Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:21:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240245.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_SRR6240245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:21:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,937,523
Mapped reads	1,364,923 / 70.45%
Unmapped reads	572,600 / 29.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,551 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	309,575 / 15.98%
Duplication rate	13.74%
Clipped reads	852,472 / 44%

2.2. ACGT Content

Number/percentage of A's	23,069,598 / 27.15%
Number/percentage of C's	14,634,079 / 17.22%
Number/percentage of T's	27,347,986 / 32.18%
Number/percentage of G's	19,915,214 / 23.44%
Number/percentage of N's	7,032 / 0.01%
GC Percentage	40.66%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.4619

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

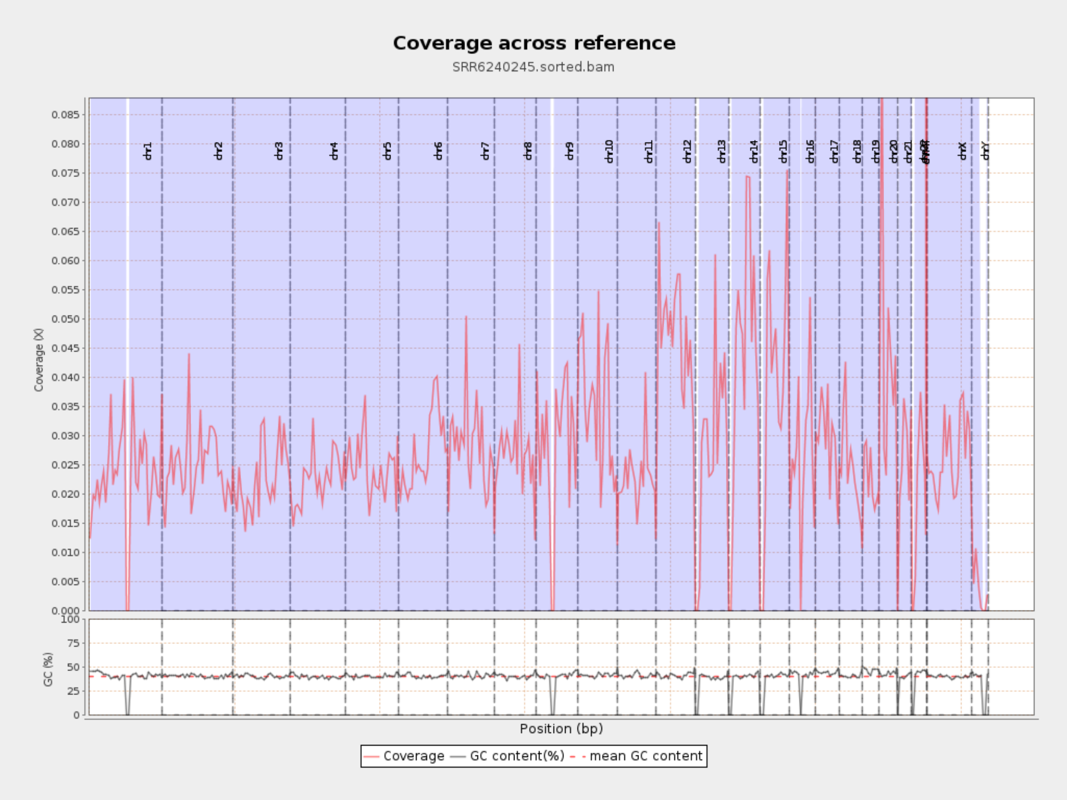
General error rate	1.01%
Mismatches	850,333
Insertions	6,036
Mapped reads with at least one insertion	0.44%
Deletions	29,946
Mapped reads with at least one deletion	2.16%
Homopolymer indels	47.93%

2.6. Chromosome stats

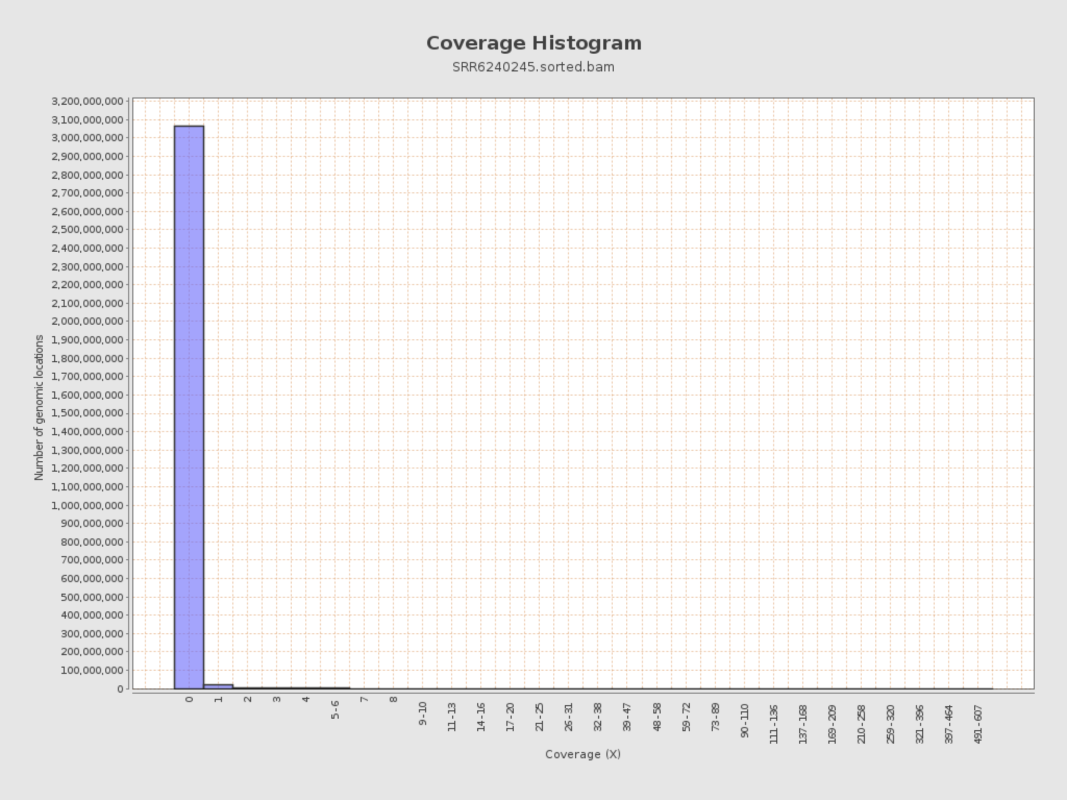
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5715907	0.0229	0.5233
chr2	243199373	6028780	0.0248	0.4464
chr3	198022430	4474442	0.0226	0.3734
chr4	191154276	4299166	0.0225	0.3798
chr5	180915260	4372211	0.0242	0.3864
chr6	171115067	4631538	0.0271	0.4196
chr7	159138663	4531790	0.0285	0.5619

chr8	146364022	3919191	0.0268	0.5373
chr9	141213431	3910068	0.0277	0.4615
chr10	135534747	4755672	0.0351	0.4952
chr11	135006516	3105430	0.023	0.3921
chr12	133851895	6204308	0.0464	0.5634
chr13	115169878	3192402	0.0277	0.44
chr14	107349540	4569478	0.0426	0.5606
chr15	102531392	3934280	0.0384	0.5437
chr16	90354753	2413534	0.0267	0.4047
chr17	81195210	2350453	0.0289	0.4249
chr18	78077248	1970801	0.0252	0.586
chr19	59128983	1316282	0.0223	0.3954
chr20	63025520	2857993	0.0453	0.5414
chr21	48129895	1168865	0.0243	0.388
chr22	51304566	960002	0.0187	0.3372
chrMT	16571	34239	2.0662	2.893
chrX	155270560	4088458	0.0263	0.4172
chrY	59373566	220053	0.0037	0.1589

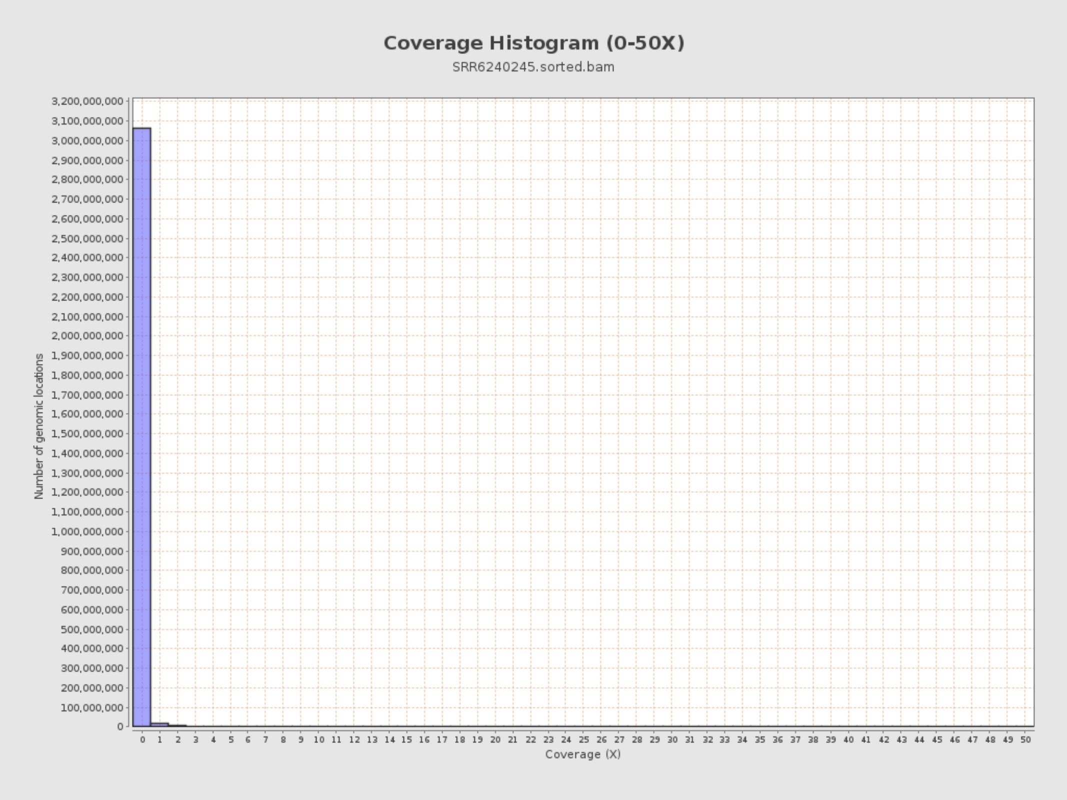
3. Results : Coverage across reference



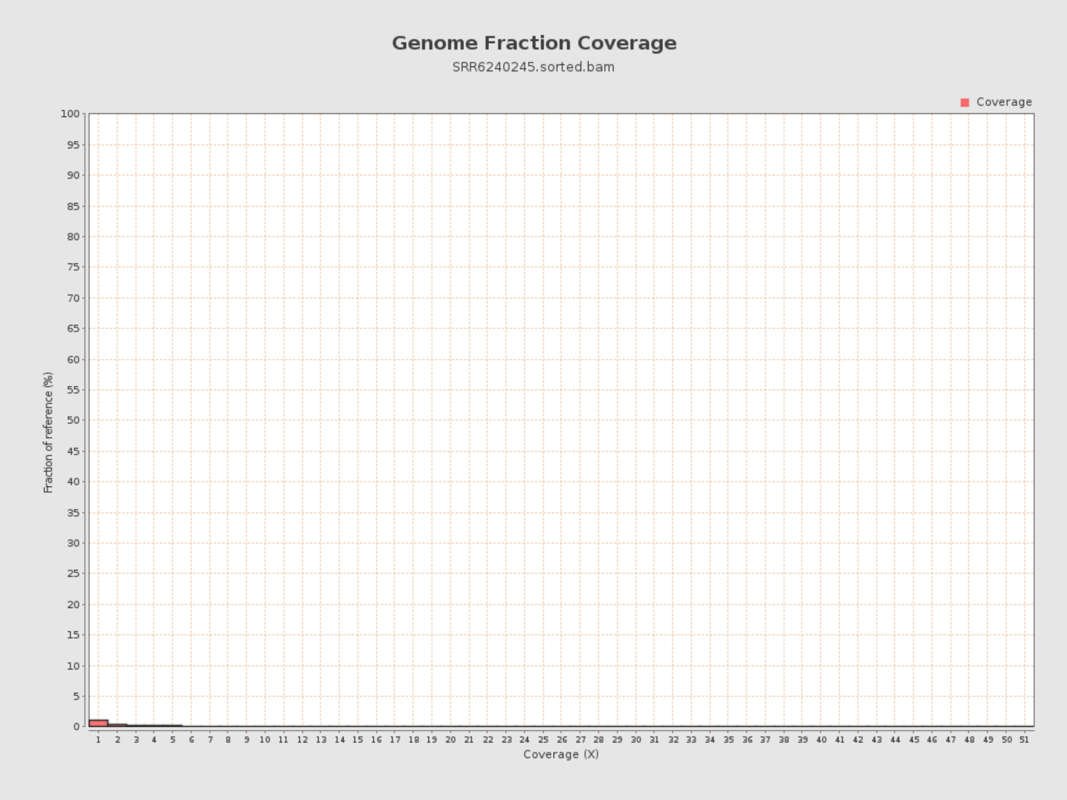
4. Results : Coverage Histogram



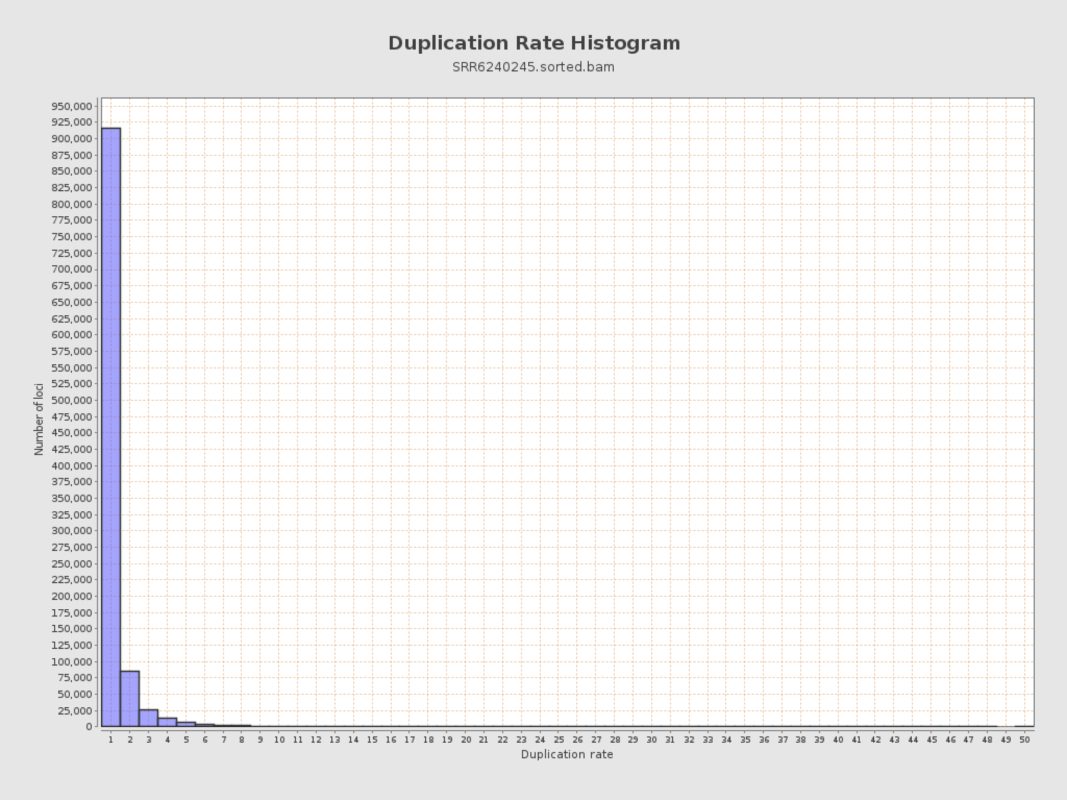
5. Results : Coverage Histogram (0-50X)



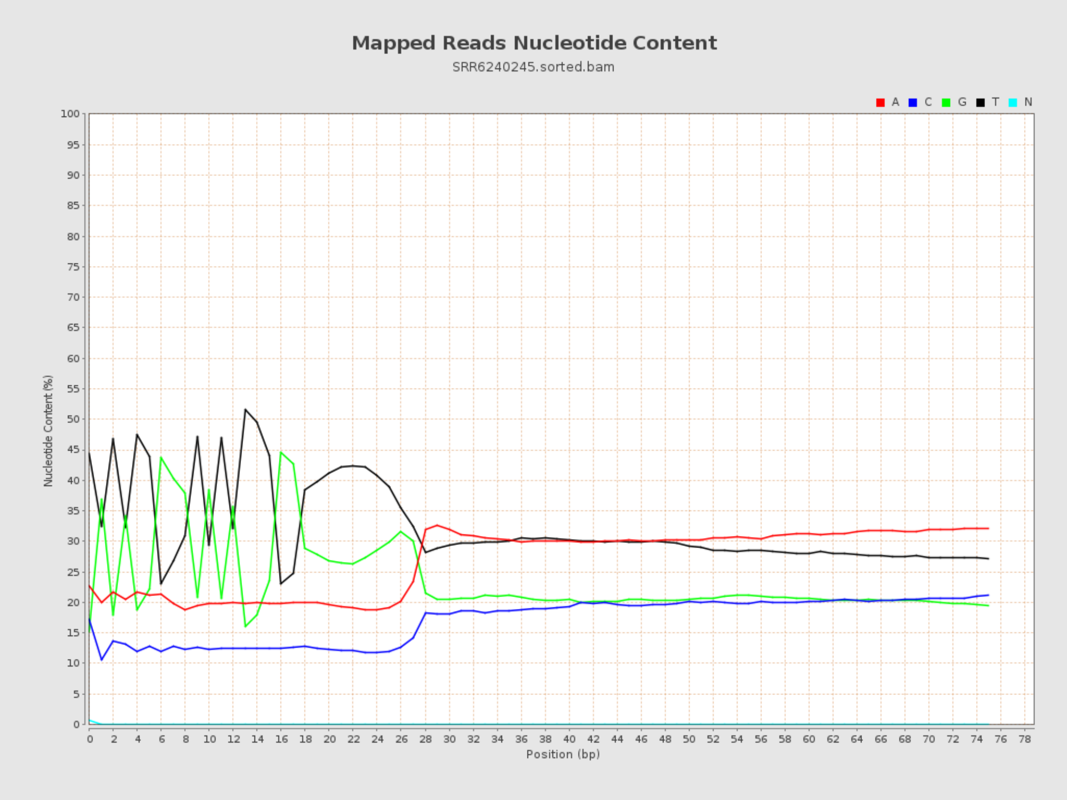
6. Results : Genome Fraction Coverage



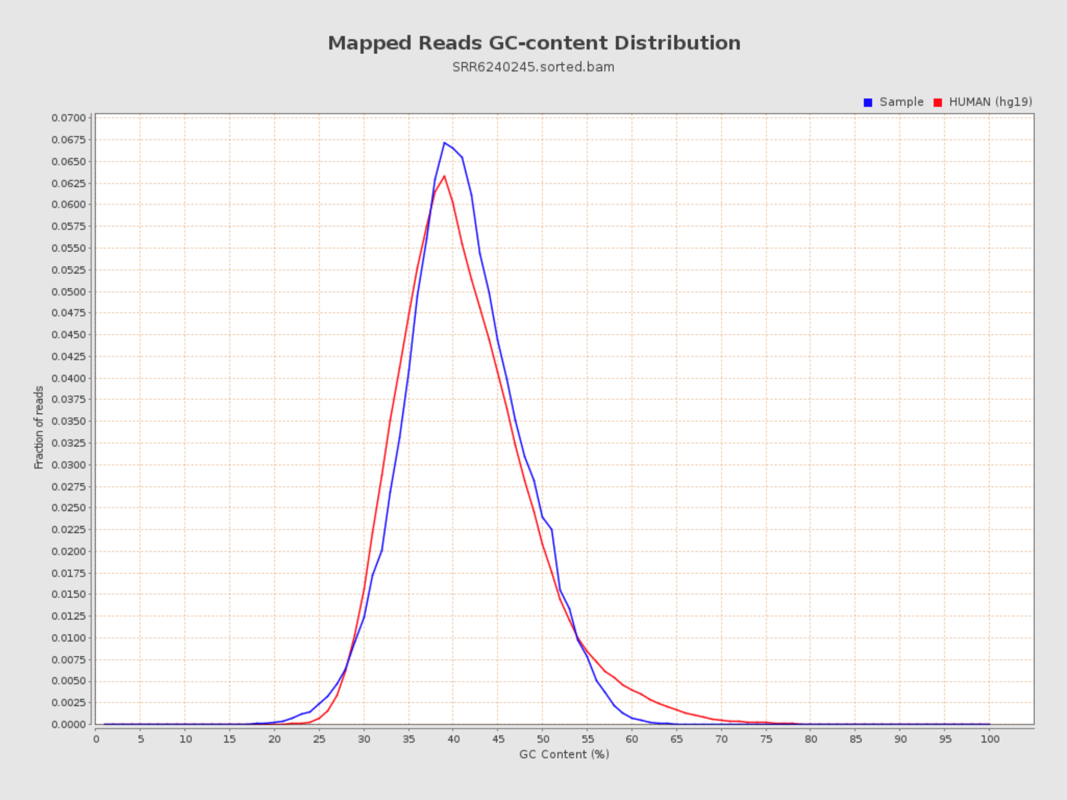
7. Results : Duplication Rate Histogram



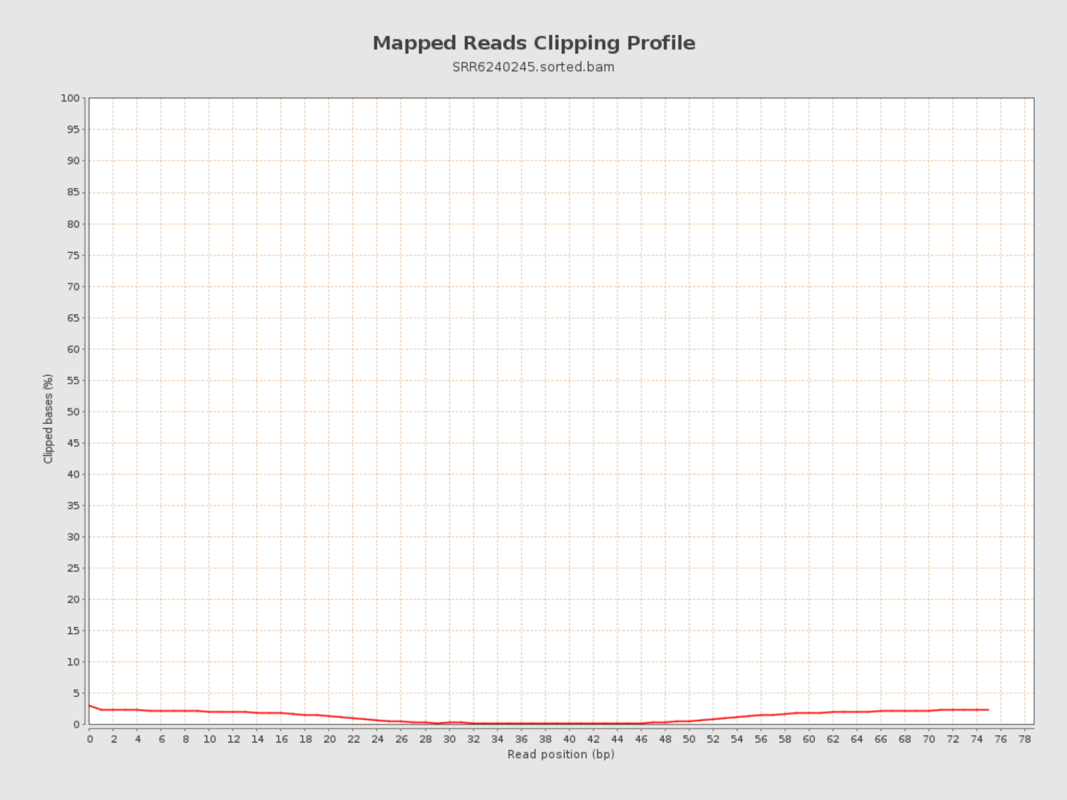
8. Results : Mapped Reads Nucleotide Content



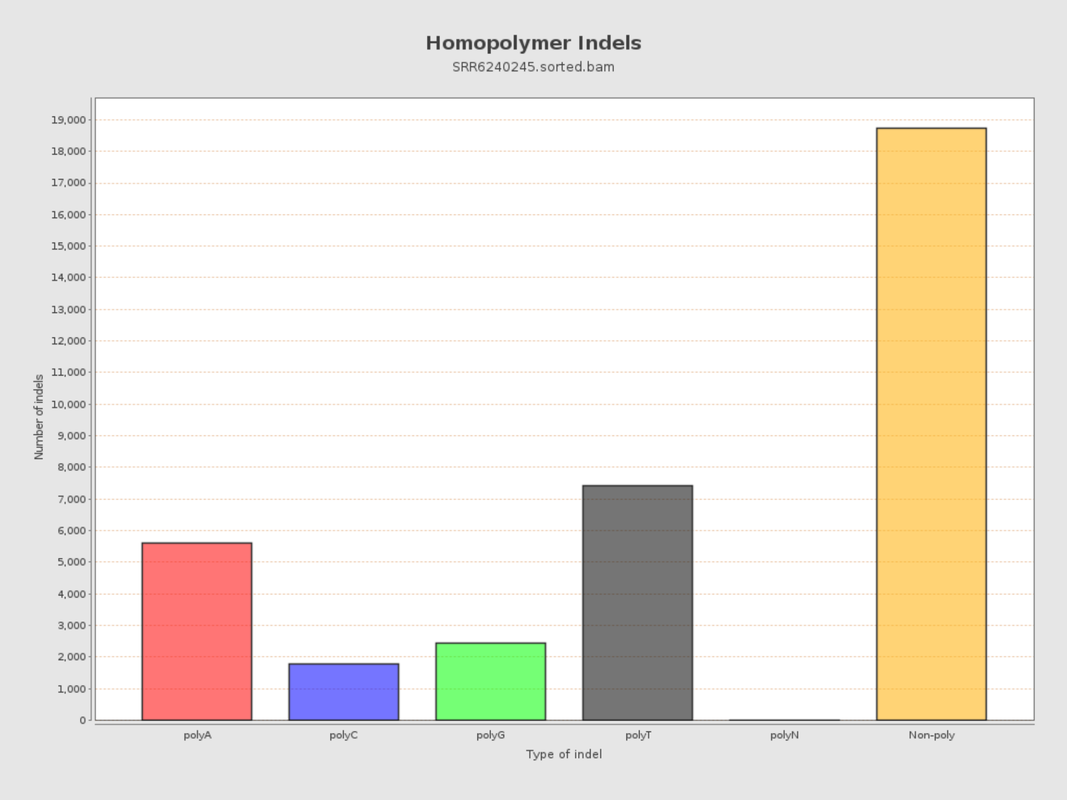
9. Results : Mapped Reads GC-content Distribution



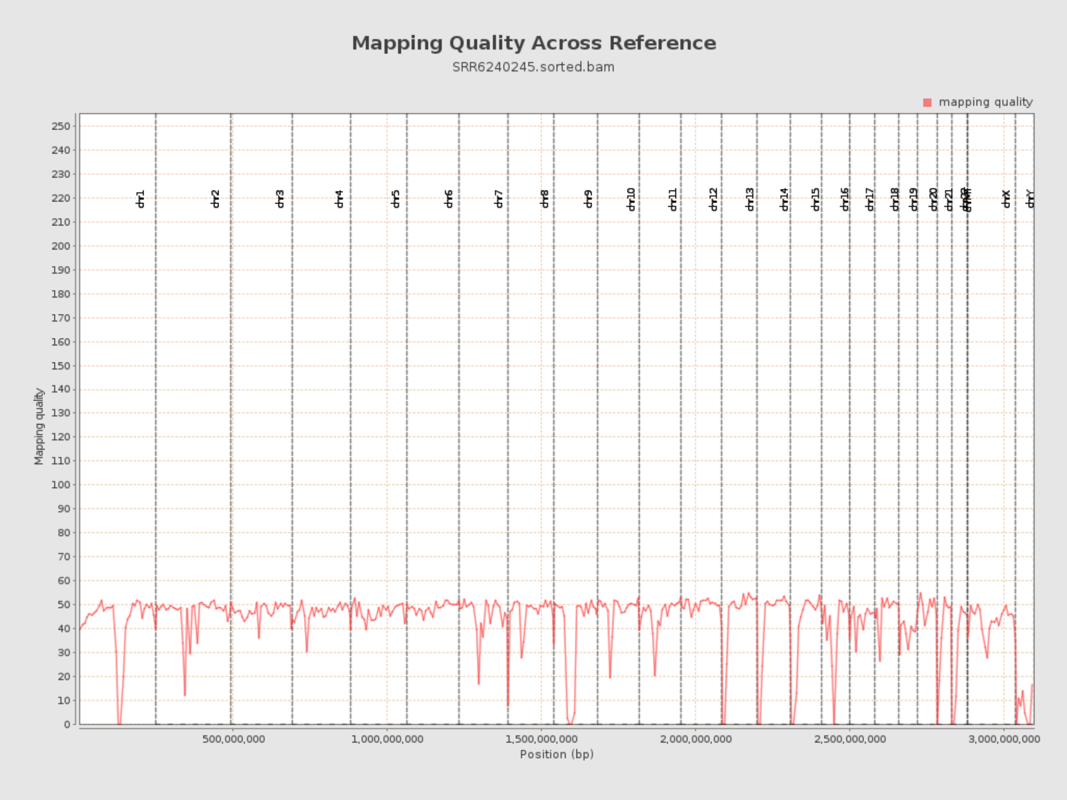
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram