Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:23:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716859.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_SRR9716859 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716859.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:23:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716859.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,363,754
Mapped reads	1,285,026 / 94.23%
Unmapped reads	78,728 / 5.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	31,824 / 2.33%
Read min/max/mean length	30 / 101 / 101.84
Duplicated reads (estimated)	49,956 / 3.66%
Duplication rate	3%
Clipped reads	1,316,335 / 96.52%

2.2. ACGT Content

Number/percentage of A's	24,422,927 / 24.7%
Number/percentage of C's	20,869,124 / 21.11%
Number/percentage of T's	28,964,226 / 29.3%
Number/percentage of G's	24,603,317 / 24.89%
Number/percentage of N's	3,729 / 0%
GC Percentage	46%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.282

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

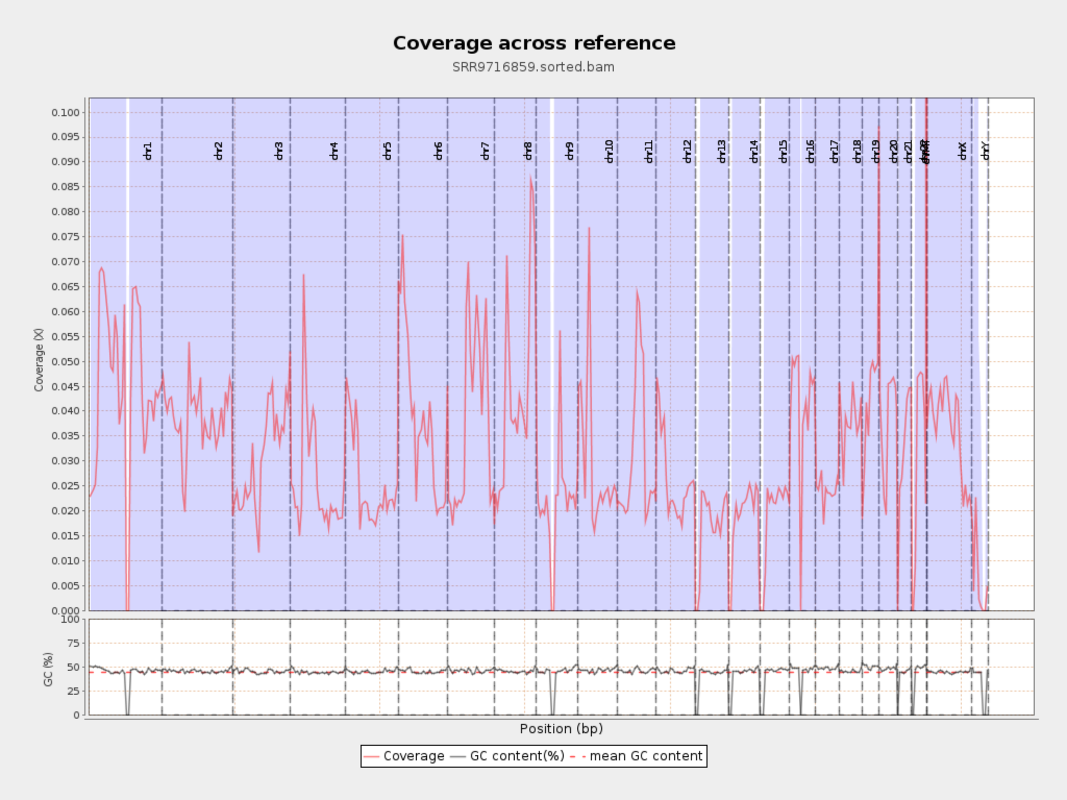
General error rate	0.67%
Mismatches	638,459
Insertions	7,661
Mapped reads with at least one insertion	0.59%
Deletions	18,981
Mapped reads with at least one deletion	1.45%
Homopolymer indels	39.17%

2.6. Chromosome stats

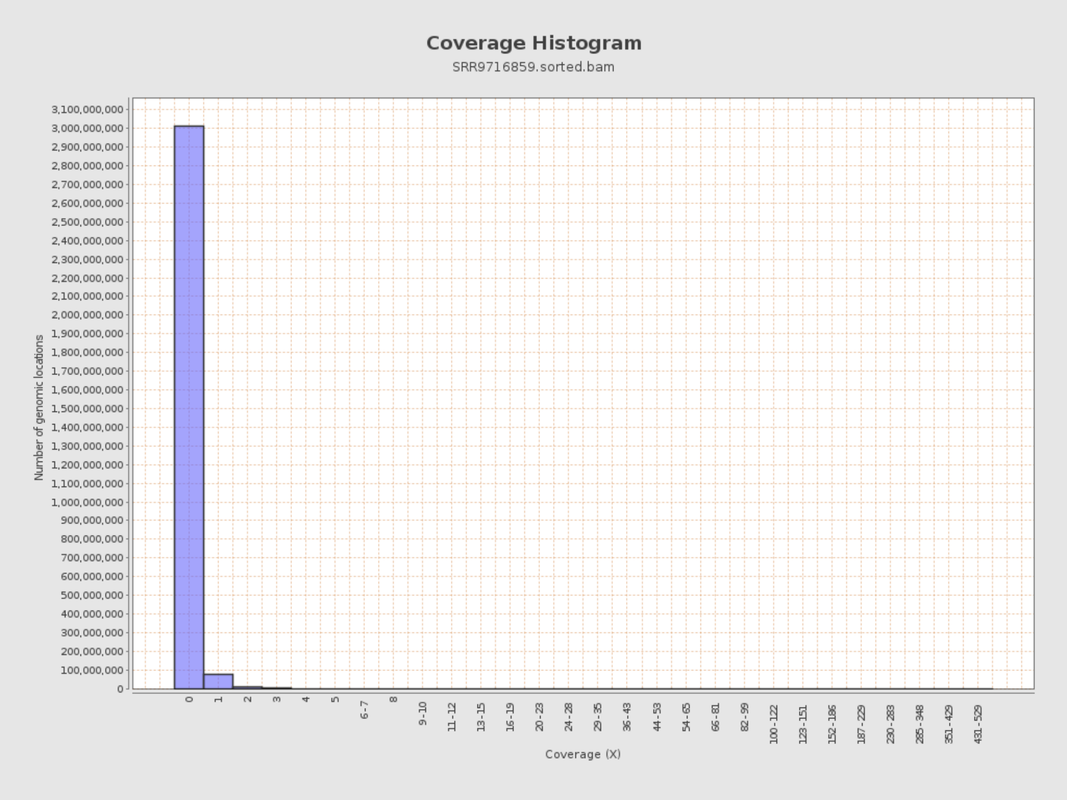
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11211911	0.045	0.5132
chr2	243199373	9434522	0.0388	0.296
chr3	198022430	6035352	0.0305	0.2018
chr4	191154276	4931994	0.0258	0.2552
chr5	180915260	4632862	0.0256	0.1807
chr6	171115067	6605949	0.0386	0.2301
chr7	159138663	6198634	0.039	0.3438

chr8	146364022	6467226	0.0442	0.3119
chr9	141213431	3011769	0.0213	0.1964
chr10	135534747	4030443	0.0297	0.3848
chr11	135006516	4267485	0.0316	0.2442
chr12	133851895	3535449	0.0264	0.1824
chr13	115169878	1922649	0.0167	0.1432
chr14	107349540	2002789	0.0187	0.1626
chr15	102531392	1918959	0.0187	0.1526
chr16	90354753	3743444	0.0414	0.2479
chr17	81195210	1947098	0.024	0.1906
chr18	78077248	2963883	0.038	0.3006
chr19	59128983	2582686	0.0437	0.4105
chr20	63025520	2366595	0.0375	0.24
chr21	48129895	1540970	0.032	0.2431
chr22	51304566	1510208	0.0294	0.1992
chrMT	16571	28566	1.7239	1.868
chrX	155270560	5658202	0.0364	0.2249
chrY	59373566	353151	0.0059	0.2171

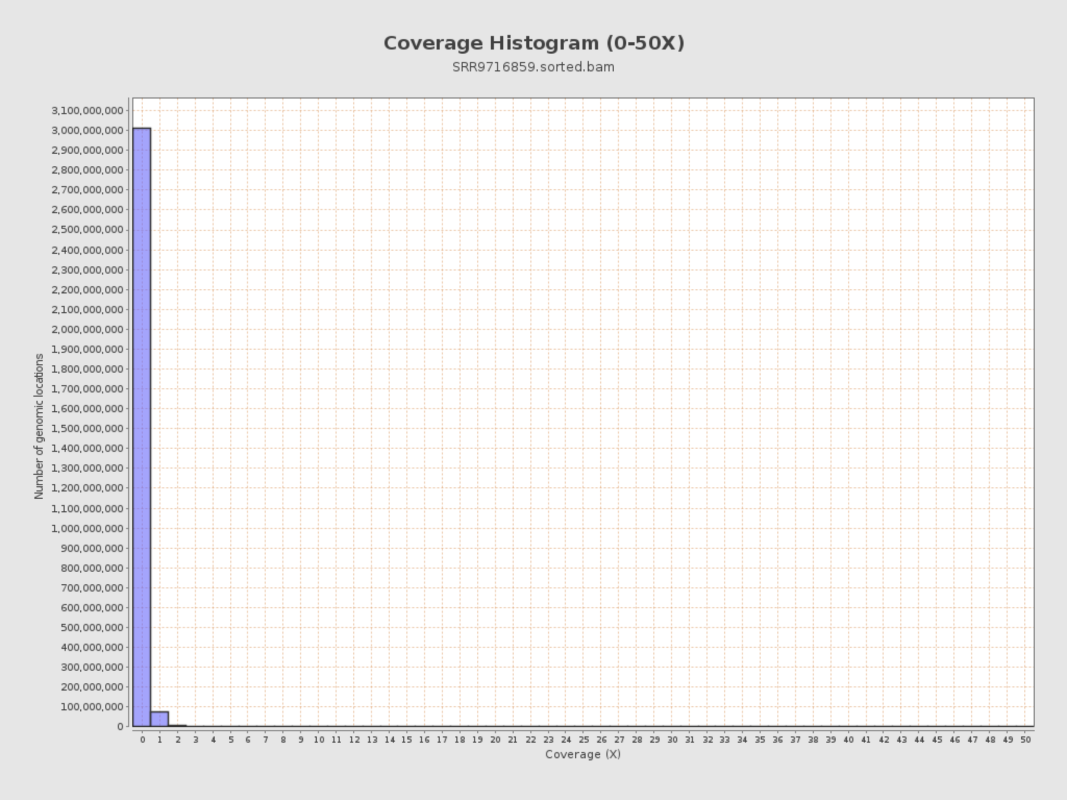
3. Results : Coverage across reference



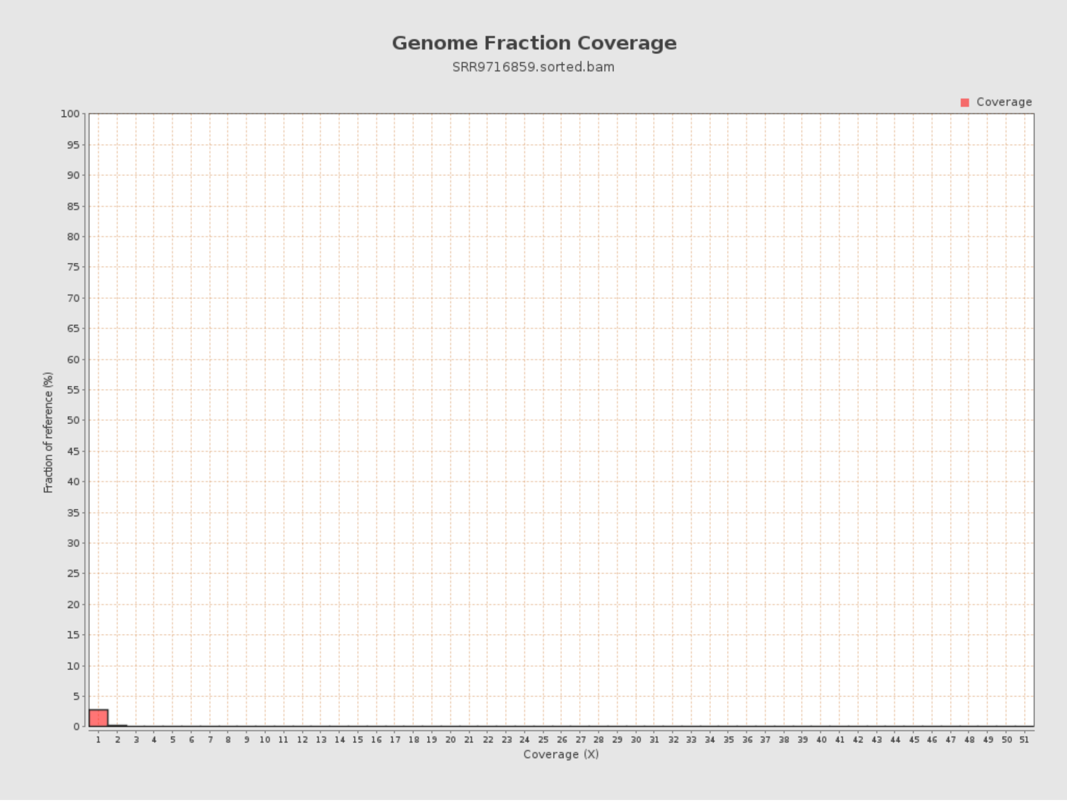
4. Results : Coverage Histogram



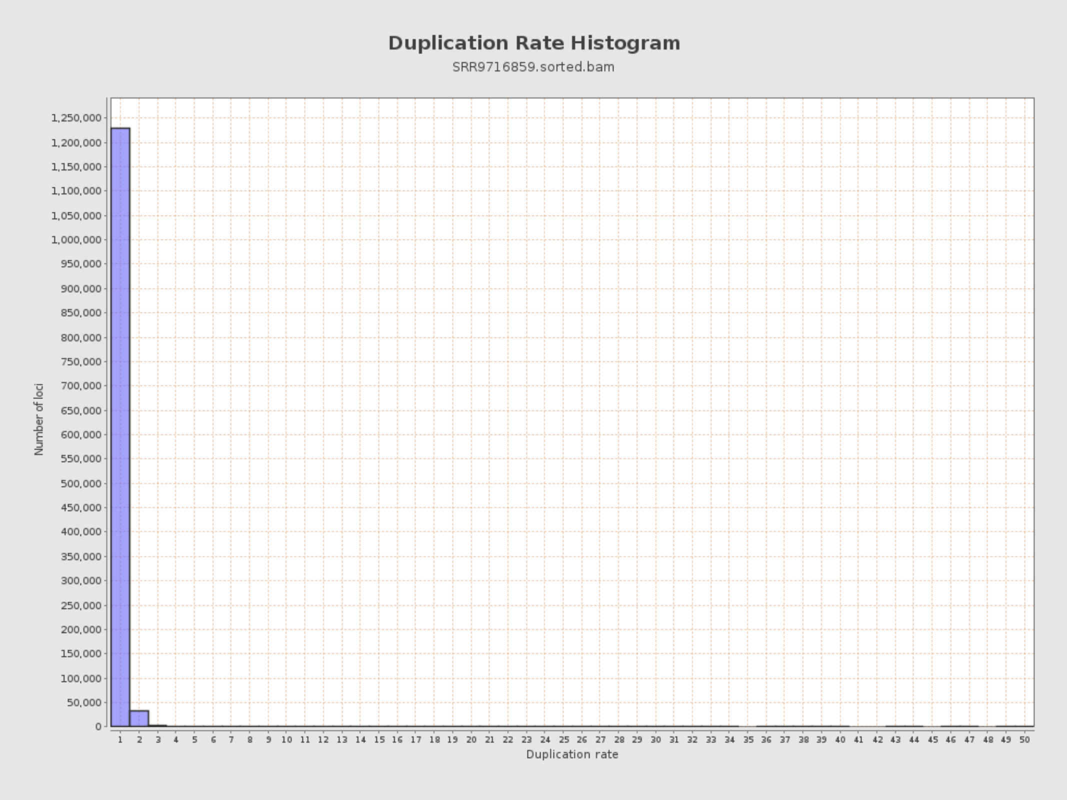
5. Results : Coverage Histogram (0-50X)



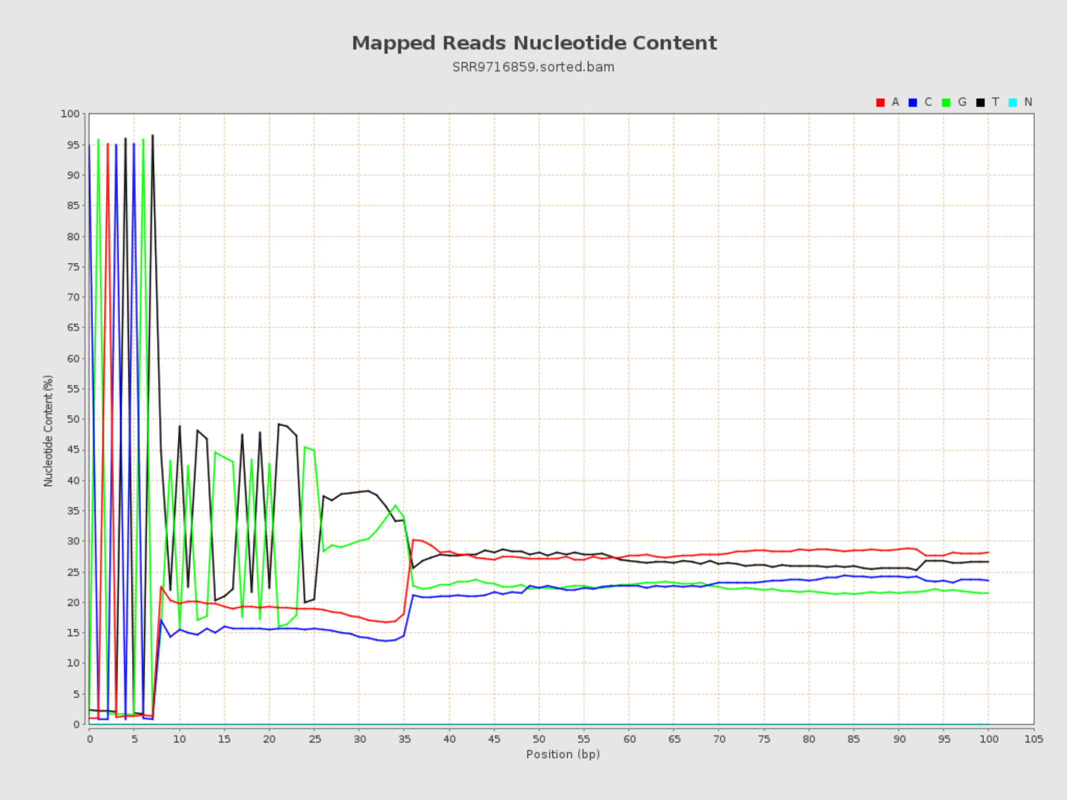
6. Results : Genome Fraction Coverage



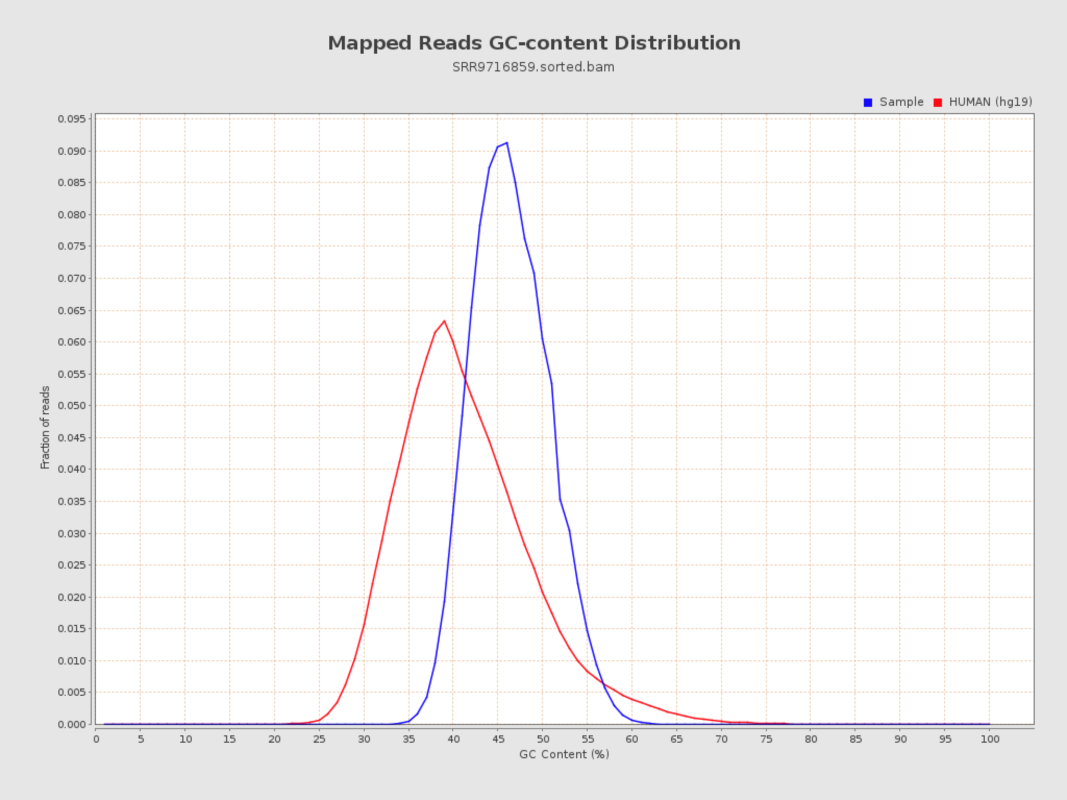
7. Results : Duplication Rate Histogram



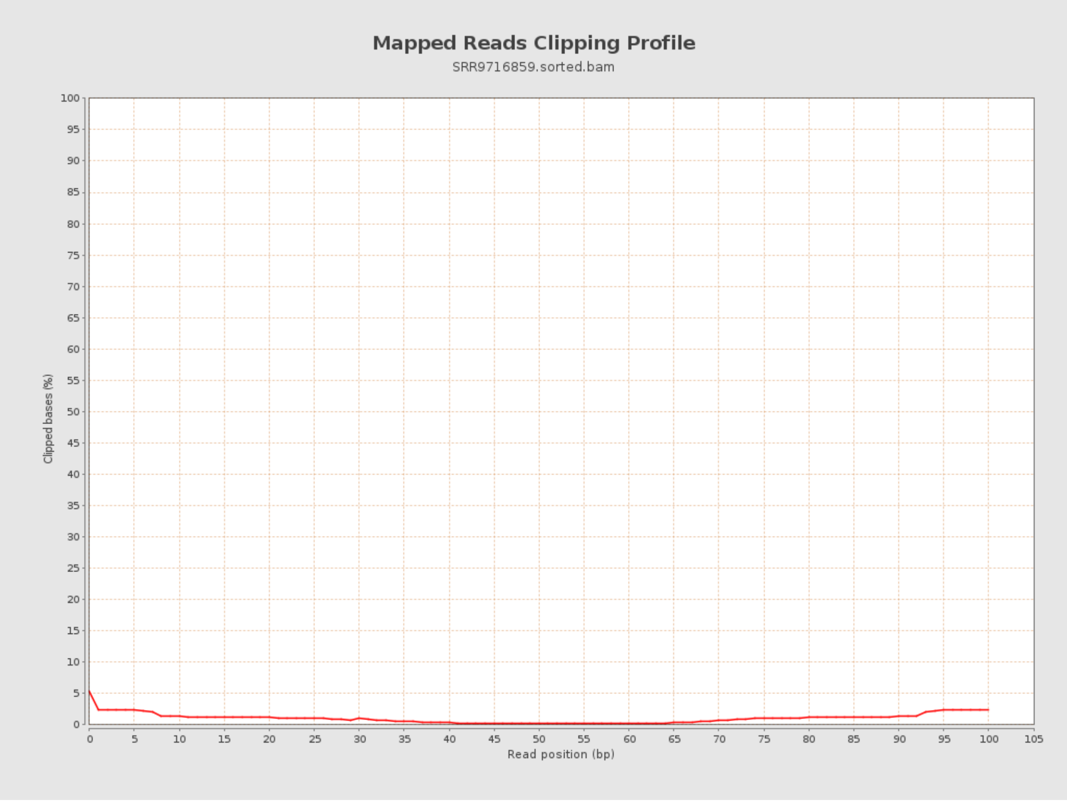
8. Results : Mapped Reads Nucleotide Content



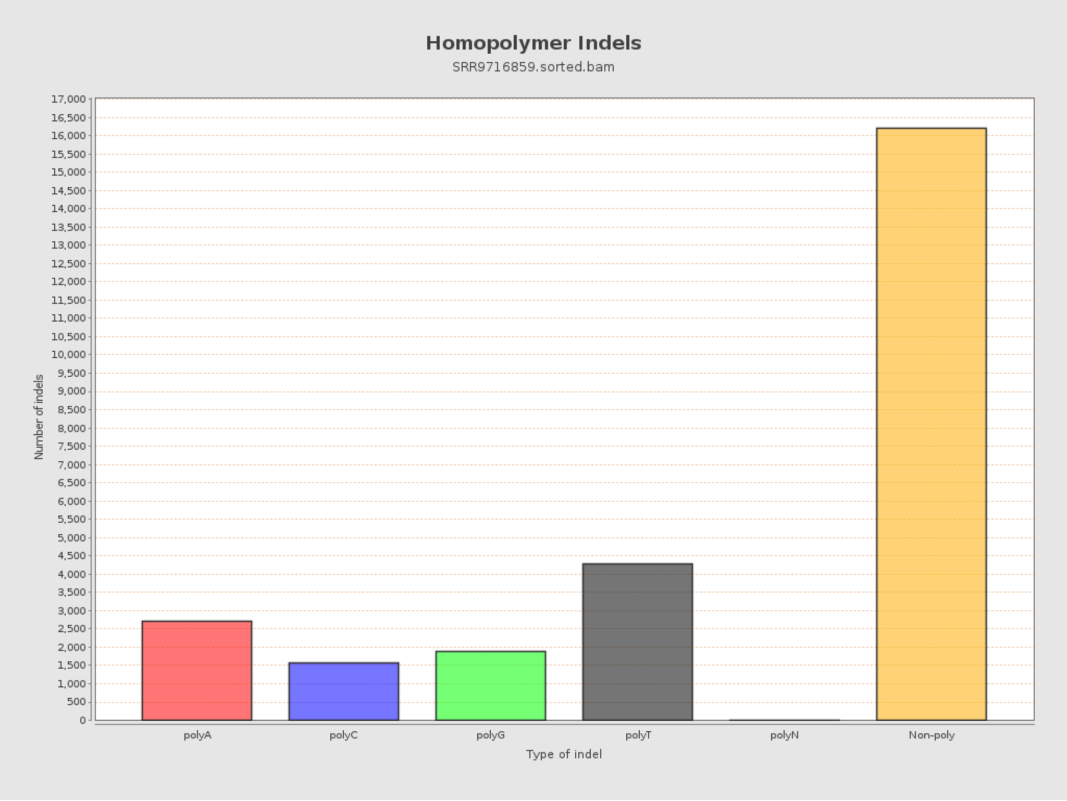
9. Results : Mapped Reads GC-content Distribution



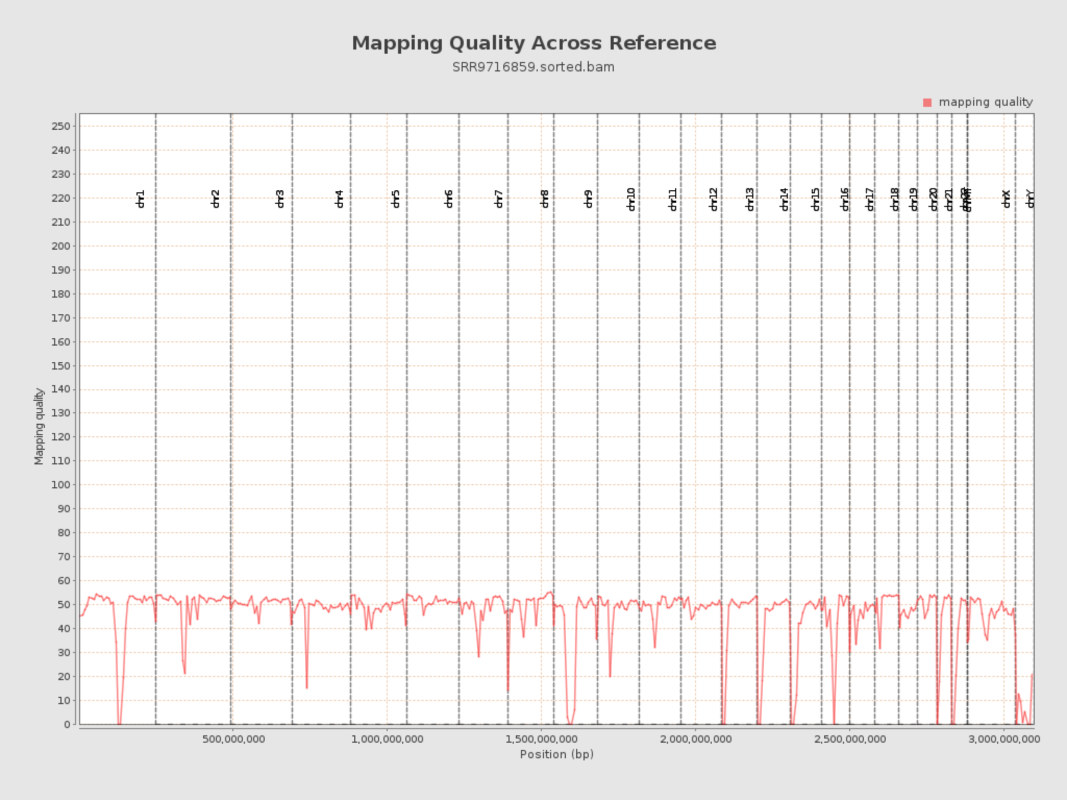
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram