Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:34:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818758.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_SRR1818758 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818758.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:34:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818758.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,581,538
Mapped reads	3,484,854 / 97.3%
Unmapped reads	96,684 / 2.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,607 / 0.69%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	1,940,110 / 54.17%
Duplication rate	46.76%
Clipped reads	3,486,880 / 97.36%

2.2. ACGT Content

Number/percentage of A's	68,430,688 / 28.88%
Number/percentage of C's	49,920,635 / 21.07%
Number/percentage of T's	69,118,714 / 29.17%
Number/percentage of G's	49,479,197 / 20.88%
Number/percentage of N's	14,406 / 0.01%
GC Percentage	41.95%

2.3. Coverage

Mean	0.0766

Standard Deviation	0.9142

2.4. Mapping Quality

Mean Mapping Quality	47.48

2.5. Mismatches and indels

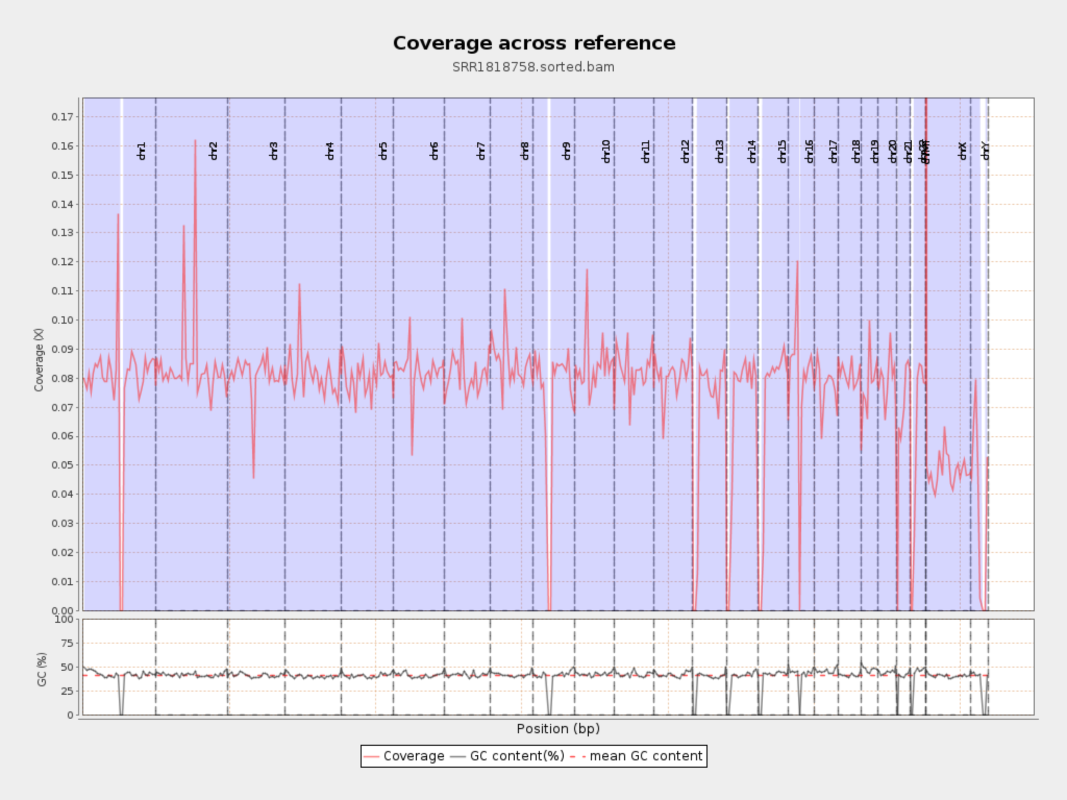
General error rate	0.54%
Mismatches	1,215,172
Insertions	28,870
Mapped reads with at least one insertion	0.82%
Deletions	59,764
Mapped reads with at least one deletion	1.7%
Homopolymer indels	40.54%

2.6. Chromosome stats

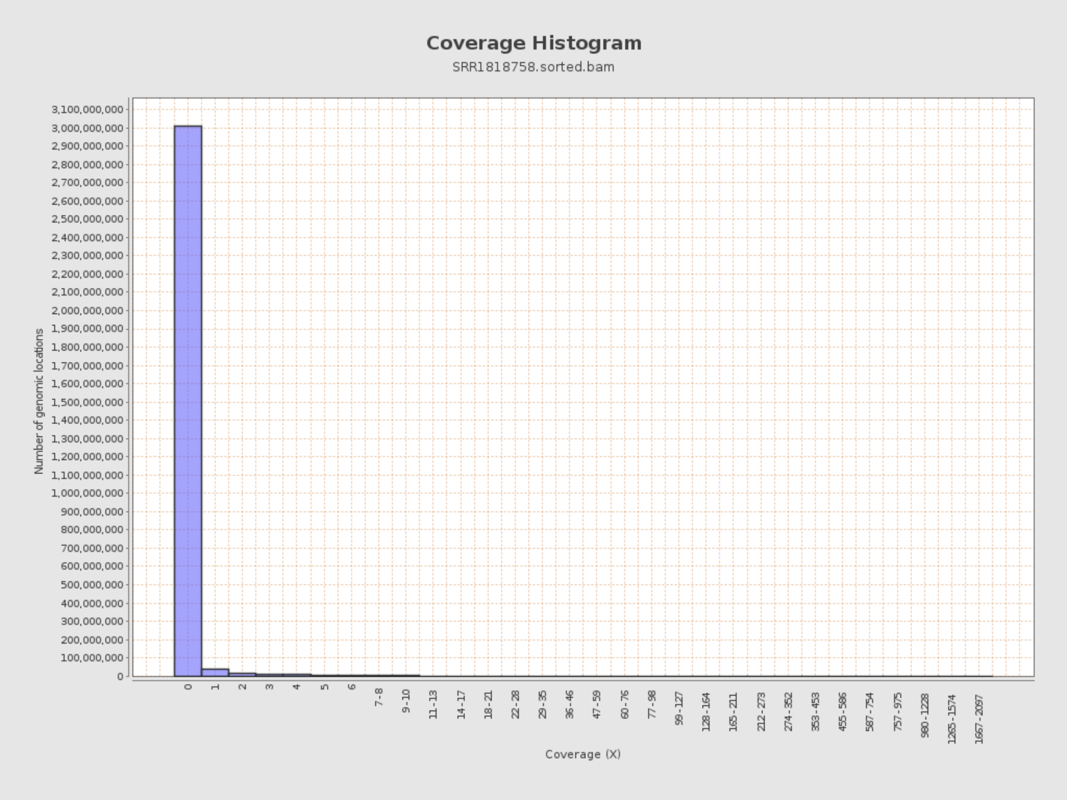
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19543637	0.0784	1.4279
chr2	243199373	20721308	0.0852	1.485
chr3	198022430	16020428	0.0809	0.6165
chr4	191154276	15675032	0.082	0.7202
chr5	180915260	14573360	0.0806	0.6353
chr6	171115067	14094074	0.0824	0.7093
chr7	159138663	12935840	0.0813	0.8118

chr8	146364022	12524593	0.0856	0.7791
chr9	141213431	10170632	0.072	0.7462
chr10	135534747	11429564	0.0843	0.9468
chr11	135006516	11189118	0.0829	0.7336
chr12	133851895	10923878	0.0816	0.8052
chr13	115169878	7627515	0.0662	0.5622
chr14	107349540	7289468	0.0679	0.6558
chr15	102531392	6883031	0.0671	0.5667
chr16	90354753	7072671	0.0783	1.0143
chr17	81195210	6312597	0.0777	0.6556
chr18	78077248	6341515	0.0812	1.0058
chr19	59128983	4627859	0.0783	1.1397
chr20	63025520	5029672	0.0798	0.6647
chr21	48129895	3205232	0.0666	0.5967
chr22	51304566	2894105	0.0564	0.5736
chrMT	16571	310387	18.7307	16.9706
chrX	155270560	7489221	0.0482	0.5717
chrY	59373566	2176530	0.0367	1.4988

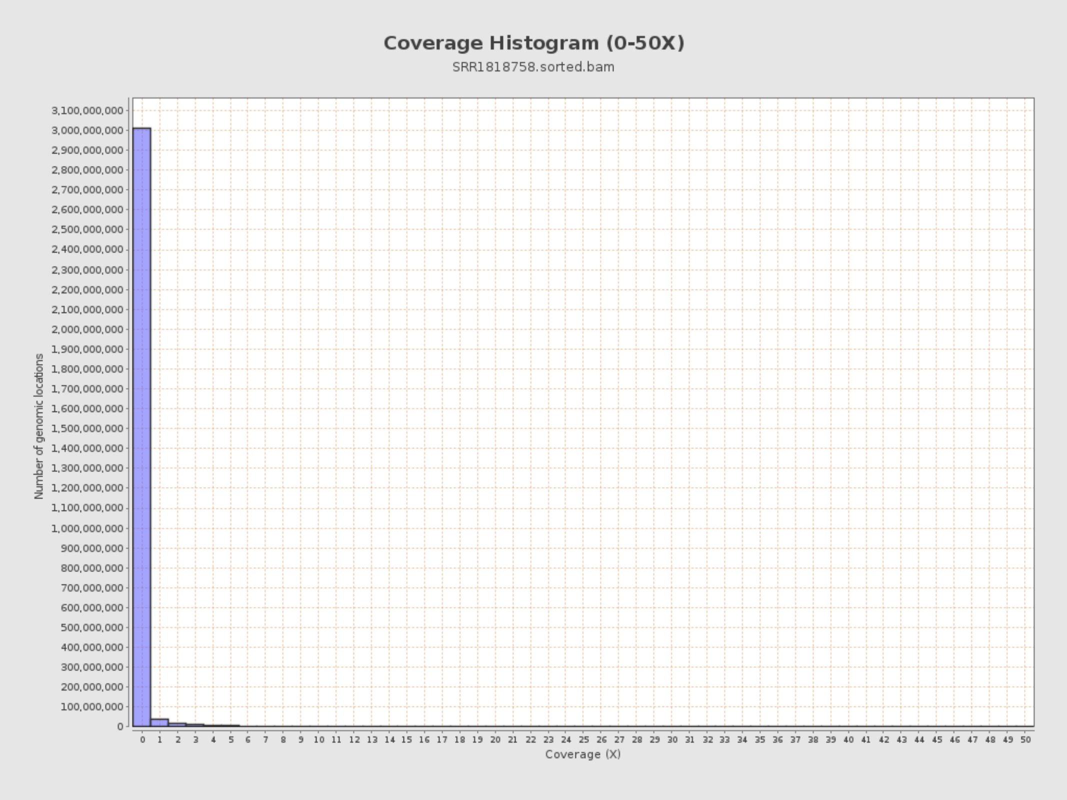
3. Results : Coverage across reference



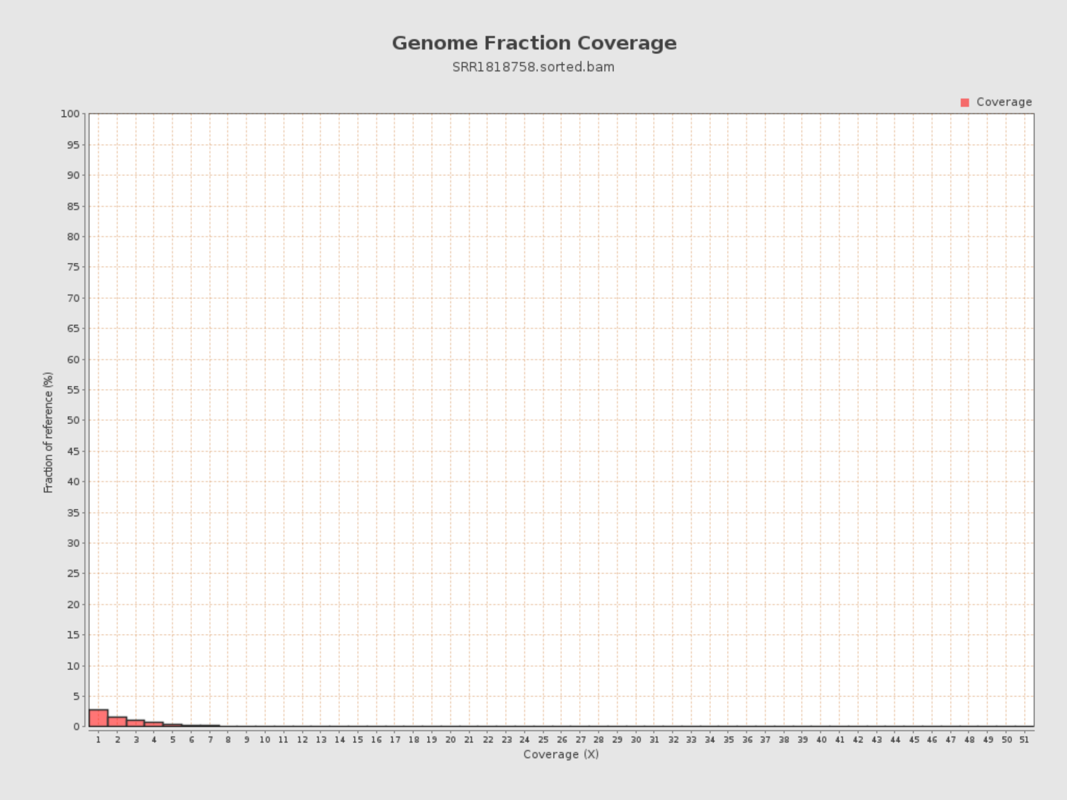
4. Results : Coverage Histogram



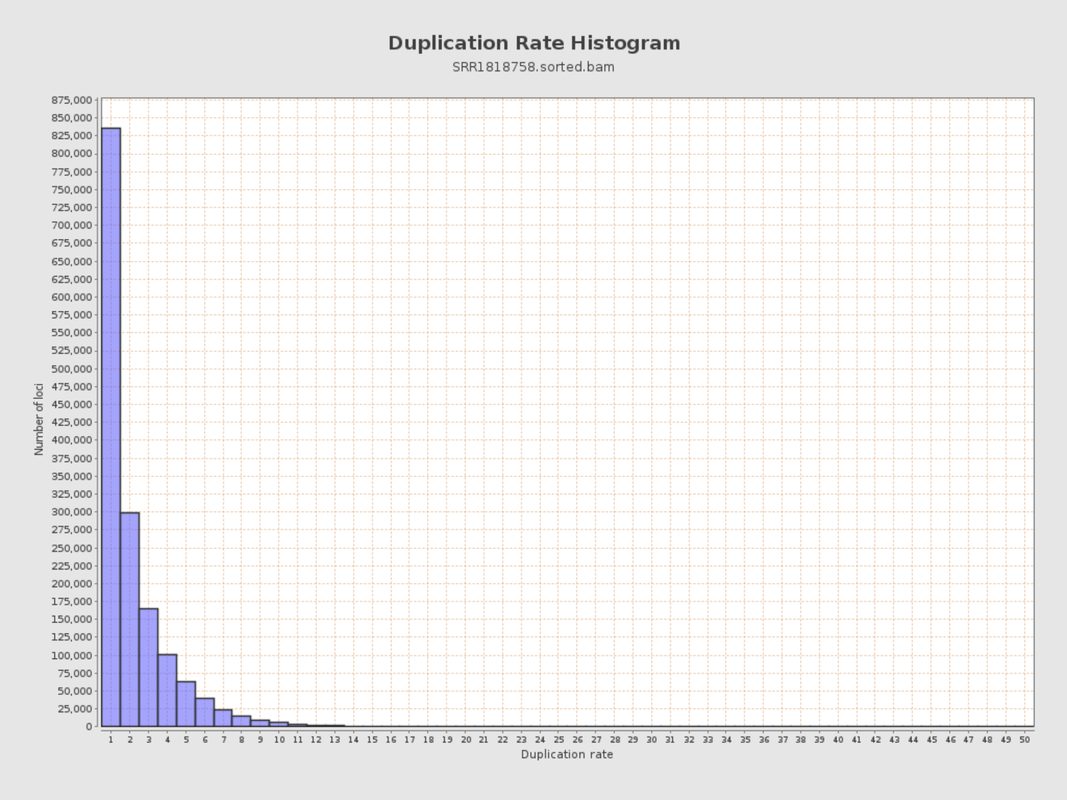
5. Results : Coverage Histogram (0-50X)



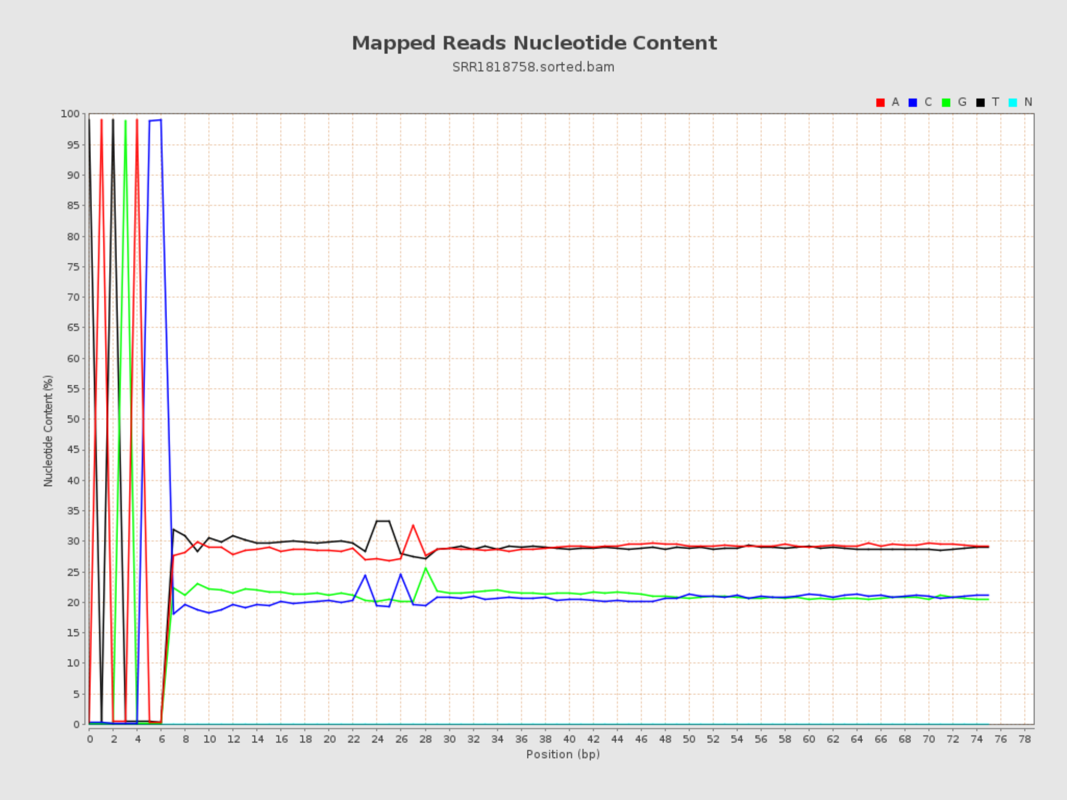
6. Results : Genome Fraction Coverage



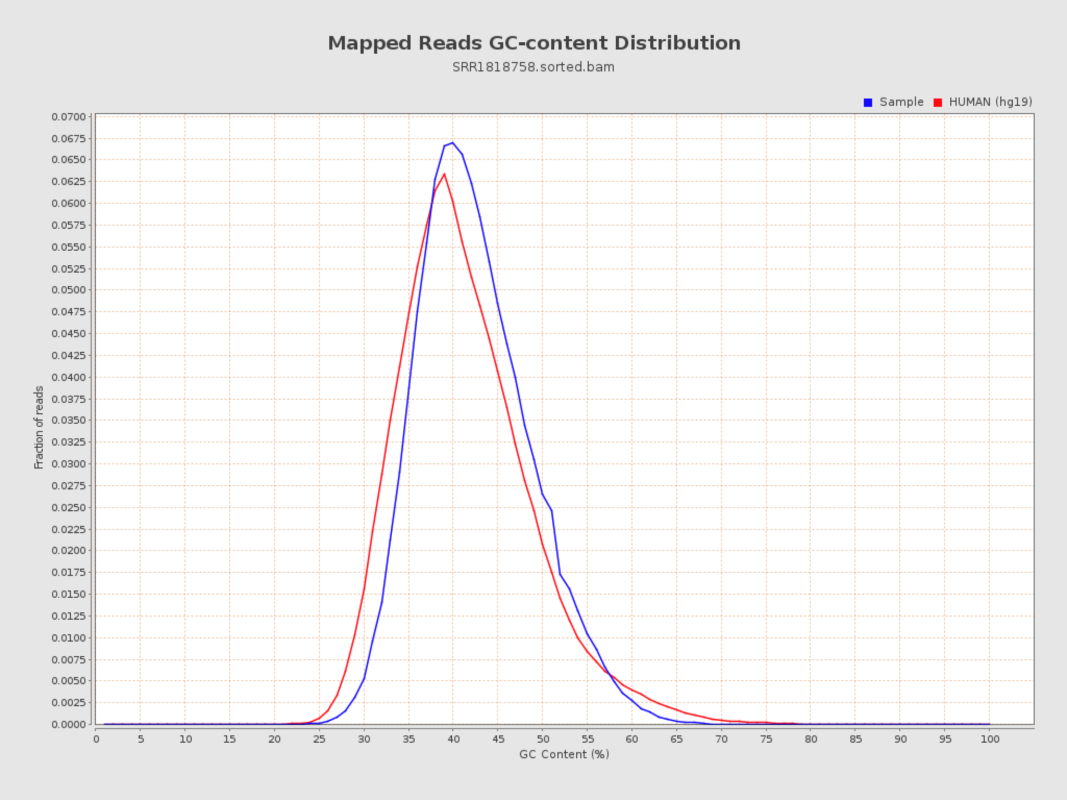
7. Results : Duplication Rate Histogram



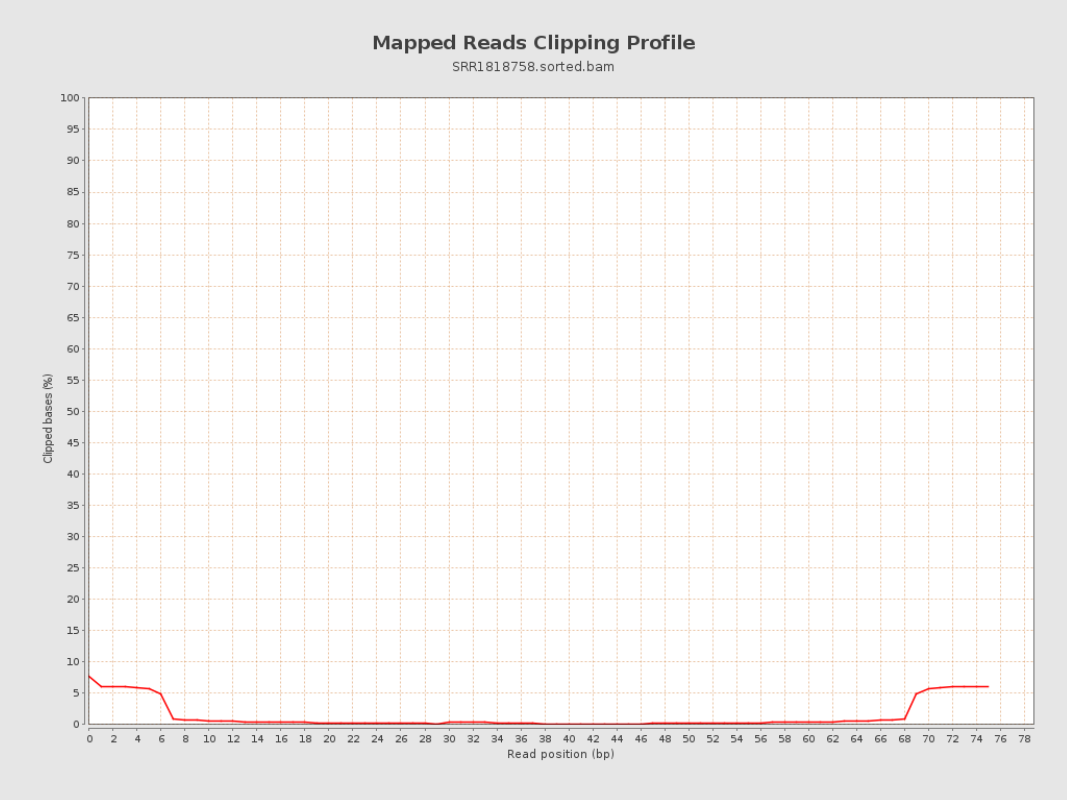
8. Results : Mapped Reads Nucleotide Content



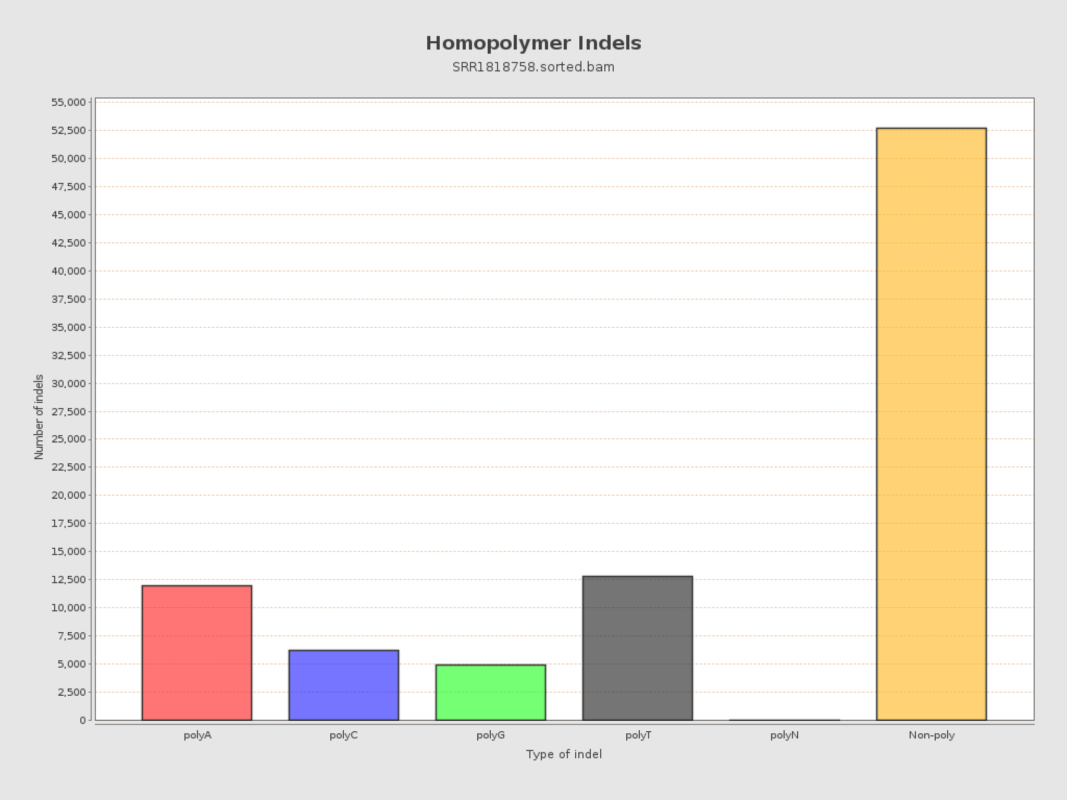
9. Results : Mapped Reads GC-content Distribution



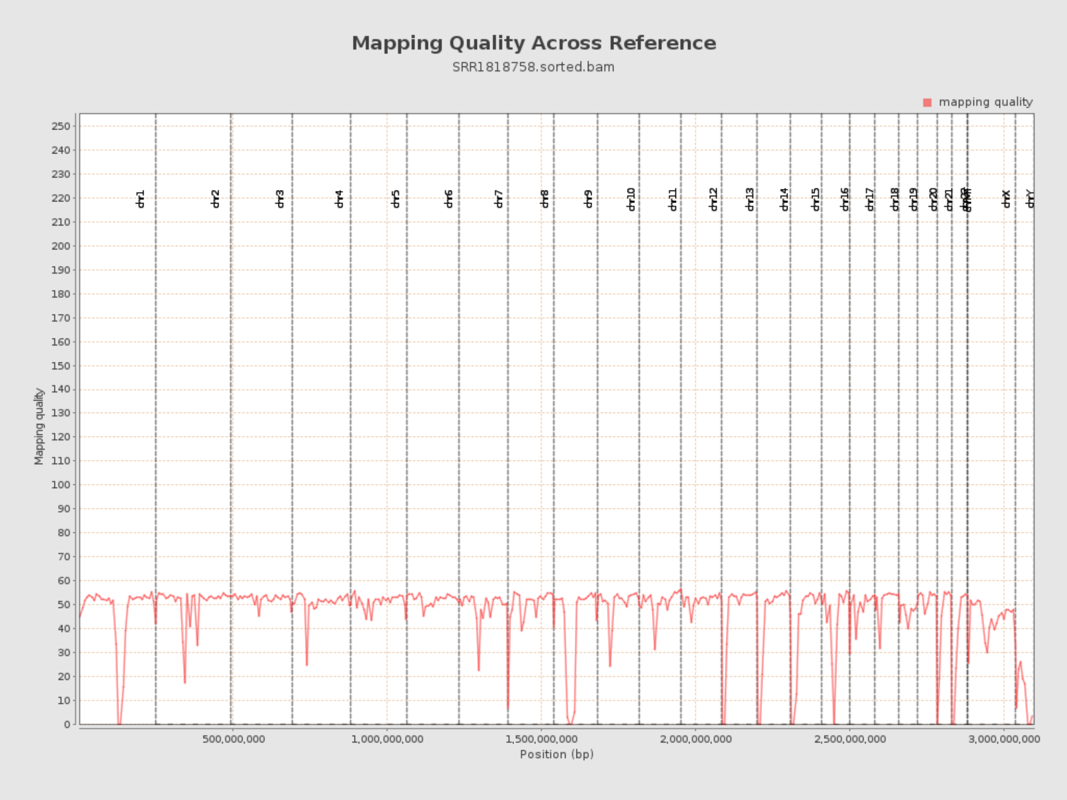
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram