Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:03:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716645.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_SRR9716645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716645.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:03:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716645.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,116,911
Mapped reads	1,005,834 / 90.05%
Unmapped reads	111,077 / 9.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,075 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	30,086 / 2.69%
Duplication rate	2.12%
Clipped reads	1,007,160 / 90.17%

2.2. ACGT Content

Number/percentage of A's	14,340,336 / 24.94%
Number/percentage of C's	10,458,822 / 18.19%
Number/percentage of T's	18,854,606 / 32.79%
Number/percentage of G's	13,850,724 / 24.09%
Number/percentage of N's	1,049 / 0%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0186

Standard Deviation	0.1972

2.4. Mapping Quality

Mean Mapping Quality	44.14

2.5. Mismatches and indels

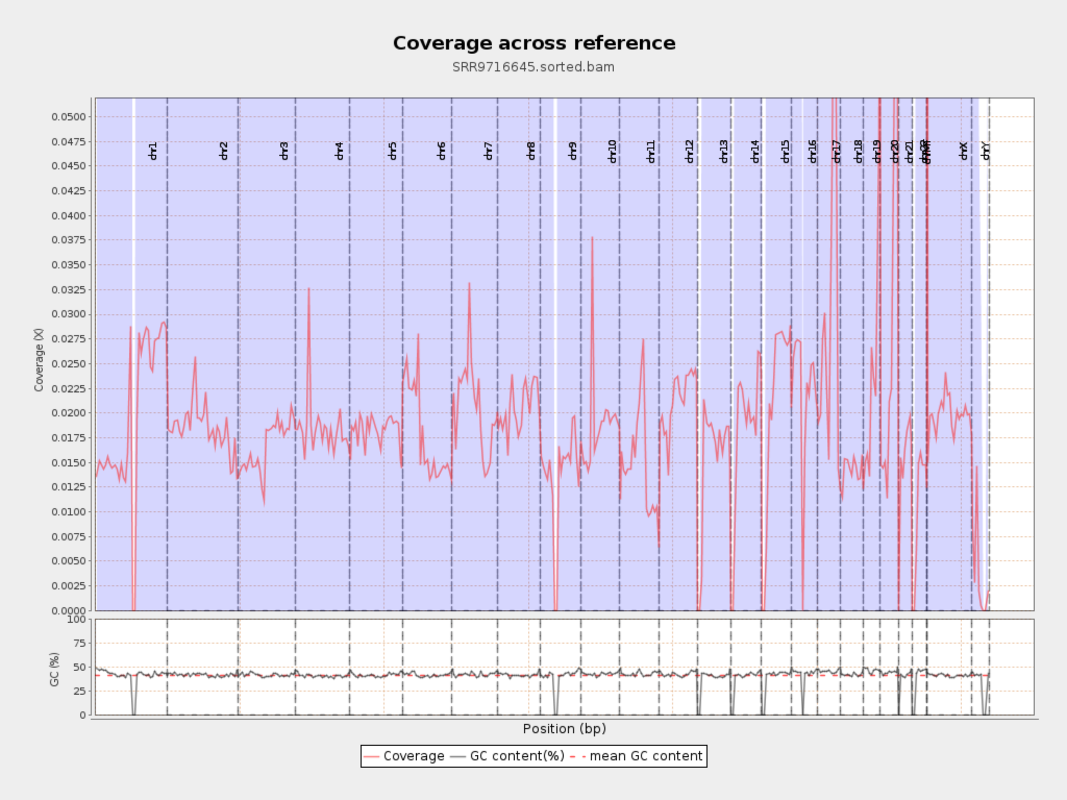
General error rate	0.53%
Mismatches	300,156
Insertions	3,820
Mapped reads with at least one insertion	0.38%
Deletions	10,815
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.71%

2.6. Chromosome stats

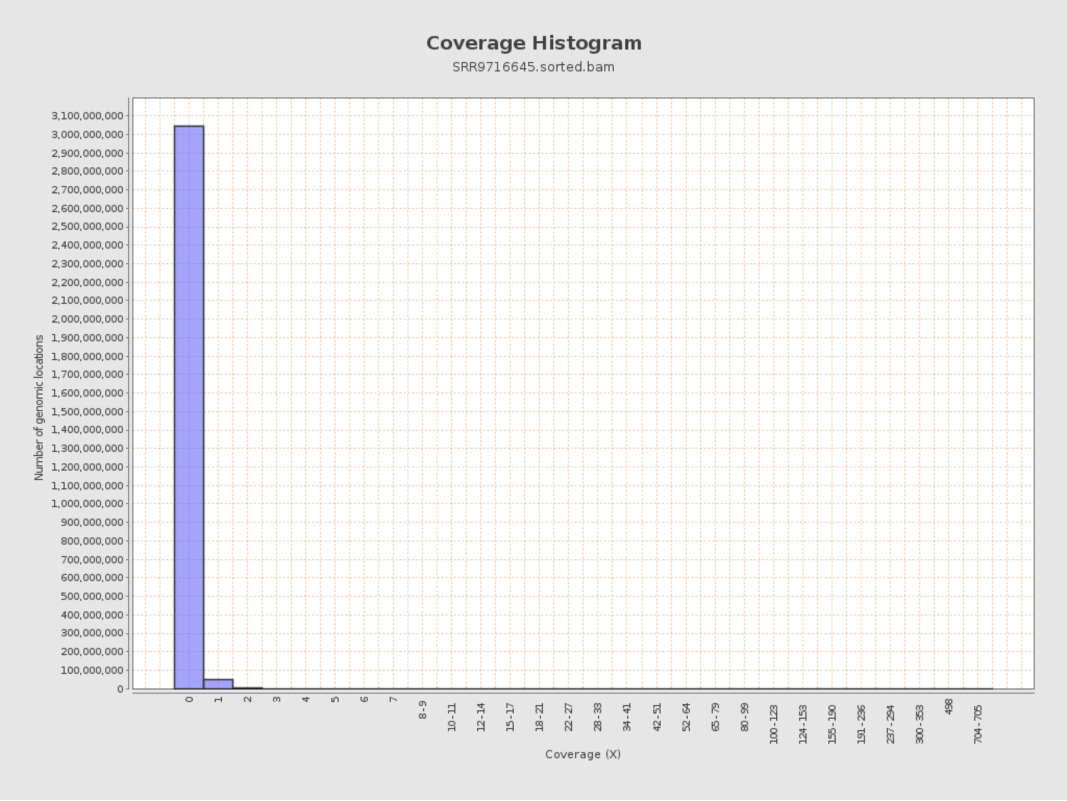
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4856694	0.0195	0.2756
chr2	243199373	4505511	0.0185	0.3124
chr3	198022430	3288280	0.0166	0.1372
chr4	191154276	3539231	0.0185	0.1625
chr5	180915260	3330315	0.0184	0.1438
chr6	171115067	3053897	0.0178	0.1621
chr7	159138663	3286410	0.0207	0.2376

chr8	146364022	3012400	0.0206	0.2314
chr9	141213431	1922968	0.0136	0.1467
chr10	135534747	2561461	0.0189	0.2058
chr11	135006516	2045448	0.0152	0.1555
chr12	133851895	2848475	0.0213	0.1552
chr13	115169878	1737113	0.0151	0.1301
chr14	107349540	1935213	0.018	0.1436
chr15	102531392	2121826	0.0207	0.154
chr16	90354753	1968059	0.0218	0.1625
chr17	81195210	2479747	0.0305	0.1906
chr18	78077248	1102581	0.0141	0.2145
chr19	59128983	1465398	0.0248	0.2402
chr20	63025520	1859516	0.0295	0.187
chr21	48129895	728368	0.0151	0.1491
chr22	51304566	538122	0.0105	0.1085
chrMT	16571	42862	2.5866	2.2026
chrX	155270560	3079103	0.0198	0.1587
chrY	59373566	213850	0.0036	0.1644

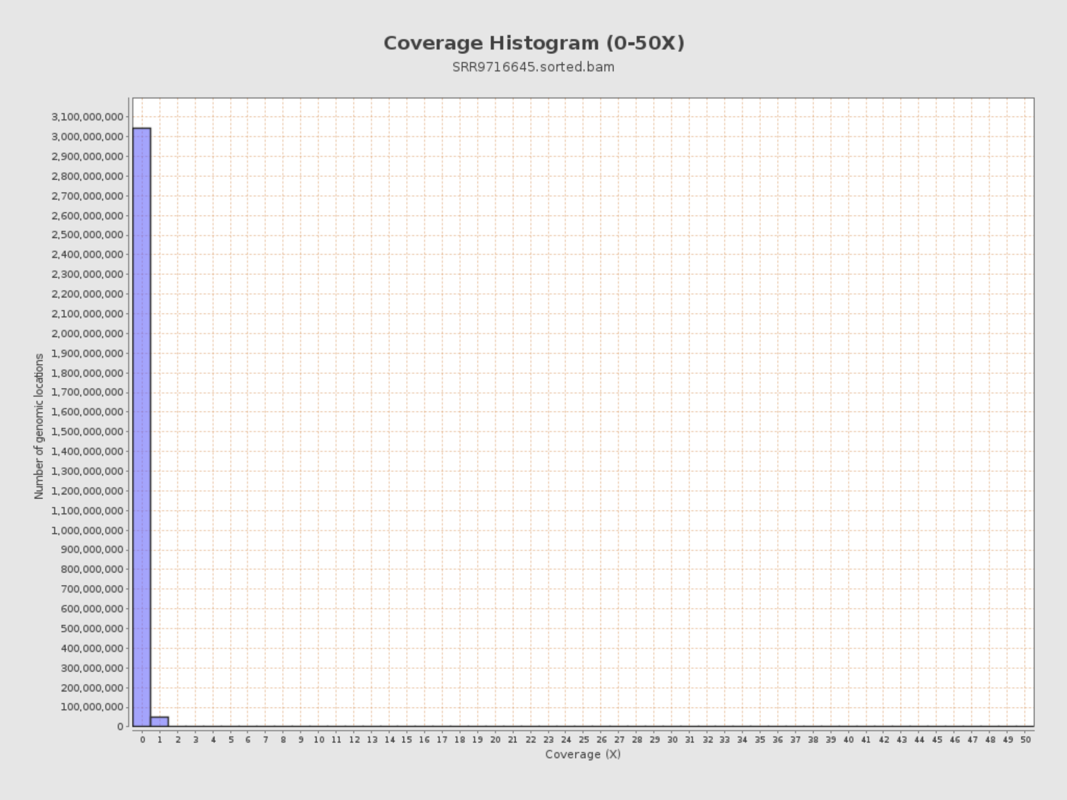
3. Results : Coverage across reference



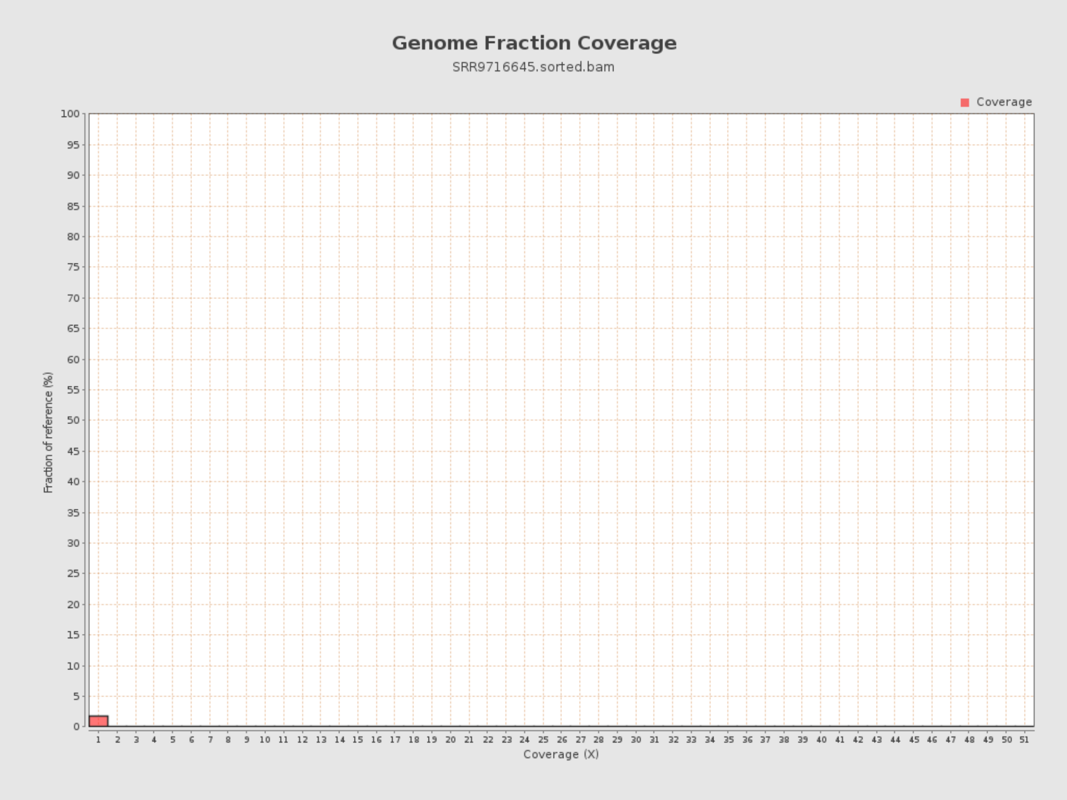
4. Results : Coverage Histogram



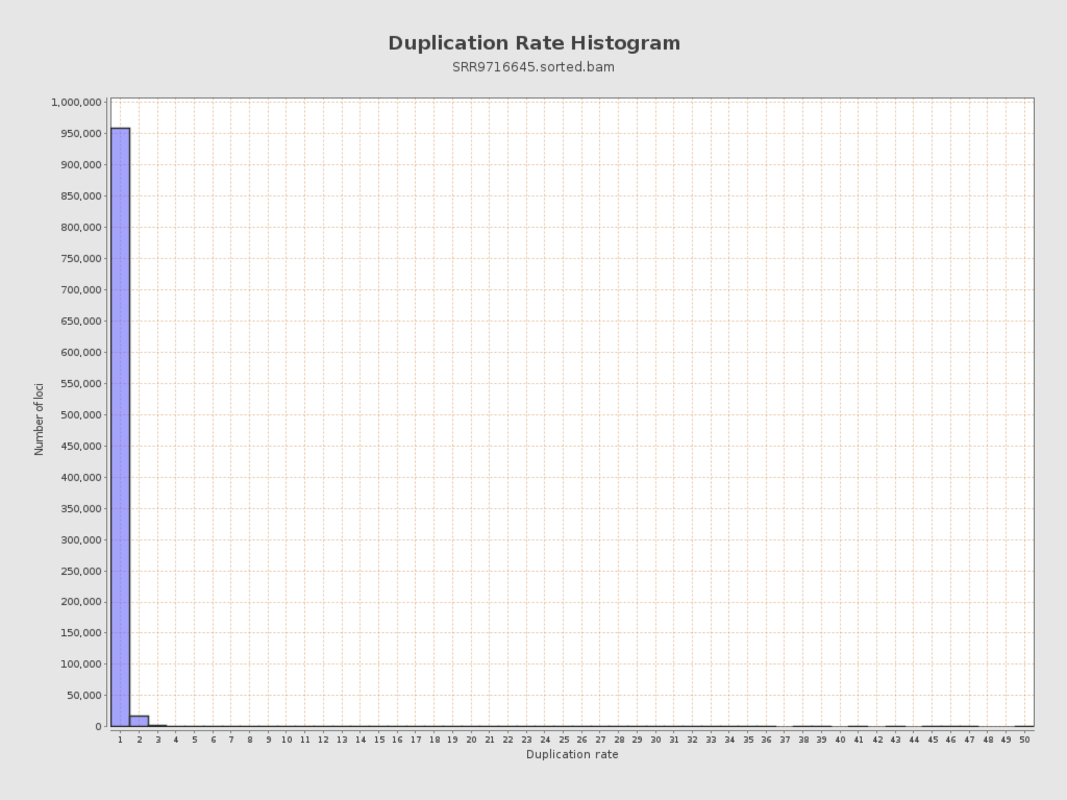
5. Results : Coverage Histogram (0-50X)



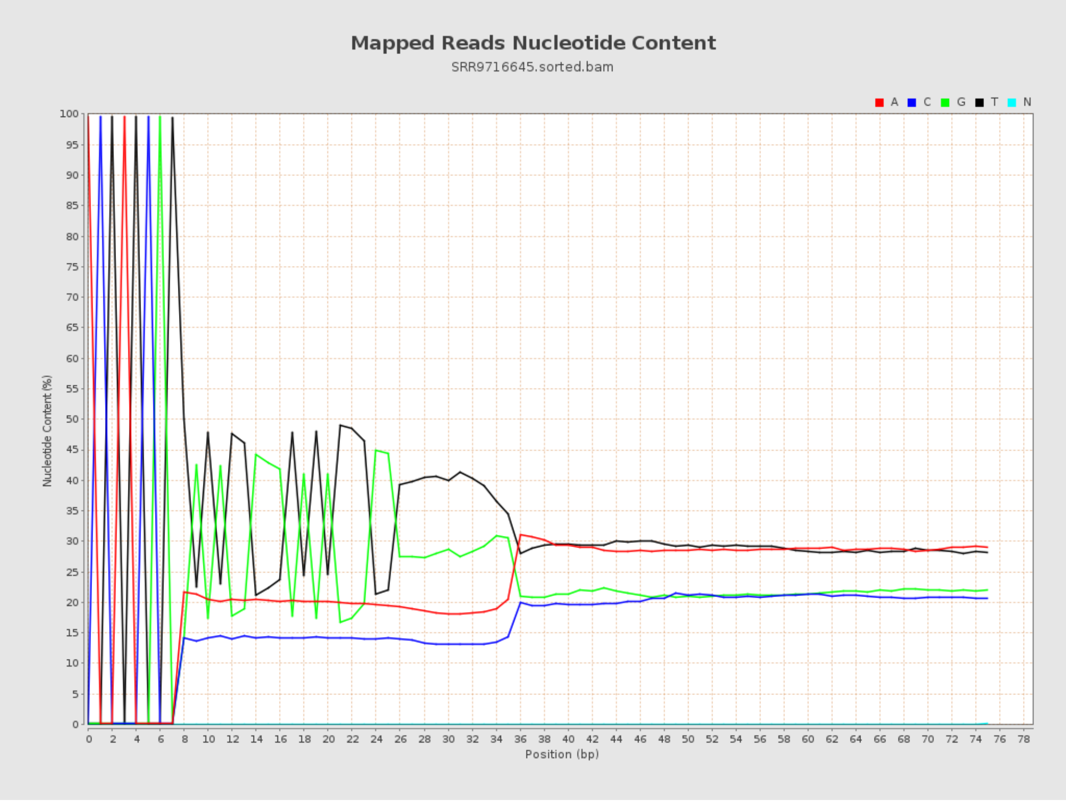
6. Results : Genome Fraction Coverage



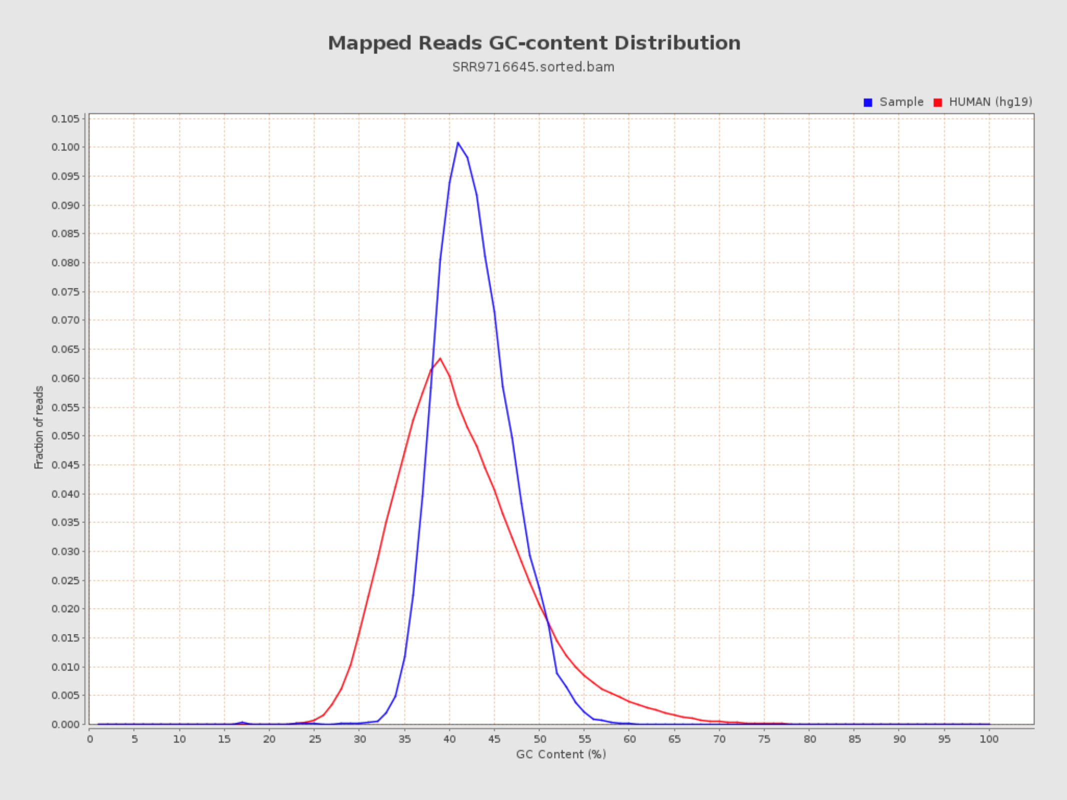
7. Results : Duplication Rate Histogram



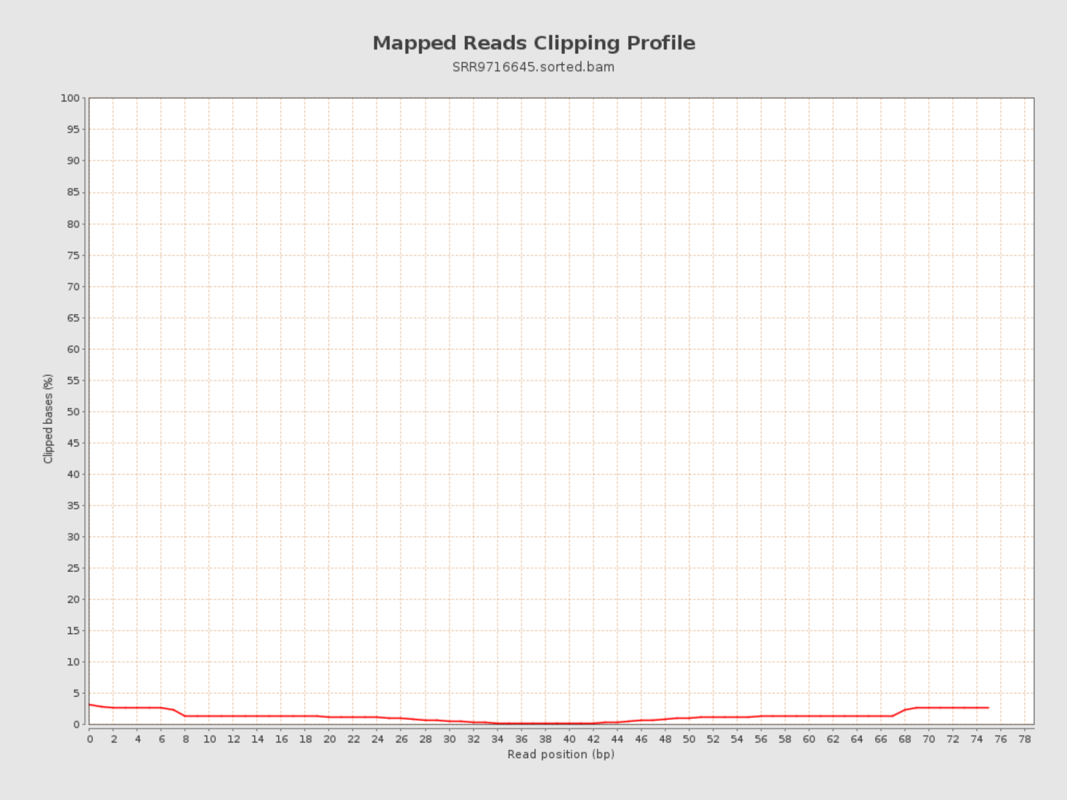
8. Results : Mapped Reads Nucleotide Content



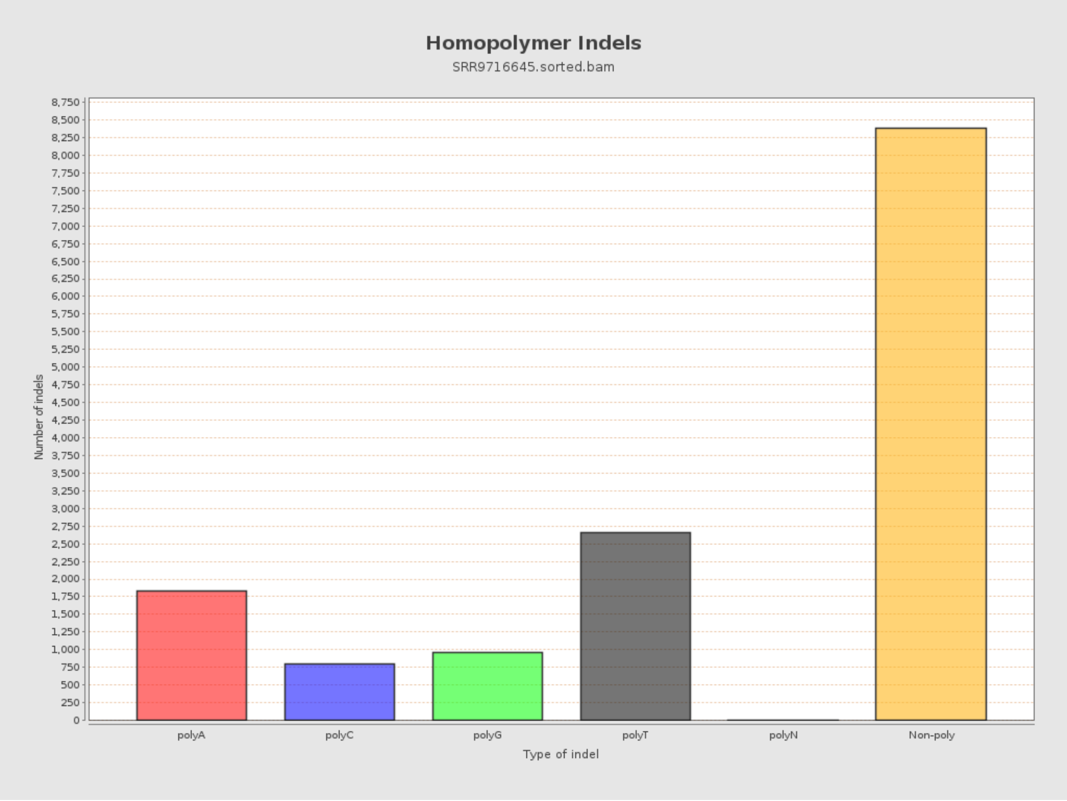
9. Results : Mapped Reads GC-content Distribution



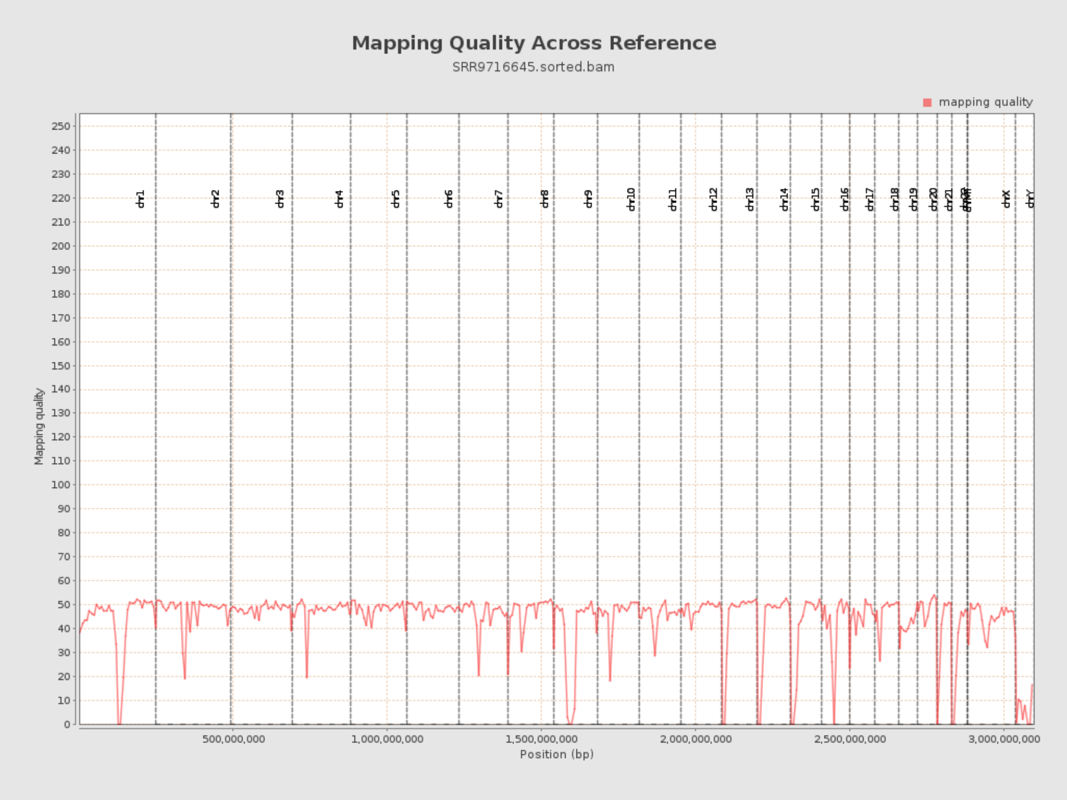
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram