Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:30:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818871.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_SRR1818871 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818871.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:30:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818871.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	804,183
Mapped reads	792,952 / 98.6%
Unmapped reads	11,231 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,731 / 1.58%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	135,580 / 16.86%
Duplication rate	14.41%
Clipped reads	799,695 / 99.44%

2.2. ACGT Content

Number/percentage of A's	21,372,212 / 29.14%
Number/percentage of C's	15,593,439 / 21.26%
Number/percentage of T's	20,620,963 / 28.12%
Number/percentage of G's	15,743,248 / 21.47%
Number/percentage of N's	1,073 / 0%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0237

Standard Deviation	0.2953

2.4. Mapping Quality

Mean Mapping Quality	49.4

2.5. Mismatches and indels

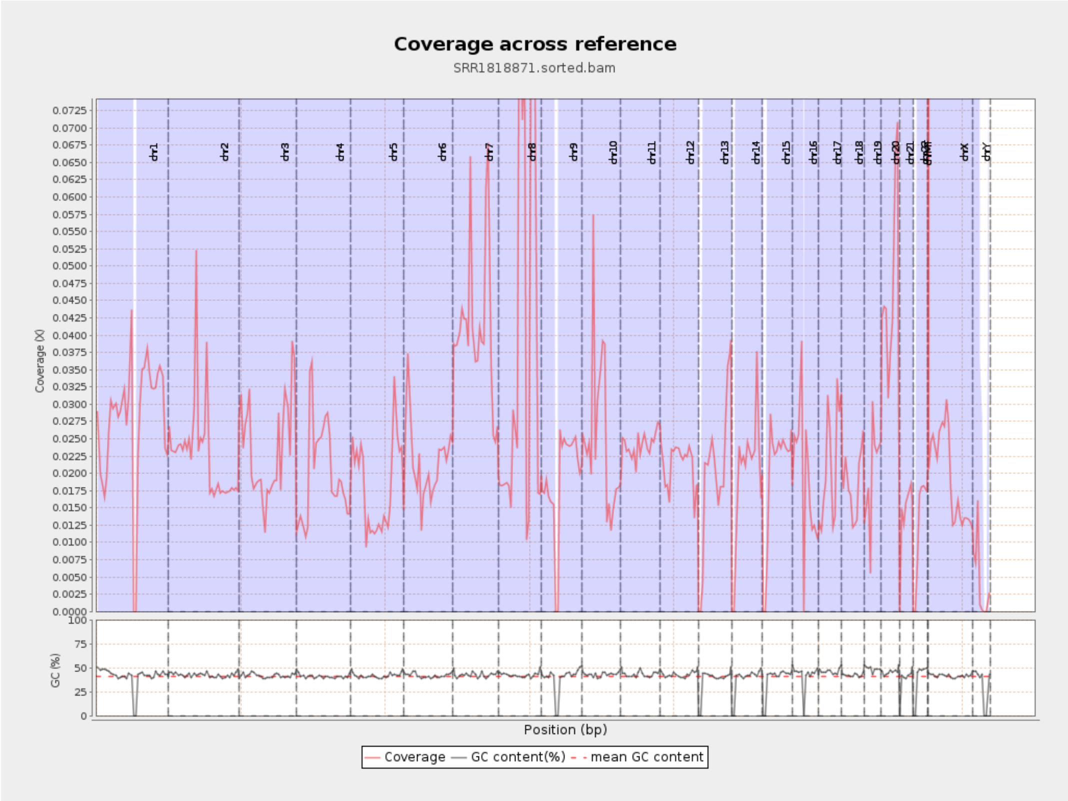
General error rate	0.63%
Mismatches	435,837
Insertions	9,303
Mapped reads with at least one insertion	1.14%
Deletions	23,727
Mapped reads with at least one deletion	2.92%
Homopolymer indels	40.63%

2.6. Chromosome stats

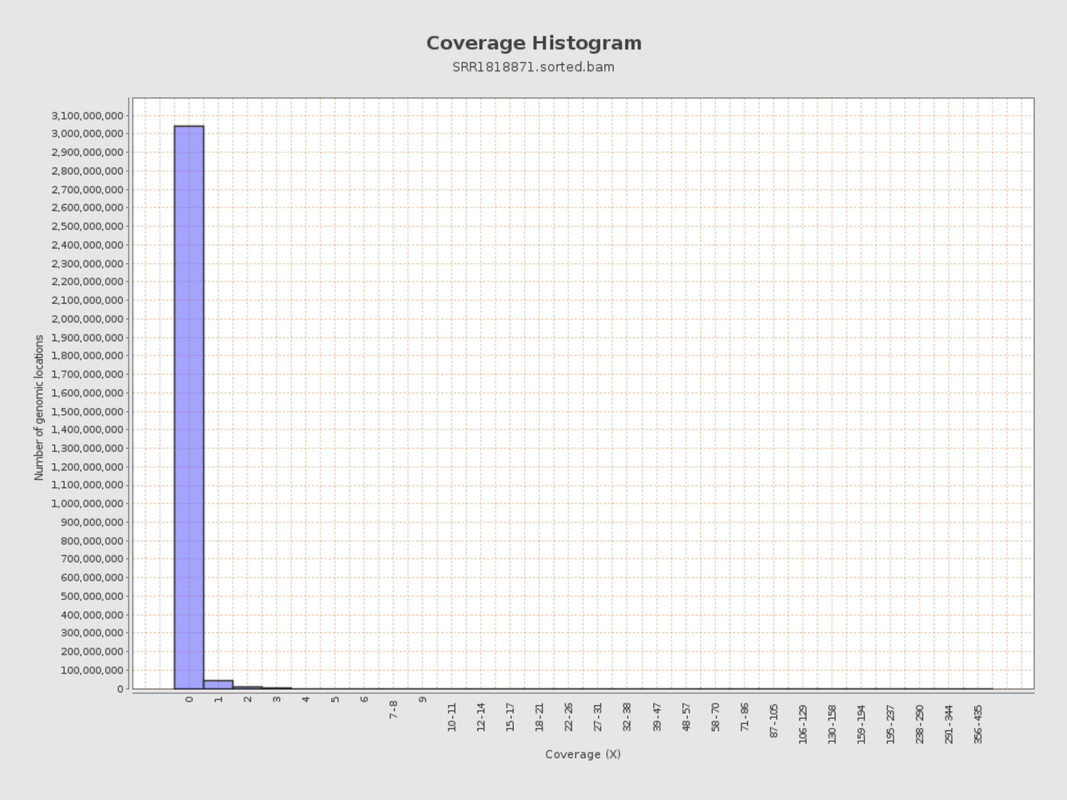
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6879184	0.0276	0.4149
chr2	243199373	5542386	0.0228	0.3903
chr3	198022430	4680668	0.0236	0.1905
chr4	191154276	3833031	0.0201	0.2091
chr5	180915260	3277322	0.0181	0.1689
chr6	171115067	3682663	0.0215	0.1926
chr7	159138663	6549384	0.0412	0.5988

chr8	146364022	6538114	0.0447	0.2966
chr9	141213431	2682430	0.019	0.2512
chr10	135534747	3396231	0.0251	0.364
chr11	135006516	3250551	0.0241	0.2107
chr12	133851895	2822708	0.0211	0.1815
chr13	115169878	2311390	0.0201	0.1768
chr14	107349540	2113098	0.0197	0.1798
chr15	102531392	2015780	0.0197	0.1742
chr16	90354753	1739826	0.0193	0.2716
chr17	81195210	1724101	0.0212	0.2073
chr18	78077248	1417081	0.0181	0.2692
chr19	59128983	1175120	0.0199	0.368
chr20	63025520	2940772	0.0467	0.2792
chr21	48129895	688053	0.0143	0.1613
chr22	51304566	641562	0.0125	0.1494
chrMT	16571	184470	11.1321	8.8721
chrX	155270560	3036121	0.0196	0.1915
chrY	59373566	253317	0.0043	0.2947

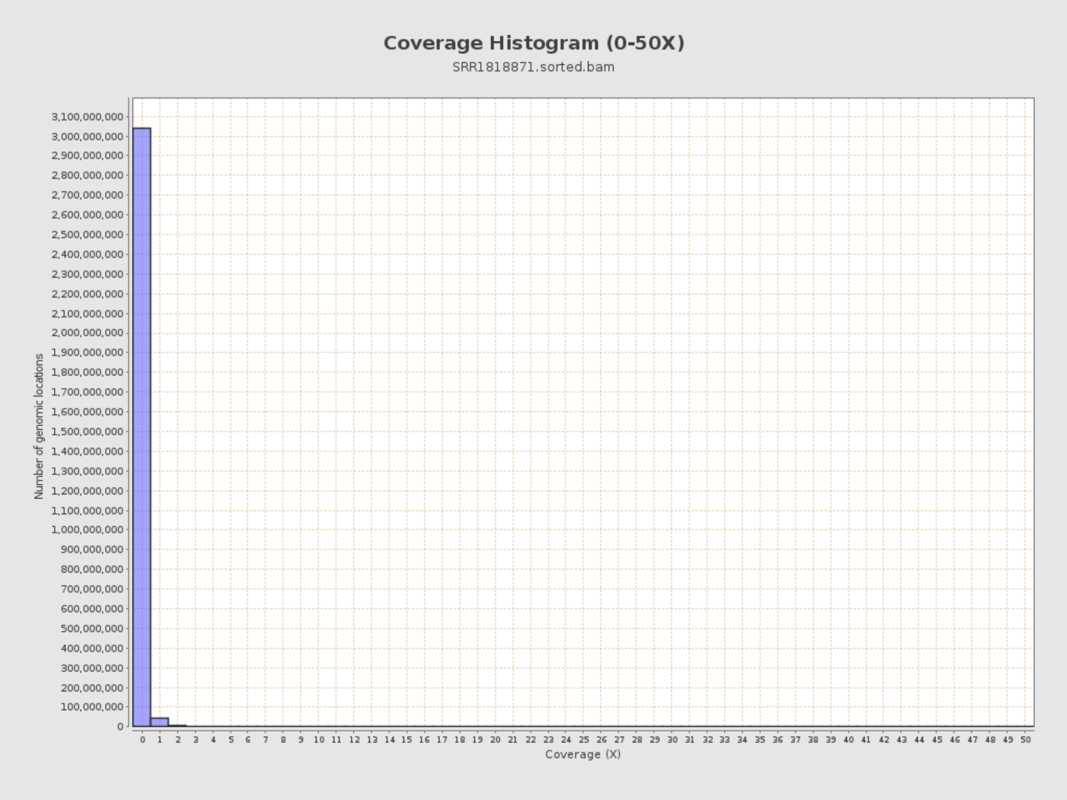
3. Results : Coverage across reference



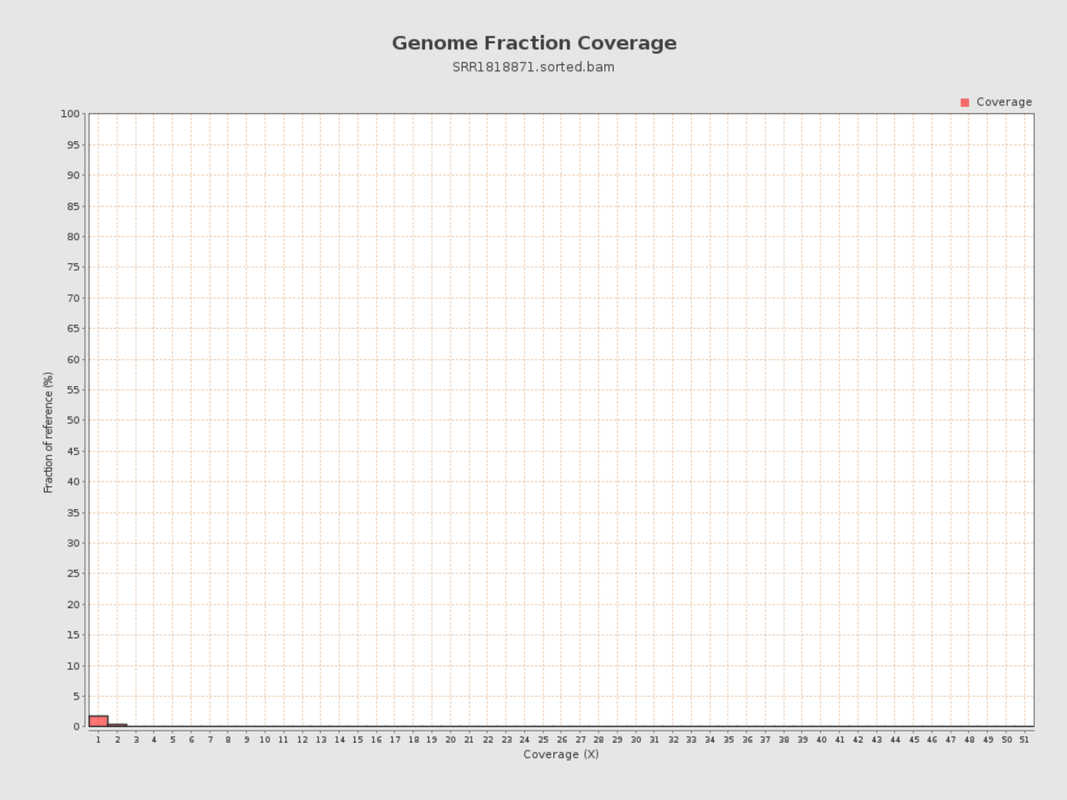
4. Results : Coverage Histogram



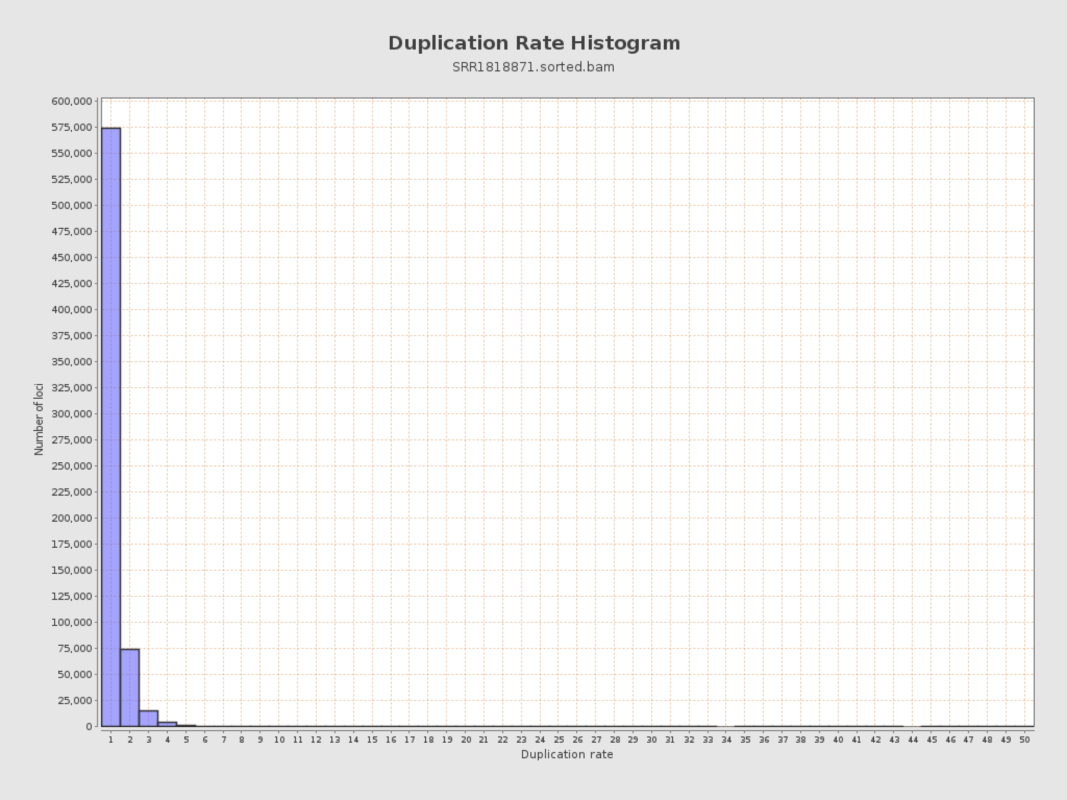
5. Results : Coverage Histogram (0-50X)



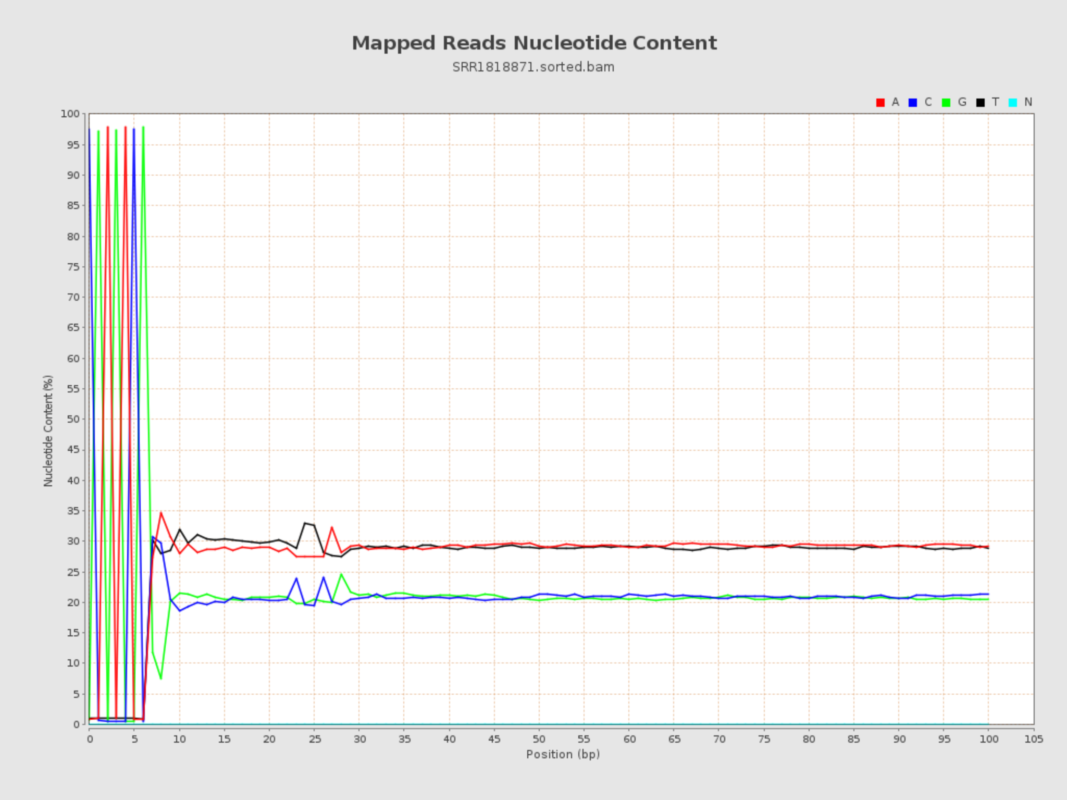
6. Results : Genome Fraction Coverage



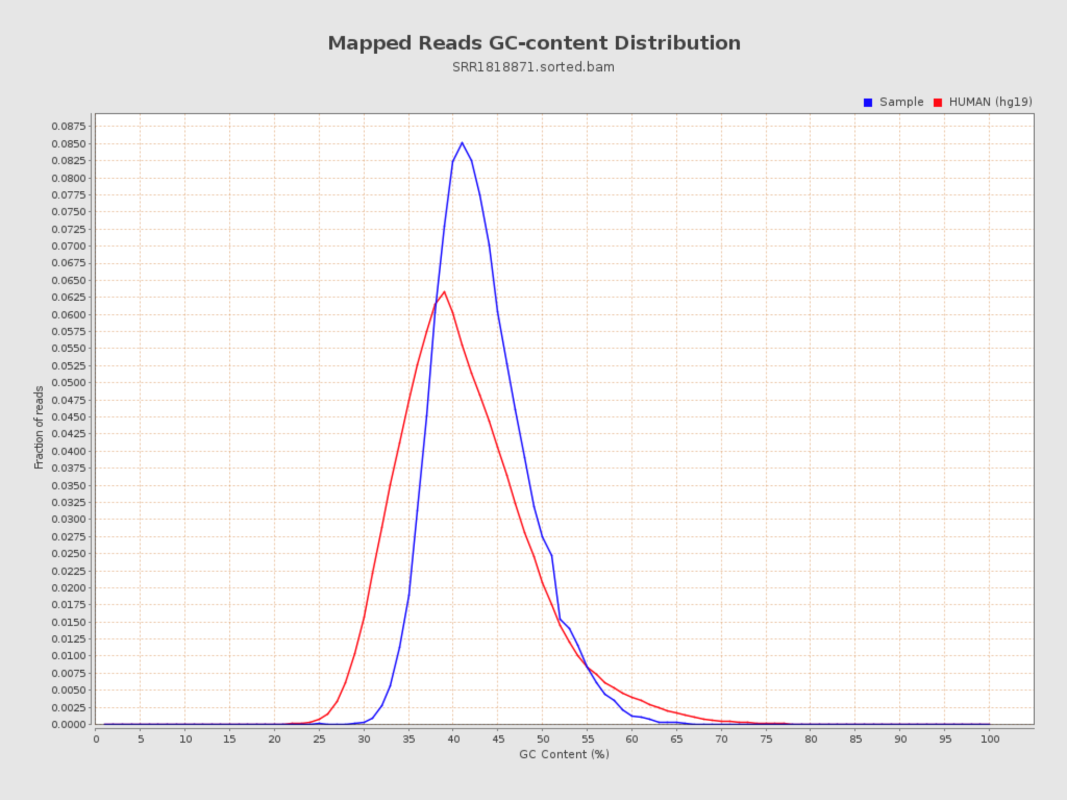
7. Results : Duplication Rate Histogram



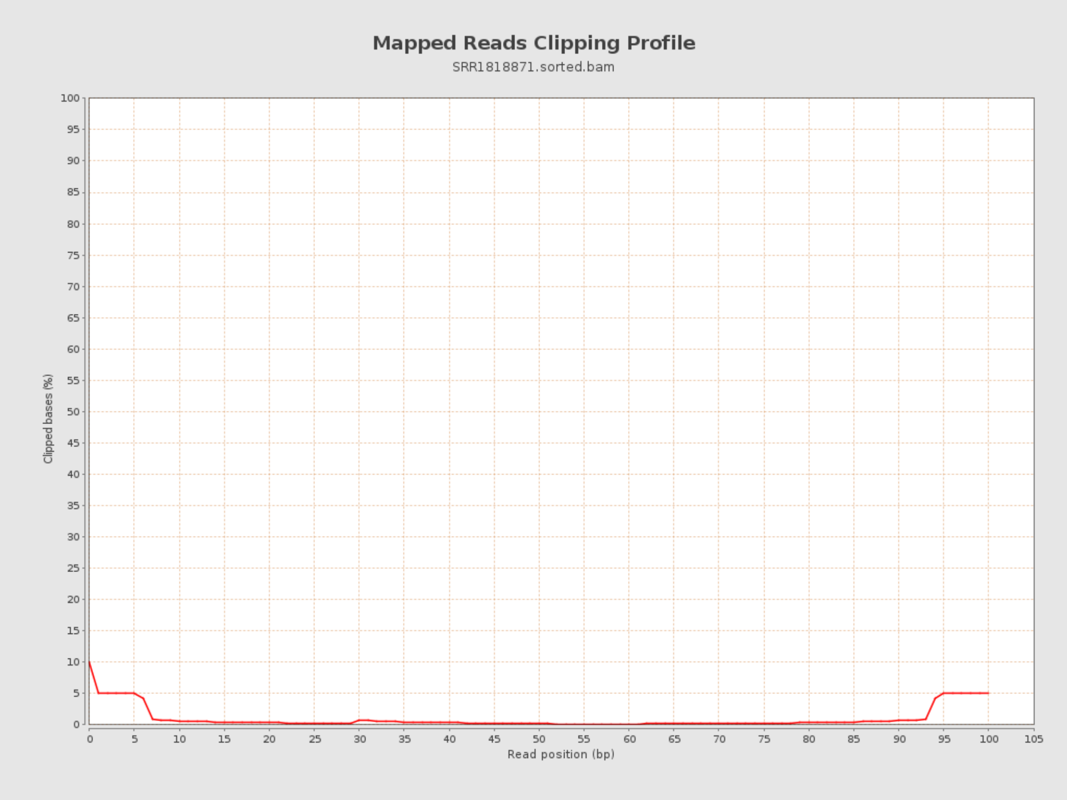
8. Results : Mapped Reads Nucleotide Content



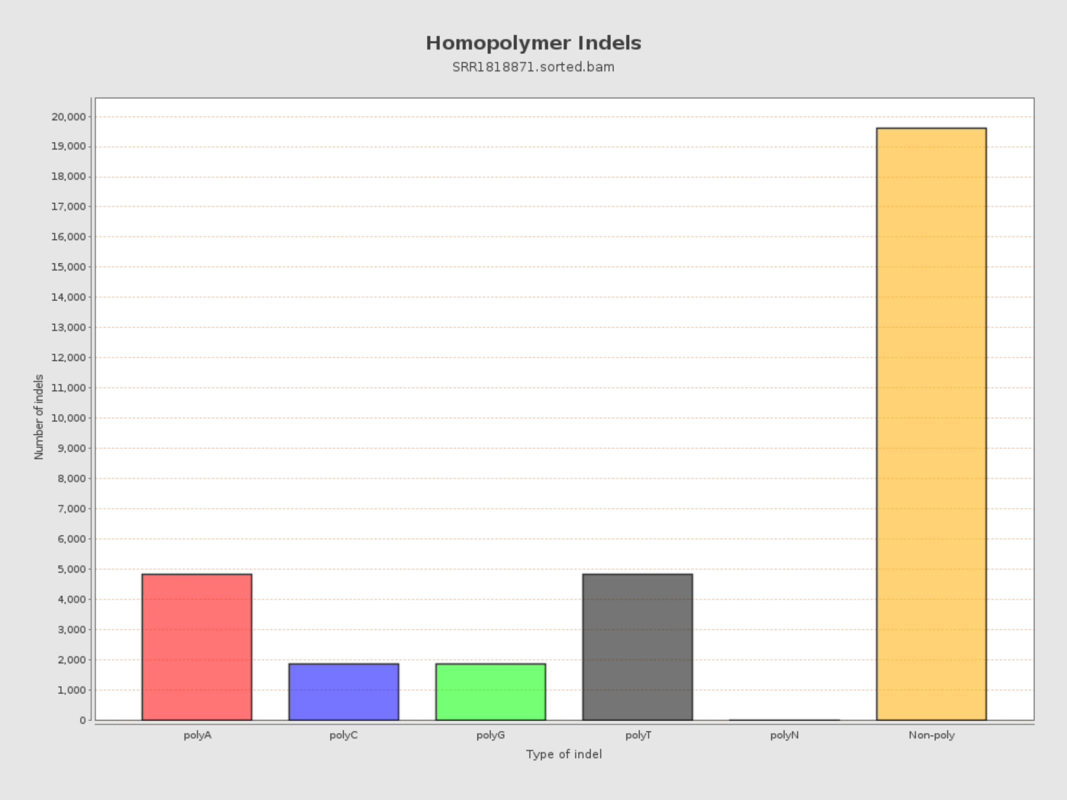
9. Results : Mapped Reads GC-content Distribution



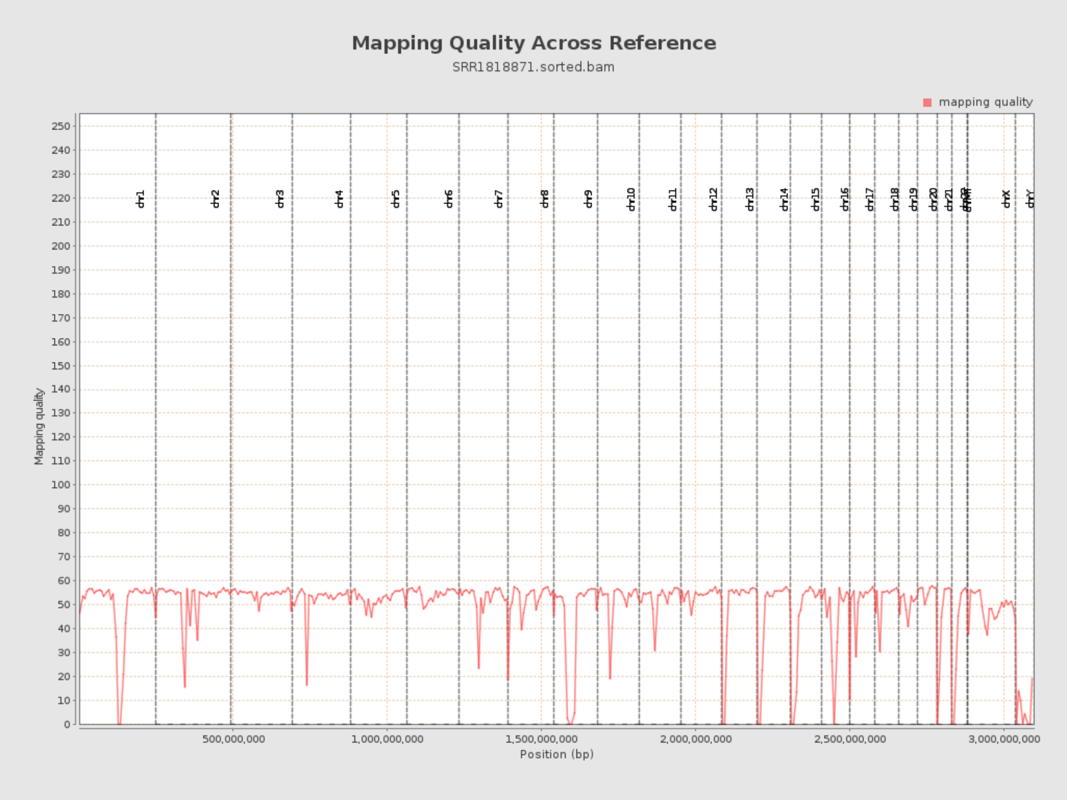
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram