Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:35:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716862.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_SRR9716862 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716862.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:35:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716862.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	917,313
Mapped reads	872,454 / 95.11%
Unmapped reads	44,859 / 4.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,816 / 2.05%
Read min/max/mean length	30 / 101 / 101.74
Duplicated reads (estimated)	26,836 / 2.93%
Duplication rate	2.41%
Clipped reads	890,649 / 97.09%

2.2. ACGT Content

Number/percentage of A's	17,406,285 / 25.48%
Number/percentage of C's	14,810,695 / 21.68%
Number/percentage of T's	19,663,247 / 28.78%
Number/percentage of G's	16,444,052 / 24.07%
Number/percentage of N's	2,586 / 0%
GC Percentage	45.74%

2.3. Coverage

Mean	0.0221

Standard Deviation	0.2135

2.4. Mapping Quality

Mean Mapping Quality	46.82

2.5. Mismatches and indels

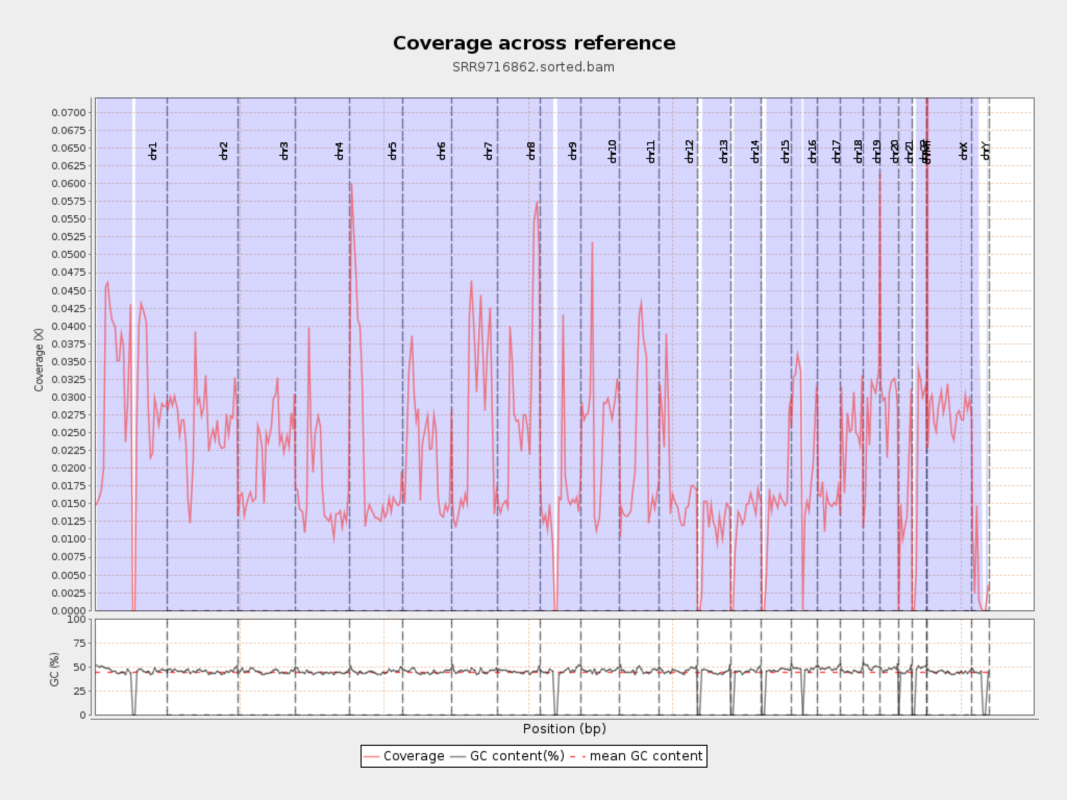
General error rate	0.64%
Mismatches	420,169
Insertions	5,348
Mapped reads with at least one insertion	0.6%
Deletions	12,858
Mapped reads with at least one deletion	1.45%
Homopolymer indels	40.54%

2.6. Chromosome stats

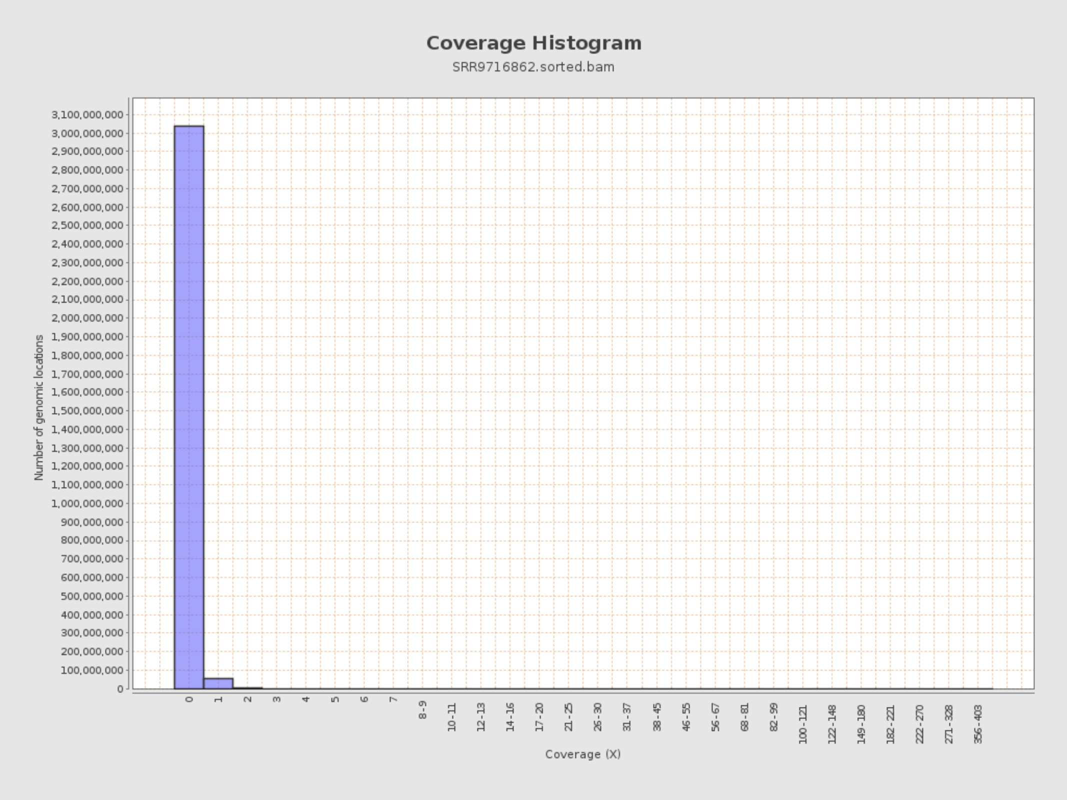
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7491870	0.0301	0.3846
chr2	243199373	6400768	0.0263	0.2255
chr3	198022430	4361306	0.022	0.1637
chr4	191154276	3255738	0.017	0.1826
chr5	180915260	4059140	0.0224	0.1651
chr6	171115067	3851051	0.0225	0.1698
chr7	159138663	4235879	0.0266	0.2656

chr8	146364022	4239360	0.029	0.2267
chr9	141213431	2044050	0.0145	0.15
chr10	135534747	3656757	0.027	0.2891
chr11	135006516	2901808	0.0215	0.1844
chr12	133851895	2574503	0.0192	0.1515
chr13	115169878	1262698	0.011	0.1126
chr14	107349540	1316647	0.0123	0.1268
chr15	102531392	1421527	0.0139	0.1271
chr16	90354753	2058246	0.0228	0.1706
chr17	81195210	1248369	0.0154	0.1488
chr18	78077248	2005826	0.0257	0.2143
chr19	59128983	1688472	0.0286	0.2804
chr20	63025520	1871249	0.0297	0.1944
chr21	48129895	744196	0.0155	0.1645
chr22	51304566	1084347	0.0211	0.1618
chrMT	16571	16177	0.9762	1.2988
chrX	155270560	4334234	0.0279	0.187
chrY	59373566	229130	0.0039	0.1501

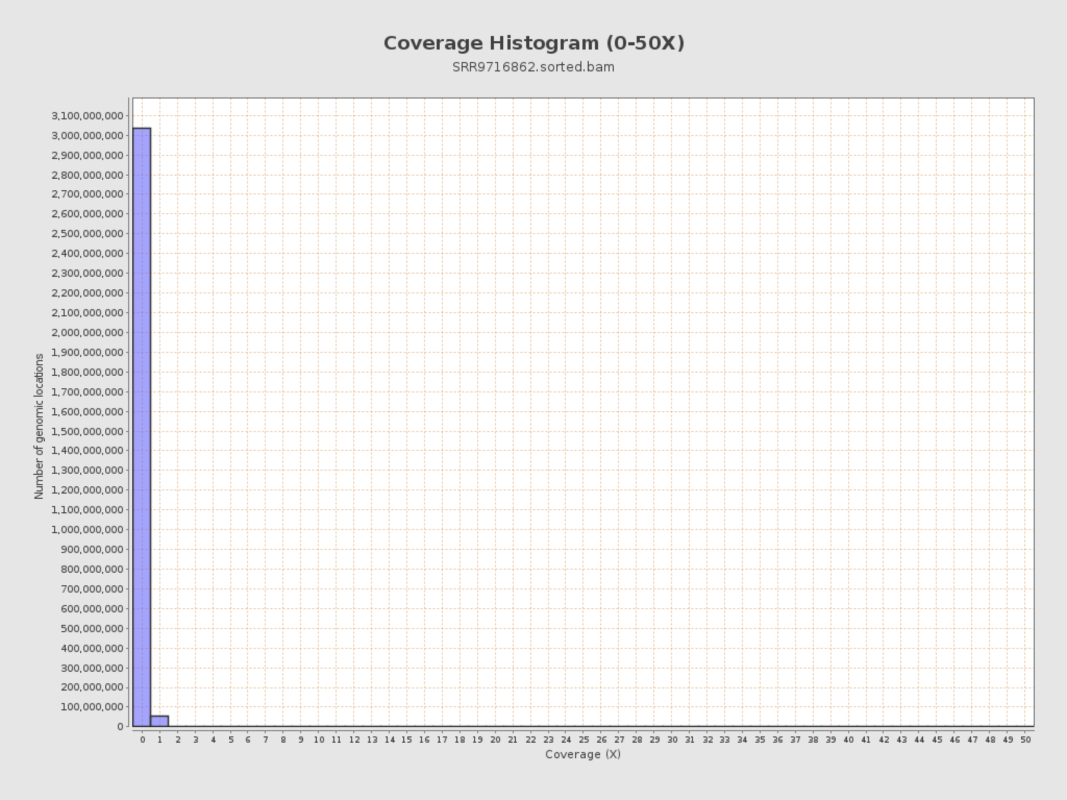
3. Results : Coverage across reference



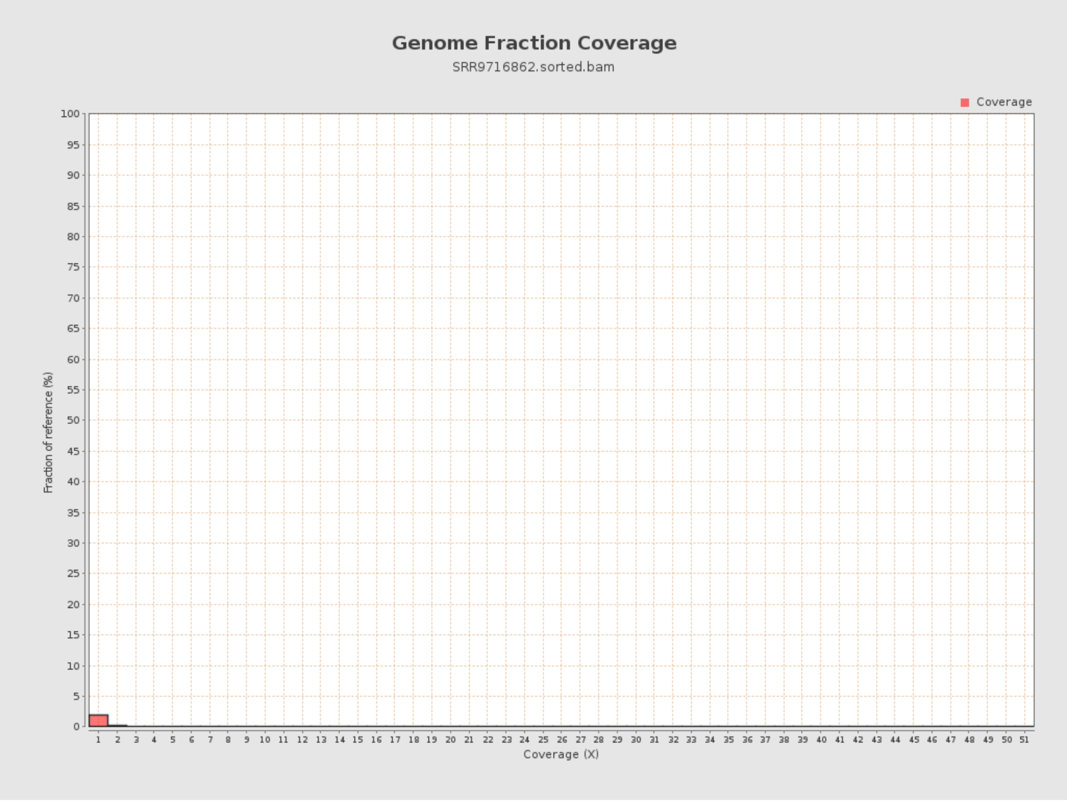
4. Results : Coverage Histogram



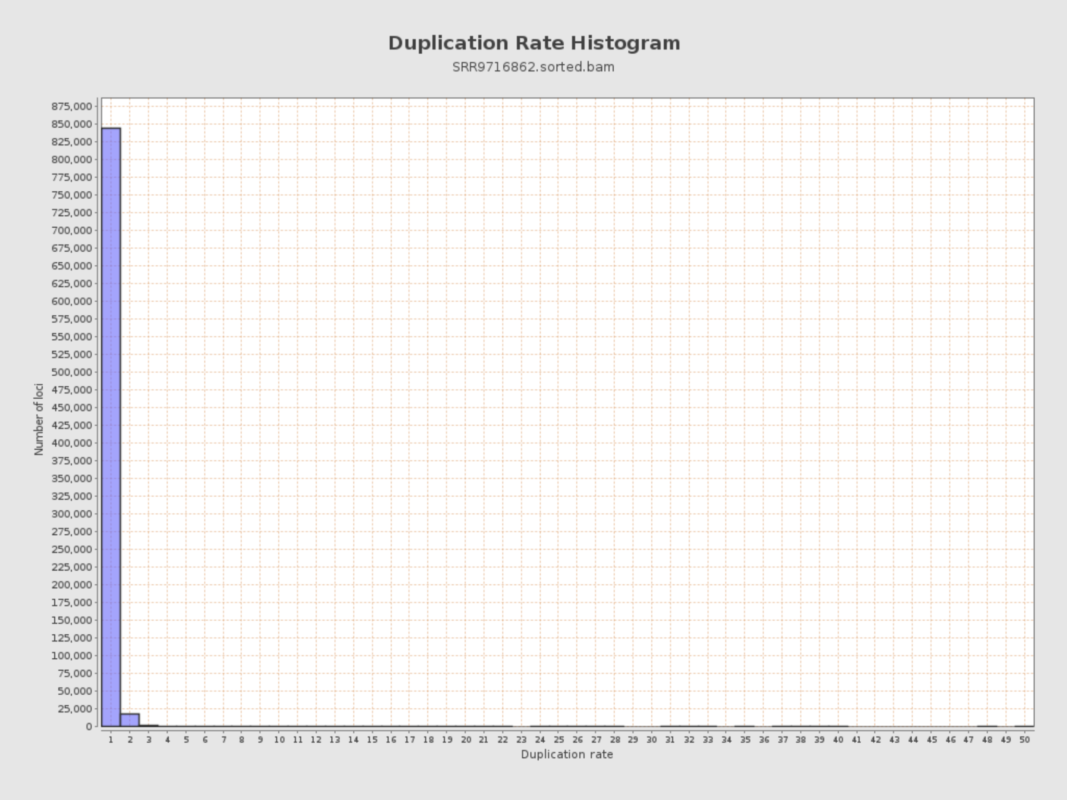
5. Results : Coverage Histogram (0-50X)



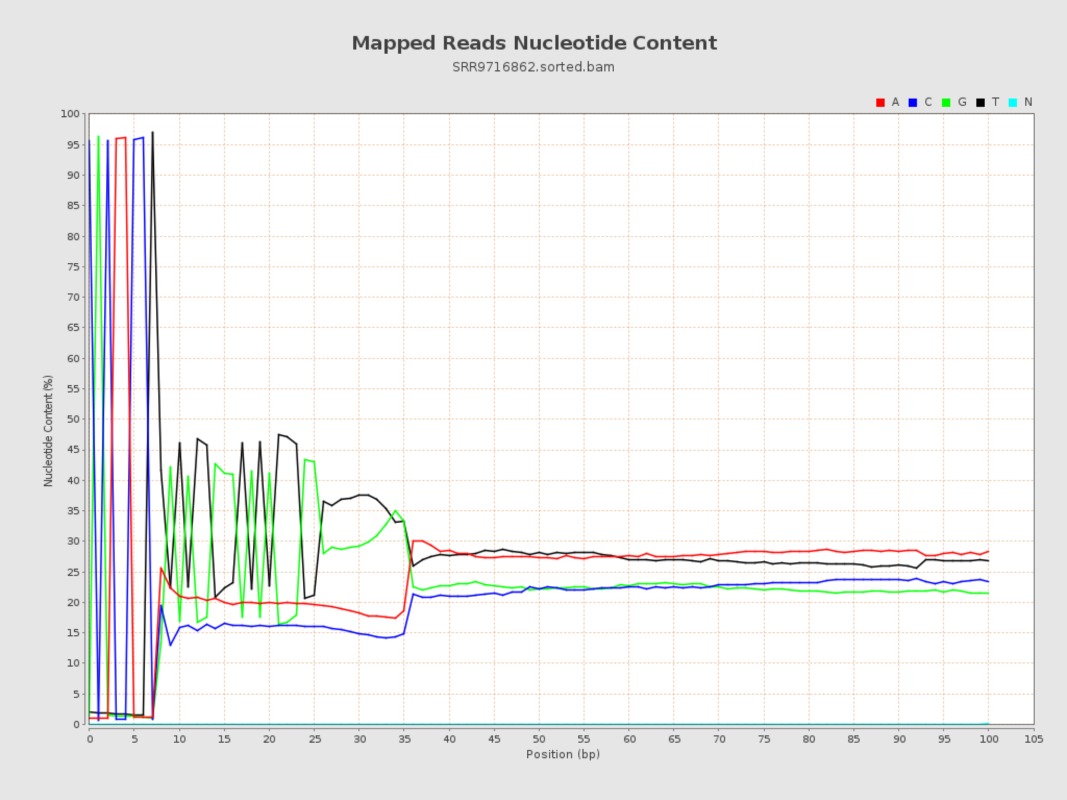
6. Results : Genome Fraction Coverage



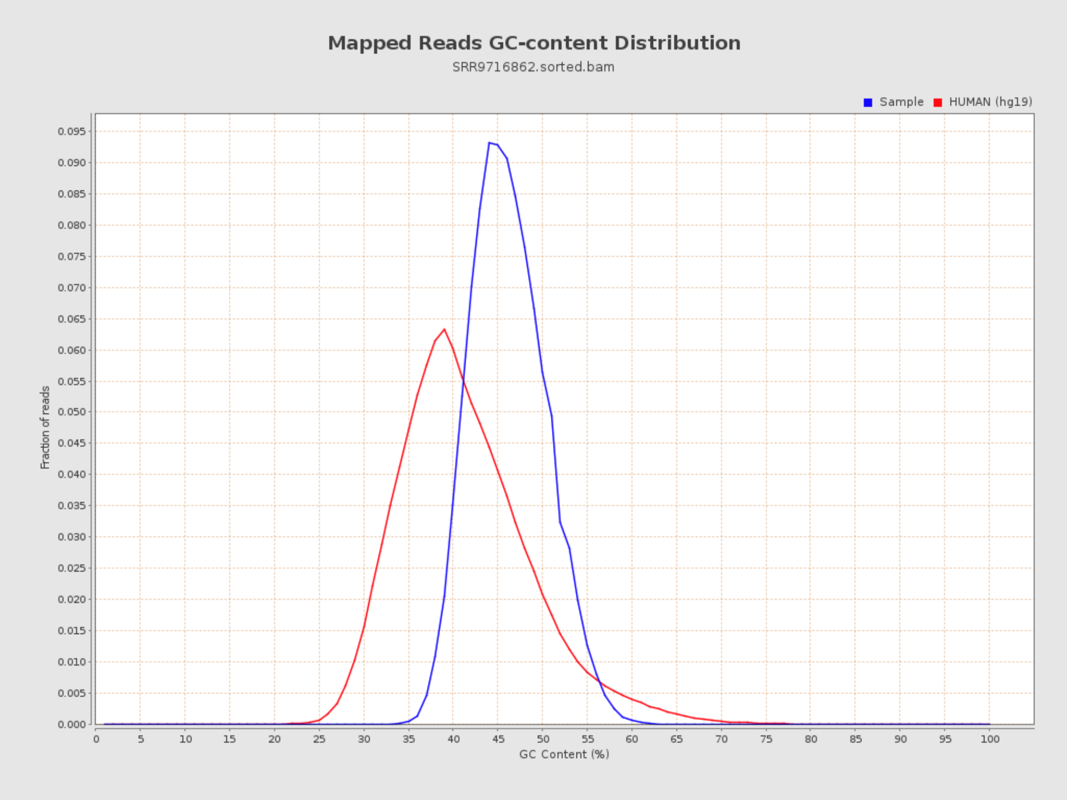
7. Results : Duplication Rate Histogram



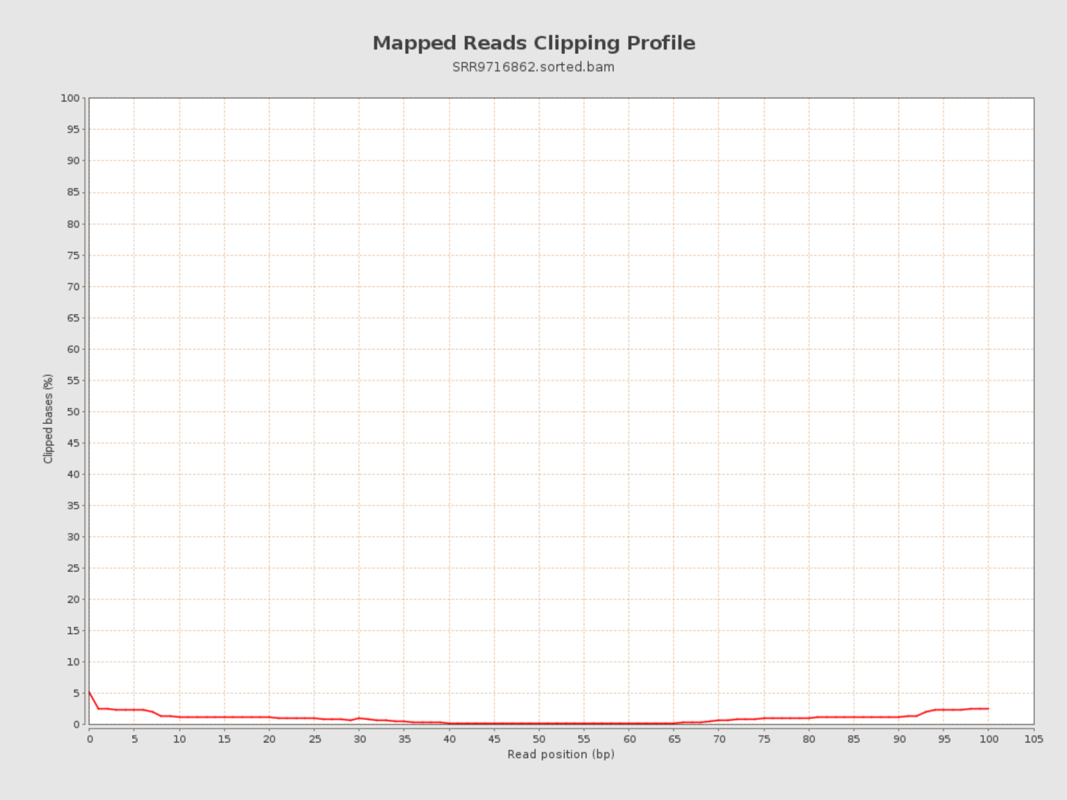
8. Results : Mapped Reads Nucleotide Content



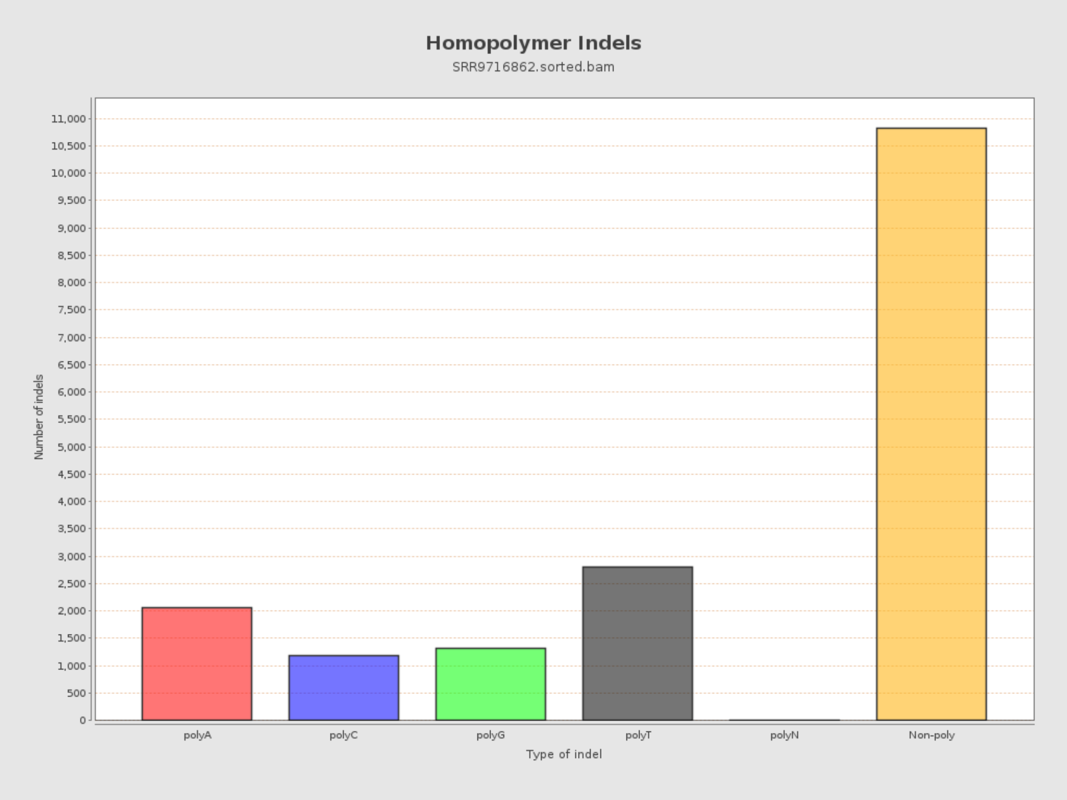
9. Results : Mapped Reads GC-content Distribution



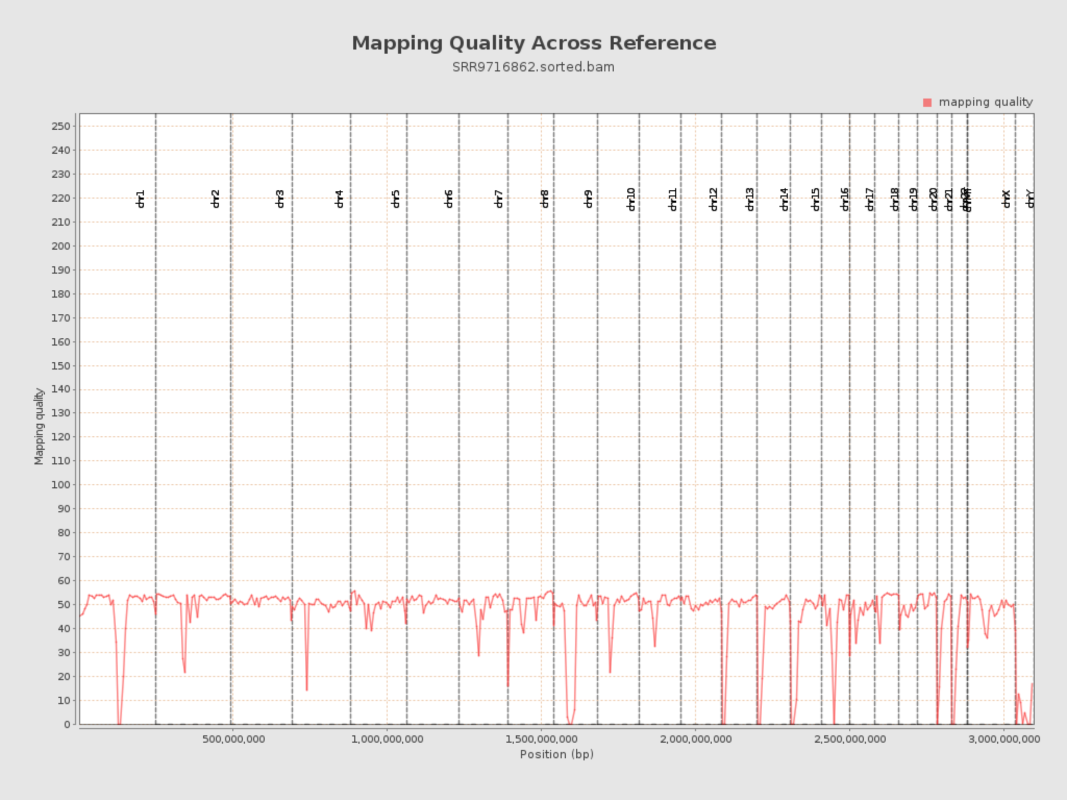
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram