Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:20:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240205.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_SRR6240205 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240205.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:20:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240205.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,177,998
Mapped reads	1,770,584 / 81.29%
Unmapped reads	407,414 / 18.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,615 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	165,806 / 7.61%
Duplication rate	7.77%
Clipped reads	1,124,865 / 51.65%

2.2. ACGT Content

Number/percentage of A's	30,061,427 / 27.34%
Number/percentage of C's	19,258,979 / 17.51%
Number/percentage of T's	35,808,564 / 32.57%
Number/percentage of G's	24,802,578 / 22.56%
Number/percentage of N's	26,233 / 0.02%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0355

Standard Deviation	0.348

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

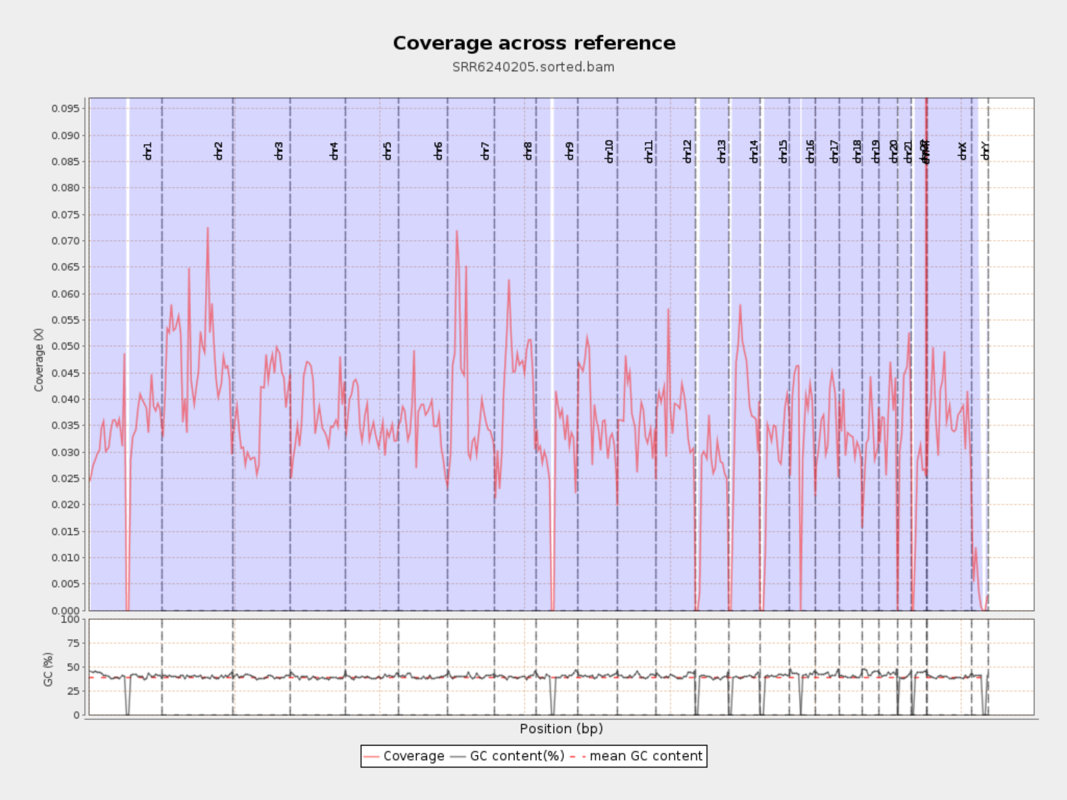
General error rate	0.94%
Mismatches	1,016,317
Insertions	7,823
Mapped reads with at least one insertion	0.44%
Deletions	34,776
Mapped reads with at least one deletion	1.94%
Homopolymer indels	49.65%

2.6. Chromosome stats

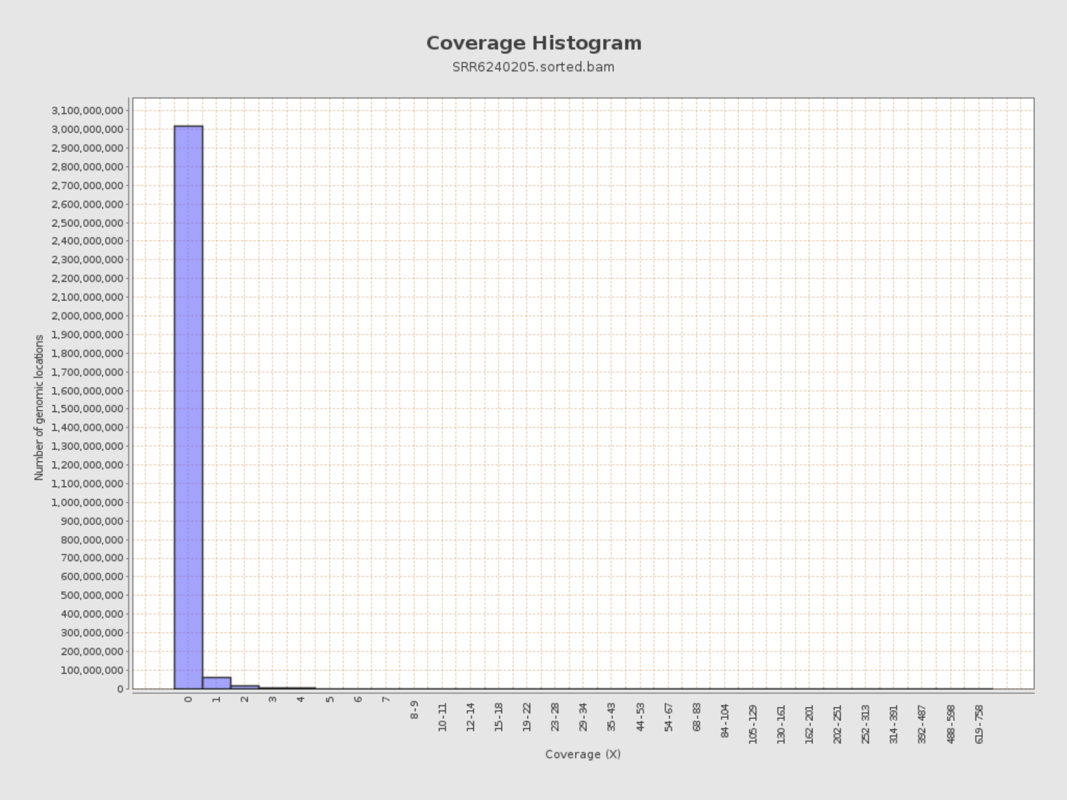
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8215639	0.033	0.5493
chr2	243199373	11649699	0.0479	0.3955
chr3	198022430	7532296	0.038	0.2553
chr4	191154276	7098360	0.0371	0.2588
chr5	180915260	6435128	0.0356	0.2493
chr6	171115067	6097967	0.0356	0.2954
chr7	159138663	6447802	0.0405	0.5472

chr8	146364022	6309029	0.0431	0.5272
chr9	141213431	4072158	0.0288	0.2973
chr10	135534747	5131634	0.0379	0.3024
chr11	135006516	4846095	0.0359	0.3029
chr12	133851895	5064948	0.0378	0.2568
chr13	115169878	2736978	0.0238	0.2025
chr14	107349540	3902399	0.0364	0.2587
chr15	102531392	2817126	0.0275	0.2217
chr16	90354753	3204016	0.0355	0.2533
chr17	81195210	2809315	0.0346	0.259
chr18	78077248	2575931	0.033	0.4682
chr19	59128983	1897989	0.0321	0.3802
chr20	63025520	2294998	0.0364	0.253
chr21	48129895	1779139	0.037	0.2579
chr22	51304566	1018554	0.0199	0.178
chrMT	16571	43425	2.6205	3.4768
chrX	155270560	5789162	0.0373	0.2739
chrY	59373566	248016	0.0042	0.0917

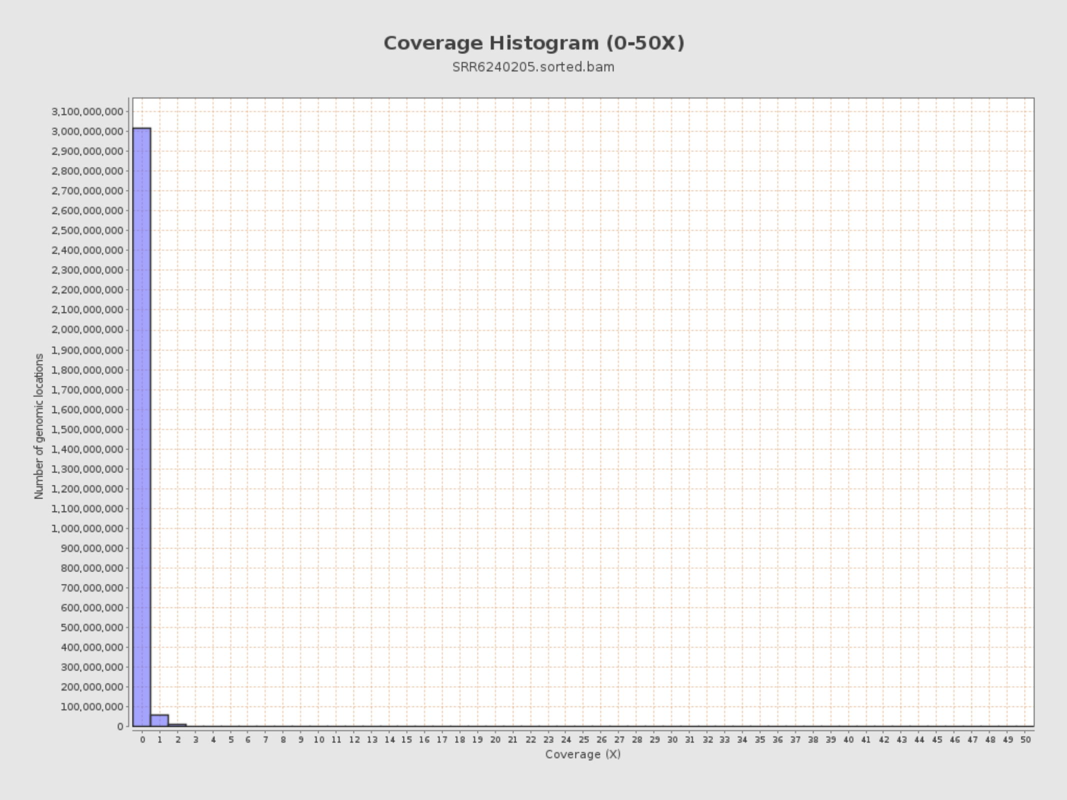
3. Results : Coverage across reference



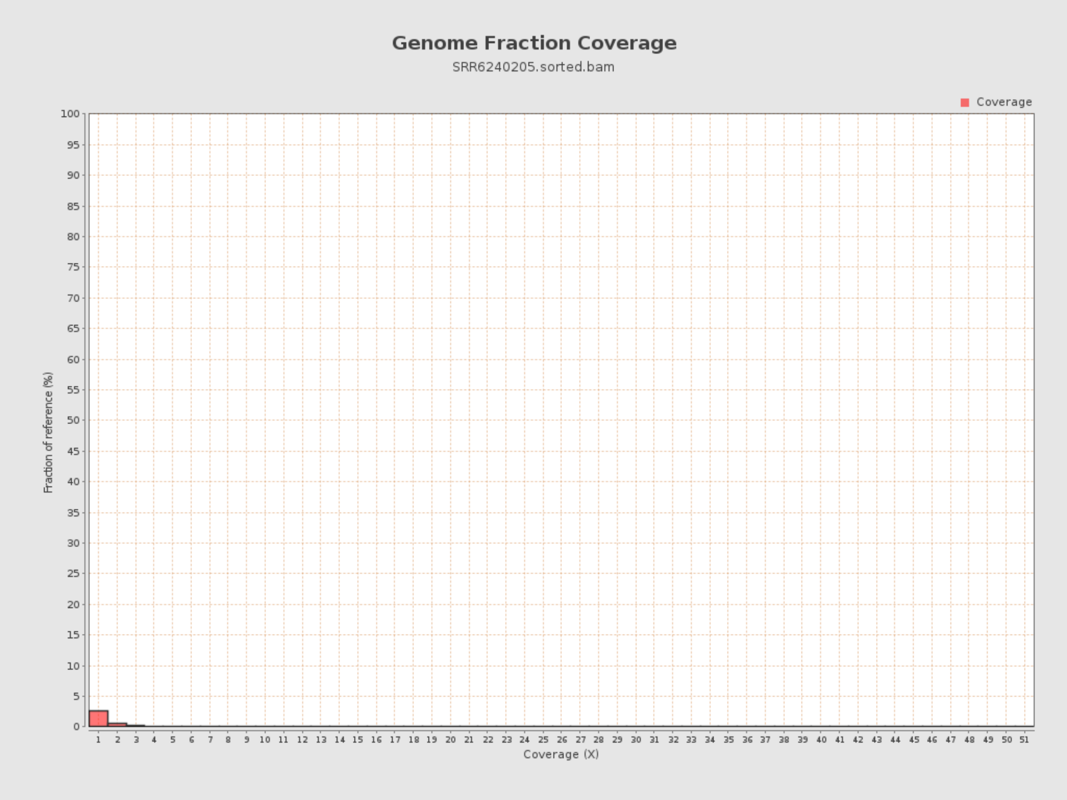
4. Results : Coverage Histogram



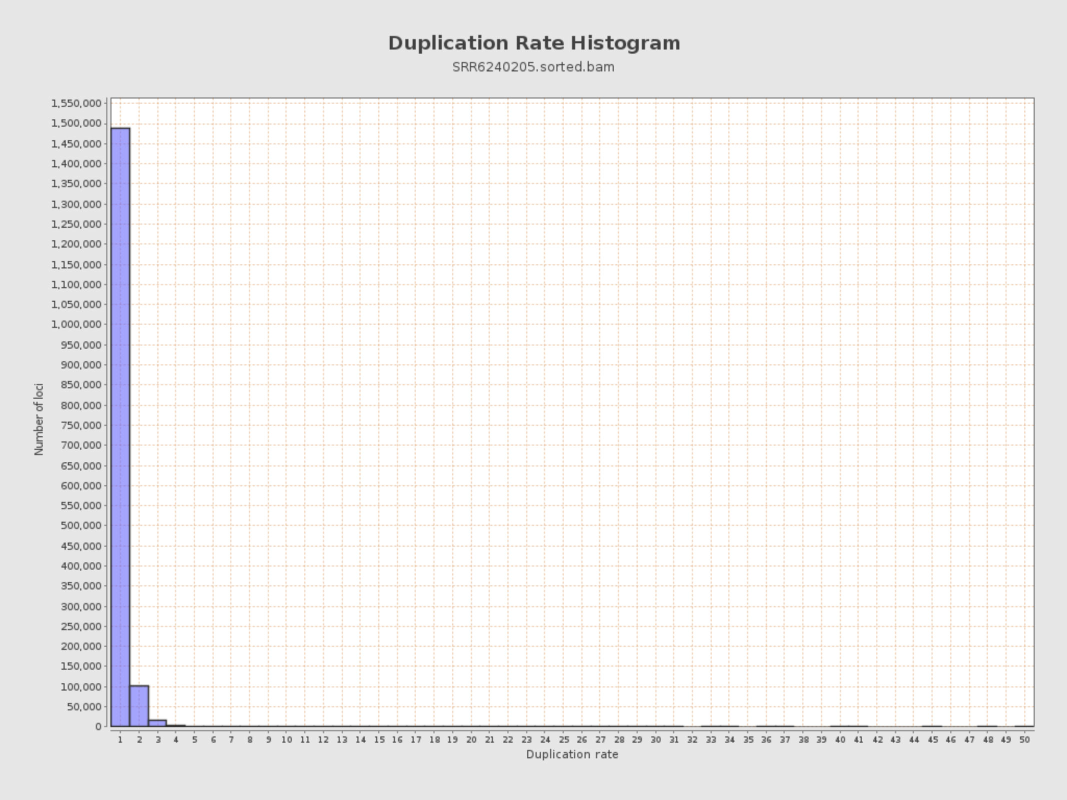
5. Results : Coverage Histogram (0-50X)



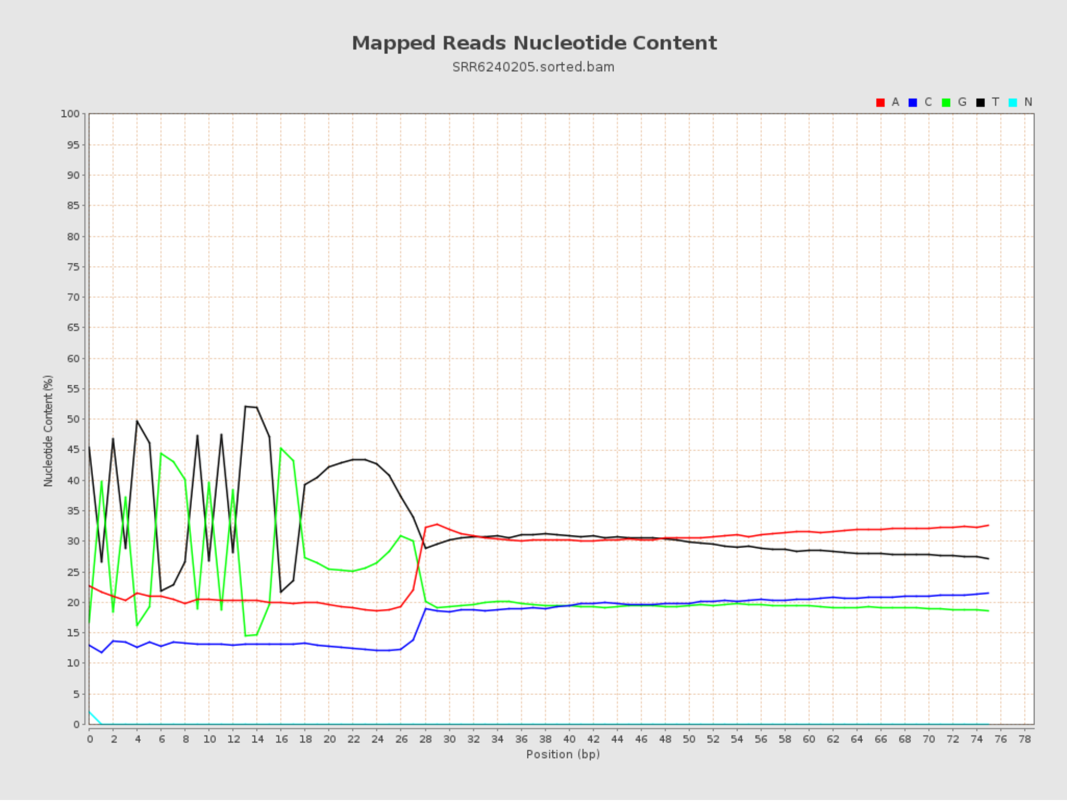
6. Results : Genome Fraction Coverage



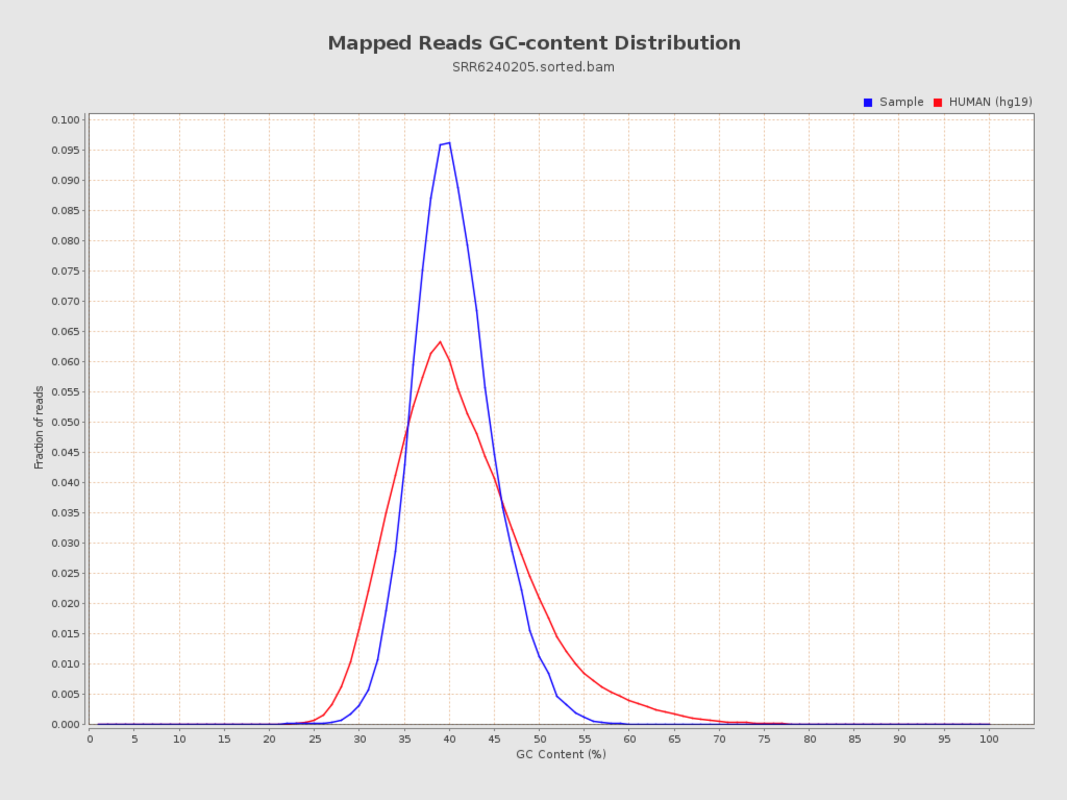
7. Results : Duplication Rate Histogram



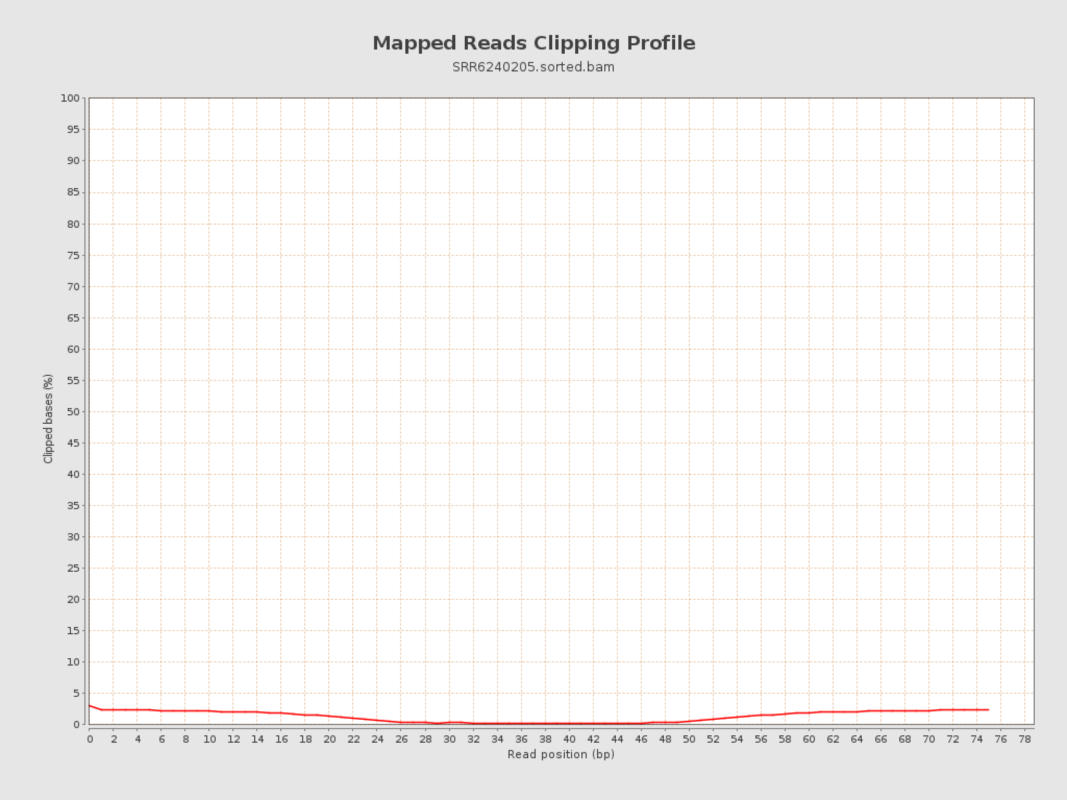
8. Results : Mapped Reads Nucleotide Content



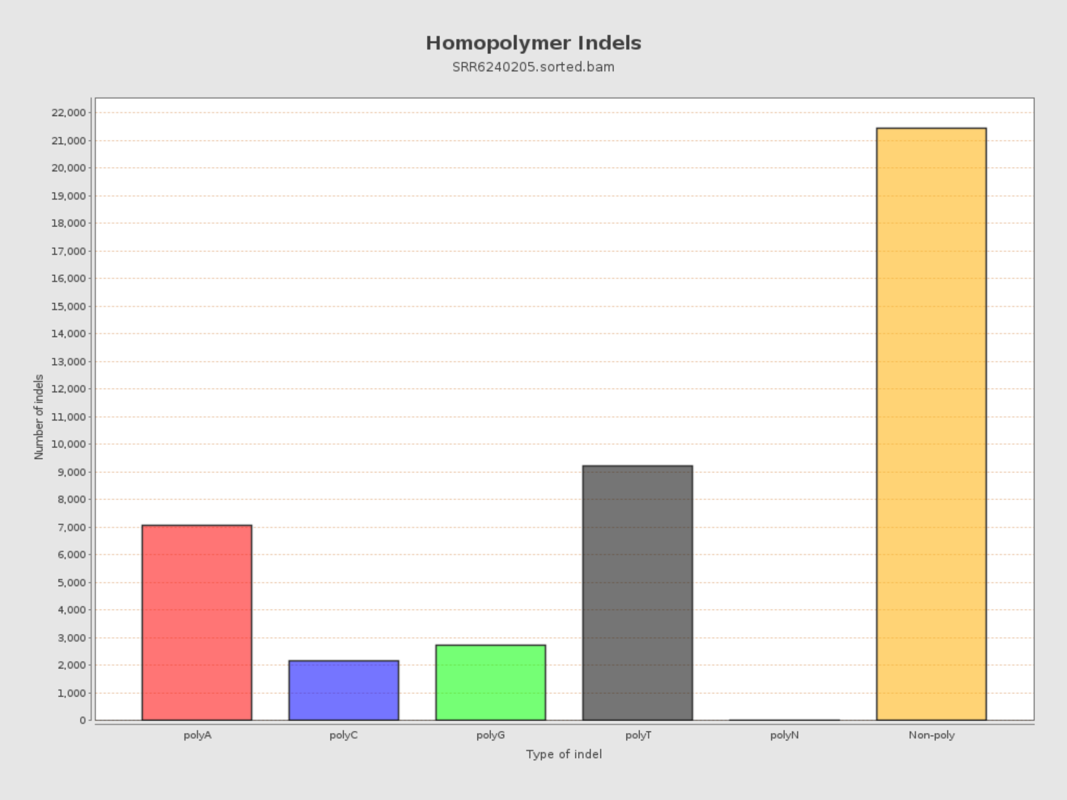
9. Results : Mapped Reads GC-content Distribution



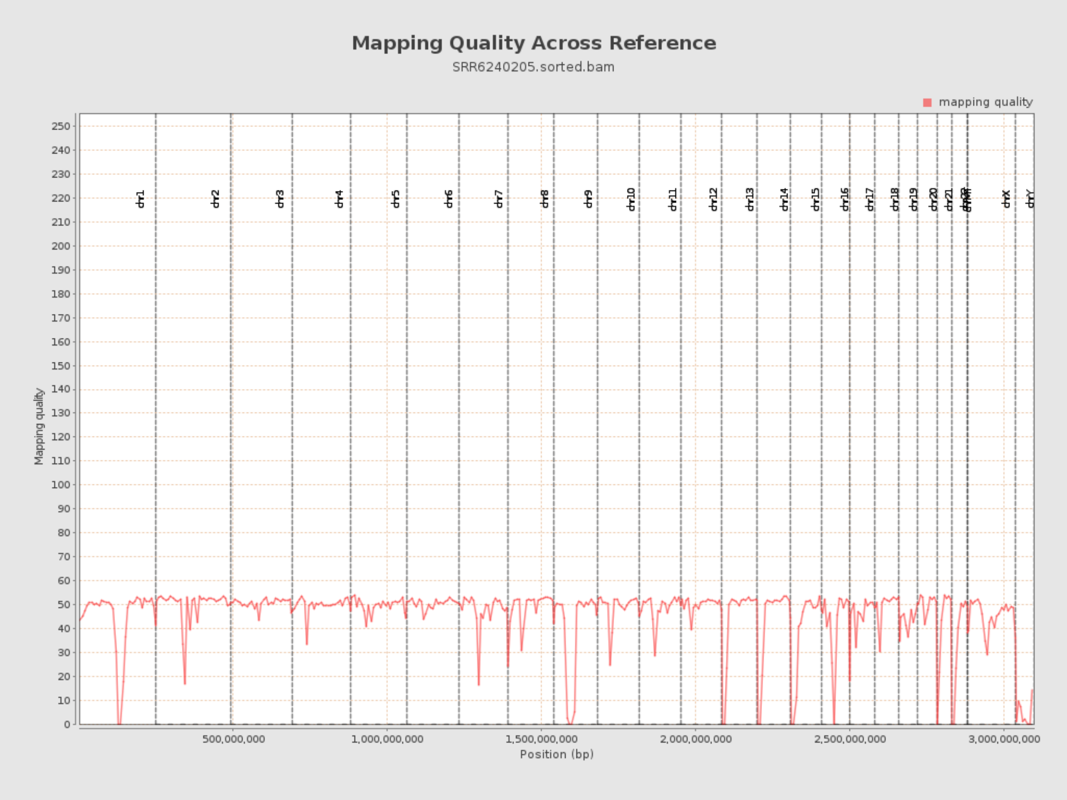
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram