Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:46:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716866.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_SRR9716866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716866.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:46:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,680,122
Mapped reads	2,322,656 / 86.66%
Unmapped reads	357,466 / 13.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,870 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	92,779 / 3.46%
Duplication rate	2.97%
Clipped reads	2,328,517 / 86.88%

2.2. ACGT Content

Number/percentage of A's	32,701,209 / 24.56%
Number/percentage of C's	26,721,612 / 20.07%
Number/percentage of T's	40,917,959 / 30.74%
Number/percentage of G's	32,779,698 / 24.62%
Number/percentage of N's	2,042 / 0%
GC Percentage	44.7%

2.3. Coverage

Mean	0.043

Standard Deviation	0.3309

2.4. Mapping Quality

Mean Mapping Quality	43.57

2.5. Mismatches and indels

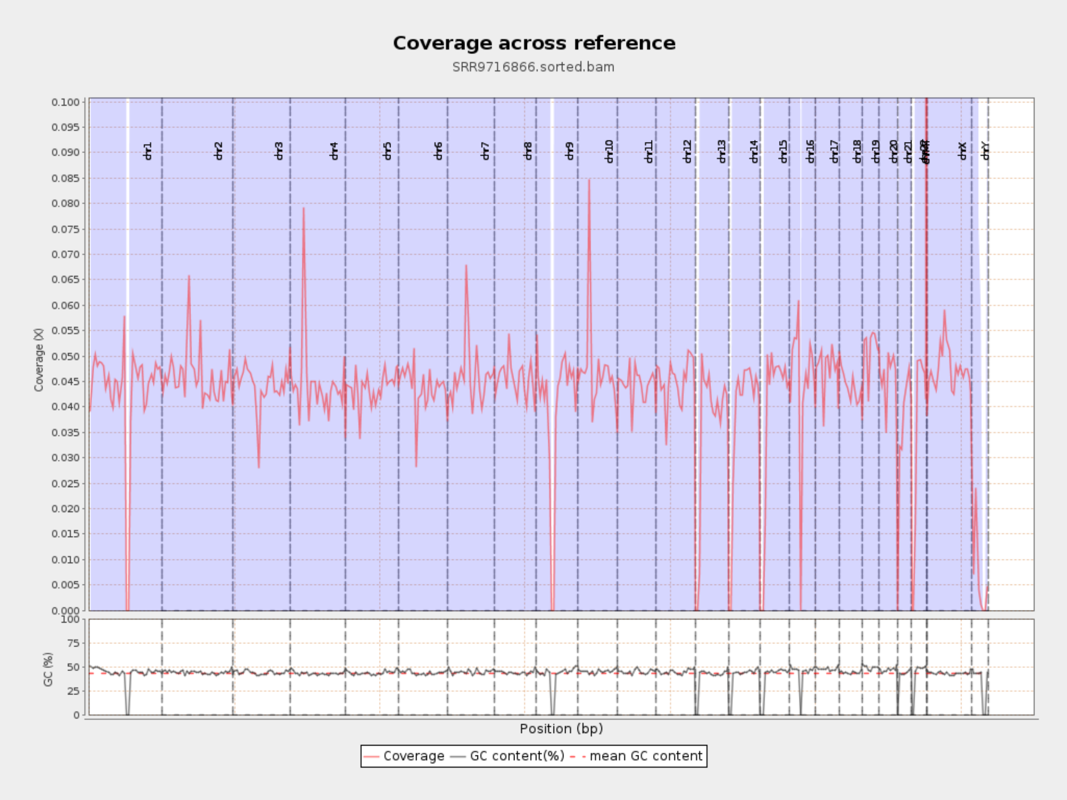
General error rate	0.52%
Mismatches	680,326
Insertions	8,359
Mapped reads with at least one insertion	0.36%
Deletions	25,512
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.15%

2.6. Chromosome stats

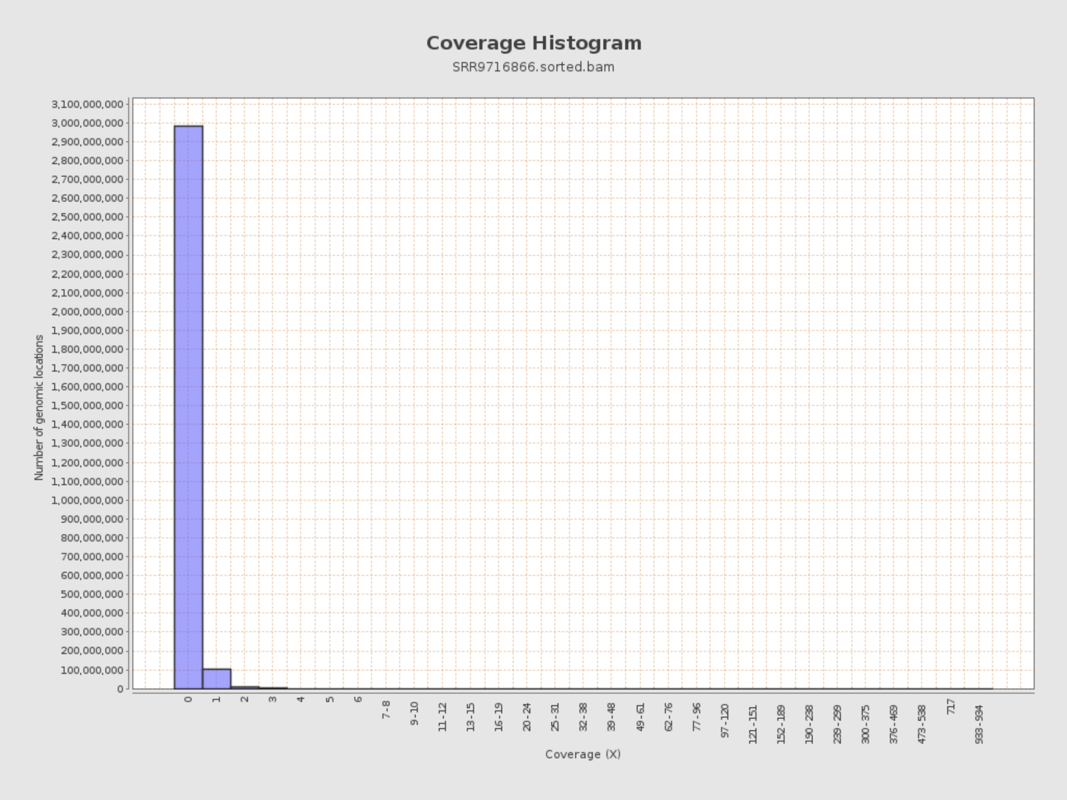
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10706853	0.043	0.472
chr2	243199373	11241290	0.0462	0.4899
chr3	198022430	8751142	0.0442	0.2412
chr4	191154276	8518050	0.0446	0.2865
chr5	180915260	7902650	0.0437	0.2355
chr6	171115067	7508739	0.0439	0.2751
chr7	159138663	7358584	0.0462	0.4293

chr8	146364022	6654725	0.0455	0.3203
chr9	141213431	5528612	0.0392	0.2749
chr10	135534747	6420010	0.0474	0.3969
chr11	135006516	5981678	0.0443	0.2986
chr12	133851895	6048822	0.0452	0.2436
chr13	115169878	4087562	0.0355	0.2132
chr14	107349540	4048716	0.0377	0.2288
chr15	102531392	3925336	0.0383	0.2267
chr16	90354753	4064925	0.045	0.2646
chr17	81195210	3843741	0.0473	0.268
chr18	78077248	3449399	0.0442	0.4706
chr19	59128983	3015812	0.051	0.4068
chr20	63025520	2874209	0.0456	0.2508
chr21	48129895	1733420	0.036	0.2484
chr22	51304566	1706531	0.0333	0.2086
chrMT	16571	8953	0.5403	0.9737
chrX	155270560	7363945	0.0474	0.2728
chrY	59373566	420684	0.0071	0.194

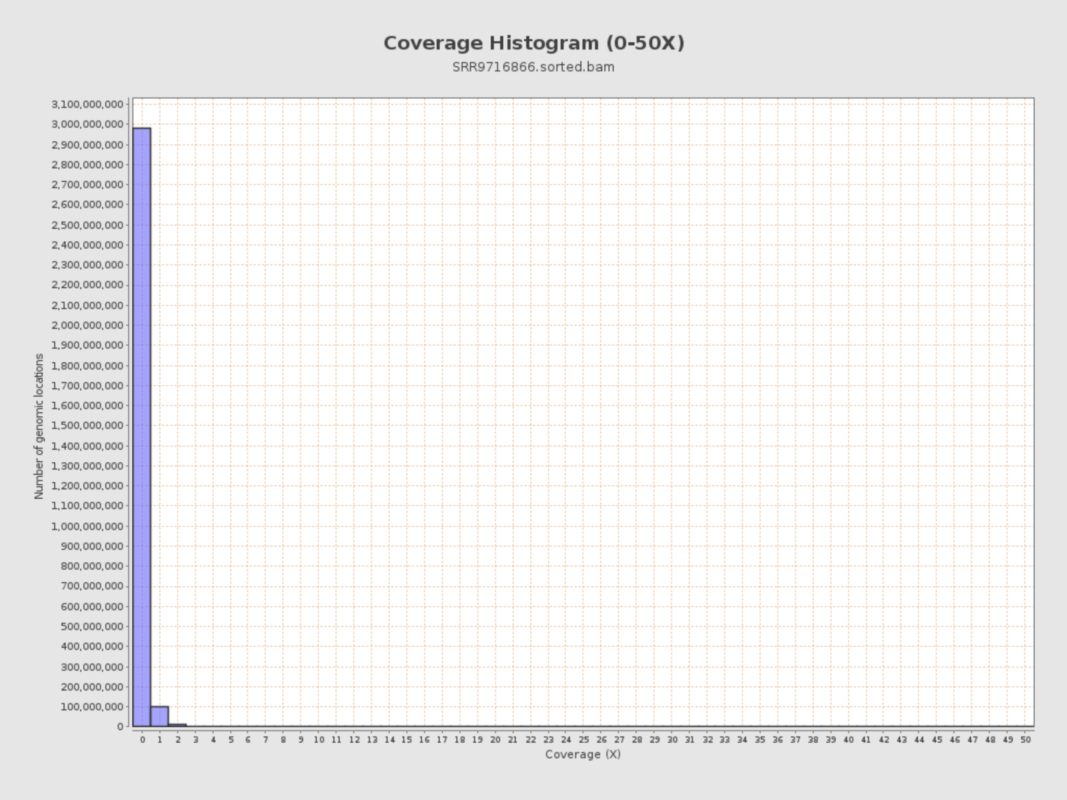
3. Results : Coverage across reference



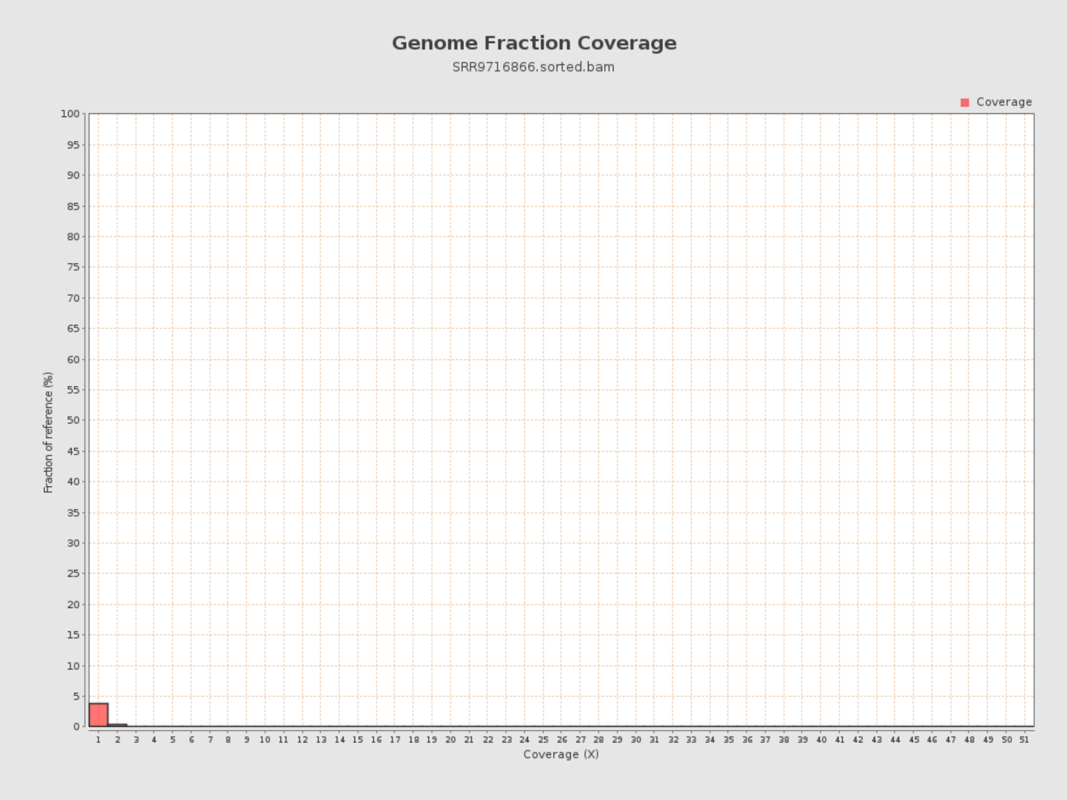
4. Results : Coverage Histogram



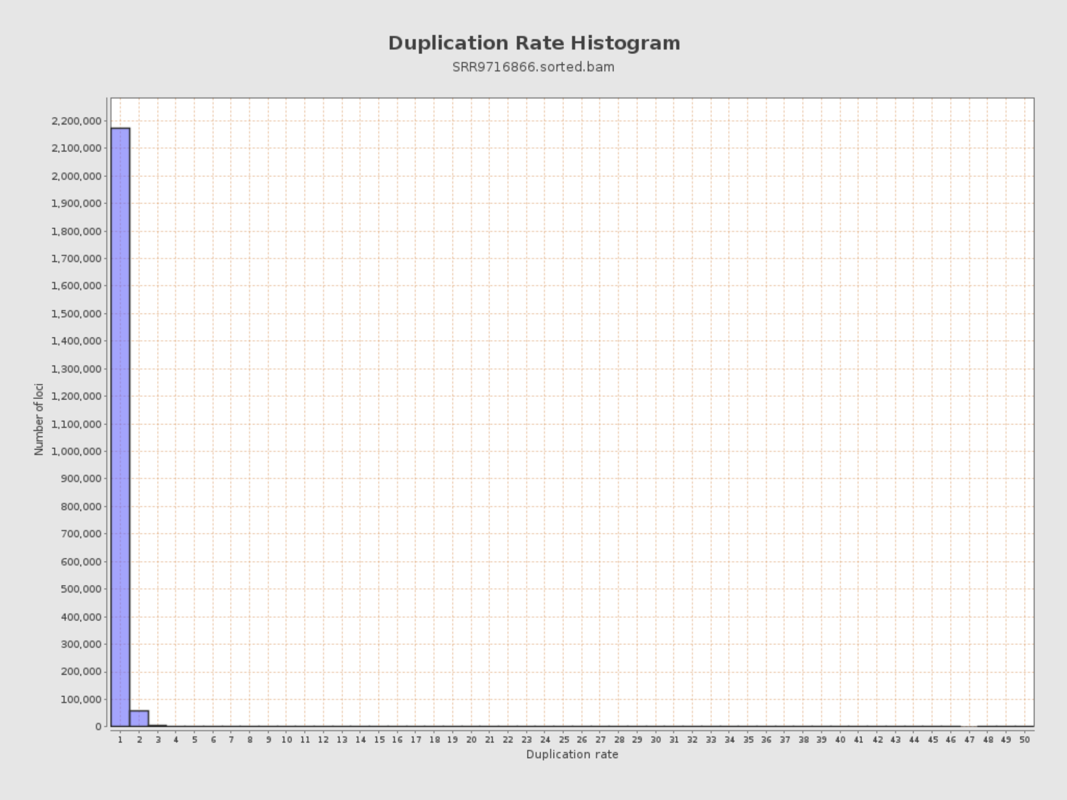
5. Results : Coverage Histogram (0-50X)



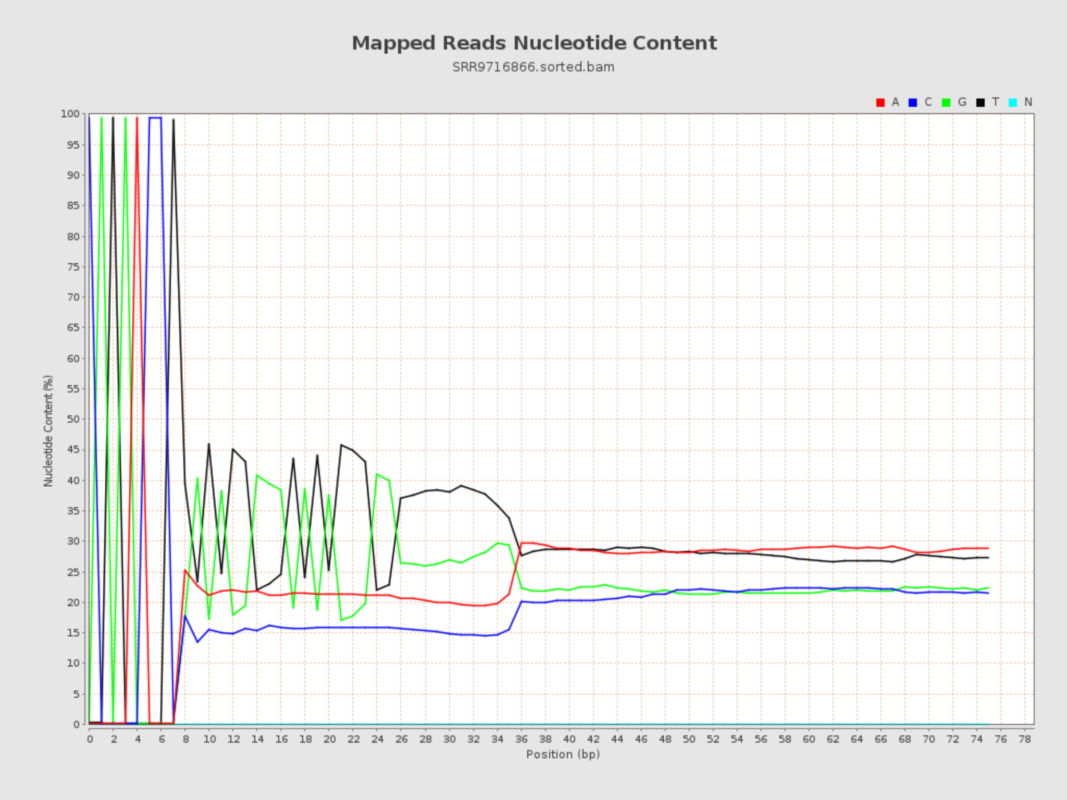
6. Results : Genome Fraction Coverage



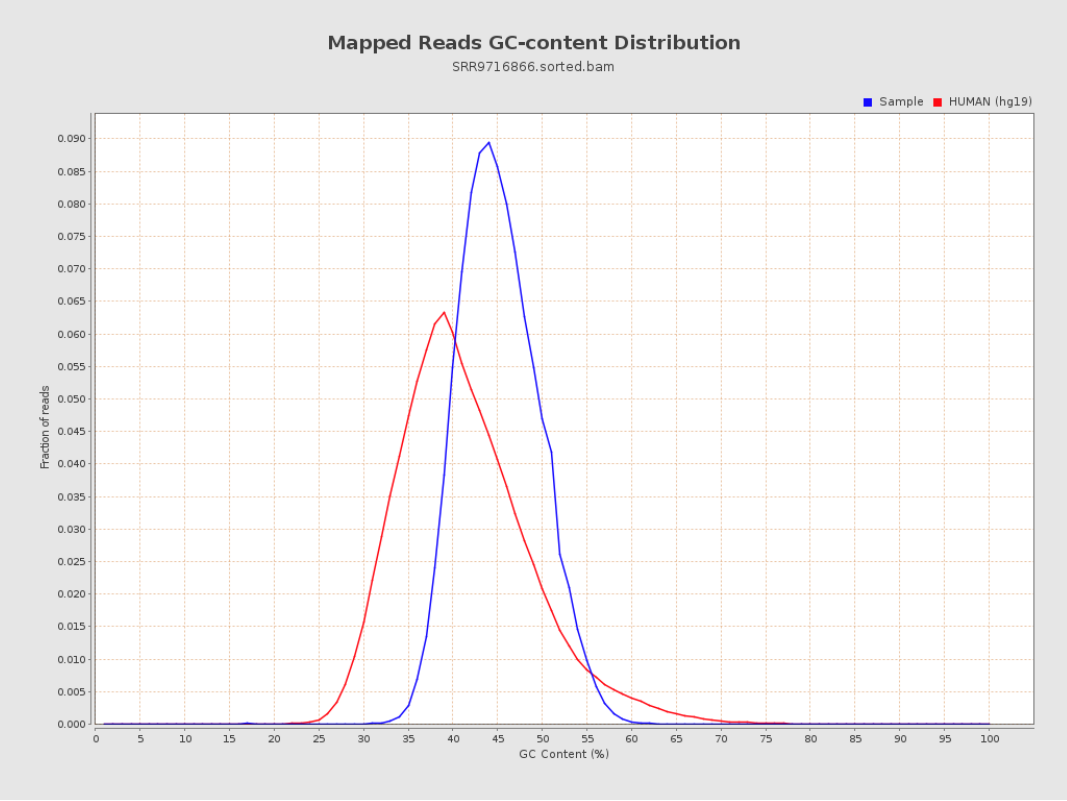
7. Results : Duplication Rate Histogram



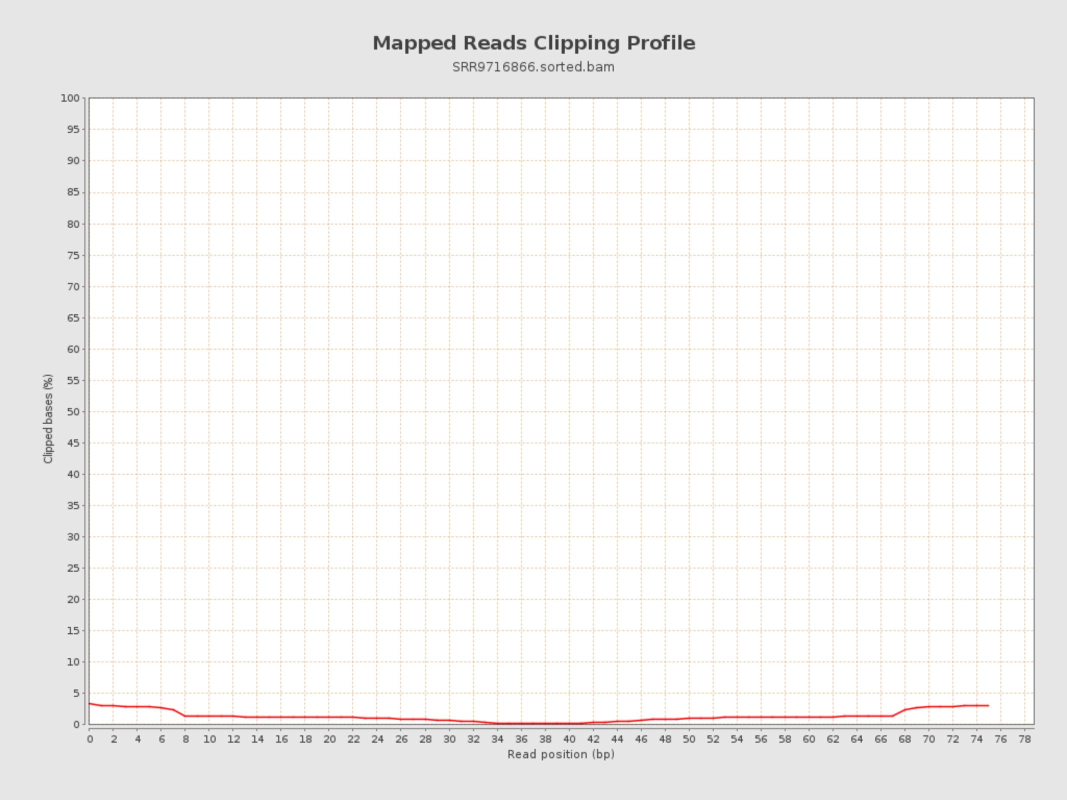
8. Results : Mapped Reads Nucleotide Content



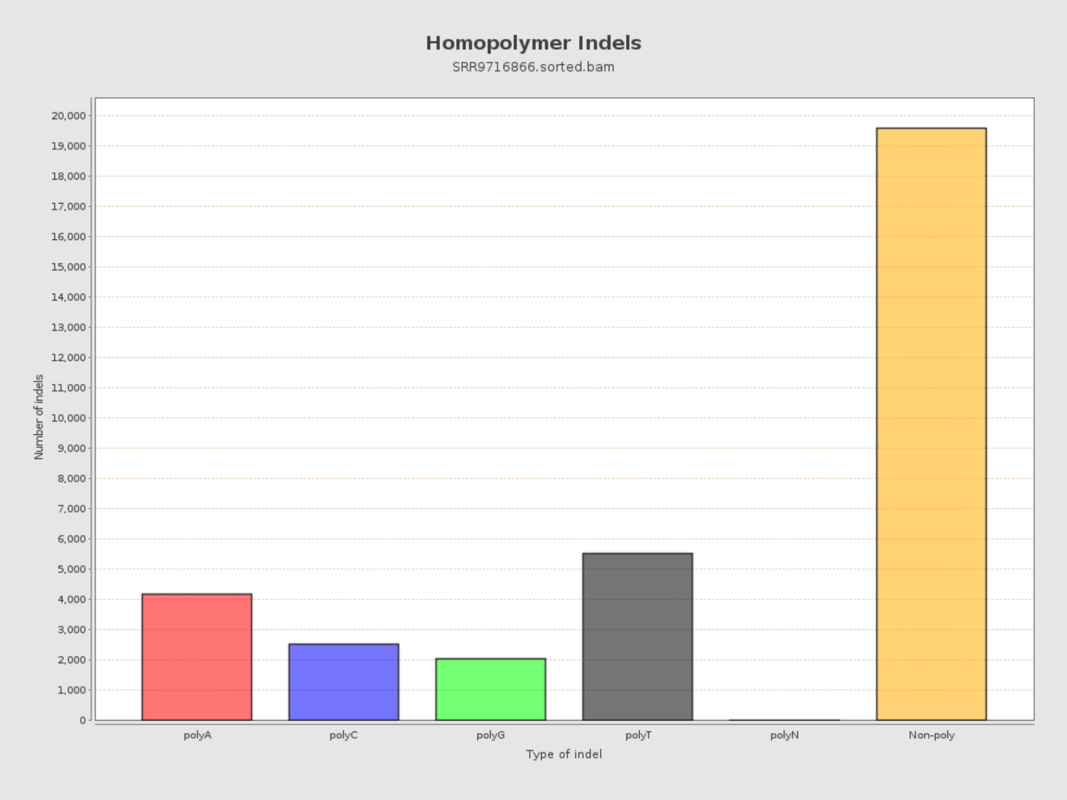
9. Results : Mapped Reads GC-content Distribution



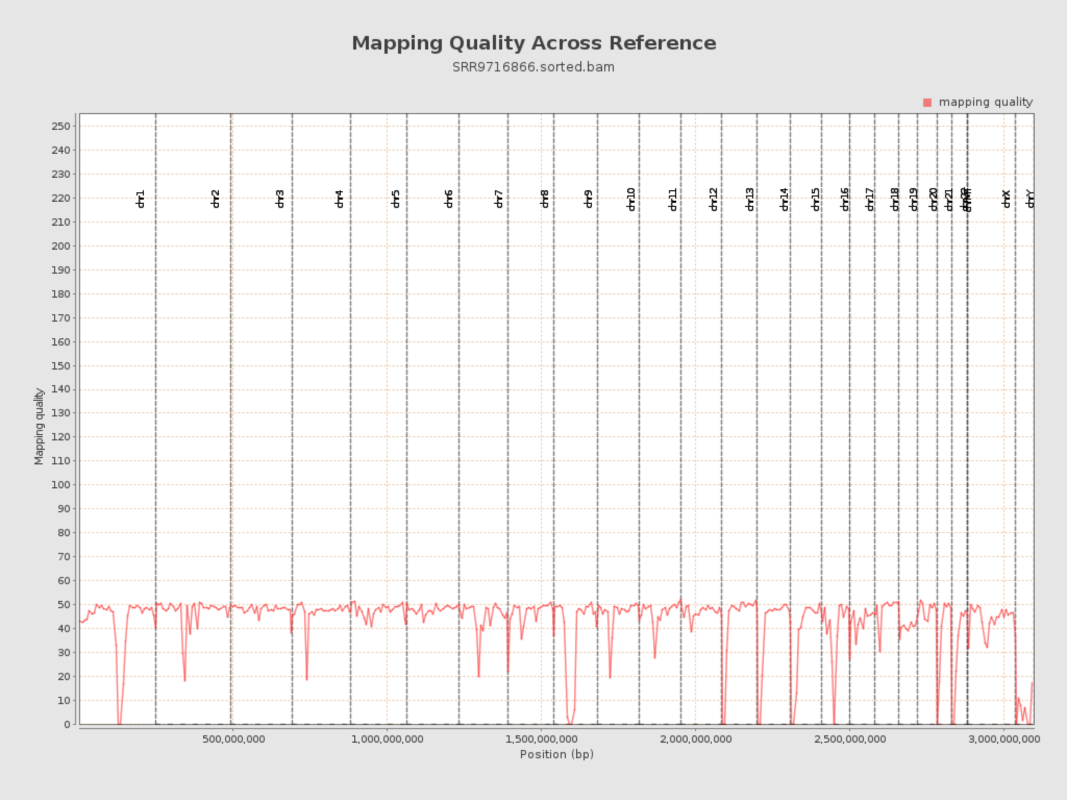
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram