Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 10:31:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818950.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_SRR1818950 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818950.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 10:31:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818950.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,377,841
Mapped reads	3,325,062 / 98.44%
Unmapped reads	52,779 / 1.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	45,545 / 1.35%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	1,769,244 / 52.38%
Duplication rate	42.01%
Clipped reads	3,364,861 / 99.62%

2.2. ACGT Content

Number/percentage of A's	89,494,628 / 29.13%
Number/percentage of C's	66,556,602 / 21.67%
Number/percentage of T's	86,428,423 / 28.13%
Number/percentage of G's	64,703,015 / 21.06%
Number/percentage of N's	14,612 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0993

Standard Deviation	1.1294

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

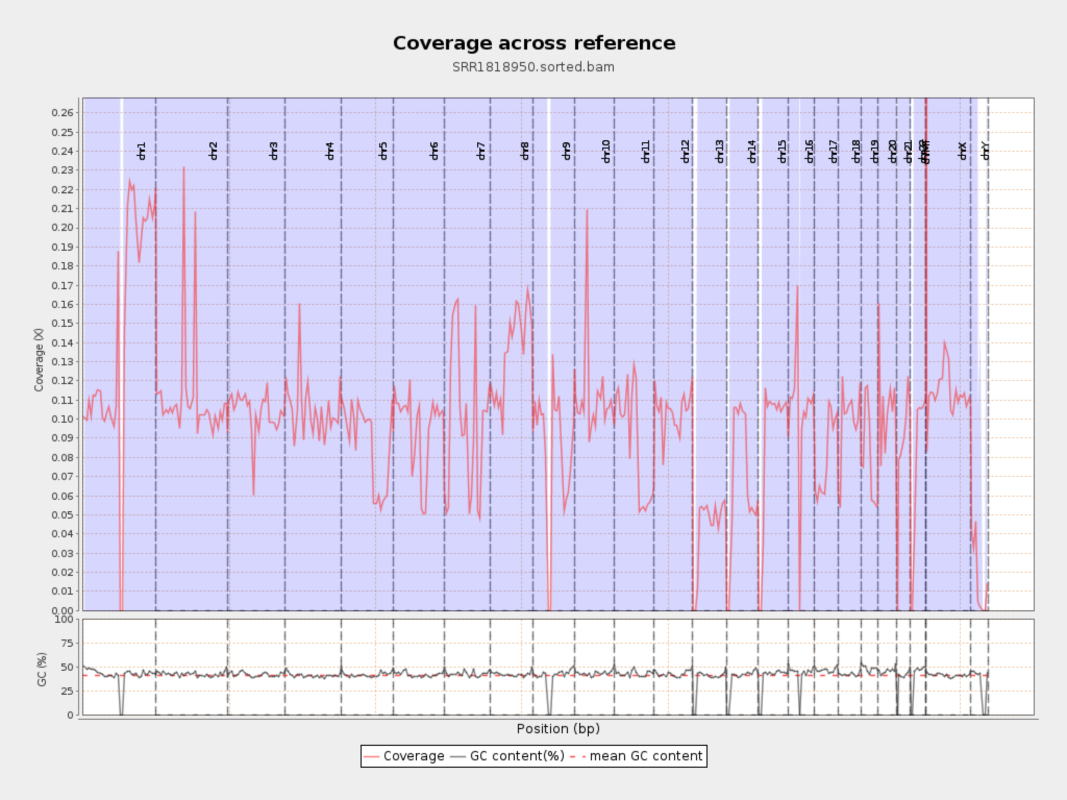
General error rate	0.69%
Mismatches	2,030,154
Insertions	36,943
Mapped reads with at least one insertion	1.07%
Deletions	94,408
Mapped reads with at least one deletion	2.78%
Homopolymer indels	43.35%

2.6. Chromosome stats

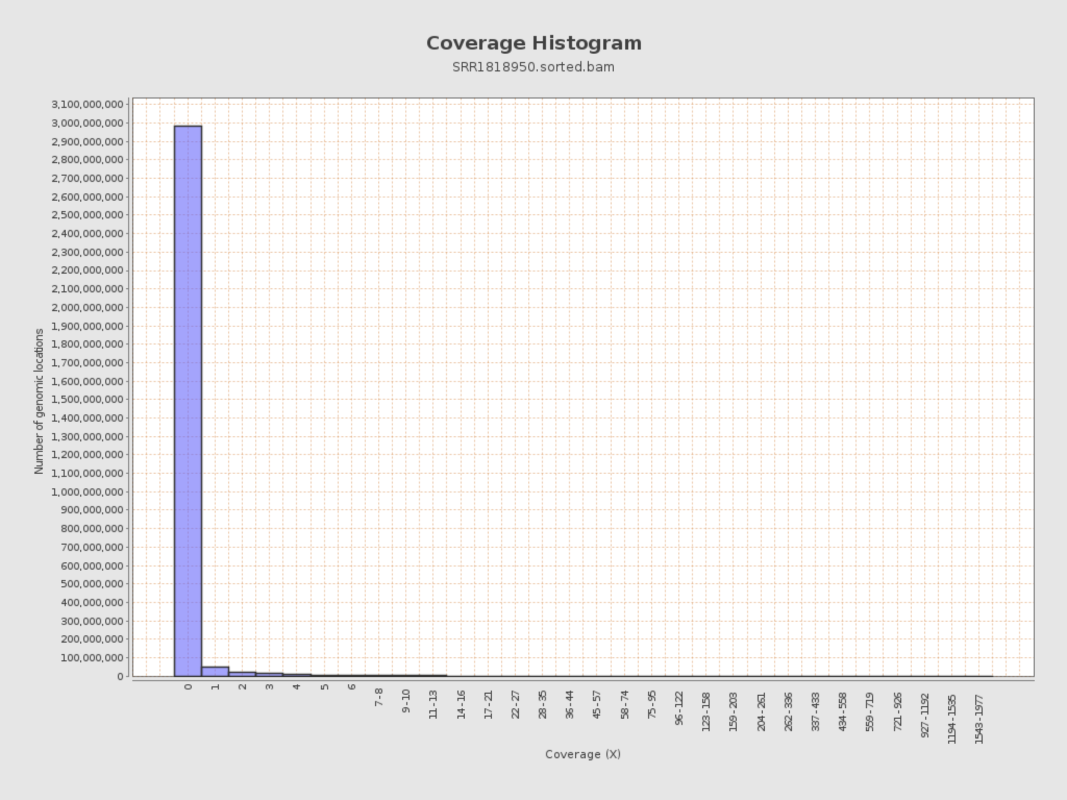
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36085120	0.1448	1.9585
chr2	243199373	27200977	0.1118	1.7248
chr3	198022430	20469414	0.1034	0.7179
chr4	191154276	20102499	0.1052	0.8196
chr5	180915260	15874095	0.0877	0.6878
chr6	171115067	16386367	0.0958	0.765
chr7	159138663	15692623	0.0986	0.9302

chr8	146364022	19954905	0.1363	0.9644
chr9	141213431	11650893	0.0825	1.2793
chr10	135534747	15038645	0.111	1.3514
chr11	135006516	11803777	0.0874	0.7952
chr12	133851895	13979969	0.1044	0.7509
chr13	115169878	4964043	0.0431	0.4536
chr14	107349540	7343712	0.0684	0.6582
chr15	102531392	8956948	0.0874	0.6659
chr16	90354753	9295638	0.1029	1.2973
chr17	81195210	6557396	0.0808	0.7187
chr18	78077248	7699776	0.0986	1.5985
chr19	59128983	4794714	0.0811	1.5956
chr20	63025520	6720036	0.1066	0.7918
chr21	48129895	4169784	0.0866	0.758
chr22	51304566	3788648	0.0738	0.6881
chrMT	16571	80518	4.859	5.2336
chrX	155270560	17770261	0.1144	0.8849
chrY	59373566	990222	0.0167	1.0376

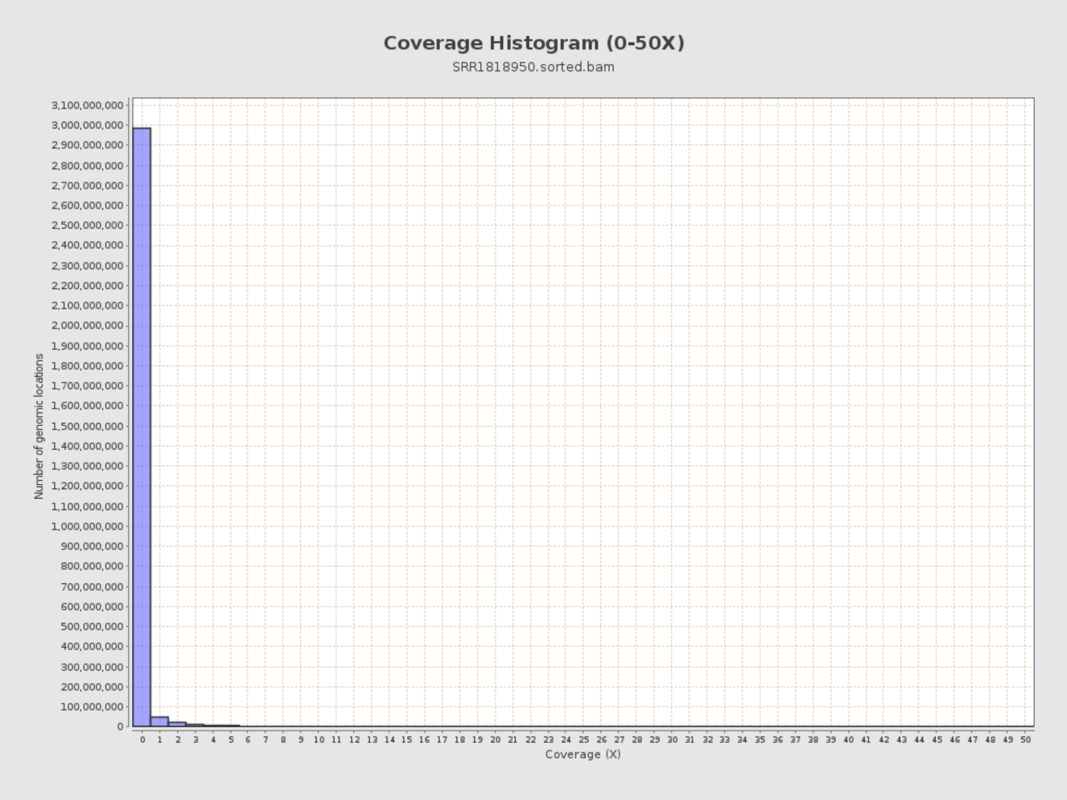
3. Results : Coverage across reference



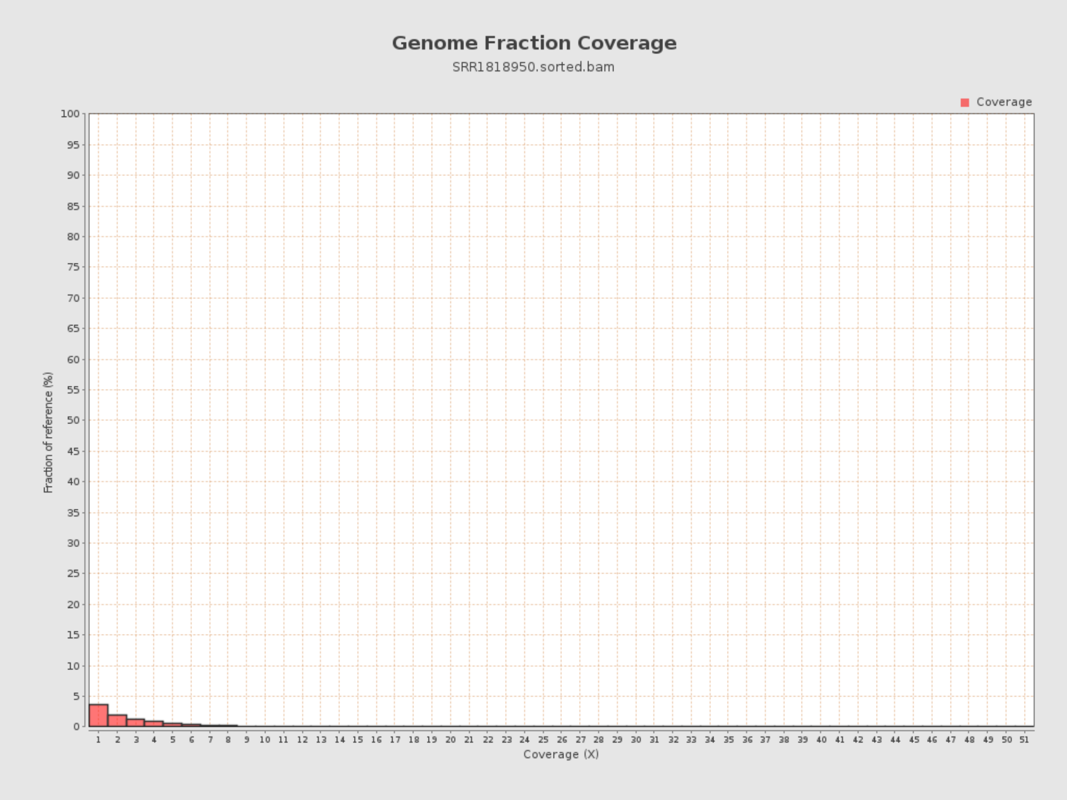
4. Results : Coverage Histogram



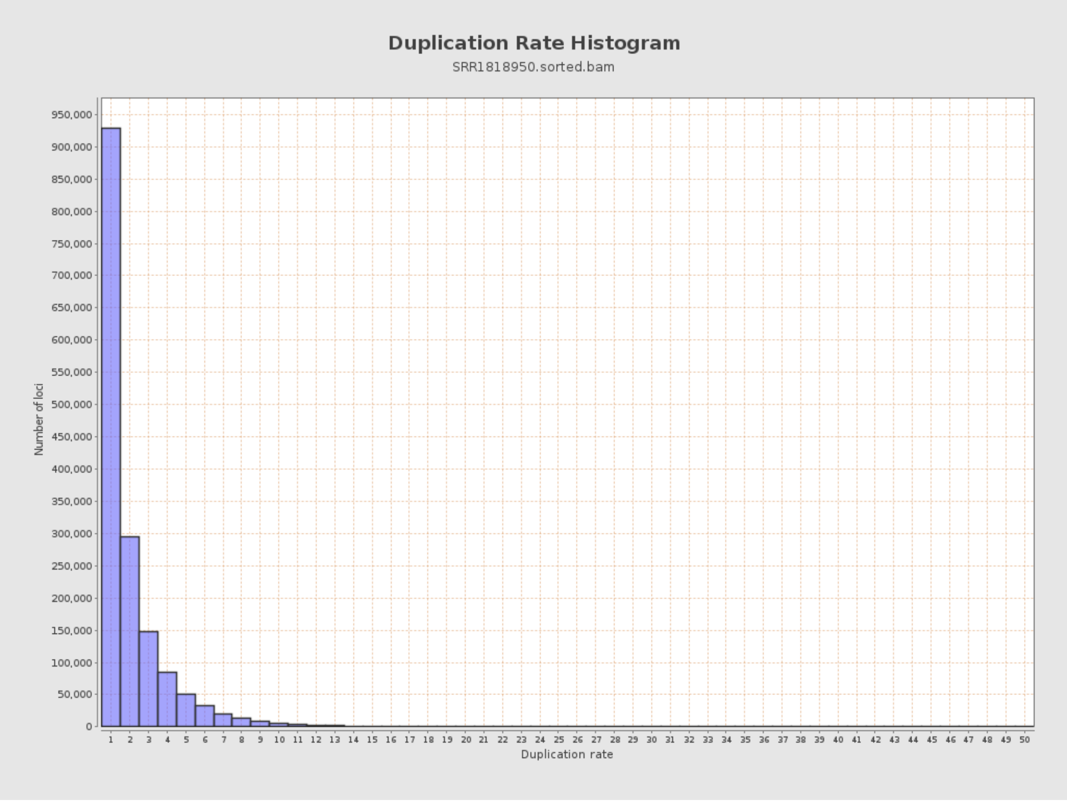
5. Results : Coverage Histogram (0-50X)



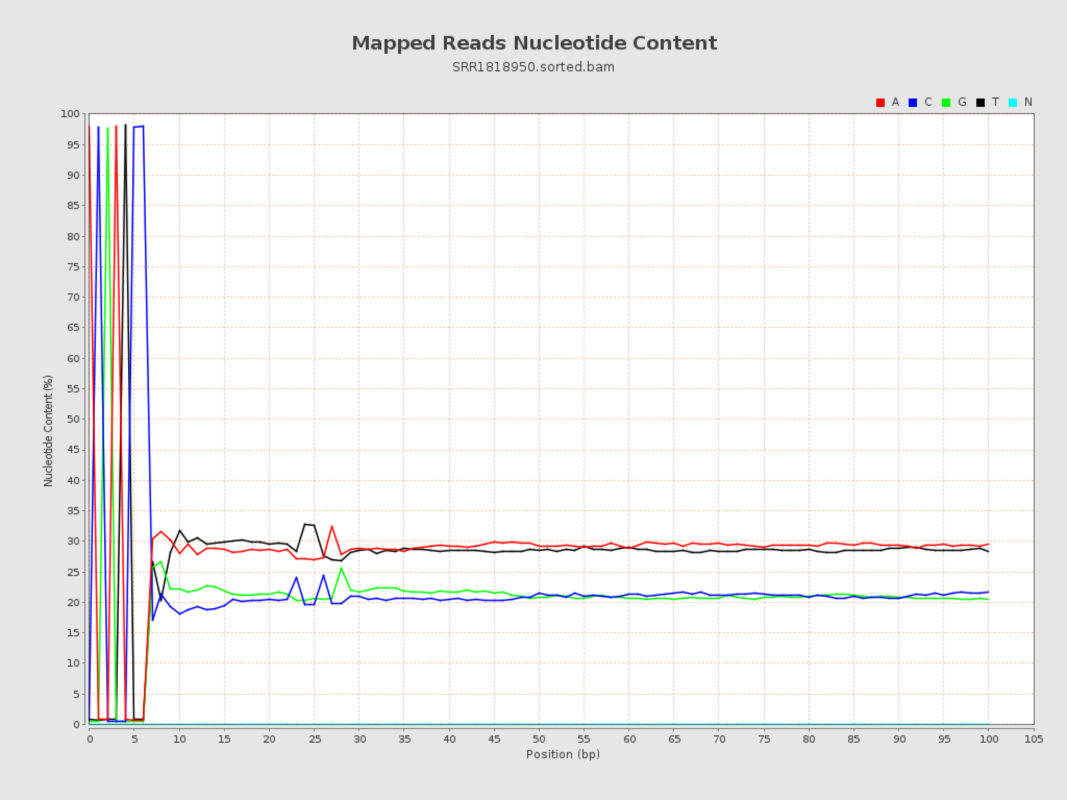
6. Results : Genome Fraction Coverage



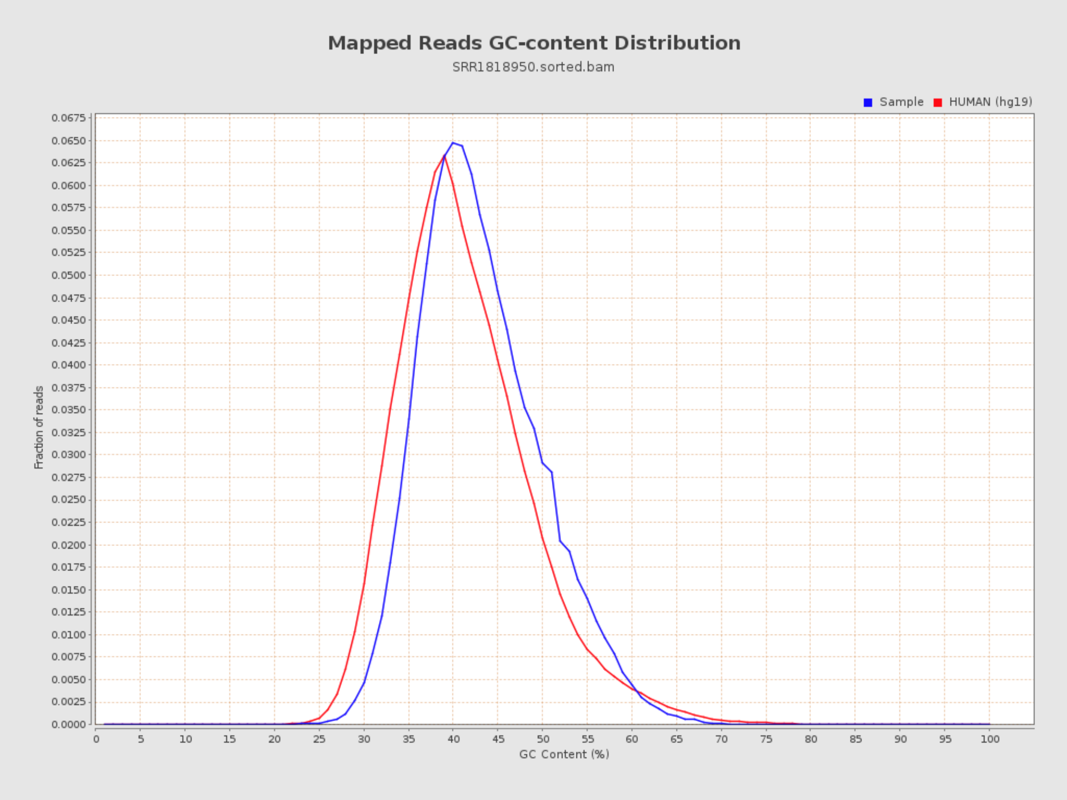
7. Results : Duplication Rate Histogram



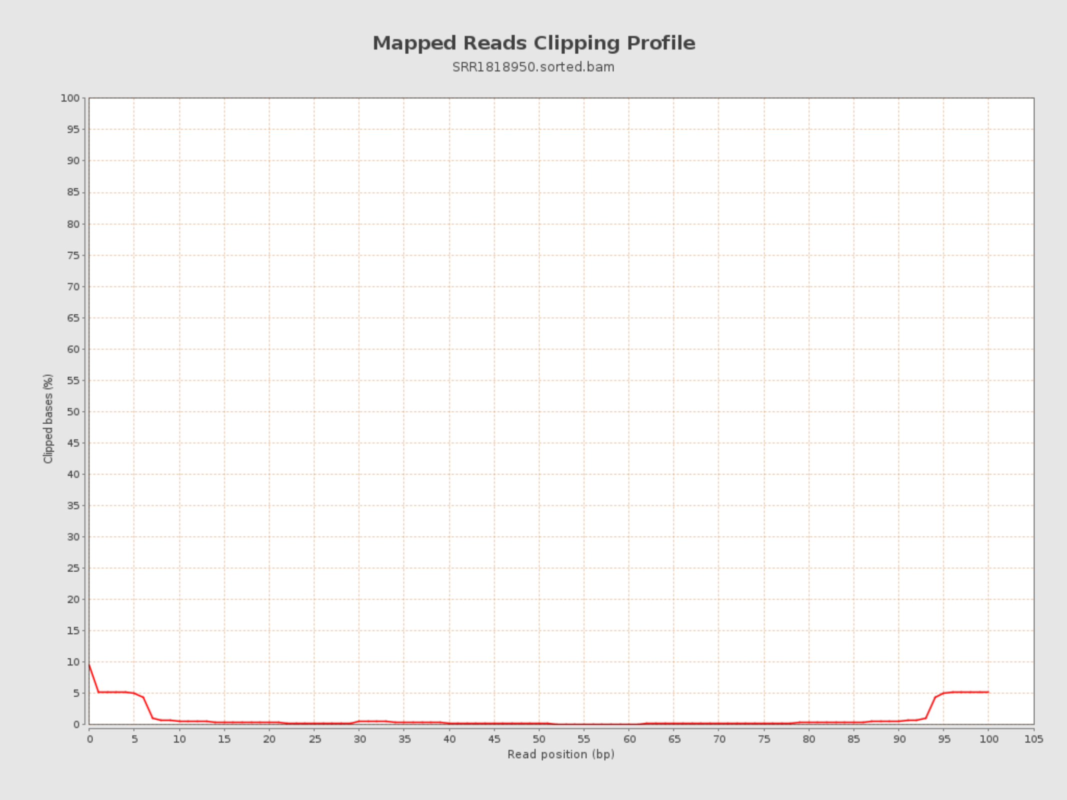
8. Results : Mapped Reads Nucleotide Content



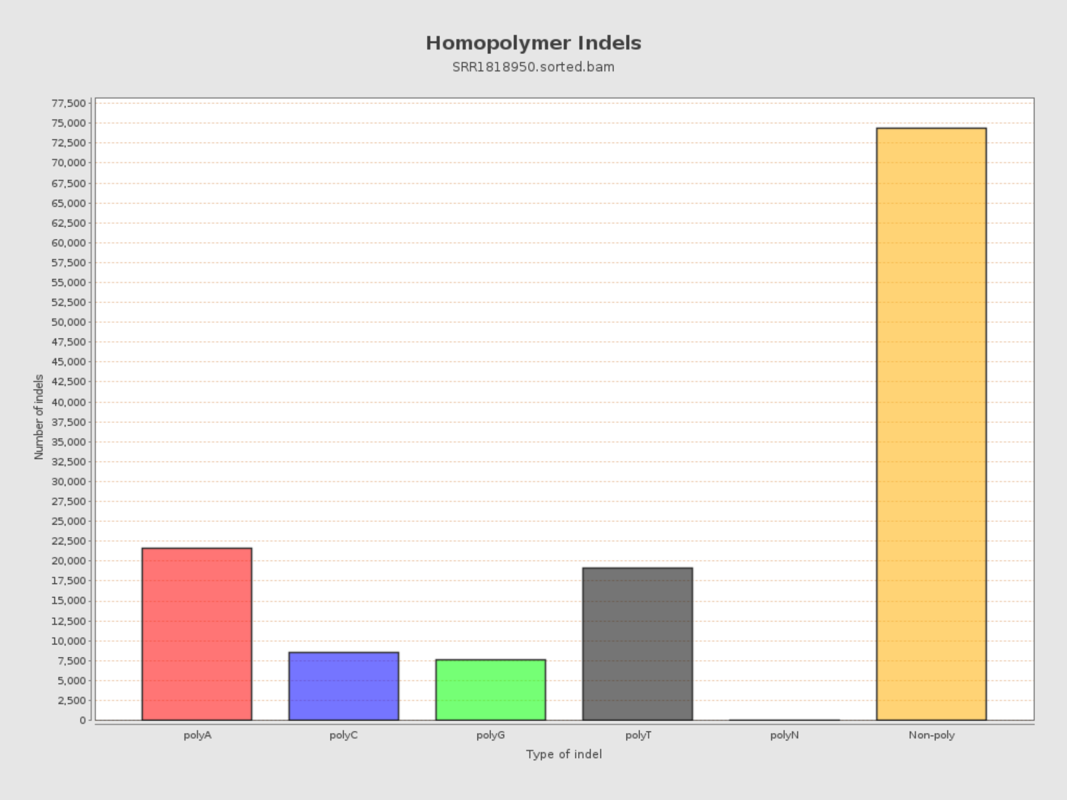
9. Results : Mapped Reads GC-content Distribution



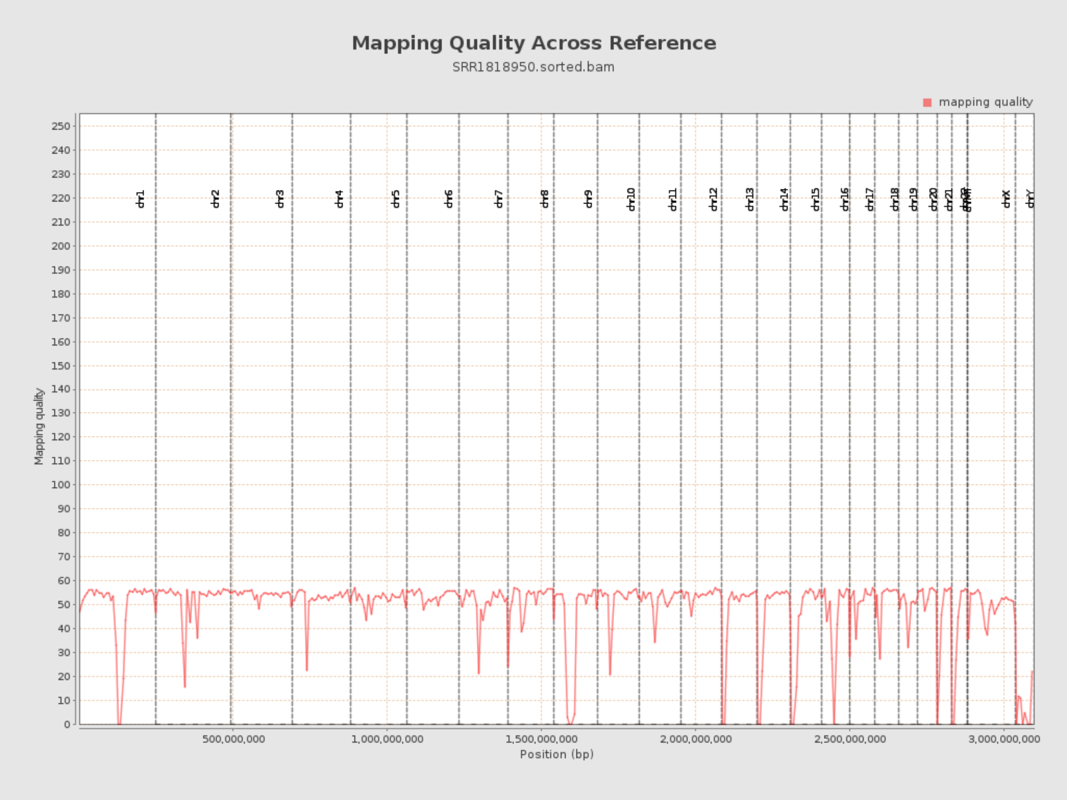
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram