Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:44:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819010.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_SRR1819010 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819010.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:44:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819010.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,030,017
Mapped reads	1,994,941 / 98.27%
Unmapped reads	35,076 / 1.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,894 / 1.52%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	846,655 / 41.71%
Duplication rate	35.5%
Clipped reads	2,019,847 / 99.5%

2.2. ACGT Content

Number/percentage of A's	52,623,054 / 28.54%
Number/percentage of C's	39,328,008 / 21.33%
Number/percentage of T's	52,382,755 / 28.41%
Number/percentage of G's	40,014,434 / 21.7%
Number/percentage of N's	9,060 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0596

Standard Deviation	0.7461

2.4. Mapping Quality

Mean Mapping Quality	49.14

2.5. Mismatches and indels

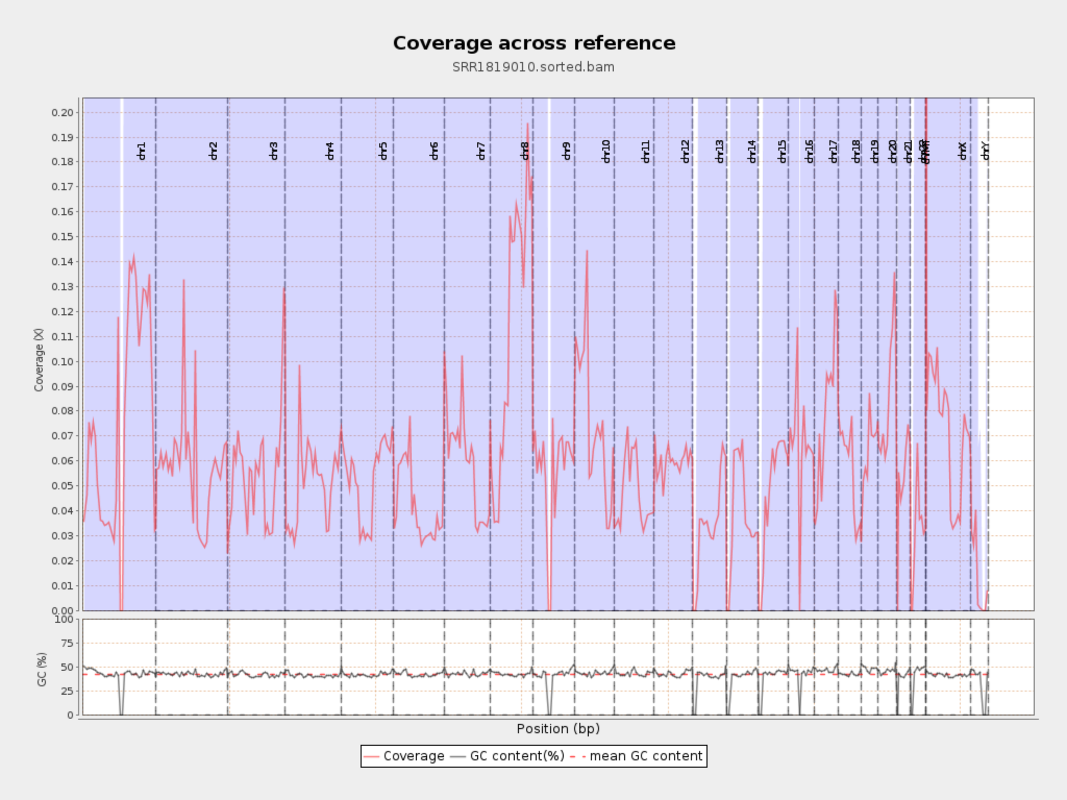
General error rate	0.67%
Mismatches	1,171,033
Insertions	27,034
Mapped reads with at least one insertion	1.31%
Deletions	59,439
Mapped reads with at least one deletion	2.91%
Homopolymer indels	41.05%

2.6. Chromosome stats

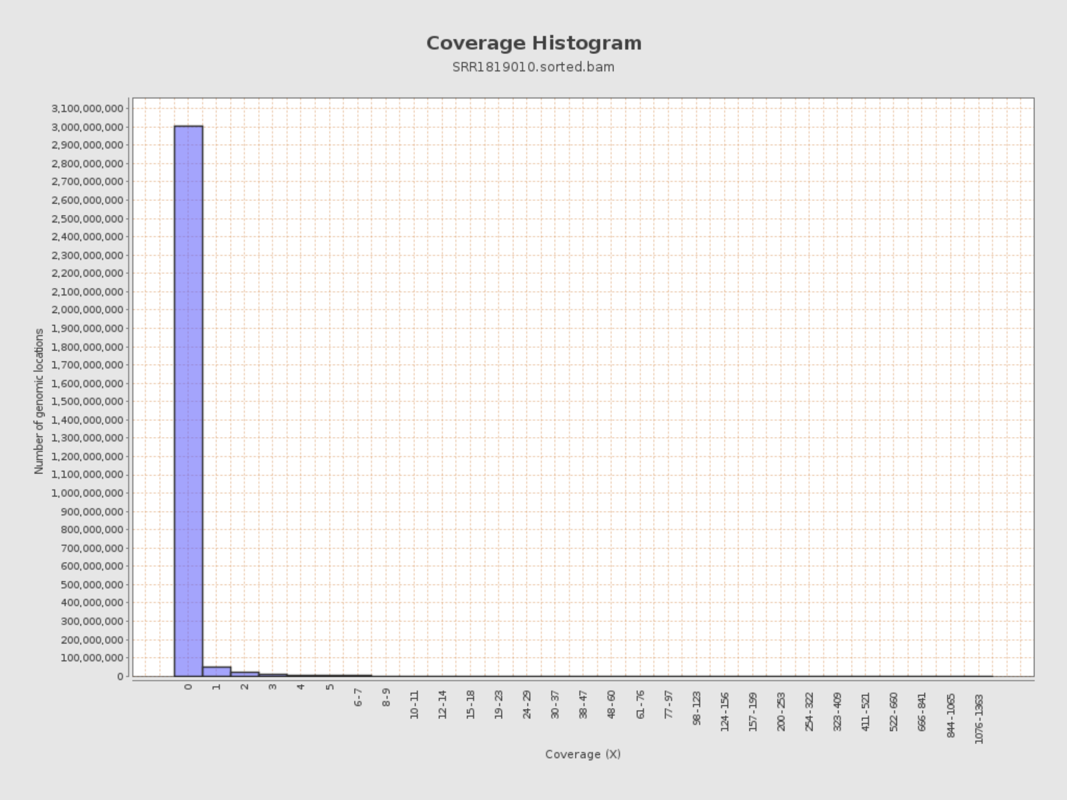
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18772647	0.0753	1.2619
chr2	243199373	14113194	0.058	1.2018
chr3	198022430	10923641	0.0552	0.4158
chr4	191154276	9792960	0.0512	0.4944
chr5	180915260	9698577	0.0536	0.4449
chr6	171115067	7141061	0.0417	0.4647
chr7	159138663	9475572	0.0595	0.8051

chr8	146364022	16922506	0.1156	0.6707
chr9	141213431	7807843	0.0553	0.6871
chr10	135534747	10147747	0.0749	0.9453
chr11	135006516	6312081	0.0468	0.473
chr12	133851895	8044563	0.0601	0.4435
chr13	115169878	4010034	0.0348	0.3271
chr14	107349540	4219025	0.0393	0.3794
chr15	102531392	4806019	0.0469	0.3855
chr16	90354753	5881902	0.0651	0.987
chr17	81195210	6407542	0.0789	0.5689
chr18	78077248	4449776	0.057	0.7546
chr19	59128983	3818429	0.0646	1.1106
chr20	63025520	5520301	0.0876	0.5701
chr21	48129895	2584117	0.0537	0.4658
chr22	51304566	1571327	0.0306	0.3631
chrMT	16571	19790	1.1943	1.9719
chrX	155270560	11261795	0.0725	0.5665
chrY	59373566	769326	0.013	0.8698

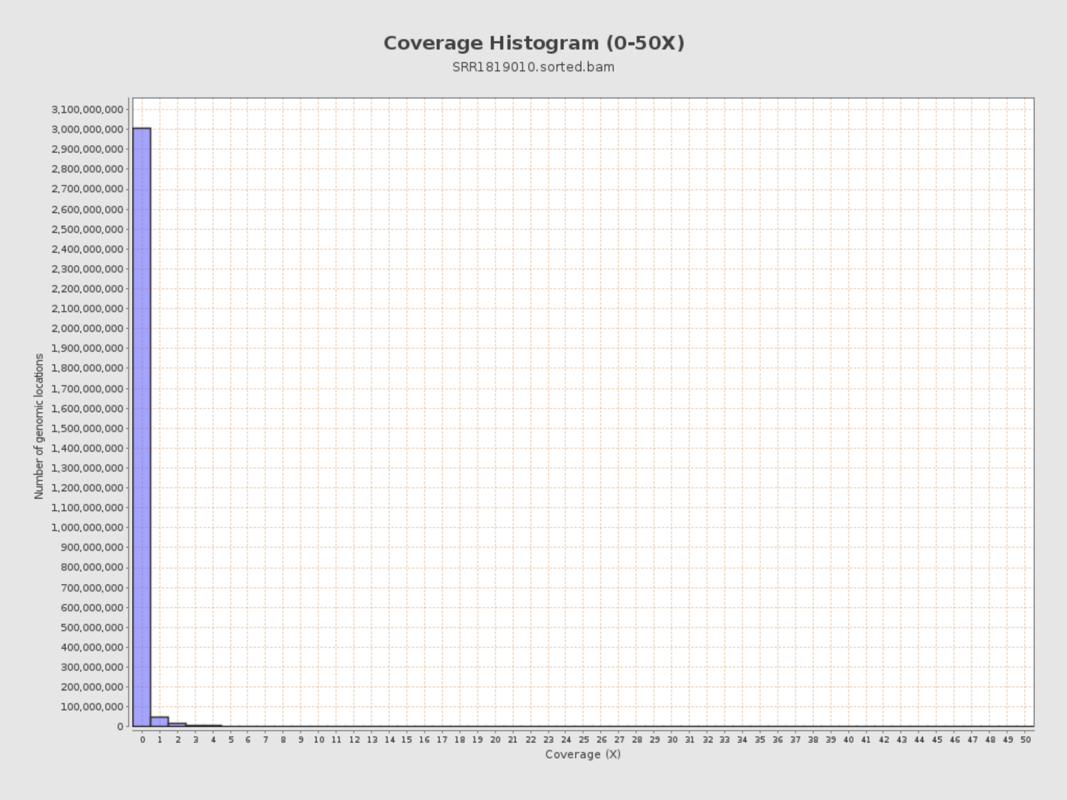
3. Results : Coverage across reference



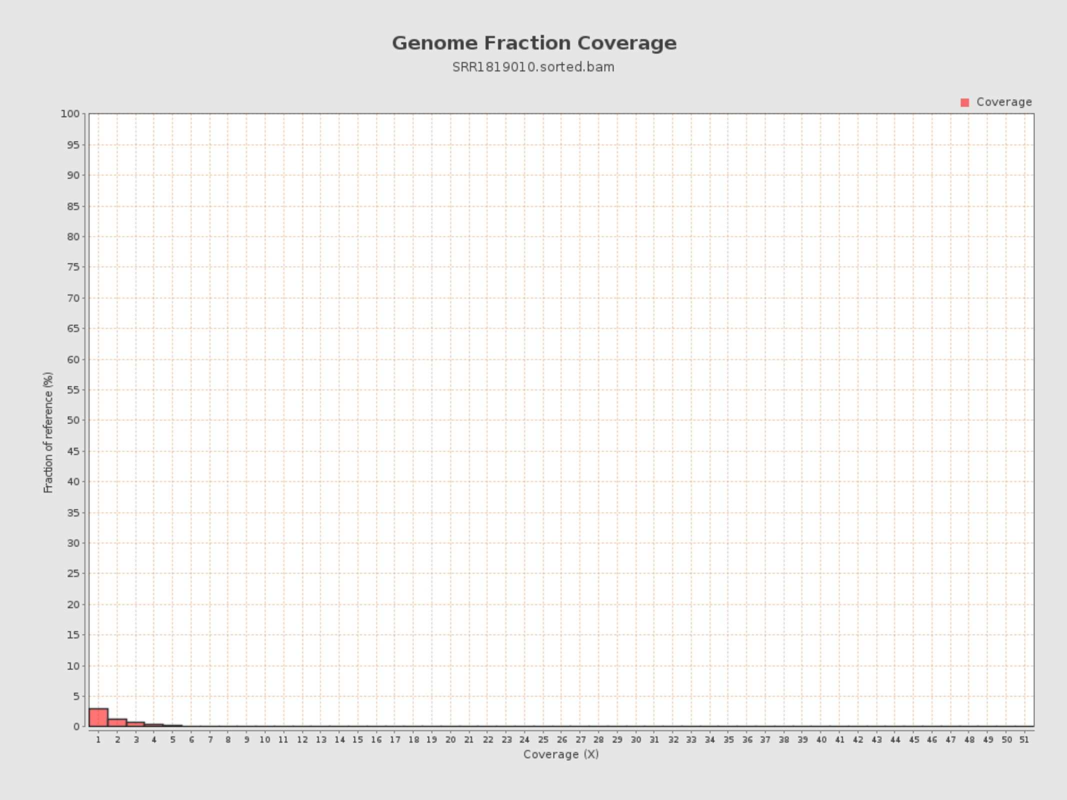
4. Results : Coverage Histogram



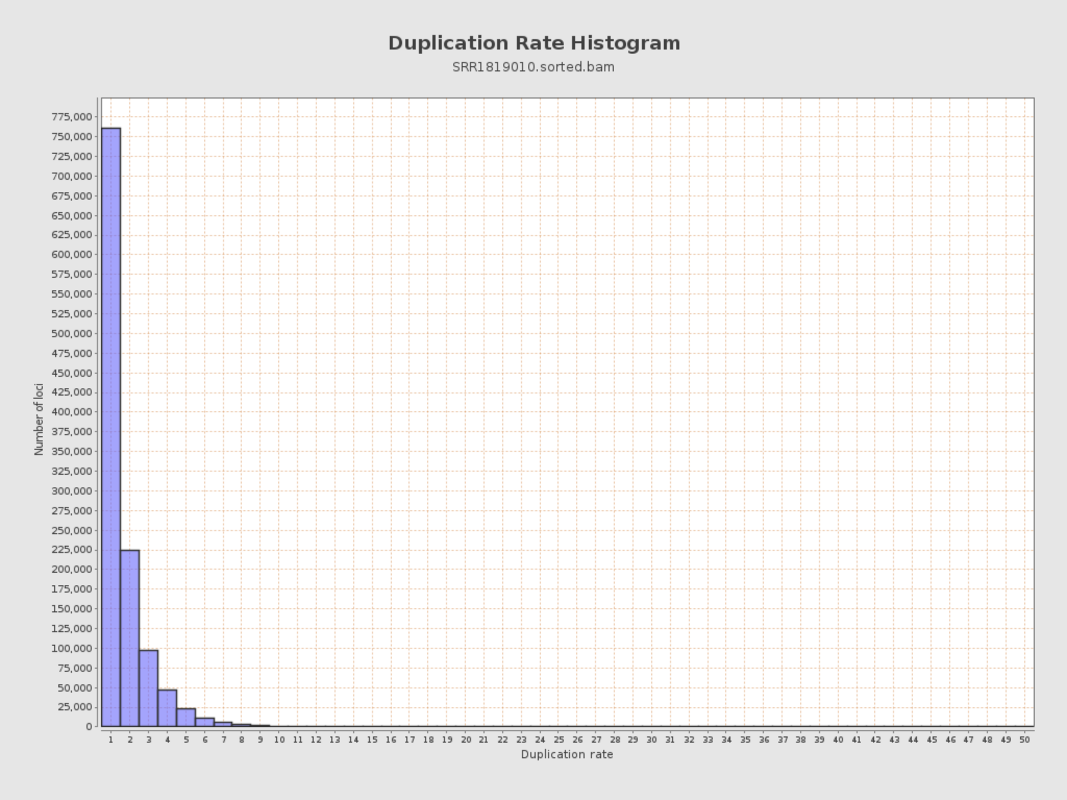
5. Results : Coverage Histogram (0-50X)



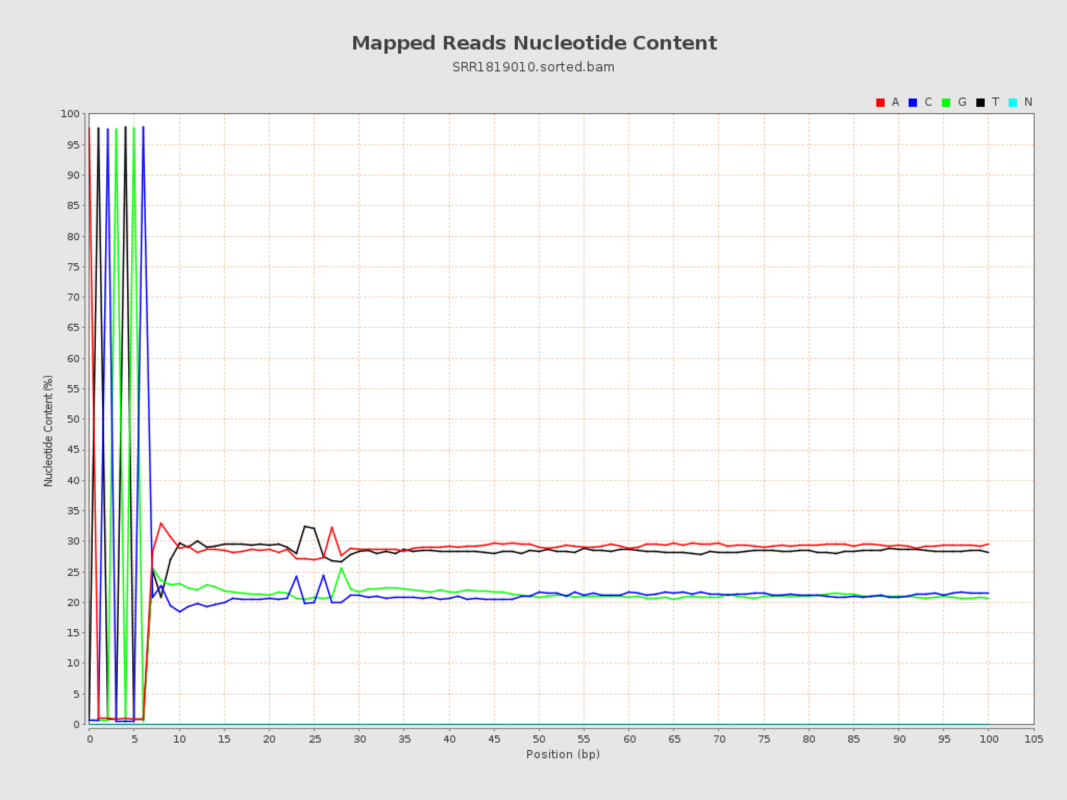
6. Results : Genome Fraction Coverage



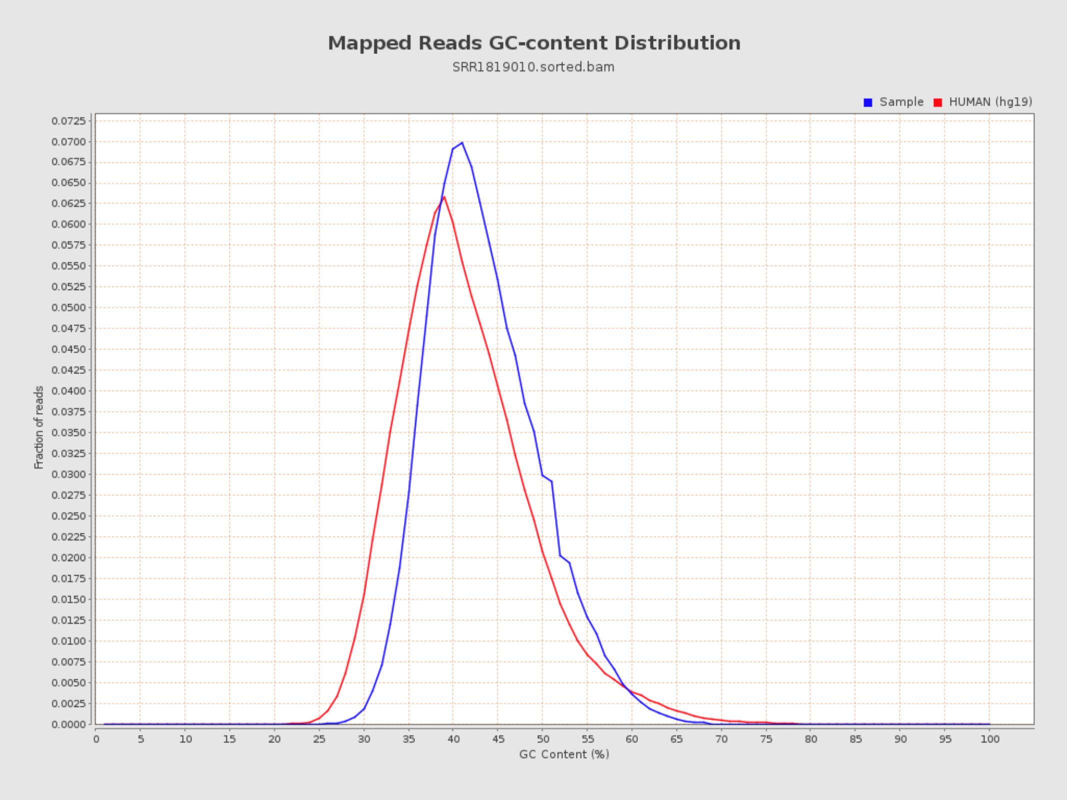
7. Results : Duplication Rate Histogram



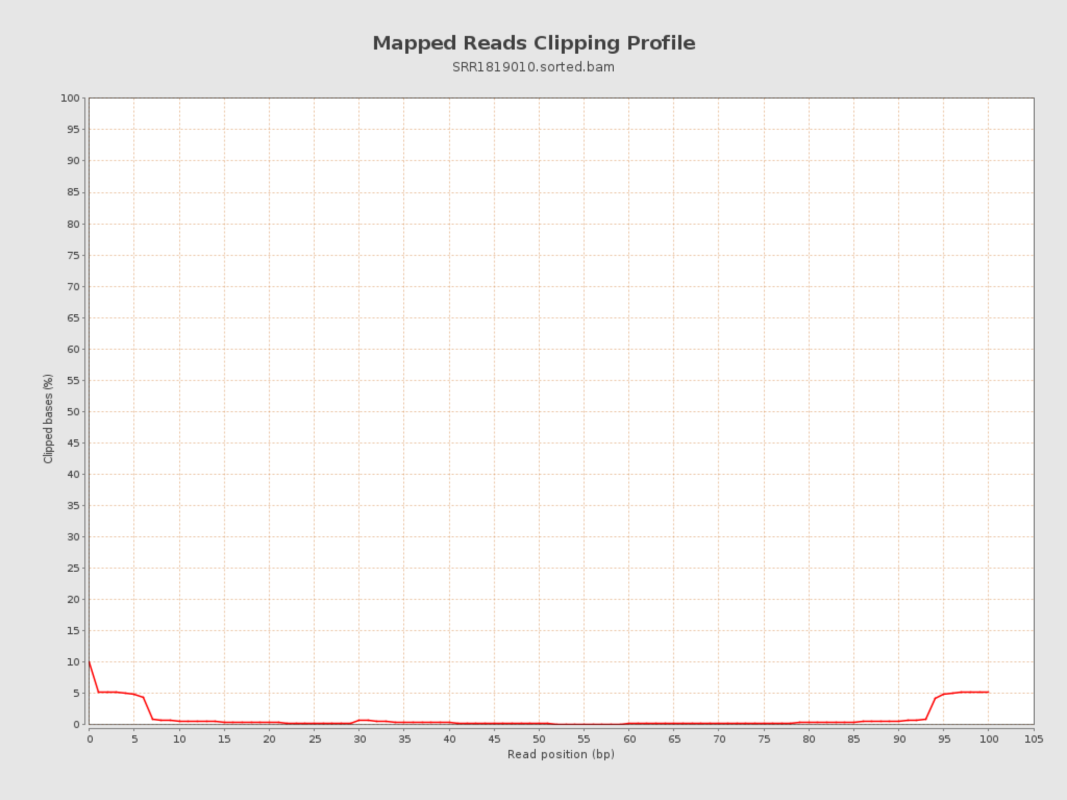
8. Results : Mapped Reads Nucleotide Content



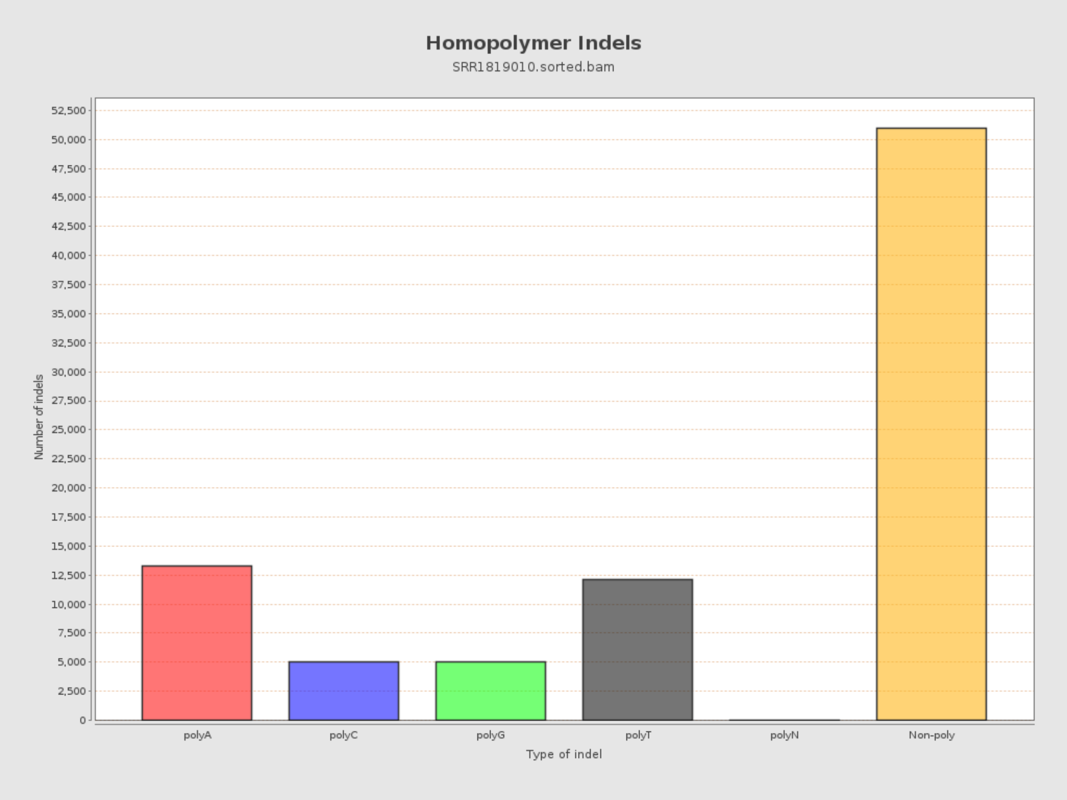
9. Results : Mapped Reads GC-content Distribution



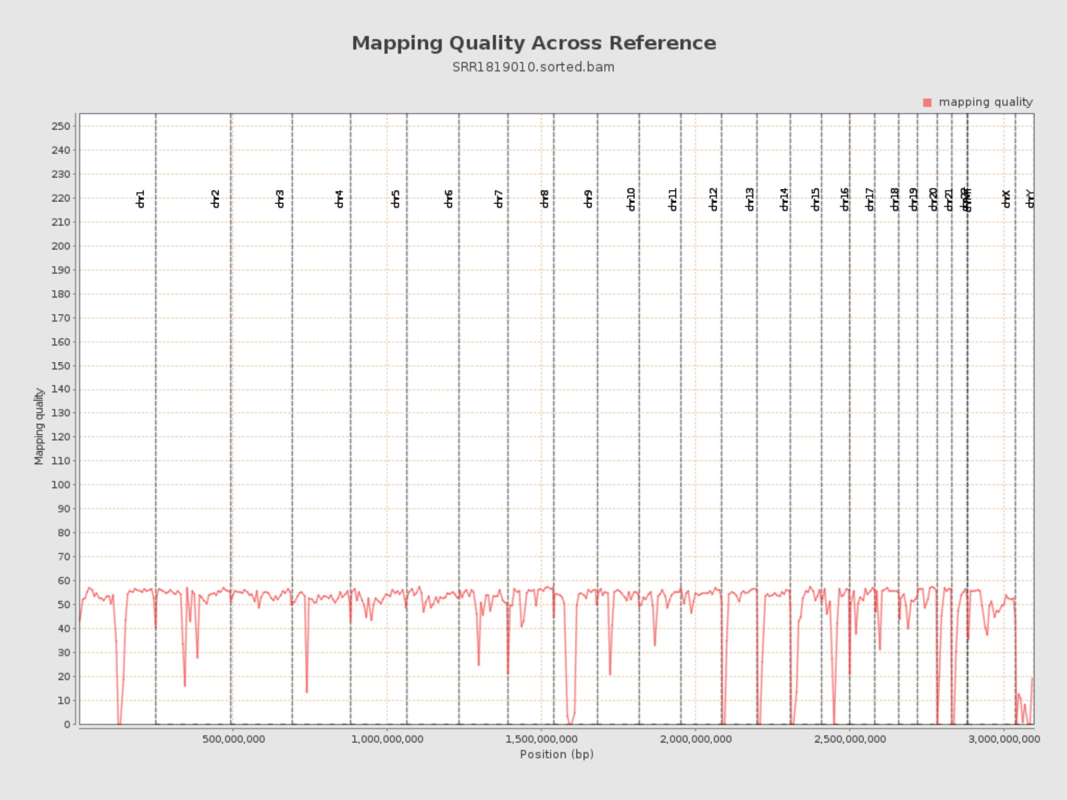
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram