Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:59:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240218.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_SRR6240218 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240218.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:59:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240218.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,315,257
Mapped reads	2,918,853 / 88.04%
Unmapped reads	396,404 / 11.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,821 / 0.75%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	226,589 / 6.83%
Duplication rate	5.93%
Clipped reads	1,184,519 / 35.73%

2.2. ACGT Content

Number/percentage of A's	56,135,615 / 28.41%
Number/percentage of C's	36,422,666 / 18.43%
Number/percentage of T's	62,918,462 / 31.84%
Number/percentage of G's	42,115,934 / 21.31%
Number/percentage of N's	19,284 / 0.01%
GC Percentage	39.74%

2.3. Coverage

Mean	0.0639

Standard Deviation	0.6392

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Mismatches and indels

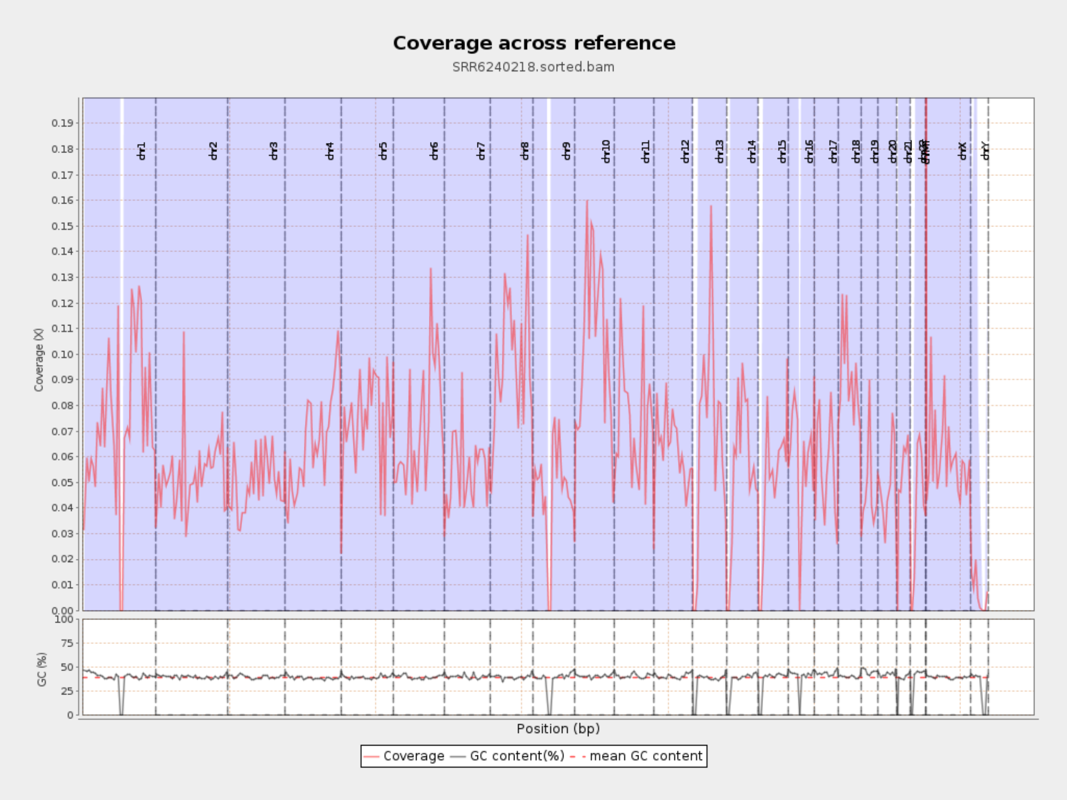
General error rate	0.77%
Mismatches	1,492,768
Insertions	13,920
Mapped reads with at least one insertion	0.47%
Deletions	43,311
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.22%

2.6. Chromosome stats

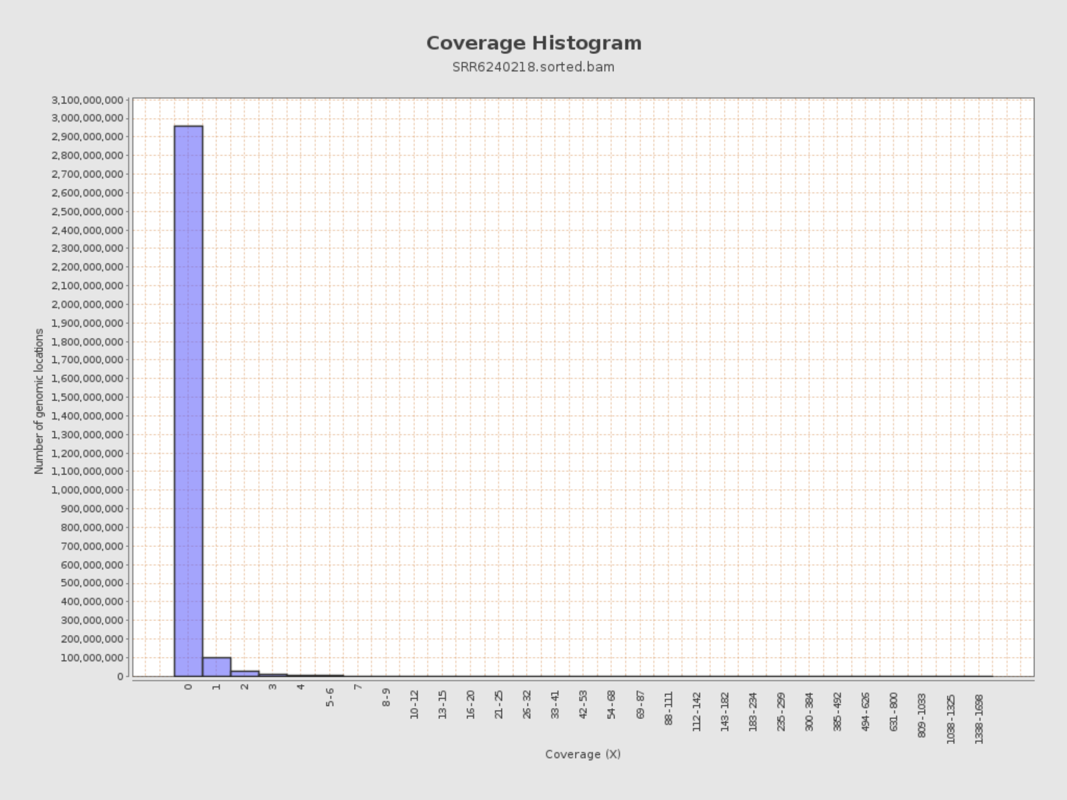
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18143298	0.0728	1.2108
chr2	243199373	12913350	0.0531	0.6391
chr3	198022430	9867742	0.0498	0.3059
chr4	191154276	12584564	0.0658	0.3634
chr5	180915260	13421707	0.0742	0.373
chr6	171115067	12375097	0.0723	0.4441
chr7	159138663	8627796	0.0542	0.6572

chr8	146364022	14312342	0.0978	1.1161
chr9	141213431	6583480	0.0466	0.5034
chr10	135534747	14311037	0.1056	0.7892
chr11	135006516	10131760	0.075	0.6912
chr12	133851895	8498120	0.0635	0.3543
chr13	115169878	7986641	0.0693	0.3592
chr14	107349540	5969501	0.0556	0.3504
chr15	102531392	4985754	0.0486	0.3127
chr16	90354753	5159487	0.0571	0.356
chr17	81195210	4584752	0.0565	0.4007
chr18	78077248	7180635	0.092	1.1286
chr19	59128983	2825976	0.0478	0.8011
chr20	63025520	3113473	0.0494	0.3154
chr21	48129895	2425146	0.0504	0.322
chr22	51304566	2000255	0.039	0.2635
chrMT	16571	8057	0.4862	0.9601
chrX	155270560	9279053	0.0598	0.4232
chrY	59373566	398329	0.0067	0.1411

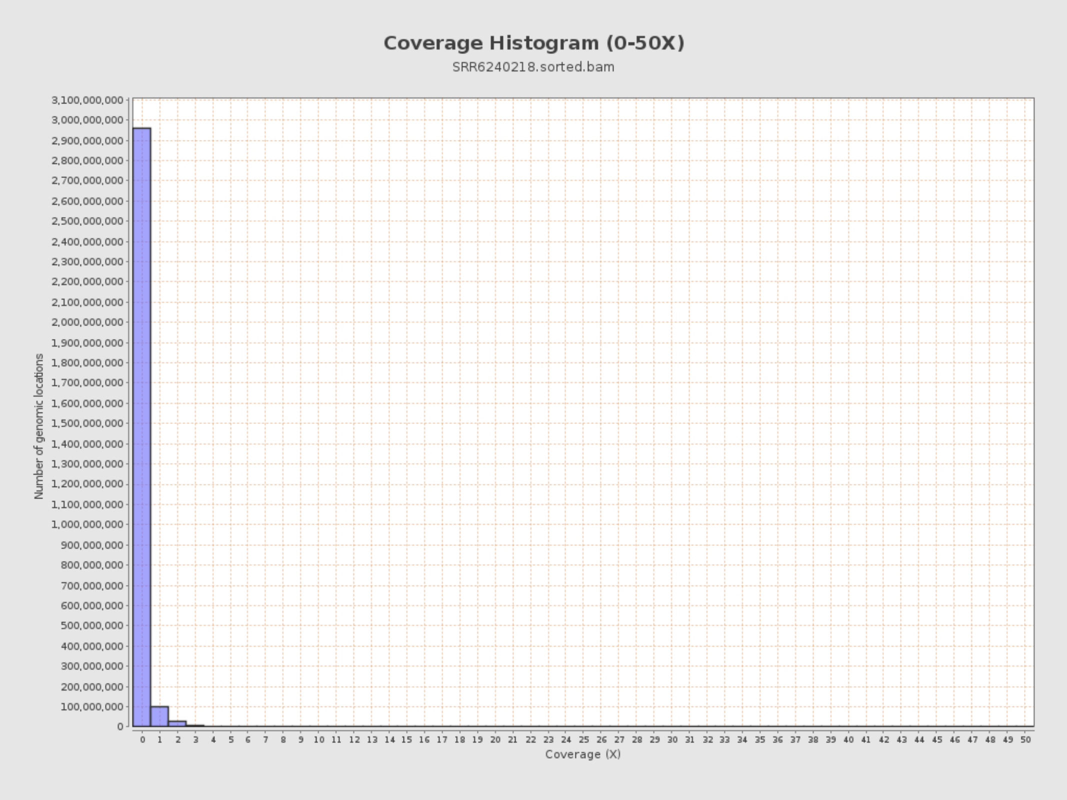
3. Results : Coverage across reference



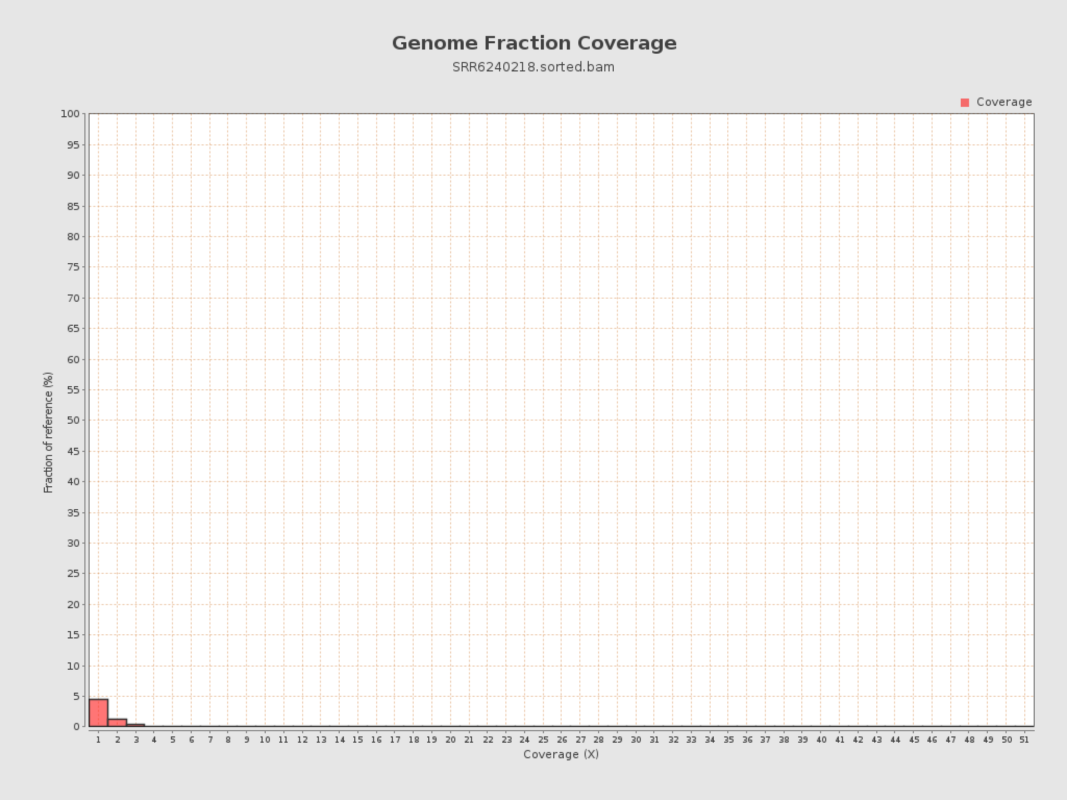
4. Results : Coverage Histogram



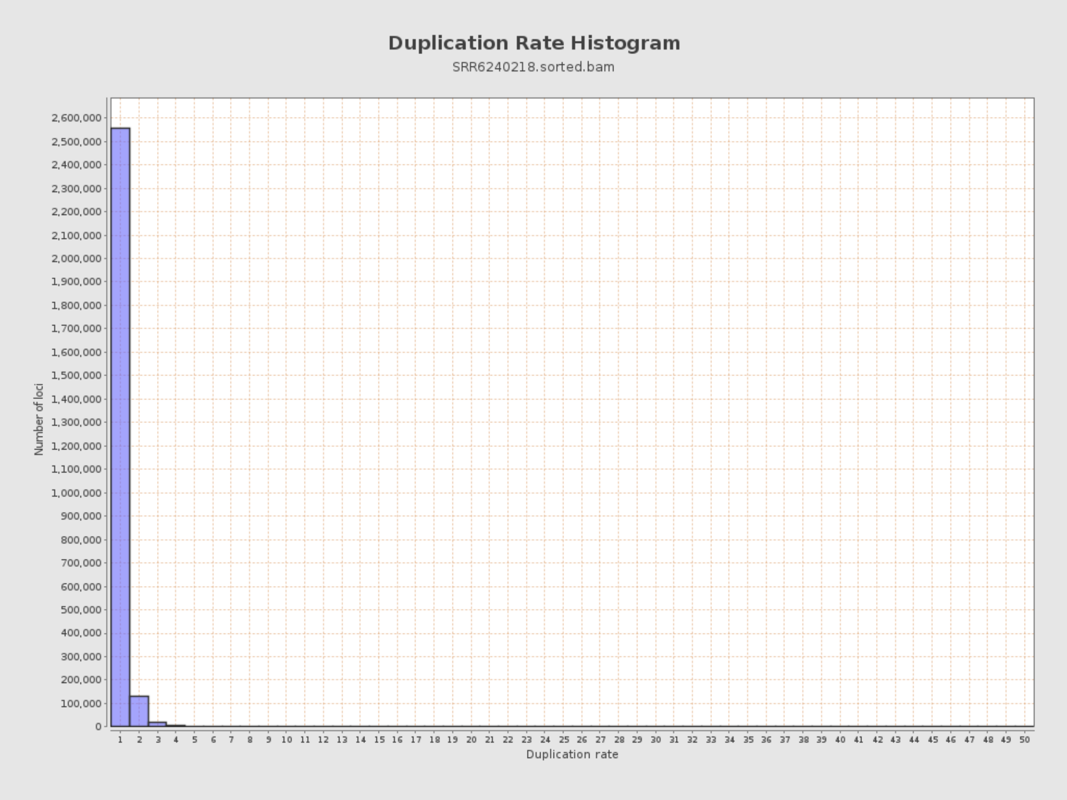
5. Results : Coverage Histogram (0-50X)



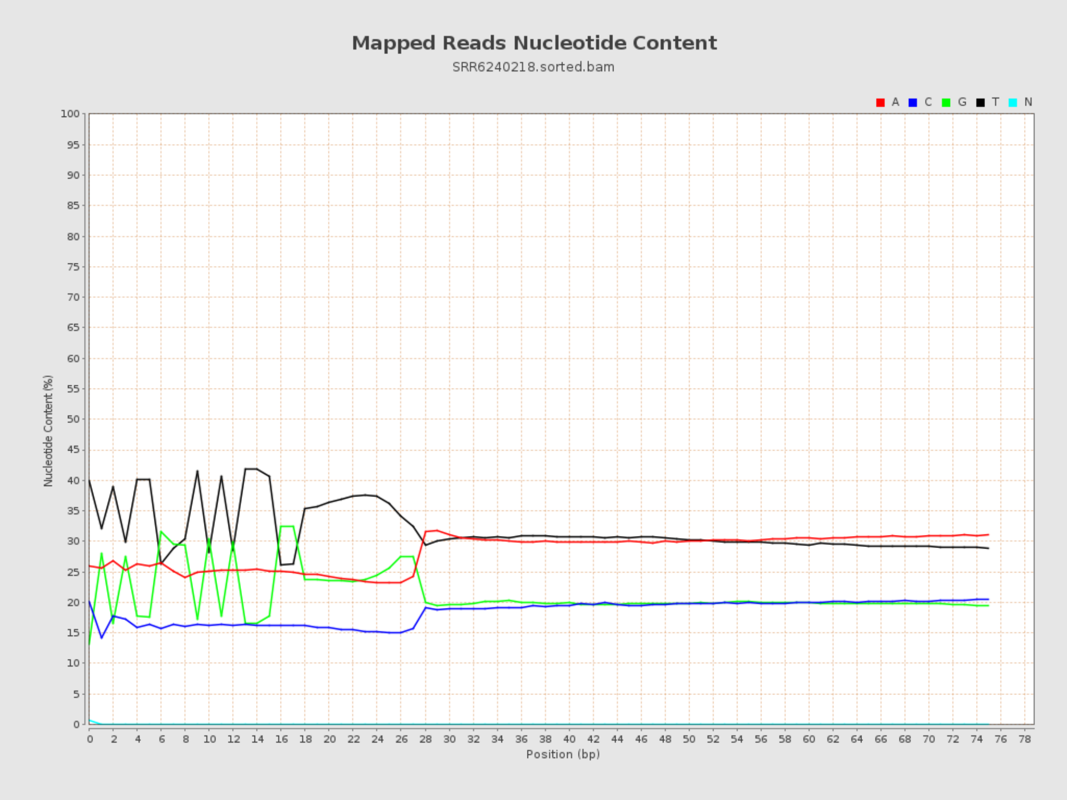
6. Results : Genome Fraction Coverage



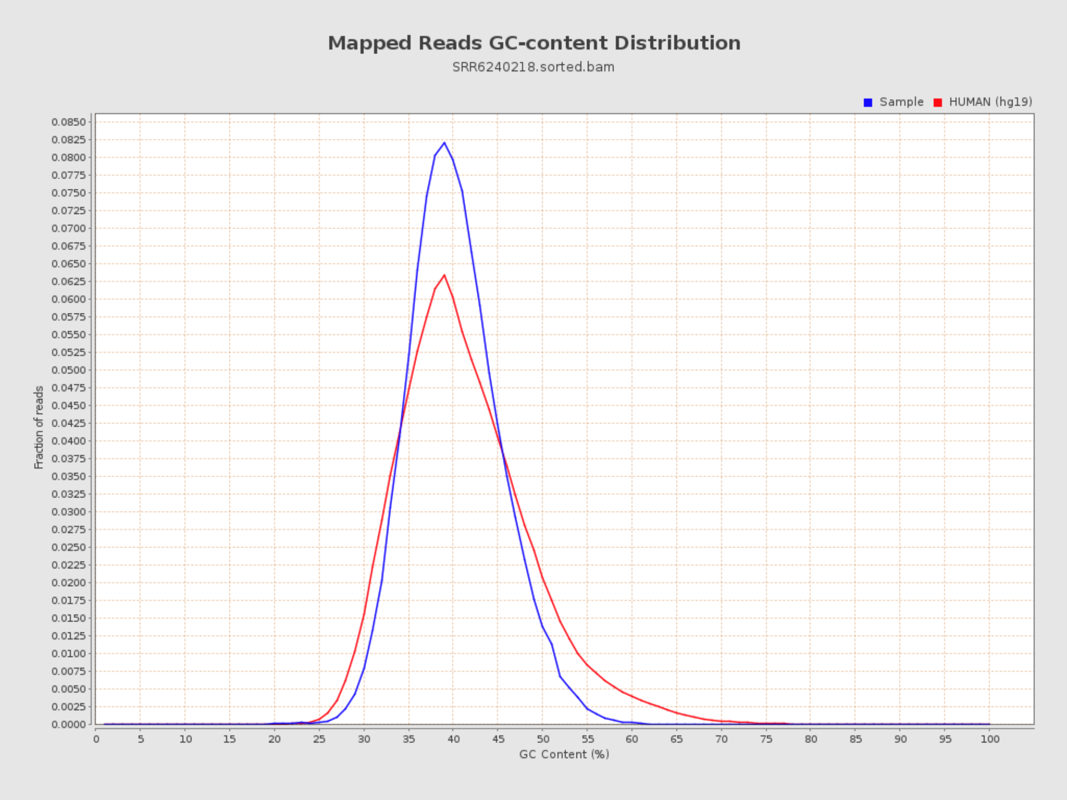
7. Results : Duplication Rate Histogram



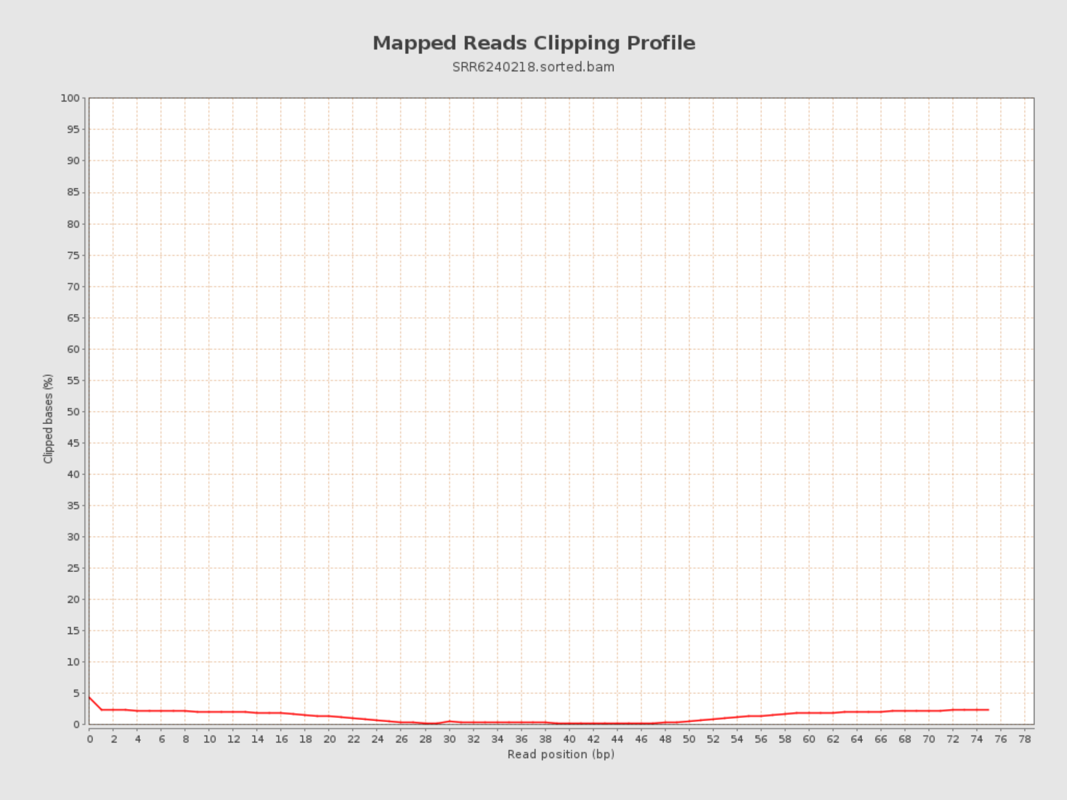
8. Results : Mapped Reads Nucleotide Content



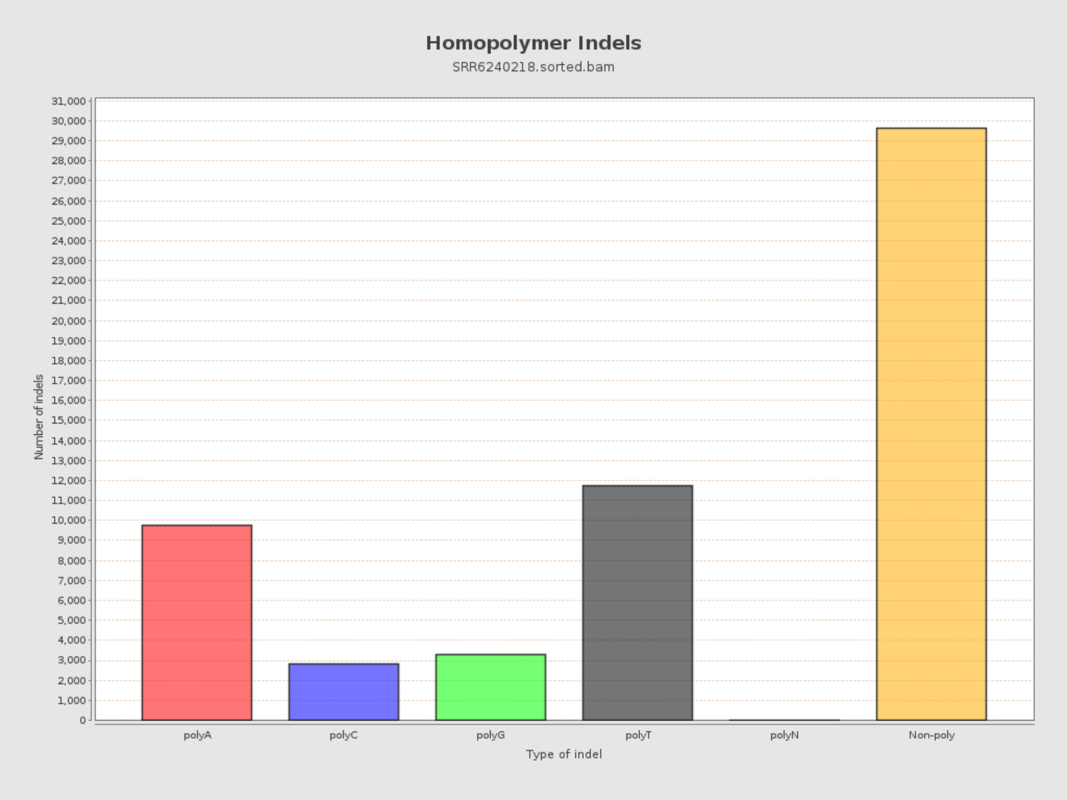
9. Results : Mapped Reads GC-content Distribution



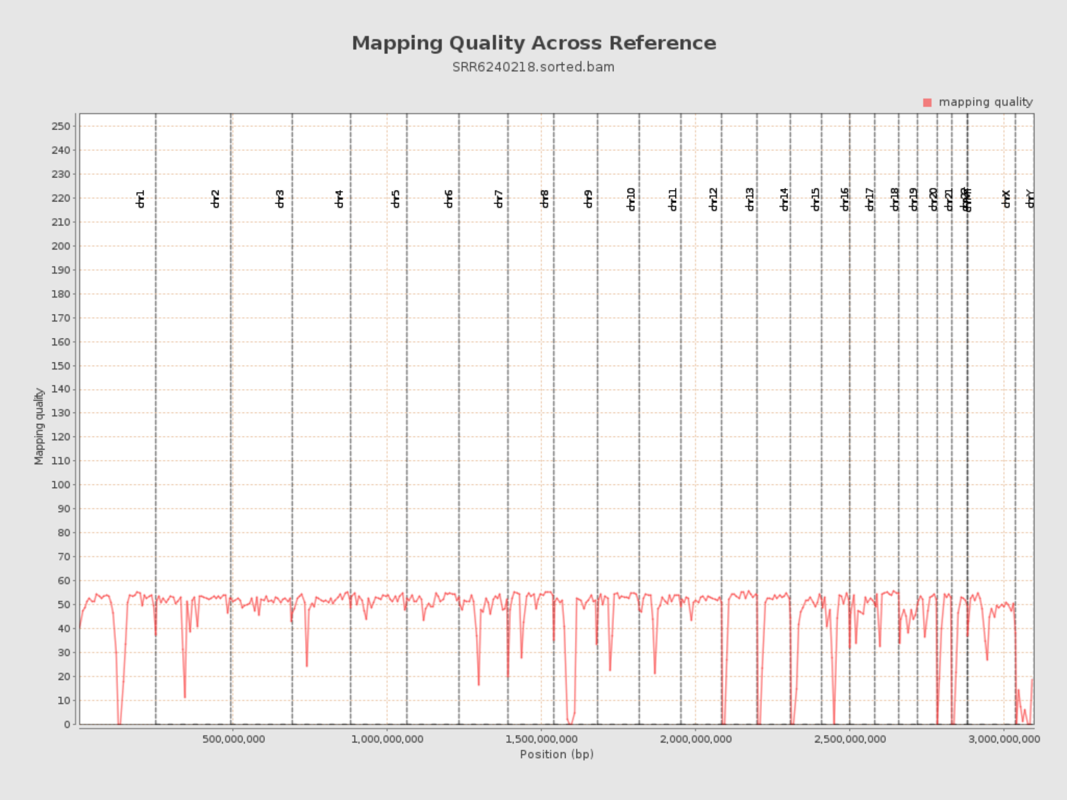
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram