Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:19:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716588.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_SRR9716588 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716588.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:19:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716588.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,517,451
Mapped reads	2,114,967 / 84.01%
Unmapped reads	402,484 / 15.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,534 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	63,281 / 2.51%
Duplication rate	2.06%
Clipped reads	2,120,100 / 84.22%

2.2. ACGT Content

Number/percentage of A's	29,865,721 / 24.96%
Number/percentage of C's	23,181,245 / 19.38%
Number/percentage of T's	37,619,949 / 31.45%
Number/percentage of G's	28,964,530 / 24.21%
Number/percentage of N's	891 / 0%
GC Percentage	43.59%

2.3. Coverage

Mean	0.0387

Standard Deviation	0.3076

2.4. Mapping Quality

Mean Mapping Quality	41.82

2.5. Mismatches and indels

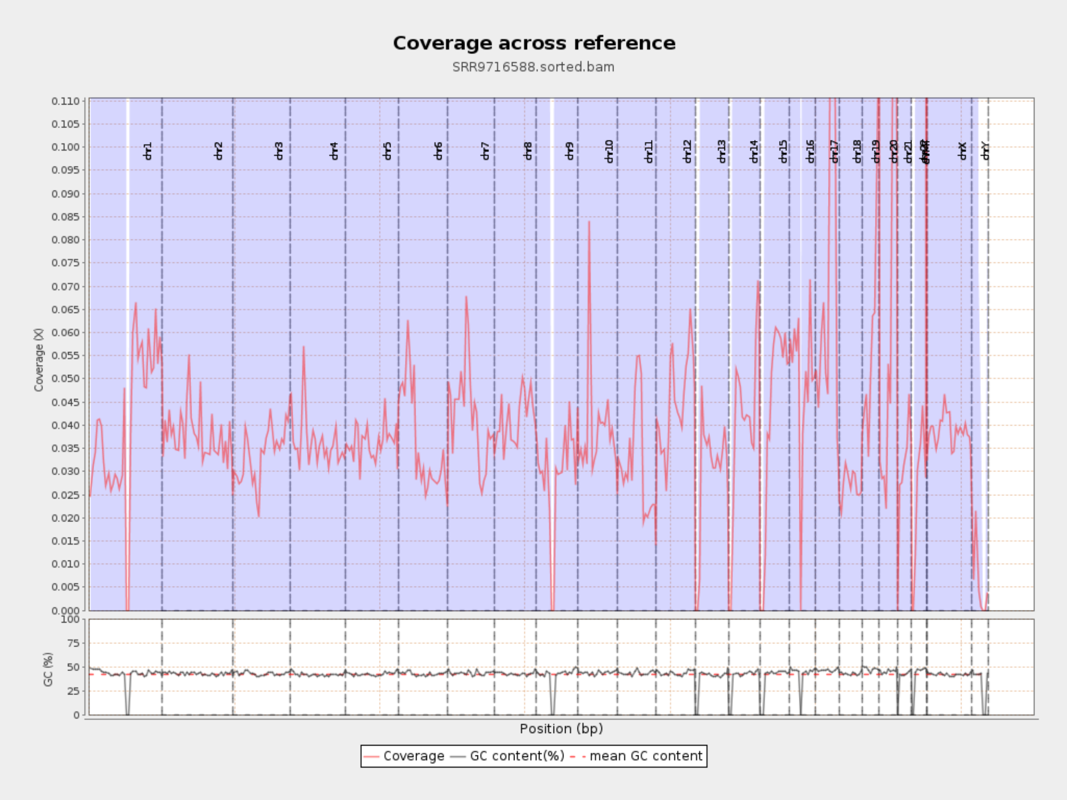
General error rate	0.54%
Mismatches	630,643
Insertions	8,317
Mapped reads with at least one insertion	0.39%
Deletions	21,721
Mapped reads with at least one deletion	1.02%
Homopolymer indels	39.22%

2.6. Chromosome stats

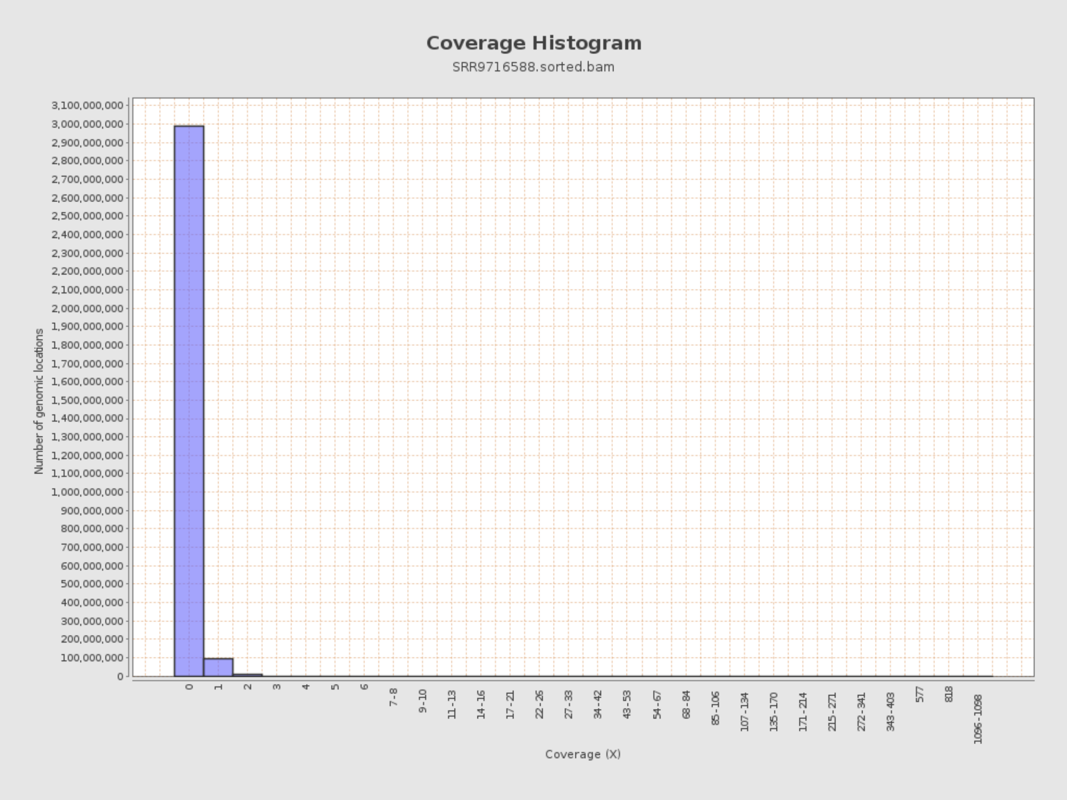
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10052141	0.0403	0.3878
chr2	243199373	9243093	0.038	0.4939
chr3	198022430	6667290	0.0337	0.2096
chr4	191154276	6921736	0.0362	0.2336
chr5	180915260	6584693	0.0364	0.2105
chr6	171115067	6242140	0.0365	0.2594
chr7	159138663	6733799	0.0423	0.4261

chr8	146364022	6051740	0.0413	0.2805
chr9	141213431	4047136	0.0287	0.2271
chr10	135534747	5298312	0.0391	0.4179
chr11	135006516	4348461	0.0322	0.2531
chr12	133851895	6061590	0.0453	0.2382
chr13	115169878	3400786	0.0295	0.19
chr14	107349540	4241652	0.0395	0.2304
chr15	102531392	4362532	0.0425	0.2344
chr16	90354753	4481610	0.0496	0.2744
chr17	81195210	5851113	0.0721	0.3178
chr18	78077248	2115502	0.0271	0.3522
chr19	59128983	3638088	0.0615	0.3864
chr20	63025520	4165775	0.0661	0.3086
chr21	48129895	1483269	0.0308	0.2125
chr22	51304566	1270007	0.0248	0.1758
chrMT	16571	9120	0.5504	0.895
chrX	155270560	6024891	0.0388	0.2383
chrY	59373566	370907	0.0062	0.1766

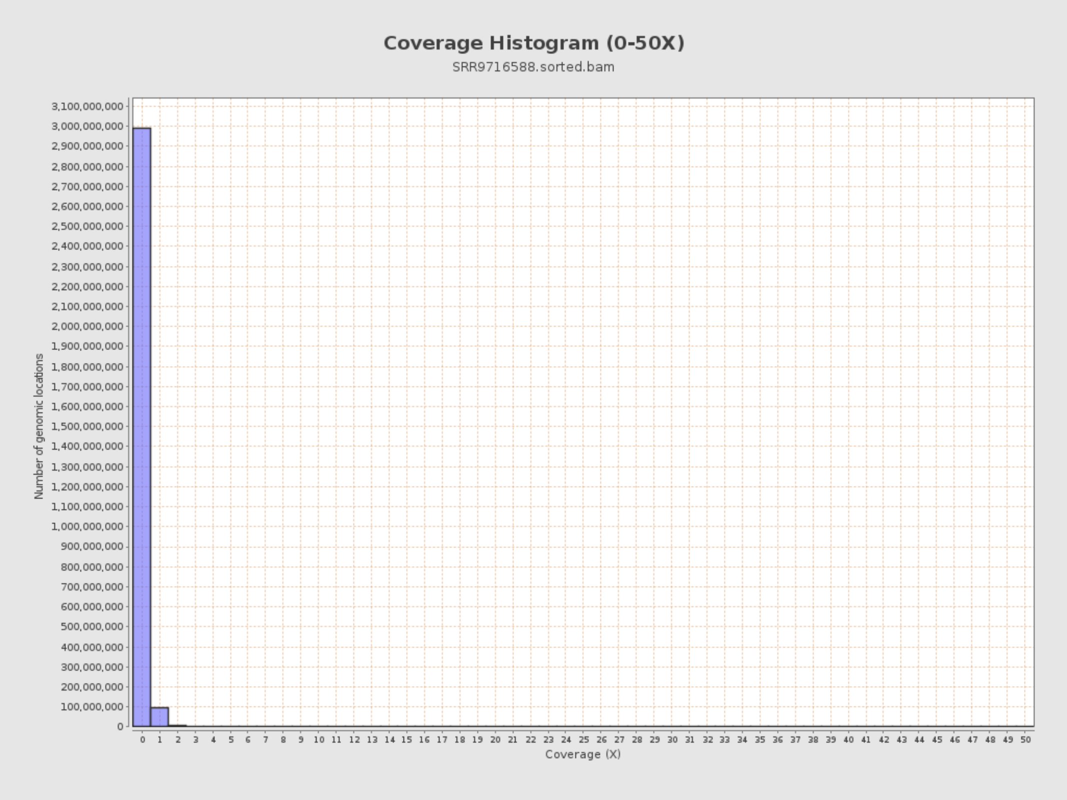
3. Results : Coverage across reference



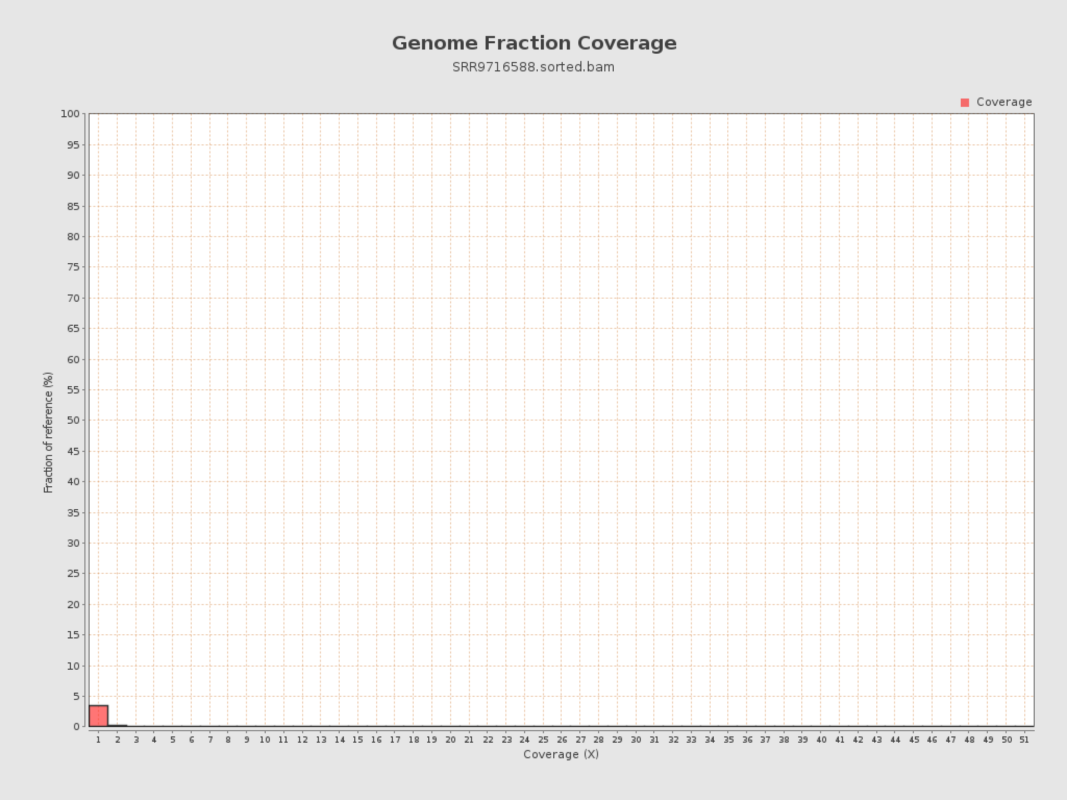
4. Results : Coverage Histogram



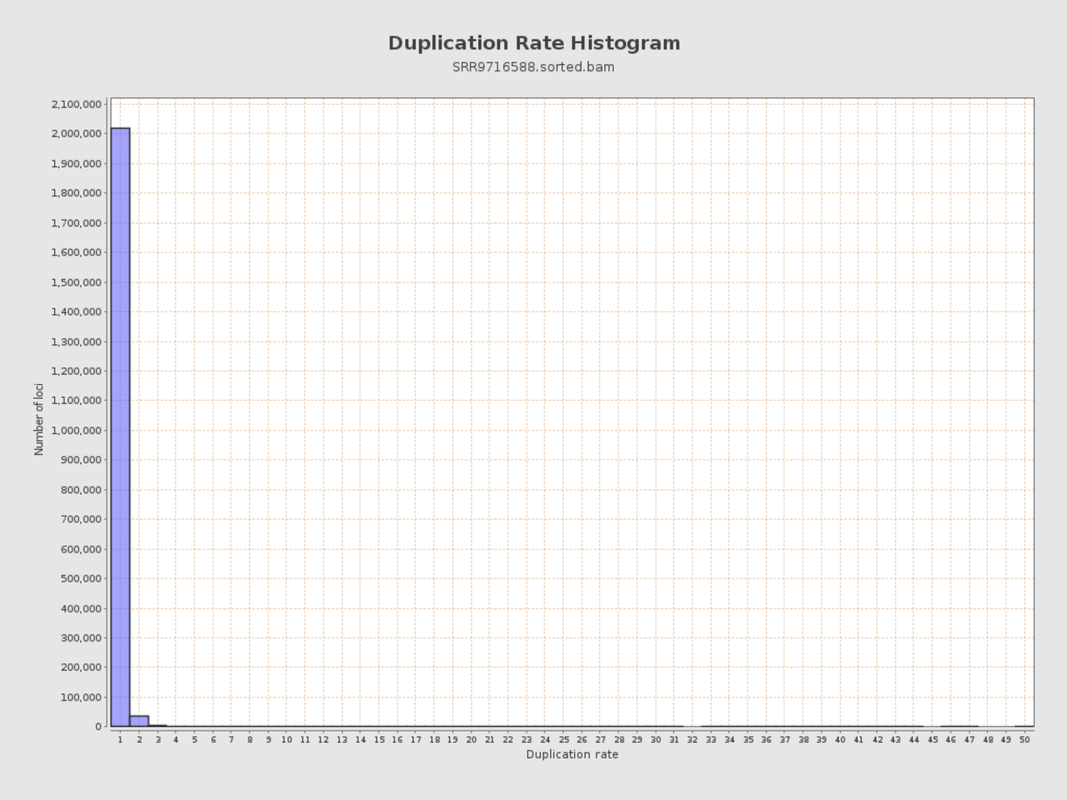
5. Results : Coverage Histogram (0-50X)



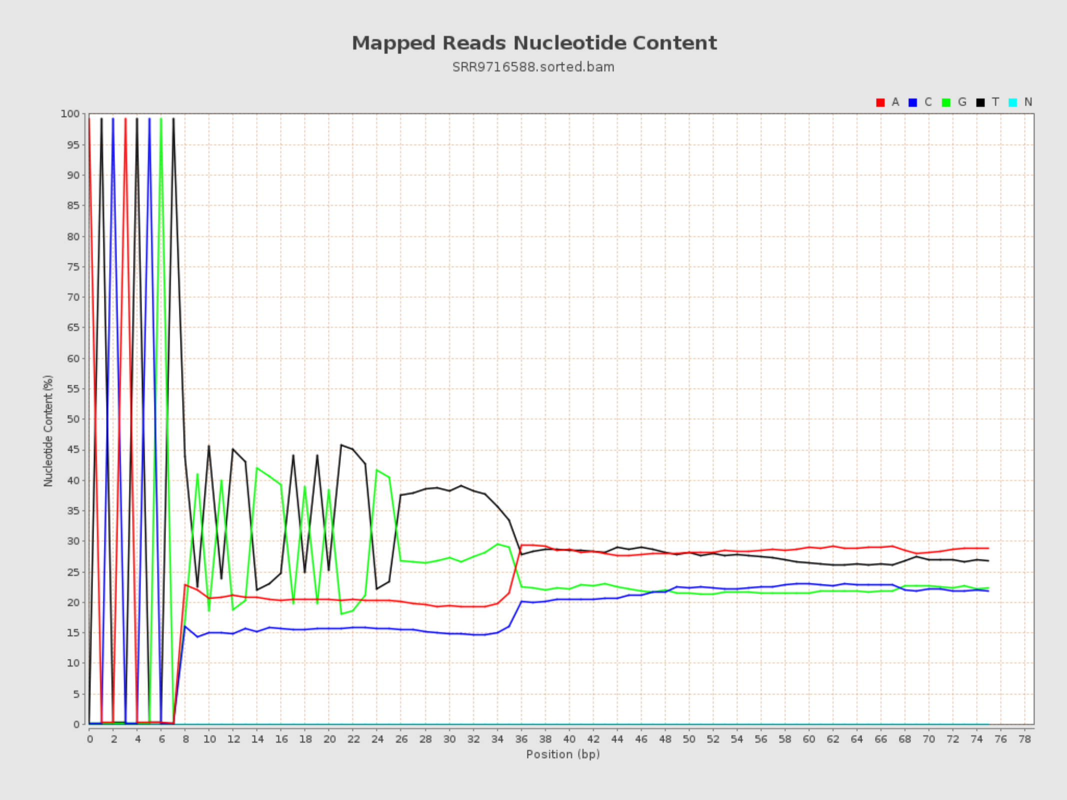
6. Results : Genome Fraction Coverage



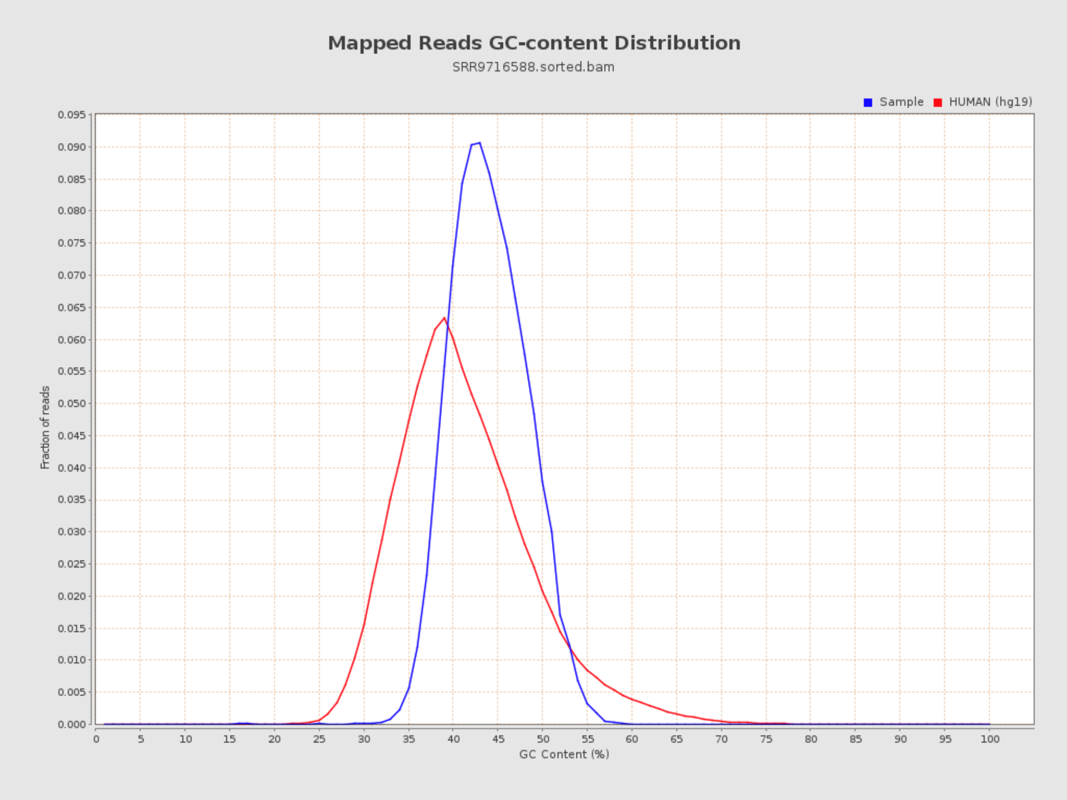
7. Results : Duplication Rate Histogram



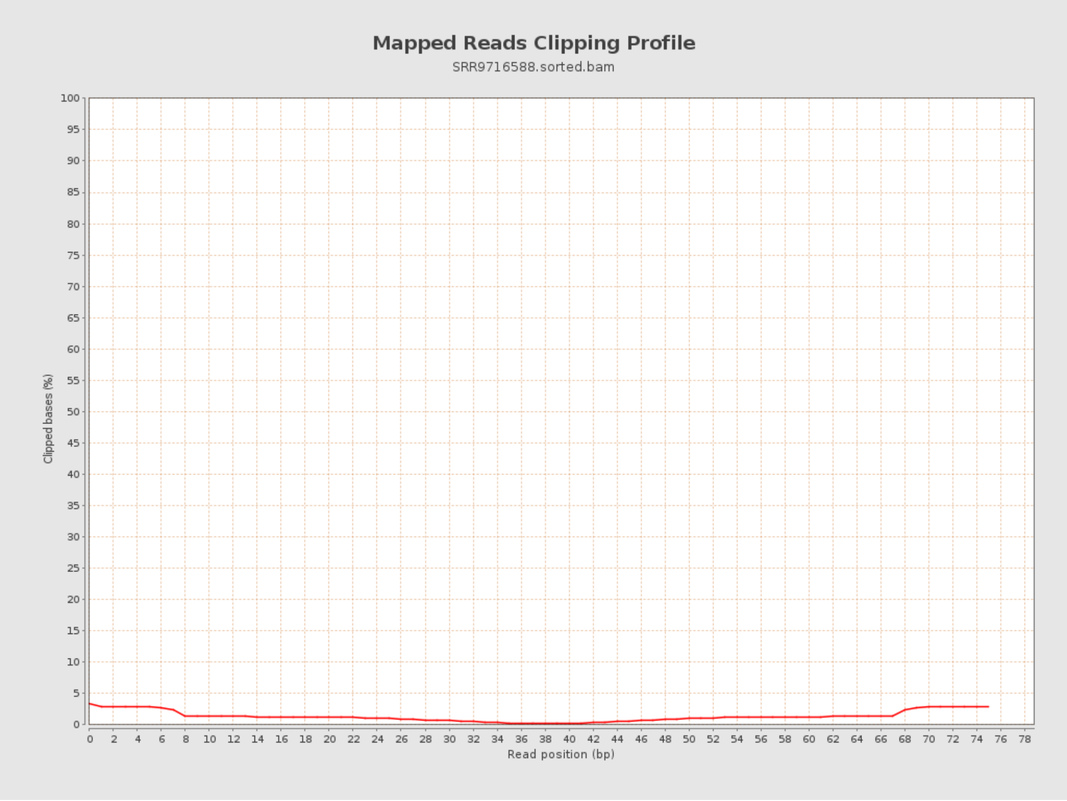
8. Results : Mapped Reads Nucleotide Content



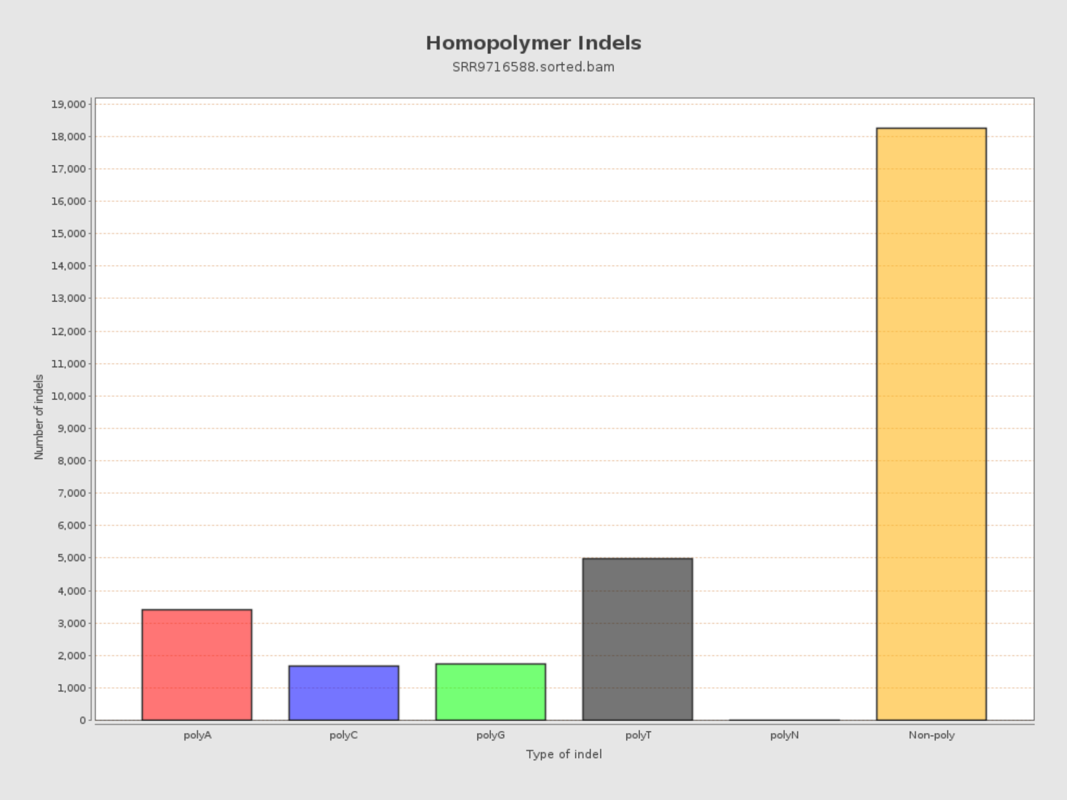
9. Results : Mapped Reads GC-content Distribution



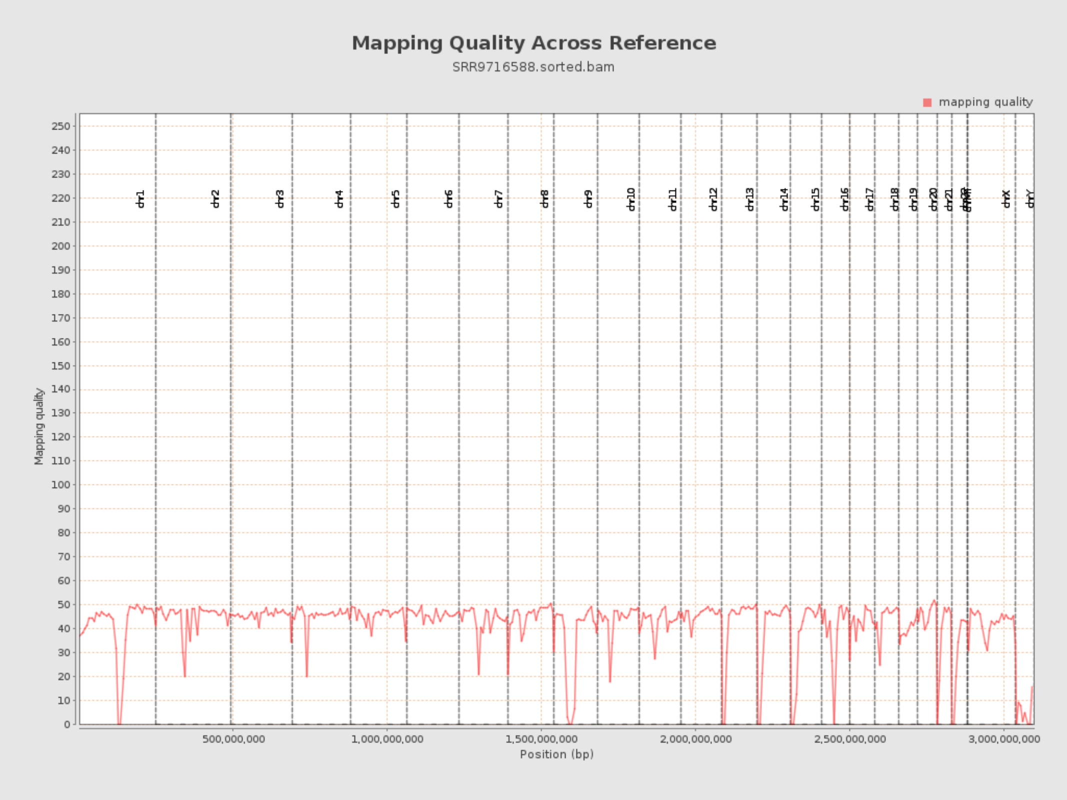
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram