Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:23:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240246.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_SRR6240246 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240246.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:23:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240246.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,757,192
Mapped reads	1,176,152 / 66.93%
Unmapped reads	581,040 / 33.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,010 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	220,152 / 12.53%
Duplication rate	13.01%
Clipped reads	725,165 / 41.27%

2.2. ACGT Content

Number/percentage of A's	20,048,779 / 27.27%
Number/percentage of C's	12,860,442 / 17.49%
Number/percentage of T's	24,198,074 / 32.92%
Number/percentage of G's	16,399,746 / 22.31%
Number/percentage of N's	6,811 / 0.01%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.3373

2.4. Mapping Quality

Mean Mapping Quality	45.65

2.5. Mismatches and indels

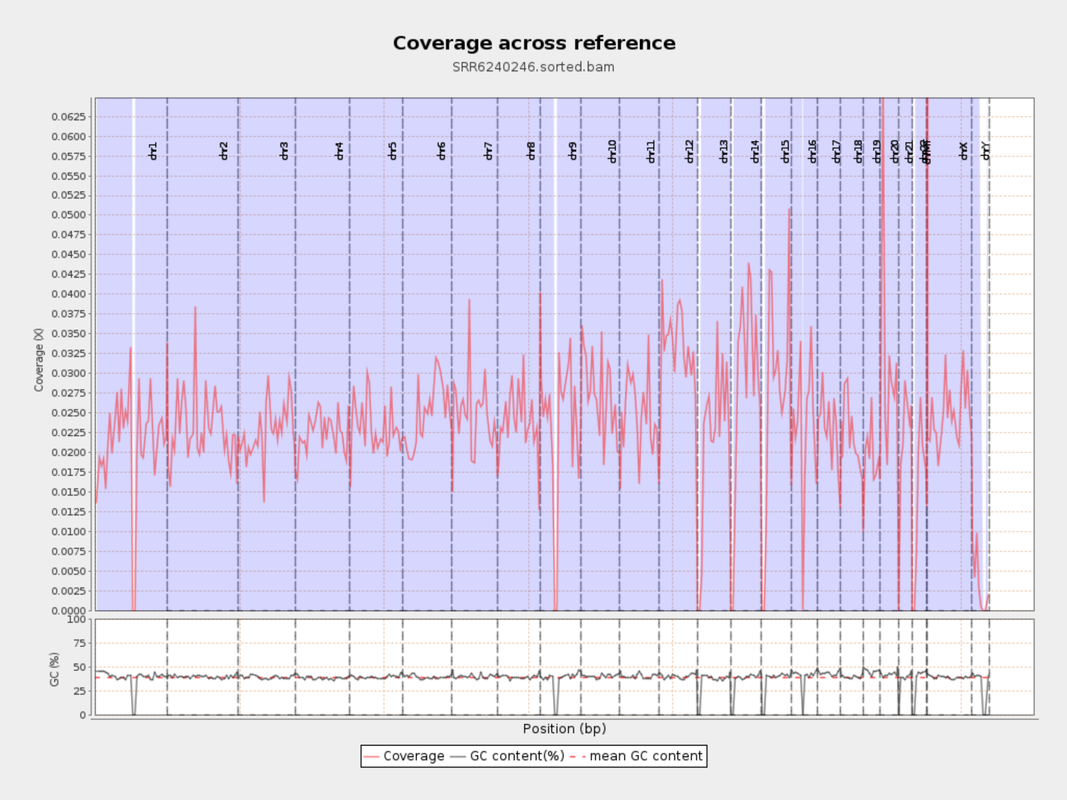
General error rate	0.91%
Mismatches	658,157
Insertions	5,119
Mapped reads with at least one insertion	0.43%
Deletions	22,234
Mapped reads with at least one deletion	1.87%
Homopolymer indels	48.48%

2.6. Chromosome stats

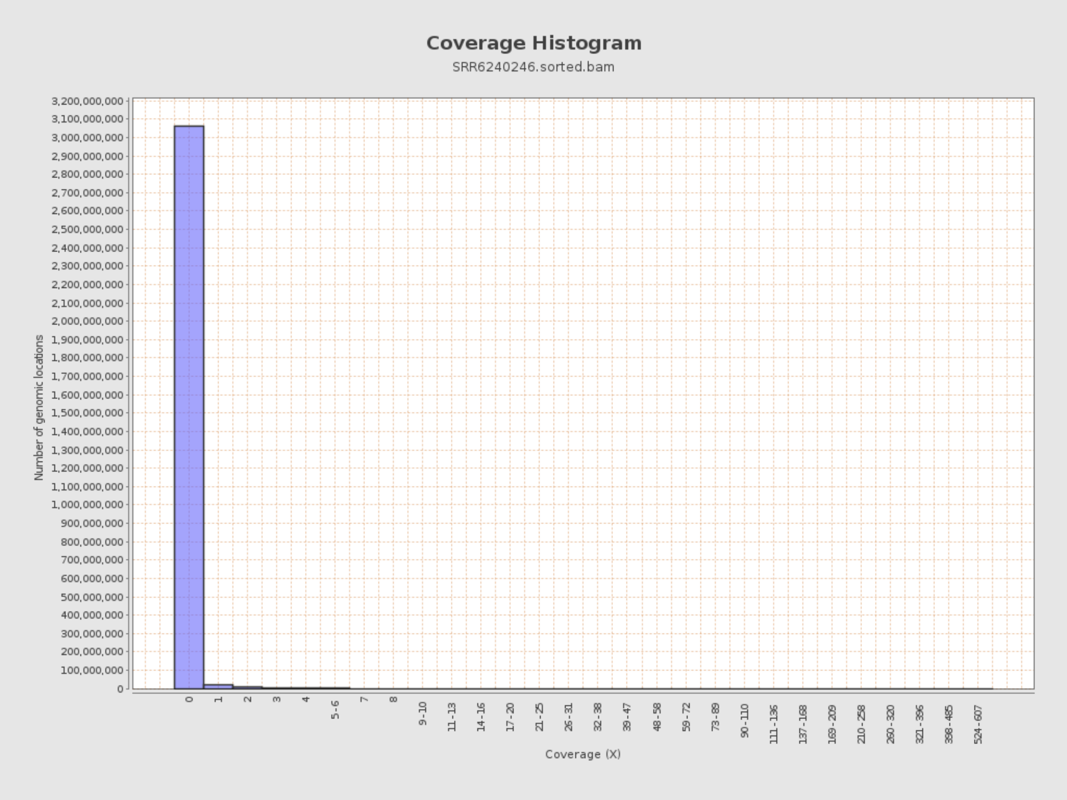
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5285892	0.0212	0.4041
chr2	243199373	5633043	0.0232	0.3441
chr3	198022430	4506482	0.0228	0.2824
chr4	191154276	4278463	0.0224	0.2896
chr5	180915260	4237599	0.0234	0.2995
chr6	171115067	4266597	0.0249	0.3171
chr7	159138663	3978090	0.025	0.3779

chr8	146364022	3500980	0.0239	0.445
chr9	141213431	3298477	0.0234	0.3267
chr10	135534747	3734546	0.0276	0.3443
chr11	135006516	3367137	0.0249	0.3199
chr12	133851895	4415362	0.033	0.3685
chr13	115169878	2485091	0.0216	0.2979
chr14	107349540	3045446	0.0284	0.3554
chr15	102531392	2798957	0.0273	0.3501
chr16	90354753	2052011	0.0227	0.2917
chr17	81195210	1874261	0.0231	0.2979
chr18	78077248	1722759	0.0221	0.4361
chr19	59128983	1158006	0.0196	0.3098
chr20	63025520	2014804	0.032	0.3727
chr21	48129895	1041092	0.0216	0.2844
chr22	51304566	747285	0.0146	0.2256
chrMT	16571	32345	1.9519	3.0439
chrX	155270560	3885175	0.025	0.3074
chrY	59373566	192040	0.0032	0.111

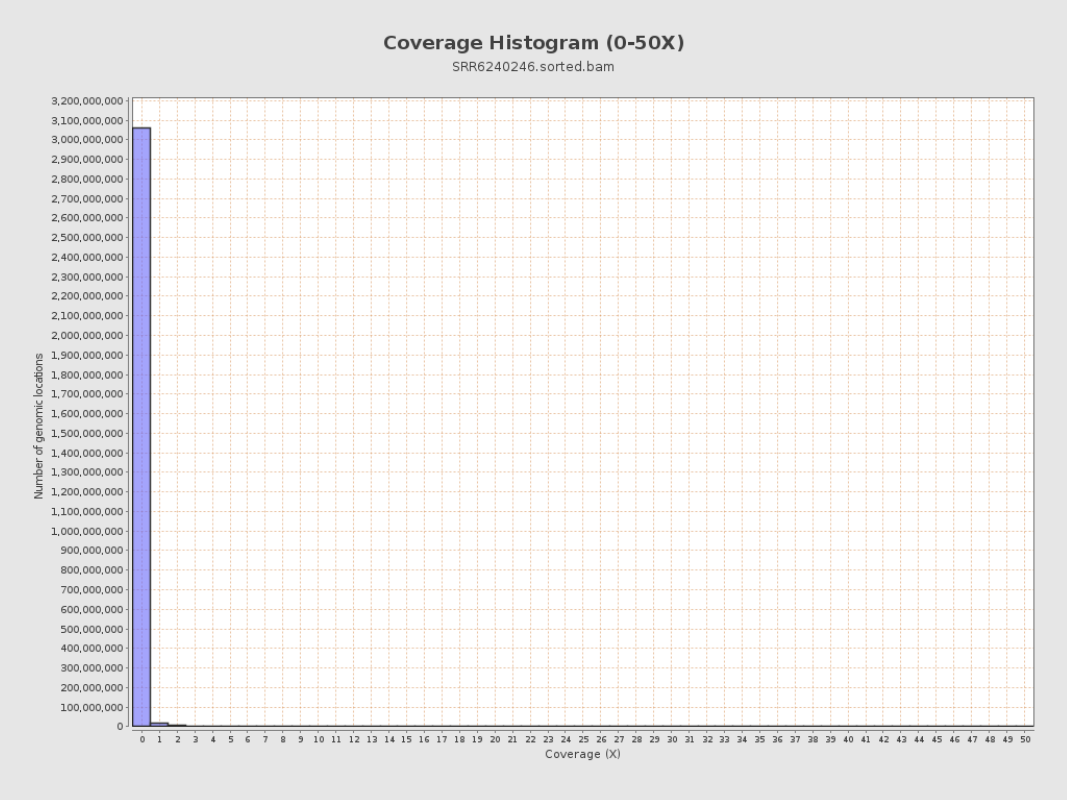
3. Results : Coverage across reference



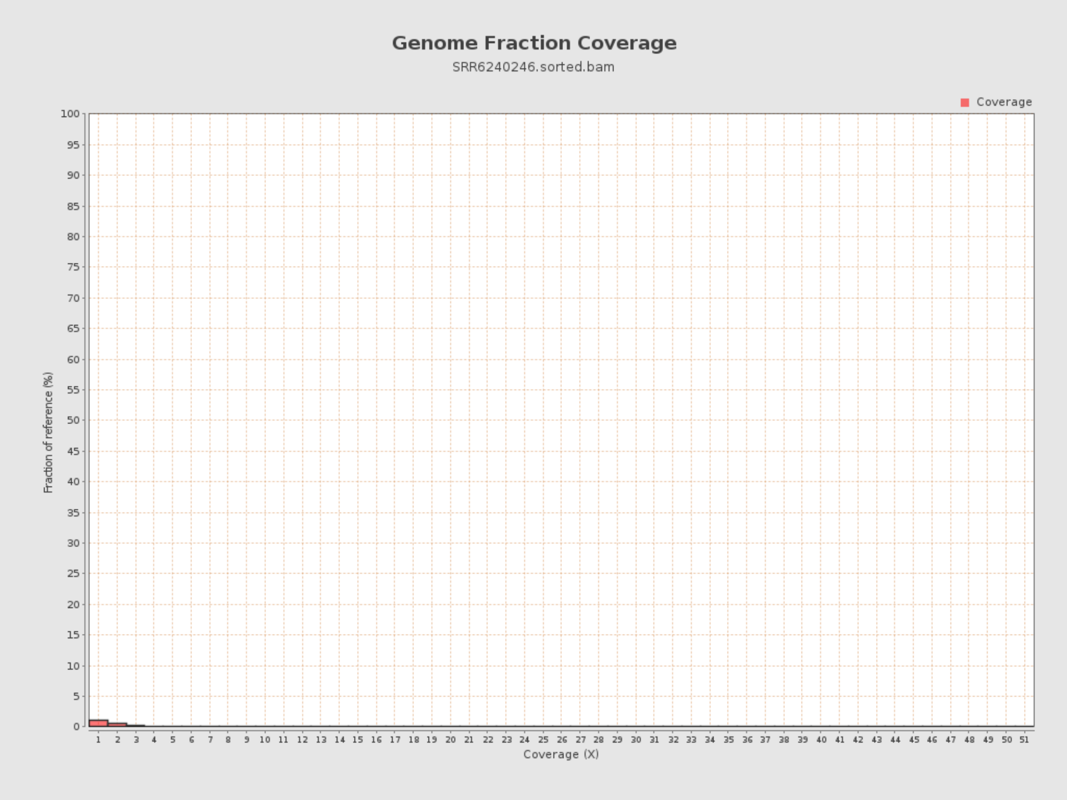
4. Results : Coverage Histogram



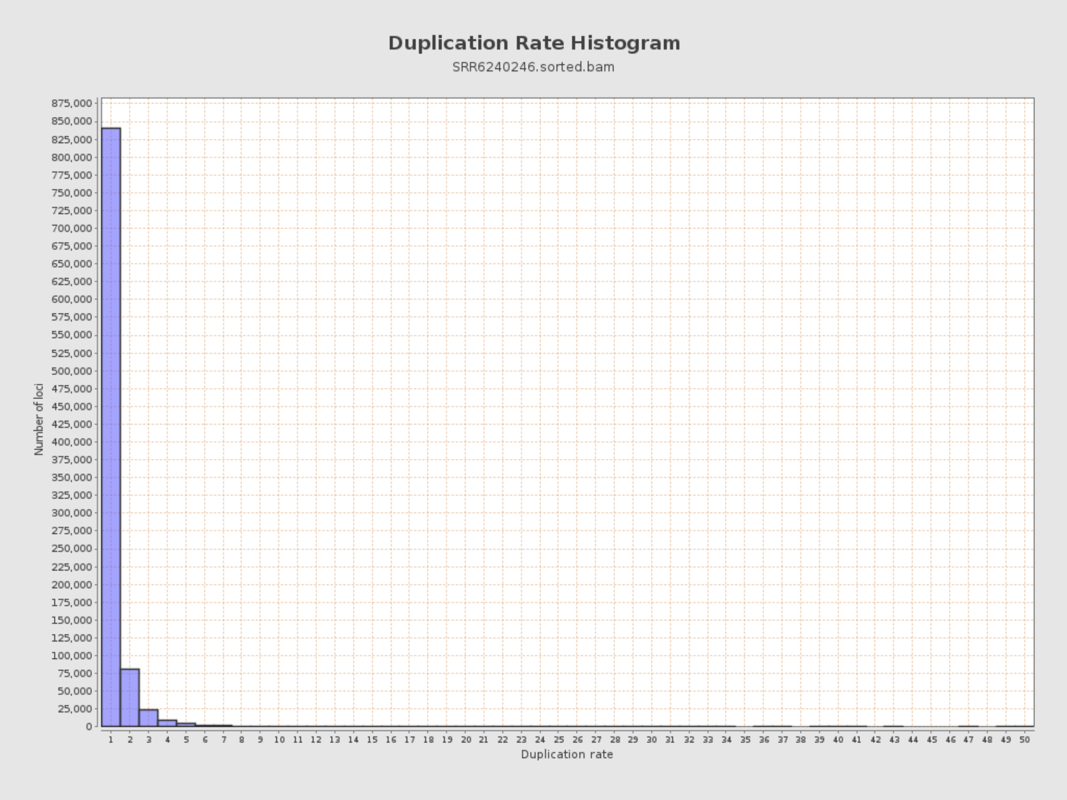
5. Results : Coverage Histogram (0-50X)



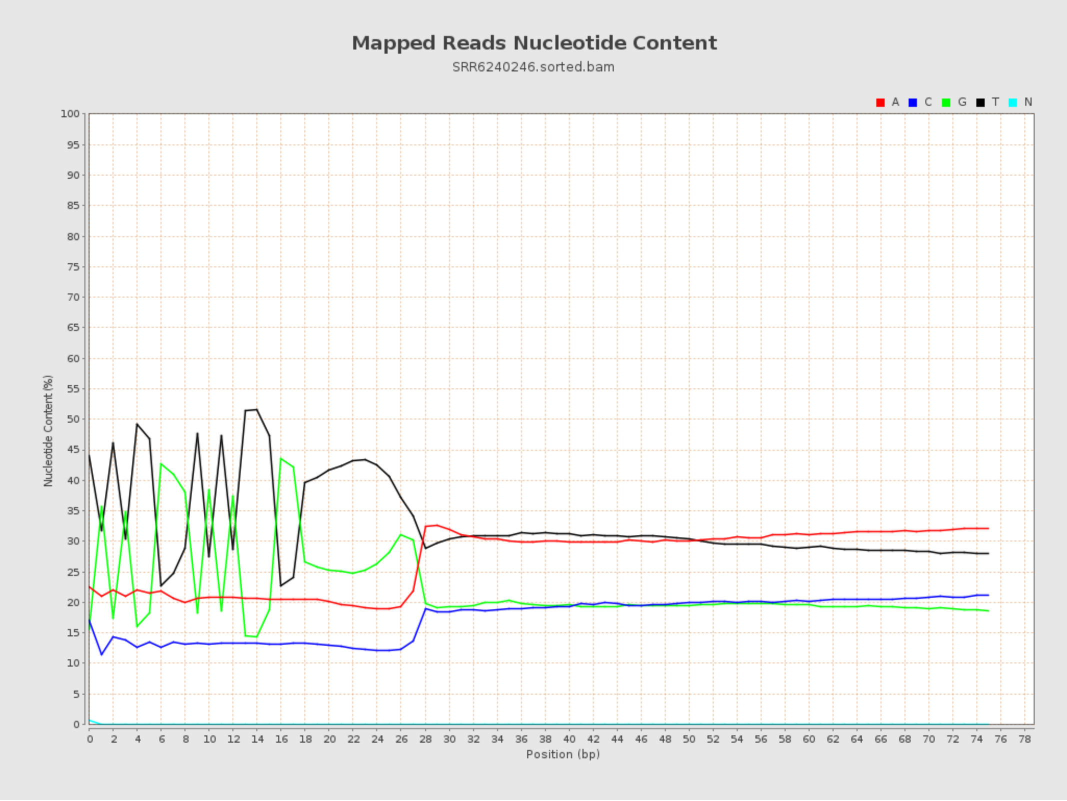
6. Results : Genome Fraction Coverage



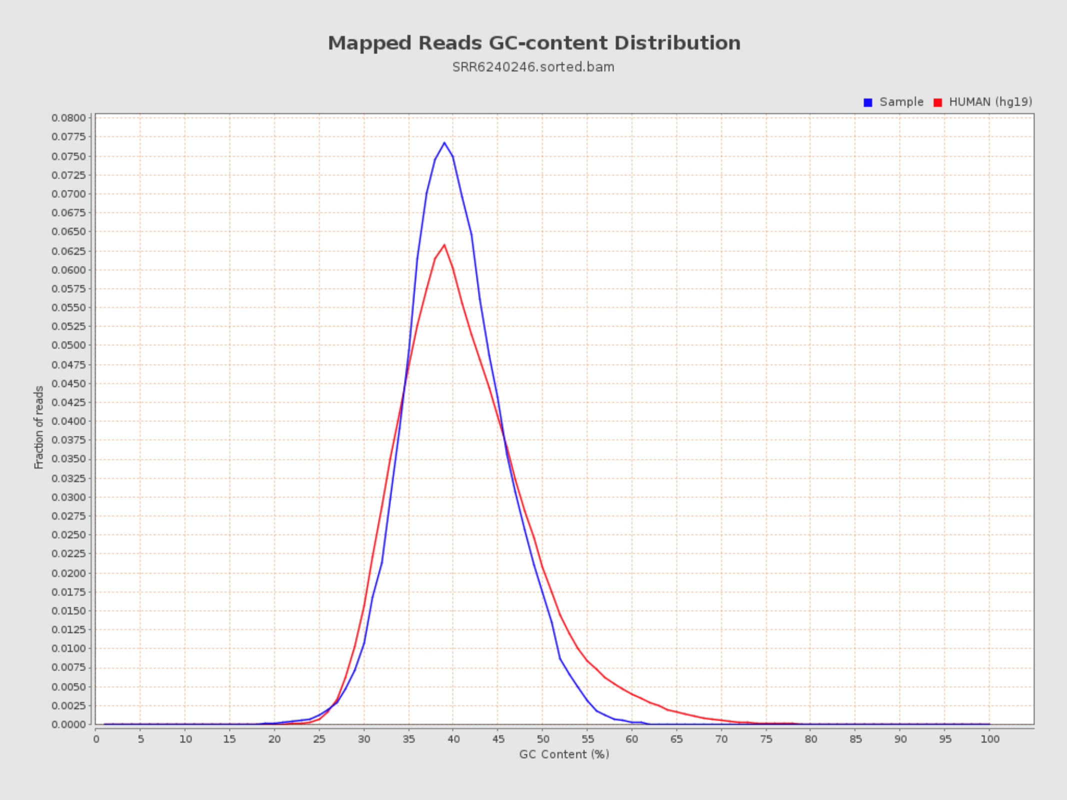
7. Results : Duplication Rate Histogram



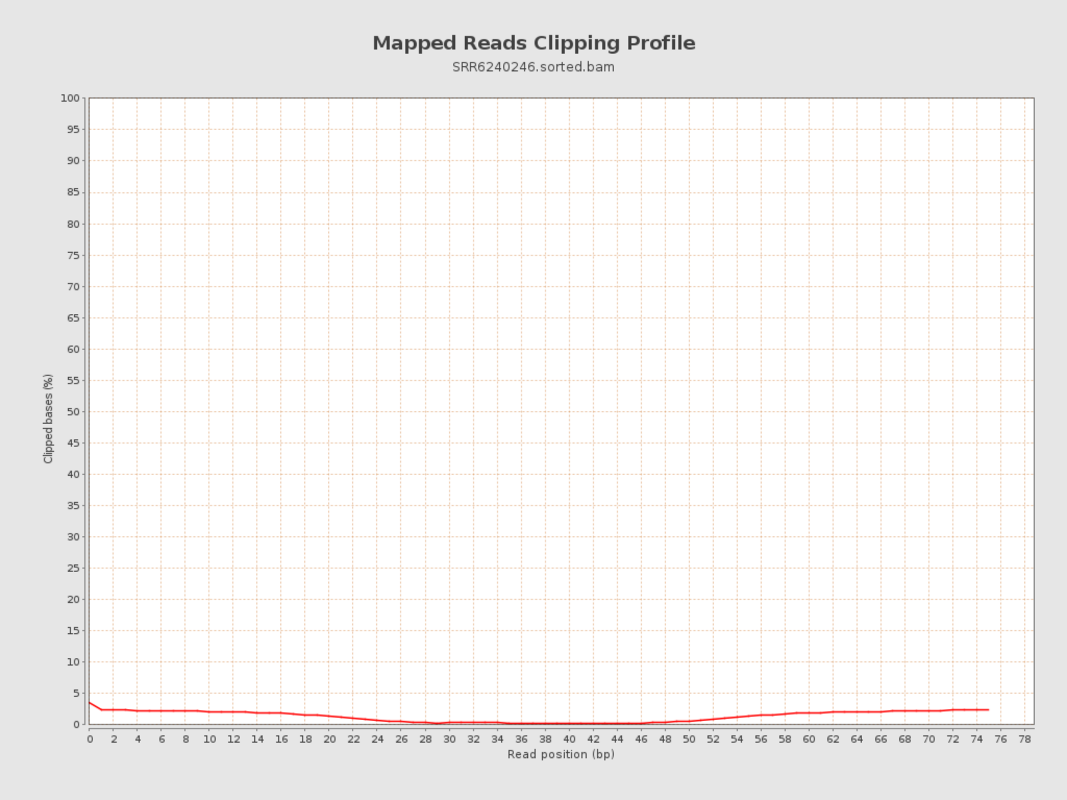
8. Results : Mapped Reads Nucleotide Content



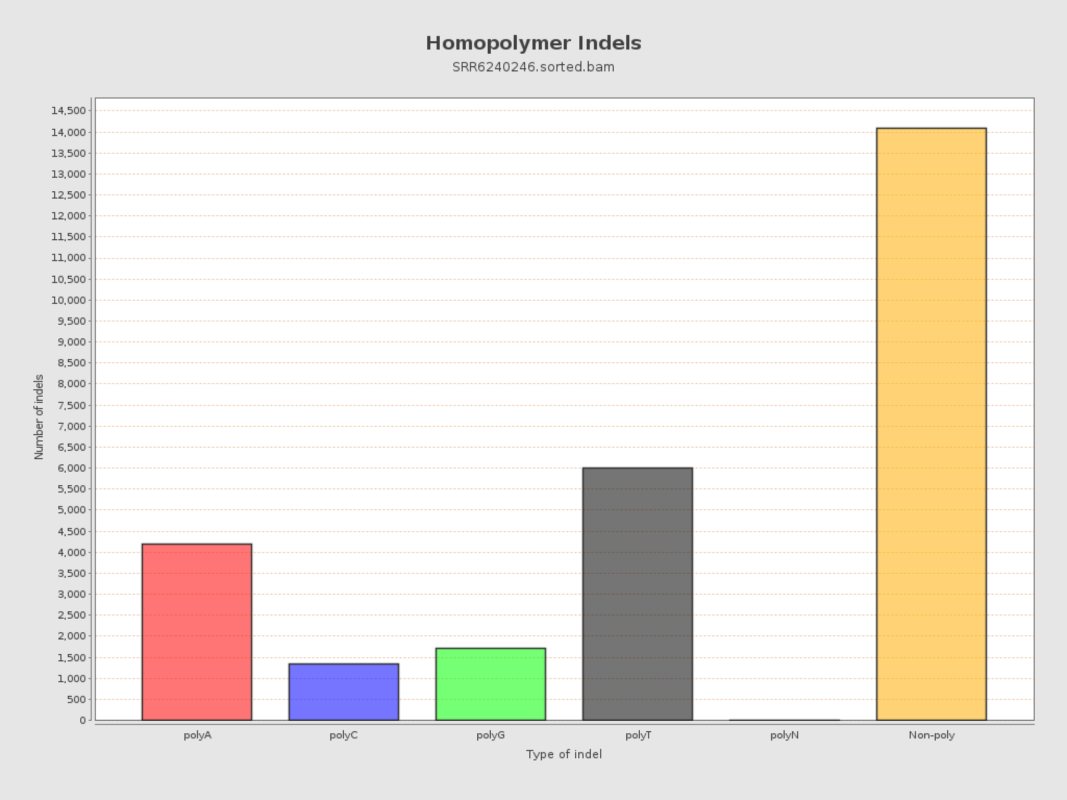
9. Results : Mapped Reads GC-content Distribution



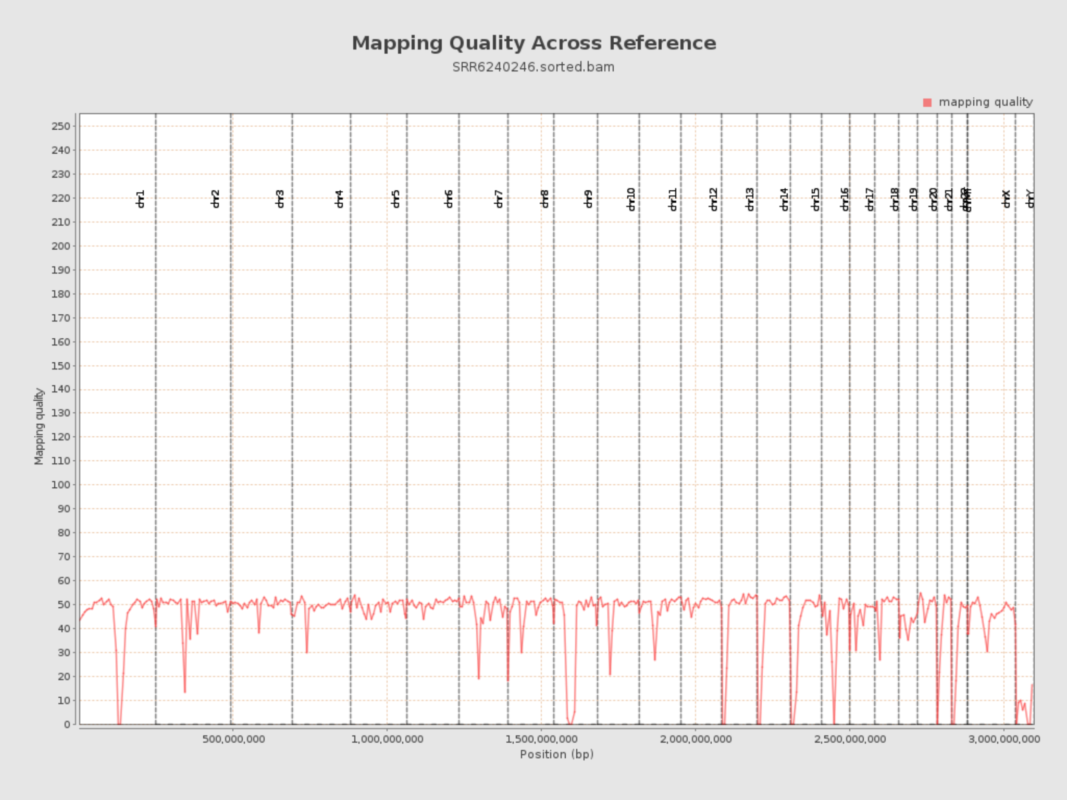
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram