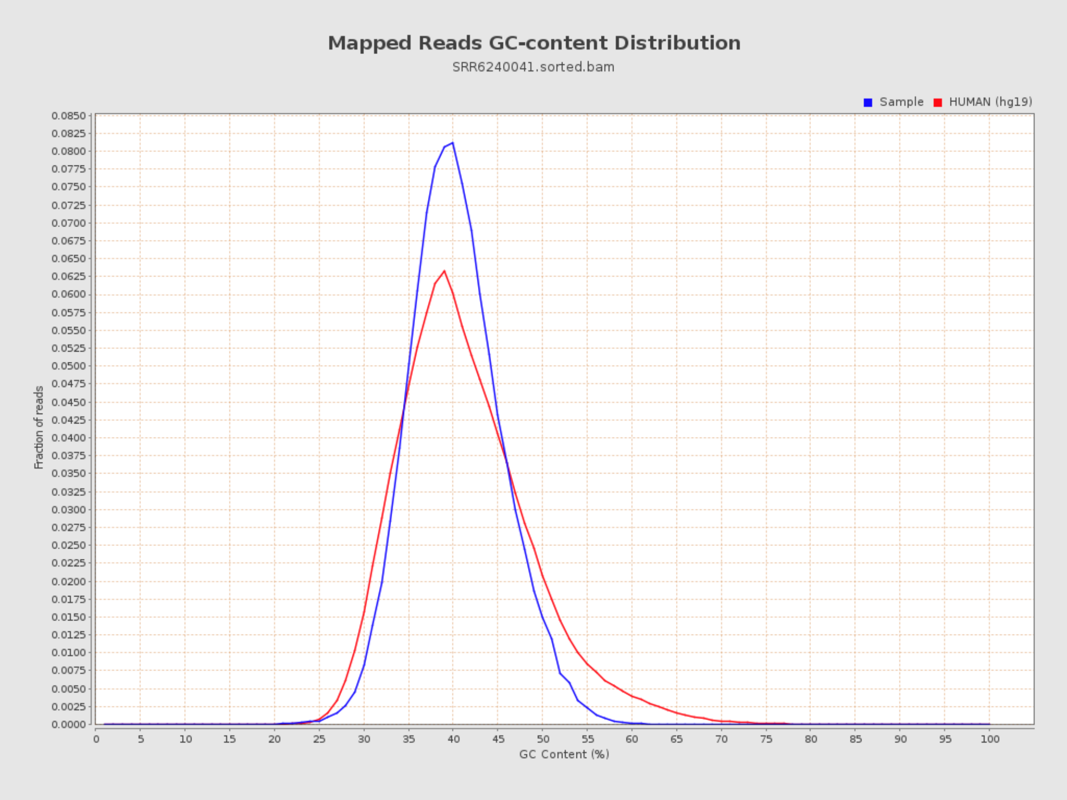
7. Results : Duplication Rate Histogram



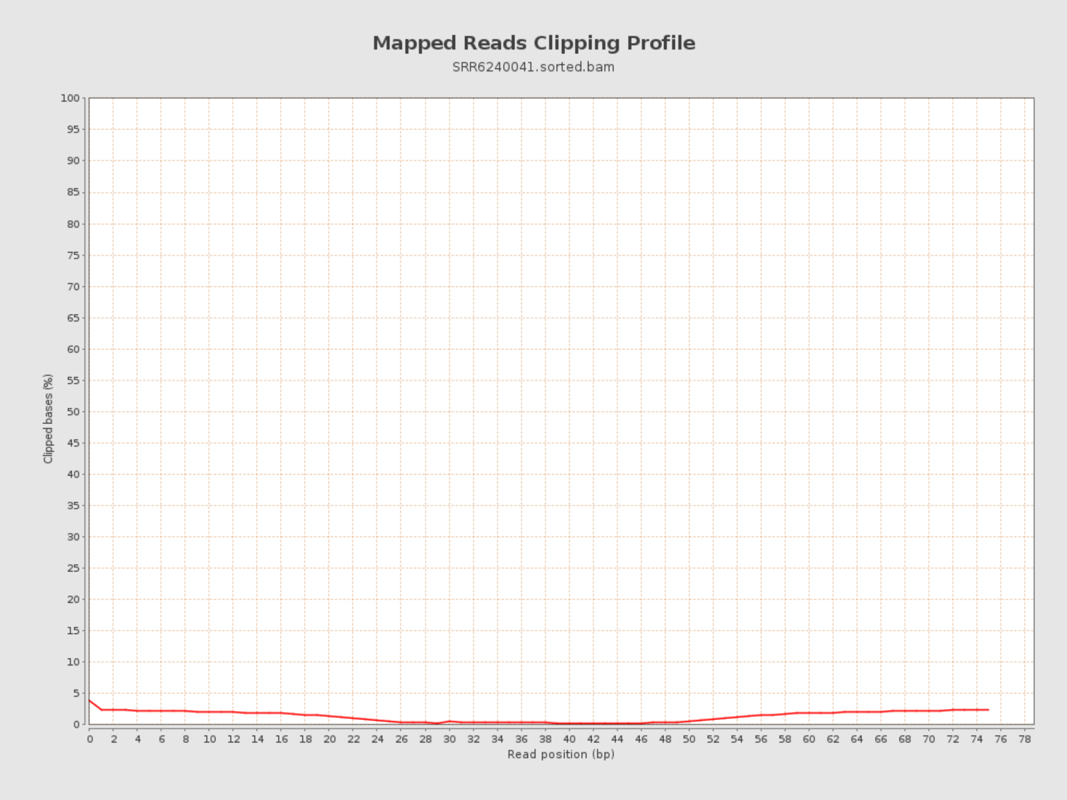
8. Results : Mapped Reads Nucleotide Content



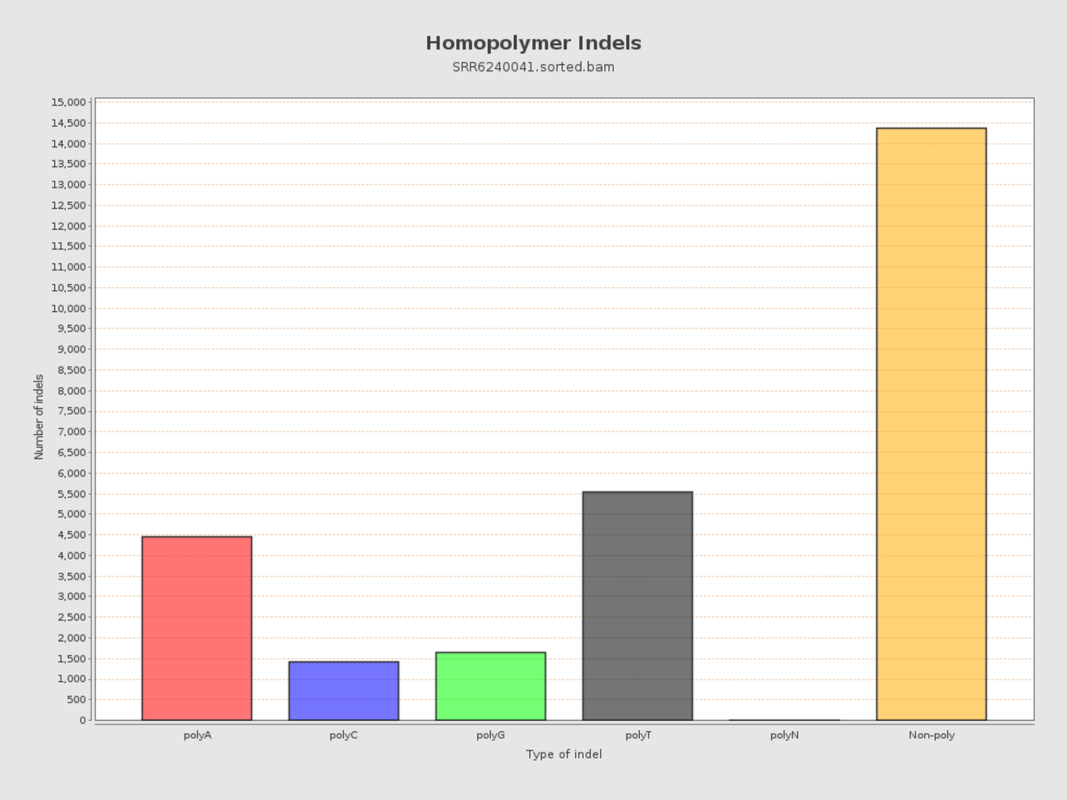
9. Results : Mapped Reads GC-content Distribution



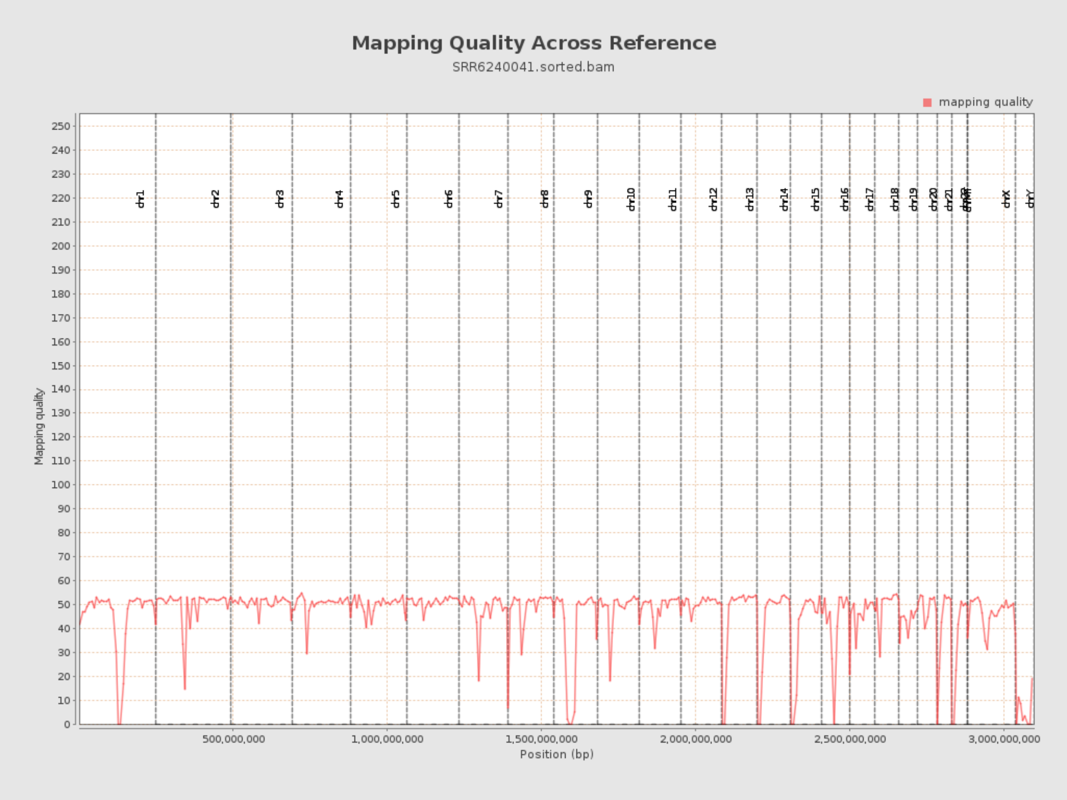
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram