Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:05:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240240.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_SRR6240240 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240240.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:05:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240240.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	672,741
Mapped reads	511,526 / 76.04%
Unmapped reads	161,215 / 23.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,449 / 0.36%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	40,198 / 5.98%
Duplication rate	6.11%
Clipped reads	313,740 / 46.64%

2.2. ACGT Content

Number/percentage of A's	8,282,167 / 25.92%
Number/percentage of C's	5,484,846 / 17.16%
Number/percentage of T's	10,548,143 / 33.01%
Number/percentage of G's	7,622,349 / 23.85%
Number/percentage of N's	17,030 / 0.05%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1451

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

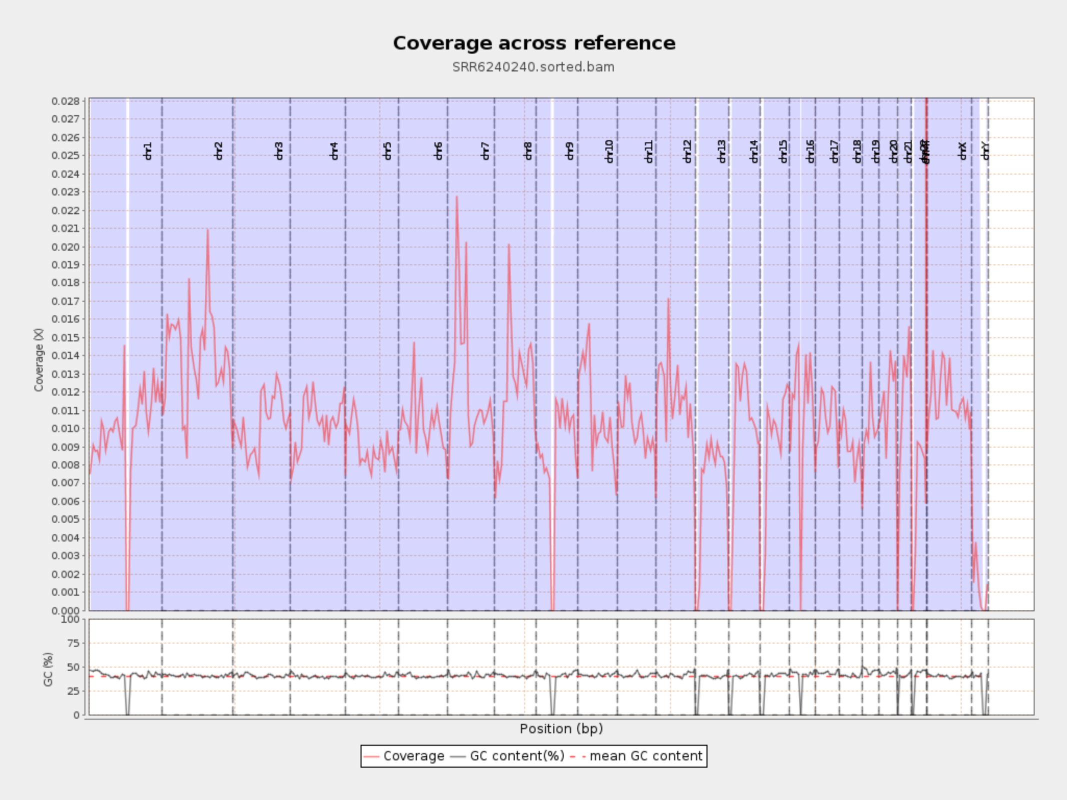
General error rate	0.93%
Mismatches	293,278
Insertions	2,239
Mapped reads with at least one insertion	0.43%
Deletions	10,792
Mapped reads with at least one deletion	2.09%
Homopolymer indels	49.7%

2.6. Chromosome stats

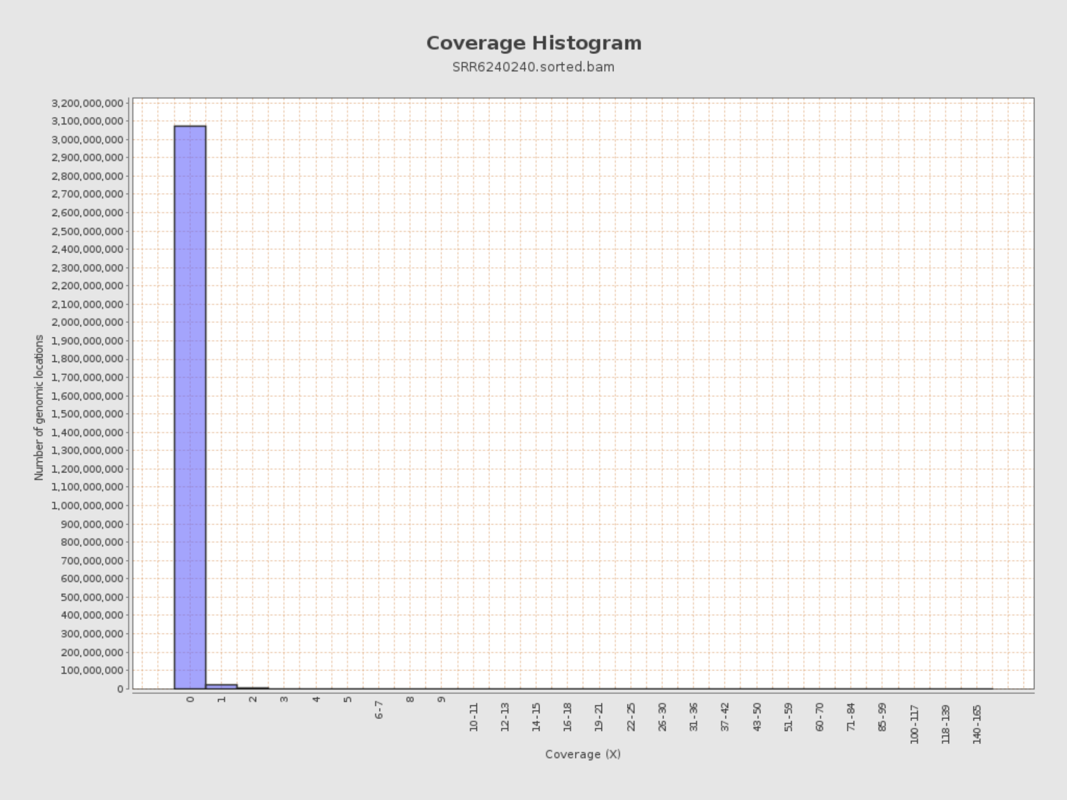
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2435662	0.0098	0.1736
chr2	243199373	3410680	0.014	0.179
chr3	198022430	2026355	0.0102	0.1307
chr4	191154276	1965440	0.0103	0.1315
chr5	180915260	1624654	0.009	0.1189
chr6	171115067	1765483	0.0103	0.1381
chr7	159138663	1991802	0.0125	0.198

chr8	146364022	1782967	0.0122	0.1613
chr9	141213431	1209927	0.0086	0.132
chr10	135534747	1482999	0.0109	0.1423
chr11	135006516	1369420	0.0101	0.1387
chr12	133851895	1576650	0.0118	0.1431
chr13	115169878	793929	0.0069	0.1049
chr14	107349540	1043147	0.0097	0.1274
chr15	102531392	879071	0.0086	0.1242
chr16	90354753	990292	0.011	0.1373
chr17	81195210	855071	0.0105	0.135
chr18	78077248	712136	0.0091	0.1543
chr19	59128983	596946	0.0101	0.1481
chr20	63025520	732297	0.0116	0.1413
chr21	48129895	525959	0.0109	0.1364
chr22	51304566	309526	0.006	0.0992
chrMT	16571	13584	0.8197	1.2137
chrX	155270560	1797691	0.0116	0.1398
chrY	59373566	81949	0.0014	0.0453

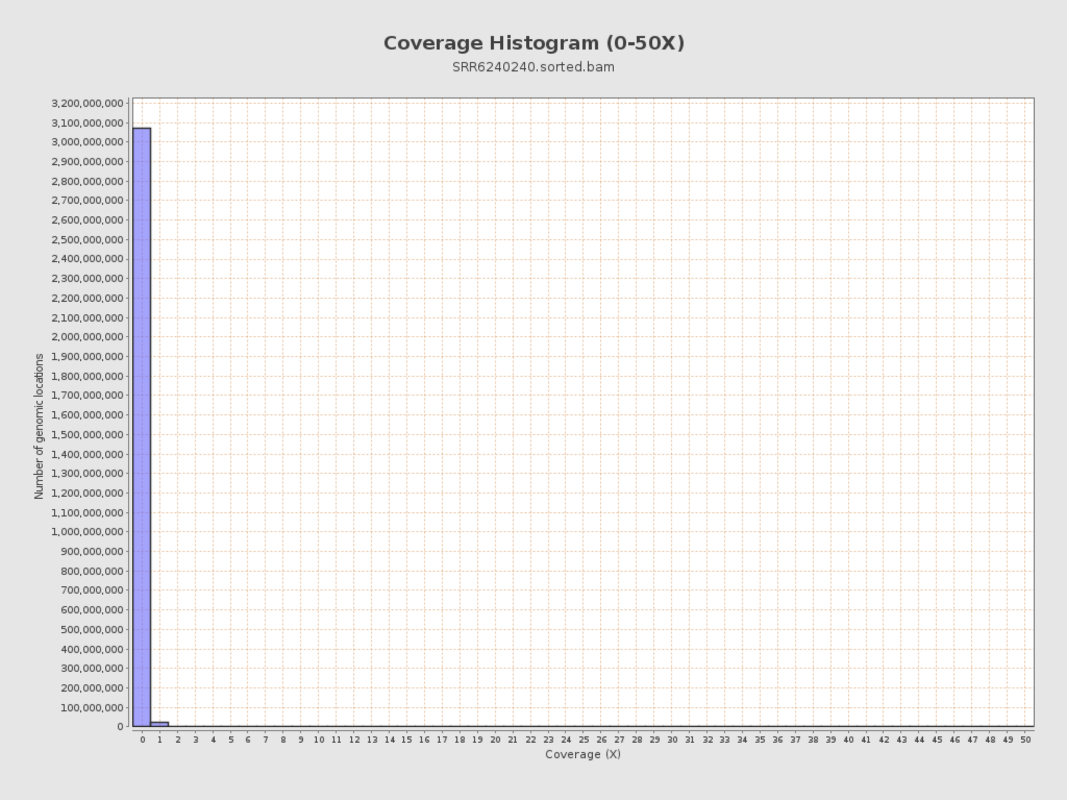
3. Results : Coverage across reference



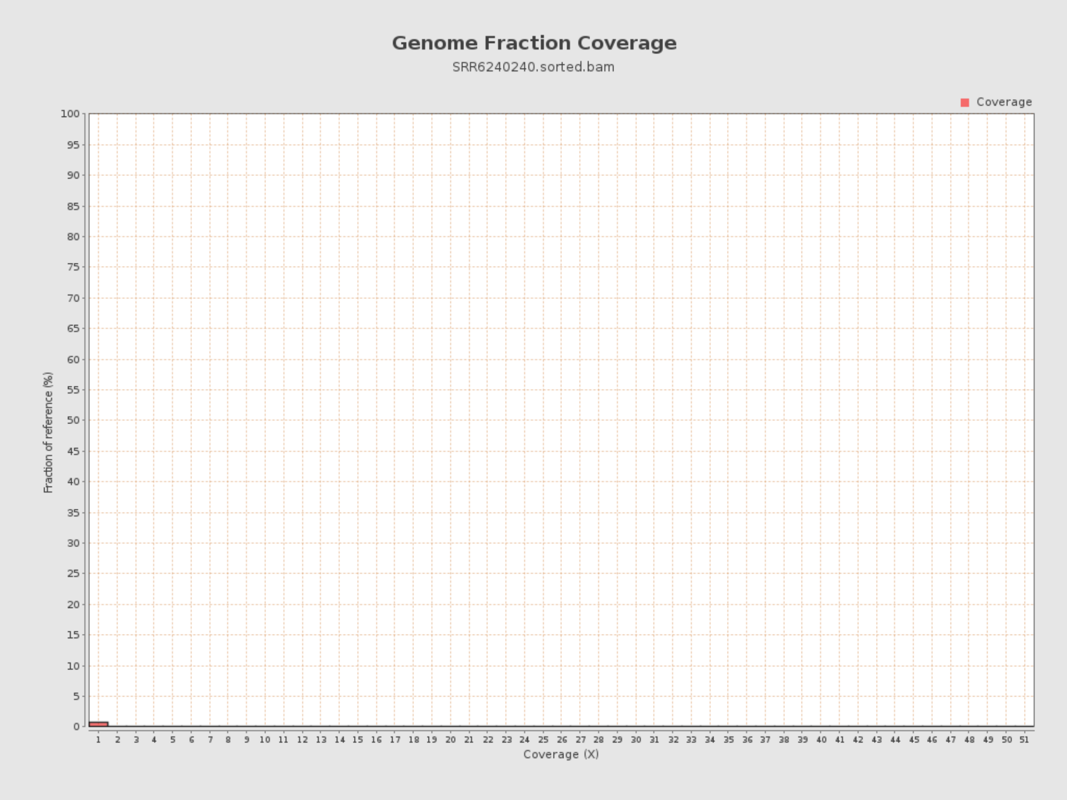
4. Results : Coverage Histogram



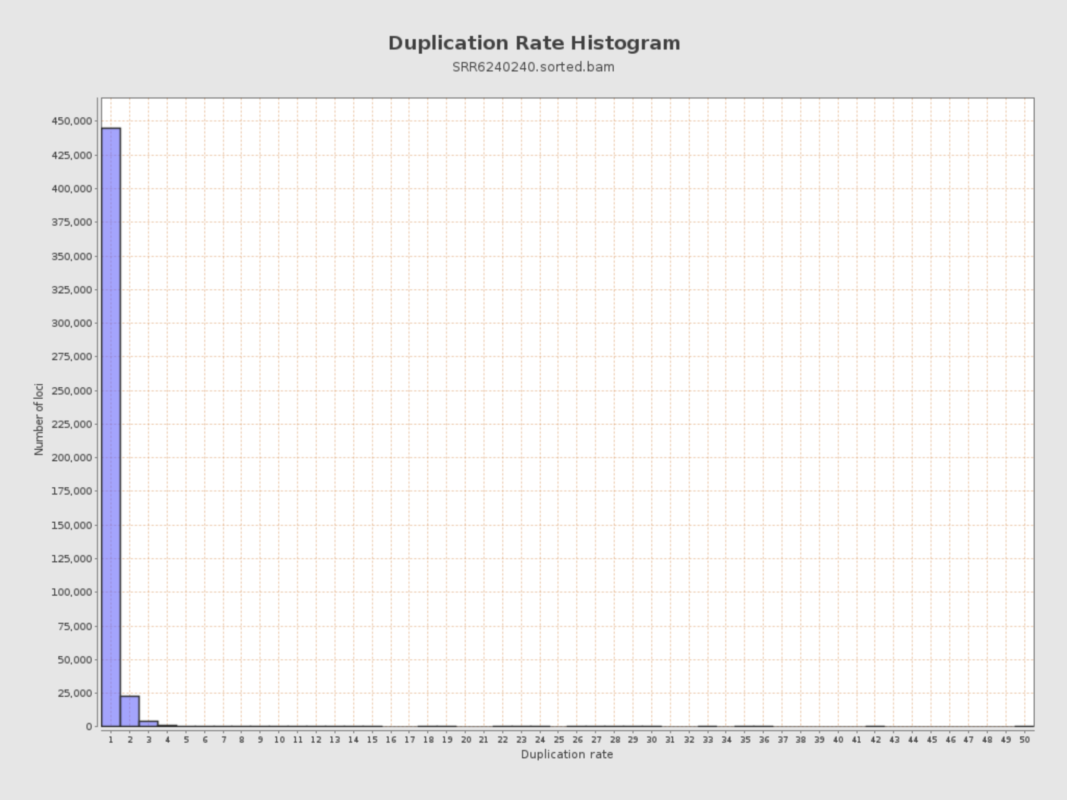
5. Results : Coverage Histogram (0-50X)



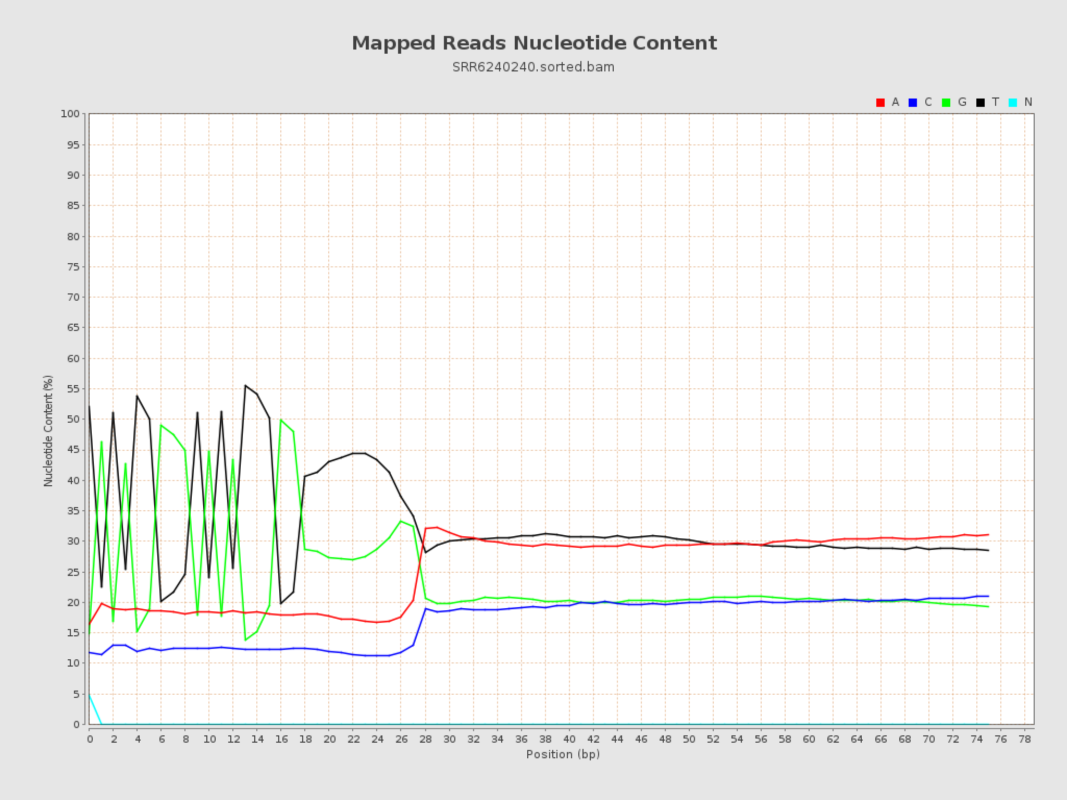
6. Results : Genome Fraction Coverage



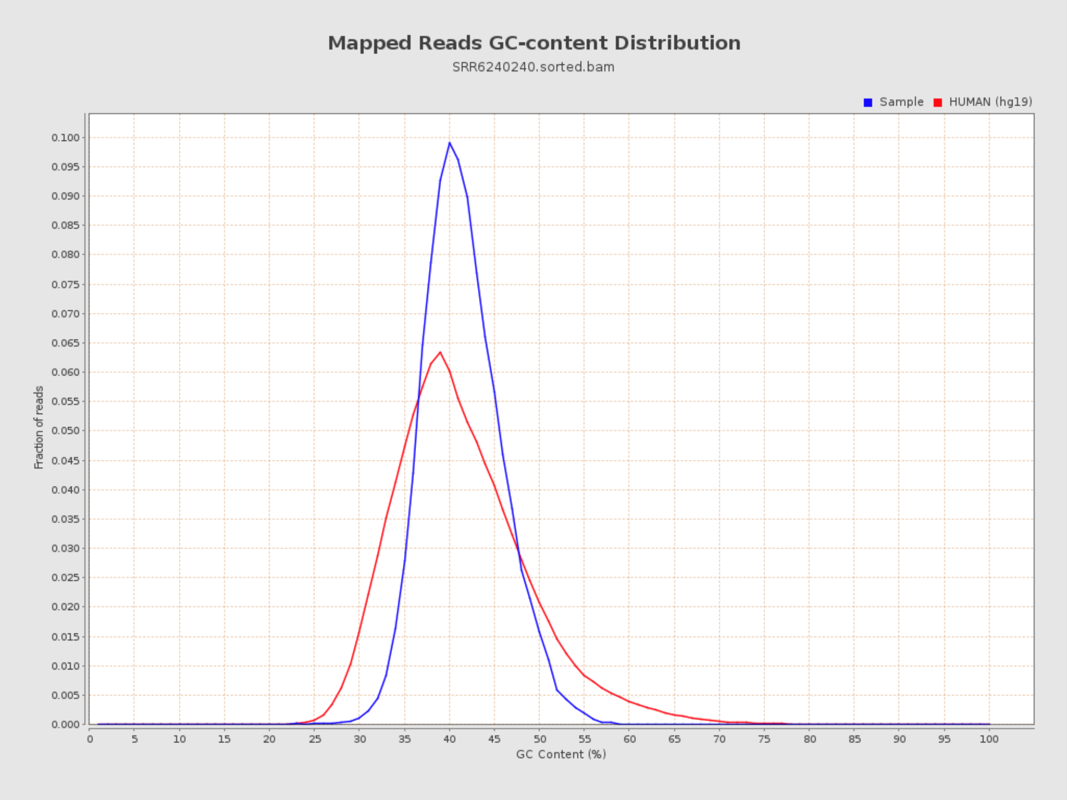
7. Results : Duplication Rate Histogram



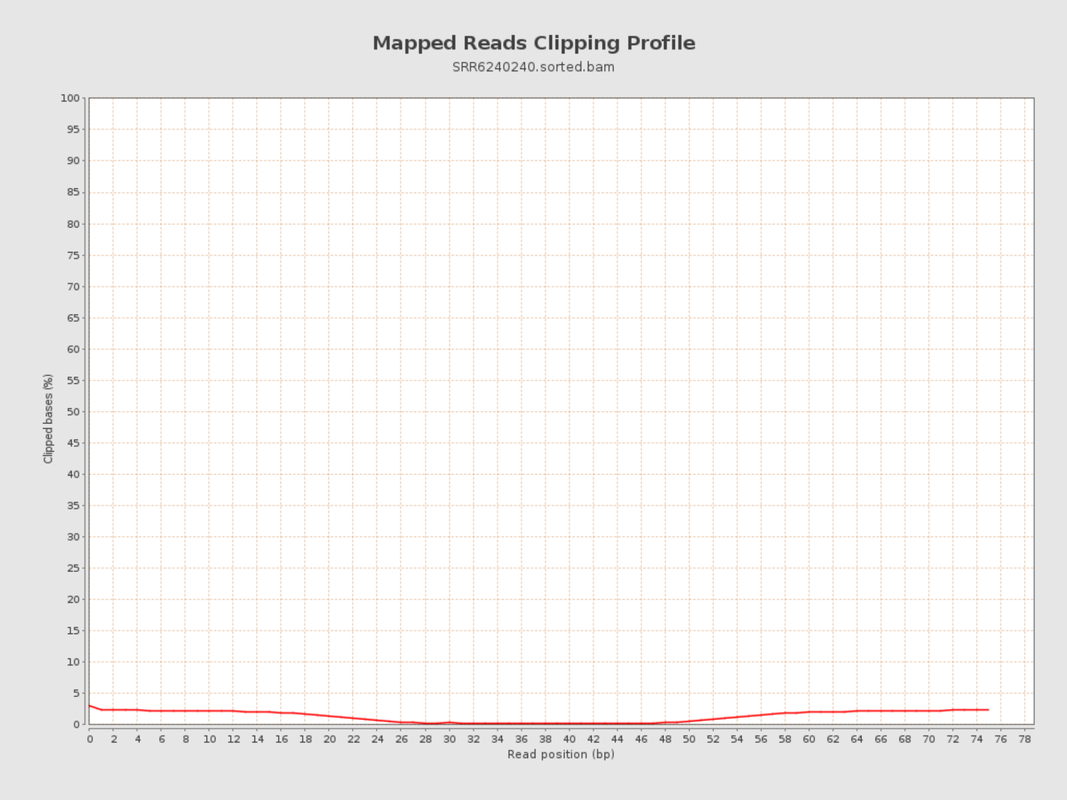
8. Results : Mapped Reads Nucleotide Content



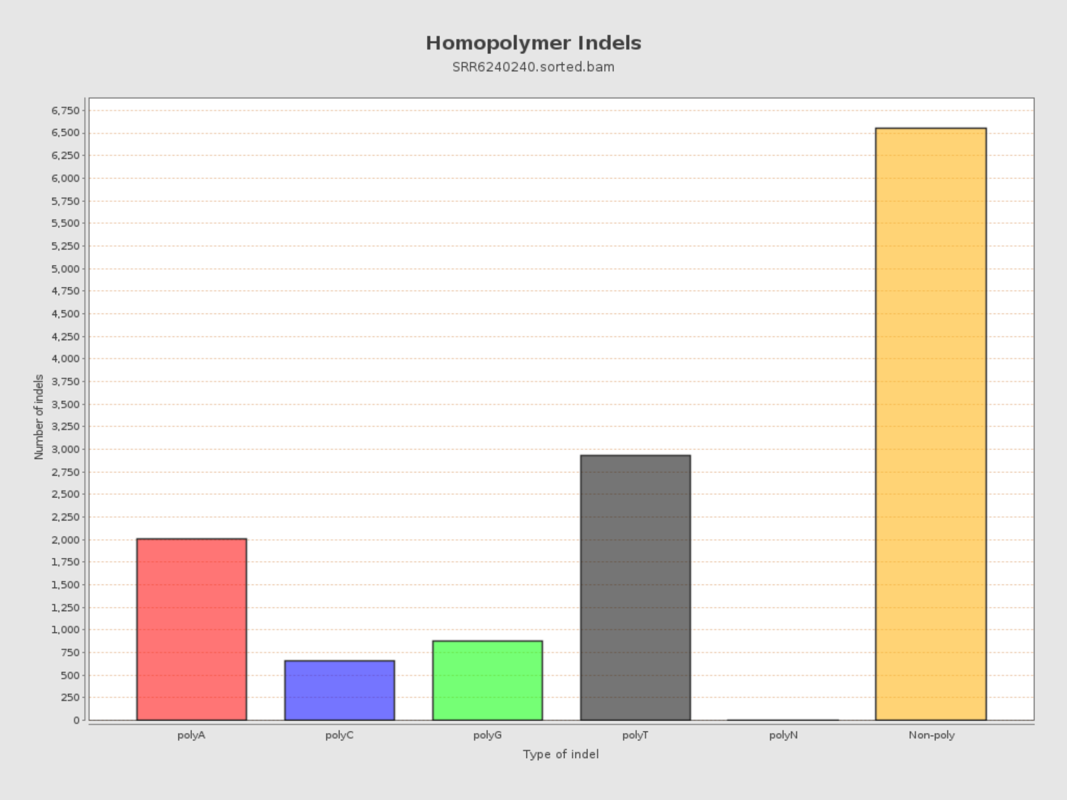
9. Results : Mapped Reads GC-content Distribution



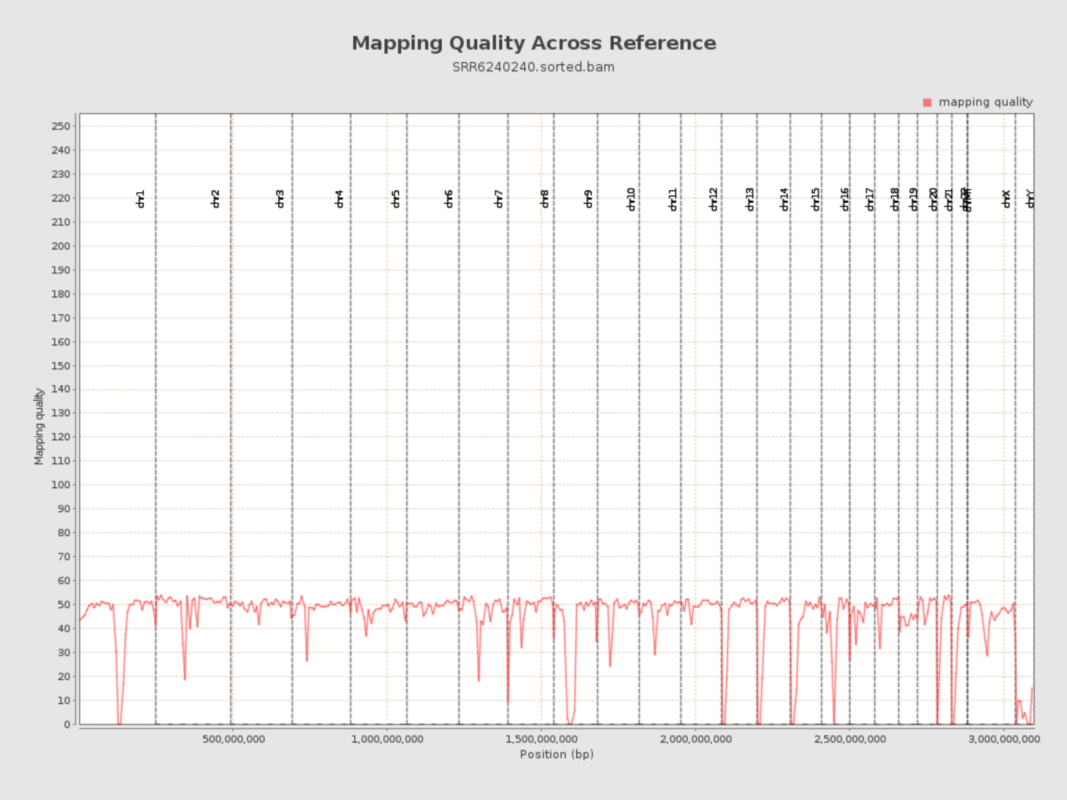
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram