Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:51:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240257.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_SRR6240257 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240257.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:51:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240257.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,175,084
Mapped reads	886,372 / 75.43%
Unmapped reads	288,712 / 24.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,428 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	27,657 / 2.35%
Duplication rate	2.39%
Clipped reads	513,167 / 43.67%

2.2. ACGT Content

Number/percentage of A's	16,023,103 / 28.57%
Number/percentage of C's	9,731,087 / 17.35%
Number/percentage of T's	17,617,687 / 31.41%
Number/percentage of G's	12,707,404 / 22.65%
Number/percentage of N's	13,624 / 0.02%
GC Percentage	40%

2.3. Coverage

Mean	0.0181

Standard Deviation	0.2077

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

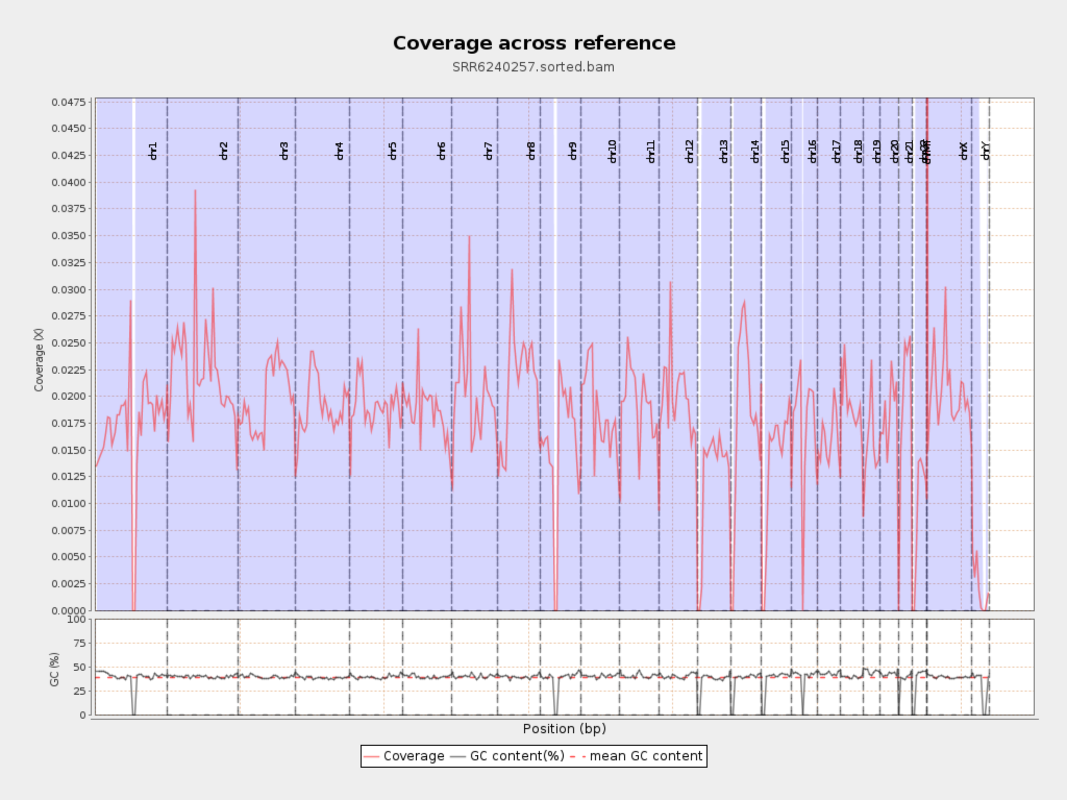
General error rate	1.03%
Mismatches	568,334
Insertions	4,109
Mapped reads with at least one insertion	0.46%
Deletions	17,922
Mapped reads with at least one deletion	2%
Homopolymer indels	48.92%

2.6. Chromosome stats

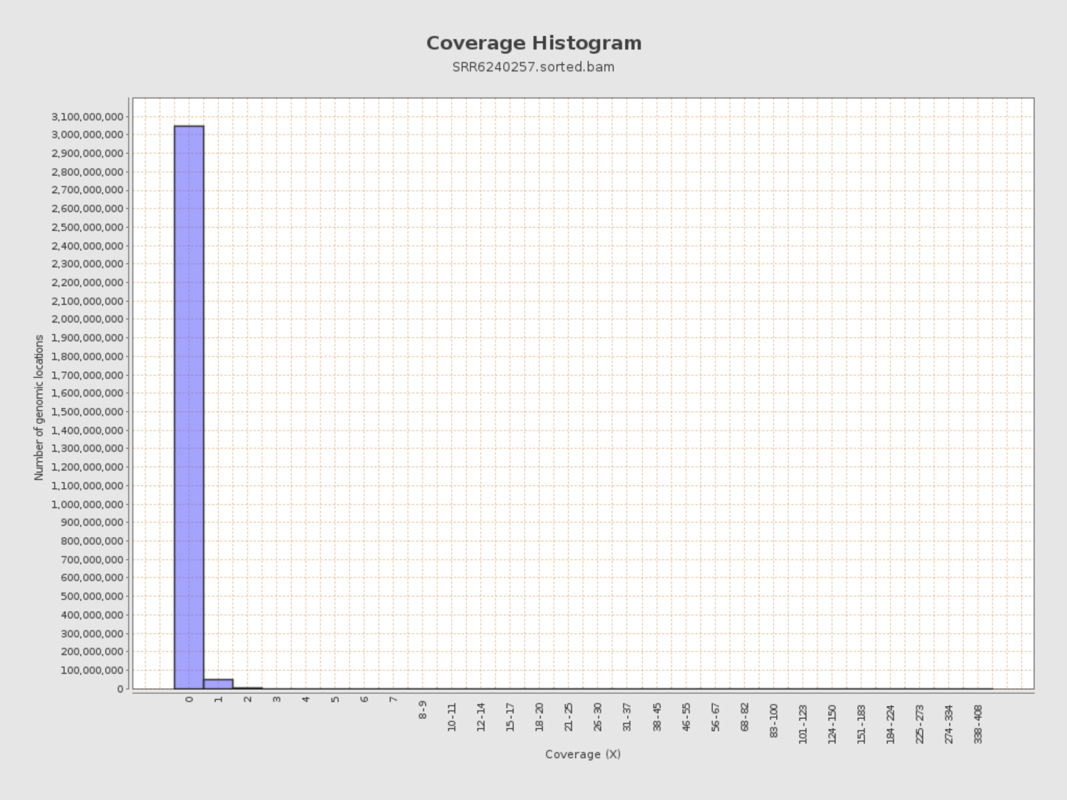
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4236360	0.017	0.3291
chr2	243199373	5407130	0.0222	0.2457
chr3	198022430	3935697	0.0199	0.153
chr4	191154276	3631210	0.019	0.1522
chr5	180915260	3459949	0.0191	0.1509
chr6	171115067	3196778	0.0187	0.1728
chr7	159138663	3235040	0.0203	0.3081

chr8	146364022	3133478	0.0214	0.2984
chr9	141213431	2172437	0.0154	0.1911
chr10	135534747	2501168	0.0185	0.1679
chr11	135006516	2604029	0.0193	0.194
chr12	133851895	2679633	0.02	0.1558
chr13	115169878	1417109	0.0123	0.1195
chr14	107349540	1964794	0.0183	0.1526
chr15	102531392	1396198	0.0136	0.1307
chr16	90354753	1524864	0.0169	0.1471
chr17	81195210	1304174	0.0161	0.1481
chr18	78077248	1499212	0.0192	0.3112
chr19	59128983	932396	0.0158	0.2265
chr20	63025520	1148858	0.0182	0.1505
chr21	48129895	932402	0.0194	0.1566
chr22	51304566	481172	0.0094	0.1043
chrMT	16571	15679	0.9462	1.2159
chrX	155270560	3187967	0.0205	0.1689
chrY	59373566	126158	0.0021	0.0536

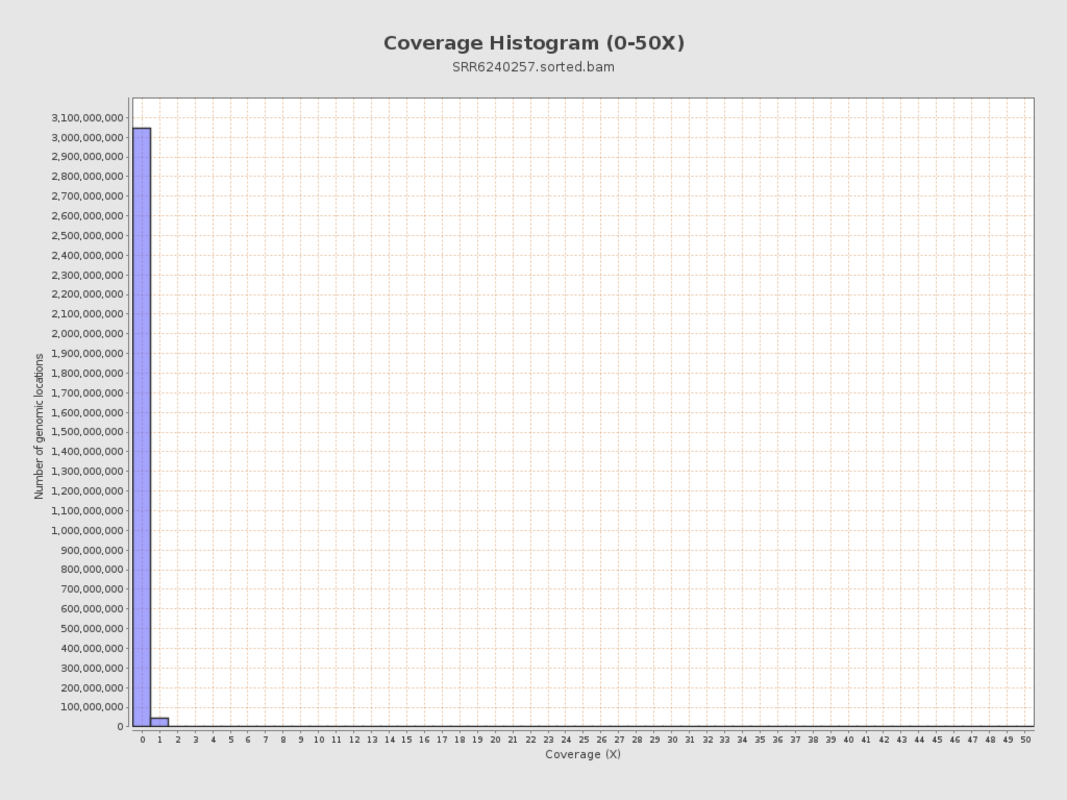
3. Results : Coverage across reference



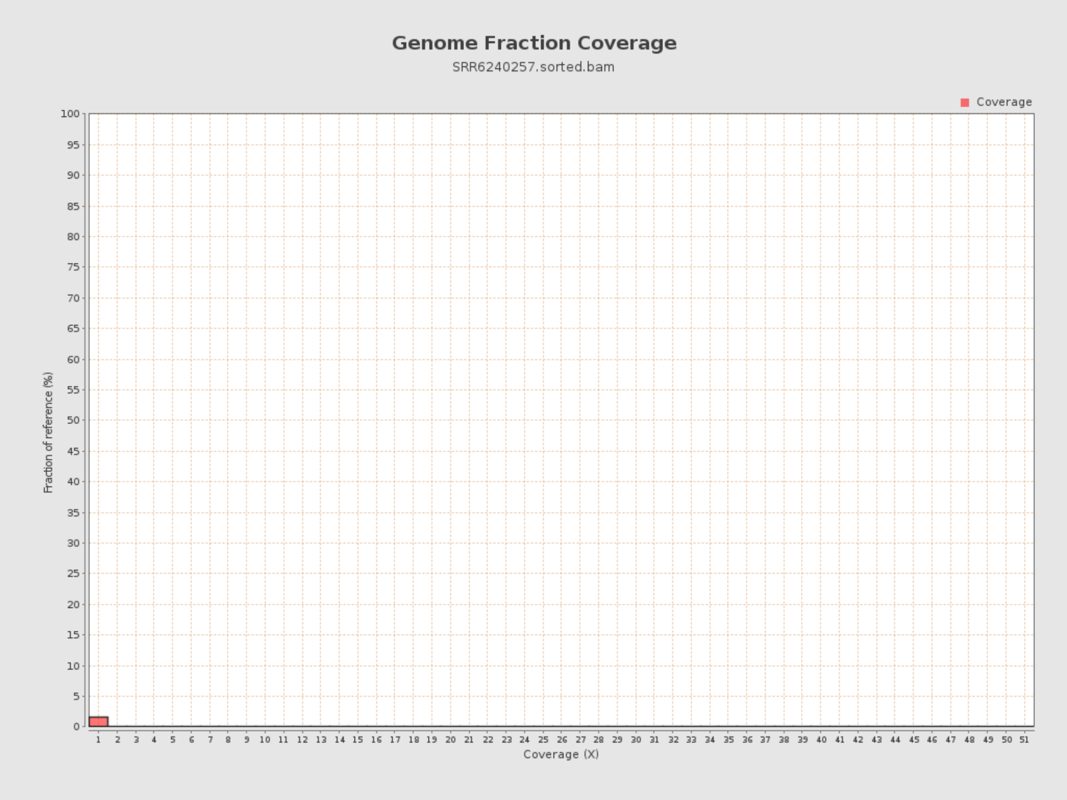
4. Results : Coverage Histogram



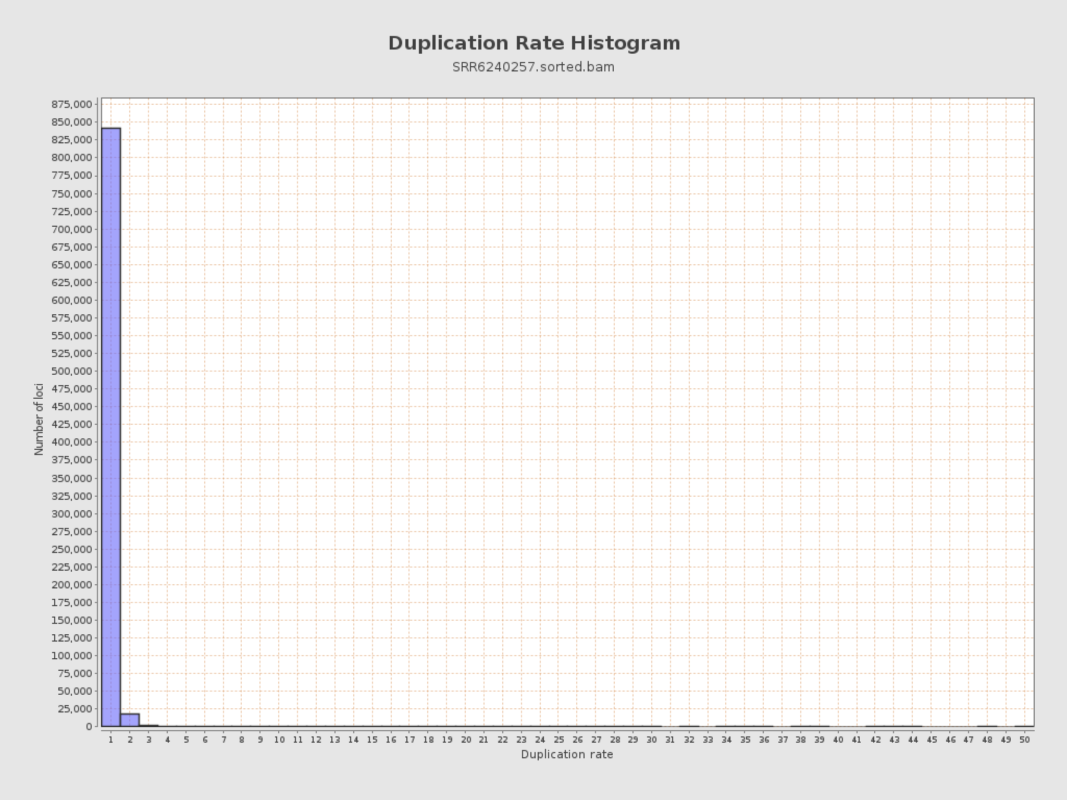
5. Results : Coverage Histogram (0-50X)



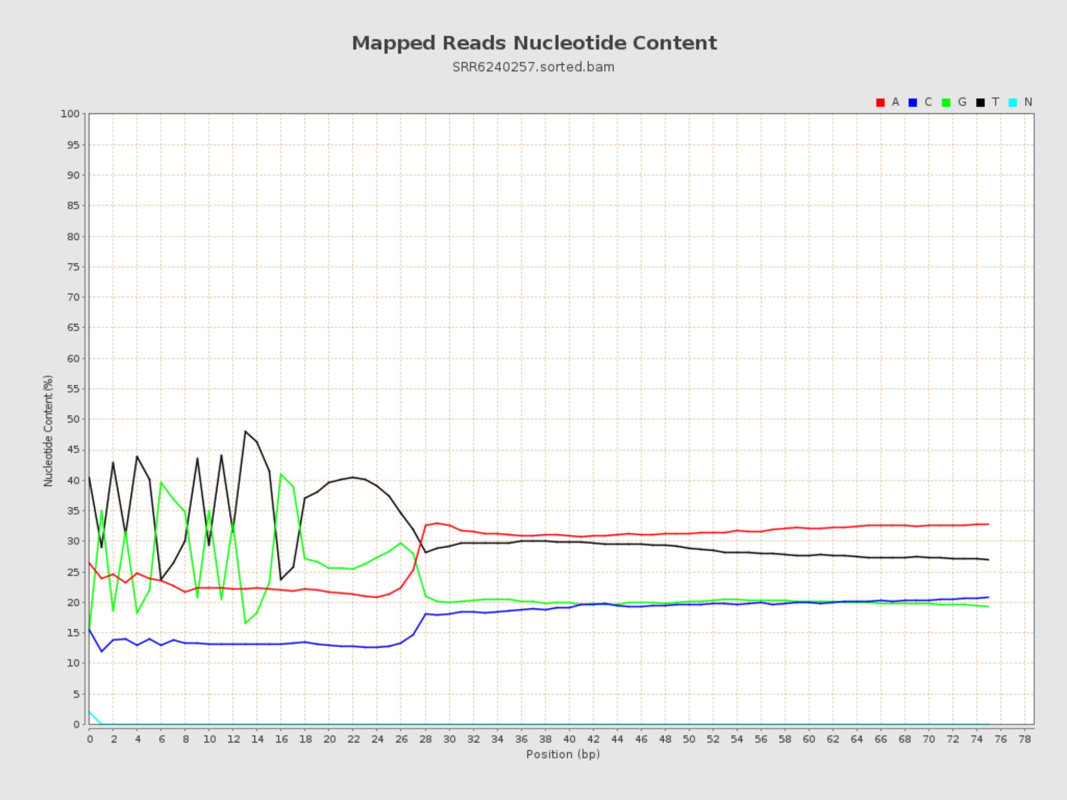
6. Results : Genome Fraction Coverage



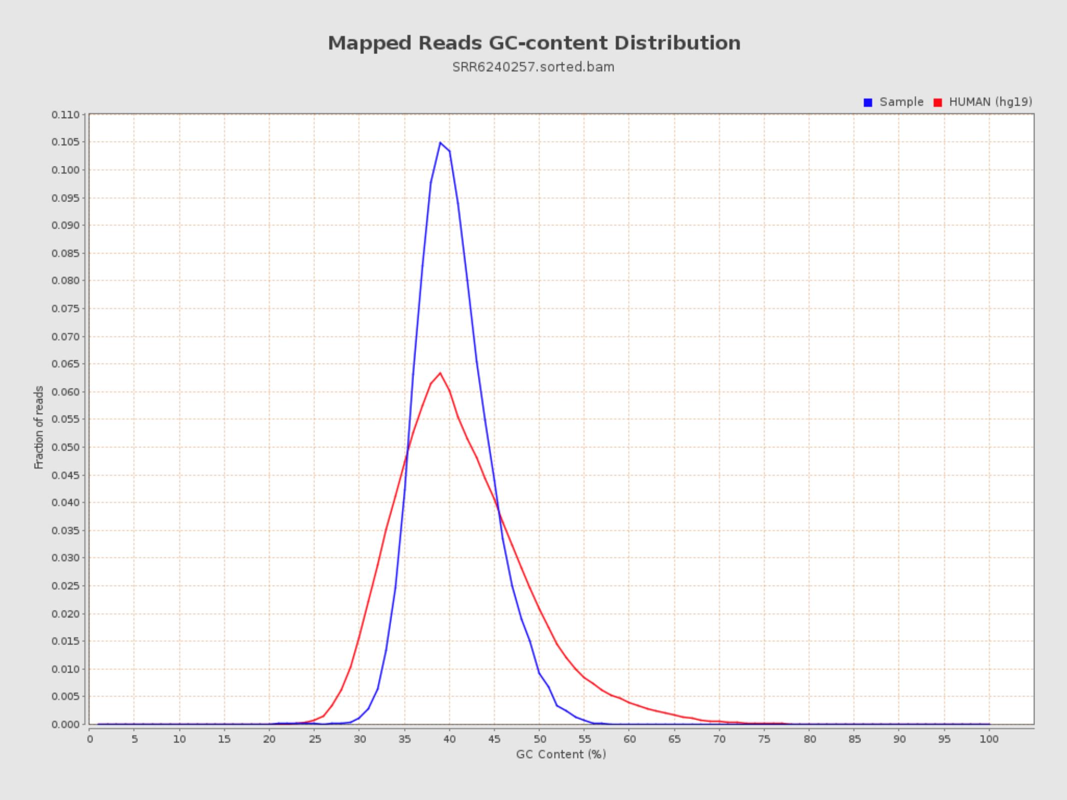
7. Results : Duplication Rate Histogram



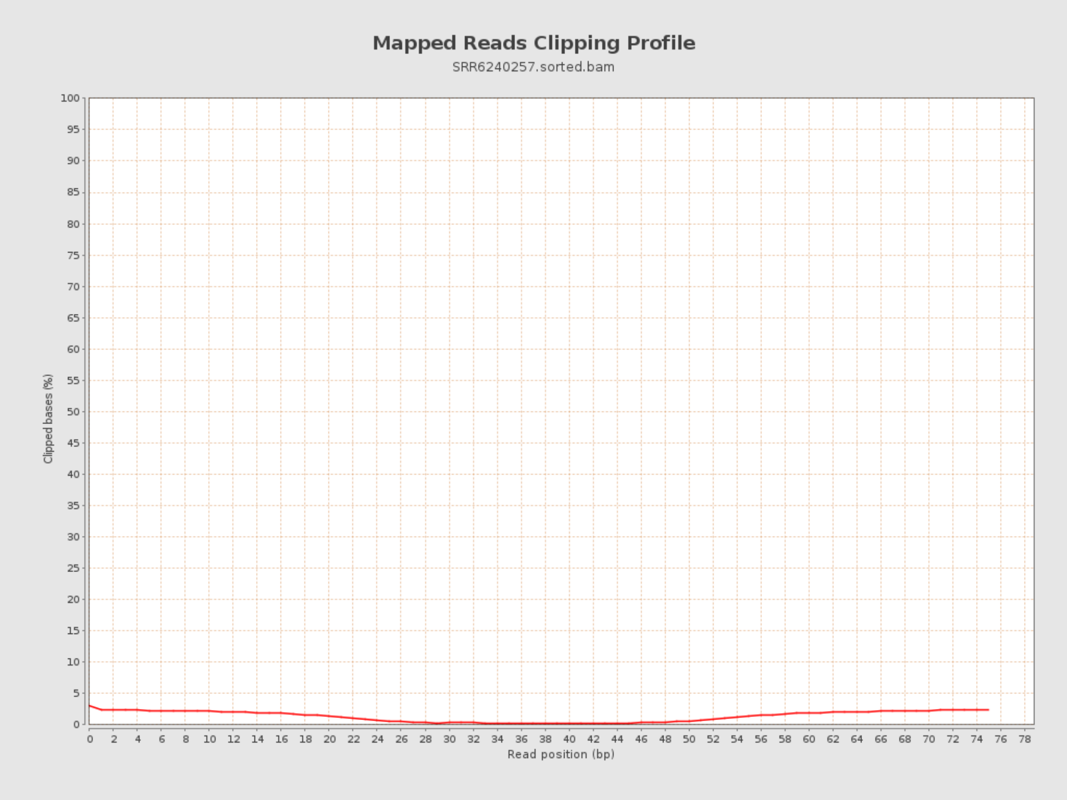
8. Results : Mapped Reads Nucleotide Content



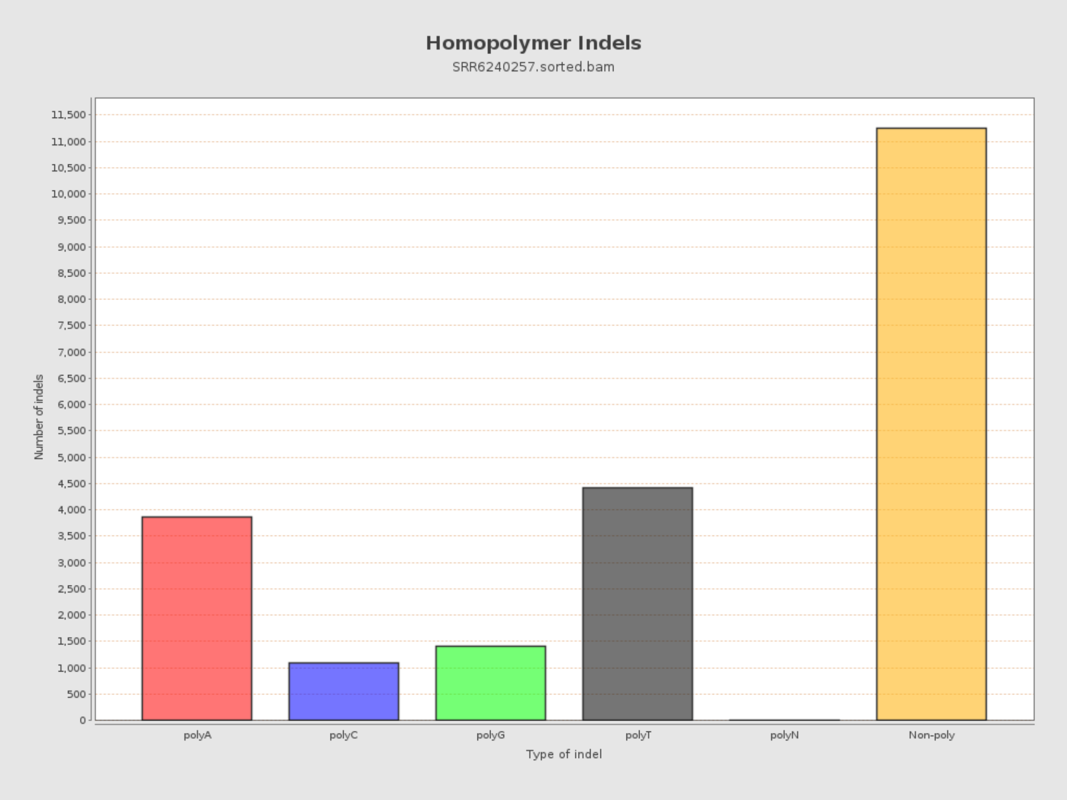
9. Results : Mapped Reads GC-content Distribution



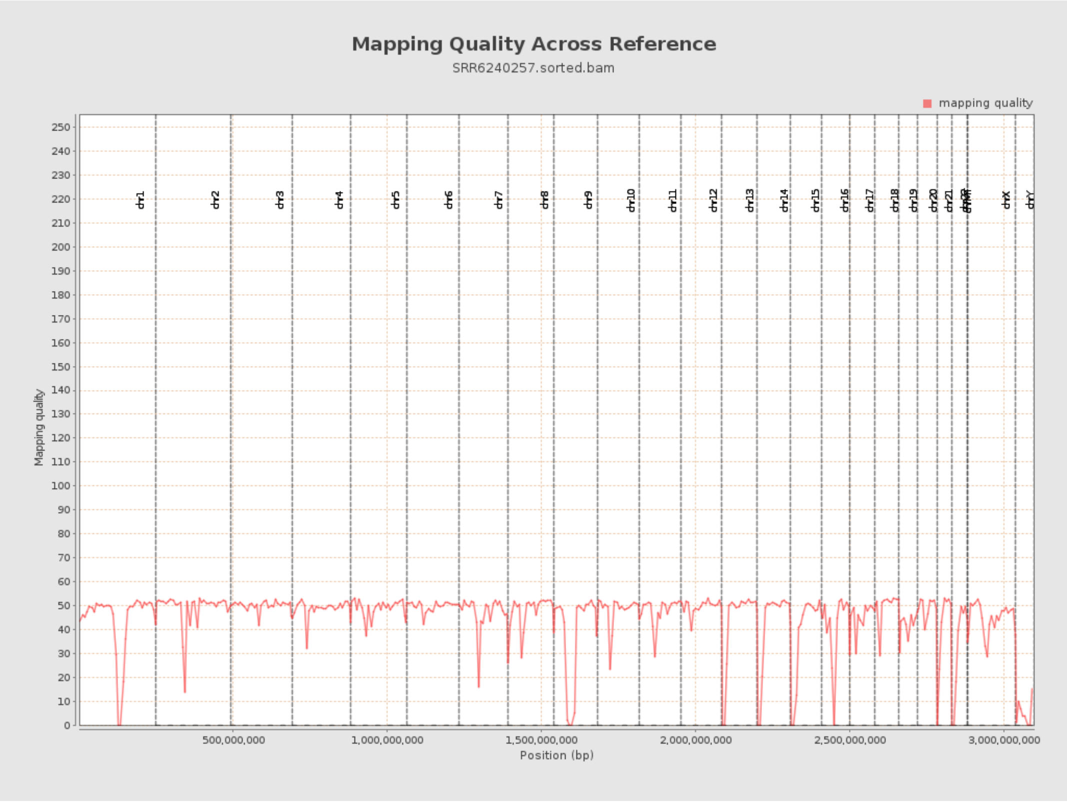
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram