Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:37:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234079.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_SRR6234079 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234079.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:37:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234079.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,655,149
Mapped reads	1,368,258 / 51.53%
Unmapped reads	1,286,891 / 48.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,727 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	122,446 / 4.61%
Duplication rate	7.27%
Clipped reads	769,491 / 28.98%

2.2. ACGT Content

Number/percentage of A's	24,086,826 / 27.83%
Number/percentage of C's	14,588,506 / 16.86%
Number/percentage of T's	28,877,710 / 33.37%
Number/percentage of G's	18,961,685 / 21.91%
Number/percentage of N's	22,003 / 0.03%
GC Percentage	38.77%

2.3. Coverage

Mean	0.028

Standard Deviation	0.3326

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

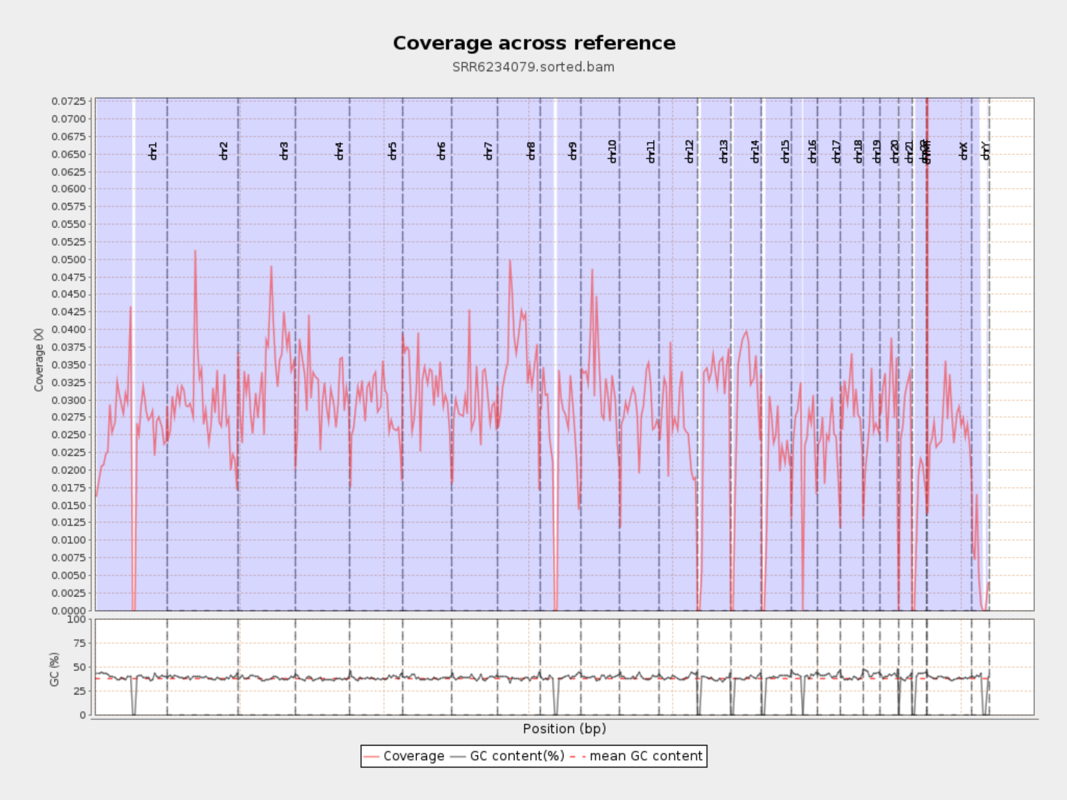
General error rate	0.98%
Mismatches	835,960
Insertions	7,509
Mapped reads with at least one insertion	0.54%
Deletions	27,921
Mapped reads with at least one deletion	2.01%
Homopolymer indels	45.87%

2.6. Chromosome stats

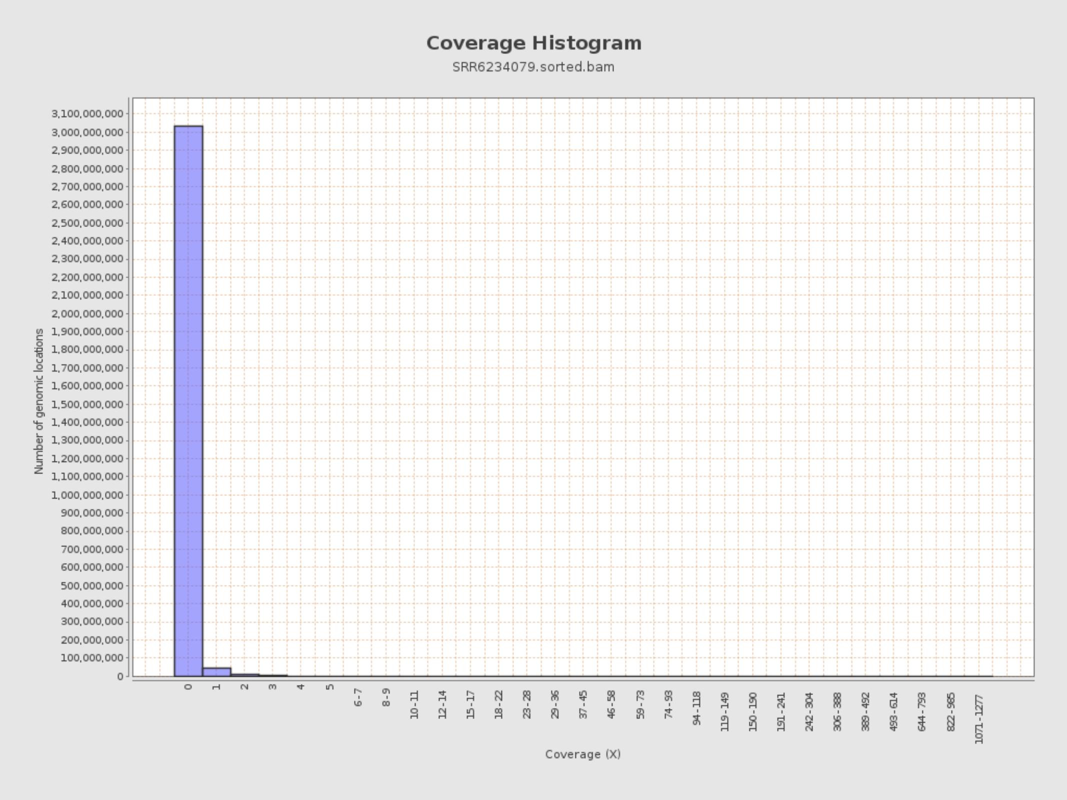
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6254141	0.0251	0.4522
chr2	243199373	7069841	0.0291	0.3354
chr3	198022430	6711028	0.0339	0.25
chr4	191154276	5925862	0.031	0.2531
chr5	180915260	5245613	0.029	0.2352
chr6	171115067	5452052	0.0319	0.2709
chr7	159138663	4679724	0.0294	0.3129

chr8	146364022	5257114	0.0359	0.7846
chr9	141213431	3470295	0.0246	0.2887
chr10	135534747	4436160	0.0327	0.2953
chr11	135006516	3843654	0.0285	0.2677
chr12	133851895	3539906	0.0264	0.2292
chr13	115169878	3265389	0.0284	0.2368
chr14	107349540	3125203	0.0291	0.2385
chr15	102531392	2039655	0.0199	0.194
chr16	90354753	2111159	0.0234	0.2078
chr17	81195210	1915825	0.0236	0.2168
chr18	78077248	2328471	0.0298	0.5296
chr19	59128983	1506457	0.0255	0.3208
chr20	63025520	1920206	0.0305	0.2409
chr21	48129895	1254952	0.0261	0.2216
chr22	51304566	712212	0.0139	0.1522
chrMT	16571	142811	8.6181	7.1204
chrX	155270560	4071271	0.0262	0.2347
chrY	59373566	306896	0.0052	0.1229

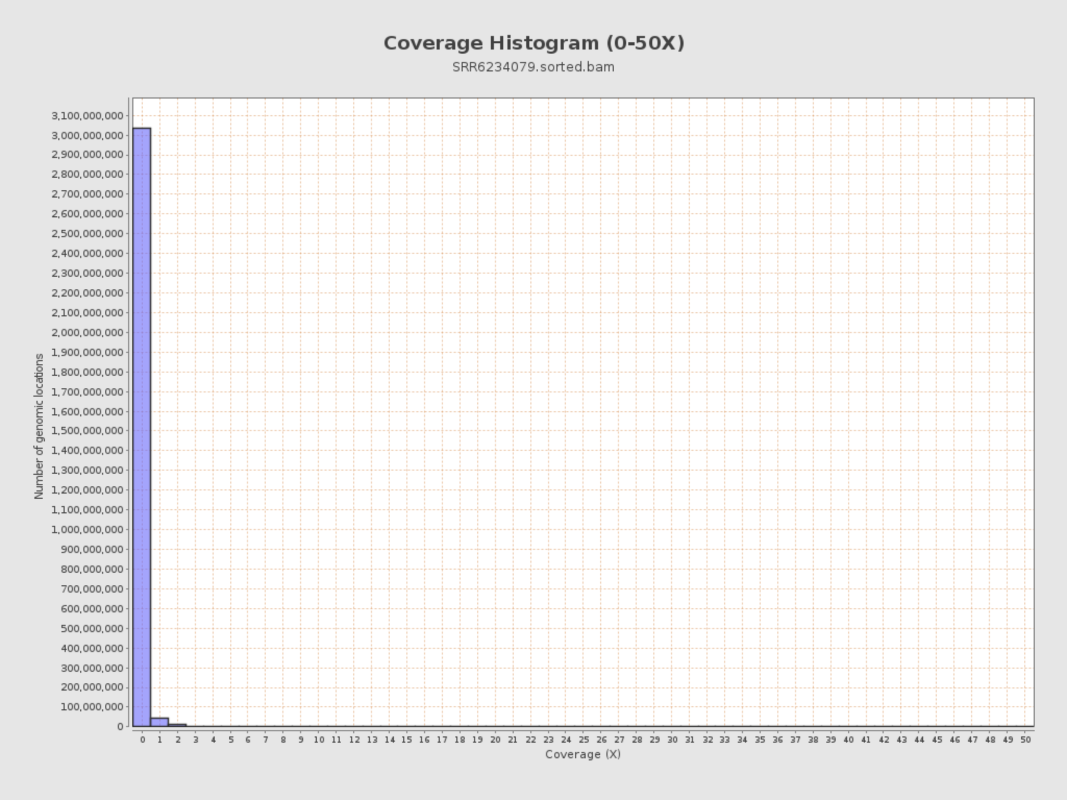
3. Results : Coverage across reference



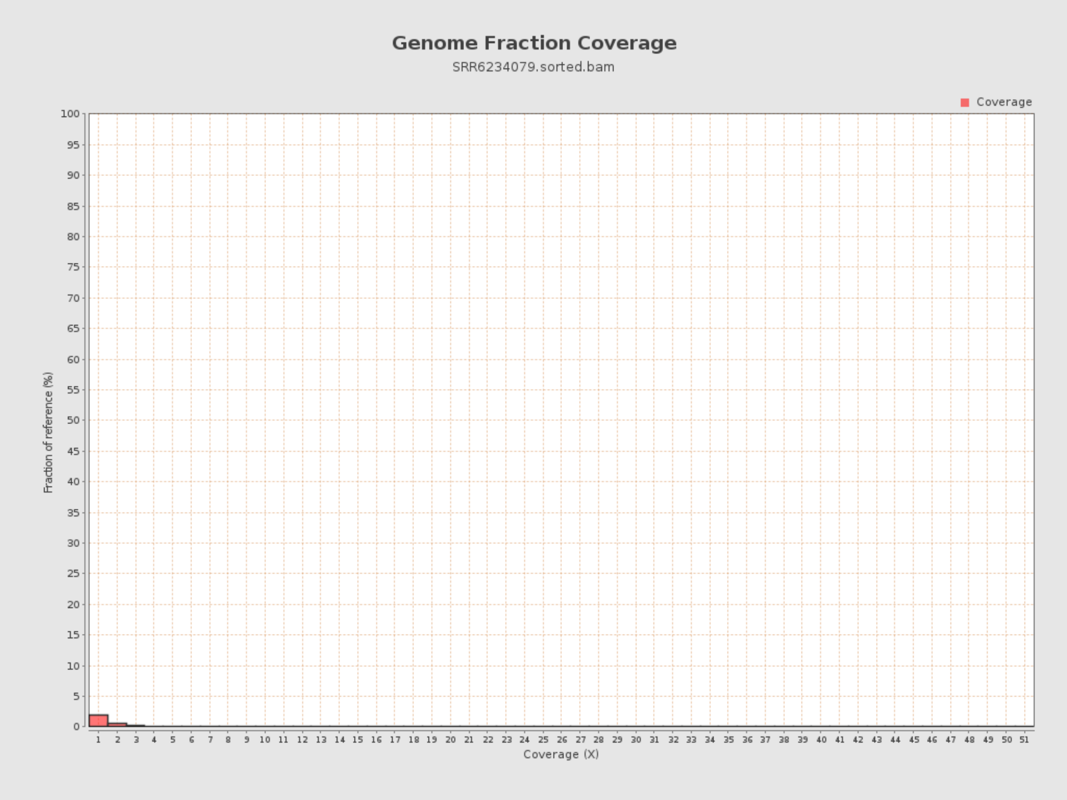
4. Results : Coverage Histogram



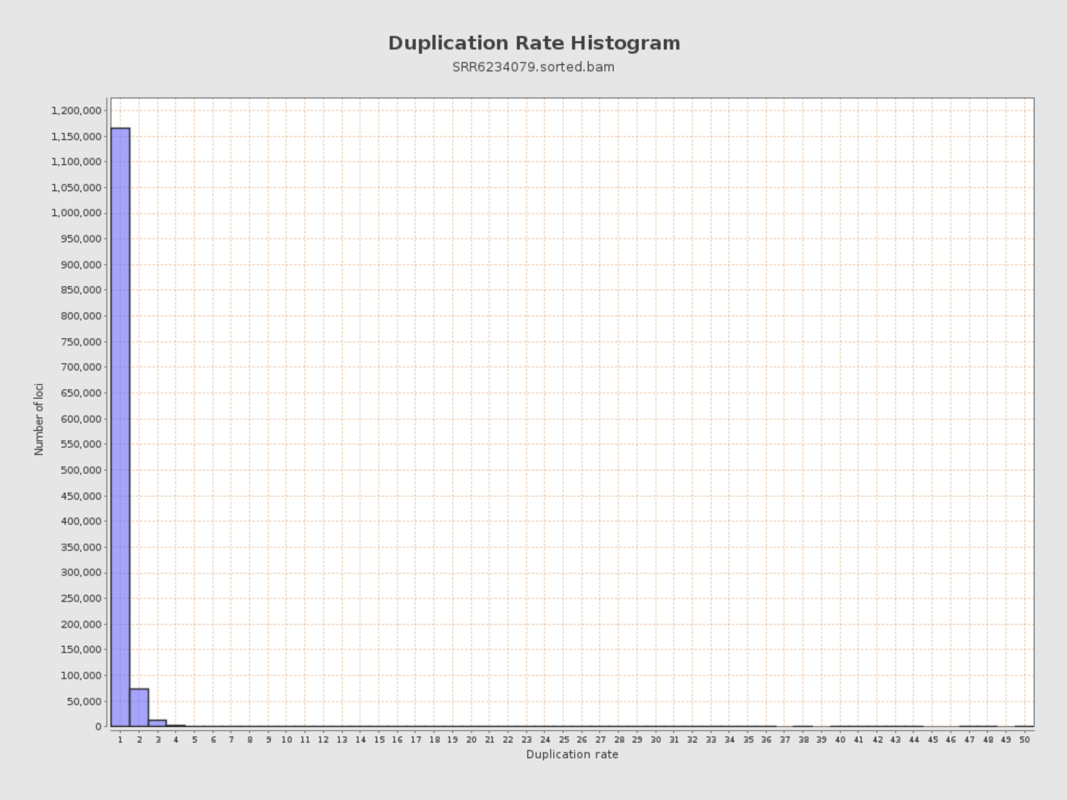
5. Results : Coverage Histogram (0-50X)



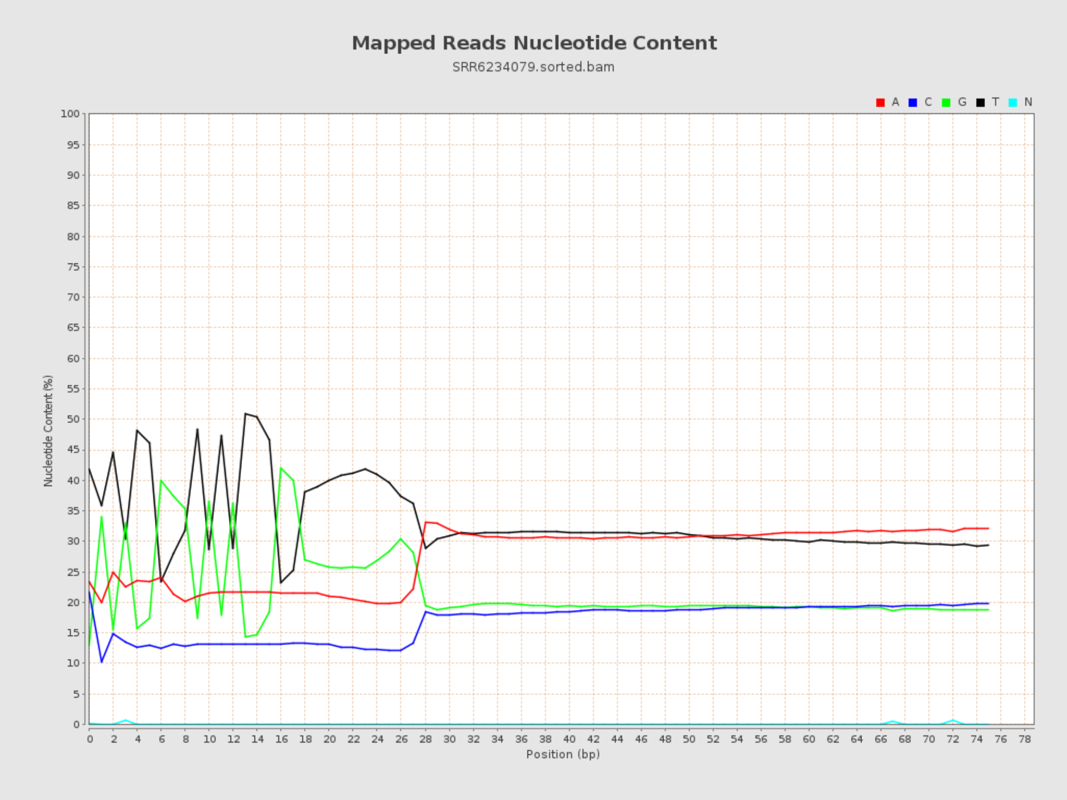
6. Results : Genome Fraction Coverage



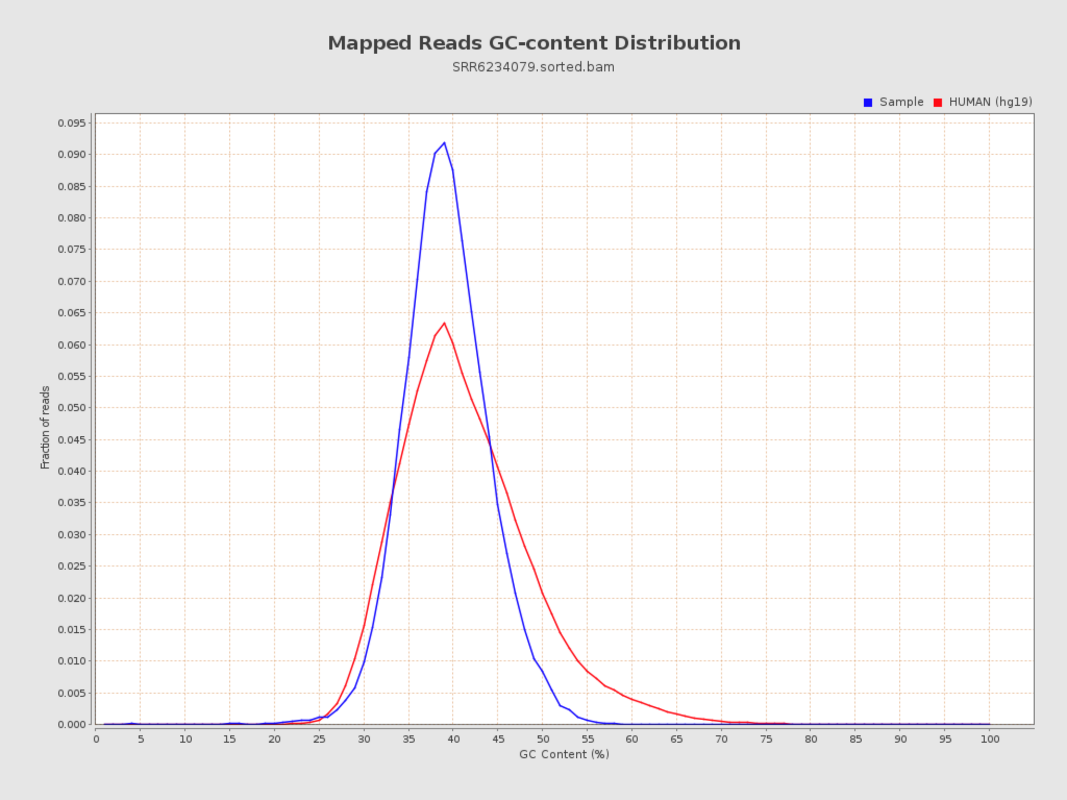
7. Results : Duplication Rate Histogram



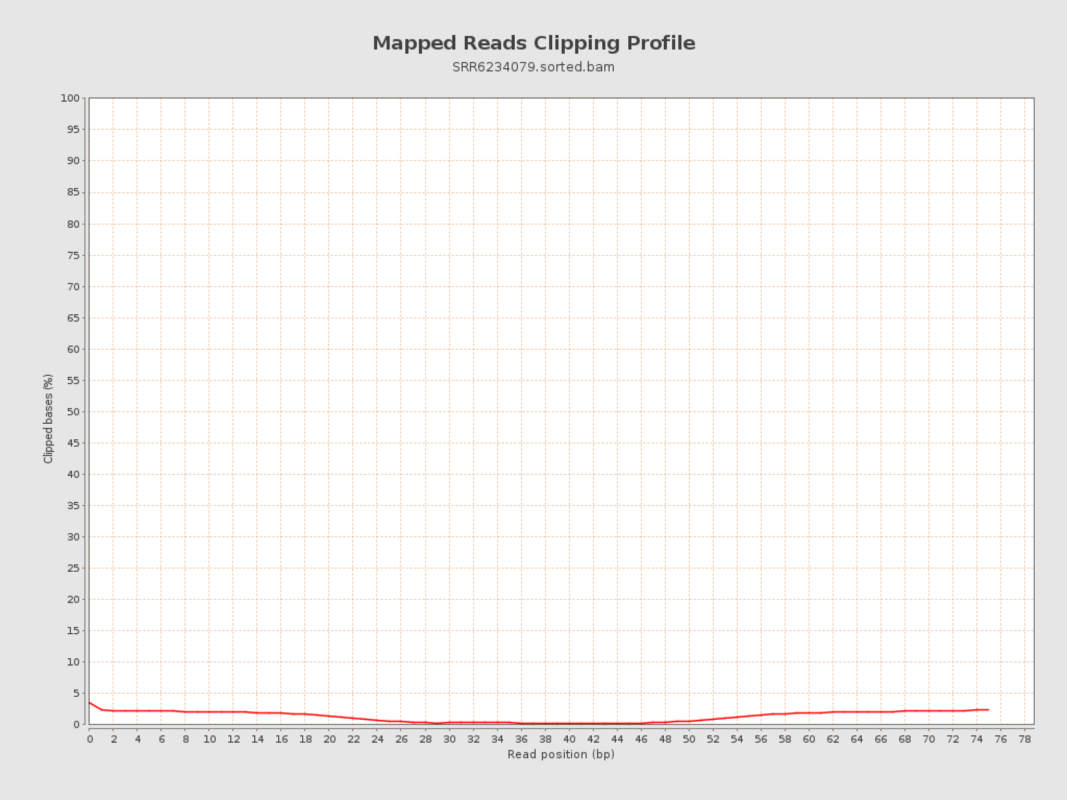
8. Results : Mapped Reads Nucleotide Content



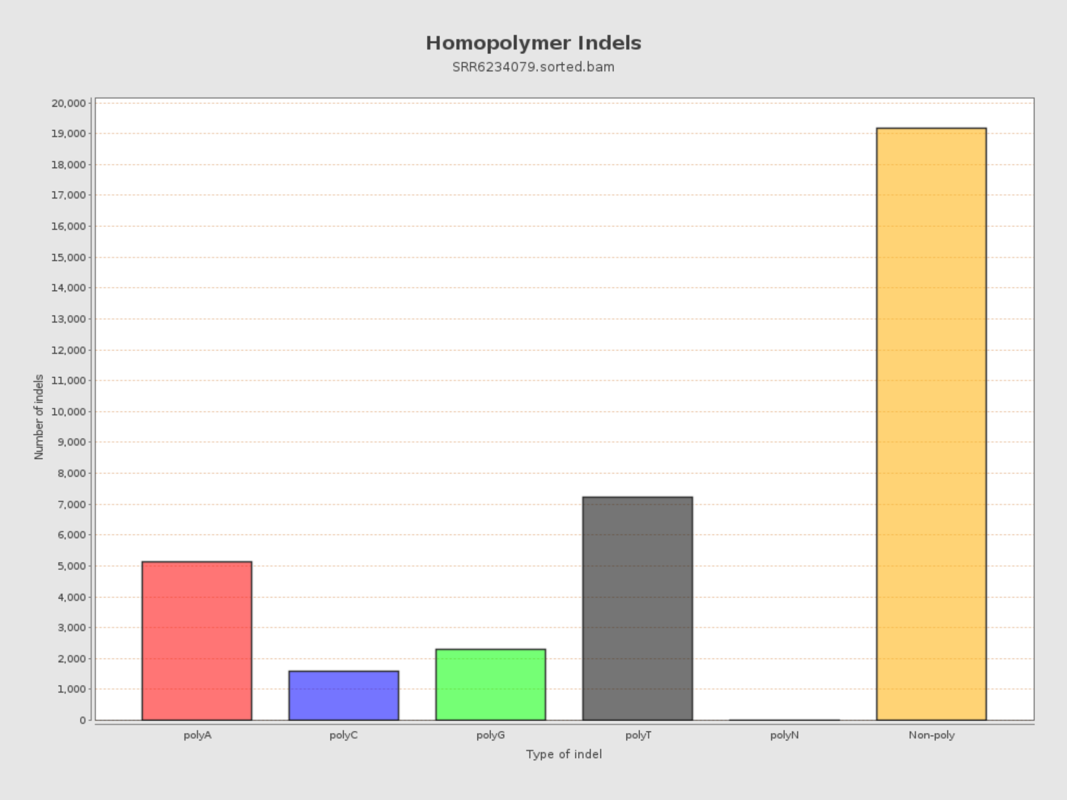
9. Results : Mapped Reads GC-content Distribution



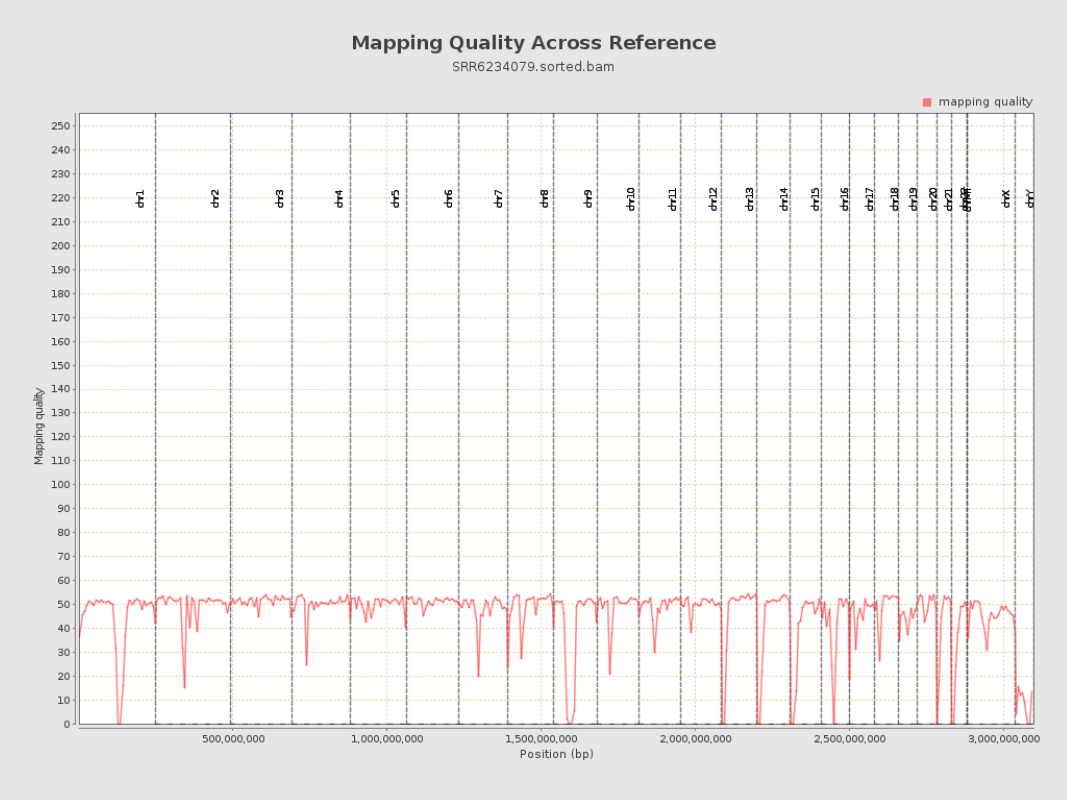
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram