Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818864.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_SRR1818864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818864.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:31:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818864.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,704,266
Mapped reads	1,610,705 / 94.51%
Unmapped reads	93,561 / 5.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,026 / 1.47%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	372,515 / 21.86%
Duplication rate	19.97%
Clipped reads	1,618,097 / 94.94%

2.2. ACGT Content

Number/percentage of A's	43,338,472 / 29.06%
Number/percentage of C's	30,468,416 / 20.43%
Number/percentage of T's	42,326,087 / 28.38%
Number/percentage of G's	33,009,244 / 22.13%
Number/percentage of N's	2,023 / 0%
GC Percentage	42.56%

2.3. Coverage

Mean	0.0482

Standard Deviation	0.5702

2.4. Mapping Quality

Mean Mapping Quality	49.36

2.5. Mismatches and indels

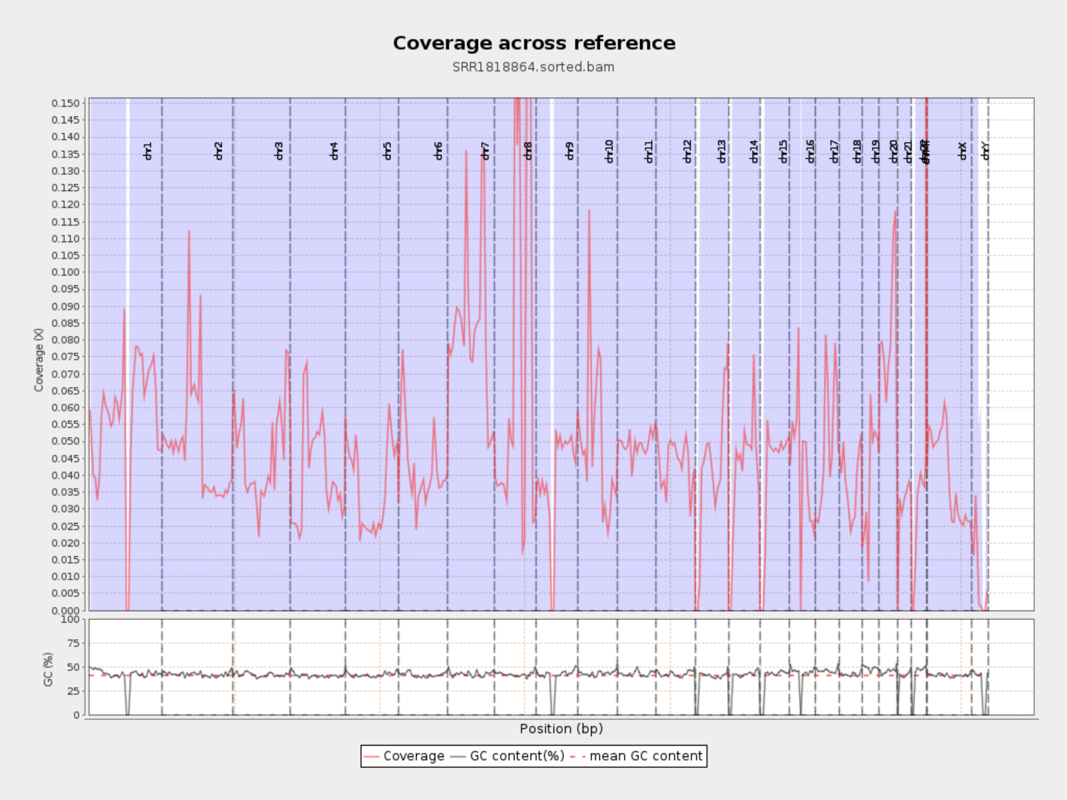
General error rate	0.64%
Mismatches	904,858
Insertions	21,411
Mapped reads with at least one insertion	1.29%
Deletions	48,847
Mapped reads with at least one deletion	2.96%
Homopolymer indels	41.08%

2.6. Chromosome stats

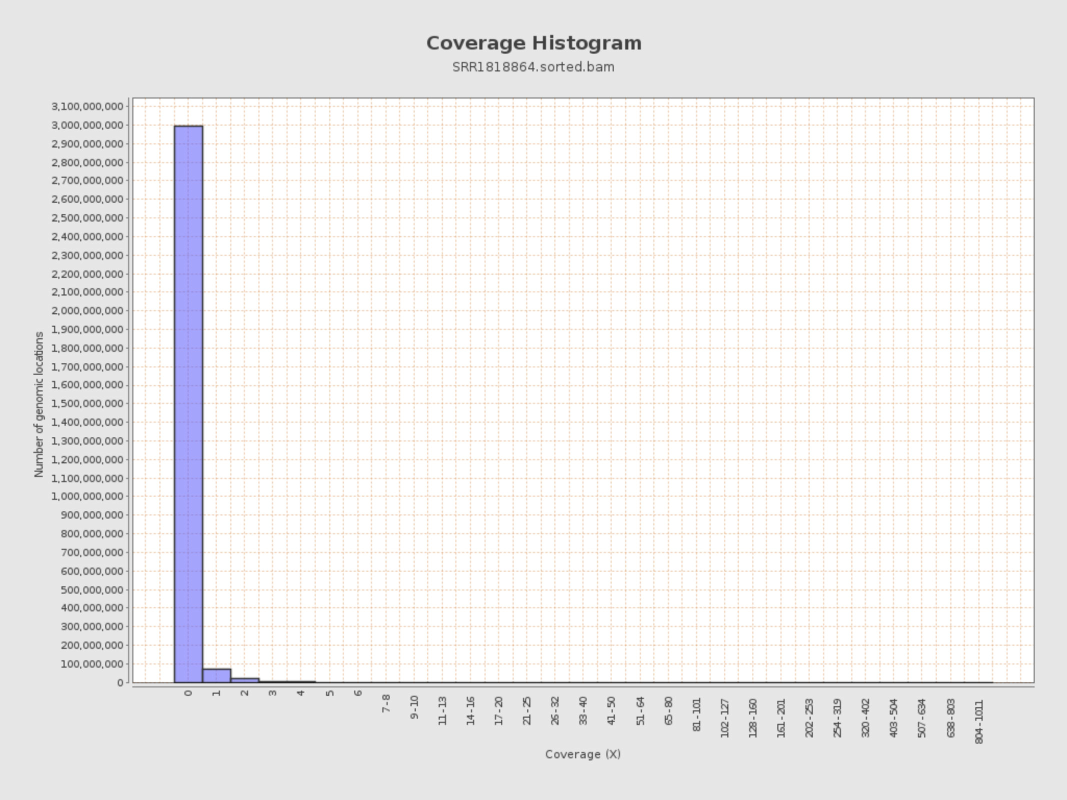
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14226706	0.0571	0.8479
chr2	243199373	11883725	0.0489	0.8306
chr3	198022430	9303320	0.047	0.2935
chr4	191154276	7650800	0.04	0.3473
chr5	180915260	6614429	0.0366	0.2715
chr6	171115067	7180470	0.042	0.3058
chr7	159138663	13572740	0.0853	1.1922

chr8	146364022	12673880	0.0866	0.4994
chr9	141213431	5547834	0.0393	0.4669
chr10	135534747	6760353	0.0499	0.7471
chr11	135006516	6640633	0.0492	0.3532
chr12	133851895	5897189	0.0441	0.2893
chr13	115169878	4661427	0.0405	0.2689
chr14	107349540	4396667	0.041	0.3086
chr15	102531392	4081238	0.0398	0.2675
chr16	90354753	3755426	0.0416	0.6294
chr17	81195210	4104047	0.0505	0.3676
chr18	78077248	2962214	0.0379	0.5459
chr19	59128983	2299827	0.0389	0.7306
chr20	63025520	5224102	0.0829	0.4166
chr21	48129895	1470638	0.0306	0.2808
chr22	51304566	1352406	0.0264	0.2538
chrMT	16571	199038	12.0112	7.763
chrX	155270560	6224625	0.0401	0.3387
chrY	59373566	554624	0.0093	0.6564

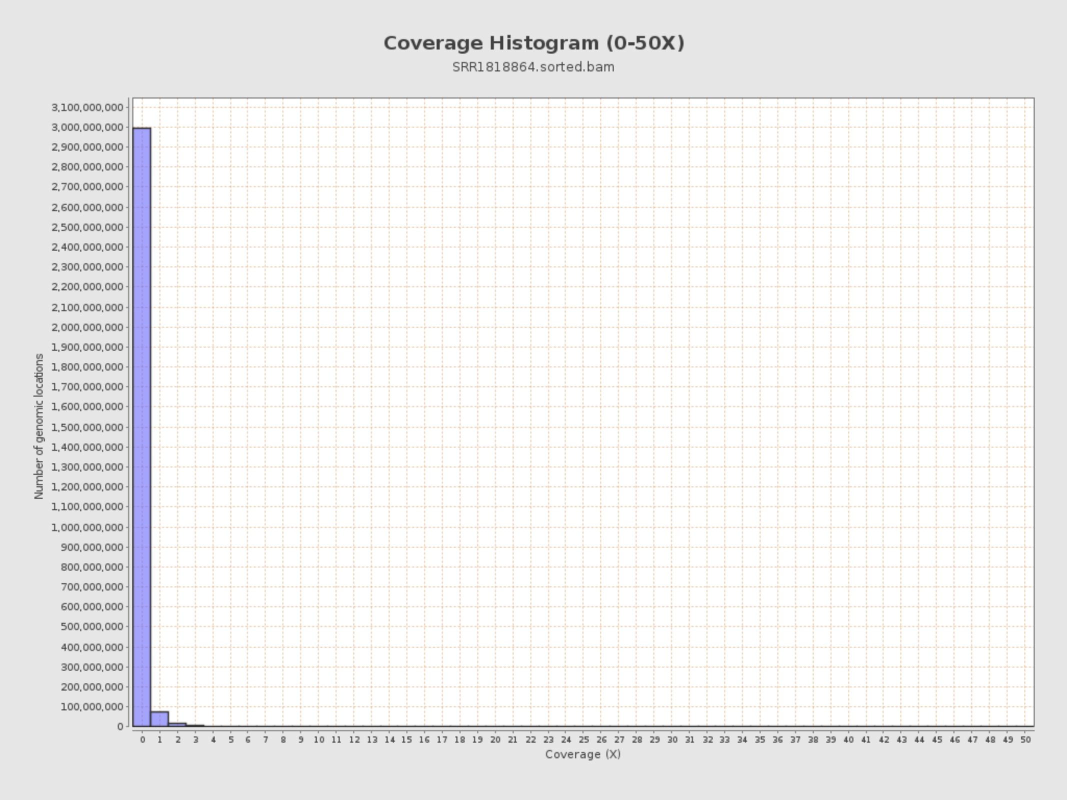
3. Results : Coverage across reference



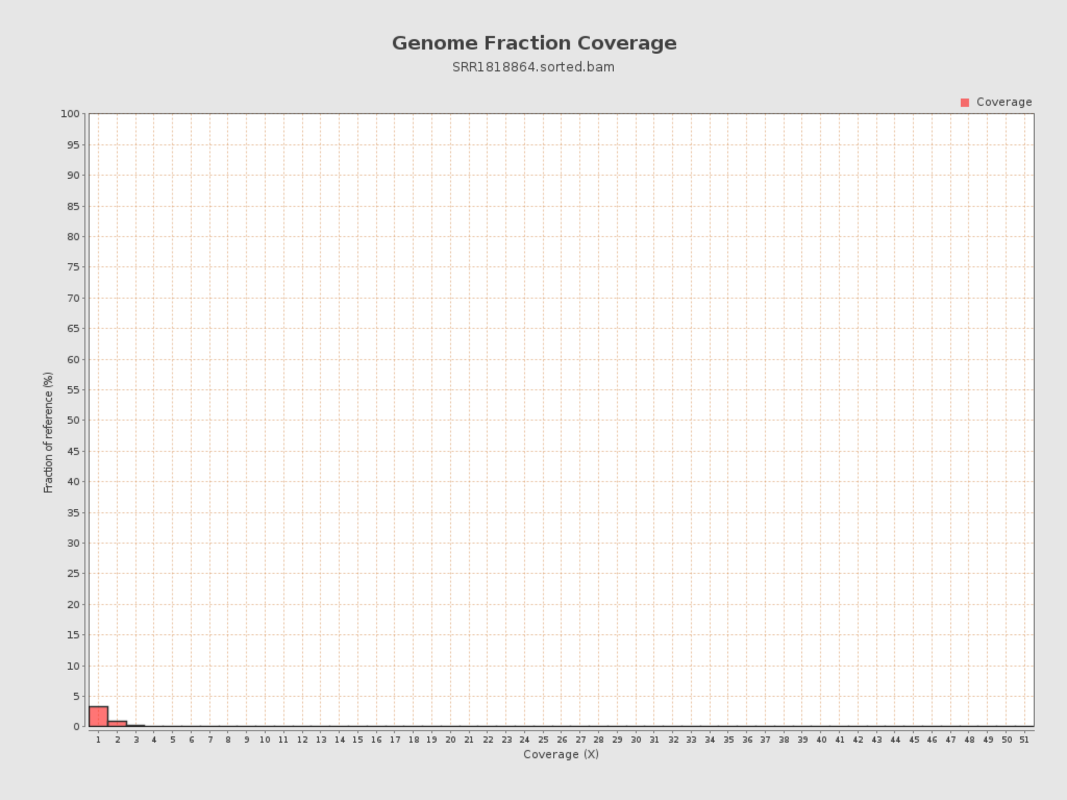
4. Results : Coverage Histogram



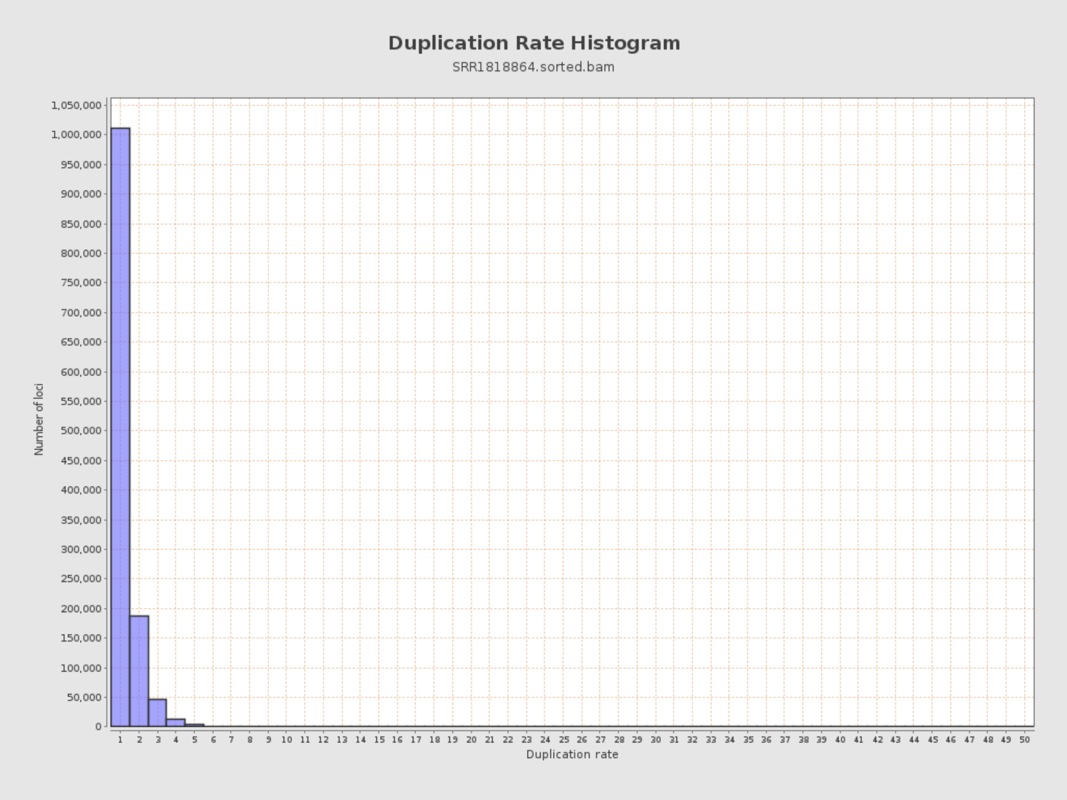
5. Results : Coverage Histogram (0-50X)



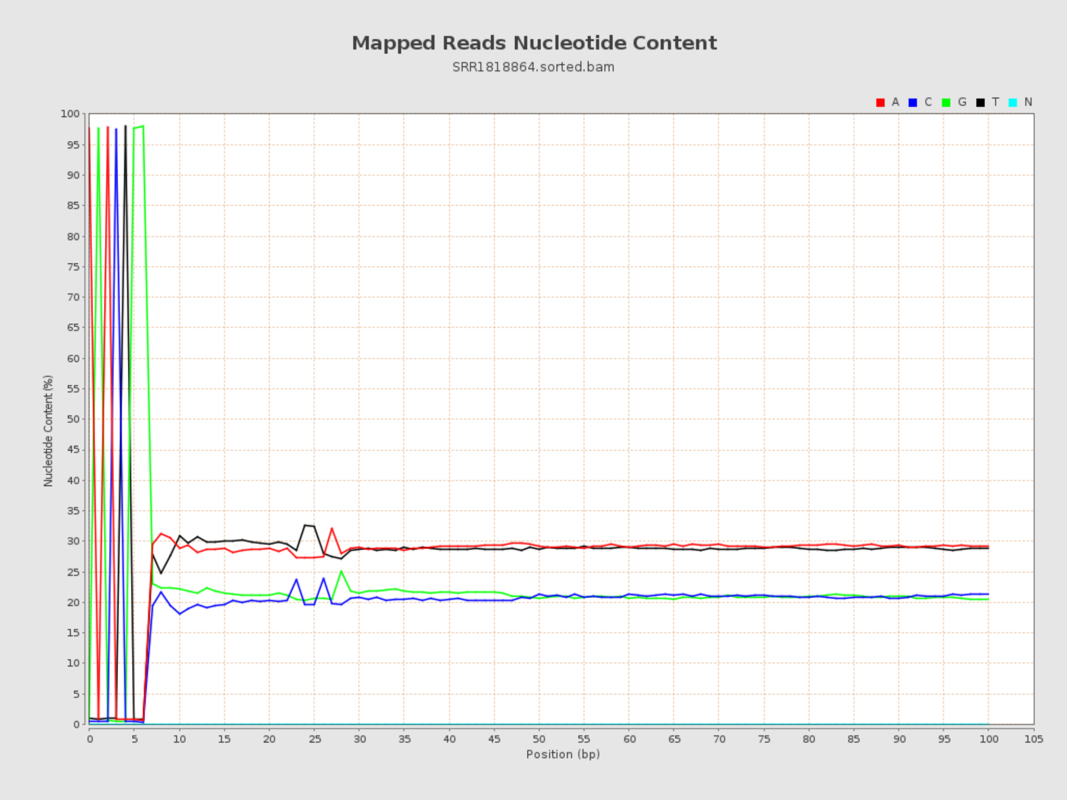
6. Results : Genome Fraction Coverage



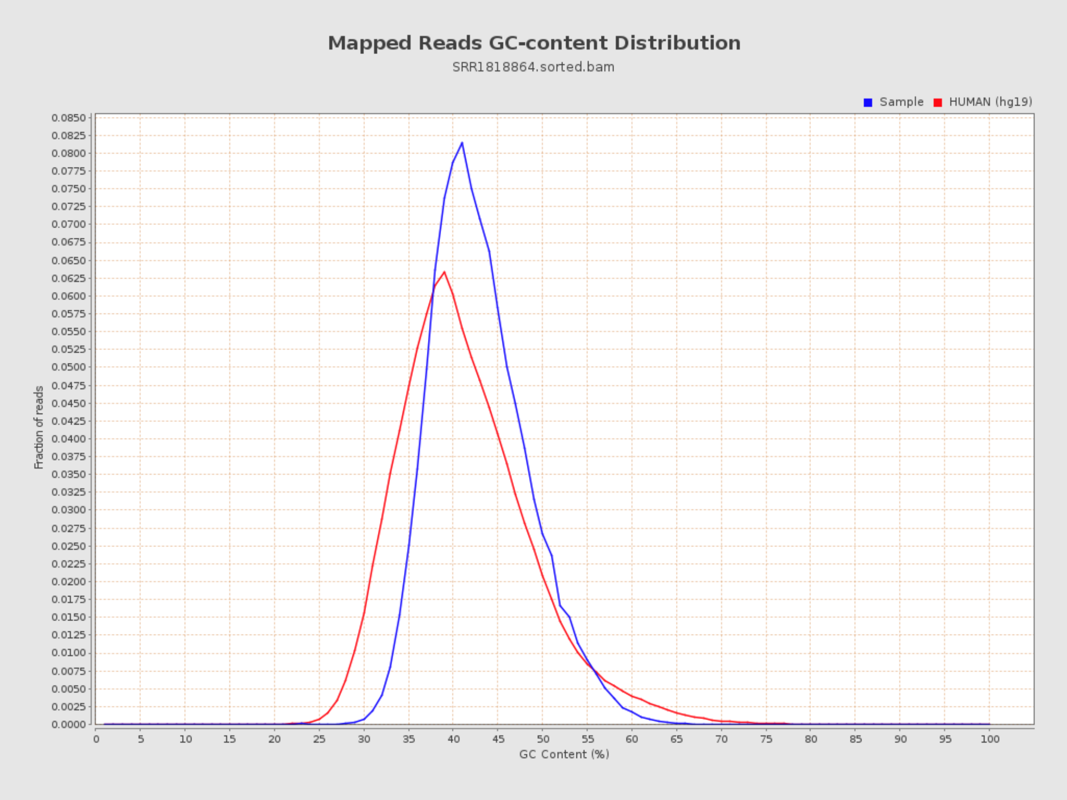
7. Results : Duplication Rate Histogram



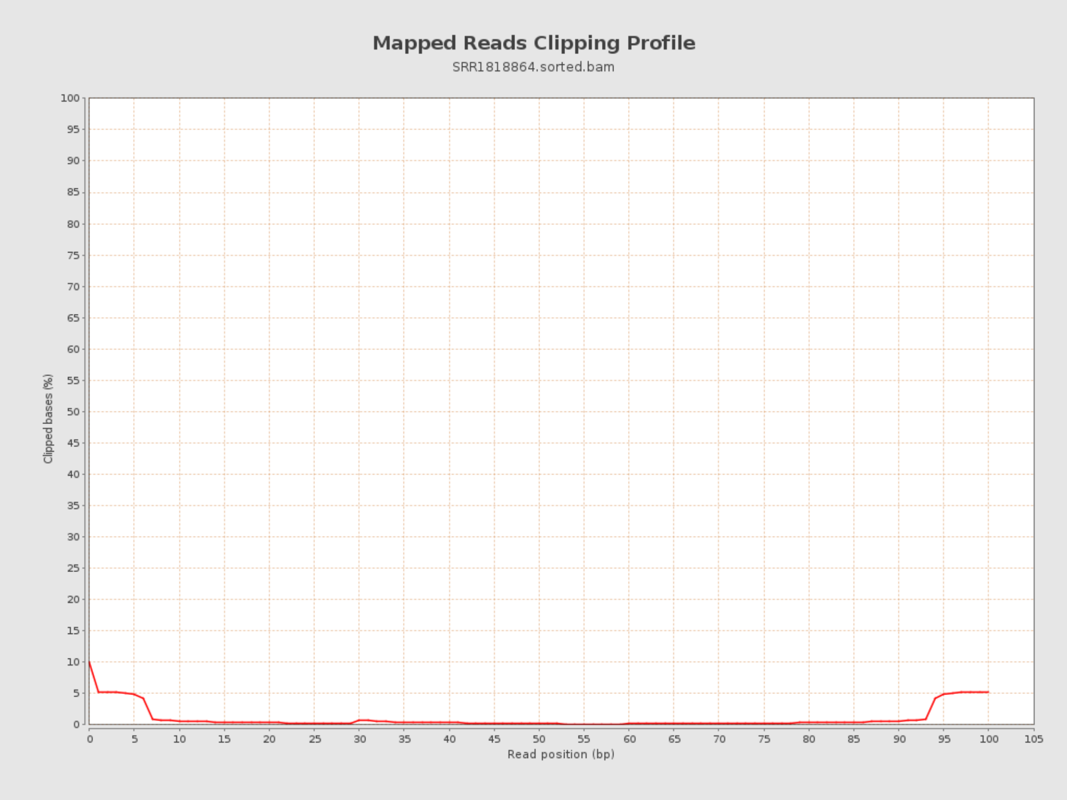
8. Results : Mapped Reads Nucleotide Content



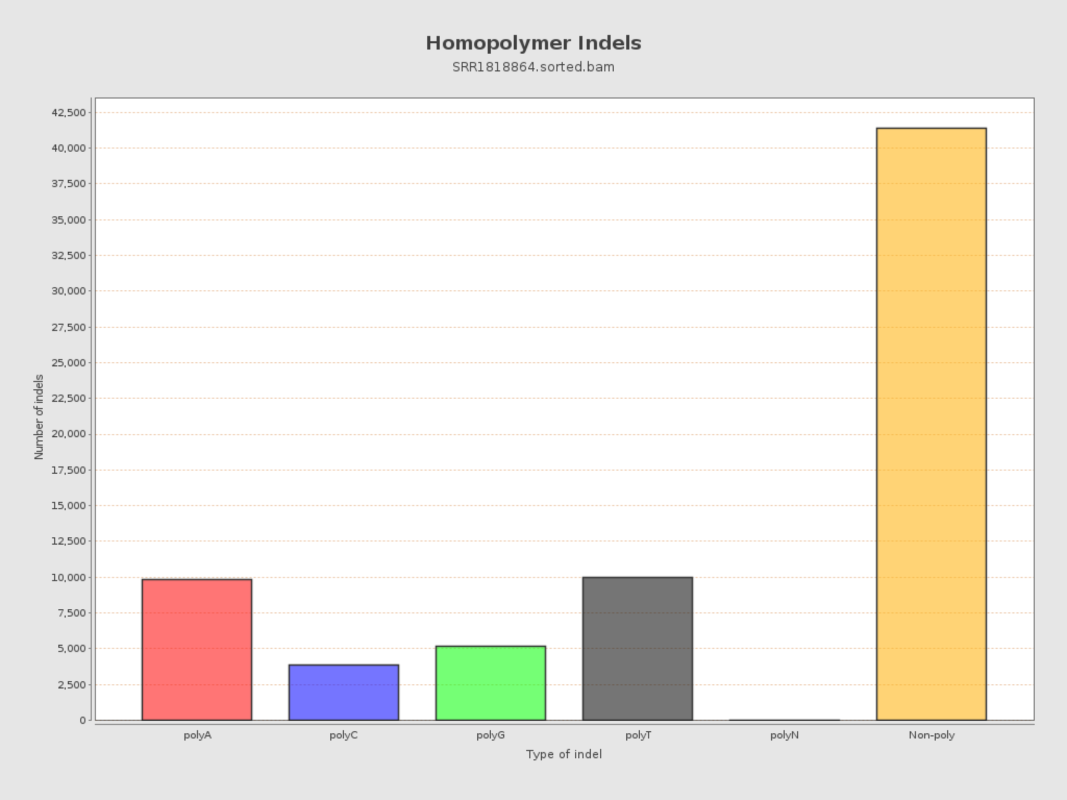
9. Results : Mapped Reads GC-content Distribution



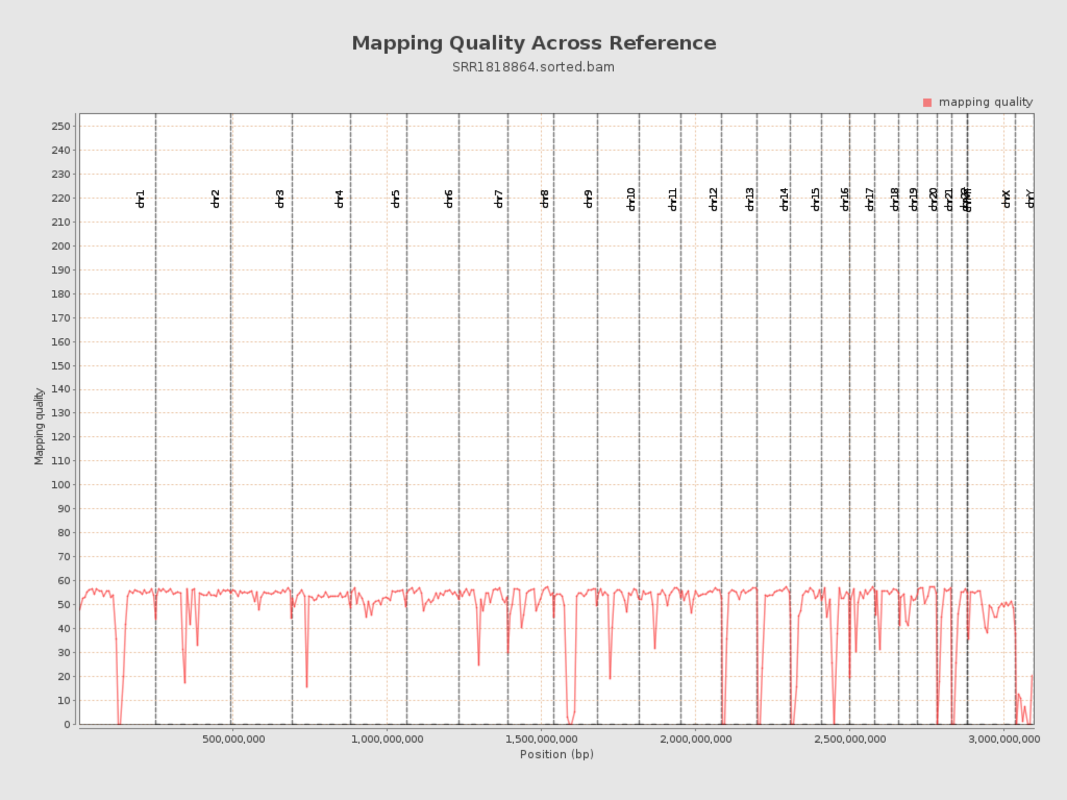
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram