Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:40:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230346.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_SRR6230346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230346.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:40:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230346.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,011,721
Mapped reads	942,966 / 93.2%
Unmapped reads	68,755 / 6.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,088 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	28,186 / 2.79%
Duplication rate	2.22%
Clipped reads	294,273 / 29.09%

2.2. ACGT Content

Number/percentage of A's	20,237,662 / 30.33%
Number/percentage of C's	13,085,813 / 19.61%
Number/percentage of T's	20,023,075 / 30.01%
Number/percentage of G's	13,341,663 / 20%
Number/percentage of N's	36,214 / 0.05%
GC Percentage	39.61%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2536

2.4. Mapping Quality

Mean Mapping Quality	47.95

2.5. Mismatches and indels

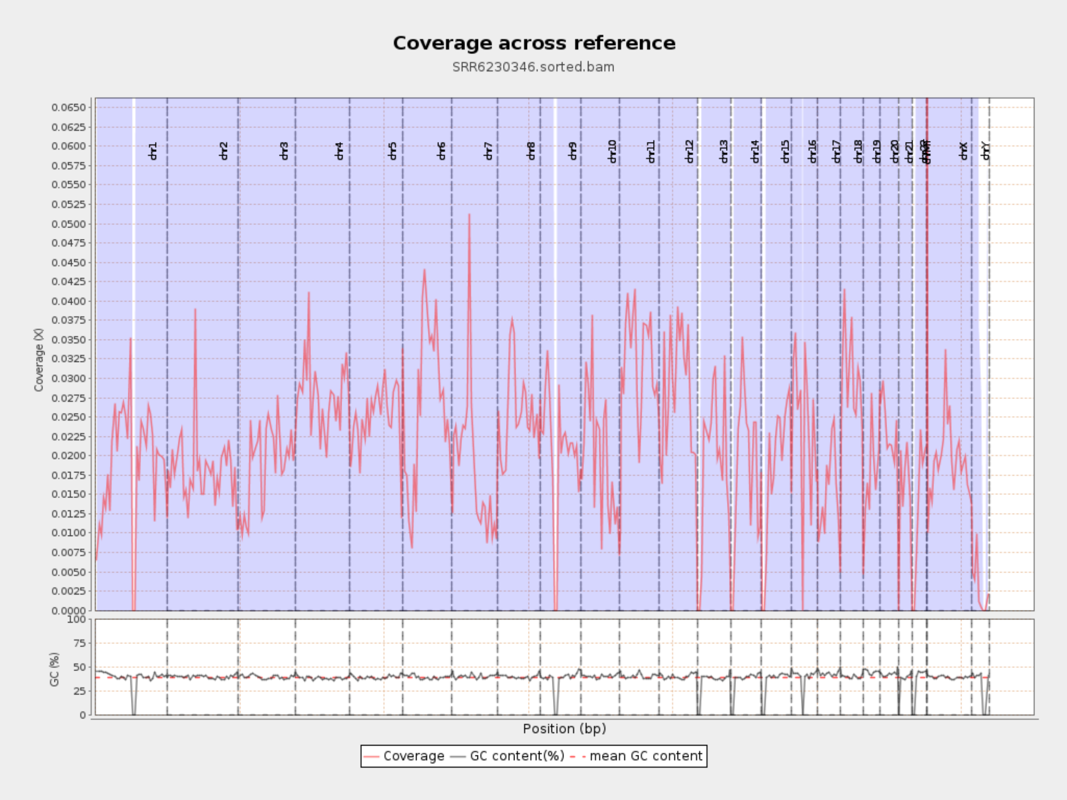
General error rate	0.95%
Mismatches	623,713
Insertions	6,036
Mapped reads with at least one insertion	0.64%
Deletions	21,921
Mapped reads with at least one deletion	2.29%
Homopolymer indels	45.75%

2.6. Chromosome stats

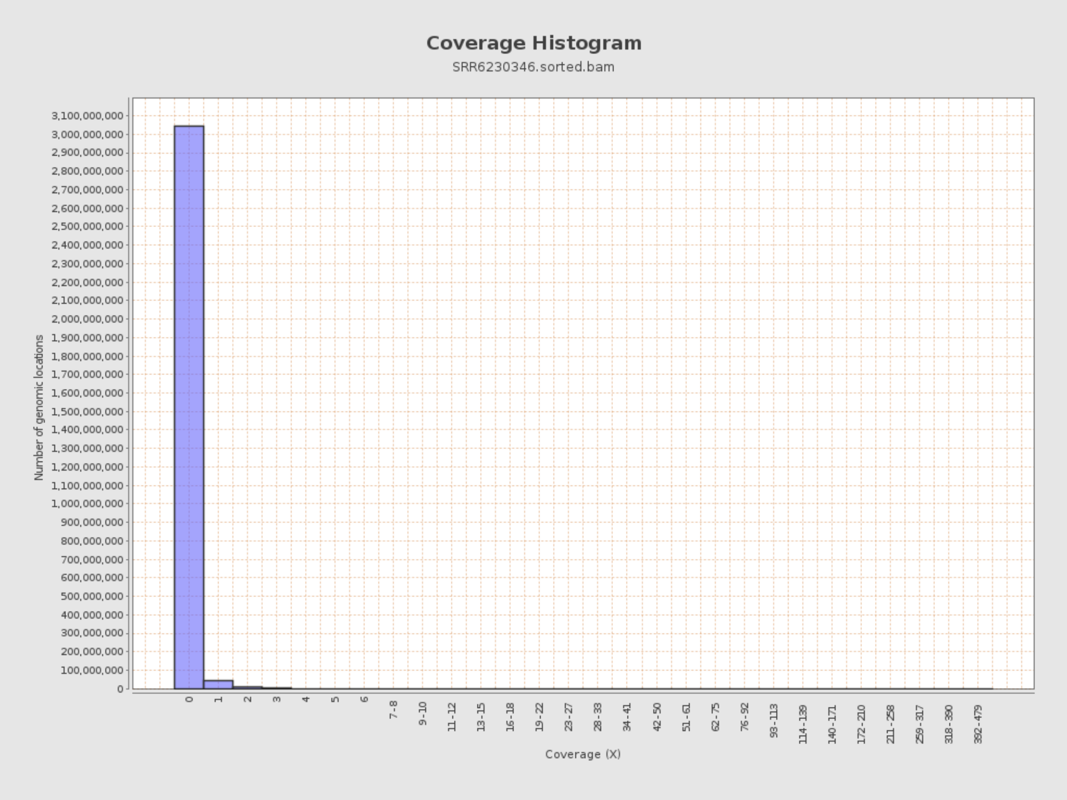
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4701084	0.0189	0.366
chr2	243199373	4462619	0.0183	0.2382
chr3	198022430	3736514	0.0189	0.1651
chr4	191154276	5305222	0.0278	0.2053
chr5	180915260	4540125	0.0251	0.1897
chr6	171115067	4621448	0.027	0.2525
chr7	159138663	2948430	0.0185	0.3872

chr8	146364022	3781924	0.0258	0.2531
chr9	141213431	2903630	0.0206	0.2452
chr10	135534747	2716433	0.02	0.2466
chr11	135006516	4363703	0.0323	0.3354
chr12	133851895	3781627	0.0283	0.2032
chr13	115169878	2173209	0.0189	0.1641
chr14	107349540	1965638	0.0183	0.1699
chr15	102531392	1890507	0.0184	0.1609
chr16	90354753	2119602	0.0235	0.2187
chr17	81195210	1216394	0.015	0.1719
chr18	78077248	2391640	0.0306	0.5057
chr19	59128983	1057207	0.0179	0.2735
chr20	63025520	1463930	0.0232	0.1866
chr21	48129895	717597	0.0149	0.1611
chr22	51304566	699758	0.0136	0.1361
chrMT	16571	2416	0.1458	0.4101
chrX	155270560	3038066	0.0196	0.1864
chrY	59373566	162388	0.0027	0.0923

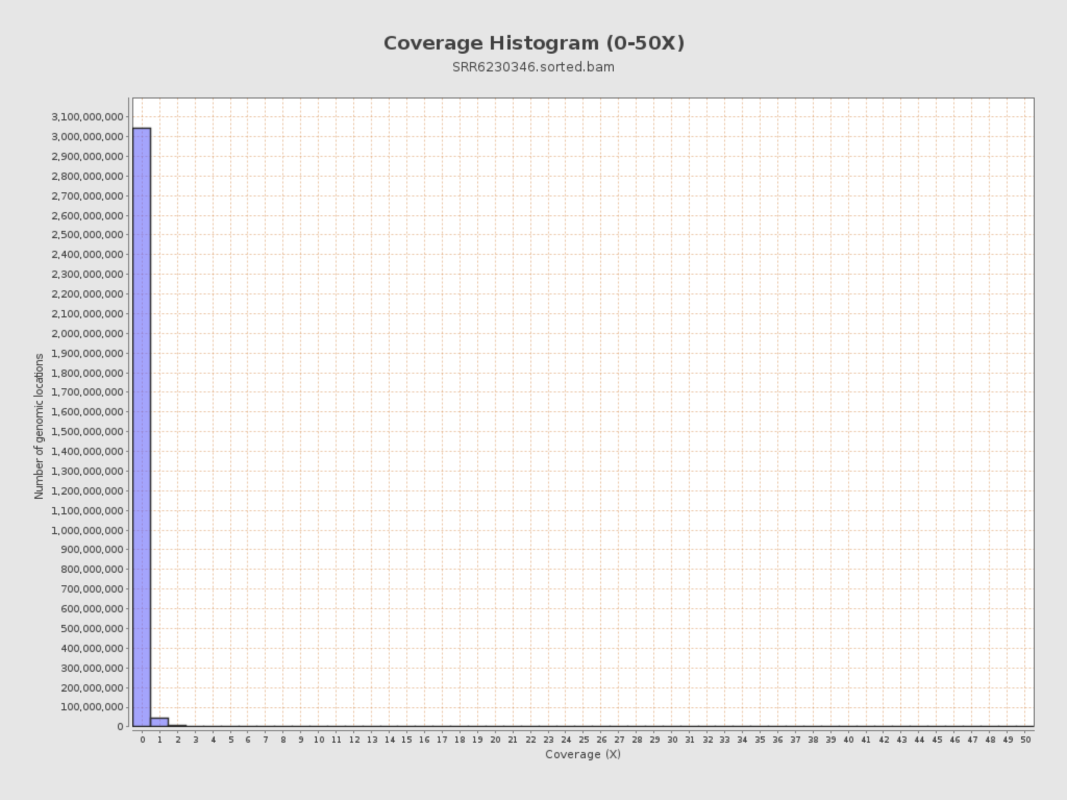
3. Results : Coverage across reference



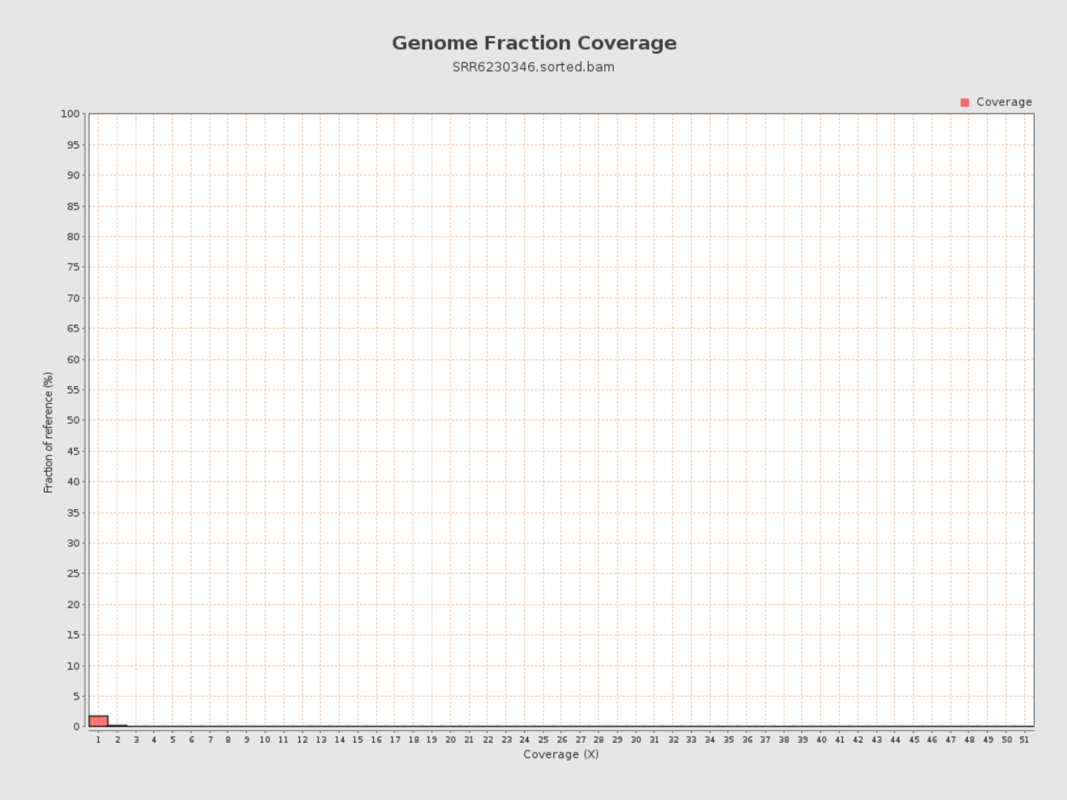
4. Results : Coverage Histogram



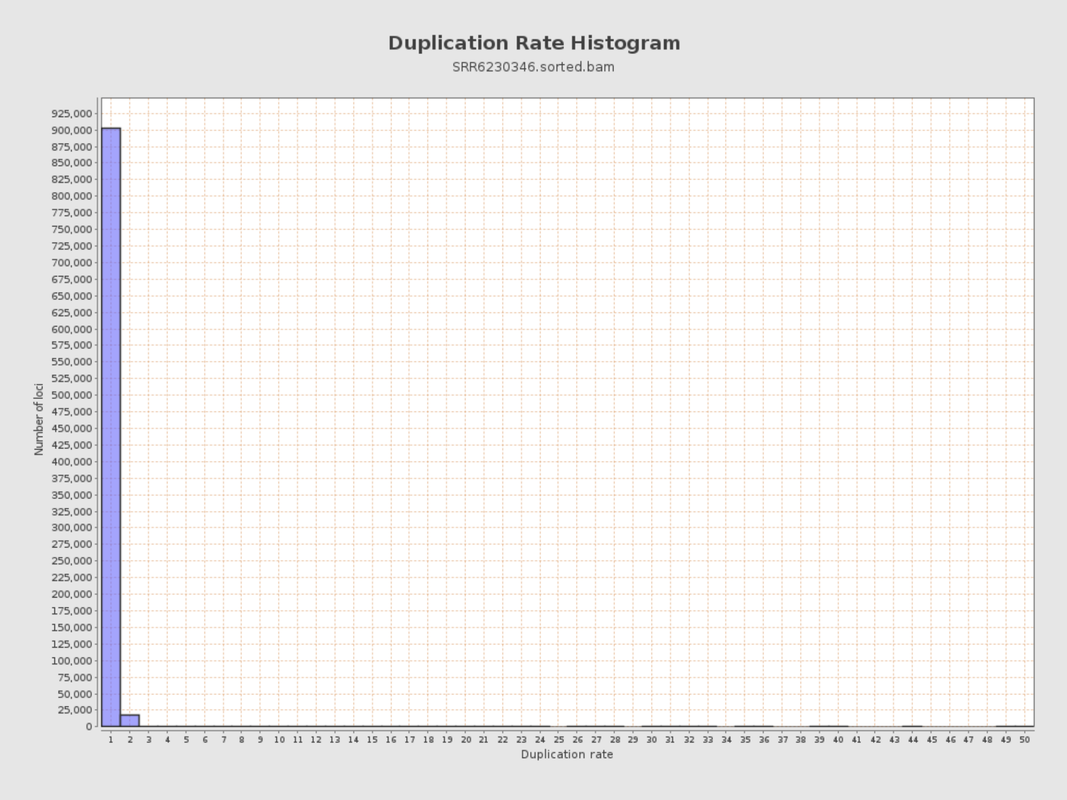
5. Results : Coverage Histogram (0-50X)



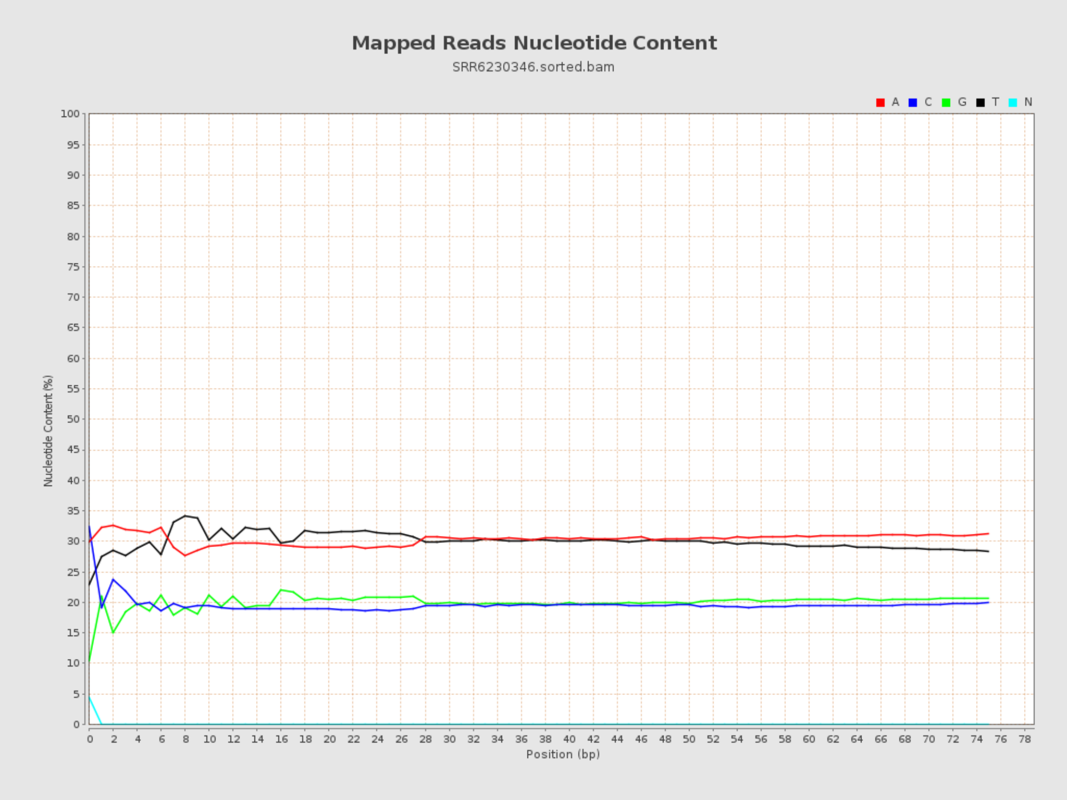
6. Results : Genome Fraction Coverage



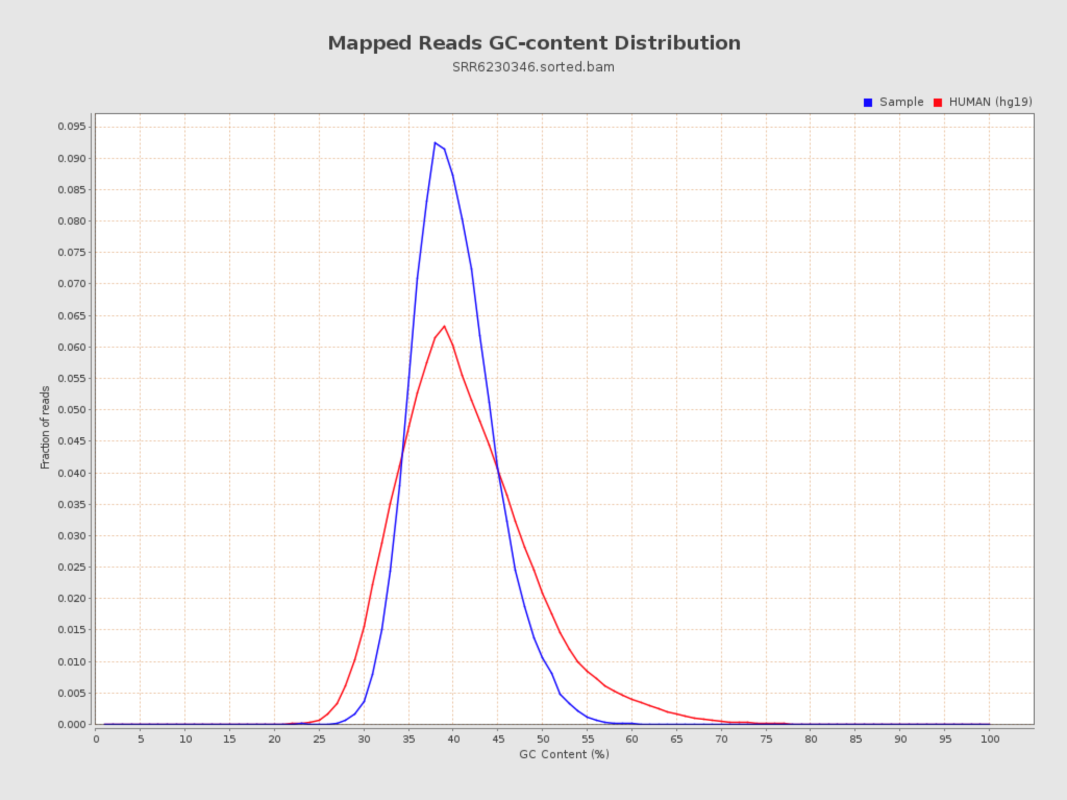
7. Results : Duplication Rate Histogram



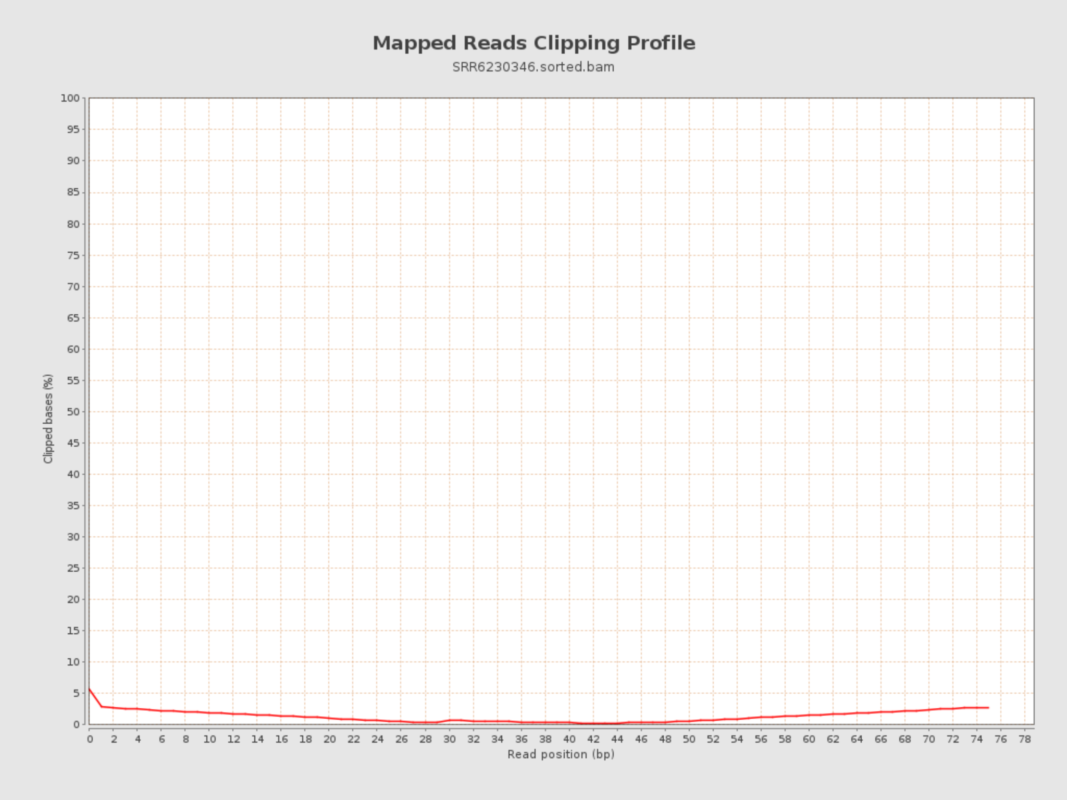
8. Results : Mapped Reads Nucleotide Content



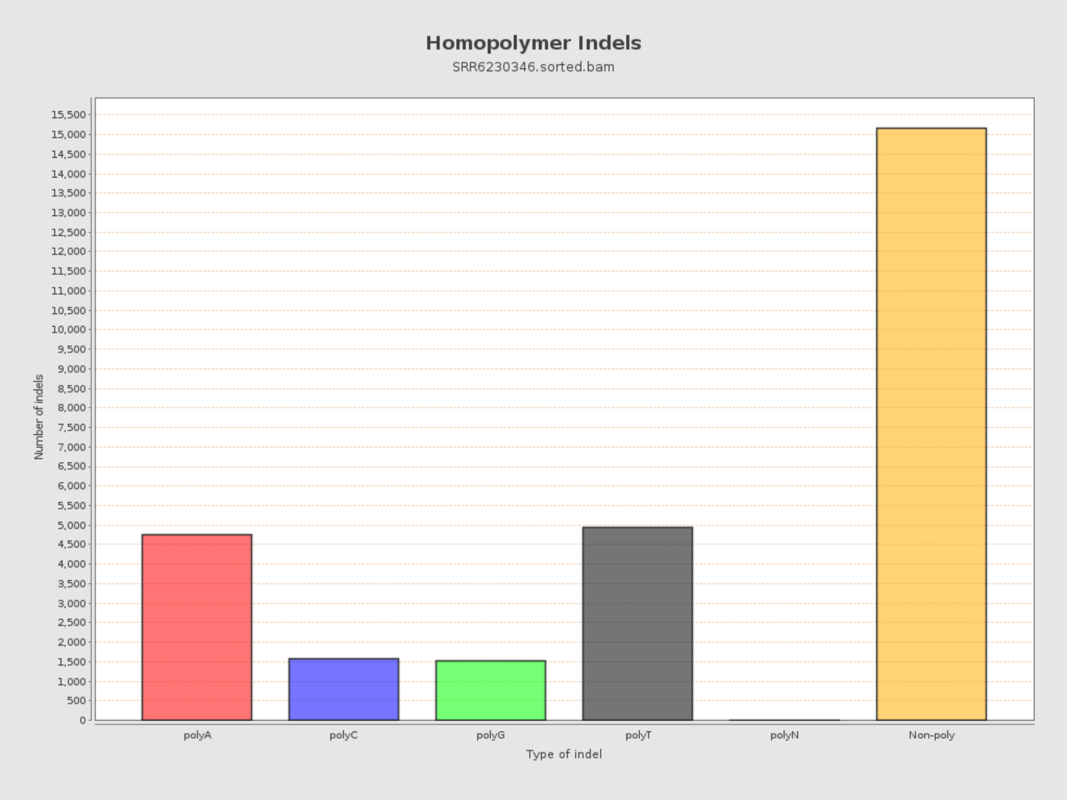
9. Results : Mapped Reads GC-content Distribution



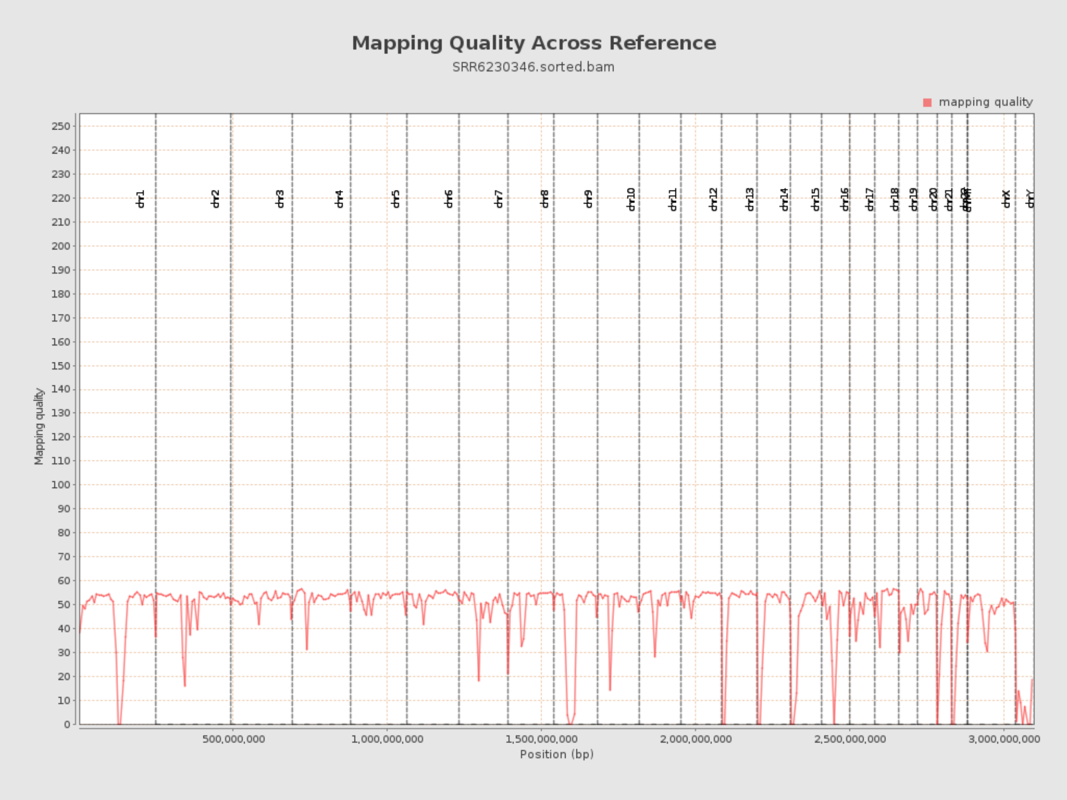
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram