Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:18:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818862.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_SRR1818862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:18:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	679,255
Mapped reads	667,658 / 98.29%
Unmapped reads	11,597 / 1.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,386 / 1.53%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	90,383 / 13.31%
Duplication rate	11.39%
Clipped reads	673,820 / 99.2%

2.2. ACGT Content

Number/percentage of A's	17,863,049 / 28.93%
Number/percentage of C's	13,505,846 / 21.87%
Number/percentage of T's	17,473,049 / 28.3%
Number/percentage of G's	12,907,563 / 20.9%
Number/percentage of N's	915 / 0%
GC Percentage	42.77%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2595

2.4. Mapping Quality

Mean Mapping Quality	49.45

2.5. Mismatches and indels

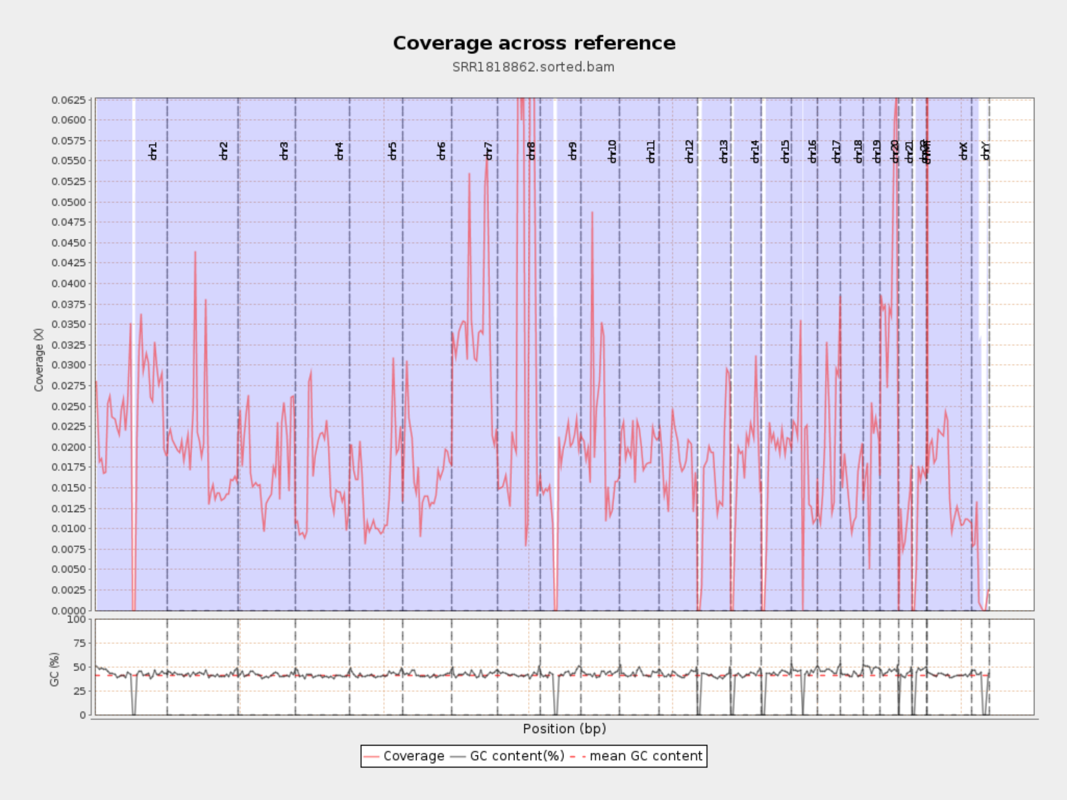
General error rate	0.64%
Mismatches	375,129
Insertions	8,183
Mapped reads with at least one insertion	1.18%
Deletions	19,960
Mapped reads with at least one deletion	2.92%
Homopolymer indels	39.81%

2.6. Chromosome stats

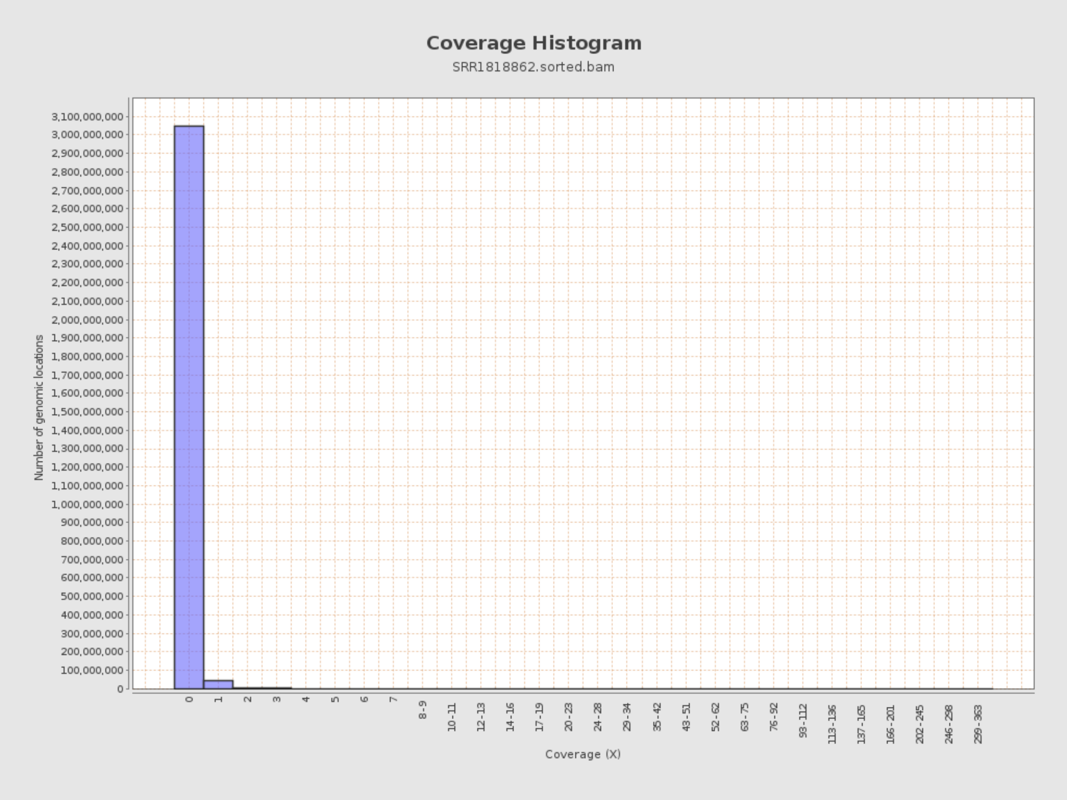
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5948723	0.0239	0.3356
chr2	243199373	4678322	0.0192	0.3792
chr3	198022430	3685267	0.0186	0.1619
chr4	191154276	3062449	0.016	0.1769
chr5	180915260	2714773	0.015	0.1487
chr6	171115067	2886414	0.0169	0.1602
chr7	159138663	5496974	0.0345	0.4926

chr8	146364022	5326517	0.0364	0.254
chr9	141213431	2299602	0.0163	0.2101
chr10	135534747	2898557	0.0214	0.3473
chr11	135006516	2720743	0.0202	0.1826
chr12	133851895	2435974	0.0182	0.1606
chr13	115169878	1852800	0.0161	0.1489
chr14	107349540	1858706	0.0173	0.1623
chr15	102531392	1730064	0.0169	0.1547
chr16	90354753	1613406	0.0179	0.2895
chr17	81195210	1698423	0.0209	0.1908
chr18	78077248	1166005	0.0149	0.2285
chr19	59128983	1085831	0.0184	0.3013
chr20	63025520	2627499	0.0417	0.2507
chr21	48129895	503330	0.0105	0.1356
chr22	51304566	605738	0.0118	0.138
chrMT	16571	182715	11.0262	7.346
chrX	155270560	2472244	0.0159	0.1645
chrY	59373566	237477	0.004	0.3294

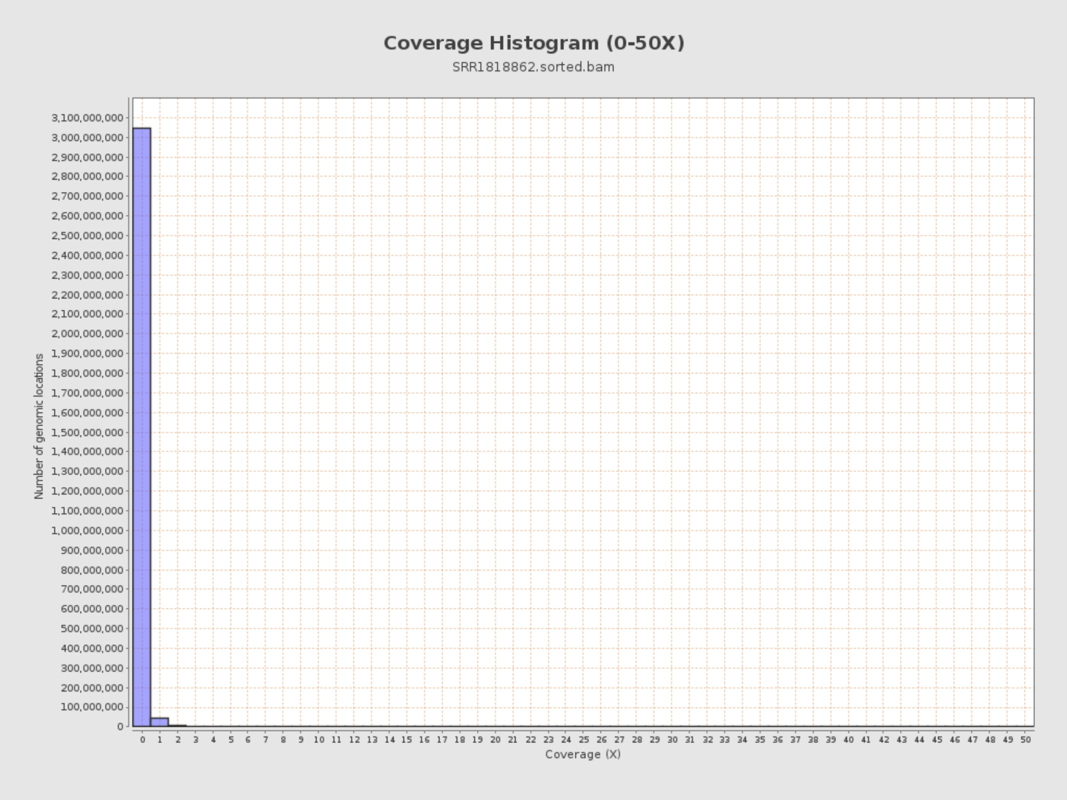
3. Results : Coverage across reference



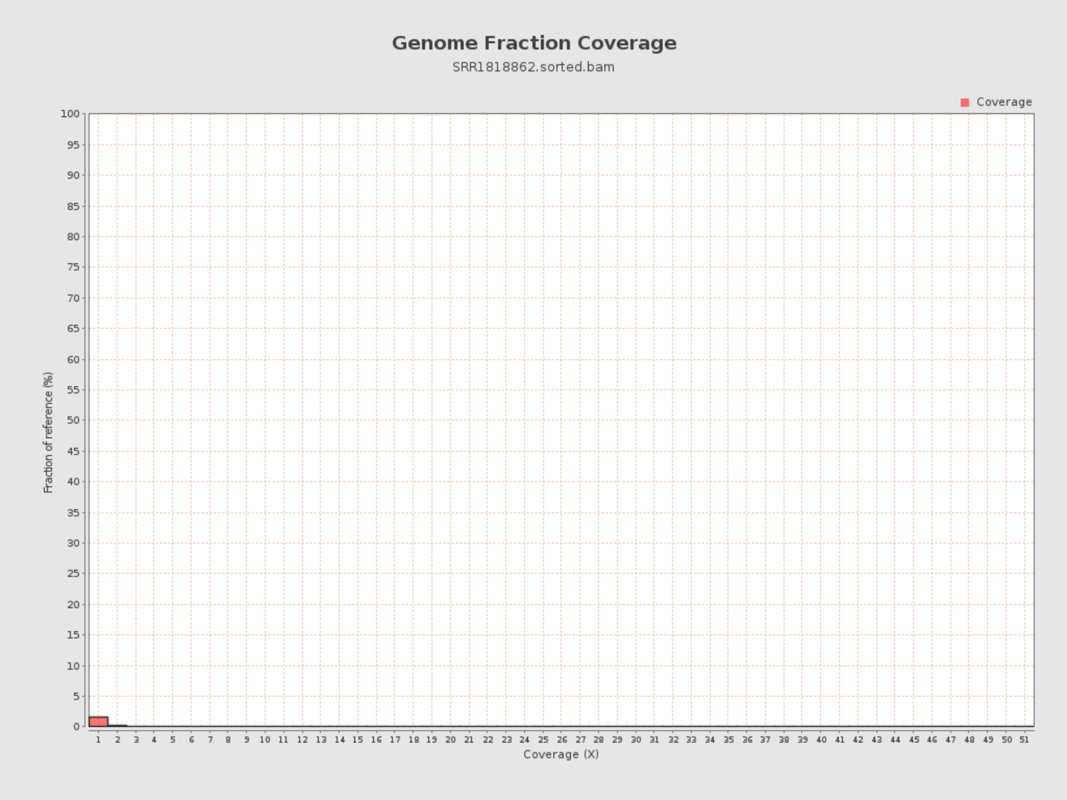
4. Results : Coverage Histogram



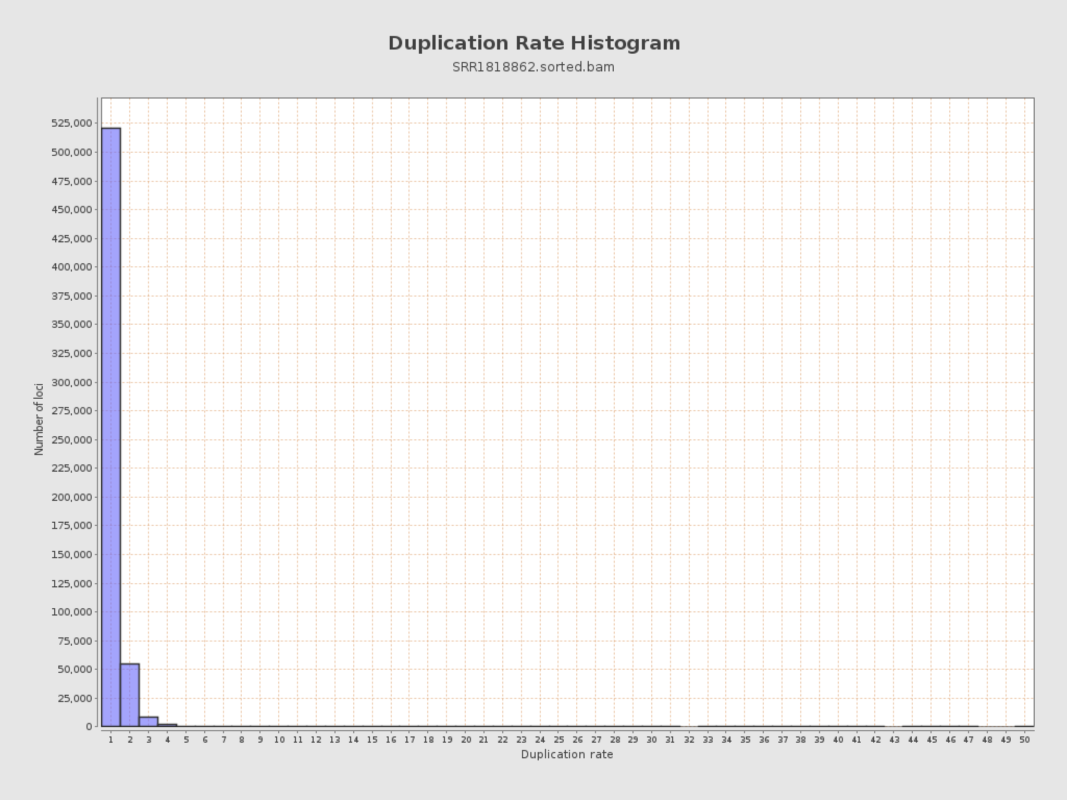
5. Results : Coverage Histogram (0-50X)



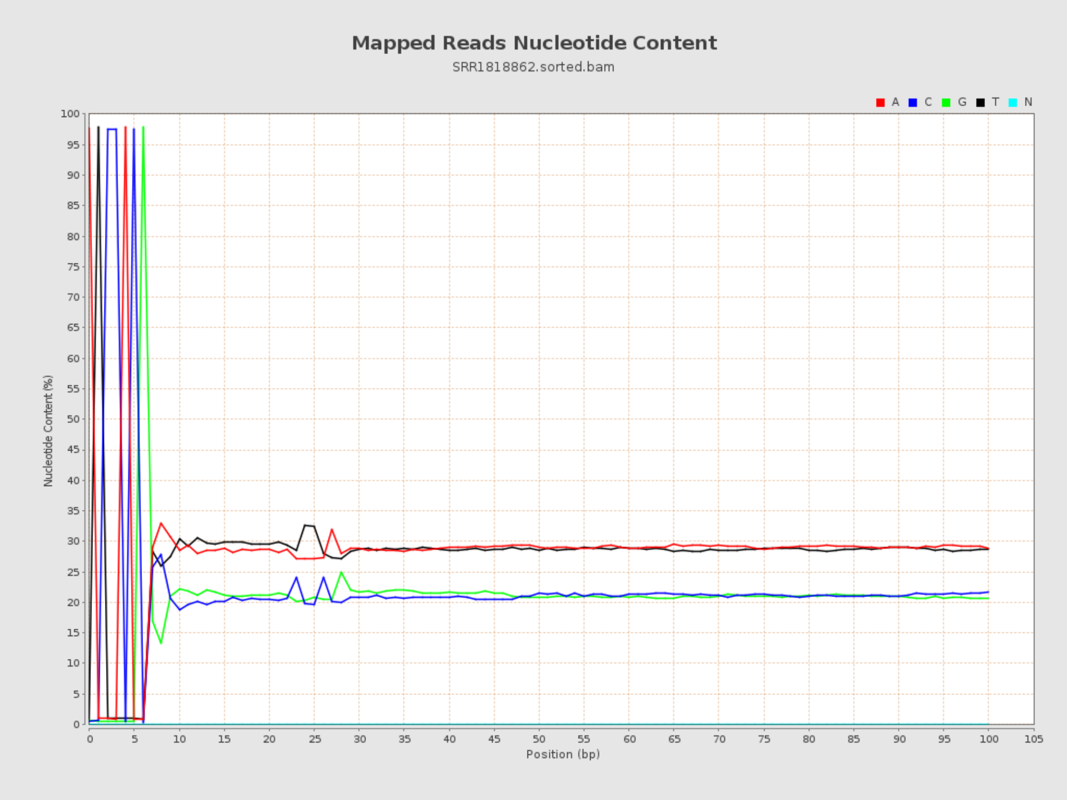
6. Results : Genome Fraction Coverage



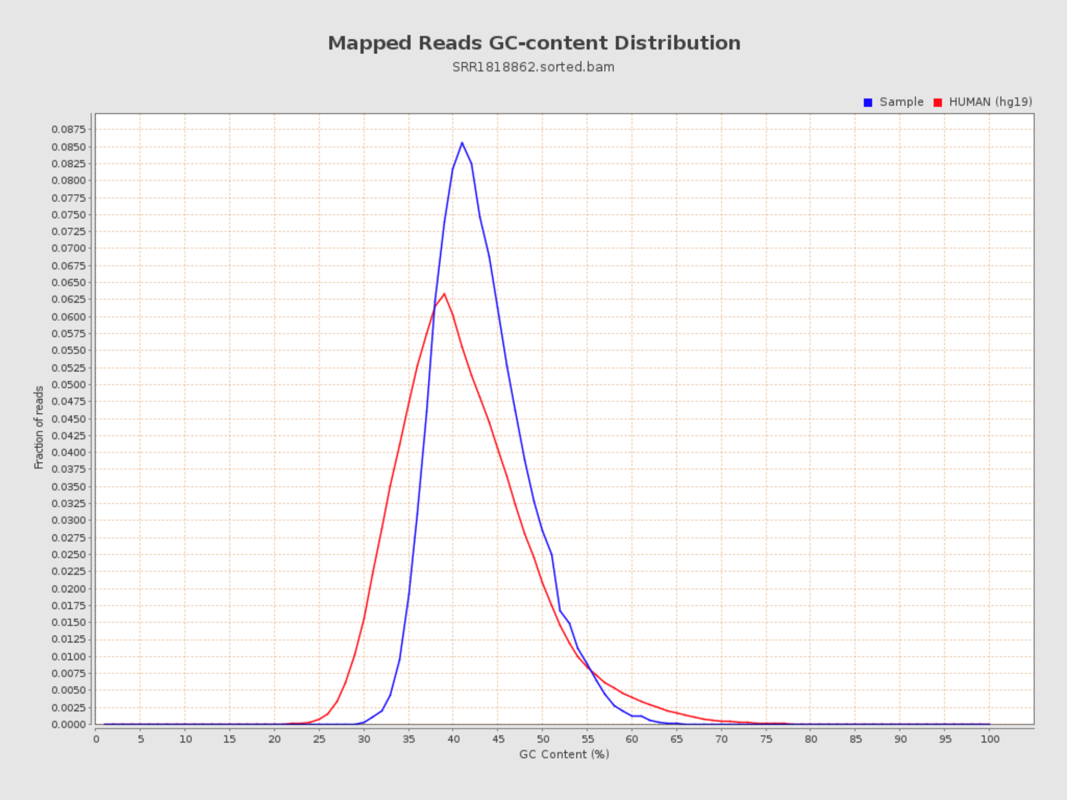
7. Results : Duplication Rate Histogram



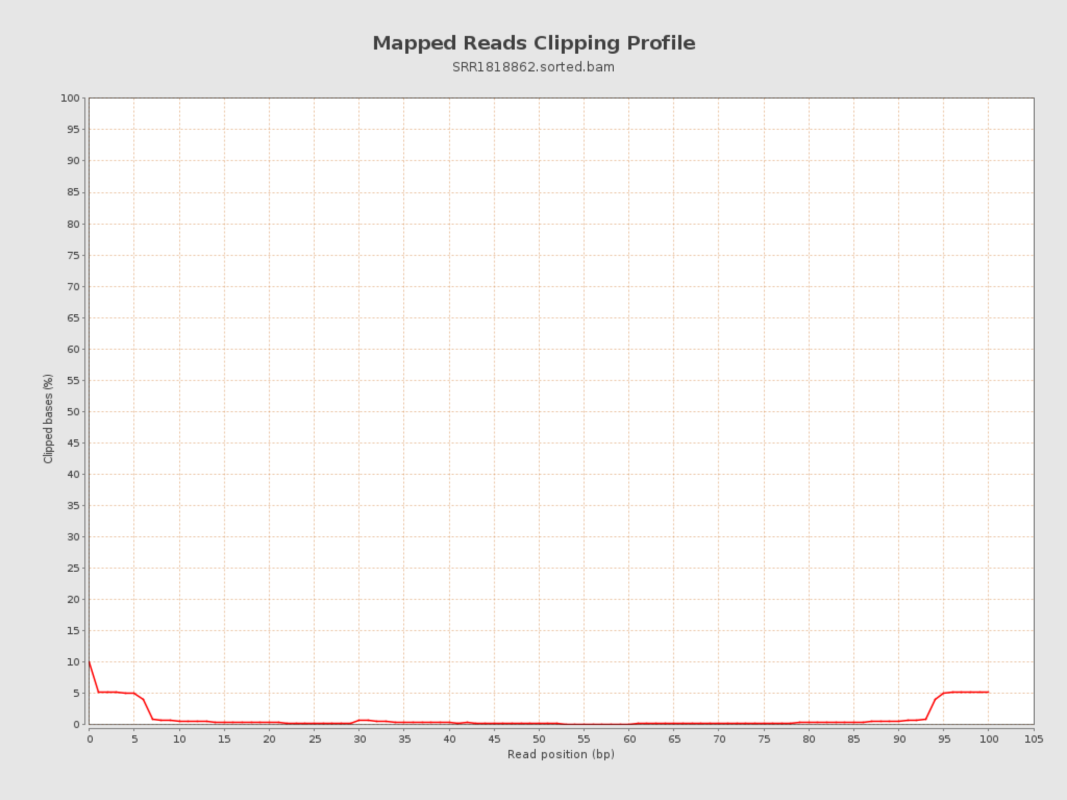
8. Results : Mapped Reads Nucleotide Content



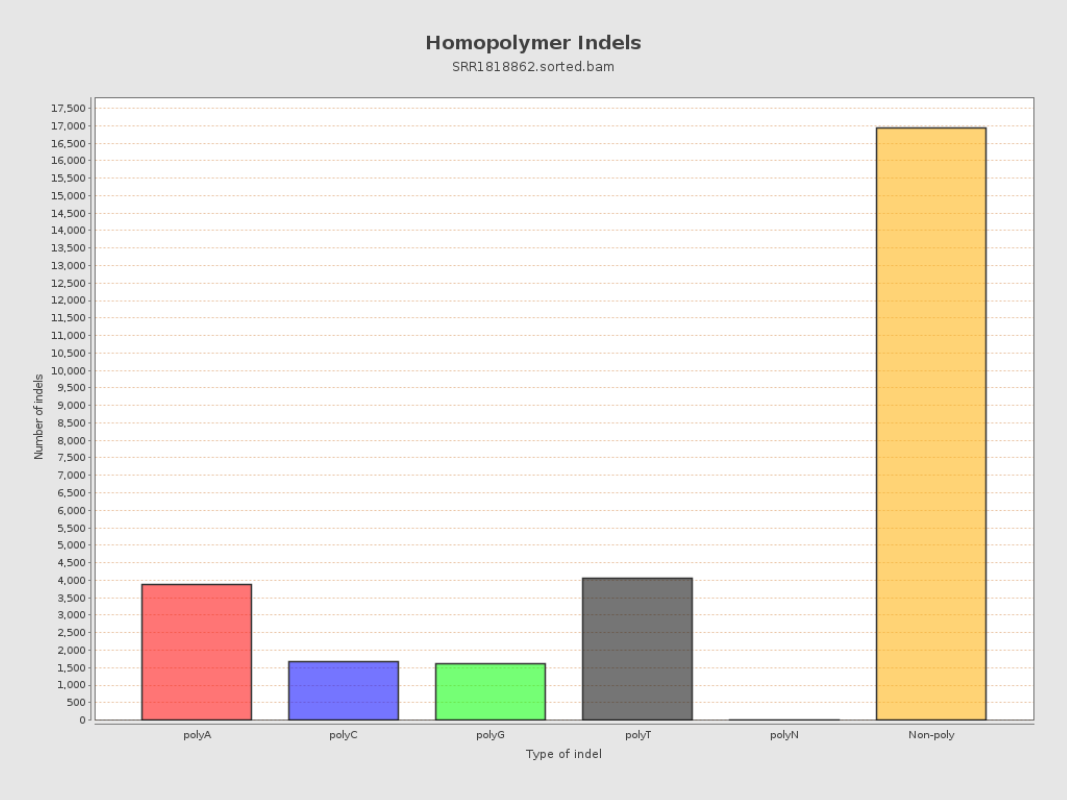
9. Results : Mapped Reads GC-content Distribution



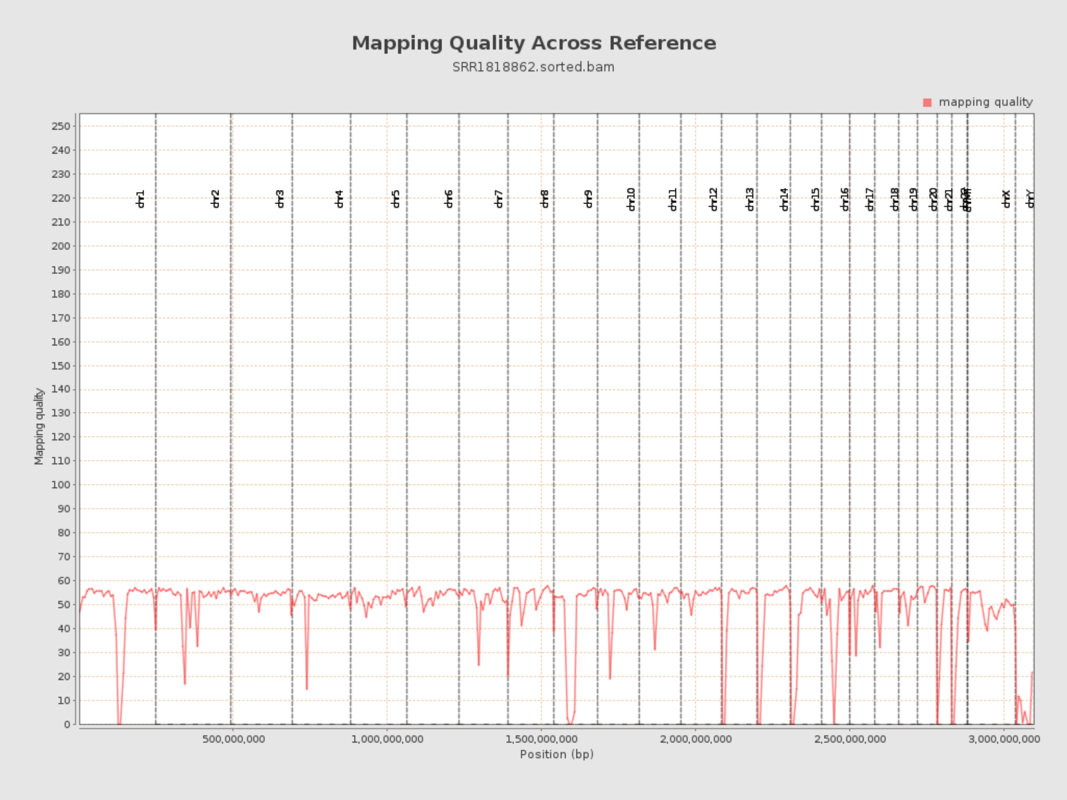
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram