Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:37:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240251.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_SRR6240251 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240251.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:37:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240251.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,965,707
Mapped reads	1,289,076 / 65.58%
Unmapped reads	676,631 / 34.42%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,221 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	170,115 / 8.65%
Duplication rate	10.24%
Clipped reads	680,275 / 34.61%

2.2. ACGT Content

Number/percentage of A's	23,319,547 / 27.9%
Number/percentage of C's	15,261,303 / 18.26%
Number/percentage of T's	26,836,040 / 32.11%
Number/percentage of G's	18,154,441 / 21.72%
Number/percentage of N's	7,515 / 0.01%
GC Percentage	39.98%

2.3. Coverage

Mean	0.027

Standard Deviation	0.3282

2.4. Mapping Quality

Mean Mapping Quality	46.49

2.5. Mismatches and indels

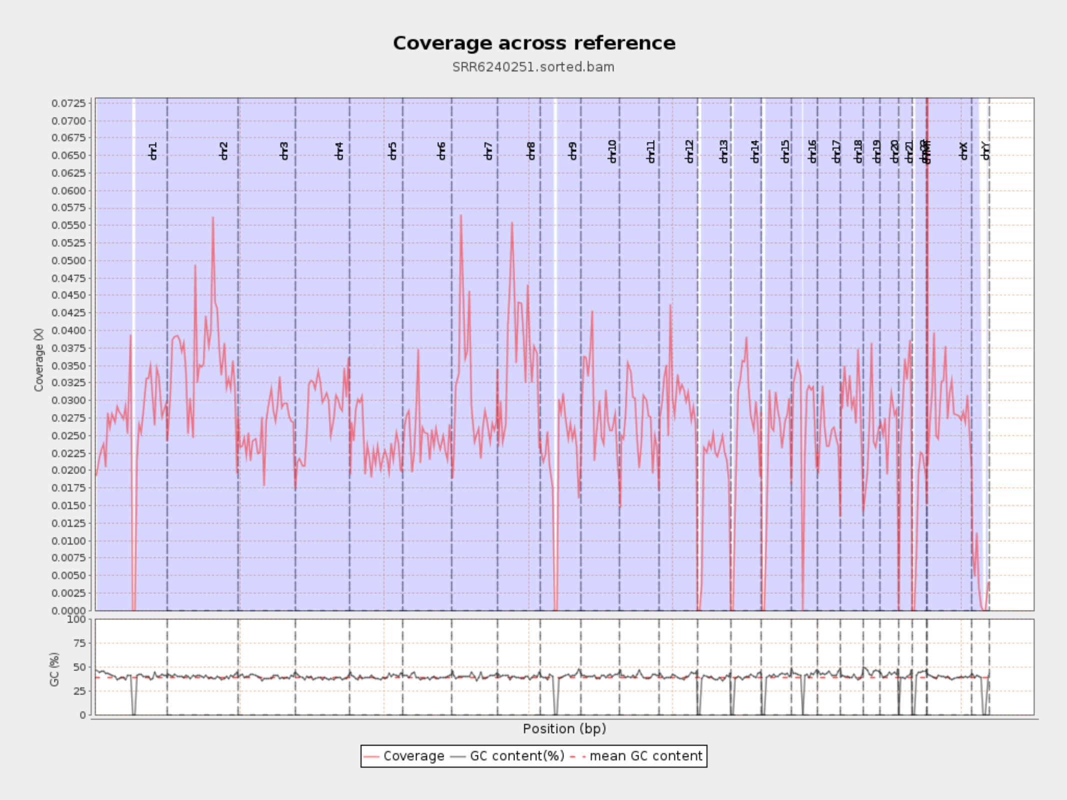
General error rate	0.85%
Mismatches	703,265
Insertions	5,879
Mapped reads with at least one insertion	0.45%
Deletions	22,562
Mapped reads with at least one deletion	1.73%
Homopolymer indels	48.16%

2.6. Chromosome stats

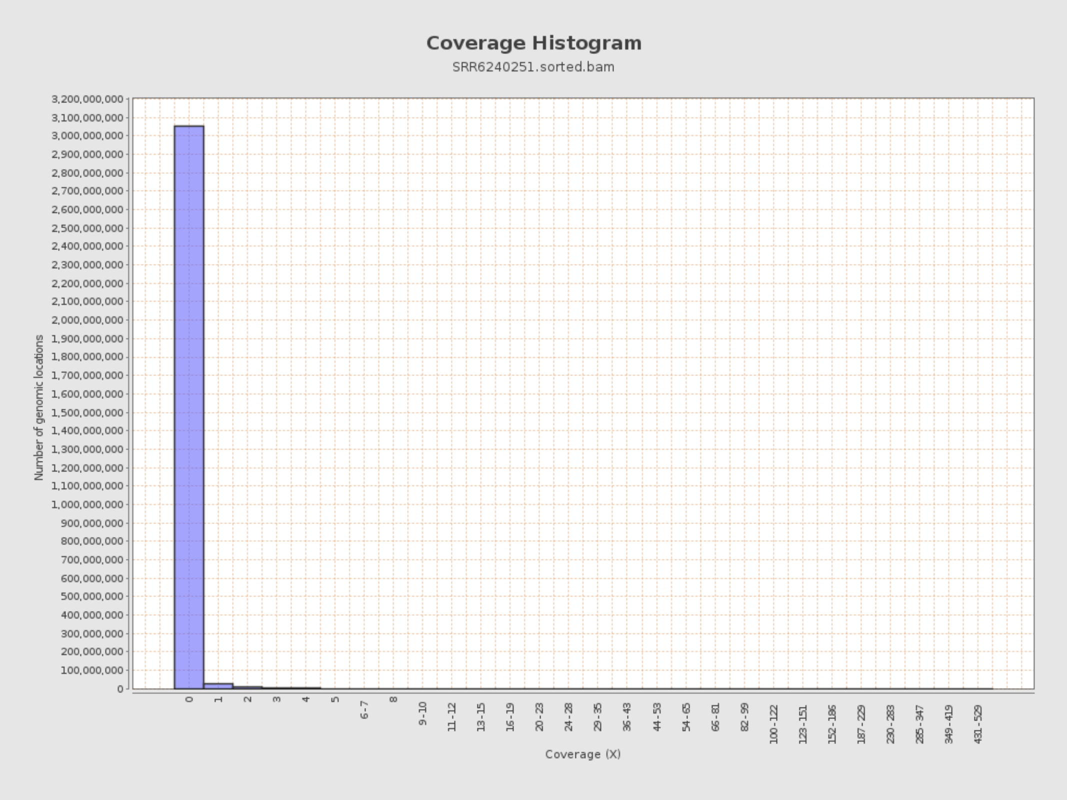
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6530242	0.0262	0.454
chr2	243199373	8768886	0.0361	0.3776
chr3	198022430	5190308	0.0262	0.2741
chr4	191154276	5492841	0.0287	0.2882
chr5	180915260	4260736	0.0236	0.2554
chr6	171115067	4286684	0.0251	0.2858
chr7	159138663	4881295	0.0307	0.431

chr8	146364022	5436130	0.0371	0.4596
chr9	141213431	3051355	0.0216	0.2838
chr10	135534747	3933225	0.029	0.3247
chr11	135006516	3615656	0.0268	0.3031
chr12	133851895	4107999	0.0307	0.2946
chr13	115169878	2168131	0.0188	0.232
chr14	107349540	2737559	0.0255	0.2735
chr15	102531392	2308750	0.0225	0.2585
chr16	90354753	2457917	0.0272	0.276
chr17	81195210	1997159	0.0246	0.2724
chr18	78077248	2383551	0.0305	0.4352
chr19	59128983	1449643	0.0245	0.3505
chr20	63025520	1649526	0.0262	0.2713
chr21	48129895	1387723	0.0288	0.2845
chr22	51304566	738298	0.0144	0.1878
chrMT	16571	18385	1.1095	1.8253
chrX	155270560	4535924	0.0292	0.2961
chrY	59373566	230053	0.0039	0.1013

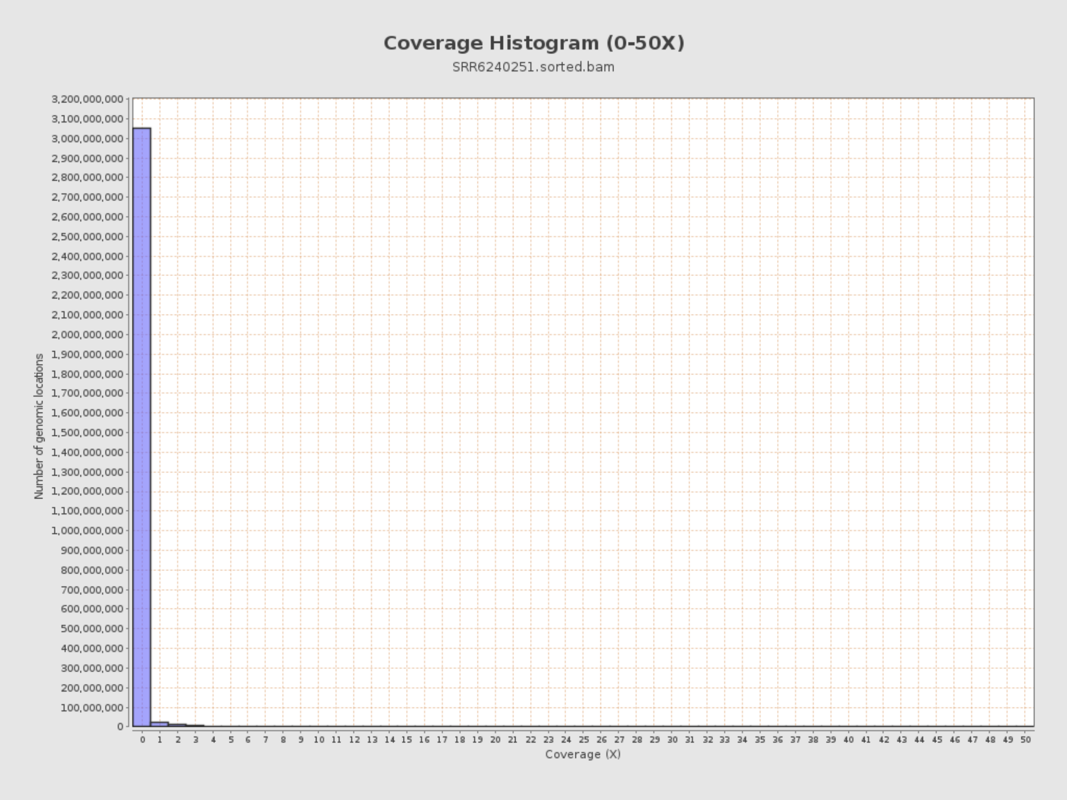
3. Results : Coverage across reference



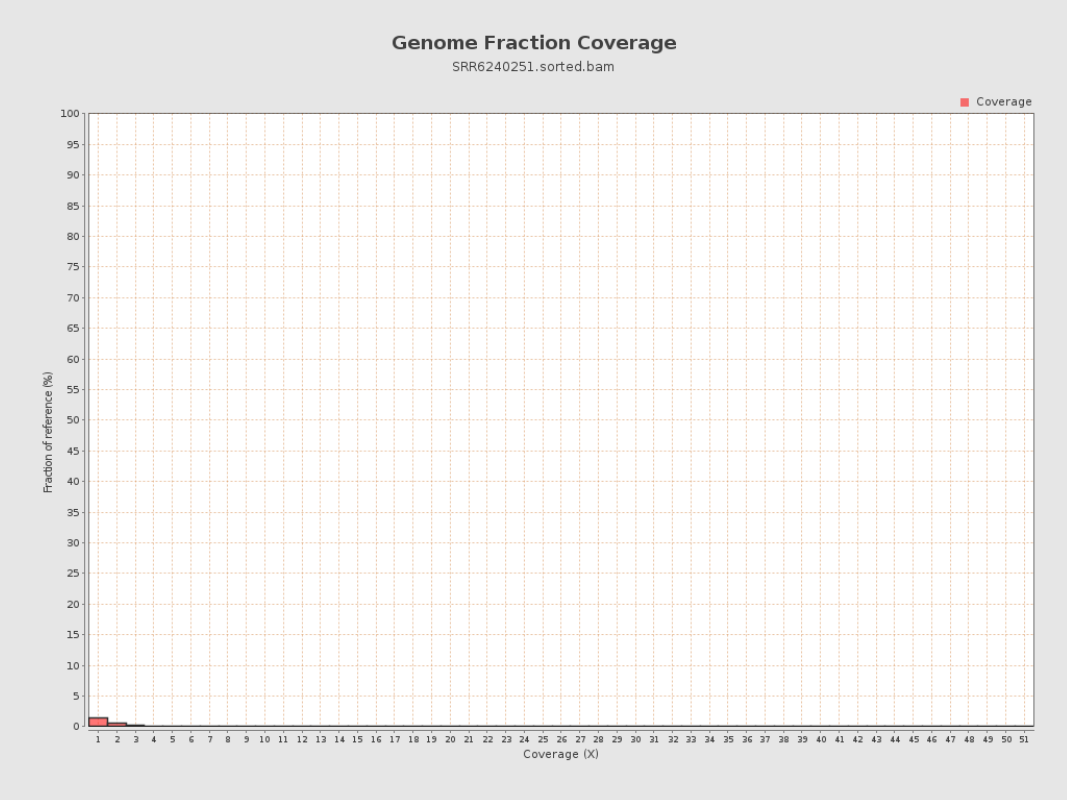
4. Results : Coverage Histogram



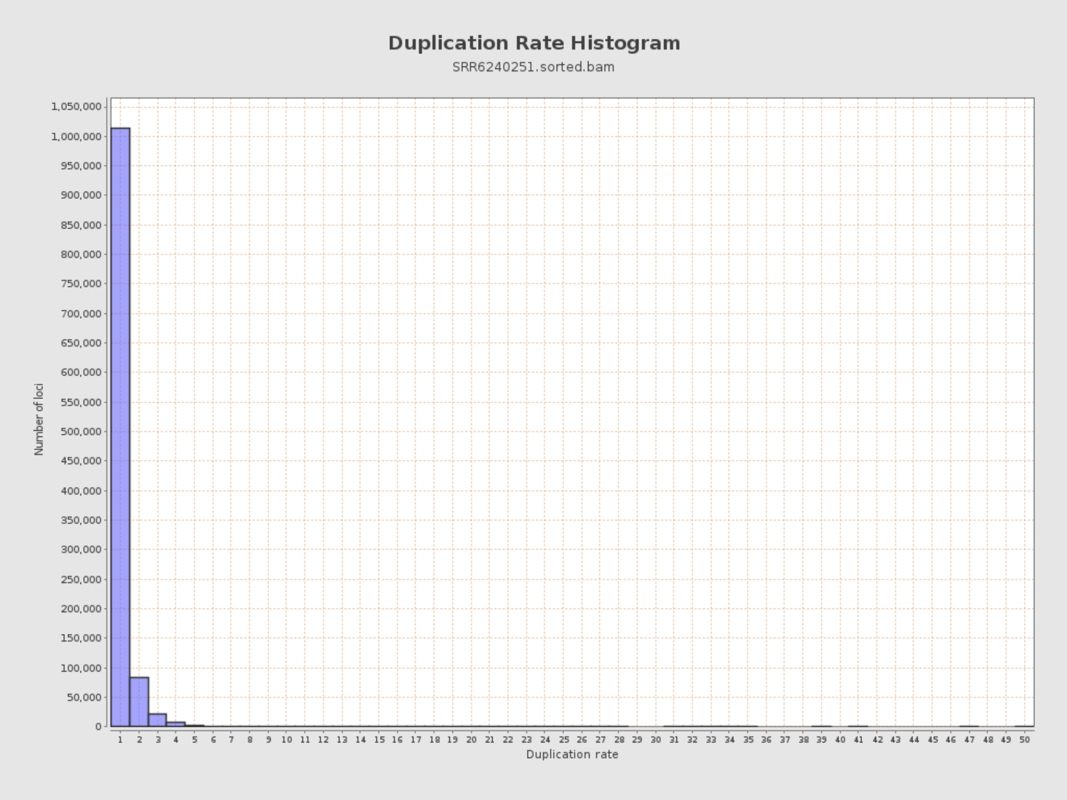
5. Results : Coverage Histogram (0-50X)



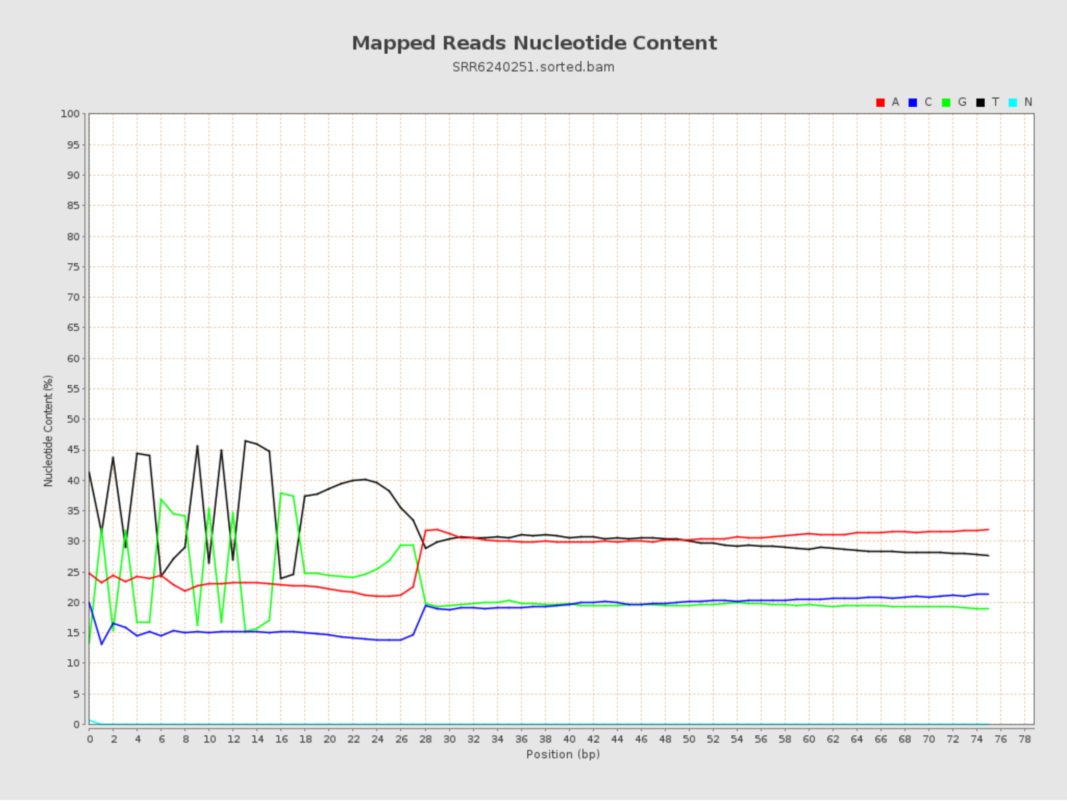
6. Results : Genome Fraction Coverage



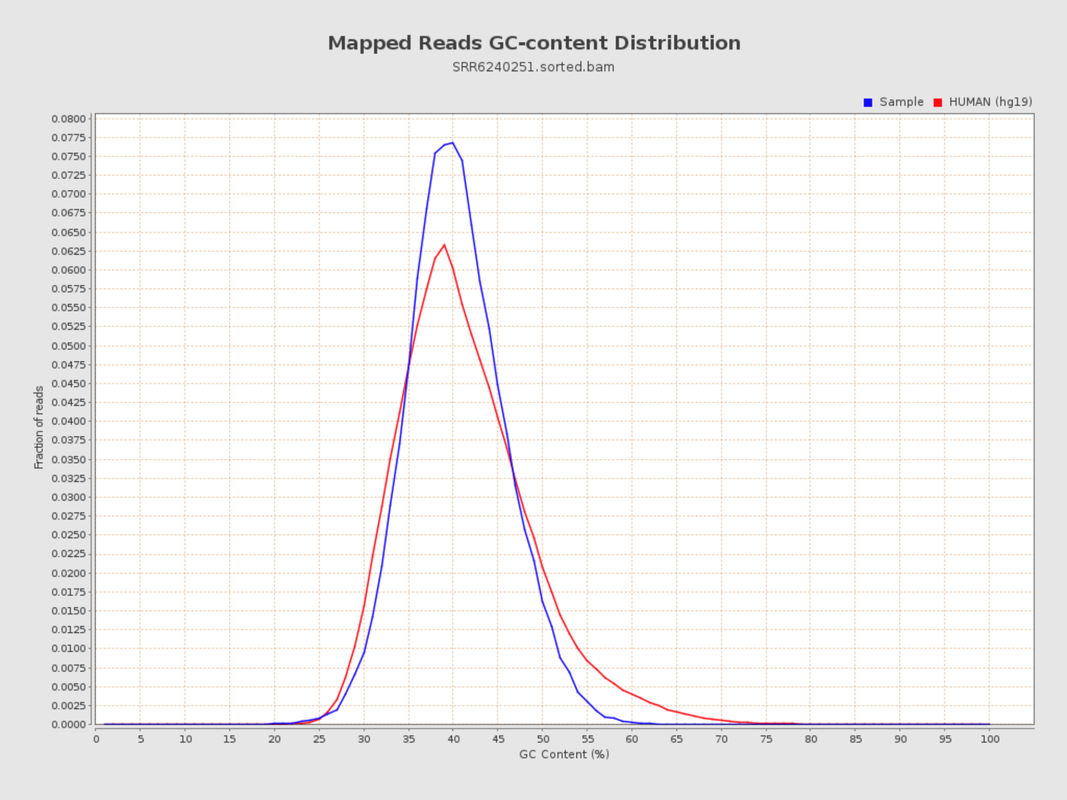
7. Results : Duplication Rate Histogram



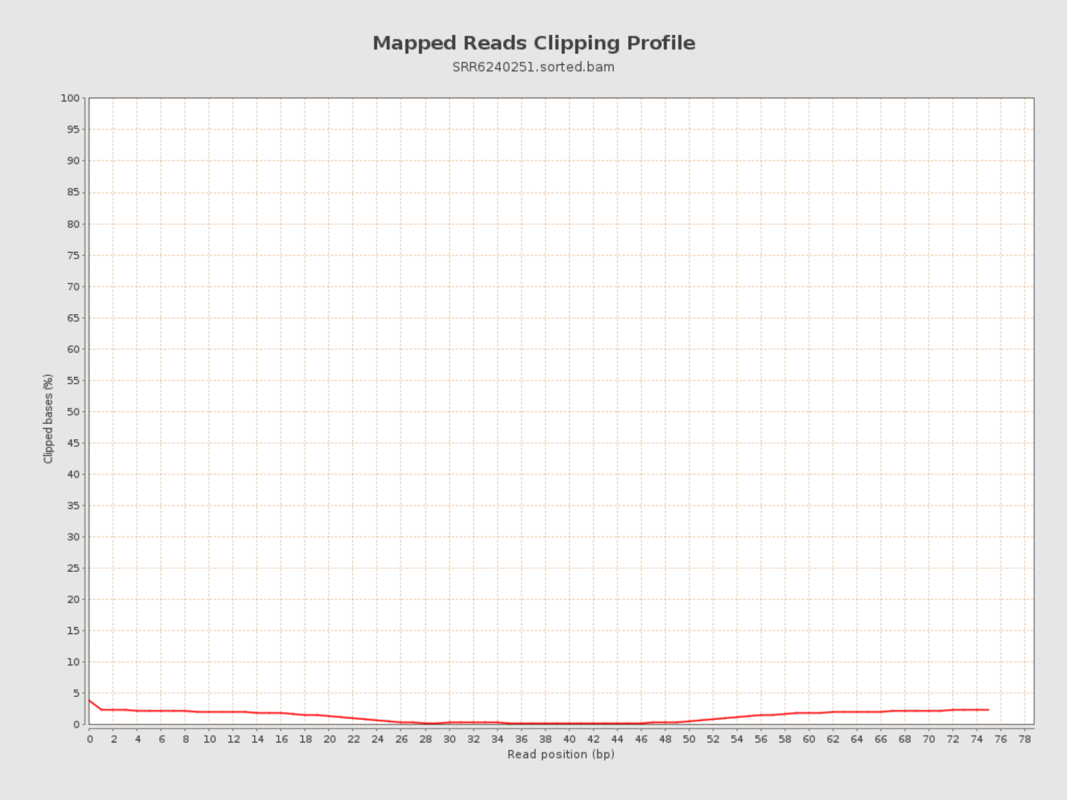
8. Results : Mapped Reads Nucleotide Content



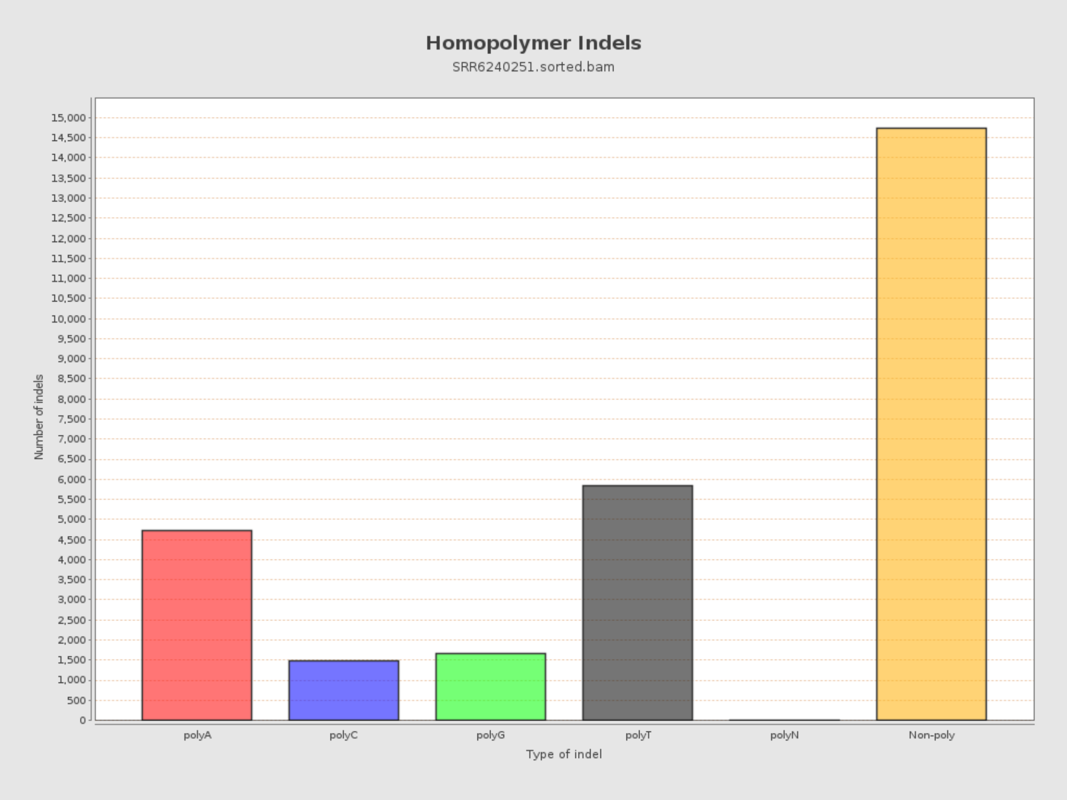
9. Results : Mapped Reads GC-content Distribution



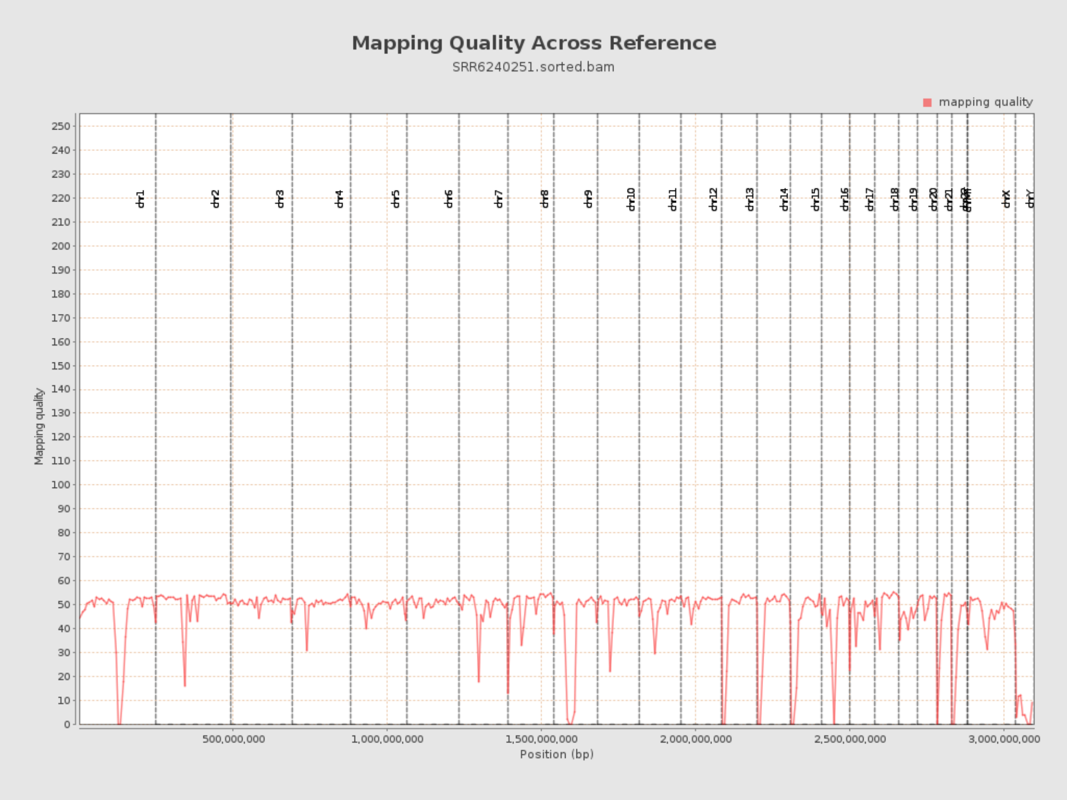
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram