Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:59:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818867.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_SRR1818867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818867.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:59:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818867.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,300,381
Mapped reads	2,271,676 / 98.75%
Unmapped reads	28,705 / 1.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,584 / 1.33%
Read min/max/mean length	30 / 101 / 101.51
Duplicated reads (estimated)	602,565 / 26.19%
Duplication rate	22.57%
Clipped reads	2,290,893 / 99.59%

2.2. ACGT Content

Number/percentage of A's	59,841,131 / 28.39%
Number/percentage of C's	44,137,562 / 20.94%
Number/percentage of T's	58,101,891 / 27.57%
Number/percentage of G's	48,669,192 / 23.09%
Number/percentage of N's	3,369 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0681

Standard Deviation	0.7954

2.4. Mapping Quality

Mean Mapping Quality	49.37

2.5. Mismatches and indels

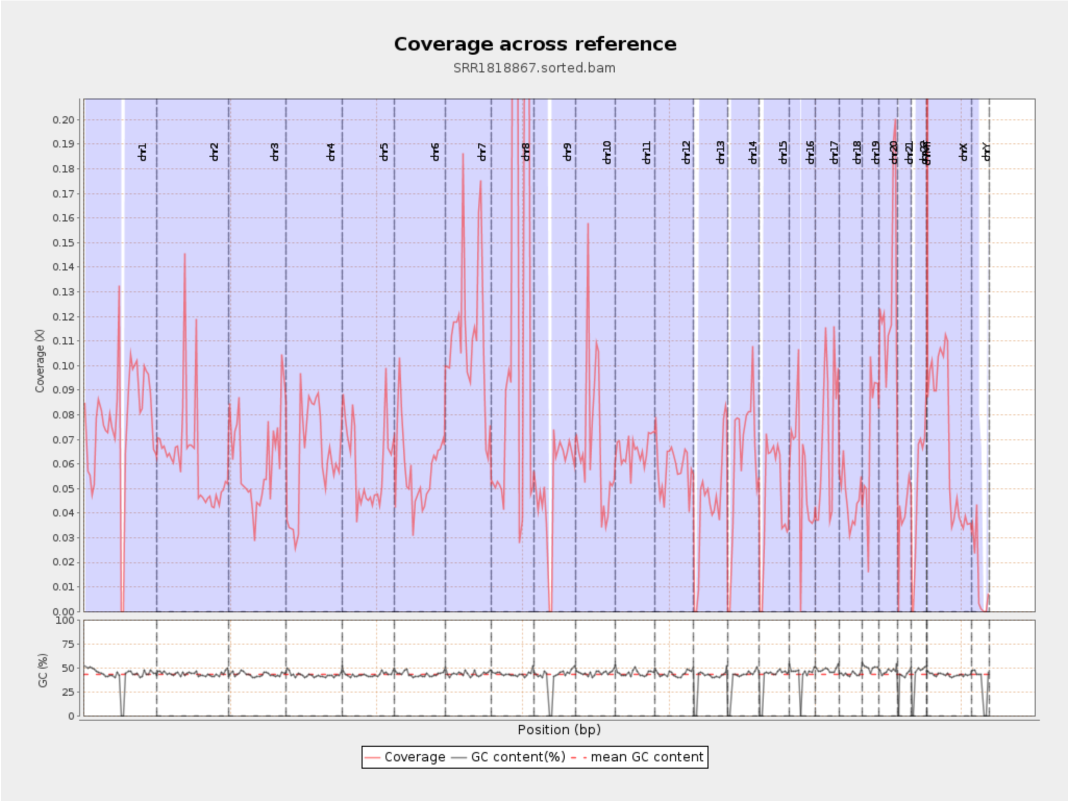
General error rate	0.62%
Mismatches	1,248,324
Insertions	24,726
Mapped reads with at least one insertion	1.05%
Deletions	66,740
Mapped reads with at least one deletion	2.87%
Homopolymer indels	42.97%

2.6. Chromosome stats

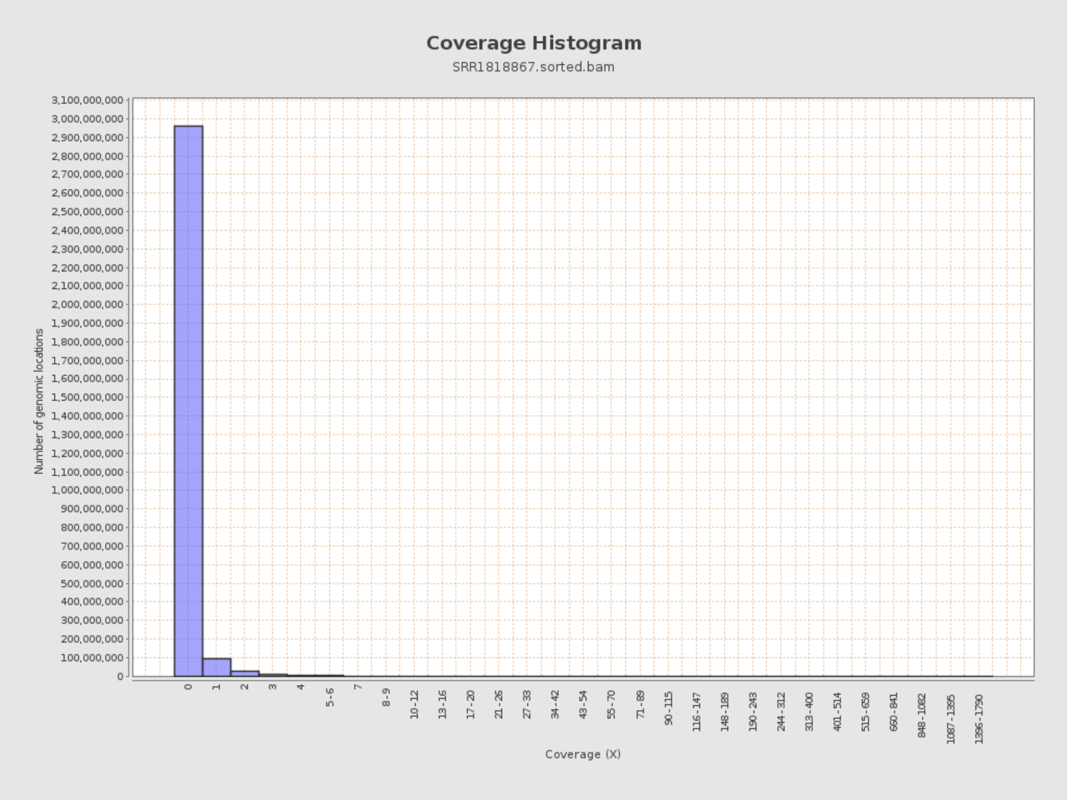
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19032209	0.0764	1.3135
chr2	243199373	15112813	0.0621	1.0829
chr3	198022430	12255667	0.0619	0.3577
chr4	191154276	12031627	0.0629	0.4851
chr5	180915260	10900424	0.0603	0.3691
chr6	171115067	9942988	0.0581	0.3875
chr7	159138663	17822802	0.112	1.7093

chr8	146364022	21110936	0.1442	0.7128
chr9	141213431	7287382	0.0516	0.6251
chr10	135534747	9219155	0.068	0.9436
chr11	135006516	8843455	0.0655	0.4665
chr12	133851895	7840375	0.0586	0.3544
chr13	115169878	5073113	0.044	0.2952
chr14	107349540	6766841	0.063	0.3903
chr15	102531392	4674968	0.0456	0.3034
chr16	90354753	4987543	0.0552	0.7062
chr17	81195210	5723187	0.0705	0.5132
chr18	78077248	3564809	0.0457	0.7617
chr19	59128983	4111836	0.0695	1.1844
chr20	63025520	8383812	0.133	0.5781
chr21	48129895	1933388	0.0402	0.3572
chr22	51304566	2495035	0.0486	0.3551
chrMT	16571	322129	19.4393	12.511
chrX	155270560	10652503	0.0686	0.4609
chrY	59373566	793257	0.0134	0.9473

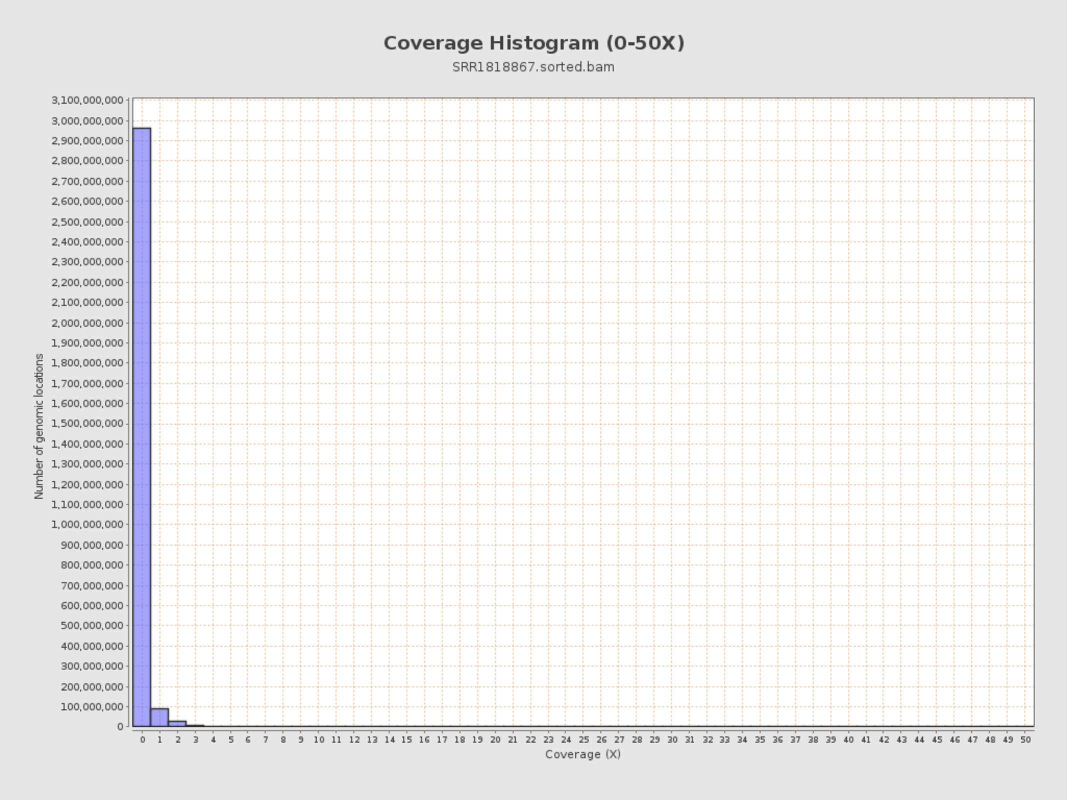
3. Results : Coverage across reference



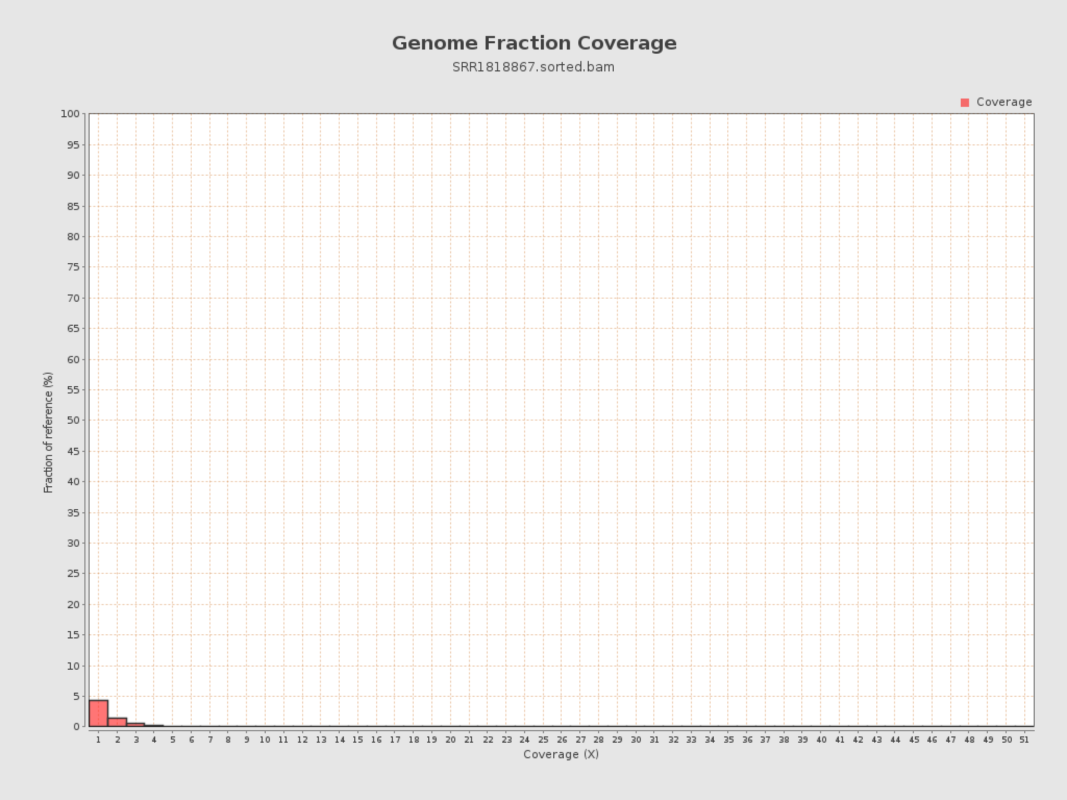
4. Results : Coverage Histogram



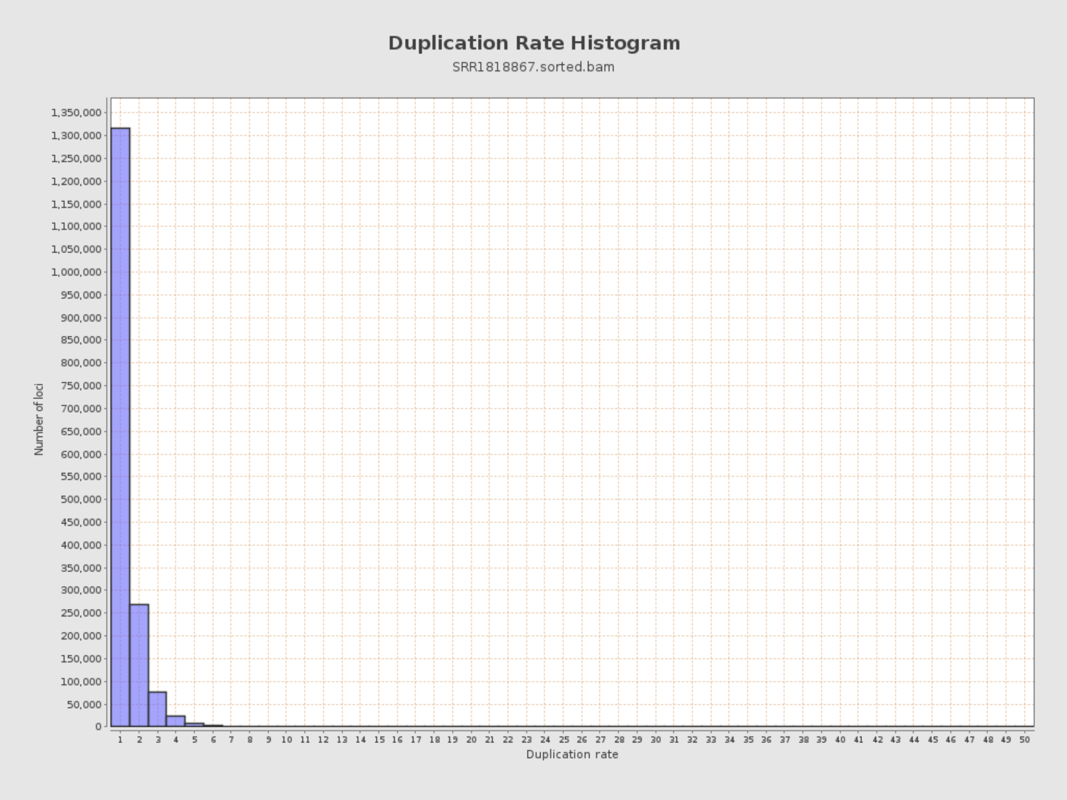
5. Results : Coverage Histogram (0-50X)



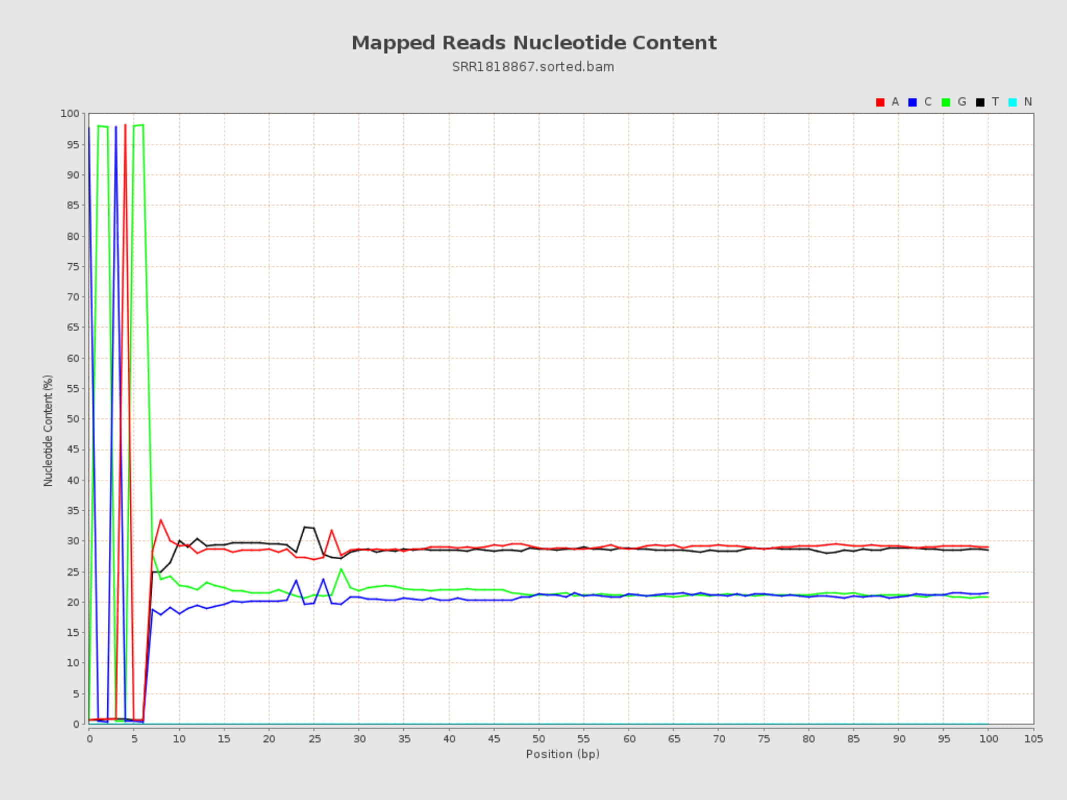
6. Results : Genome Fraction Coverage



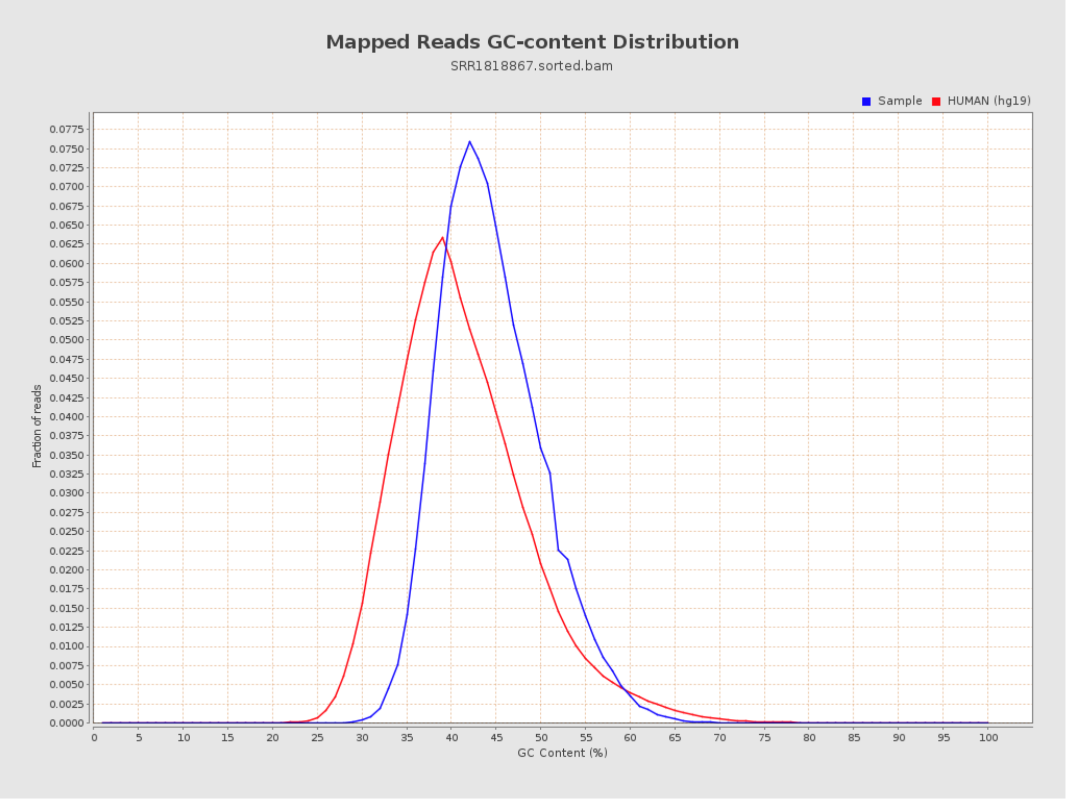
7. Results : Duplication Rate Histogram



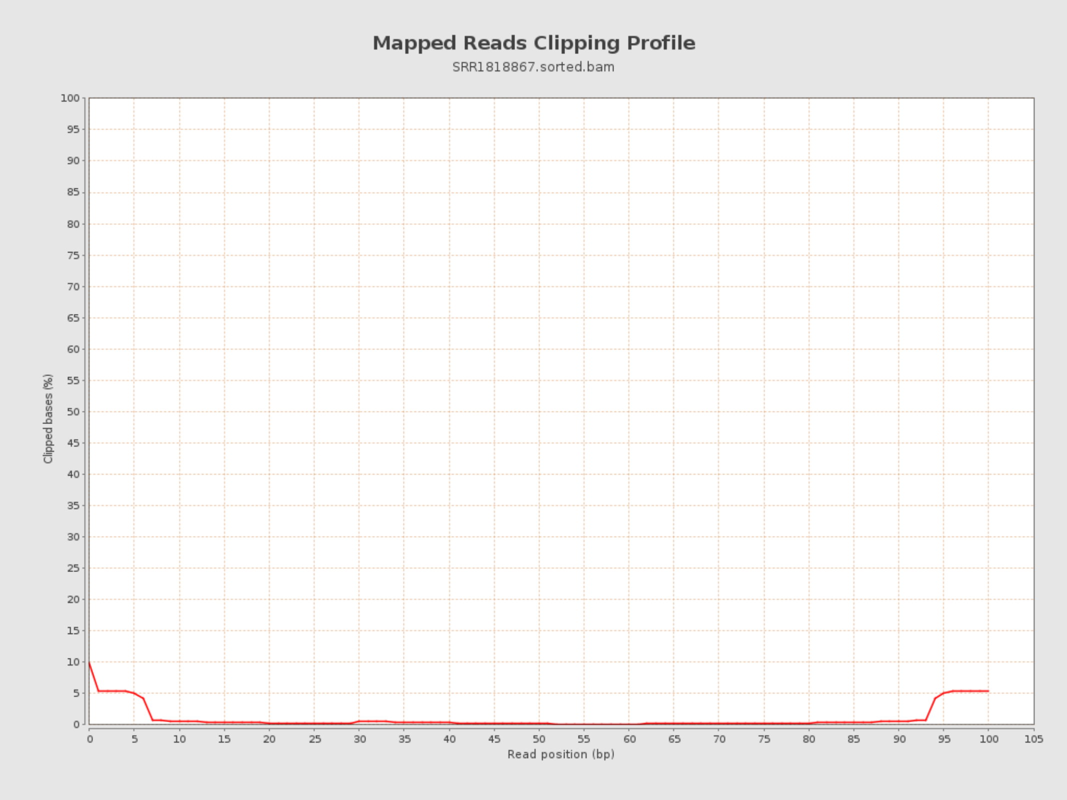
8. Results : Mapped Reads Nucleotide Content



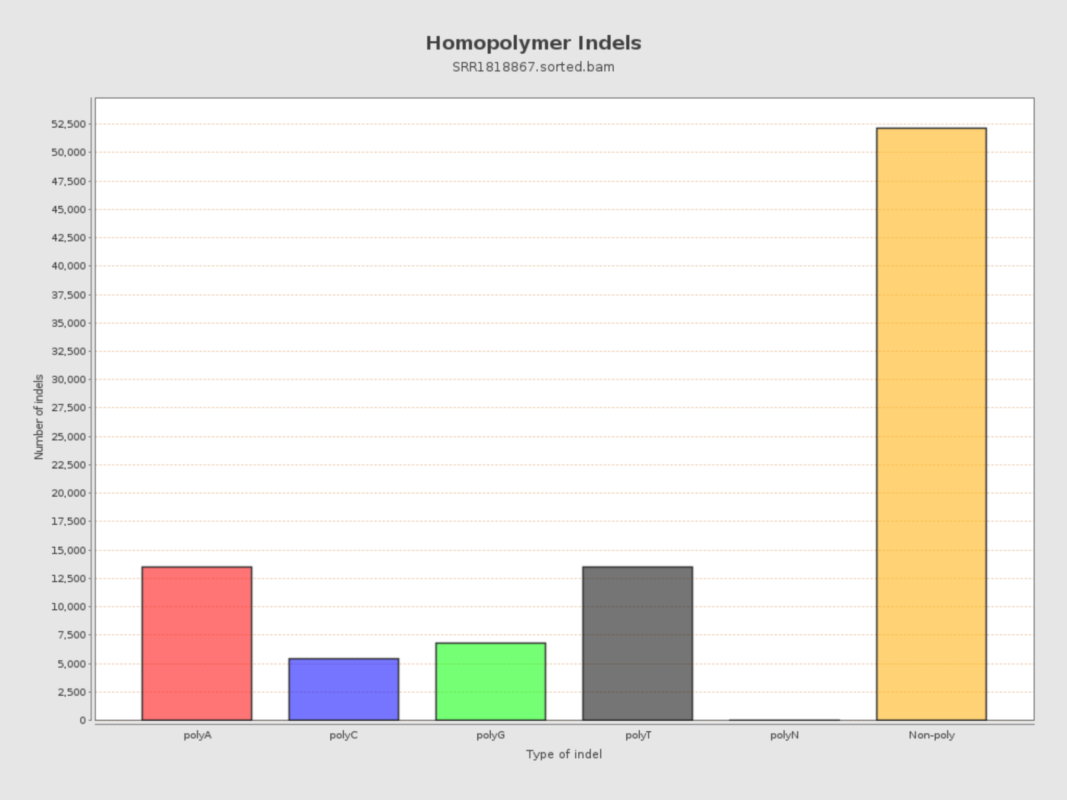
9. Results : Mapped Reads GC-content Distribution



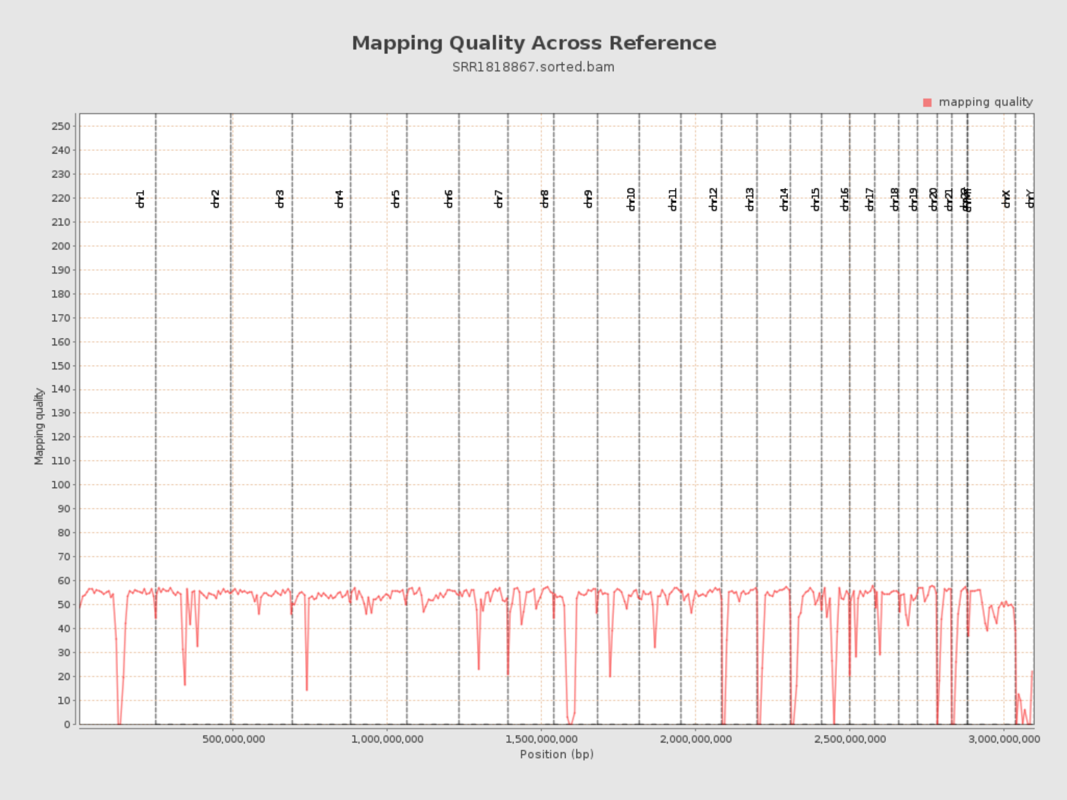
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram