Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:55:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818995.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_SRR1818995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818995.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:55:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818995.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,707,223
Mapped reads	1,660,104 / 97.24%
Unmapped reads	47,119 / 2.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,636 / 1.44%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	676,294 / 39.61%
Duplication rate	34.1%
Clipped reads	1,659,240 / 97.19%

2.2. ACGT Content

Number/percentage of A's	44,107,022 / 28.7%
Number/percentage of C's	31,425,037 / 20.45%
Number/percentage of T's	44,678,713 / 29.07%
Number/percentage of G's	33,462,118 / 21.77%
Number/percentage of N's	7,955 / 0.01%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0497

Standard Deviation	0.5803

2.4. Mapping Quality

Mean Mapping Quality	47.92

2.5. Mismatches and indels

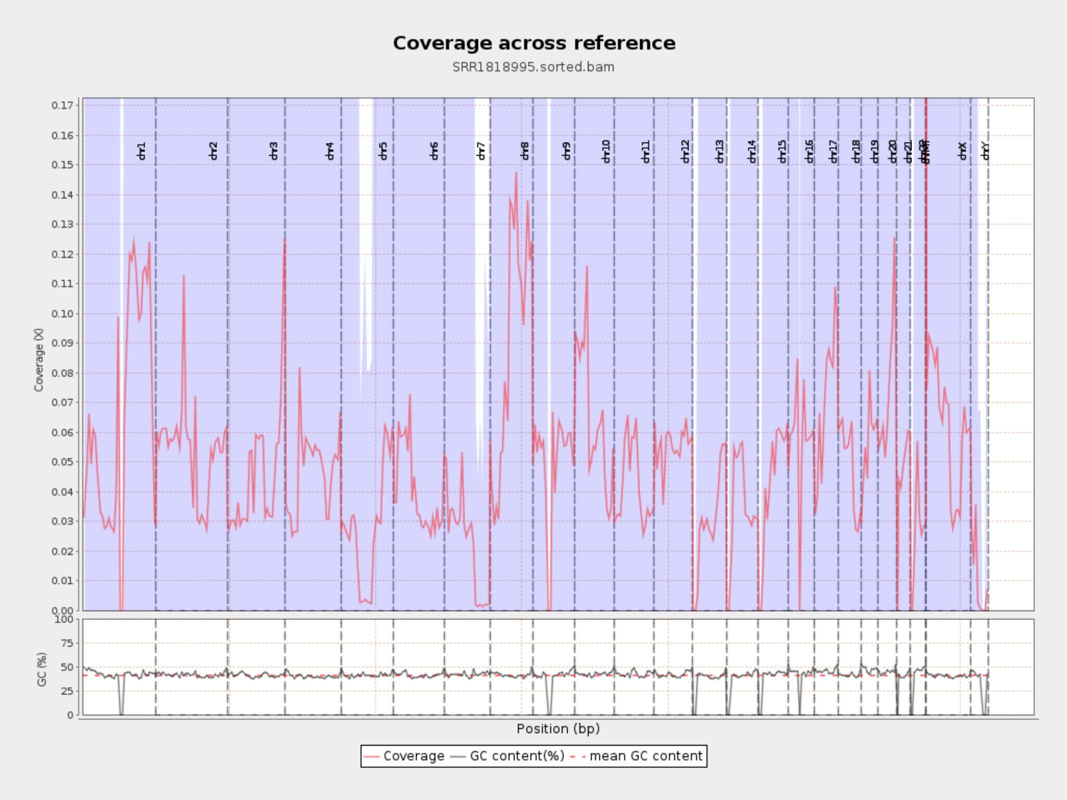
General error rate	0.68%
Mismatches	995,835
Insertions	25,598
Mapped reads with at least one insertion	1.51%
Deletions	49,225
Mapped reads with at least one deletion	2.9%
Homopolymer indels	40.95%

2.6. Chromosome stats

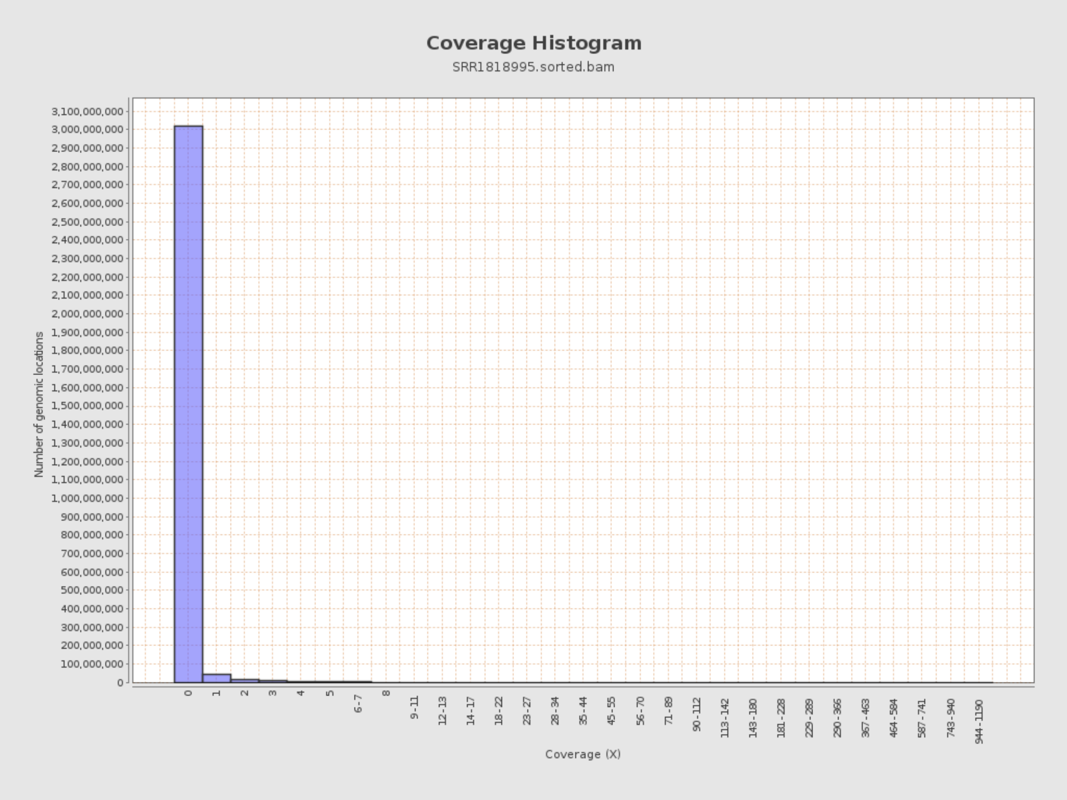
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16336625	0.0655	1.0315
chr2	243199373	13238951	0.0544	0.7812
chr3	198022430	8982205	0.0454	0.3697
chr4	191154276	8977495	0.047	0.4372
chr5	180915260	5042558	0.0279	0.3064
chr6	171115067	6851055	0.04	0.4133
chr7	159138663	3602811	0.0226	0.4447

chr8	146364022	13458246	0.092	0.5837
chr9	141213431	7013921	0.0497	0.5535
chr10	135534747	8748917	0.0646	0.7479
chr11	135006516	5634912	0.0417	0.4376
chr12	133851895	7459114	0.0557	0.4201
chr13	115169878	3461057	0.0301	0.3009
chr14	107349540	3740184	0.0348	0.3381
chr15	102531392	4274850	0.0417	0.3615
chr16	90354753	5127461	0.0567	0.6309
chr17	81195210	5812427	0.0716	0.5224
chr18	78077248	3803445	0.0487	0.6469
chr19	59128983	3397804	0.0575	0.9533
chr20	63025520	4779981	0.0758	0.5125
chr21	48129895	2239745	0.0465	0.4097
chr22	51304566	1292025	0.0252	0.3084
chrMT	16571	45668	2.7559	3.3213
chrX	155270560	9829675	0.0633	0.4929
chrY	59373566	620786	0.0105	0.5814

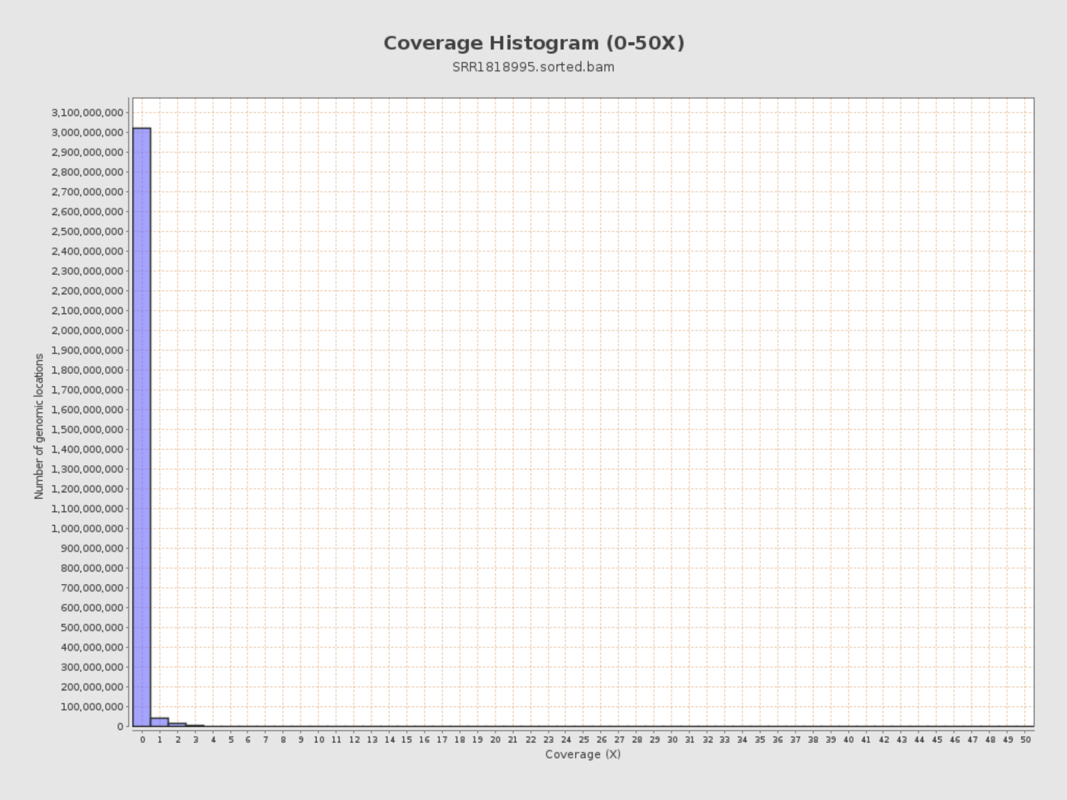
3. Results : Coverage across reference



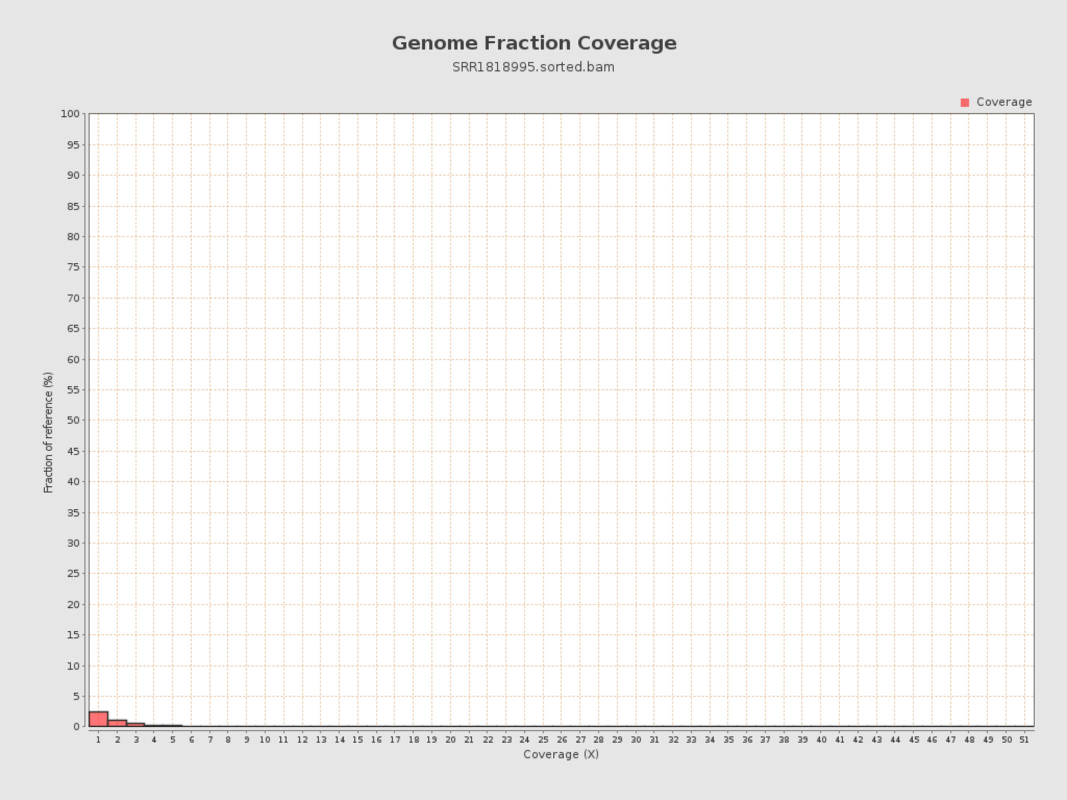
4. Results : Coverage Histogram



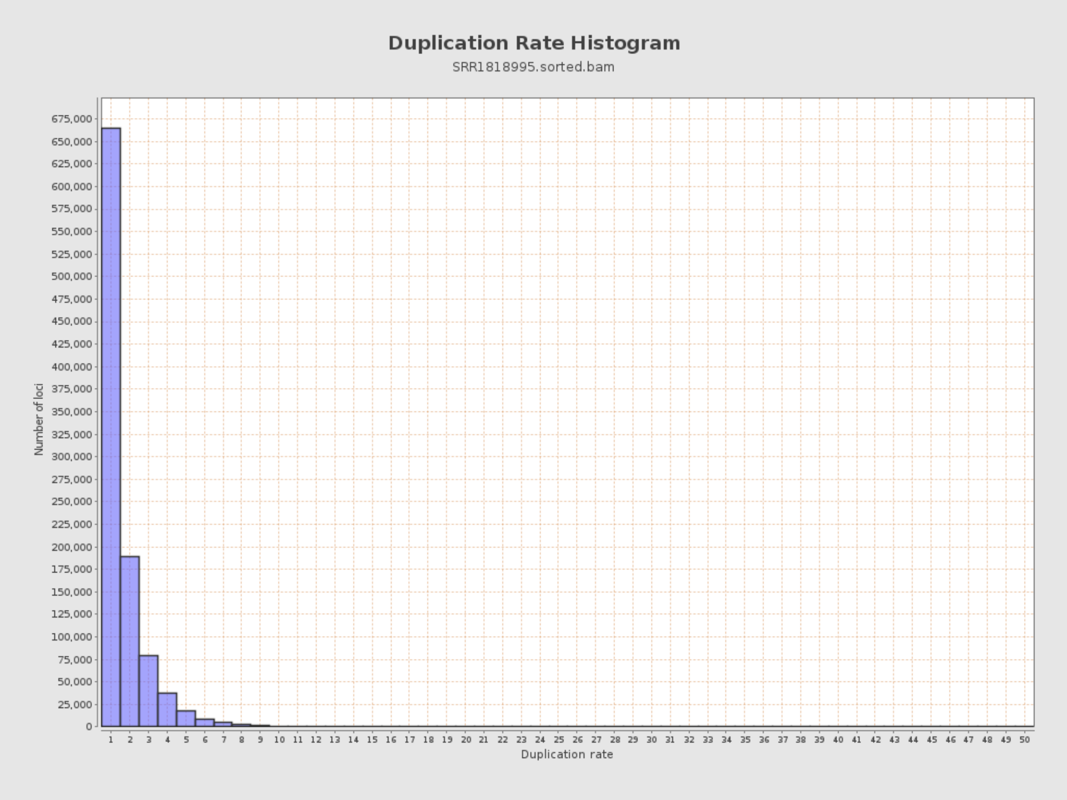
5. Results : Coverage Histogram (0-50X)



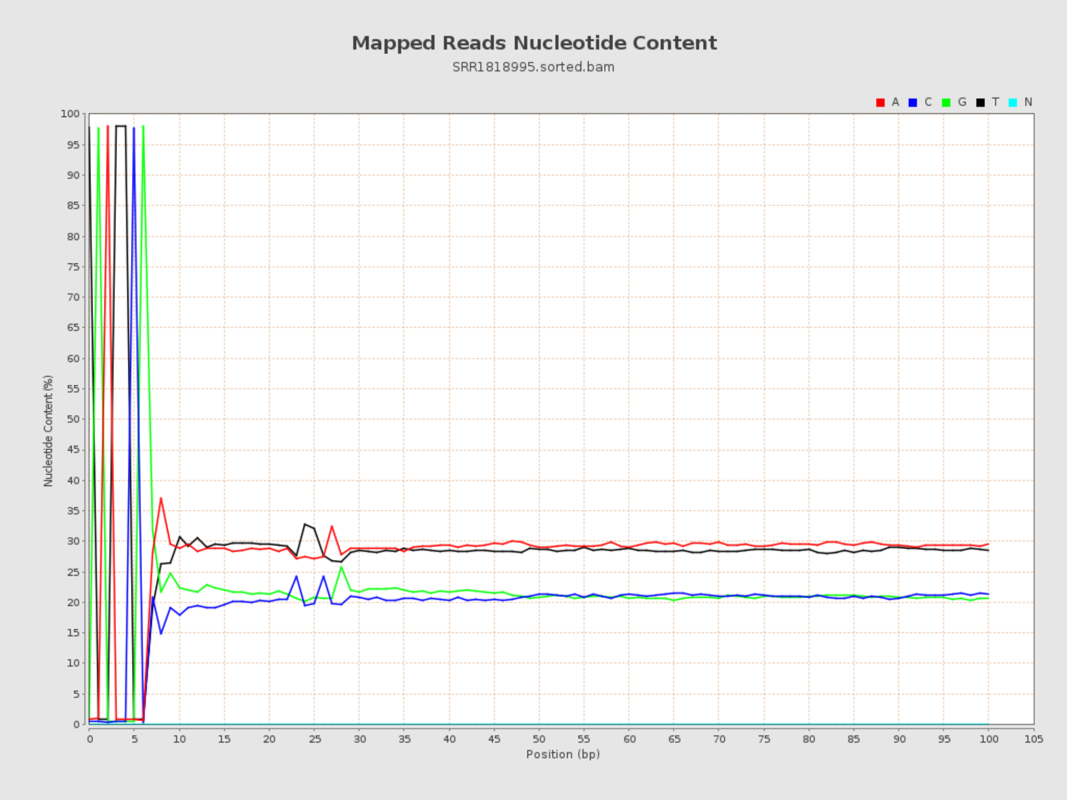
6. Results : Genome Fraction Coverage



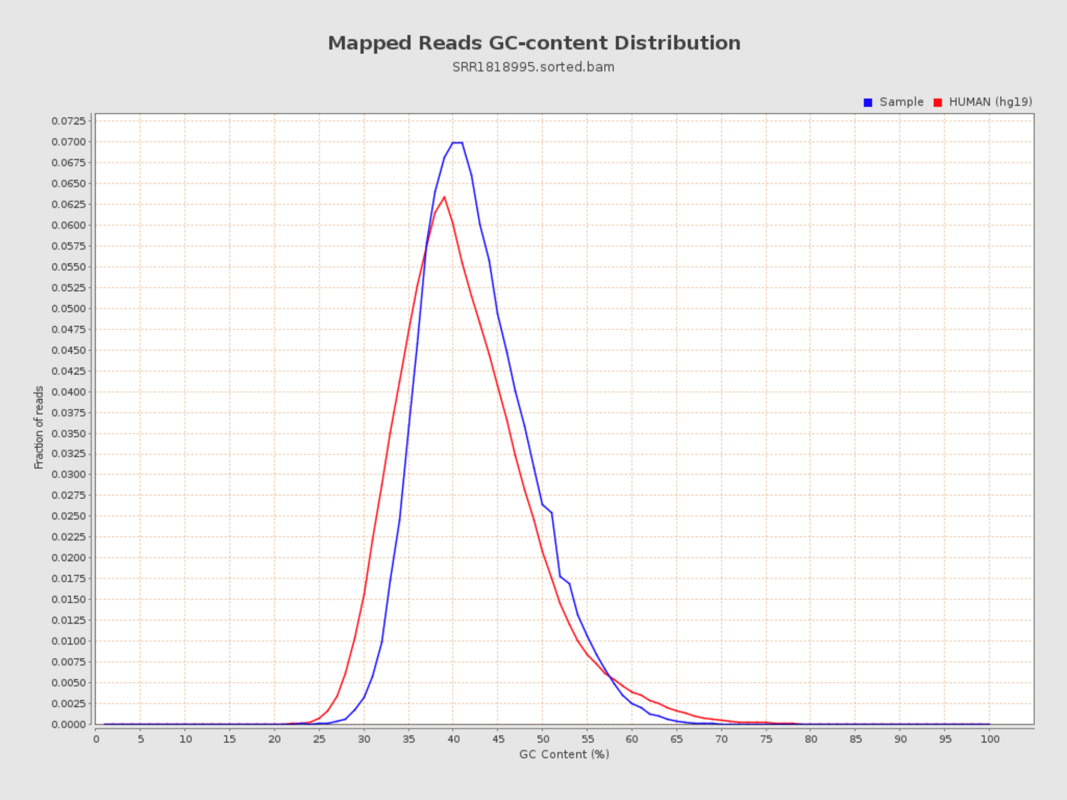
7. Results : Duplication Rate Histogram



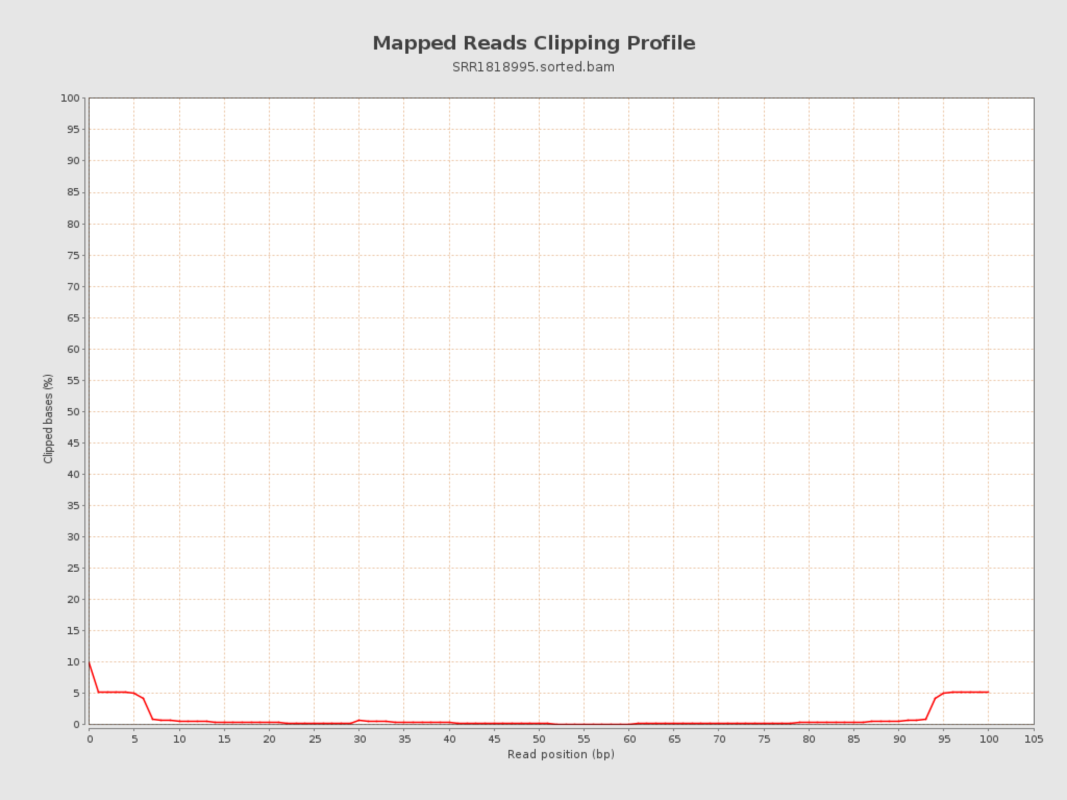
8. Results : Mapped Reads Nucleotide Content



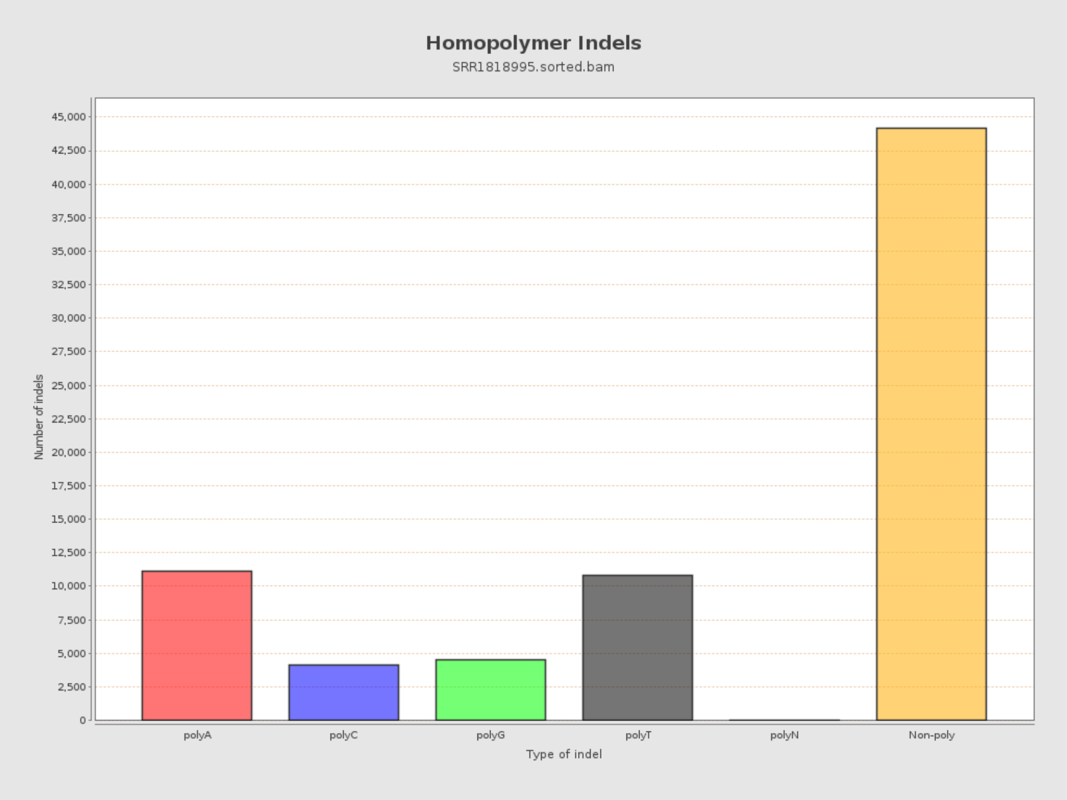
9. Results : Mapped Reads GC-content Distribution



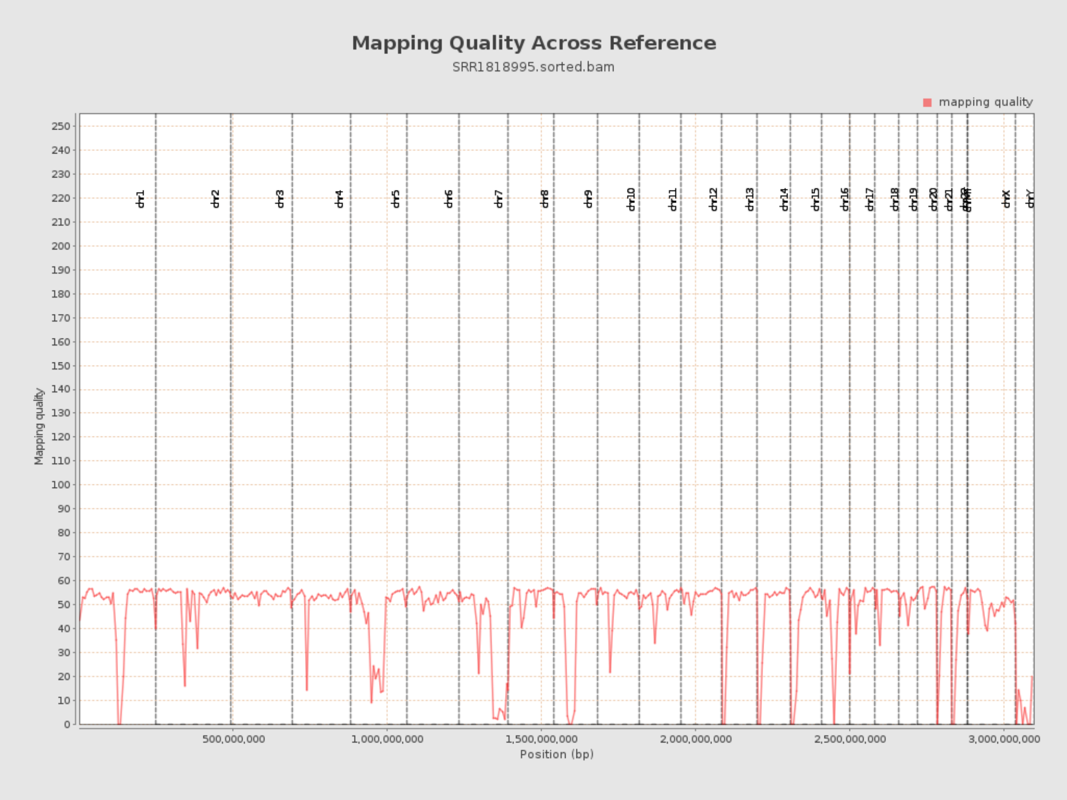
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram