Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:44:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818941.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_SRR1818941 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818941.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:44:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818941.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,830,099
Mapped reads	2,657,509 / 93.9%
Unmapped reads	172,590 / 6.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,048 / 1.2%
Read min/max/mean length	30 / 101 / 101.46
Duplicated reads (estimated)	1,338,331 / 47.29%
Duplication rate	41.5%
Clipped reads	2,678,993 / 94.66%

2.2. ACGT Content

Number/percentage of A's	72,067,698 / 29.28%
Number/percentage of C's	51,521,838 / 20.93%
Number/percentage of T's	71,113,681 / 28.89%
Number/percentage of G's	51,402,932 / 20.89%
Number/percentage of N's	10,456 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0795

Standard Deviation	0.8438

2.4. Mapping Quality

Mean Mapping Quality	49.46

2.5. Mismatches and indels

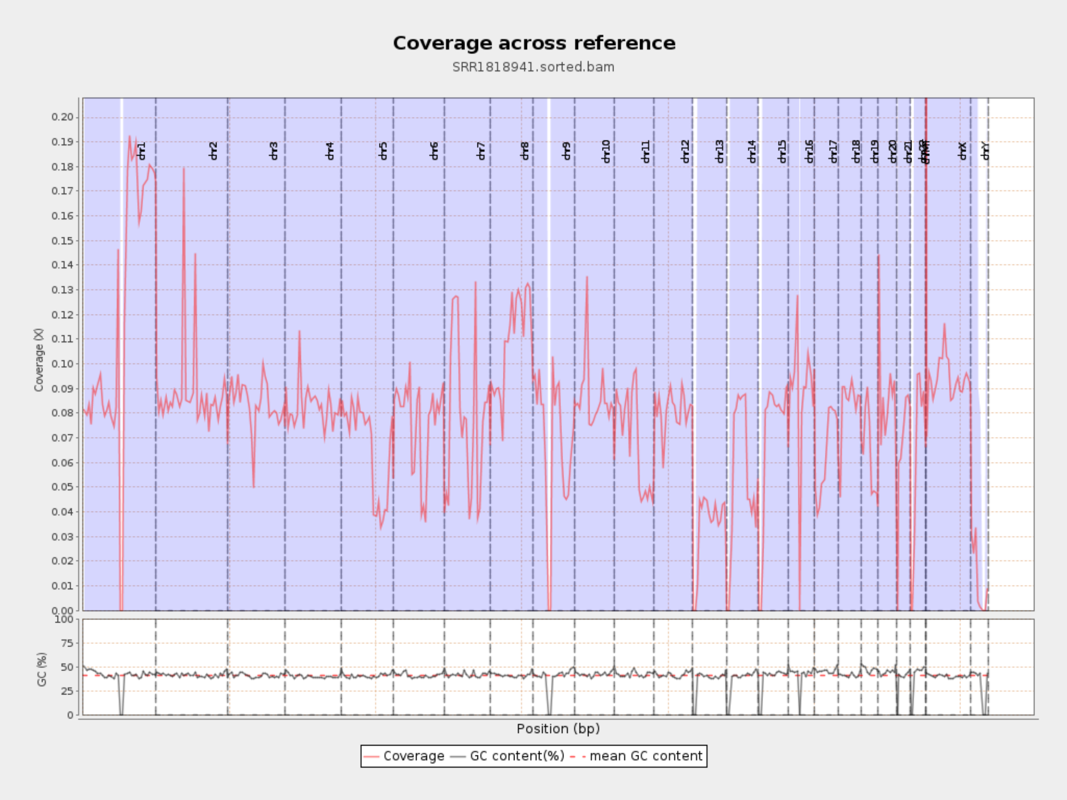
General error rate	0.66%
Mismatches	1,539,227
Insertions	34,041
Mapped reads with at least one insertion	1.25%
Deletions	75,151
Mapped reads with at least one deletion	2.77%
Homopolymer indels	42.44%

2.6. Chromosome stats

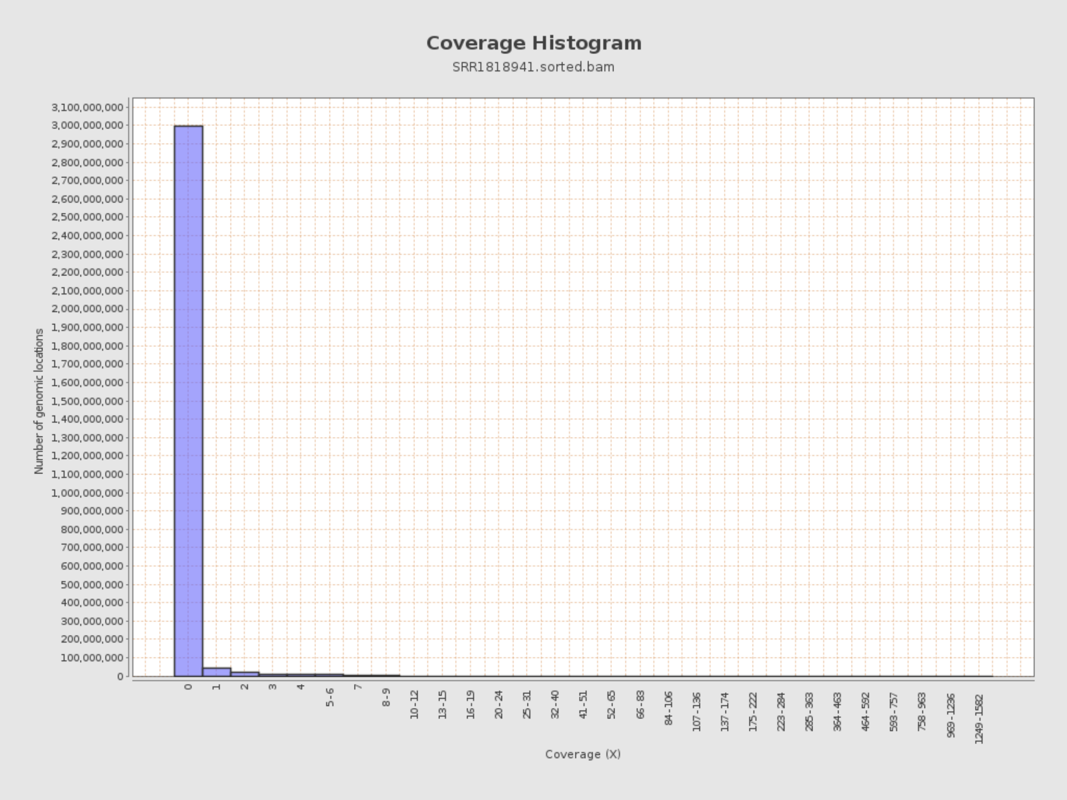
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29823819	0.1197	1.514
chr2	243199373	21671364	0.0891	1.1771
chr3	198022430	16553883	0.0836	0.5963
chr4	191154276	15859632	0.083	0.6323
chr5	180915260	12006052	0.0664	0.5395
chr6	171115067	13179318	0.077	0.6107
chr7	159138663	12467634	0.0783	0.7273

chr8	146364022	16052818	0.1097	0.7658
chr9	141213431	9503176	0.0673	0.9485
chr10	135534747	11706947	0.0864	0.9222
chr11	135006516	9274155	0.0687	0.6095
chr12	133851895	10927749	0.0816	0.5965
chr13	115169878	3927378	0.0341	0.3755
chr14	107349540	5868082	0.0547	0.519
chr15	102531392	6992627	0.0682	0.5362
chr16	90354753	7735863	0.0856	0.8646
chr17	81195210	5171794	0.0637	0.5717
chr18	78077248	6436726	0.0824	1.1338
chr19	59128983	3829219	0.0648	1.1898
chr20	63025520	5530368	0.0877	0.6494
chr21	48129895	3275106	0.068	0.584
chr22	51304566	3158436	0.0616	0.5557
chrMT	16571	14885	0.8983	1.8666
chrX	155270560	14580150	0.0939	0.7456
chrY	59373566	706280	0.0119	0.6236

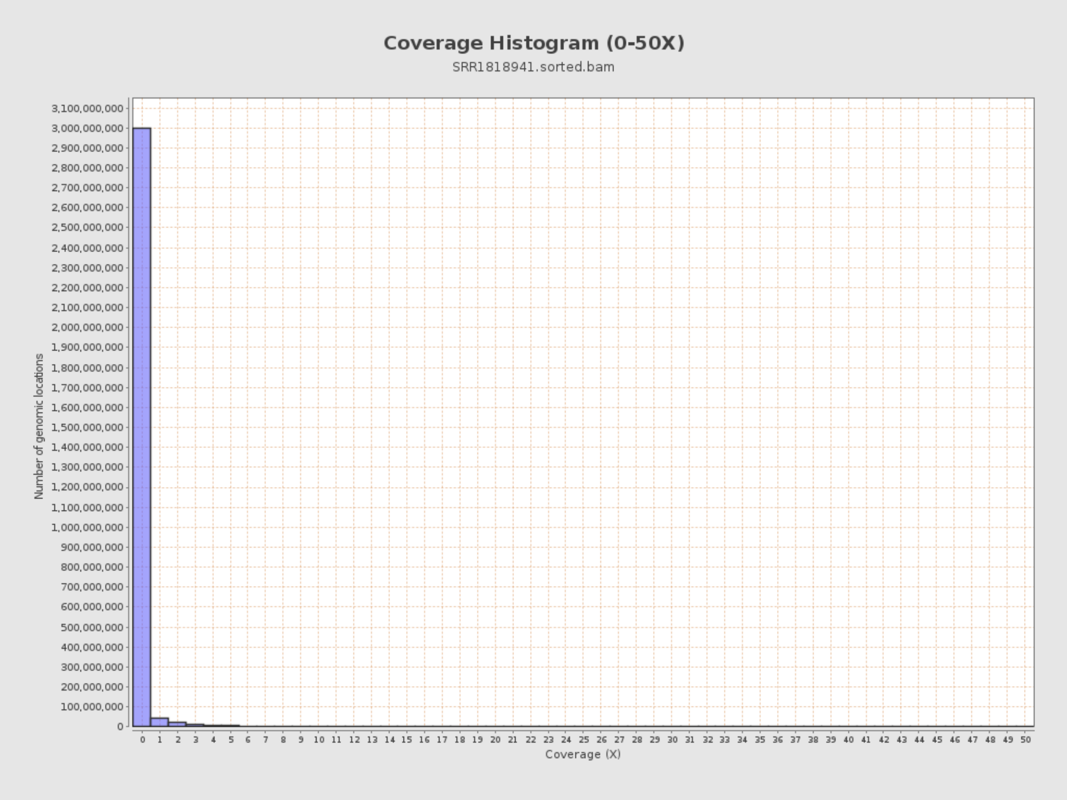
3. Results : Coverage across reference



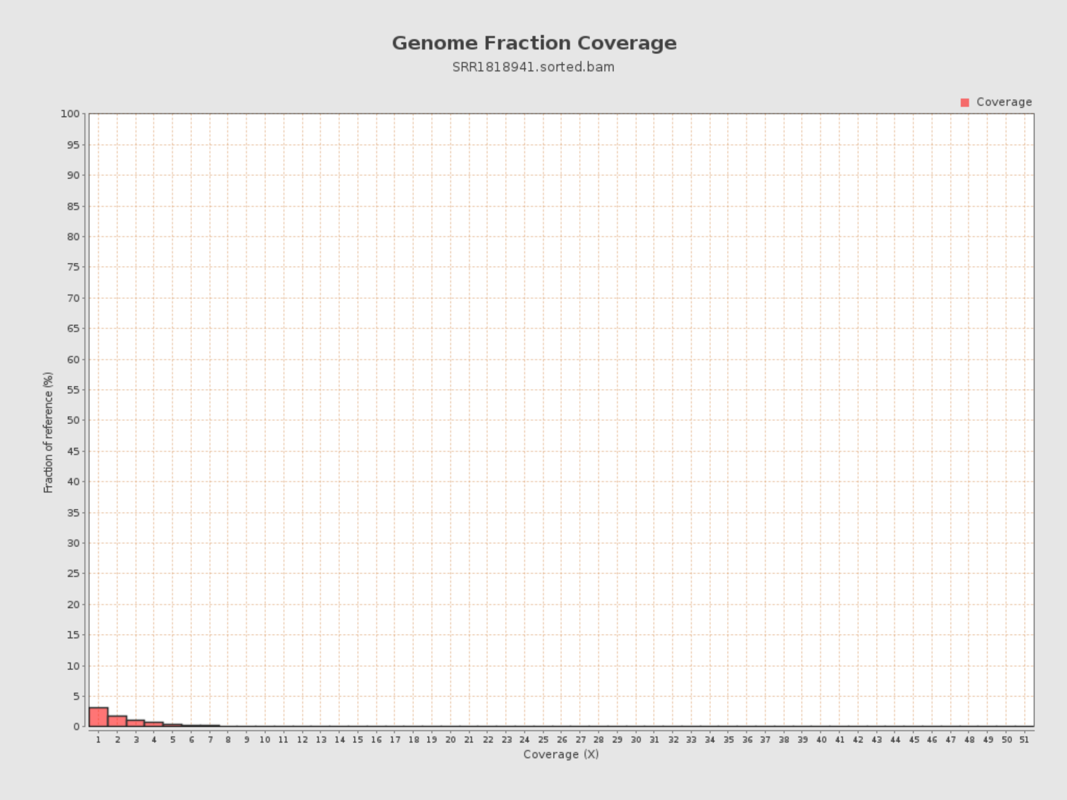
4. Results : Coverage Histogram



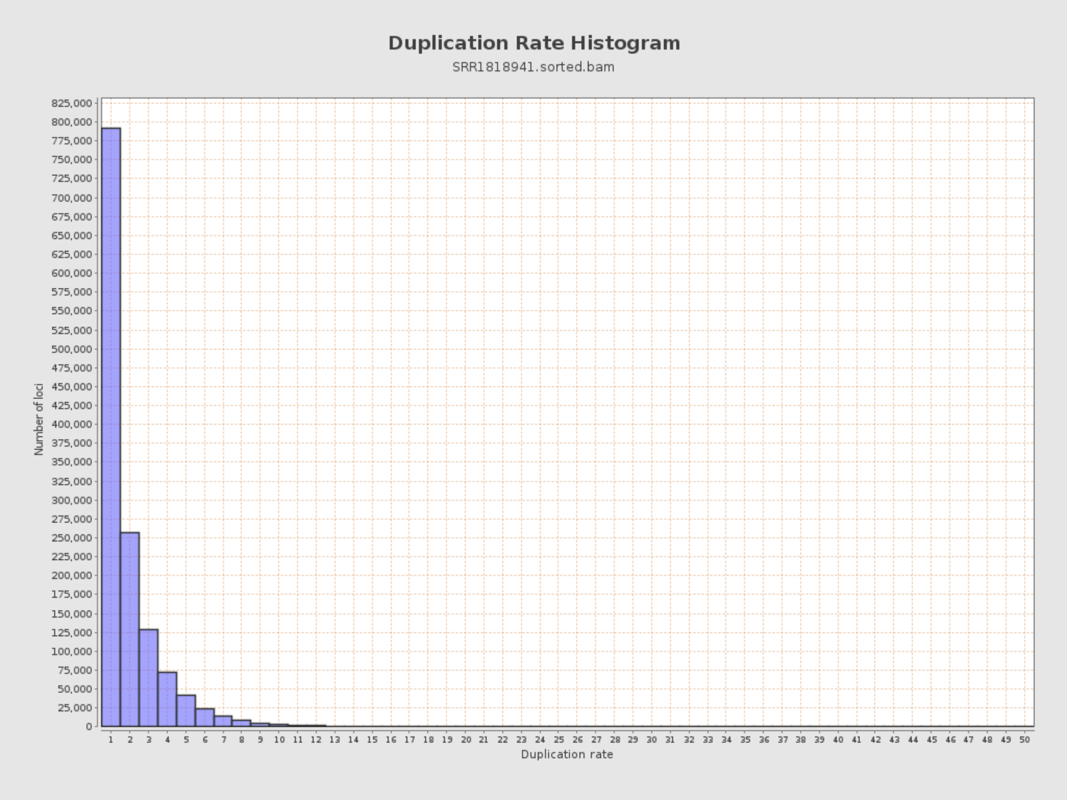
5. Results : Coverage Histogram (0-50X)



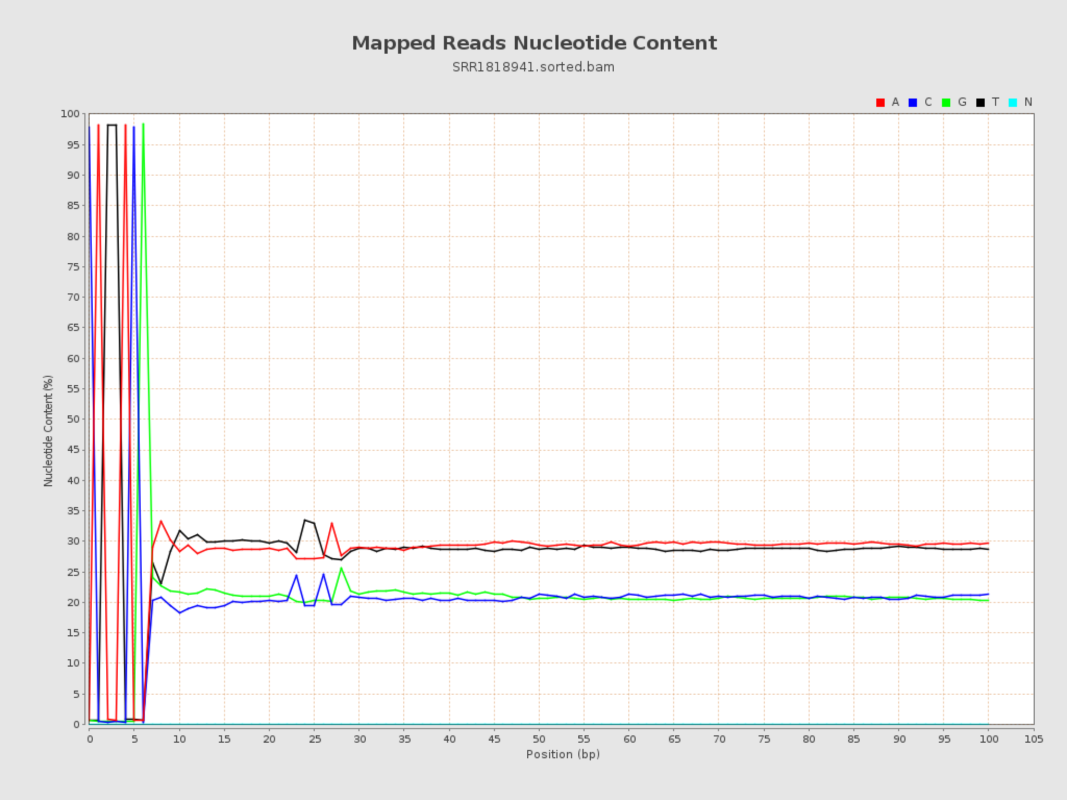
6. Results : Genome Fraction Coverage



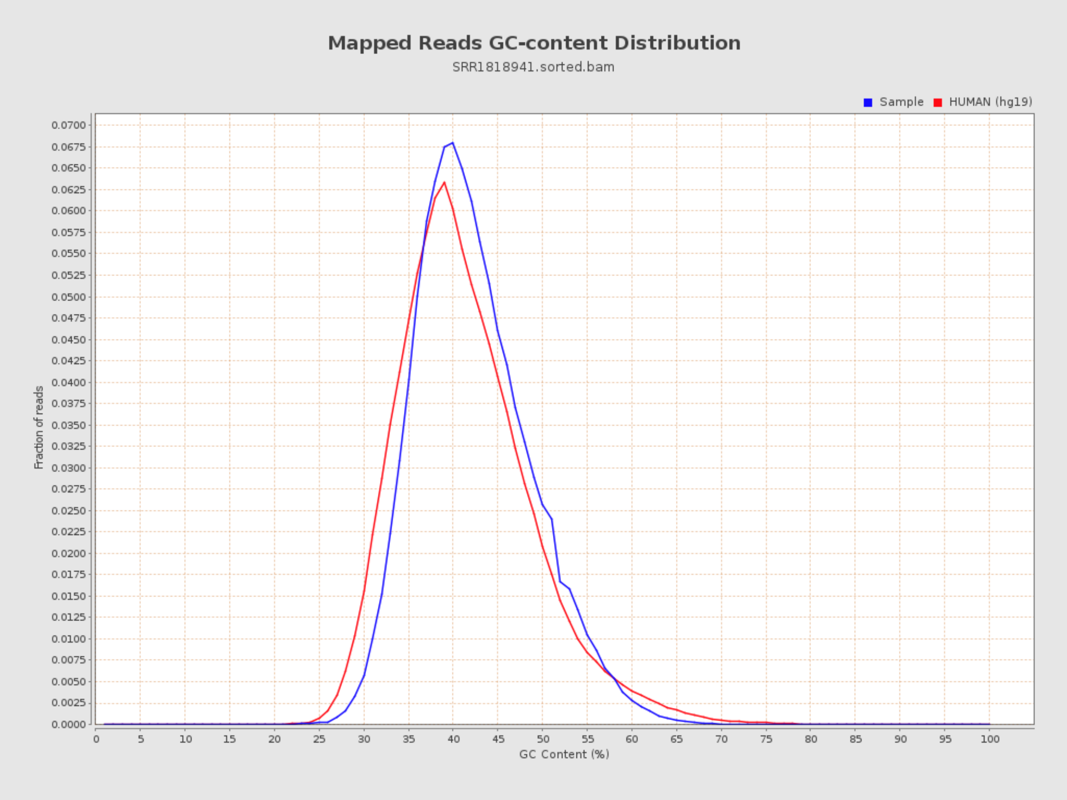
7. Results : Duplication Rate Histogram



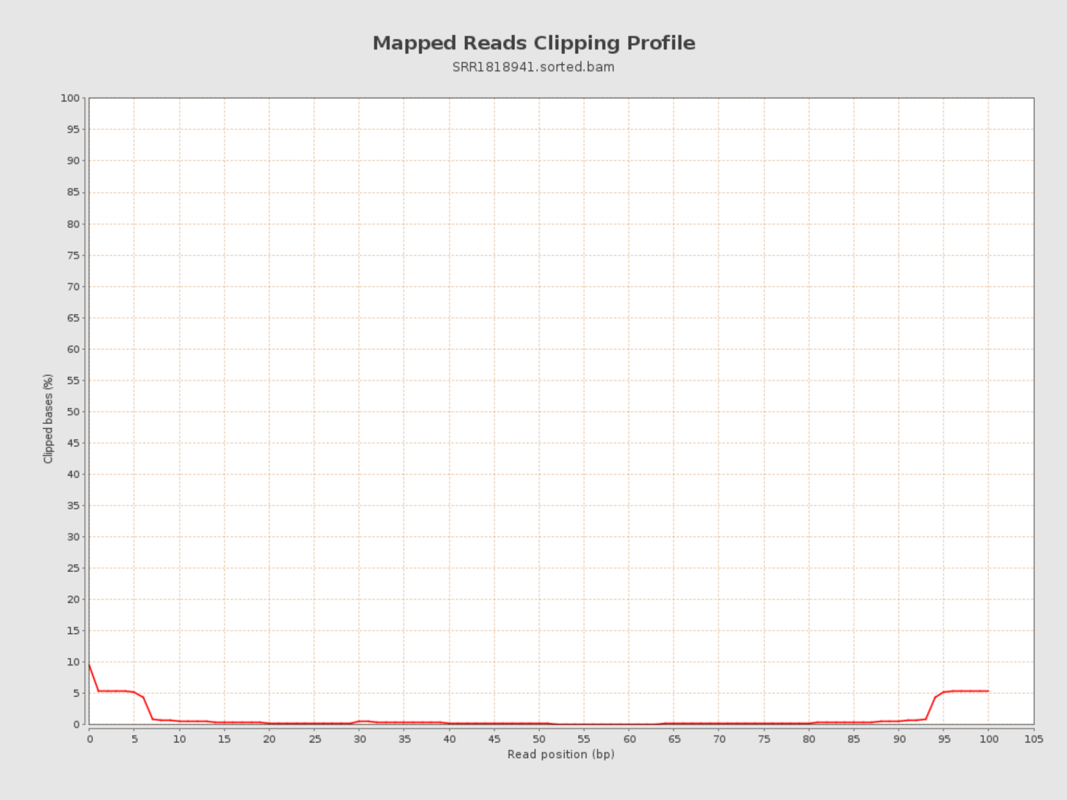
8. Results : Mapped Reads Nucleotide Content



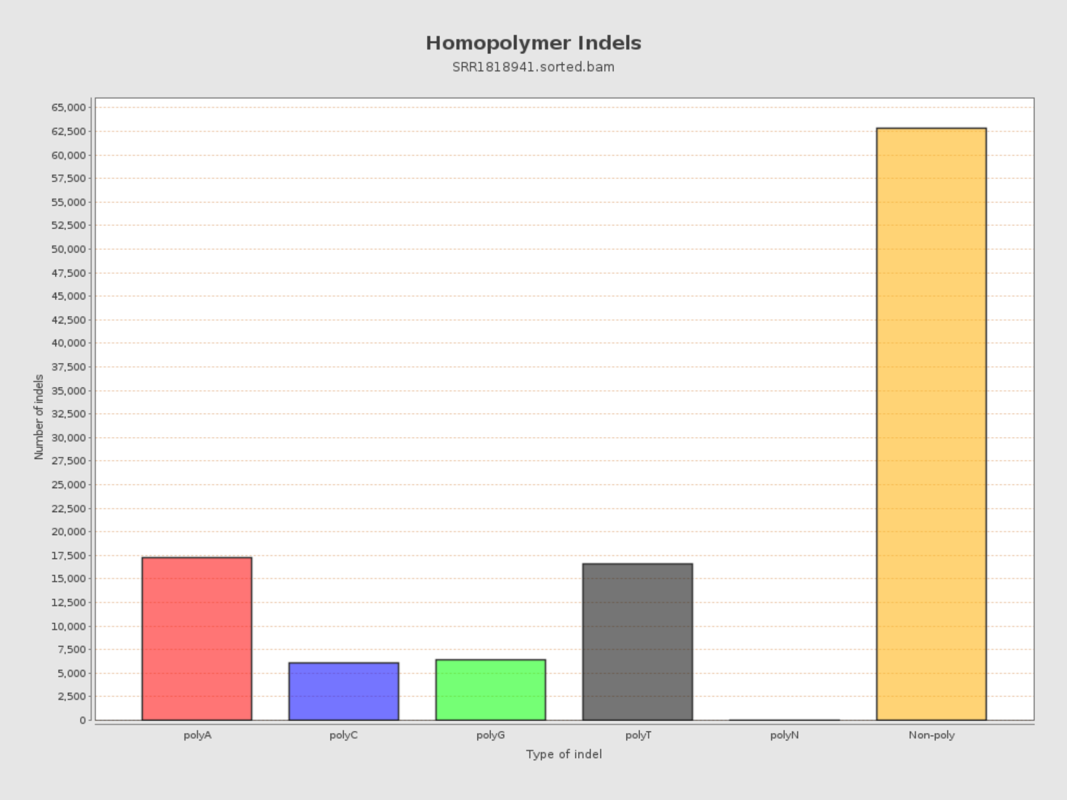
9. Results : Mapped Reads GC-content Distribution



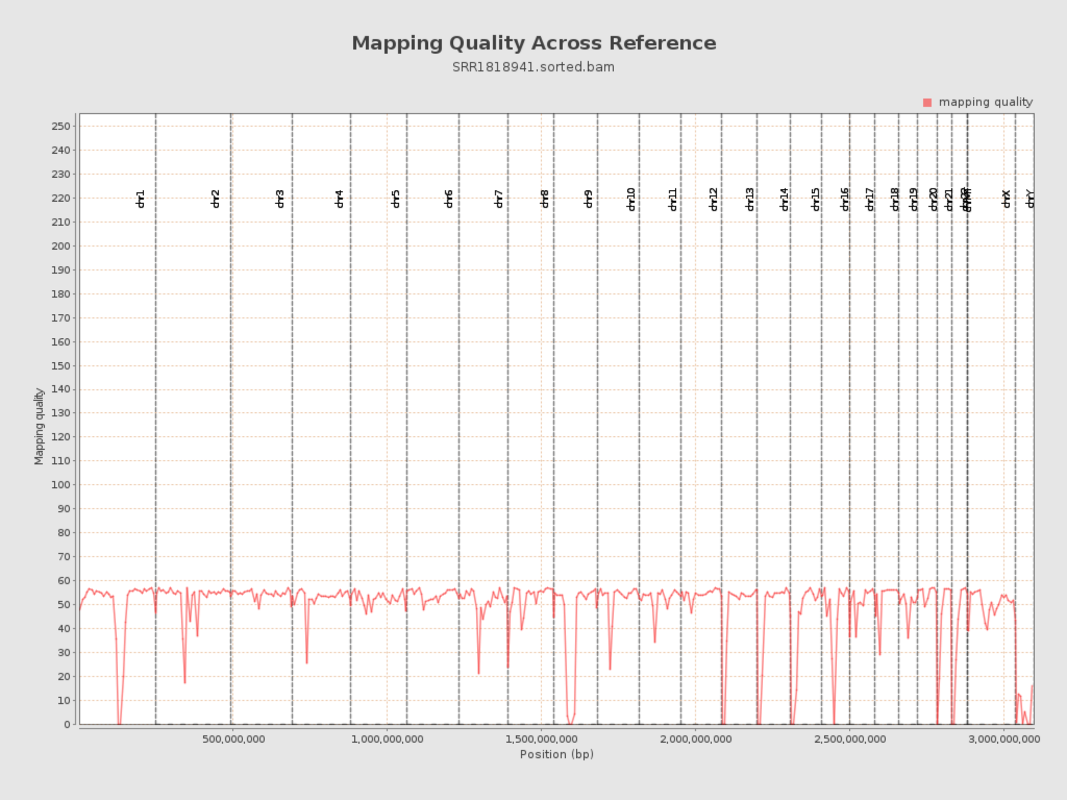
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram