Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:10:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240052.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_SRR6240052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240052.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:10:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240052.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,069,819
Mapped reads	1,664,885 / 80.44%
Unmapped reads	404,934 / 19.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,205 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	154,289 / 7.45%
Duplication rate	7.71%
Clipped reads	1,063,827 / 51.4%

2.2. ACGT Content

Number/percentage of A's	28,043,229 / 27.19%
Number/percentage of C's	18,079,366 / 17.53%
Number/percentage of T's	33,488,486 / 32.47%
Number/percentage of G's	23,444,727 / 22.74%
Number/percentage of N's	65,444 / 0.06%
GC Percentage	40.27%

2.3. Coverage

Mean	0.0333

Standard Deviation	0.3231

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

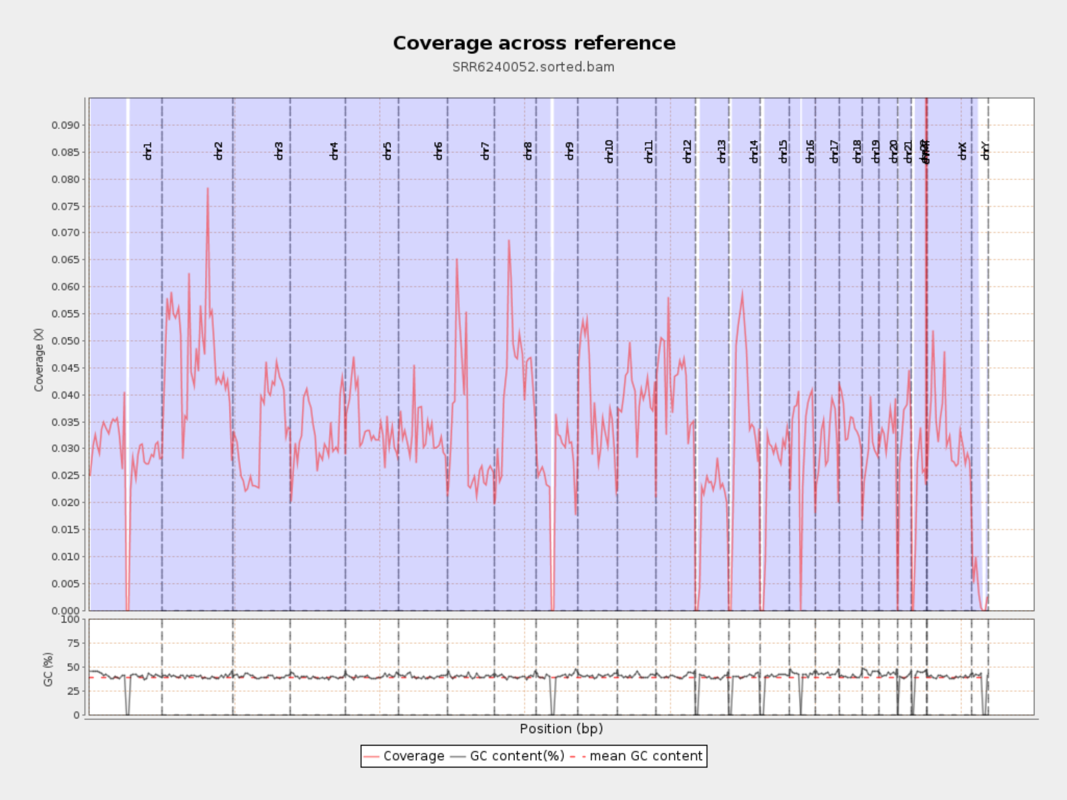
General error rate	0.98%
Mismatches	1,000,853
Insertions	7,224
Mapped reads with at least one insertion	0.43%
Deletions	31,975
Mapped reads with at least one deletion	1.9%
Homopolymer indels	49.59%

2.6. Chromosome stats

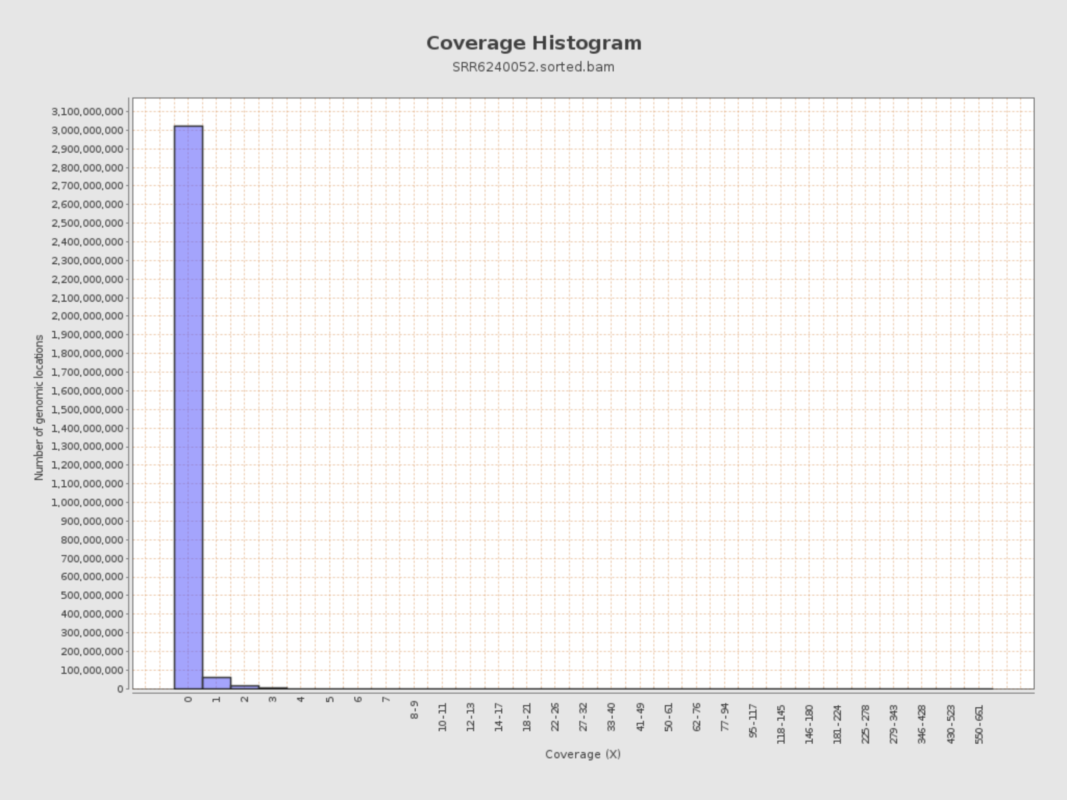
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7157659	0.0287	0.4409
chr2	243199373	11657974	0.0479	0.4088
chr3	198022430	6572928	0.0332	0.2421
chr4	191154276	6226665	0.0326	0.2416
chr5	180915260	6221375	0.0344	0.2425
chr6	171115067	5561681	0.0325	0.2771
chr7	159138663	5258691	0.033	0.4727

chr8	146364022	6261047	0.0428	0.478
chr9	141213431	3566699	0.0253	0.2847
chr10	135534747	5205414	0.0384	0.2995
chr11	135006516	5359517	0.0397	0.3624
chr12	133851895	5696518	0.0426	0.2726
chr13	115169878	2225794	0.0193	0.1781
chr14	107349540	3878871	0.0361	0.2542
chr15	102531392	2520528	0.0246	0.2174
chr16	90354753	2869470	0.0318	0.2373
chr17	81195210	2510359	0.0309	0.2526
chr18	78077248	2719487	0.0348	0.4545
chr19	59128983	1739943	0.0294	0.3317
chr20	63025520	2078047	0.033	0.2393
chr21	48129895	1554629	0.0323	0.2405
chr22	51304566	1010186	0.0197	0.1767
chrMT	16571	23594	1.4238	2.0103
chrX	155270560	5089973	0.0328	0.2565
chrY	59373566	209727	0.0035	0.0821

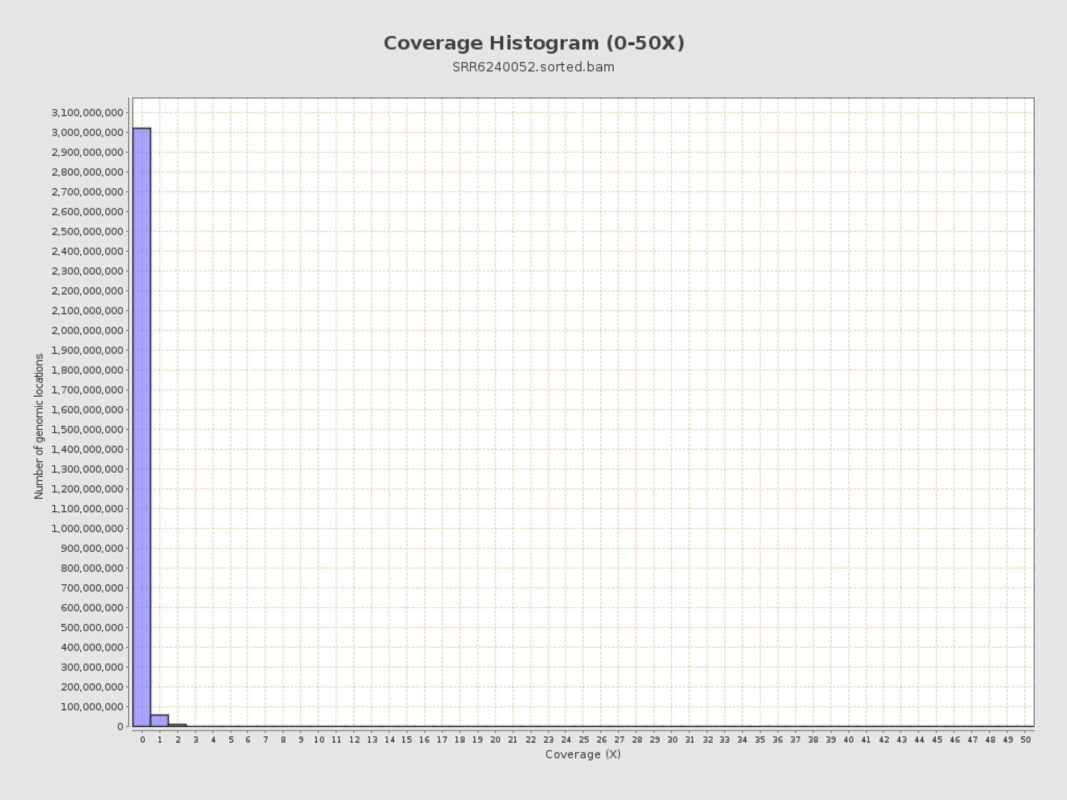
3. Results : Coverage across reference



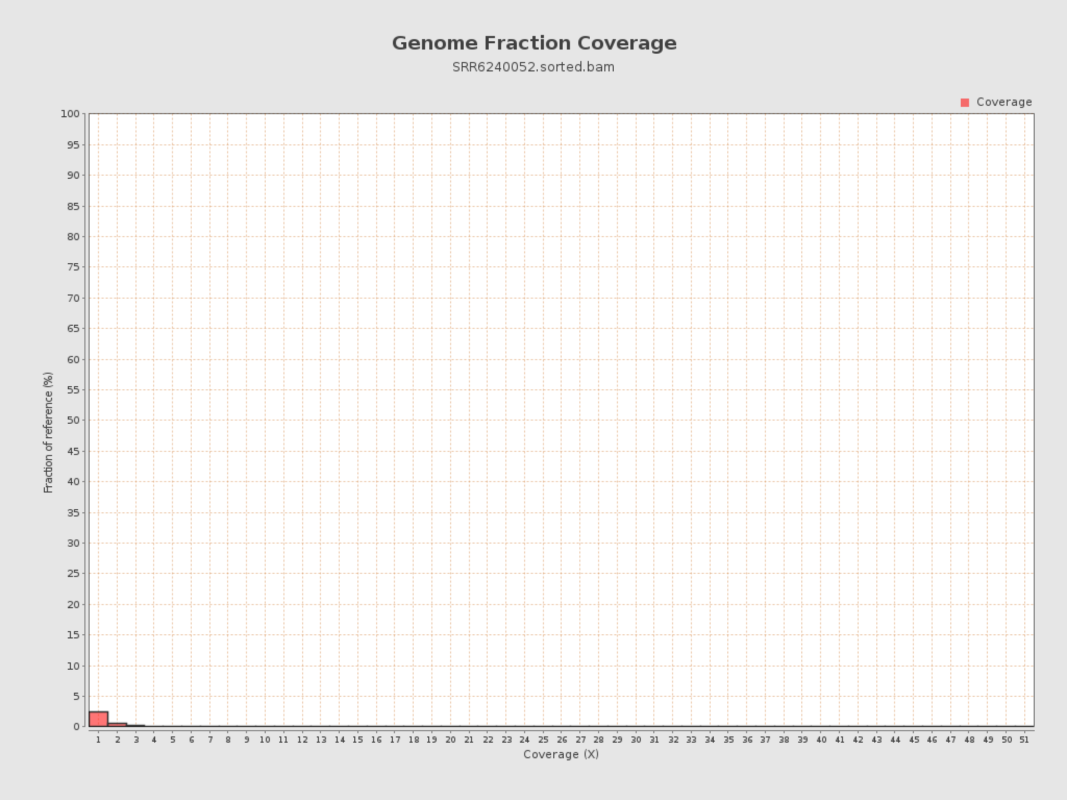
4. Results : Coverage Histogram



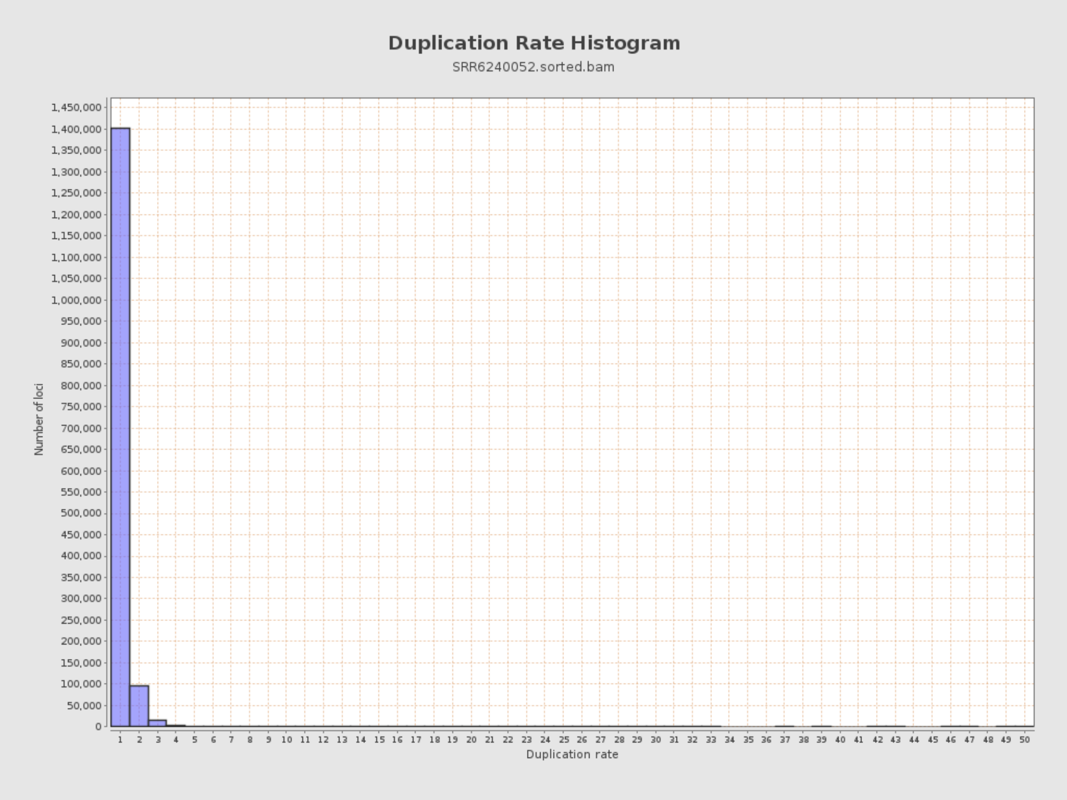
5. Results : Coverage Histogram (0-50X)



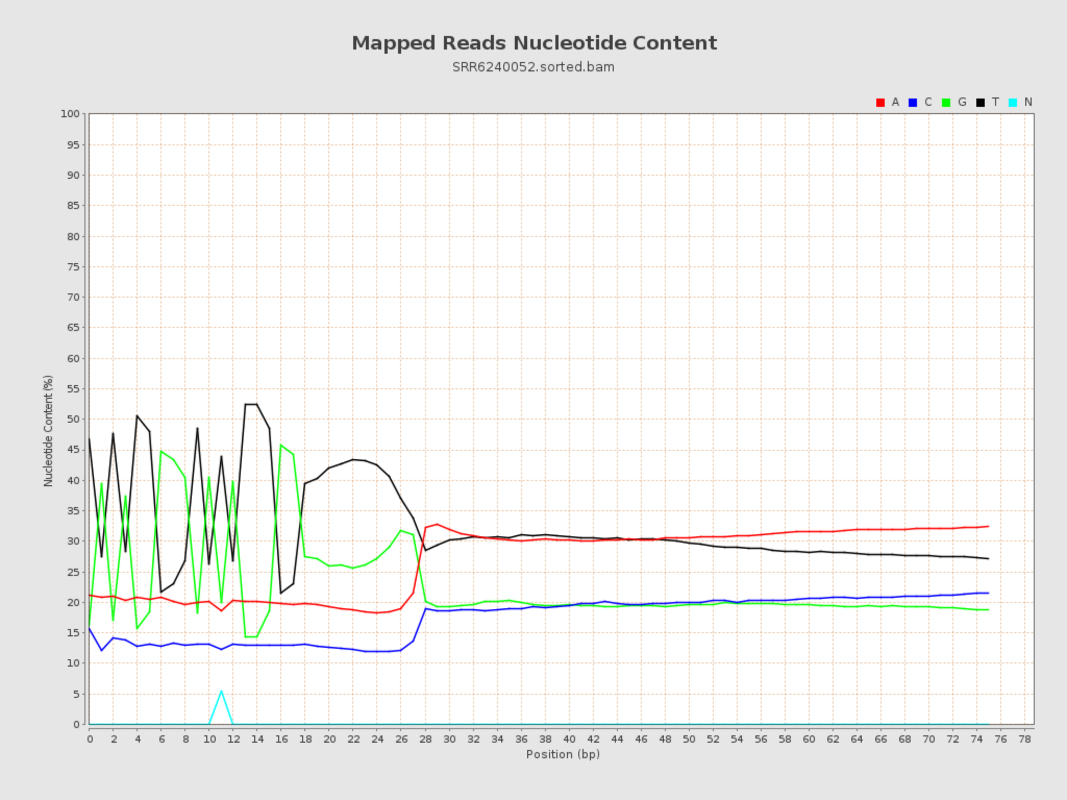
6. Results : Genome Fraction Coverage



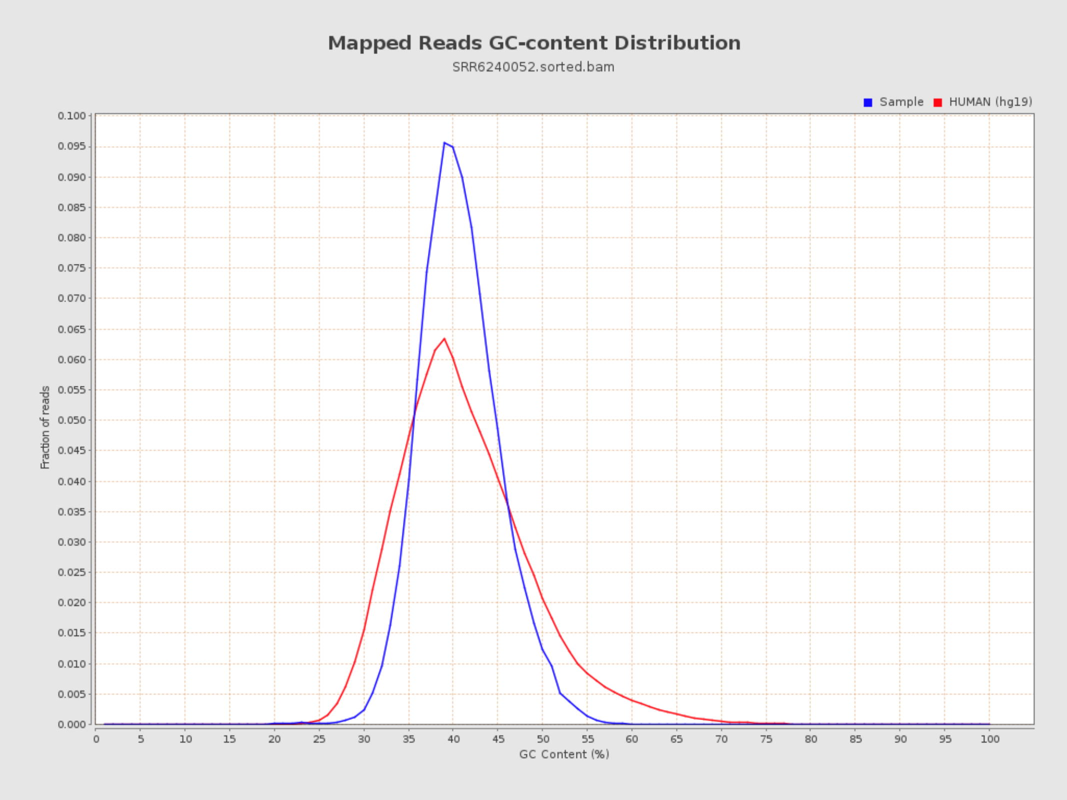
7. Results : Duplication Rate Histogram



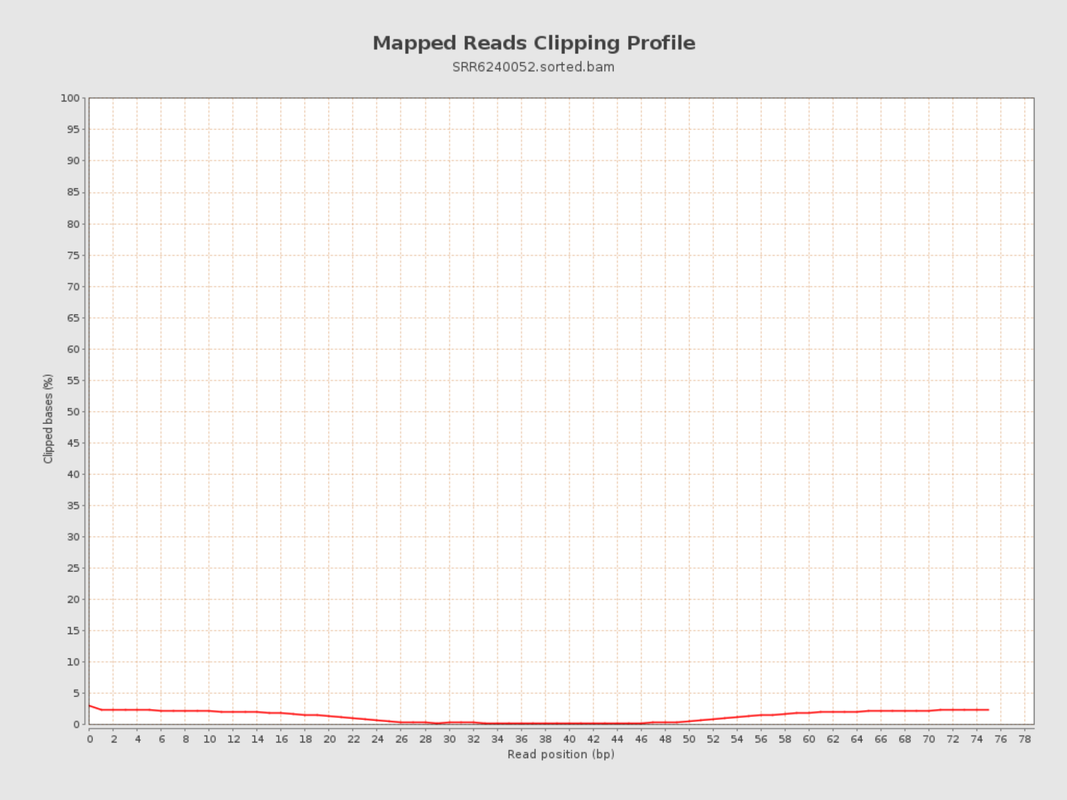
8. Results : Mapped Reads Nucleotide Content



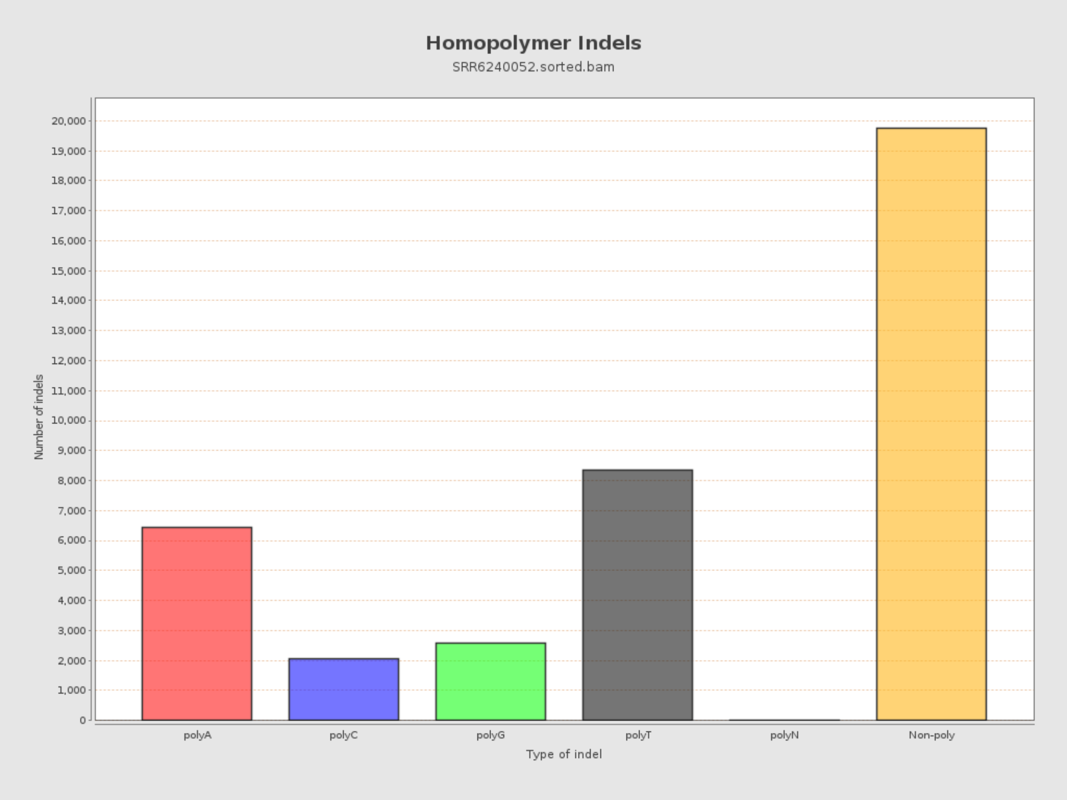
9. Results : Mapped Reads GC-content Distribution



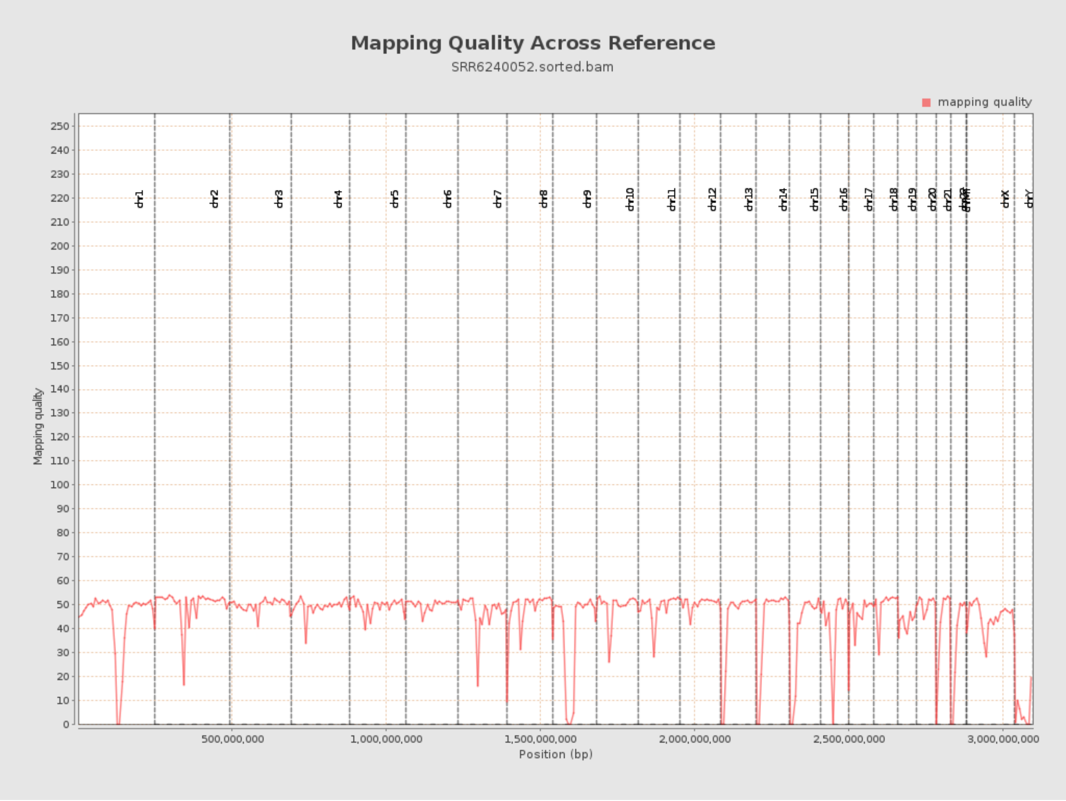
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram