Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 22:58:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716188.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_SRR9716188 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716188.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 22:58:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716188.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,348,352
Mapped reads	1,201,852 / 89.13%
Unmapped reads	146,500 / 10.87%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,735 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	26,072 / 1.93%
Duplication rate	1.5%
Clipped reads	1,203,027 / 89.22%

2.2. ACGT Content

Number/percentage of A's	16,297,089 / 23.7%
Number/percentage of C's	13,319,687 / 19.37%
Number/percentage of T's	21,701,105 / 31.56%
Number/percentage of G's	17,447,737 / 25.37%
Number/percentage of N's	532 / 0%
GC Percentage	44.74%

2.3. Coverage

Mean	0.0222

Standard Deviation	0.204

2.4. Mapping Quality

Mean Mapping Quality	42.39

2.5. Mismatches and indels

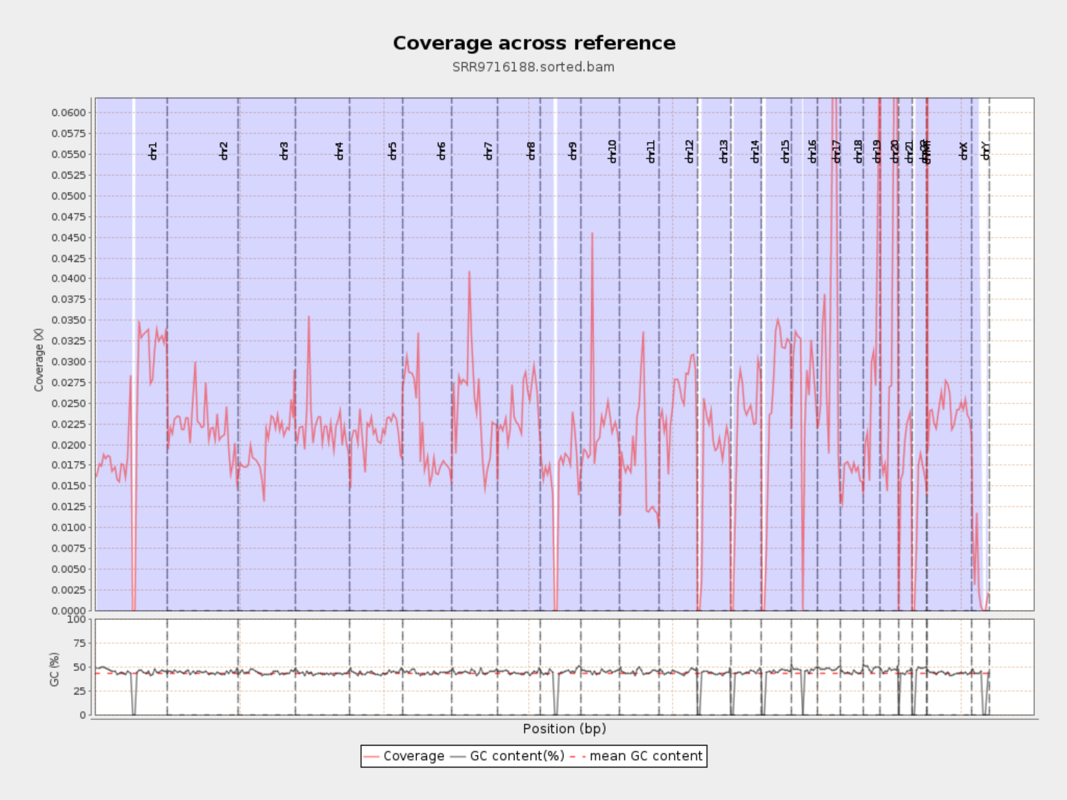
General error rate	0.55%
Mismatches	366,794
Insertions	4,974
Mapped reads with at least one insertion	0.41%
Deletions	13,403
Mapped reads with at least one deletion	1.11%
Homopolymer indels	41.98%

2.6. Chromosome stats

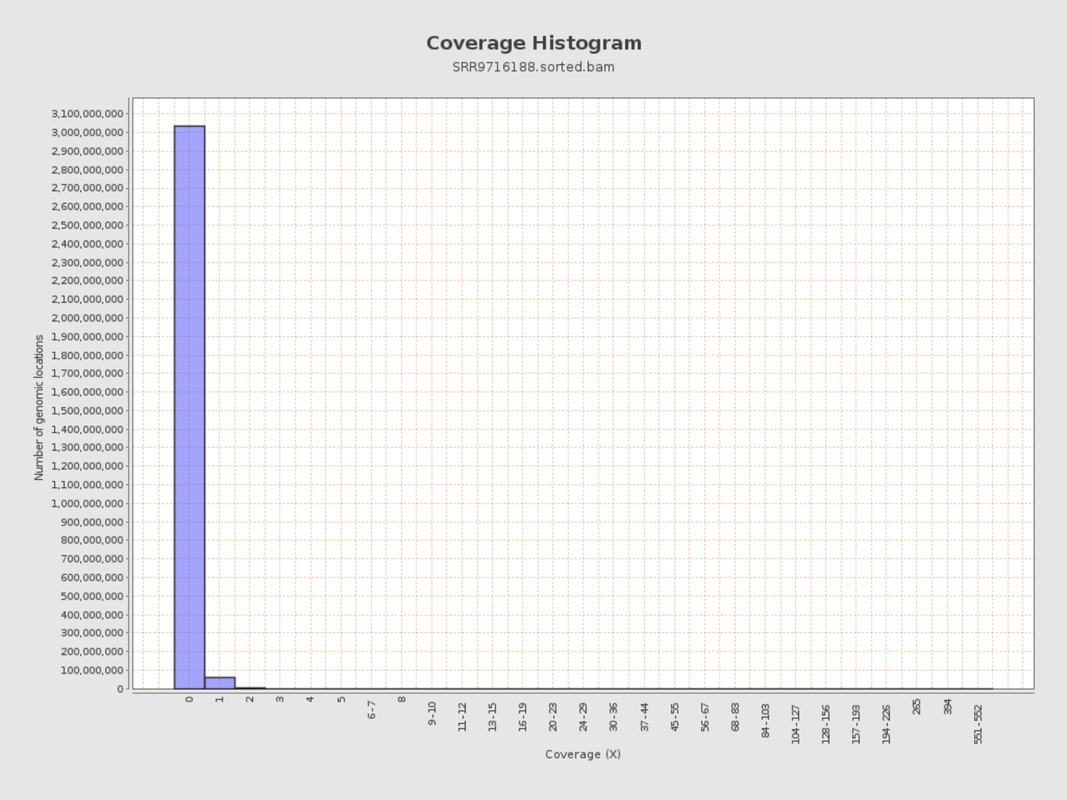
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5723032	0.023	0.2459
chr2	243199373	5356482	0.022	0.2772
chr3	198022430	3972176	0.0201	0.1552
chr4	191154276	4258668	0.0223	0.1705
chr5	180915260	3906116	0.0216	0.1558
chr6	171115067	3677680	0.0215	0.1853
chr7	159138663	3926900	0.0247	0.2844

chr8	146364022	3556301	0.0243	0.1988
chr9	141213431	2261581	0.016	0.1525
chr10	135534747	3032592	0.0224	0.2581
chr11	135006516	2440906	0.0181	0.1689
chr12	133851895	3422998	0.0256	0.1708
chr13	115169878	2050056	0.0178	0.1417
chr14	107349540	2311315	0.0215	0.1634
chr15	102531392	2523726	0.0246	0.1685
chr16	90354753	2387480	0.0264	0.1853
chr17	81195210	3033298	0.0374	0.2144
chr18	78077248	1288314	0.0165	0.2333
chr19	59128983	1817842	0.0307	0.2508
chr20	63025520	2216050	0.0352	0.2066
chr21	48129895	865996	0.018	0.1528
chr22	51304566	623446	0.0122	0.1171
chrMT	16571	186527	11.2562	7.6214
chrX	155270560	3744547	0.0241	0.1725
chrY	59373566	203699	0.0034	0.0996

3. Results : Coverage across reference



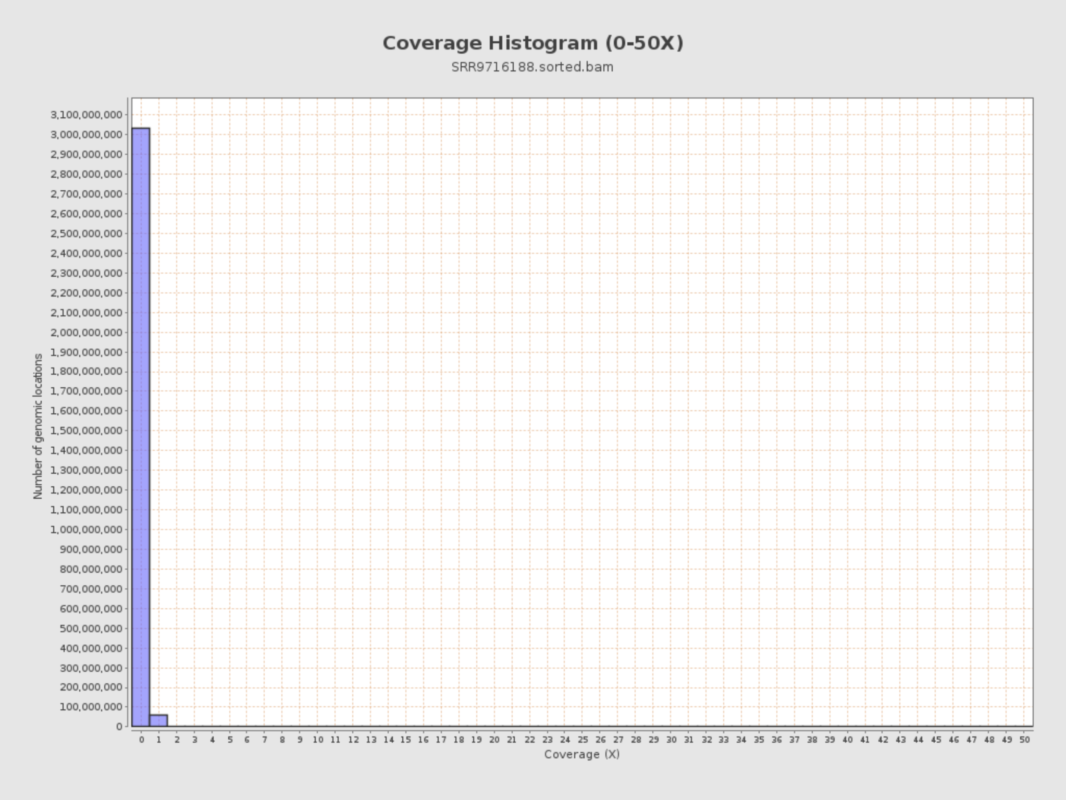
4. Results : Coverage Histogram



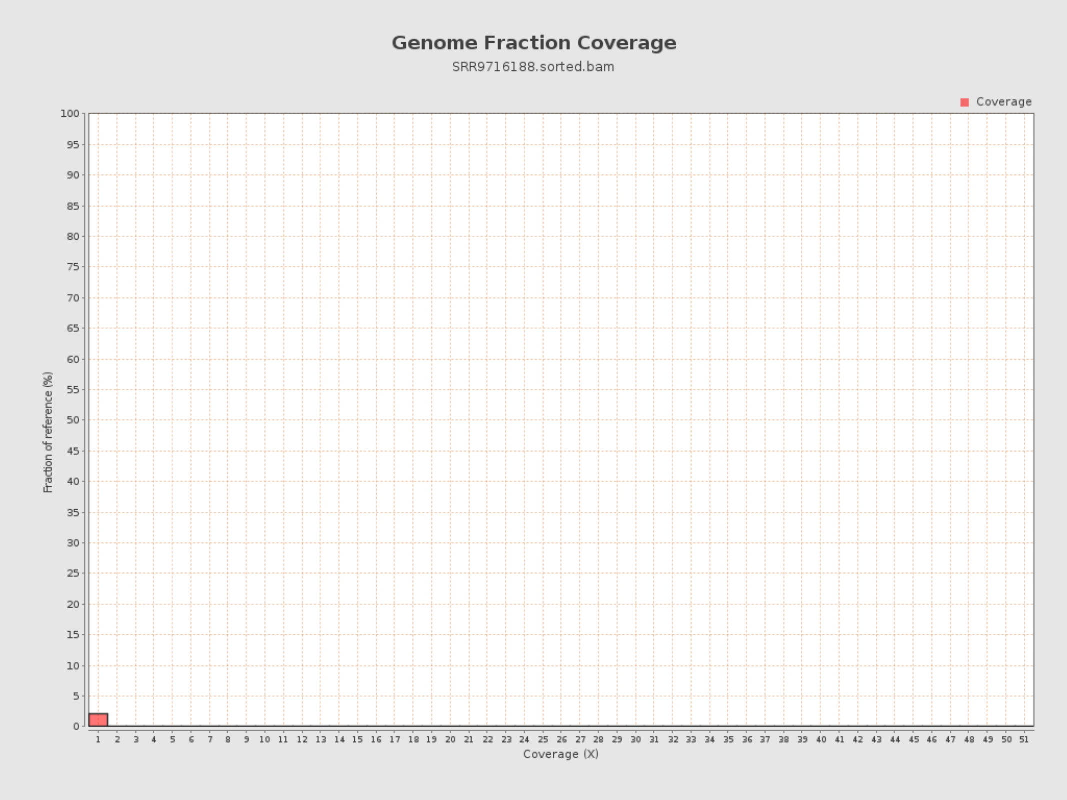
Coverage Histogram

SRR9716188.sorted.bam

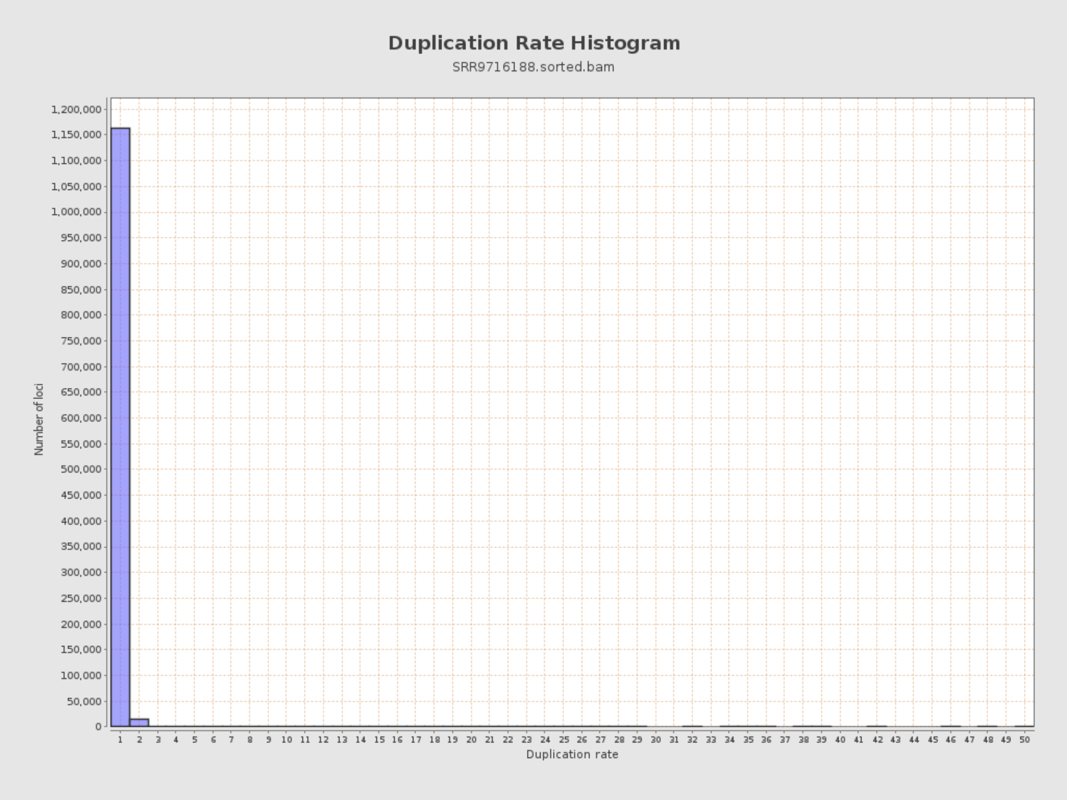
5. Results : Coverage Histogram (0-50X)



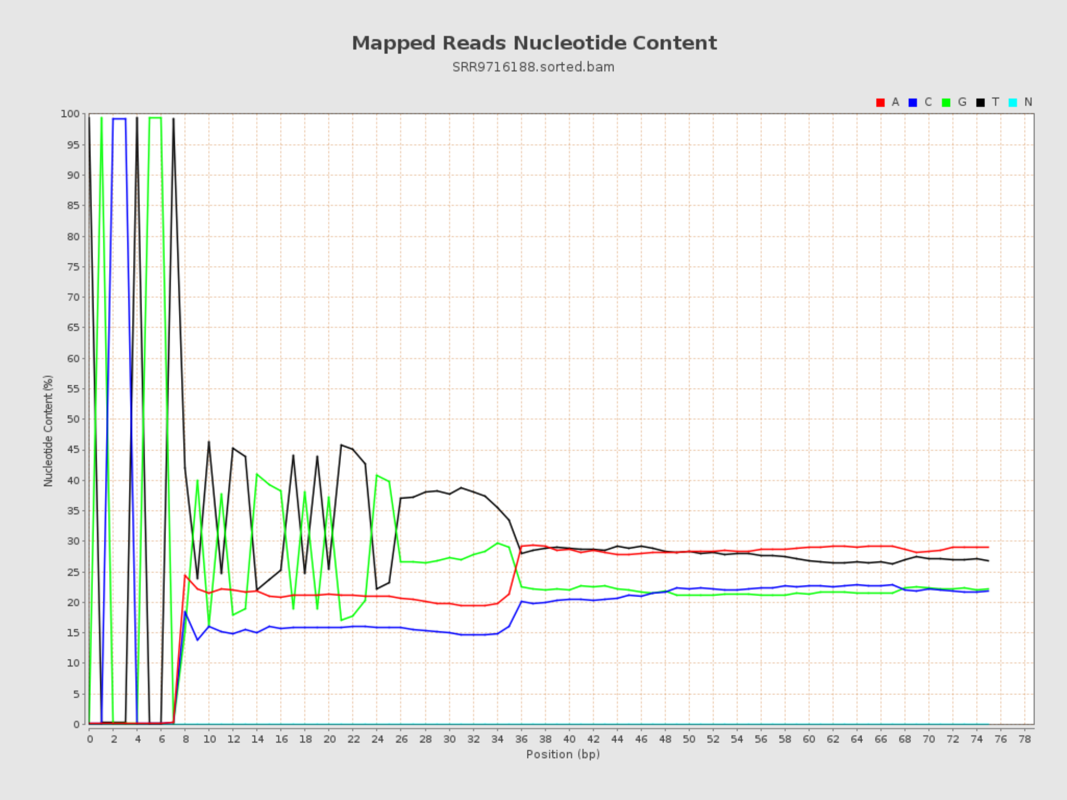
6. Results : Genome Fraction Coverage



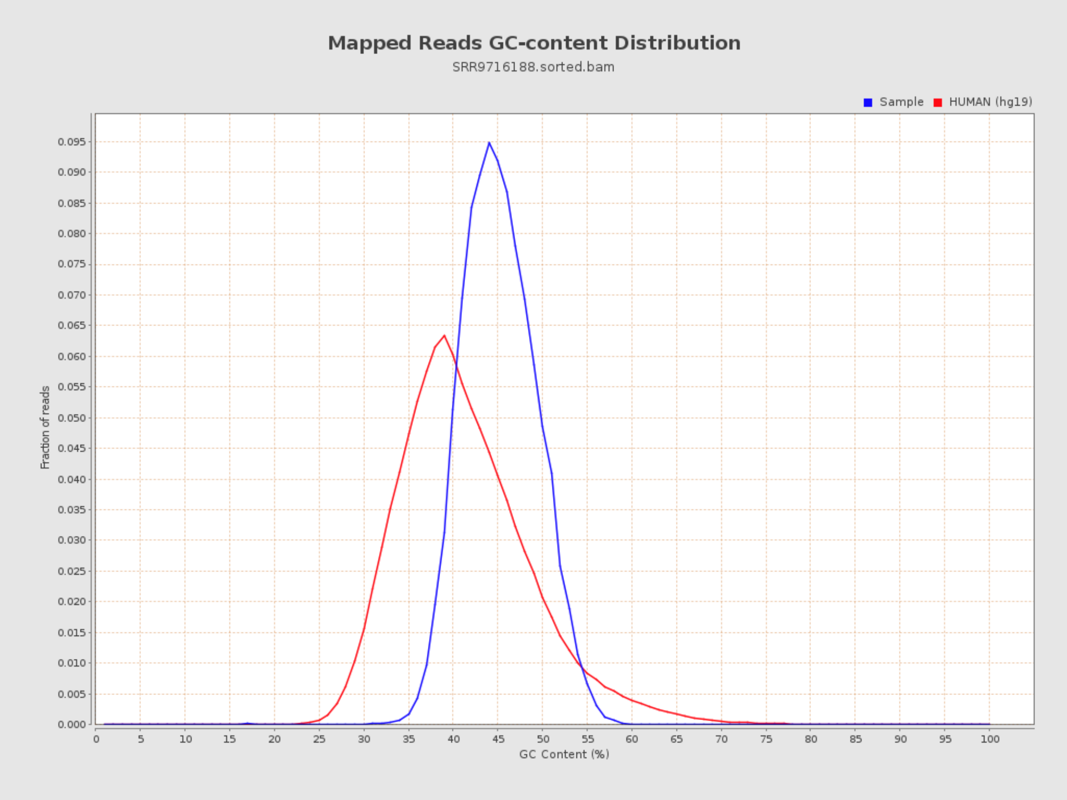
7. Results : Duplication Rate Histogram



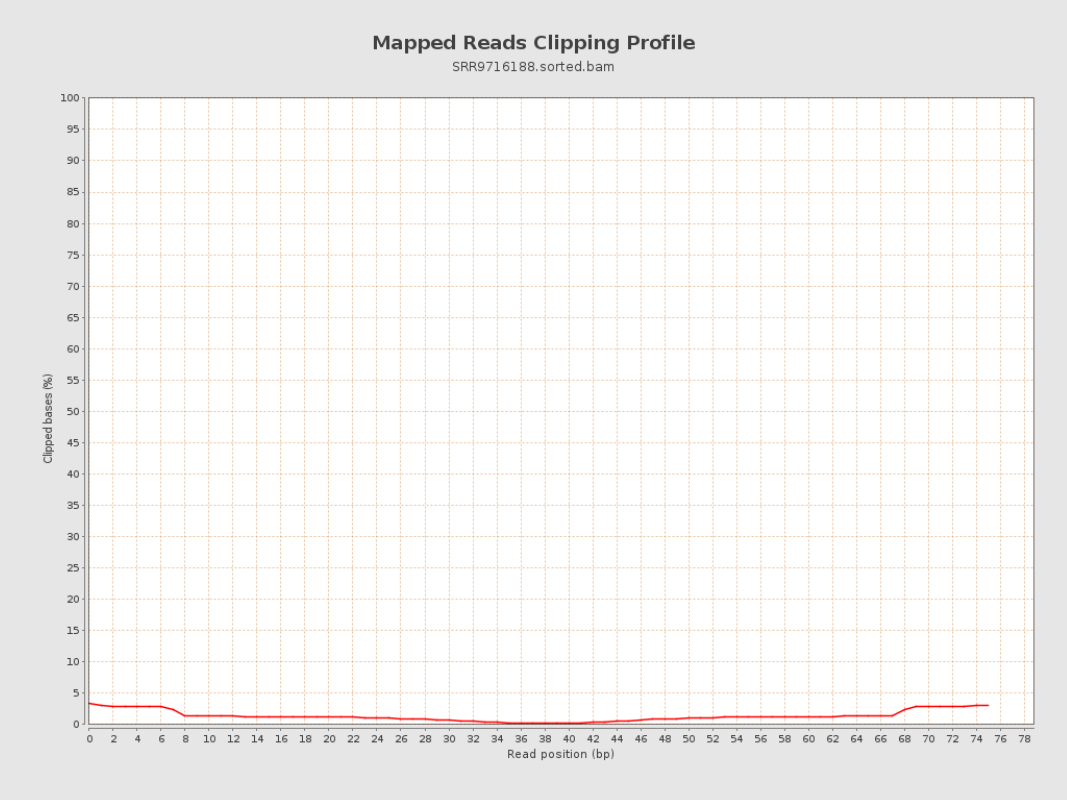
8. Results : Mapped Reads Nucleotide Content



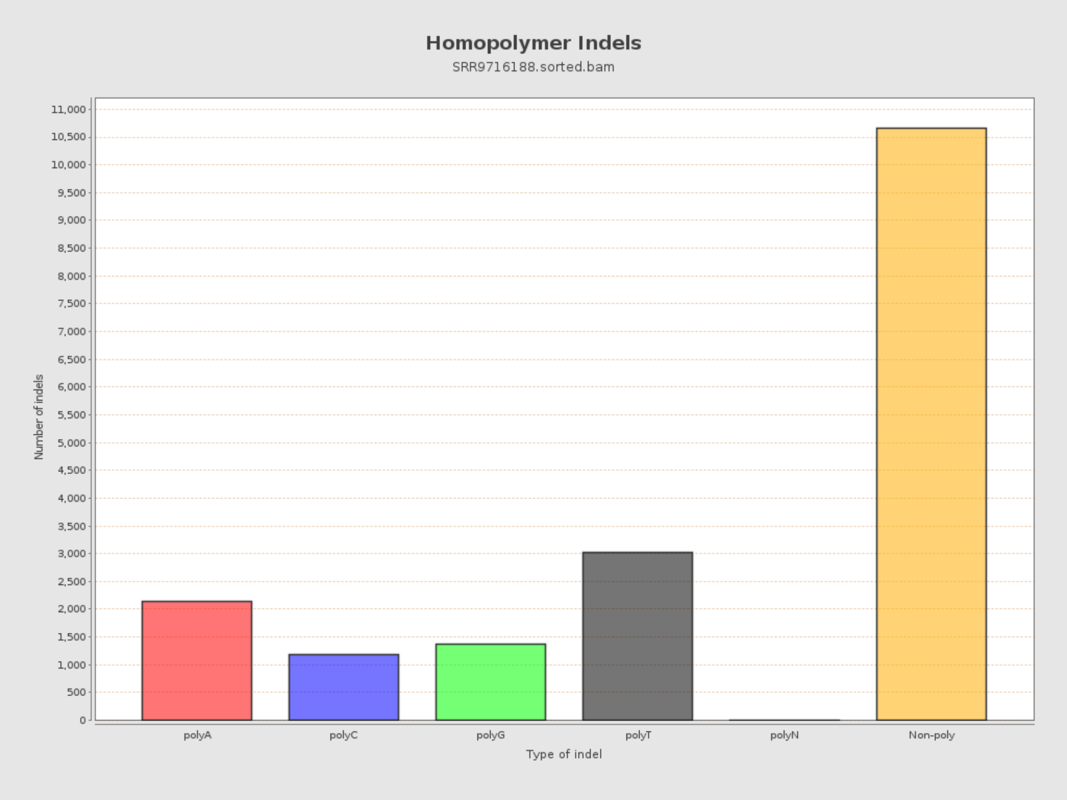
9. Results : Mapped Reads GC-content Distribution



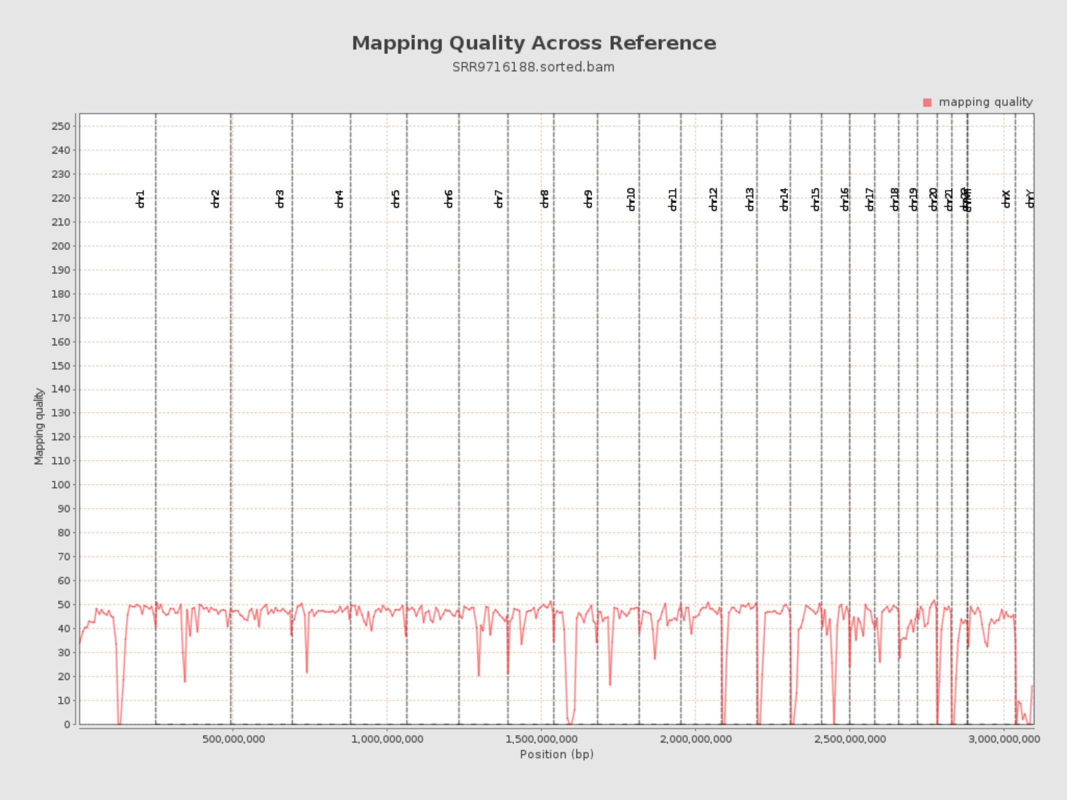
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram