Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:24:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818863.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_SRR1818863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818863.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:24:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818863.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	326,367
Mapped reads	317,788 / 97.37%
Unmapped reads	8,579 / 2.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,059 / 1.55%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	29,510 / 9.04%
Duplication rate	7.74%
Clipped reads	321,475 / 98.5%

2.2. ACGT Content

Number/percentage of A's	8,514,365 / 28.99%
Number/percentage of C's	6,467,727 / 22.02%
Number/percentage of T's	8,263,784 / 28.14%
Number/percentage of G's	6,123,160 / 20.85%
Number/percentage of N's	565 / 0%
GC Percentage	42.87%

2.3. Coverage

Mean	0.0095

Standard Deviation	0.1486

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

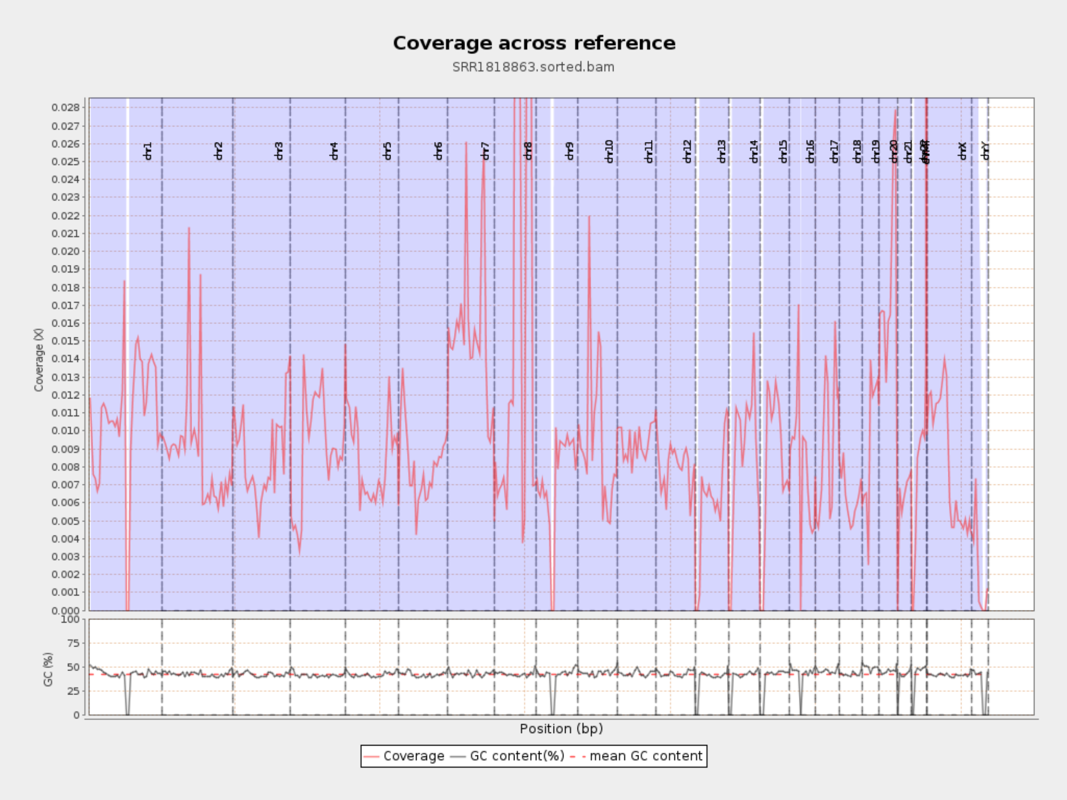
General error rate	0.65%
Mismatches	179,643
Insertions	4,409
Mapped reads with at least one insertion	1.33%
Deletions	9,746
Mapped reads with at least one deletion	3%
Homopolymer indels	39.77%

2.6. Chromosome stats

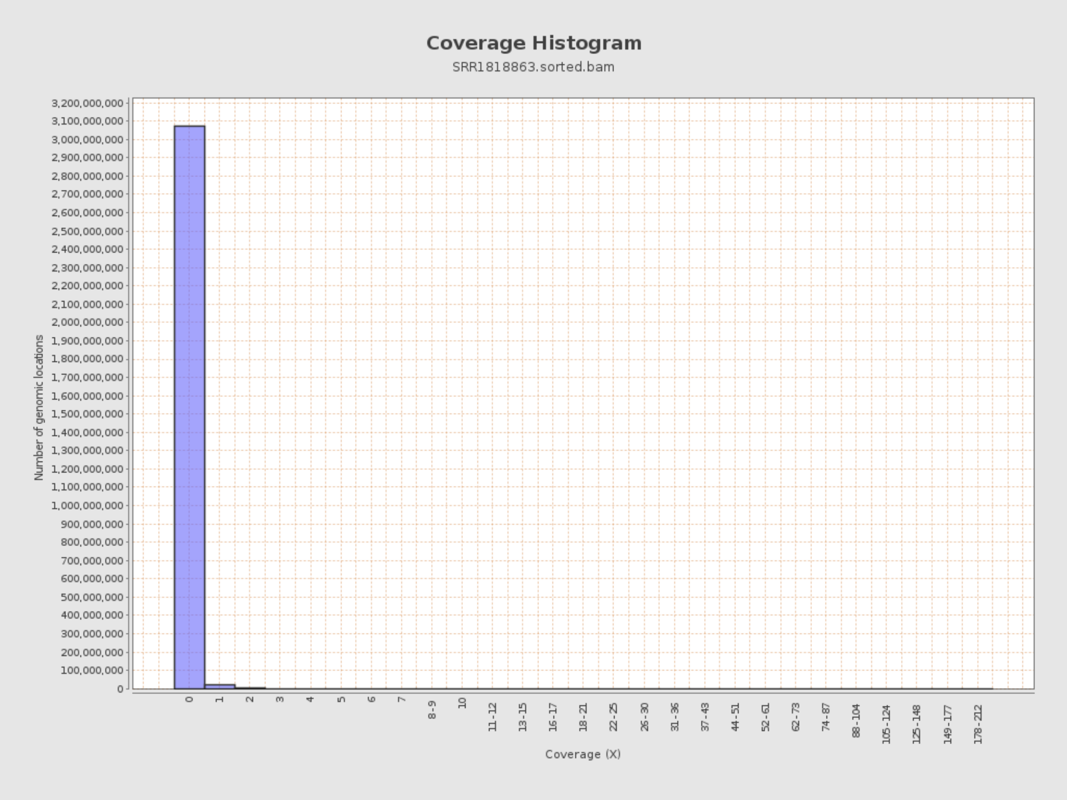
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2669164	0.0107	0.2024
chr2	243199373	2146696	0.0088	0.2113
chr3	198022430	1709492	0.0086	0.1031
chr4	191154276	1702936	0.0089	0.1148
chr5	180915260	1525209	0.0084	0.1033
chr6	171115067	1380717	0.0081	0.1013
chr7	159138663	2515950	0.0158	0.2573

chr8	146364022	2814353	0.0192	0.1626
chr9	141213431	1019921	0.0072	0.1171
chr10	135534747	1295898	0.0096	0.1755
chr11	135006516	1265620	0.0094	0.1137
chr12	133851895	1073618	0.008	0.0994
chr13	115169878	695601	0.006	0.0852
chr14	107349540	936754	0.0087	0.1059
chr15	102531392	844865	0.0082	0.0999
chr16	90354753	716212	0.0079	0.1547
chr17	81195210	766826	0.0094	0.115
chr18	78077248	494951	0.0063	0.1251
chr19	59128983	555789	0.0094	0.1776
chr20	63025520	1160099	0.0184	0.1561
chr21	48129895	294214	0.0061	0.0951
chr22	51304566	345878	0.0067	0.0931
chrMT	16571	31646	1.9097	1.7263
chrX	155270560	1303146	0.0084	0.1074
chrY	59373566	123166	0.0021	0.1646

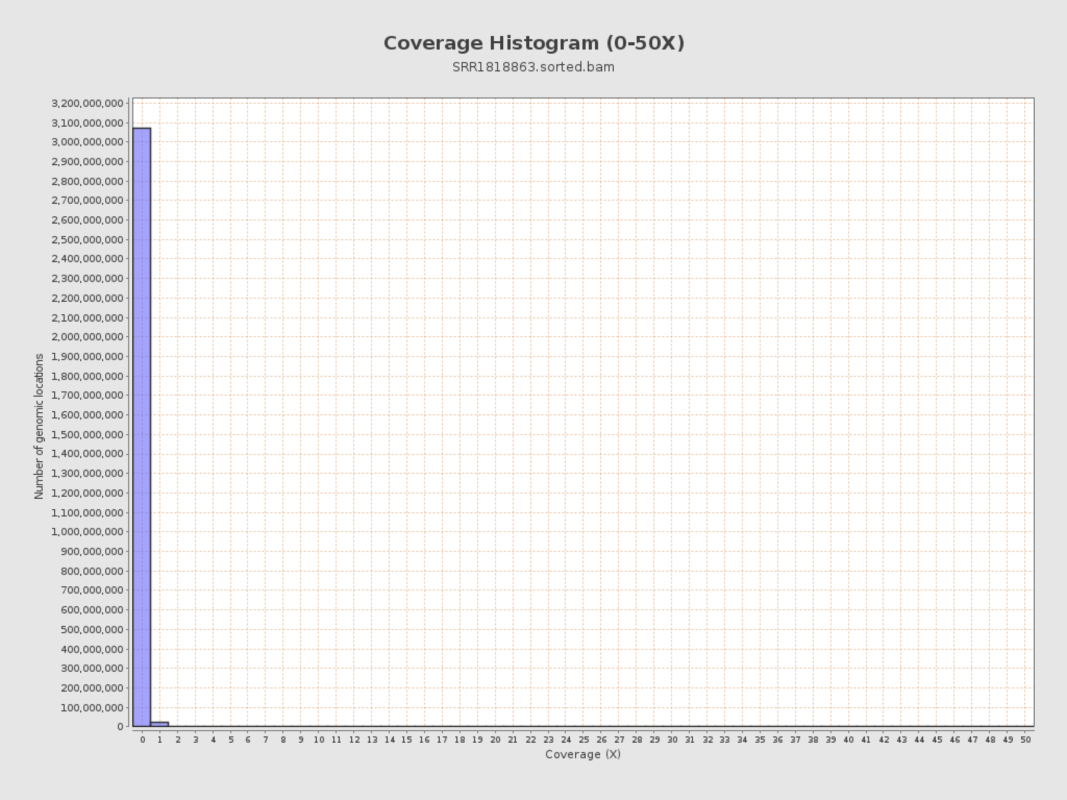
3. Results : Coverage across reference



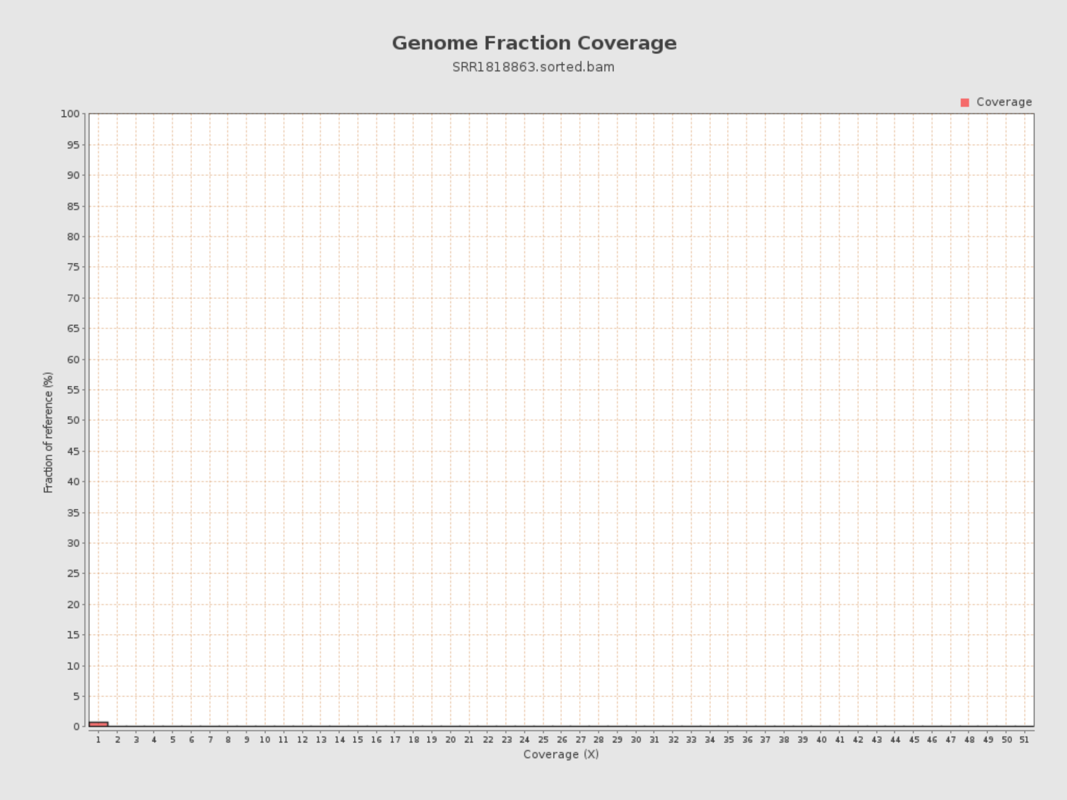
4. Results : Coverage Histogram



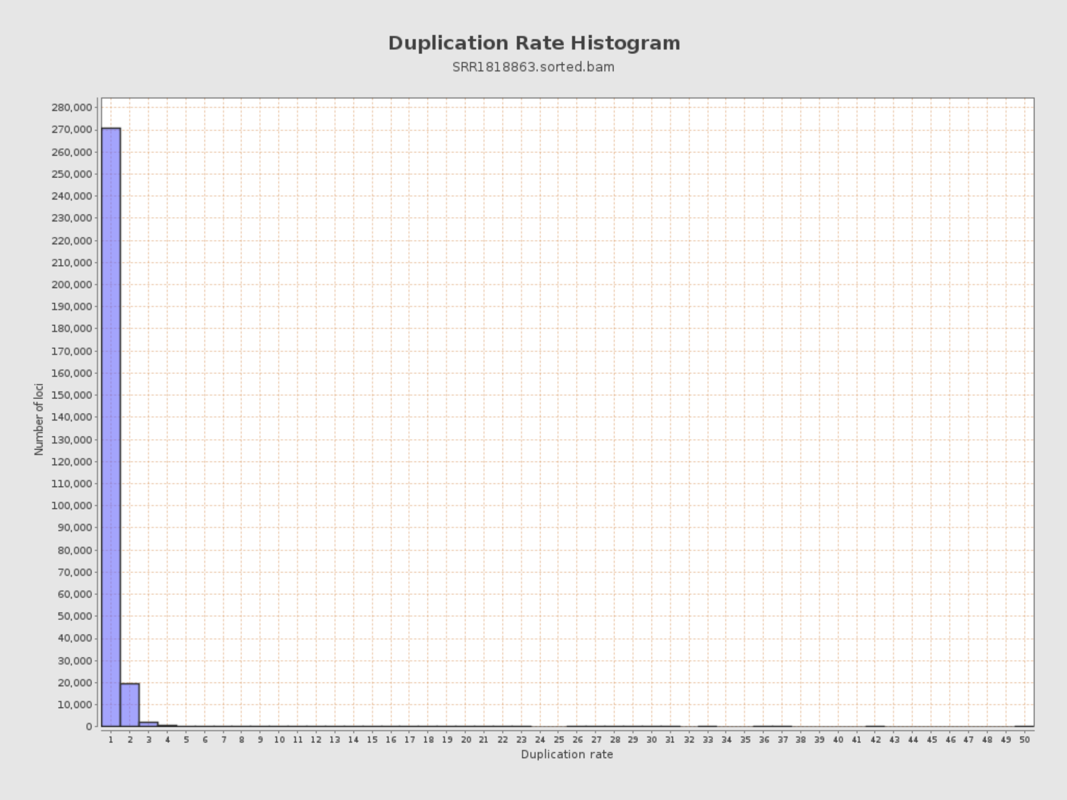
5. Results : Coverage Histogram (0-50X)



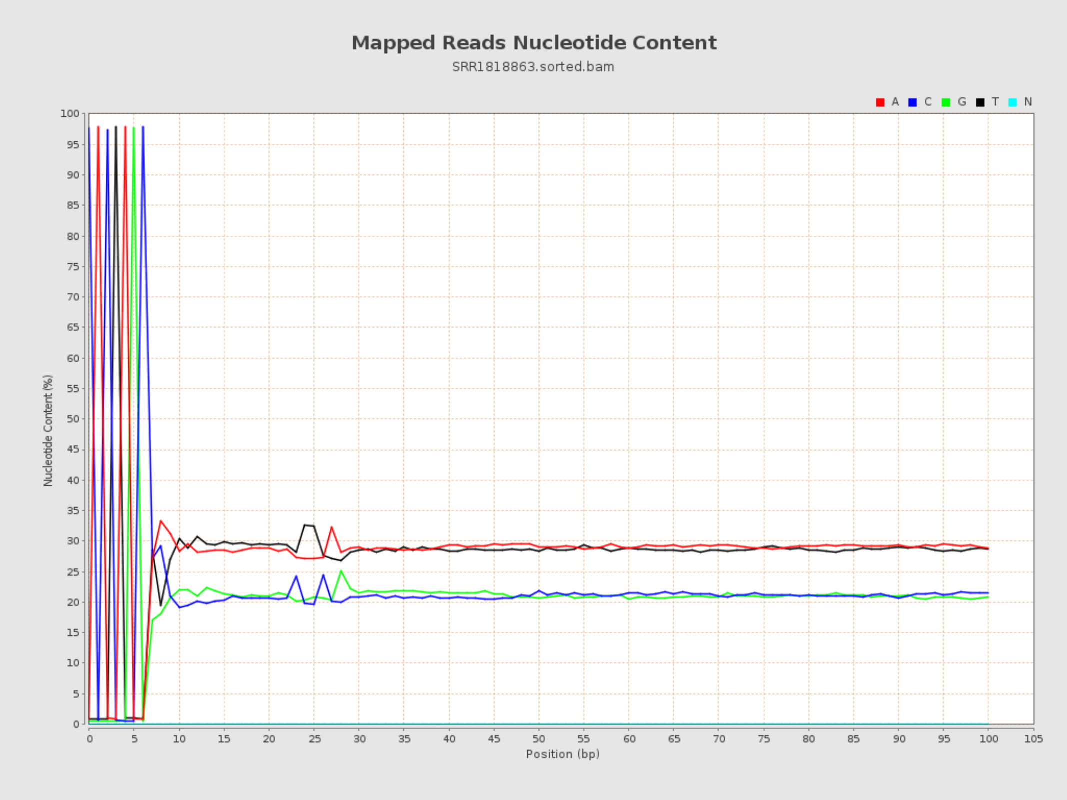
6. Results : Genome Fraction Coverage



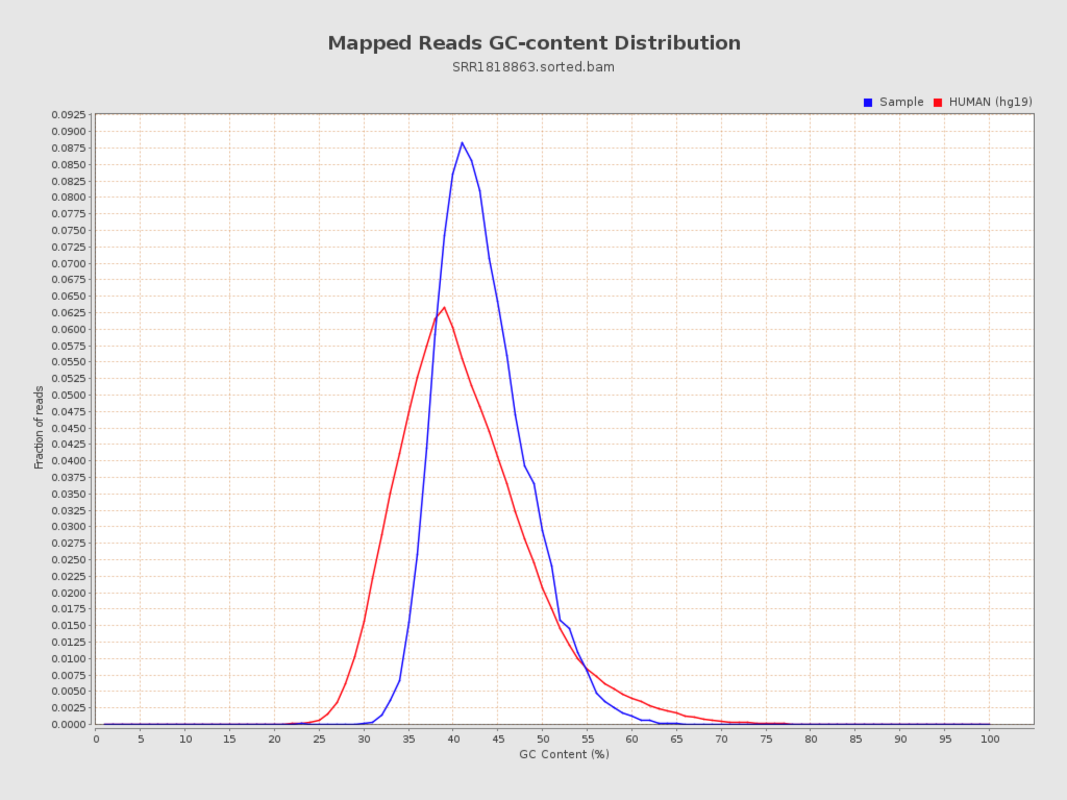
7. Results : Duplication Rate Histogram



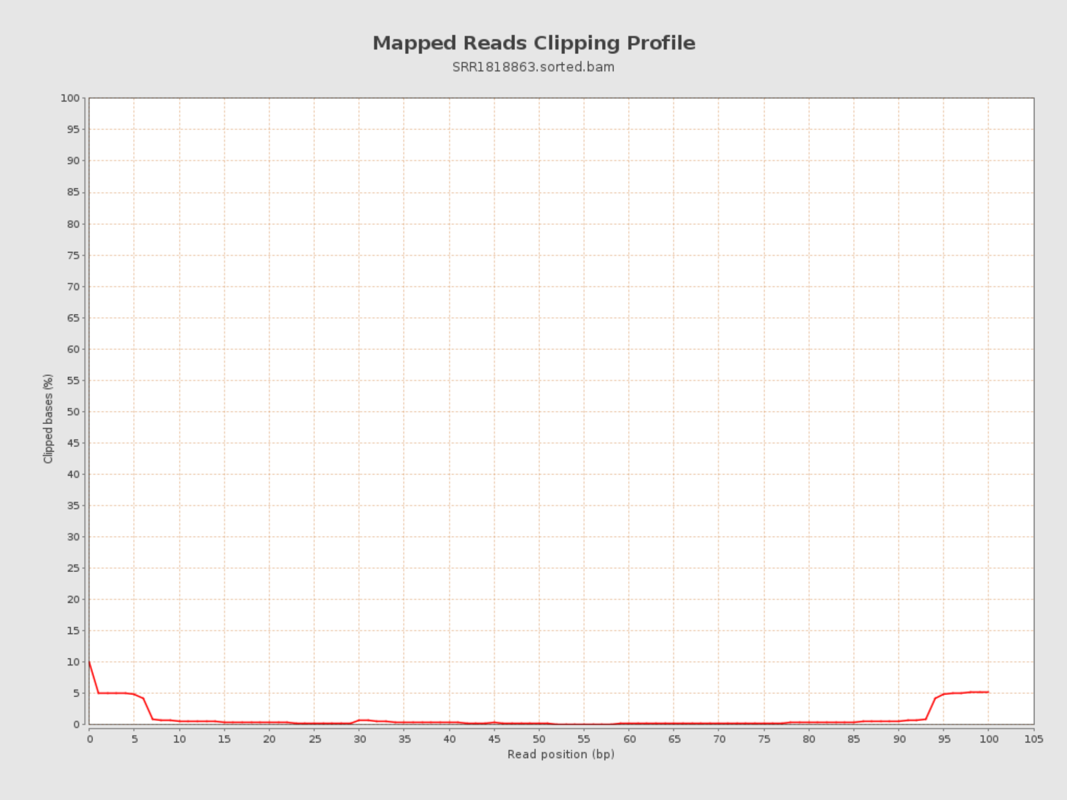
8. Results : Mapped Reads Nucleotide Content



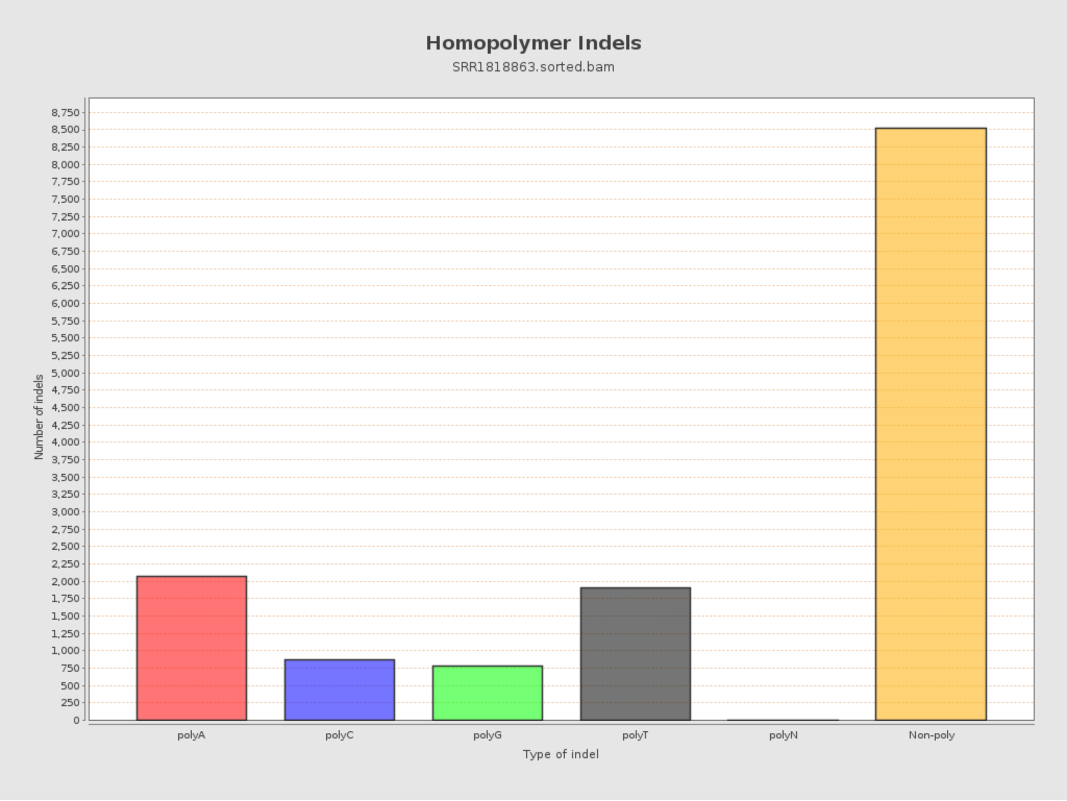
9. Results : Mapped Reads GC-content Distribution



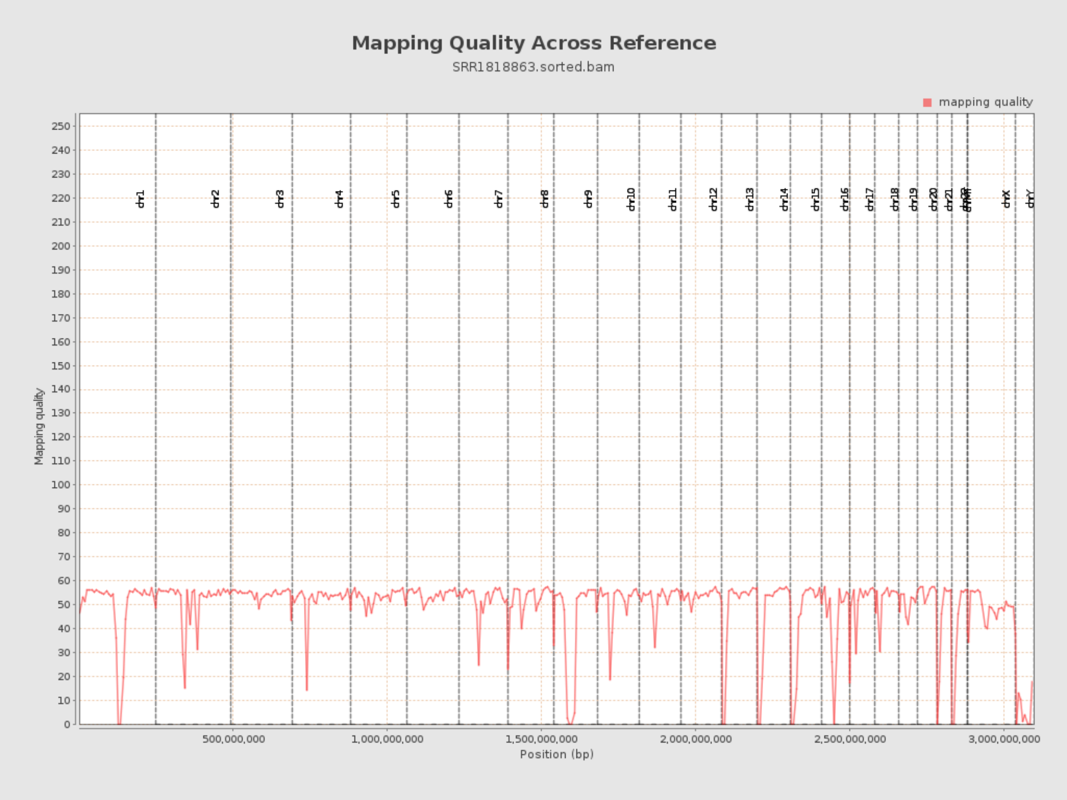
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram