Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:44:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751219.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_SRR8751219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:44:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,983,503
Mapped reads	2,932,673 / 58.85%
Unmapped reads	2,050,830 / 41.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	165,187 / 3.31%
Read min/max/mean length	30 / 101 / 102.37
Duplicated reads (estimated)	108,556 / 2.18%
Duplication rate	1.81%
Clipped reads	696,159 / 13.97%

2.2. ACGT Content

Number/percentage of A's	85,101,209 / 29.53%
Number/percentage of C's	58,960,296 / 20.46%
Number/percentage of T's	85,668,422 / 29.72%
Number/percentage of G's	58,489,339 / 20.29%
Number/percentage of N's	2,105 / 0%
GC Percentage	40.75%

2.3. Coverage

Mean	0.0931

Standard Deviation	1.1307

2.4. Mapping Quality

Mean Mapping Quality	50.97

2.5. Mismatches and indels

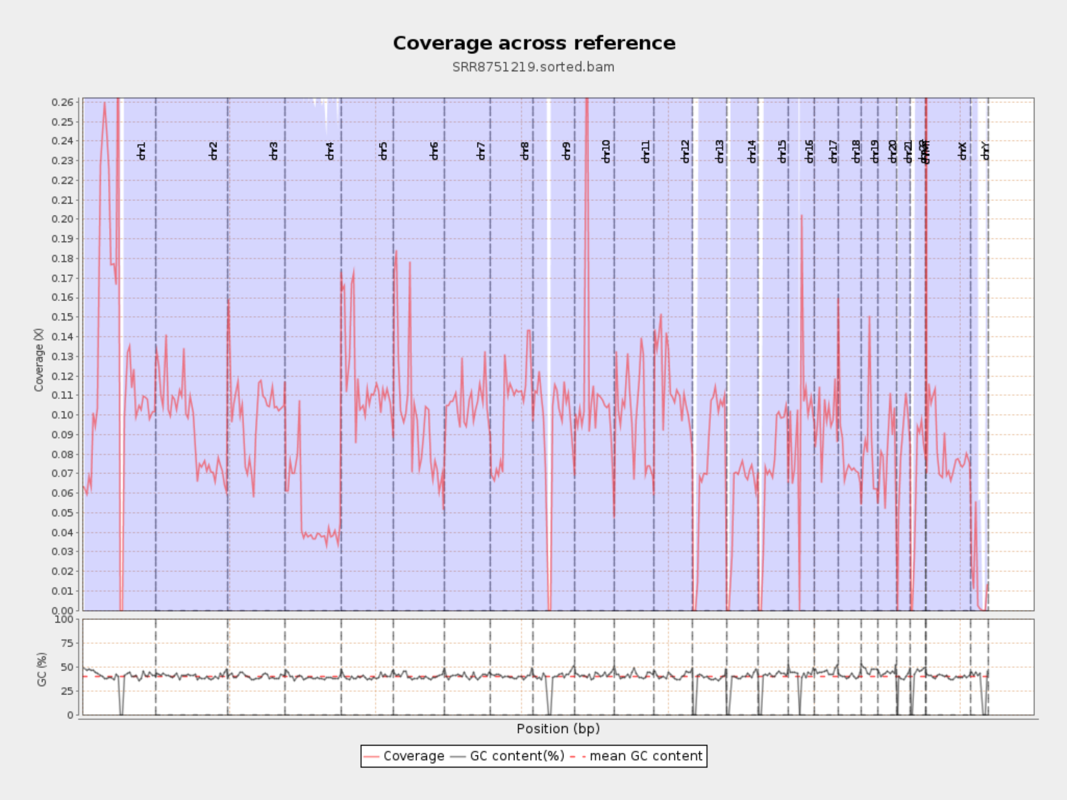
General error rate	0.51%
Mismatches	1,162,398
Insertions	230,223
Mapped reads with at least one insertion	7.49%
Deletions	44,273
Mapped reads with at least one deletion	1.48%
Homopolymer indels	53.52%

2.6. Chromosome stats

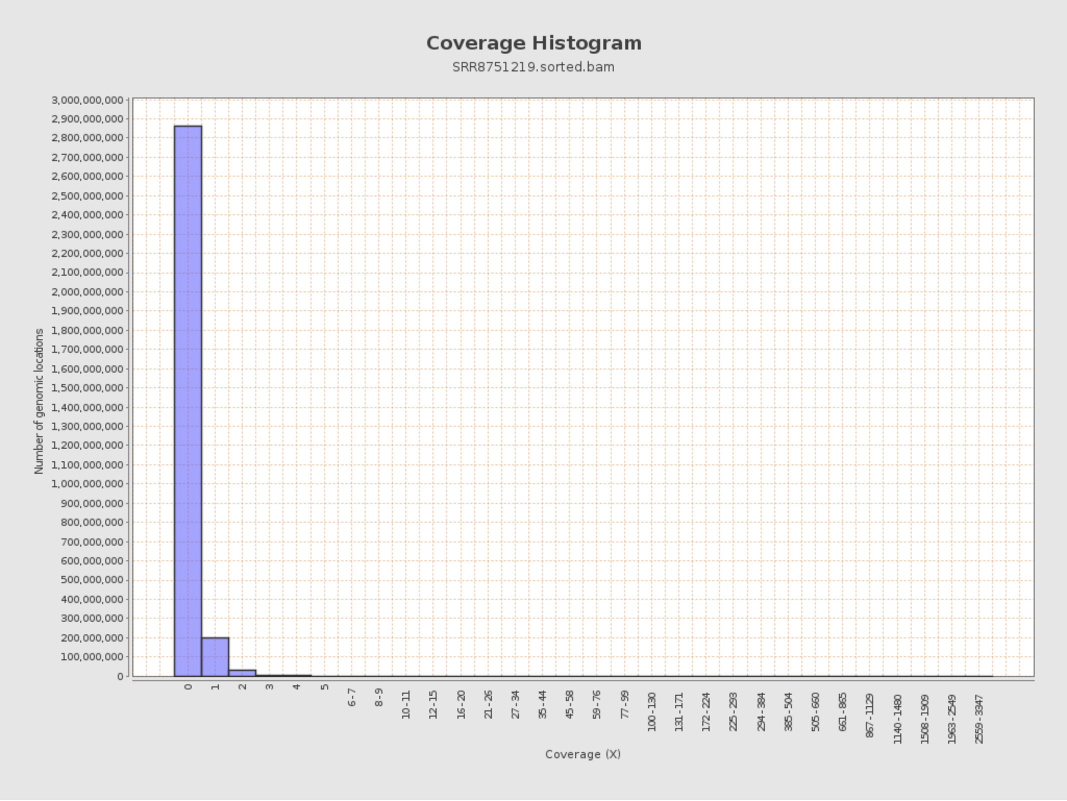
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	32174219	0.1291	3.093
chr2	243199373	22666883	0.0932	0.5166
chr3	198022430	20187046	0.1019	0.4605
chr4	191154276	9303629	0.0487	0.3759
chr5	180915260	21418526	0.1184	0.4575
chr6	171115067	16917866	0.0989	0.8052
chr7	159138663	16789724	0.1055	0.7455

chr8	146364022	15114485	0.1033	0.4801
chr9	141213431	13101280	0.0928	0.5693
chr10	135534747	15388186	0.1135	1.9606
chr11	135006516	13472844	0.0998	0.6265
chr12	133851895	15569666	0.1163	0.4212
chr13	115169878	8894461	0.0772	0.3195
chr14	107349540	6253687	0.0583	0.2971
chr15	102531392	7189723	0.0701	0.3067
chr16	90354753	8657977	0.0958	0.8497
chr17	81195210	7901098	0.0973	0.5363
chr18	78077248	6164699	0.079	1.0304
chr19	59128983	4986556	0.0843	2.0125
chr20	63025520	5186512	0.0823	0.3484
chr21	48129895	3807014	0.0791	0.3794
chr22	51304566	3204677	0.0625	0.289
chrMT	16571	528784	31.9102	18.0814
chrX	155270560	12669513	0.0816	0.3897
chrY	59373566	769020	0.013	0.528

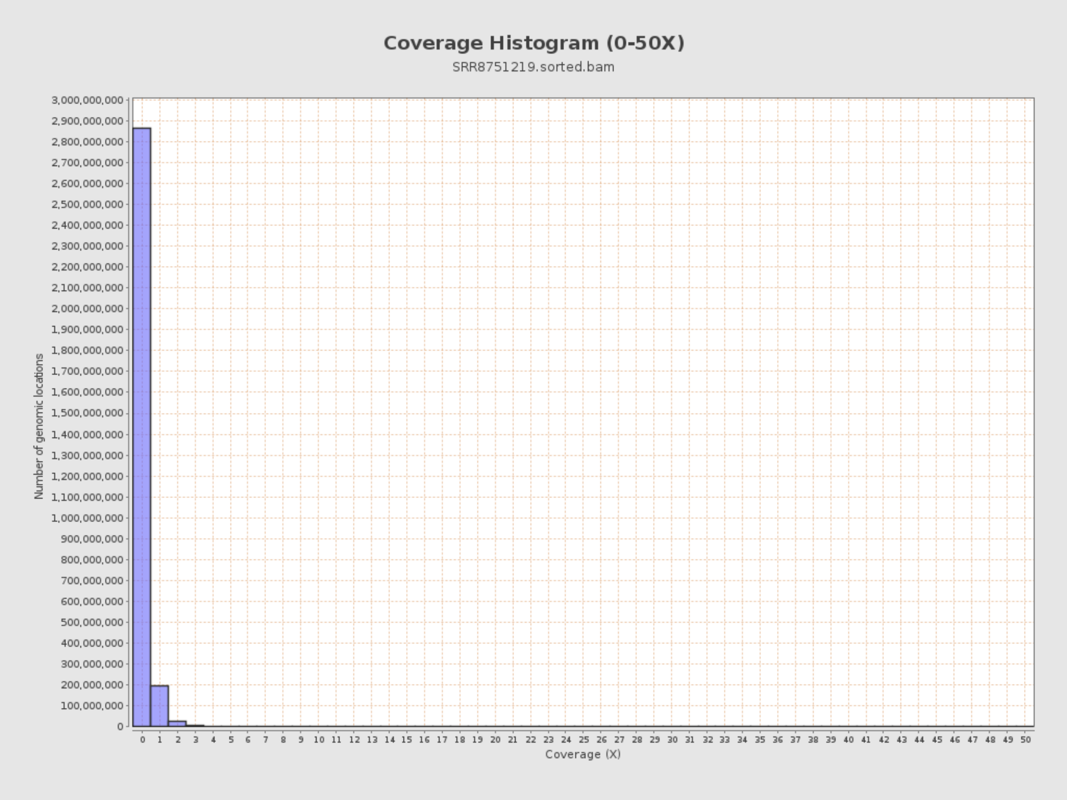
3. Results : Coverage across reference



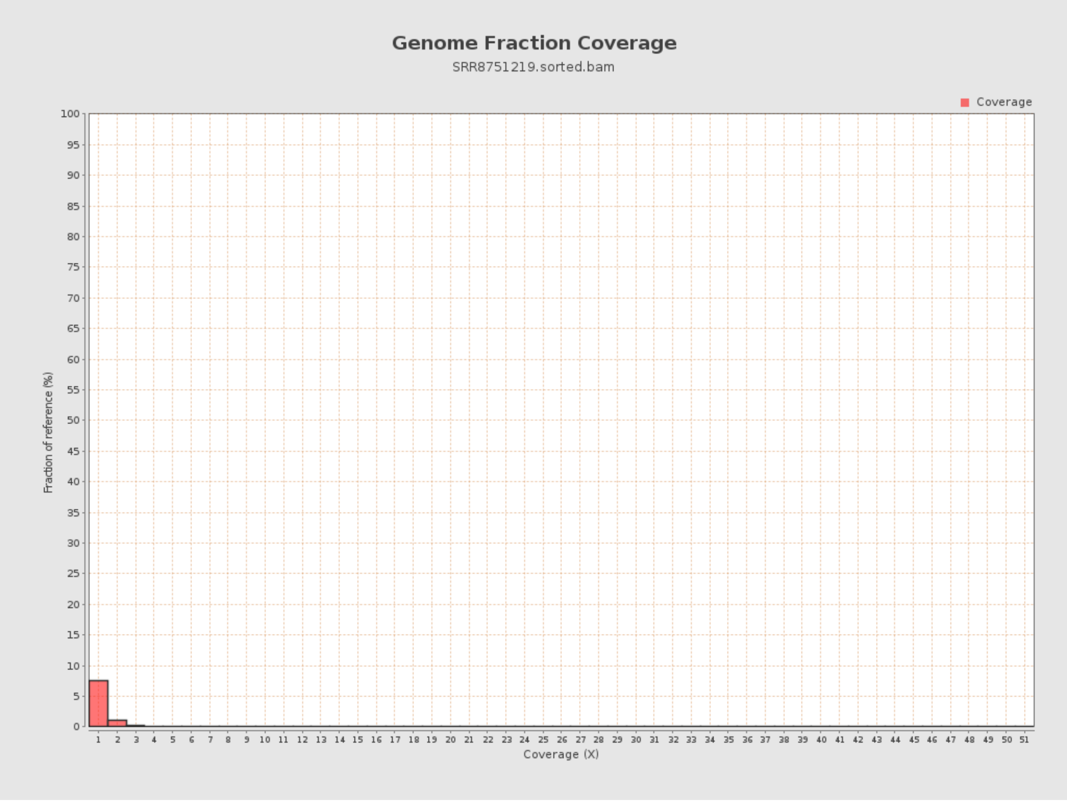
4. Results : Coverage Histogram



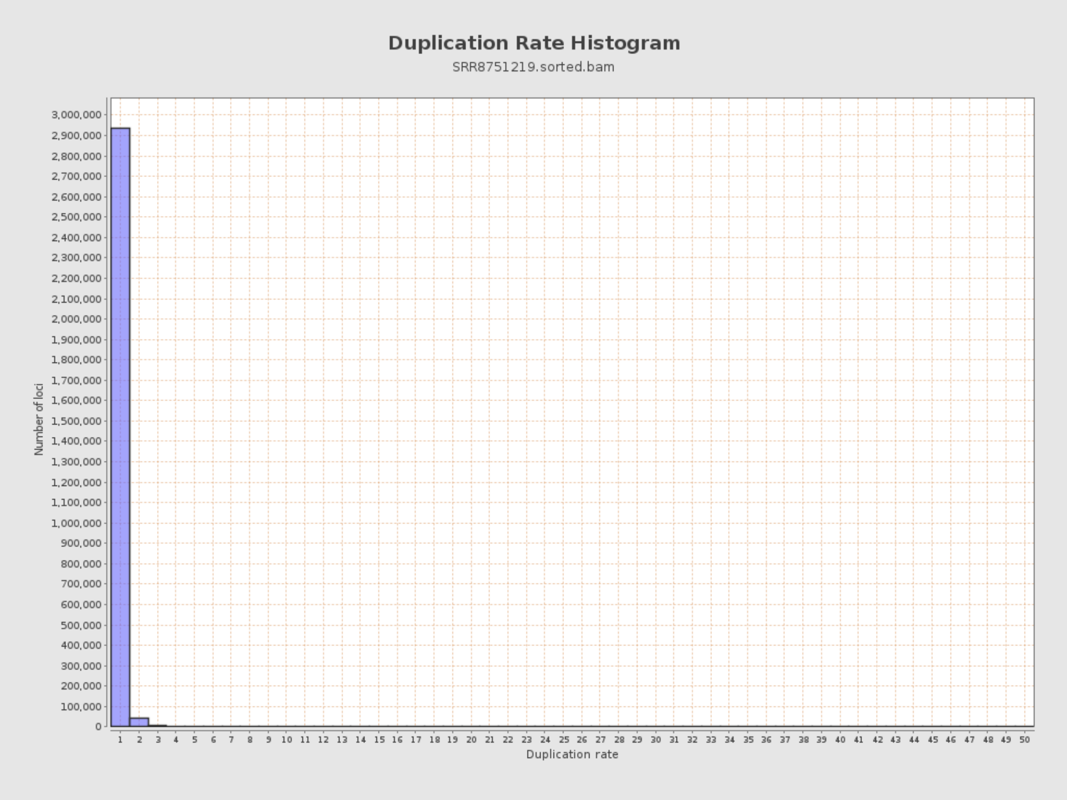
5. Results : Coverage Histogram (0-50X)



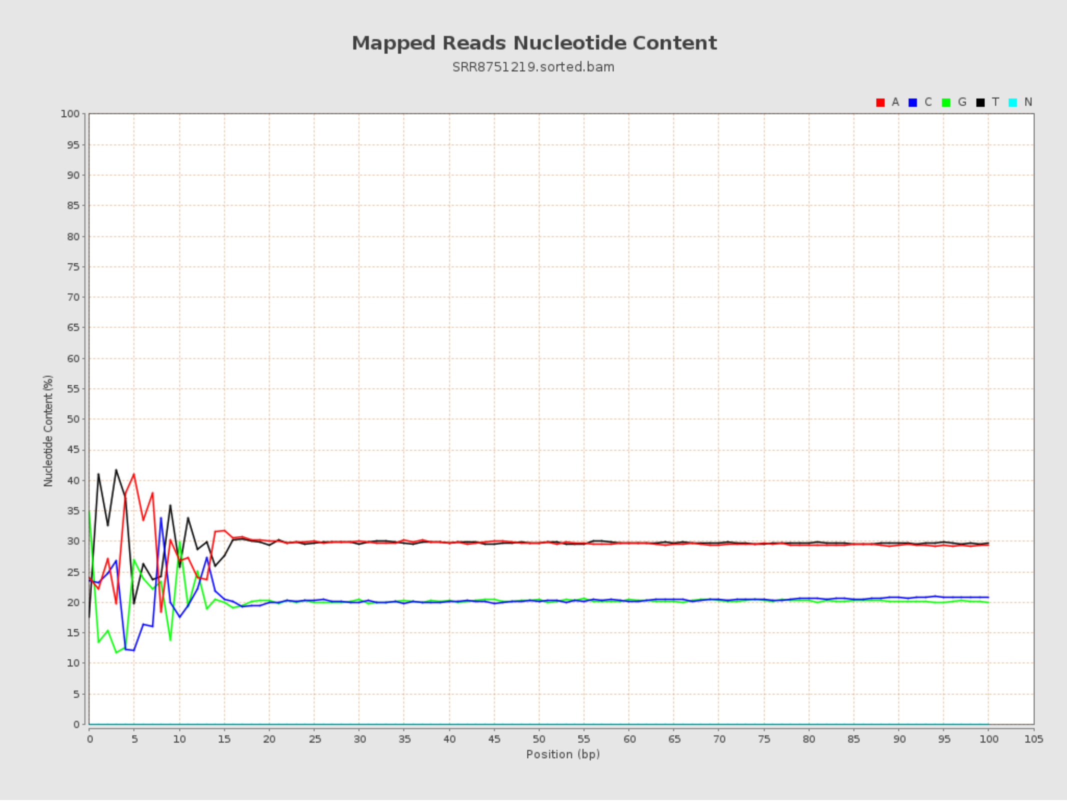
6. Results : Genome Fraction Coverage



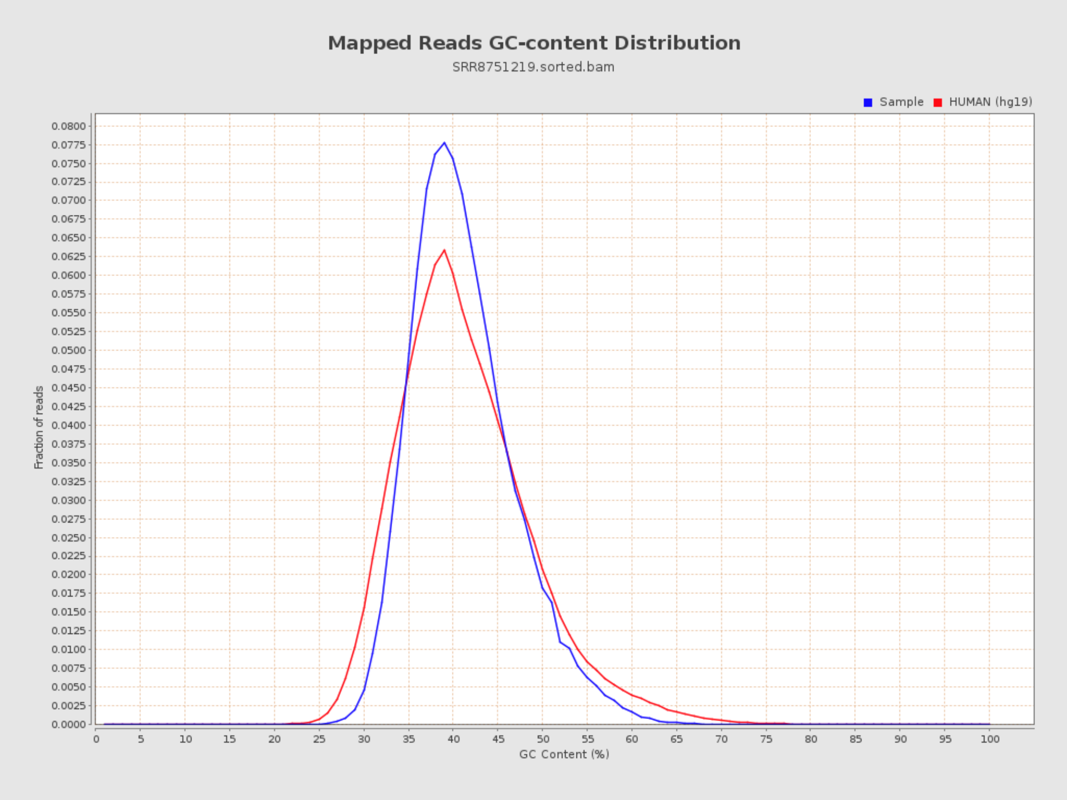
7. Results : Duplication Rate Histogram



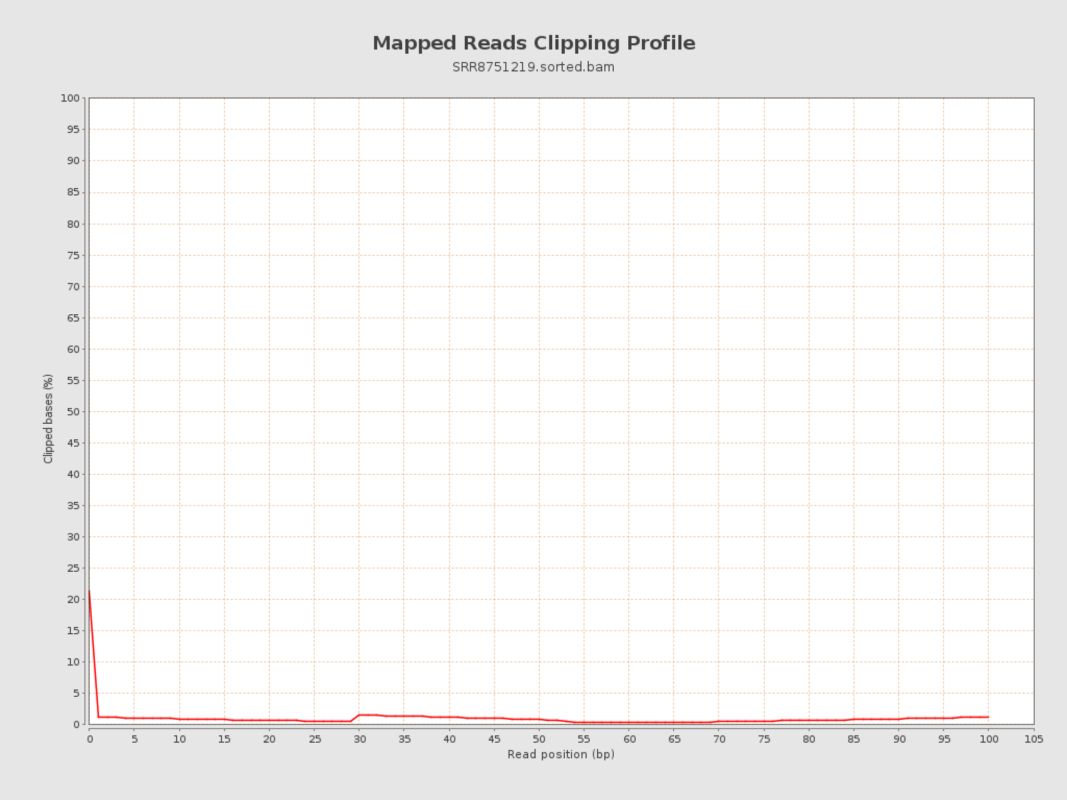
8. Results : Mapped Reads Nucleotide Content



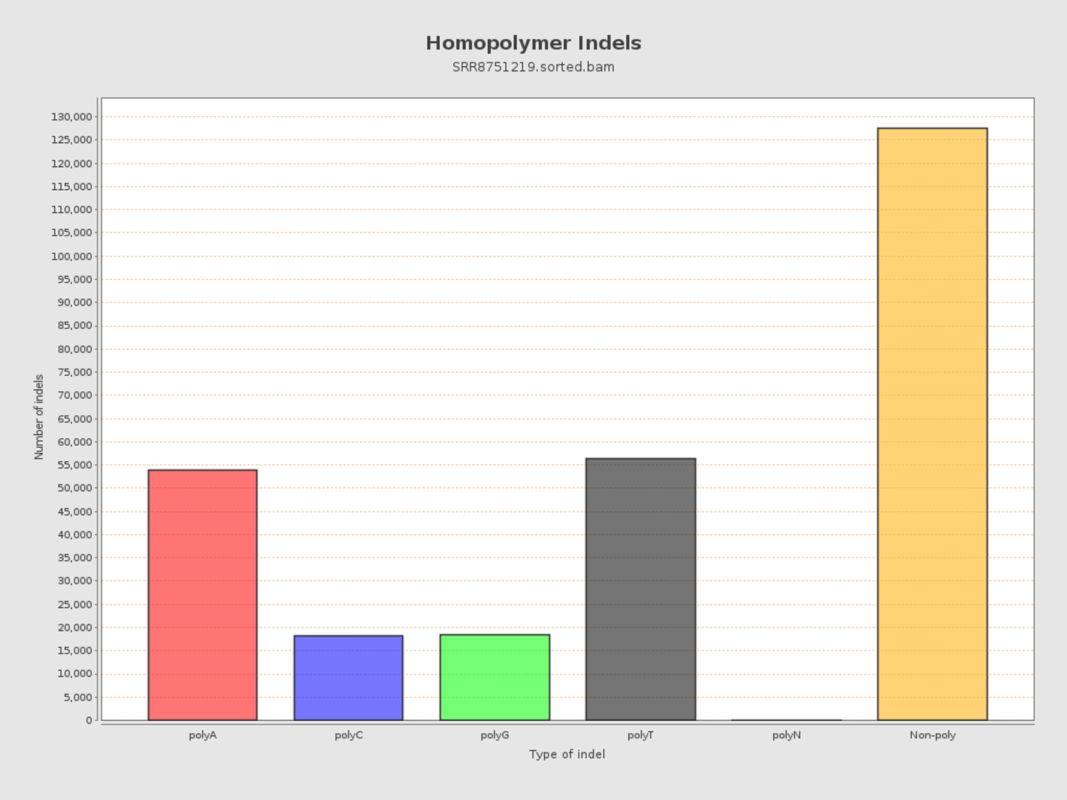
9. Results : Mapped Reads GC-content Distribution



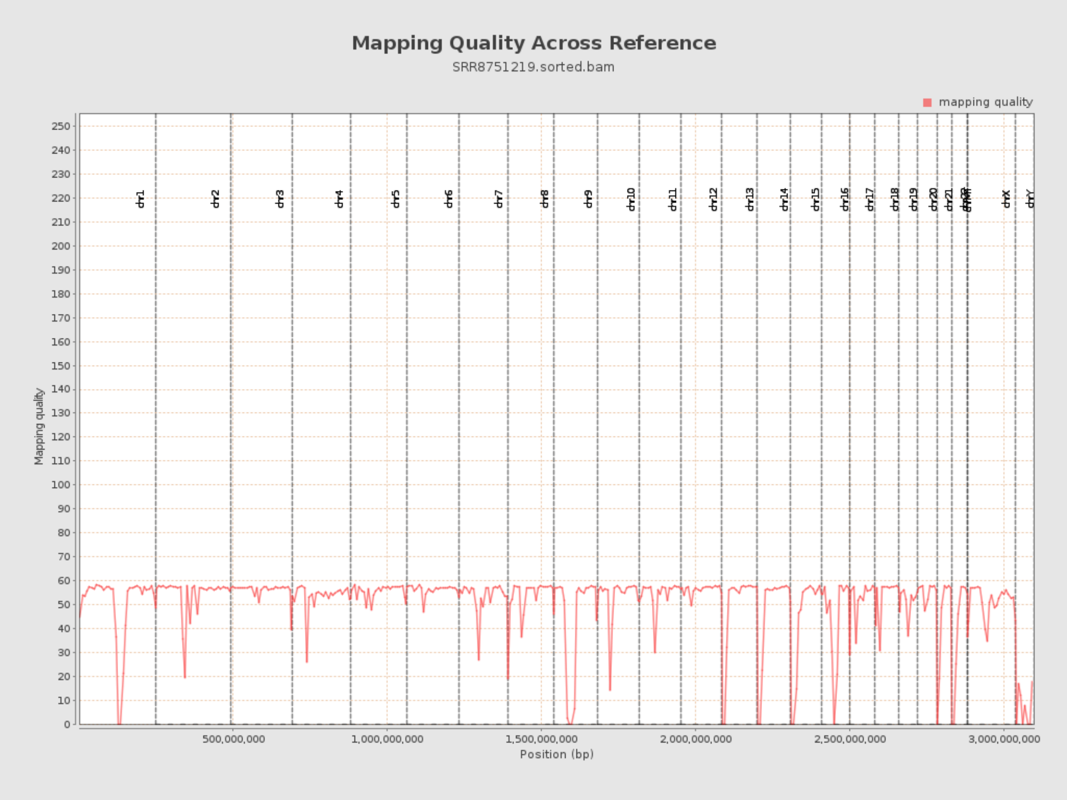
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram