Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:13:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716648.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_SRR9716648 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716648.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:13:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716648.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,392,354
Mapped reads	2,101,337 / 87.84%
Unmapped reads	291,017 / 12.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	58,364 / 2.44%
Read min/max/mean length	30 / 101 / 101.88
Duplicated reads (estimated)	68,784 / 2.88%
Duplication rate	2.15%
Clipped reads	2,156,331 / 90.13%

2.2. ACGT Content

Number/percentage of A's	41,659,955 / 26.23%
Number/percentage of C's	32,666,956 / 20.57%
Number/percentage of T's	47,708,915 / 30.04%
Number/percentage of G's	36,765,590 / 23.15%
Number/percentage of N's	19,523 / 0.01%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.4277

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

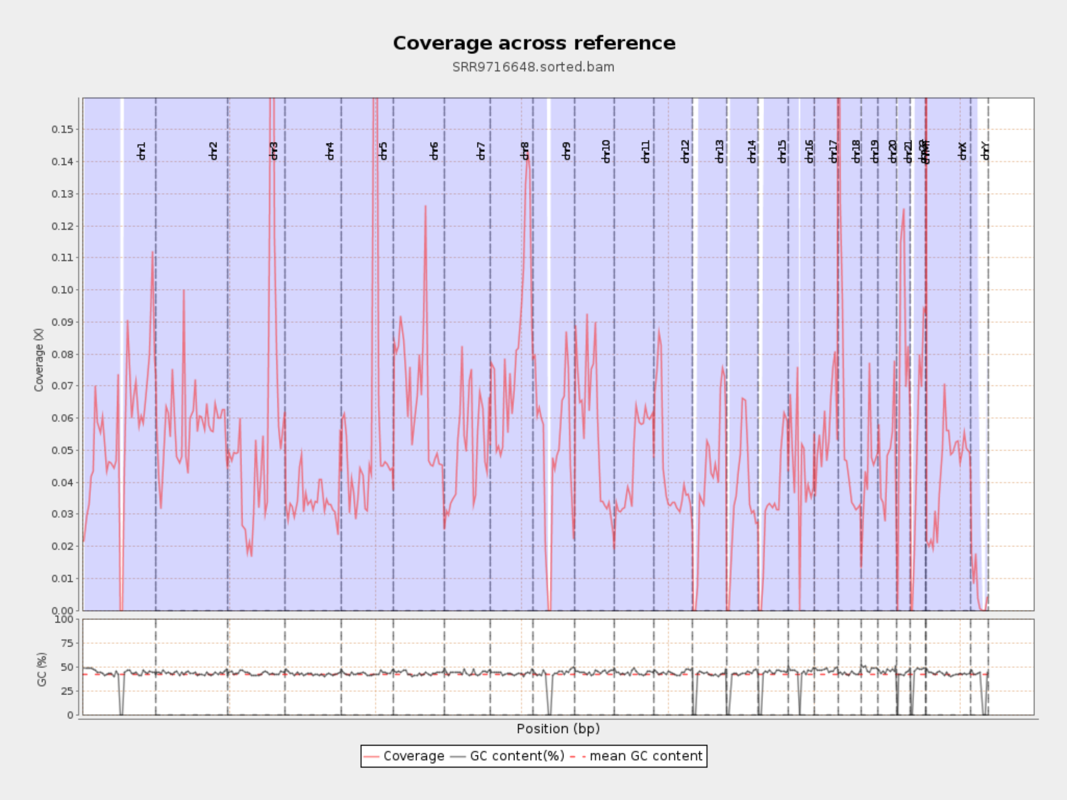
General error rate	0.78%
Mismatches	1,220,930
Insertions	12,574
Mapped reads with at least one insertion	0.59%
Deletions	34,974
Mapped reads with at least one deletion	1.64%
Homopolymer indels	40.91%

2.6. Chromosome stats

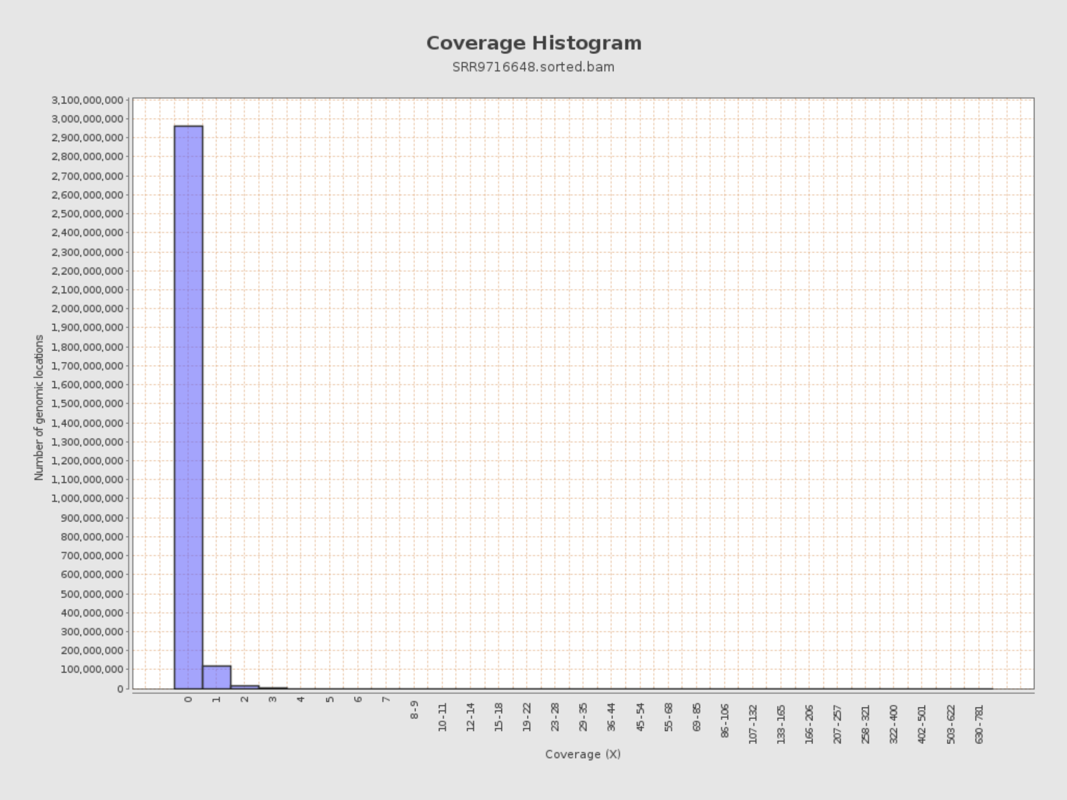
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13740582	0.0551	0.6449
chr2	243199373	14031358	0.0577	0.6348
chr3	198022430	11449168	0.0578	0.2822
chr4	191154276	6666464	0.0349	0.2238
chr5	180915260	10079297	0.0557	0.2726
chr6	171115067	11507757	0.0673	0.3436
chr7	159138663	8044193	0.0505	0.6056

chr8	146364022	11995151	0.082	0.5557
chr9	141213431	7016080	0.0497	0.3922
chr10	135534747	7775671	0.0574	0.4225
chr11	135006516	6298971	0.0467	0.346
chr12	133851895	5968601	0.0446	0.24
chr13	115169878	4790741	0.0416	0.2268
chr14	107349540	3782446	0.0352	0.2398
chr15	102531392	3325924	0.0324	0.2012
chr16	90354753	3937575	0.0436	0.2775
chr17	81195210	4611927	0.0568	0.3101
chr18	78077248	4823076	0.0618	0.8369
chr19	59128983	2692705	0.0455	0.5334
chr20	63025520	3015550	0.0478	0.3024
chr21	48129895	3606370	0.0749	0.3261
chr22	51304566	2632325	0.0513	0.2592
chrMT	16571	11173	0.6743	1.2468
chrX	155270560	6716712	0.0433	0.2953
chrY	59373566	360399	0.0061	0.1562

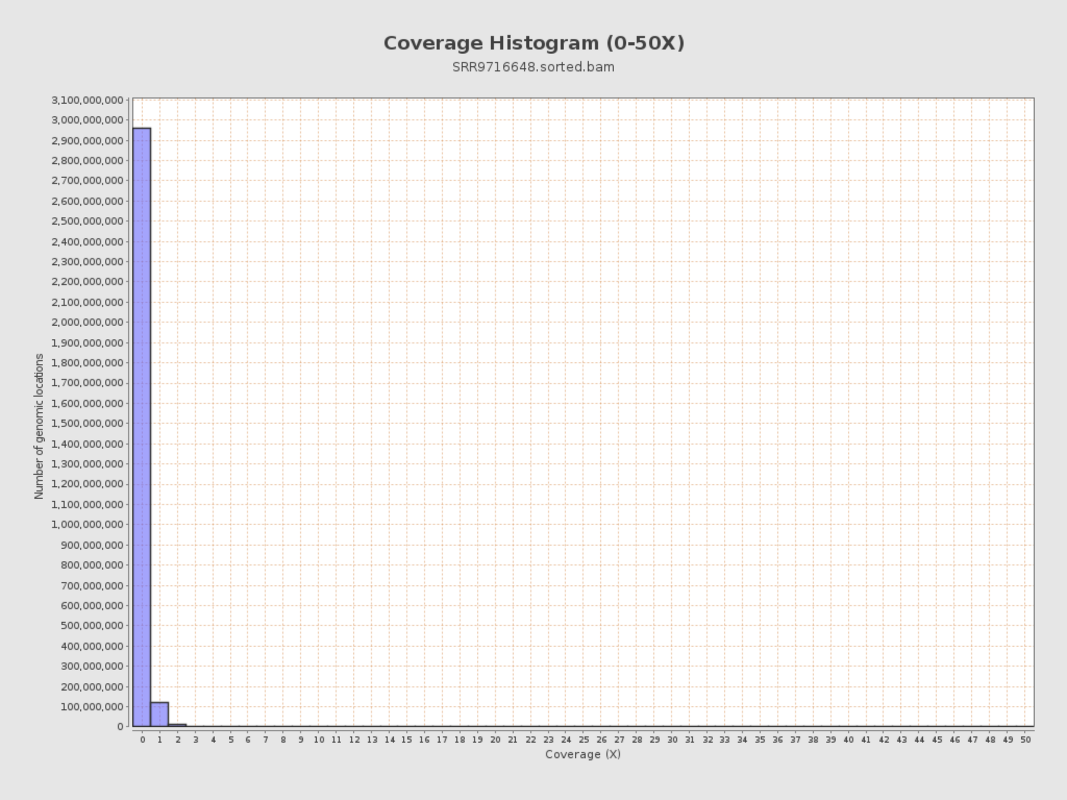
3. Results : Coverage across reference



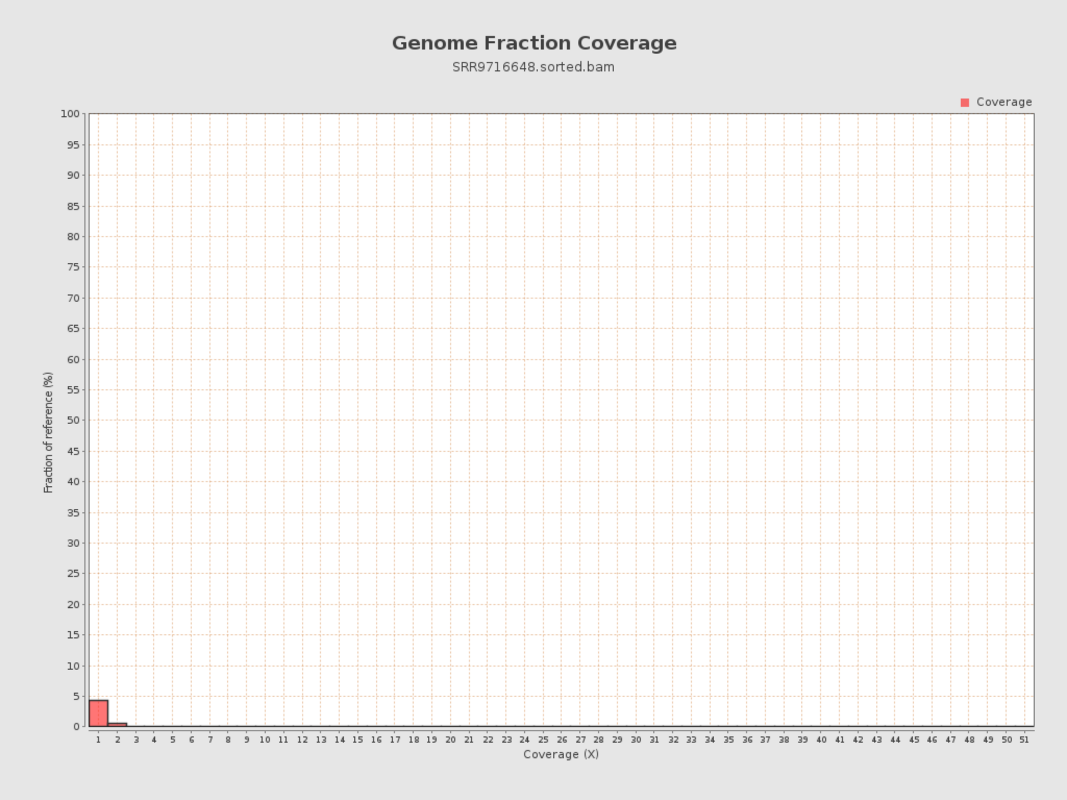
4. Results : Coverage Histogram



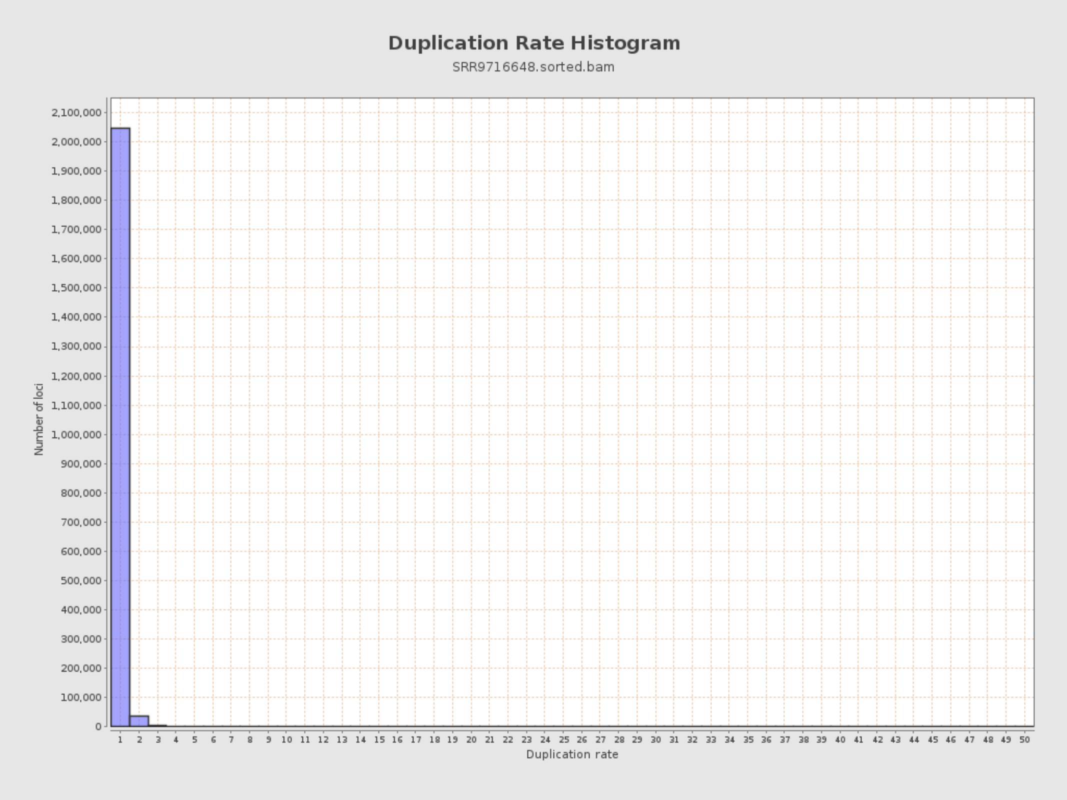
5. Results : Coverage Histogram (0-50X)



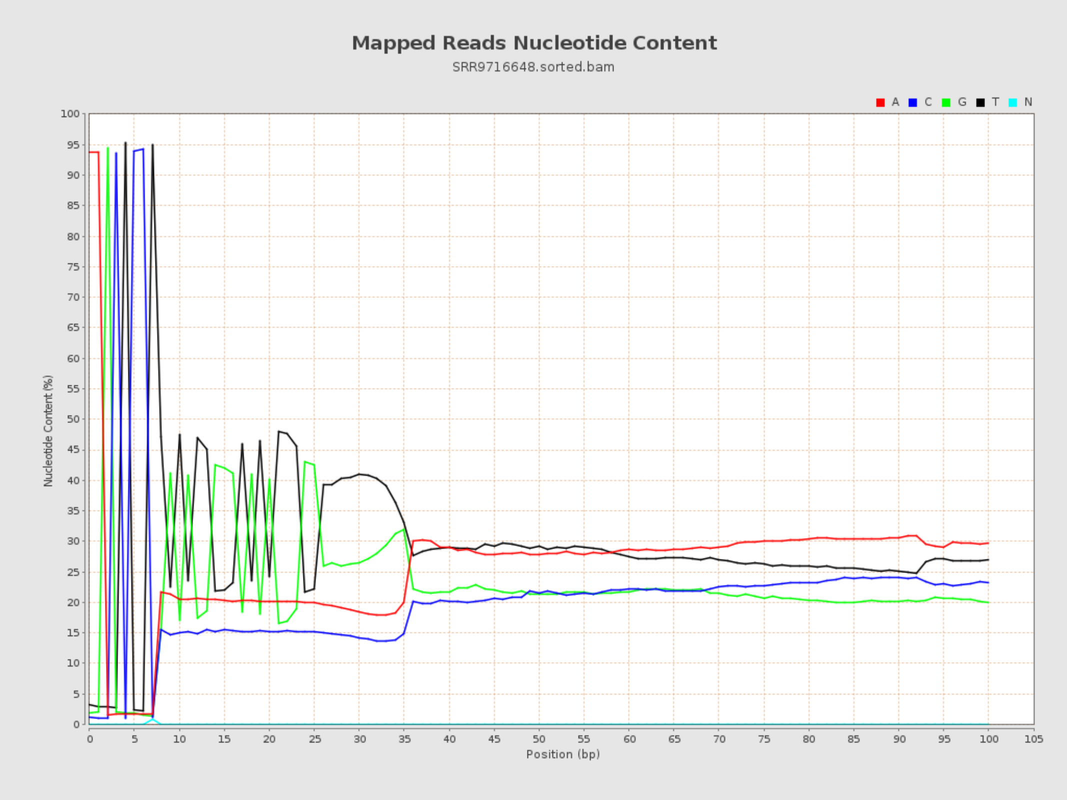
6. Results : Genome Fraction Coverage



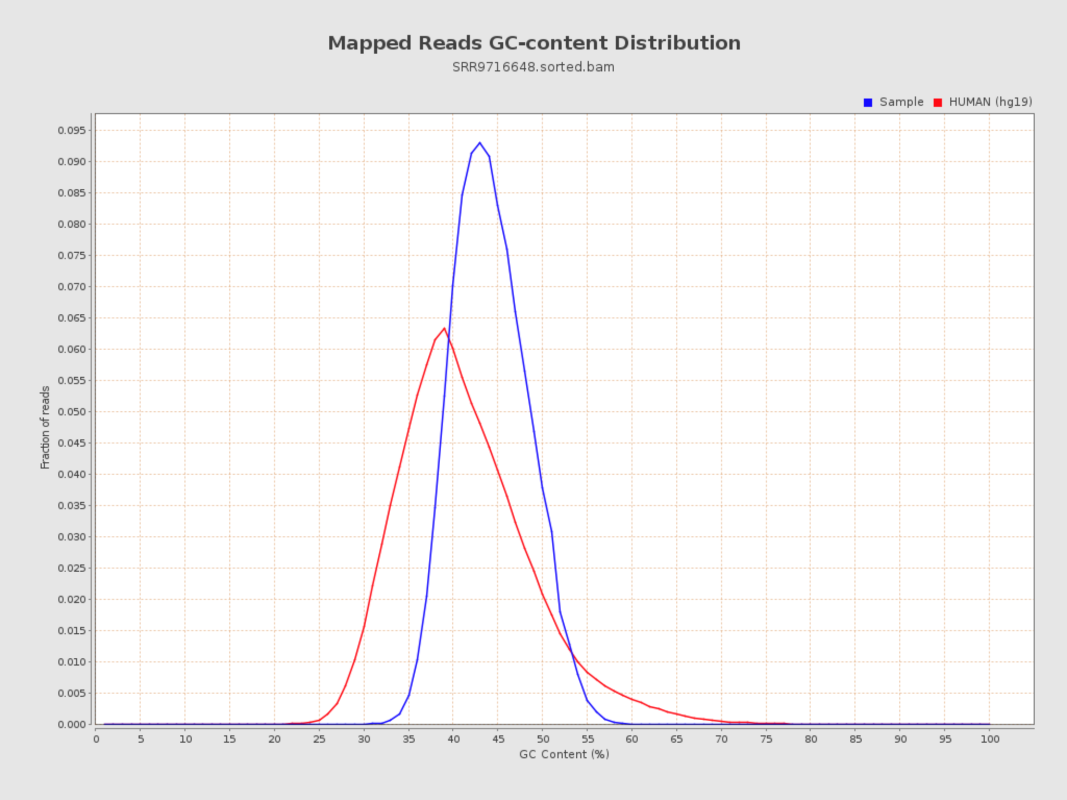
7. Results : Duplication Rate Histogram



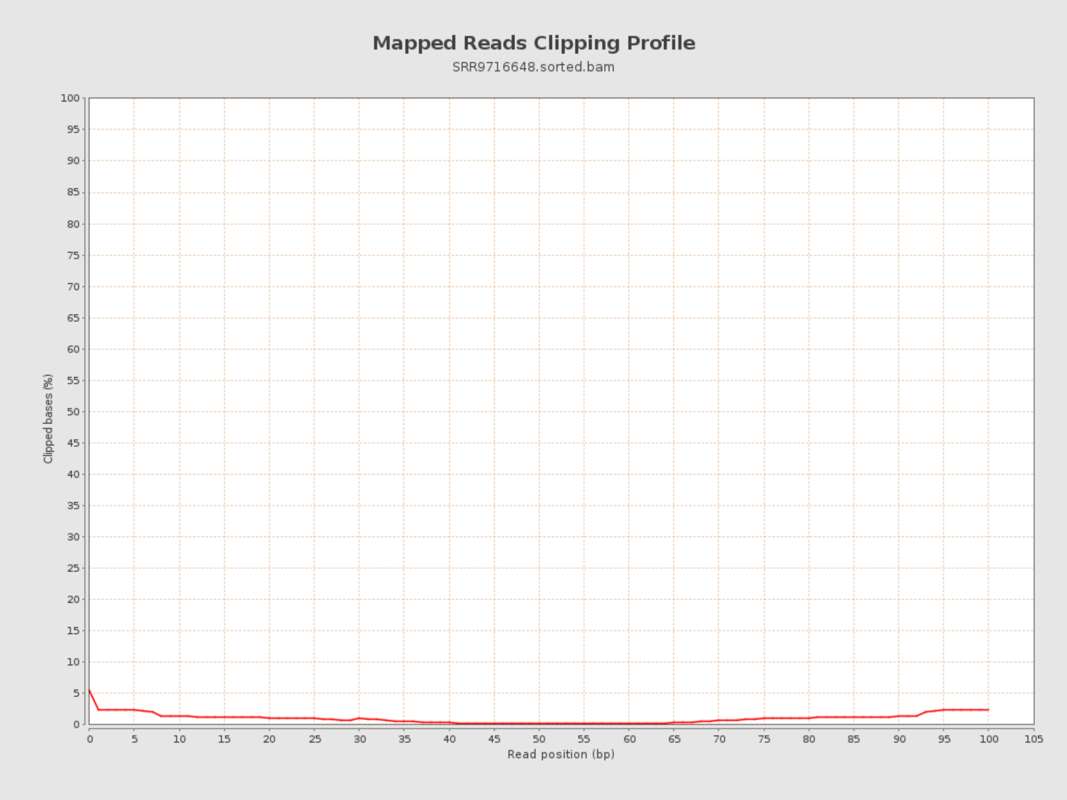
8. Results : Mapped Reads Nucleotide Content



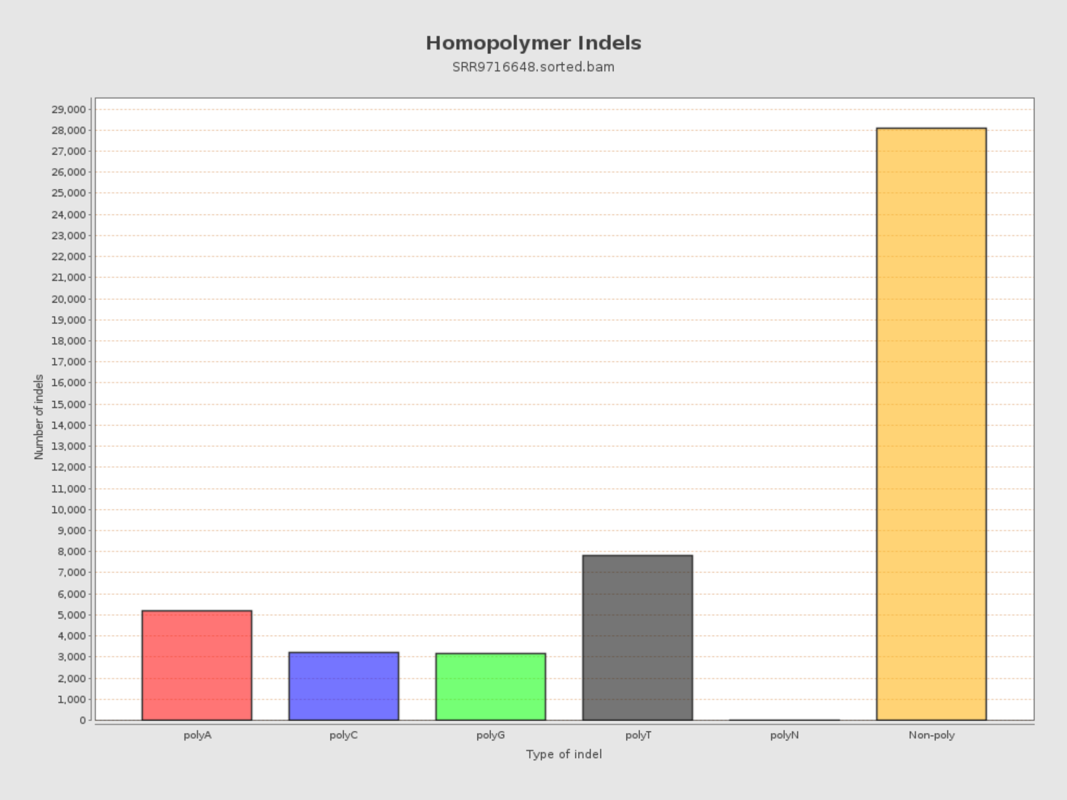
9. Results : Mapped Reads GC-content Distribution



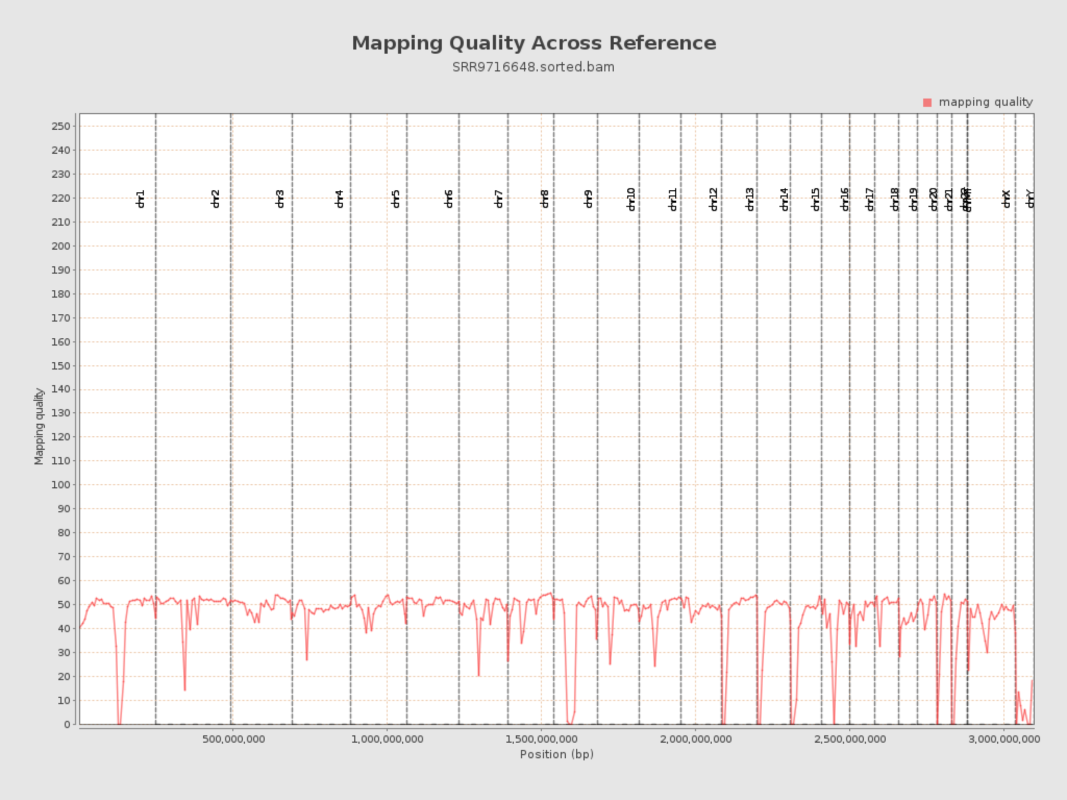
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram