Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 15:58:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819019.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_SRR1819019 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819019.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 15:58:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819019.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,232,899
Mapped reads	1,147,225 / 93.05%
Unmapped reads	85,674 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,196 / 1.39%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	333,370 / 27.04%
Duplication rate	25.07%
Clipped reads	1,149,677 / 93.25%

2.2. ACGT Content

Number/percentage of A's	31,490,691 / 29.68%
Number/percentage of C's	21,932,978 / 20.67%
Number/percentage of T's	29,793,608 / 28.08%
Number/percentage of G's	22,864,640 / 21.55%
Number/percentage of N's	5,278 / 0%
GC Percentage	42.23%

2.3. Coverage

Mean	0.0343

Standard Deviation	0.4501

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

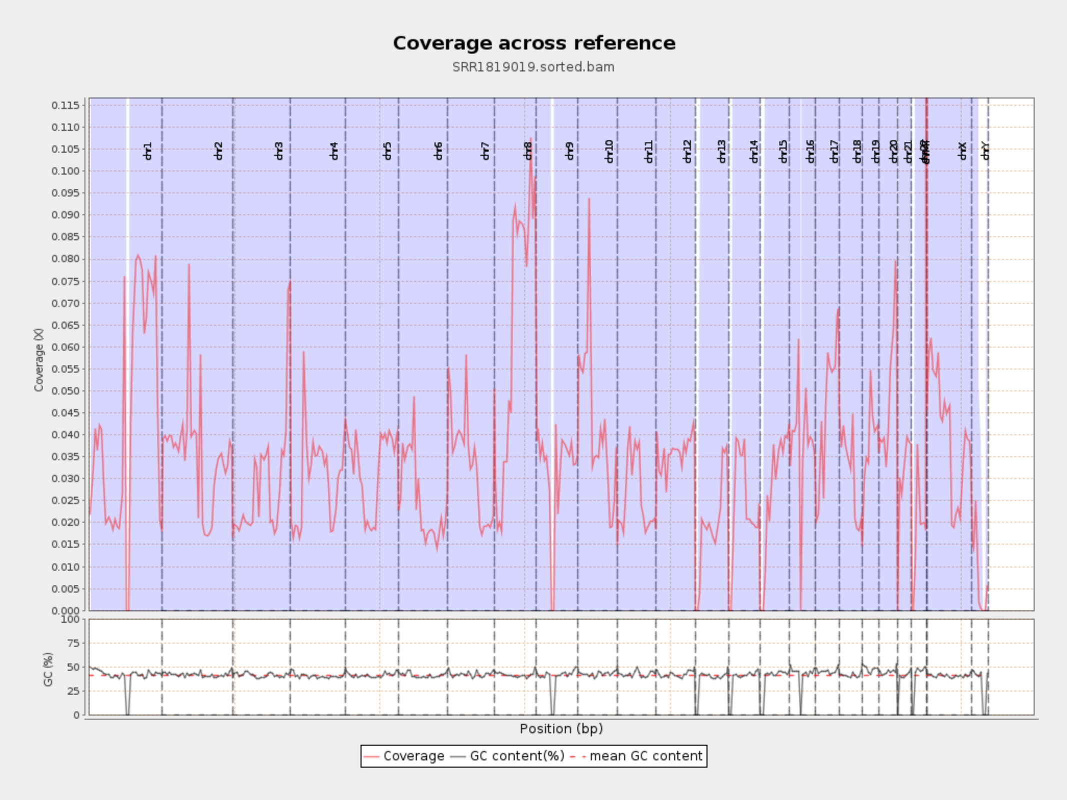
General error rate	0.69%
Mismatches	688,961
Insertions	18,510
Mapped reads with at least one insertion	1.57%
Deletions	34,094
Mapped reads with at least one deletion	2.91%
Homopolymer indels	40.91%

2.6. Chromosome stats

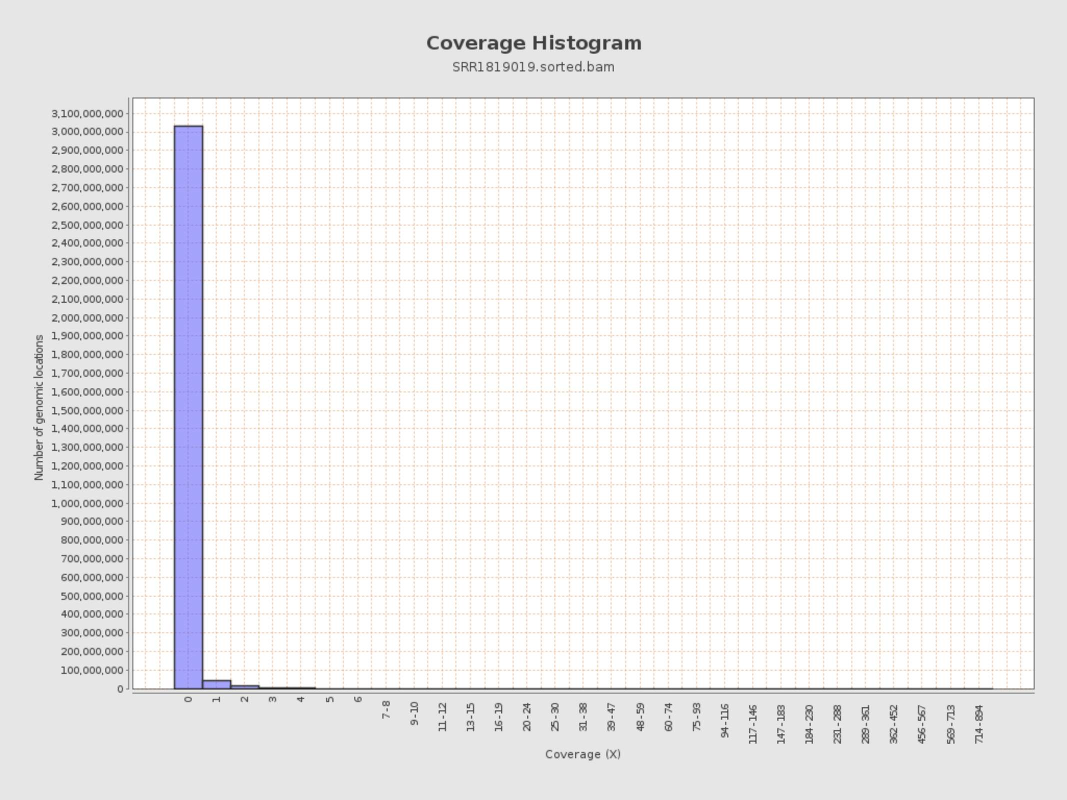
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10941823	0.0439	0.8386
chr2	243199373	8647207	0.0356	0.6214
chr3	198022430	5584918	0.0282	0.2444
chr4	191154276	5689564	0.0298	0.3122
chr5	180915260	5866510	0.0324	0.2715
chr6	171115067	4273835	0.025	0.2786
chr7	159138663	5270583	0.0331	0.503

chr8	146364022	9506827	0.065	0.4075
chr9	141213431	4403075	0.0312	0.3787
chr10	135534747	5793815	0.0427	0.5923
chr11	135006516	3548270	0.0263	0.2871
chr12	133851895	4824447	0.036	0.2825
chr13	115169878	2261566	0.0196	0.2027
chr14	107349540	2507505	0.0234	0.2436
chr15	102531392	2770267	0.027	0.2402
chr16	90354753	3449737	0.0382	0.5211
chr17	81195210	3756873	0.0463	0.3515
chr18	78077248	2479315	0.0318	0.4491
chr19	59128983	2288088	0.0387	0.7281
chr20	63025520	3158272	0.0501	0.3494
chr21	48129895	1477936	0.0307	0.2838
chr22	51304566	877007	0.0171	0.2193
chrMT	16571	11338	0.6842	1.2029
chrX	155270560	6320266	0.0407	0.3385
chrY	59373566	442633	0.0075	0.5179

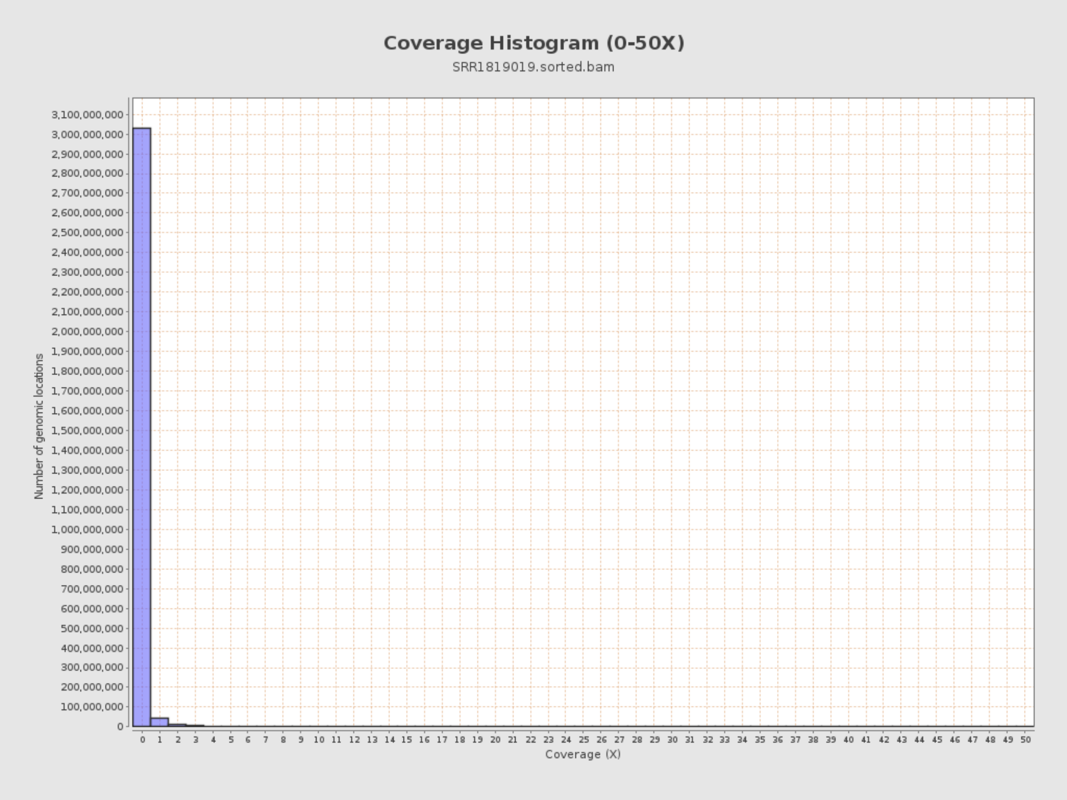
3. Results : Coverage across reference



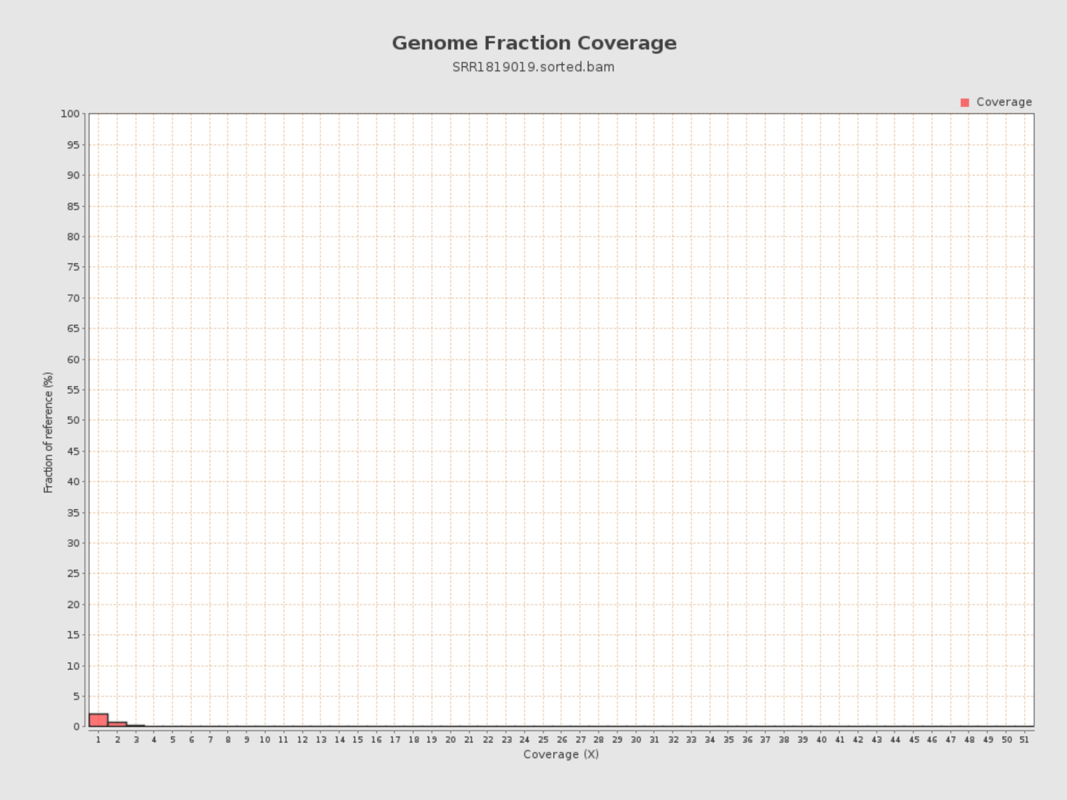
4. Results : Coverage Histogram



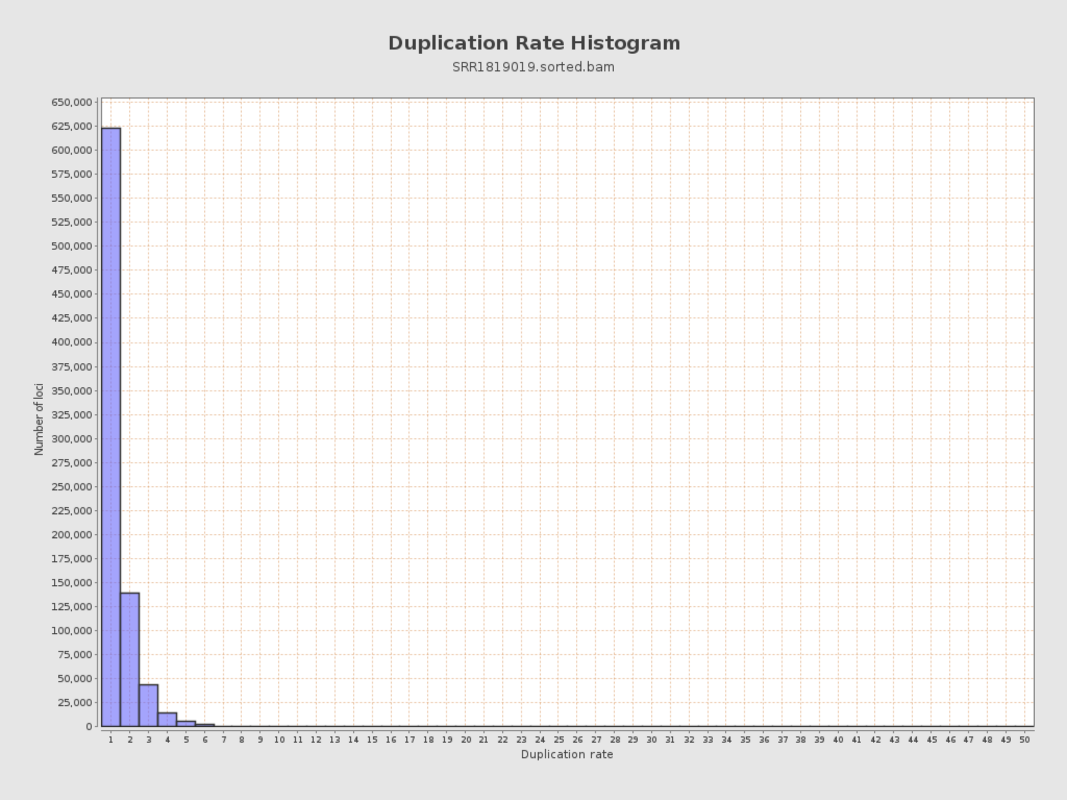
5. Results : Coverage Histogram (0-50X)



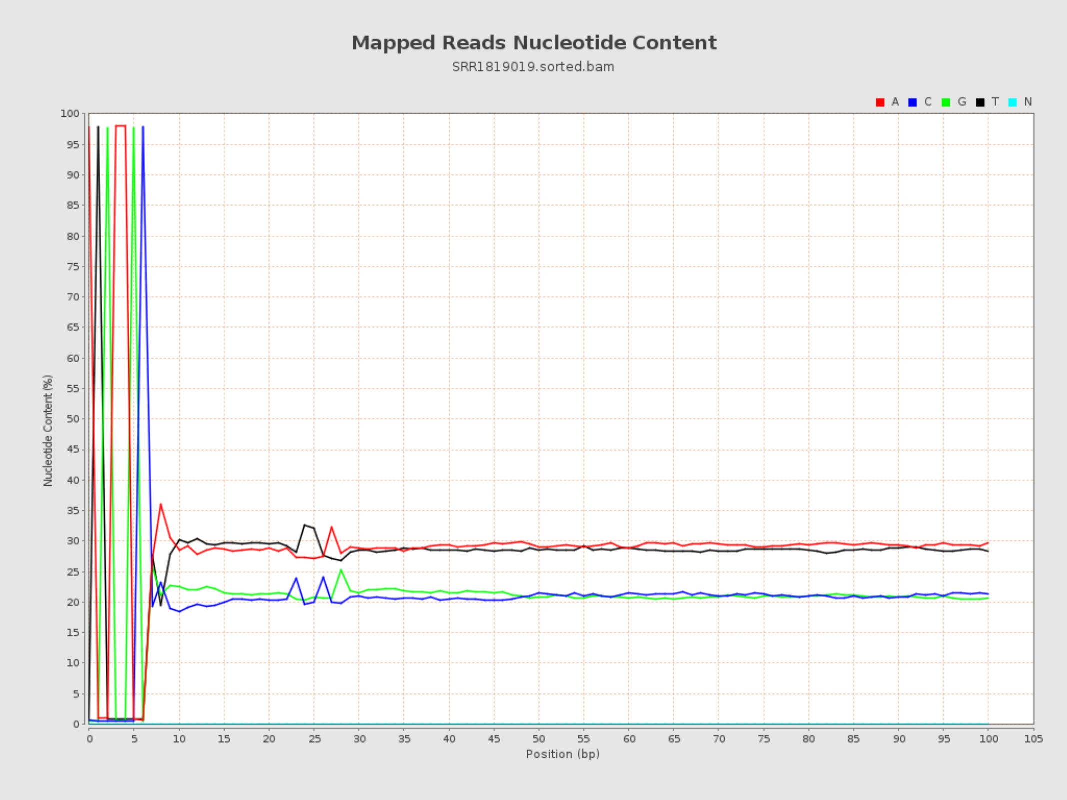
6. Results : Genome Fraction Coverage



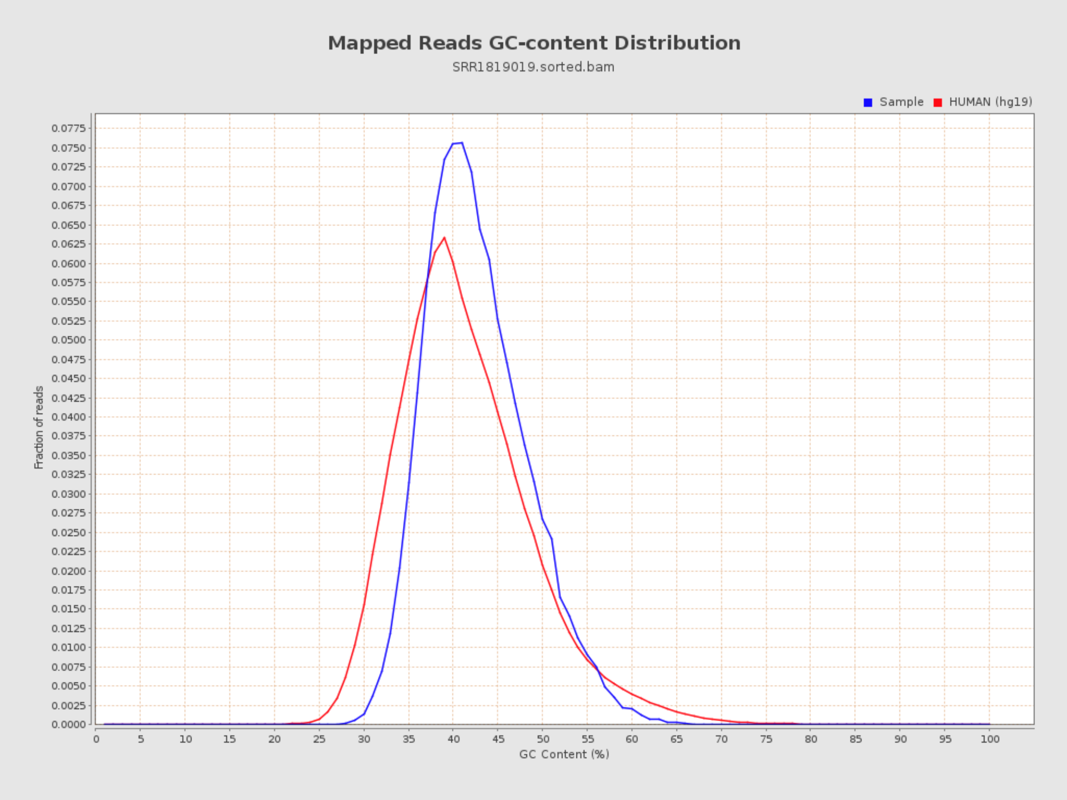
7. Results : Duplication Rate Histogram



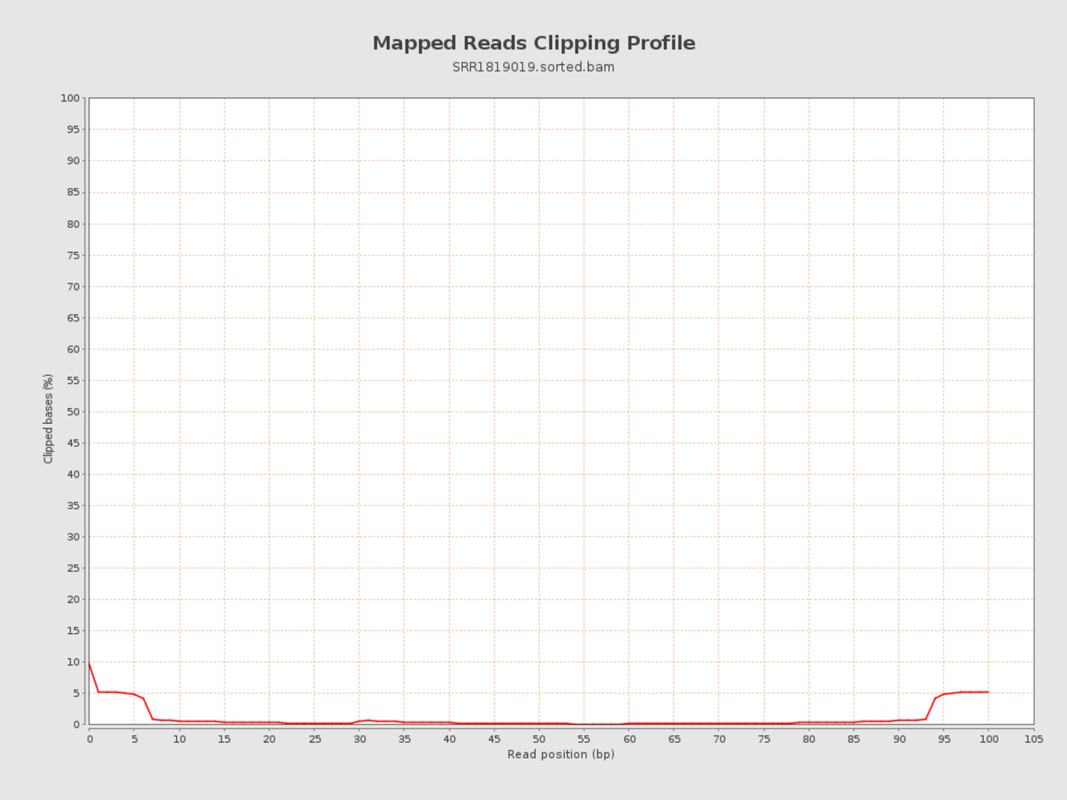
8. Results : Mapped Reads Nucleotide Content



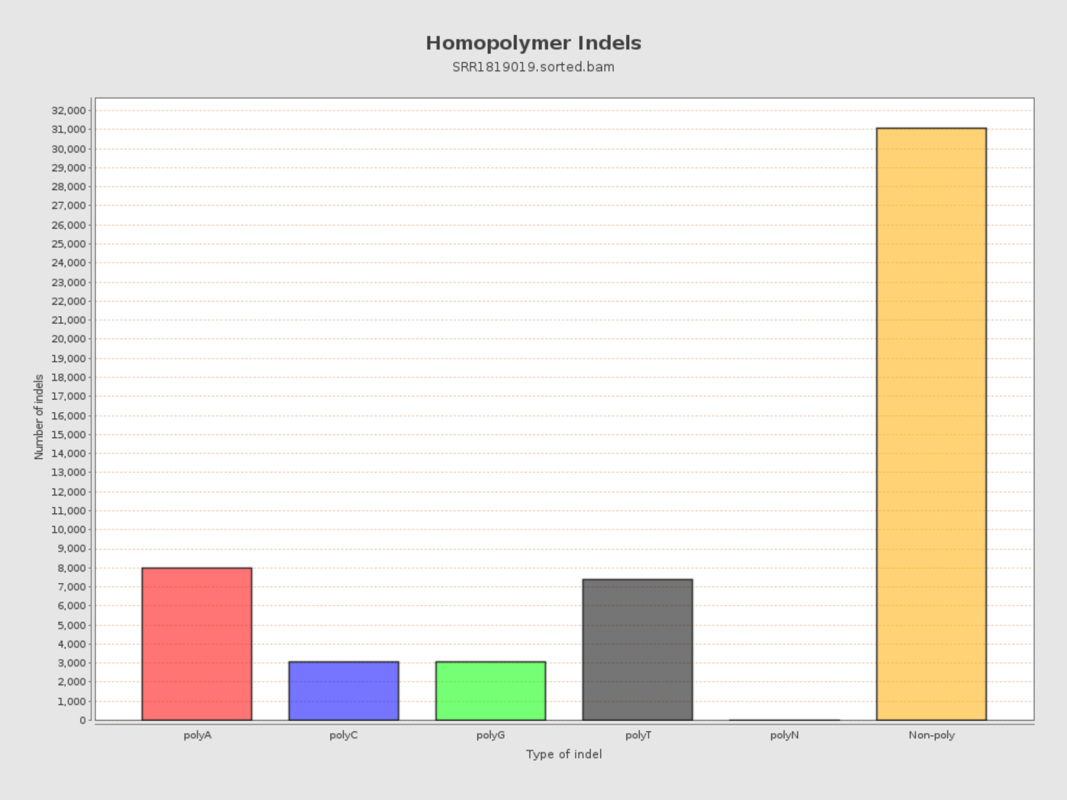
9. Results : Mapped Reads GC-content Distribution



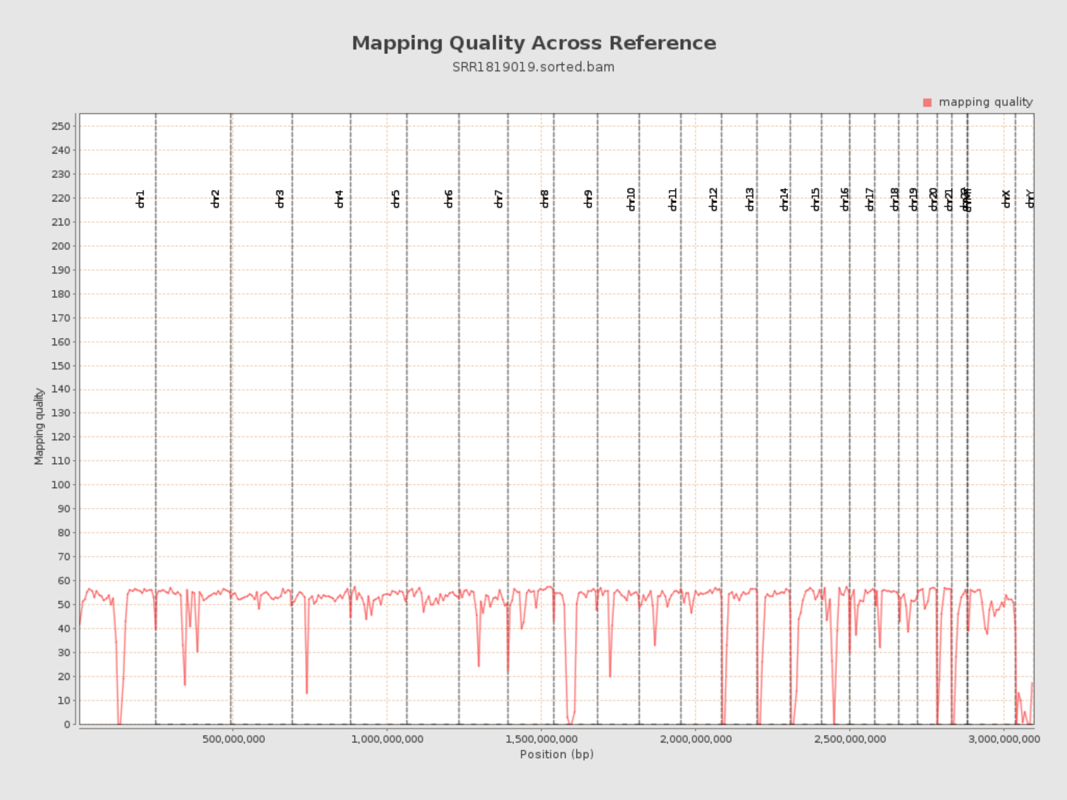
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram