Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 12:21:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716415.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_SRR9716415 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716415.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 12:21:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716415.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,232,030
Mapped reads	2,056,492 / 92.14%
Unmapped reads	175,538 / 7.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,153 / 0.63%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	134,631 / 6.03%
Duplication rate	5.09%
Clipped reads	2,066,299 / 92.57%

2.2. ACGT Content

Number/percentage of A's	30,079,776 / 24.84%
Number/percentage of C's	22,869,898 / 18.89%
Number/percentage of T's	36,573,164 / 30.21%
Number/percentage of G's	31,550,375 / 26.06%
Number/percentage of N's	1,457 / 0%
GC Percentage	44.95%

2.3. Coverage

Mean	0.0391

Standard Deviation	0.3354

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

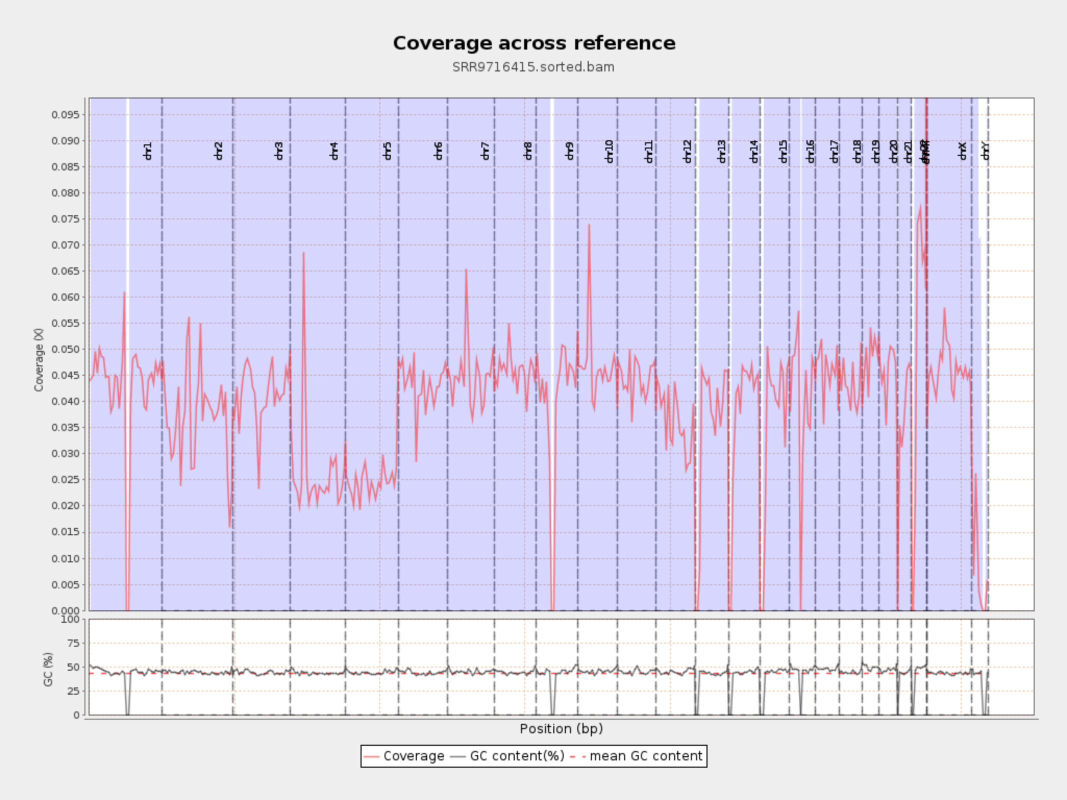
General error rate	0.52%
Mismatches	610,382
Insertions	8,460
Mapped reads with at least one insertion	0.41%
Deletions	21,312
Mapped reads with at least one deletion	1.03%
Homopolymer indels	41.58%

2.6. Chromosome stats

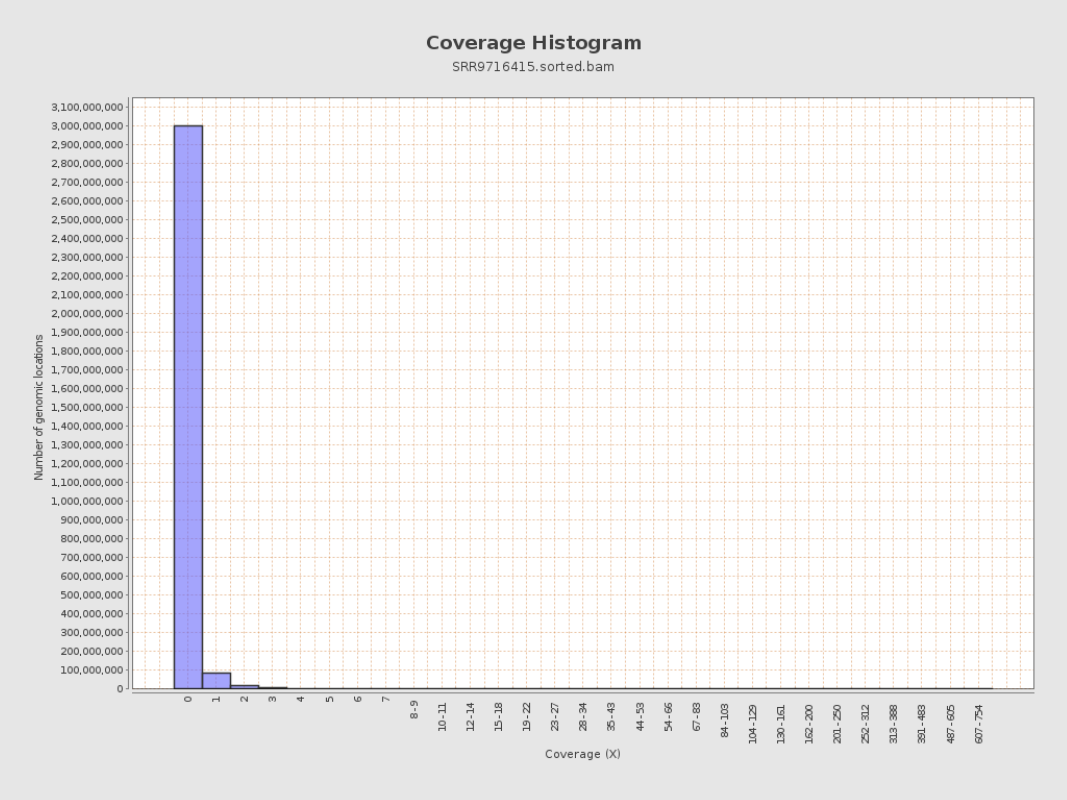
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10601012	0.0425	0.5244
chr2	243199373	9044307	0.0372	0.4321
chr3	198022430	8180770	0.0413	0.2406
chr4	191154276	4952432	0.0259	0.2547
chr5	180915260	4453960	0.0246	0.187
chr6	171115067	7415086	0.0433	0.2696
chr7	159138663	7140866	0.0449	0.4524

chr8	146364022	6702531	0.0458	0.3585
chr9	141213431	5501473	0.039	0.284
chr10	135534747	6351426	0.0469	0.3744
chr11	135006516	5998951	0.0444	0.3268
chr12	133851895	4801094	0.0359	0.2285
chr13	115169878	3991606	0.0347	0.2241
chr14	107349540	3975164	0.037	0.2359
chr15	102531392	3620771	0.0353	0.2265
chr16	90354753	3674658	0.0407	0.2553
chr17	81195210	3744922	0.0461	0.2782
chr18	78077248	3368050	0.0431	0.544
chr19	59128983	2857179	0.0483	0.4002
chr20	63025520	2881080	0.0457	0.2632
chr21	48129895	1734895	0.036	0.2657
chr22	51304566	2512682	0.049	0.268
chrMT	16571	29051	1.7531	1.9107
chrX	155270560	7143687	0.046	0.2787
chrY	59373566	431424	0.0073	0.2204

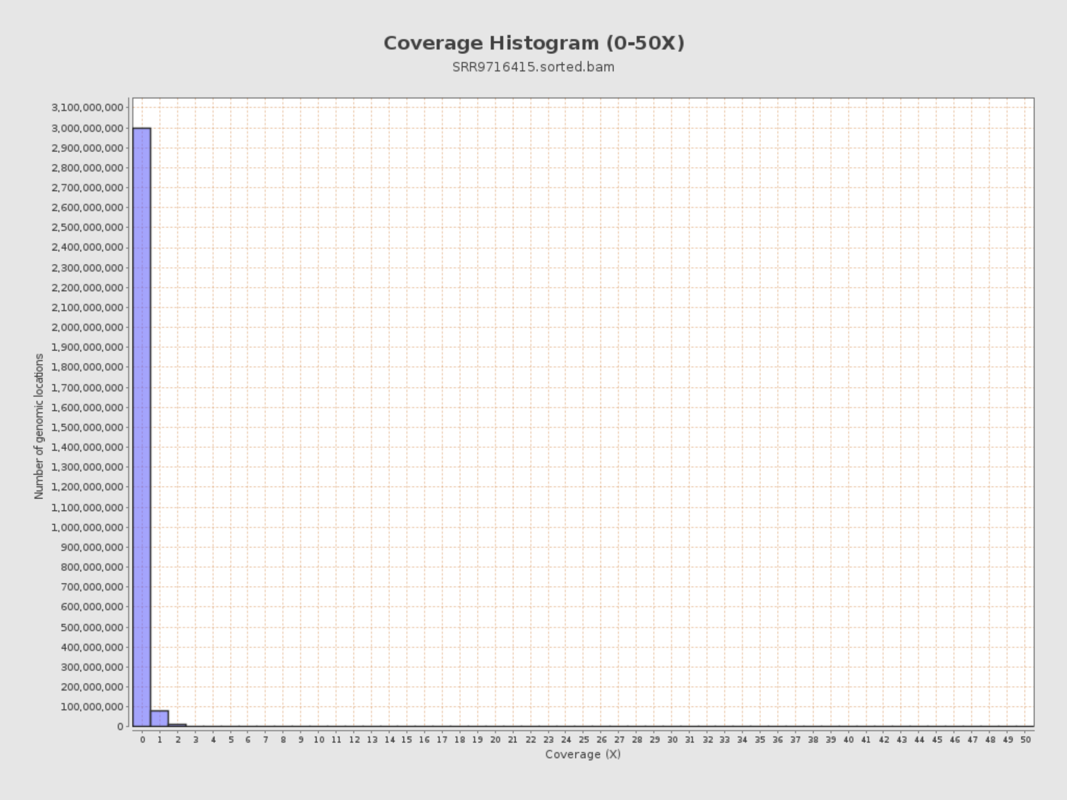
3. Results : Coverage across reference



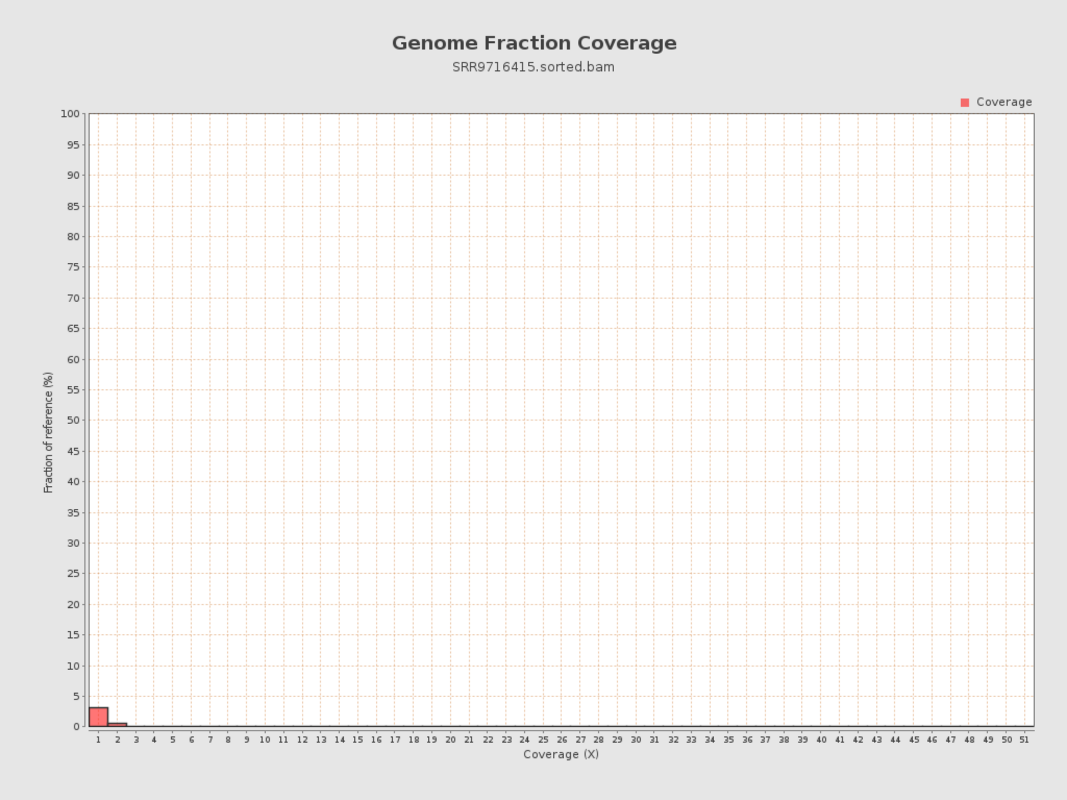
4. Results : Coverage Histogram



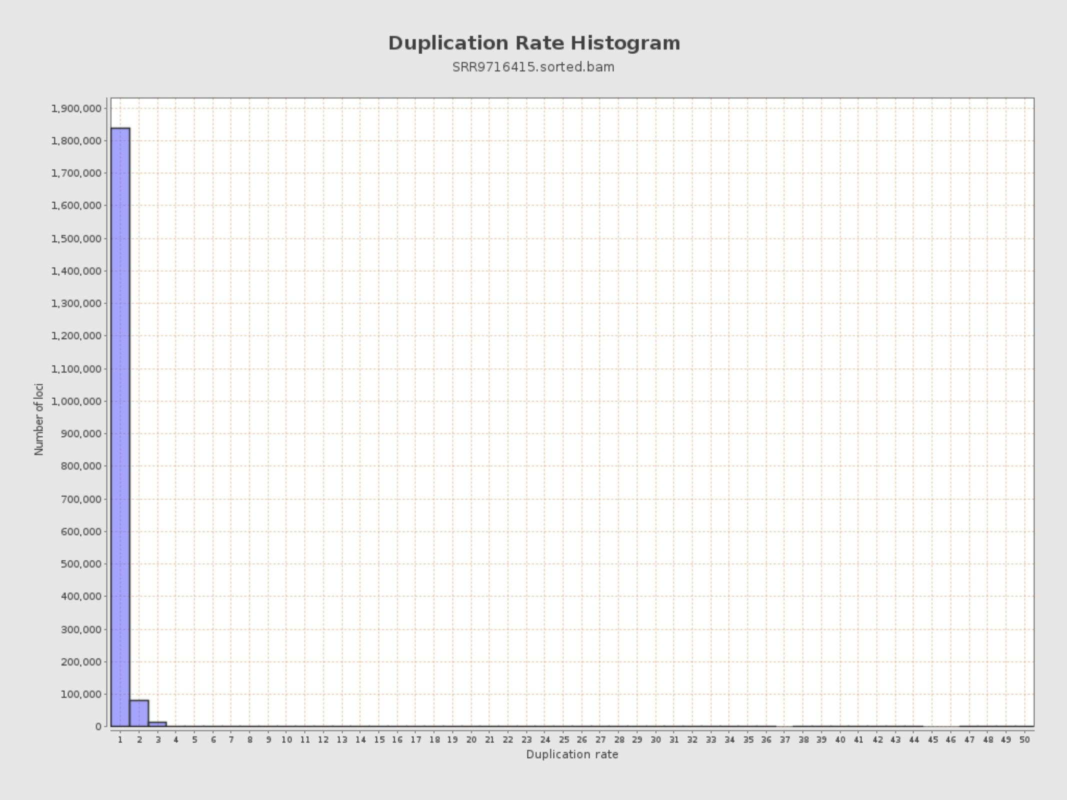
5. Results : Coverage Histogram (0-50X)



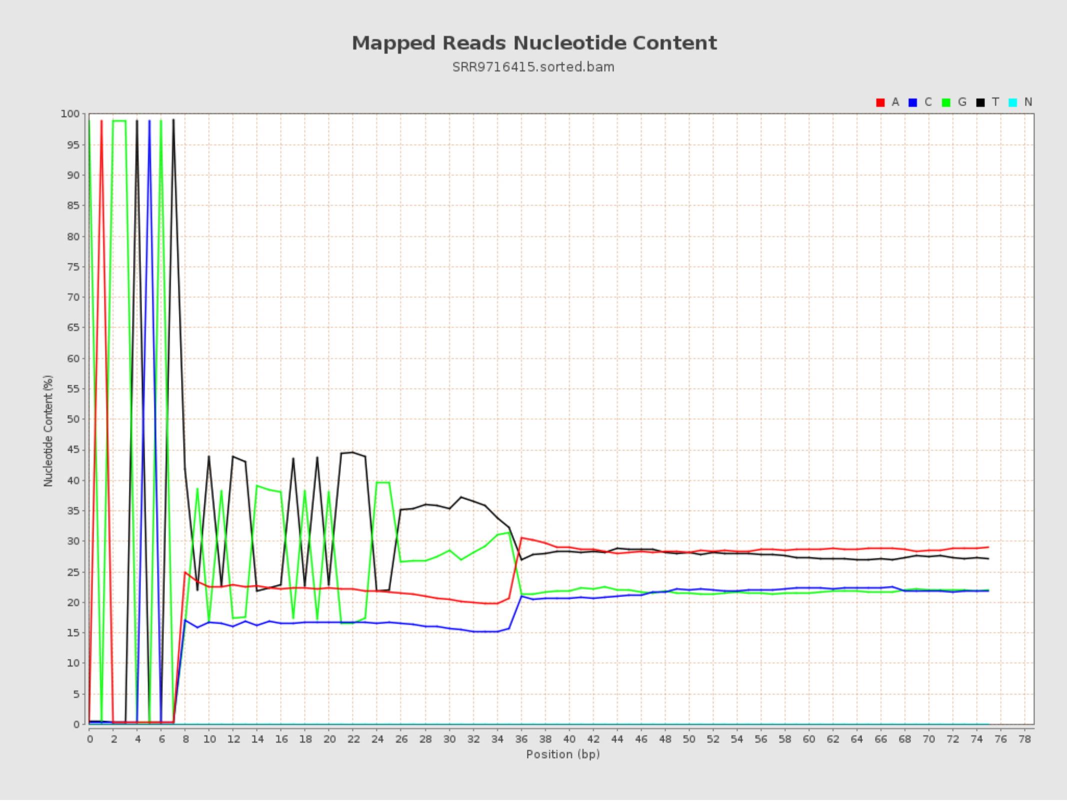
6. Results : Genome Fraction Coverage



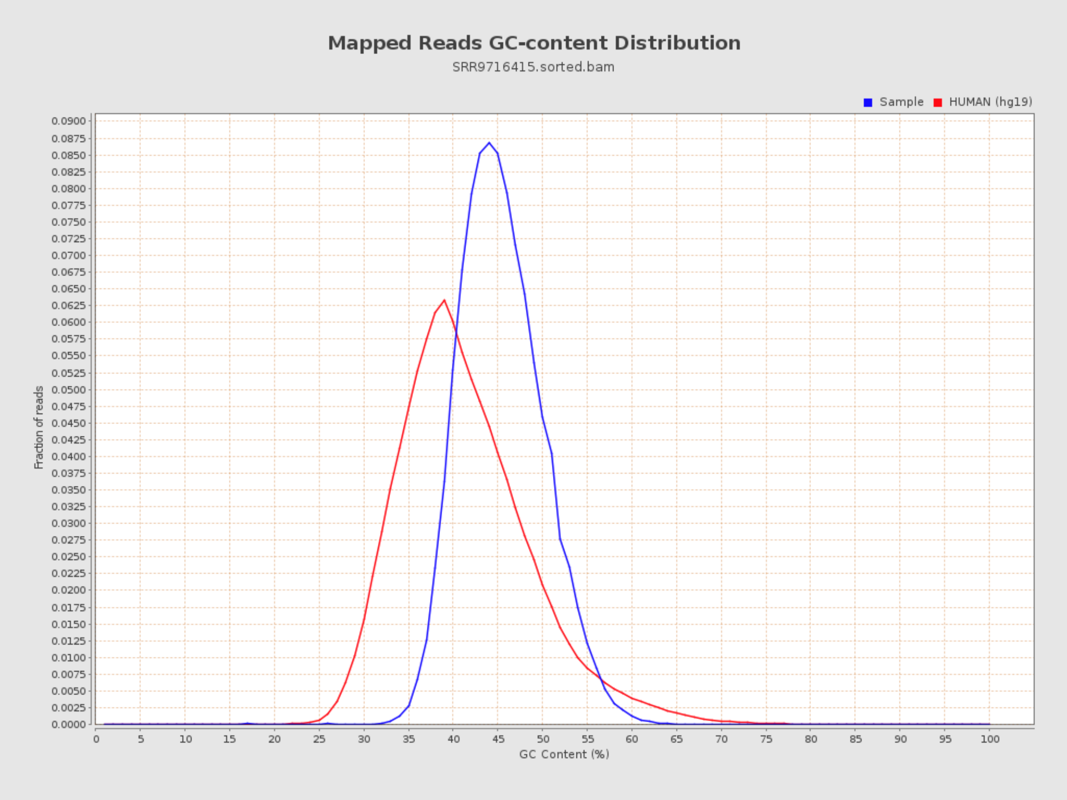
7. Results : Duplication Rate Histogram



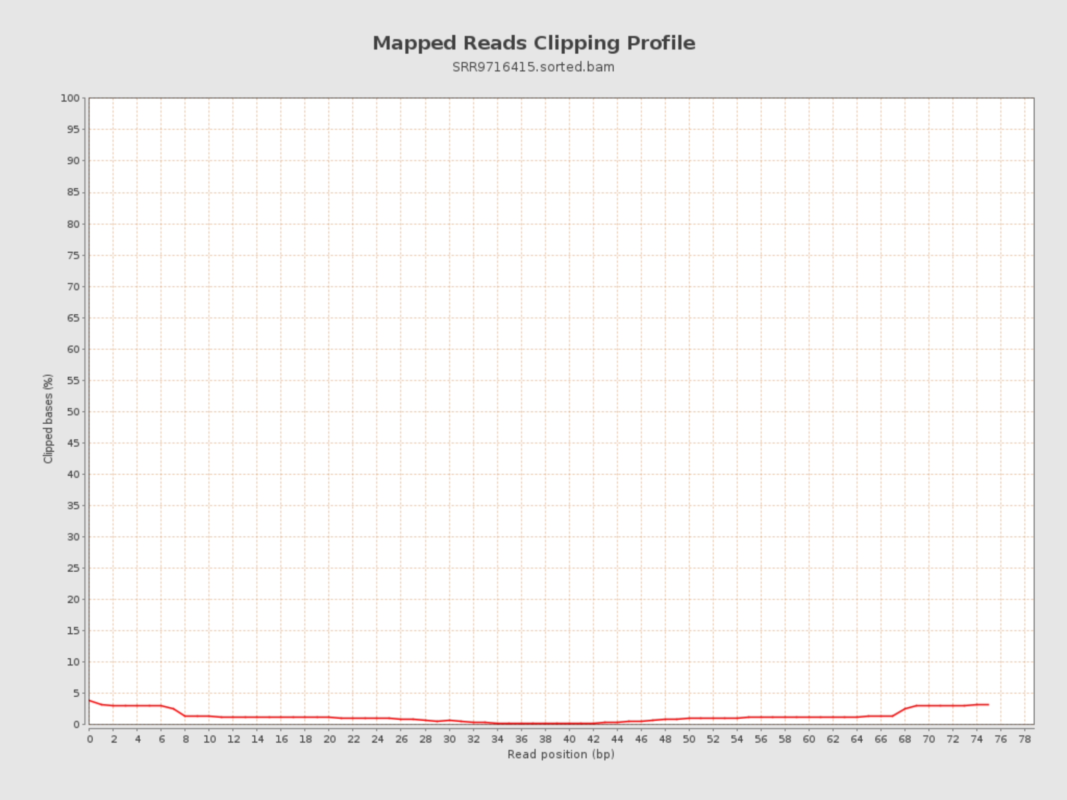
8. Results : Mapped Reads Nucleotide Content



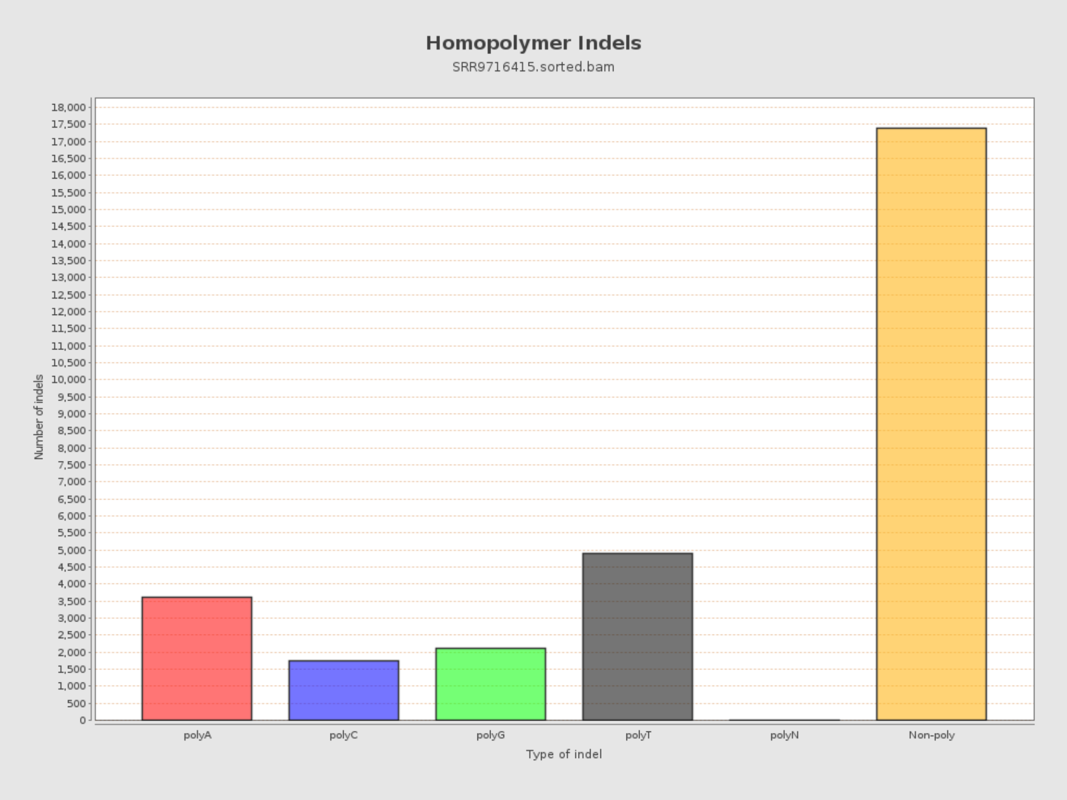
9. Results : Mapped Reads GC-content Distribution



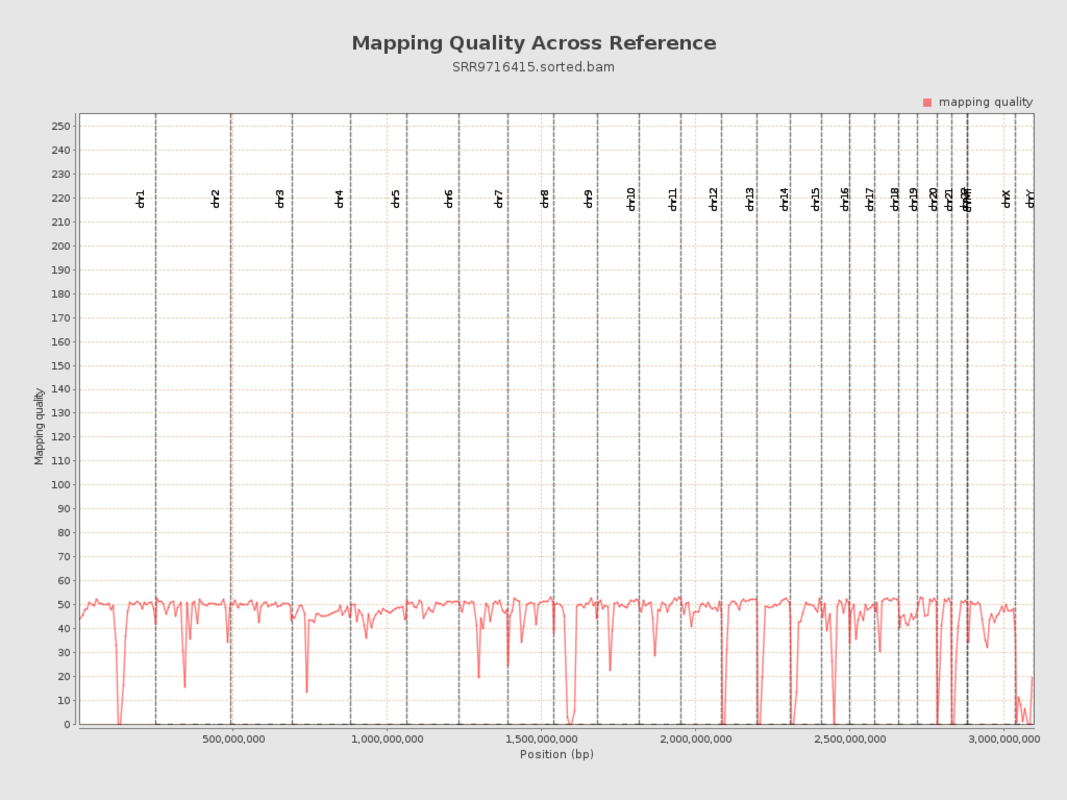
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram