Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 04:16:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716263.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_SRR9716263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 04:16:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,584,129
Mapped reads	1,257,927 / 79.41%
Unmapped reads	326,202 / 20.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,200 / 0.08%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	99,703 / 6.29%
Duplication rate	6.82%
Clipped reads	1,256,482 / 79.32%

2.2. ACGT Content

Number/percentage of A's	13,149,485 / 20.1%
Number/percentage of C's	11,310,036 / 17.29%
Number/percentage of T's	22,155,498 / 33.87%
Number/percentage of G's	18,806,485 / 28.75%
Number/percentage of N's	1,063 / 0%
GC Percentage	46.03%

2.3. Coverage

Mean	0.0211

Standard Deviation	0.1971

2.4. Mapping Quality

Mean Mapping Quality	42.86

2.5. Mismatches and indels

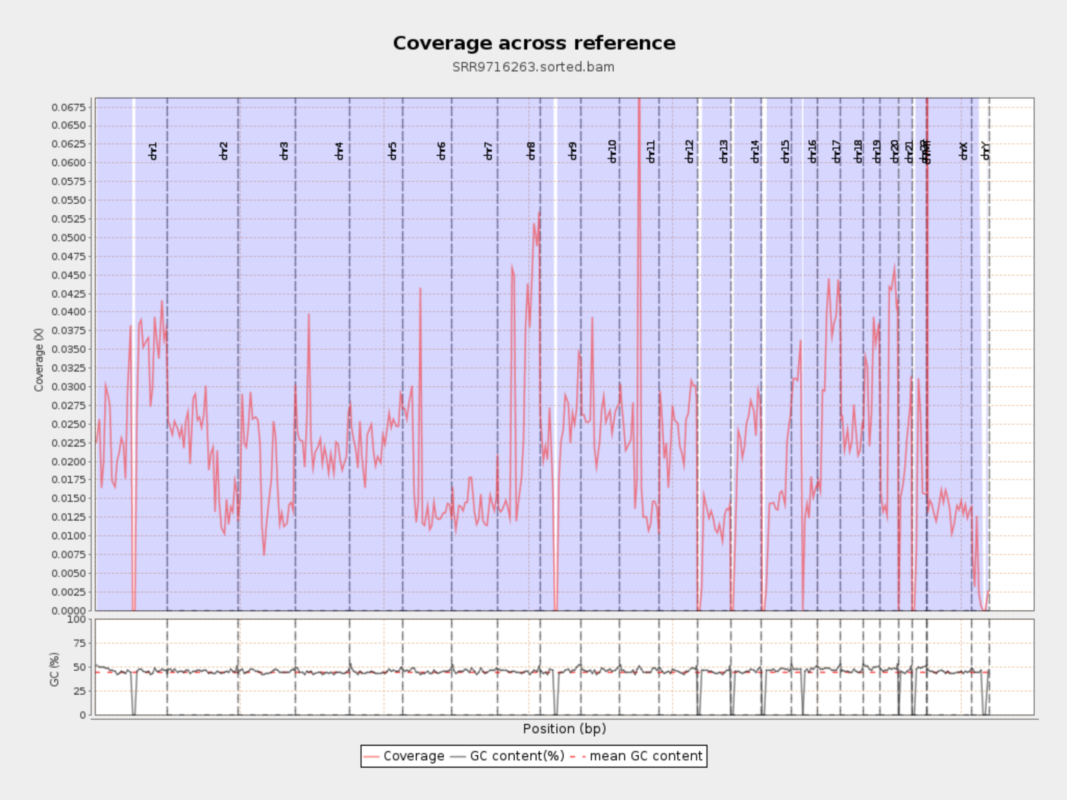
General error rate	0.65%
Mismatches	419,555
Insertions	4,195
Mapped reads with at least one insertion	0.33%
Deletions	10,410
Mapped reads with at least one deletion	0.82%
Homopolymer indels	38.88%

2.6. Chromosome stats

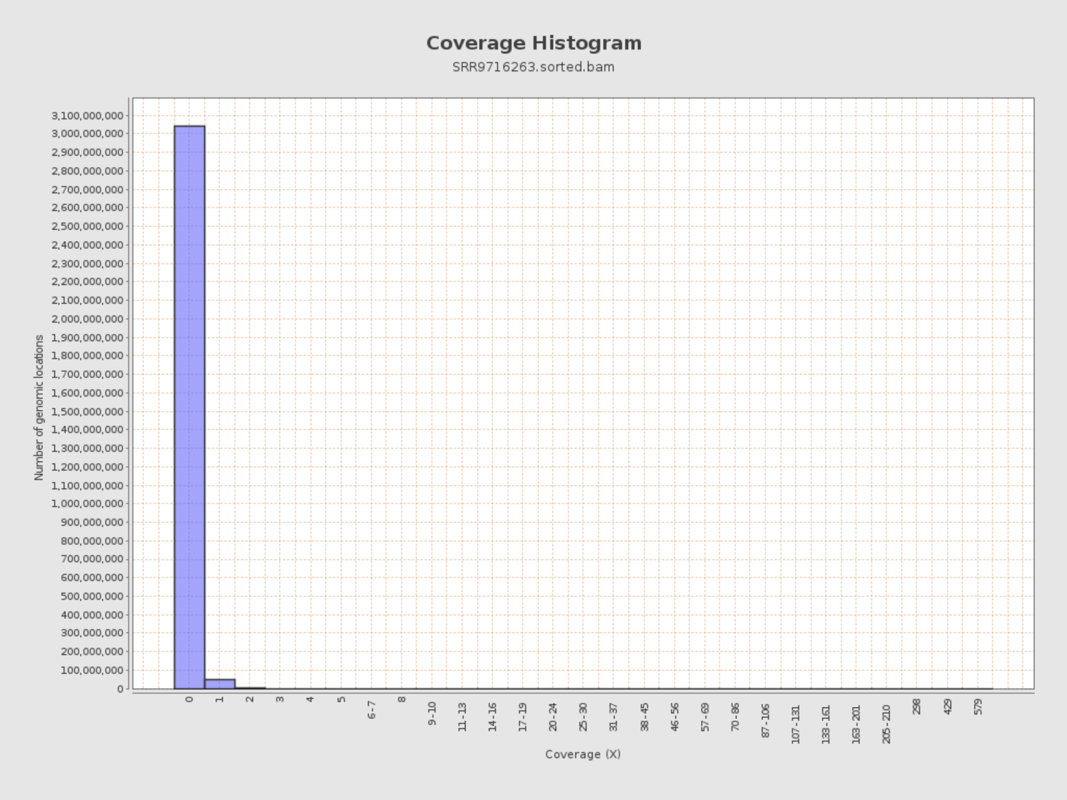
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6794566	0.0273	0.2412
chr2	243199373	5128147	0.0211	0.2911
chr3	198022430	3630212	0.0183	0.1621
chr4	191154276	4293213	0.0225	0.1864
chr5	180915260	4184170	0.0231	0.176
chr6	171115067	2987170	0.0175	0.1729
chr7	159138663	2212287	0.0139	0.1575

chr8	146364022	4273497	0.0292	0.2089
chr9	141213431	3060409	0.0217	0.1847
chr10	135534747	3538301	0.0261	0.236
chr11	135006516	2950895	0.0219	0.1981
chr12	133851895	3314463	0.0248	0.1841
chr13	115169878	1205900	0.0105	0.12
chr14	107349540	2237542	0.0208	0.1687
chr15	102531392	1372517	0.0134	0.1346
chr16	90354753	1830586	0.0203	0.1775
chr17	81195210	2766444	0.0341	0.2238
chr18	78077248	1833806	0.0235	0.2178
chr19	59128983	1904543	0.0322	0.2469
chr20	63025520	1870571	0.0297	0.2093
chr21	48129895	941459	0.0196	0.1724
chr22	51304566	779932	0.0152	0.1484
chrMT	16571	6068	0.3662	0.6958
chrX	155270560	2122179	0.0137	0.1447
chrY	59373566	201373	0.0034	0.102

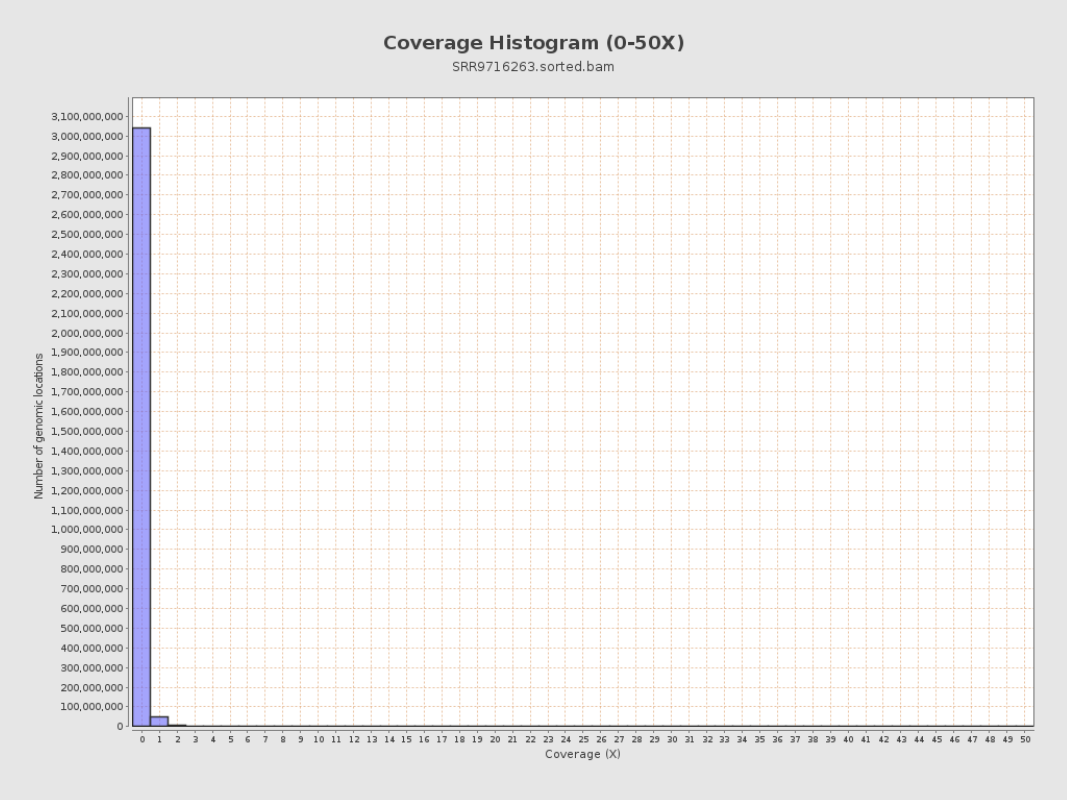
3. Results : Coverage across reference



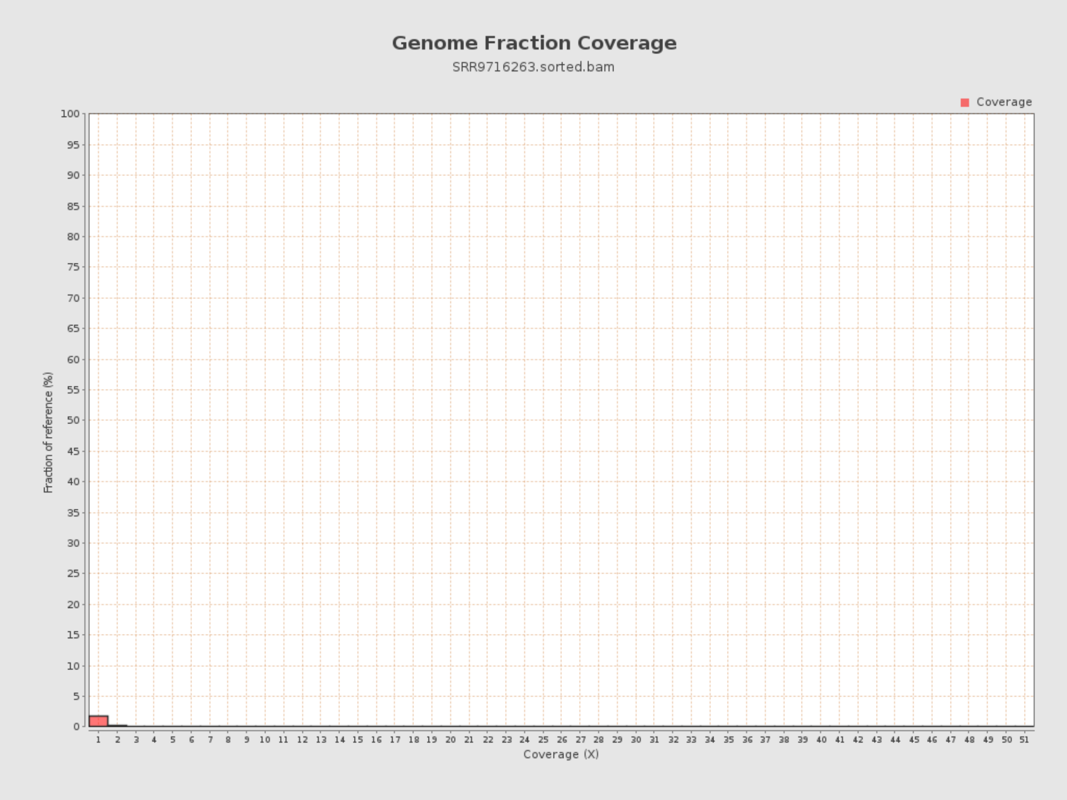
4. Results : Coverage Histogram



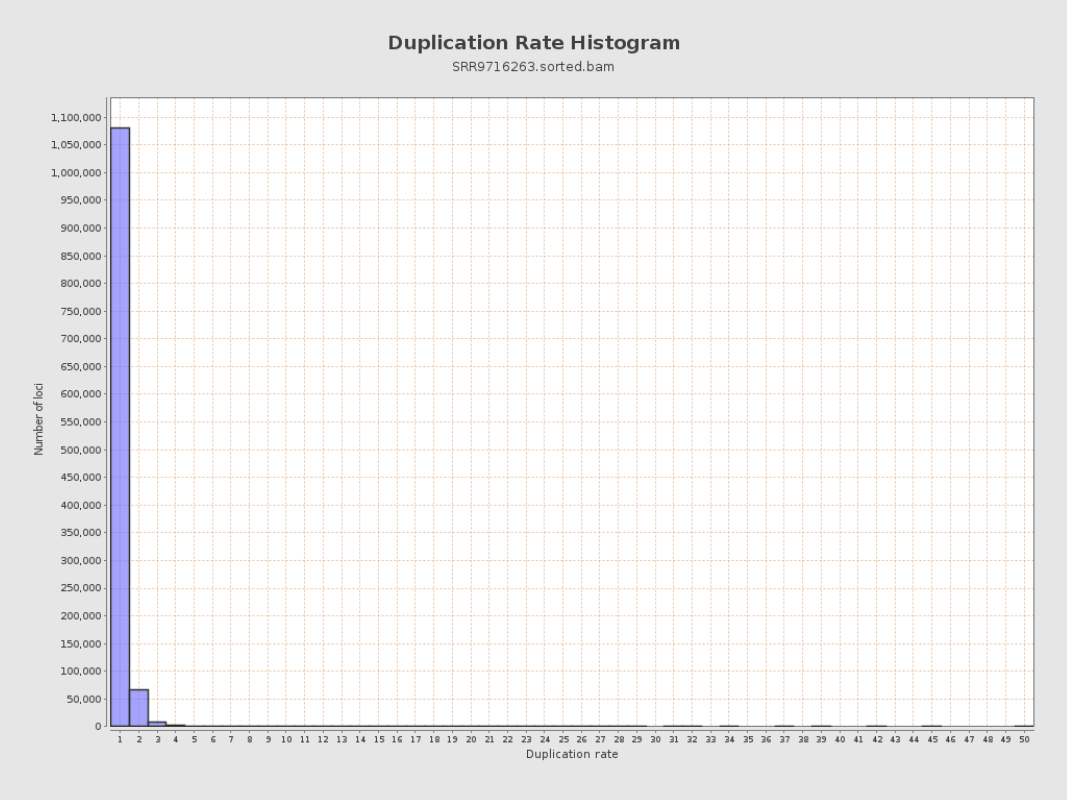
5. Results : Coverage Histogram (0-50X)



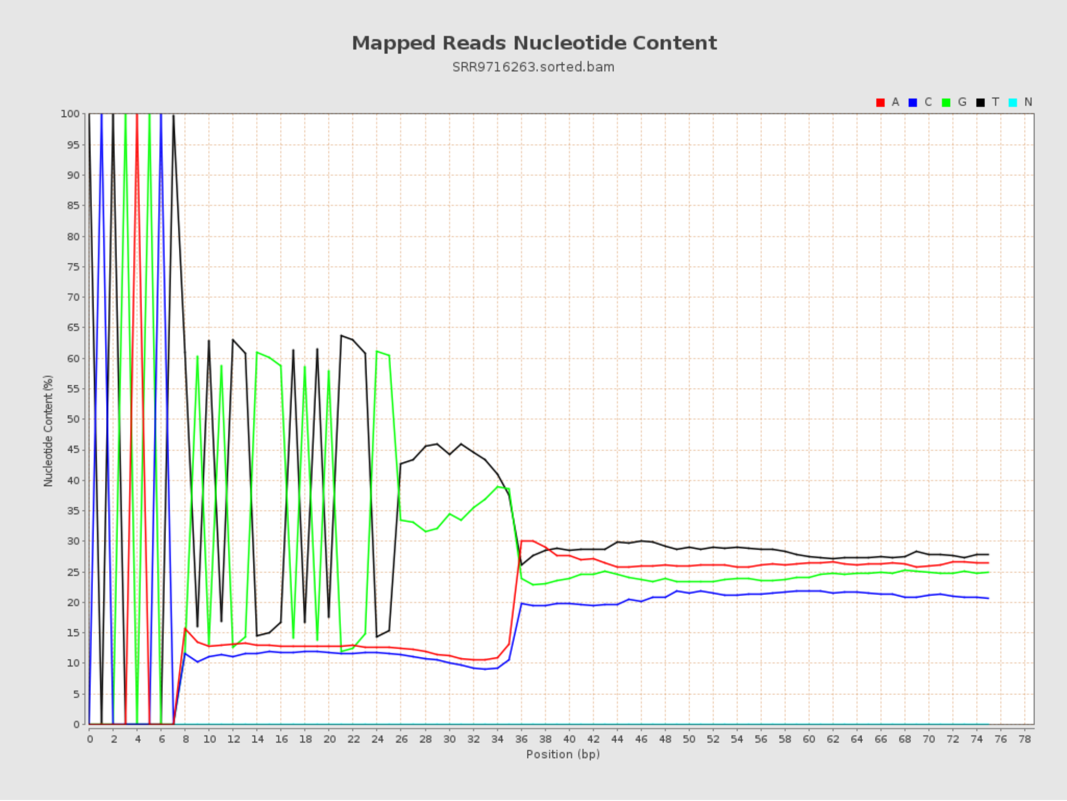
6. Results : Genome Fraction Coverage



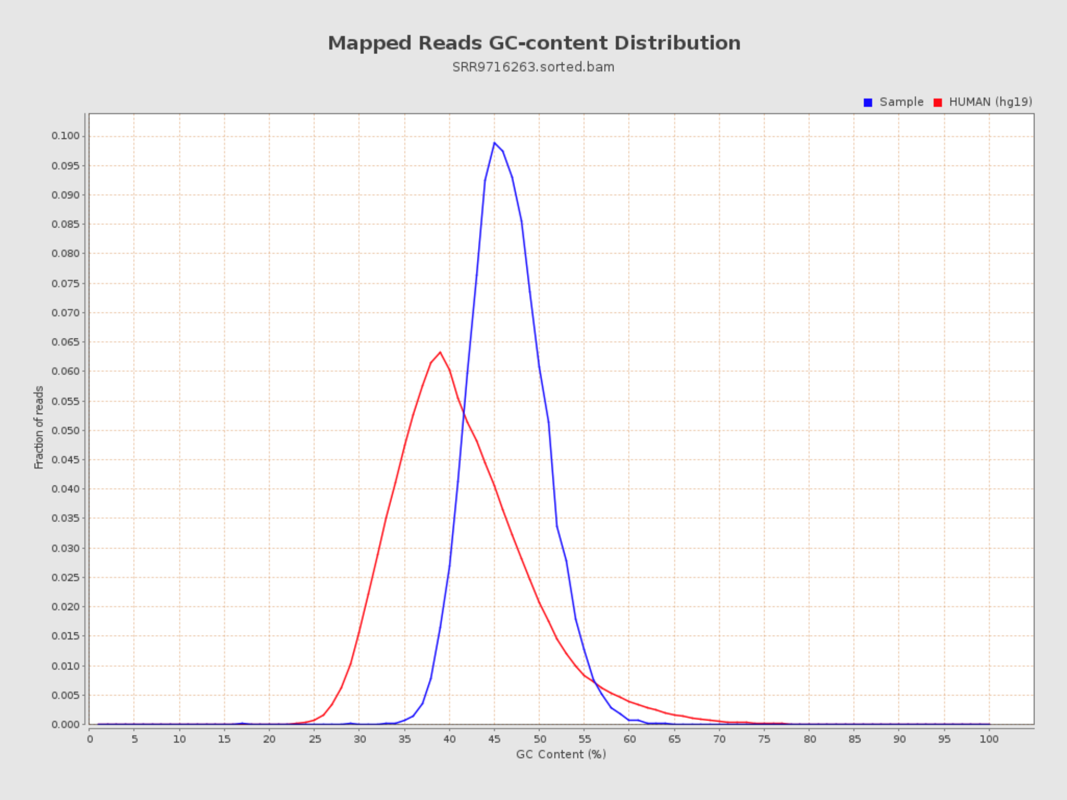
7. Results : Duplication Rate Histogram



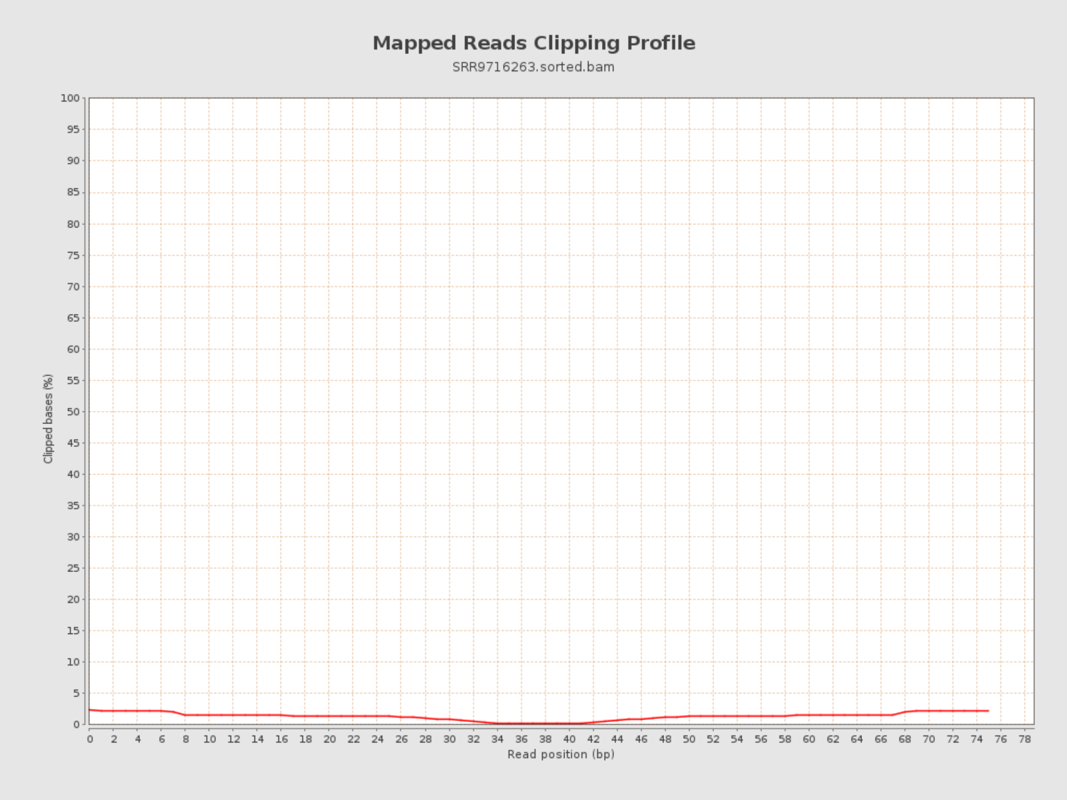
8. Results : Mapped Reads Nucleotide Content



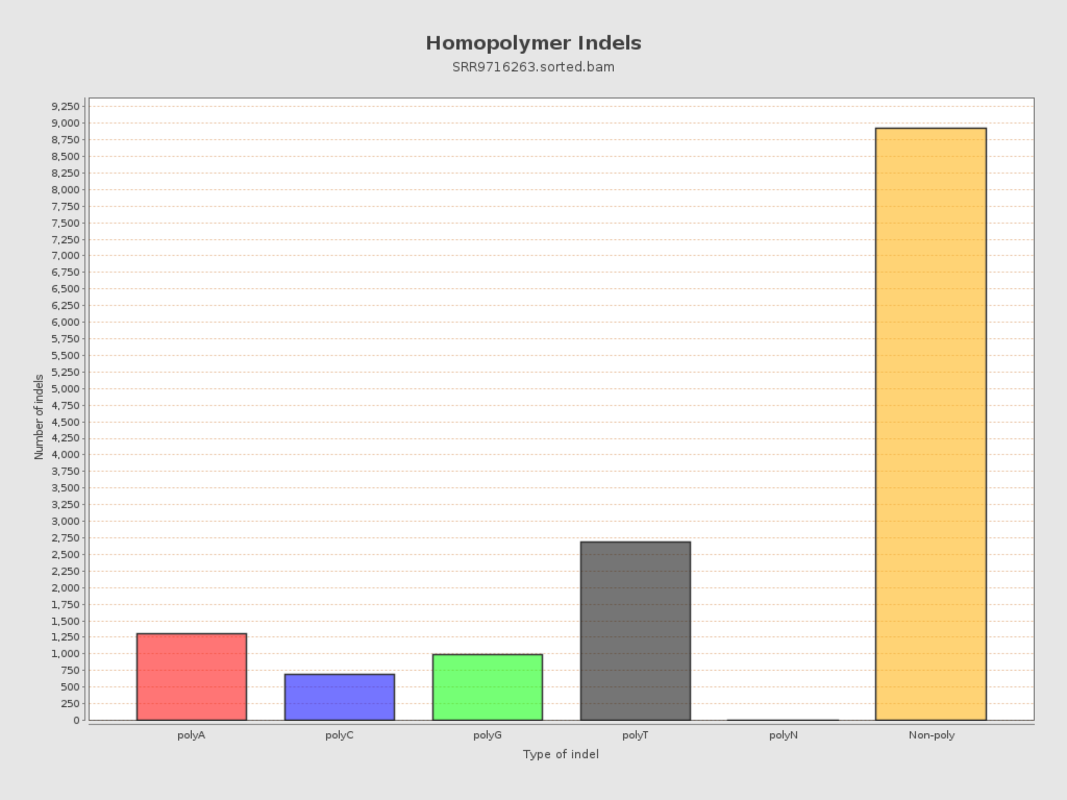
9. Results : Mapped Reads GC-content Distribution



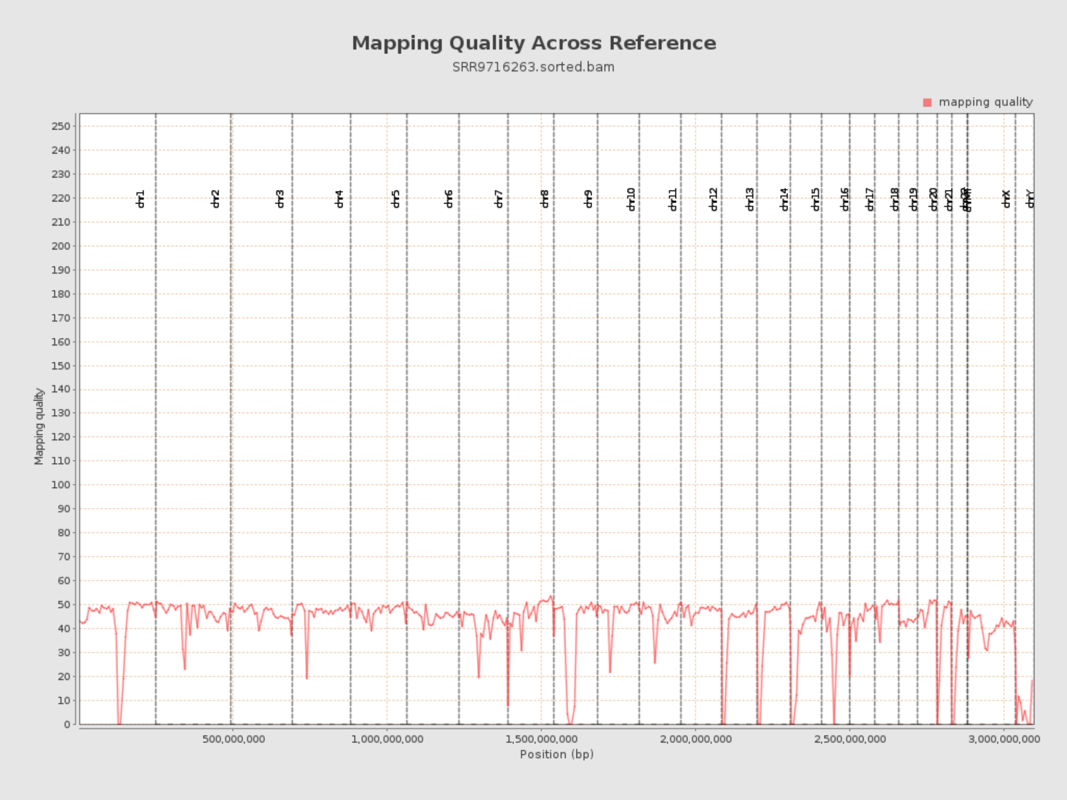
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram