Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:23:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716175.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_SRR9716175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:23:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,252,616
Mapped reads	1,964,682 / 87.22%
Unmapped reads	287,934 / 12.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	55,786 / 2.48%
Read min/max/mean length	30 / 101 / 101.89
Duplicated reads (estimated)	61,188 / 2.72%
Duplication rate	2.03%
Clipped reads	2,017,174 / 89.55%

2.2. ACGT Content

Number/percentage of A's	37,320,145 / 25.51%
Number/percentage of C's	28,902,357 / 19.75%
Number/percentage of T's	45,002,263 / 30.76%
Number/percentage of G's	35,071,568 / 23.97%
Number/percentage of N's	17,385 / 0.01%
GC Percentage	43.72%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.3981

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

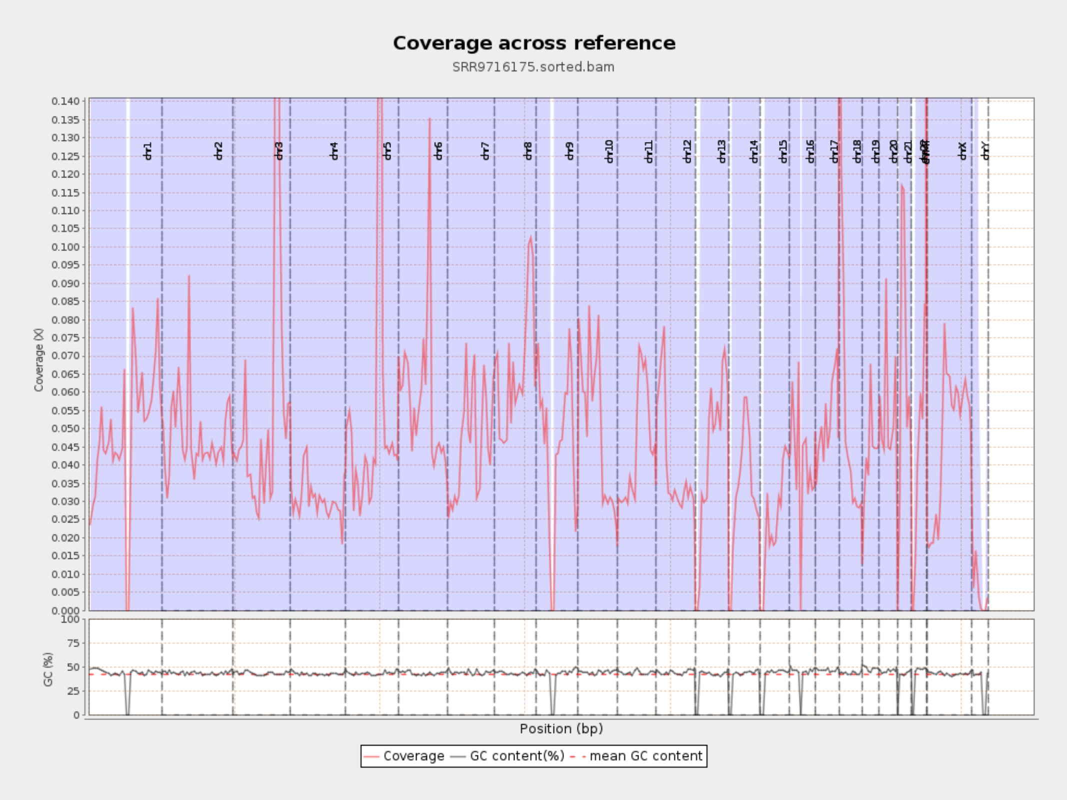
General error rate	0.75%
Mismatches	1,073,079
Insertions	12,382
Mapped reads with at least one insertion	0.62%
Deletions	31,788
Mapped reads with at least one deletion	1.6%
Homopolymer indels	40.89%

2.6. Chromosome stats

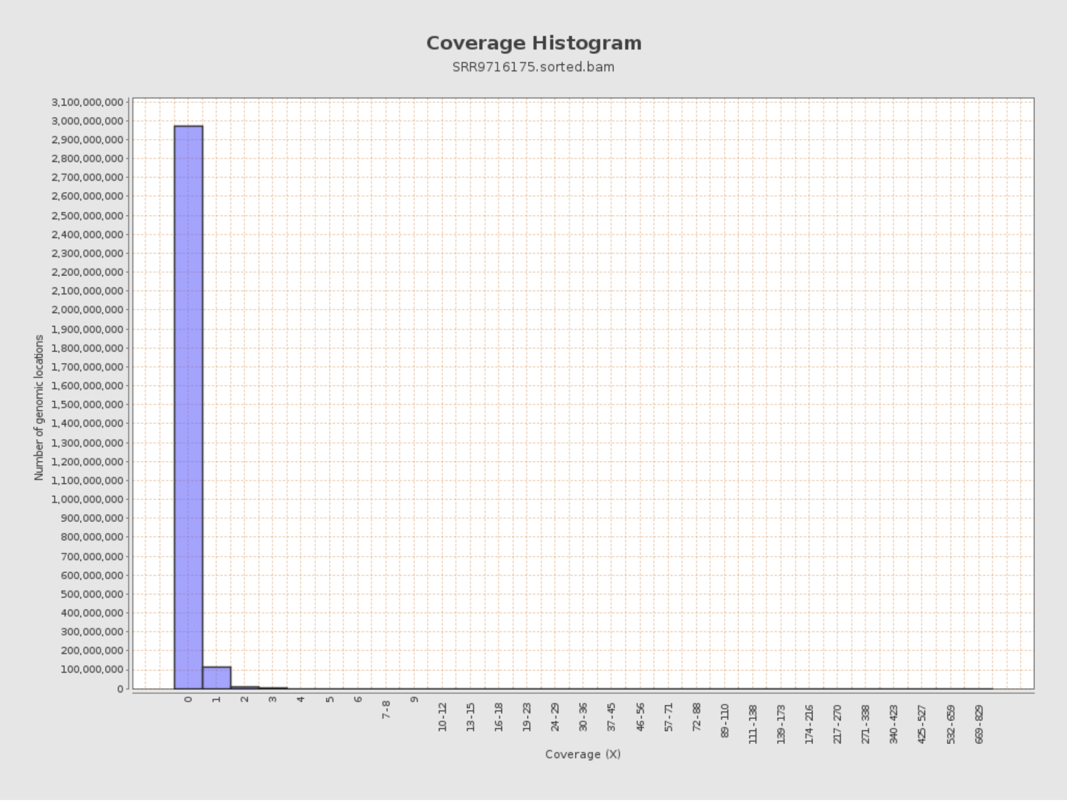
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12191927	0.0489	0.5541
chr2	243199373	11646453	0.0479	0.6135
chr3	198022430	11813797	0.0597	0.2879
chr4	191154276	5812725	0.0304	0.2085
chr5	180915260	9952366	0.055	0.2735
chr6	171115067	10154959	0.0593	0.2994
chr7	159138663	7429293	0.0467	0.5123

chr8	146364022	9829404	0.0672	0.5283
chr9	141213431	6392488	0.0453	0.3809
chr10	135534747	7085242	0.0523	0.4055
chr11	135006516	6123152	0.0454	0.3327
chr12	133851895	5360269	0.04	0.2243
chr13	115169878	4975232	0.0432	0.231
chr14	107349540	3506215	0.0327	0.2353
chr15	102531392	2553471	0.0249	0.1757
chr16	90354753	3657024	0.0405	0.2598
chr17	81195210	4246410	0.0523	0.2893
chr18	78077248	4549113	0.0583	0.7692
chr19	59128983	2554426	0.0432	0.5013
chr20	63025520	3498589	0.0555	0.2966
chr21	48129895	3091212	0.0642	0.2998
chr22	51304566	2101959	0.041	0.2303
chrMT	16571	173797	10.488	7.6007
chrX	155270560	7341743	0.0473	0.3151
chrY	59373566	327096	0.0055	0.1533

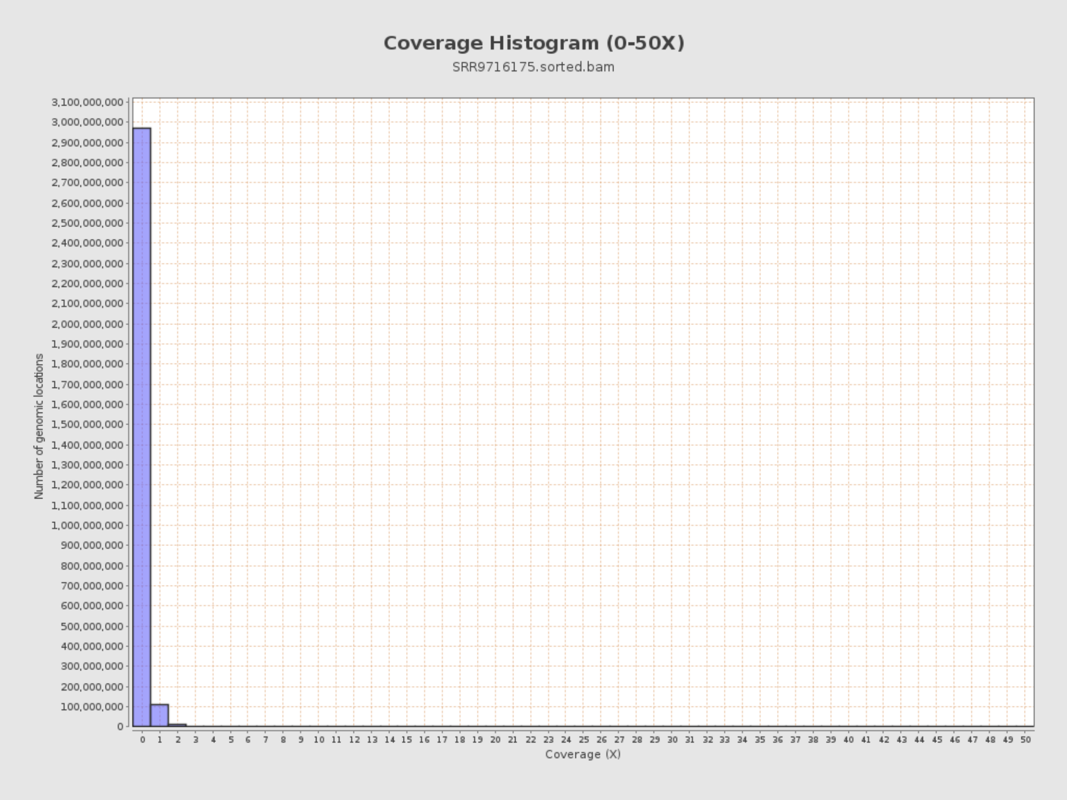
3. Results : Coverage across reference



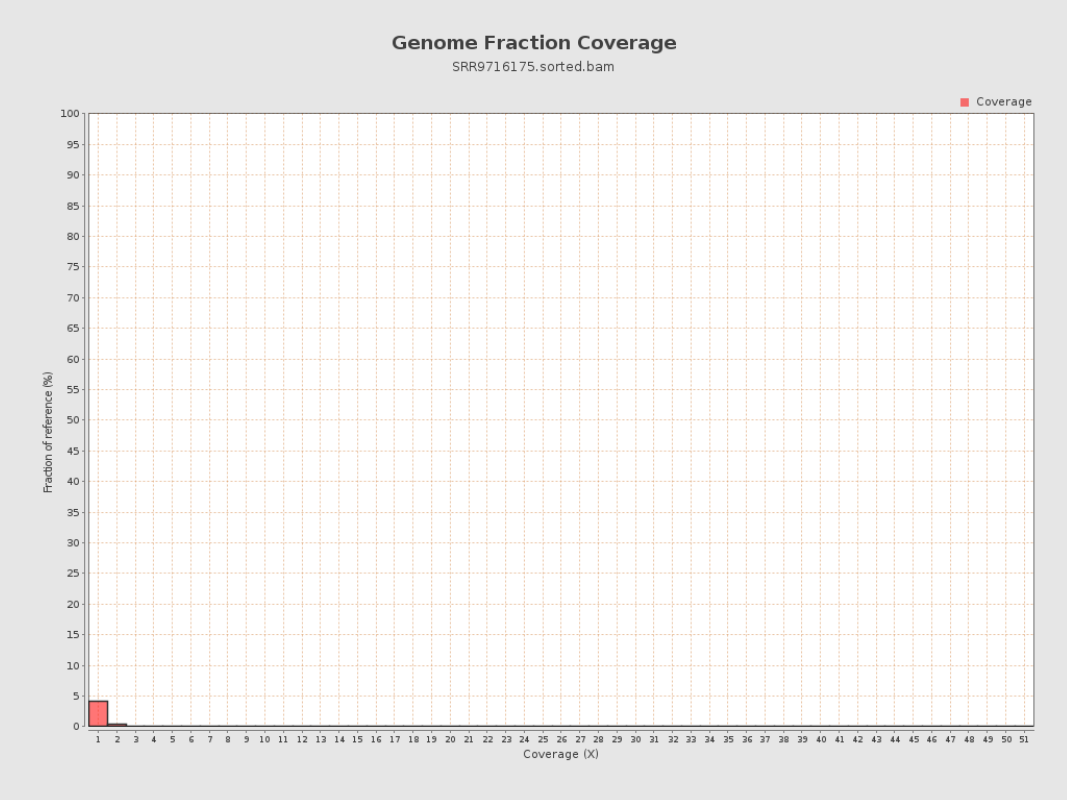
4. Results : Coverage Histogram



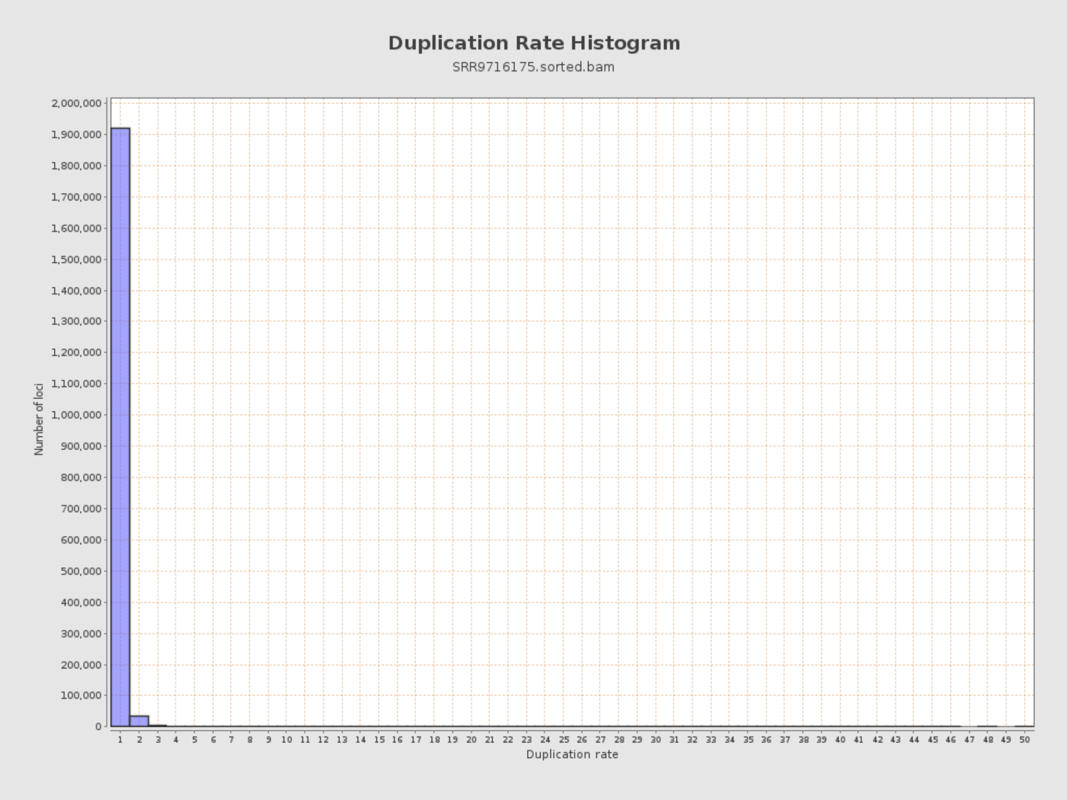
5. Results : Coverage Histogram (0-50X)



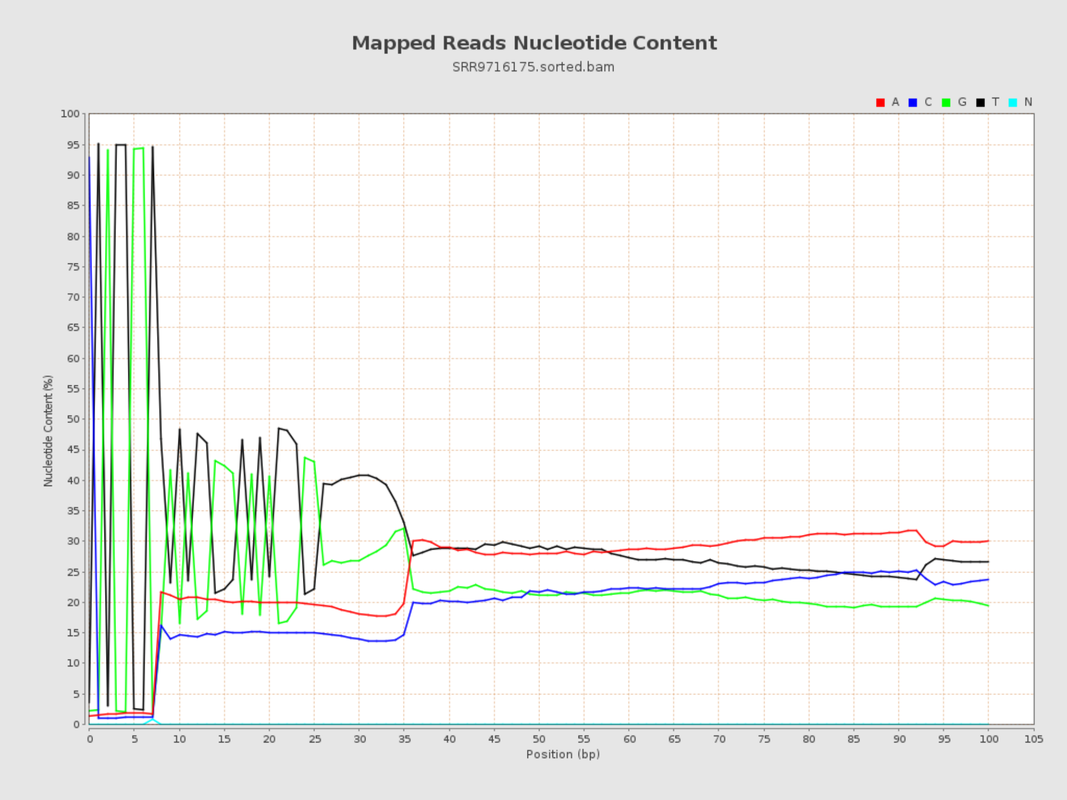
6. Results : Genome Fraction Coverage



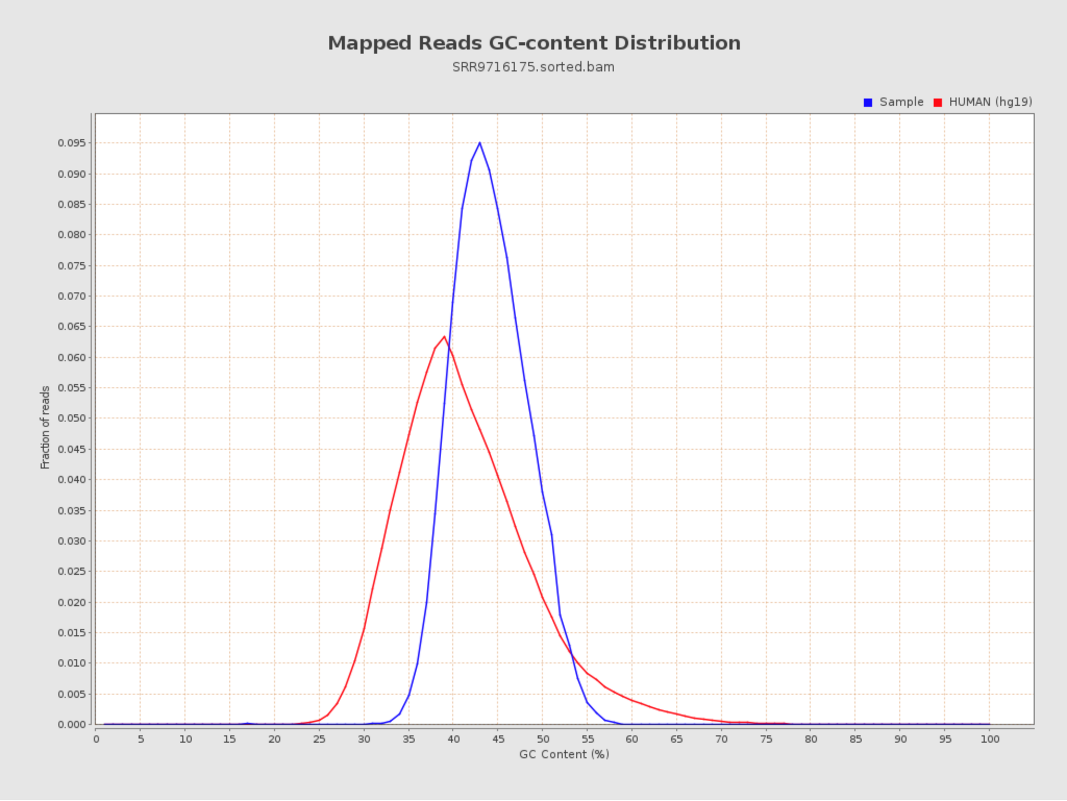
7. Results : Duplication Rate Histogram



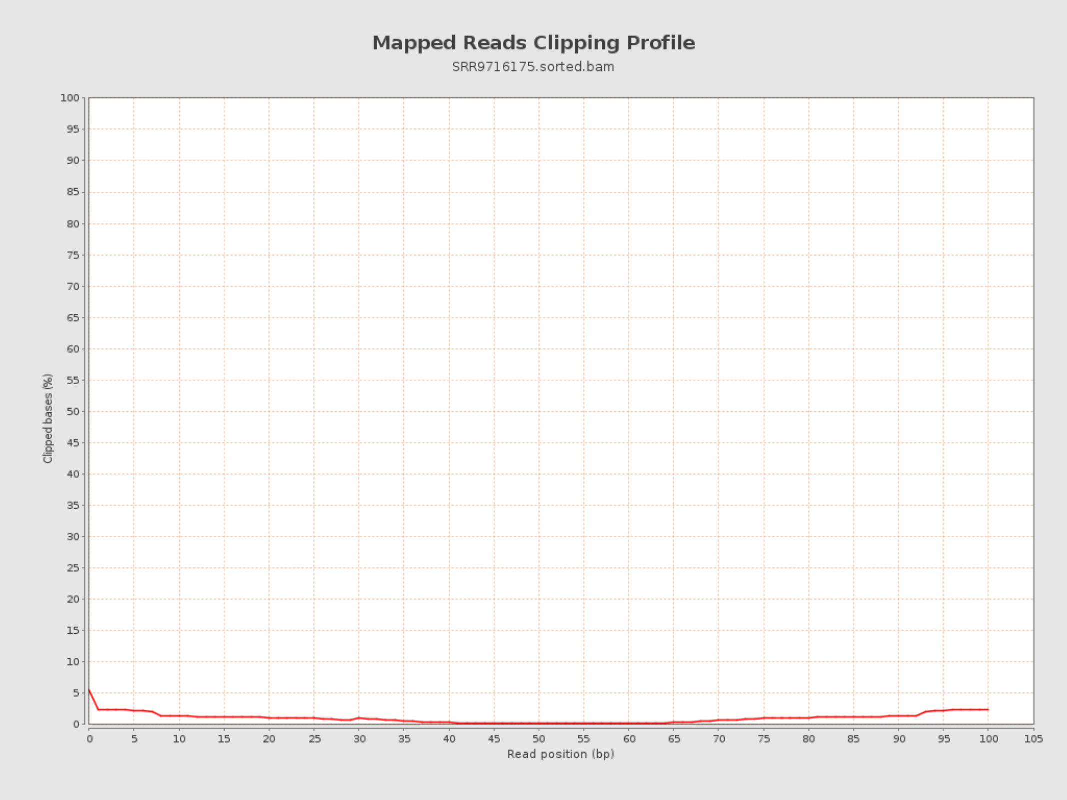
8. Results : Mapped Reads Nucleotide Content



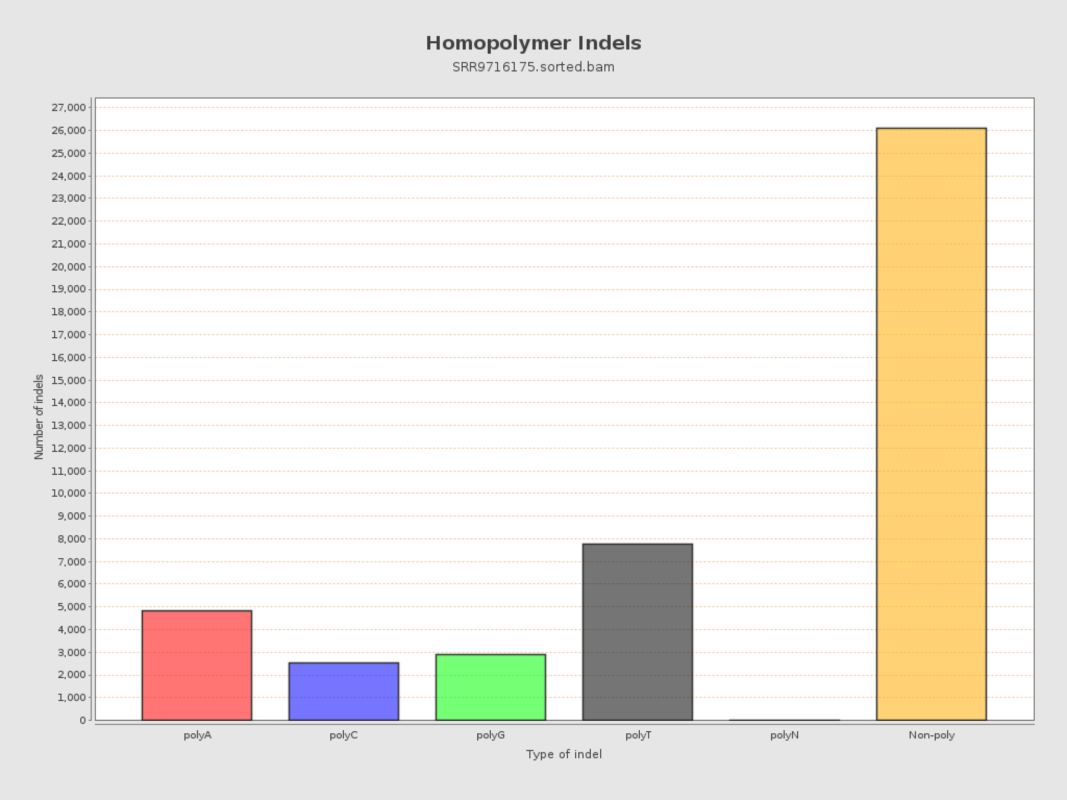
9. Results : Mapped Reads GC-content Distribution



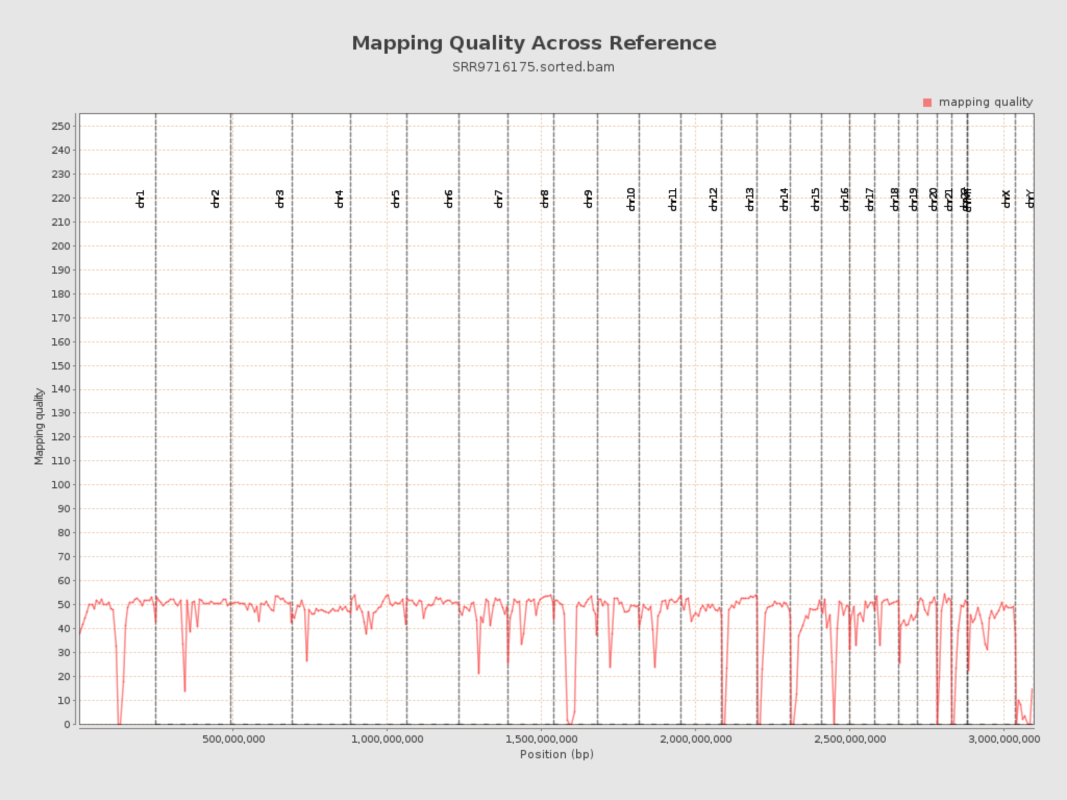
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram