Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 23:21:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716994.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_SRR9716994 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716994.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 23:20:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716994.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,415,394
Mapped reads	2,244,910 / 92.94%
Unmapped reads	170,484 / 7.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,348 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	94,619 / 3.92%
Duplication rate	3.18%
Clipped reads	2,256,727 / 93.43%

2.2. ACGT Content

Number/percentage of A's	34,215,351 / 25.9%
Number/percentage of C's	27,984,132 / 21.19%
Number/percentage of T's	39,073,731 / 29.58%
Number/percentage of G's	30,809,417 / 23.33%
Number/percentage of N's	1,732 / 0%
GC Percentage	44.51%

2.3. Coverage

Mean	0.0427

Standard Deviation	0.3489

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

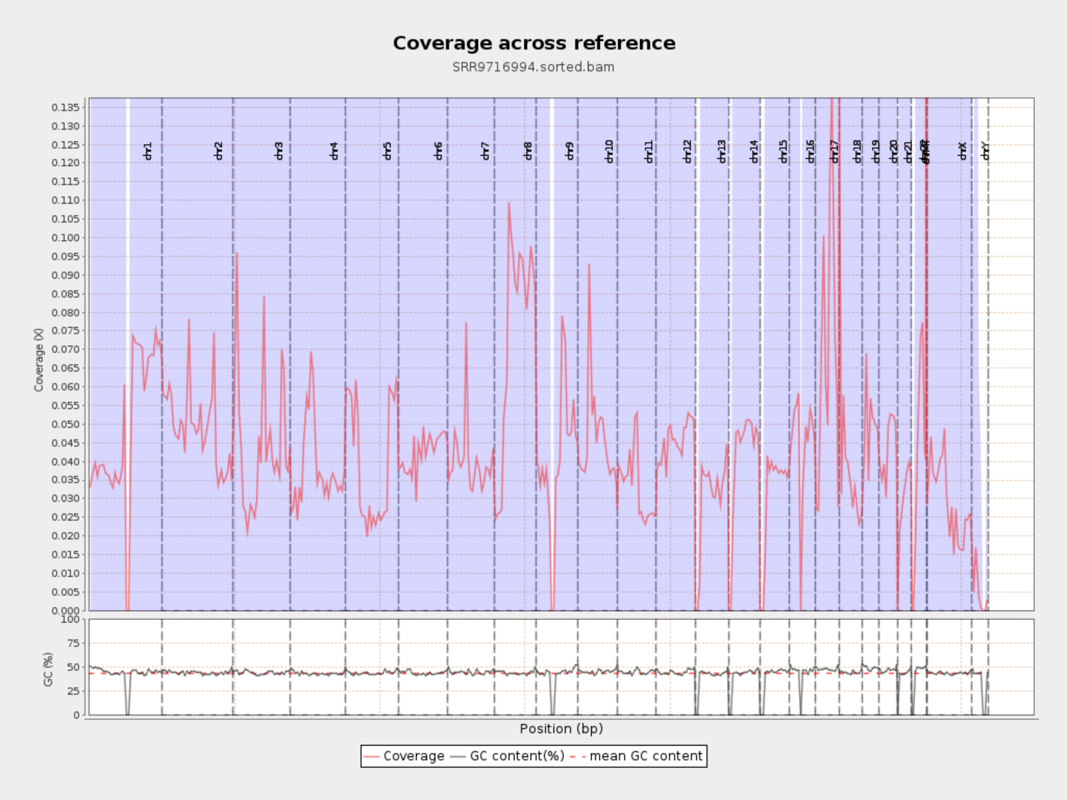
General error rate	0.49%
Mismatches	639,923
Insertions	7,418
Mapped reads with at least one insertion	0.33%
Deletions	23,707
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.97%

2.6. Chromosome stats

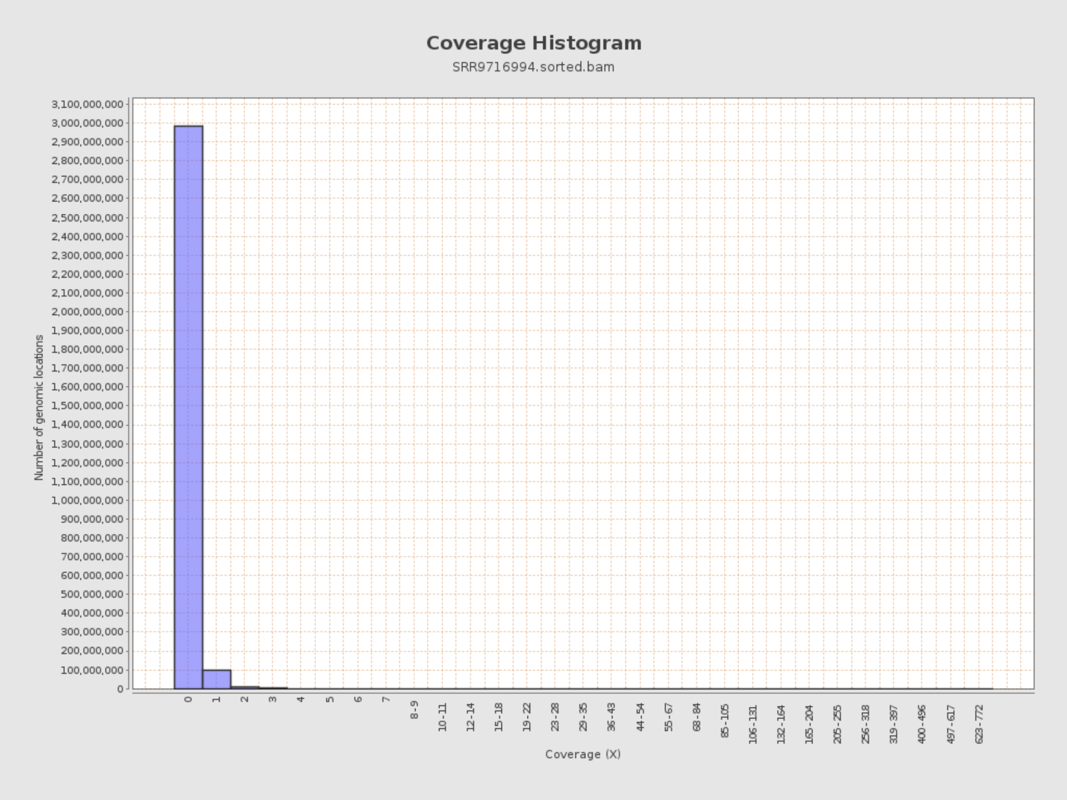
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12129924	0.0487	0.5678
chr2	243199373	12046061	0.0495	0.4347
chr3	198022430	8714461	0.044	0.24
chr4	191154276	7311143	0.0382	0.2519
chr5	180915260	7118285	0.0393	0.225
chr6	171115067	7256587	0.0424	0.2507
chr7	159138663	6398768	0.0402	0.5773

chr8	146364022	10917561	0.0746	0.4514
chr9	141213431	5631109	0.0399	0.271
chr10	135534747	6270905	0.0463	0.3887
chr11	135006516	4478615	0.0332	0.2672
chr12	133851895	6087940	0.0455	0.2514
chr13	115169878	3404235	0.0296	0.1945
chr14	107349540	4330148	0.0403	0.2346
chr15	102531392	3158324	0.0308	0.2007
chr16	90354753	4055471	0.0449	0.2517
chr17	81195210	5698557	0.0702	0.3209
chr18	78077248	3058756	0.0392	0.4359
chr19	59128983	2903574	0.0491	0.4837
chr20	63025520	2754151	0.0437	0.2445
chr21	48129895	1397028	0.029	0.2098
chr22	51304566	2052430	0.04	0.2275
chrMT	16571	17297	1.0438	1.2319
chrX	155270560	4634178	0.0298	0.2292
chrY	59373566	296388	0.005	0.1317

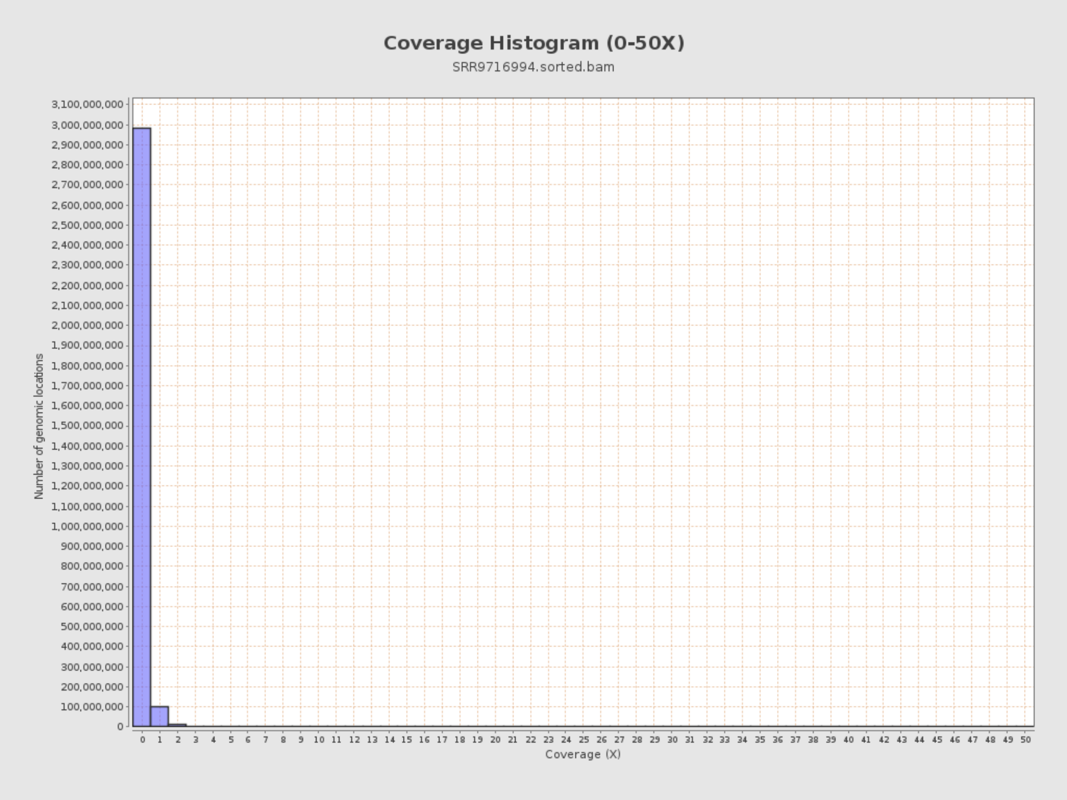
3. Results : Coverage across reference



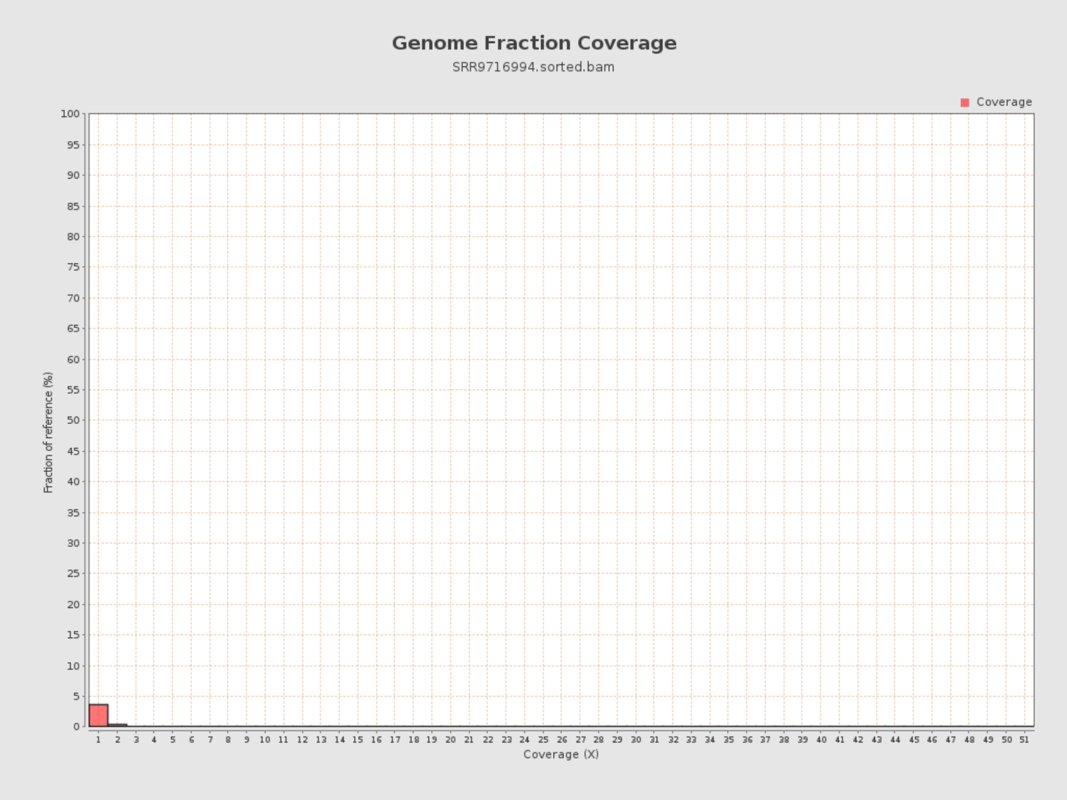
4. Results : Coverage Histogram



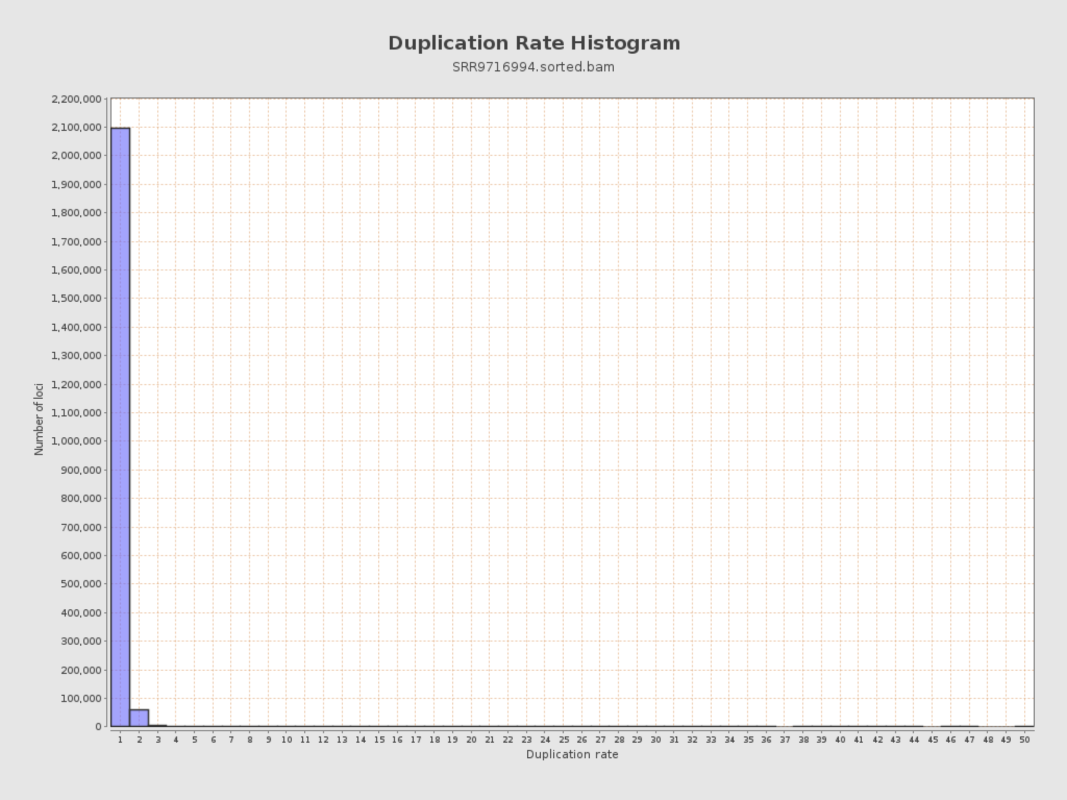
5. Results : Coverage Histogram (0-50X)



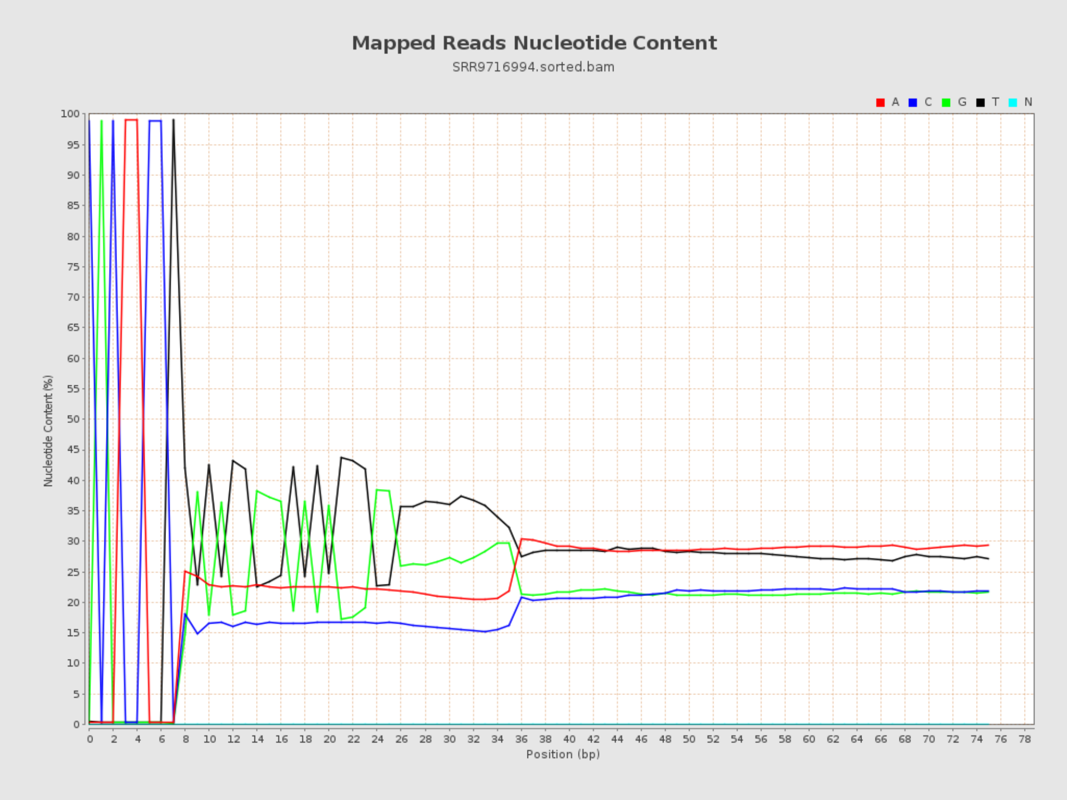
6. Results : Genome Fraction Coverage



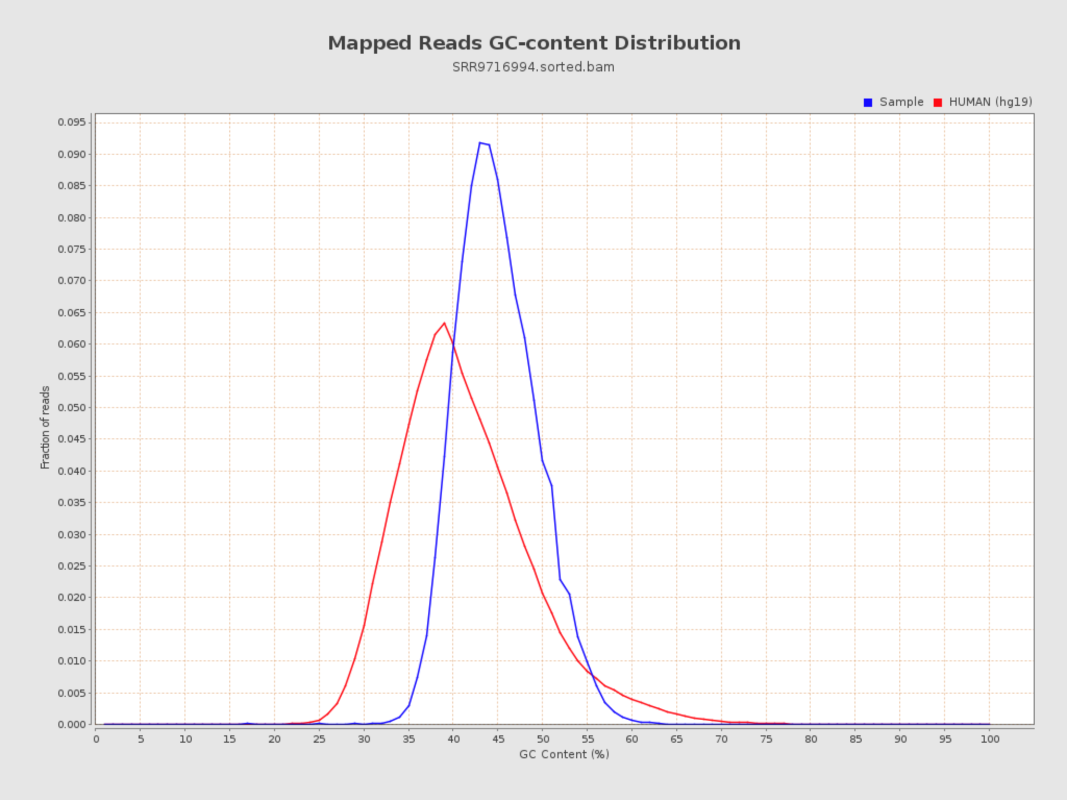
7. Results : Duplication Rate Histogram



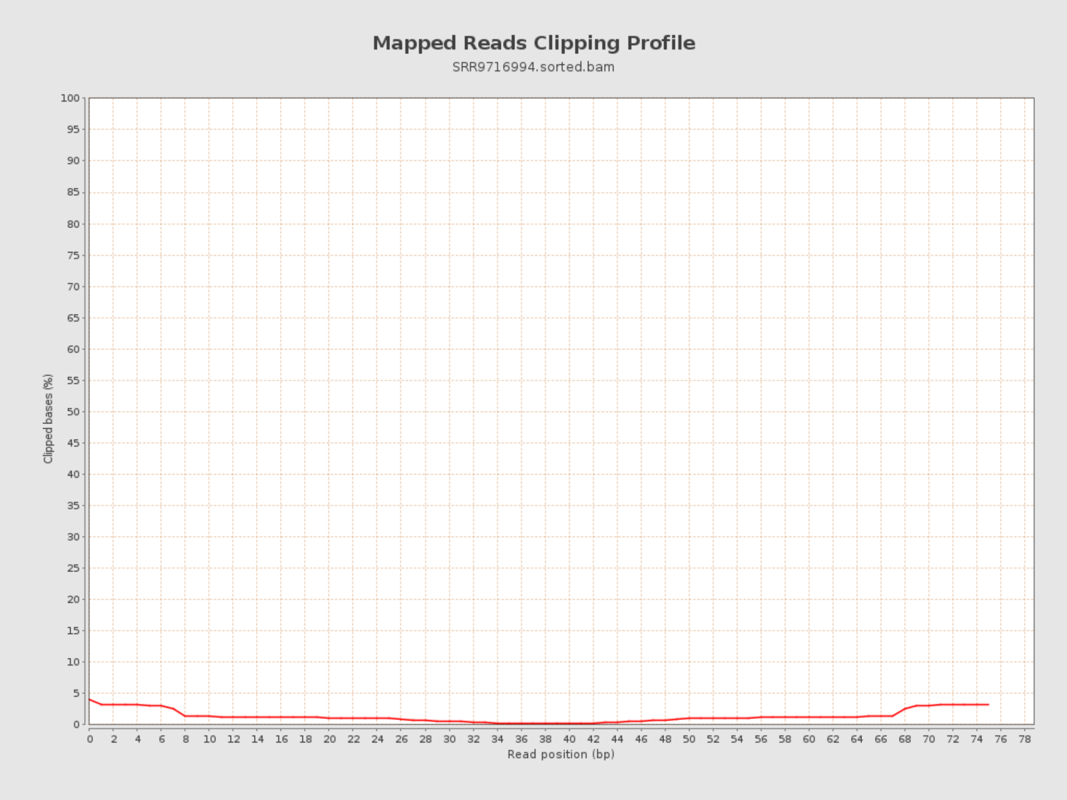
8. Results : Mapped Reads Nucleotide Content



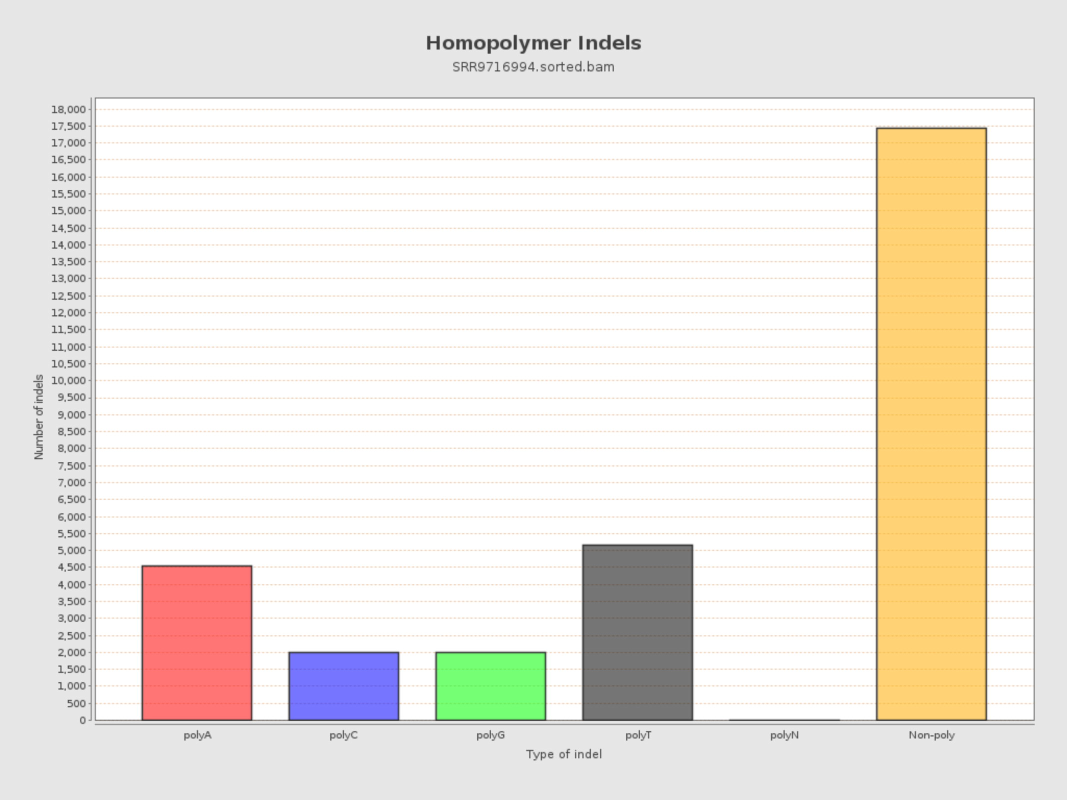
9. Results : Mapped Reads GC-content Distribution



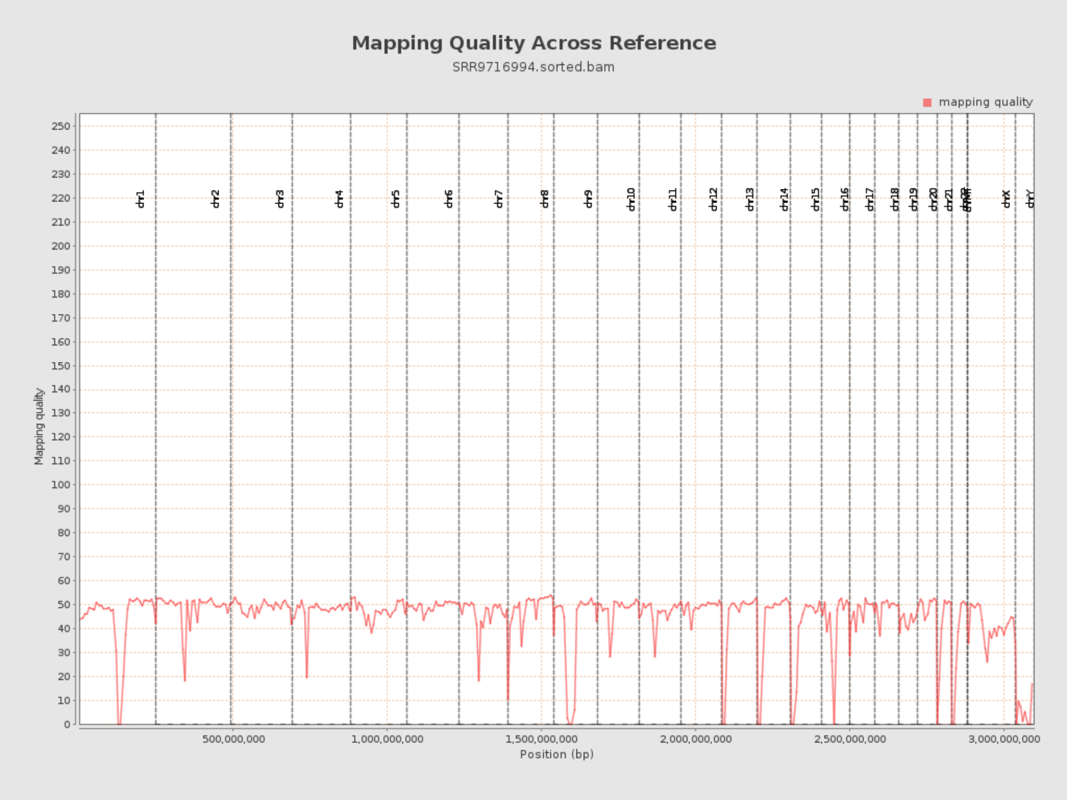
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram