Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 18:59:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716125.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_SRR9716125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 18:59:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,447
Mapped reads	2,068,685 / 93.63%
Unmapped reads	140,762 / 6.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	40,652 / 1.84%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	95,349 / 4.32%
Duplication rate	3.33%
Clipped reads	2,108,490 / 95.43%

2.2. ACGT Content

Number/percentage of A's	41,877,003 / 25.55%
Number/percentage of C's	32,863,804 / 20.05%
Number/percentage of T's	49,493,167 / 30.19%
Number/percentage of G's	39,683,810 / 24.21%
Number/percentage of N's	11,418 / 0.01%
GC Percentage	44.26%

2.3. Coverage

Mean	0.053

Standard Deviation	0.4741

2.4. Mapping Quality

Mean Mapping Quality	47.46

2.5. Mismatches and indels

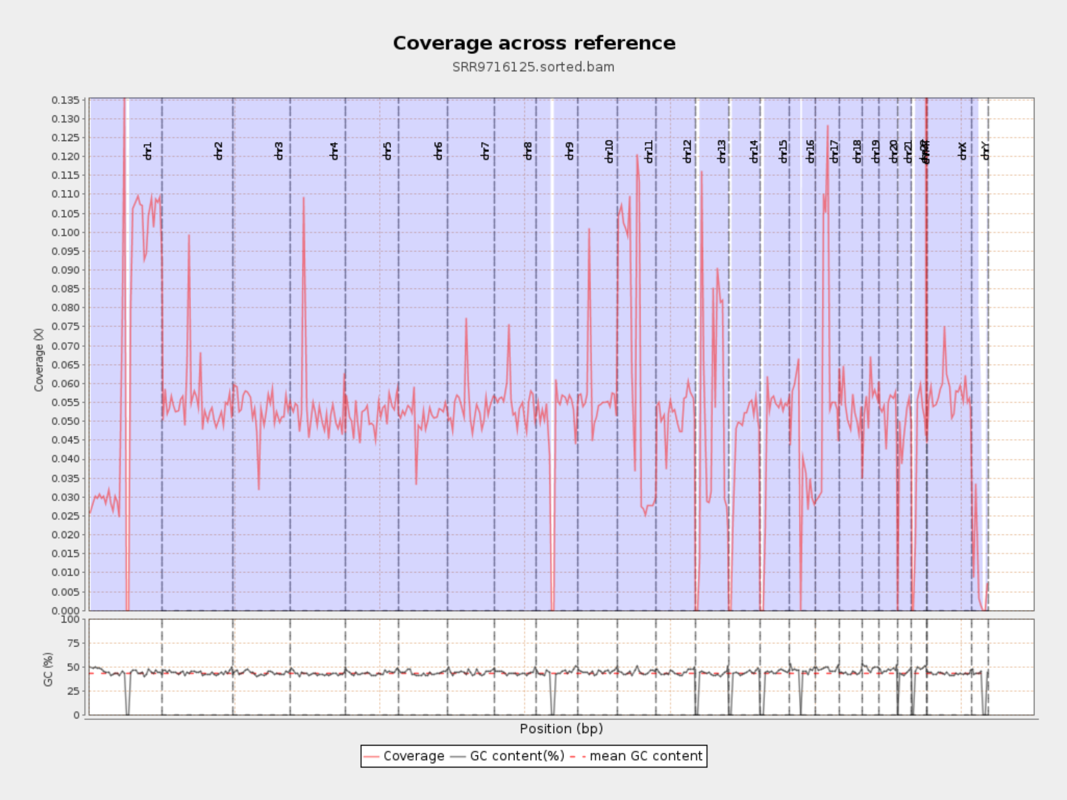
General error rate	0.66%
Mismatches	1,055,352
Insertions	13,037
Mapped reads with at least one insertion	0.62%
Deletions	40,411
Mapped reads with at least one deletion	1.92%
Homopolymer indels	43.46%

2.6. Chromosome stats

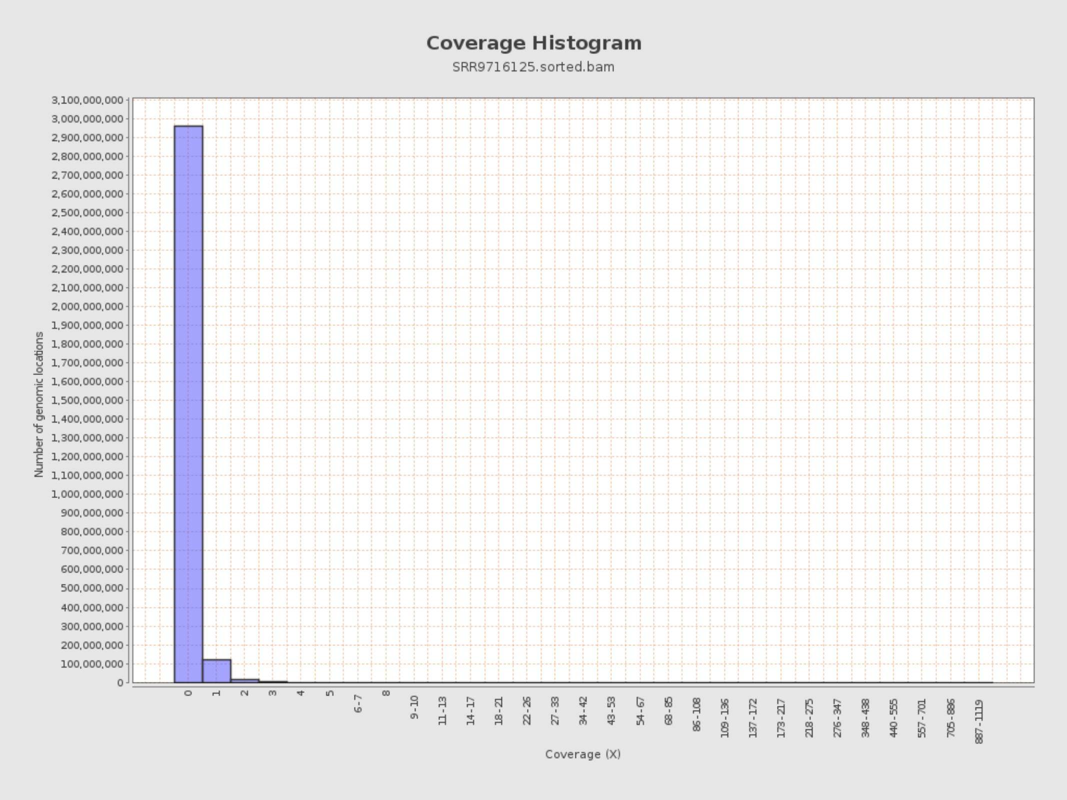
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16137849	0.0647	0.9984
chr2	243199373	13493067	0.0555	0.4956
chr3	198022430	10517995	0.0531	0.2625
chr4	191154276	10255883	0.0537	0.3579
chr5	180915260	9380263	0.0518	0.2627
chr6	171115067	8779845	0.0513	0.2842
chr7	159138663	8586516	0.054	0.5585

chr8	146364022	8097653	0.0553	0.5219
chr9	141213431	6702522	0.0475	0.4053
chr10	135534747	7696540	0.0568	0.4723
chr11	135006516	9129624	0.0676	0.5264
chr12	133851895	7015633	0.0524	0.2623
chr13	115169878	5703463	0.0495	0.2555
chr14	107349540	4636271	0.0432	0.26
chr15	102531392	4613705	0.045	0.2425
chr16	90354753	3657885	0.0405	0.2625
chr17	81195210	5210014	0.0642	0.3561
chr18	78077248	4184188	0.0536	0.665
chr19	59128983	3277410	0.0554	0.6793
chr20	63025520	3349707	0.0531	0.2819
chr21	48129895	2136513	0.0444	0.2965
chr22	51304566	1932566	0.0377	0.2252
chrMT	16571	91593	5.5273	3.6189
chrX	155270560	8908365	0.0574	0.3281
chrY	59373566	512319	0.0086	0.2913

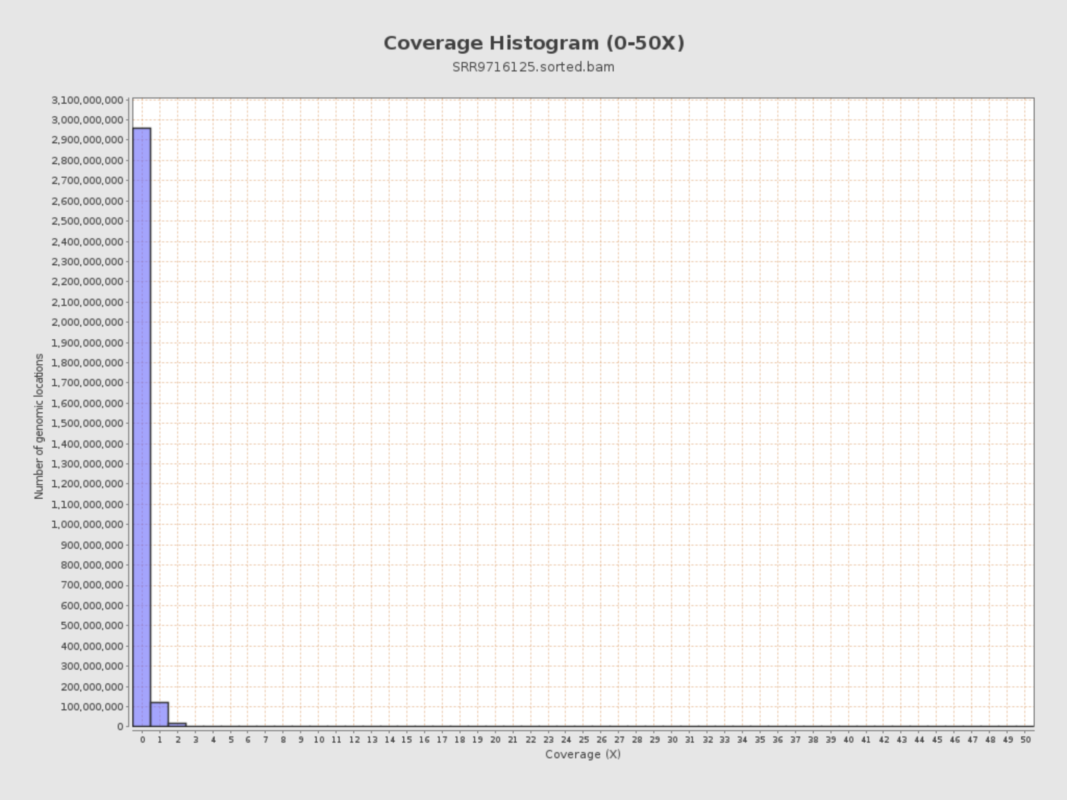
3. Results : Coverage across reference



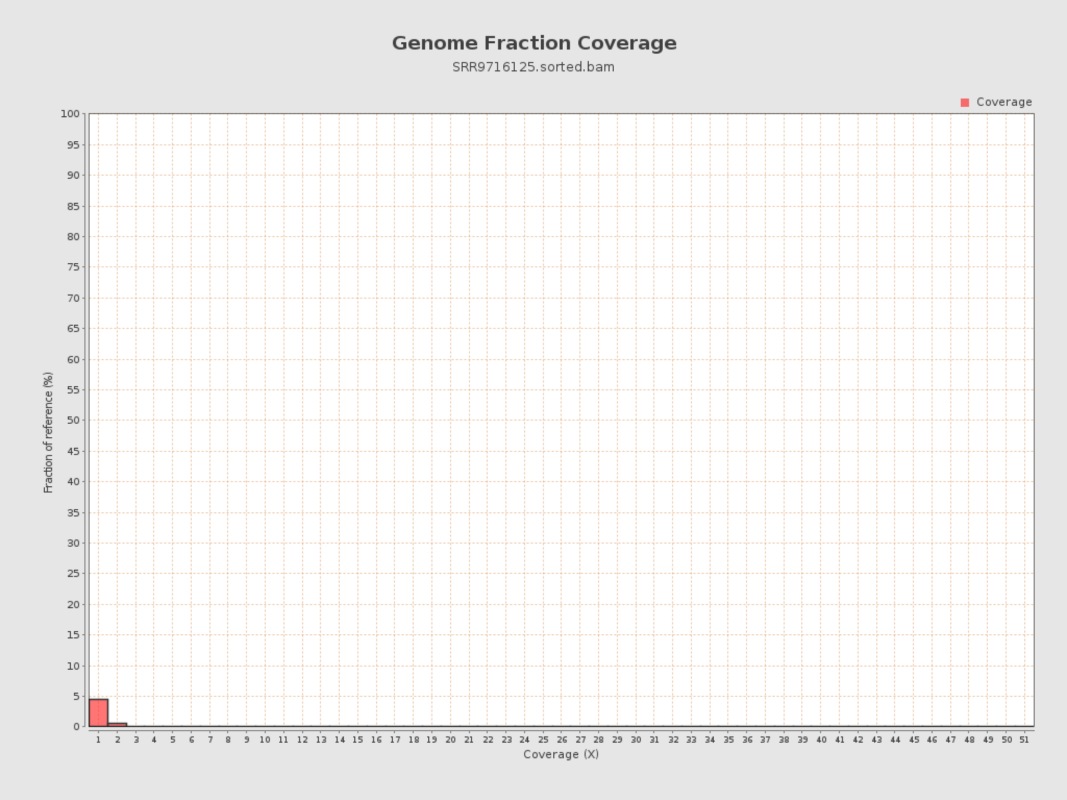
4. Results : Coverage Histogram



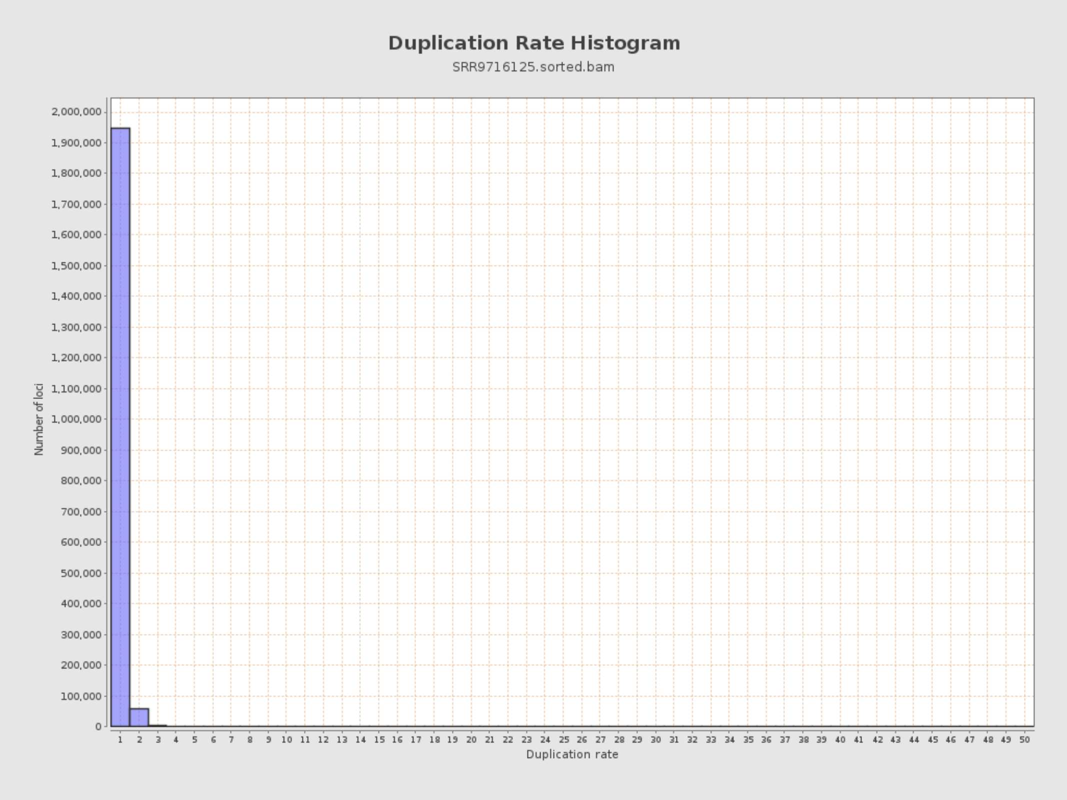
5. Results : Coverage Histogram (0-50X)



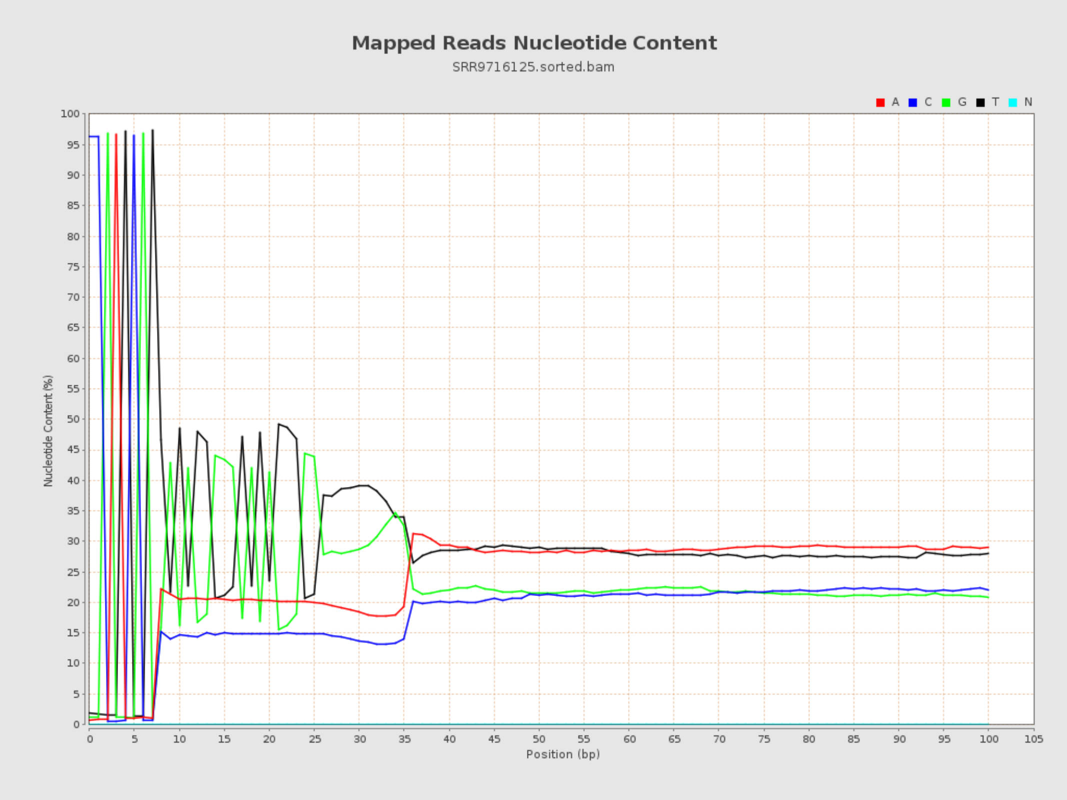
6. Results : Genome Fraction Coverage



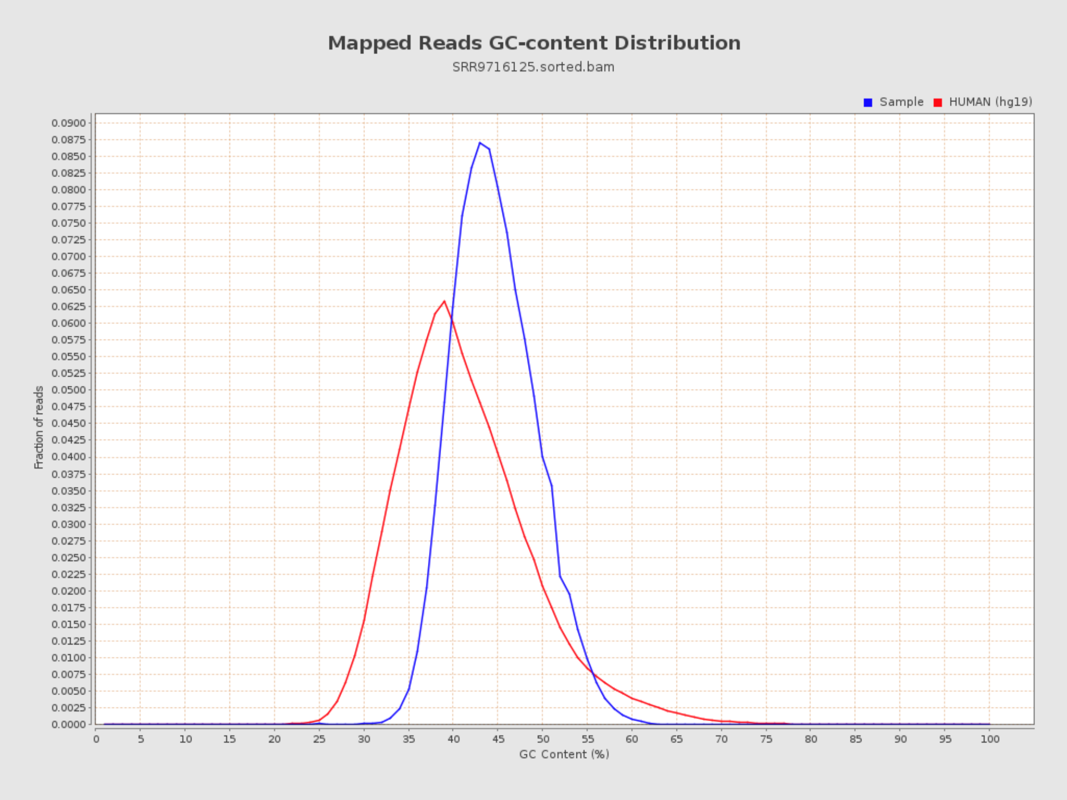
7. Results : Duplication Rate Histogram



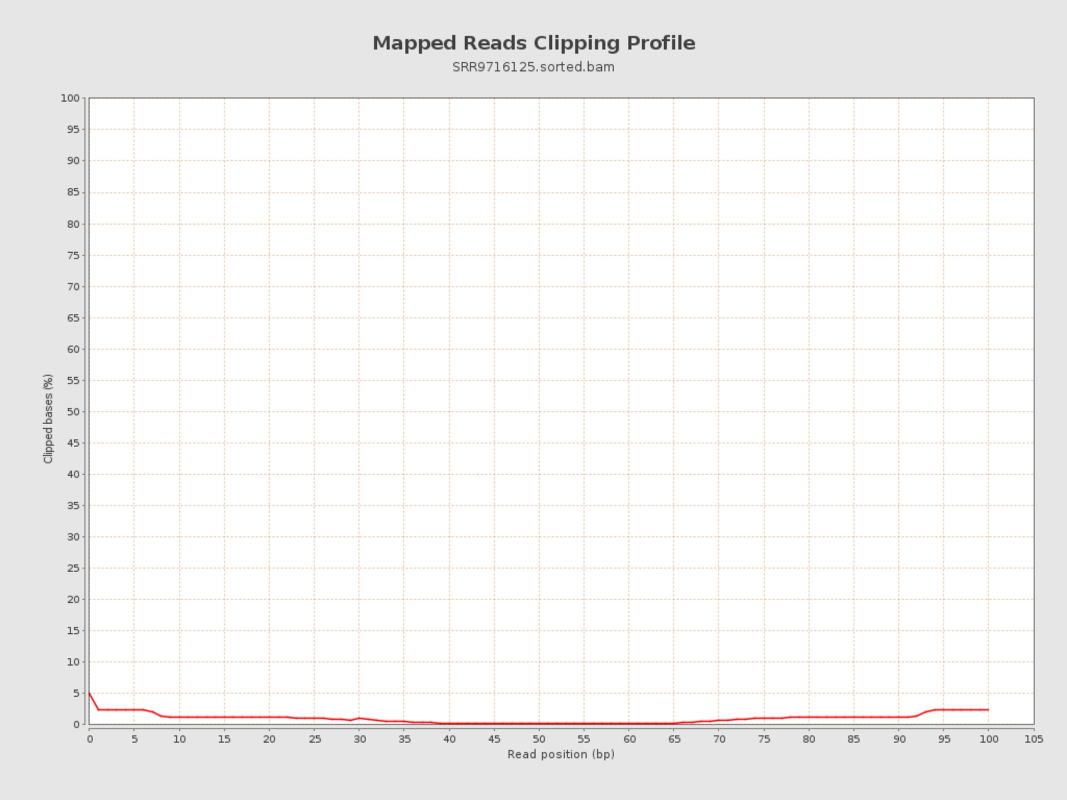
8. Results : Mapped Reads Nucleotide Content



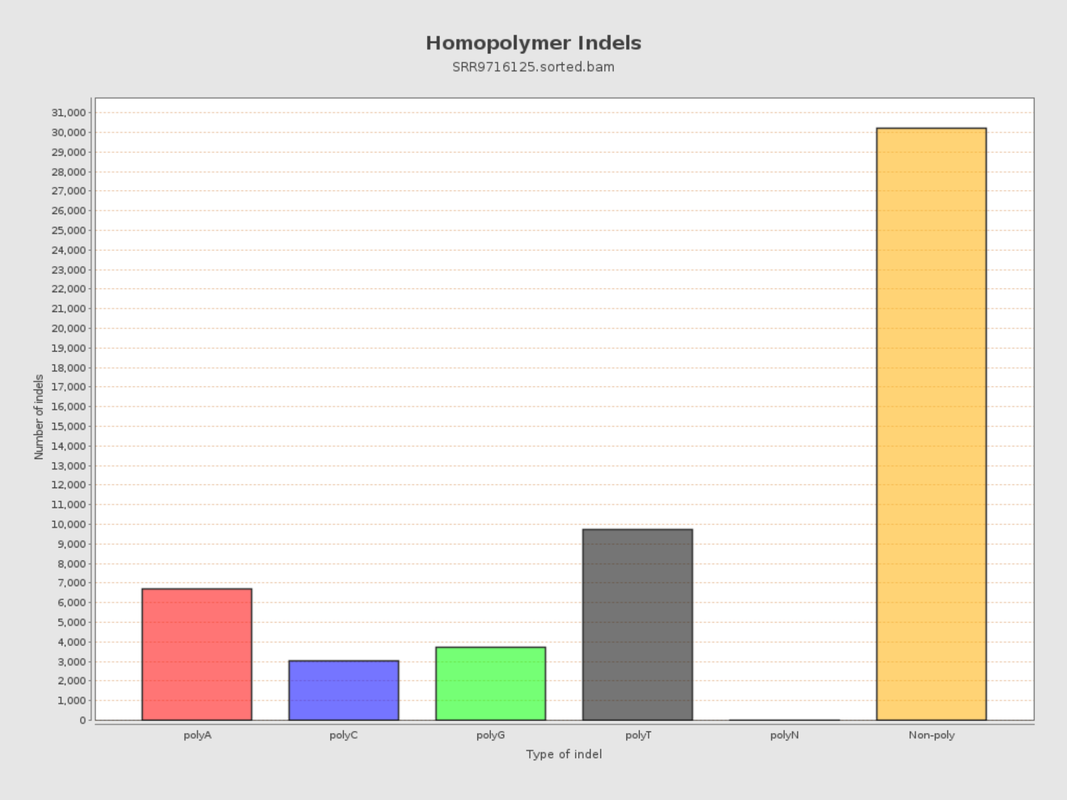
9. Results : Mapped Reads GC-content Distribution



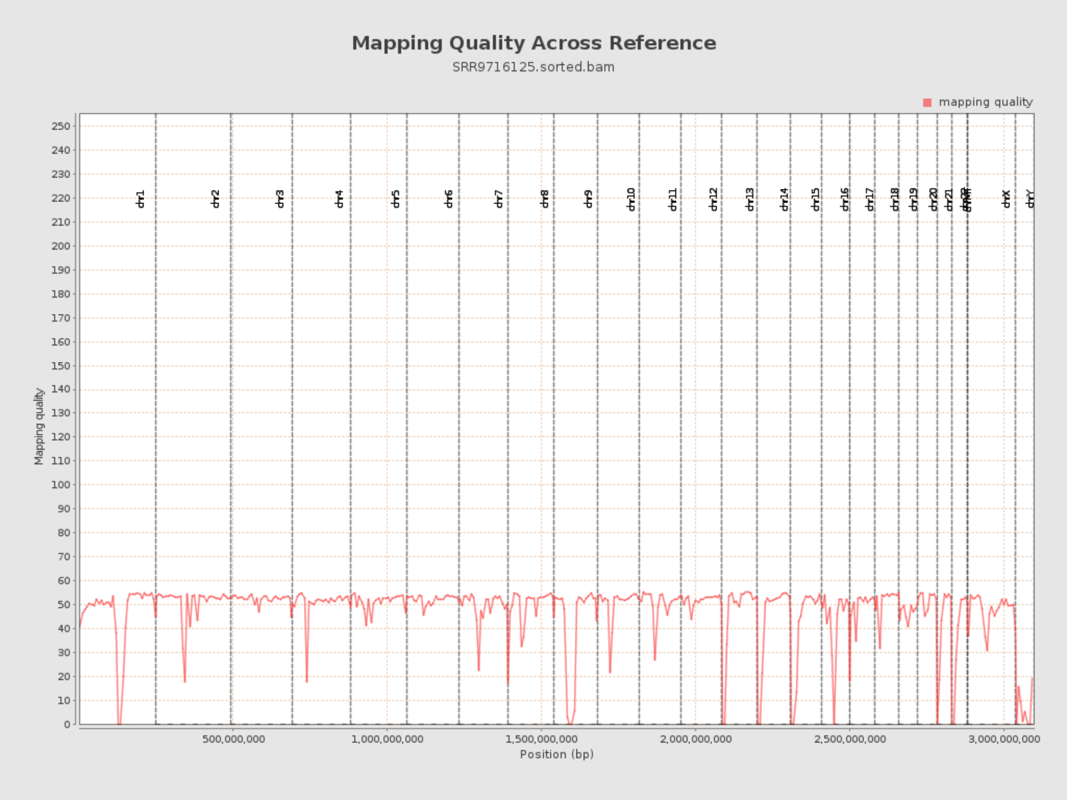
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram