Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:47:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716426.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_SRR9716426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716426.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:47:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716426.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,583,676
Mapped reads	1,456,243 / 91.95%
Unmapped reads	127,433 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,217 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,116 / 3.67%
Duplication rate	2.87%
Clipped reads	1,457,547 / 92.04%

2.2. ACGT Content

Number/percentage of A's	20,662,719 / 24.44%
Number/percentage of C's	15,021,854 / 17.77%
Number/percentage of T's	28,095,632 / 33.23%
Number/percentage of G's	20,772,900 / 24.57%
Number/percentage of N's	1,599 / 0%
GC Percentage	42.33%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2672

2.4. Mapping Quality

Mean Mapping Quality	44.6

2.5. Mismatches and indels

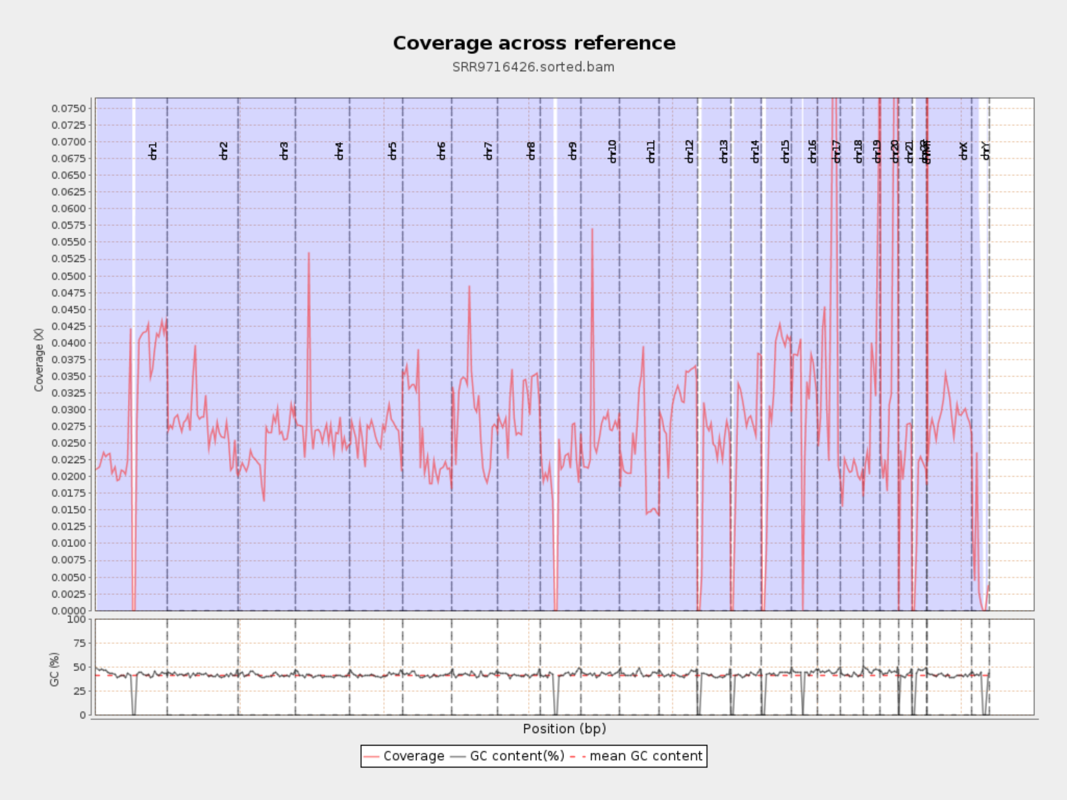
General error rate	0.52%
Mismatches	430,181
Insertions	6,313
Mapped reads with at least one insertion	0.43%
Deletions	16,390
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.26%

2.6. Chromosome stats

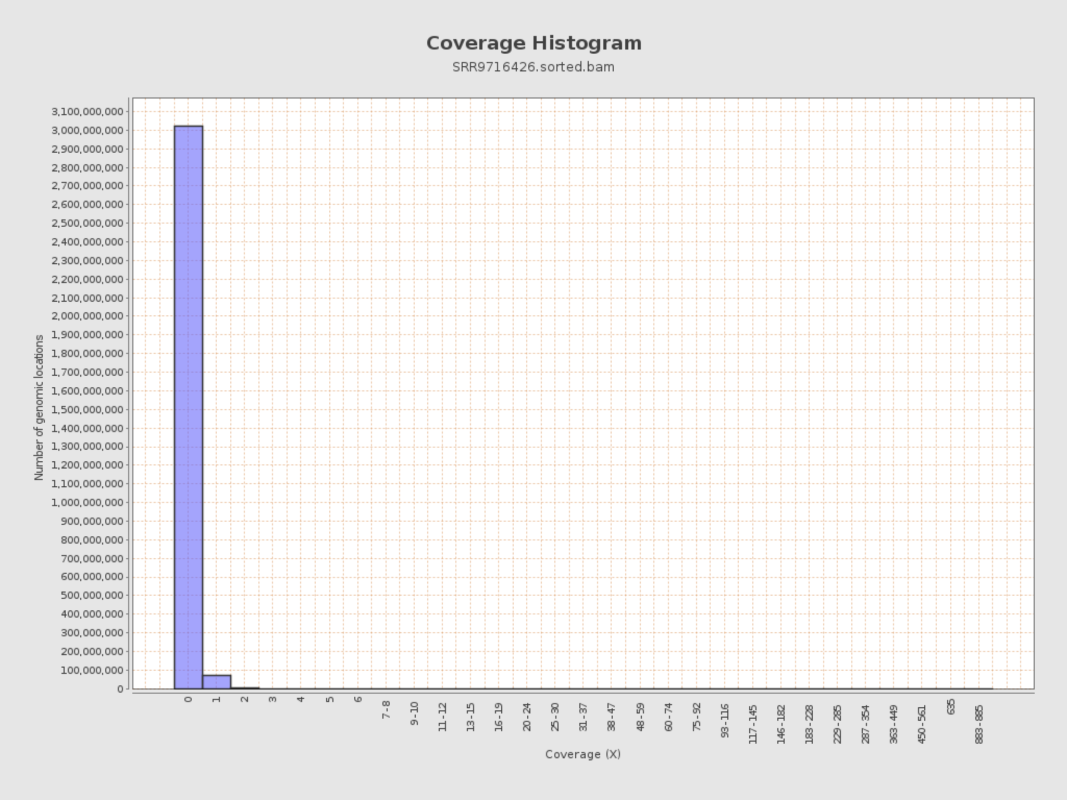
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7196624	0.0289	0.4067
chr2	243199373	6723658	0.0276	0.4052
chr3	198022430	4866297	0.0246	0.1712
chr4	191154276	5239106	0.0274	0.2269
chr5	180915260	4810855	0.0266	0.1771
chr6	171115067	4459653	0.0261	0.2066
chr7	159138663	4717495	0.0296	0.3205

chr8	146364022	4461377	0.0305	0.3362
chr9	141213431	2787240	0.0197	0.1877
chr10	135534747	3734770	0.0276	0.2978
chr11	135006516	3000737	0.0222	0.2048
chr12	133851895	4193615	0.0313	0.1943
chr13	115169878	2524649	0.0219	0.1618
chr14	107349540	2806601	0.0261	0.178
chr15	102531392	3109378	0.0303	0.1901
chr16	90354753	2880414	0.0319	0.2012
chr17	81195210	3657177	0.045	0.2406
chr18	78077248	1597166	0.0205	0.3225
chr19	59128983	2189433	0.037	0.3264
chr20	63025520	2817180	0.0447	0.2402
chr21	48129895	1082399	0.0225	0.2105
chr22	51304566	789297	0.0154	0.1352
chrMT	16571	76546	4.6193	3.2296
chrX	155270560	4524246	0.0291	0.1991
chrY	59373566	335469	0.0057	0.267

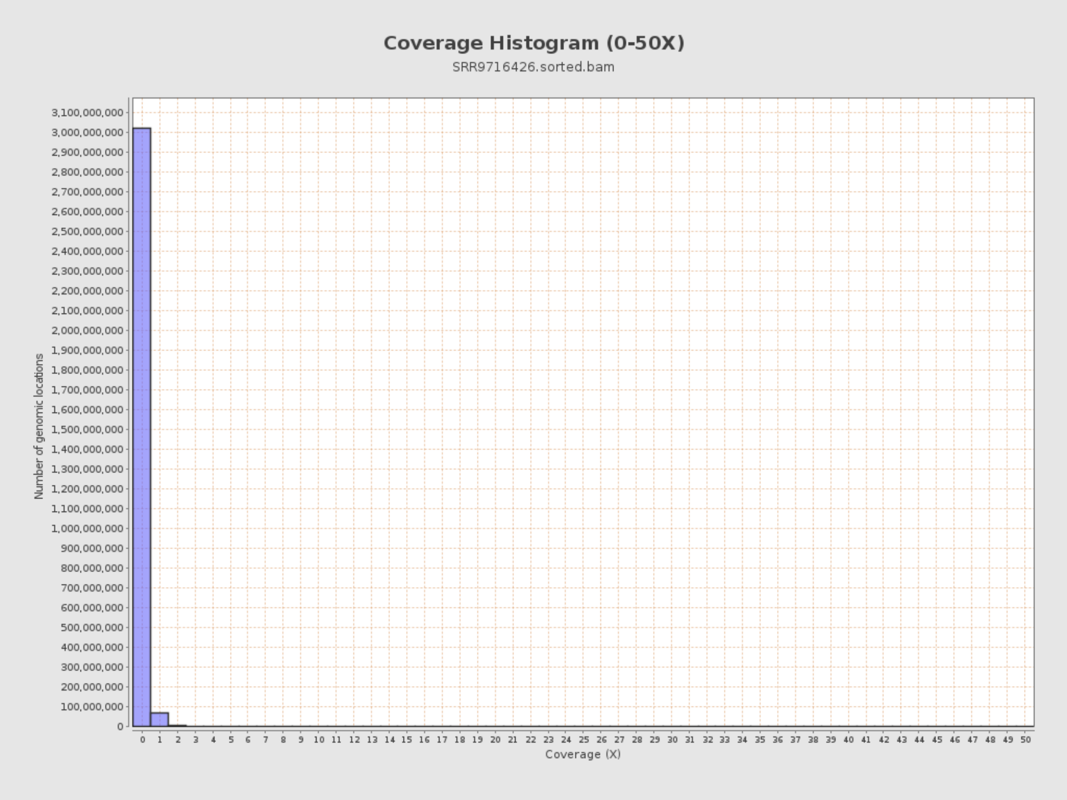
3. Results : Coverage across reference



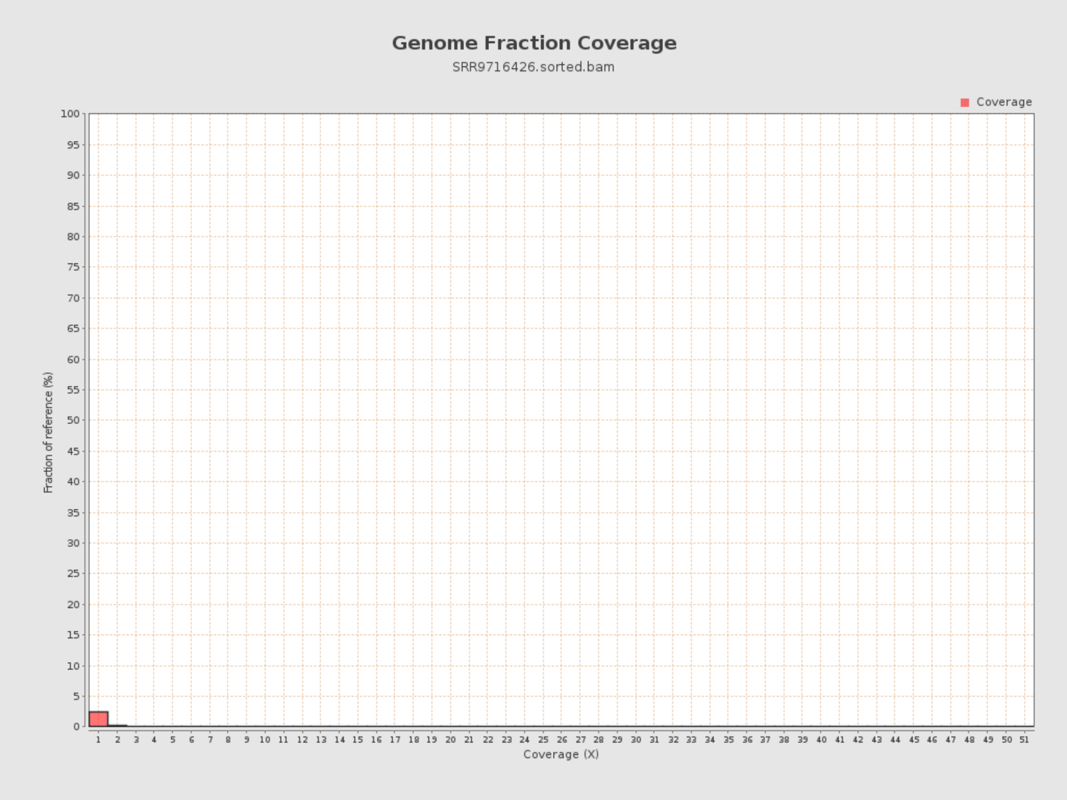
4. Results : Coverage Histogram



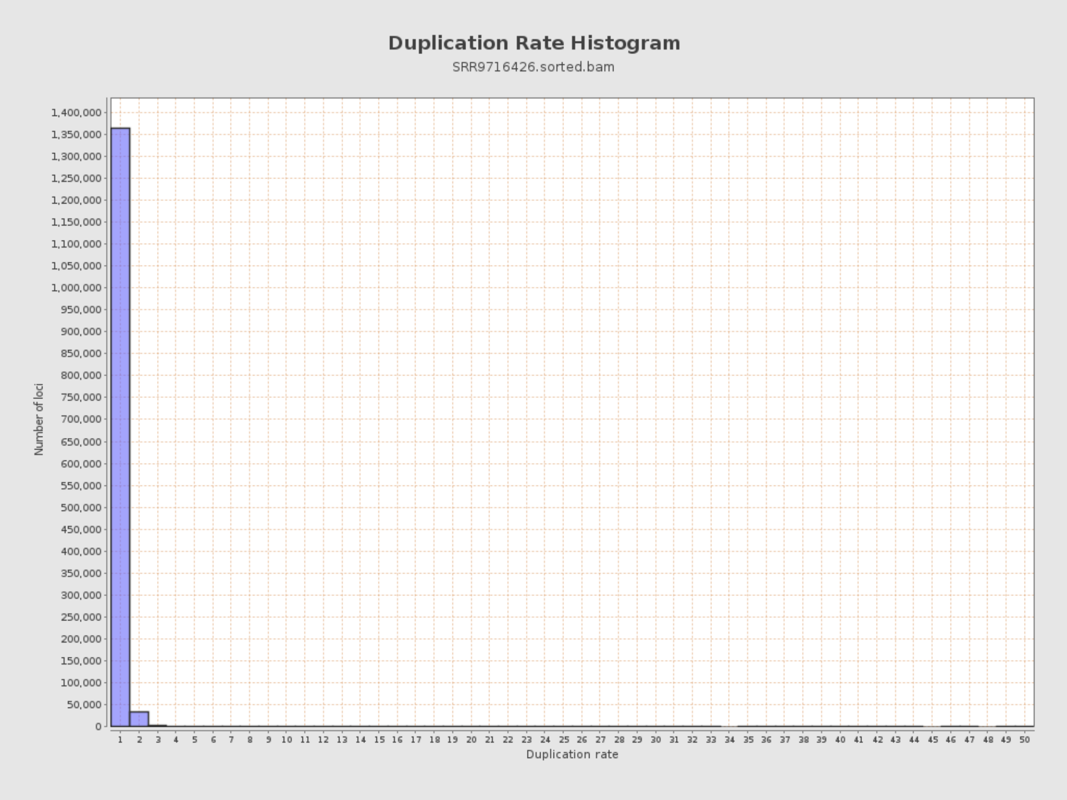
5. Results : Coverage Histogram (0-50X)



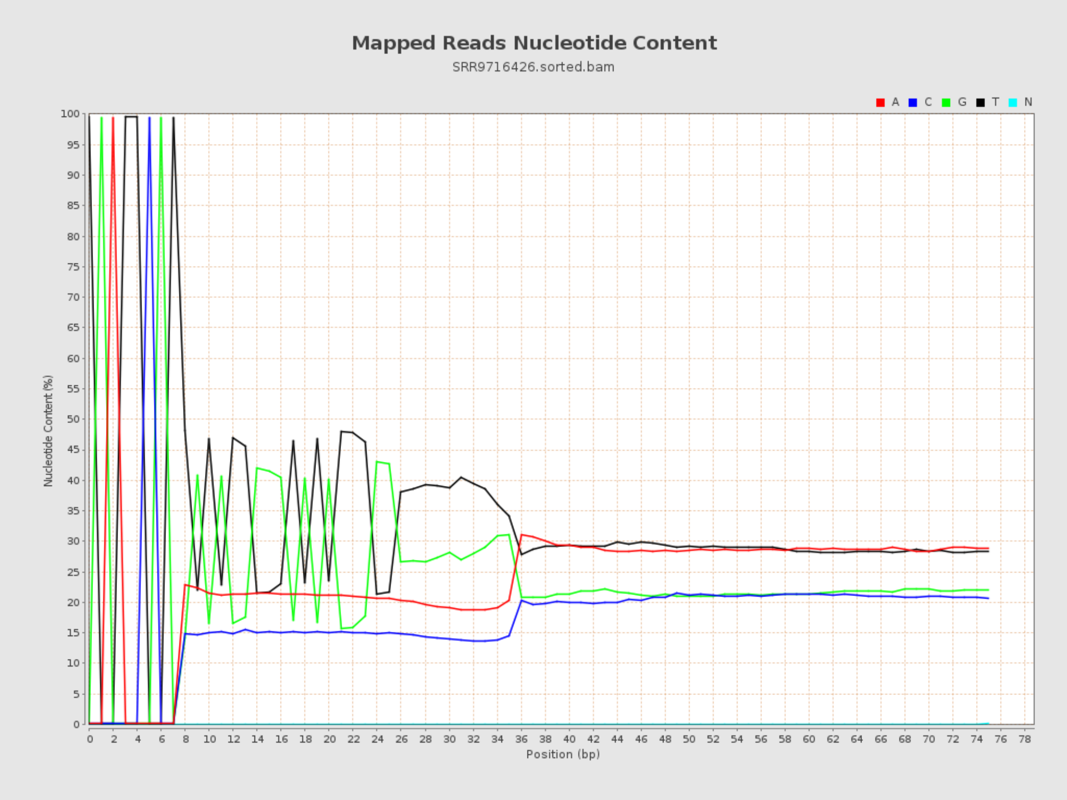
6. Results : Genome Fraction Coverage



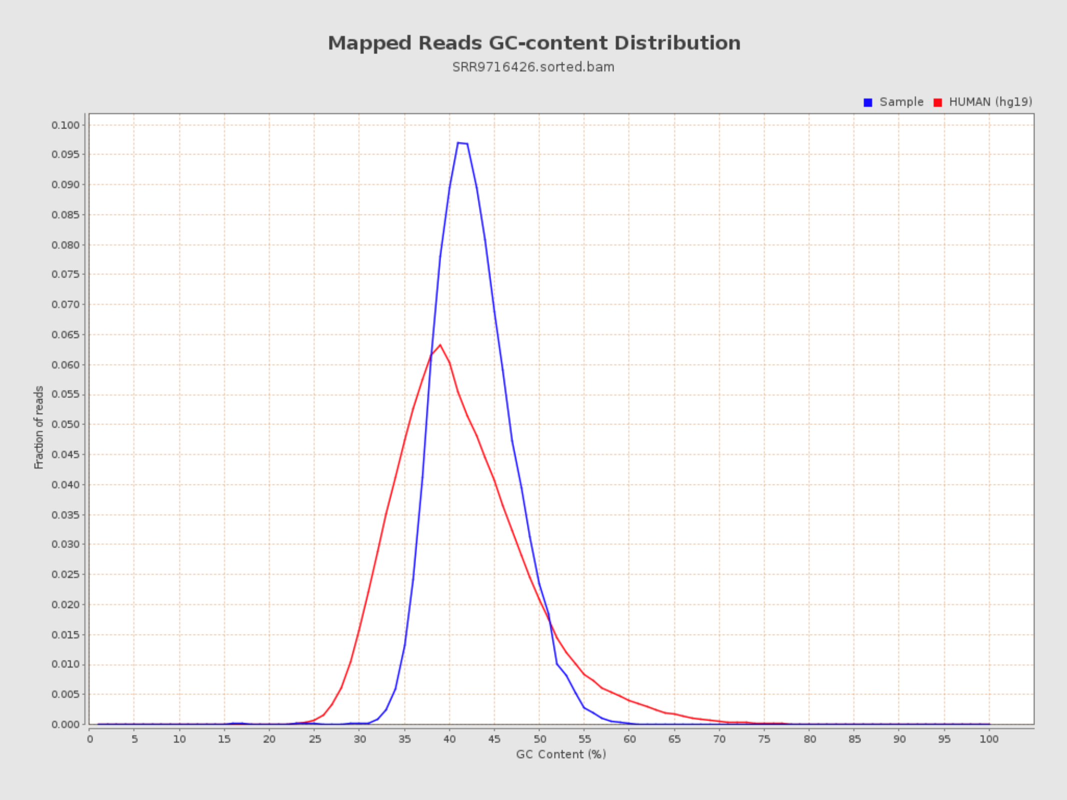
7. Results : Duplication Rate Histogram



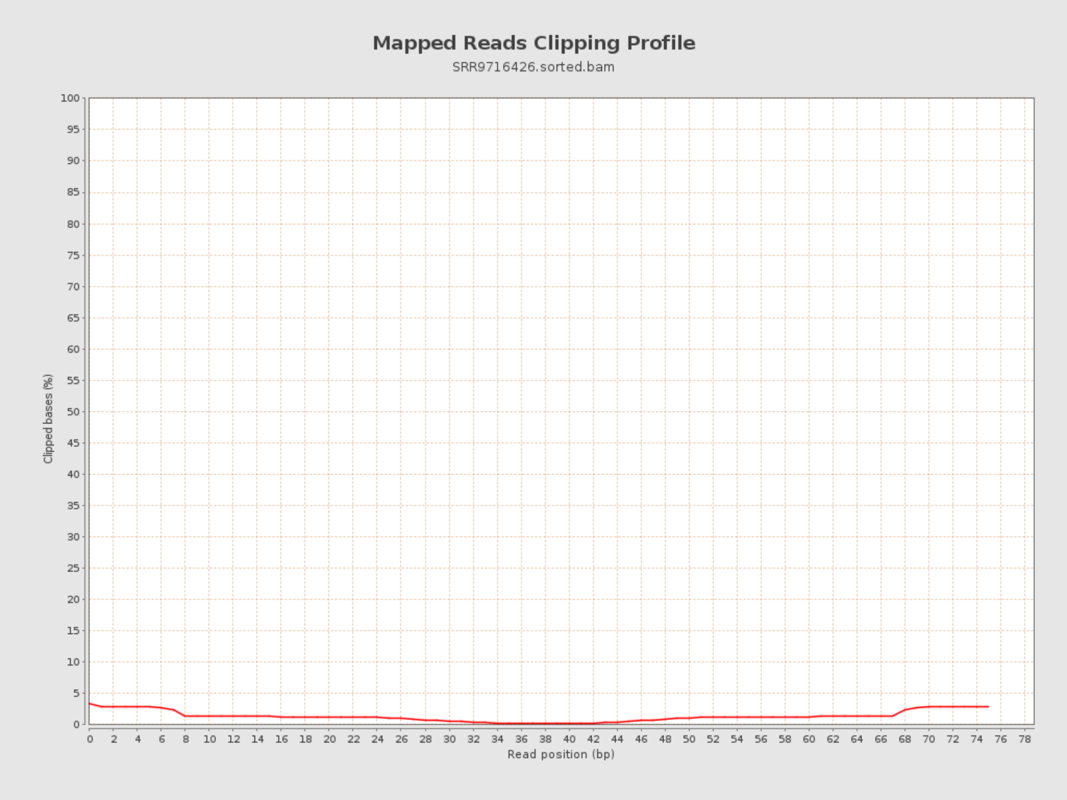
8. Results : Mapped Reads Nucleotide Content



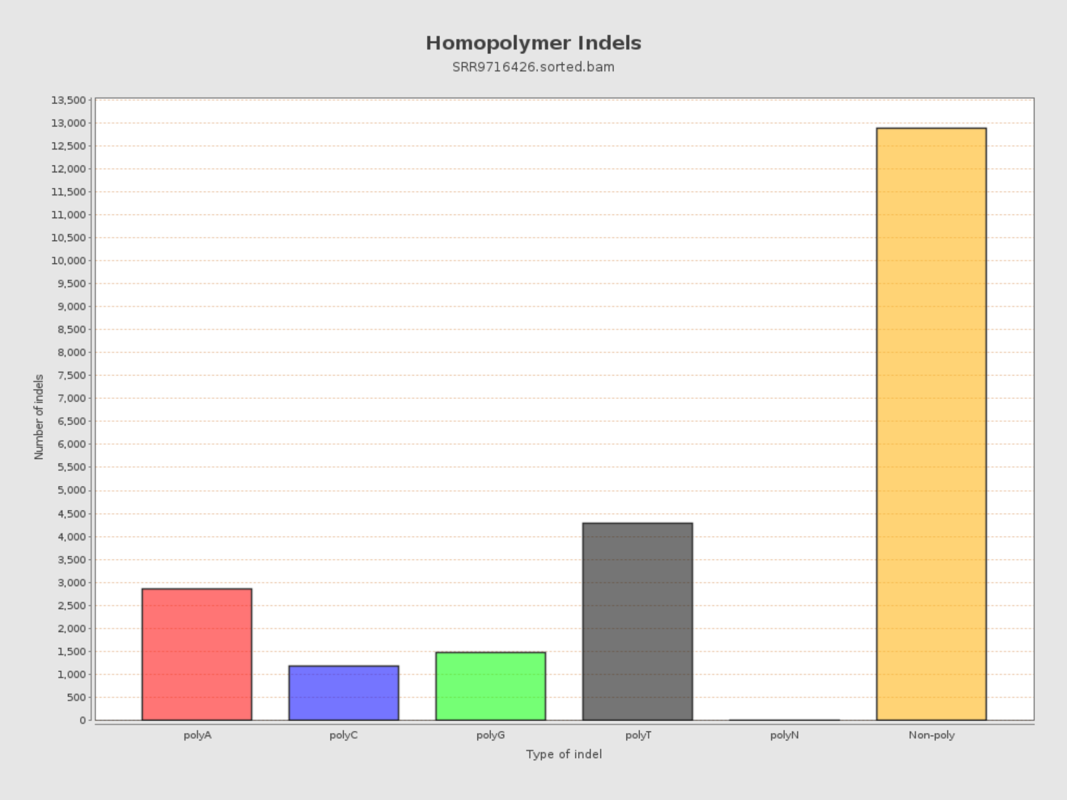
9. Results : Mapped Reads GC-content Distribution



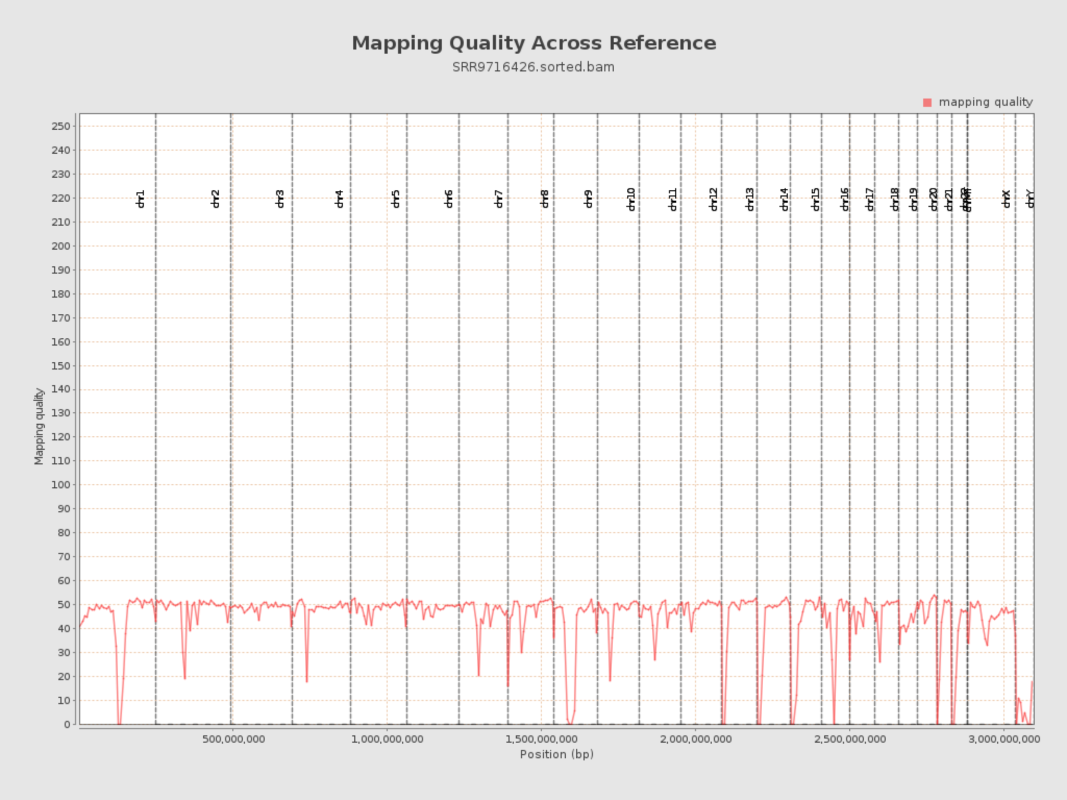
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram