Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:22:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751216.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_SRR8751216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:22:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,885,229
Mapped reads	3,686,836 / 62.65%
Unmapped reads	2,198,393 / 37.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	212,473 / 3.61%
Read min/max/mean length	30 / 101 / 102.49
Duplicated reads (estimated)	136,509 / 2.32%
Duplication rate	1.87%
Clipped reads	897,535 / 15.25%

2.2. ACGT Content

Number/percentage of A's	107,572,691 / 29.67%
Number/percentage of C's	73,693,287 / 20.32%
Number/percentage of T's	108,321,212 / 29.87%
Number/percentage of G's	73,012,312 / 20.14%
Number/percentage of N's	2,597 / 0%
GC Percentage	40.46%

2.3. Coverage

Mean	0.1172

Standard Deviation	1.3364

2.4. Mapping Quality

Mean Mapping Quality	51.06

2.5. Mismatches and indels

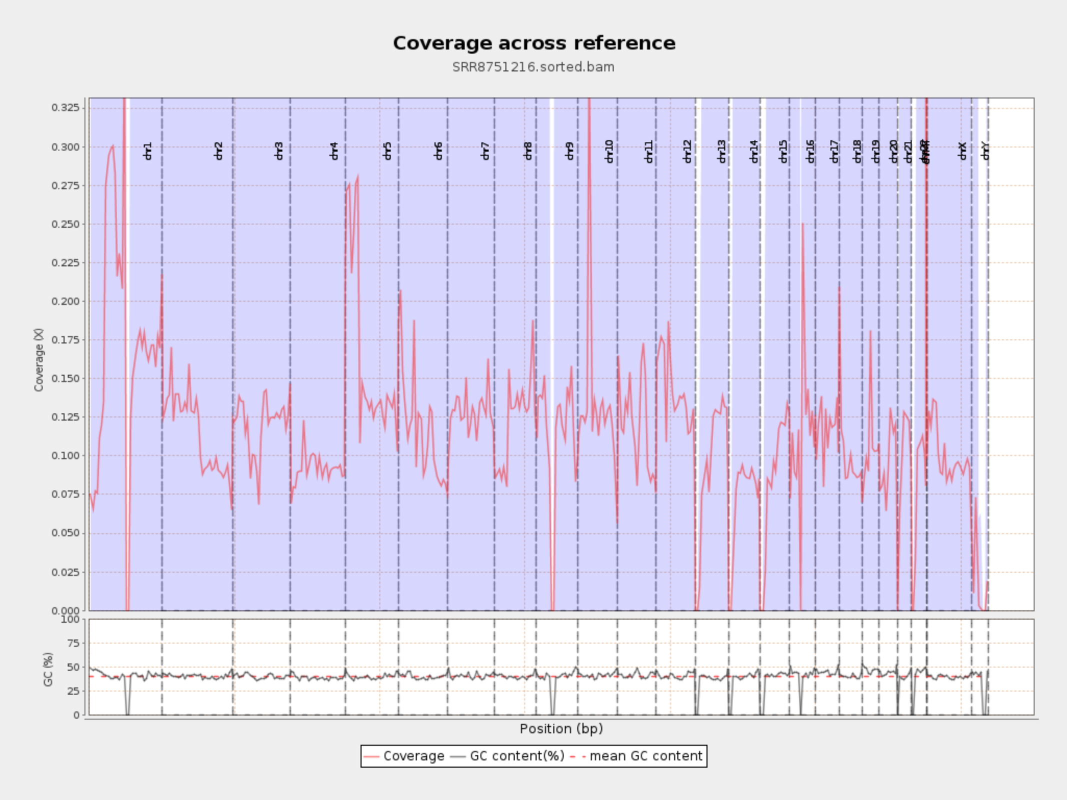
General error rate	0.5%
Mismatches	1,421,425
Insertions	286,837
Mapped reads with at least one insertion	7.43%
Deletions	55,531
Mapped reads with at least one deletion	1.47%
Homopolymer indels	53.48%

2.6. Chromosome stats

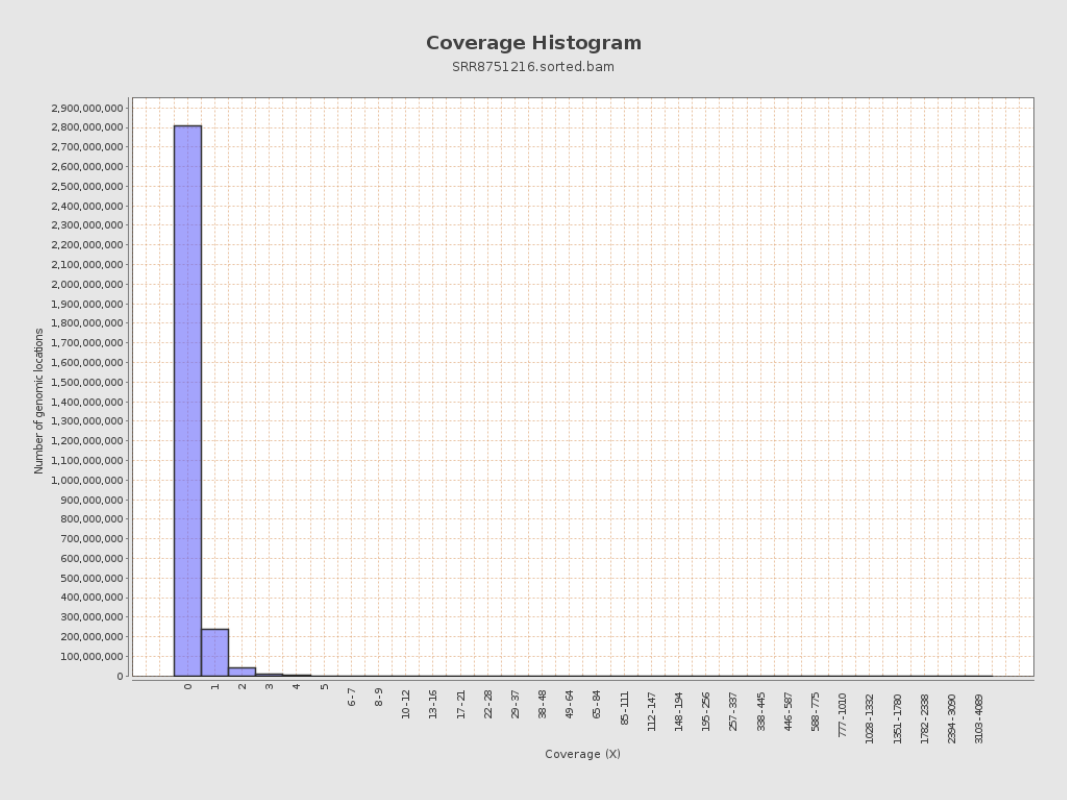
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	42694236	0.1713	3.7474
chr2	243199373	27885162	0.1147	0.5972
chr3	198022430	23724650	0.1198	0.4977
chr4	191154276	17519975	0.0917	0.4608
chr5	180915260	29703326	0.1642	0.541
chr6	171115067	20206074	0.1181	0.7424
chr7	159138663	20532615	0.129	0.8125

chr8	146364022	18087569	0.1236	0.6325
chr9	141213431	15920561	0.1127	0.6553
chr10	135534747	18361479	0.1355	2.0456
chr11	135006516	16296887	0.1207	0.6694
chr12	133851895	19097751	0.1427	0.4801
chr13	115169878	10723935	0.0931	0.3569
chr14	107349540	7632835	0.0711	0.3296
chr15	102531392	8684232	0.0847	0.3395
chr16	90354753	10274581	0.1137	1.0426
chr17	81195210	9476947	0.1167	0.6094
chr18	78077248	7745823	0.0992	1.3354
chr19	59128983	6371102	0.1077	2.5187
chr20	63025520	6049833	0.096	0.3844
chr21	48129895	4592769	0.0954	0.4177
chr22	51304566	3719743	0.0725	0.3178
chrMT	16571	880527	53.1366	24.642
chrX	155270560	15548265	0.1001	0.4358
chrY	59373566	994487	0.0167	0.7059

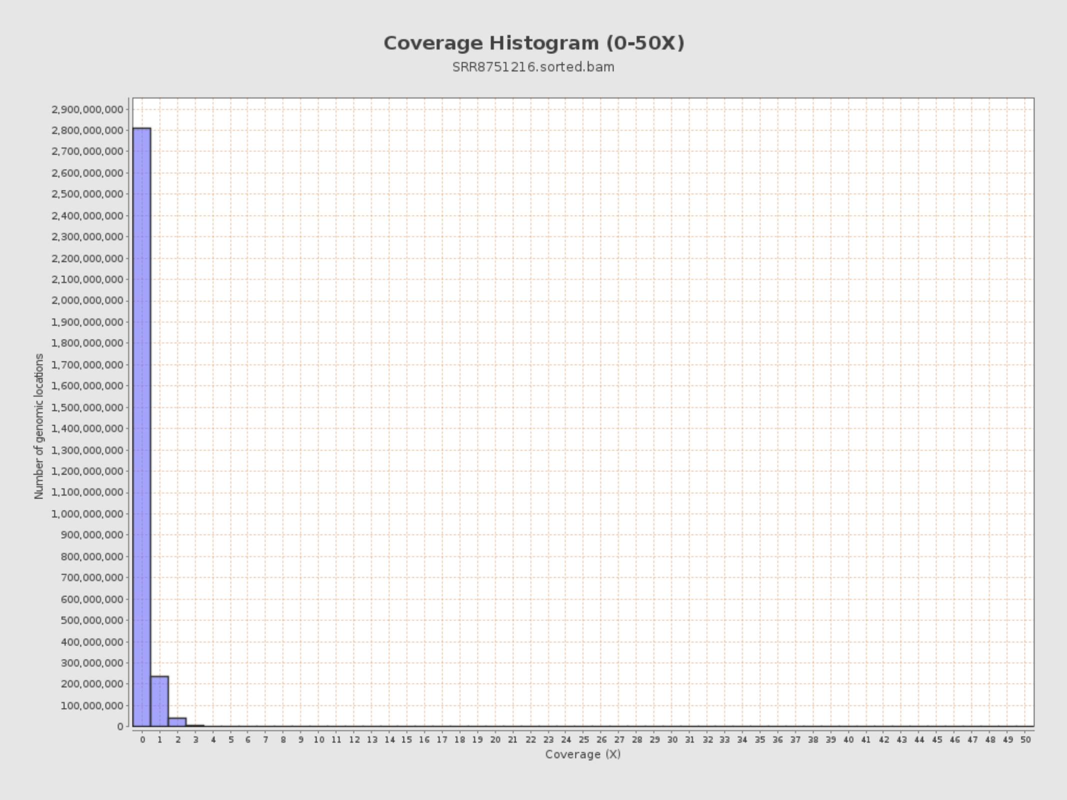
3. Results : Coverage across reference



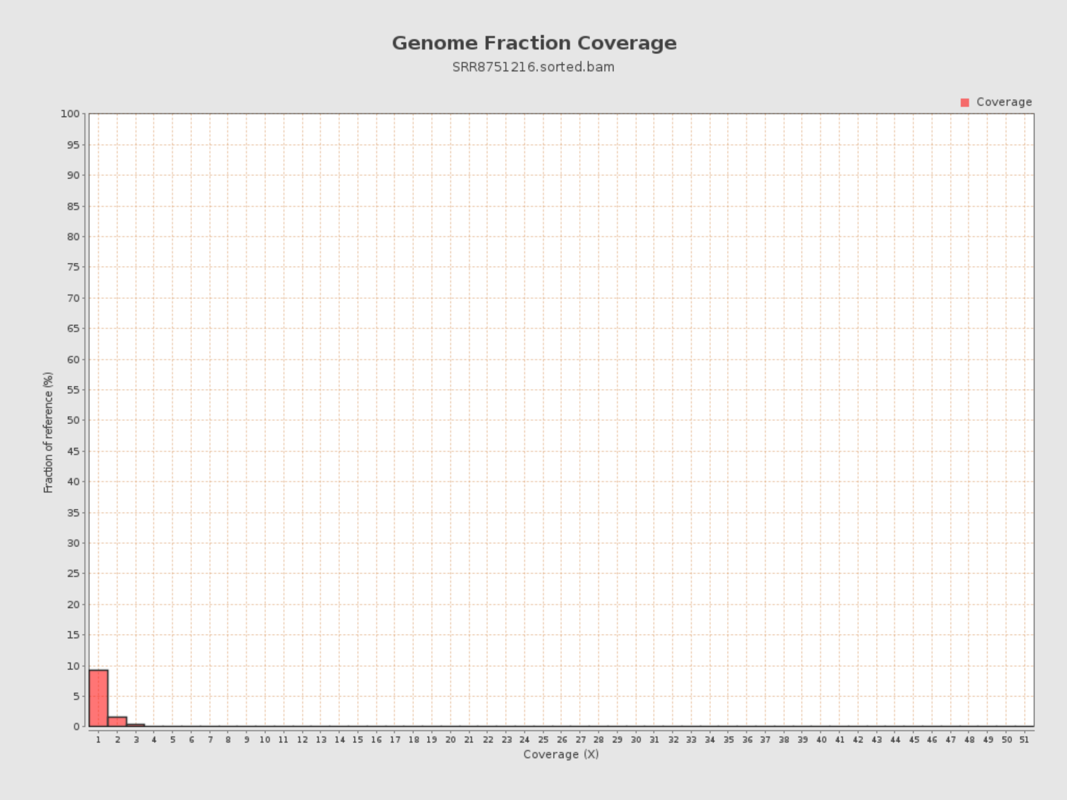
4. Results : Coverage Histogram



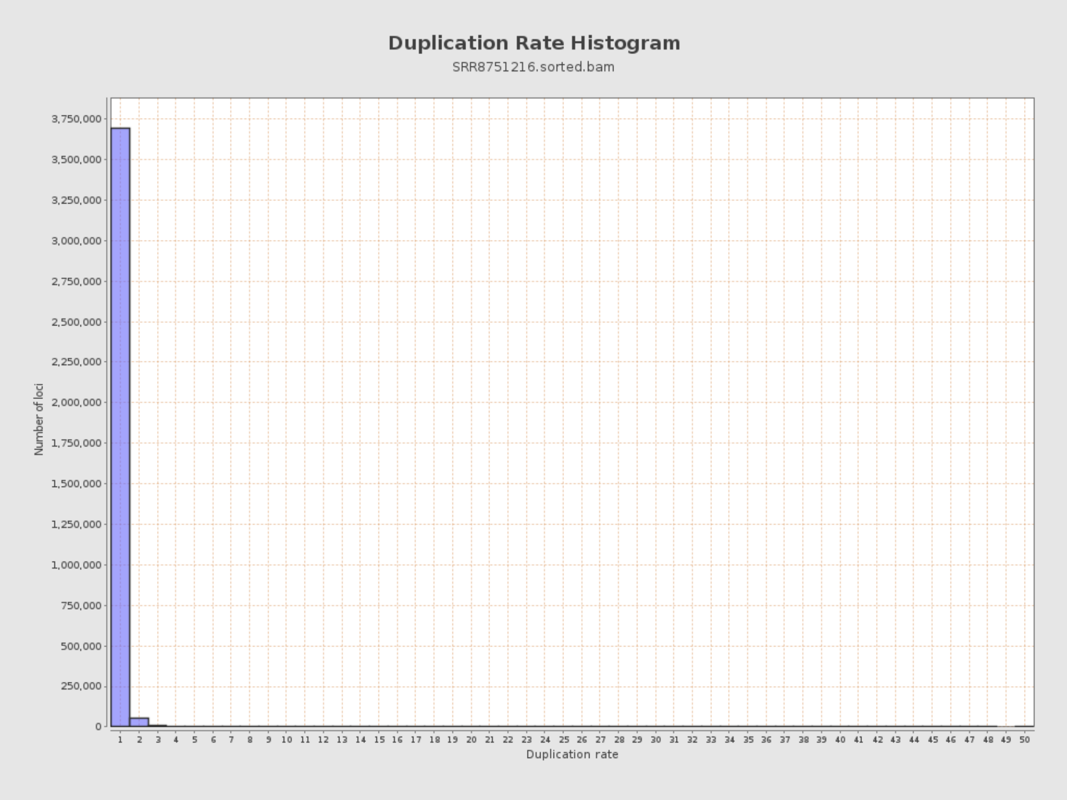
5. Results : Coverage Histogram (0-50X)



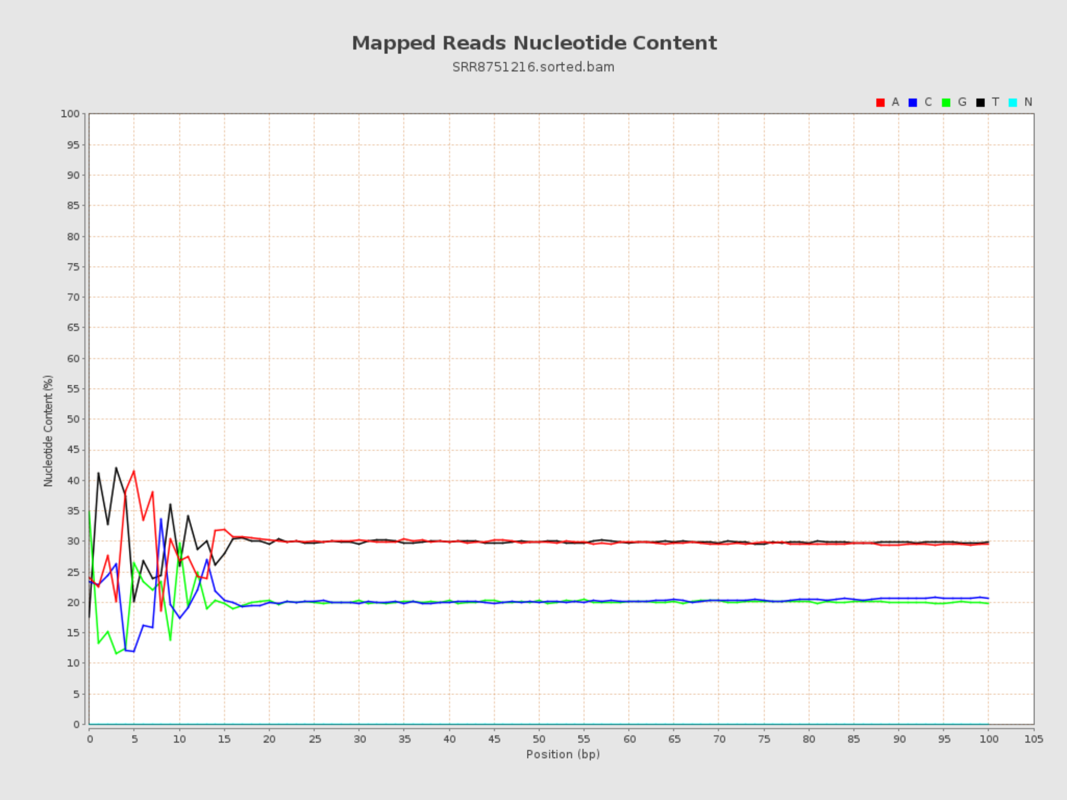
6. Results : Genome Fraction Coverage



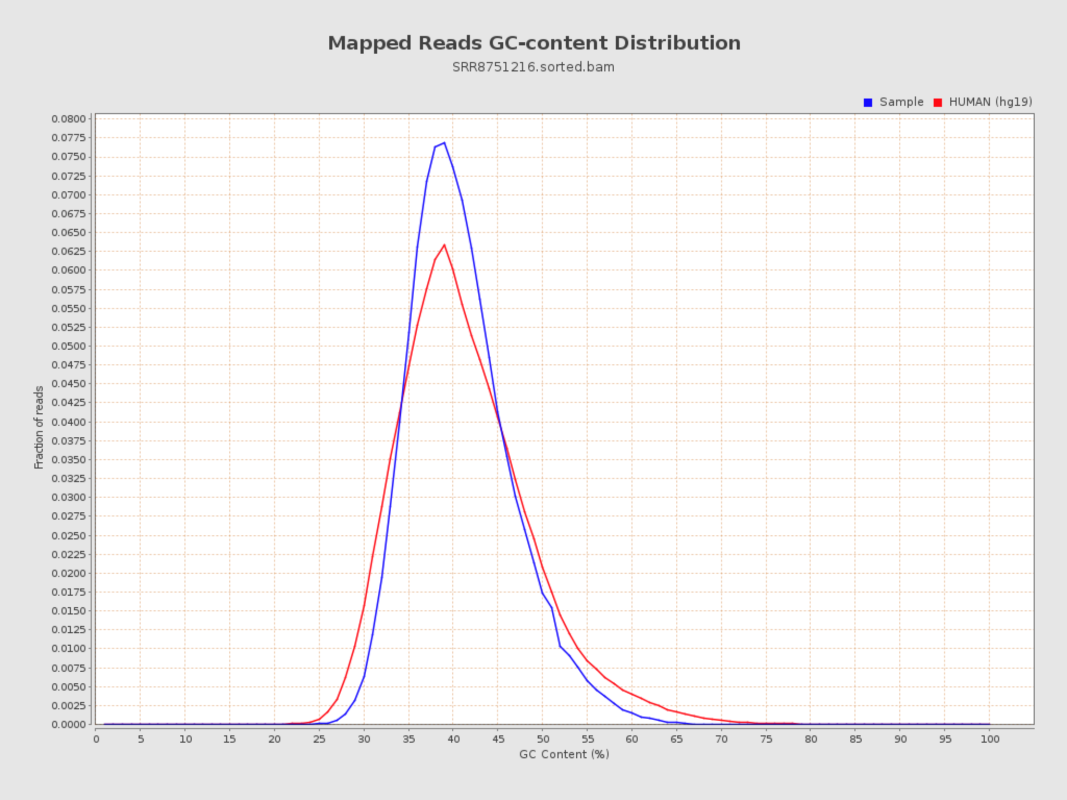
7. Results : Duplication Rate Histogram



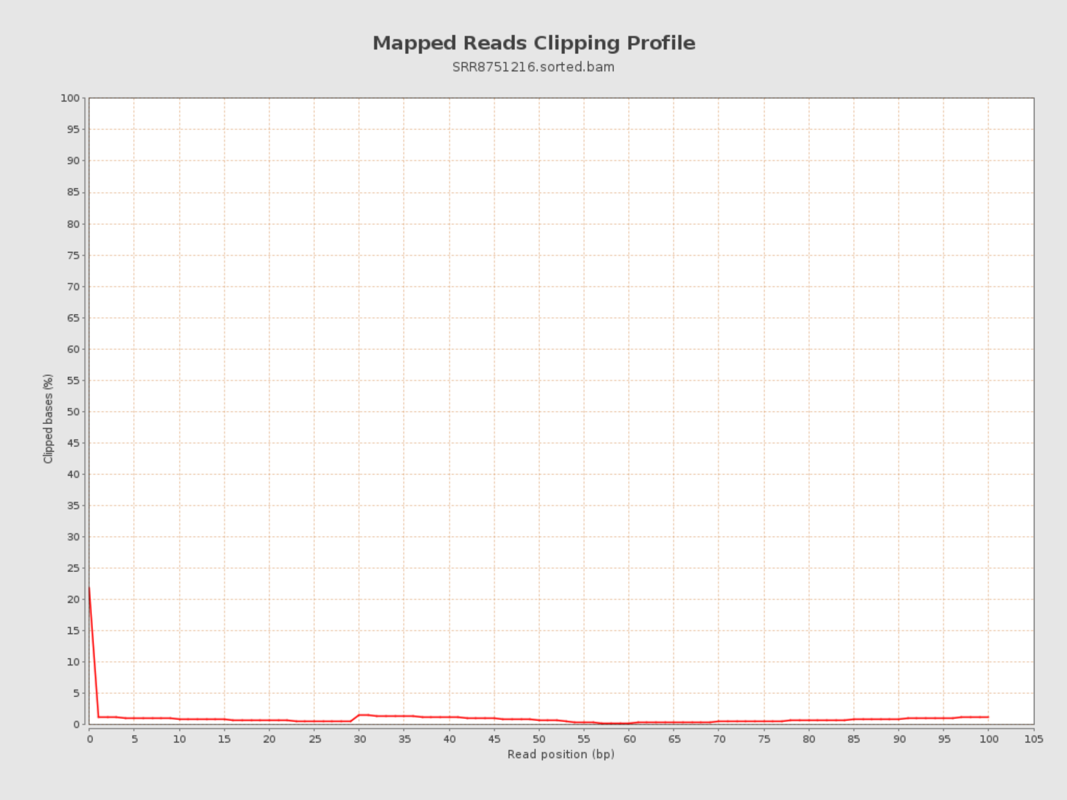
8. Results : Mapped Reads Nucleotide Content



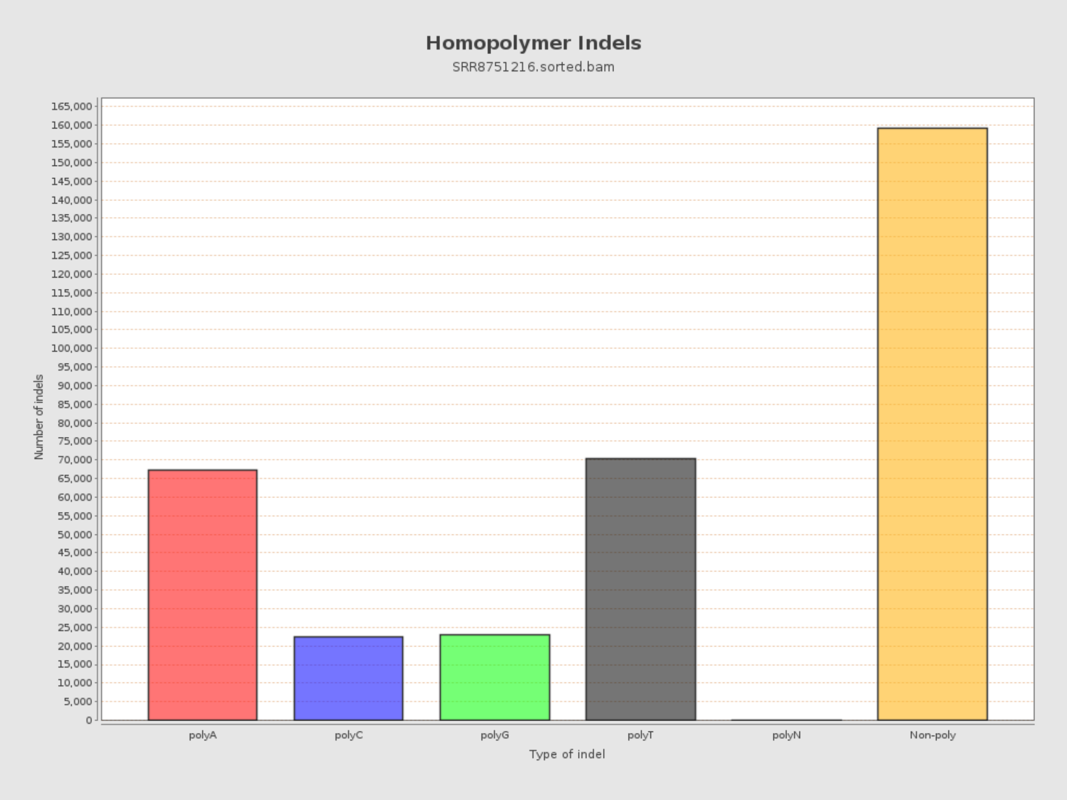
9. Results : Mapped Reads GC-content Distribution



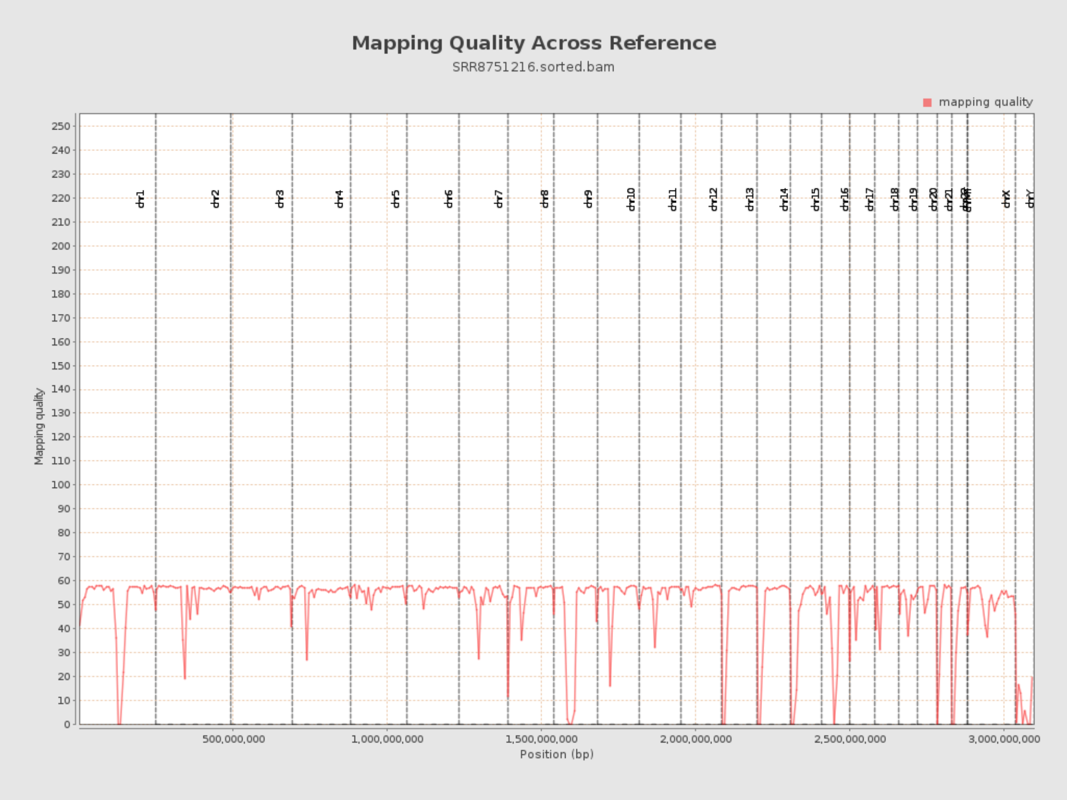
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram