Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:23:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240012.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_SRR6240012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:23:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	886,074
Mapped reads	707,899 / 79.89%
Unmapped reads	178,175 / 20.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,900 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	26,704 / 3.01%
Duplication rate	3.11%
Clipped reads	477,173 / 53.85%

2.2. ACGT Content

Number/percentage of A's	11,795,297 / 27.39%
Number/percentage of C's	7,249,122 / 16.83%
Number/percentage of T's	13,856,128 / 32.18%
Number/percentage of G's	10,133,021 / 23.53%
Number/percentage of N's	27,212 / 0.06%
GC Percentage	40.37%

2.3. Coverage

Mean	0.0139

Standard Deviation	0.1588

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

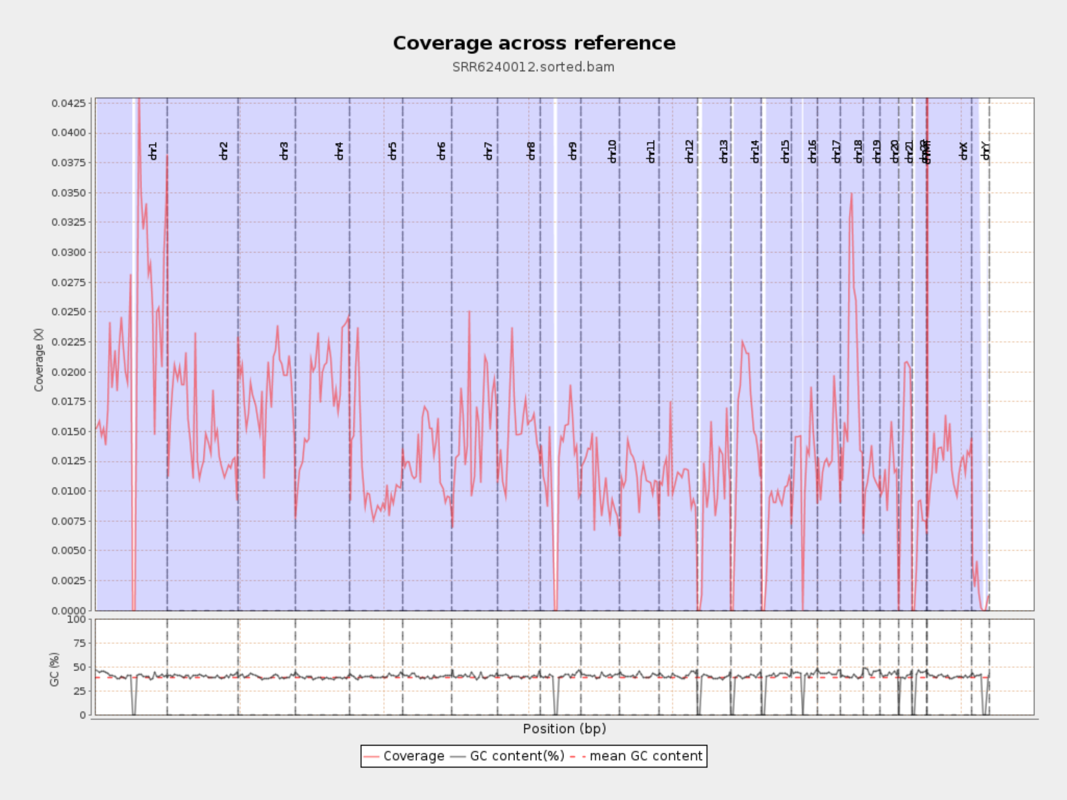
General error rate	0.99%
Mismatches	421,983
Insertions	2,953
Mapped reads with at least one insertion	0.41%
Deletions	13,702
Mapped reads with at least one deletion	1.92%
Homopolymer indels	49.31%

2.6. Chromosome stats

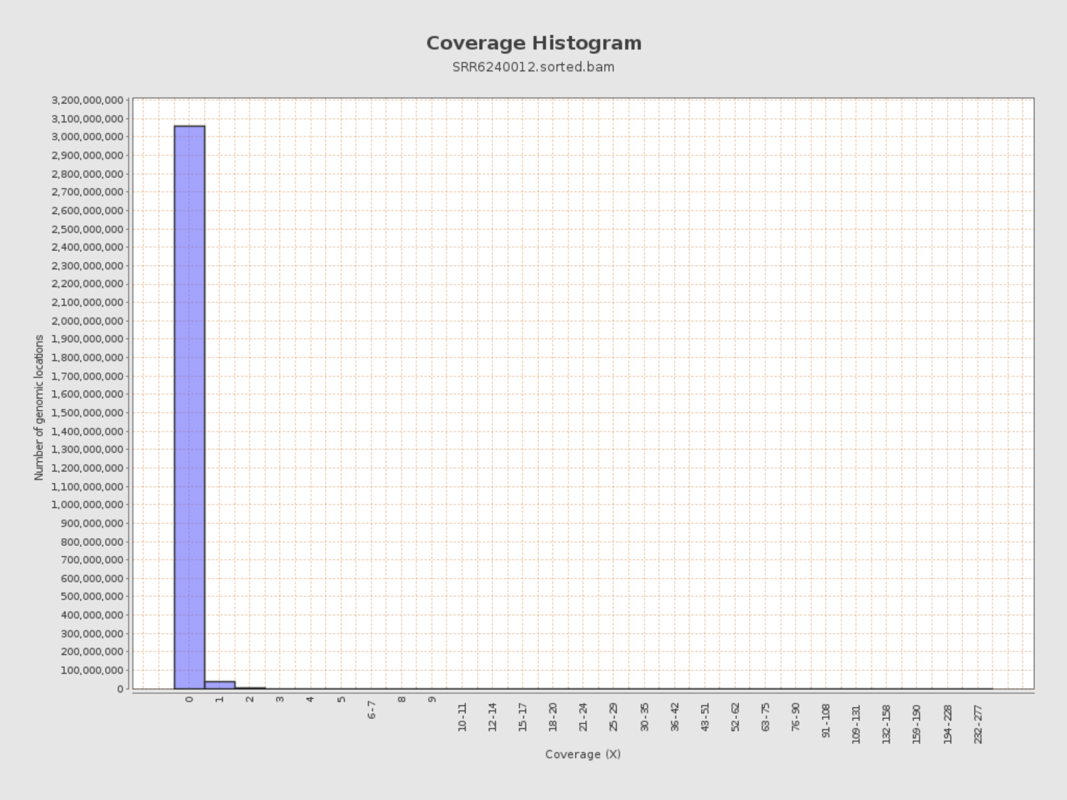
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5550906	0.0223	0.2349
chr2	243199373	3629071	0.0149	0.1727
chr3	198022430	3680765	0.0186	0.1488
chr4	191154276	3517068	0.0184	0.1491
chr5	180915260	2027409	0.0112	0.1158
chr6	171115067	2180075	0.0127	0.1326
chr7	159138663	2467165	0.0155	0.2639

chr8	146364022	2229287	0.0152	0.2054
chr9	141213431	1656925	0.0117	0.137
chr10	135534747	1425309	0.0105	0.121
chr11	135006516	1506585	0.0112	0.1283
chr12	133851895	1476223	0.011	0.1155
chr13	115169878	1122331	0.0097	0.1064
chr14	107349540	1585612	0.0148	0.1348
chr15	102531392	808475	0.0079	0.1042
chr16	90354753	1090493	0.0121	0.1217
chr17	81195210	1062790	0.0131	0.1271
chr18	78077248	1618638	0.0207	0.2151
chr19	59128983	652939	0.011	0.1622
chr20	63025520	705490	0.0112	0.1182
chr21	48129895	741560	0.0154	0.1359
chr22	51304566	298809	0.0058	0.083
chrMT	16571	24950	1.5056	1.9525
chrX	155270560	1936618	0.0125	0.1284
chrY	59373566	88566	0.0015	0.0438

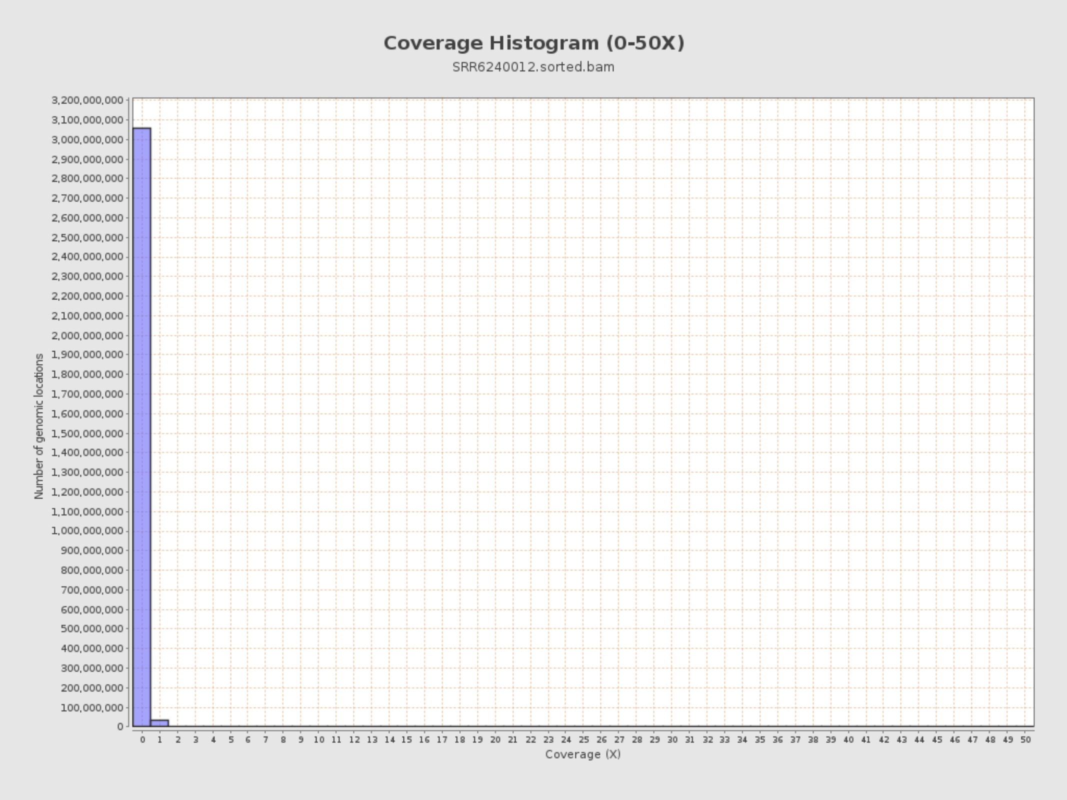
3. Results : Coverage across reference



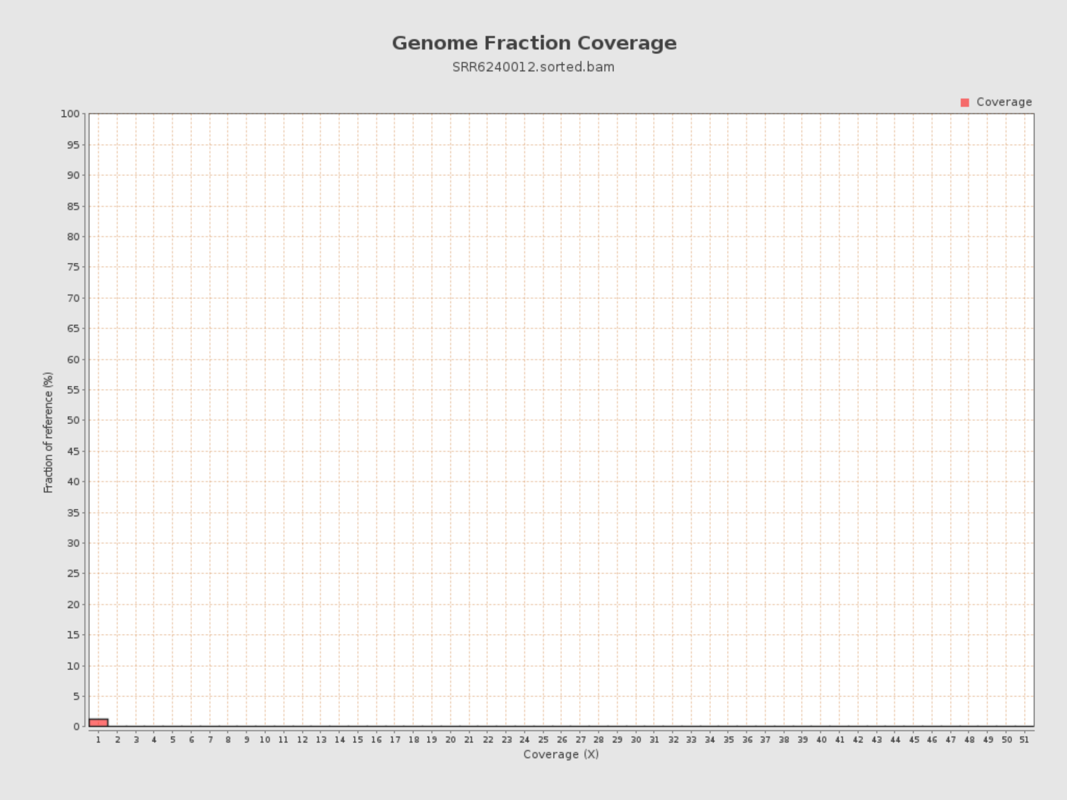
4. Results : Coverage Histogram



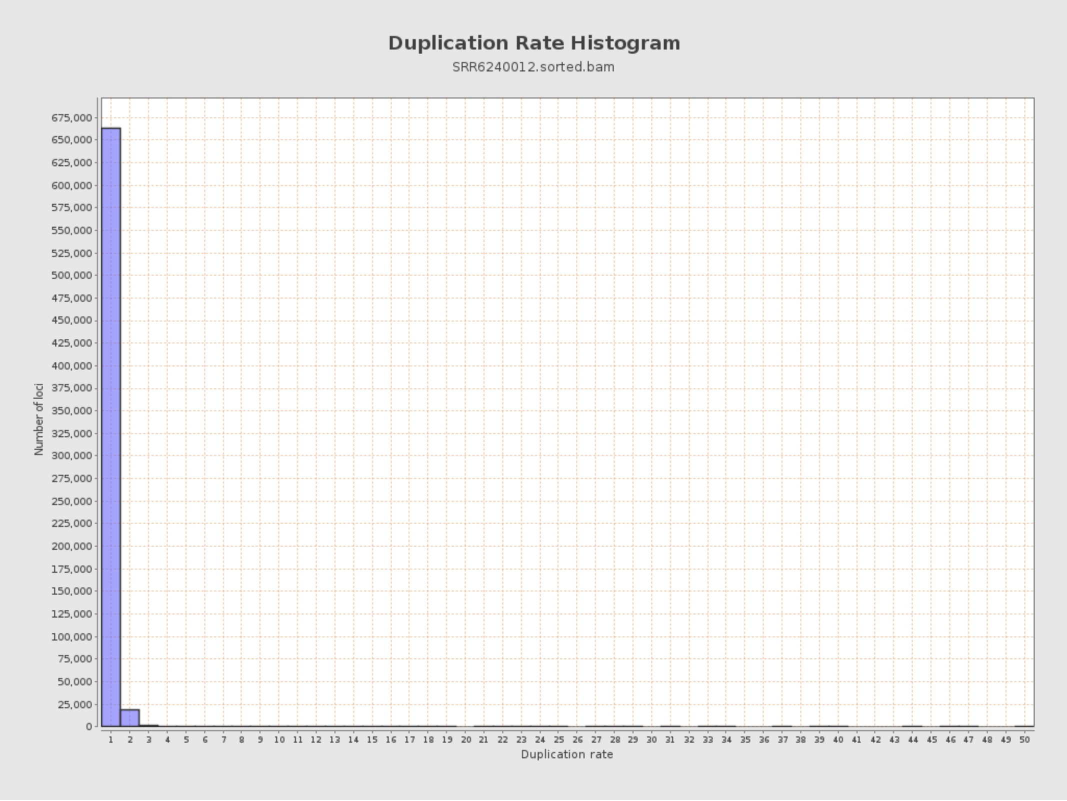
5. Results : Coverage Histogram (0-50X)



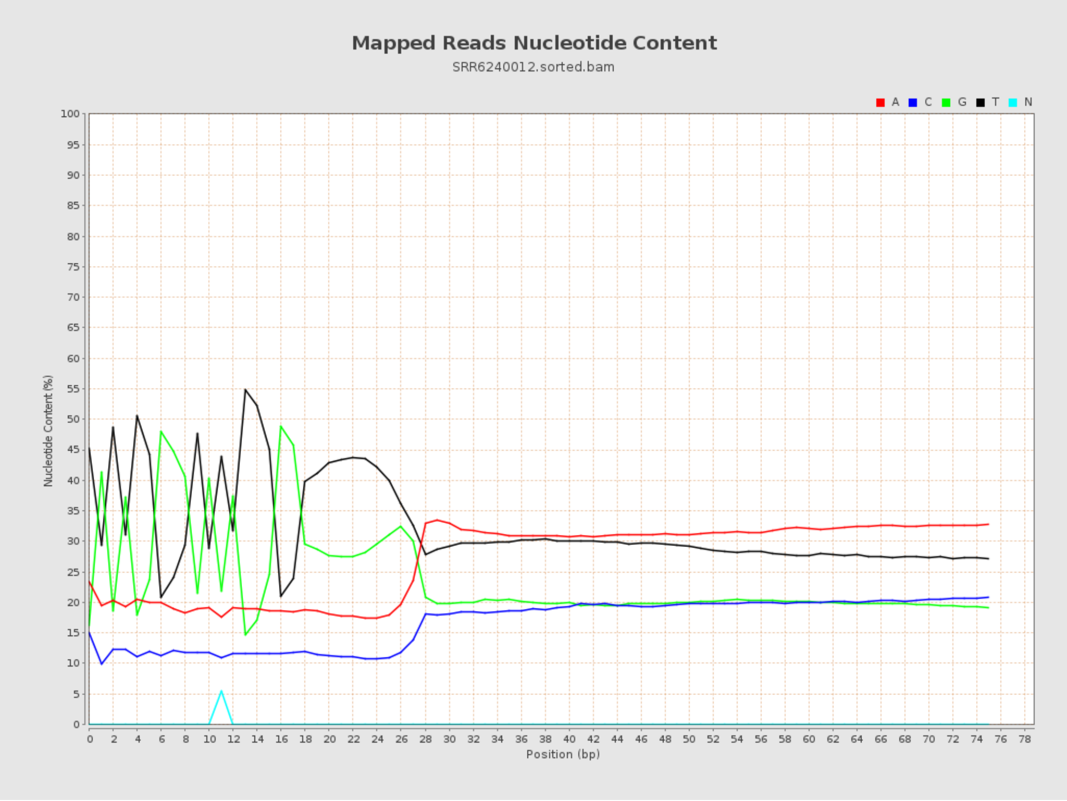
6. Results : Genome Fraction Coverage



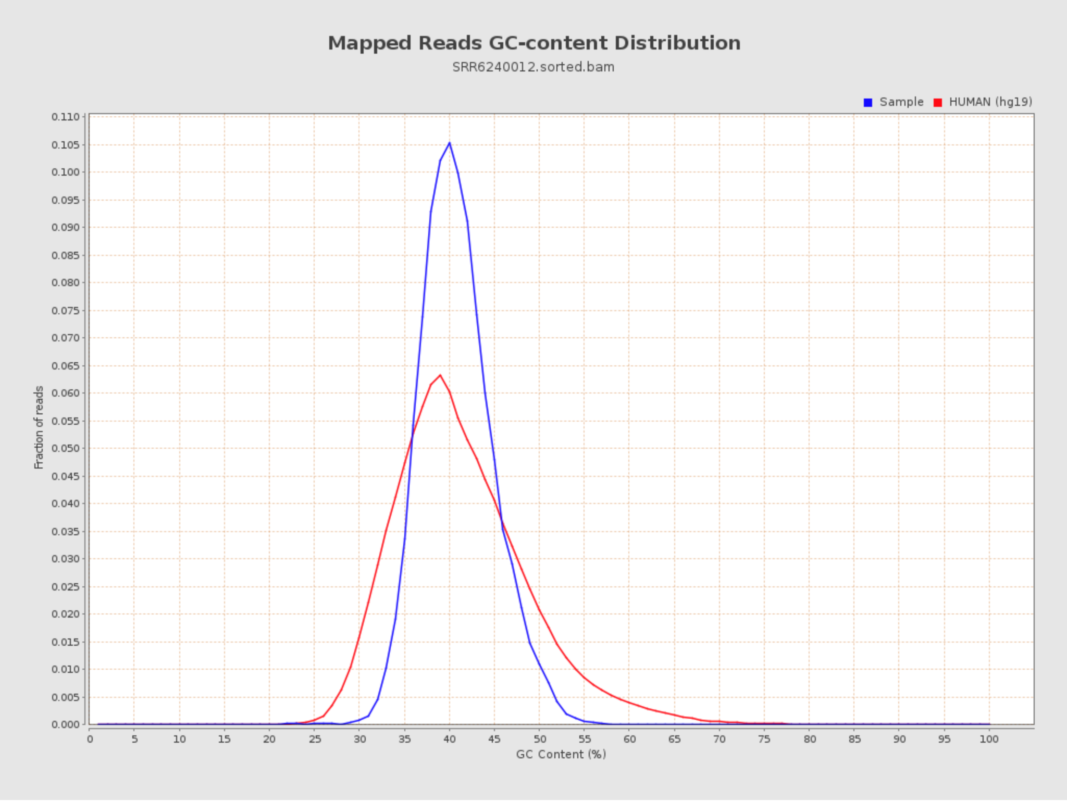
7. Results : Duplication Rate Histogram



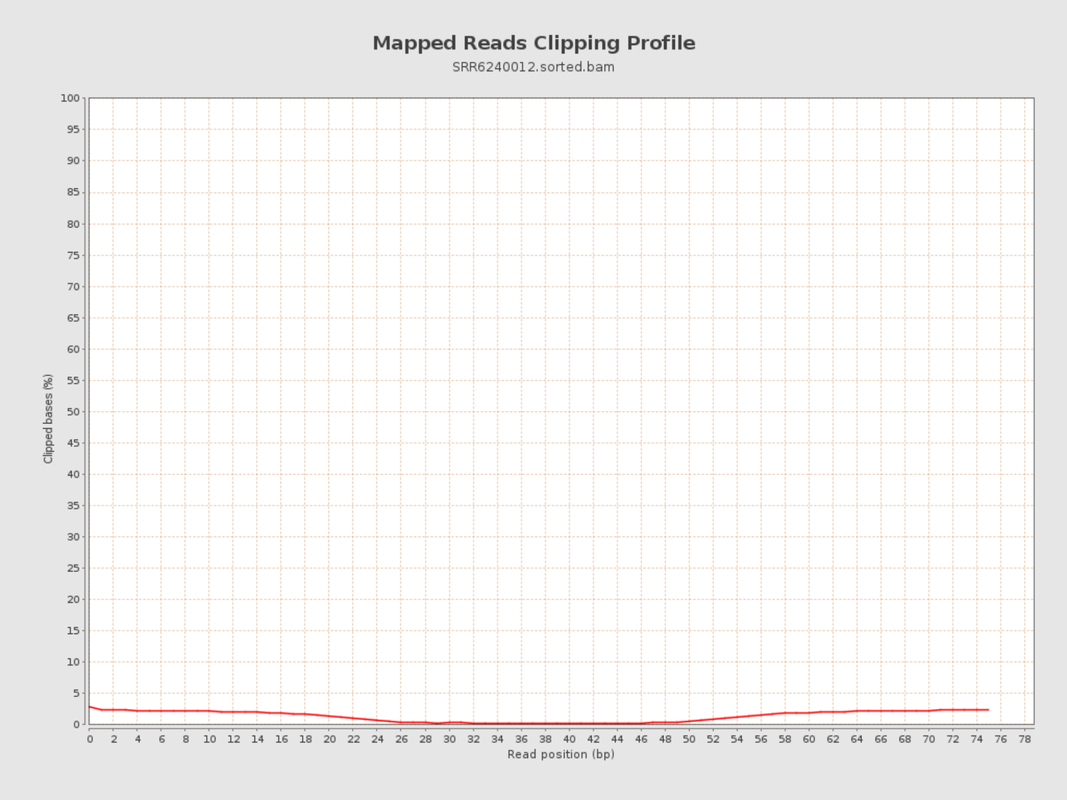
8. Results : Mapped Reads Nucleotide Content



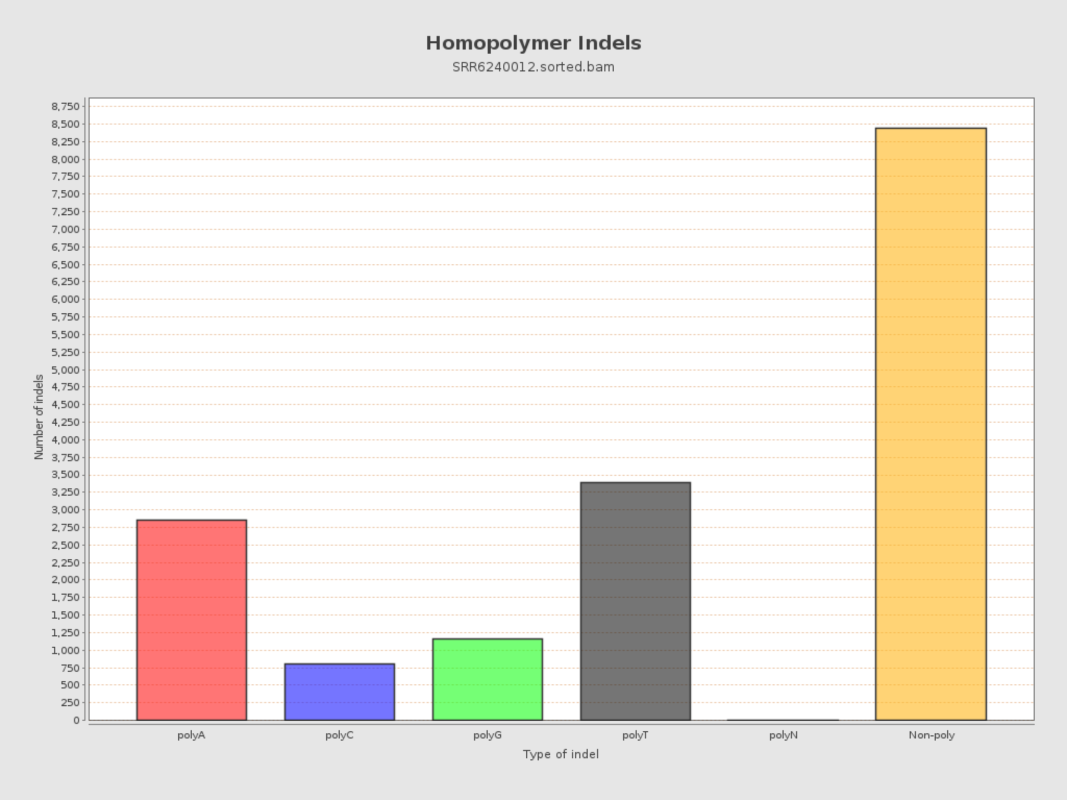
9. Results : Mapped Reads GC-content Distribution



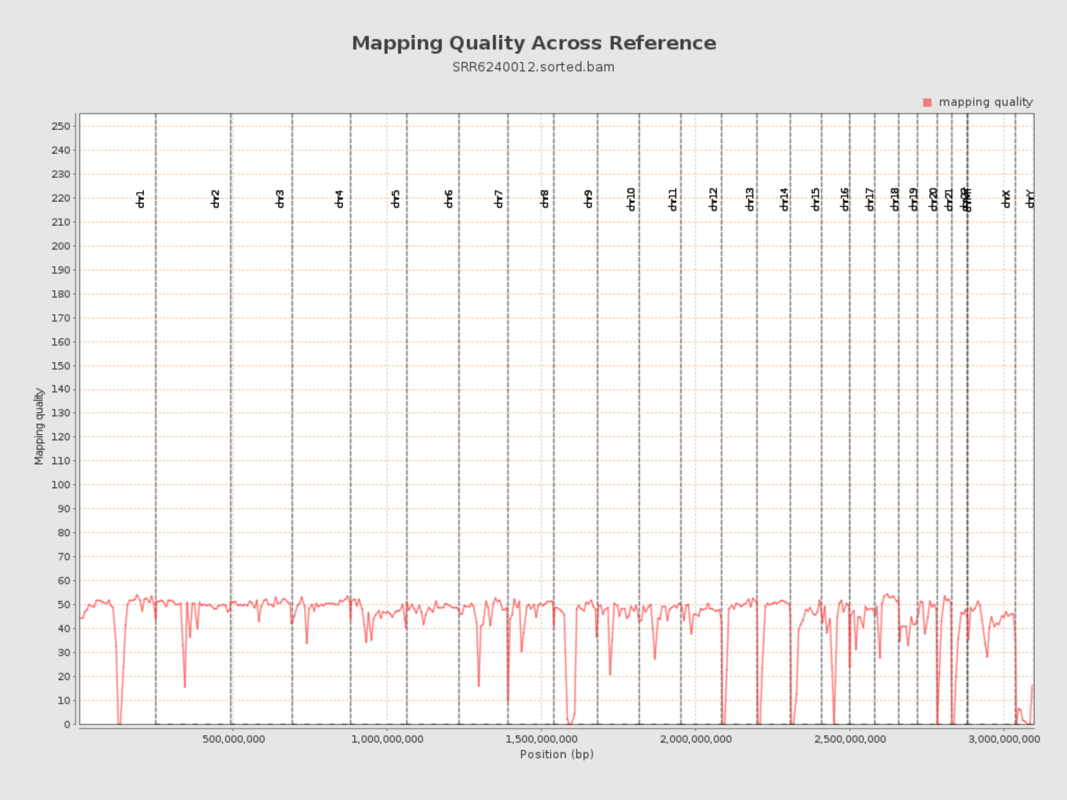
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram