

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 07:26:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716705.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_SRR9716705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716705.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 07:26:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716705.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,446,343
Mapped reads	2,182,078 / 89.2%
Unmapped reads	264,265 / 10.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,732 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	68,389 / 2.8%
Duplication rate	2.25%
Clipped reads	2,184,356 / 89.29%

2.2. ACGT Content

Number/percentage of A's	32,498,288 / 26.16%
Number/percentage of C's	26,246,818 / 21.13%
Number/percentage of T's	37,094,634 / 29.86%
Number/percentage of G's	28,377,803 / 22.85%
Number/percentage of N's	965 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3102
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2.4. Mapping Quality

Mean Mapping Quality	42.54
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2.5. Mismatches and indels

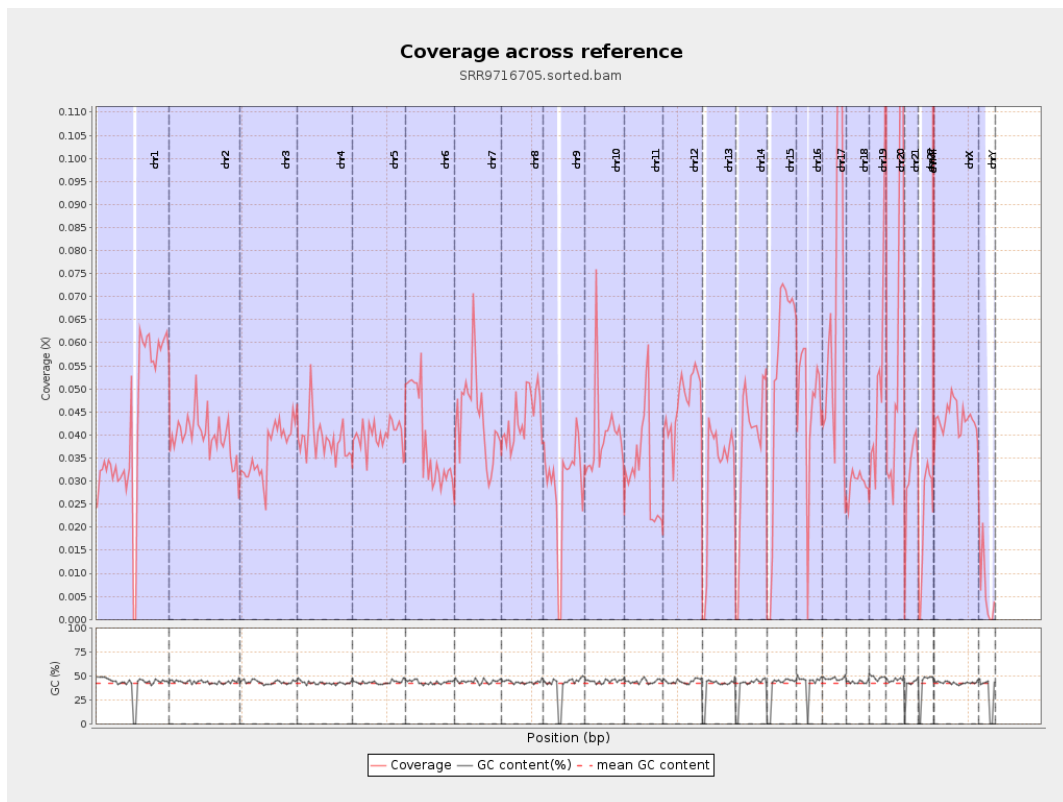
General error rate	0.53%
Mismatches	640,792
Insertions	9,595
Mapped reads with at least one insertion	0.44%
Deletions	23,256
Mapped reads with at least one deletion	1.06%
Homopolymer indels	39.96%

2.6. Chromosome stats

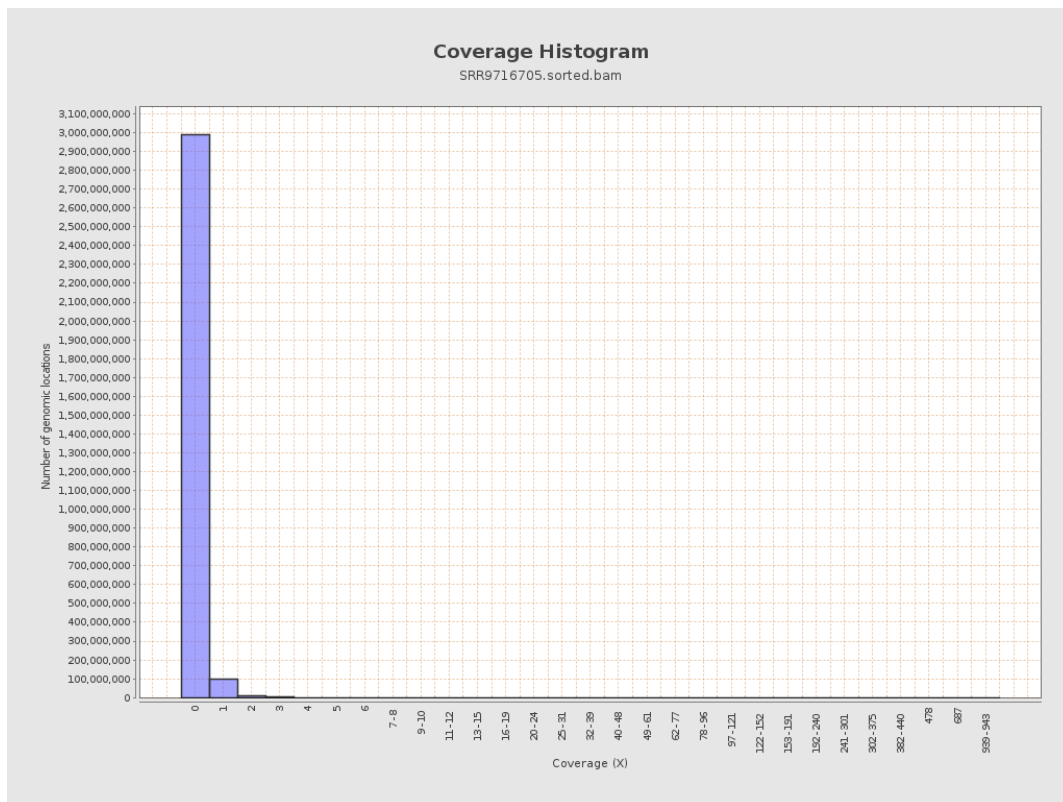
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10468051	0.042	0.4147
chr2	243199373	9661023	0.0397	0.4432
chr3	198022430	7217047	0.0364	0.2185
chr4	191154276	7426516	0.0389	0.2374
chr5	180915260	7214806	0.0399	0.221
chr6	171115067	6629207	0.0387	0.2669
chr7	159138663	7014596	0.0441	0.4655

chr8	146364022	6411481	0.0438	0.313
chr9	141213431	4128731	0.0292	0.2307
chr10	135534747	5394069	0.0398	0.3855
chr11	135006516	4384997	0.0325	0.2584
chr12	133851895	6280335	0.0469	0.243
chr13	115169878	3642831	0.0316	0.1978
chr14	107349540	4067244	0.0379	0.2313
chr15	102531392	5365951	0.0523	0.2644
chr16	90354753	4213915	0.0466	0.2594
chr17	81195210	5451017	0.0671	0.3102
chr18	78077248	2305683	0.0295	0.3712
chr19	59128983	3215079	0.0544	0.3942
chr20	63025520	3965043	0.0629	0.2985
chr21	48129895	1498716	0.0311	0.2143
chr22	51304566	1124386	0.0219	0.1667
chrMT	16571	60320	3.6401	3.0848
chrX	155270560	6744860	0.0434	0.2501
chrY	59373566	369689	0.0062	0.1729

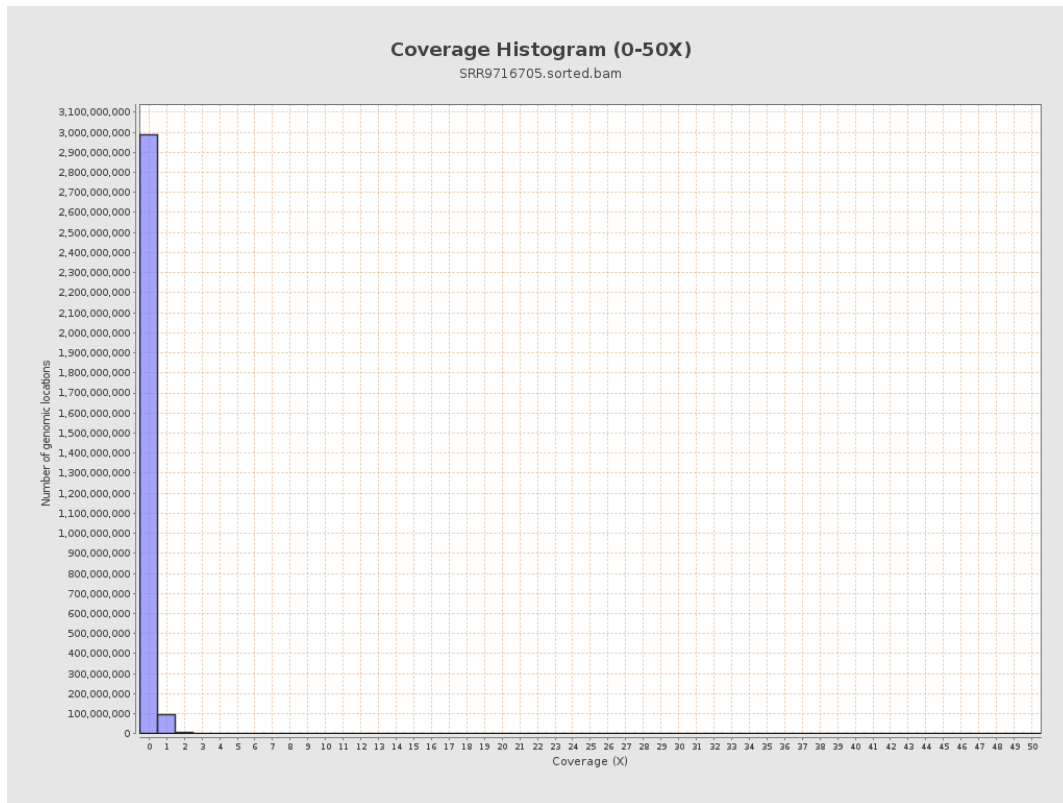
3. Results : Coverage across reference



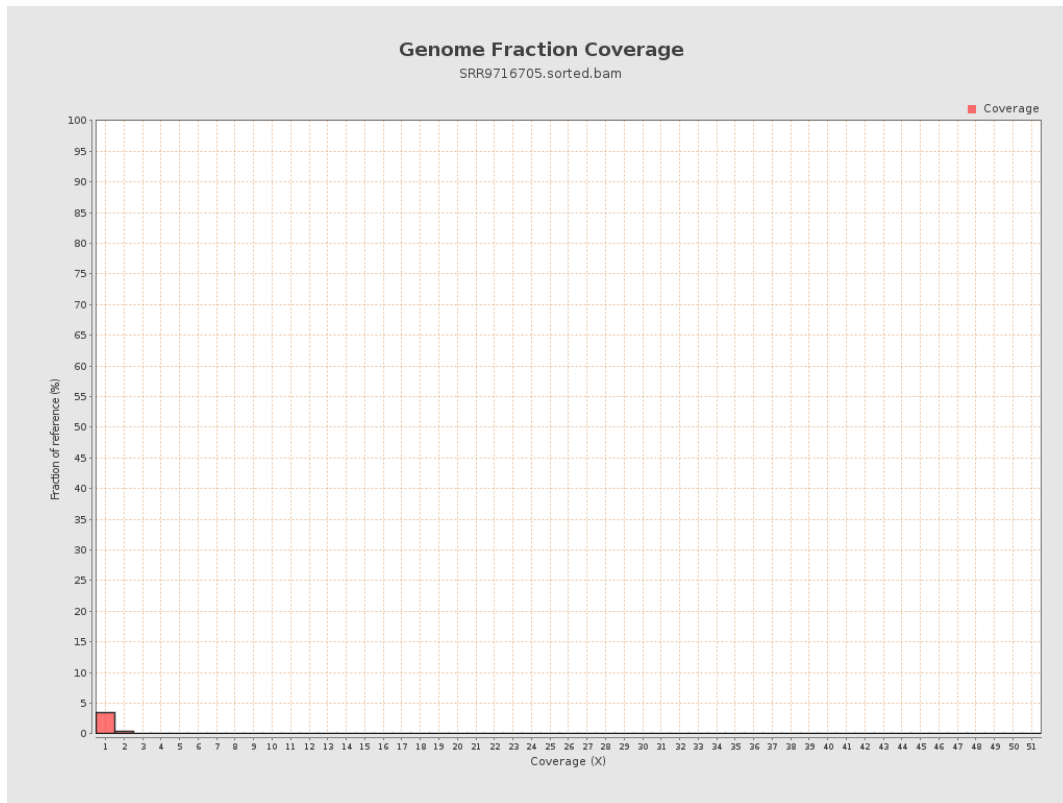
4. Results : Coverage Histogram



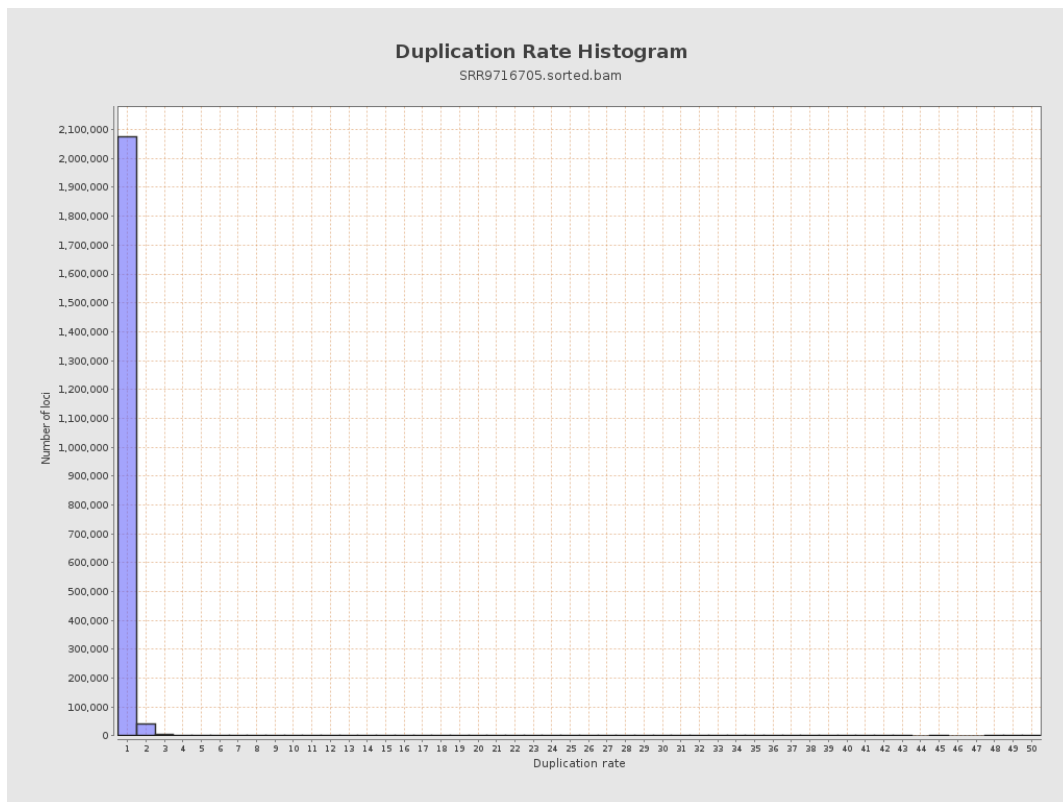
5. Results : Coverage Histogram (0-50X)



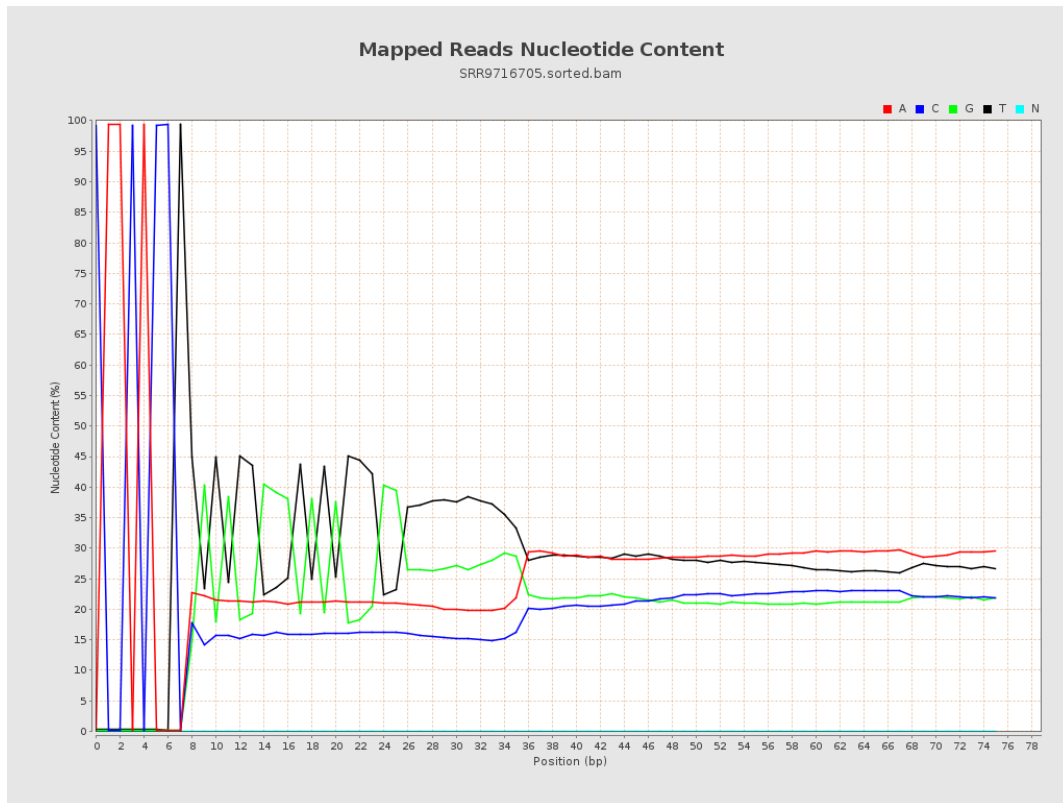
6. Results : Genome Fraction Coverage



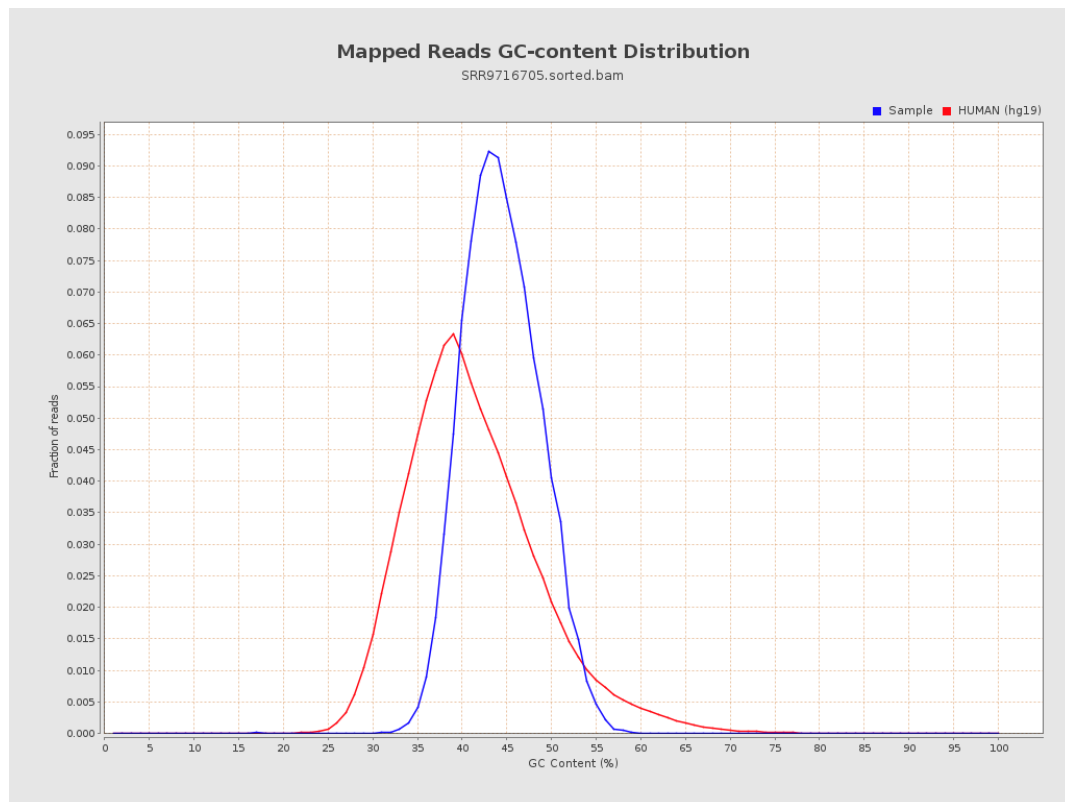
7. Results : Duplication Rate Histogram



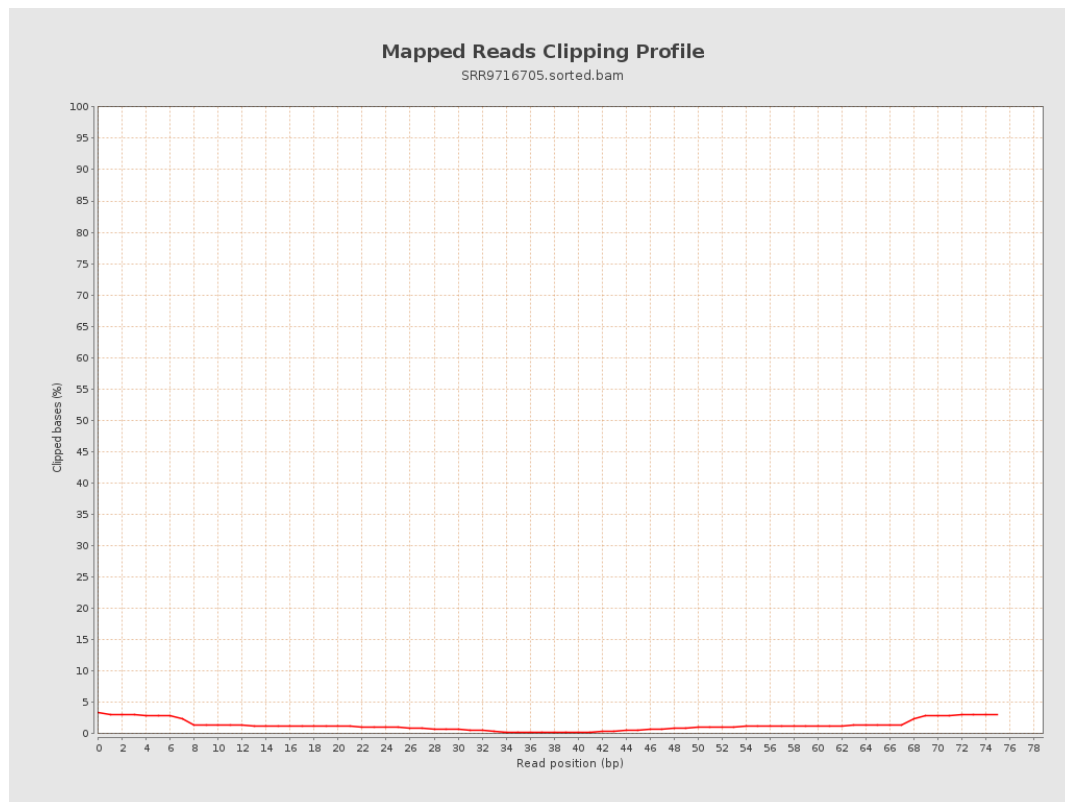
8. Results : Mapped Reads Nucleotide Content



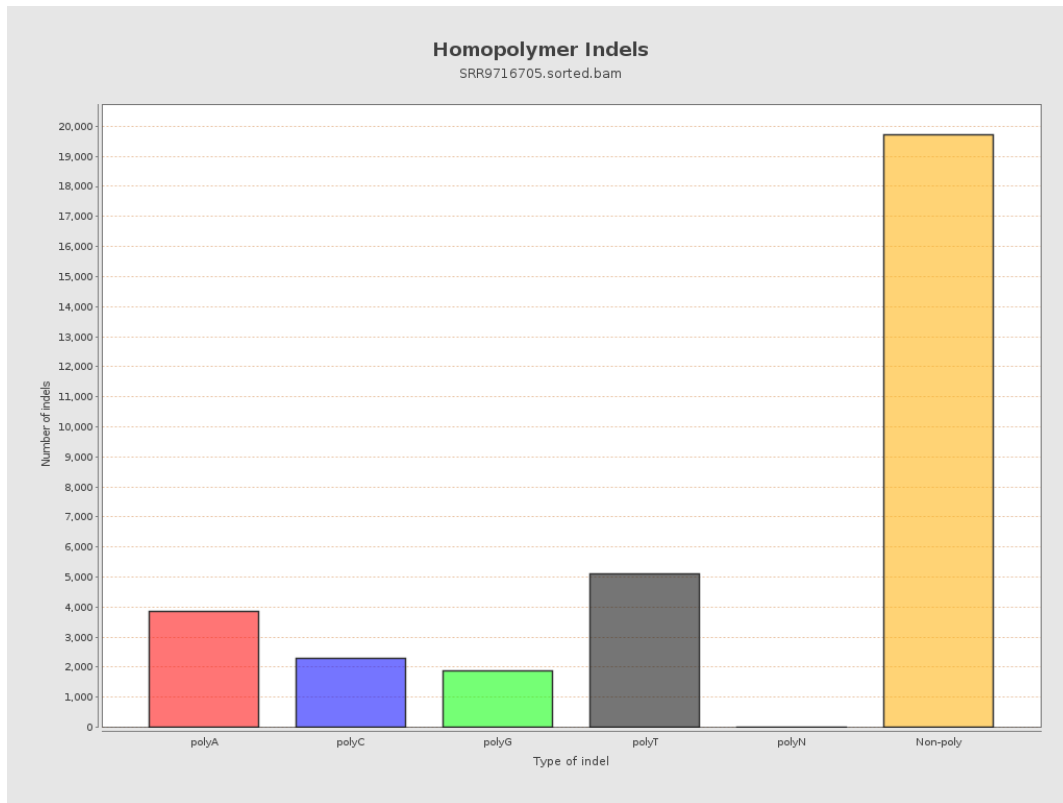
9. Results : Mapped Reads GC-content Distribution



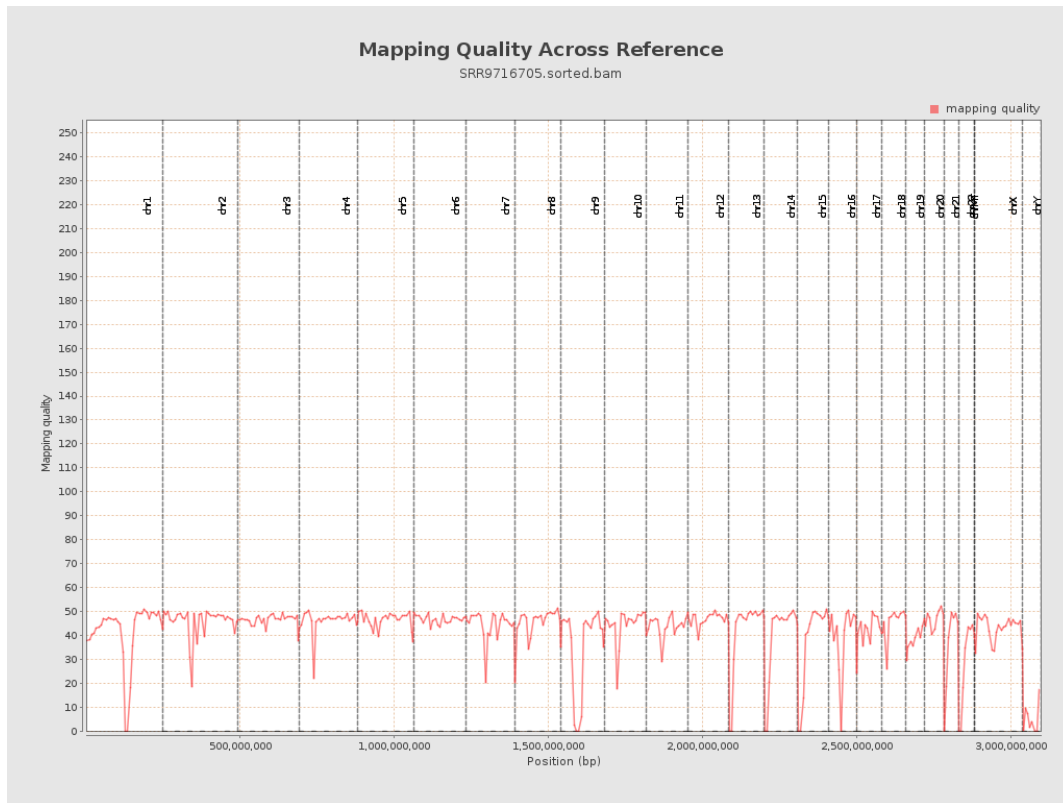
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

