Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 08:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716712.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_SRR9716712 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716712.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 08:17:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716712.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,370,063
Mapped reads	4,129,429 / 94.49%
Unmapped reads	240,634 / 5.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	90,647 / 2.07%
Read min/max/mean length	30 / 101 / 101.75
Duplicated reads (estimated)	330,824 / 7.57%
Duplication rate	6.11%
Clipped reads	4,214,713 / 96.45%

2.2. ACGT Content

Number/percentage of A's	79,654,097 / 25.07%
Number/percentage of C's	64,699,477 / 20.36%
Number/percentage of T's	92,213,092 / 29.02%
Number/percentage of G's	81,162,999 / 25.54%
Number/percentage of N's	12,271 / 0%
GC Percentage	45.91%

2.3. Coverage

Mean	0.1027

Standard Deviation	0.6621

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

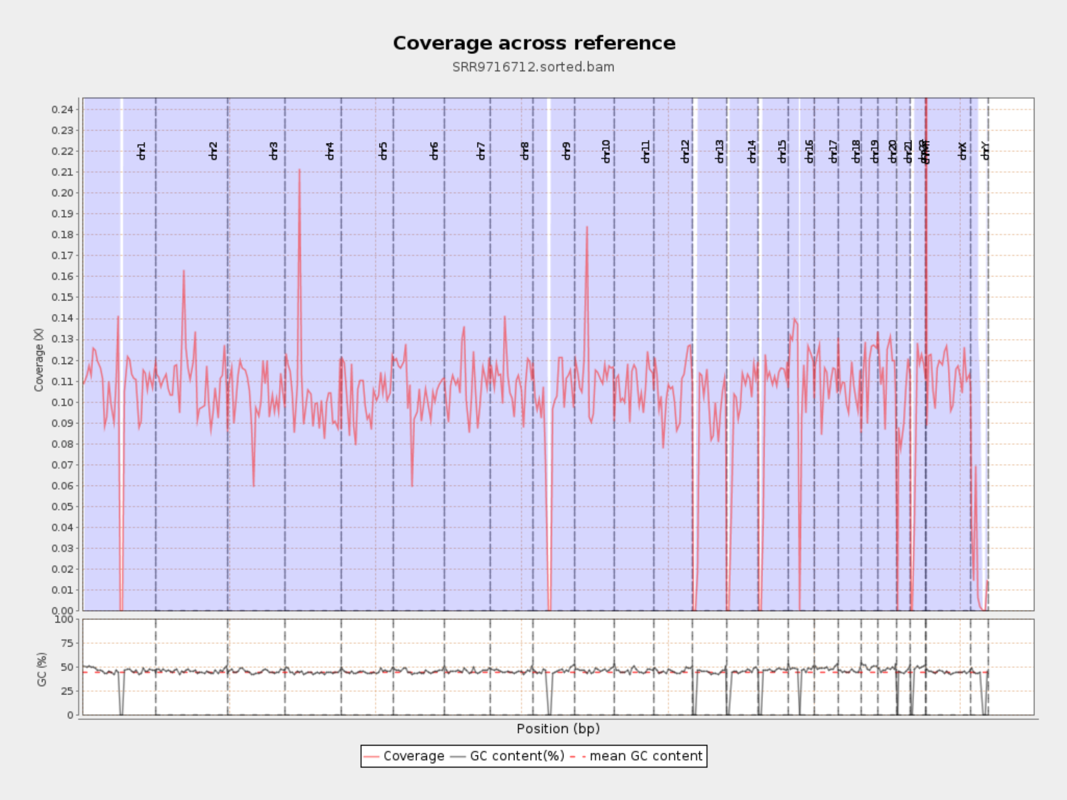
General error rate	0.65%
Mismatches	2,003,697
Insertions	26,581
Mapped reads with at least one insertion	0.63%
Deletions	56,848
Mapped reads with at least one deletion	1.35%
Homopolymer indels	38.49%

2.6. Chromosome stats

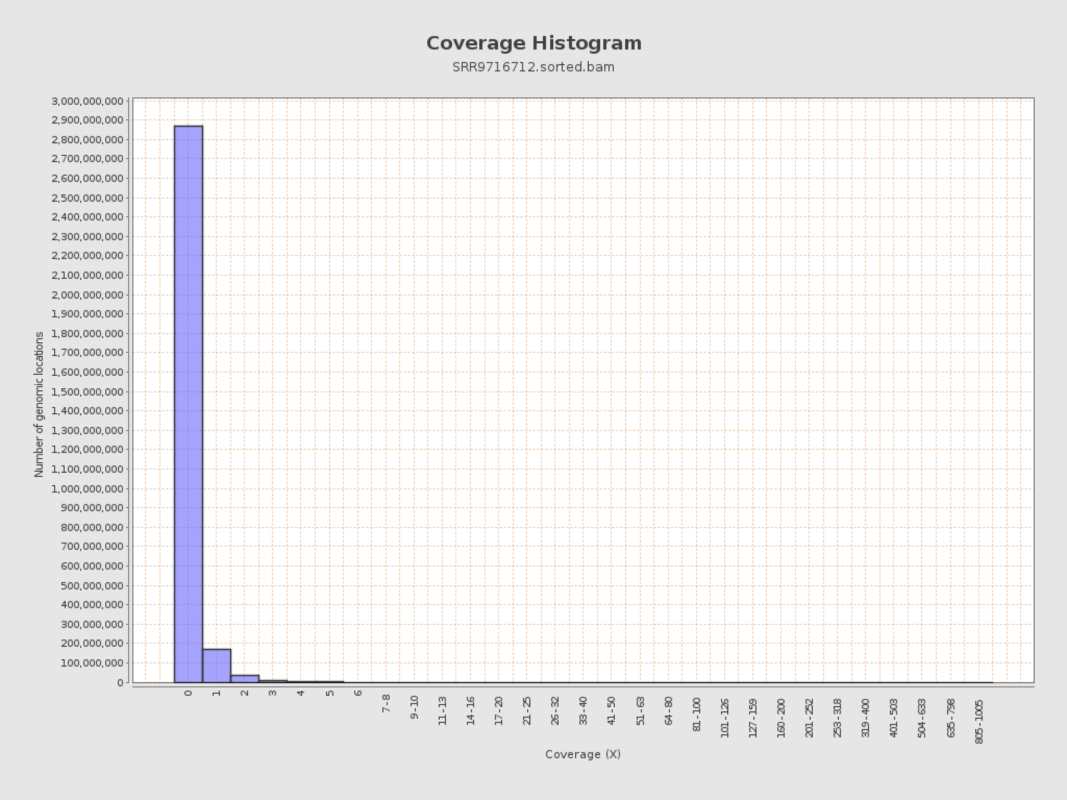
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25820098	0.1036	0.9935
chr2	243199373	26856206	0.1104	0.7787
chr3	198022430	20422287	0.1031	0.4266
chr4	191154276	20057138	0.1049	0.6794
chr5	180915260	18742967	0.1036	0.4321
chr6	171115067	17813049	0.1041	0.4589
chr7	159138663	17188212	0.108	0.7885

chr8	146364022	16152444	0.1104	0.71
chr9	141213431	12982120	0.0919	0.6144
chr10	135534747	15465513	0.1141	0.9187
chr11	135006516	14555042	0.1078	0.734
chr12	133851895	14242954	0.1064	0.4459
chr13	115169878	9646264	0.0838	0.3879
chr14	107349540	9654057	0.0899	0.4768
chr15	102531392	9464631	0.0923	0.4091
chr16	90354753	9945946	0.1101	0.5116
chr17	81195210	9110928	0.1122	0.5419
chr18	78077248	8307934	0.1064	1.0094
chr19	59128983	6974476	0.118	0.7643
chr20	63025520	7292766	0.1157	0.5107
chr21	48129895	4296161	0.0893	0.5866
chr22	51304566	4290437	0.0836	0.4142
chrMT	16571	33619	2.0288	2.2002
chrX	155270560	17511594	0.1128	0.5222
chrY	59373566	1033842	0.0174	0.6412

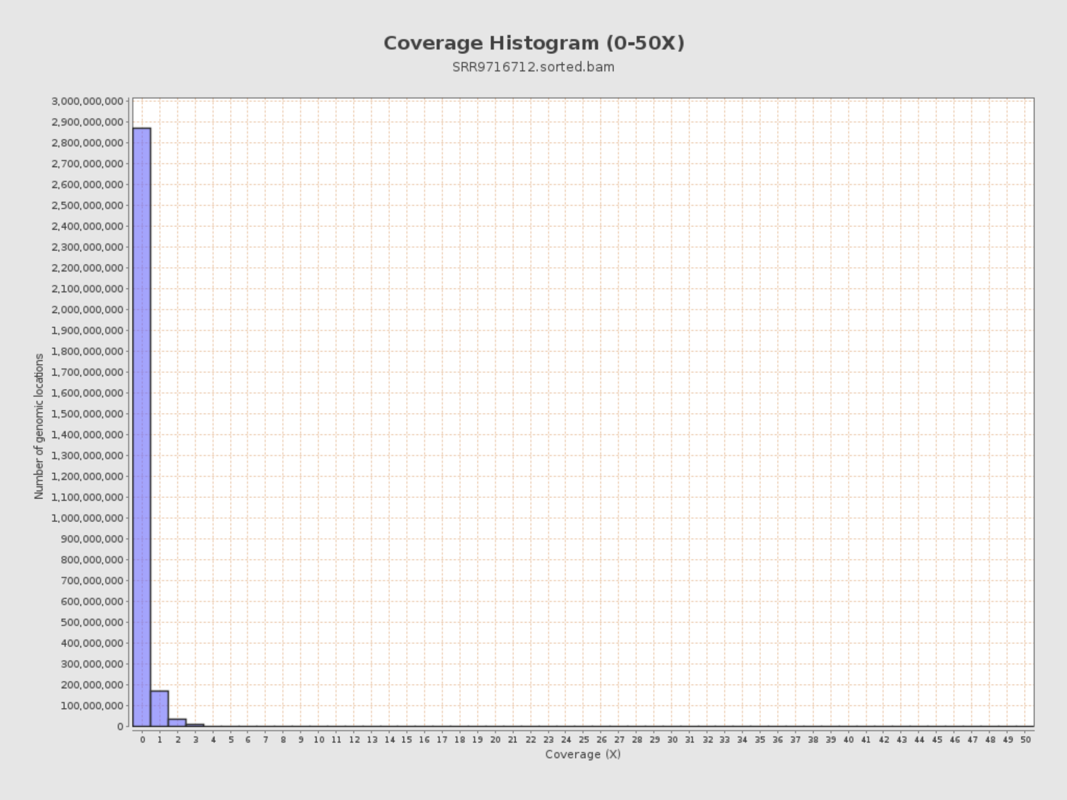
3. Results : Coverage across reference



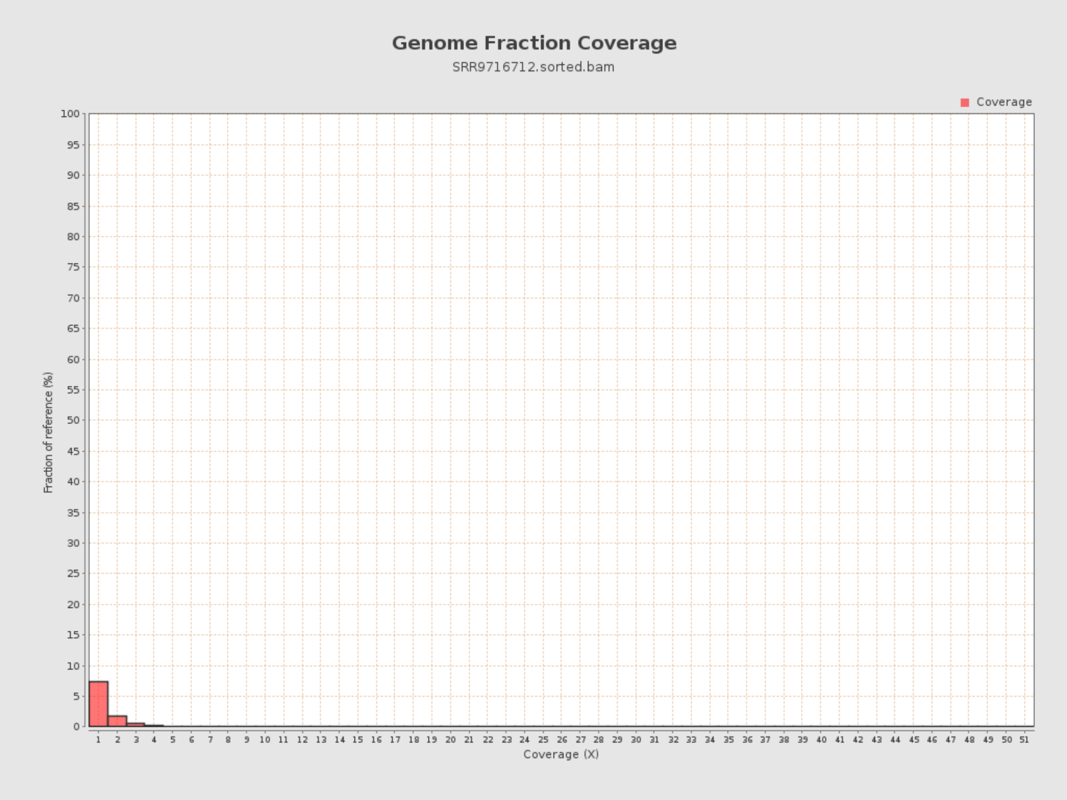
4. Results : Coverage Histogram



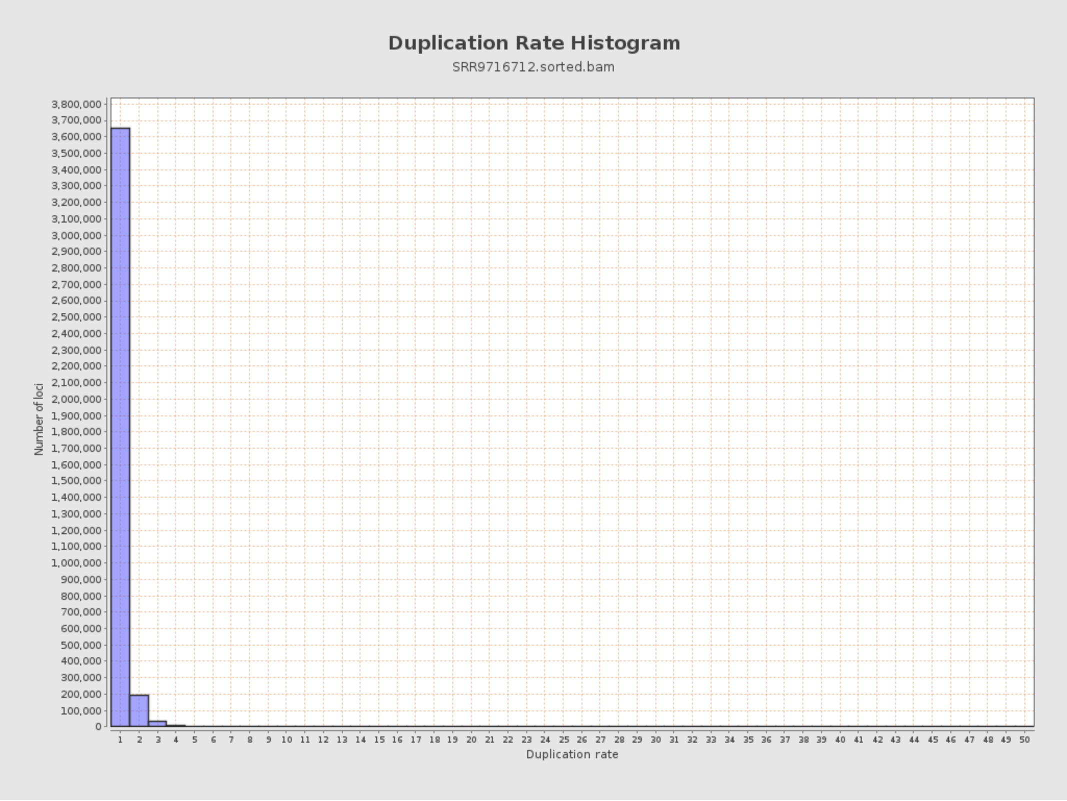
5. Results : Coverage Histogram (0-50X)



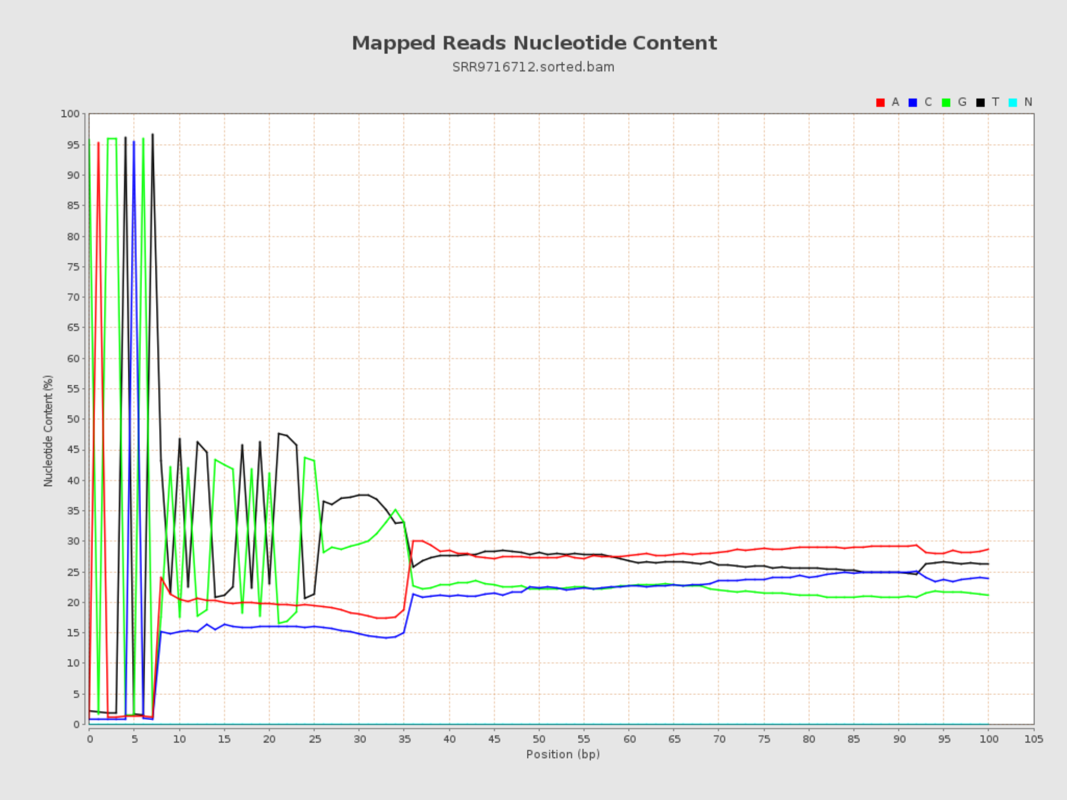
6. Results : Genome Fraction Coverage



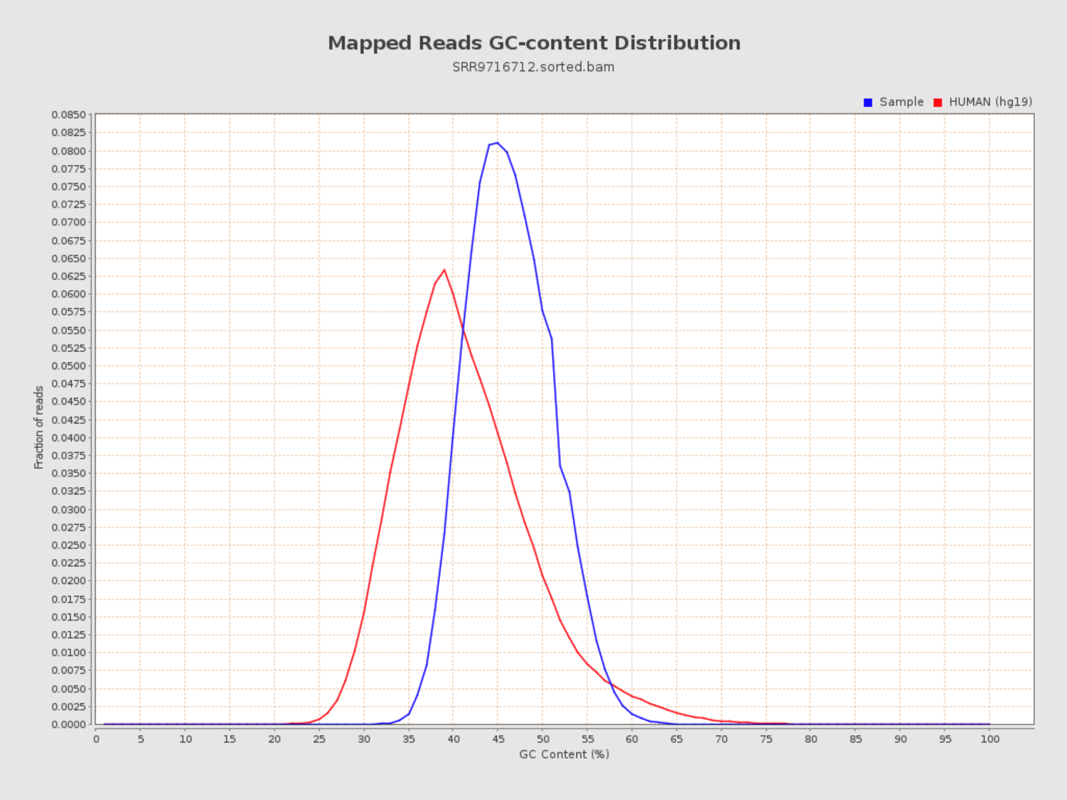
7. Results : Duplication Rate Histogram



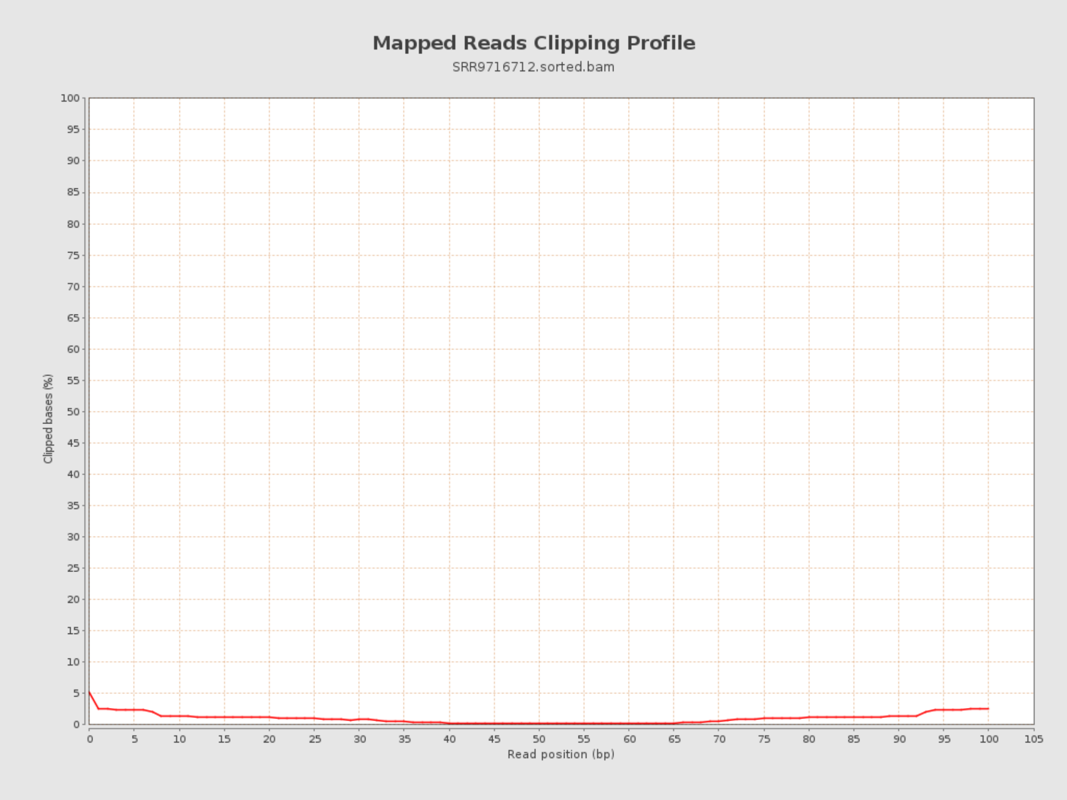
8. Results : Mapped Reads Nucleotide Content



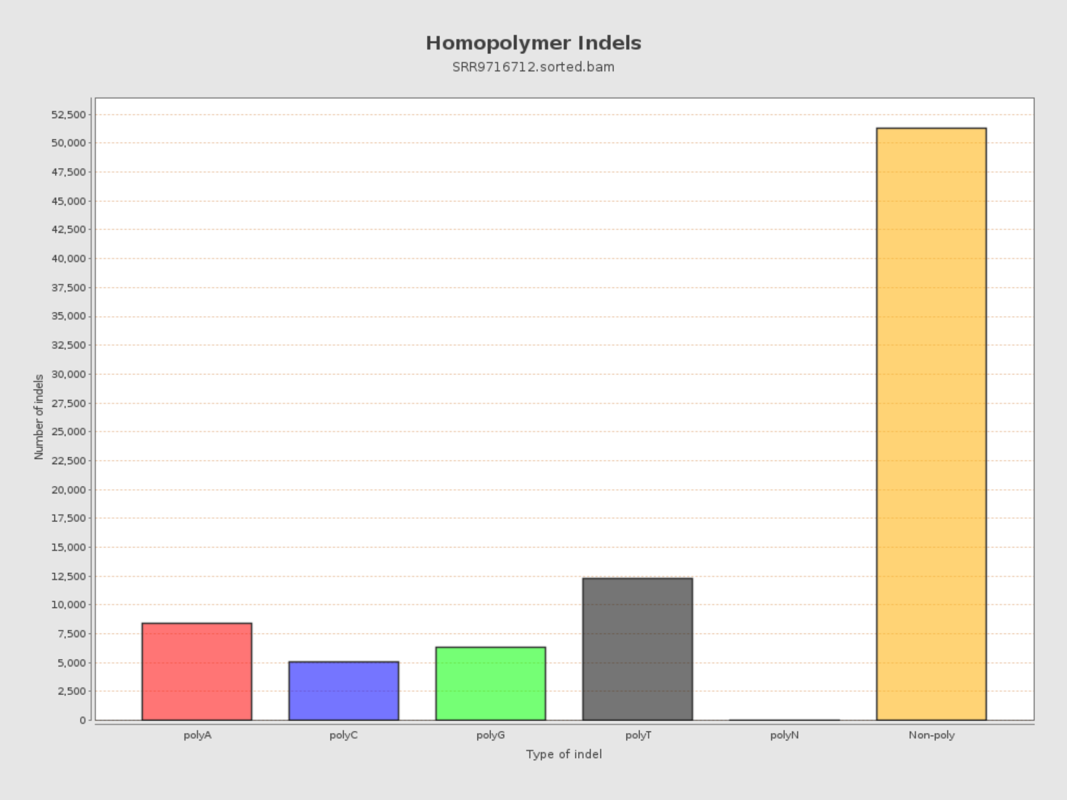
9. Results : Mapped Reads GC-content Distribution



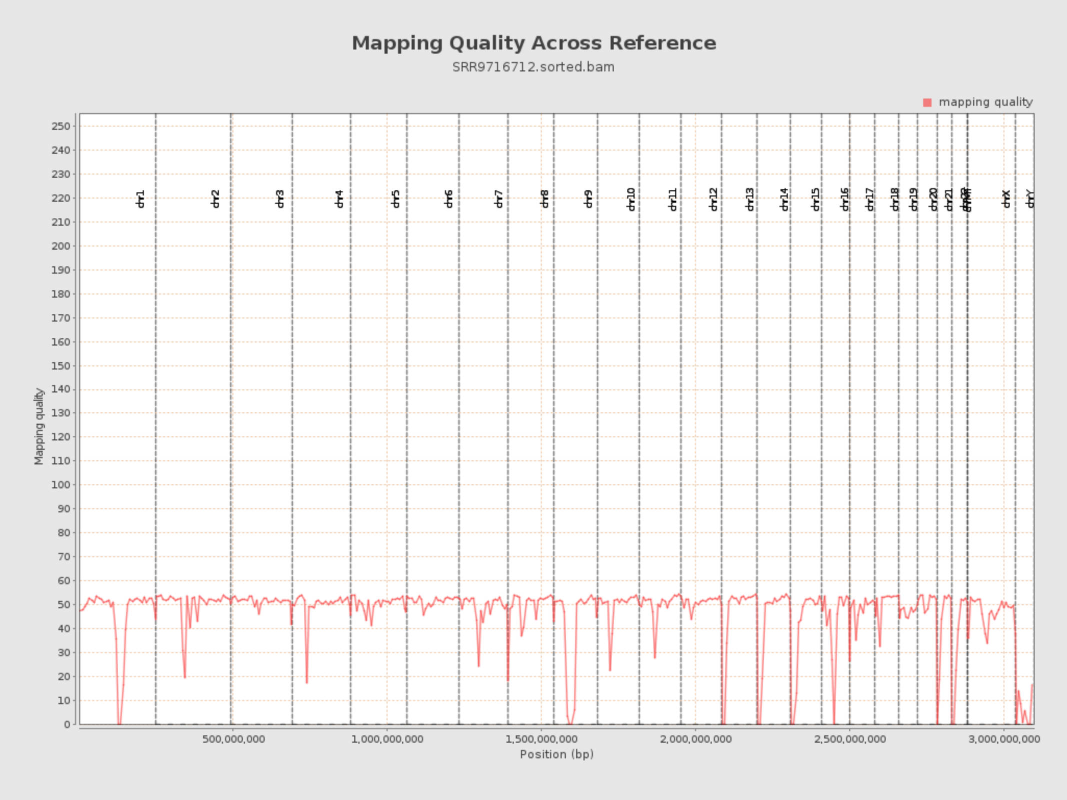
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram