Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:31:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751230.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_SRR8751230 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751230.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:31:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751230.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,247,109
Mapped reads	3,754,873 / 71.56%
Unmapped reads	1,492,236 / 28.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	211,799 / 4.04%
Read min/max/mean length	30 / 101 / 102.66
Duplicated reads (estimated)	122,912 / 2.34%
Duplication rate	1.85%
Clipped reads	936,021 / 17.84%

2.2. ACGT Content

Number/percentage of A's	107,861,381 / 29.32%
Number/percentage of C's	75,964,482 / 20.65%
Number/percentage of T's	108,777,660 / 29.57%
Number/percentage of G's	75,247,880 / 20.46%
Number/percentage of N's	2,514 / 0%
GC Percentage	41.11%

2.3. Coverage

Mean	0.1189

Standard Deviation	1.0743

2.4. Mapping Quality

Mean Mapping Quality	51.12

2.5. Mismatches and indels

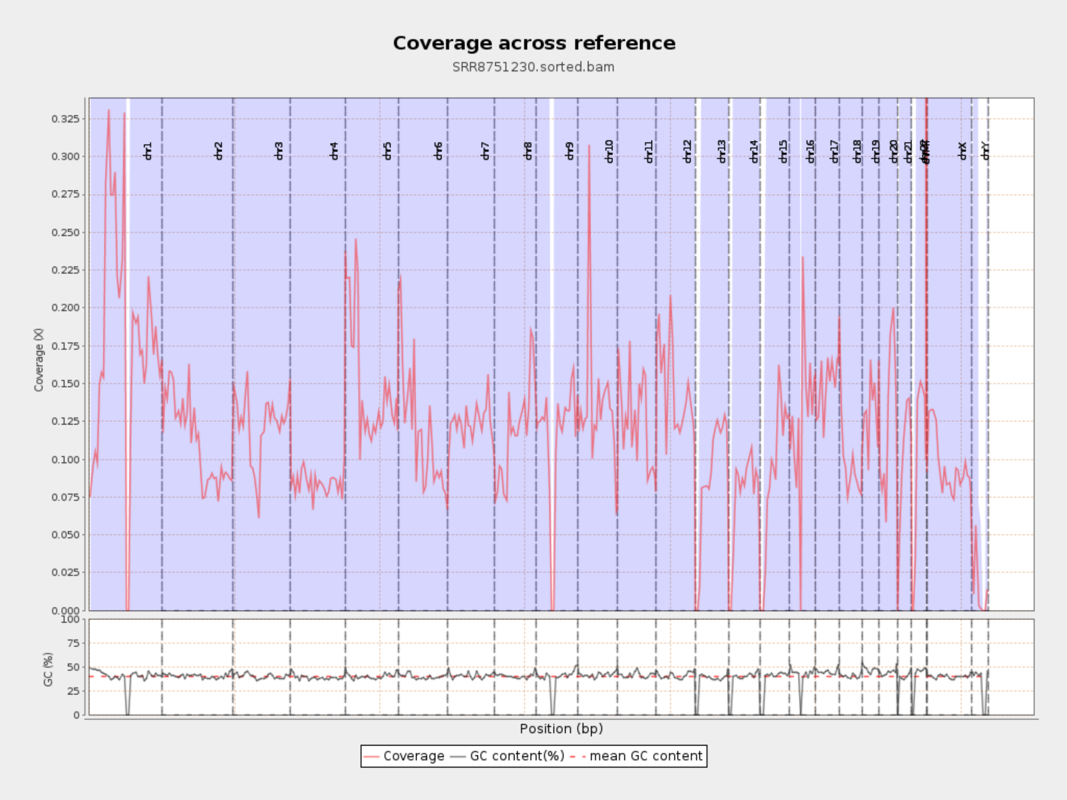
General error rate	0.49%
Mismatches	1,338,850
Insertions	338,002
Mapped reads with at least one insertion	8.55%
Deletions	55,789
Mapped reads with at least one deletion	1.46%
Homopolymer indels	54.52%

2.6. Chromosome stats

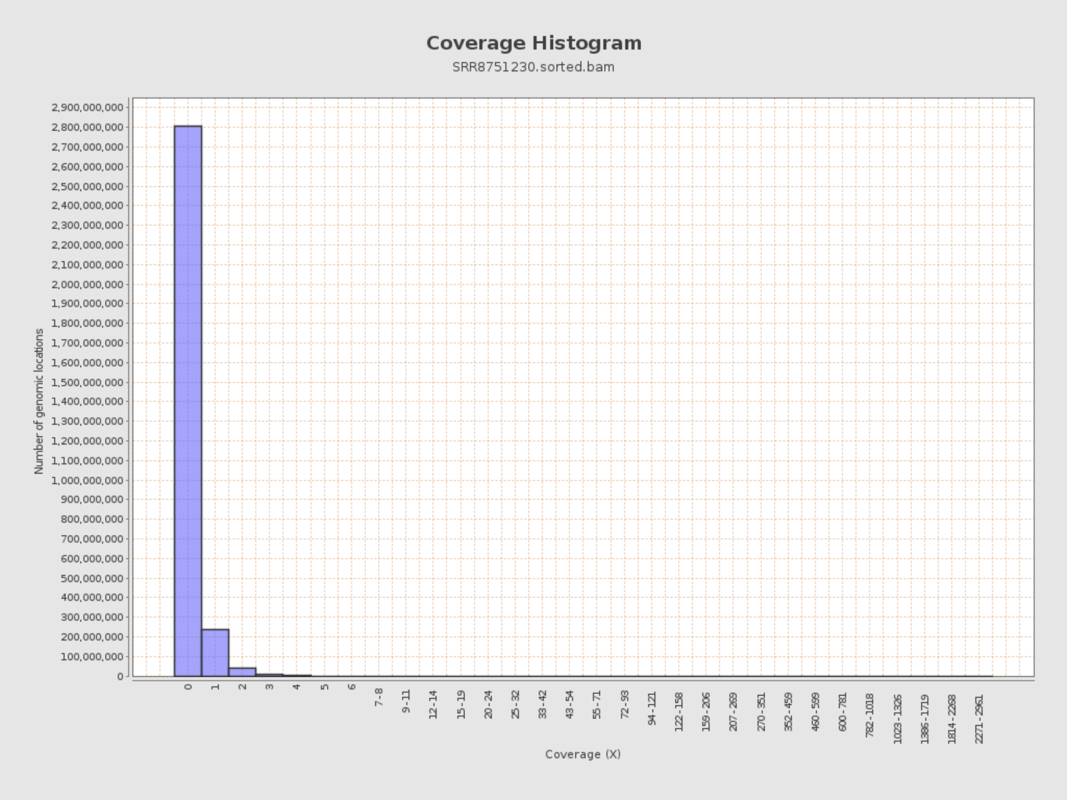
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	44630190	0.1791	2.8297
chr2	243199373	27252262	0.1121	0.5473
chr3	198022430	24027991	0.1213	0.4956
chr4	191154276	16057291	0.084	0.4059
chr5	180915260	26910067	0.1487	0.5006
chr6	171115067	20358717	0.119	0.7457
chr7	159138663	19843503	0.1247	0.7108

chr8	146364022	17424091	0.119	0.4988
chr9	141213431	15996090	0.1133	0.5895
chr10	135534747	18527651	0.1367	1.8118
chr11	135006516	16899066	0.1252	0.6098
chr12	133851895	19772329	0.1477	0.4755
chr13	115169878	10096985	0.0877	0.3575
chr14	107349540	8002797	0.0745	0.342
chr15	102531392	9231234	0.09	0.362
chr16	90354753	11359522	0.1257	0.8947
chr17	81195210	12040045	0.1483	0.6487
chr18	78077248	7643849	0.0979	1.1049
chr19	59128983	7761320	0.1313	1.9764
chr20	63025520	7979478	0.1266	0.4585
chr21	48129895	4701430	0.0977	0.4067
chr22	51304566	4948461	0.0965	0.4096
chrMT	16571	769117	46.4134	17.8489
chrX	155270560	14938503	0.0962	0.4202
chrY	59373566	802981	0.0135	0.5459

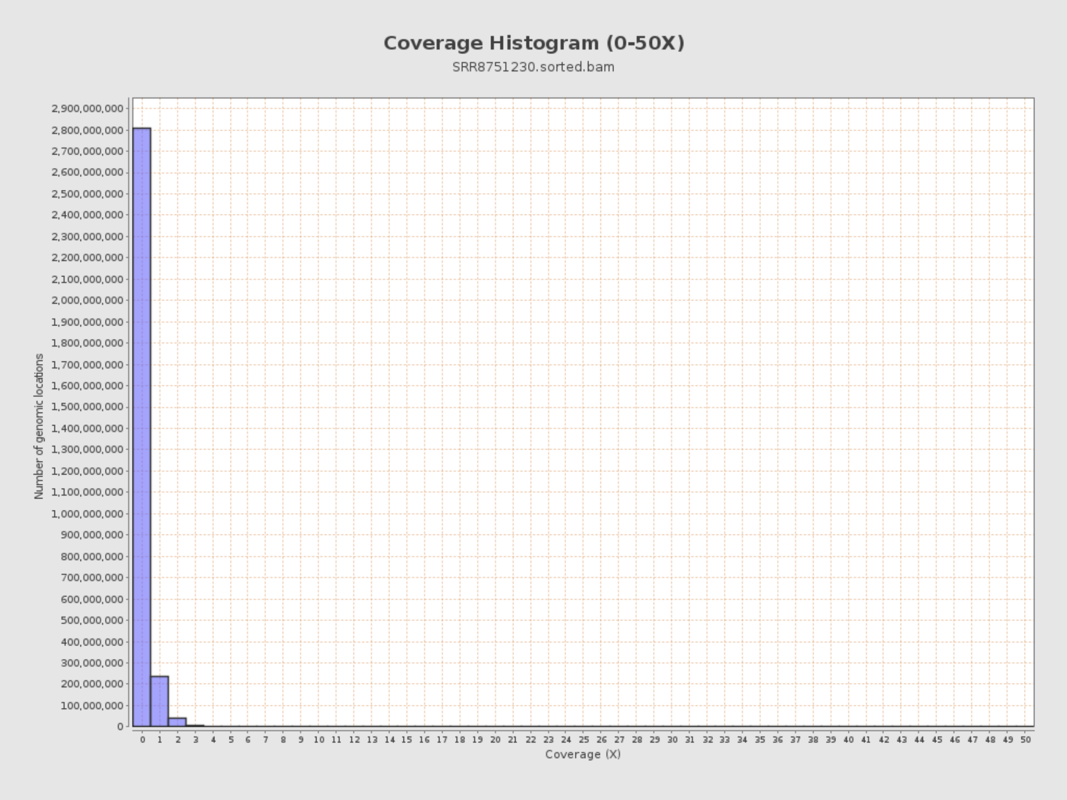
3. Results : Coverage across reference



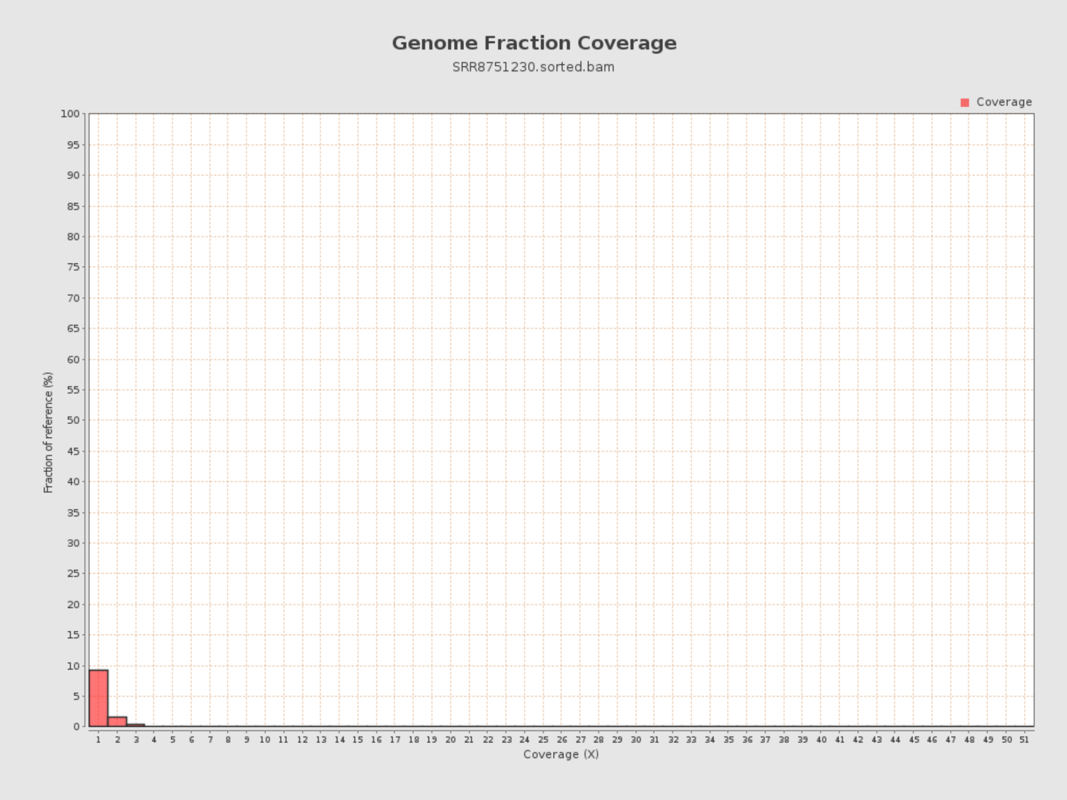
4. Results : Coverage Histogram



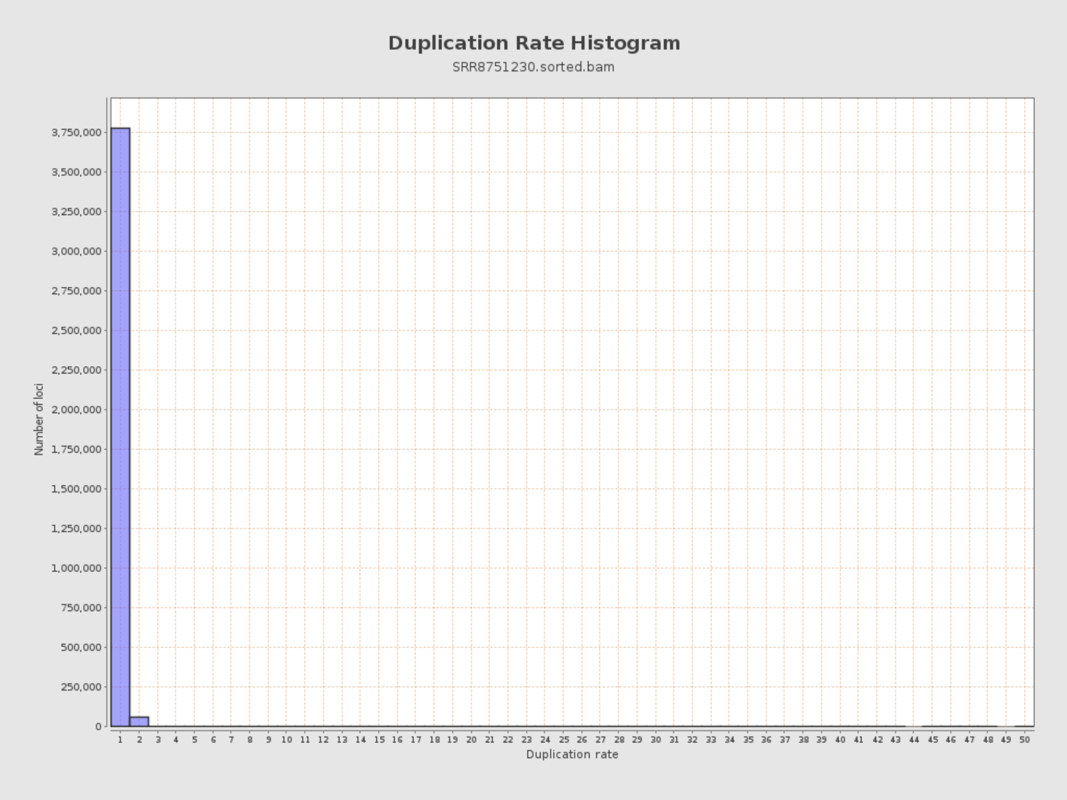
5. Results : Coverage Histogram (0-50X)



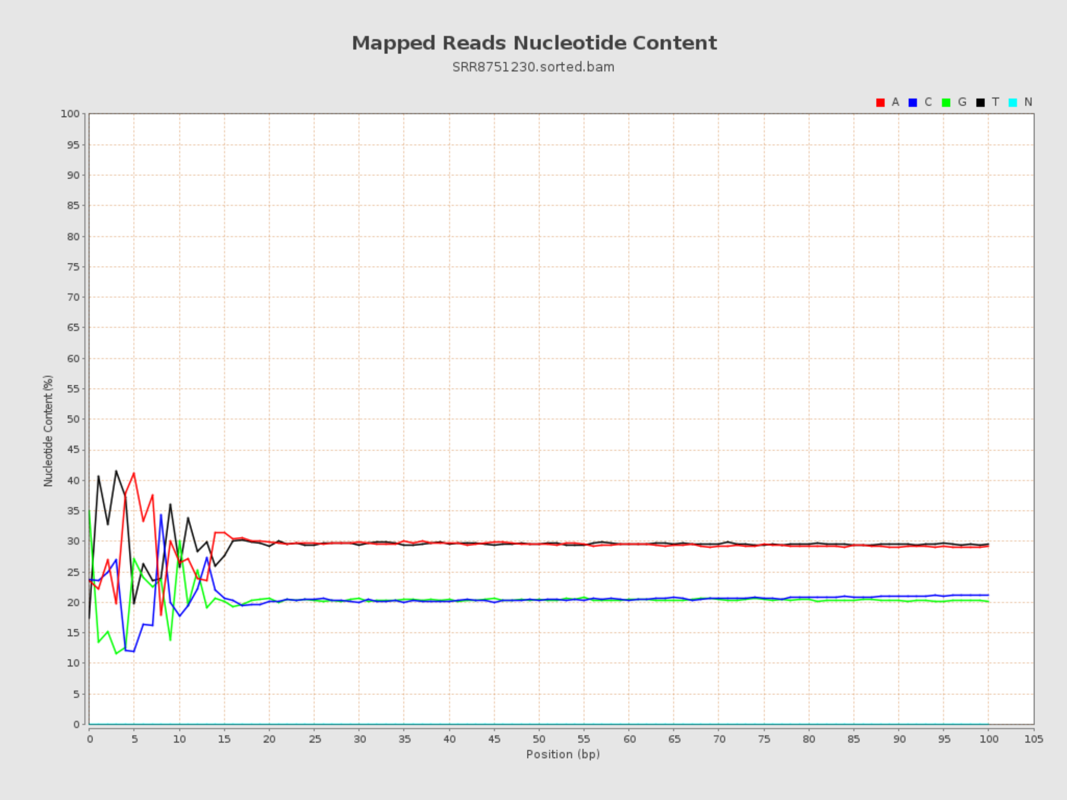
6. Results : Genome Fraction Coverage



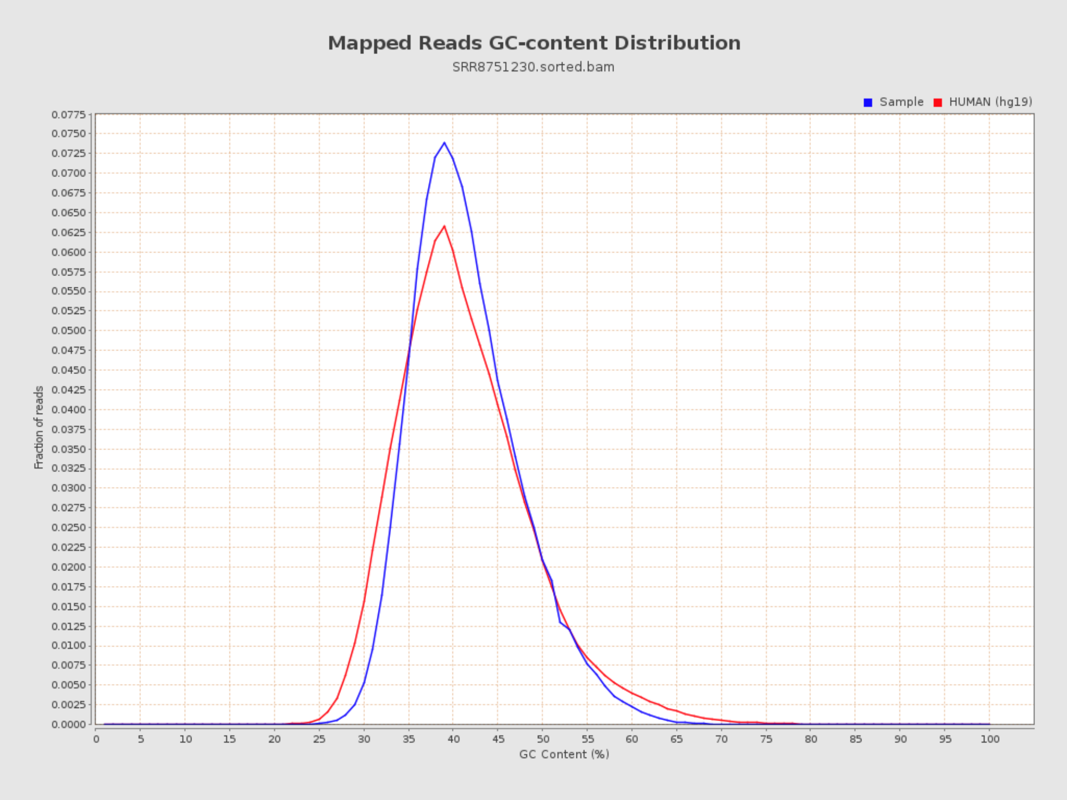
7. Results : Duplication Rate Histogram



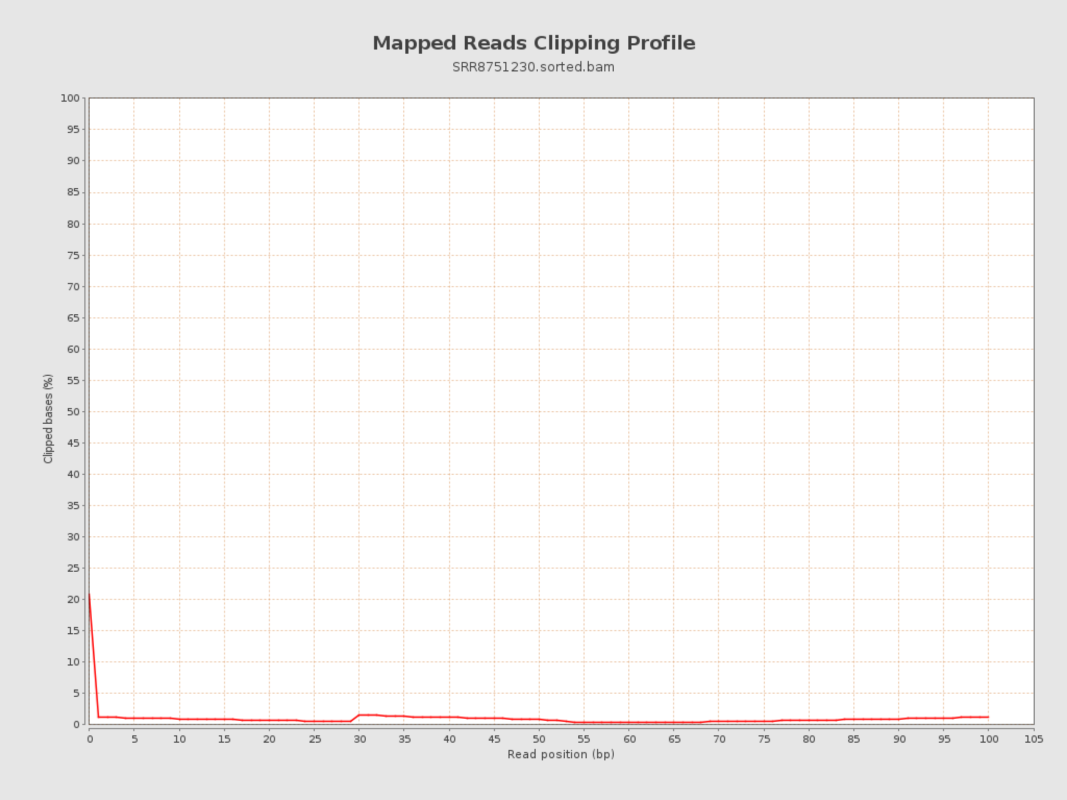
8. Results : Mapped Reads Nucleotide Content



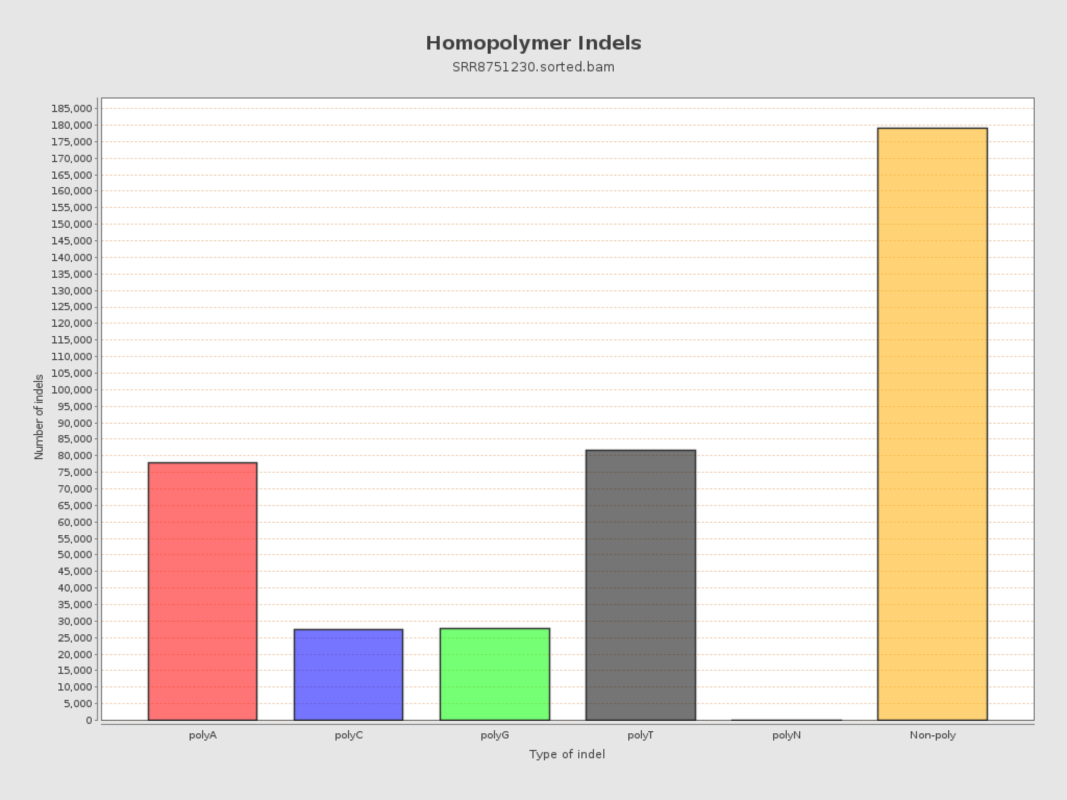
9. Results : Mapped Reads GC-content Distribution



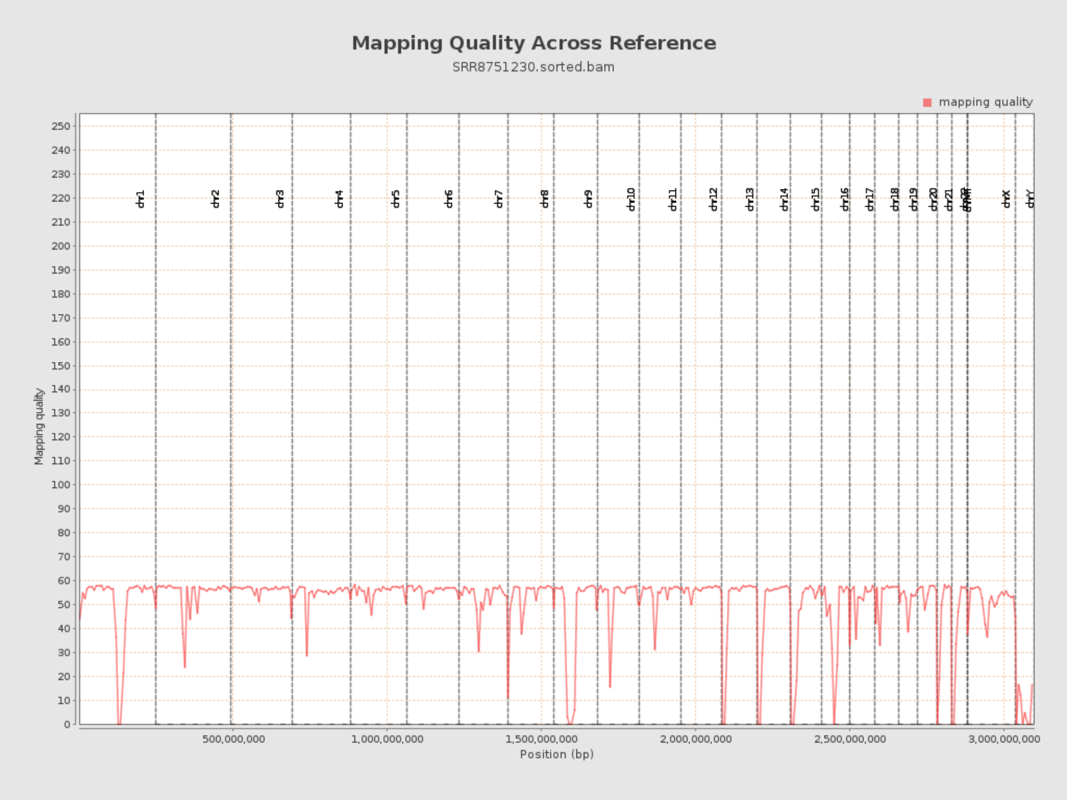
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram