Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:46:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716825.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_SRR9716825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:46:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,643,367
Mapped reads	1,211,233 / 73.7%
Unmapped reads	432,134 / 26.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,430 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	122,040 / 7.43%
Duplication rate	8.69%
Clipped reads	1,210,601 / 73.67%

2.2. ACGT Content

Number/percentage of A's	13,973,475 / 22.14%
Number/percentage of C's	10,846,810 / 17.18%
Number/percentage of T's	20,214,281 / 32.02%
Number/percentage of G's	18,086,680 / 28.65%
Number/percentage of N's	1,158 / 0%
GC Percentage	45.84%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.1964

2.4. Mapping Quality

Mean Mapping Quality	43

2.5. Mismatches and indels

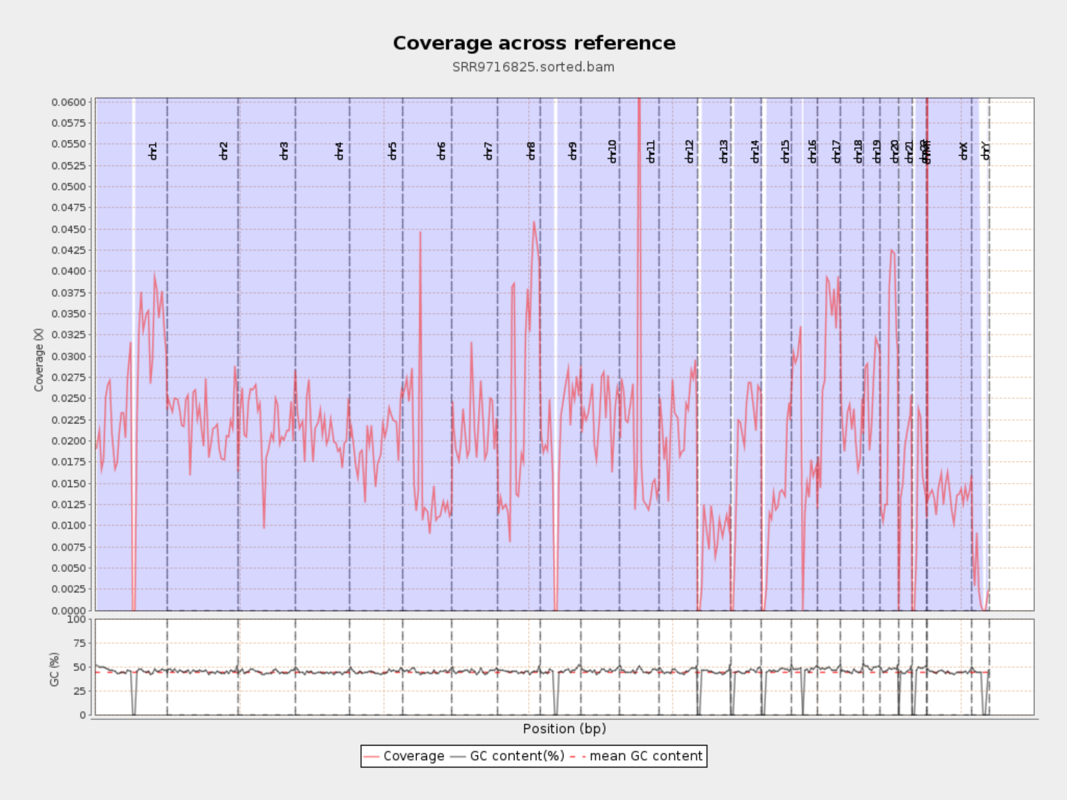
General error rate	0.67%
Mismatches	416,020
Insertions	3,747
Mapped reads with at least one insertion	0.31%
Deletions	8,618
Mapped reads with at least one deletion	0.71%
Homopolymer indels	40.71%

2.6. Chromosome stats

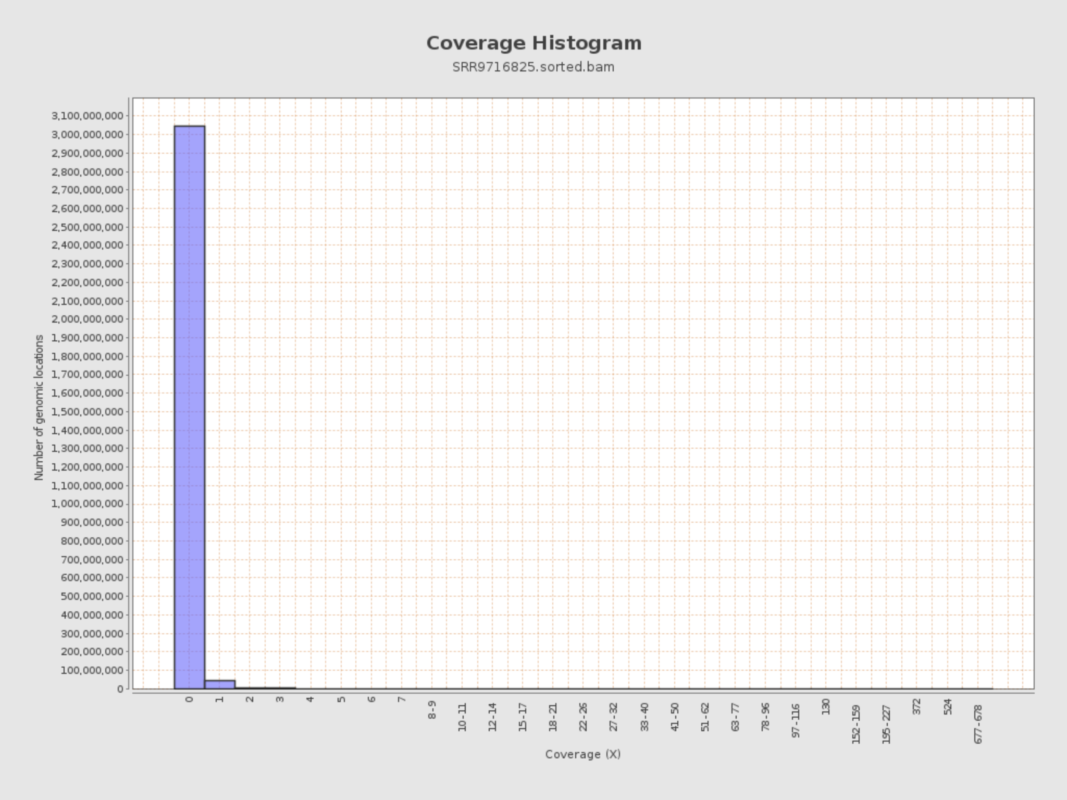
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6407500	0.0257	0.2109
chr2	243199373	5457549	0.0224	0.3191
chr3	198022430	4306858	0.0217	0.1797
chr4	191154276	4096559	0.0214	0.1796
chr5	180915260	3586453	0.0198	0.1707
chr6	171115067	2835770	0.0166	0.1872
chr7	159138663	3447170	0.0217	0.1897

chr8	146364022	3710432	0.0254	0.1989
chr9	141213431	2865004	0.0203	0.1831
chr10	135534747	3192613	0.0236	0.2004
chr11	135006516	2950282	0.0219	0.1954
chr12	133851895	3006393	0.0225	0.1832
chr13	115169878	946195	0.0082	0.1119
chr14	107349540	2098682	0.0195	0.1704
chr15	102531392	1240205	0.0121	0.1347
chr16	90354753	1782500	0.0197	0.1755
chr17	81195210	2530040	0.0312	0.2215
chr18	78077248	1659664	0.0213	0.1996
chr19	59128983	1589103	0.0269	0.2393
chr20	63025520	1641731	0.026	0.2038
chr21	48129895	834820	0.0173	0.1627
chr22	51304566	659645	0.0129	0.1409
chrMT	16571	3881	0.2342	0.5771
chrX	155270560	2119378	0.0136	0.1459
chrY	59373566	168637	0.0028	0.0769

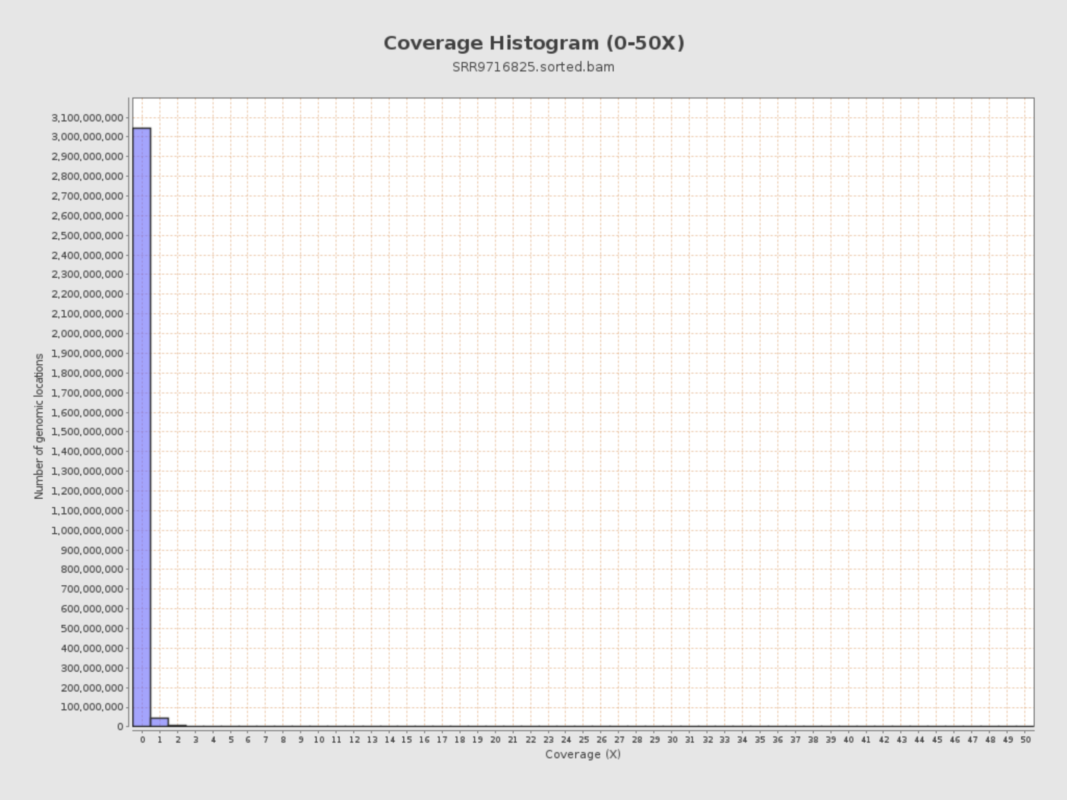
3. Results : Coverage across reference



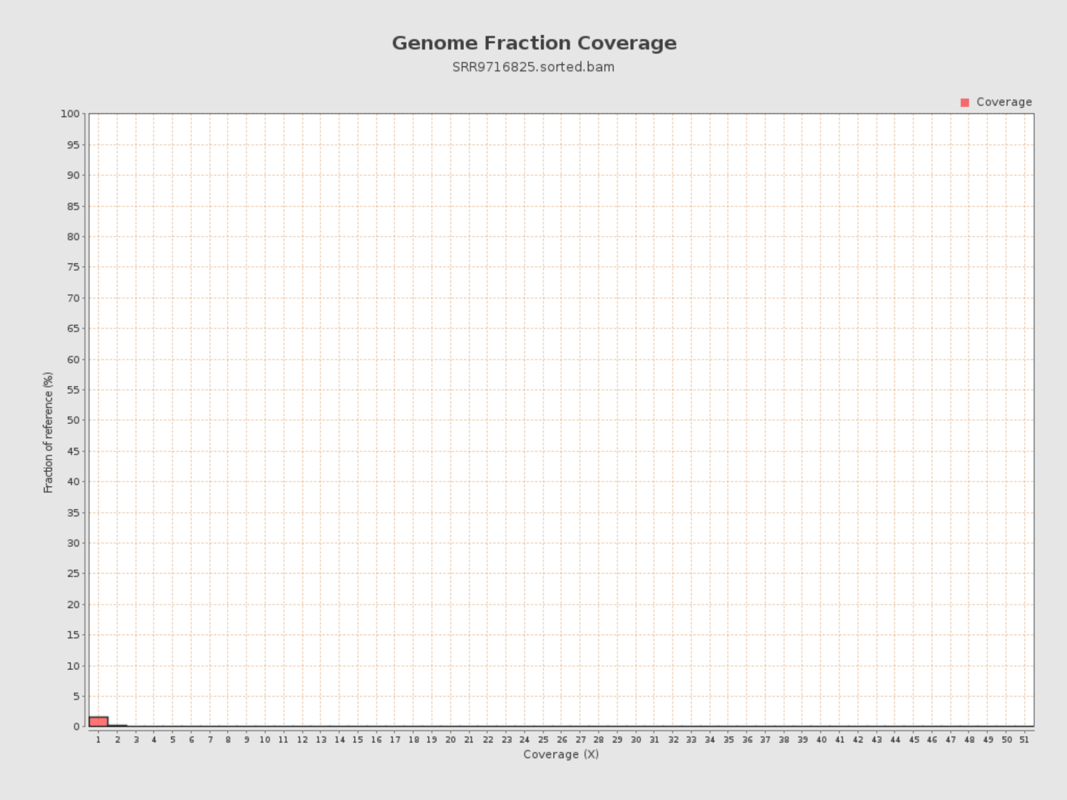
4. Results : Coverage Histogram



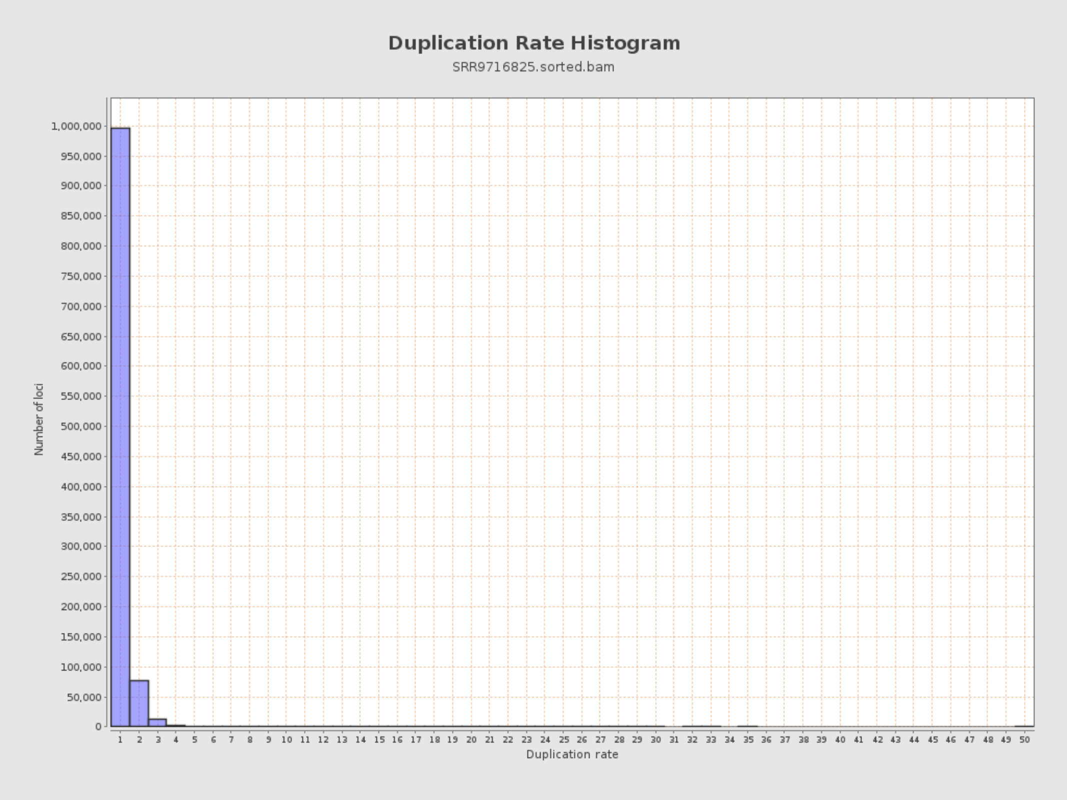
5. Results : Coverage Histogram (0-50X)



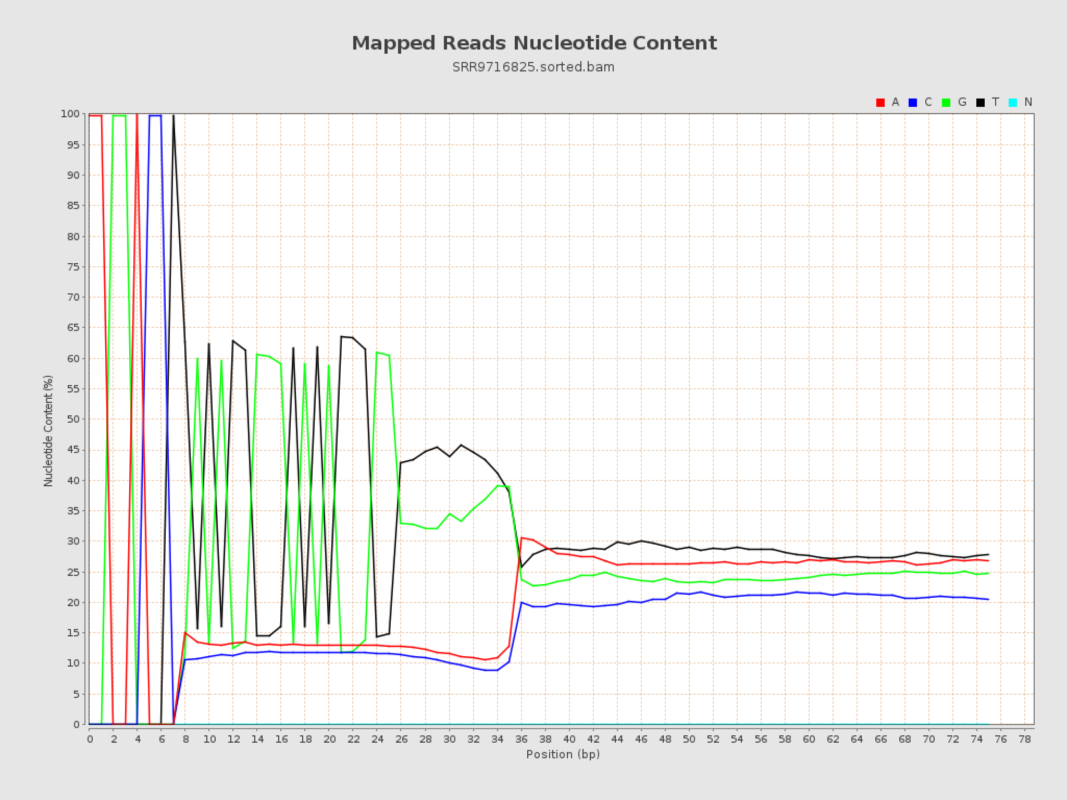
6. Results : Genome Fraction Coverage



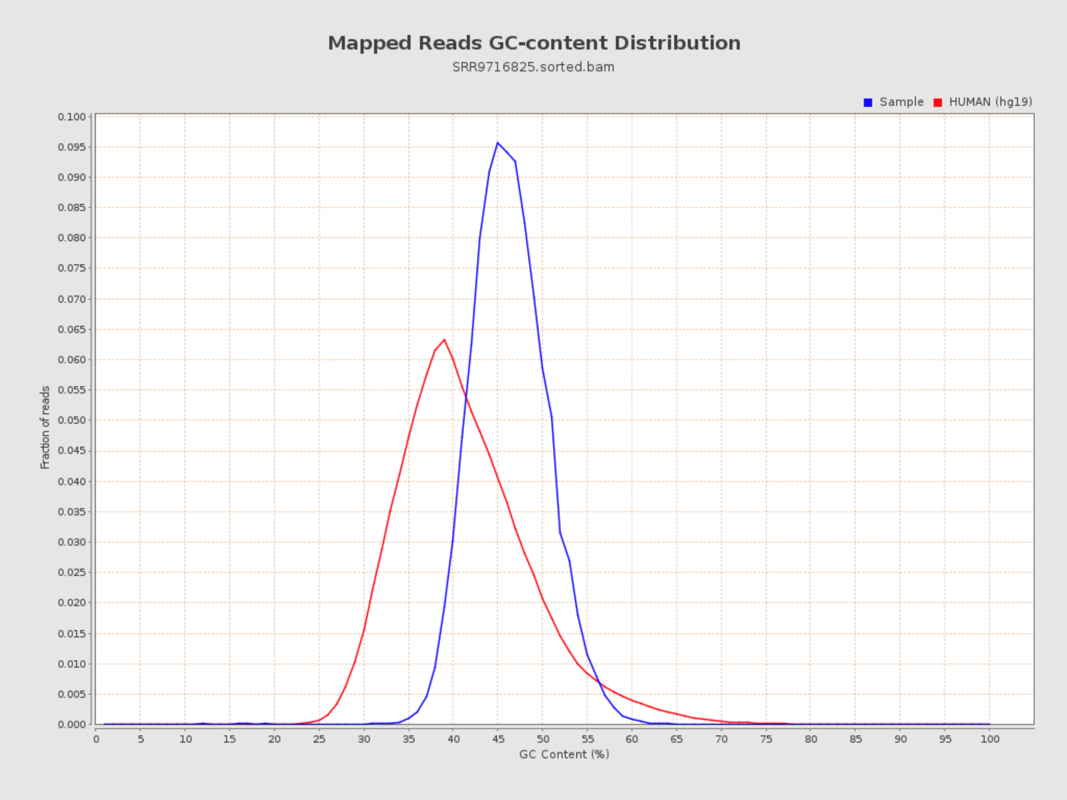
7. Results : Duplication Rate Histogram



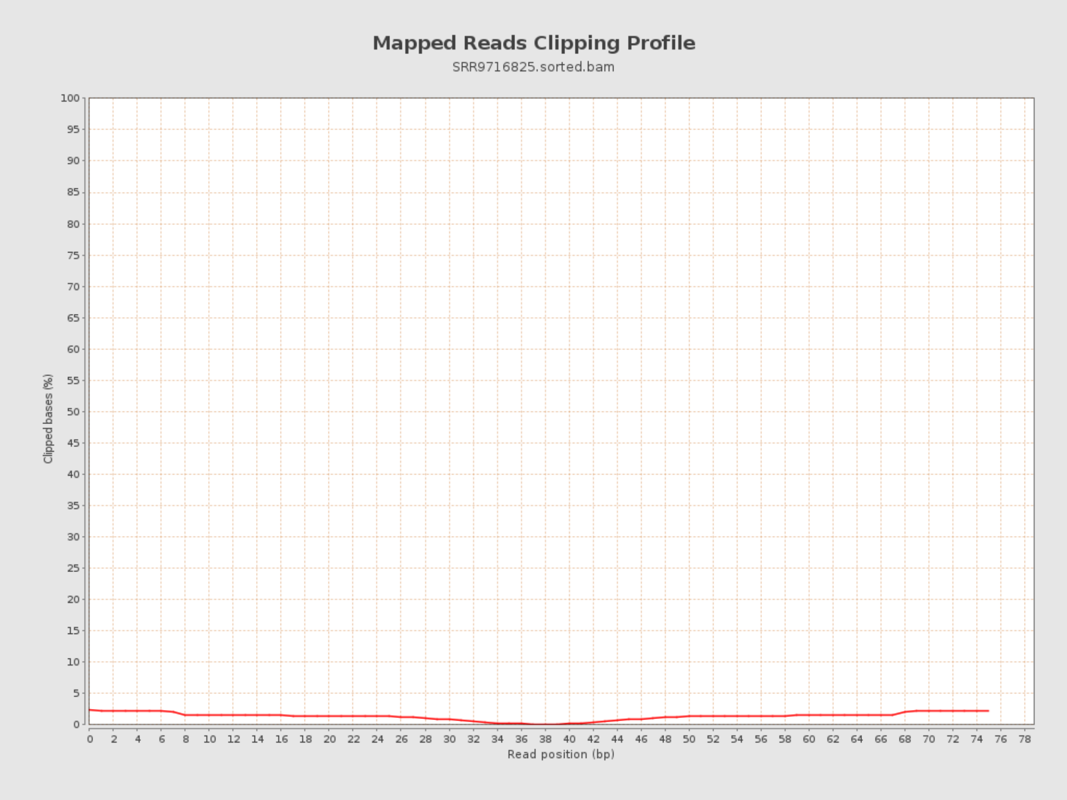
8. Results : Mapped Reads Nucleotide Content



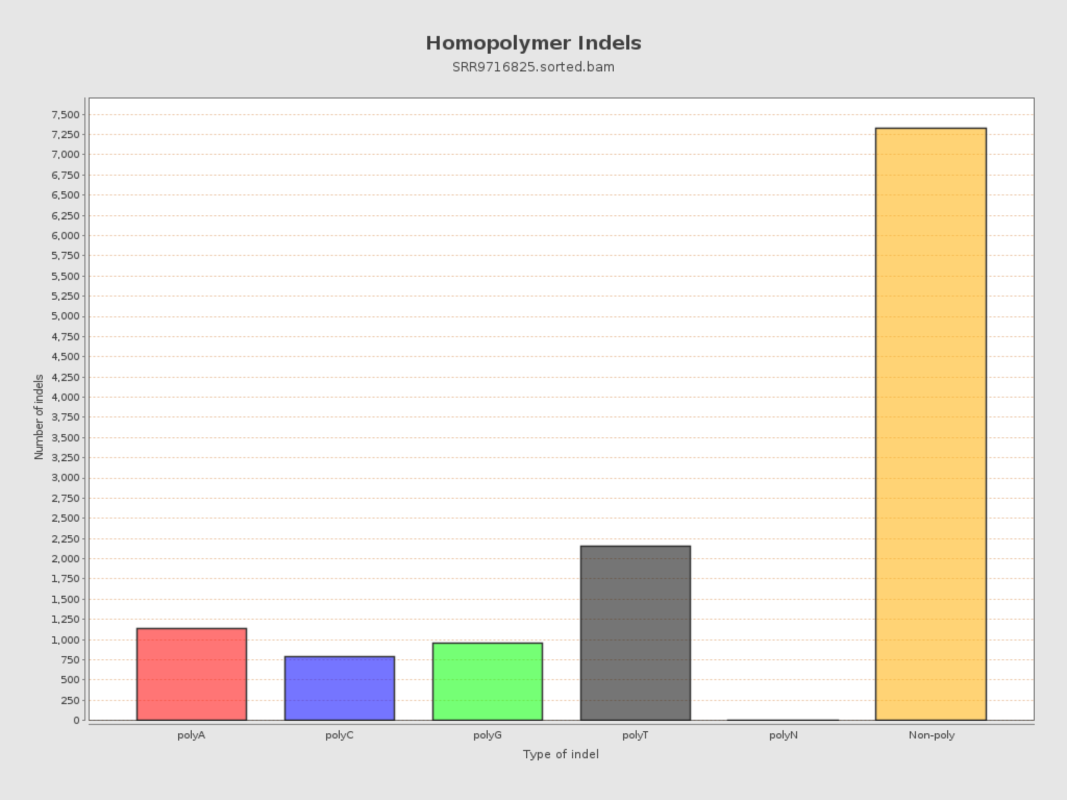
9. Results : Mapped Reads GC-content Distribution



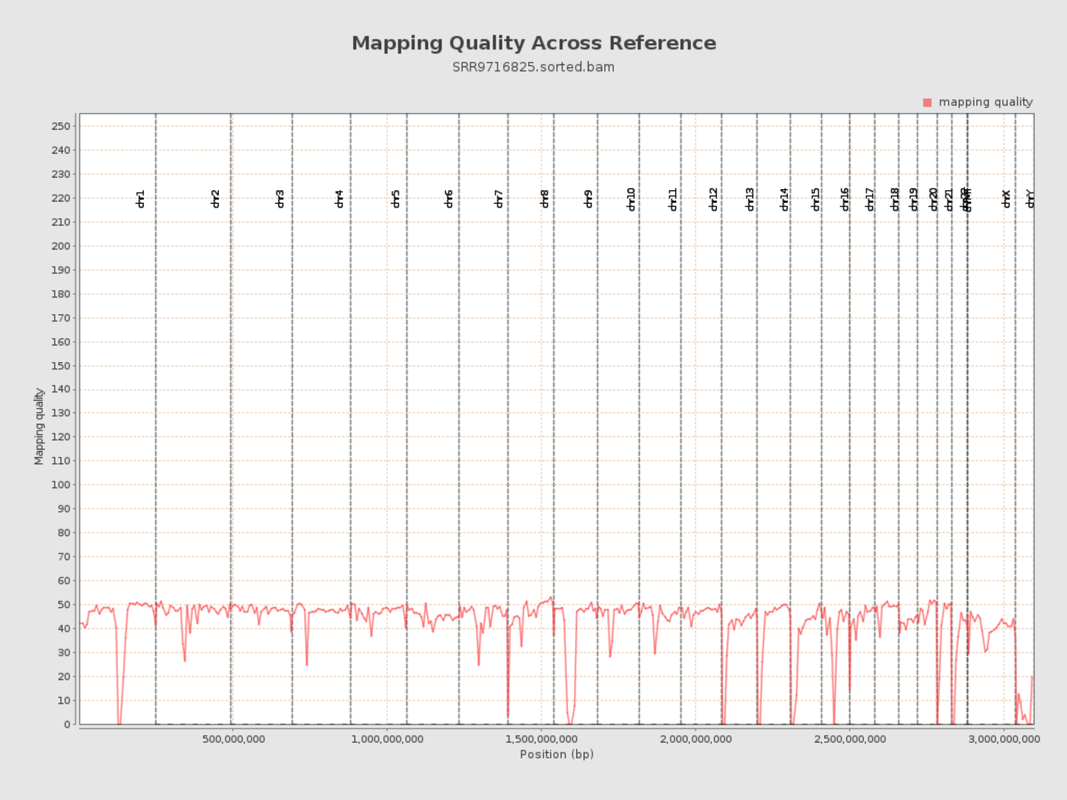
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram