Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:05:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004140.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_SRR6004140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004140.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:05:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,900,471
Mapped reads	1,484,711 / 78.12%
Unmapped reads	415,760 / 21.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,102 / 1.11%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	144,983 / 7.63%
Duplication rate	7.92%
Clipped reads	874,745 / 46.03%

2.2. ACGT Content

Number/percentage of A's	26,493,157 / 28.2%
Number/percentage of C's	16,231,104 / 17.27%
Number/percentage of T's	30,913,551 / 32.9%
Number/percentage of G's	20,279,204 / 21.58%
Number/percentage of N's	40,508 / 0.04%
GC Percentage	38.86%

2.3. Coverage

Mean	0.0304

Standard Deviation	0.3241

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

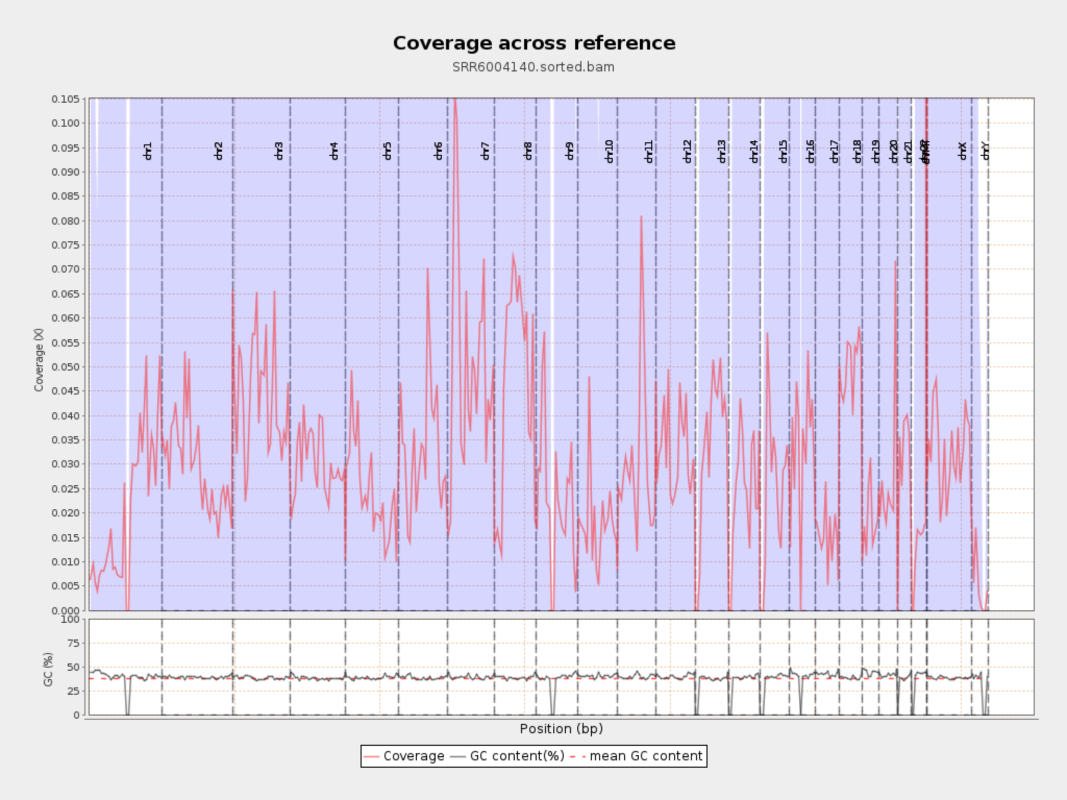
General error rate	1.02%
Mismatches	944,112
Insertions	7,214
Mapped reads with at least one insertion	0.48%
Deletions	48,433
Mapped reads with at least one deletion	3.2%
Homopolymer indels	41.75%

2.6. Chromosome stats

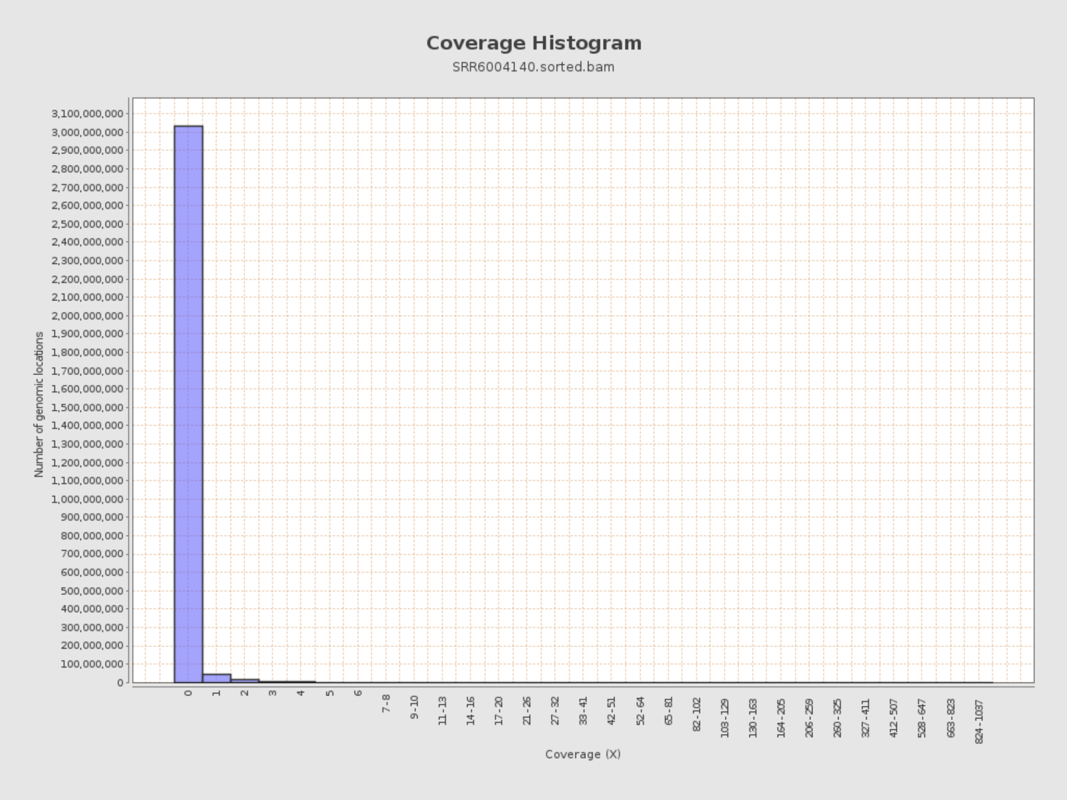
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5043355	0.0202	0.3689
chr2	243199373	7208327	0.0296	0.3416
chr3	198022430	8772535	0.0443	0.2967
chr4	191154276	5731833	0.03	0.2561
chr5	180915260	4462681	0.0247	0.2202
chr6	171115067	5677205	0.0332	0.2707
chr7	159138663	8295332	0.0521	0.466

chr8	146364022	6911310	0.0472	0.6749
chr9	141213431	3278492	0.0232	0.2544
chr10	135534747	2421447	0.0179	0.2632
chr11	135006516	4202954	0.0311	0.294
chr12	133851895	4393243	0.0328	0.2551
chr13	115169878	3857656	0.0335	0.2585
chr14	107349540	2594565	0.0242	0.2253
chr15	102531392	2623745	0.0256	0.2307
chr16	90354753	3023970	0.0335	0.2728
chr17	81195210	1239092	0.0153	0.1845
chr18	78077248	3908656	0.0501	0.4721
chr19	59128983	1114068	0.0188	0.3185
chr20	63025520	1798060	0.0285	0.2456
chr21	48129895	1451738	0.0302	0.2519
chr22	51304566	627161	0.0122	0.1485
chrMT	16571	21170	1.2775	1.8575
chrX	155270560	5076939	0.0327	0.263
chrY	59373566	304963	0.0051	0.1216

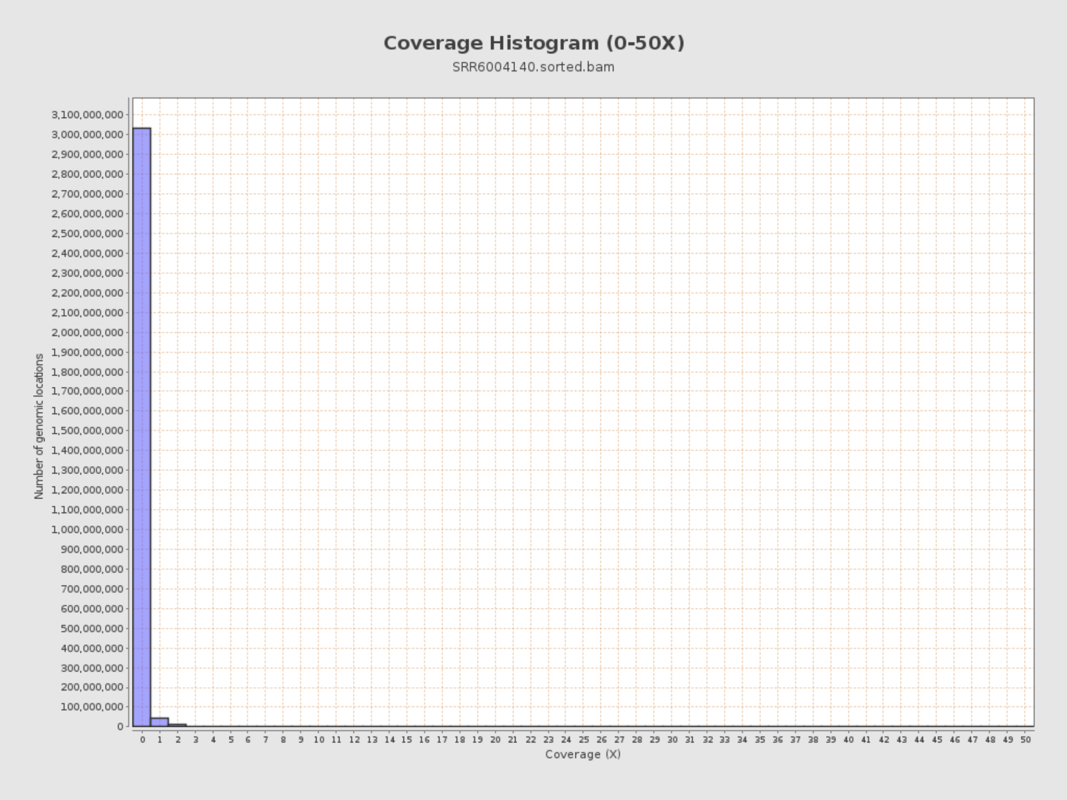
3. Results : Coverage across reference



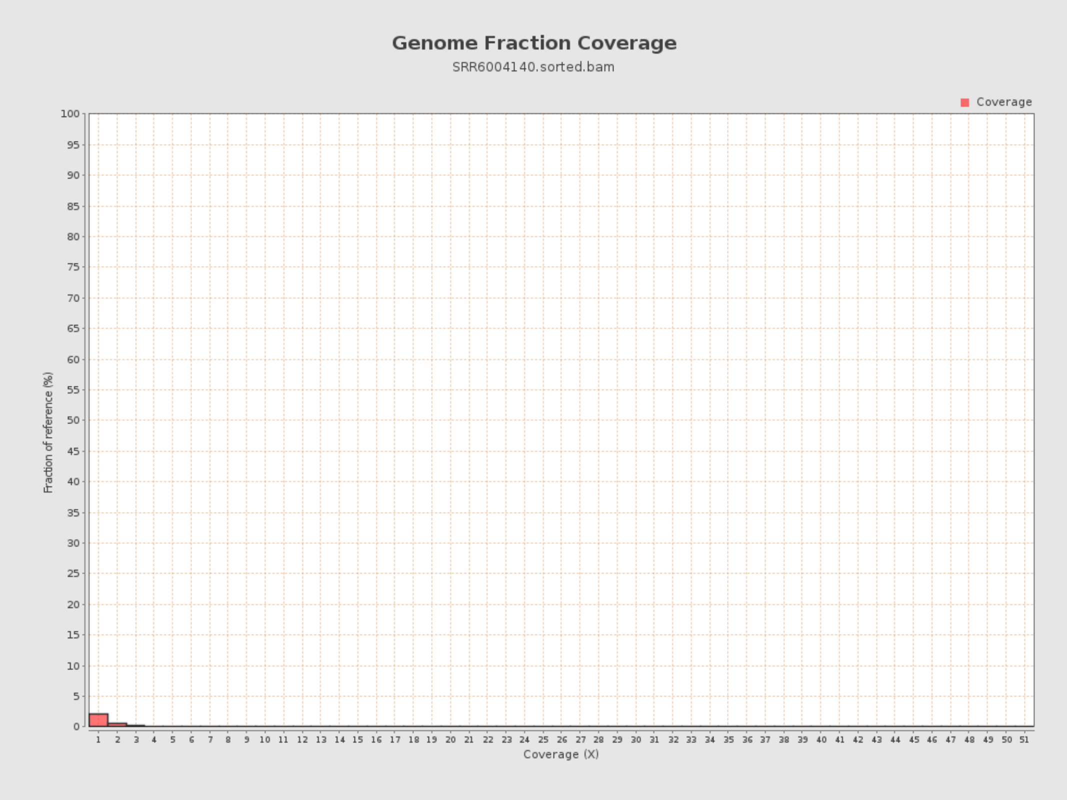
4. Results : Coverage Histogram



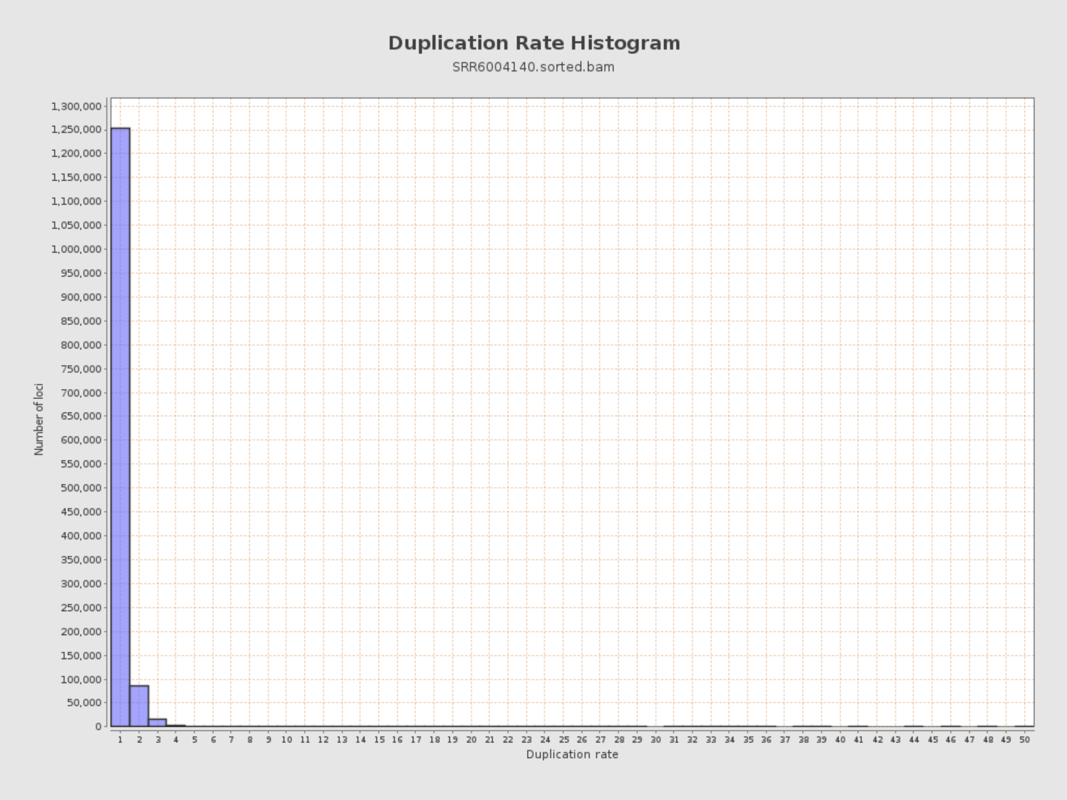
5. Results : Coverage Histogram (0-50X)



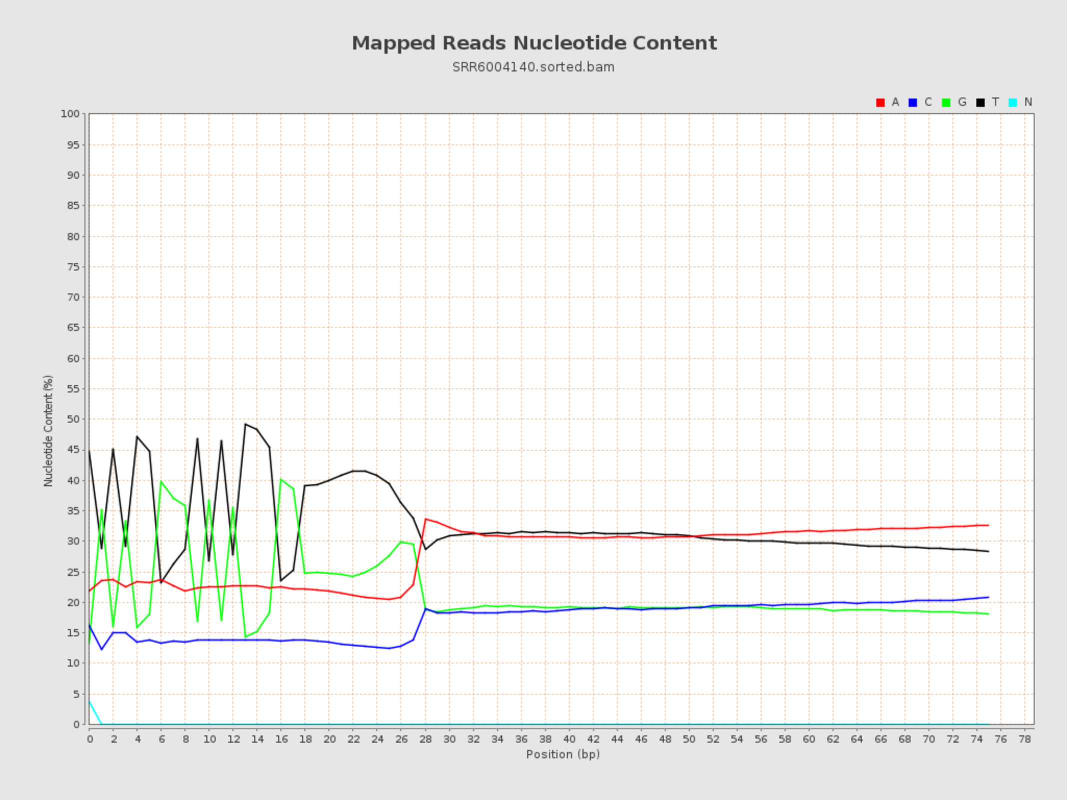
6. Results : Genome Fraction Coverage



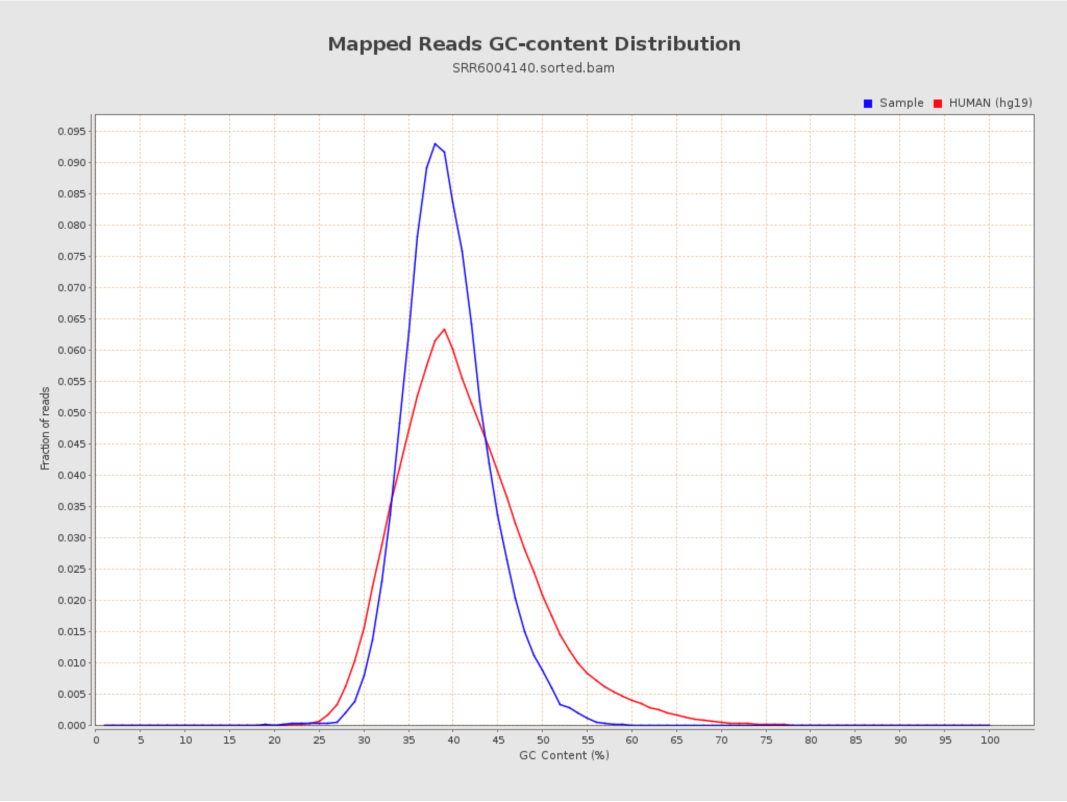
7. Results : Duplication Rate Histogram



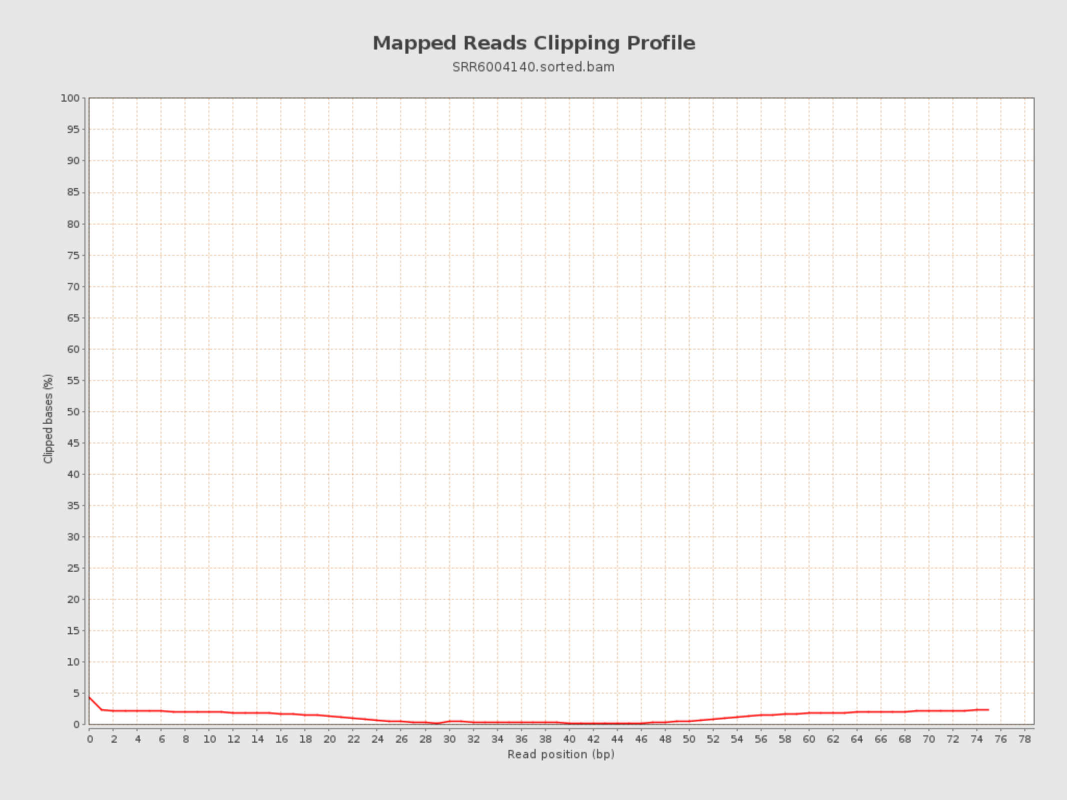
8. Results : Mapped Reads Nucleotide Content



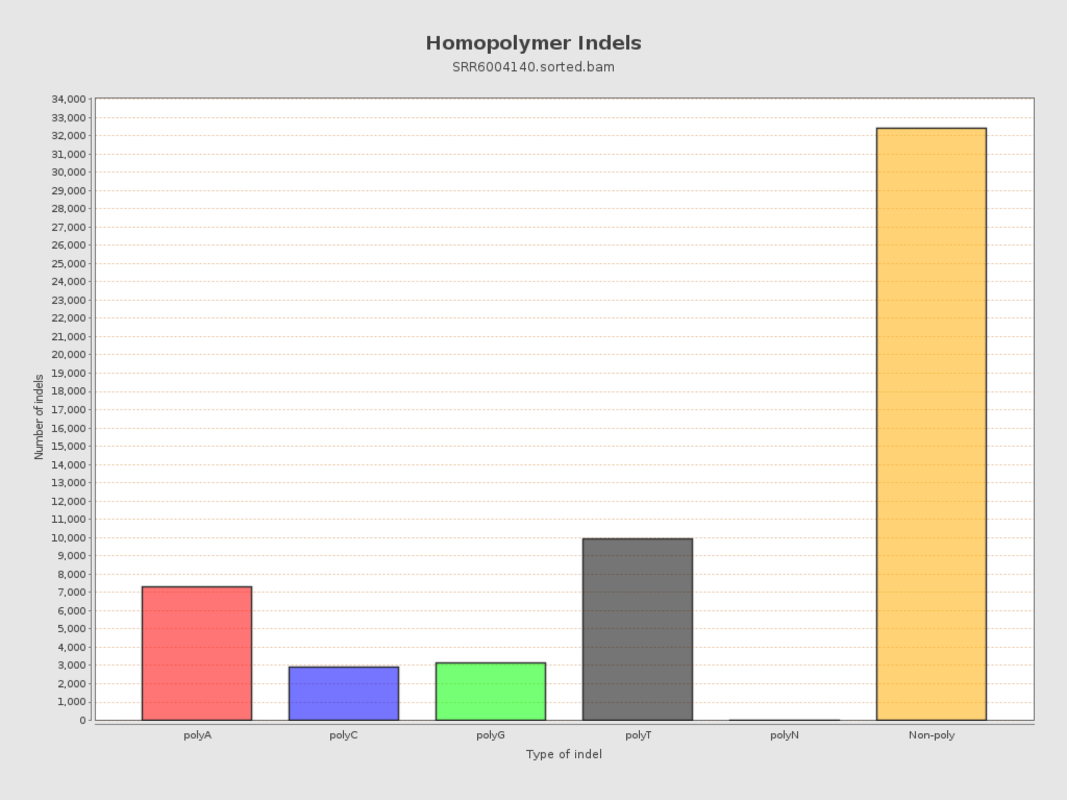
9. Results : Mapped Reads GC-content Distribution



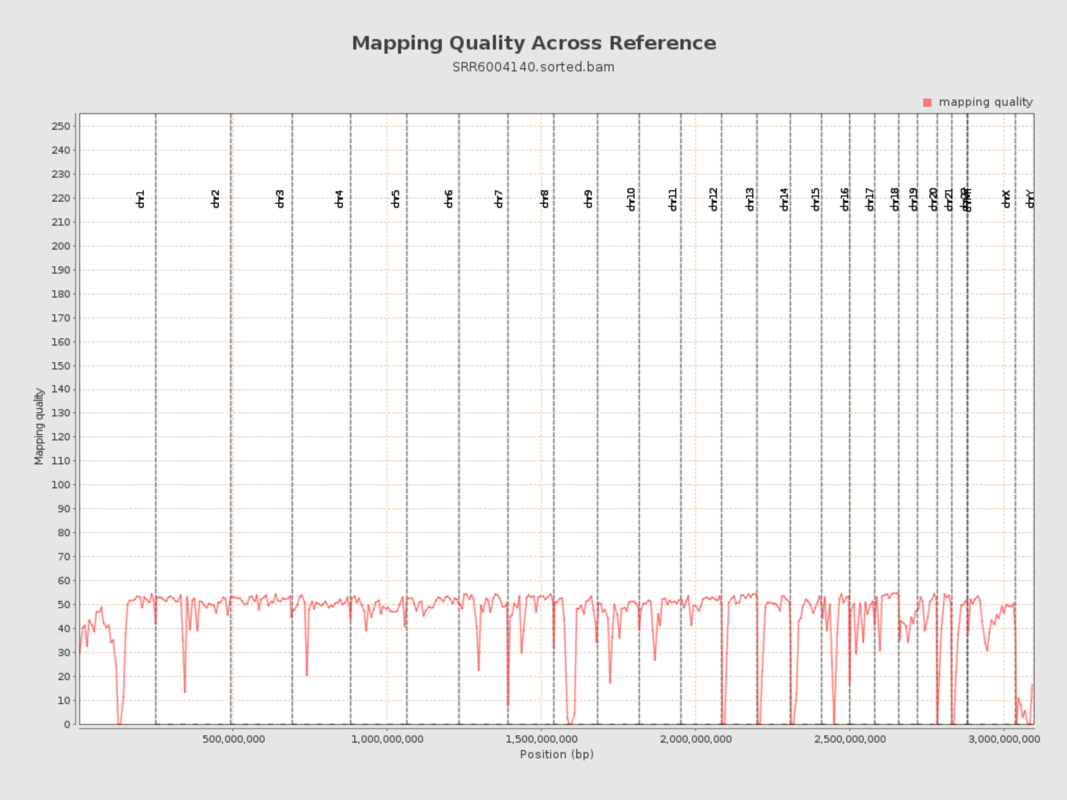
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram