Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 05:39:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240189.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_SRR6240189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 05:39:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,223,758
Mapped reads	957,406 / 78.23%
Unmapped reads	266,352 / 21.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,294 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	86,248 / 7.05%
Duplication rate	7.4%
Clipped reads	495,908 / 40.52%

2.2. ACGT Content

Number/percentage of A's	17,573,995 / 28.14%
Number/percentage of C's	11,483,145 / 18.39%
Number/percentage of T's	19,833,851 / 31.76%
Number/percentage of G's	13,524,978 / 21.66%
Number/percentage of N's	35,198 / 0.06%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0202

Standard Deviation	0.2463

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

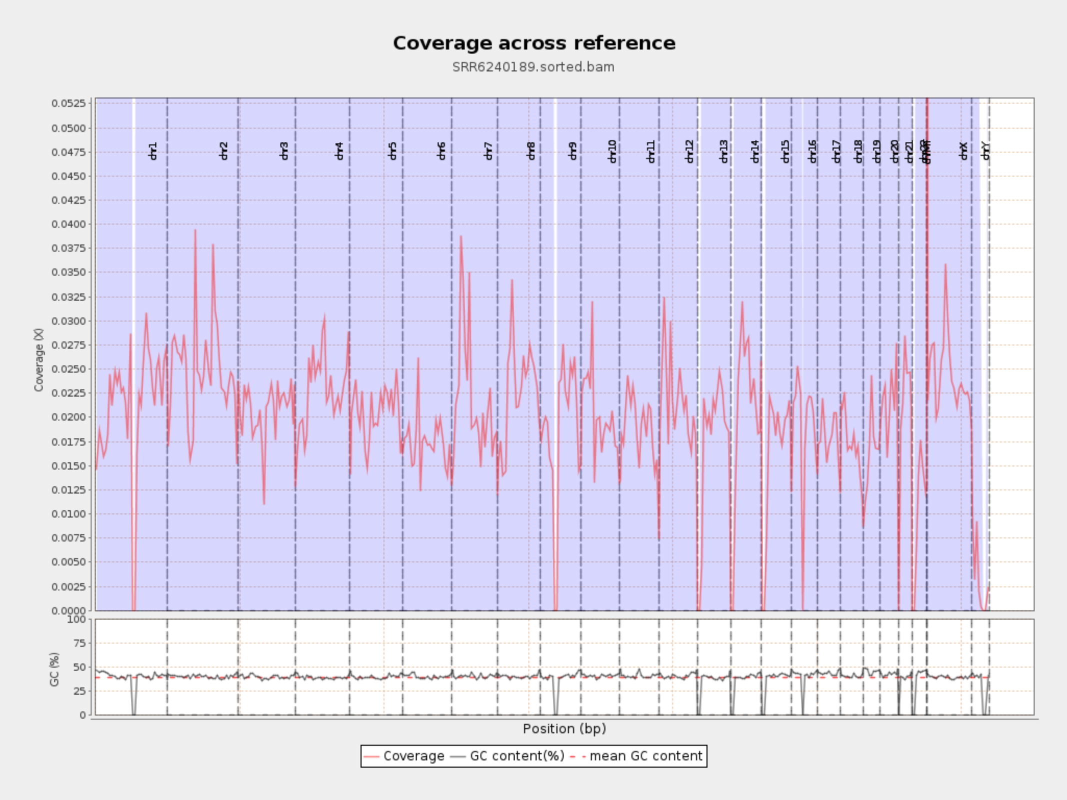
General error rate	0.92%
Mismatches	565,311
Insertions	4,431
Mapped reads with at least one insertion	0.46%
Deletions	18,104
Mapped reads with at least one deletion	1.87%
Homopolymer indels	46.87%

2.6. Chromosome stats

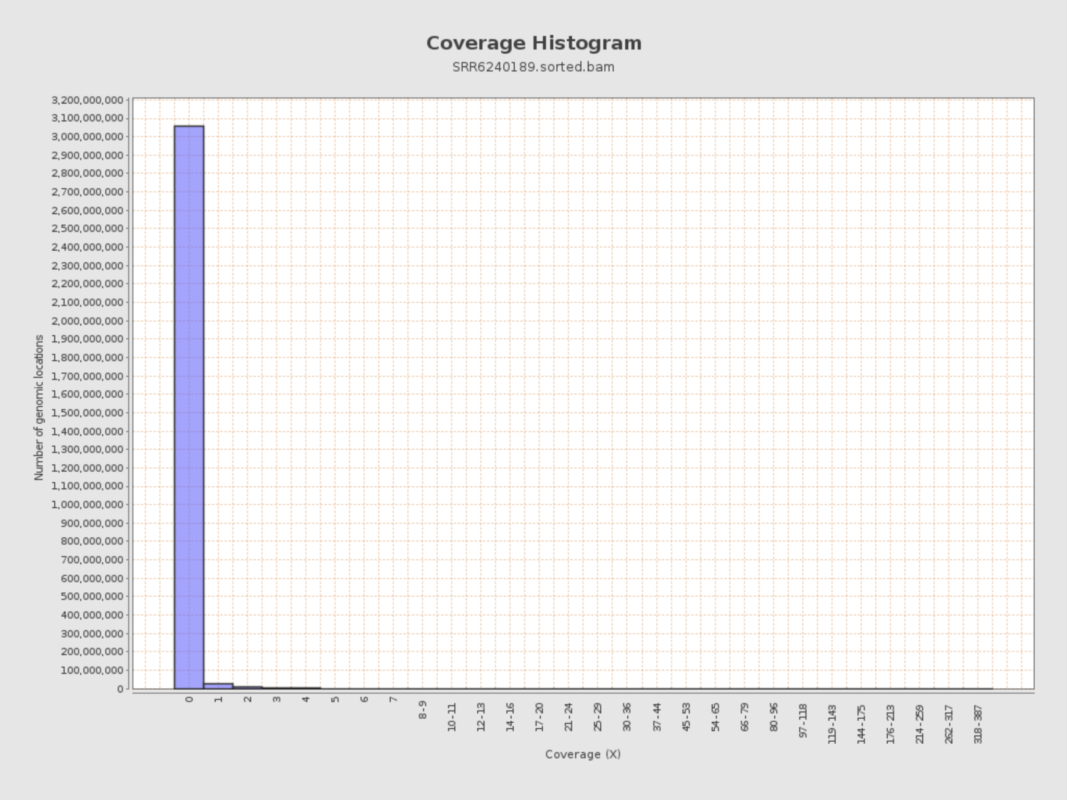
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5246862	0.0211	0.3388
chr2	243199373	6067169	0.0249	0.2803
chr3	198022430	4091774	0.0207	0.2106
chr4	191154276	4346136	0.0227	0.2219
chr5	180915260	3719349	0.0206	0.2079
chr6	171115067	2974455	0.0174	0.2134
chr7	159138663	3492184	0.0219	0.3063

chr8	146364022	3374098	0.0231	0.3222
chr9	141213431	2649304	0.0188	0.235
chr10	135534747	2750788	0.0203	0.2403
chr11	135006516	2568369	0.019	0.2322
chr12	133851895	2941947	0.022	0.2172
chr13	115169878	1989459	0.0173	0.1894
chr14	107349540	2198662	0.0205	0.214
chr15	102531392	1655496	0.0161	0.1973
chr16	90354753	1691010	0.0187	0.2003
chr17	81195210	1459642	0.018	0.2038
chr18	78077248	1363023	0.0175	0.314
chr19	59128983	971196	0.0164	0.2583
chr20	63025520	1358297	0.0216	0.2142
chr21	48129895	1017961	0.0212	0.2179
chr22	51304566	530183	0.0103	0.1425
chrMT	16571	14161	0.8546	1.3305
chrX	155270560	3827889	0.0247	0.2354
chrY	59373566	183087	0.0031	0.0792

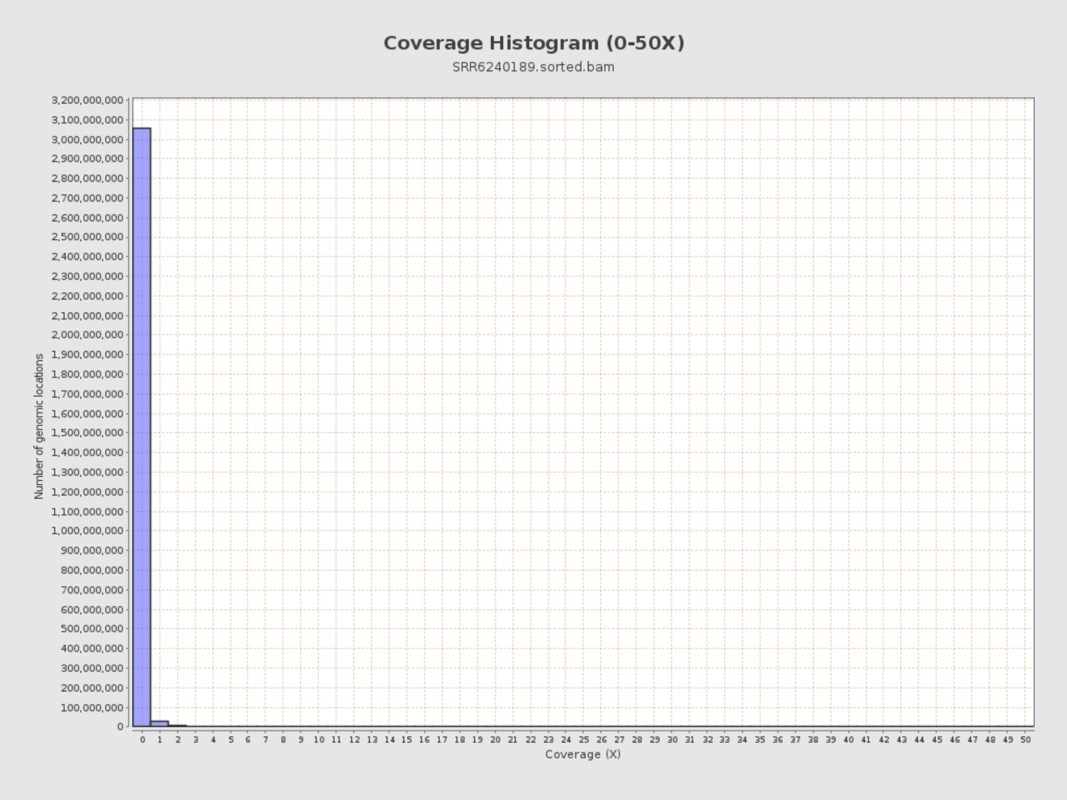
3. Results : Coverage across reference



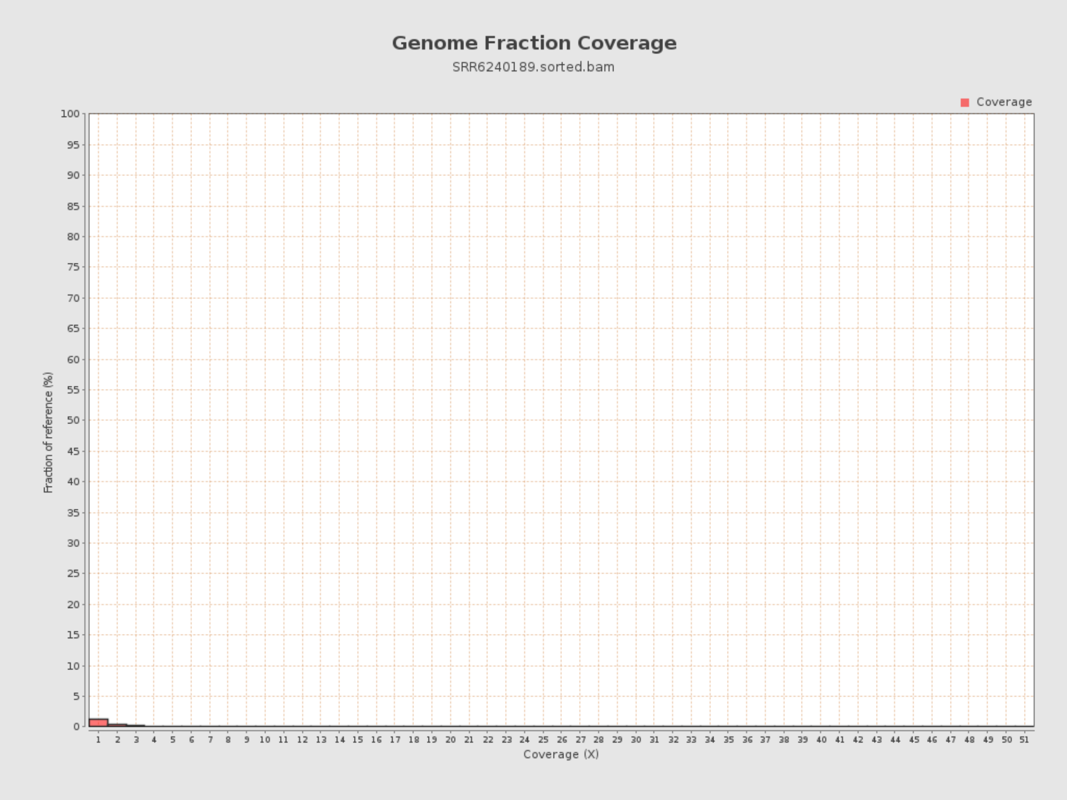
4. Results : Coverage Histogram



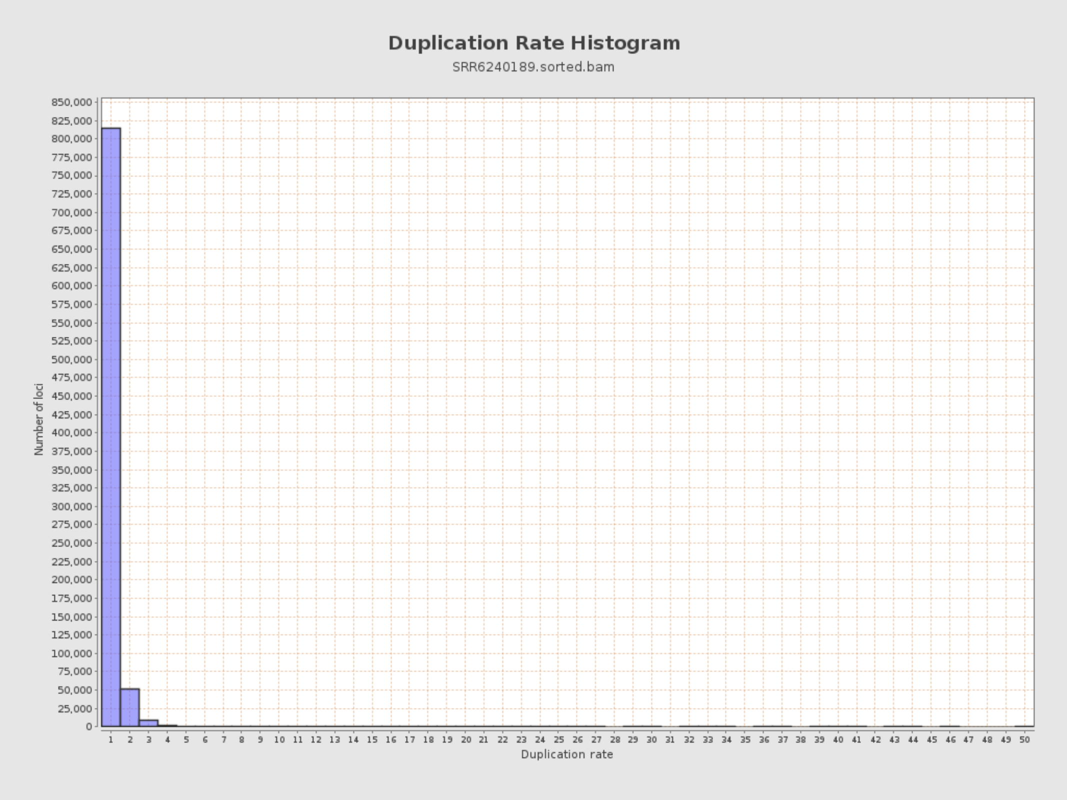
5. Results : Coverage Histogram (0-50X)



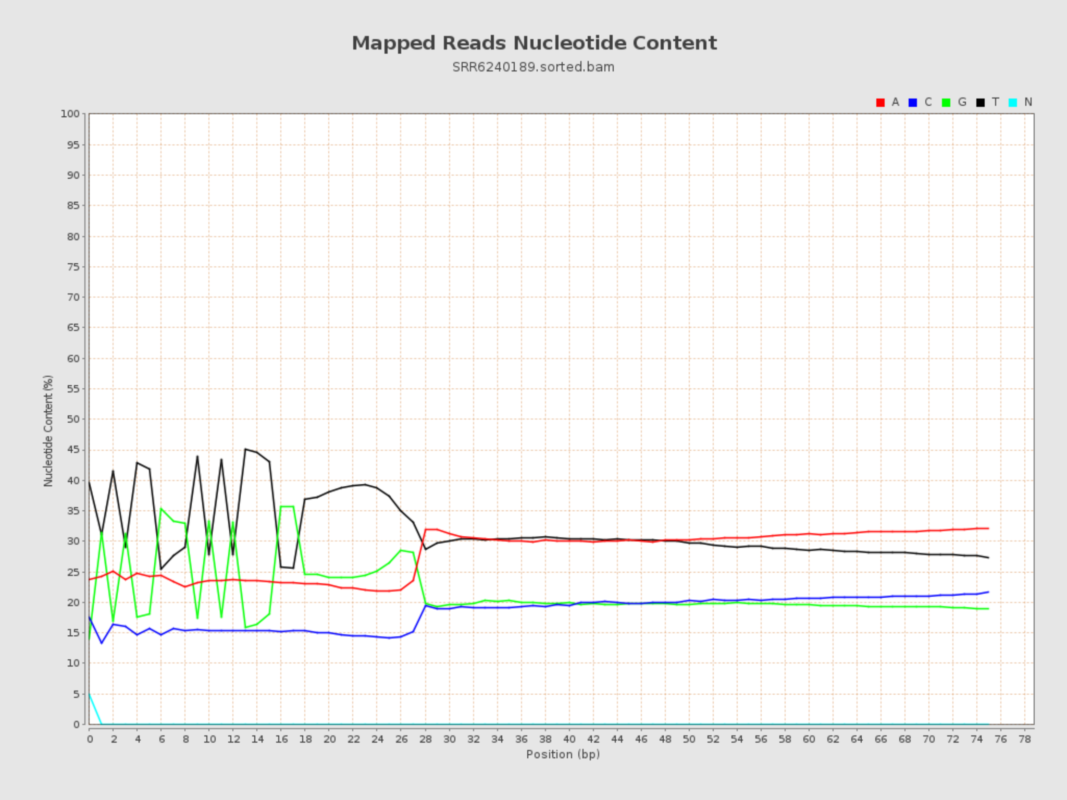
6. Results : Genome Fraction Coverage



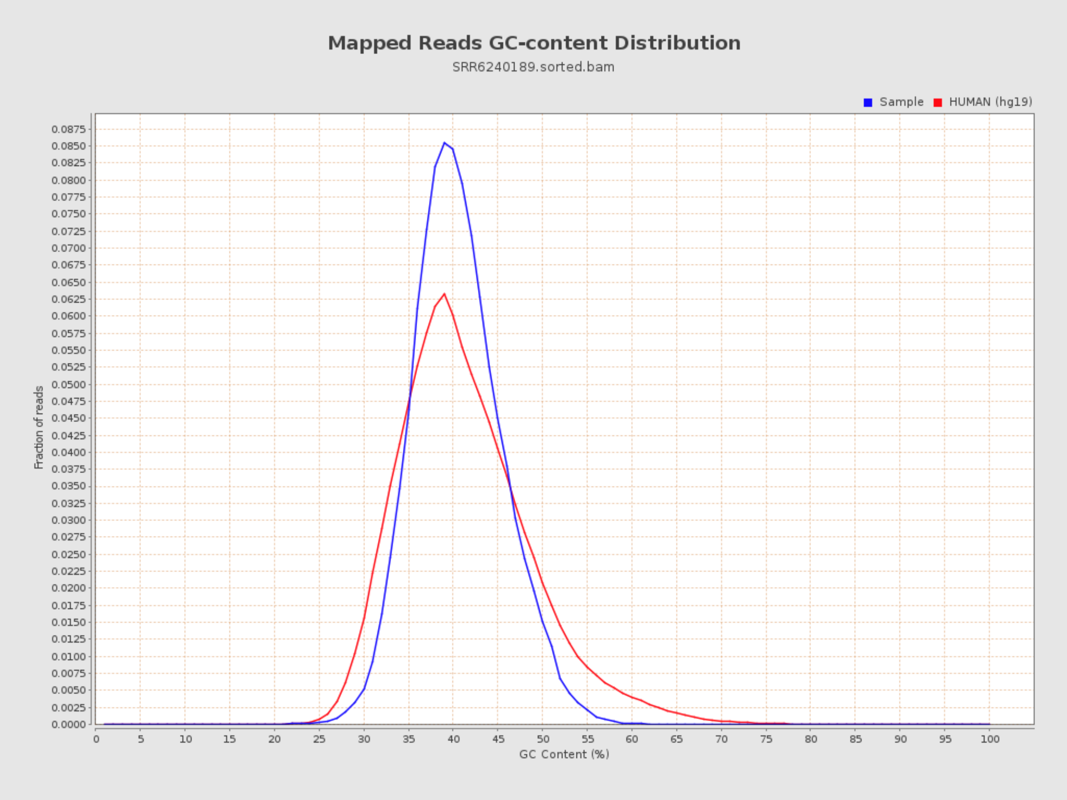
7. Results : Duplication Rate Histogram



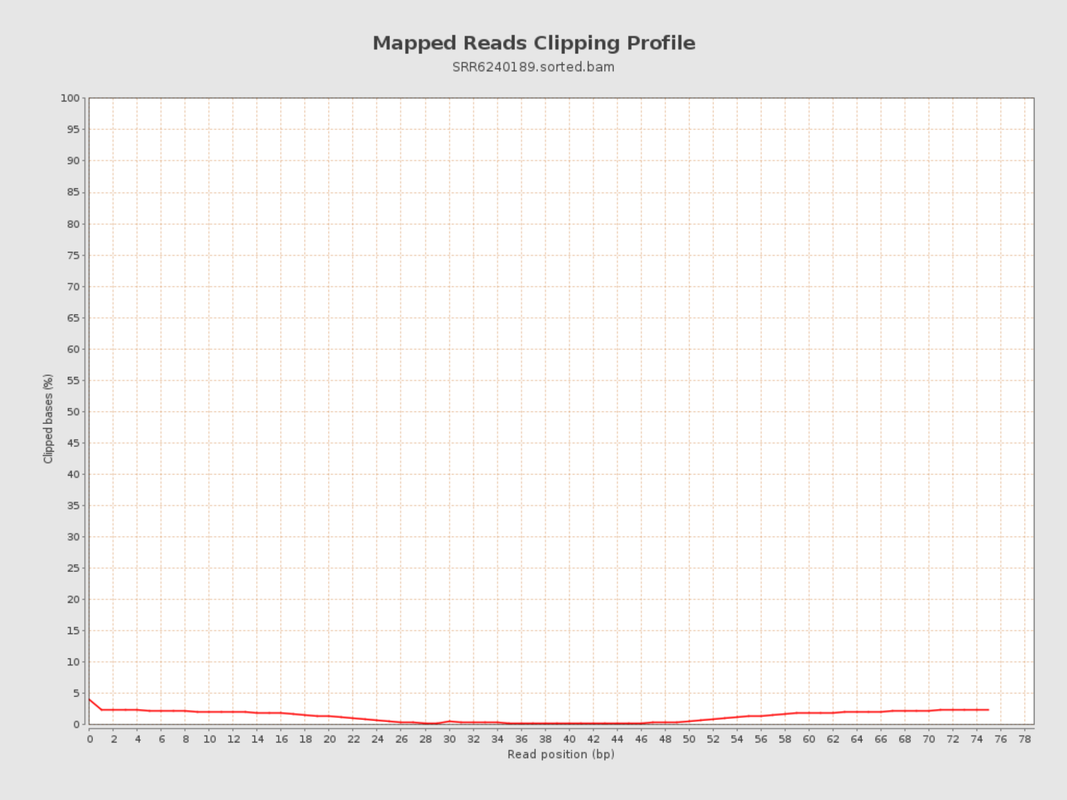
8. Results : Mapped Reads Nucleotide Content



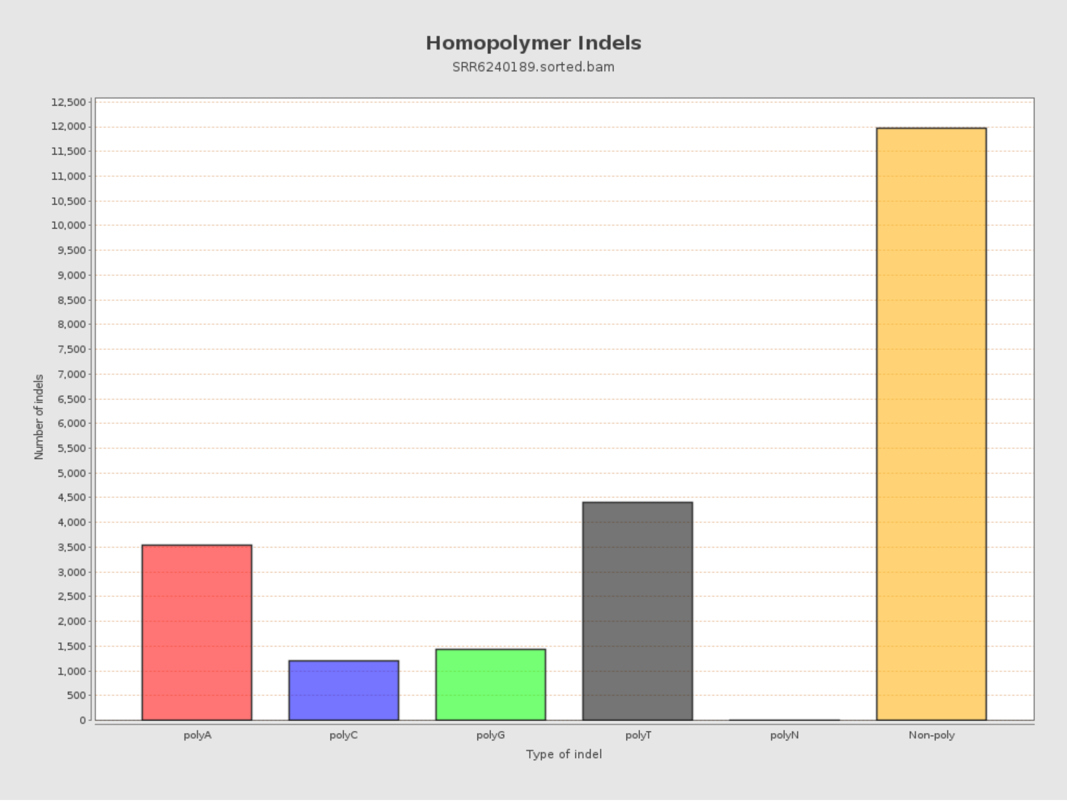
9. Results : Mapped Reads GC-content Distribution



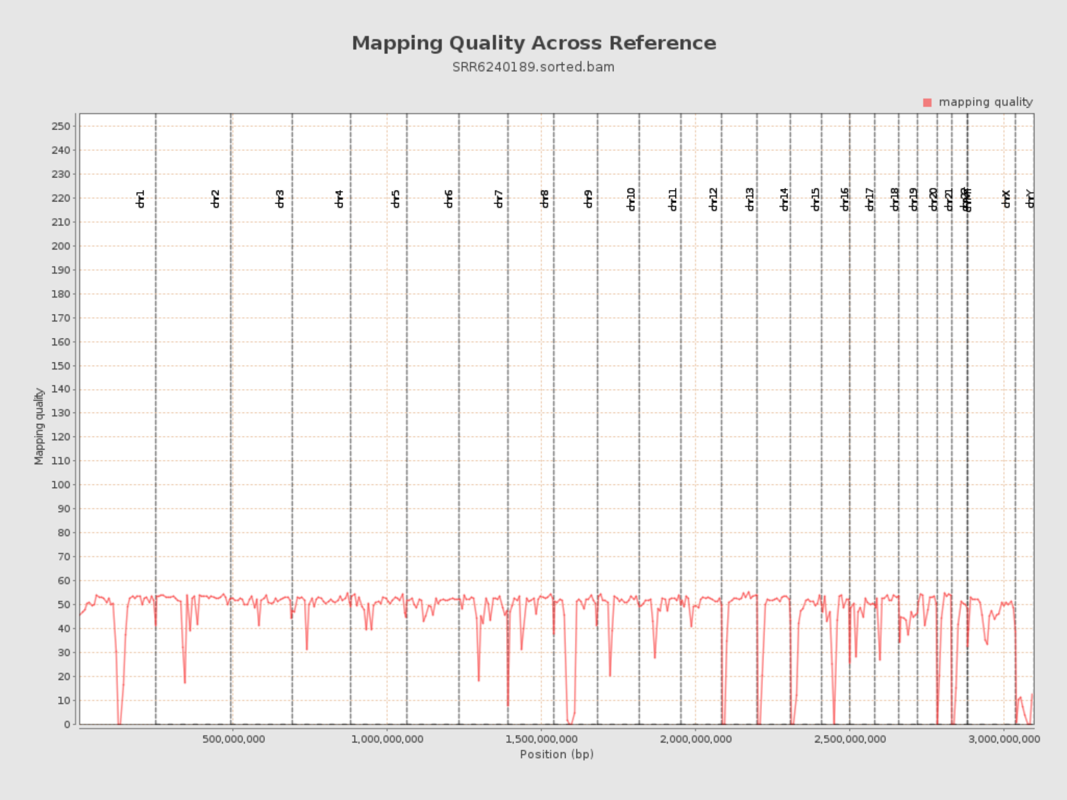
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram