Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:50:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751211.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_SRR8751211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:50:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,043,555
Mapped reads	4,211,727 / 83.51%
Unmapped reads	831,828 / 16.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237,643 / 4.71%
Read min/max/mean length	30 / 101 / 102.94
Duplicated reads (estimated)	175,891 / 3.49%
Duplication rate	2.04%
Clipped reads	1,088,150 / 21.58%

2.2. ACGT Content

Number/percentage of A's	120,405,888 / 29.25%
Number/percentage of C's	85,164,531 / 20.69%
Number/percentage of T's	121,145,974 / 29.43%
Number/percentage of G's	84,880,692 / 20.62%
Number/percentage of N's	2,188 / 0%
GC Percentage	41.31%

2.3. Coverage

Mean	0.133

Standard Deviation	1.5116

2.4. Mapping Quality

Mean Mapping Quality	50.89

2.5. Mismatches and indels

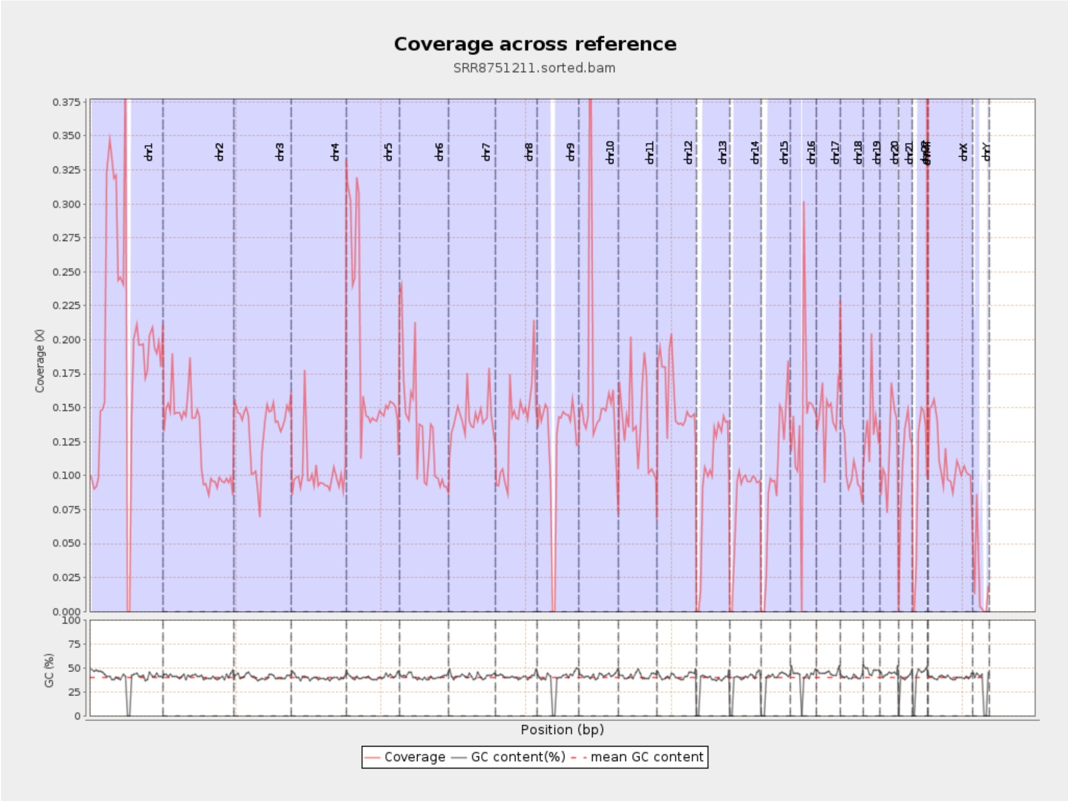
General error rate	0.56%
Mismatches	1,781,499
Insertions	375,131
Mapped reads with at least one insertion	8.47%
Deletions	67,746
Mapped reads with at least one deletion	1.57%
Homopolymer indels	54.01%

2.6. Chromosome stats

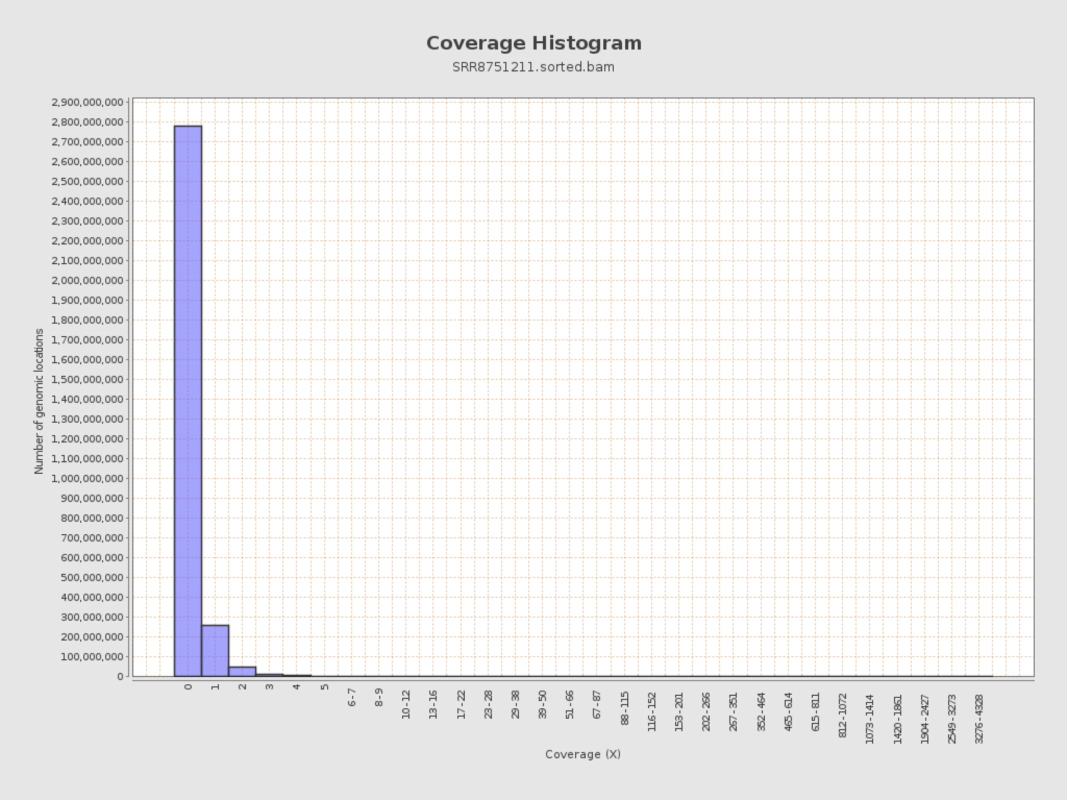
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	49038201	0.1967	4.0359
chr2	243199373	30450539	0.1252	0.6765
chr3	198022430	26562041	0.1341	0.6032
chr4	191154276	19066087	0.0997	0.6422
chr5	180915260	32911214	0.1819	0.5106
chr6	171115067	22759726	0.133	0.8699
chr7	159138663	22750192	0.143	0.9479

chr8	146364022	20027173	0.1368	0.5455
chr9	141213431	17674243	0.1252	0.7489
chr10	135534747	21914653	0.1617	2.8275
chr11	135006516	18544126	0.1374	0.7412
chr12	133851895	21203053	0.1584	0.4757
chr13	115169878	11613429	0.1008	0.3766
chr14	107349540	8661933	0.0807	0.3718
chr15	102531392	10064280	0.0982	0.62
chr16	90354753	12563009	0.139	1.256
chr17	81195210	11843674	0.1459	0.6868
chr18	78077248	8598643	0.1101	1.5245
chr19	59128983	8173951	0.1382	2.6932
chr20	63025520	7412126	0.1176	0.4555
chr21	48129895	5211393	0.1083	0.5104
chr22	51304566	4870078	0.0949	0.3696
chrMT	16571	1480091	89.3181	31.8575
chrX	155270560	17226243	0.1109	0.4755
chrY	59373566	1127781	0.019	0.818

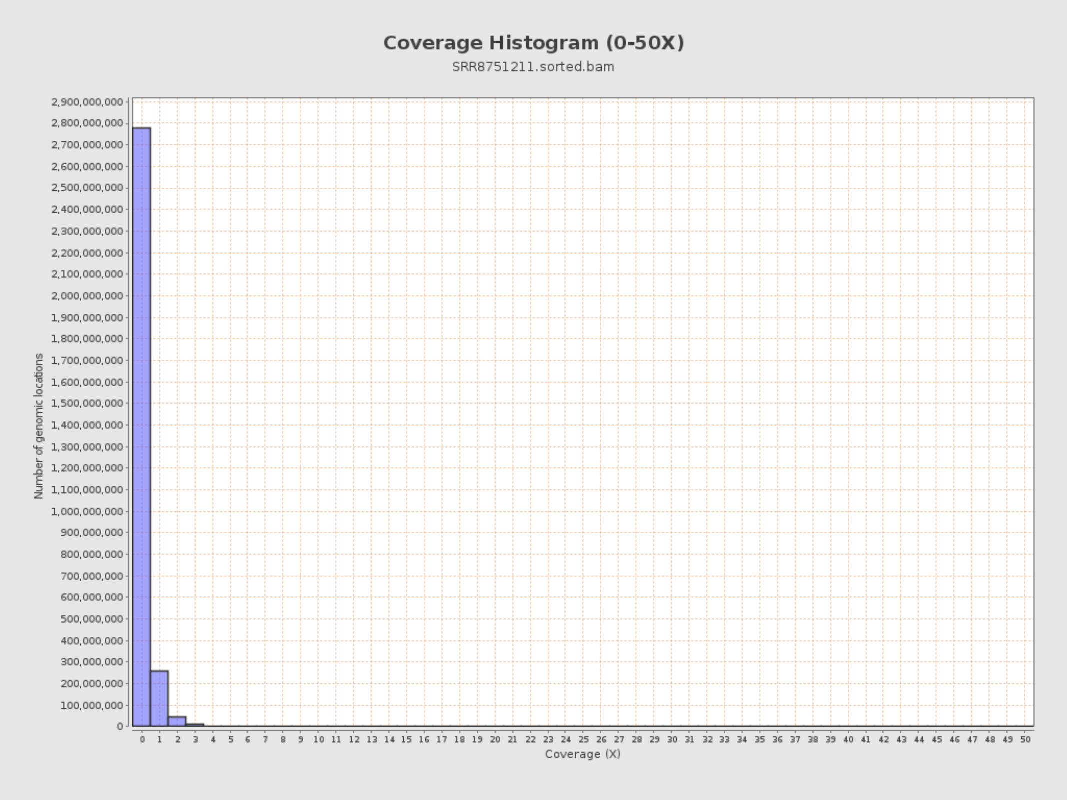
3. Results : Coverage across reference



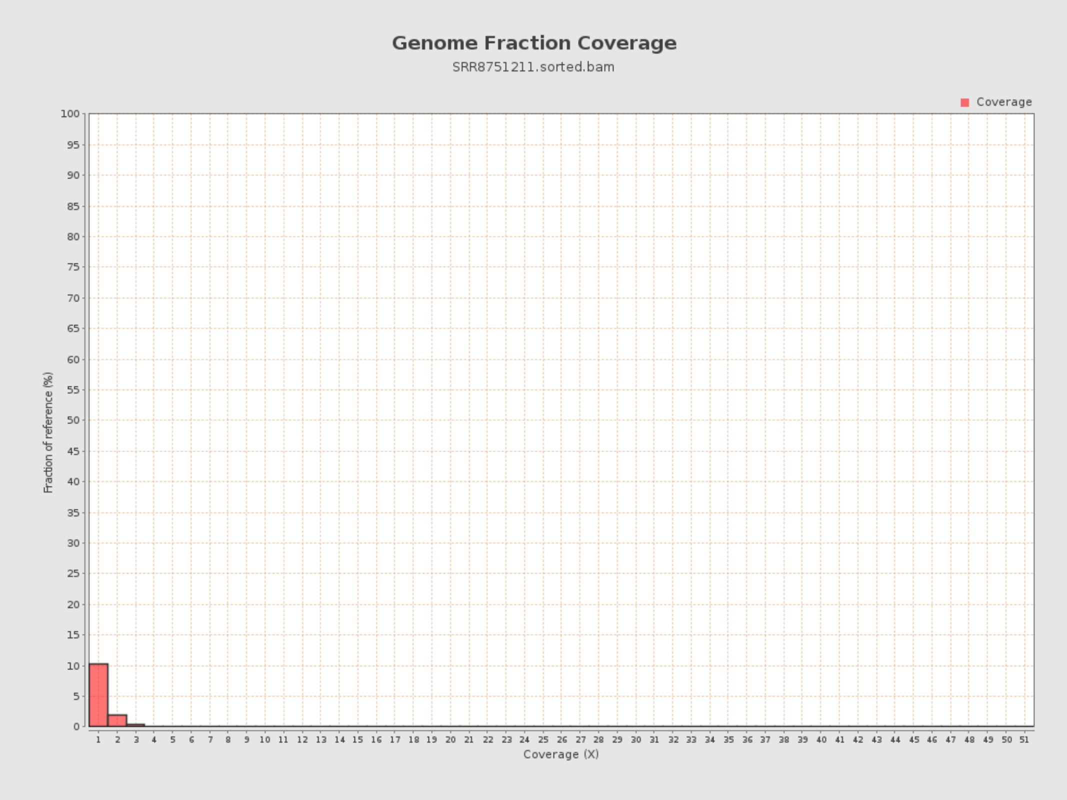
4. Results : Coverage Histogram



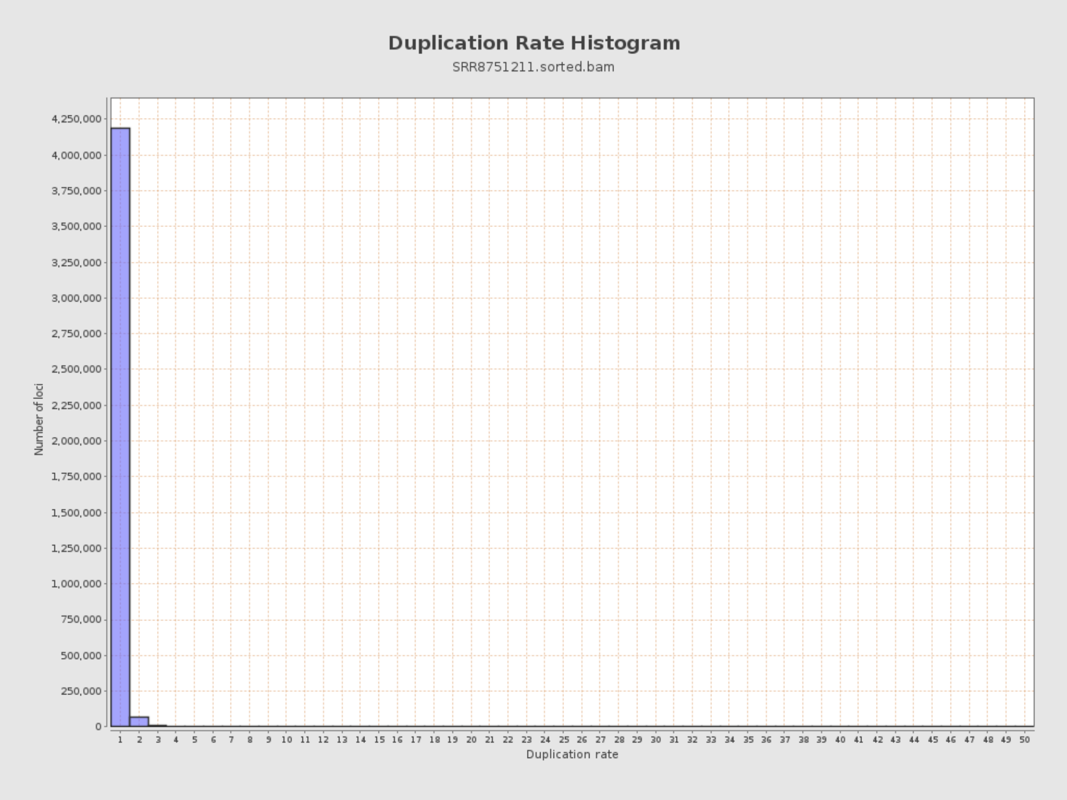
5. Results : Coverage Histogram (0-50X)



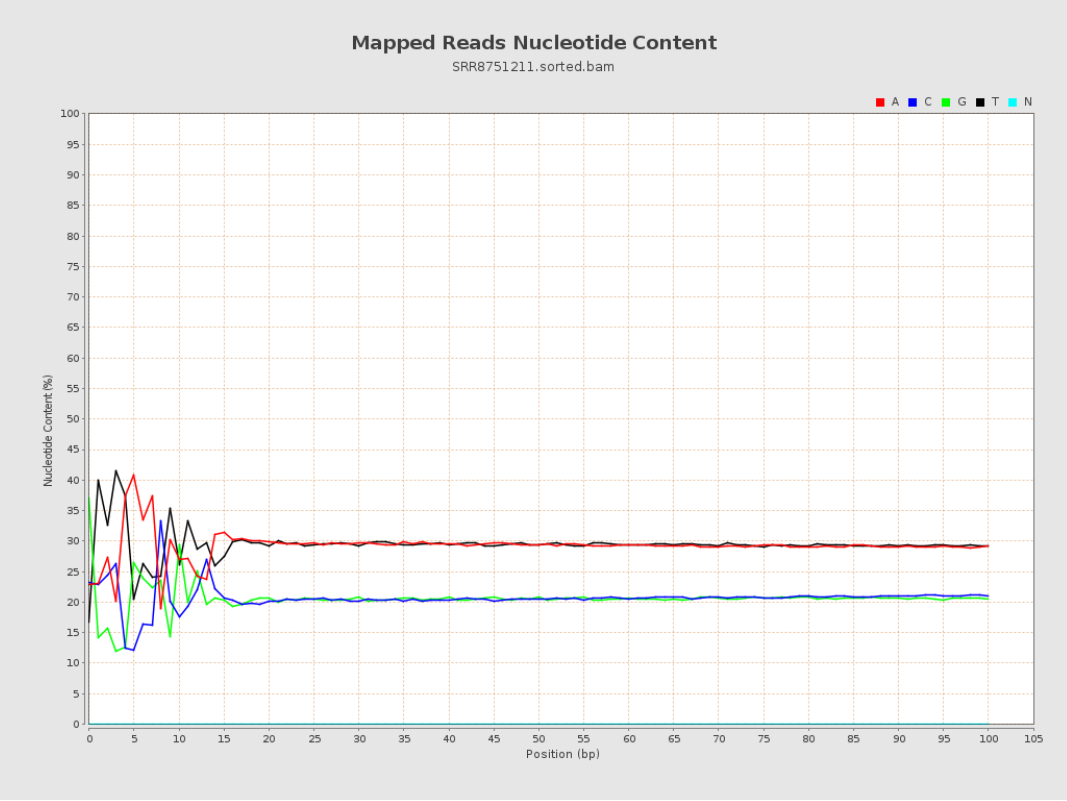
6. Results : Genome Fraction Coverage



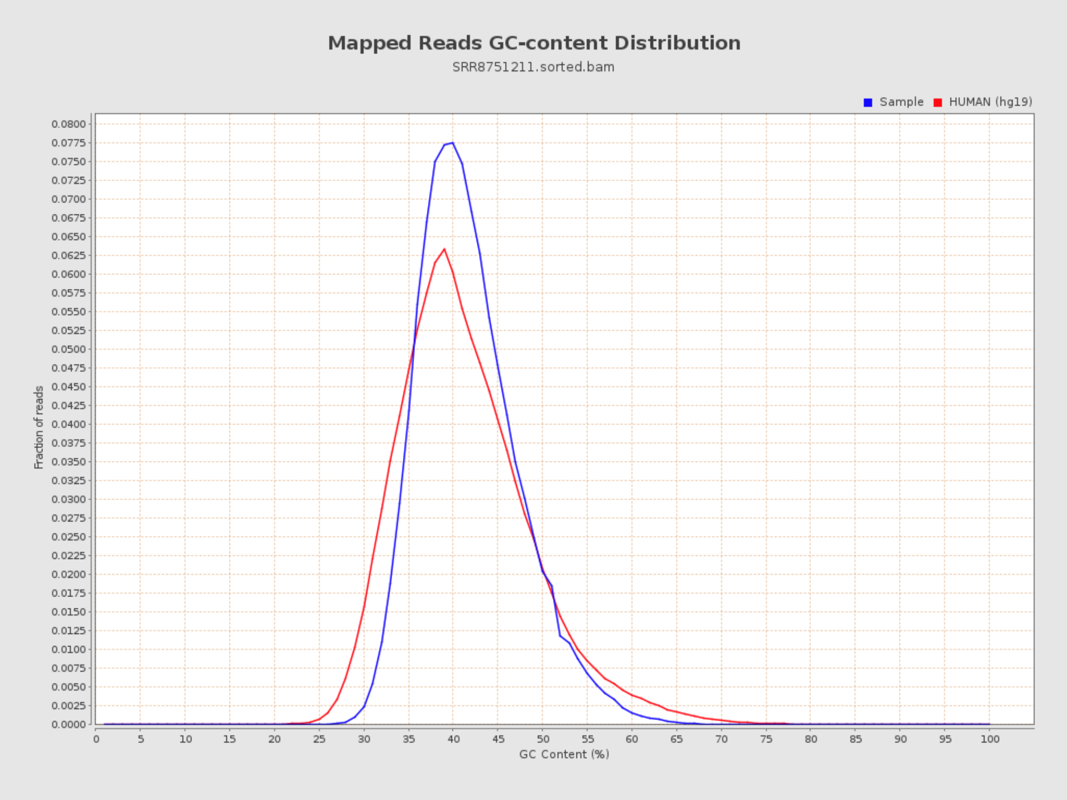
7. Results : Duplication Rate Histogram



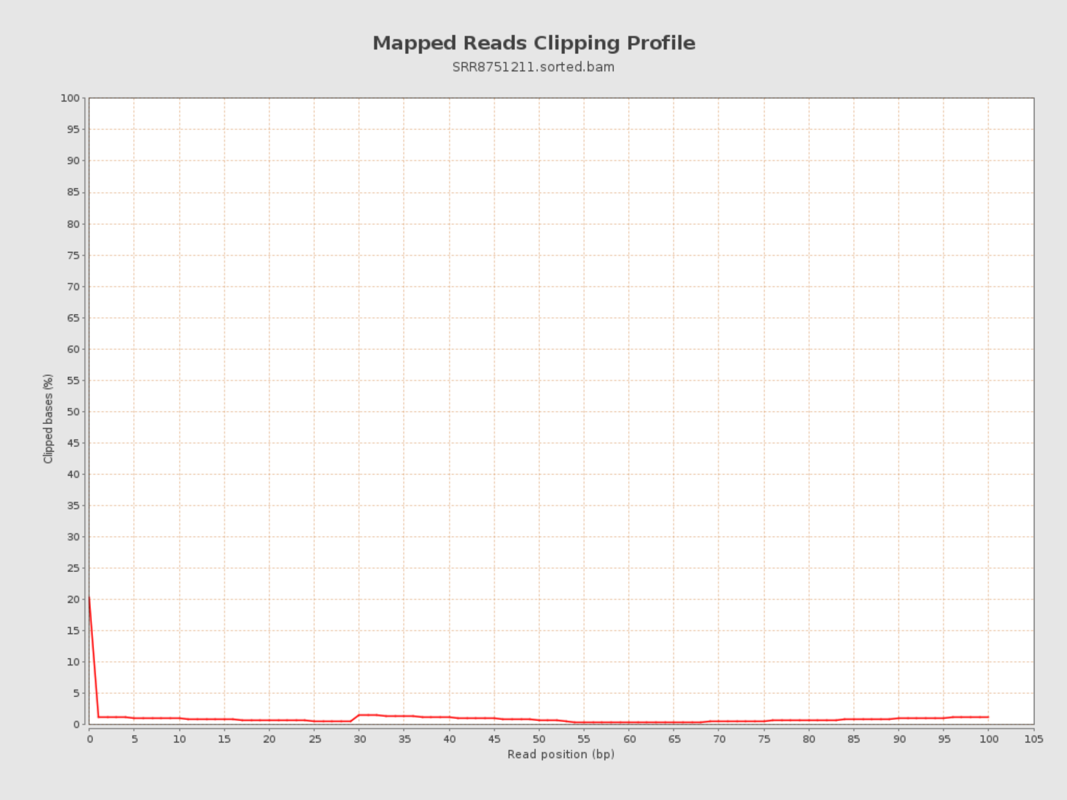
8. Results : Mapped Reads Nucleotide Content



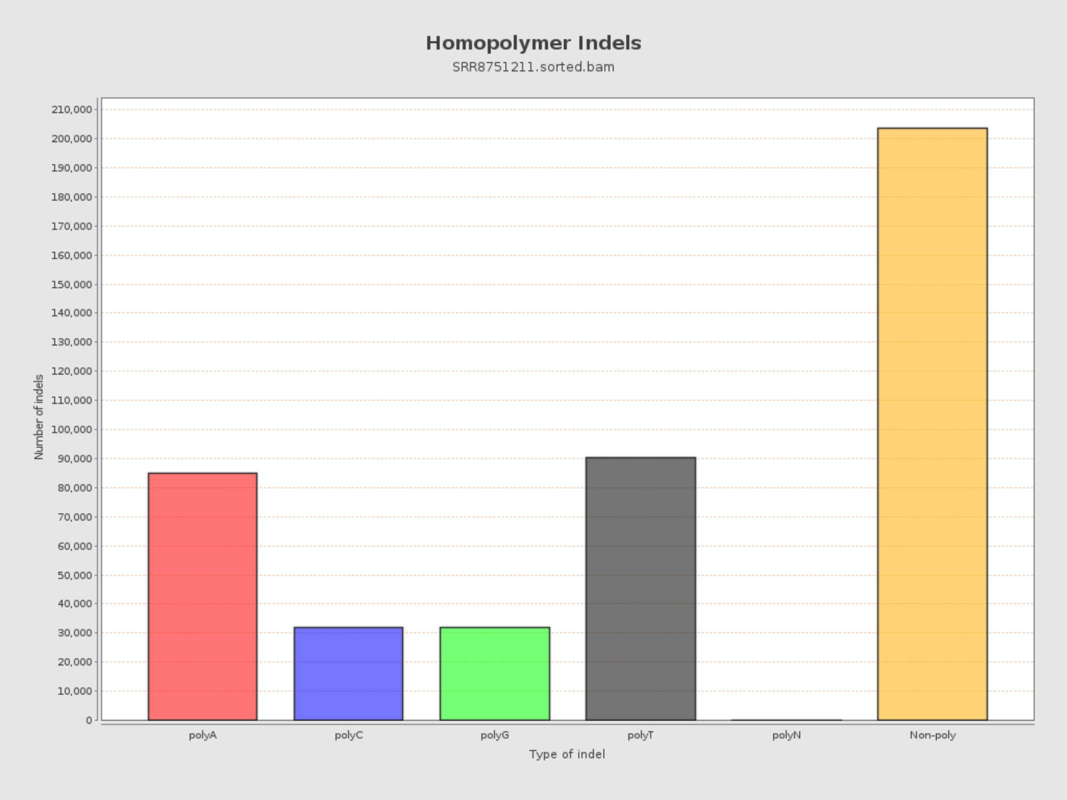
9. Results : Mapped Reads GC-content Distribution



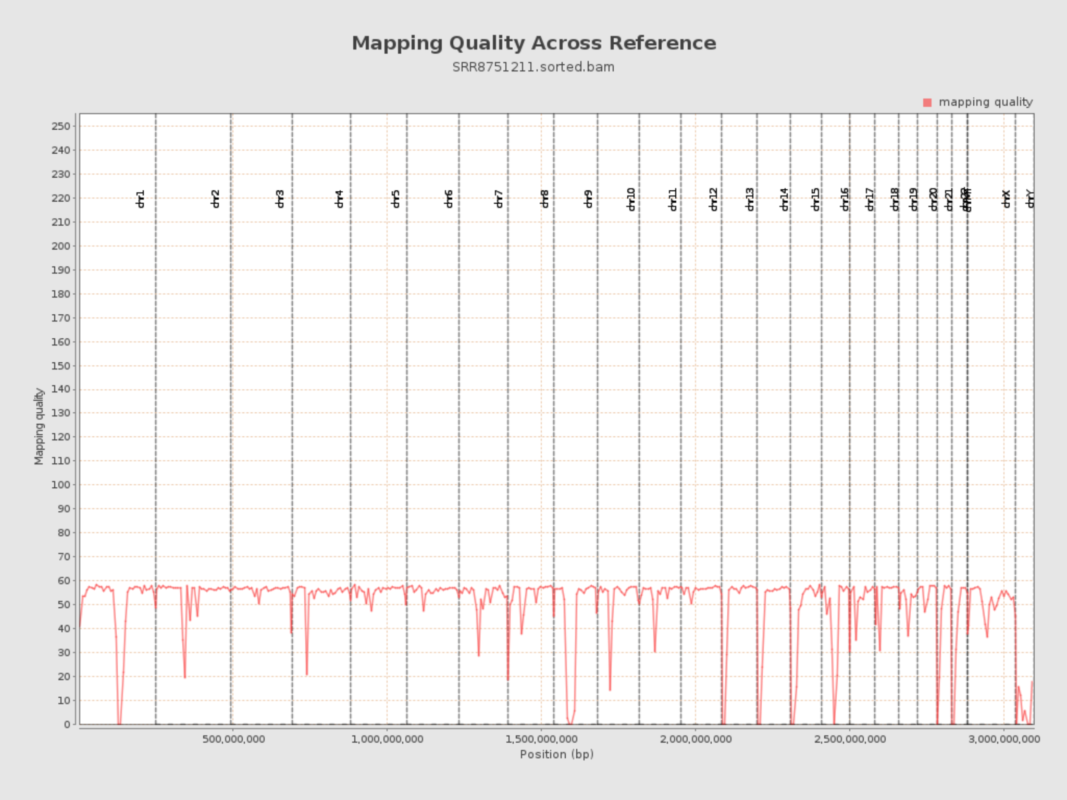
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram