Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:07:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716659.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_SRR9716659 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716659.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:07:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716659.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,011,337
Mapped reads	919,636 / 90.93%
Unmapped reads	91,701 / 9.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,399 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	23,712 / 2.34%
Duplication rate	1.89%
Clipped reads	921,665 / 91.13%

2.2. ACGT Content

Number/percentage of A's	13,366,310 / 24.98%
Number/percentage of C's	10,047,361 / 18.78%
Number/percentage of T's	17,177,986 / 32.11%
Number/percentage of G's	12,910,754 / 24.13%
Number/percentage of N's	1,671 / 0%
GC Percentage	42.91%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.1906

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

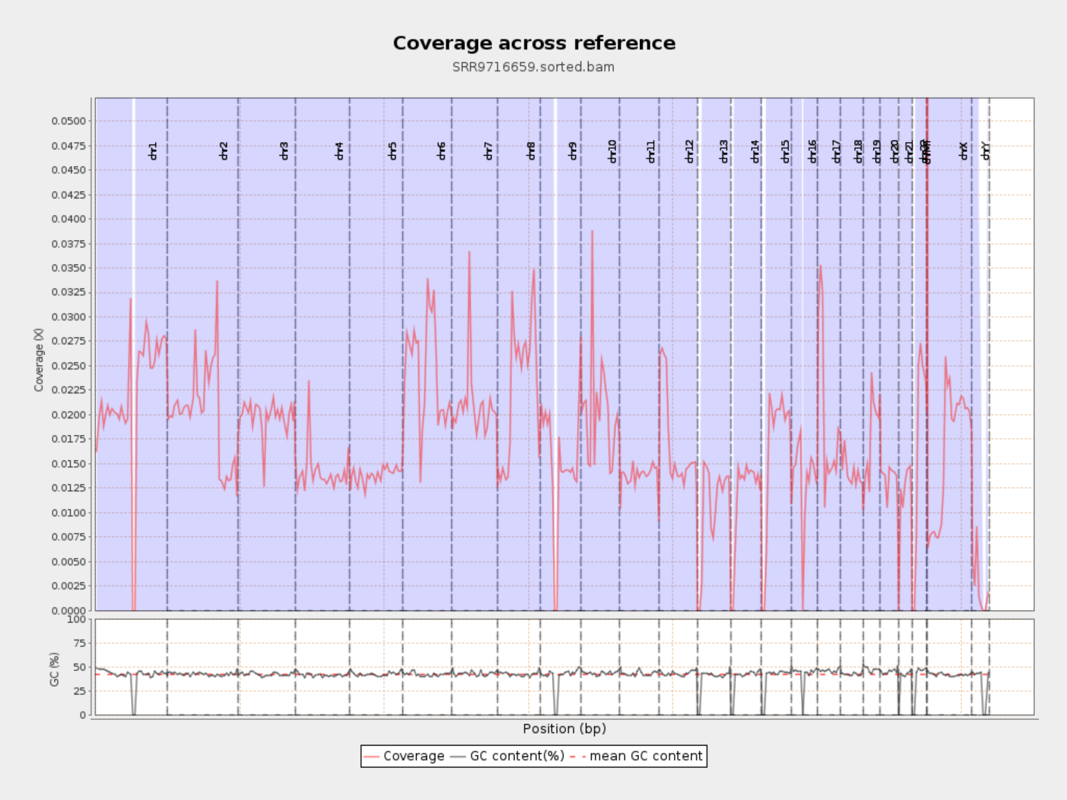
General error rate	0.51%
Mismatches	268,558
Insertions	3,665
Mapped reads with at least one insertion	0.4%
Deletions	9,789
Mapped reads with at least one deletion	1.06%
Homopolymer indels	42.2%

2.6. Chromosome stats

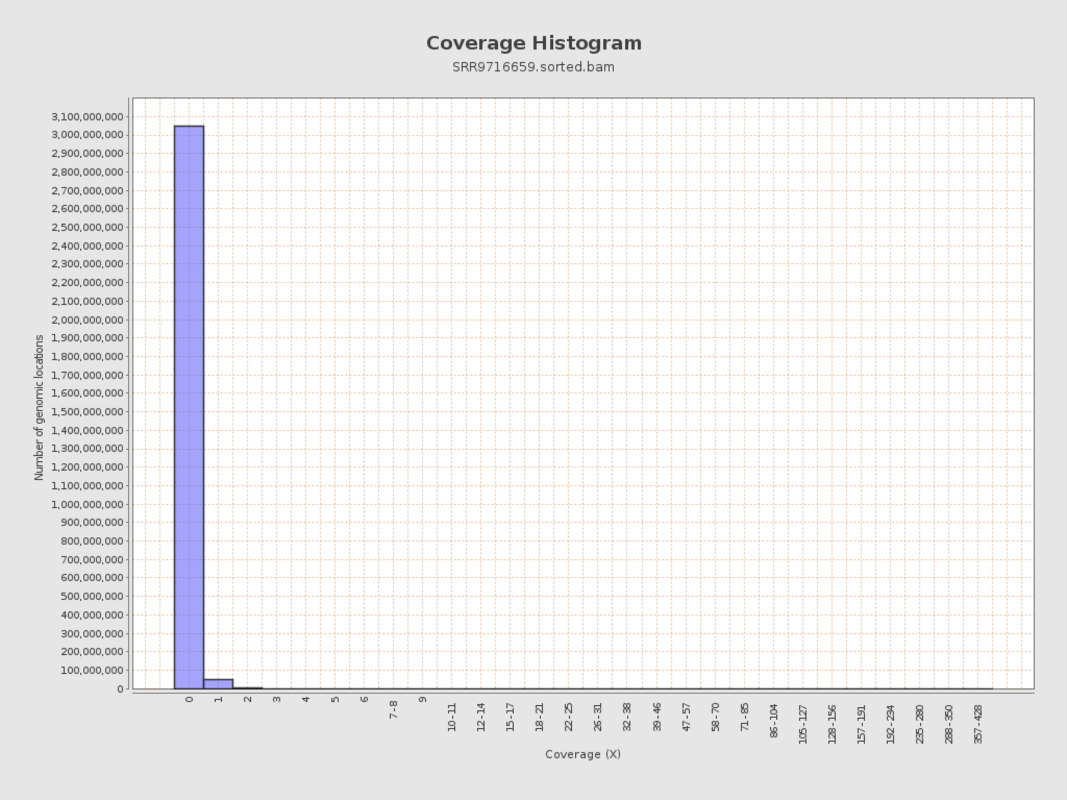
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5469635	0.0219	0.3272
chr2	243199373	4896751	0.0201	0.2281
chr3	198022430	3929816	0.0198	0.1492
chr4	191154276	2714233	0.0142	0.1321
chr5	180915260	2514385	0.0139	0.1254
chr6	171115067	4153078	0.0243	0.1859
chr7	159138663	3356717	0.0211	0.3183

chr8	146364022	3363857	0.023	0.192
chr9	141213431	2083195	0.0148	0.1487
chr10	135534747	2770446	0.0204	0.1878
chr11	135006516	1885807	0.014	0.1504
chr12	133851895	2299057	0.0172	0.1401
chr13	115169878	1191939	0.0103	0.1076
chr14	107349540	1237983	0.0115	0.1189
chr15	102531392	1686656	0.0165	0.1361
chr16	90354753	1185093	0.0131	0.1273
chr17	81195210	1619573	0.0199	0.1525
chr18	78077248	1103121	0.0141	0.2361
chr19	59128983	1054340	0.0178	0.2146
chr20	63025520	850247	0.0135	0.1232
chr21	48129895	562241	0.0117	0.1222
chr22	51304566	878761	0.0171	0.1385
chrMT	16571	18994	1.1462	1.1269
chrX	155270560	2552372	0.0164	0.1465
chrY	59373566	141235	0.0024	0.0679

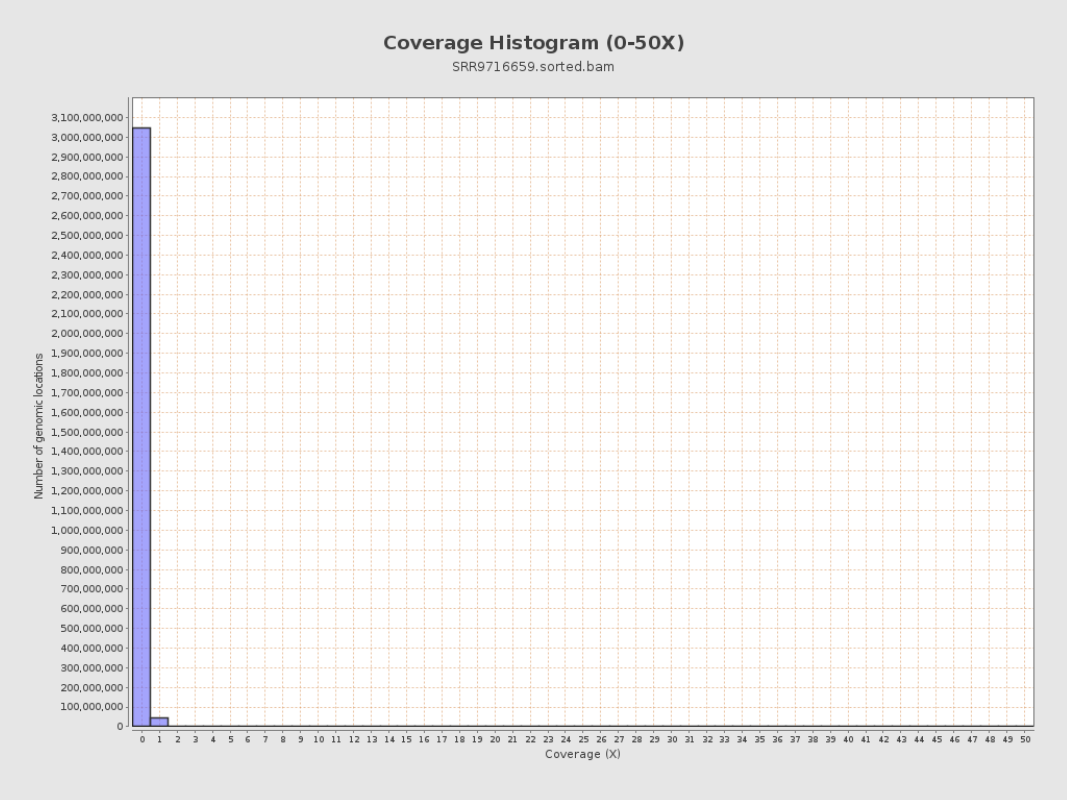
3. Results : Coverage across reference



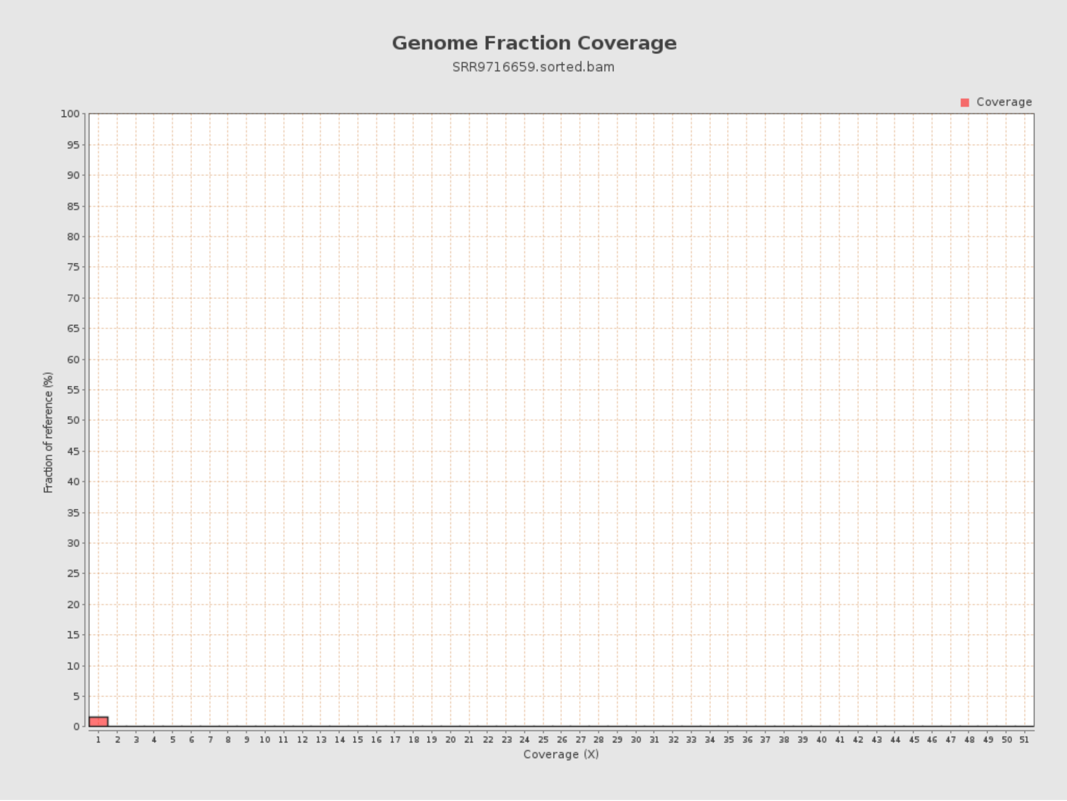
4. Results : Coverage Histogram



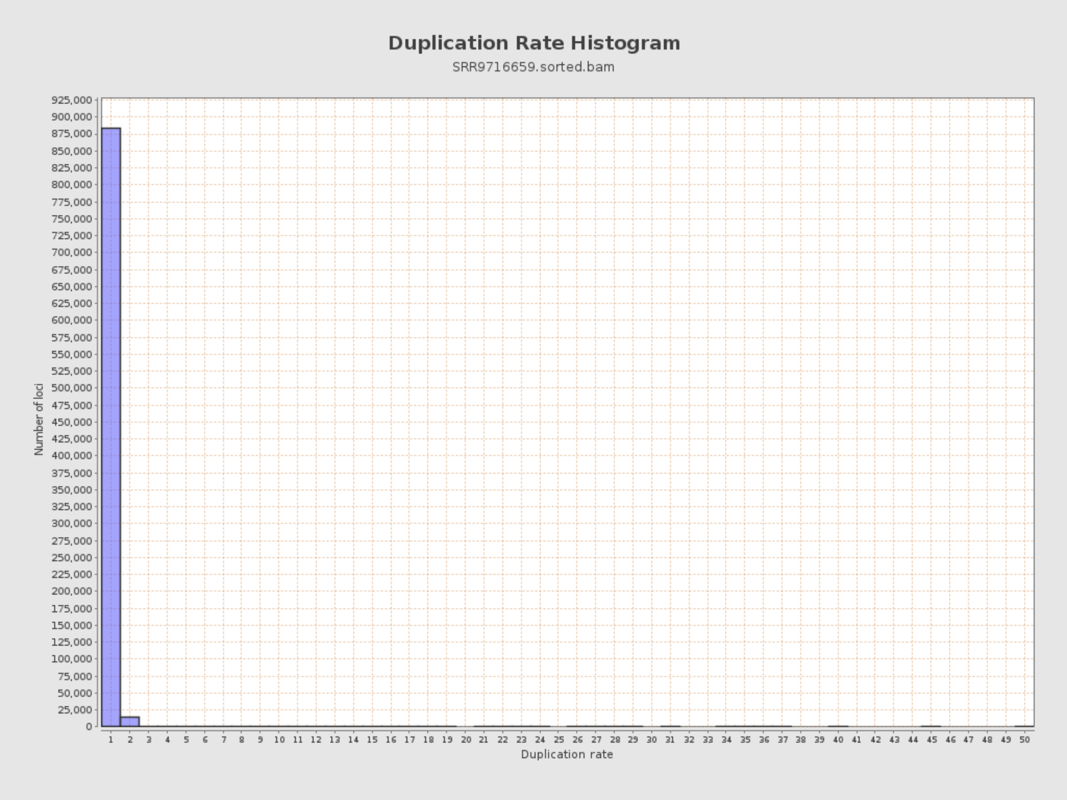
5. Results : Coverage Histogram (0-50X)



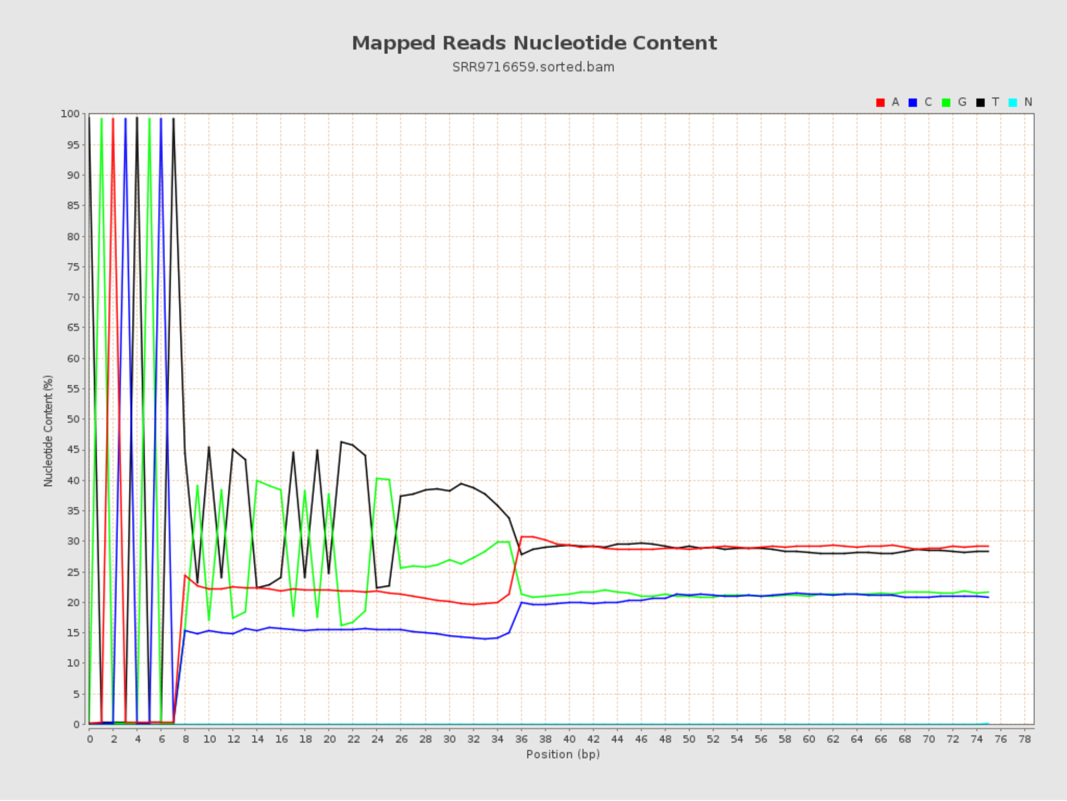
6. Results : Genome Fraction Coverage



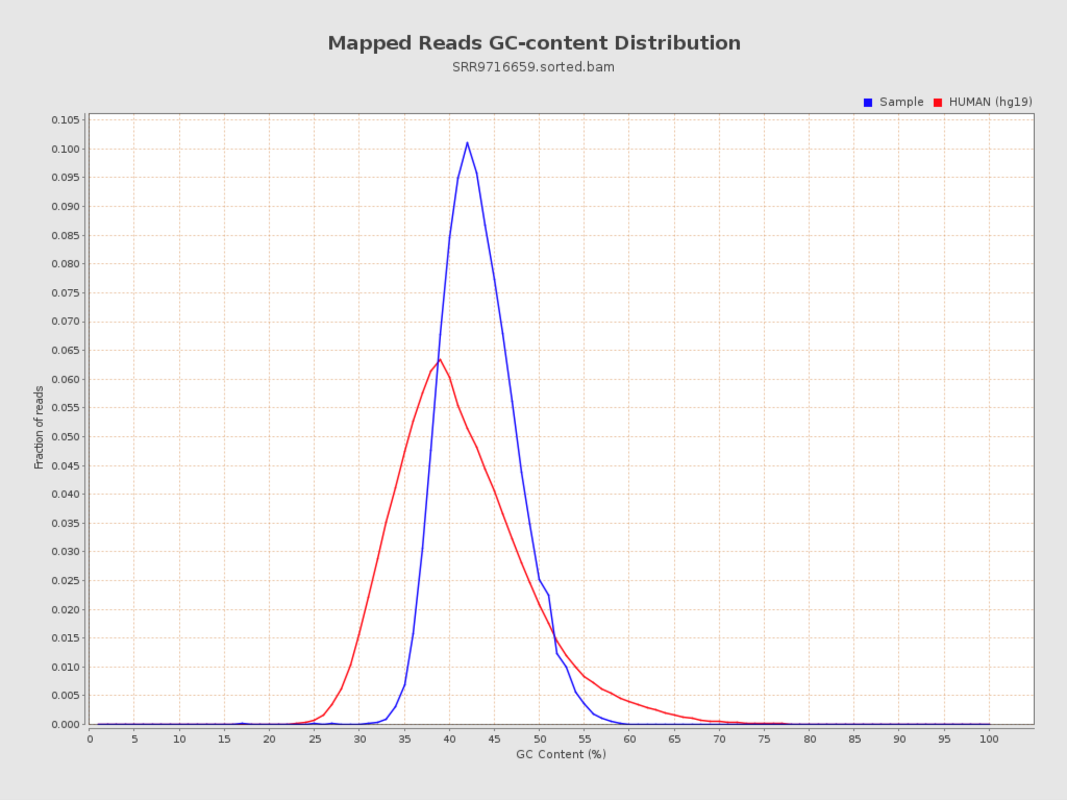
7. Results : Duplication Rate Histogram



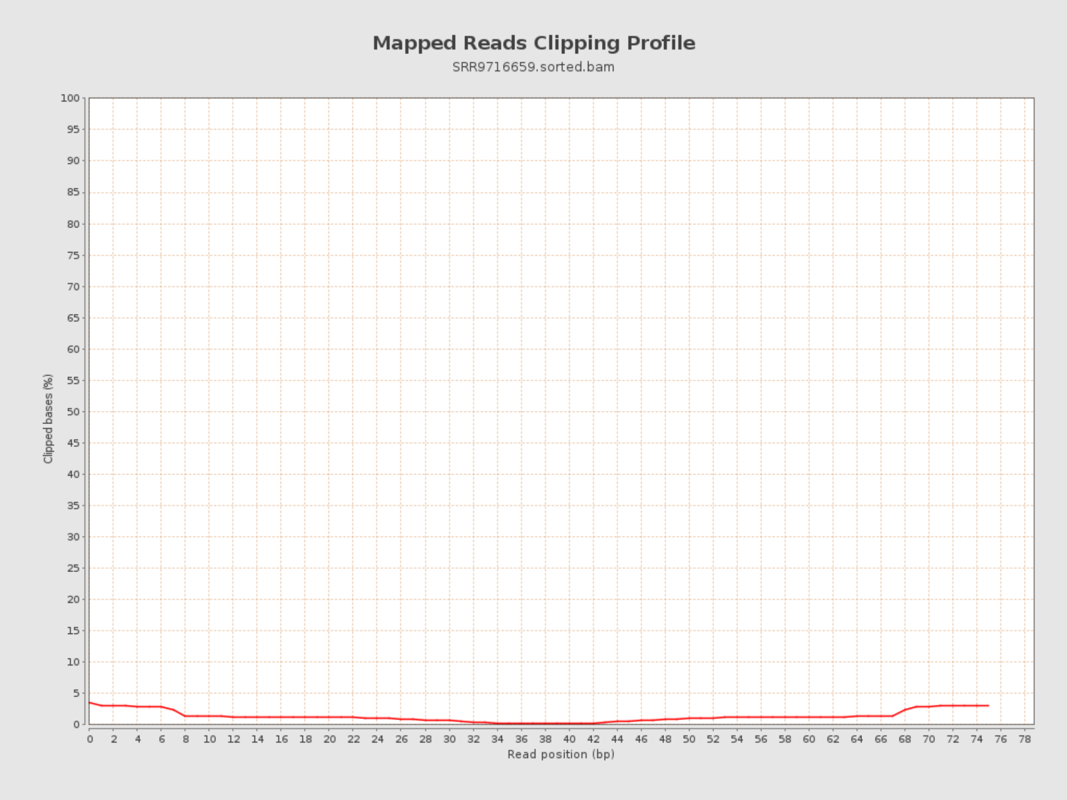
8. Results : Mapped Reads Nucleotide Content



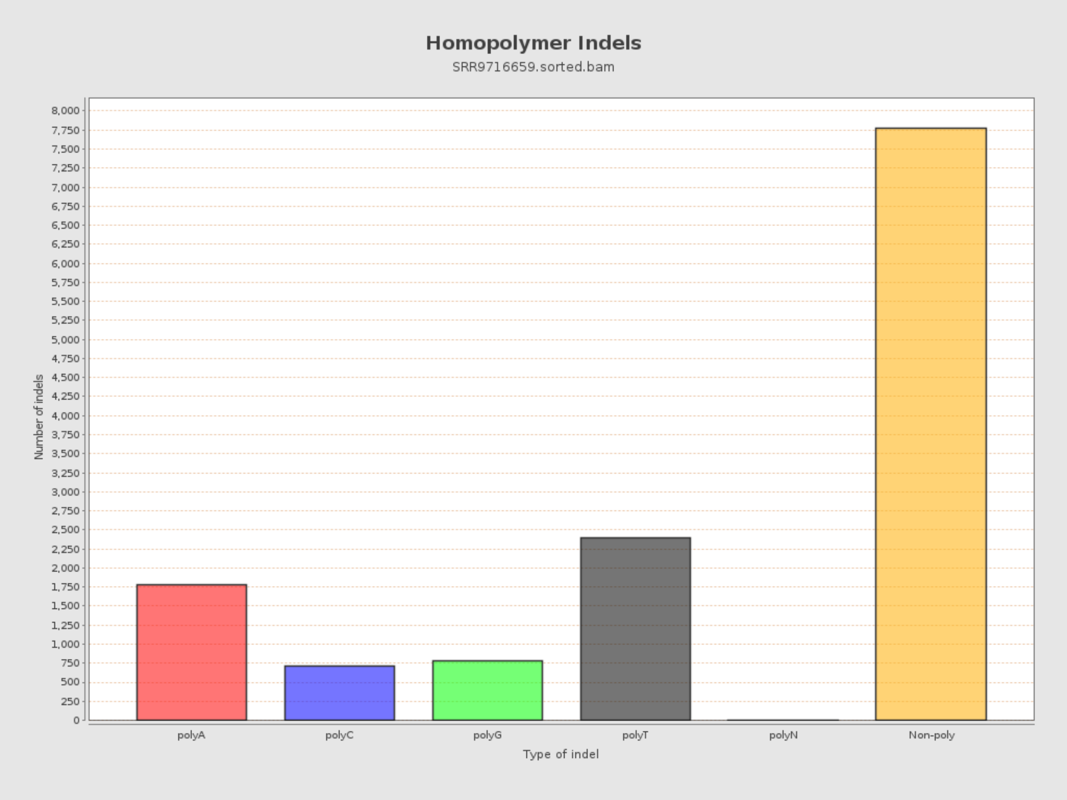
9. Results : Mapped Reads GC-content Distribution



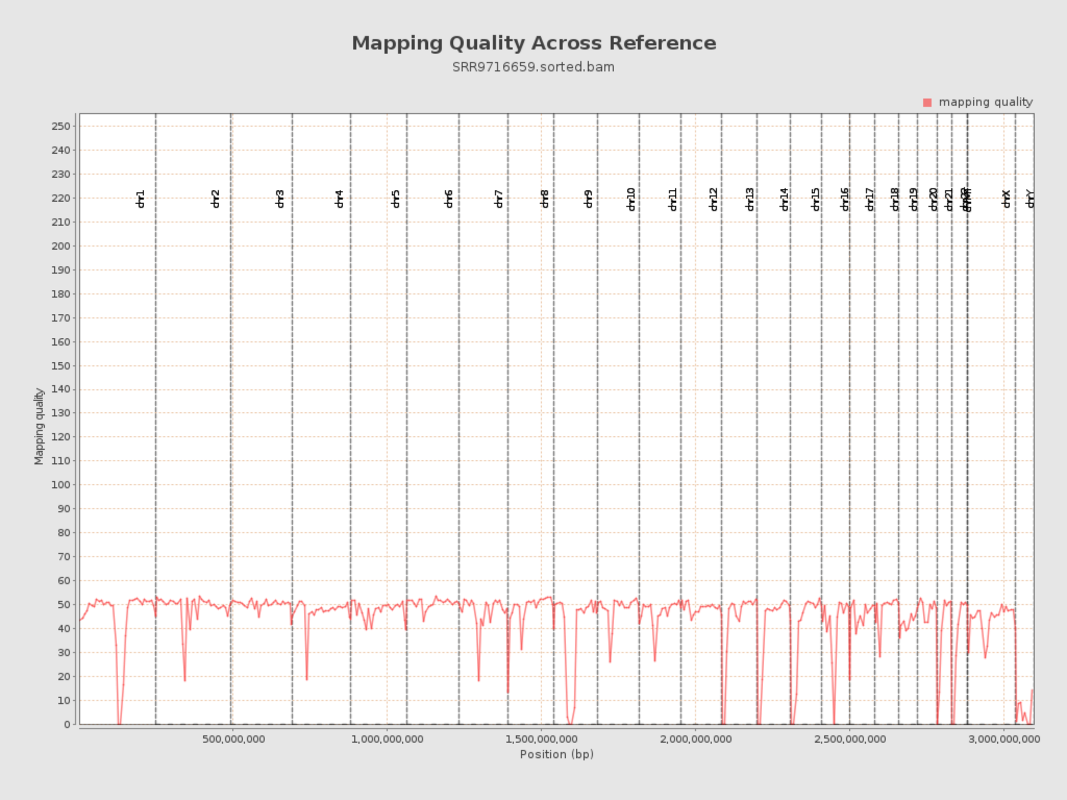
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram