Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:12:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230339.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_SRR6230339 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230339.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:12:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230339.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,205,680
Mapped reads	1,411,631 / 64%
Unmapped reads	794,049 / 36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,468 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	107,900 / 4.89%
Duplication rate	6.34%
Clipped reads	867,929 / 39.35%

2.2. ACGT Content

Number/percentage of A's	22,954,509 / 26.07%
Number/percentage of C's	14,700,435 / 16.7%
Number/percentage of T's	30,465,636 / 34.61%
Number/percentage of G's	19,768,458 / 22.45%
Number/percentage of N's	149,129 / 0.17%
GC Percentage	39.15%

2.3. Coverage

Mean	0.0285

Standard Deviation	0.2889

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

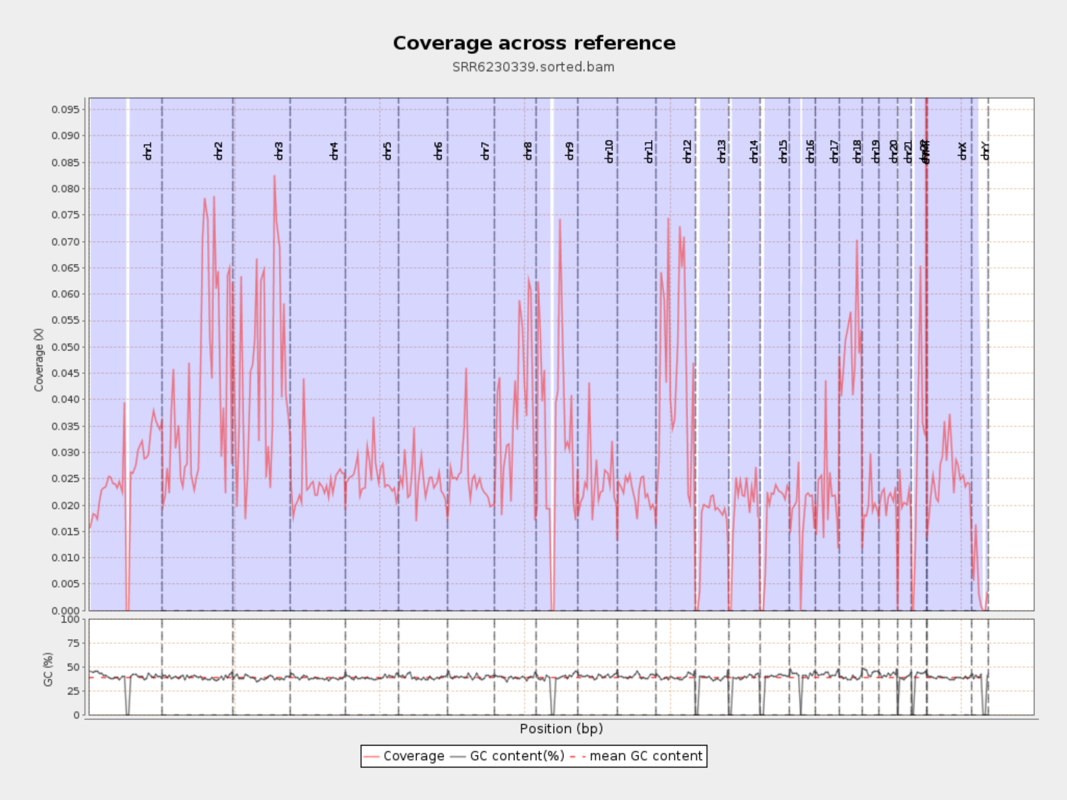
General error rate	1.23%
Mismatches	1,071,843
Insertions	7,989
Mapped reads with at least one insertion	0.56%
Deletions	27,054
Mapped reads with at least one deletion	1.89%
Homopolymer indels	48.03%

2.6. Chromosome stats

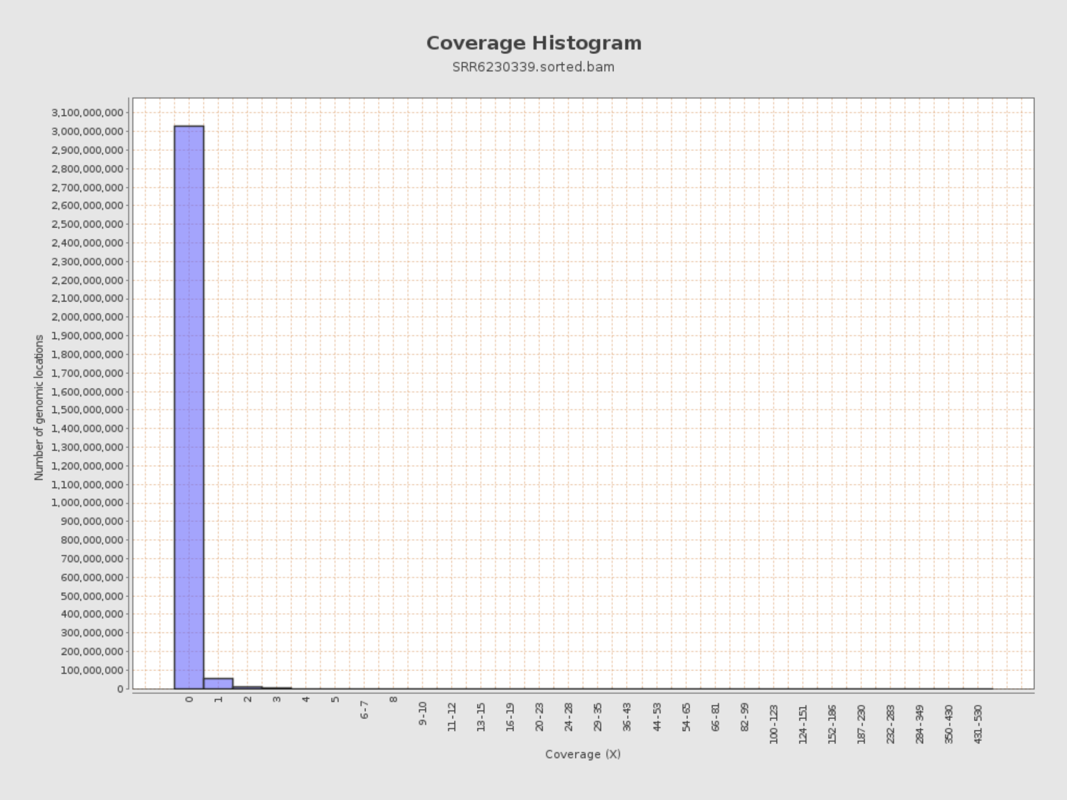
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6314267	0.0253	0.3771
chr2	243199373	9999115	0.0411	0.3682
chr3	198022430	8967075	0.0453	0.2643
chr4	191154276	4590629	0.024	0.212
chr5	180915260	4638976	0.0256	0.1985
chr6	171115067	4160292	0.0243	0.2239
chr7	159138663	4022999	0.0253	0.3453

chr8	146364022	5602981	0.0383	0.4123
chr9	141213431	4860106	0.0344	0.3356
chr10	135534747	3296357	0.0243	0.2647
chr11	135006516	3012658	0.0223	0.2435
chr12	133851895	6218287	0.0465	0.2692
chr13	115169878	1861627	0.0162	0.1541
chr14	107349540	2049158	0.0191	0.1811
chr15	102531392	1844198	0.018	0.1657
chr16	90354753	1673204	0.0185	0.1839
chr17	81195210	1792880	0.0221	0.2286
chr18	78077248	3945344	0.0505	0.608
chr19	59128983	1183211	0.02	0.2723
chr20	63025520	1337361	0.0212	0.1843
chr21	48129895	940276	0.0195	0.1898
chr22	51304566	1448883	0.0282	0.2057
chrMT	16571	81078	4.8928	4.2867
chrX	155270560	3971864	0.0256	0.2166
chrY	59373566	268912	0.0045	0.1266

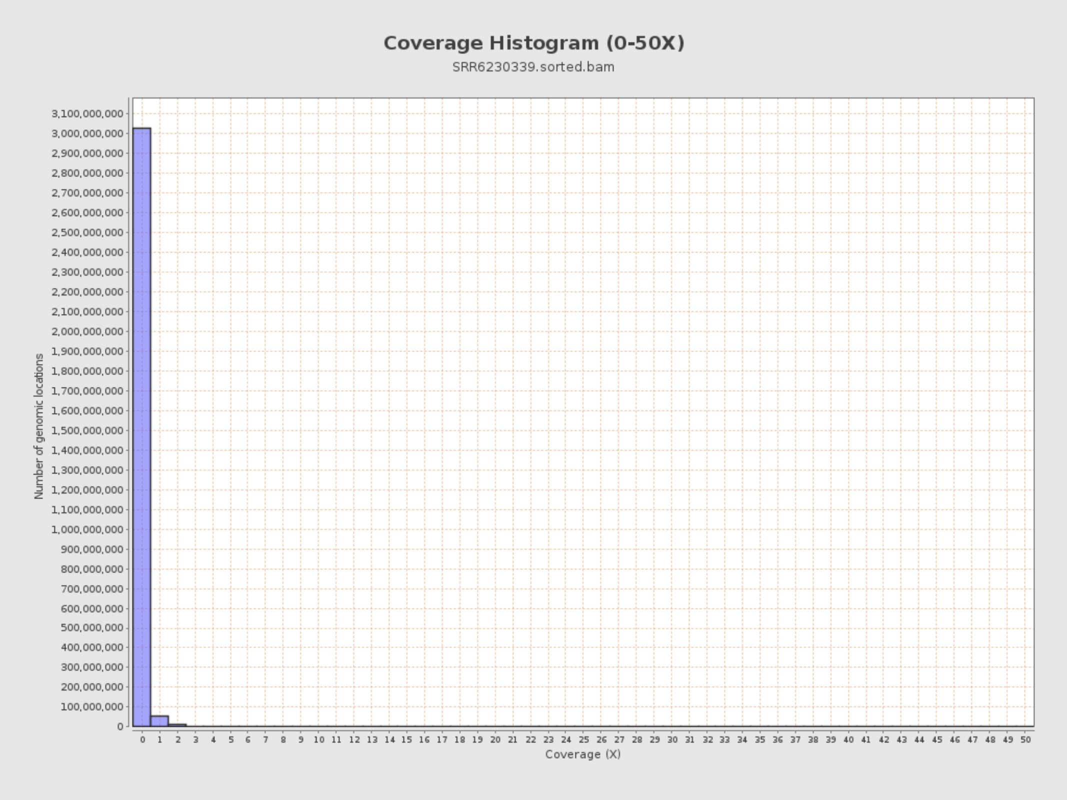
3. Results : Coverage across reference



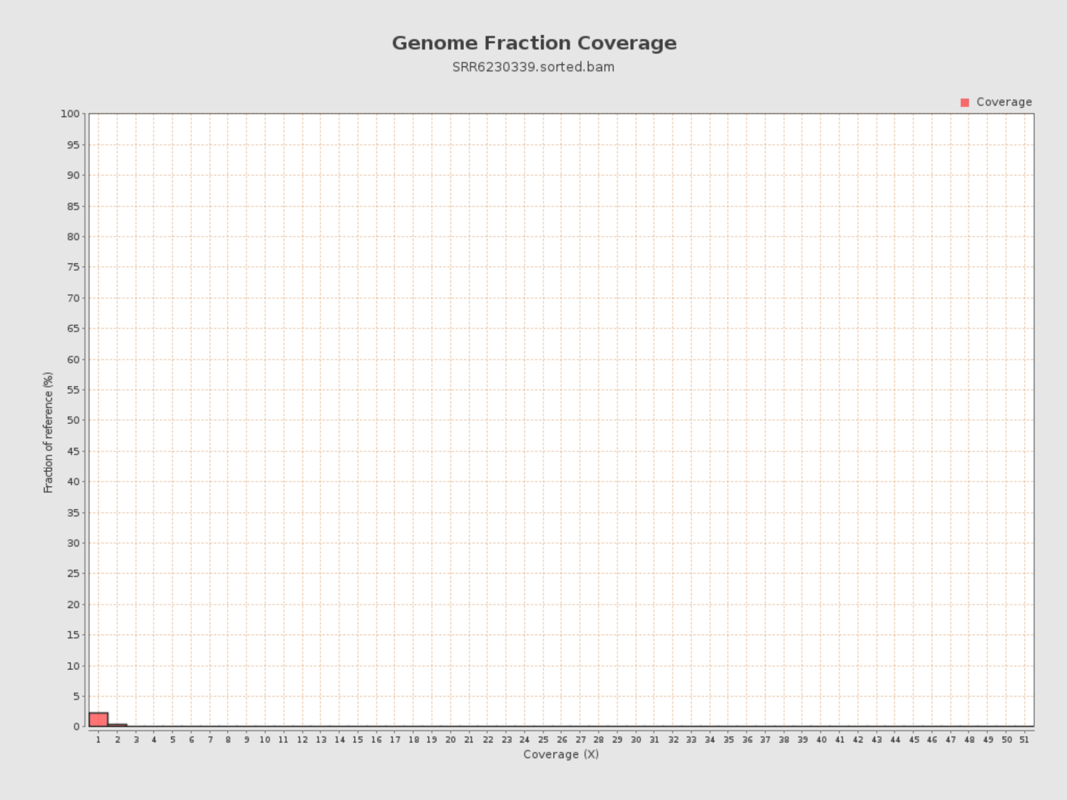
4. Results : Coverage Histogram



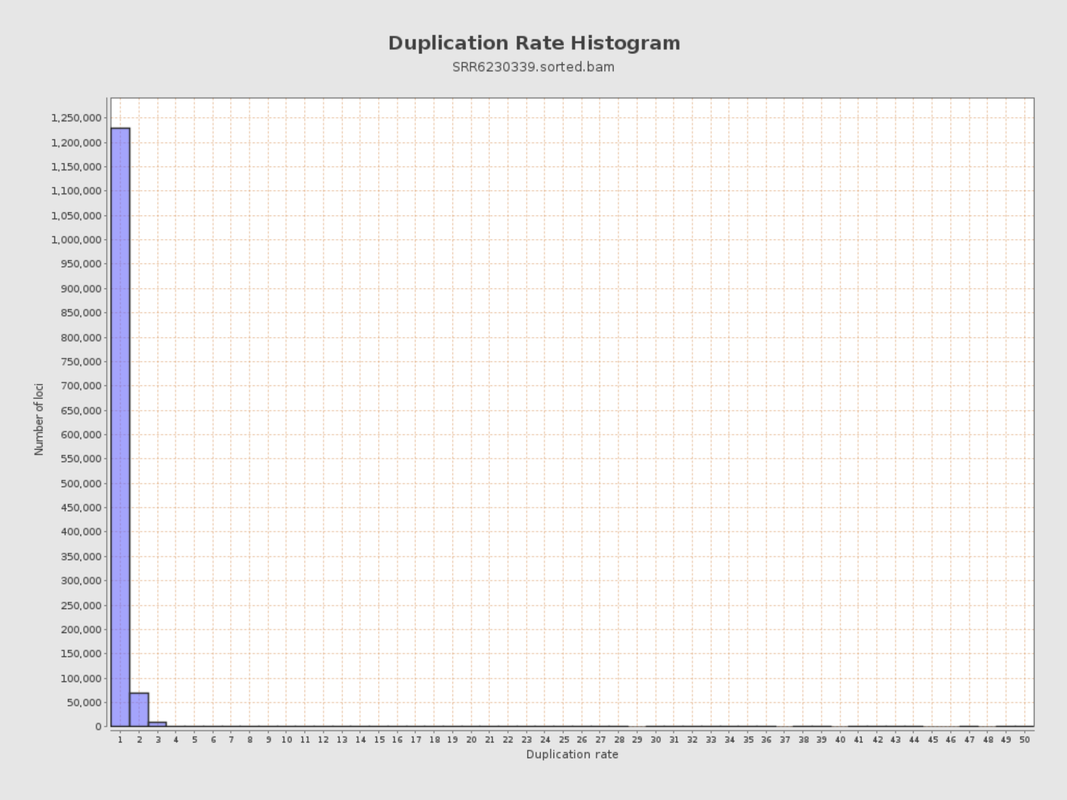
5. Results : Coverage Histogram (0-50X)



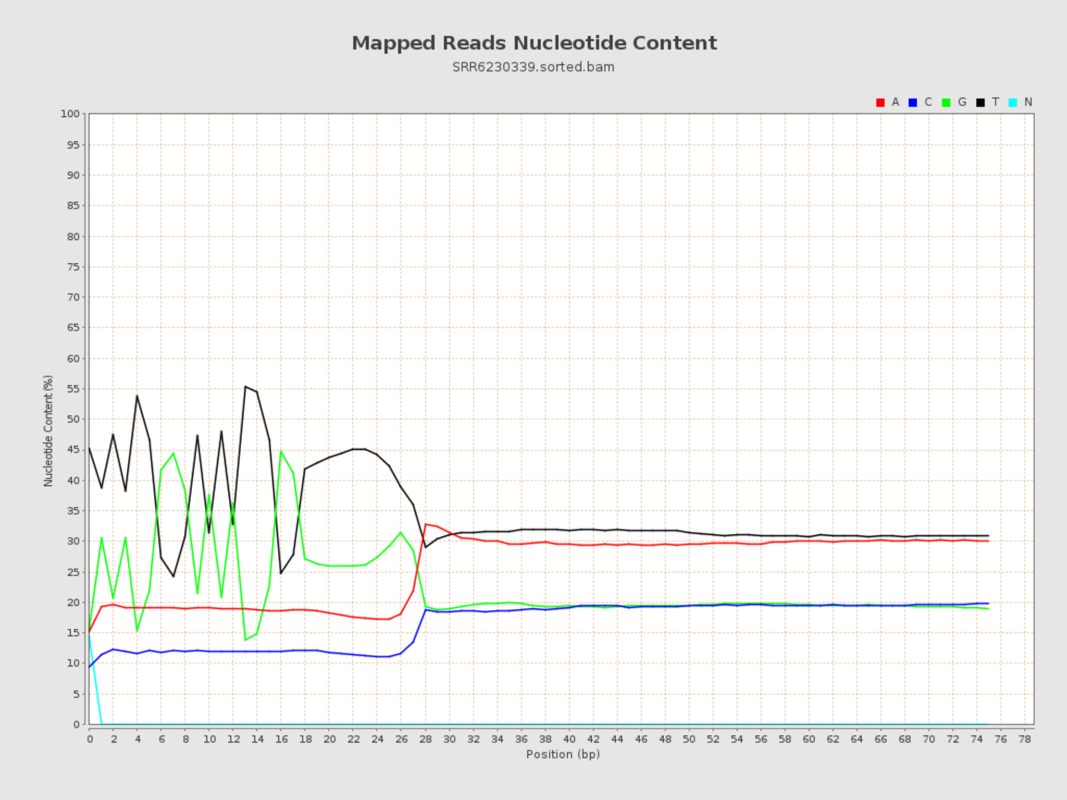
6. Results : Genome Fraction Coverage



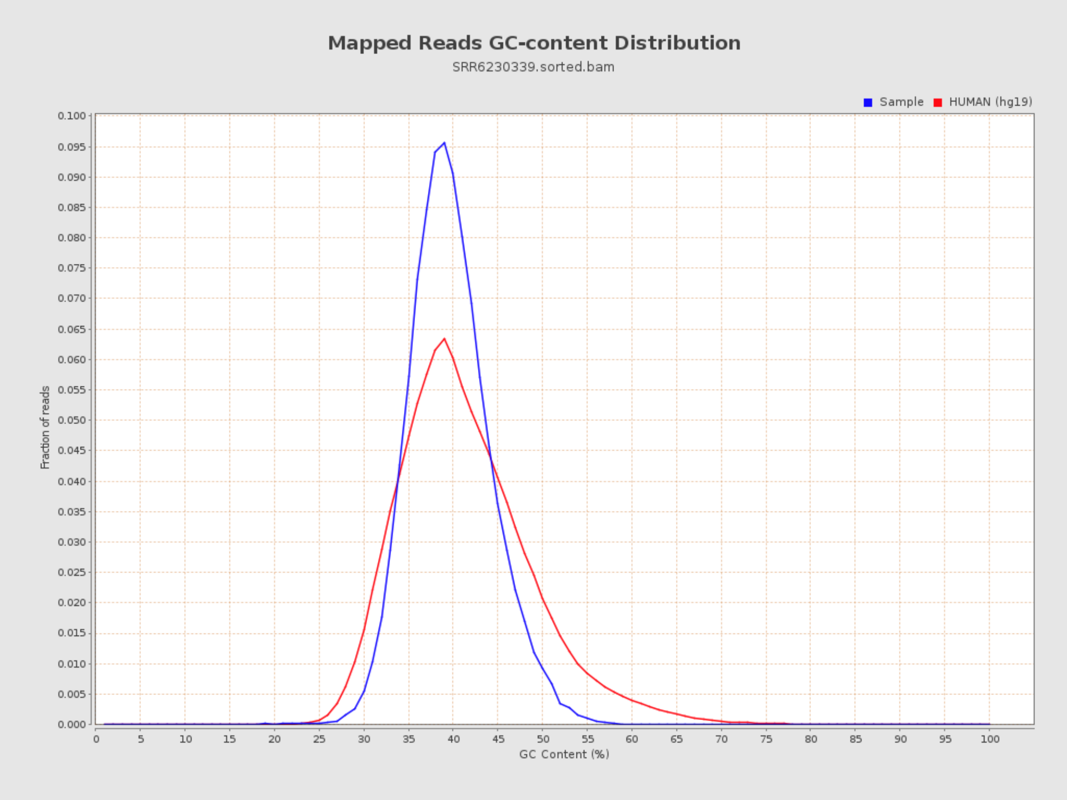
7. Results : Duplication Rate Histogram



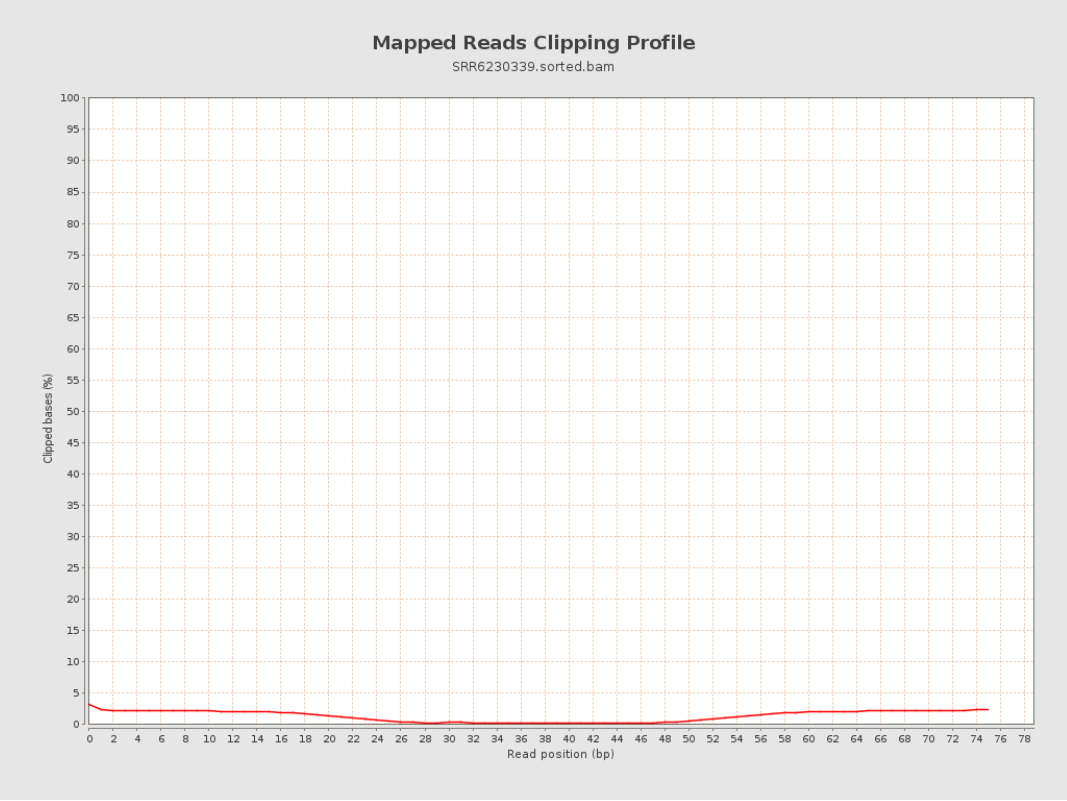
8. Results : Mapped Reads Nucleotide Content



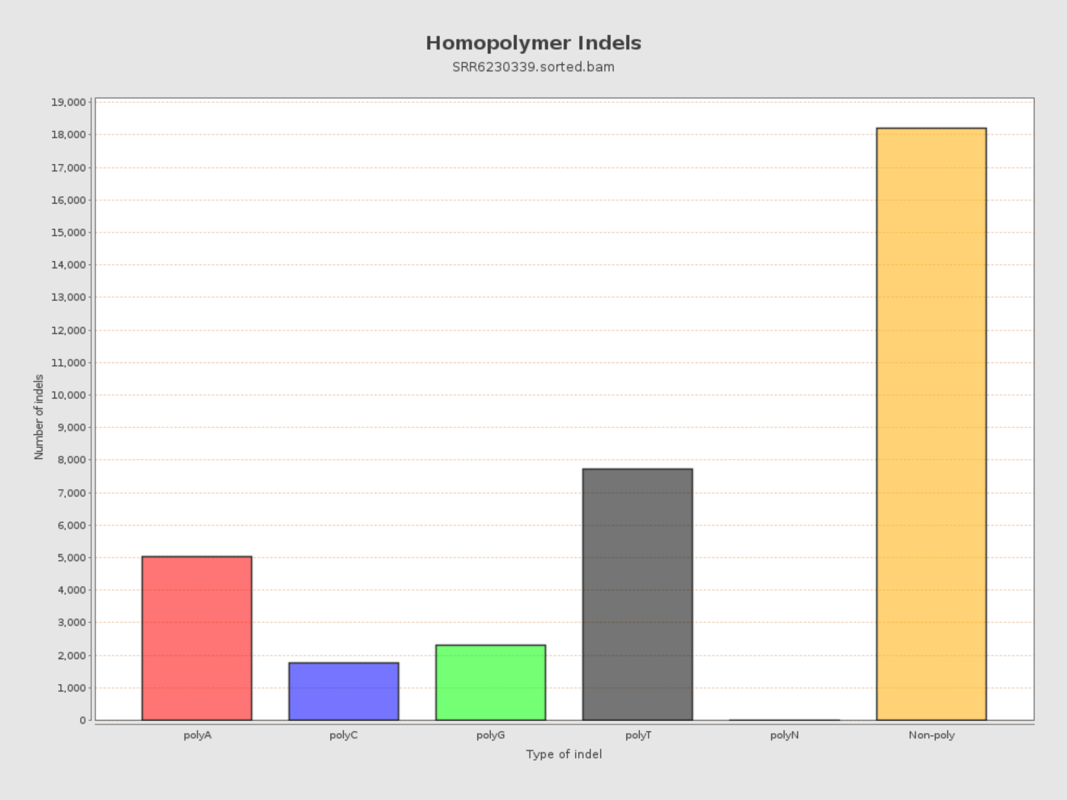
9. Results : Mapped Reads GC-content Distribution



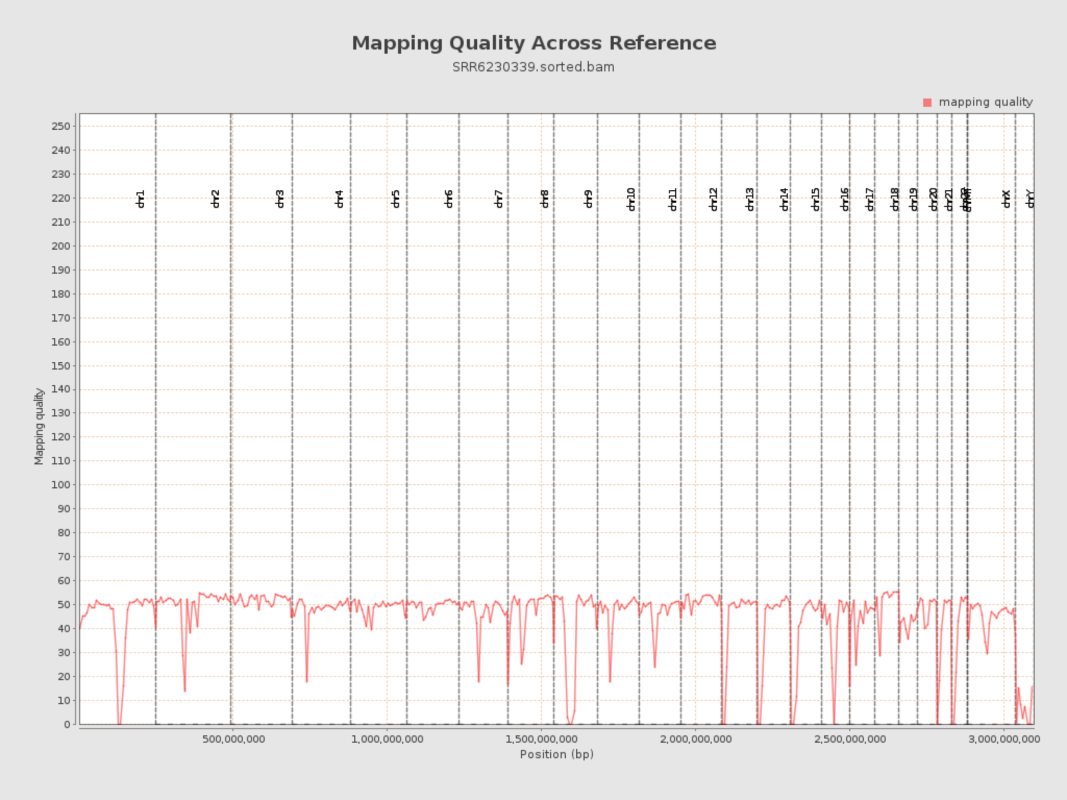
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram