Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:52:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716313.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_SRR9716313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:52:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,650,750
Mapped reads	1,506,259 / 91.25%
Unmapped reads	144,491 / 8.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,351 / 1.72%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	54,095 / 3.28%
Duplication rate	2.5%
Clipped reads	1,530,704 / 92.73%

2.2. ACGT Content

Number/percentage of A's	31,189,037 / 26.25%
Number/percentage of C's	22,790,056 / 19.18%
Number/percentage of T's	36,966,366 / 31.11%
Number/percentage of G's	27,869,789 / 23.45%
Number/percentage of N's	8,411 / 0.01%
GC Percentage	42.63%

2.3. Coverage

Mean	0.0384

Standard Deviation	0.3759

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Mismatches and indels

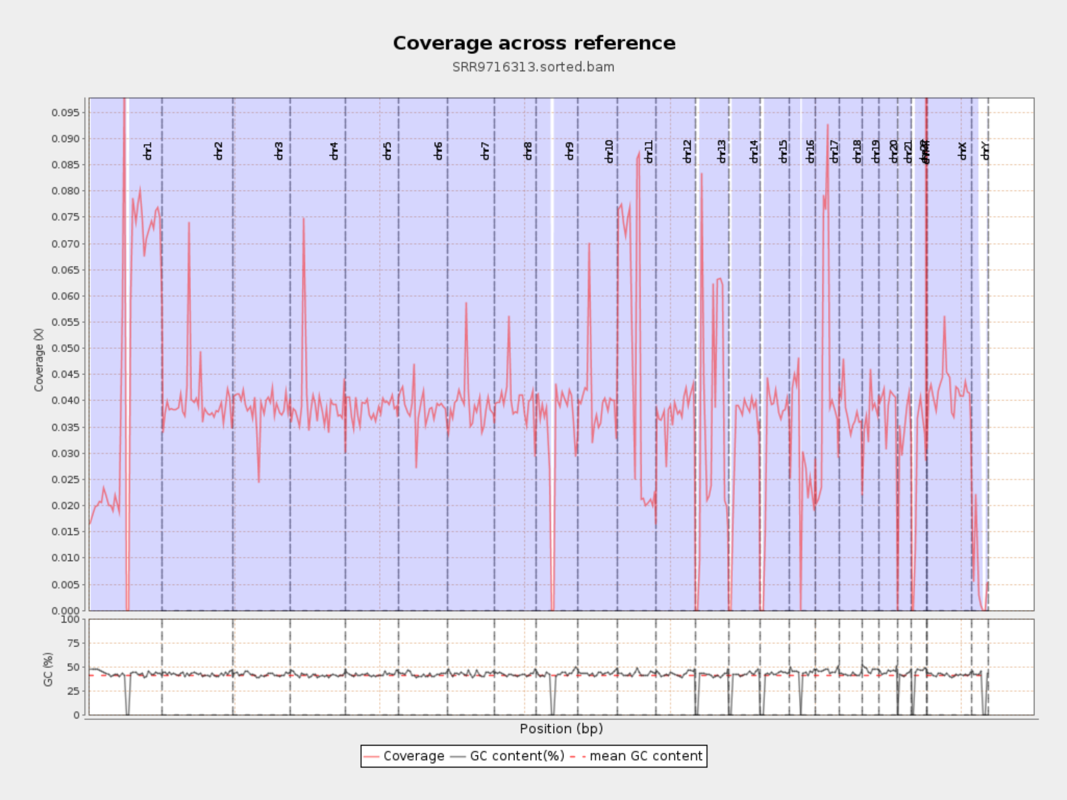
General error rate	0.71%
Mismatches	820,543
Insertions	10,054
Mapped reads with at least one insertion	0.66%
Deletions	28,957
Mapped reads with at least one deletion	1.89%
Homopolymer indels	43.46%

2.6. Chromosome stats

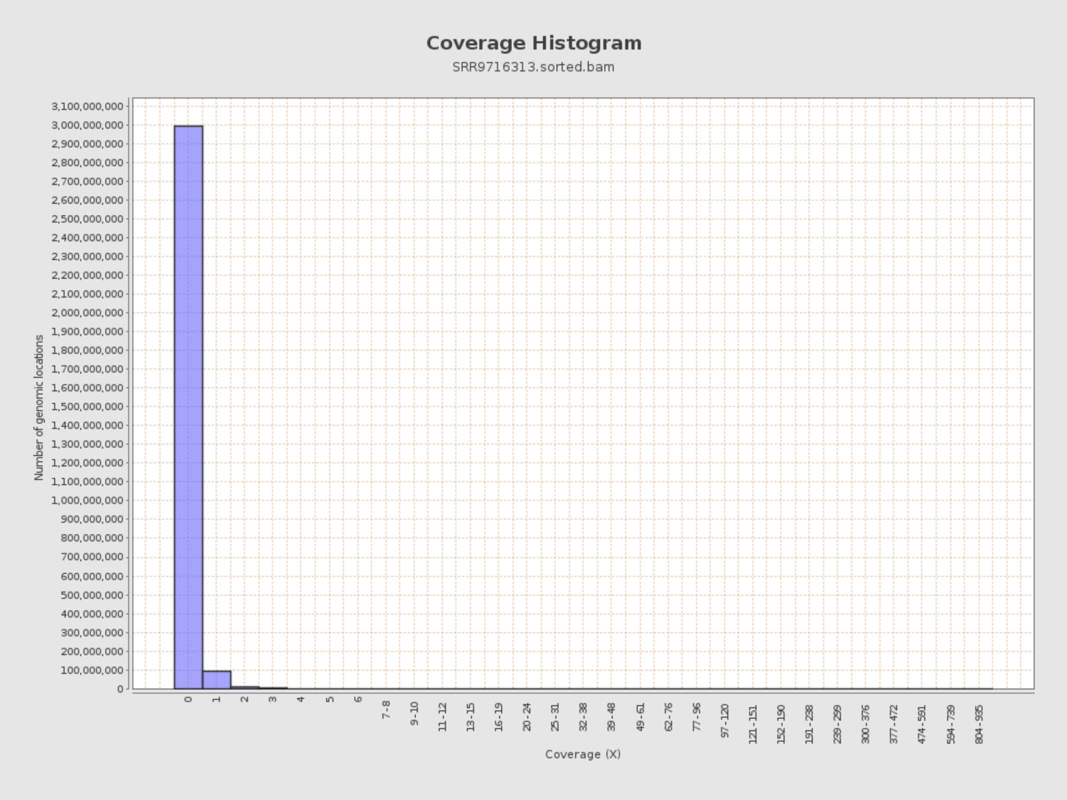
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11501560	0.0461	0.79
chr2	243199373	9730180	0.04	0.4048
chr3	198022430	7658479	0.0387	0.2168
chr4	191154276	7568766	0.0396	0.2741
chr5	180915260	6969782	0.0385	0.2186
chr6	171115067	6615203	0.0387	0.2381
chr7	159138663	6260192	0.0393	0.4445

chr8	146364022	5847828	0.04	0.4188
chr9	141213431	4800921	0.034	0.2986
chr10	135534747	5463857	0.0403	0.357
chr11	135006516	6722490	0.0498	0.4207
chr12	133851895	5092480	0.038	0.2153
chr13	115169878	4160583	0.0361	0.2102
chr14	107349540	3464277	0.0323	0.2136
chr15	102531392	3303534	0.0322	0.198
chr16	90354753	2643708	0.0293	0.2038
chr17	81195210	3728754	0.0459	0.2791
chr18	78077248	2980685	0.0382	0.5315
chr19	59128983	2200811	0.0372	0.5254
chr20	63025520	2445406	0.0388	0.2291
chr21	48129895	1542656	0.0321	0.2294
chr22	51304566	1293340	0.0252	0.1745
chrMT	16571	17010	1.0265	1.1056
chrX	155270560	6515999	0.042	0.2652
chrY	59373566	350514	0.0059	0.186

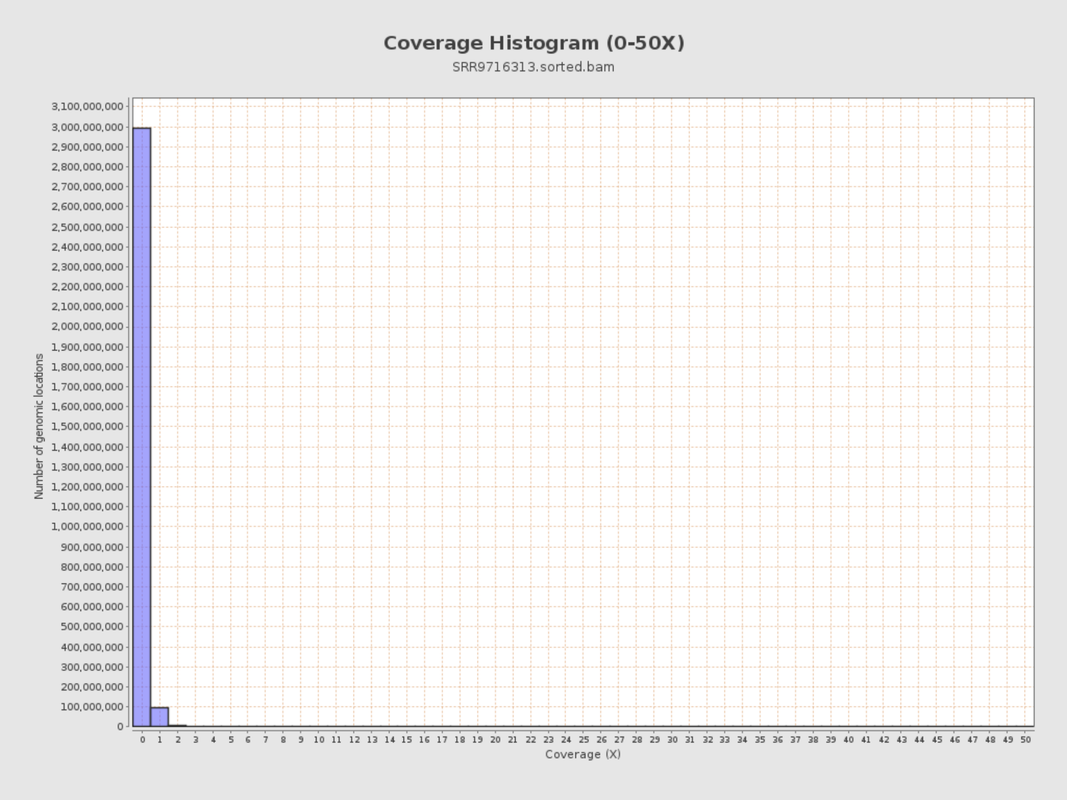
3. Results : Coverage across reference



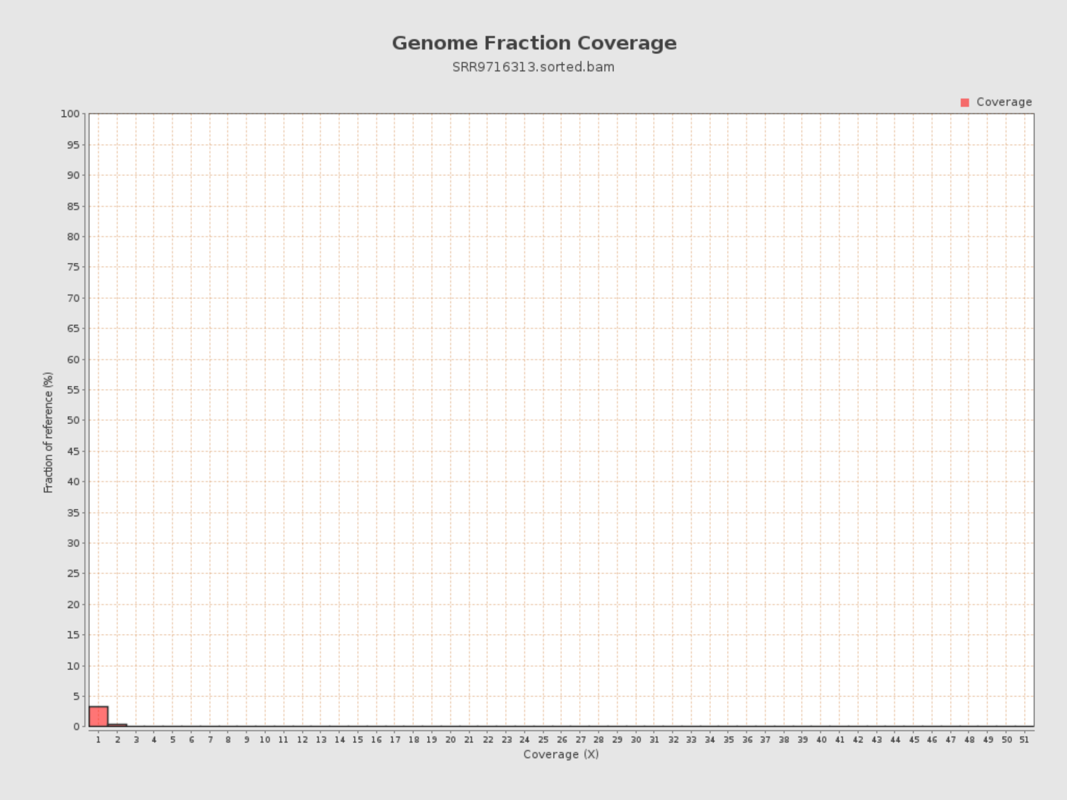
4. Results : Coverage Histogram



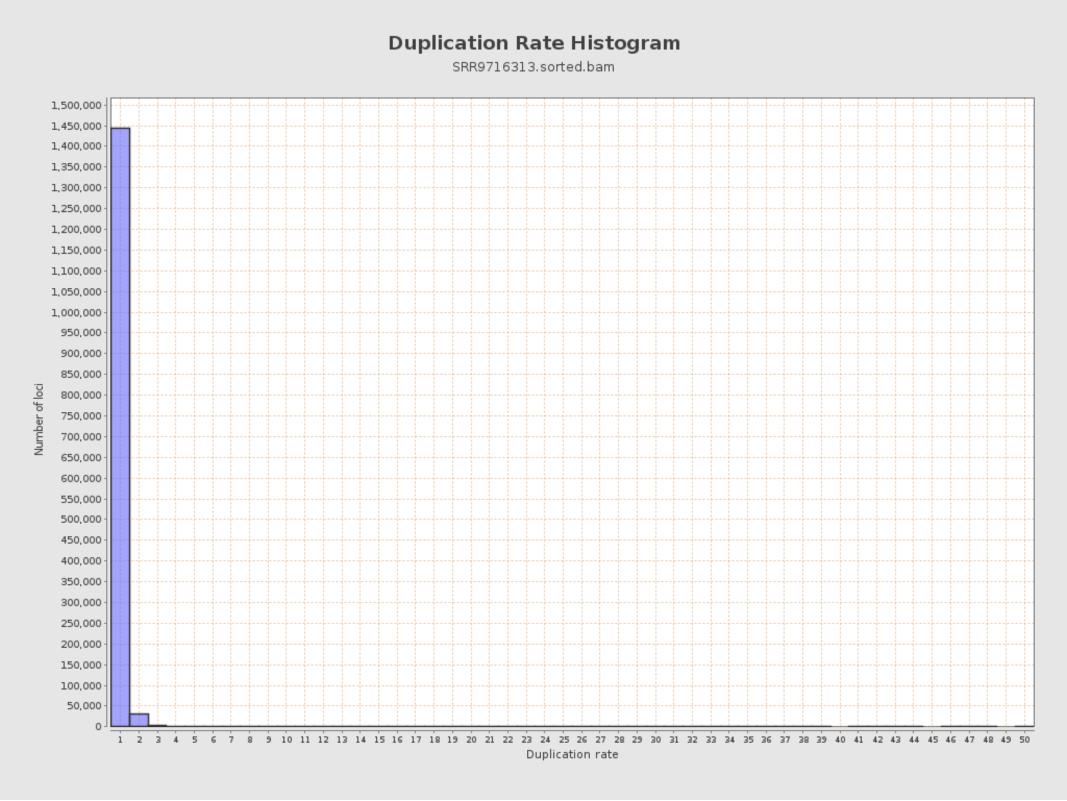
5. Results : Coverage Histogram (0-50X)



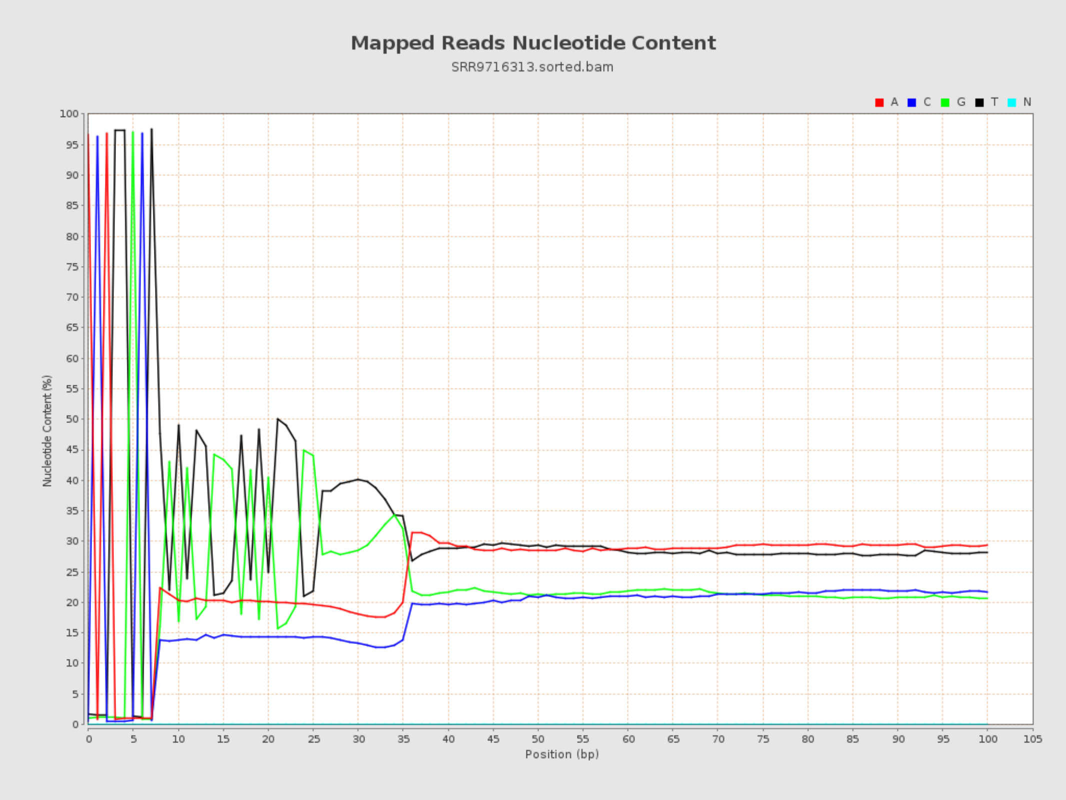
6. Results : Genome Fraction Coverage



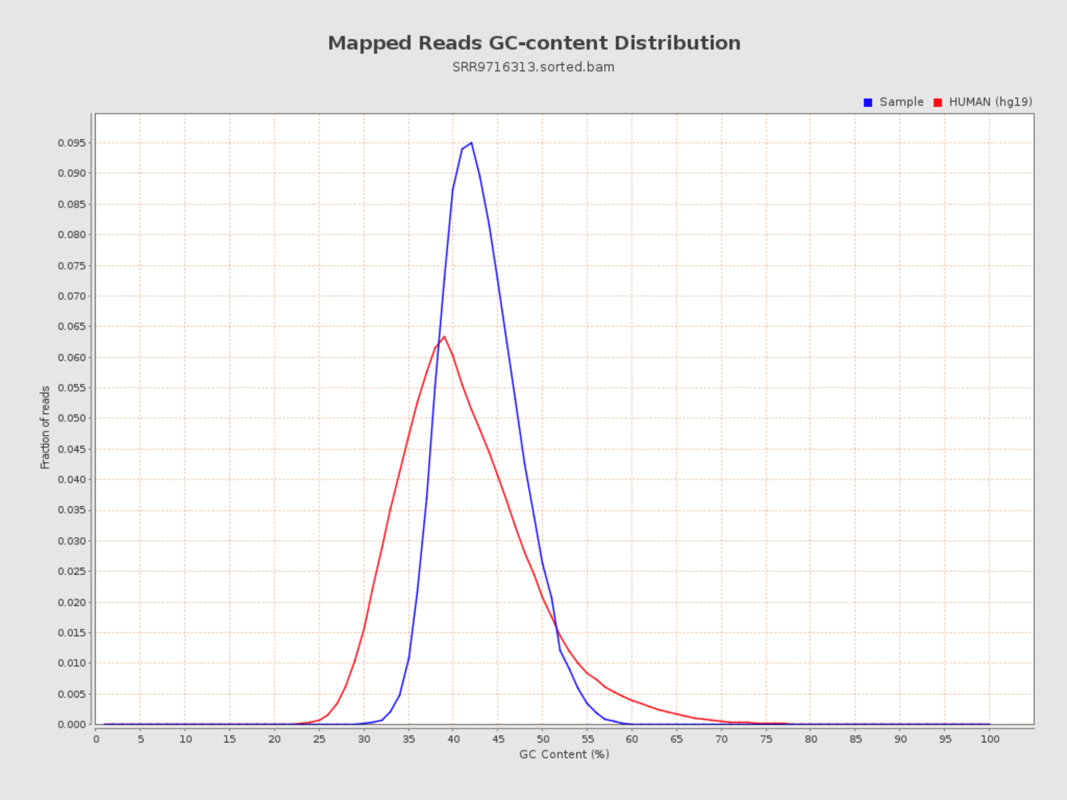
7. Results : Duplication Rate Histogram



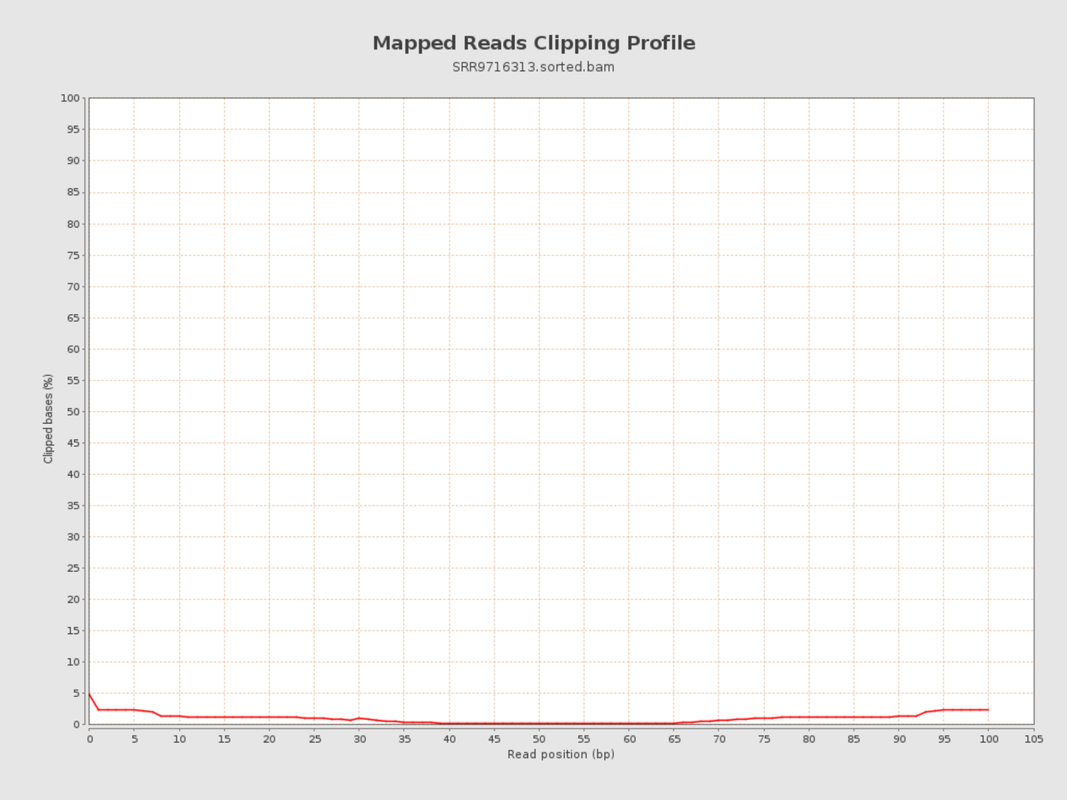
8. Results : Mapped Reads Nucleotide Content



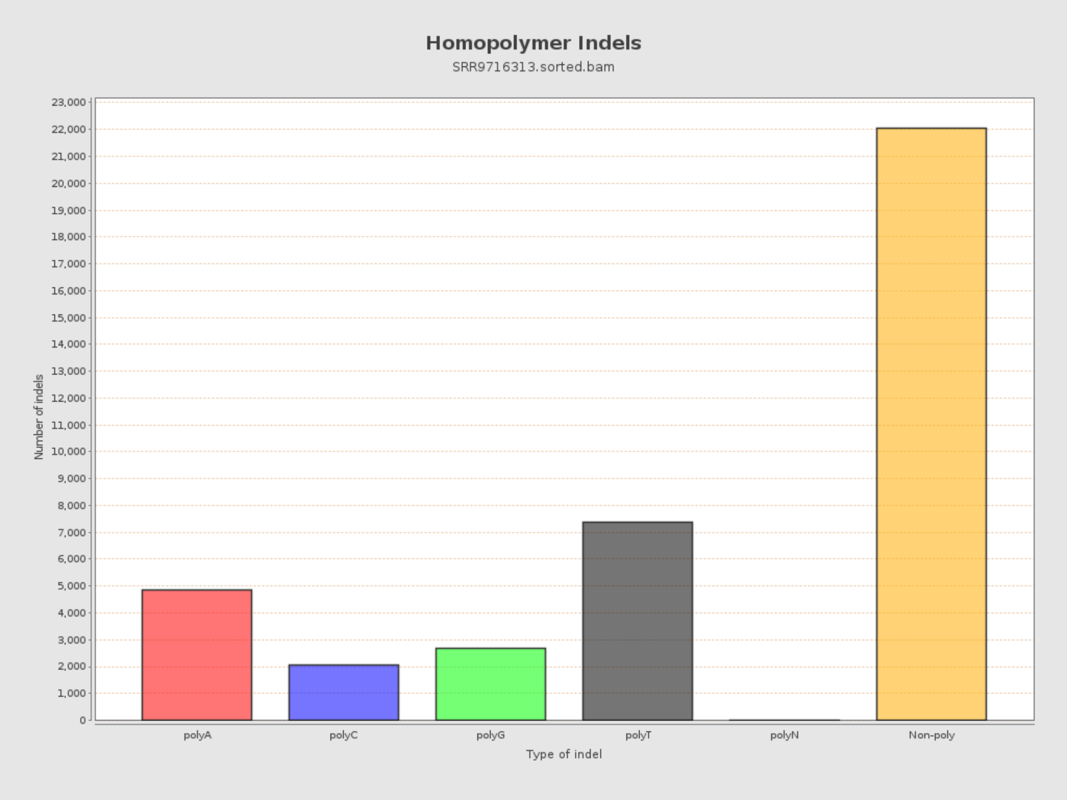
9. Results : Mapped Reads GC-content Distribution



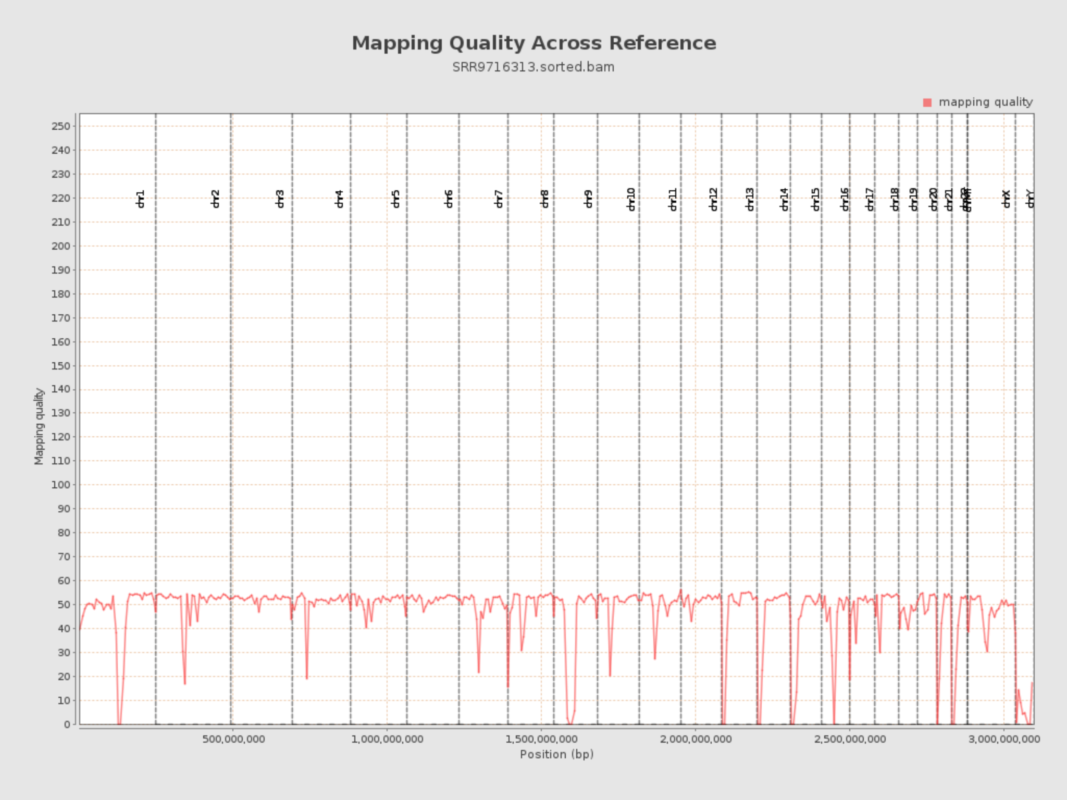
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram