Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:17:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716993.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_SRR9716993 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716993.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:17:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716993.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,794,472
Mapped reads	1,612,882 / 89.88%
Unmapped reads	181,590 / 10.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,353 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	55,249 / 3.08%
Duplication rate	2.29%
Clipped reads	1,617,948 / 90.16%

2.2. ACGT Content

Number/percentage of A's	24,014,439 / 25.73%
Number/percentage of C's	17,739,440 / 19%
Number/percentage of T's	29,659,780 / 31.77%
Number/percentage of G's	21,935,401 / 23.5%
Number/percentage of N's	1,180 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.3123

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Mismatches and indels

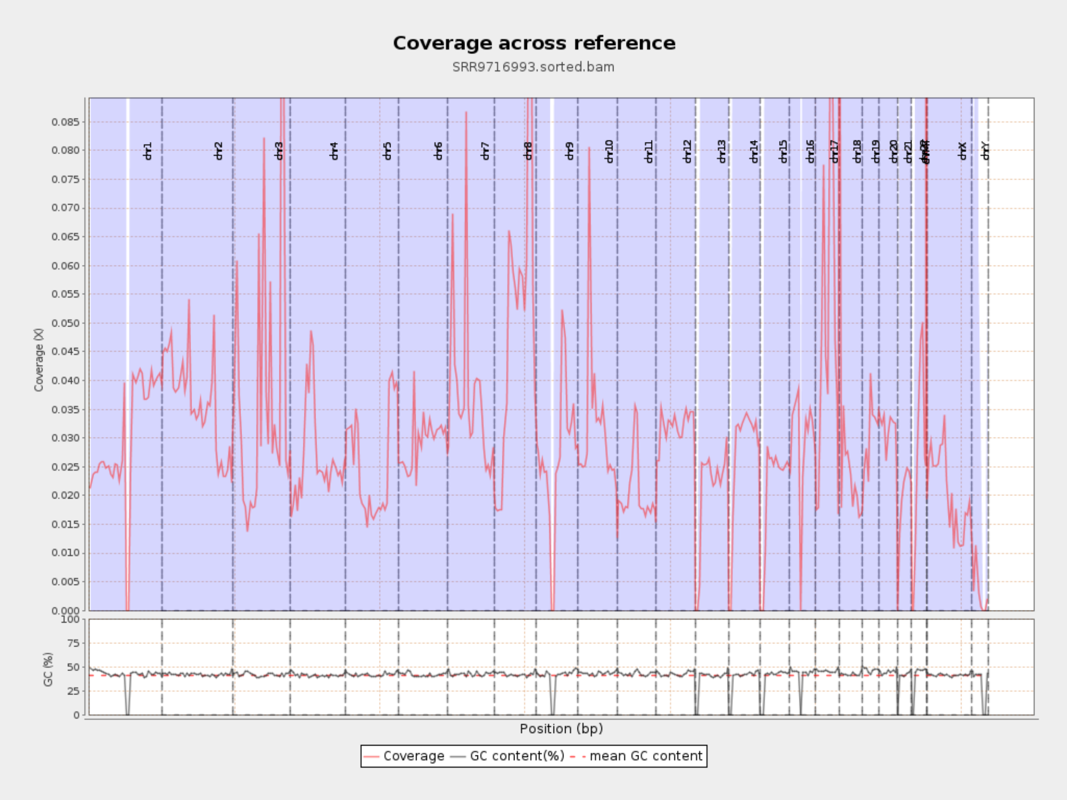
General error rate	0.52%
Mismatches	473,024
Insertions	6,560
Mapped reads with at least one insertion	0.4%
Deletions	17,046
Mapped reads with at least one deletion	1.05%
Homopolymer indels	40.65%

2.6. Chromosome stats

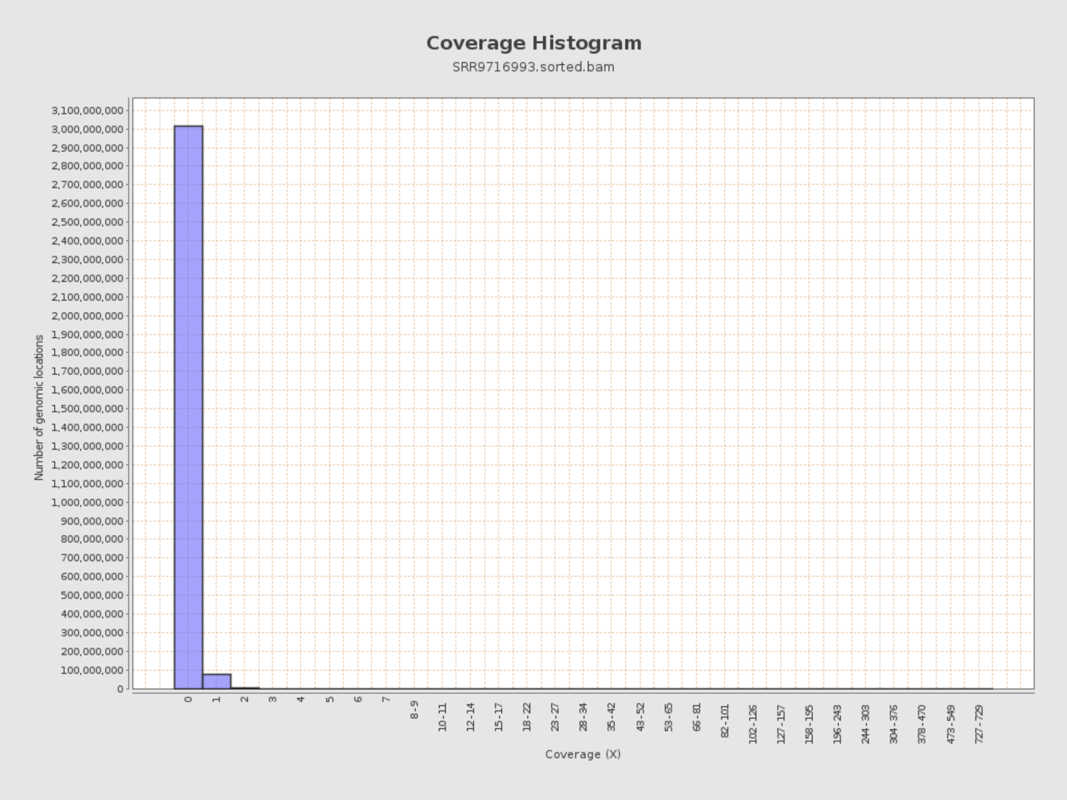
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7418802	0.0298	0.393
chr2	243199373	8861738	0.0364	0.3686
chr3	198022430	7659463	0.0387	0.2435
chr4	191154276	5087523	0.0266	0.1903
chr5	180915260	4581282	0.0253	0.1762
chr6	171115067	5015975	0.0293	0.2057
chr7	159138663	6073171	0.0382	0.726

chr8	146364022	7649400	0.0523	0.3255
chr9	141213431	3748014	0.0265	0.2044
chr10	135534747	4336892	0.032	0.4841
chr11	135006516	2748951	0.0204	0.1974
chr12	133851895	4274568	0.0319	0.2413
chr13	115169878	2377691	0.0206	0.1566
chr14	107349540	2904700	0.0271	0.1826
chr15	102531392	2155042	0.021	0.164
chr16	90354753	2692315	0.0298	0.2019
chr17	81195210	4086308	0.0503	0.2581
chr18	78077248	2213692	0.0284	0.3245
chr19	59128983	1800331	0.0304	0.4113
chr20	63025520	1989067	0.0316	0.2143
chr21	48129895	916710	0.019	0.1577
chr22	51304566	1312085	0.0256	0.1743
chrMT	16571	51981	3.1369	2.5521
chrX	155270560	3216098	0.0207	0.1903
chrY	59373566	205186	0.0035	0.0921

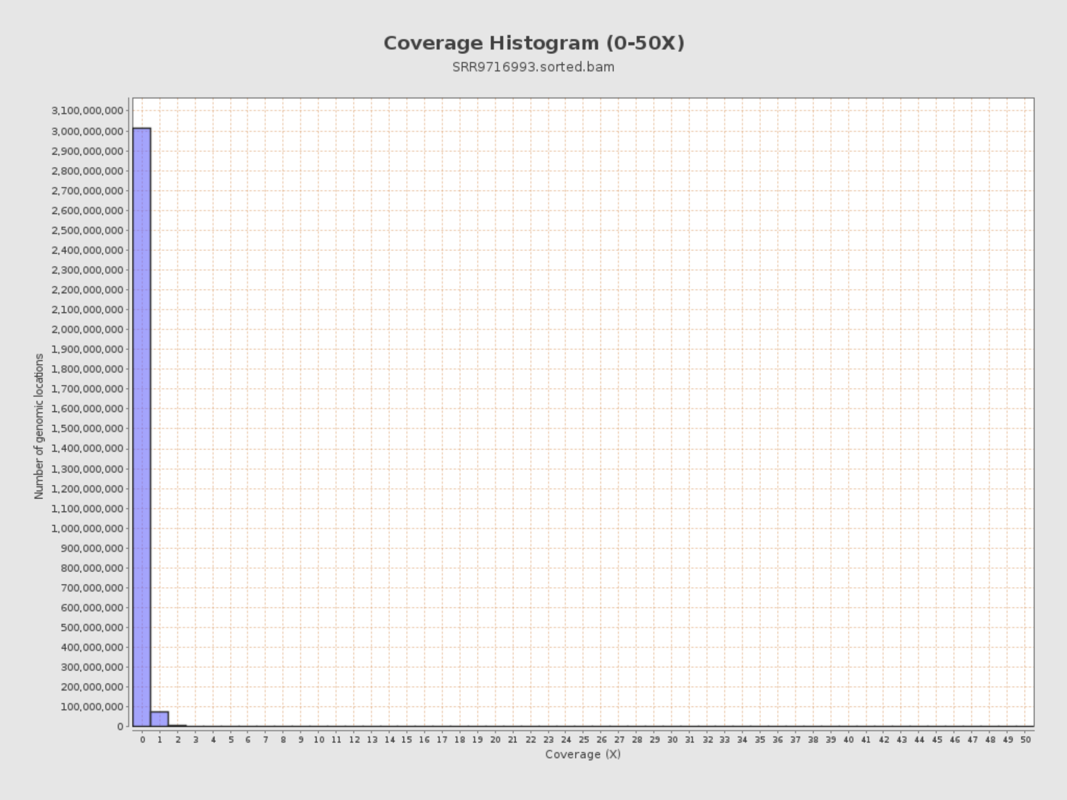
3. Results : Coverage across reference



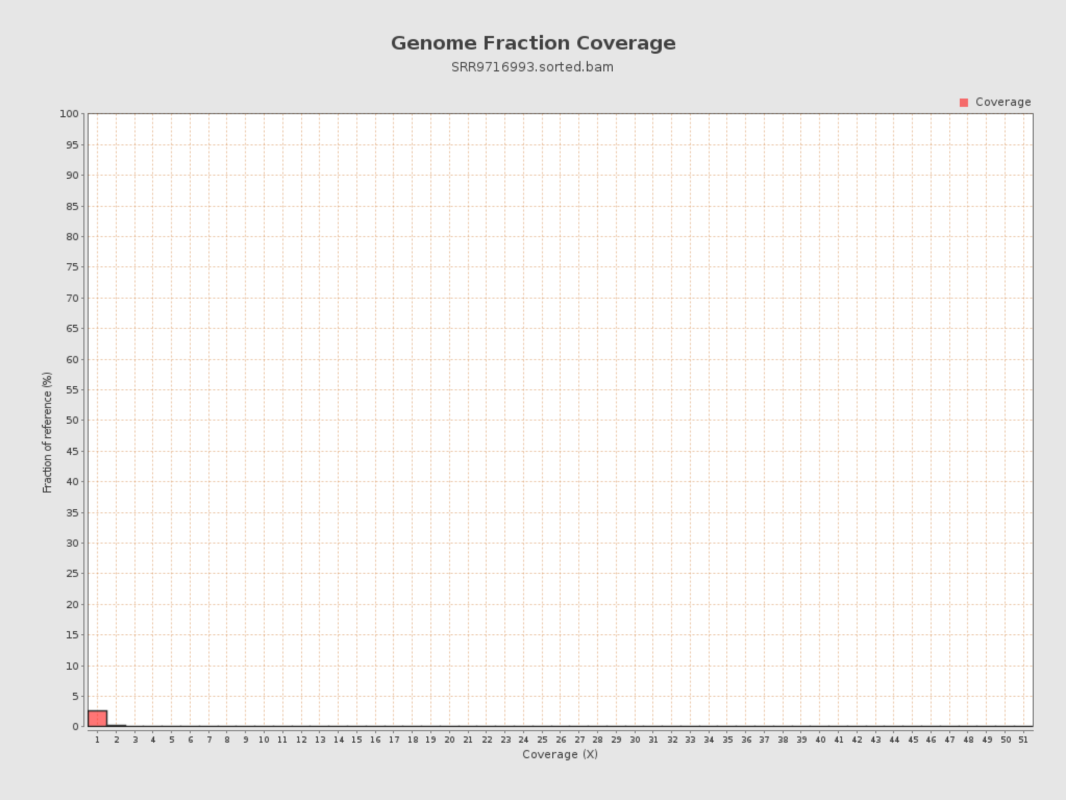
4. Results : Coverage Histogram



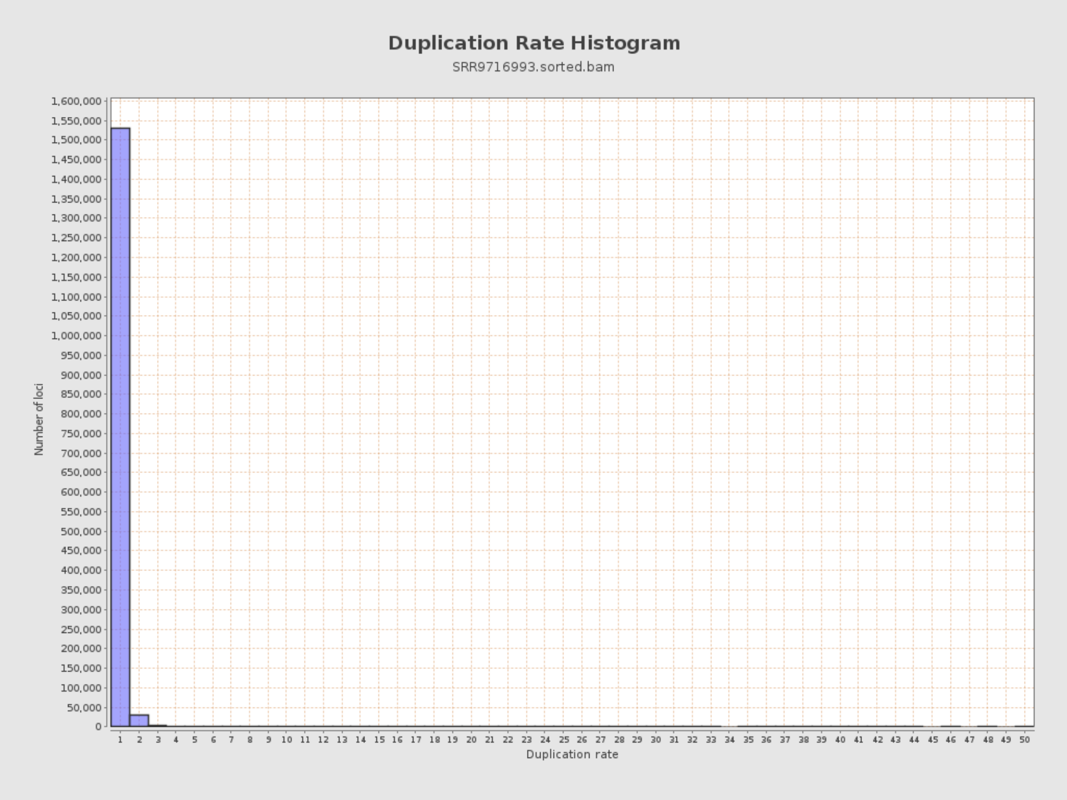
5. Results : Coverage Histogram (0-50X)



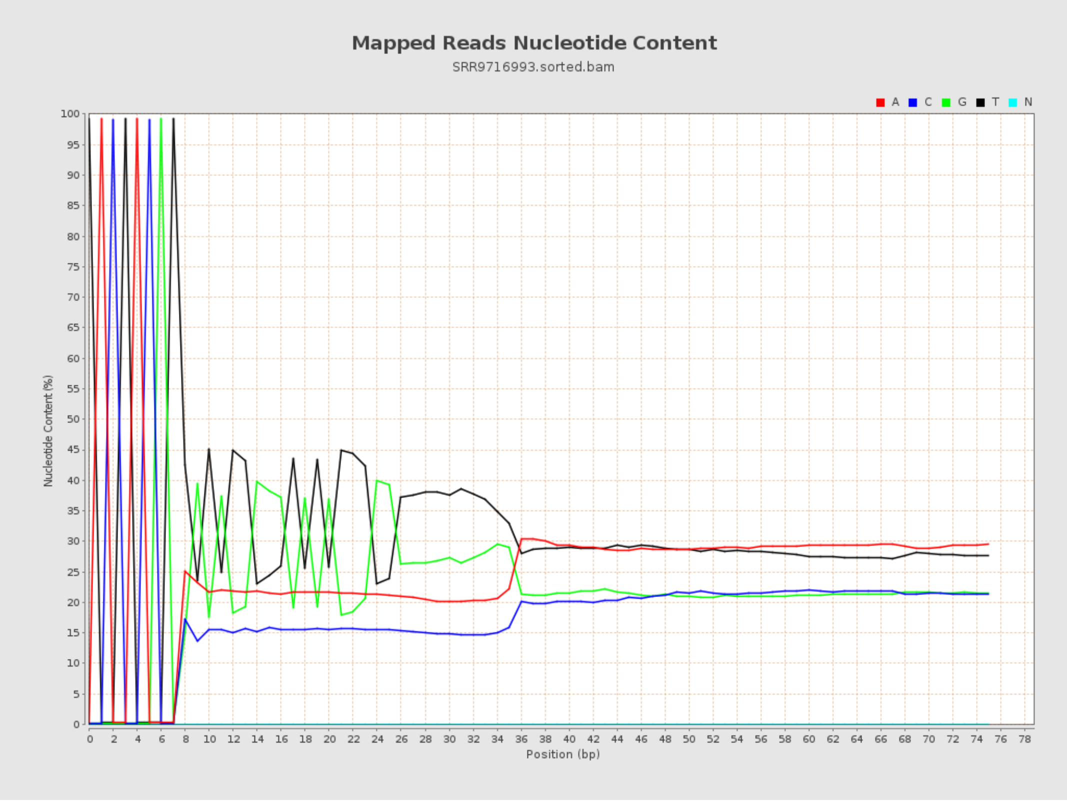
6. Results : Genome Fraction Coverage



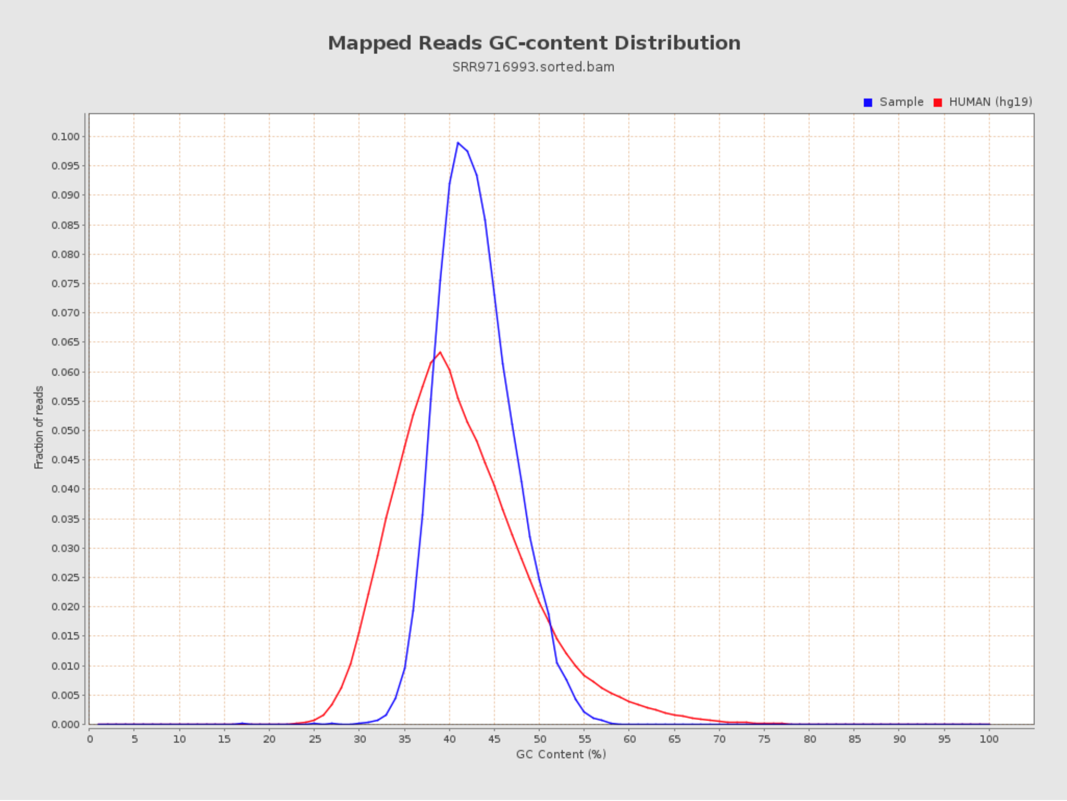
7. Results : Duplication Rate Histogram



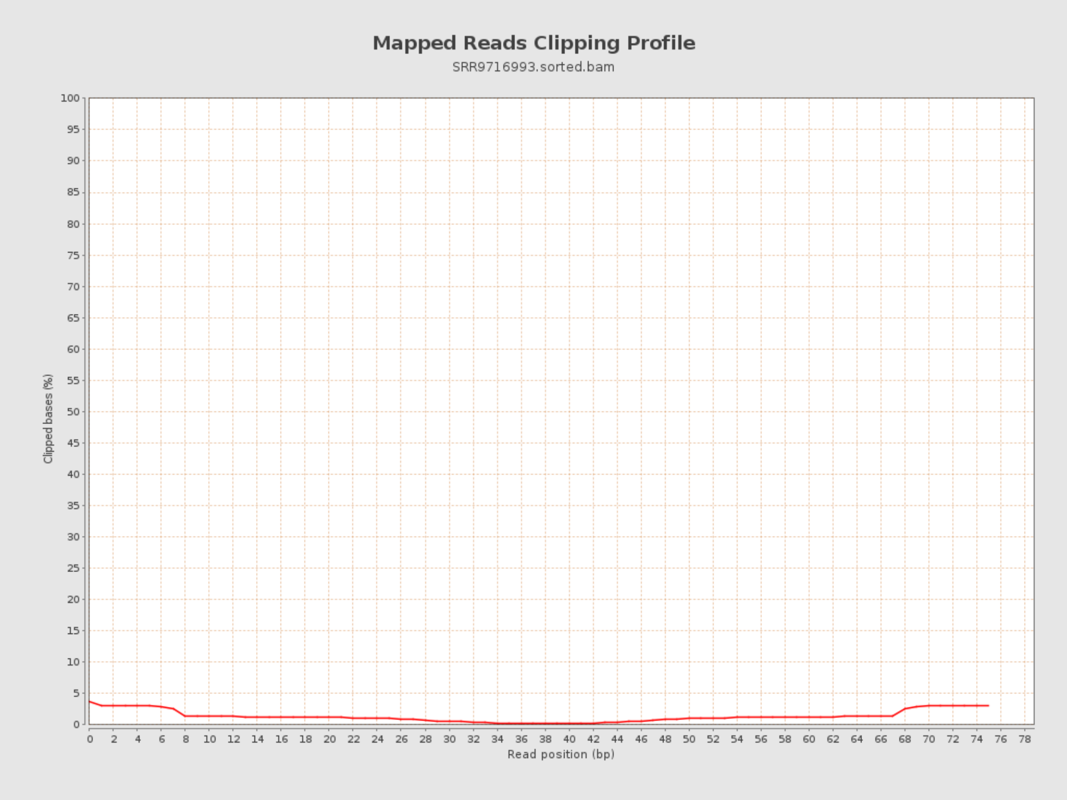
8. Results : Mapped Reads Nucleotide Content



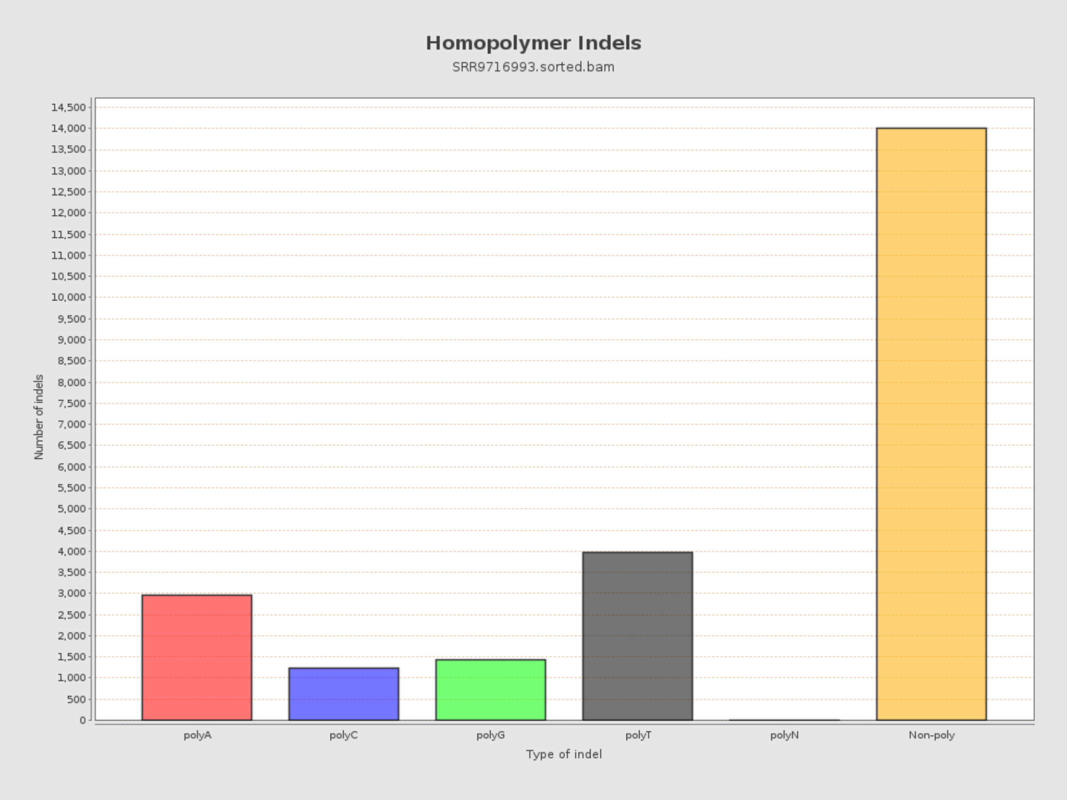
9. Results : Mapped Reads GC-content Distribution



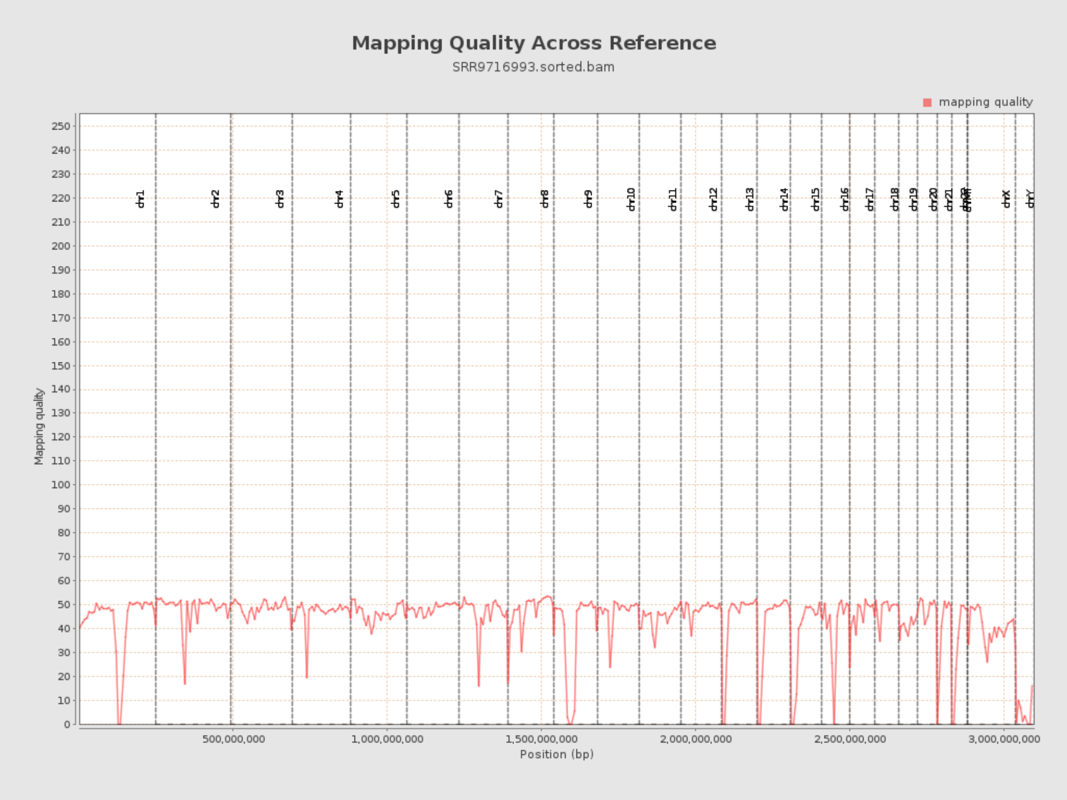
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram