Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:45:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080755.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_SRR3080755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:45:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,442,008
Mapped reads	6,238,976 / 73.9%
Unmapped reads	2,203,032 / 26.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,311 / 0.48%
Read min/max/mean length	30 / 66 / 66.16
Duplicated reads (estimated)	550,513 / 6.52%
Duplication rate	7.16%
Clipped reads	1,205,759 / 14.28%

2.2. ACGT Content

Number/percentage of A's	121,551,960 / 30.95%
Number/percentage of C's	80,267,277 / 20.44%
Number/percentage of T's	99,424,020 / 25.32%
Number/percentage of G's	90,589,424 / 23.07%
Number/percentage of N's	877,570 / 0.22%
GC Percentage	43.51%

2.3. Coverage

Mean	0.1269

Standard Deviation	0.733

2.4. Mapping Quality

Mean Mapping Quality	43.64

2.5. Mismatches and indels

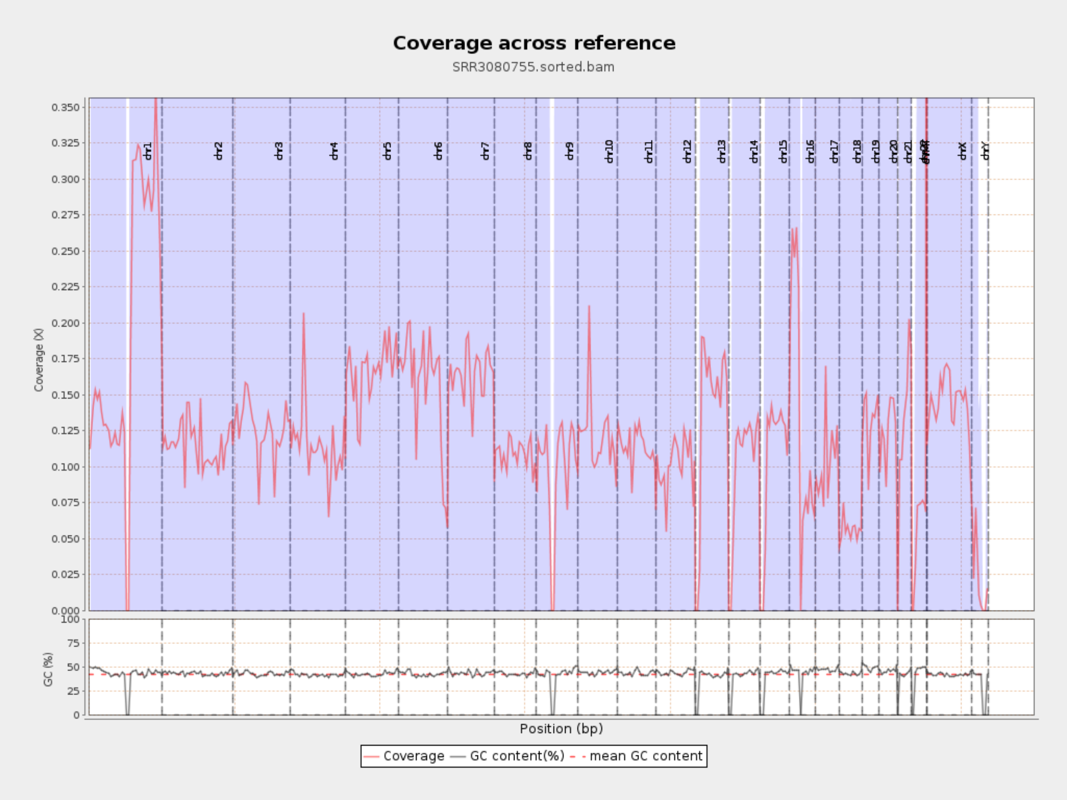
General error rate	1.05%
Mismatches	4,048,697
Insertions	29,396
Mapped reads with at least one insertion	0.47%
Deletions	68,034
Mapped reads with at least one deletion	1.08%
Homopolymer indels	41.76%

2.6. Chromosome stats

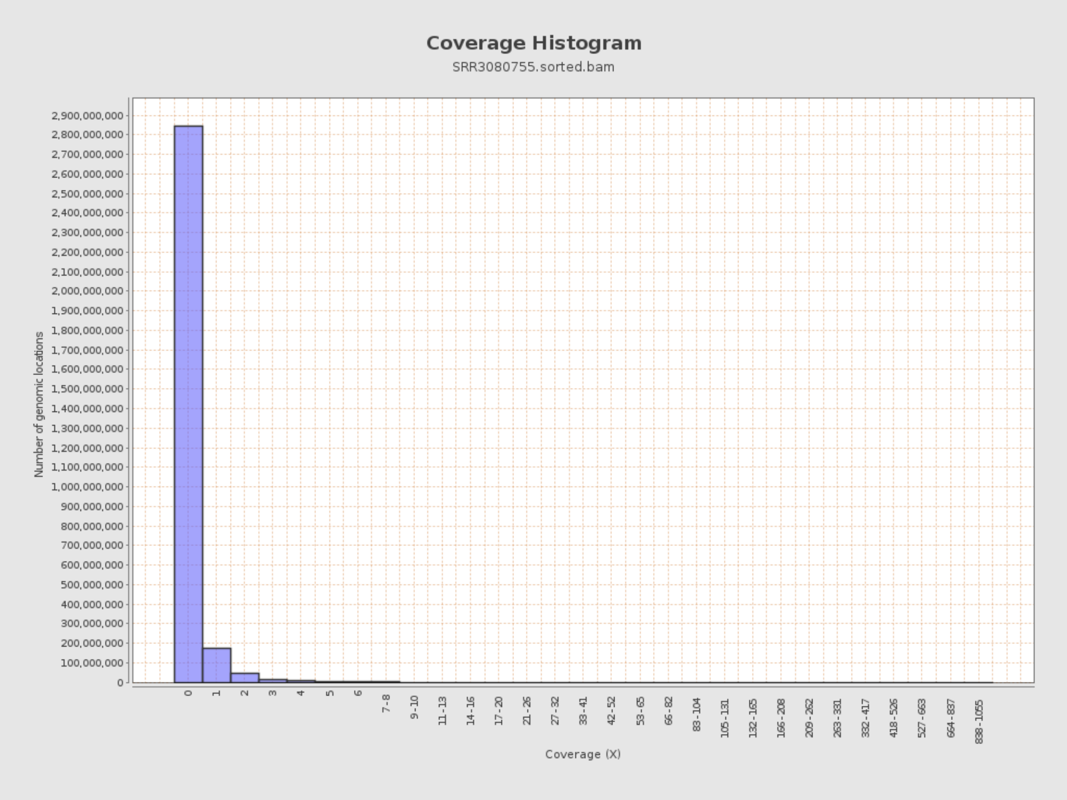
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	48339763	0.1939	0.9969
chr2	243199373	28066936	0.1154	0.744
chr3	198022430	24988934	0.1262	0.5311
chr4	191154276	21842914	0.1143	0.6762
chr5	180915260	30122939	0.1665	0.6109
chr6	171115067	26938124	0.1574	0.8203
chr7	159138663	26278615	0.1651	1.1799

chr8	146364022	16005945	0.1094	0.8479
chr9	141213431	13742561	0.0973	0.5466
chr10	135534747	16452699	0.1214	0.9511
chr11	135006516	15437107	0.1143	0.6267
chr12	133851895	13605990	0.1016	0.5044
chr13	115169878	15904264	0.1381	0.5567
chr14	107349540	10855991	0.1011	0.5556
chr15	102531392	10844622	0.1058	0.4907
chr16	90354753	12234942	0.1354	0.6581
chr17	81195210	8481045	0.1045	0.4922
chr18	78077248	4397669	0.0563	0.7574
chr19	59128983	7789348	0.1317	0.8815
chr20	63025520	7726752	0.1226	0.5554
chr21	48129895	6298163	0.1309	0.6884
chr22	51304566	2671270	0.0521	0.3299
chrMT	16571	33995	2.0515	2.5332
chrX	155270560	22522390	0.1451	0.6115
chrY	59373566	1256177	0.0212	0.6335

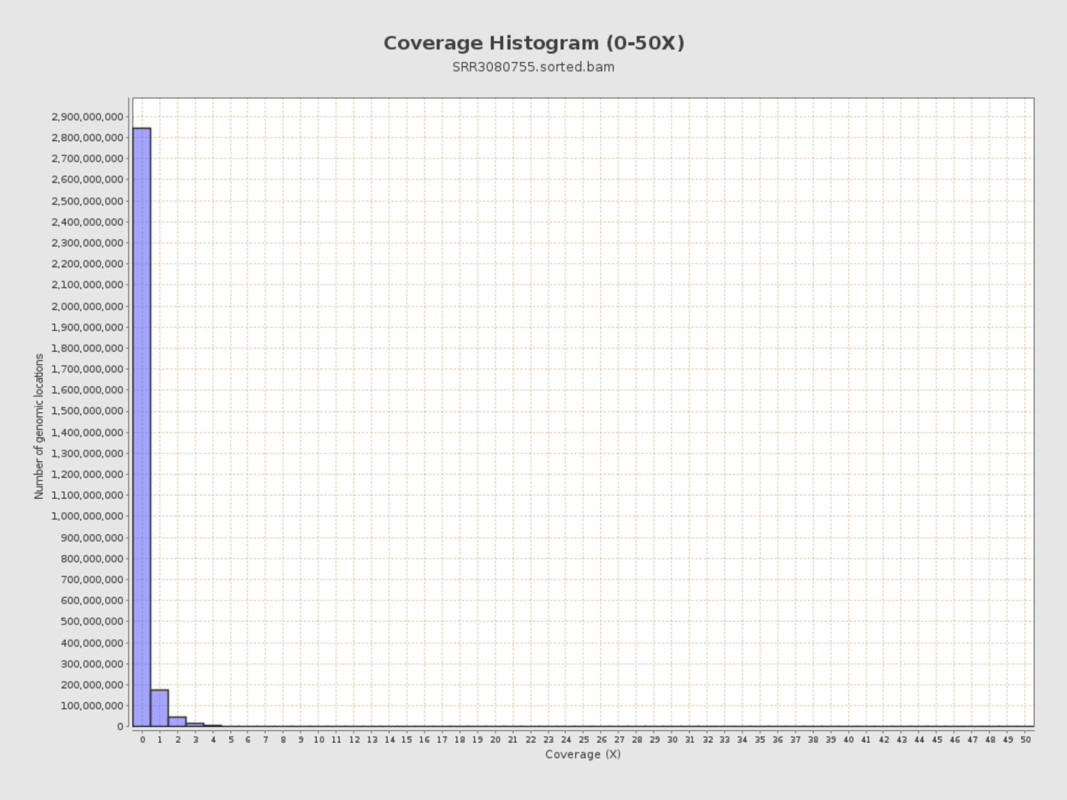
3. Results : Coverage across reference



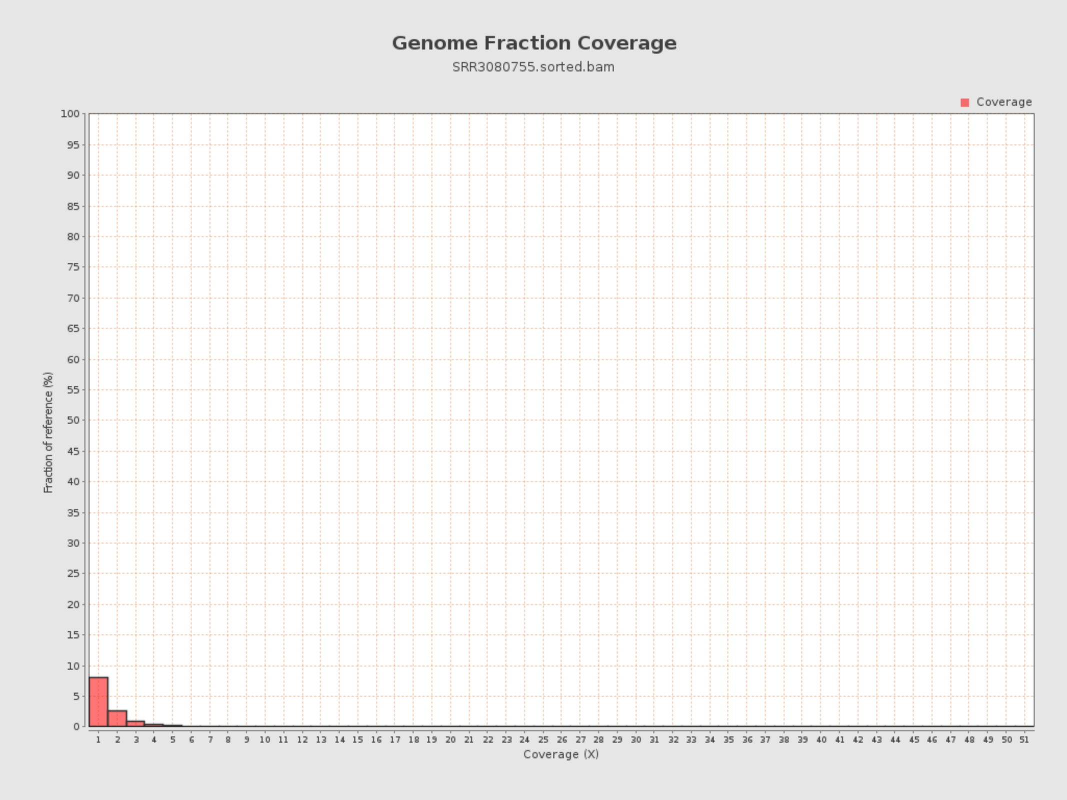
4. Results : Coverage Histogram



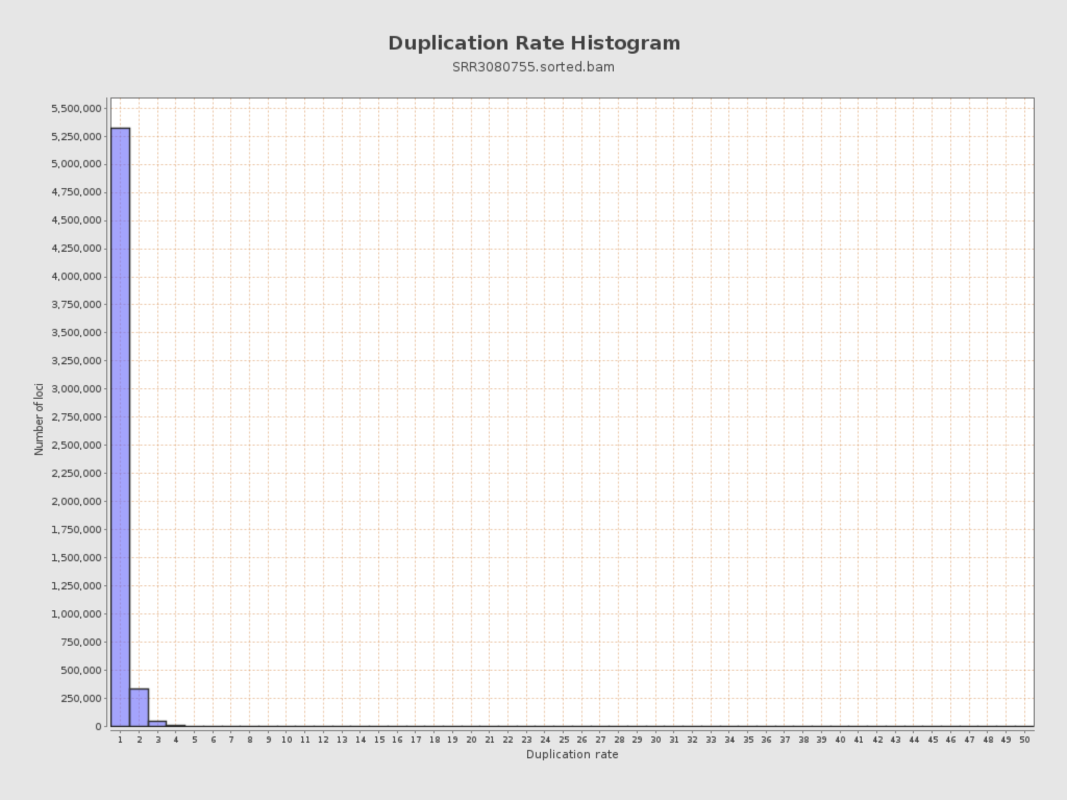
5. Results : Coverage Histogram (0-50X)



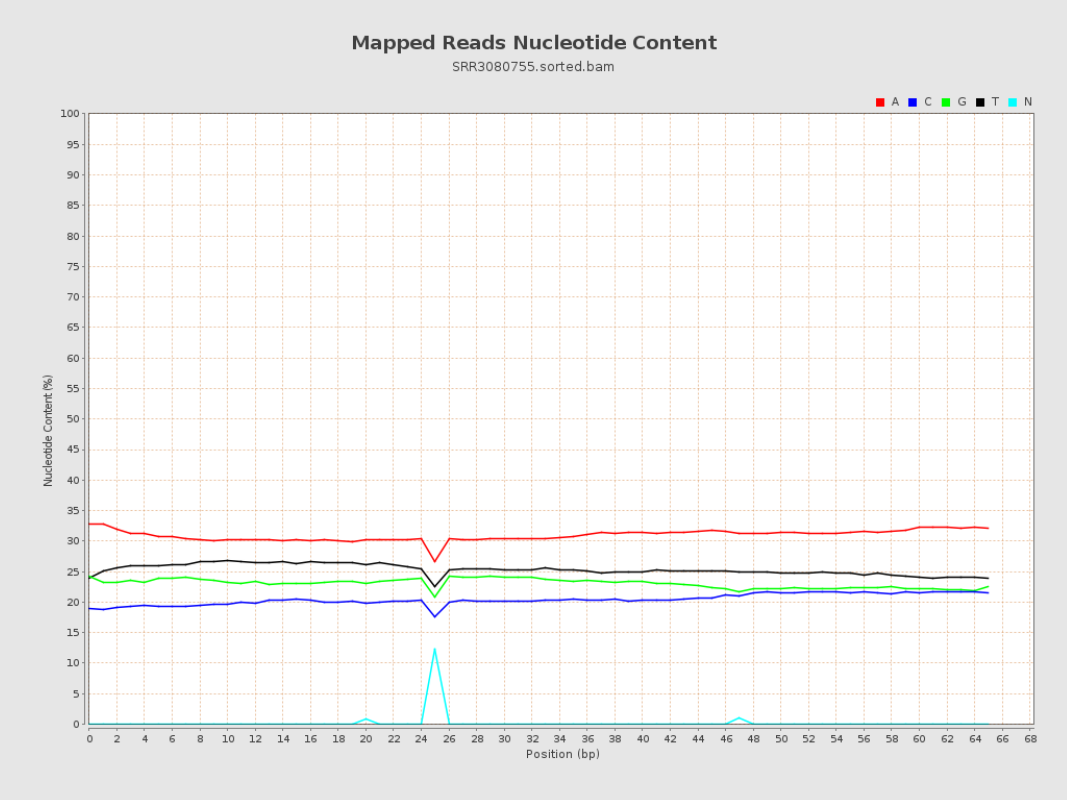
6. Results : Genome Fraction Coverage



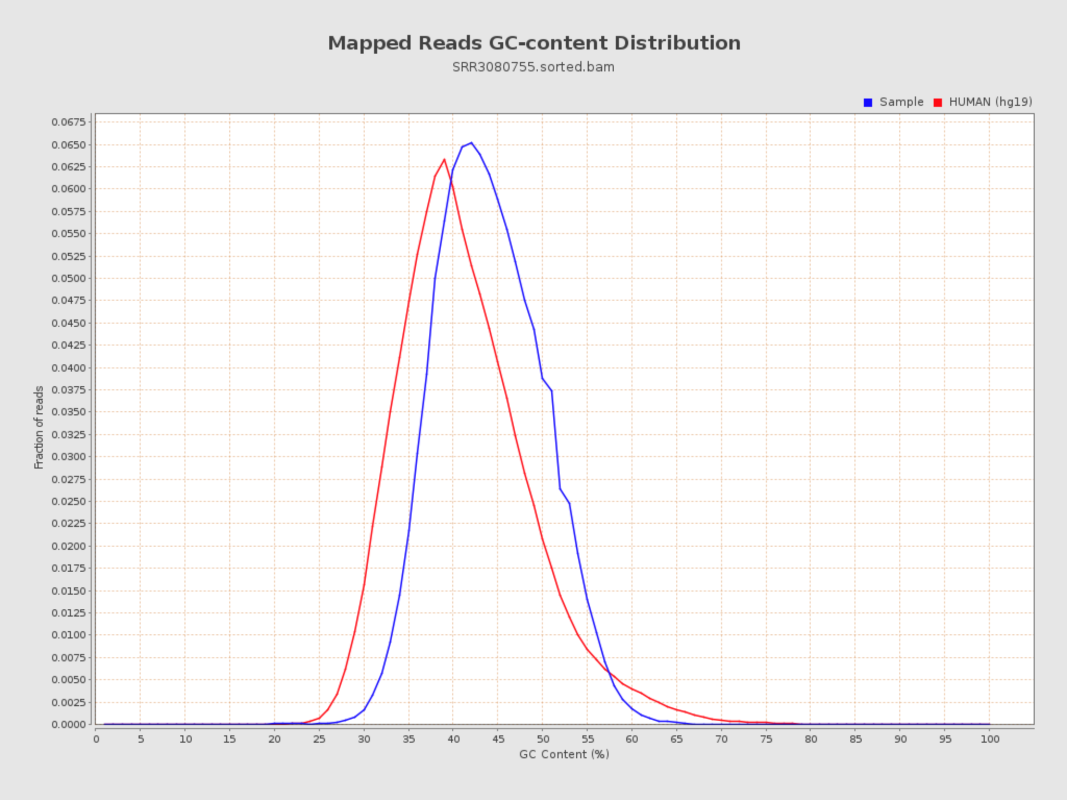
7. Results : Duplication Rate Histogram



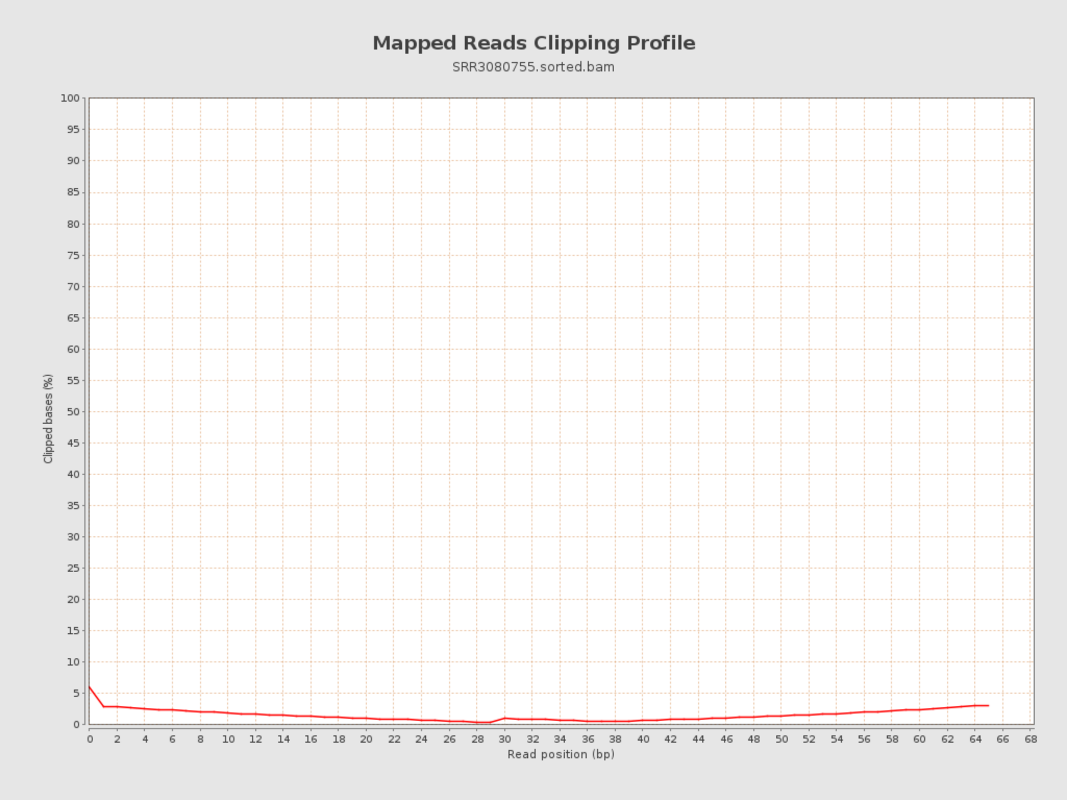
8. Results : Mapped Reads Nucleotide Content



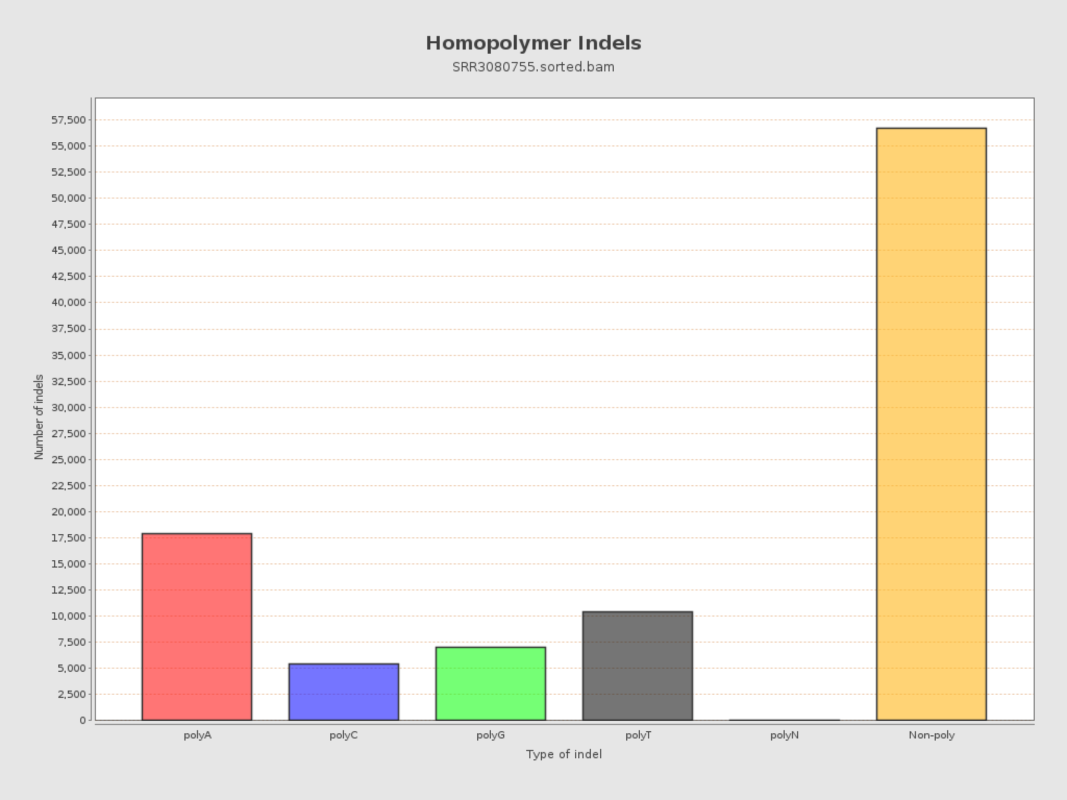
9. Results : Mapped Reads GC-content Distribution



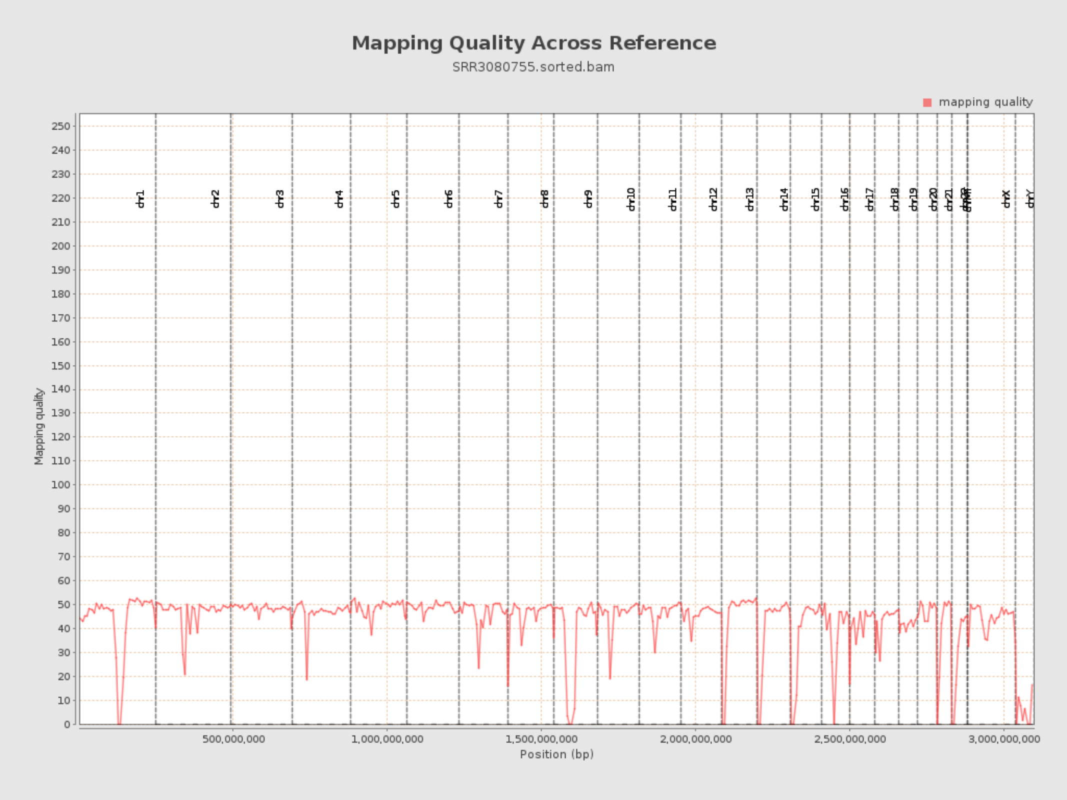
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram