Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 00:52:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716213.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_SRR9716213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716213.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 00:52:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716213.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,832,047
Mapped reads	1,621,749 / 88.52%
Unmapped reads	210,298 / 11.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,634 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	45,288 / 2.47%
Duplication rate	2.09%
Clipped reads	1,623,988 / 88.64%

2.2. ACGT Content

Number/percentage of A's	22,126,748 / 24.16%
Number/percentage of C's	19,081,535 / 20.84%
Number/percentage of T's	28,797,591 / 31.45%
Number/percentage of G's	21,563,822 / 23.55%
Number/percentage of N's	1,970 / 0%
GC Percentage	44.39%

2.3. Coverage

Mean	0.0296

Standard Deviation	0.2331

2.4. Mapping Quality

Mean Mapping Quality	43.4

2.5. Mismatches and indels

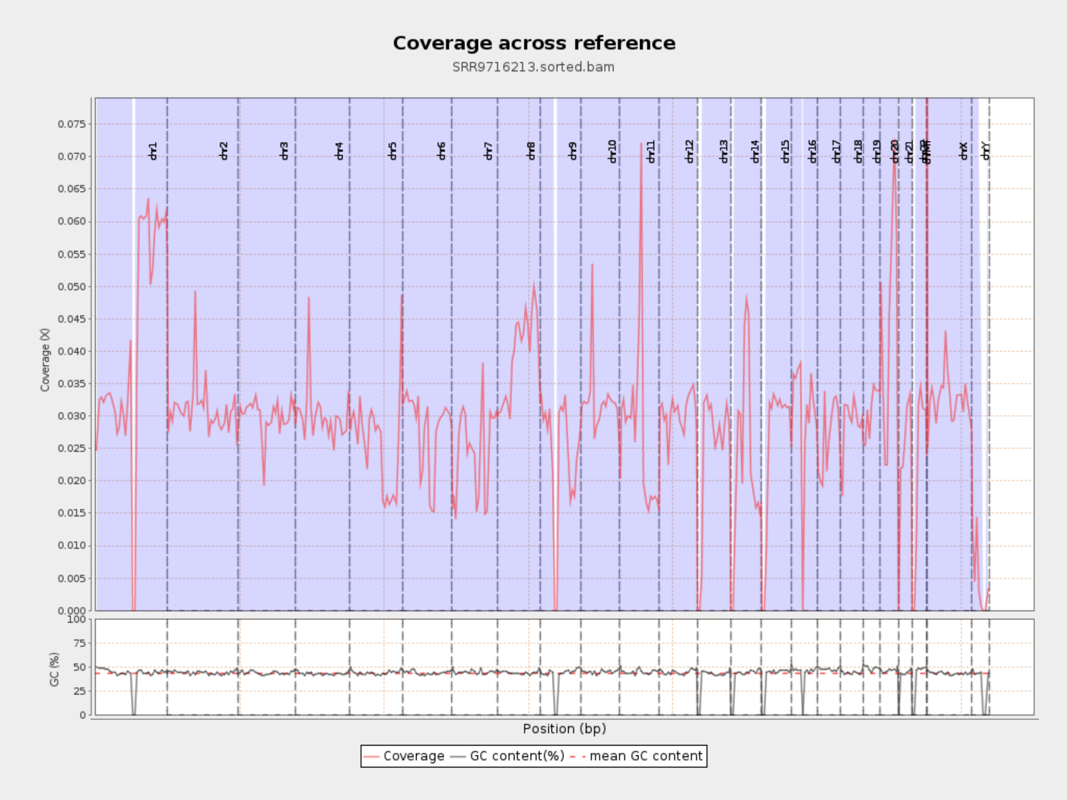
General error rate	0.51%
Mismatches	458,366
Insertions	5,389
Mapped reads with at least one insertion	0.33%
Deletions	15,313
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.87%

2.6. Chromosome stats

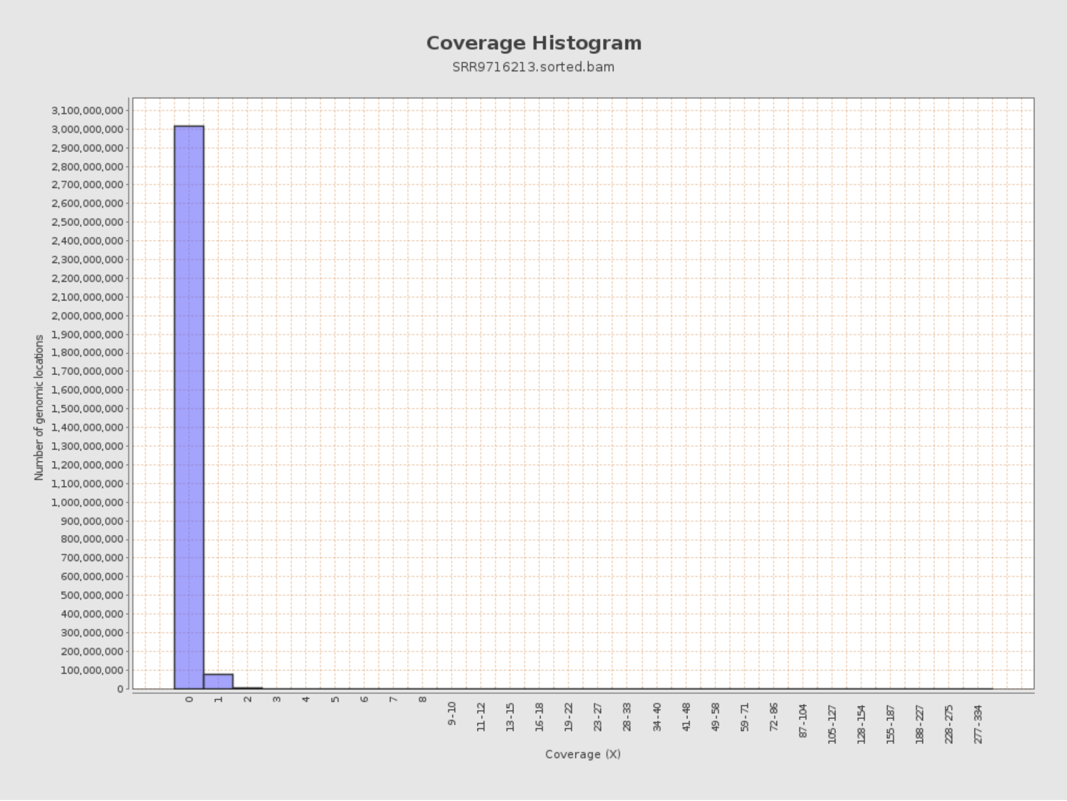
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10250482	0.0411	0.3298
chr2	243199373	7568519	0.0311	0.2688
chr3	198022430	5938873	0.03	0.189
chr4	191154276	5752333	0.0301	0.2072
chr5	180915260	4626855	0.0256	0.1755
chr6	171115067	4772269	0.0279	0.1943
chr7	159138663	3941572	0.0248	0.2064

chr8	146364022	5771737	0.0394	0.2404
chr9	141213431	3348518	0.0237	0.2411
chr10	135534747	4405710	0.0325	0.2674
chr11	135006516	3830563	0.0284	0.2402
chr12	133851895	4092702	0.0306	0.1939
chr13	115169878	2812065	0.0244	0.1687
chr14	107349540	2482762	0.0231	0.174
chr15	102531392	2625220	0.0256	0.1761
chr16	90354753	2704957	0.0299	0.2057
chr17	81195210	2175618	0.0268	0.1839
chr18	78077248	2232127	0.0286	0.4372
chr19	59128983	1827757	0.0309	0.257
chr20	63025520	2778465	0.0441	0.2378
chr21	48129895	1176927	0.0245	0.1908
chr22	51304566	1121565	0.0219	0.1624
chrMT	16571	2128	0.1284	0.379
chrX	155270560	5090555	0.0328	0.2221
chrY	59373566	267007	0.0045	0.1048

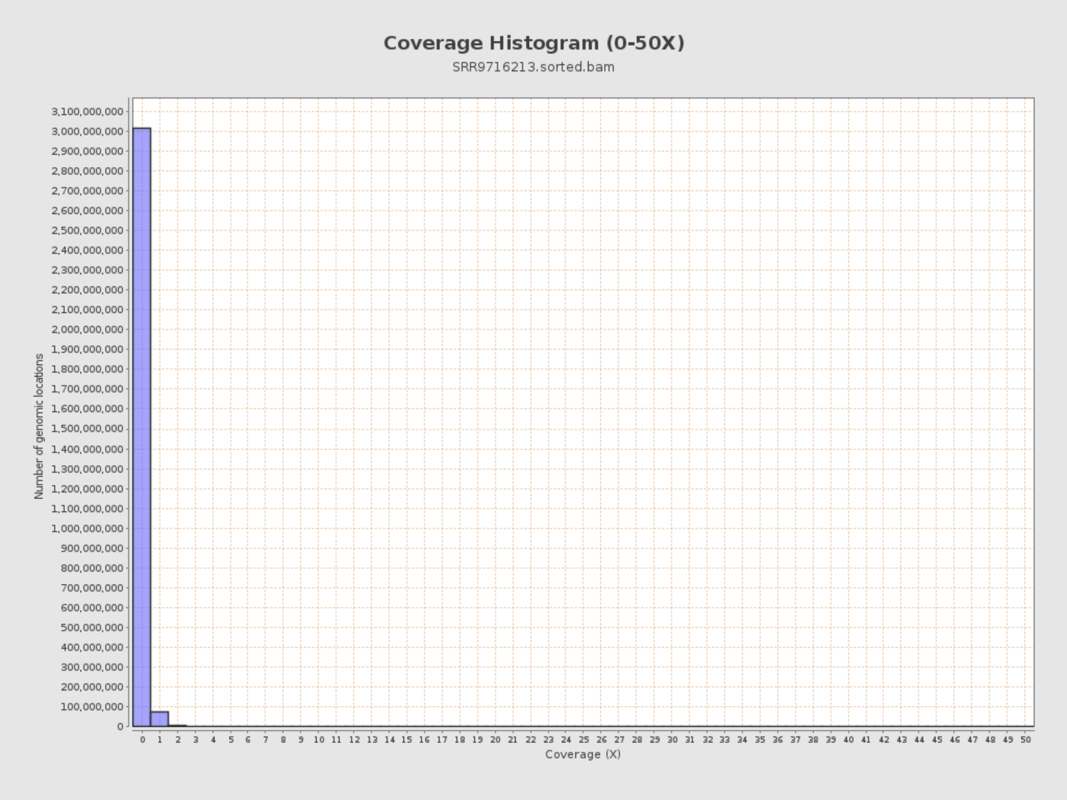
3. Results : Coverage across reference



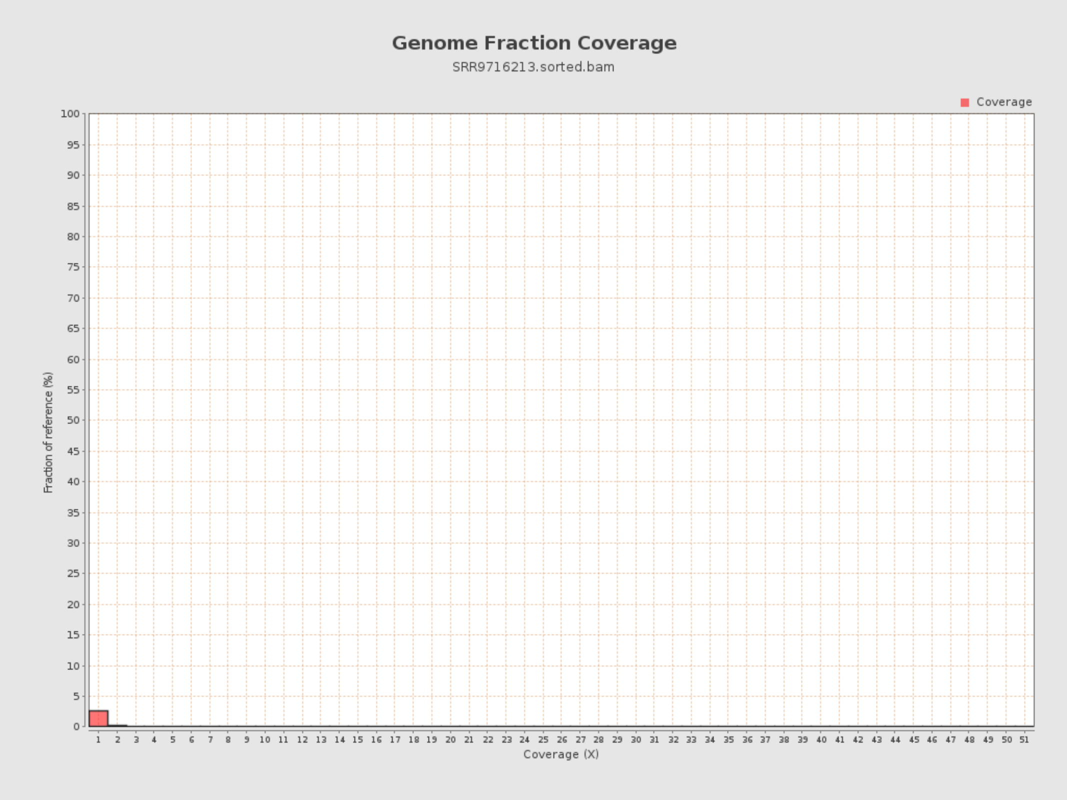
4. Results : Coverage Histogram



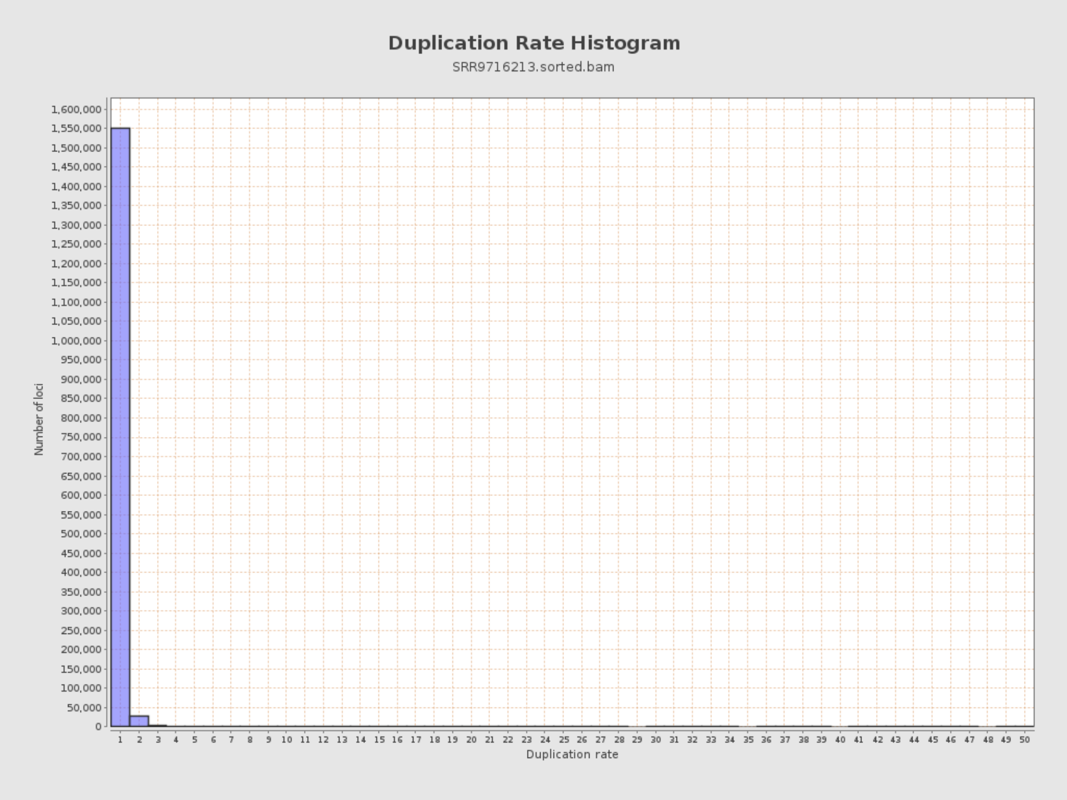
5. Results : Coverage Histogram (0-50X)



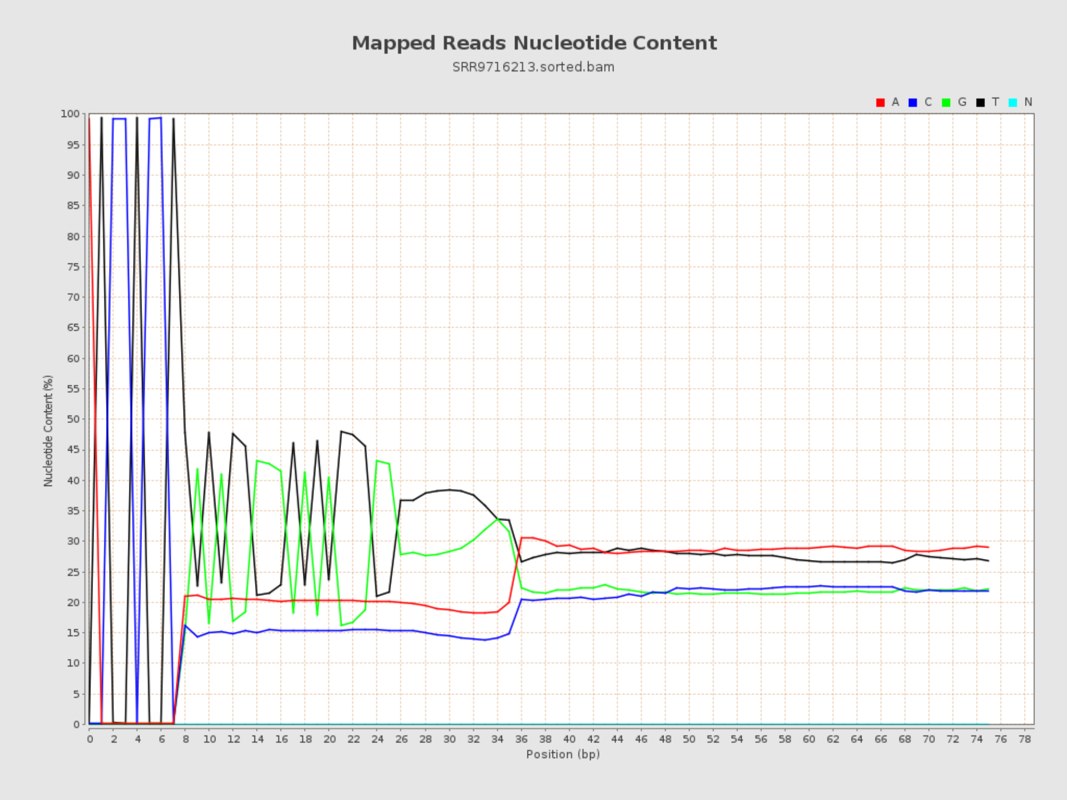
6. Results : Genome Fraction Coverage



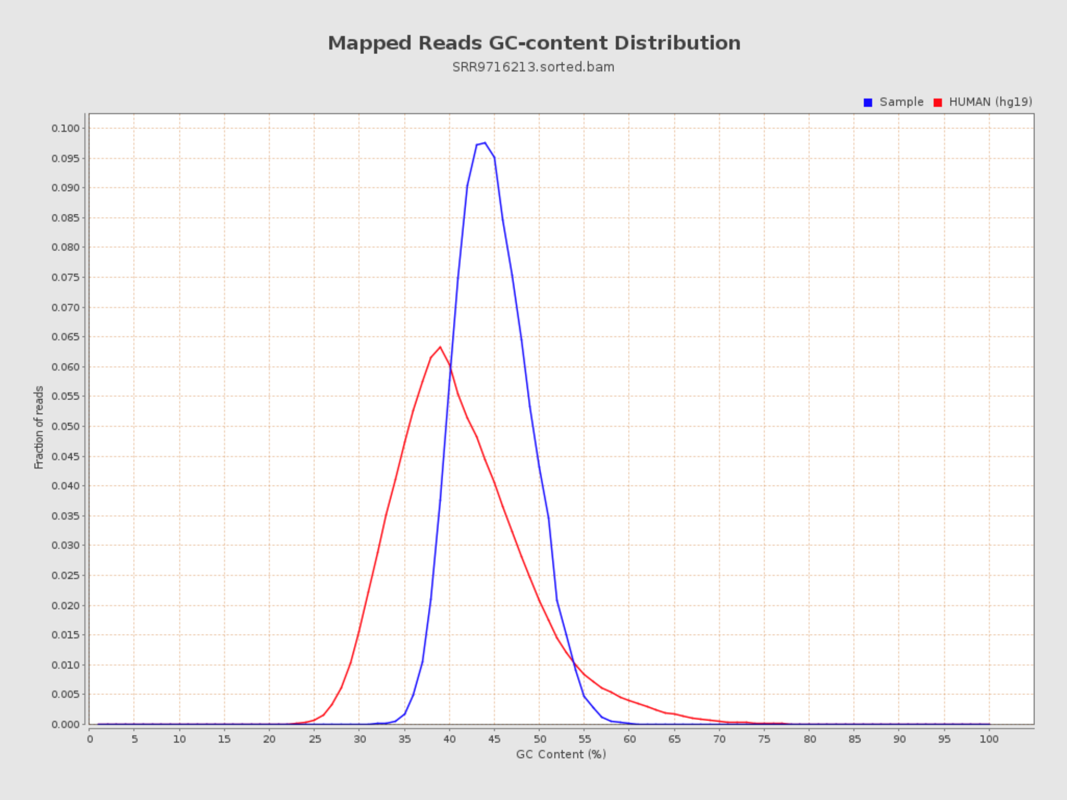
7. Results : Duplication Rate Histogram



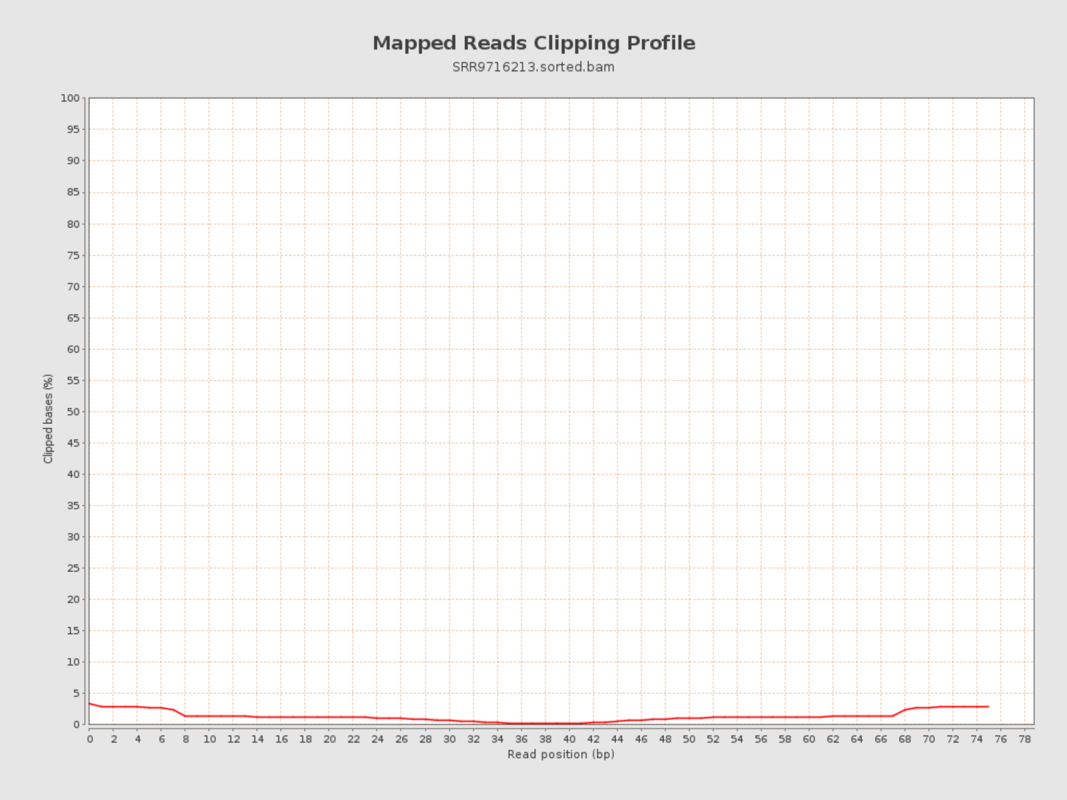
8. Results : Mapped Reads Nucleotide Content



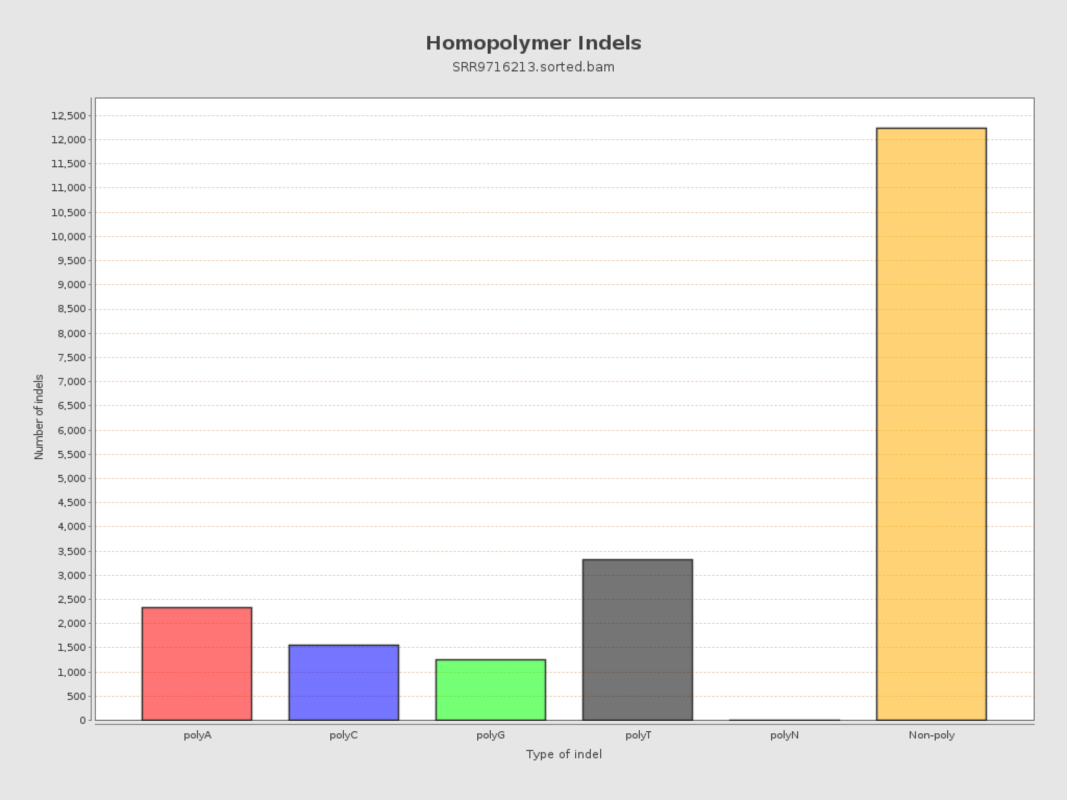
9. Results : Mapped Reads GC-content Distribution



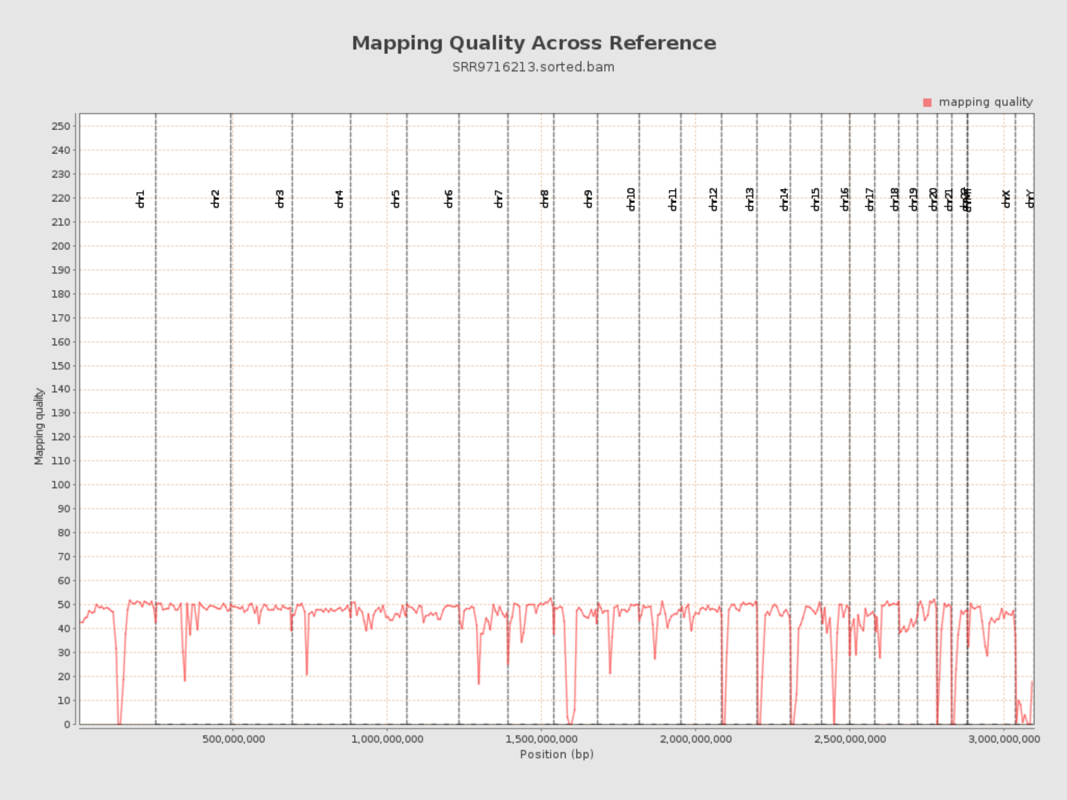
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram