Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 18:26:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751196.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_SRR8751196 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751196.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 18:26:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751196.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,374,927
Mapped reads	7,289,365 / 98.84%
Unmapped reads	85,562 / 1.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	213,789 / 2.9%
Read min/max/mean length	30 / 151 / 152.52
Duplicated reads (estimated)	1,056,482 / 14.33%
Duplication rate	13.64%
Clipped reads	1,681,797 / 22.8%

2.2. ACGT Content

Number/percentage of A's	303,224,513 / 28.6%
Number/percentage of C's	227,886,825 / 21.49%
Number/percentage of T's	303,699,950 / 28.64%
Number/percentage of G's	225,435,797 / 21.26%
Number/percentage of N's	10,025 / 0%
GC Percentage	42.76%

2.3. Coverage

Mean	0.3426

Standard Deviation	1.5474

2.4. Mapping Quality

Mean Mapping Quality	52.7

2.5. Mismatches and indels

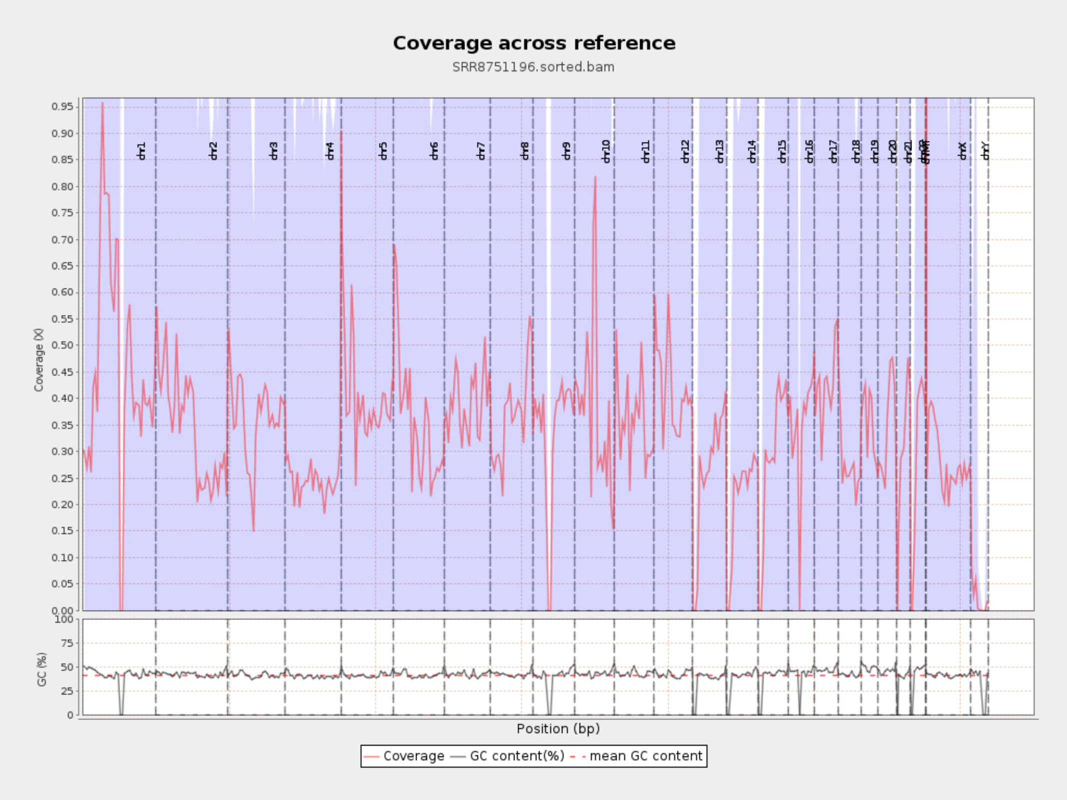
General error rate	0.84%
Mismatches	8,540,869
Insertions	224,864
Mapped reads with at least one insertion	2.99%
Deletions	132,983
Mapped reads with at least one deletion	1.78%
Homopolymer indels	49.41%

2.6. Chromosome stats

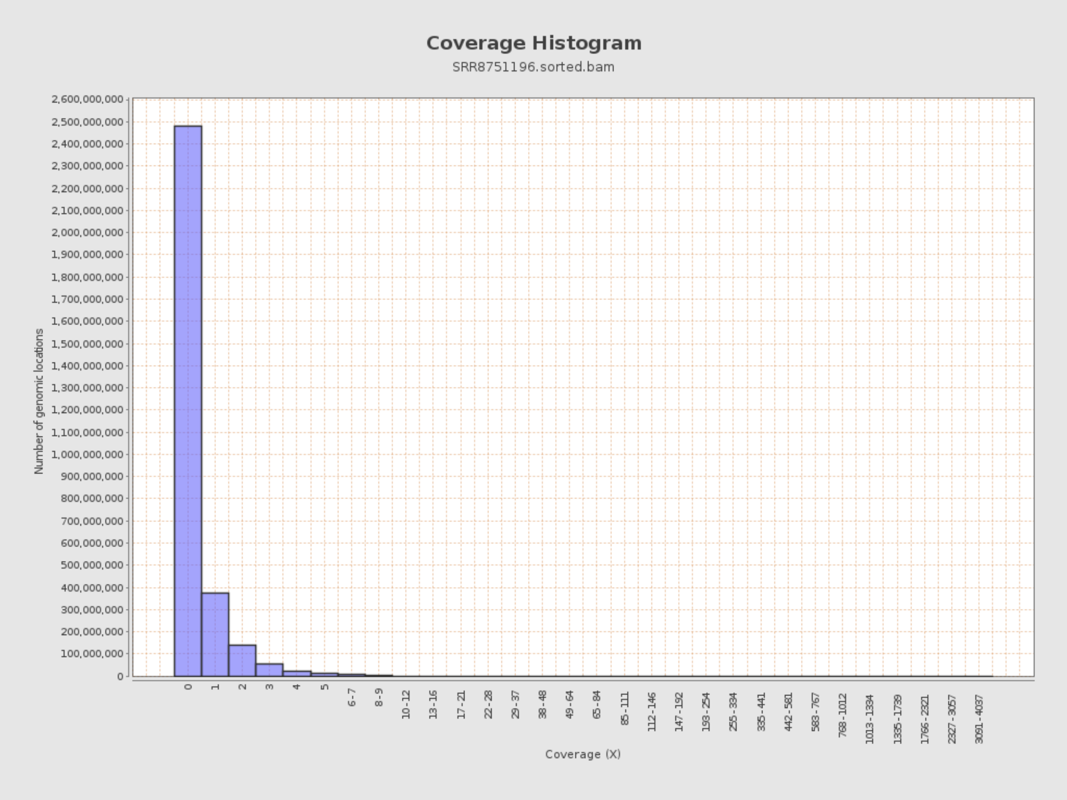
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	116019601	0.4655	3.7378
chr2	243199373	83417886	0.343	1.0715
chr3	198022430	72060815	0.3639	0.905
chr4	191154276	46690600	0.2443	0.7741
chr5	180915260	73822198	0.408	0.9367
chr6	171115067	60681188	0.3546	1.2121
chr7	159138663	62399393	0.3921	1.3023

chr8	146364022	53962505	0.3687	0.9301
chr9	141213431	47601161	0.3371	1.1347
chr10	135534747	52191845	0.3851	2.4781
chr11	135006516	48080919	0.3561	1.0943
chr12	133851895	57025303	0.426	0.9908
chr13	115169878	29894646	0.2596	0.7385
chr14	107349540	22756121	0.212	0.6813
chr15	102531392	29145178	0.2843	0.8159
chr16	90354753	31179584	0.3451	0.954
chr17	81195210	34239338	0.4217	1.3991
chr18	78077248	21392068	0.274	1.2759
chr19	59128983	20956283	0.3544	2.5265
chr20	63025520	21936597	0.3481	0.906
chr21	48129895	14602086	0.3034	0.9679
chr22	51304566	14600306	0.2846	0.823
chrMT	16571	905518	54.6447	26.5043
chrX	155270560	43774393	0.2819	0.8311
chrY	59373566	1254129	0.0211	0.5128

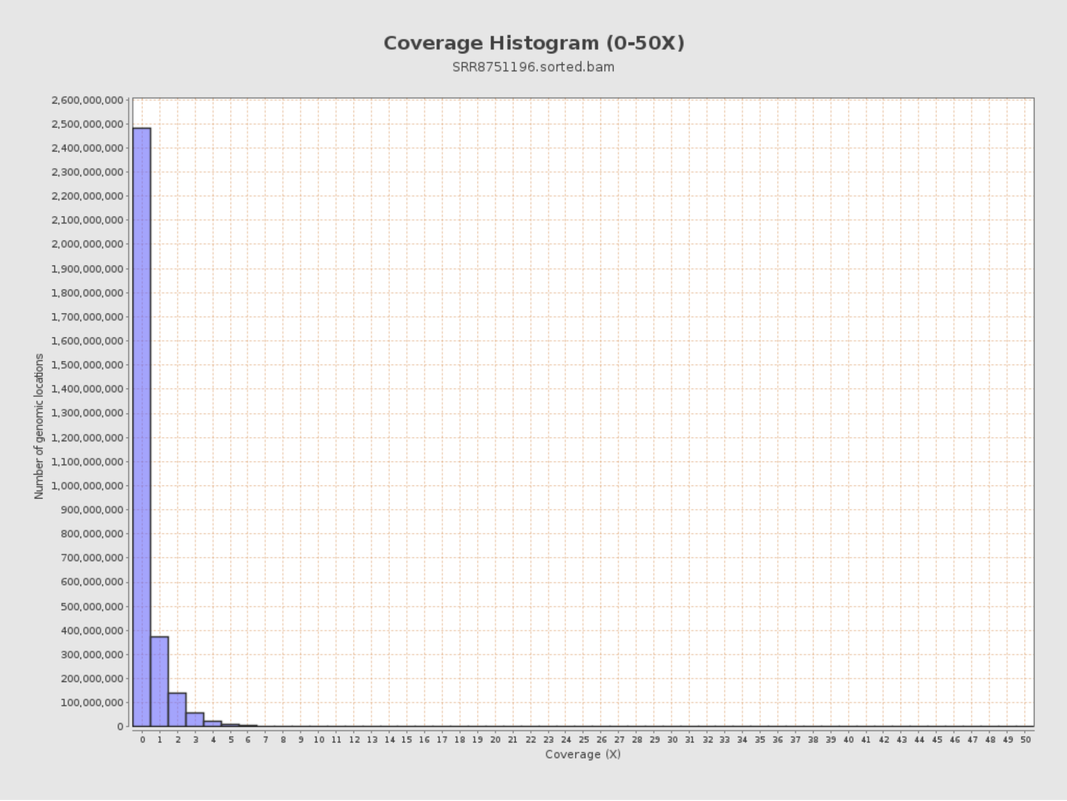
3. Results : Coverage across reference



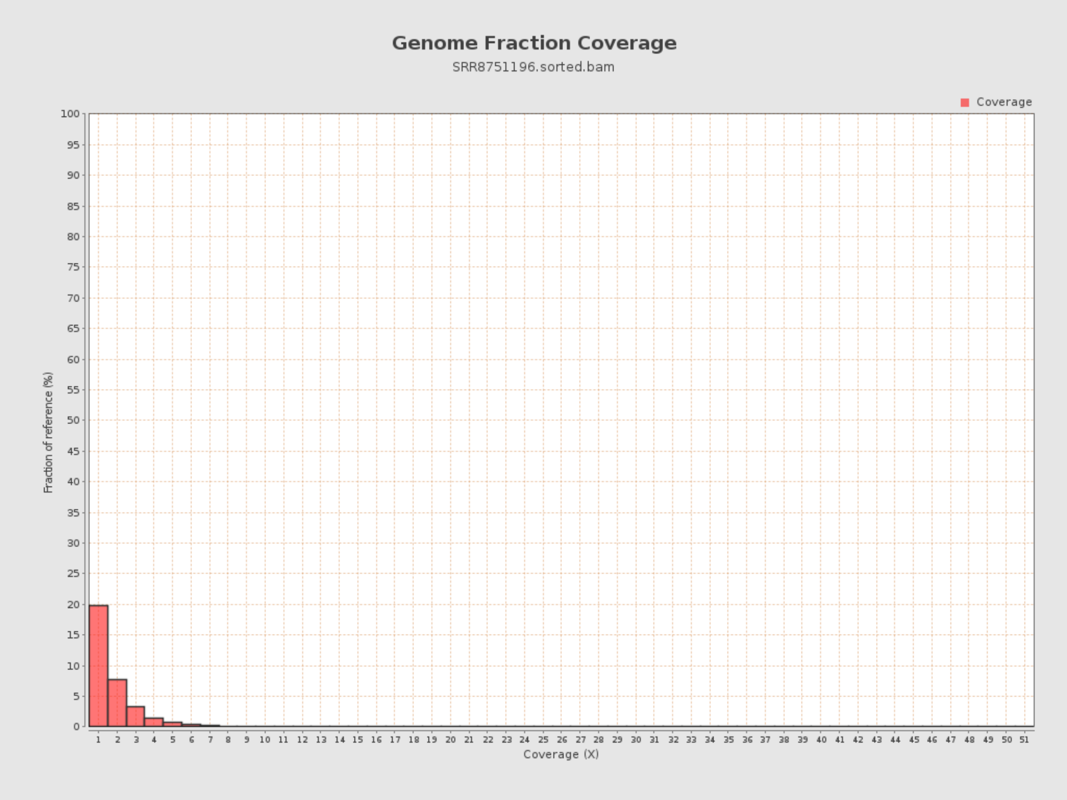
4. Results : Coverage Histogram



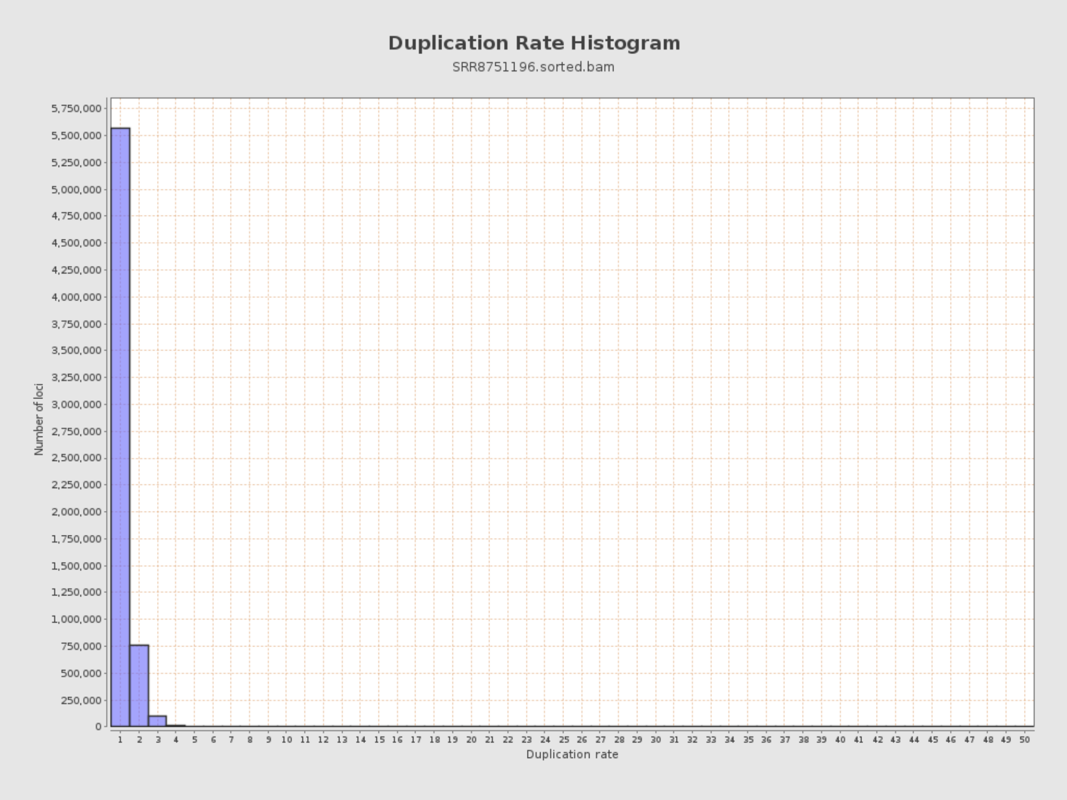
5. Results : Coverage Histogram (0-50X)



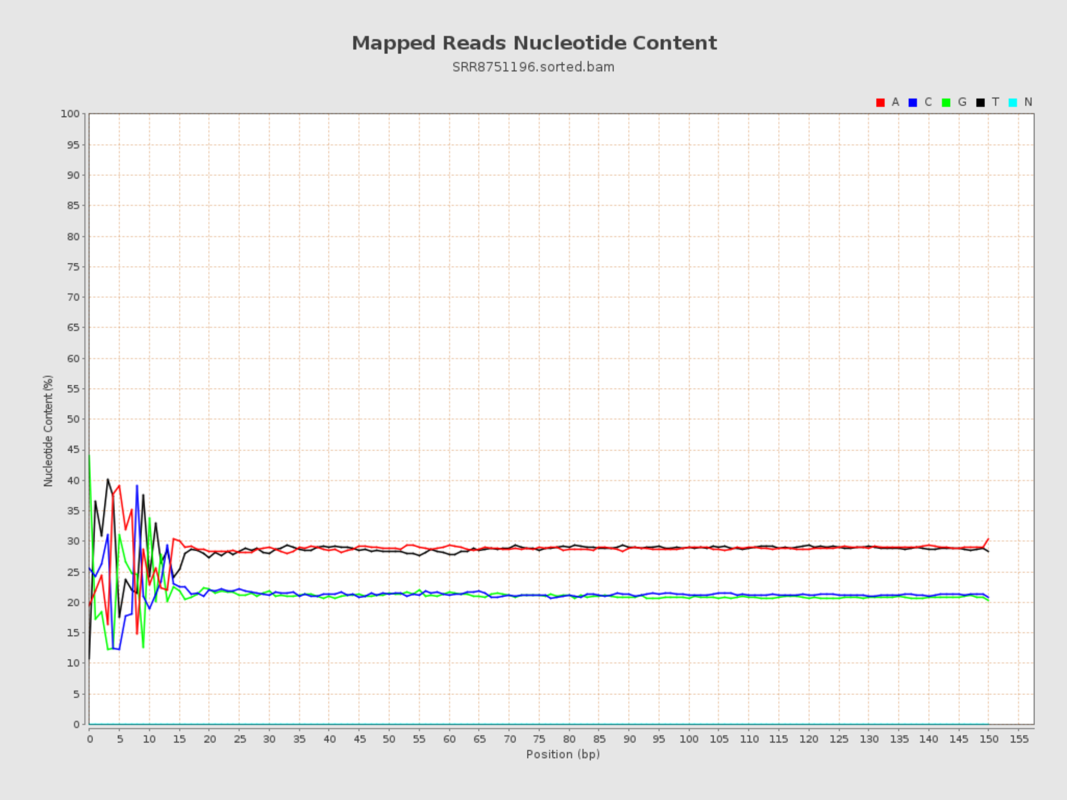
6. Results : Genome Fraction Coverage



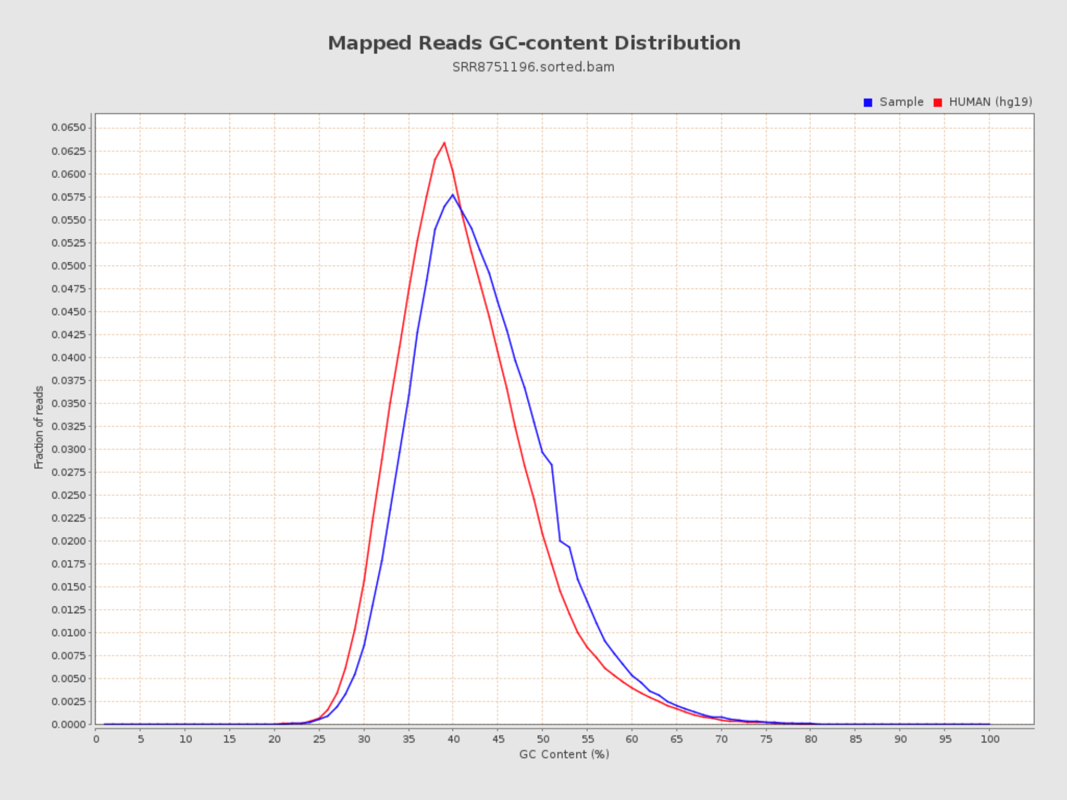
7. Results : Duplication Rate Histogram



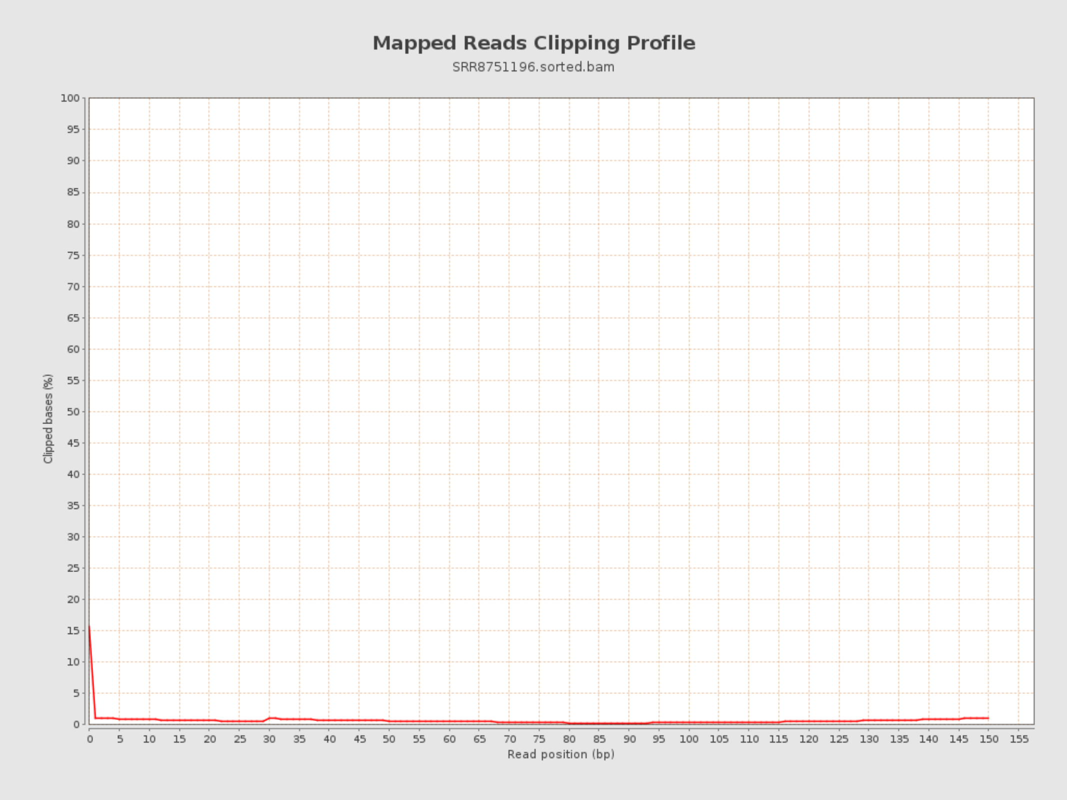
8. Results : Mapped Reads Nucleotide Content



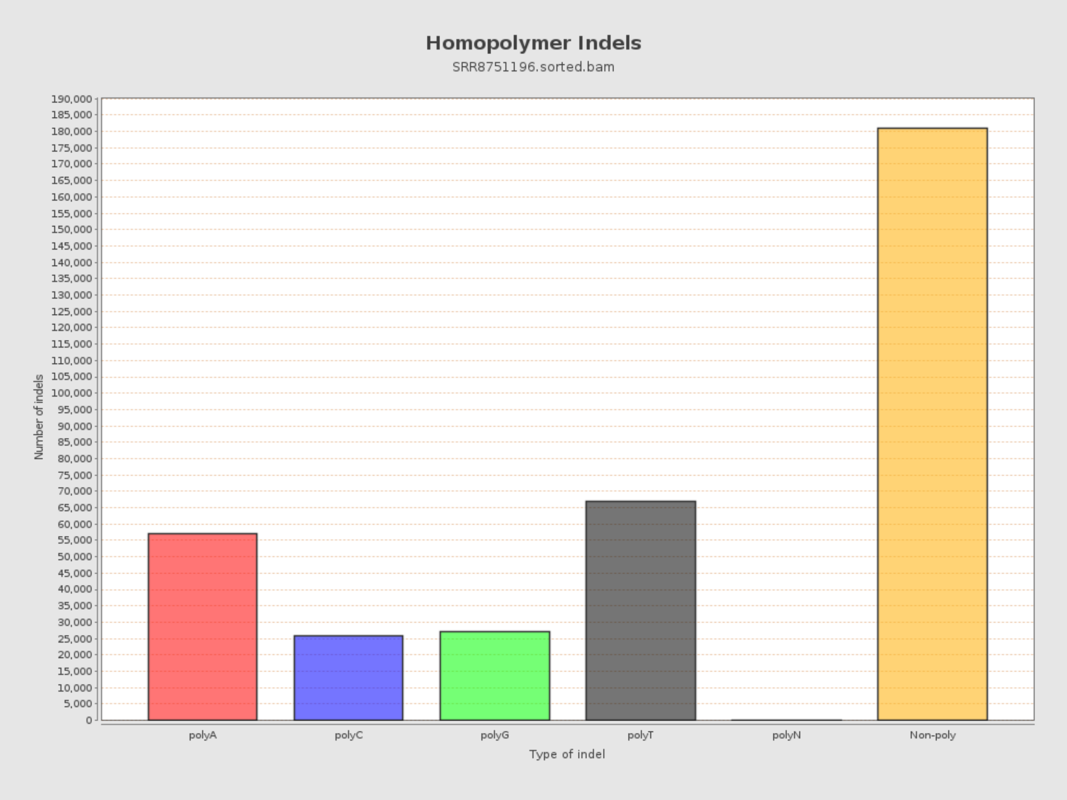
9. Results : Mapped Reads GC-content Distribution



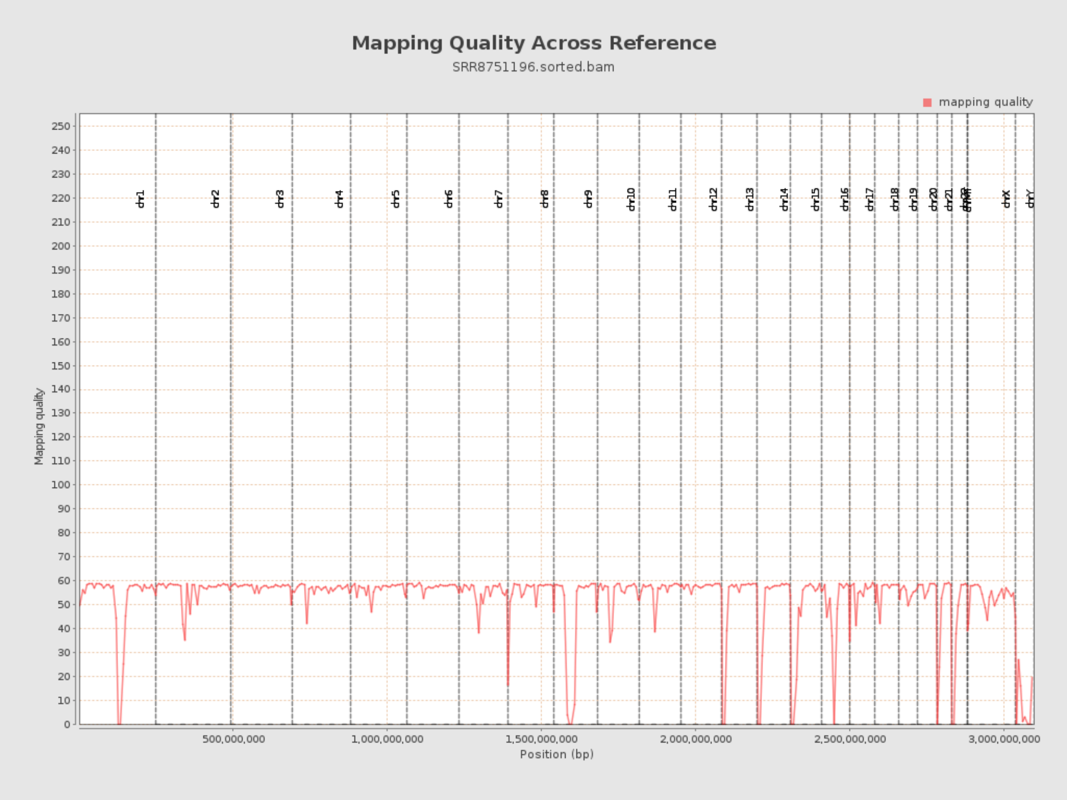
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram