Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 00:51:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818859.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_SRR1818859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 00:51:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	919,061
Mapped reads	899,429 / 97.86%
Unmapped reads	19,632 / 2.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,106 / 1.64%
Read min/max/mean length	30 / 101 / 101.63
Duplicated reads (estimated)	145,278 / 15.81%
Duplication rate	13.71%
Clipped reads	906,492 / 98.63%

2.2. ACGT Content

Number/percentage of A's	24,072,169 / 28.96%
Number/percentage of C's	17,708,572 / 21.3%
Number/percentage of T's	23,926,837 / 28.78%
Number/percentage of G's	17,422,745 / 20.96%
Number/percentage of N's	1,197 / 0%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0269

Standard Deviation	0.3415

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

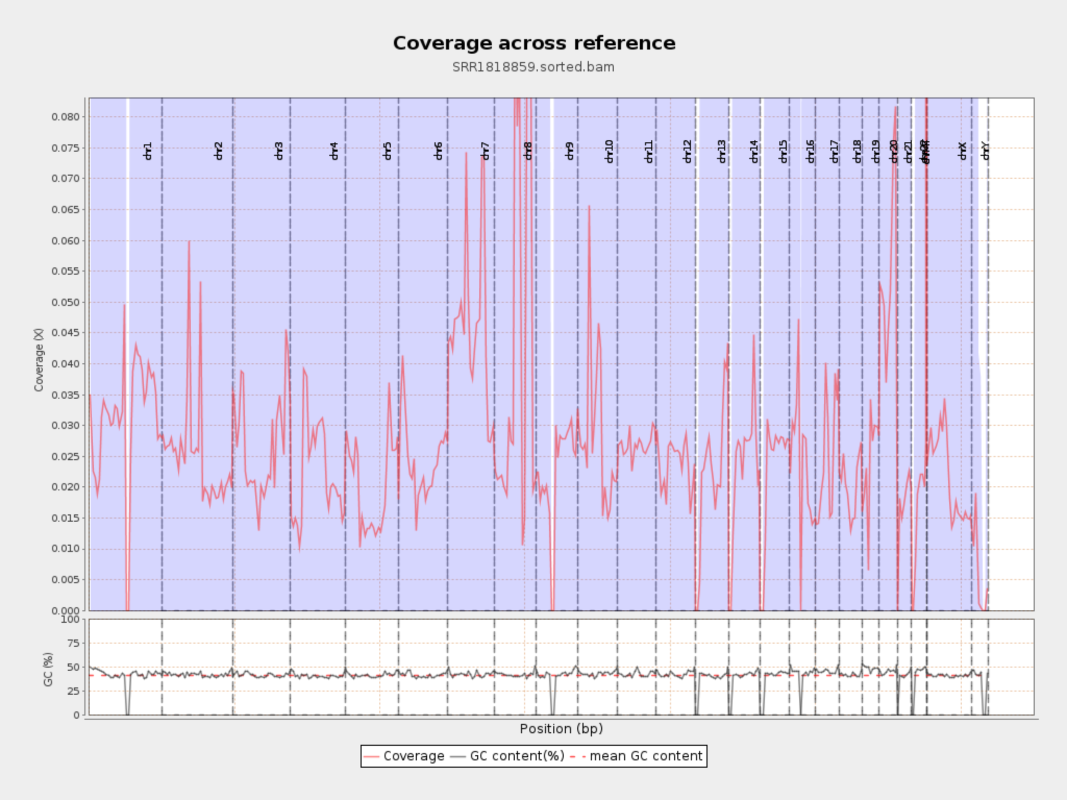
General error rate	0.66%
Mismatches	515,413
Insertions	13,162
Mapped reads with at least one insertion	1.42%
Deletions	27,464
Mapped reads with at least one deletion	2.98%
Homopolymer indels	38.9%

2.6. Chromosome stats

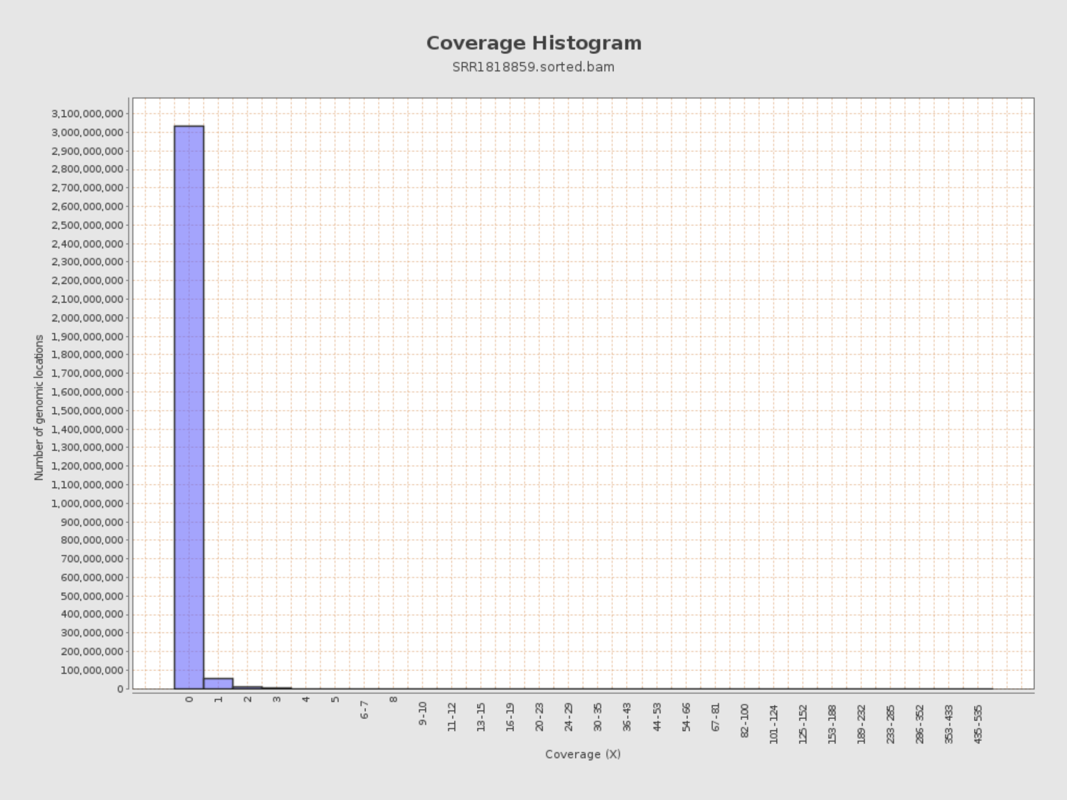
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7737006	0.031	0.4804
chr2	243199373	6171069	0.0254	0.5213
chr3	198022430	5320848	0.0269	0.2009
chr4	191154276	4219624	0.0221	0.2301
chr5	180915260	3620600	0.02	0.1811
chr6	171115067	4141124	0.0242	0.2068
chr7	159138663	7430630	0.0467	0.6458

chr8	146364022	7346066	0.0502	0.3204
chr9	141213431	3109400	0.022	0.2857
chr10	135534747	3882591	0.0286	0.4592
chr11	135006516	3621500	0.0268	0.2284
chr12	133851895	3211587	0.024	0.1905
chr13	115169878	2541310	0.0221	0.1819
chr14	107349540	2492557	0.0232	0.198
chr15	102531392	2311869	0.0225	0.183
chr16	90354753	2114415	0.0234	0.3835
chr17	81195210	2054774	0.0253	0.2292
chr18	78077248	1586088	0.0203	0.3025
chr19	59128983	1419989	0.024	0.4216
chr20	63025520	3459440	0.0549	0.3014
chr21	48129895	822256	0.0171	0.183
chr22	51304566	754332	0.0147	0.1574
chrMT	16571	87586	5.2855	4.0698
chrX	155270560	3397564	0.0219	0.2043
chrY	59373566	331157	0.0056	0.4097

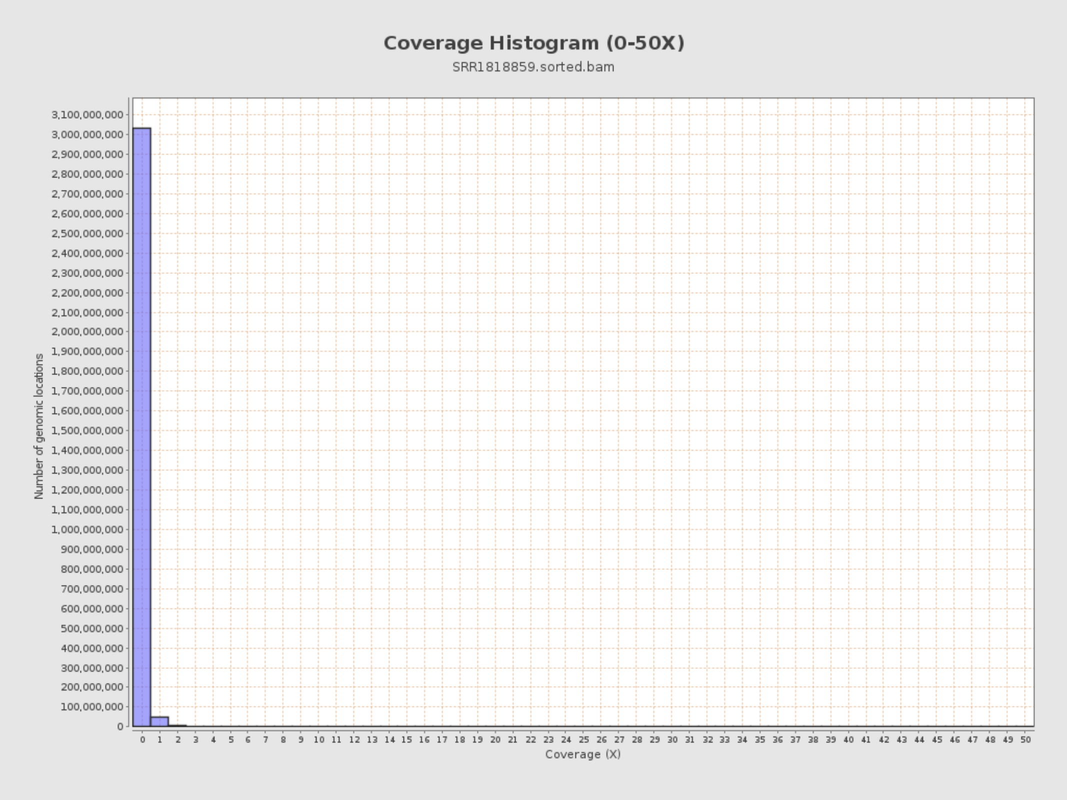
3. Results : Coverage across reference



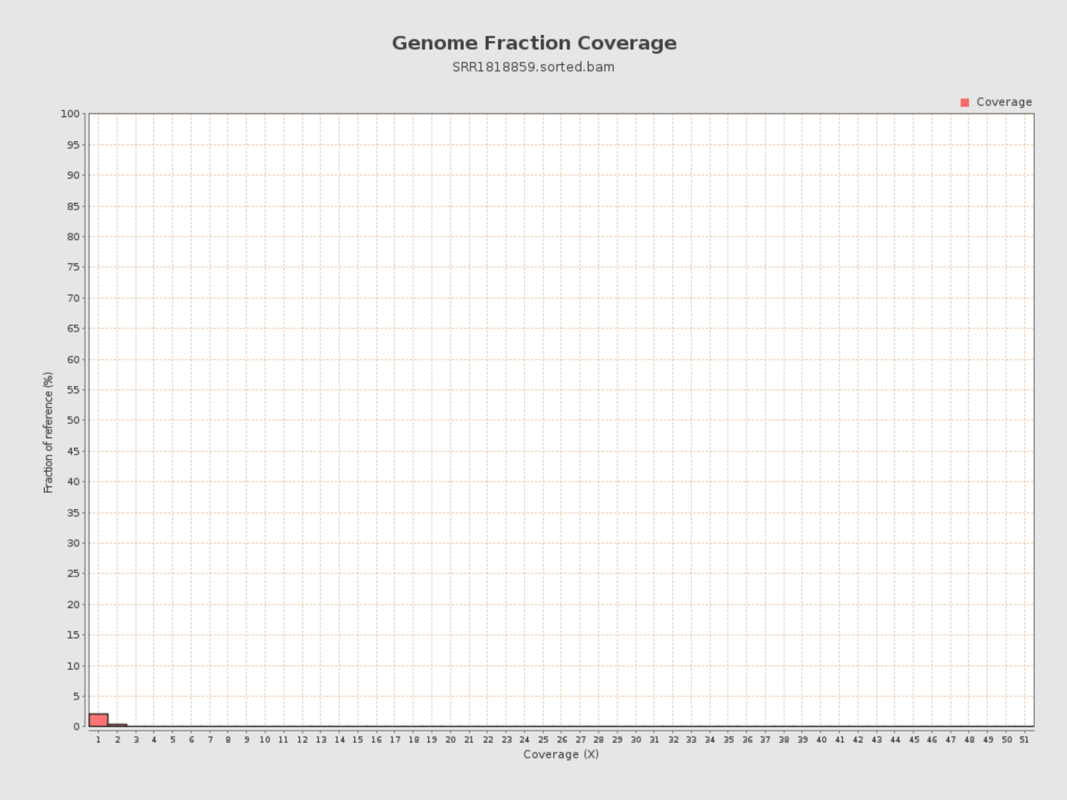
4. Results : Coverage Histogram



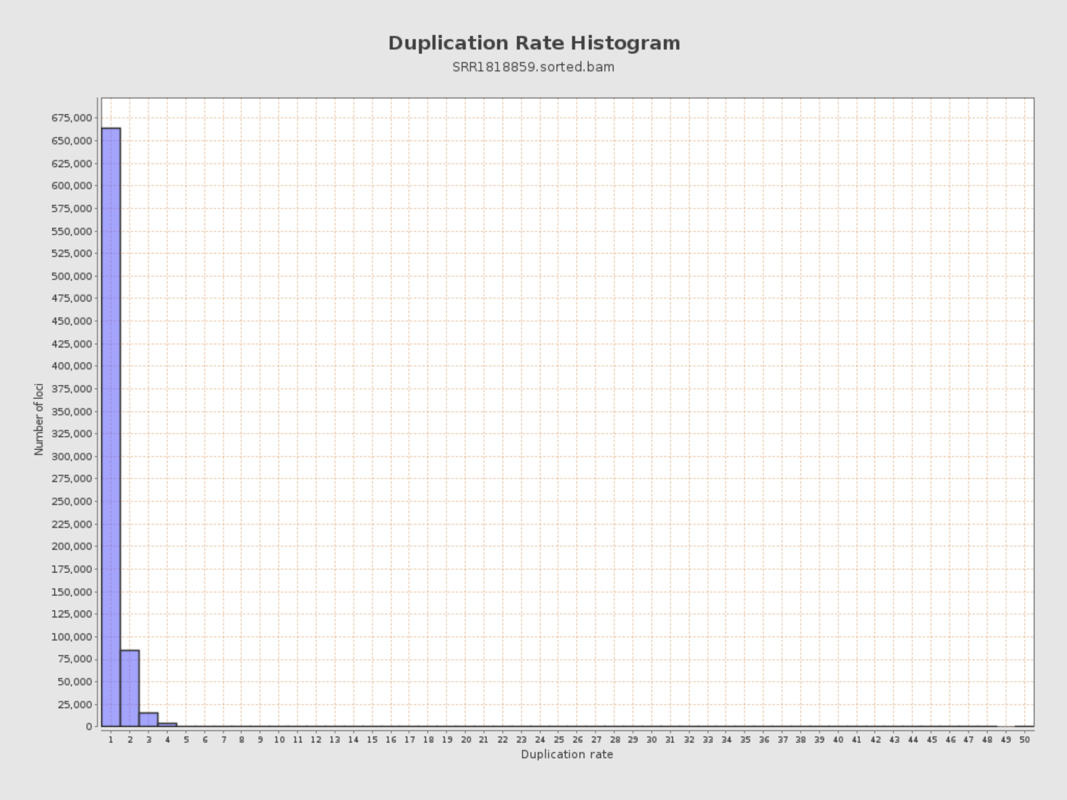
5. Results : Coverage Histogram (0-50X)



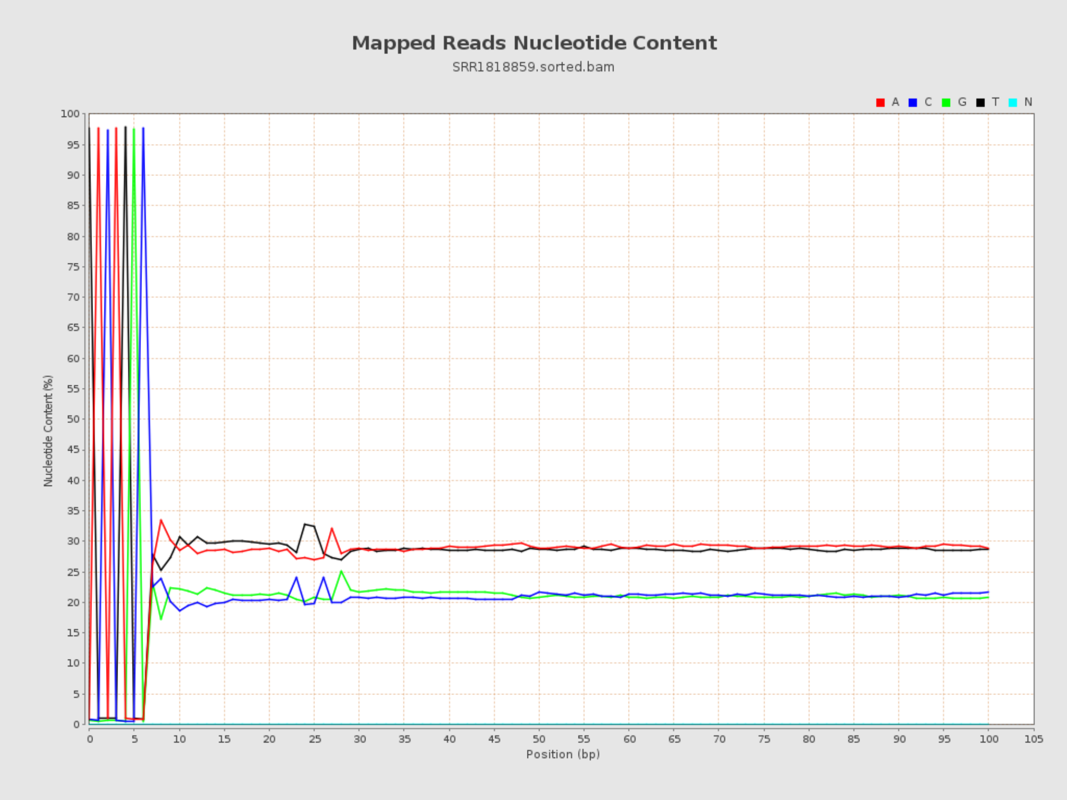
6. Results : Genome Fraction Coverage



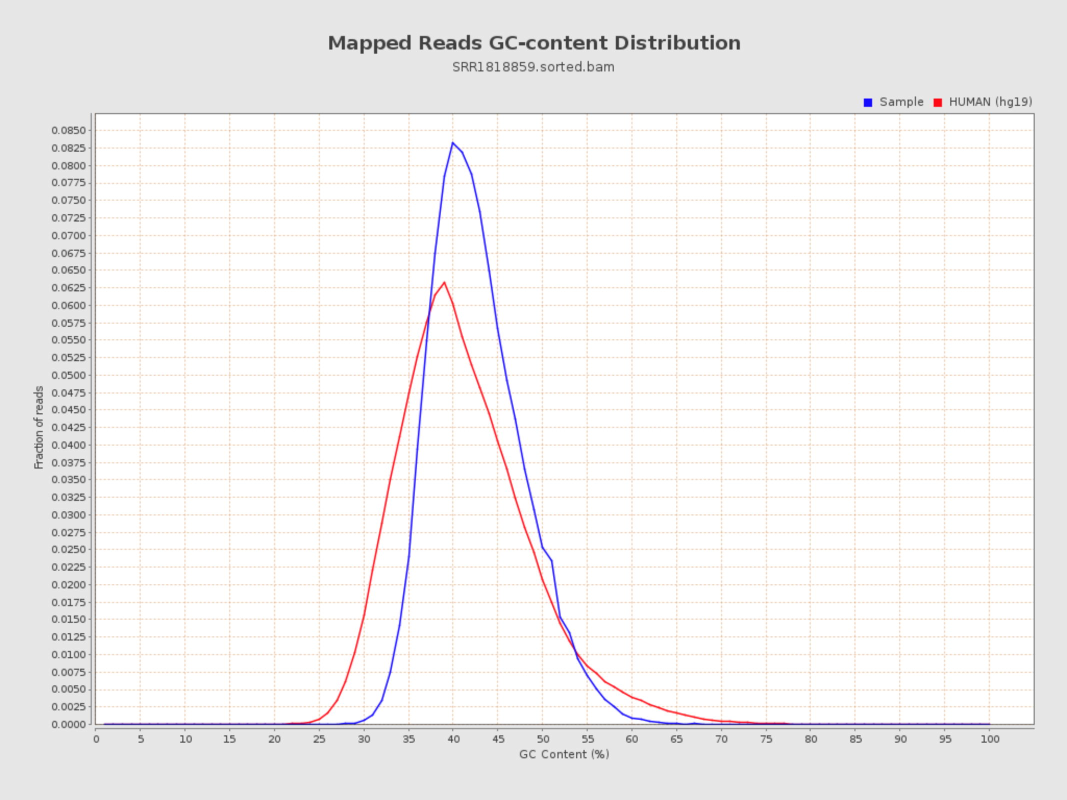
7. Results : Duplication Rate Histogram



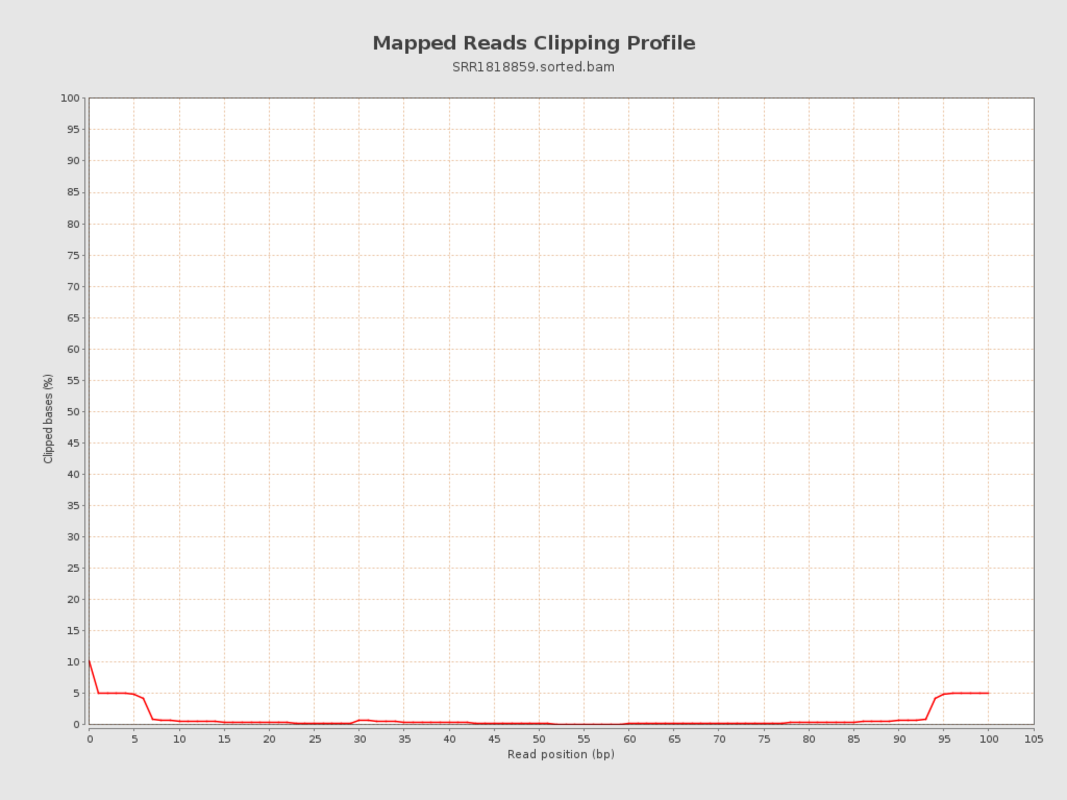
8. Results : Mapped Reads Nucleotide Content



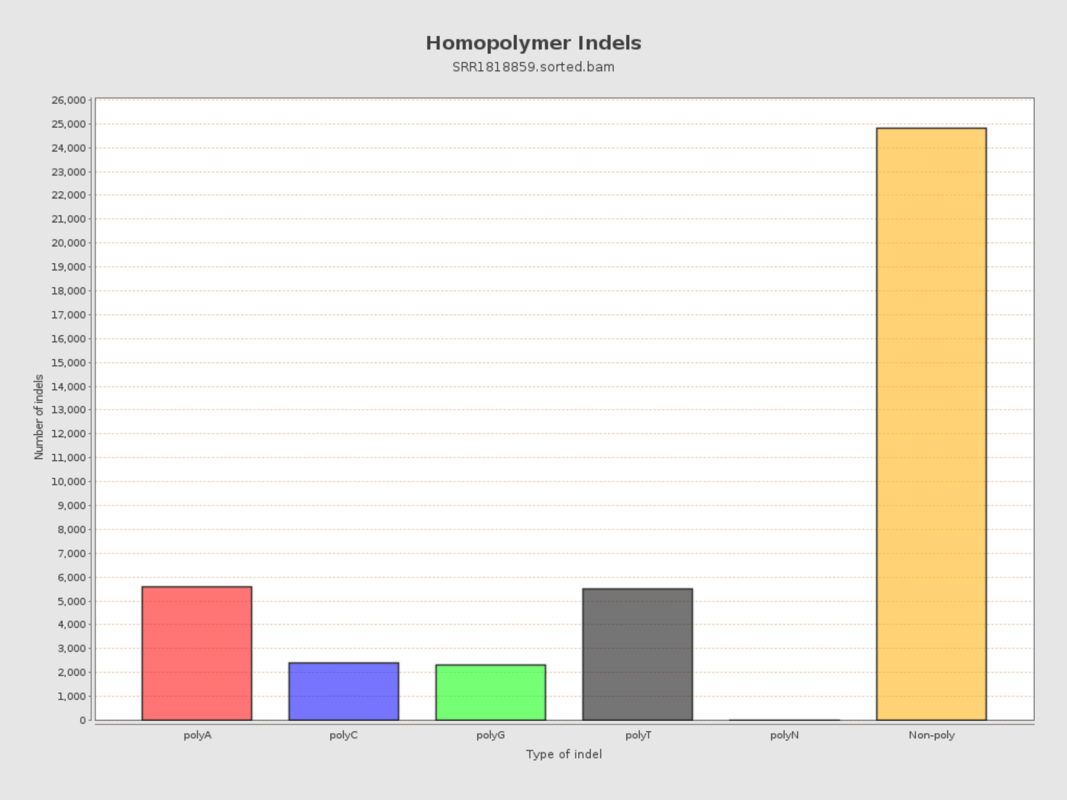
9. Results : Mapped Reads GC-content Distribution



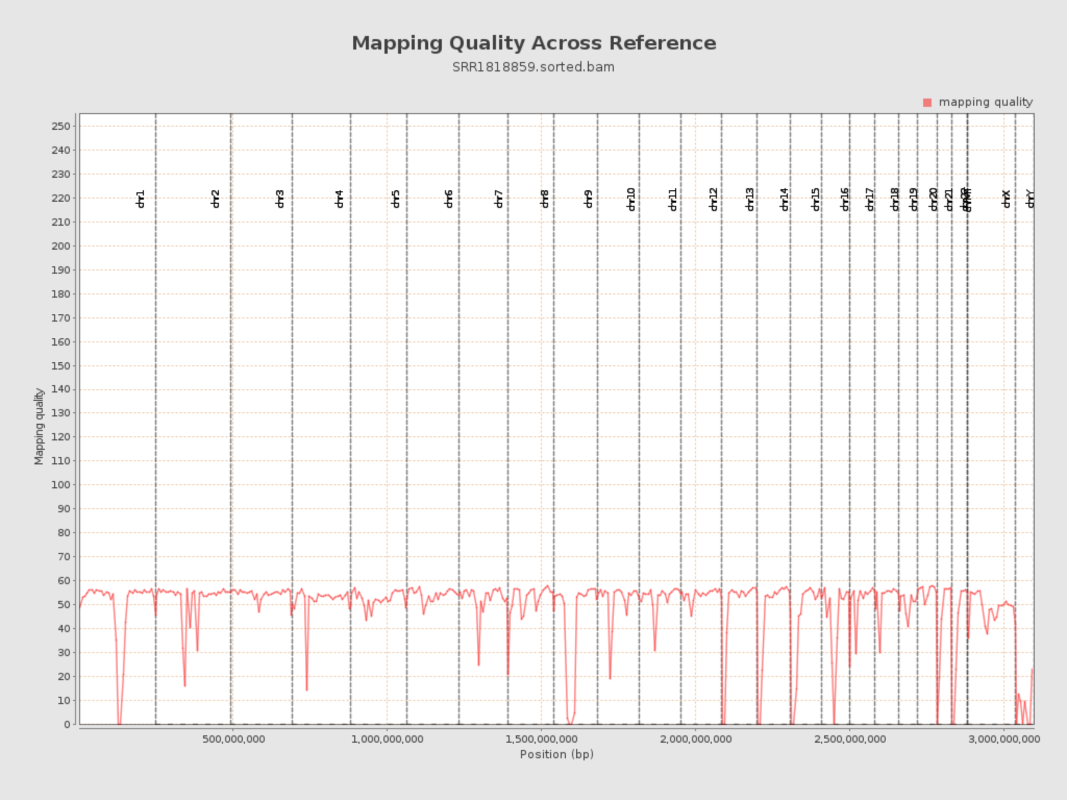
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram