Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:08:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716875.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_SRR9716875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716875.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:08:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,847,614
Mapped reads	1,550,853 / 83.94%
Unmapped reads	296,761 / 16.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,744 / 0.15%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	55,494 / 3%
Duplication rate	2.73%
Clipped reads	1,549,730 / 83.88%

2.2. ACGT Content

Number/percentage of A's	21,908,607 / 24.43%
Number/percentage of C's	16,610,249 / 18.52%
Number/percentage of T's	28,968,202 / 32.3%
Number/percentage of G's	22,184,831 / 24.74%
Number/percentage of N's	1,021 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2565

2.4. Mapping Quality

Mean Mapping Quality	44.77

2.5. Mismatches and indels

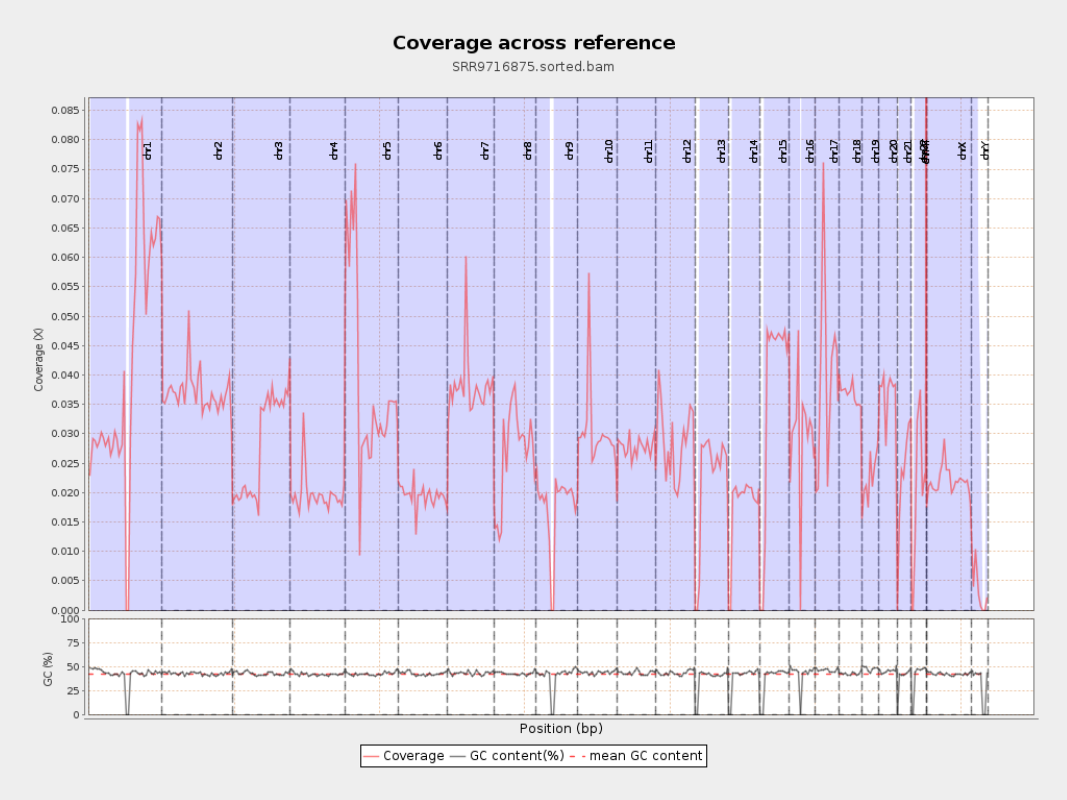
General error rate	0.49%
Mismatches	425,778
Insertions	6,213
Mapped reads with at least one insertion	0.4%
Deletions	18,098
Mapped reads with at least one deletion	1.16%
Homopolymer indels	44.19%

2.6. Chromosome stats

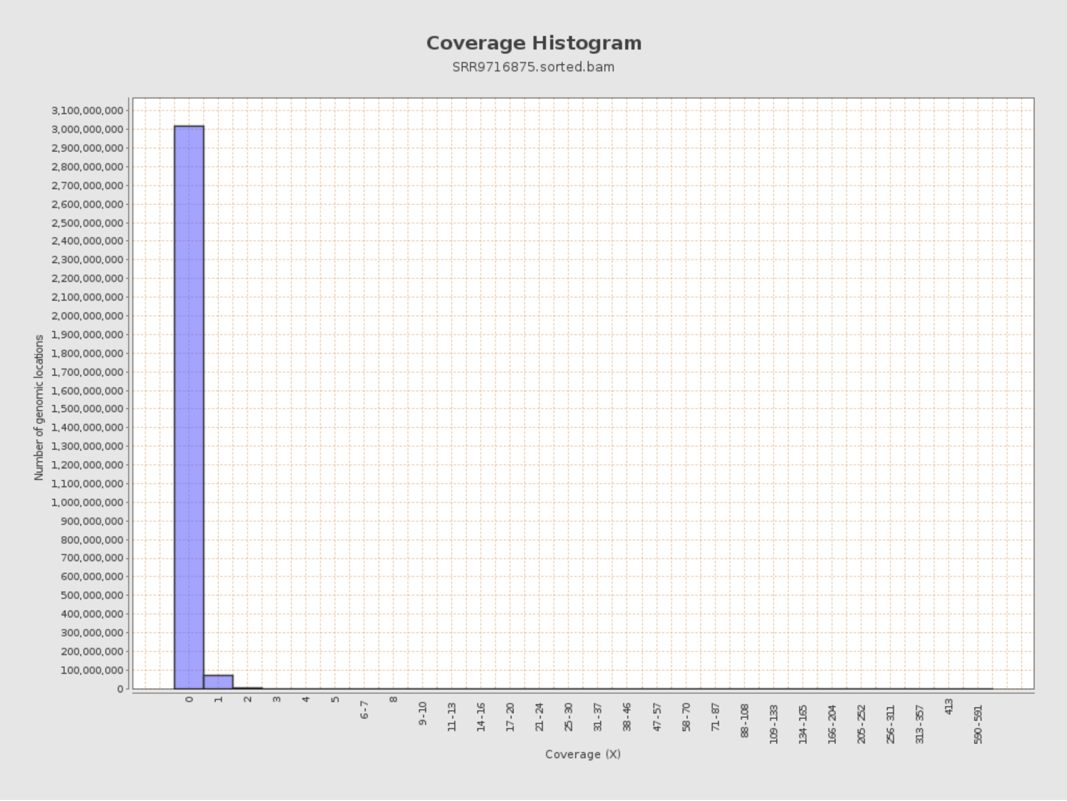
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10439861	0.0419	0.3534
chr2	243199373	9018188	0.0371	0.351
chr3	198022430	5501779	0.0278	0.1863
chr4	191154276	3750252	0.0196	0.1645
chr5	180915260	7093147	0.0392	0.2185
chr6	171115067	3336266	0.0195	0.1719
chr7	159138663	6093141	0.0383	0.45

chr8	146364022	3939744	0.0269	0.2086
chr9	141213431	2441811	0.0173	0.1929
chr10	135534747	4107732	0.0303	0.3132
chr11	135006516	3737376	0.0277	0.2385
chr12	133851895	3804596	0.0284	0.1849
chr13	115169878	2553314	0.0222	0.1623
chr14	107349540	1873488	0.0175	0.1499
chr15	102531392	3820880	0.0373	0.2147
chr16	90354753	2659708	0.0294	0.2097
chr17	81195210	3284574	0.0405	0.2375
chr18	78077248	2880578	0.0369	0.3943
chr19	59128983	1344636	0.0227	0.2792
chr20	63025520	2295878	0.0364	0.2104
chr21	48129895	1112472	0.0231	0.1741
chr22	51304566	999567	0.0195	0.1528
chrMT	16571	4549	0.2745	0.5341
chrX	155270560	3411883	0.022	0.1943
chrY	59373566	196444	0.0033	0.0871

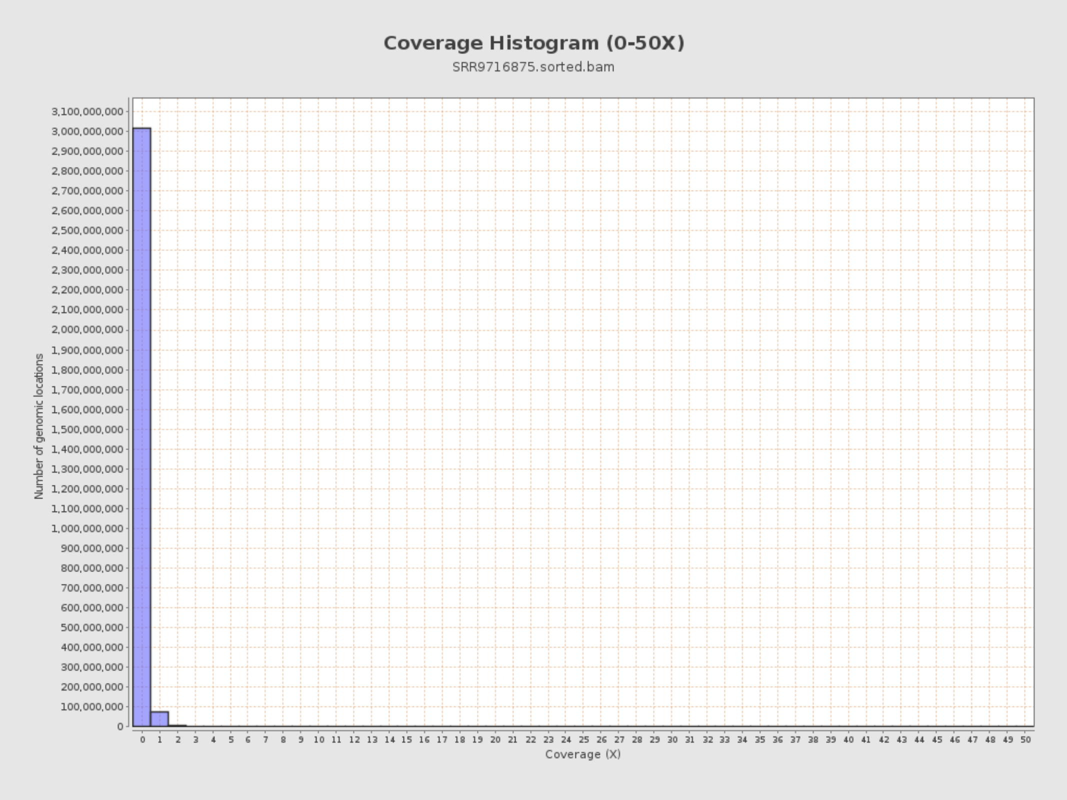
3. Results : Coverage across reference



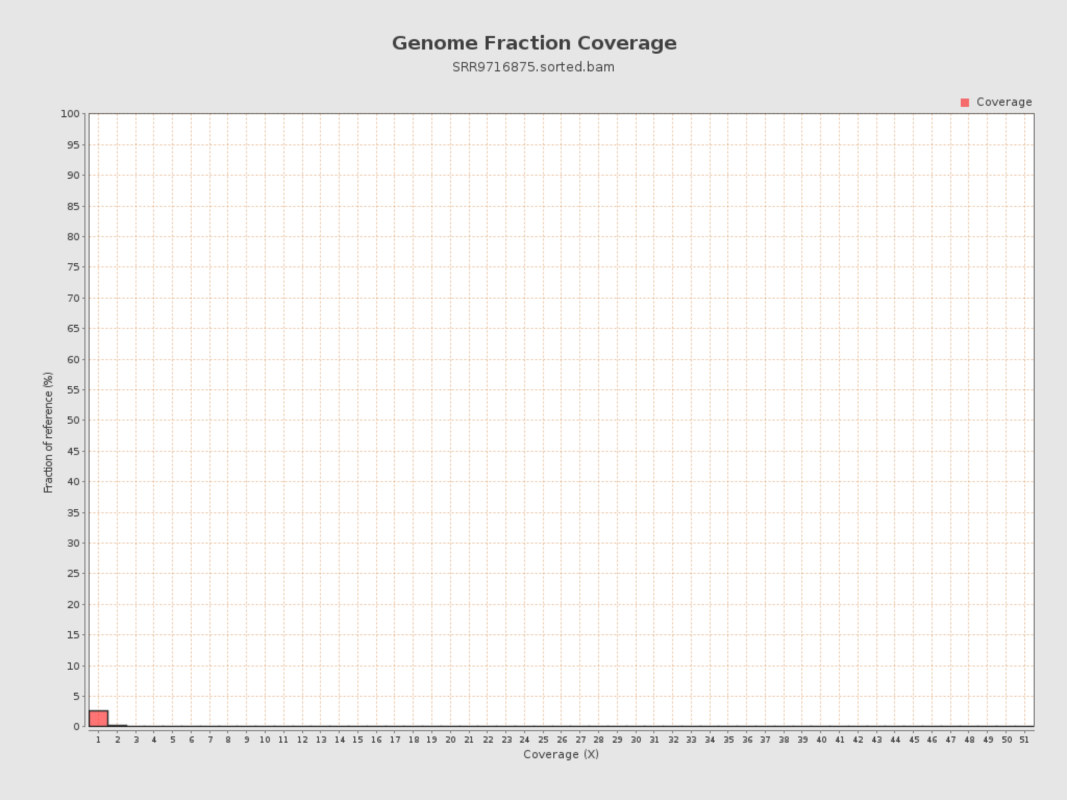
4. Results : Coverage Histogram



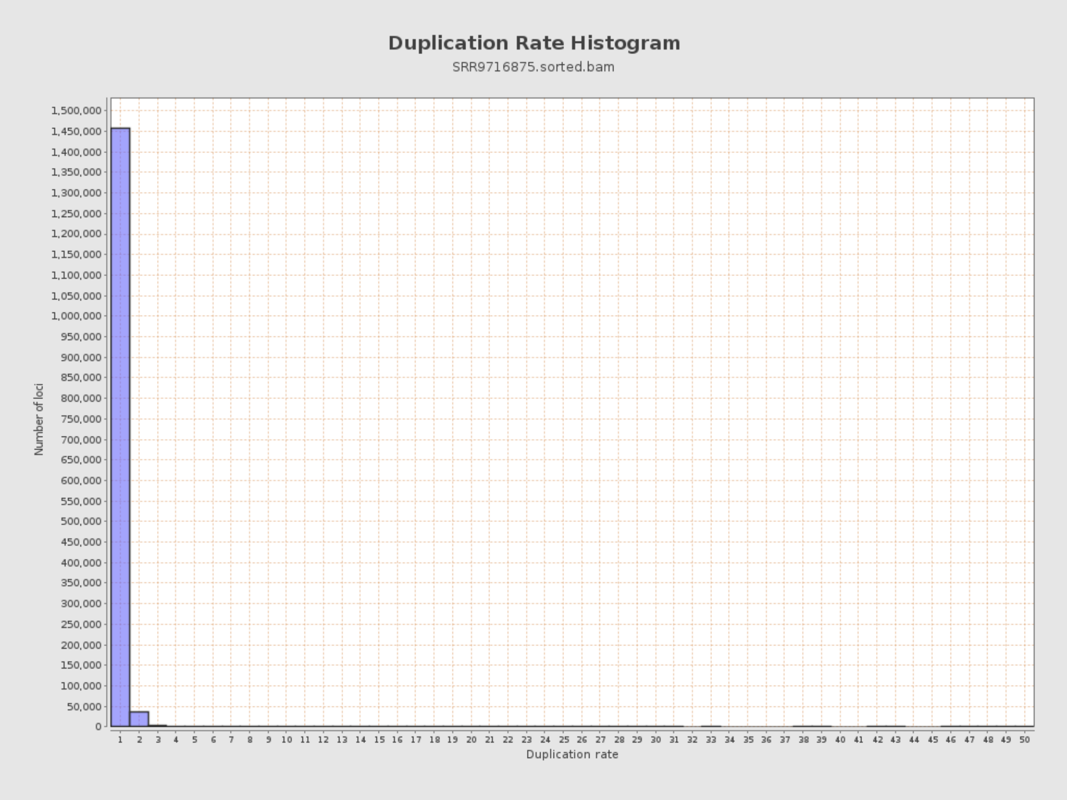
5. Results : Coverage Histogram (0-50X)



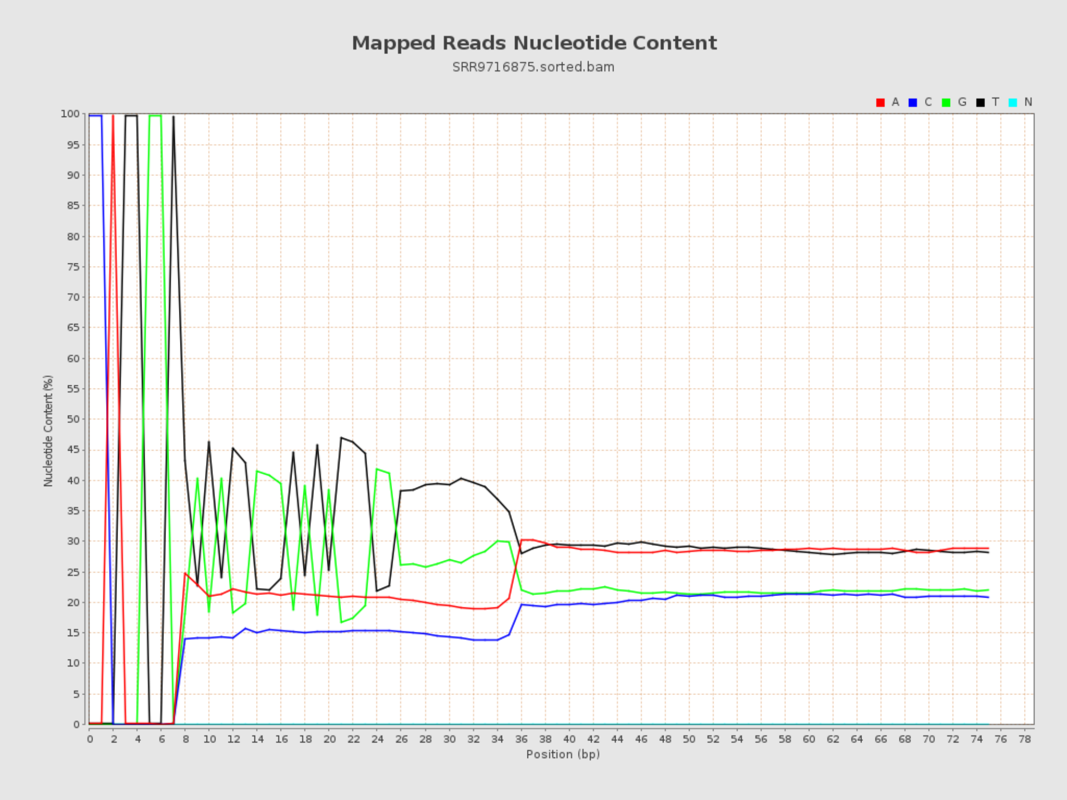
6. Results : Genome Fraction Coverage



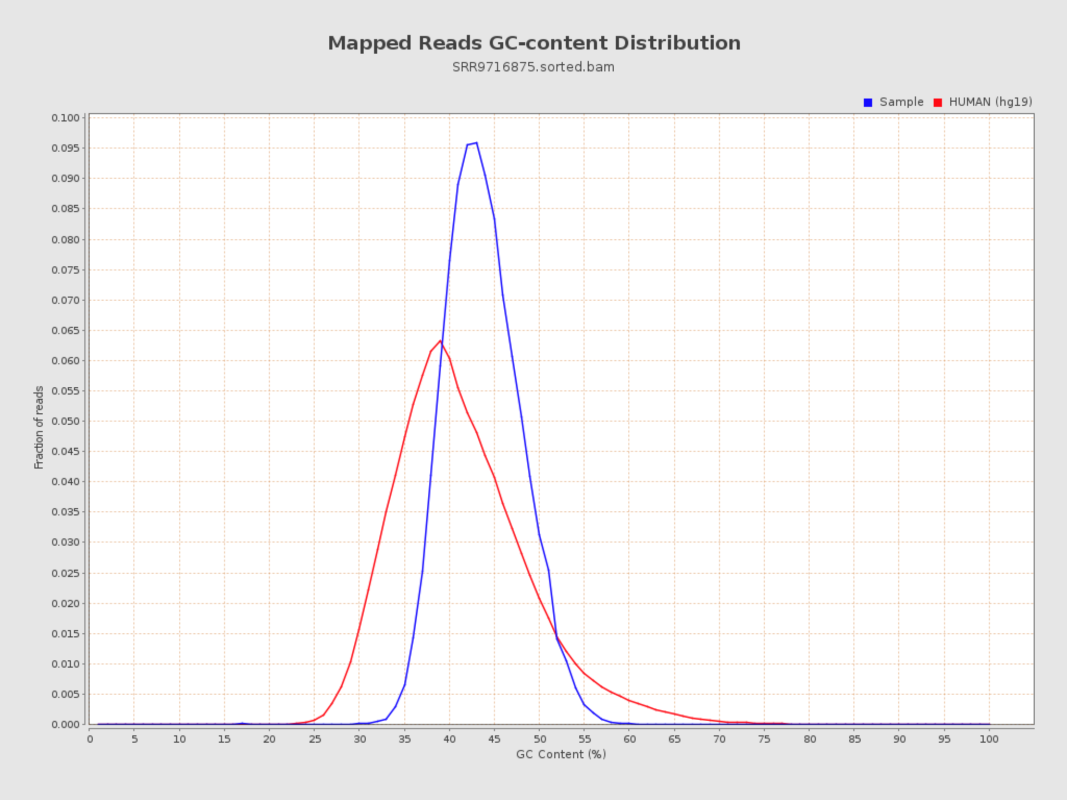
7. Results : Duplication Rate Histogram



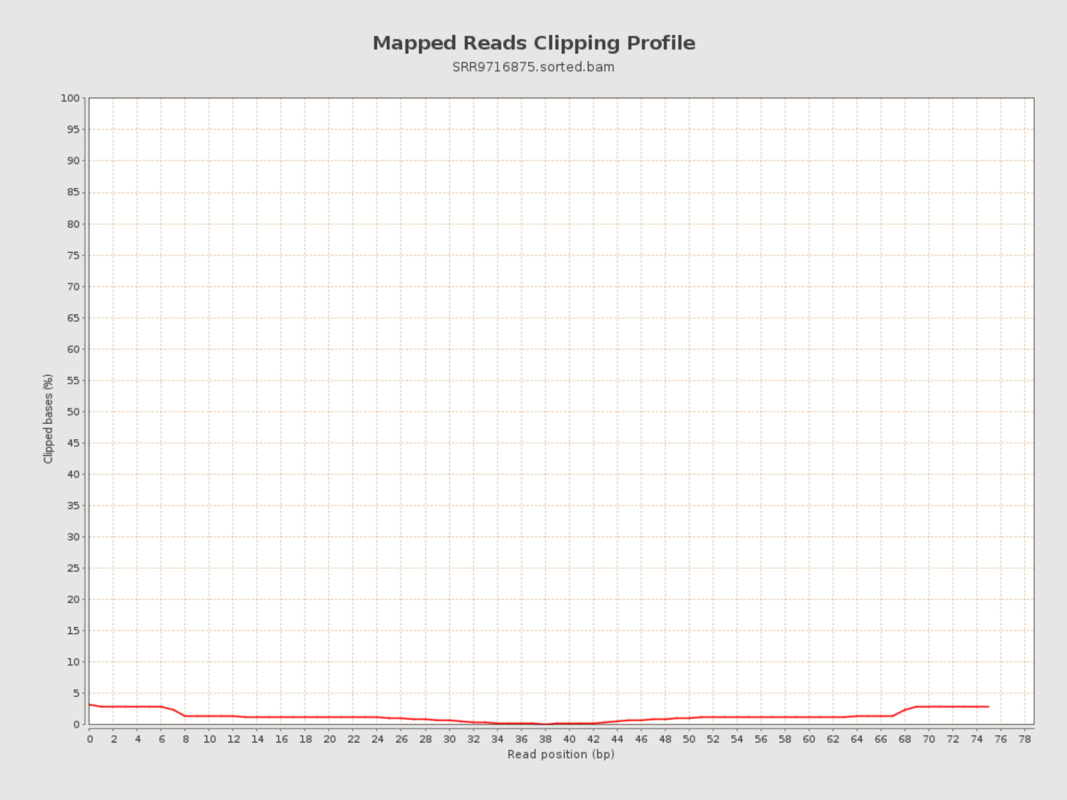
8. Results : Mapped Reads Nucleotide Content



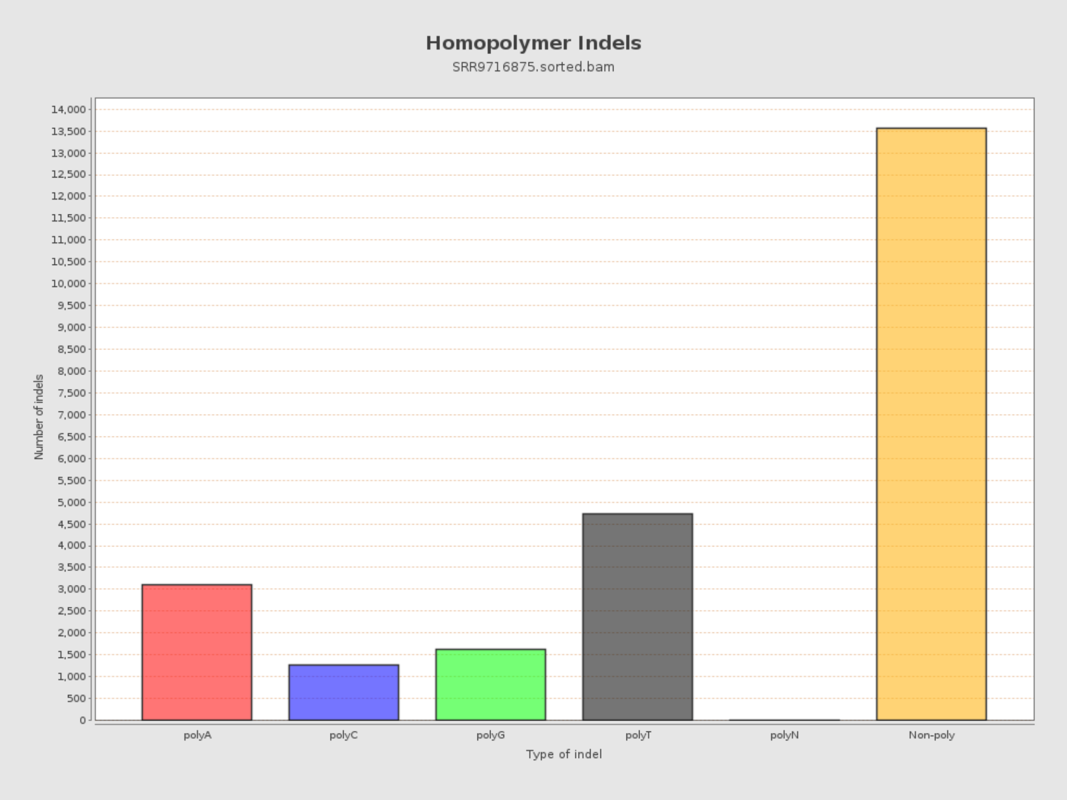
9. Results : Mapped Reads GC-content Distribution



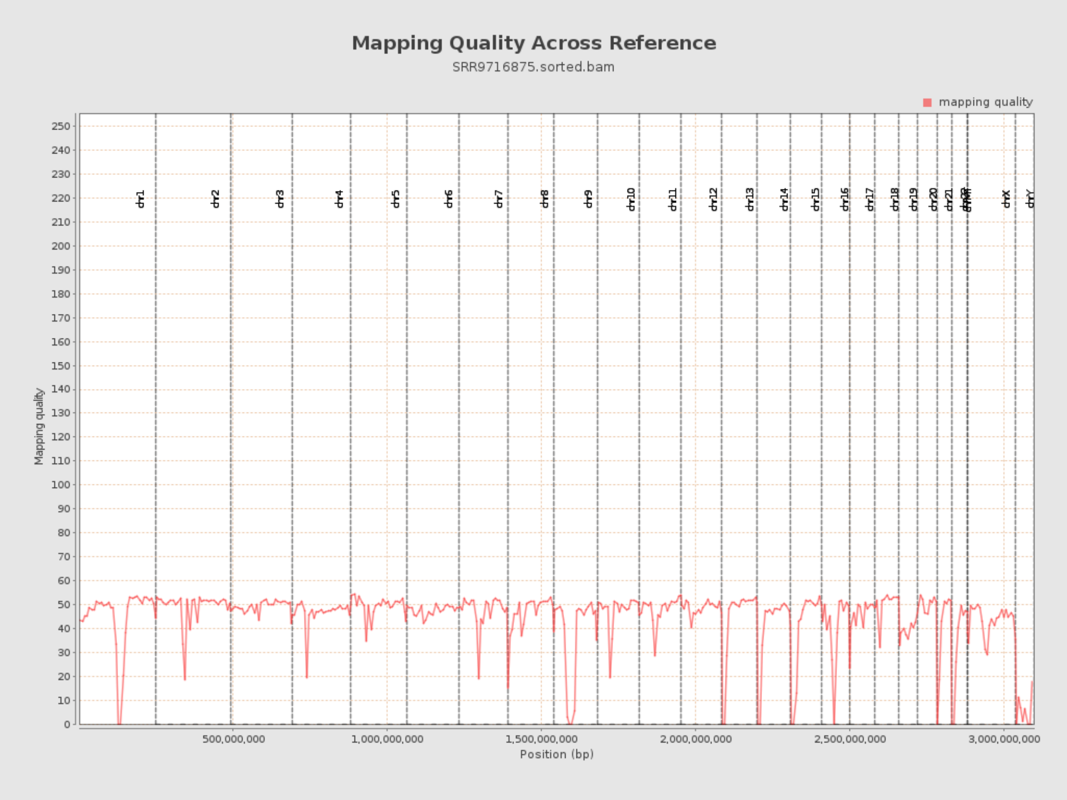
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram