Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 08:59:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240260.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_SRR6240260 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240260.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 08:59:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240260.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,941,339
Mapped reads	1,551,140 / 79.9%
Unmapped reads	390,199 / 20.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,374 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	221,140 / 11.39%
Duplication rate	11.22%
Clipped reads	1,004,800 / 51.76%

2.2. ACGT Content

Number/percentage of A's	26,328,196 / 27.53%
Number/percentage of C's	17,147,261 / 17.93%
Number/percentage of T's	30,667,471 / 32.06%
Number/percentage of G's	21,483,202 / 22.46%
Number/percentage of N's	22,520 / 0.02%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.3385

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

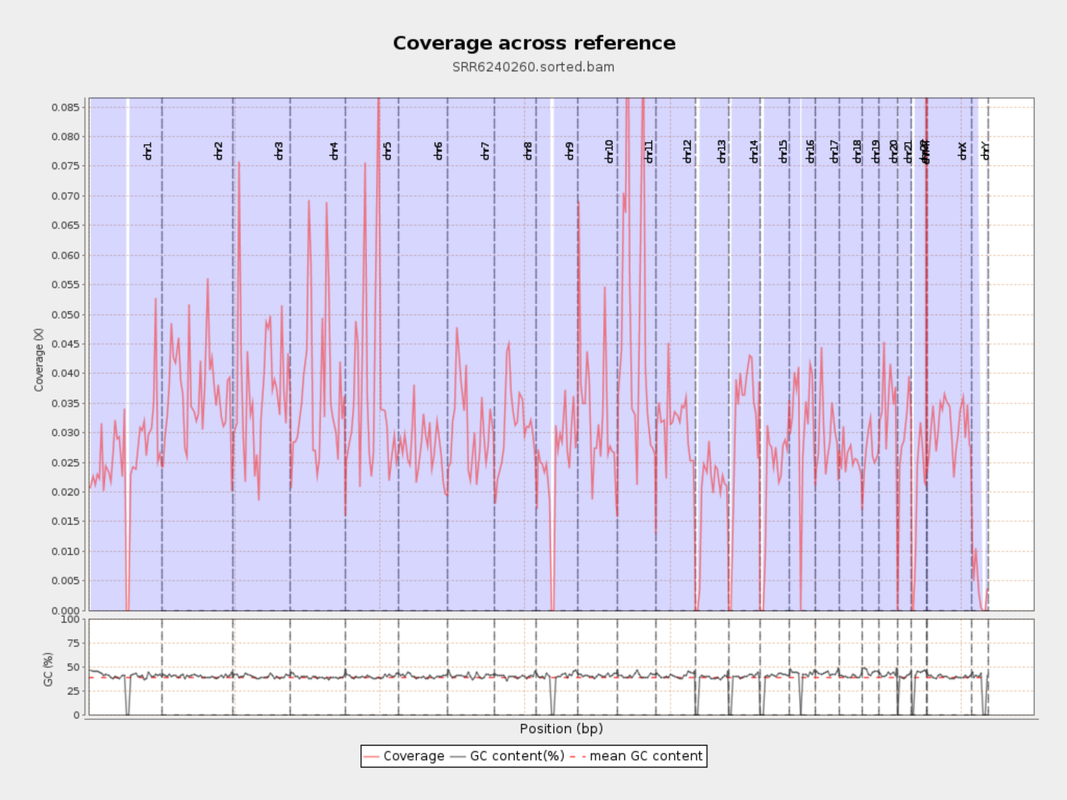
General error rate	0.89%
Mismatches	840,362
Insertions	6,933
Mapped reads with at least one insertion	0.44%
Deletions	26,438
Mapped reads with at least one deletion	1.69%
Homopolymer indels	47.88%

2.6. Chromosome stats

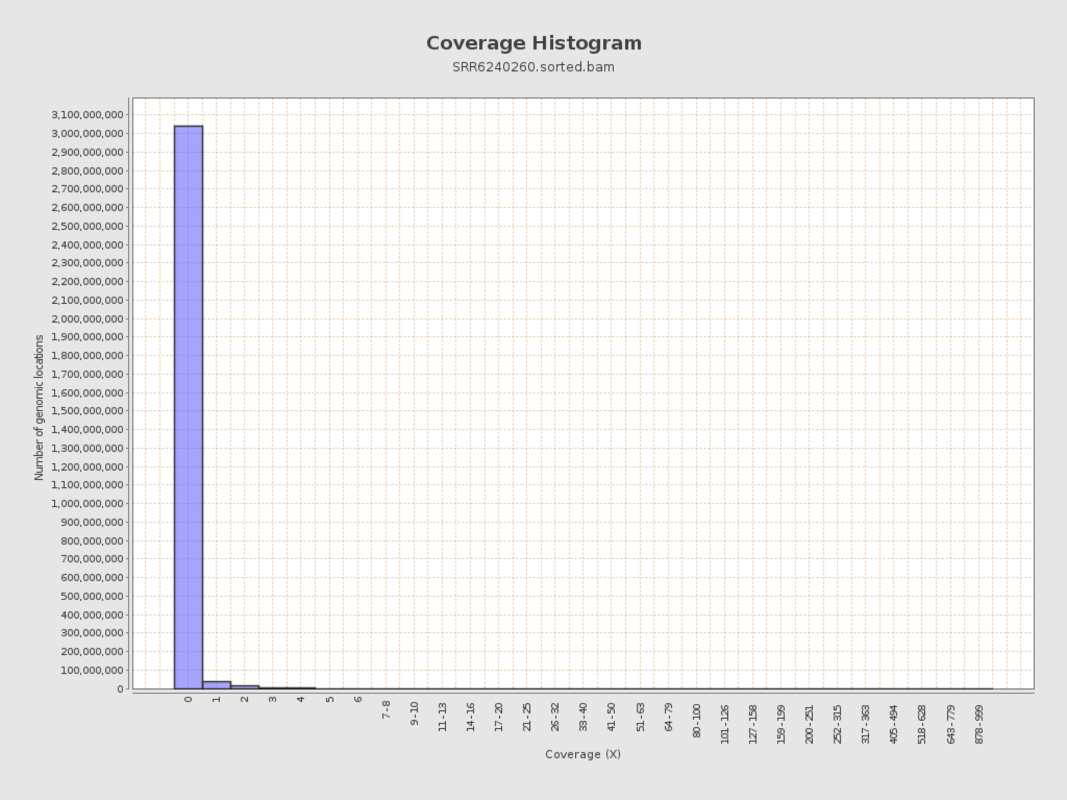
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6403934	0.0257	0.4167
chr2	243199373	8977436	0.0369	0.4195
chr3	198022430	7399591	0.0374	0.2944
chr4	191154276	7131397	0.0373	0.2985
chr5	180915260	6597074	0.0365	0.2923
chr6	171115067	4681959	0.0274	0.2795
chr7	159138663	4968807	0.0312	0.3505

chr8	146364022	4550500	0.0311	0.6187
chr9	141213431	3478710	0.0246	0.2975
chr10	135534747	4559107	0.0336	0.3033
chr11	135006516	6575403	0.0487	0.3653
chr12	133851895	4228615	0.0316	0.2778
chr13	115169878	2175507	0.0189	0.2095
chr14	107349540	3289870	0.0306	0.2823
chr15	102531392	2239804	0.0218	0.2368
chr16	90354753	2876253	0.0318	0.2718
chr17	81195210	2383276	0.0294	0.3112
chr18	78077248	2009702	0.0257	0.4011
chr19	59128983	1589144	0.0269	0.3218
chr20	63025520	2222129	0.0353	0.2903
chr21	48129895	1352610	0.0281	0.2579
chr22	51304566	923502	0.018	0.1963
chrMT	16571	54417	3.2839	3.5154
chrX	155270560	4797847	0.0309	0.2849
chrY	59373566	226761	0.0038	0.0894

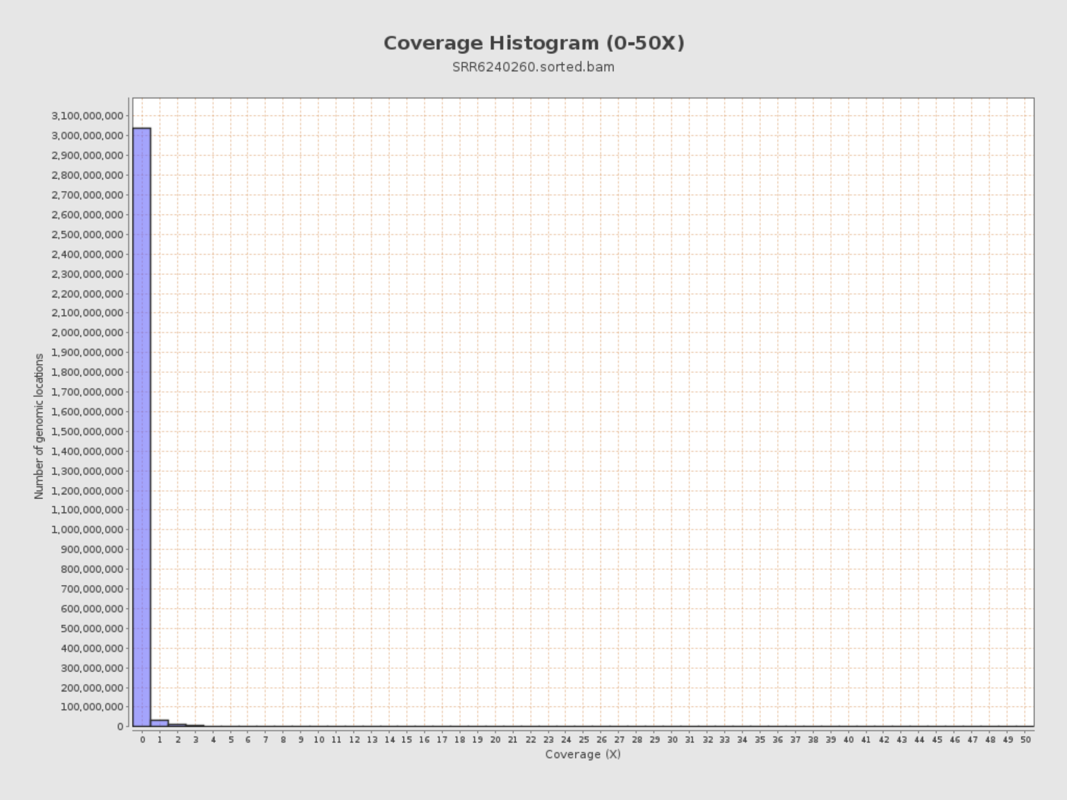
3. Results : Coverage across reference



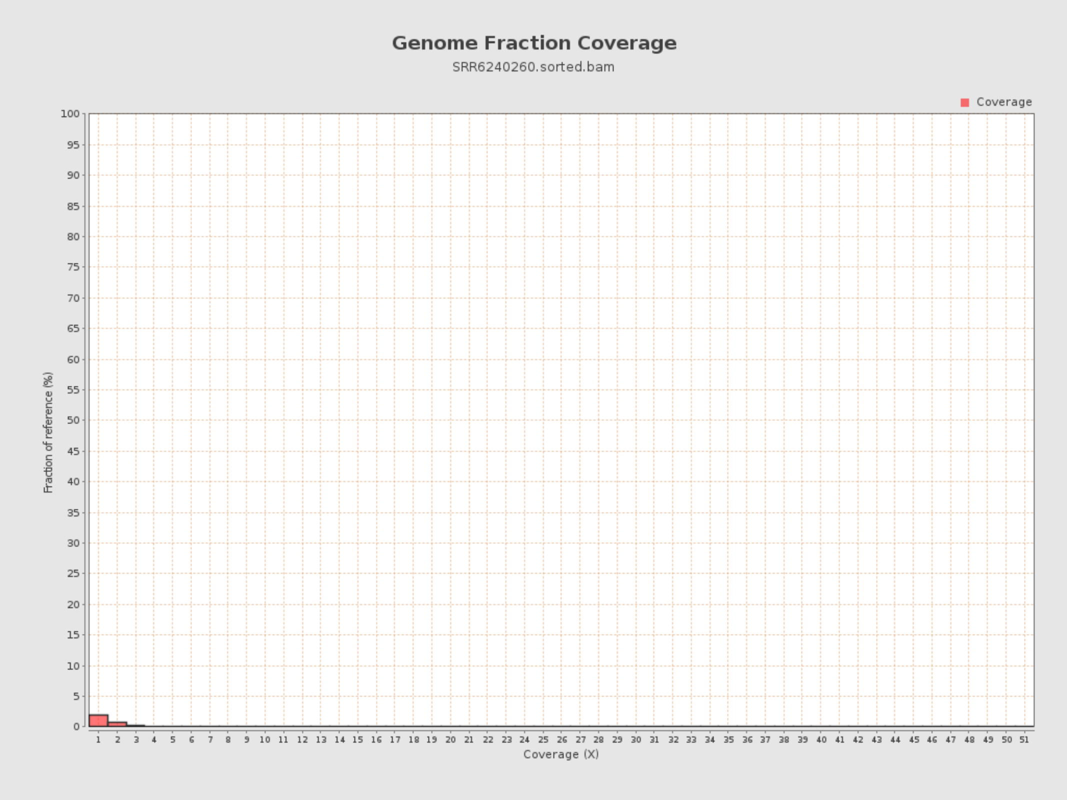
4. Results : Coverage Histogram



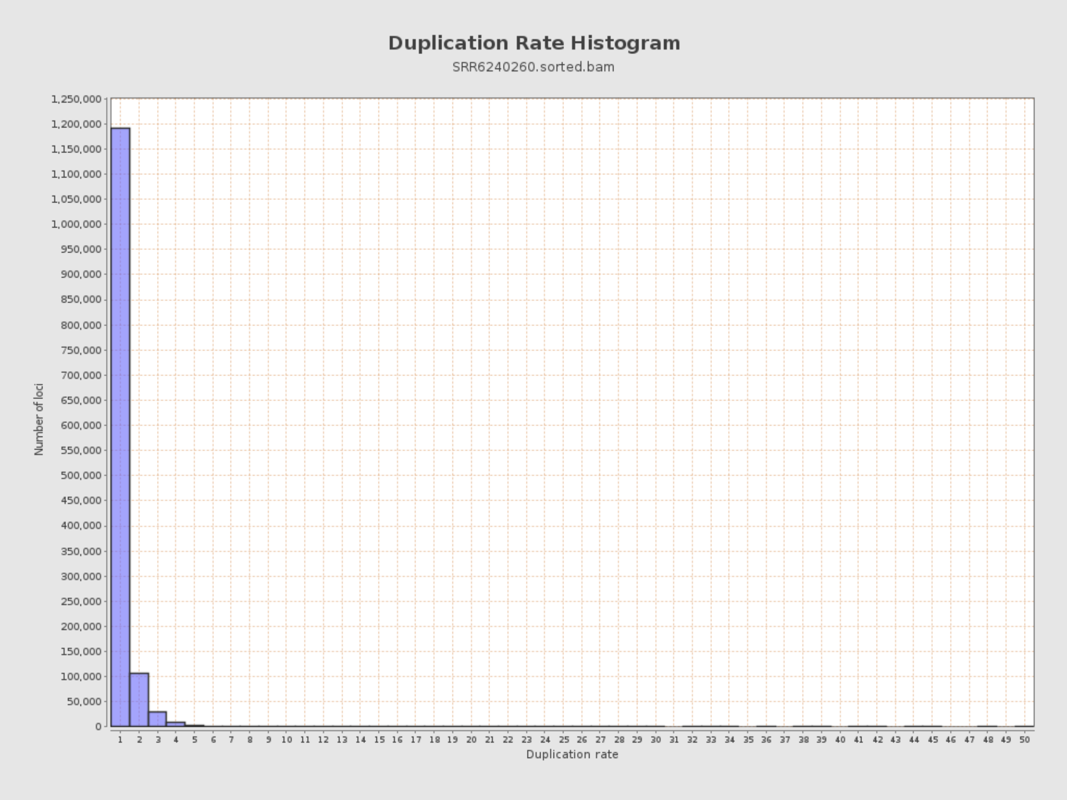
5. Results : Coverage Histogram (0-50X)



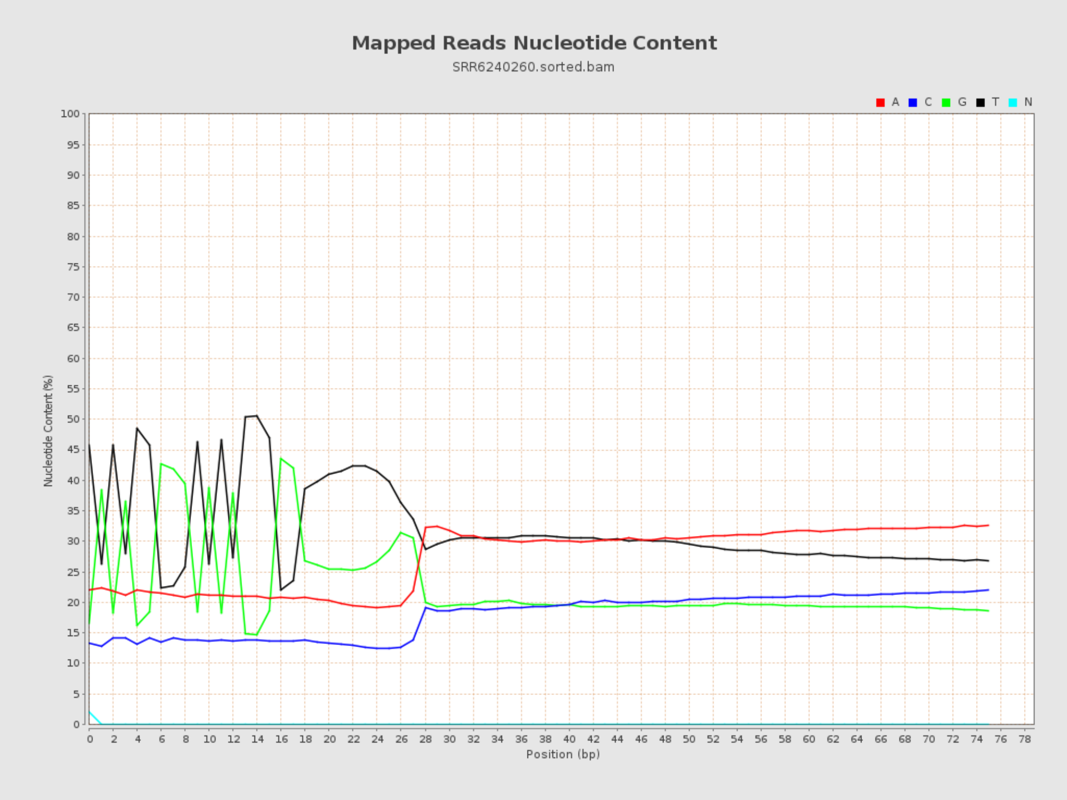
6. Results : Genome Fraction Coverage



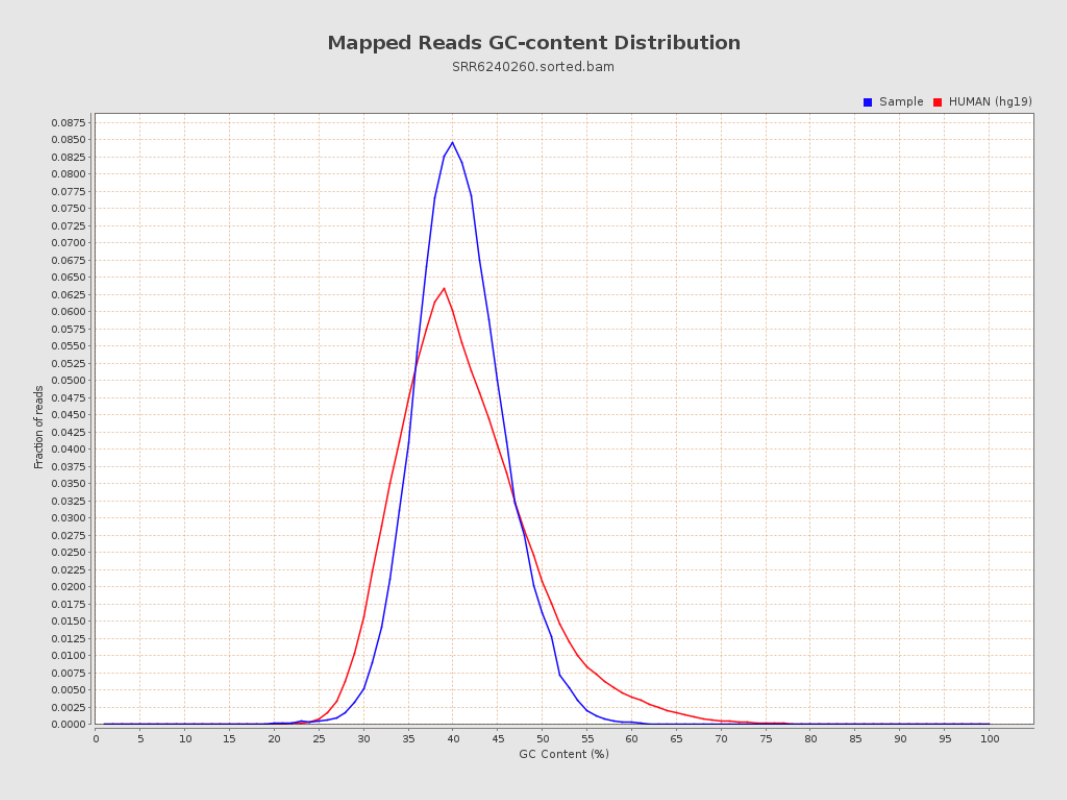
7. Results : Duplication Rate Histogram



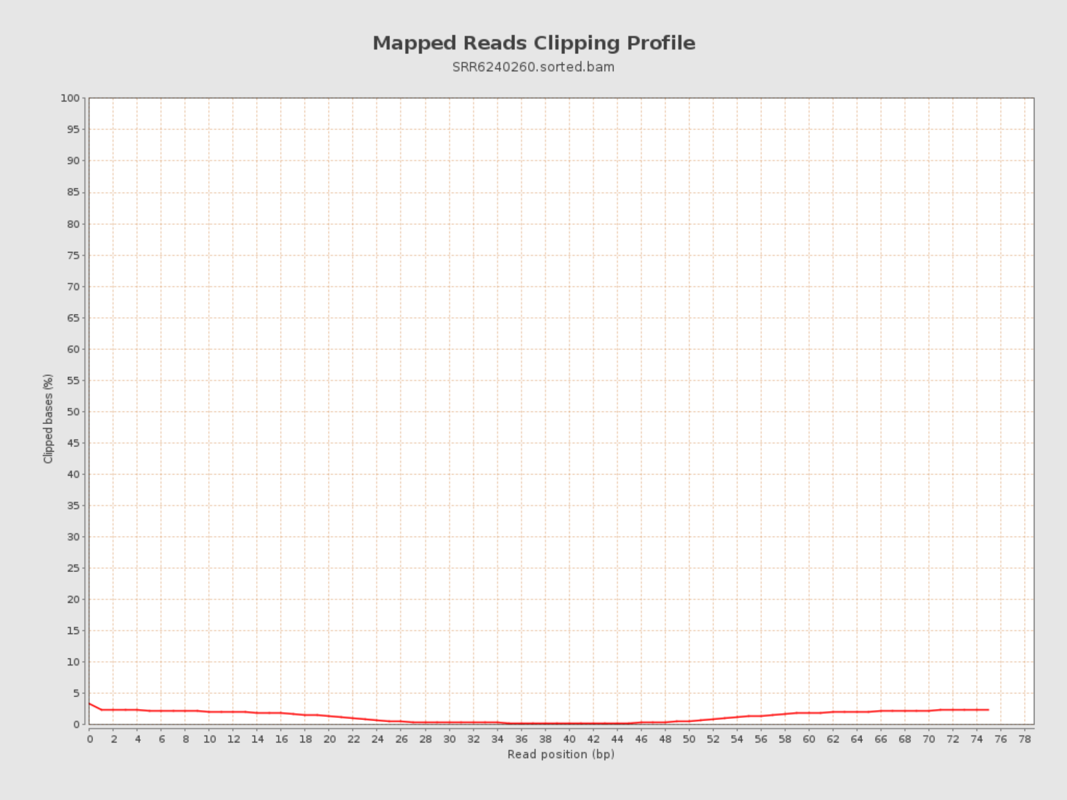
8. Results : Mapped Reads Nucleotide Content



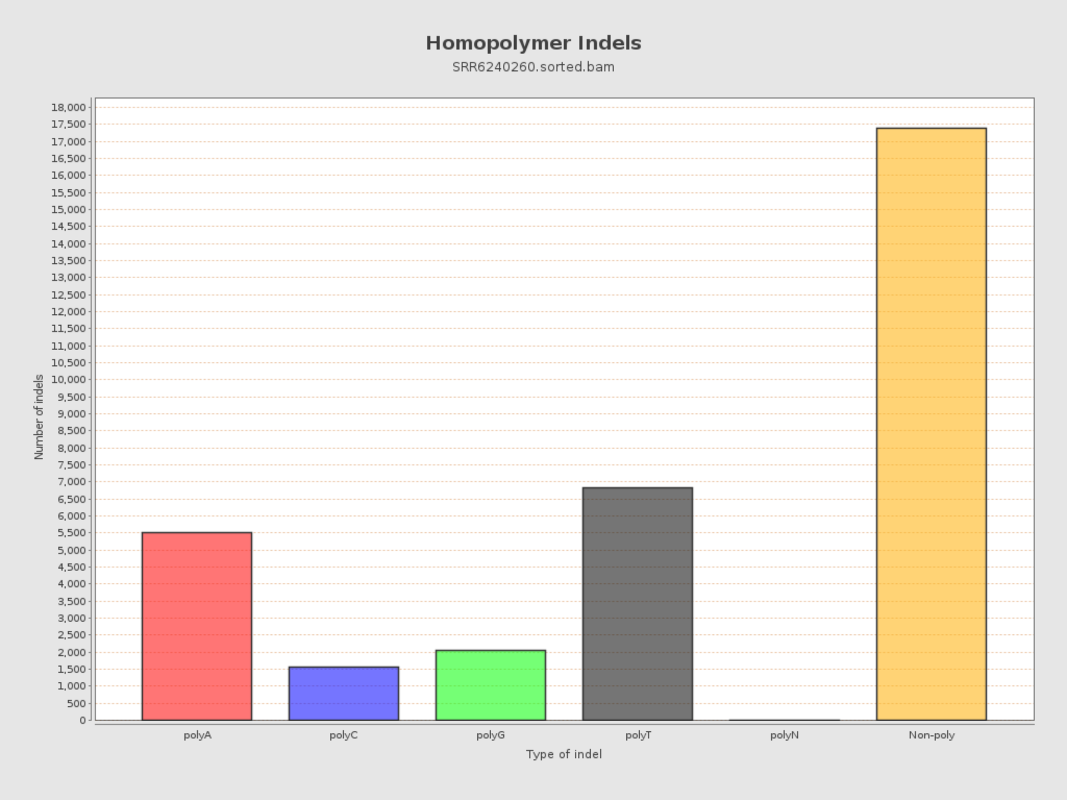
9. Results : Mapped Reads GC-content Distribution



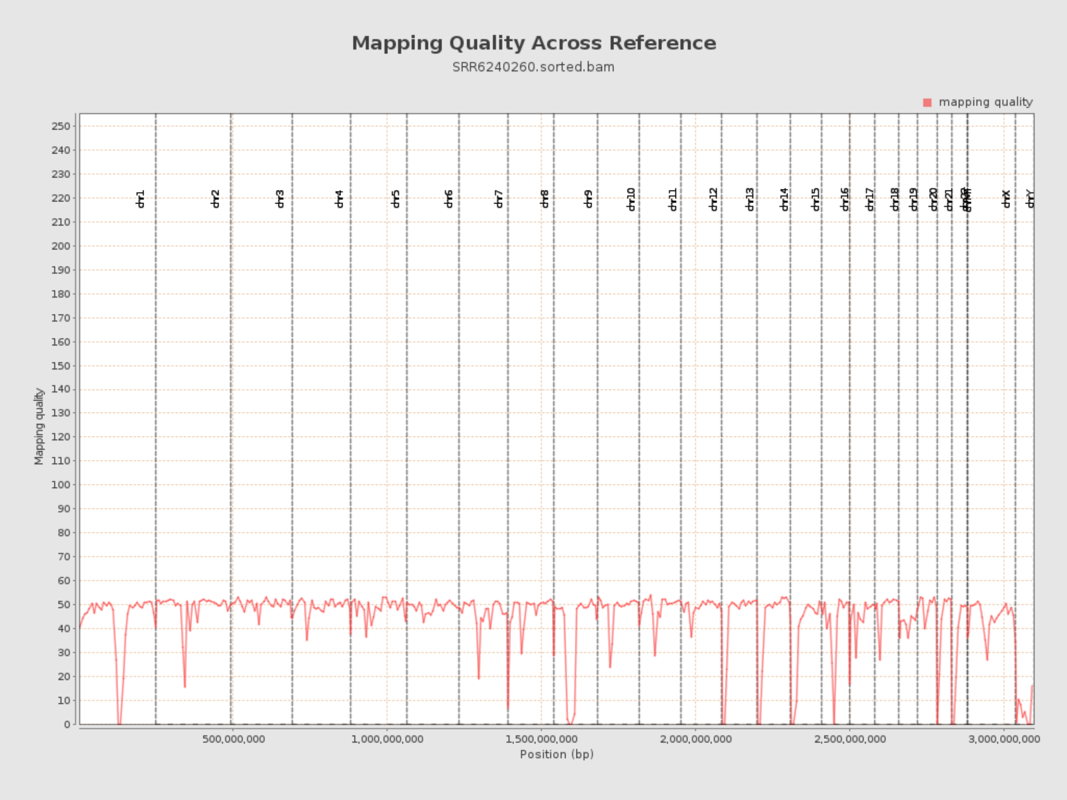
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram