Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:17:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818958.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_SRR1818958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:17:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,167,197
Mapped reads	3,034,870 / 95.82%
Unmapped reads	132,327 / 4.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,684 / 1.22%
Read min/max/mean length	30 / 101 / 101.47
Duplicated reads (estimated)	1,634,510 / 51.61%
Duplication rate	42.65%
Clipped reads	3,027,799 / 95.6%

2.2. ACGT Content

Number/percentage of A's	80,848,921 / 28.74%
Number/percentage of C's	55,963,025 / 19.89%
Number/percentage of T's	81,043,835 / 28.81%
Number/percentage of G's	63,483,046 / 22.56%
Number/percentage of N's	11,644 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0909

Standard Deviation	1.0228

2.4. Mapping Quality

Mean Mapping Quality	49.35

2.5. Mismatches and indels

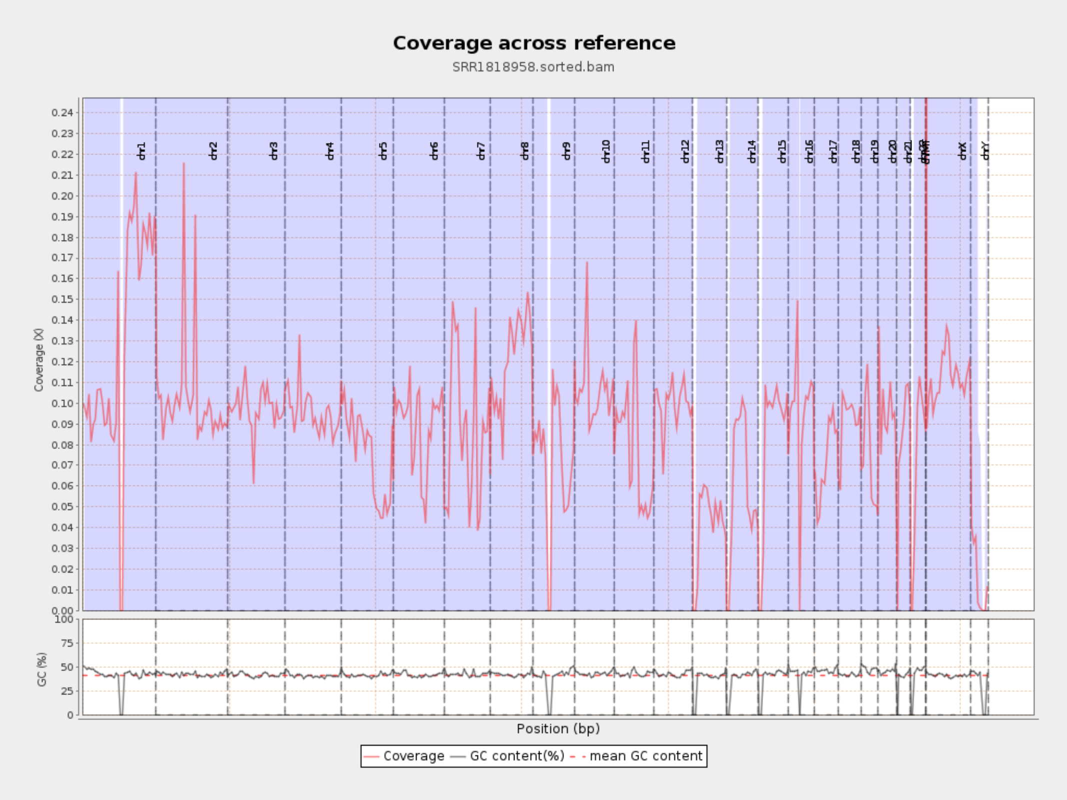
General error rate	0.66%
Mismatches	1,761,641
Insertions	38,591
Mapped reads with at least one insertion	1.23%
Deletions	87,652
Mapped reads with at least one deletion	2.83%
Homopolymer indels	42.98%

2.6. Chromosome stats

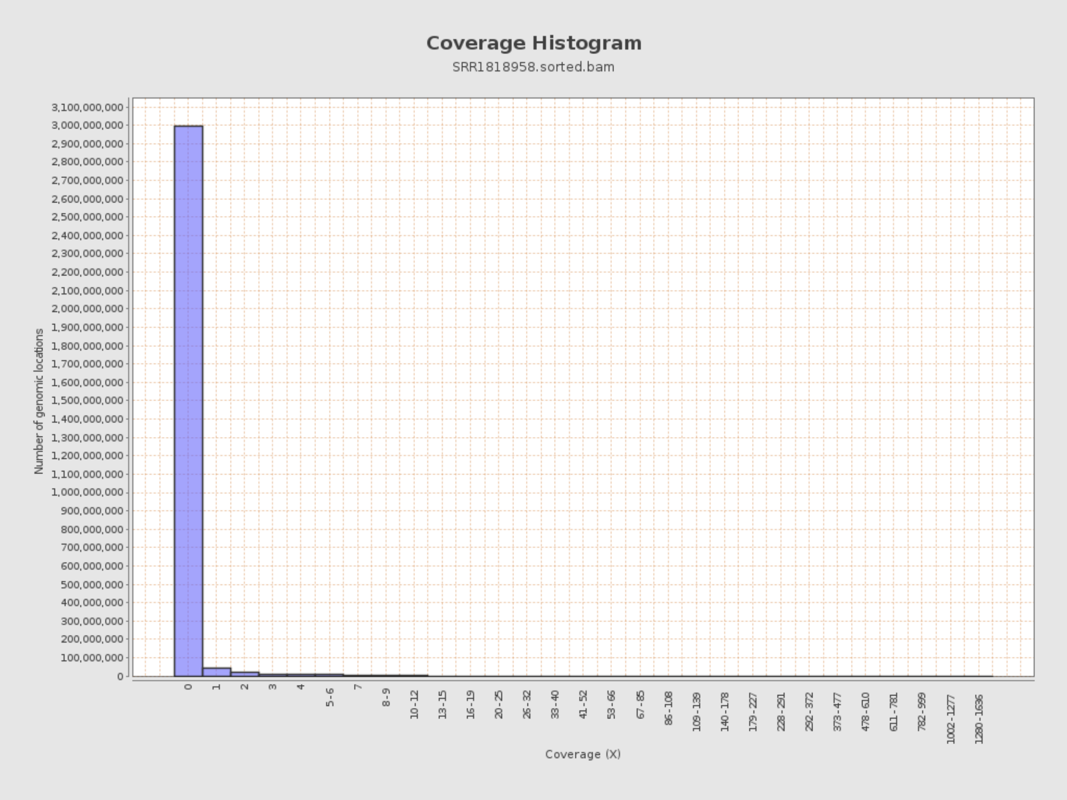
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31963967	0.1282	1.5837
chr2	243199373	24998587	0.1028	1.7136
chr3	198022430	19333218	0.0976	0.7024
chr4	191154276	18302498	0.0957	0.7645
chr5	180915260	13655566	0.0755	0.6473
chr6	171115067	15364553	0.0898	0.7197
chr7	159138663	13813993	0.0868	0.7868

chr8	146364022	17896399	0.1223	0.8897
chr9	141213431	10094896	0.0715	0.9981
chr10	135534747	14346247	0.1058	1.2311
chr11	135006516	10437996	0.0773	0.7273
chr12	133851895	13451724	0.1005	0.7362
chr13	115169878	4765238	0.0414	0.4481
chr14	107349540	6527073	0.0608	0.6141
chr15	102531392	8313124	0.0811	0.6499
chr16	90354753	8485191	0.0939	1.2735
chr17	81195210	5912093	0.0728	0.6733
chr18	78077248	7158661	0.0917	1.3471
chr19	59128983	4476717	0.0757	1.417
chr20	63025520	6123177	0.0972	0.758
chr21	48129895	4023324	0.0836	0.7146
chr22	51304566	3592084	0.07	0.6605
chrMT	16571	238476	14.3912	12.7939
chrX	155270560	17374240	0.1119	0.8554
chrY	59373566	863185	0.0145	1.0532

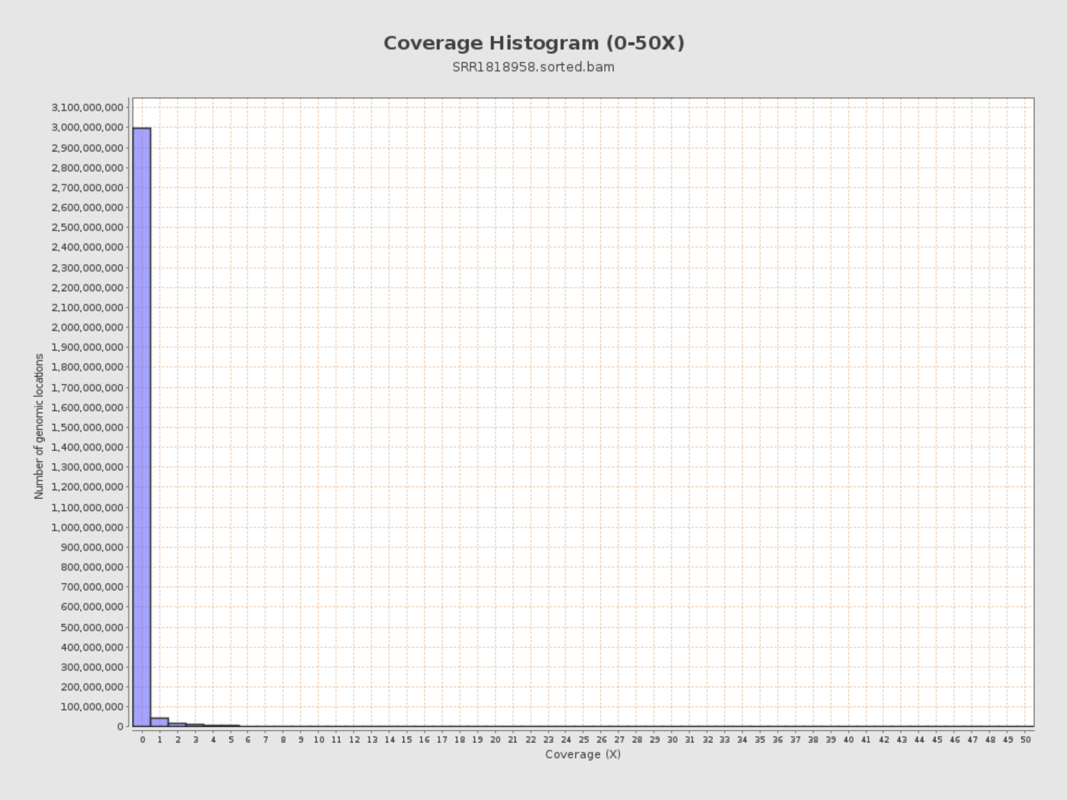
3. Results : Coverage across reference



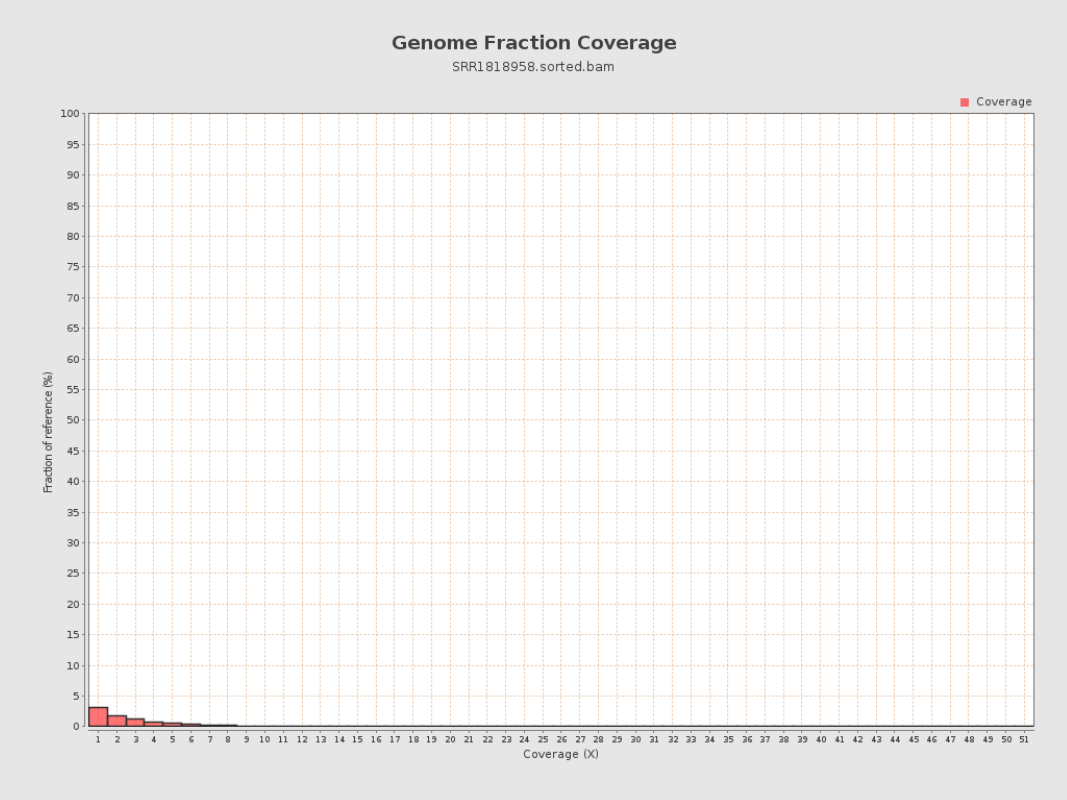
4. Results : Coverage Histogram



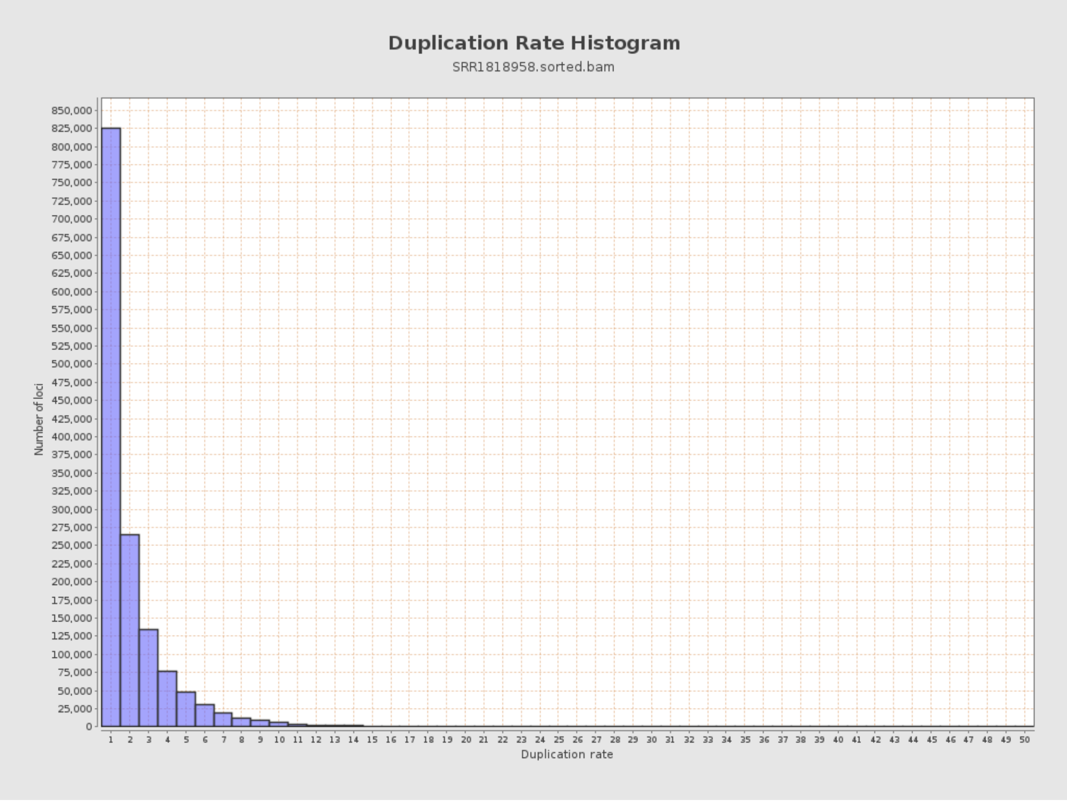
5. Results : Coverage Histogram (0-50X)



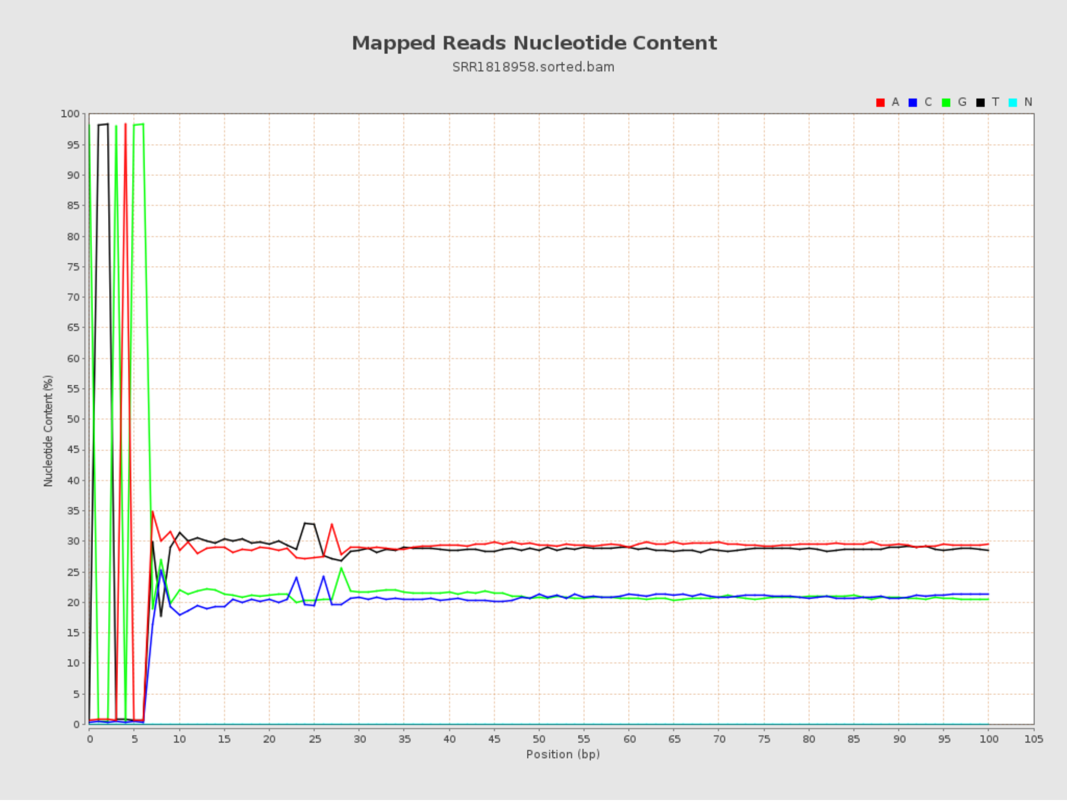
6. Results : Genome Fraction Coverage



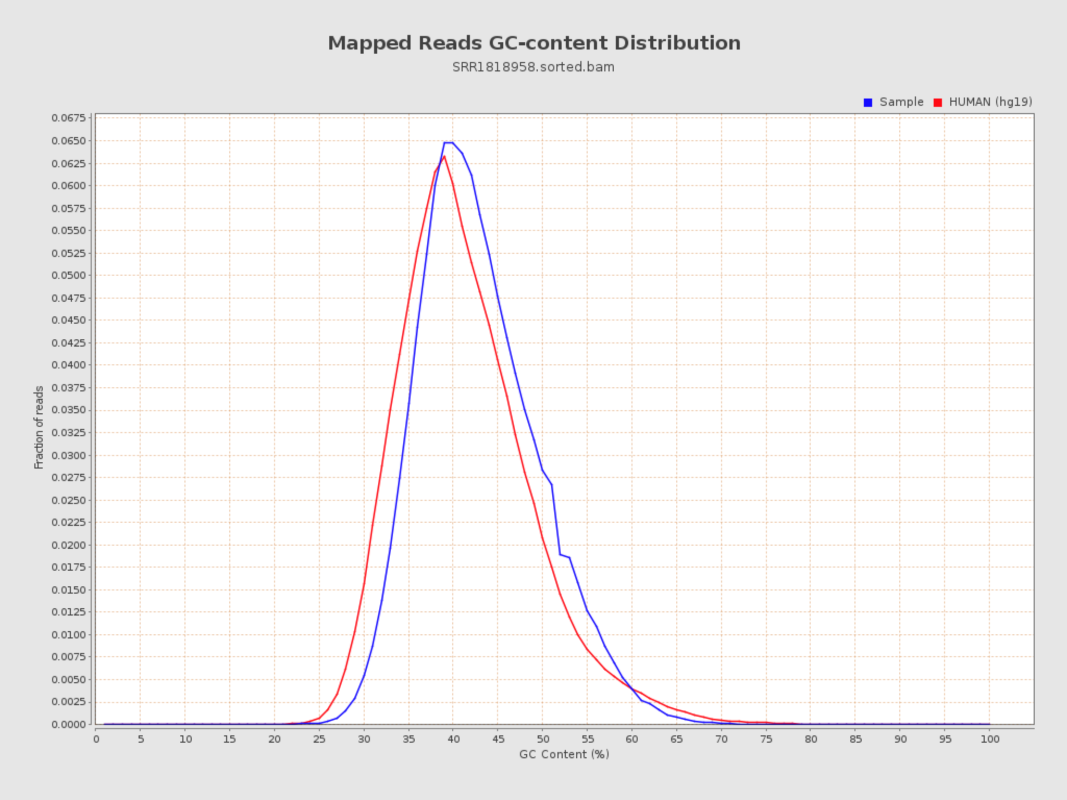
7. Results : Duplication Rate Histogram



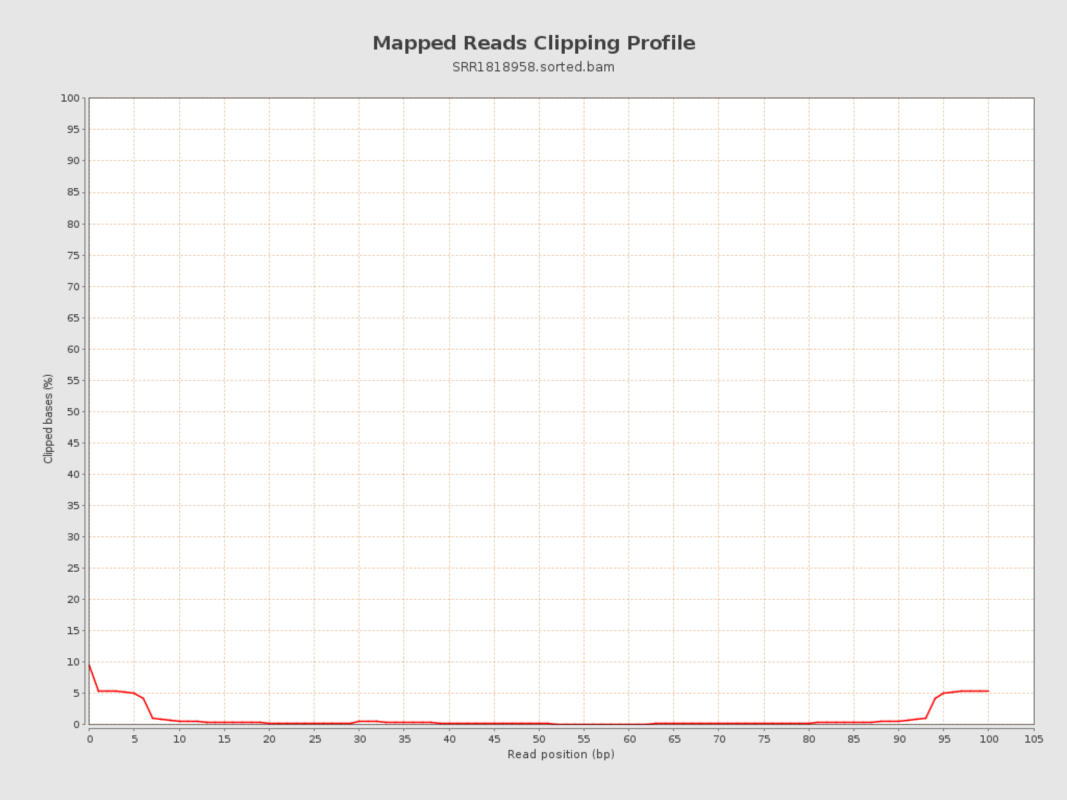
8. Results : Mapped Reads Nucleotide Content



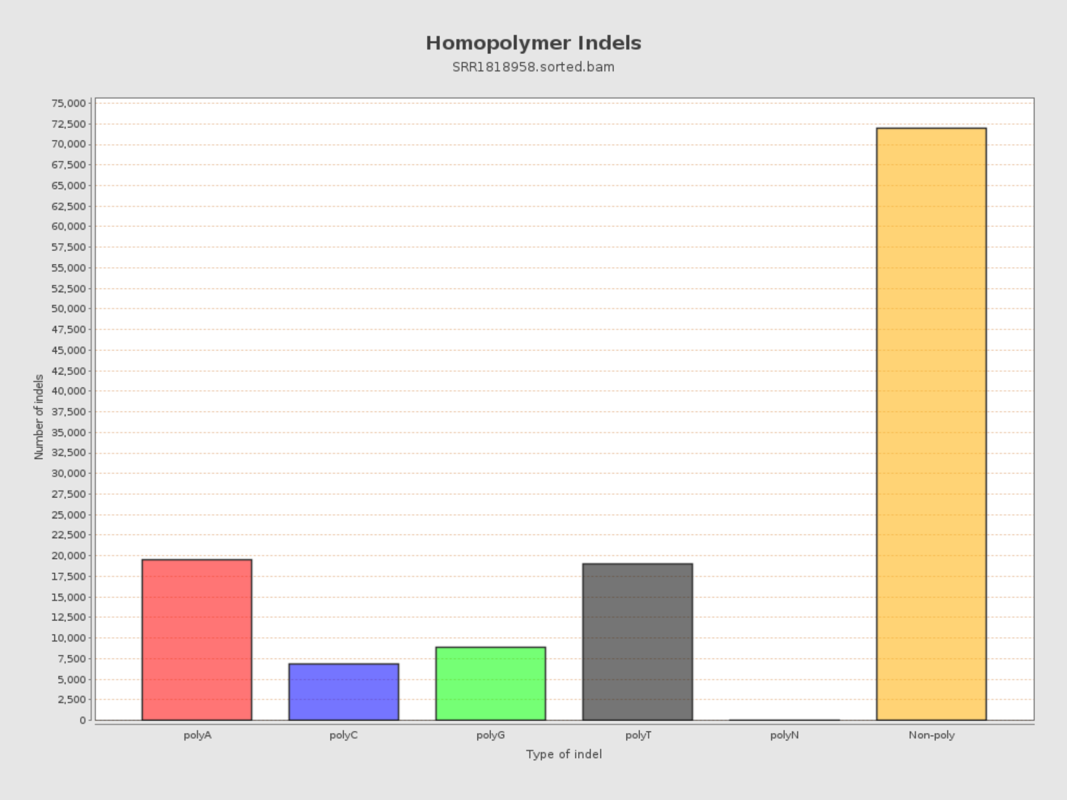
9. Results : Mapped Reads GC-content Distribution



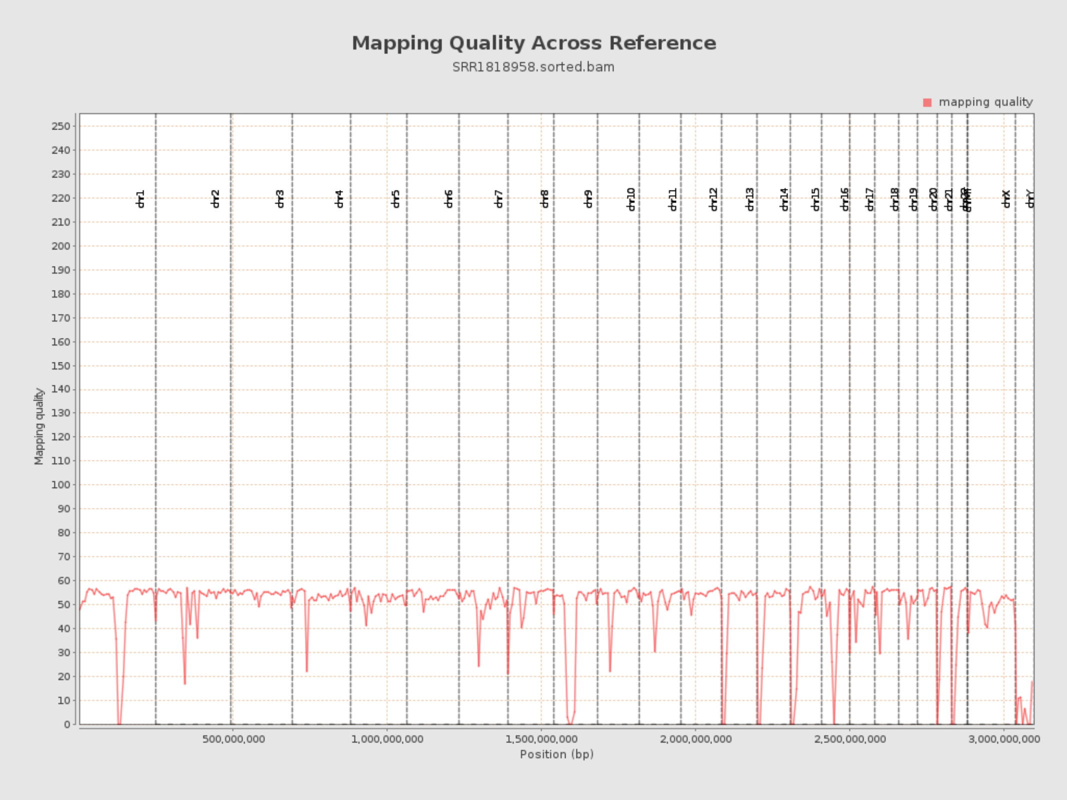
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram