Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:44:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716527.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_SRR9716527 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716527.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:44:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716527.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,058,729
Mapped reads	997,253 / 94.19%
Unmapped reads	61,476 / 5.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,380 / 1.92%
Read min/max/mean length	30 / 101 / 101.7
Duplicated reads (estimated)	27,586 / 2.61%
Duplication rate	1.88%
Clipped reads	1,016,119 / 95.98%

2.2. ACGT Content

Number/percentage of A's	20,431,653 / 25.89%
Number/percentage of C's	15,014,140 / 19.02%
Number/percentage of T's	23,866,002 / 30.24%
Number/percentage of G's	19,601,861 / 24.84%
Number/percentage of N's	5,464 / 0.01%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2736

2.4. Mapping Quality

Mean Mapping Quality	47.22

2.5. Mismatches and indels

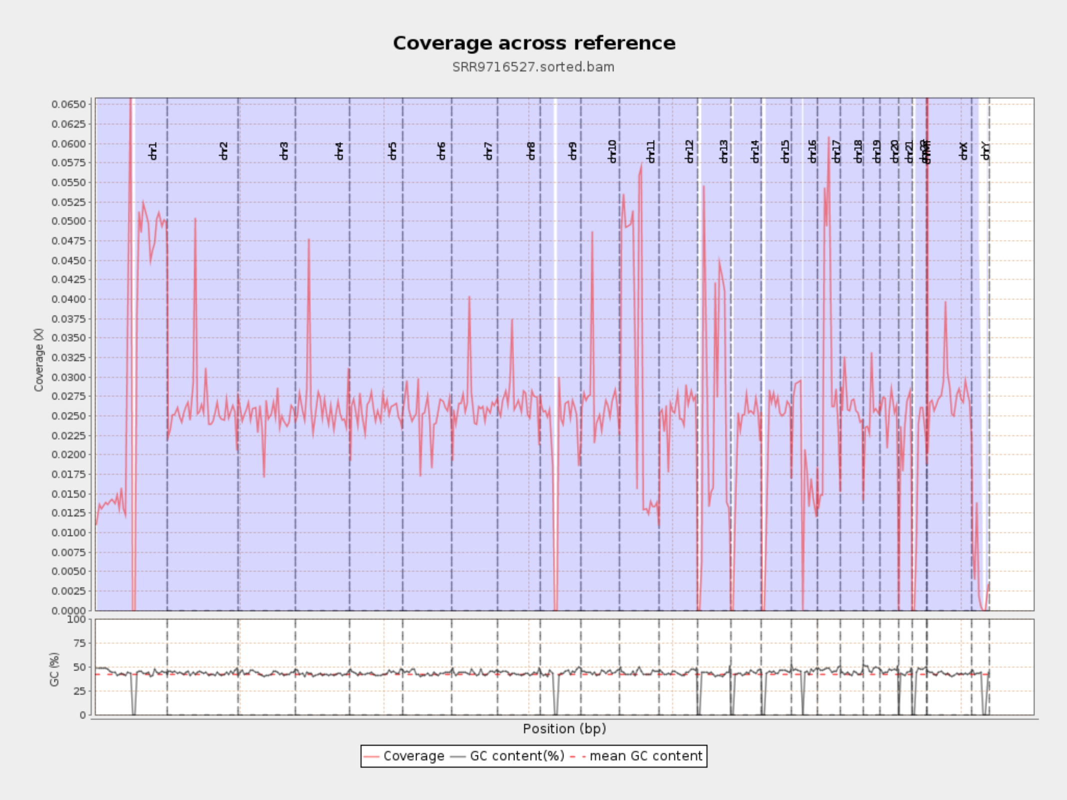
General error rate	0.65%
Mismatches	498,063
Insertions	6,544
Mapped reads with at least one insertion	0.65%
Deletions	18,716
Mapped reads with at least one deletion	1.85%
Homopolymer indels	42.2%

2.6. Chromosome stats

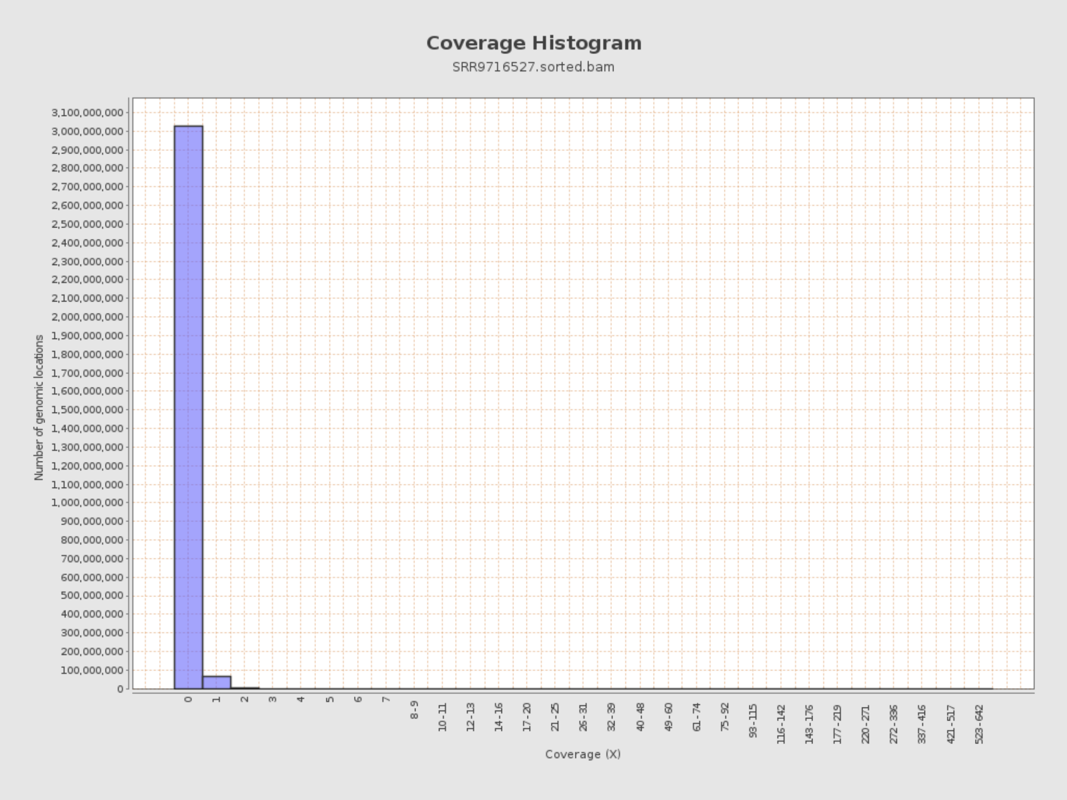
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7617644	0.0306	0.5712
chr2	243199373	6372144	0.0262	0.2826
chr3	198022430	4951679	0.025	0.1694
chr4	191154276	5082346	0.0266	0.1982
chr5	180915260	4666858	0.0258	0.1732
chr6	171115067	4325684	0.0253	0.182
chr7	159138663	4210223	0.0265	0.3052

chr8	146364022	3970003	0.0271	0.3043
chr9	141213431	3148265	0.0223	0.2238
chr10	135534747	3676697	0.0271	0.2624
chr11	135006516	4408233	0.0327	0.2977
chr12	133851895	3415653	0.0255	0.1712
chr13	115169878	2806837	0.0244	0.1676
chr14	107349540	2266638	0.0211	0.1666
chr15	102531392	2213063	0.0216	0.157
chr16	90354753	1721103	0.019	0.1575
chr17	81195210	2470241	0.0304	0.2148
chr18	78077248	2071467	0.0265	0.3747
chr19	59128983	1487342	0.0252	0.3795
chr20	63025520	1611919	0.0256	0.1795
chr21	48129895	1035050	0.0215	0.1717
chr22	51304566	864382	0.0168	0.1389
chrMT	16571	30694	1.8523	1.7204
chrX	155270560	4304904	0.0277	0.2017
chrY	59373566	224999	0.0038	0.1235

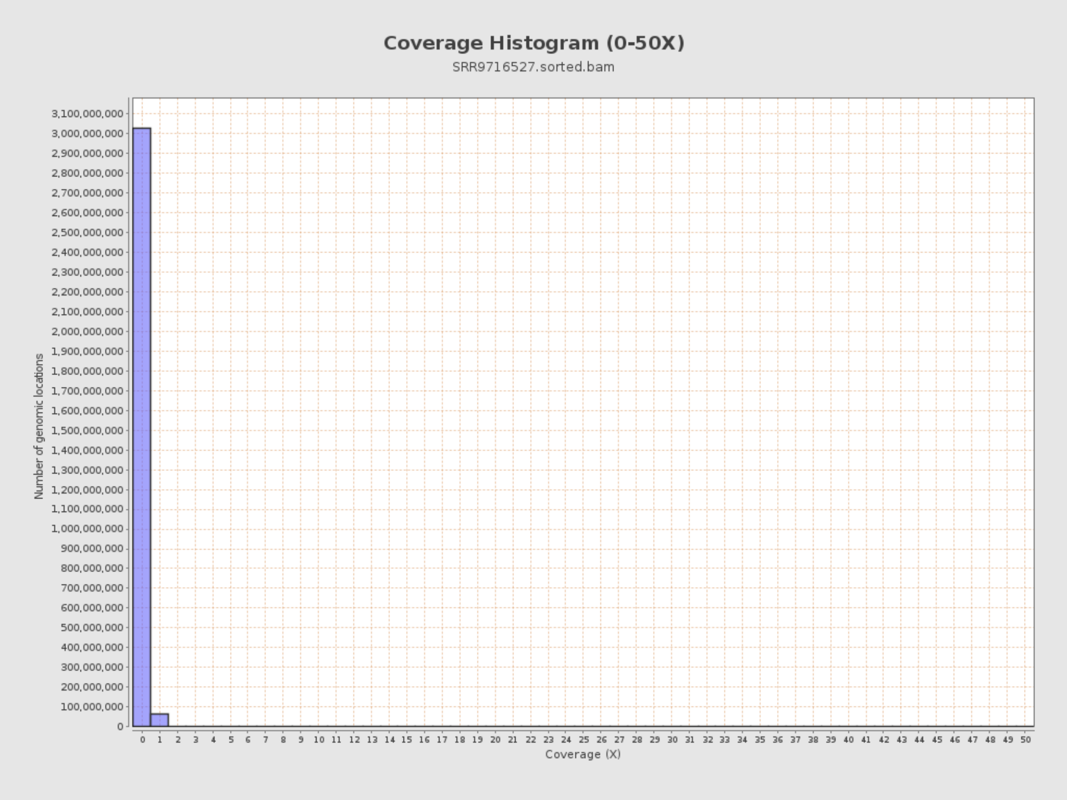
3. Results : Coverage across reference



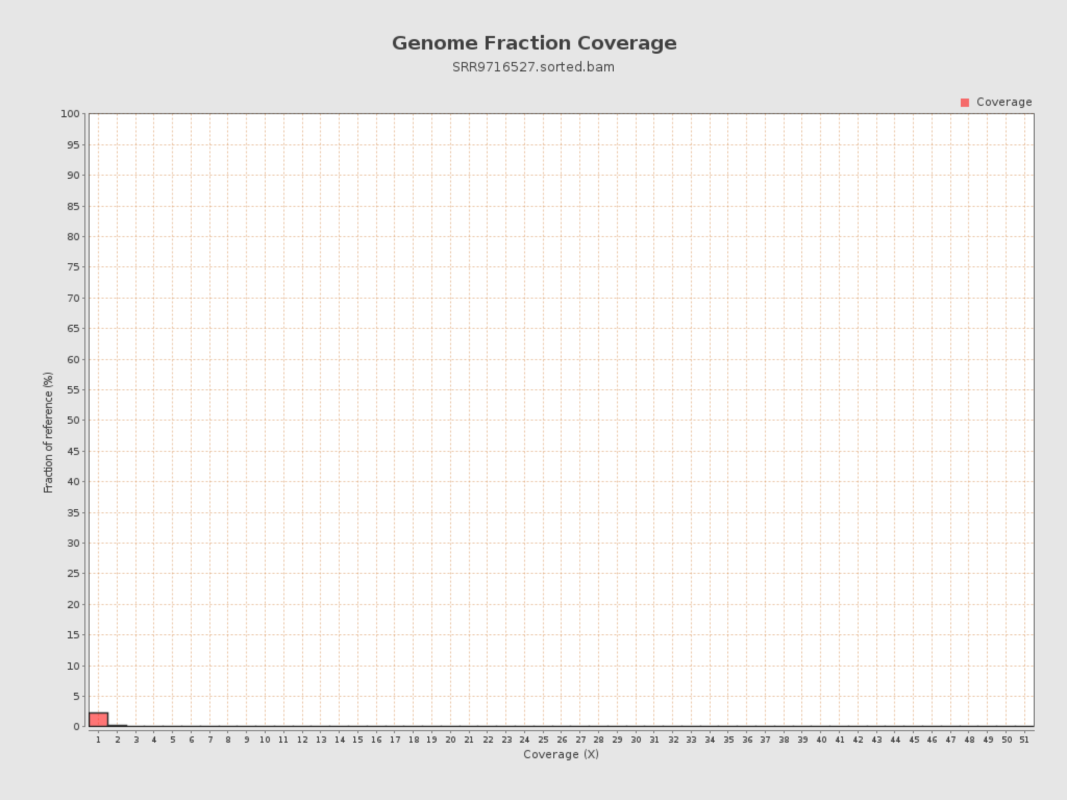
4. Results : Coverage Histogram



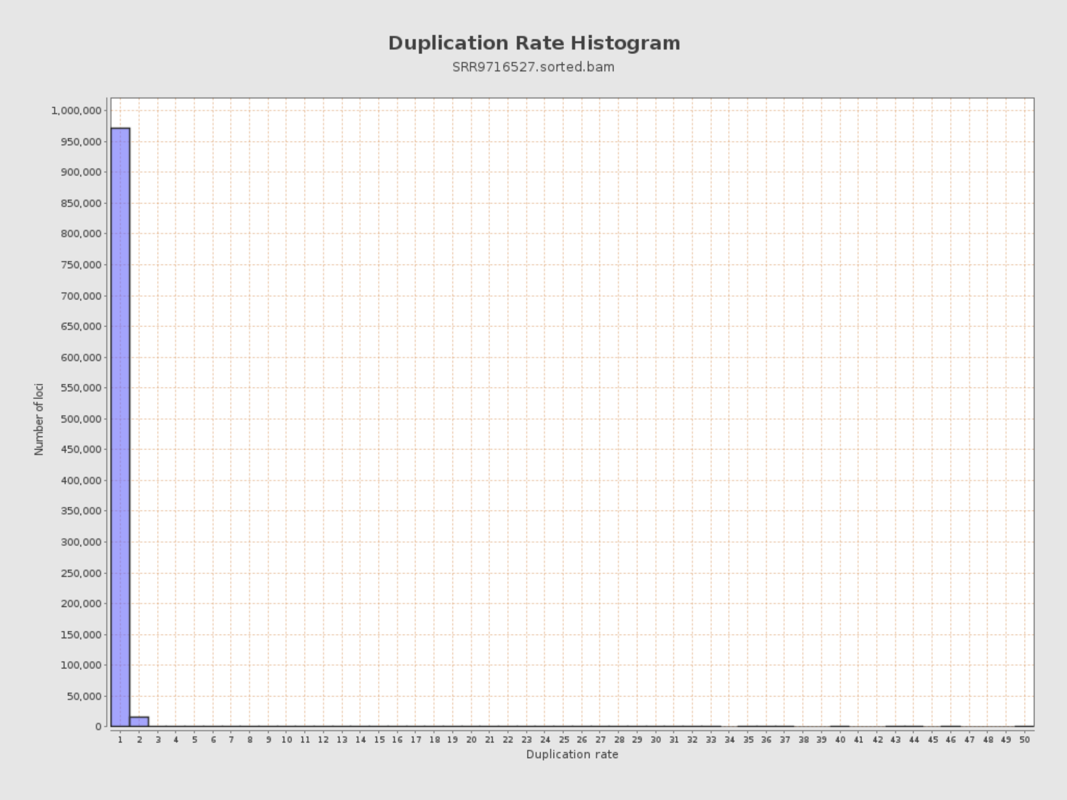
5. Results : Coverage Histogram (0-50X)



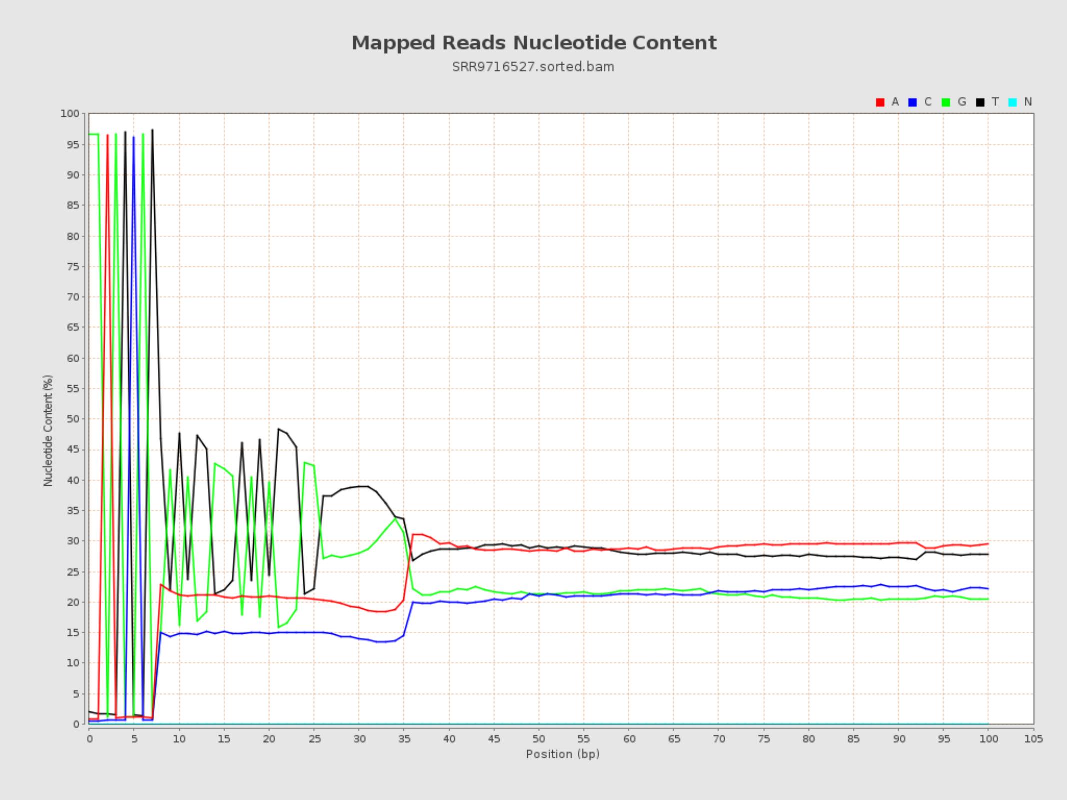
6. Results : Genome Fraction Coverage



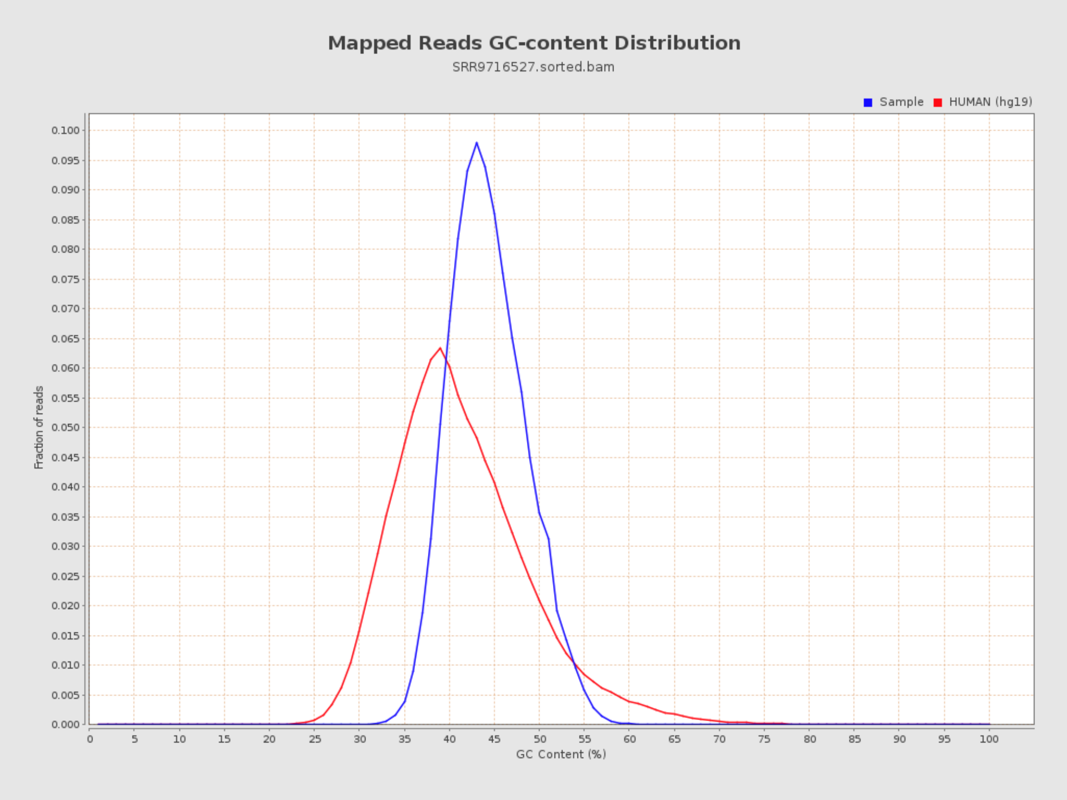
7. Results : Duplication Rate Histogram



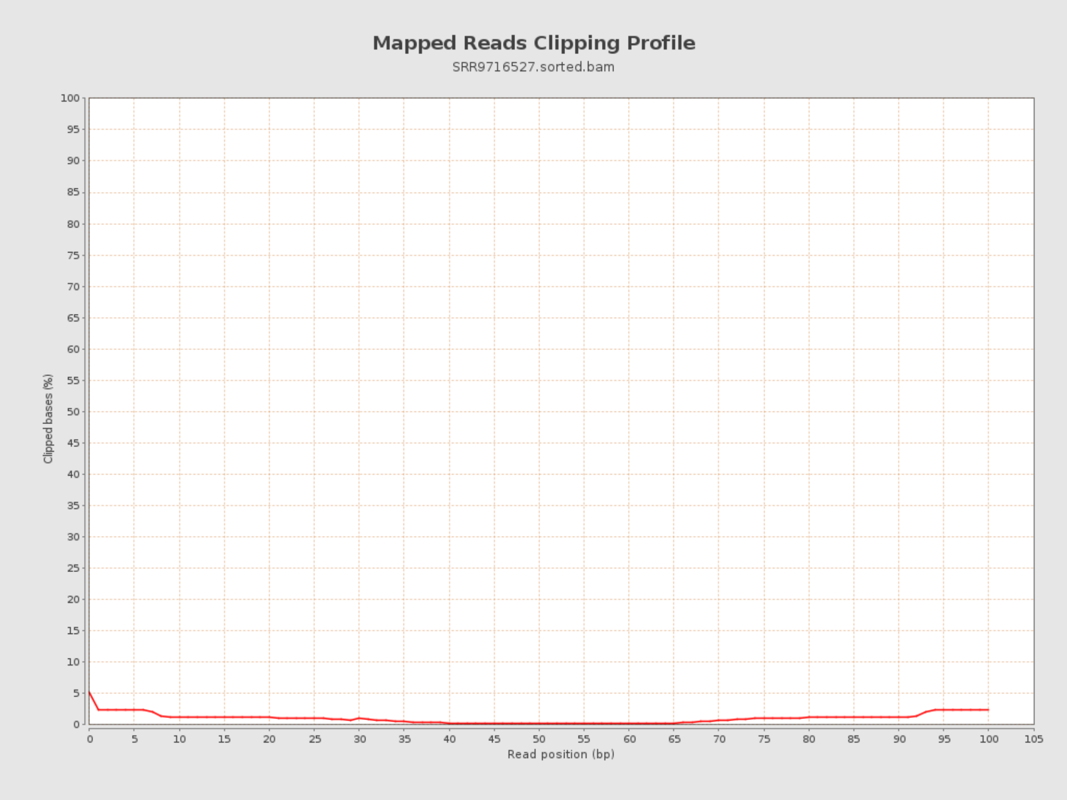
8. Results : Mapped Reads Nucleotide Content



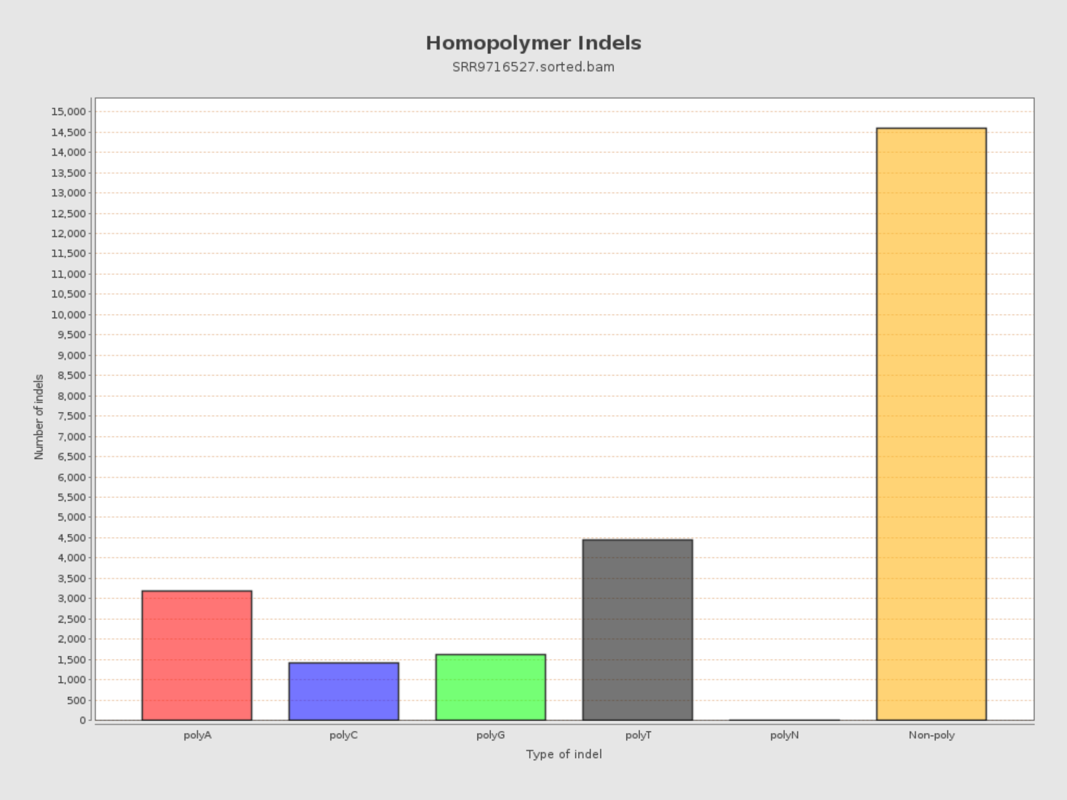
9. Results : Mapped Reads GC-content Distribution



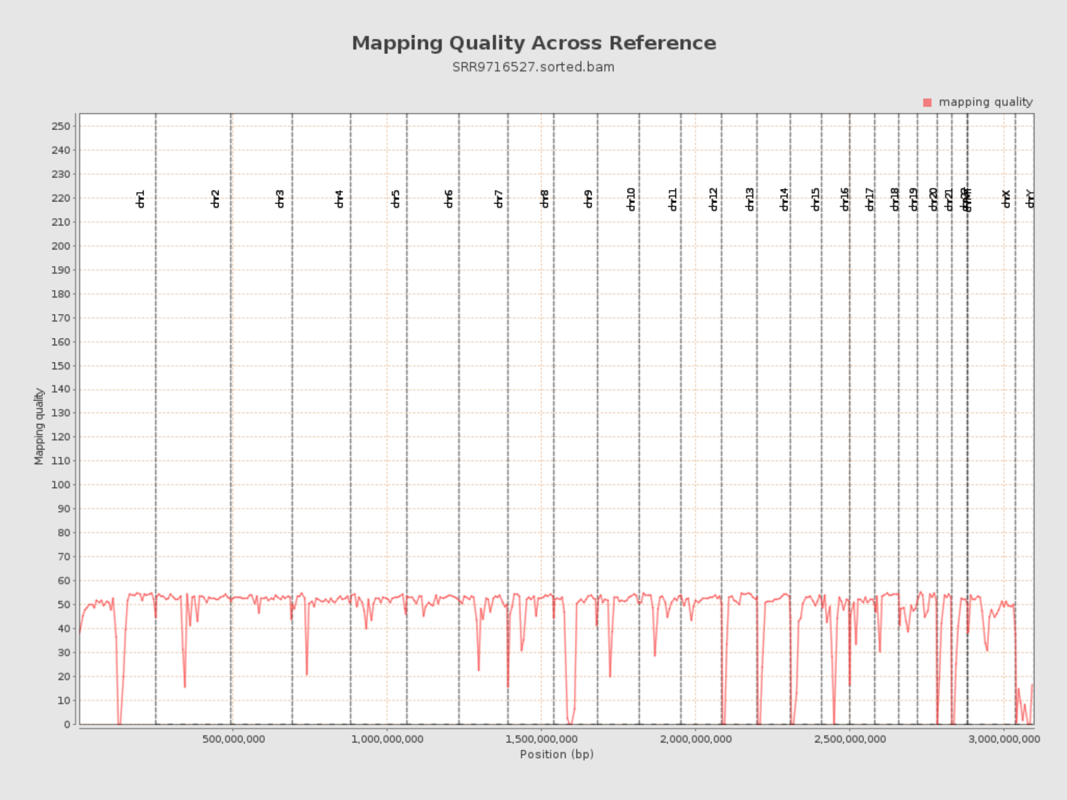
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram