Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:02:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240049.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_SRR6240049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:02:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,024,882
Mapped reads	1,732,806 / 85.58%
Unmapped reads	292,076 / 14.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,214 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	157,328 / 7.77%
Duplication rate	7.37%
Clipped reads	964,460 / 47.63%

2.2. ACGT Content

Number/percentage of A's	30,524,883 / 27.54%
Number/percentage of C's	19,813,285 / 17.88%
Number/percentage of T's	35,738,638 / 32.25%
Number/percentage of G's	24,678,463 / 22.27%
Number/percentage of N's	76,008 / 0.07%
GC Percentage	40.14%

2.3. Coverage

Mean	0.0358

Standard Deviation	0.3382

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

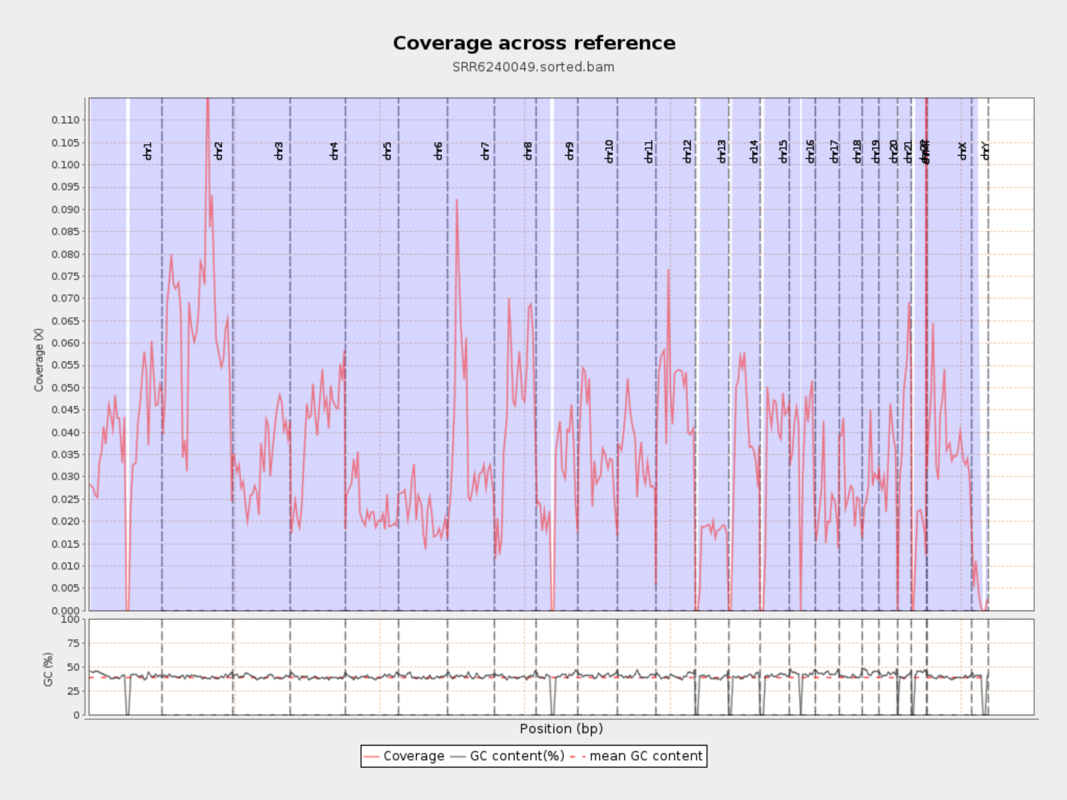
General error rate	0.93%
Mismatches	1,015,254
Insertions	7,959
Mapped reads with at least one insertion	0.46%
Deletions	33,493
Mapped reads with at least one deletion	1.91%
Homopolymer indels	49.93%

2.6. Chromosome stats

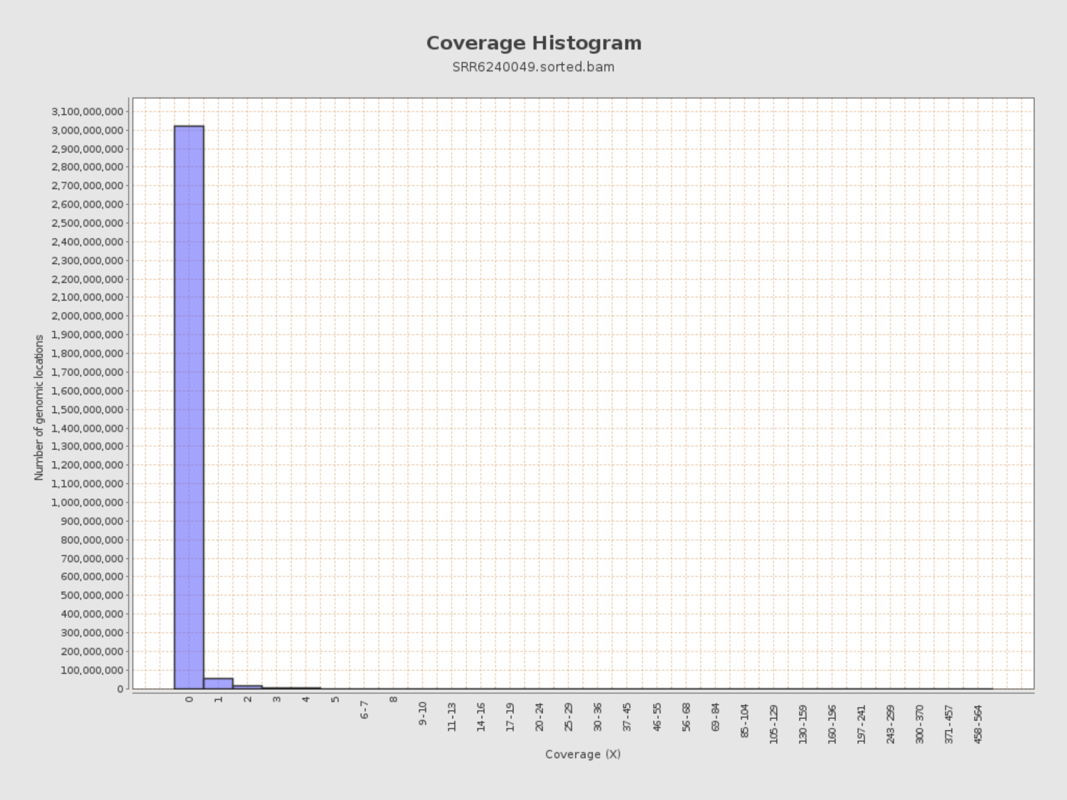
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9616874	0.0386	0.4757
chr2	243199373	15876278	0.0653	0.452
chr3	198022430	6735454	0.034	0.2491
chr4	191154276	7772466	0.0407	0.286
chr5	180915260	4176175	0.0231	0.2051
chr6	171115067	3791543	0.0222	0.219
chr7	159138663	6286495	0.0395	0.5235

chr8	146364022	6656330	0.0455	0.4545
chr9	141213431	3887972	0.0275	0.2978
chr10	135534747	4949087	0.0365	0.3268
chr11	135006516	4766411	0.0353	0.3405
chr12	133851895	6663013	0.0498	0.3084
chr13	115169878	1759108	0.0153	0.165
chr14	107349540	3980167	0.0371	0.2681
chr15	102531392	3679663	0.0359	0.274
chr16	90354753	3337053	0.0369	0.2629
chr17	81195210	1844035	0.0227	0.2259
chr18	78077248	2200534	0.0282	0.4615
chr19	59128983	1732327	0.0293	0.3253
chr20	63025520	2056809	0.0326	0.2474
chr21	48129895	2112882	0.0439	0.2947
chr22	51304566	744134	0.0145	0.1538
chrMT	16571	19842	1.1974	1.6083
chrX	155270560	6000563	0.0386	0.2876
chrY	59373566	244743	0.0041	0.0936

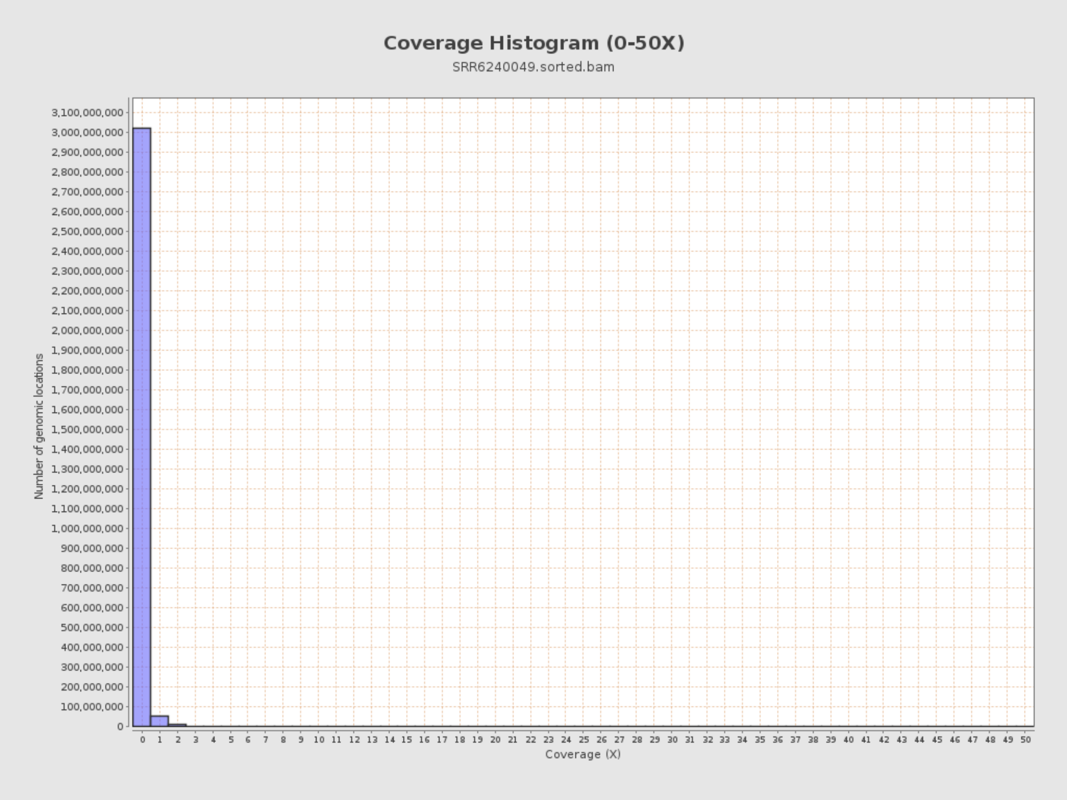
3. Results : Coverage across reference



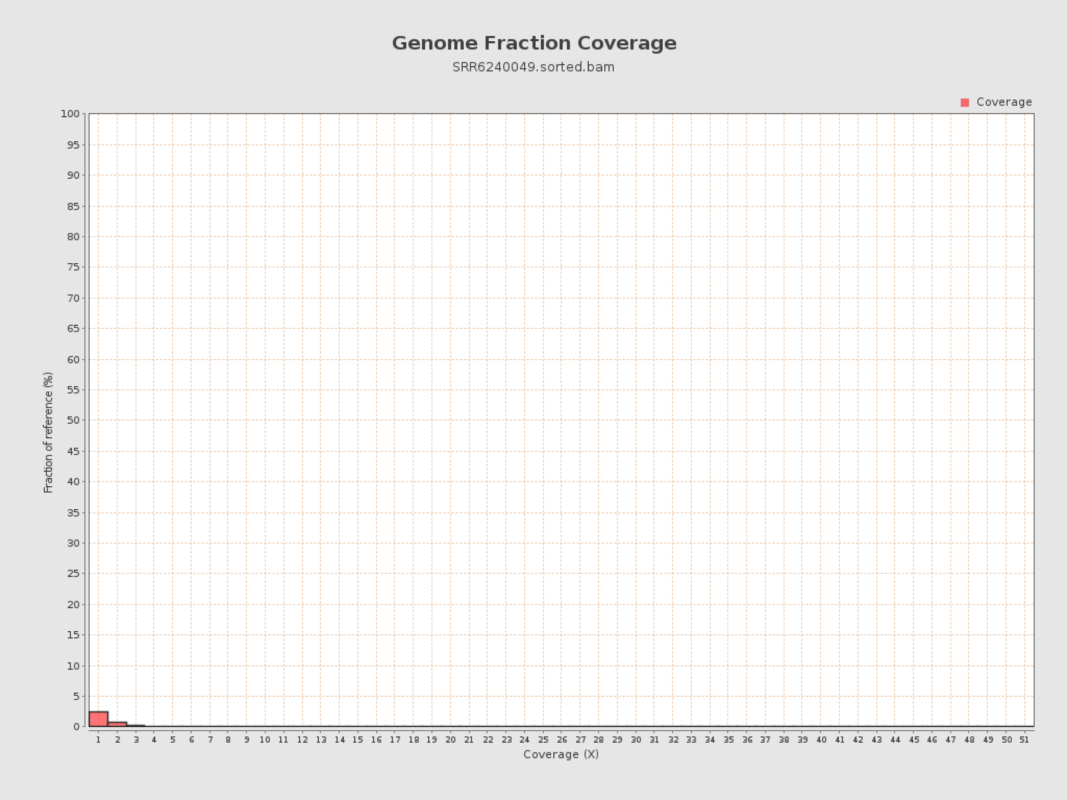
4. Results : Coverage Histogram



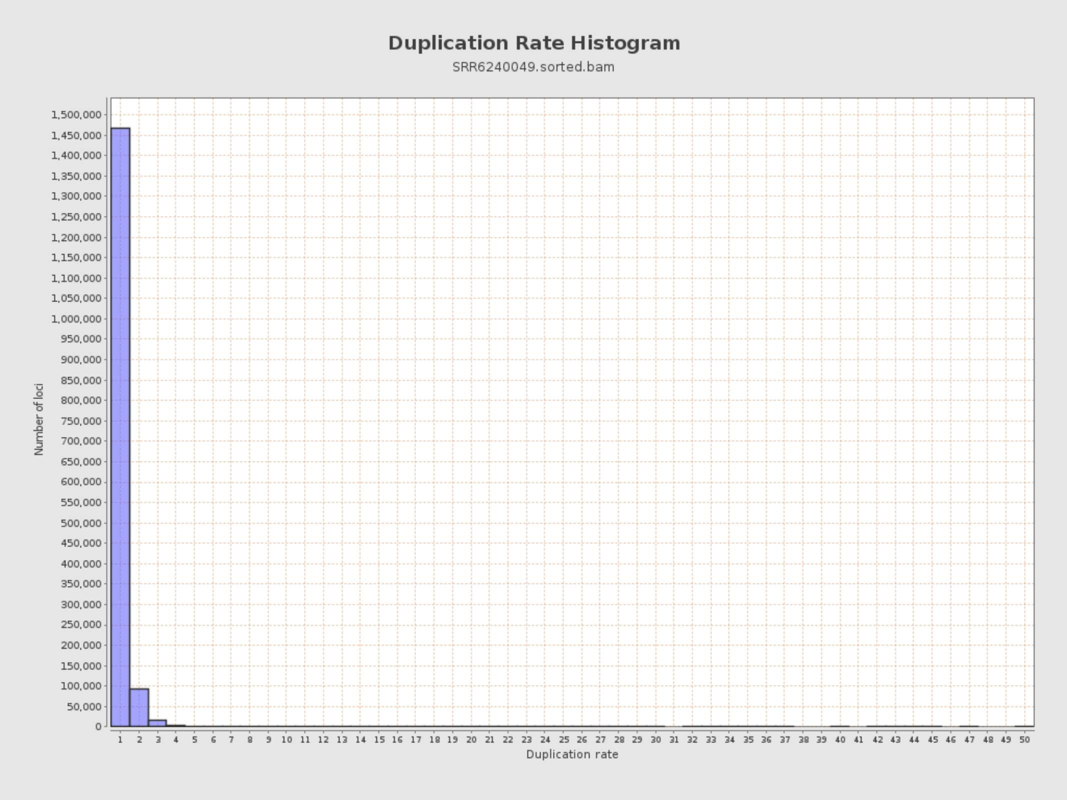
5. Results : Coverage Histogram (0-50X)



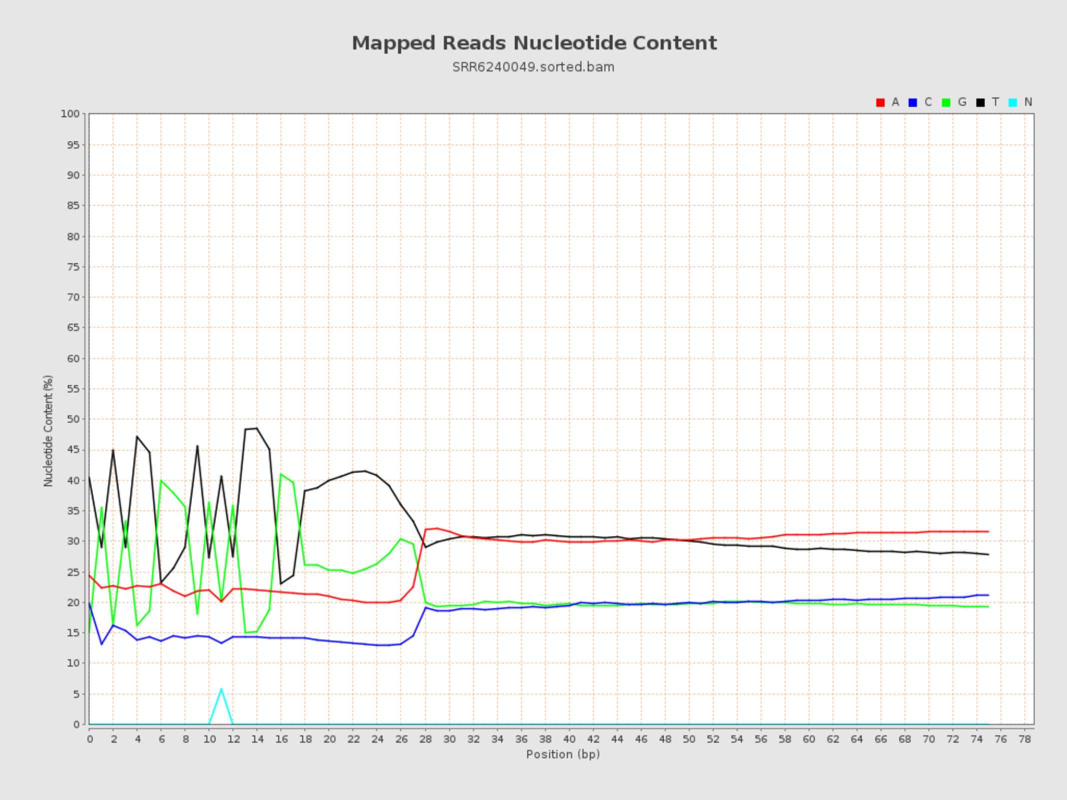
6. Results : Genome Fraction Coverage



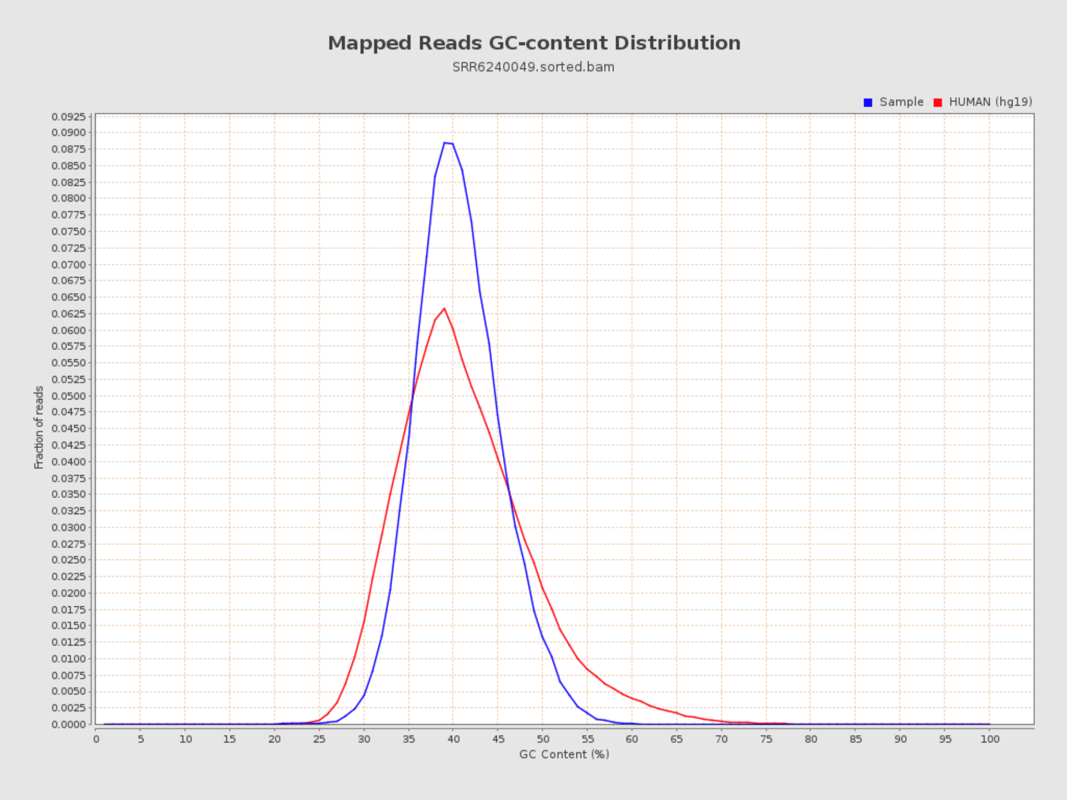
7. Results : Duplication Rate Histogram



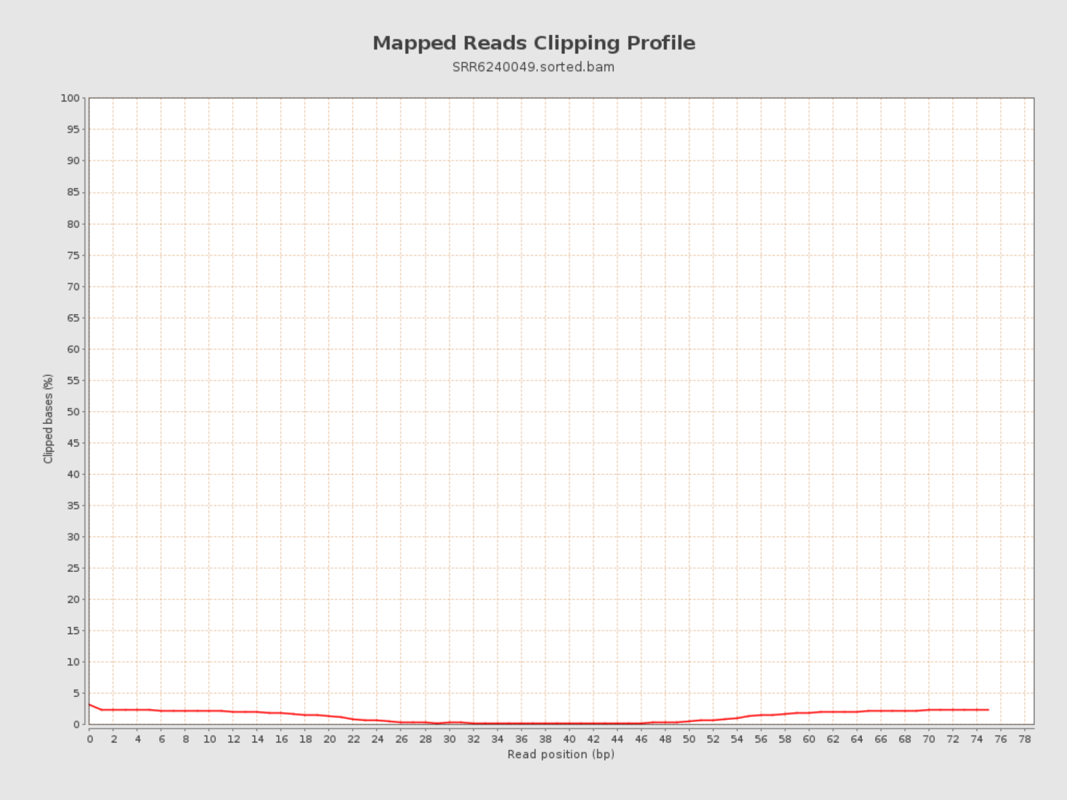
8. Results : Mapped Reads Nucleotide Content



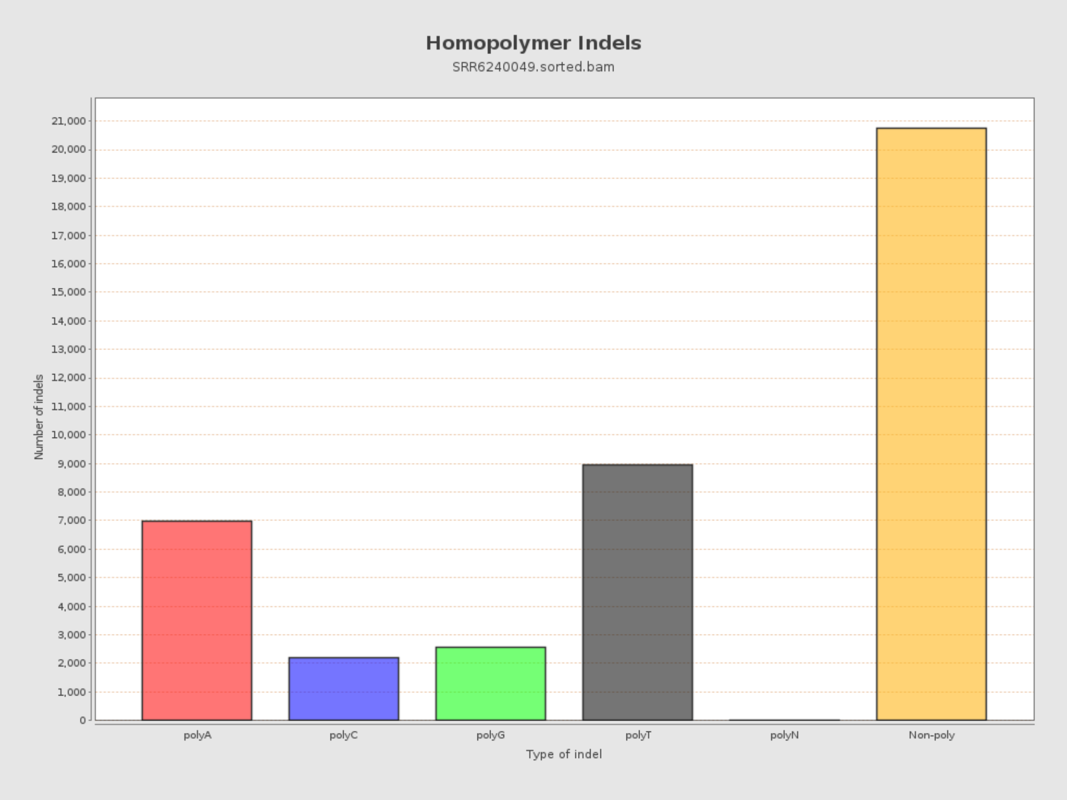
9. Results : Mapped Reads GC-content Distribution



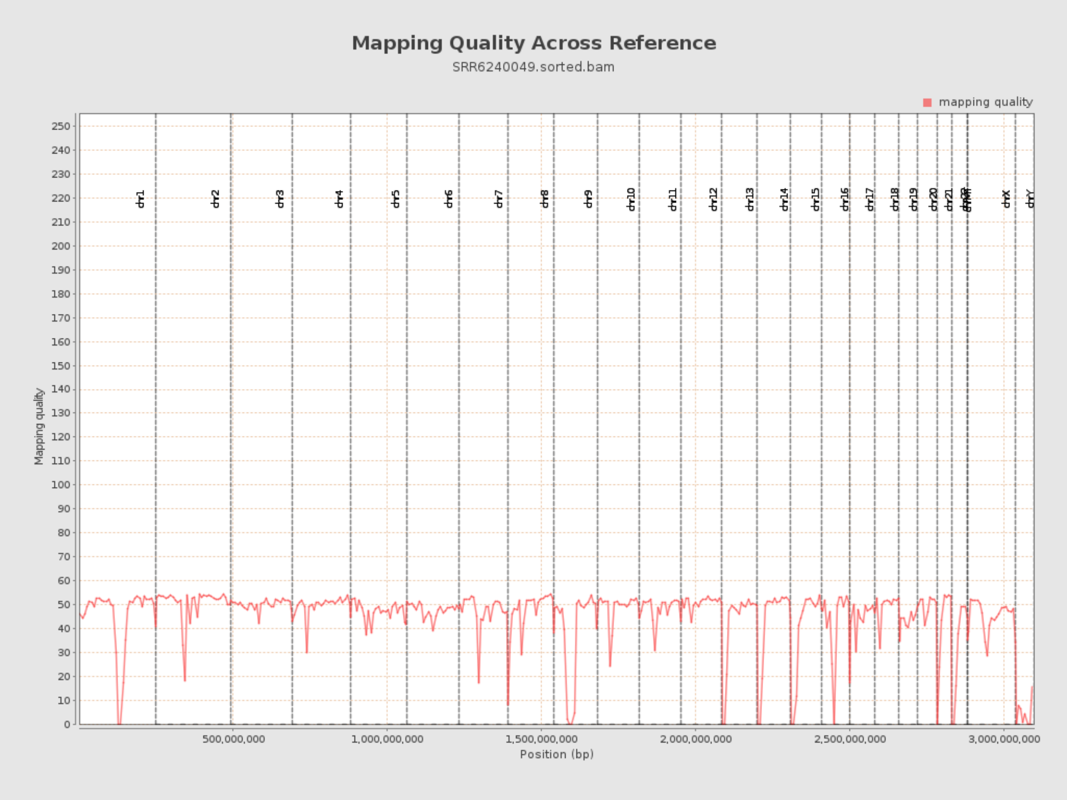
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram