Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:17:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716857.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_SRR9716857 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716857.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:17:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716857.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	634,337
Mapped reads	599,833 / 94.56%
Unmapped reads	34,504 / 5.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,454 / 2.12%
Read min/max/mean length	30 / 101 / 101.77
Duplicated reads (estimated)	13,740 / 2.17%
Duplication rate	1.76%
Clipped reads	611,577 / 96.41%

2.2. ACGT Content

Number/percentage of A's	12,027,970 / 25.69%
Number/percentage of C's	9,920,940 / 21.19%
Number/percentage of T's	13,676,769 / 29.22%
Number/percentage of G's	11,183,909 / 23.89%
Number/percentage of N's	1,677 / 0%
GC Percentage	45.08%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1648

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

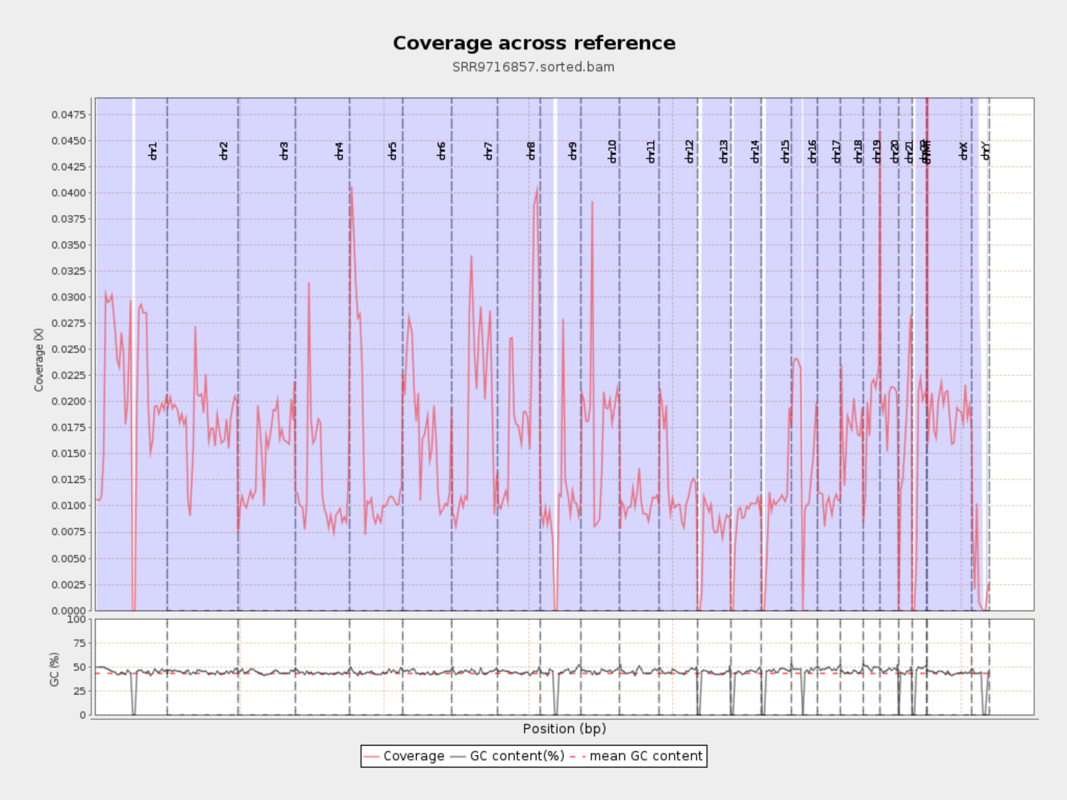
General error rate	0.65%
Mismatches	292,664
Insertions	4,549
Mapped reads with at least one insertion	0.74%
Deletions	8,696
Mapped reads with at least one deletion	1.43%
Homopolymer indels	38.17%

2.6. Chromosome stats

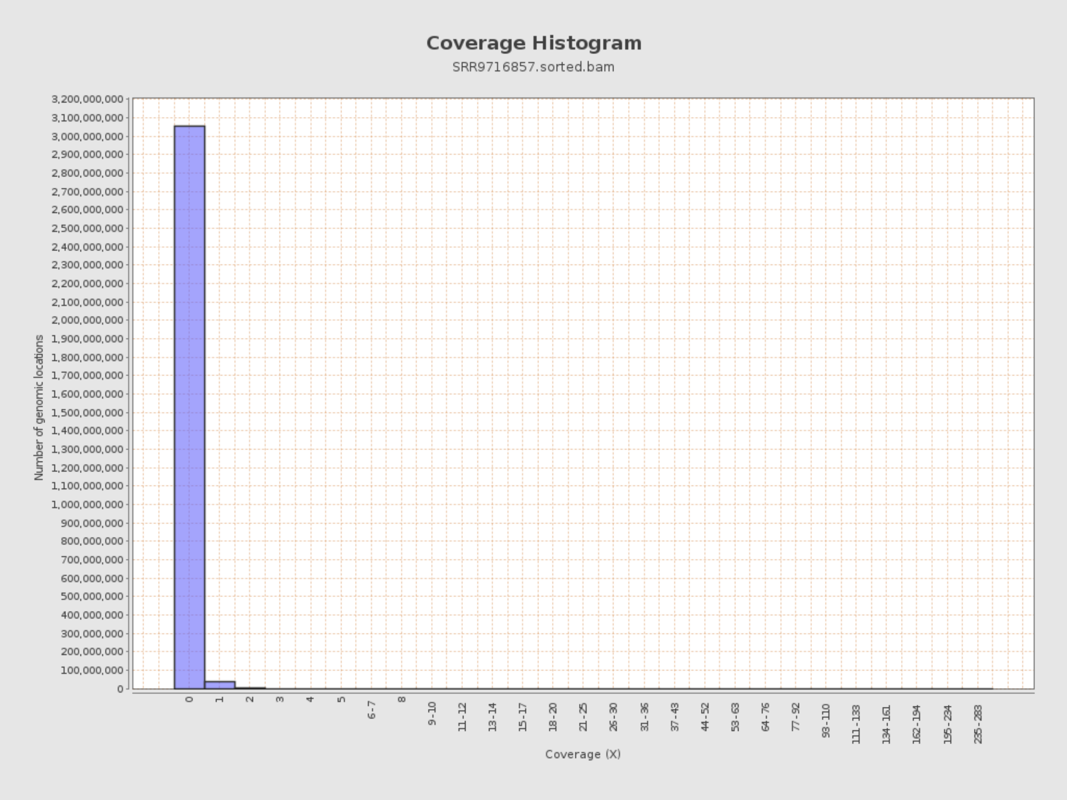
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5162045	0.0207	0.2862
chr2	243199373	4437345	0.0182	0.1733
chr3	198022430	2967041	0.015	0.131
chr4	191154276	2297313	0.012	0.146
chr5	180915260	2810797	0.0155	0.133
chr6	171115067	2899685	0.0169	0.1422
chr7	159138663	2925024	0.0184	0.1974

chr8	146364022	2917308	0.0199	0.1759
chr9	141213431	1380392	0.0098	0.1164
chr10	135534747	2499409	0.0184	0.2213
chr11	135006516	1388525	0.0103	0.1271
chr12	133851895	1674393	0.0125	0.1189
chr13	115169878	851128	0.0074	0.0902
chr14	107349540	895337	0.0083	0.0996
chr15	102531392	972794	0.0095	0.1028
chr16	90354753	1425360	0.0158	0.1374
chr17	81195210	846470	0.0104	0.114
chr18	78077248	1380462	0.0177	0.1811
chr19	59128983	1173128	0.0198	0.2131
chr20	63025520	1253700	0.0199	0.1542
chr21	48129895	812254	0.0169	0.1531
chr22	51304566	727001	0.0142	0.1284
chrMT	16571	25498	1.5387	1.6325
chrX	155270560	2944235	0.019	0.1492
chrY	59373566	163218	0.0027	0.1084

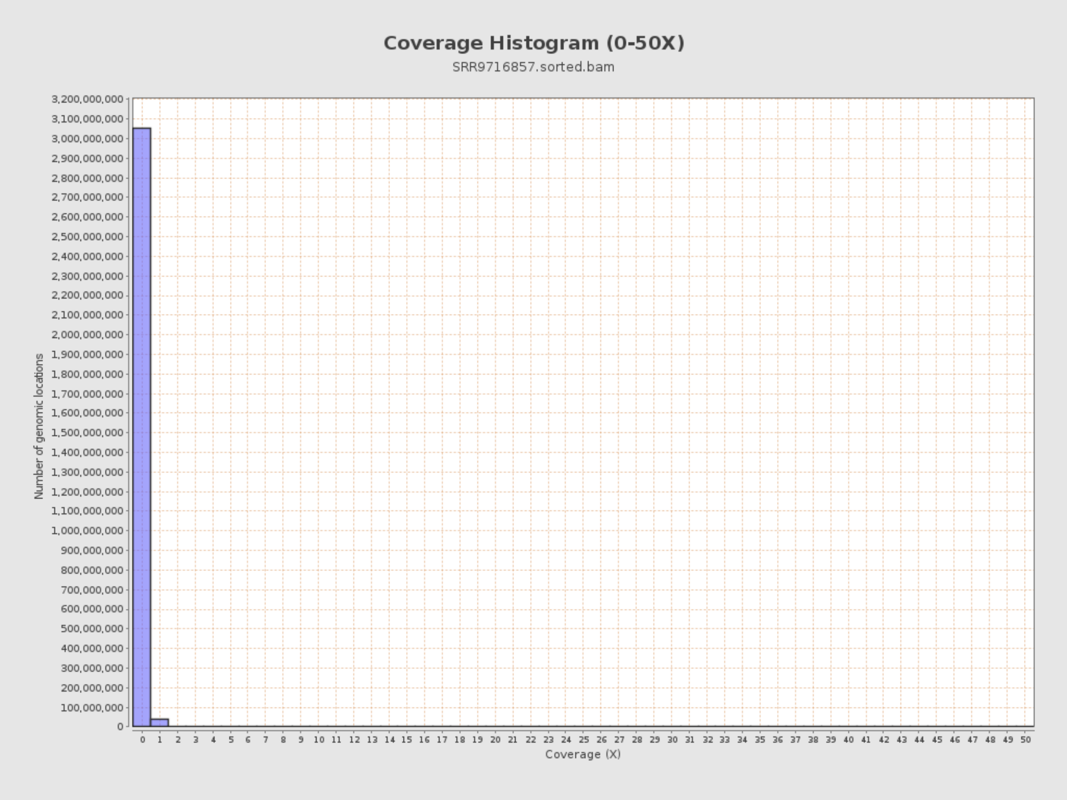
3. Results : Coverage across reference



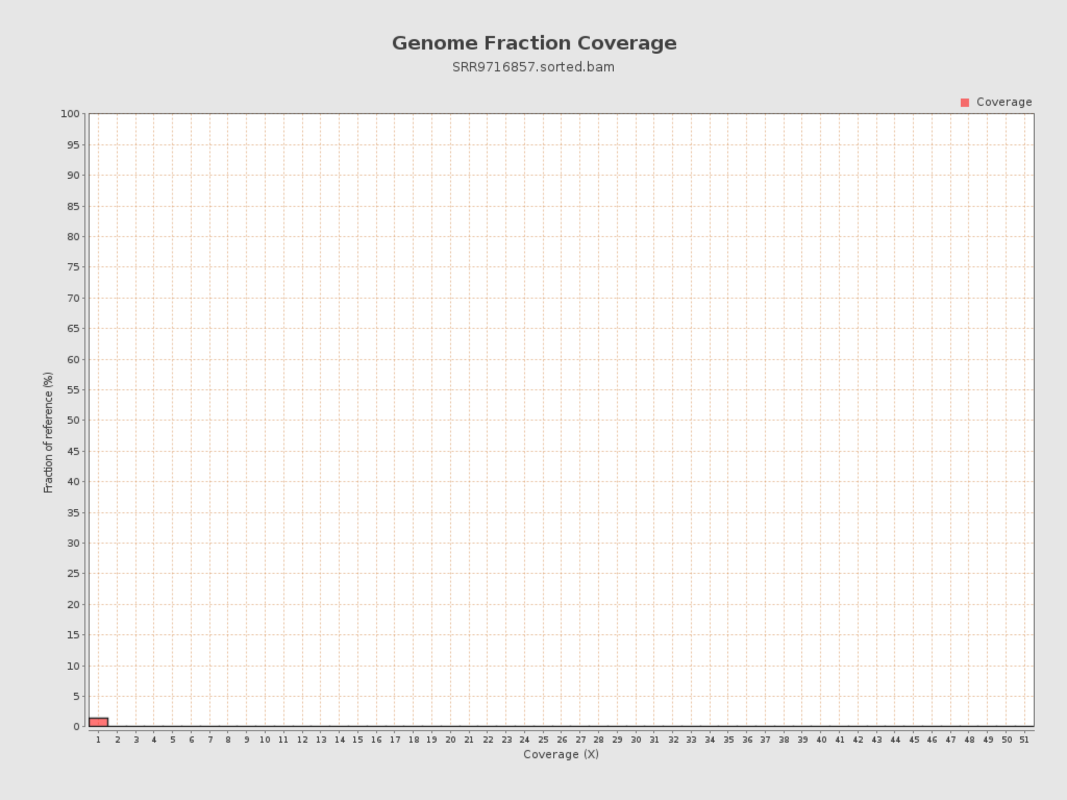
4. Results : Coverage Histogram



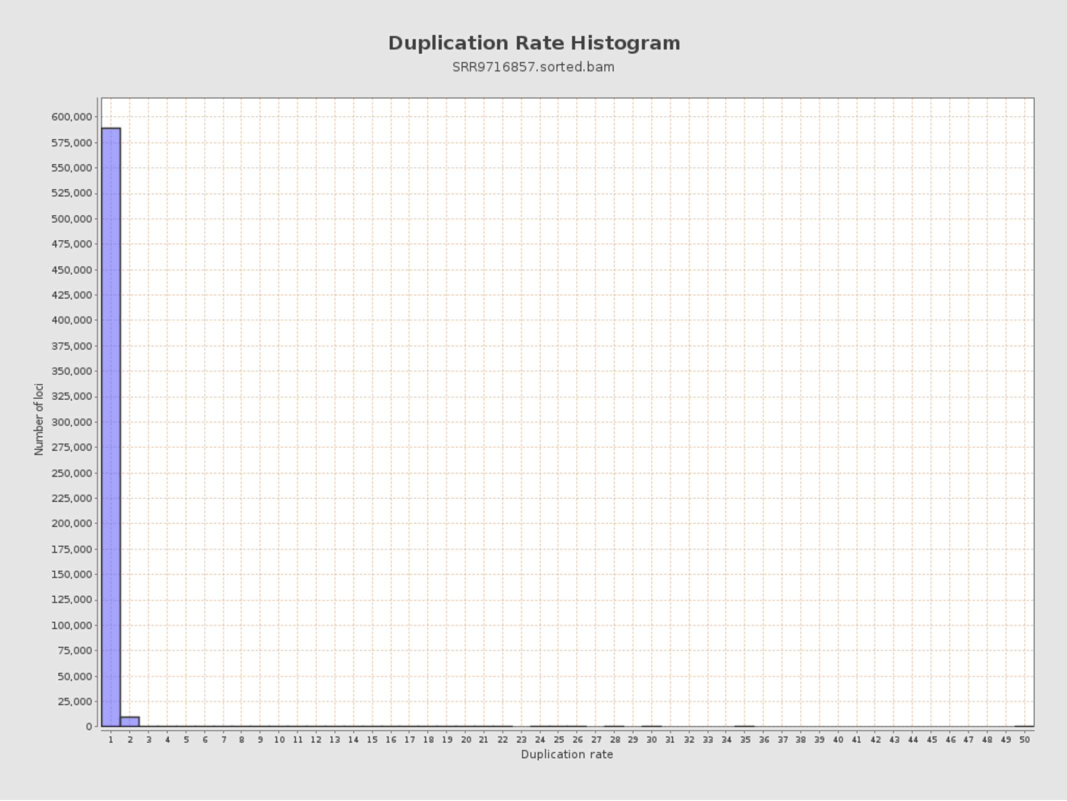
5. Results : Coverage Histogram (0-50X)



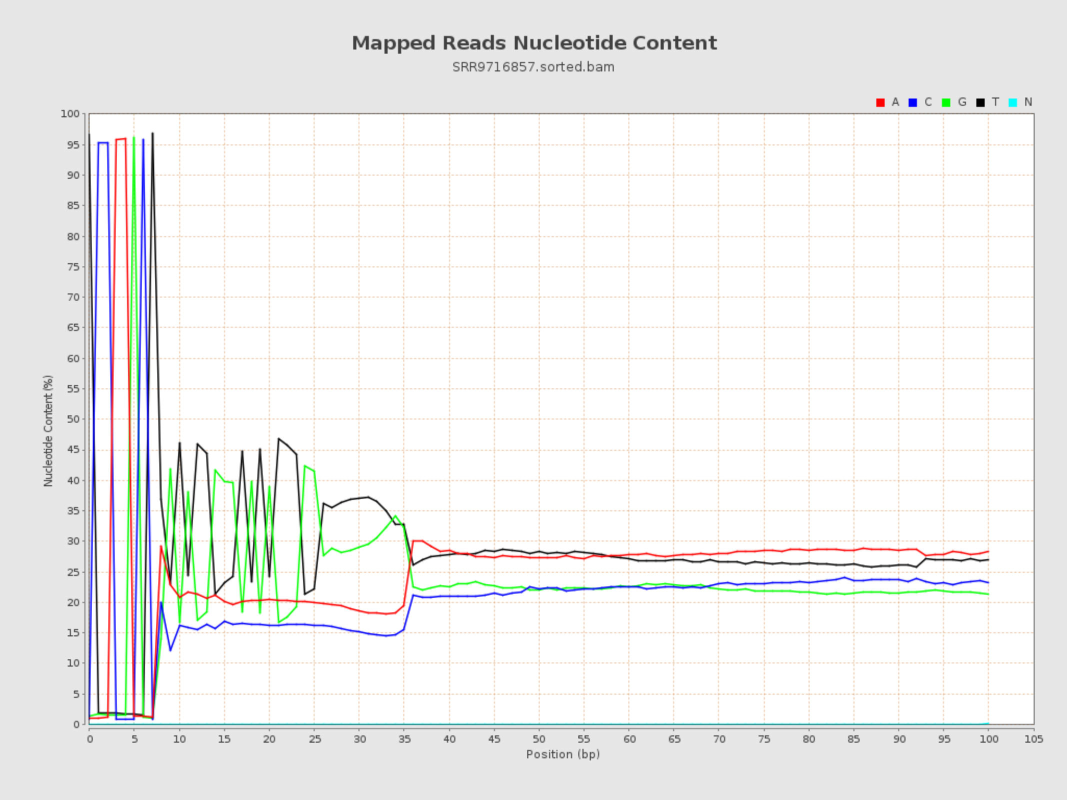
6. Results : Genome Fraction Coverage



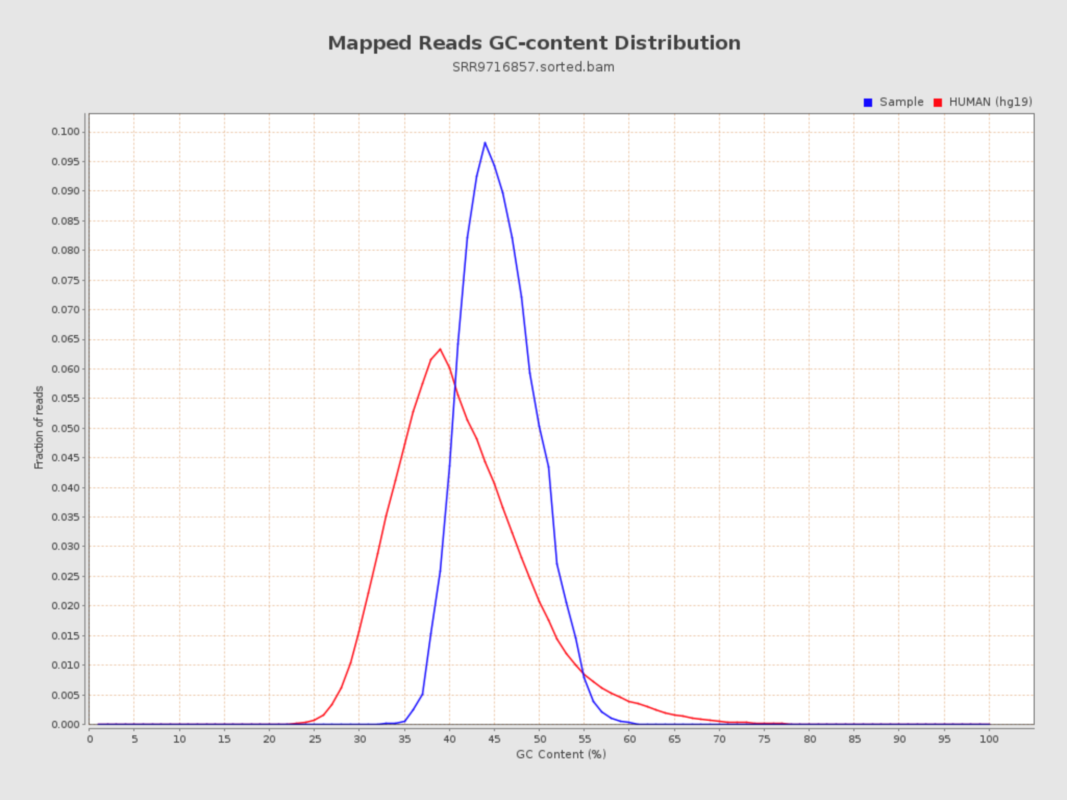
7. Results : Duplication Rate Histogram



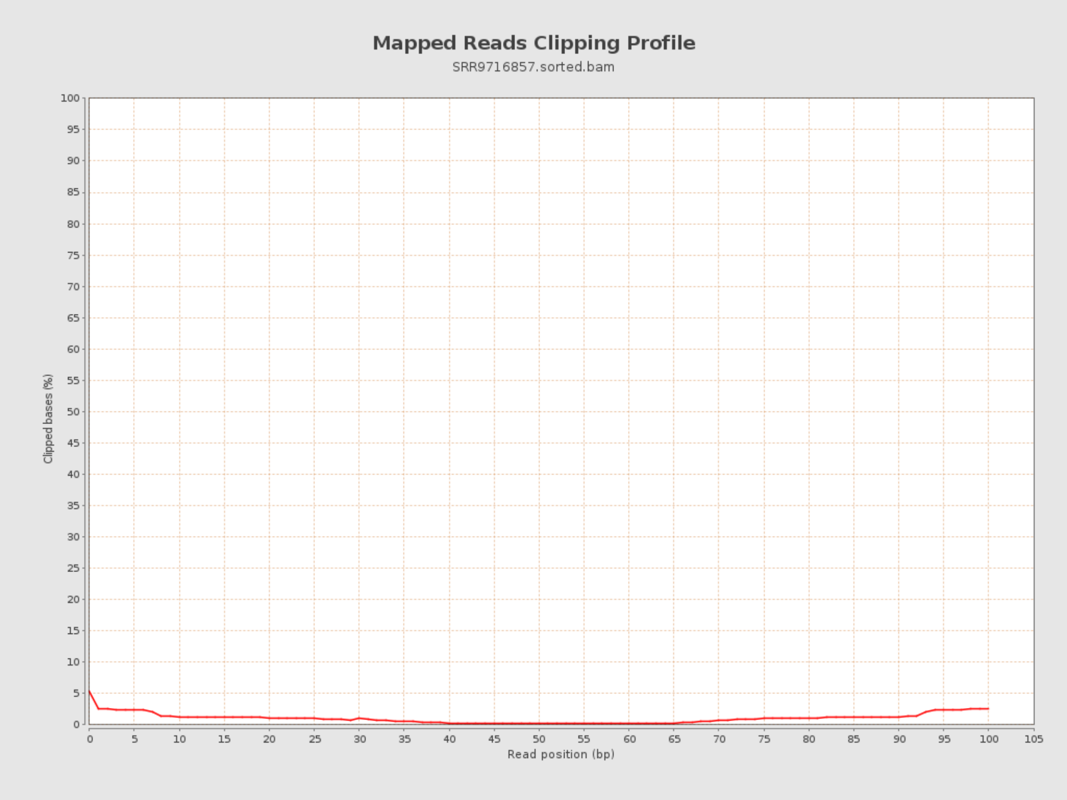
8. Results : Mapped Reads Nucleotide Content



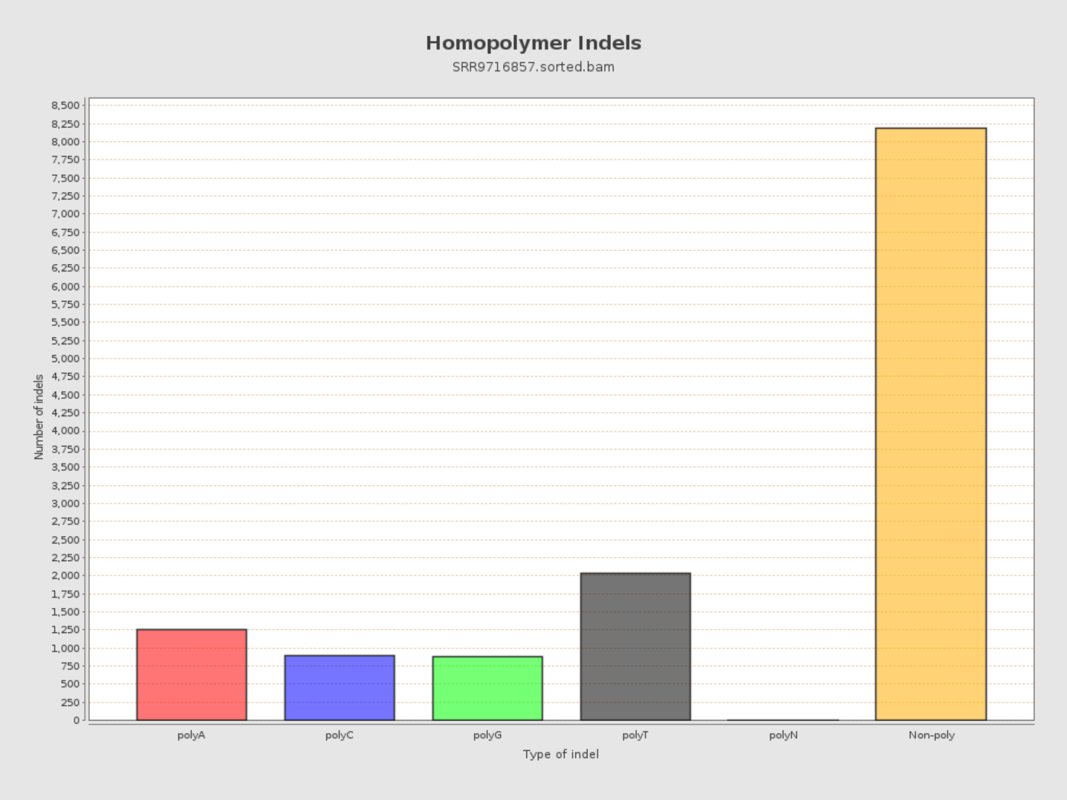
9. Results : Mapped Reads GC-content Distribution



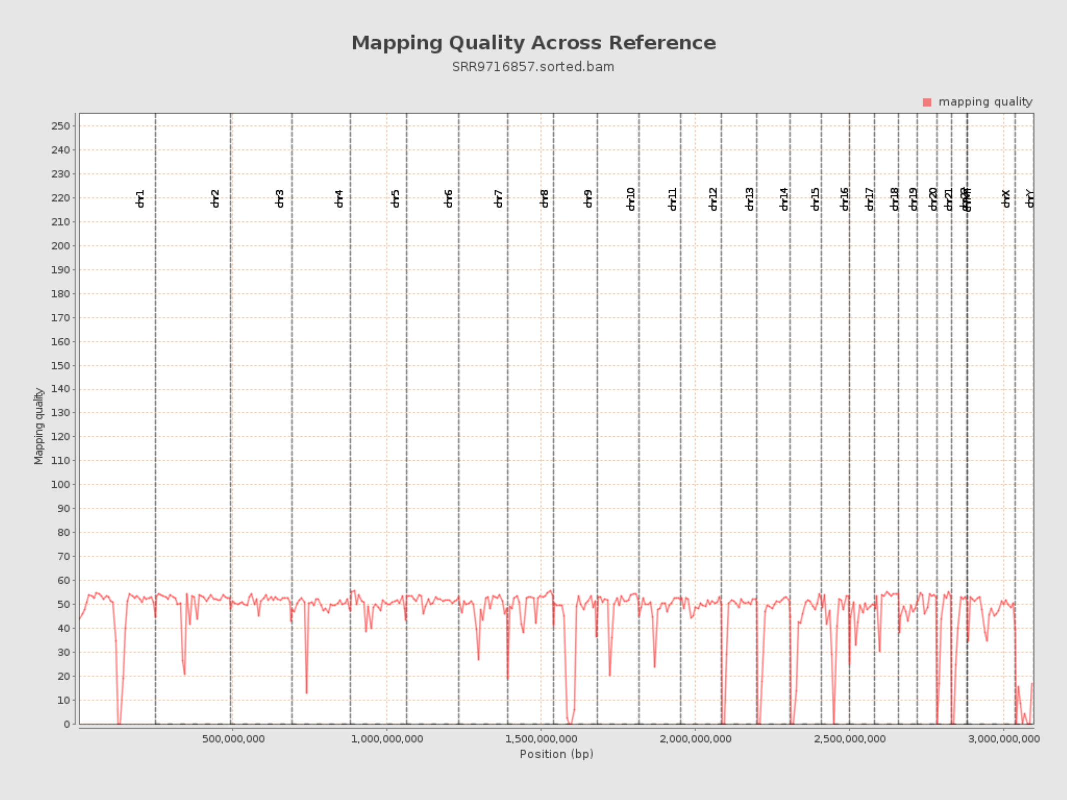
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram