Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 09:19:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818935.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_SRR1818935 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818935.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 09:18:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818935.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,505,383
Mapped reads	2,391,127 / 95.44%
Unmapped reads	114,256 / 4.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,145 / 1.16%
Read min/max/mean length	30 / 101 / 101.45
Duplicated reads (estimated)	1,482,455 / 59.17%
Duplication rate	48.92%
Clipped reads	2,396,597 / 95.66%

2.2. ACGT Content

Number/percentage of A's	66,091,805 / 29.75%
Number/percentage of C's	44,101,777 / 19.85%
Number/percentage of T's	64,171,111 / 28.88%
Number/percentage of G's	47,812,359 / 21.52%
Number/percentage of N's	10,142 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.0718

Standard Deviation	0.7775

2.4. Mapping Quality

Mean Mapping Quality	50.13

2.5. Mismatches and indels

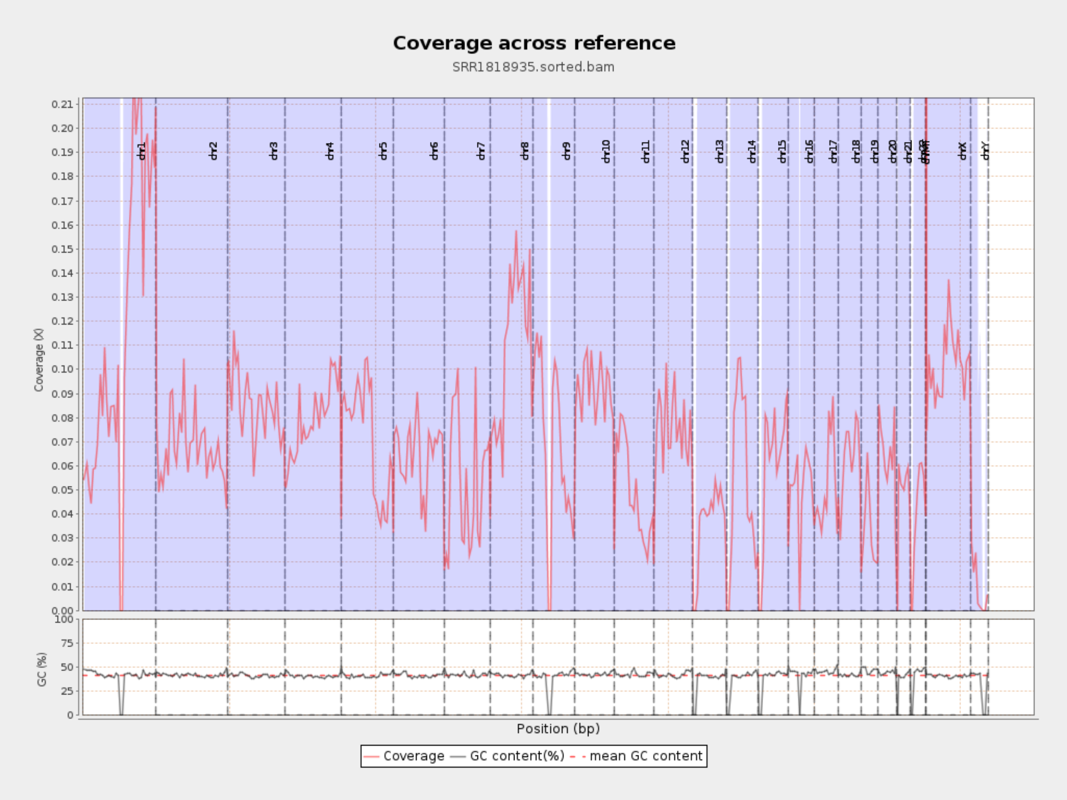
General error rate	0.61%
Mismatches	1,295,382
Insertions	27,528
Mapped reads with at least one insertion	1.13%
Deletions	66,543
Mapped reads with at least one deletion	2.73%
Homopolymer indels	44.38%

2.6. Chromosome stats

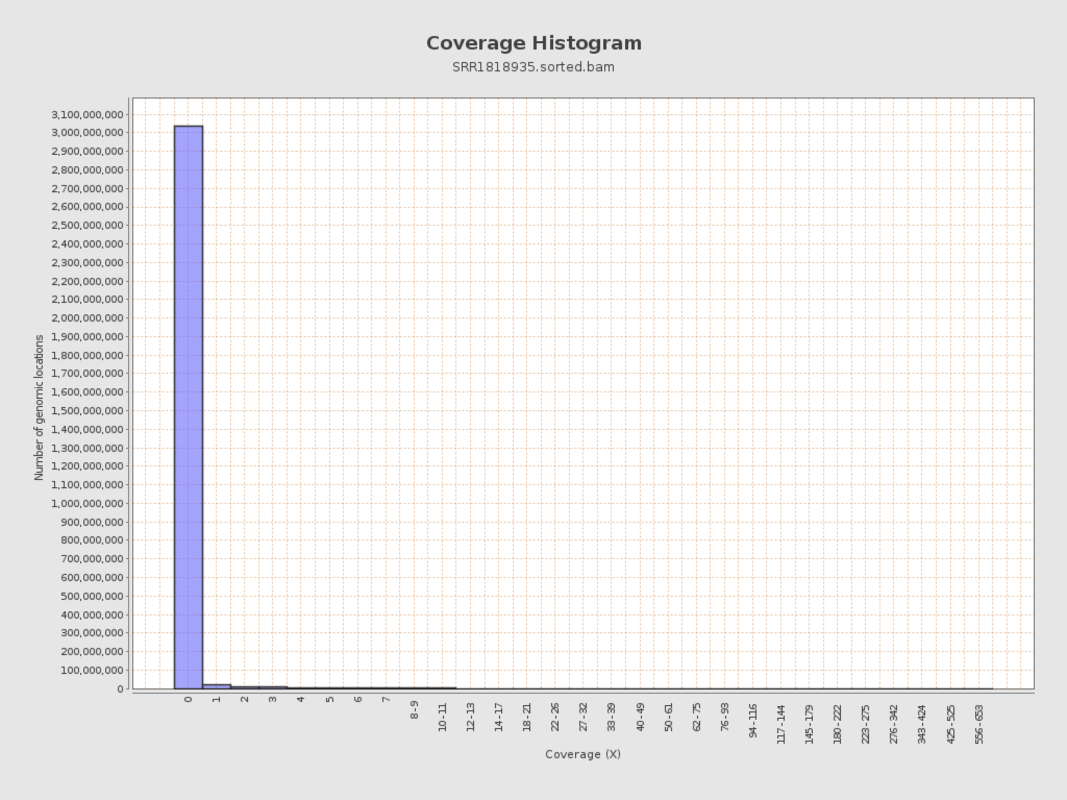
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28850050	0.1157	1.044
chr2	243199373	16414206	0.0675	0.8825
chr3	198022430	16954217	0.0856	0.7687
chr4	191154276	15272741	0.0799	0.7666
chr5	180915260	12998735	0.0718	0.7128
chr6	171115067	11156327	0.0652	0.6807
chr7	159138663	8386938	0.0527	0.6416

chr8	146364022	16213328	0.1108	0.936
chr9	141213431	9694144	0.0686	0.8087
chr10	135534747	12513855	0.0923	0.9202
chr11	135006516	6611253	0.049	0.5989
chr12	133851895	10132914	0.0757	0.7399
chr13	115169878	4177134	0.0363	0.4939
chr14	107349540	5852273	0.0545	0.6258
chr15	102531392	6035207	0.0589	0.6422
chr16	90354753	4438450	0.0491	0.6974
chr17	81195210	4308132	0.0531	0.6396
chr18	78077248	4900517	0.0628	0.8559
chr19	59128983	2028444	0.0343	0.6791
chr20	63025520	4192466	0.0665	0.7171
chr21	48129895	2348984	0.0488	0.5939
chr22	51304566	2047097	0.0399	0.5772
chrMT	16571	363249	21.9208	19.7538
chrX	155270560	15870966	0.1022	0.8637
chrY	59373566	539989	0.0091	0.4979

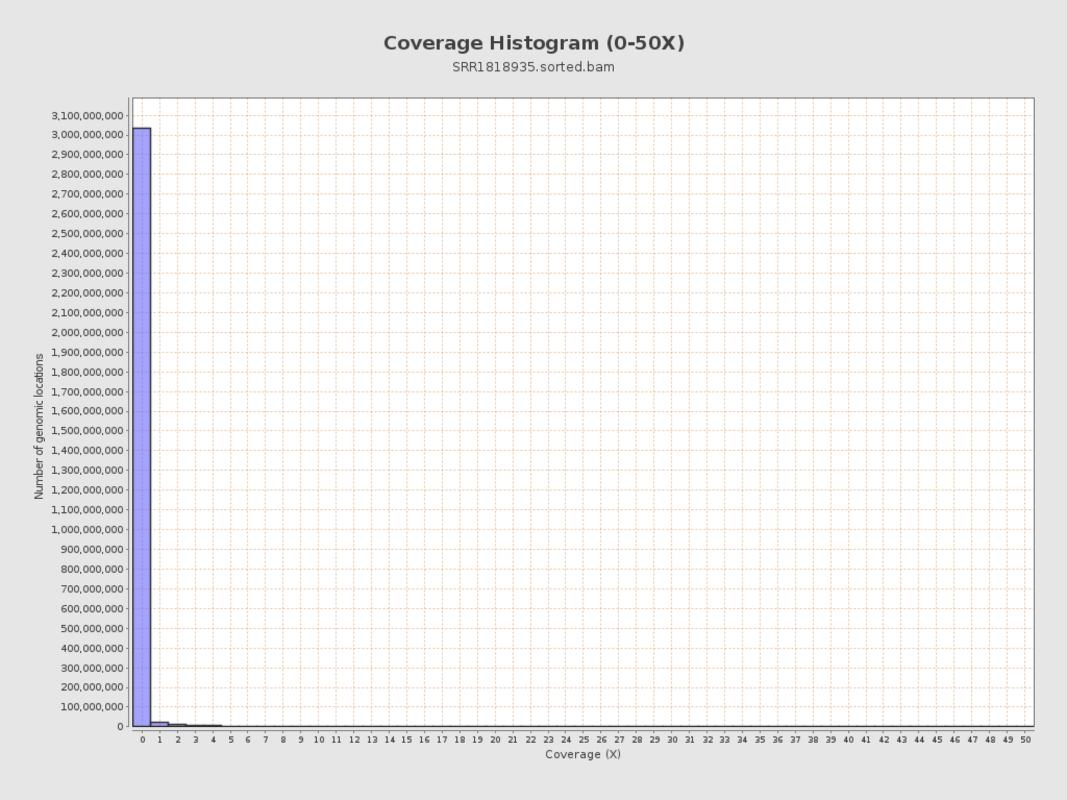
3. Results : Coverage across reference



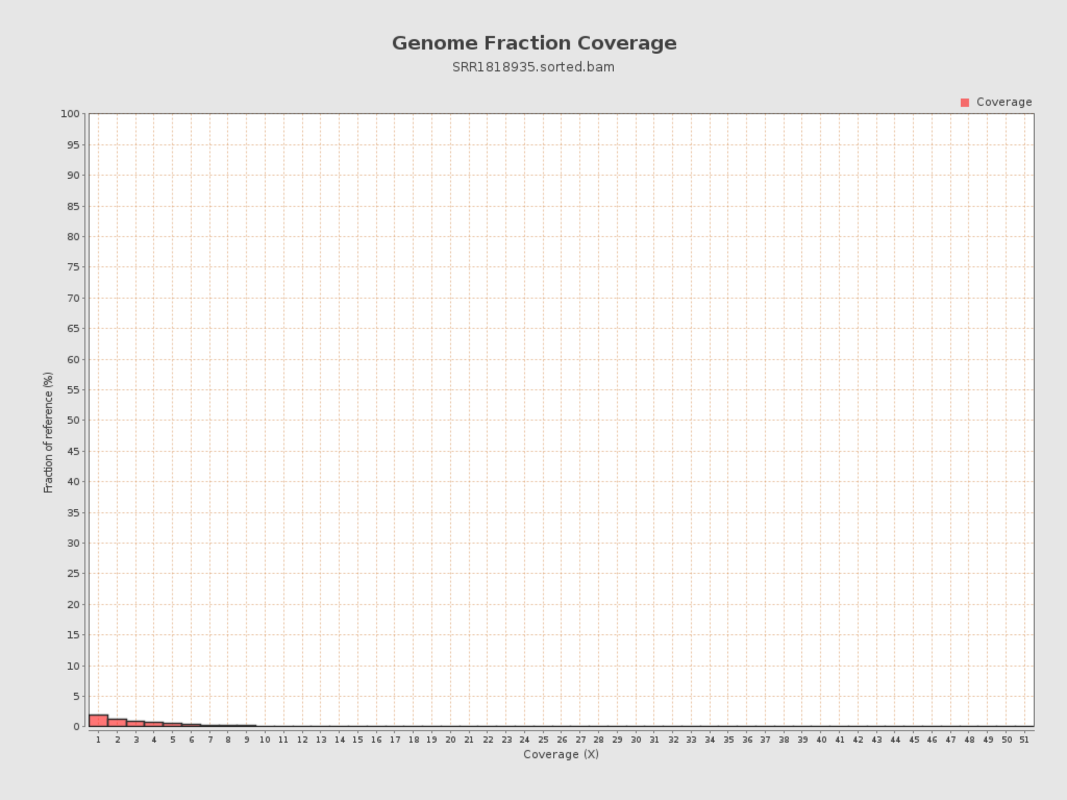
4. Results : Coverage Histogram



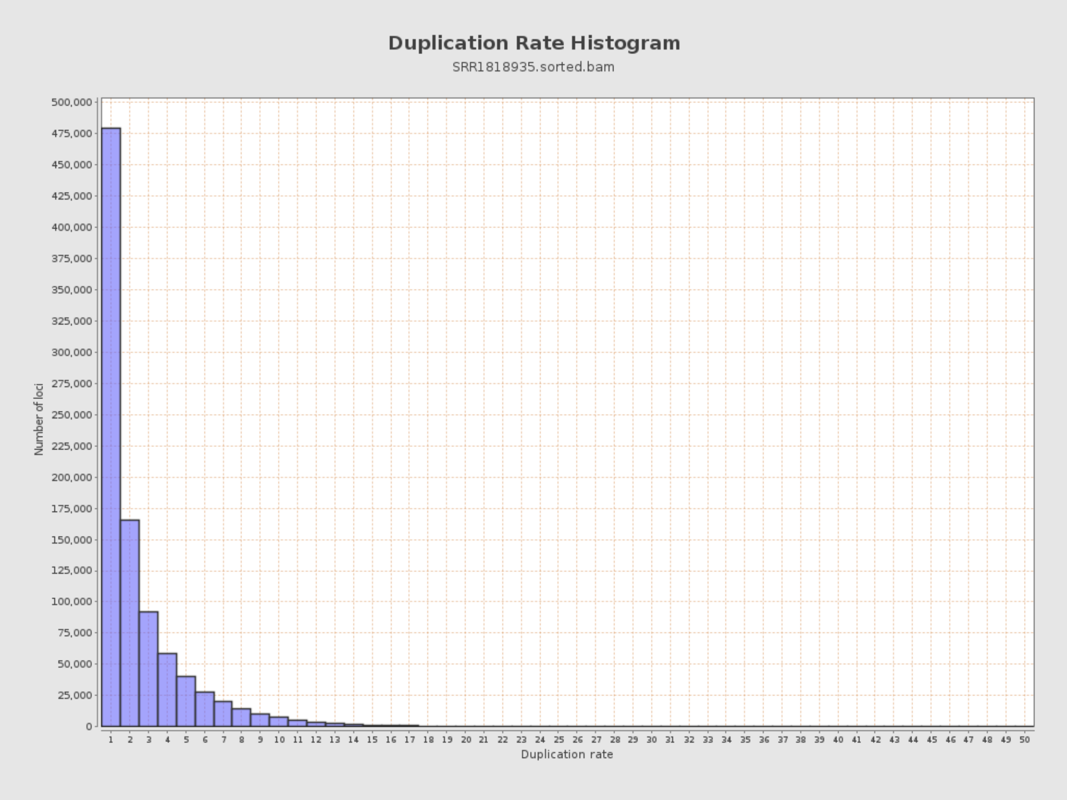
5. Results : Coverage Histogram (0-50X)



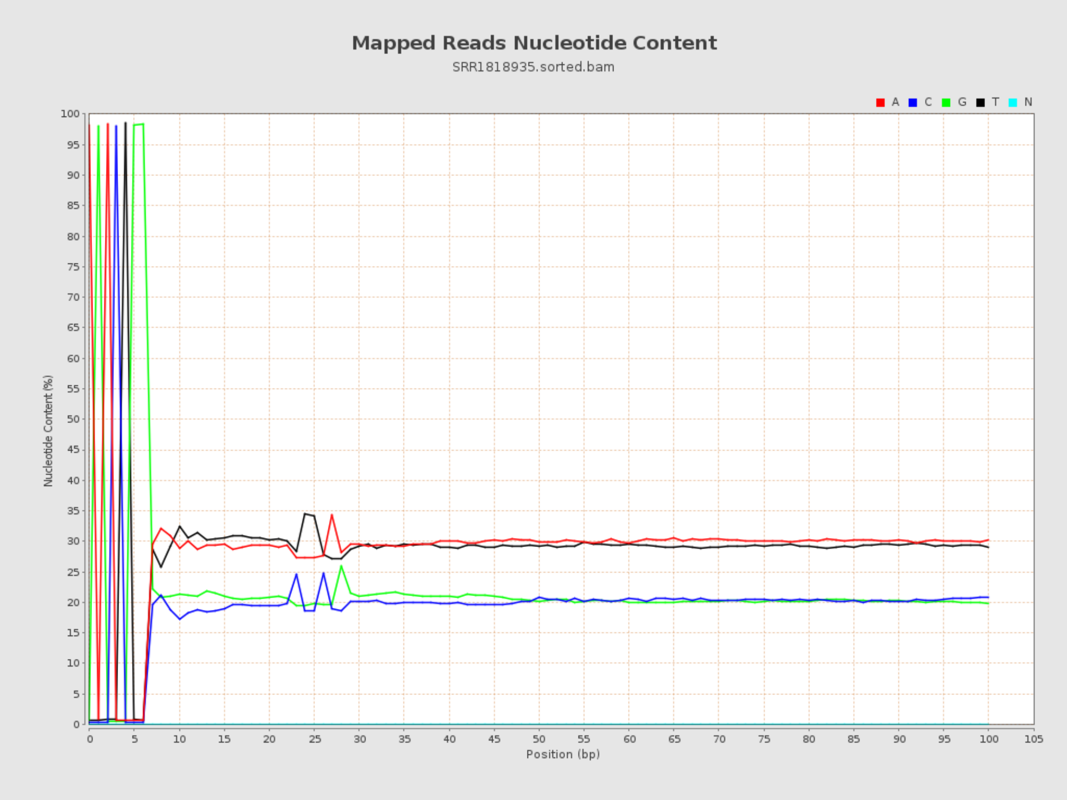
6. Results : Genome Fraction Coverage



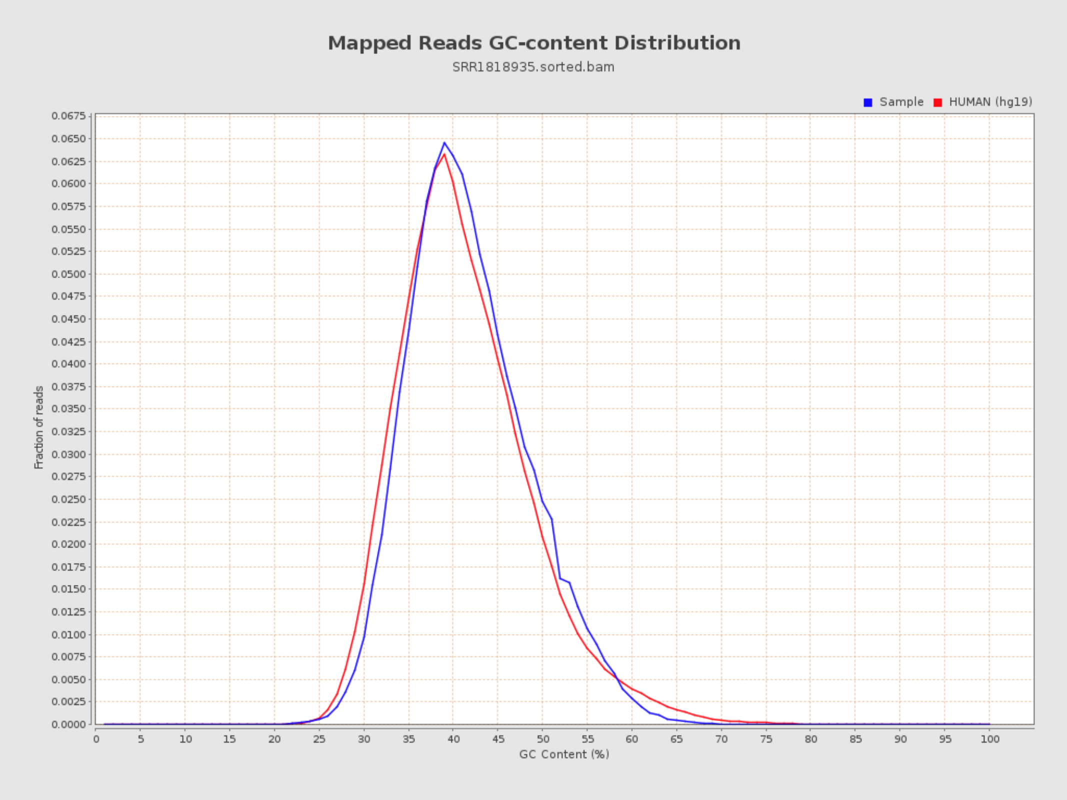
7. Results : Duplication Rate Histogram



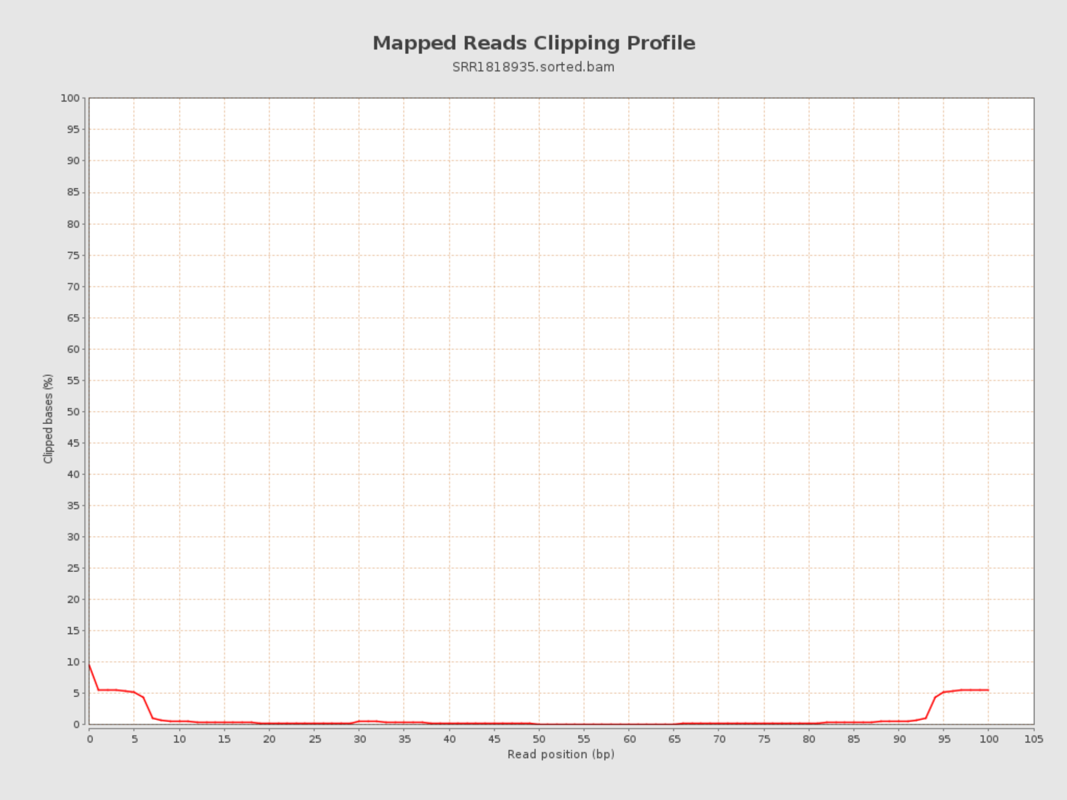
8. Results : Mapped Reads Nucleotide Content



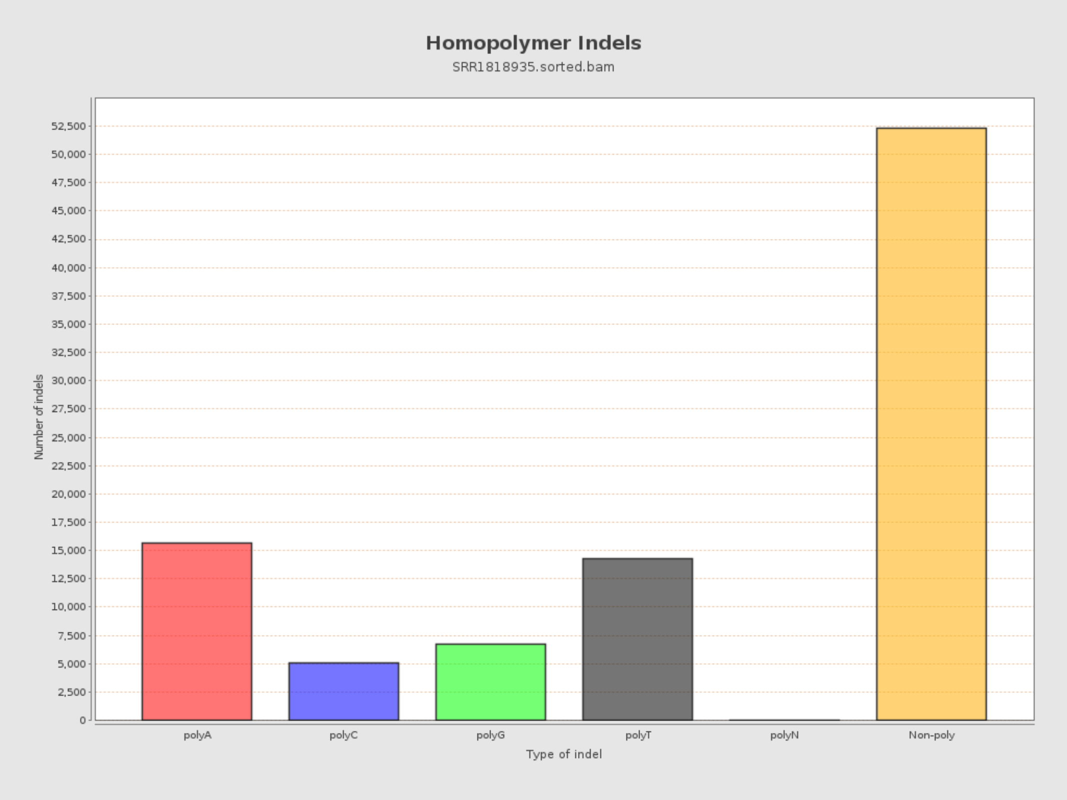
9. Results : Mapped Reads GC-content Distribution



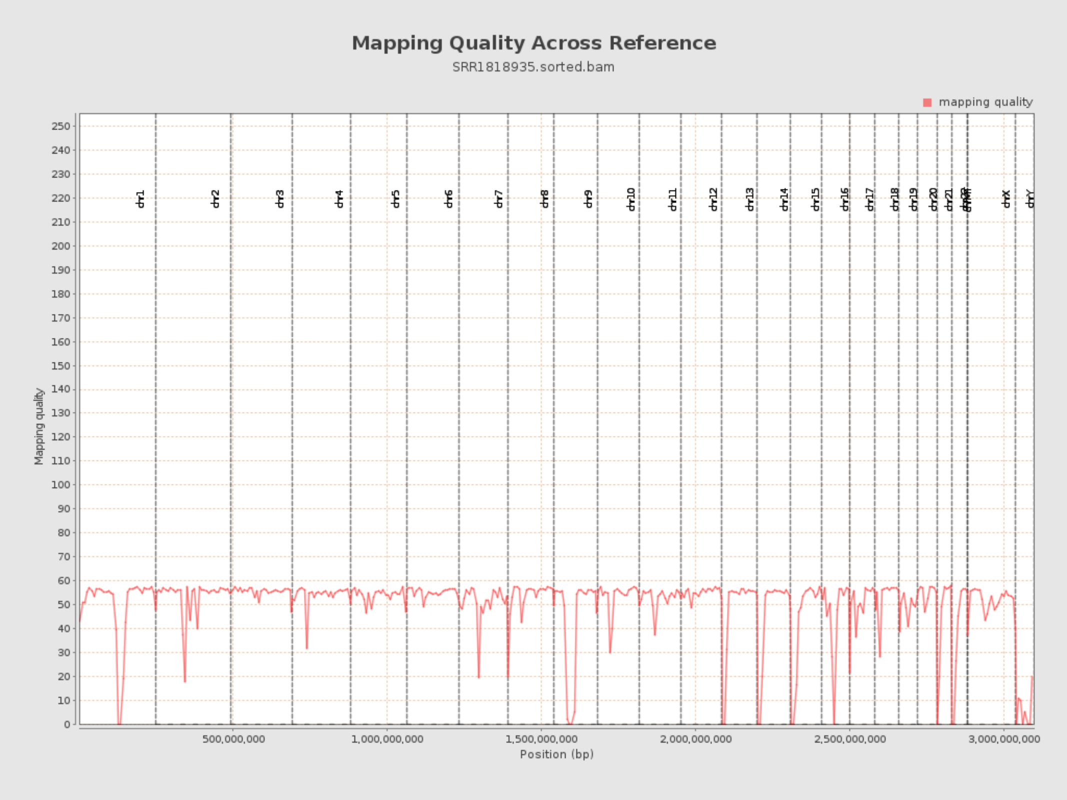
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram