

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 00:14:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717011.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_SRR9717011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717011.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 00:14:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9717011.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,043,703
Mapped reads	1,914,154 / 93.66%
Unmapped reads	129,549 / 6.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,063 / 1.57%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	81,664 / 4%
Duplication rate	2.67%
Clipped reads	1,941,801 / 95.01%

2.2. ACGT Content

Number/percentage of A's	36,270,125 / 23.91%
Number/percentage of C's	30,088,865 / 19.84%
Number/percentage of T's	46,410,614 / 30.6%
Number/percentage of G's	38,893,032 / 25.64%
Number/percentage of N's	9,008 / 0.01%
GC Percentage	45.48%

2.3. Coverage

Mean	0.049

Standard Deviation	0.5154
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.24
----------------------	-------

2.5. Mismatches and indels

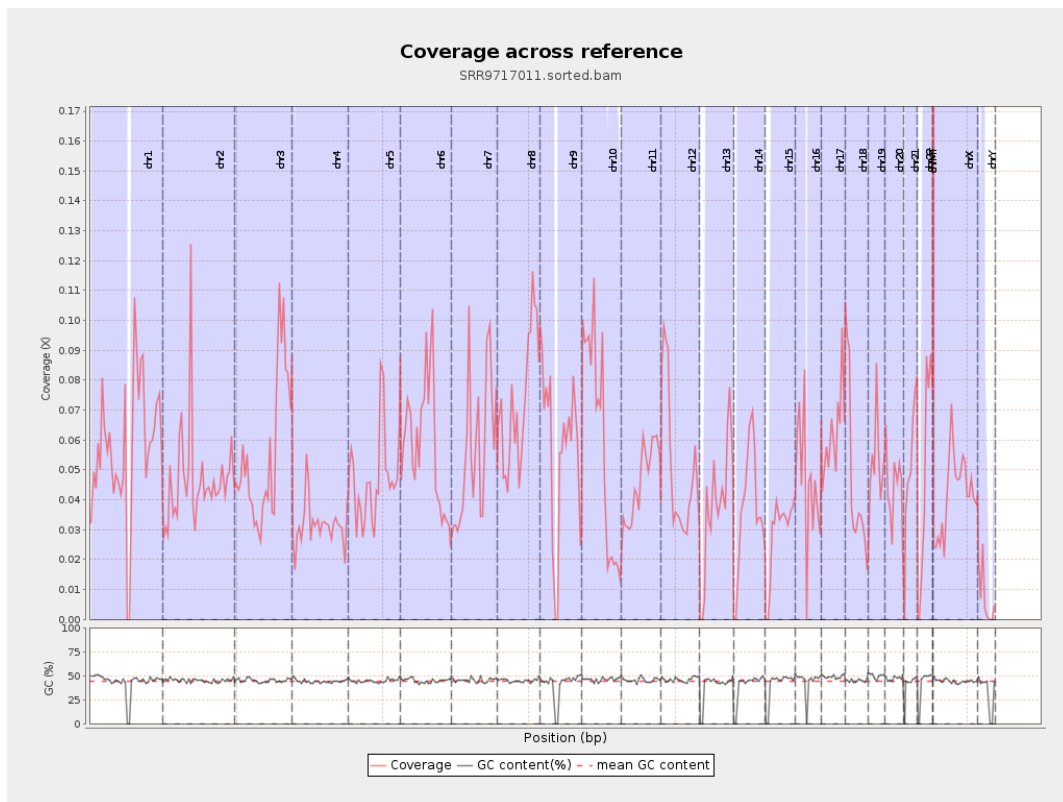
General error rate	0.81%
Mismatches	1,193,875
Insertions	14,265
Mapped reads with at least one insertion	0.73%
Deletions	37,161
Mapped reads with at least one deletion	1.91%
Homopolymer indels	43.31%

2.6. Chromosome stats

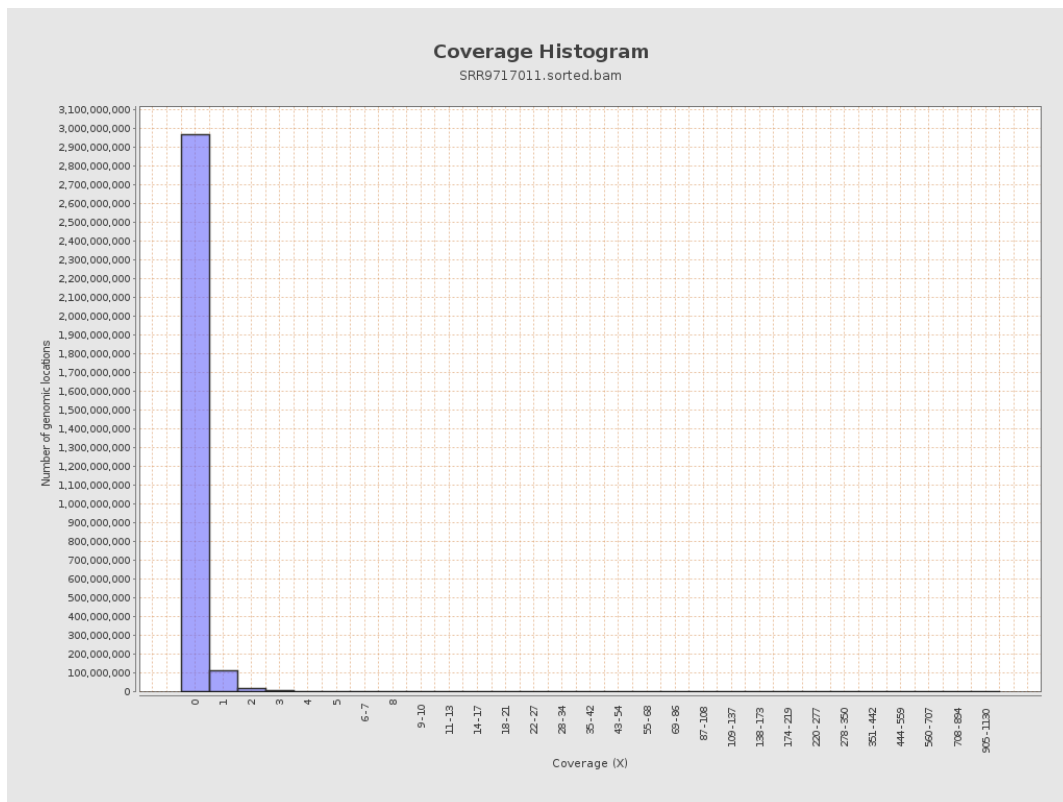
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	14246411	0.0572	0.7918
chr2	243199373	11364190	0.0467	0.8728
chr3	198022430	10894921	0.055	0.2751
chr4	191154276	6078227	0.0318	0.2542
chr5	180915260	8527806	0.0471	0.2502
chr6	171115067	9915685	0.0579	0.3303
chr7	159138663	8921040	0.0561	0.7936

chr8	146364022	10611266	0.0725	0.6997
chr9	141213431	7990299	0.0566	0.5031
chr10	135534747	8102592	0.0598	0.5322
chr11	135006516	6187818	0.0458	0.407
chr12	133851895	6861345	0.0513	0.2665
chr13	115169878	4489548	0.039	0.2243
chr14	107349540	4019958	0.0374	0.2627
chr15	102531392	2894727	0.0282	0.1989
chr16	90354753	4082559	0.0452	0.2813
chr17	81195210	5013603	0.0617	0.3412
chr18	78077248	3631628	0.0465	0.8372
chr19	59128983	3149883	0.0533	0.667
chr20	63025520	2772152	0.044	0.2684
chr21	48129895	2523310	0.0524	0.2891
chr22	51304566	2490379	0.0485	0.2629
chrMT	16571	29275	1.7666	2.2302
chrX	155270560	6514807	0.042	0.3026
chrY	59373566	424214	0.0071	0.2526

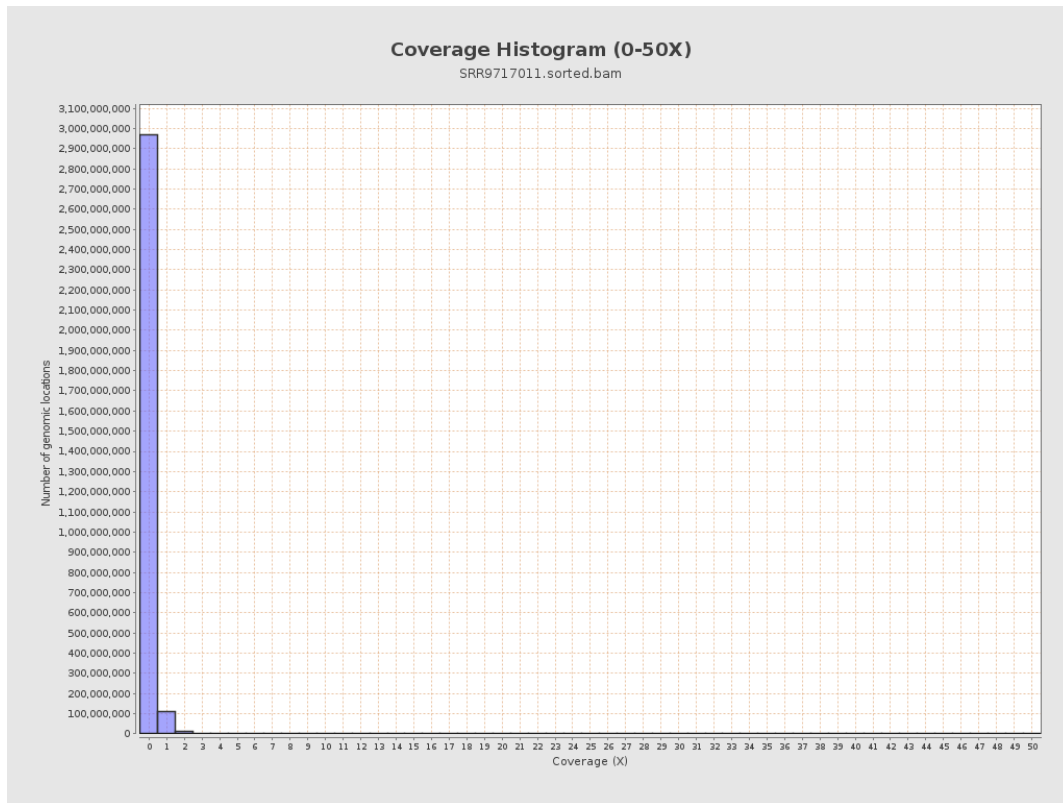
3. Results : Coverage across reference



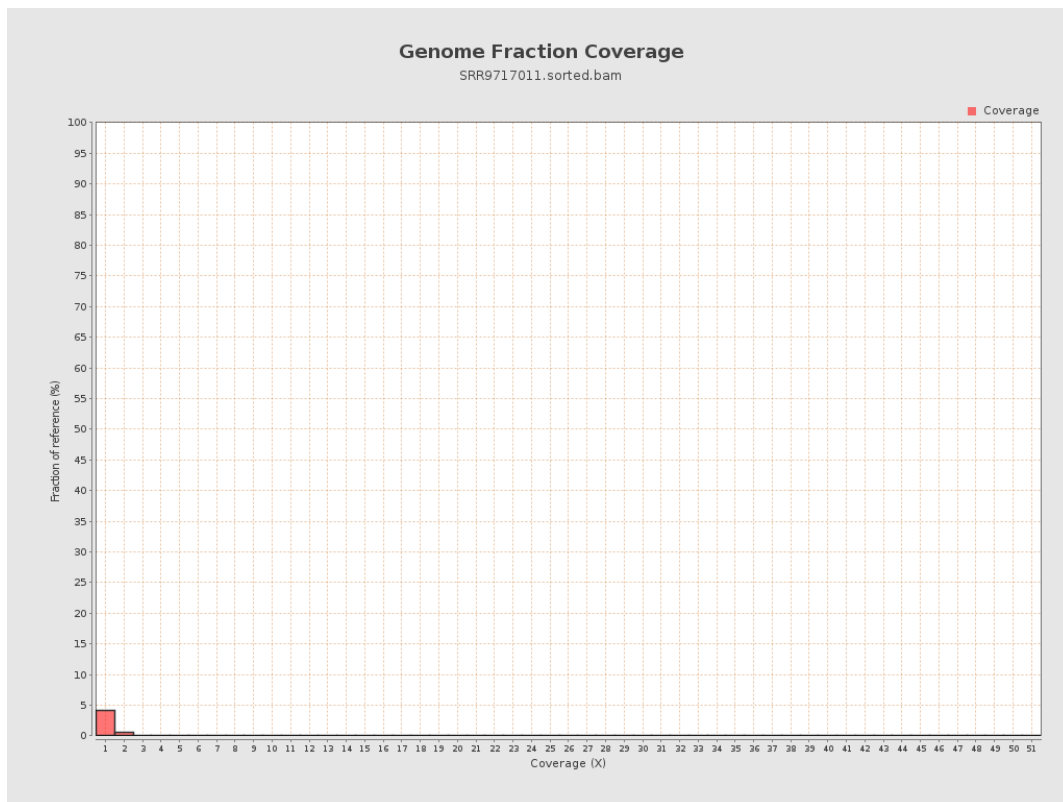
4. Results : Coverage Histogram



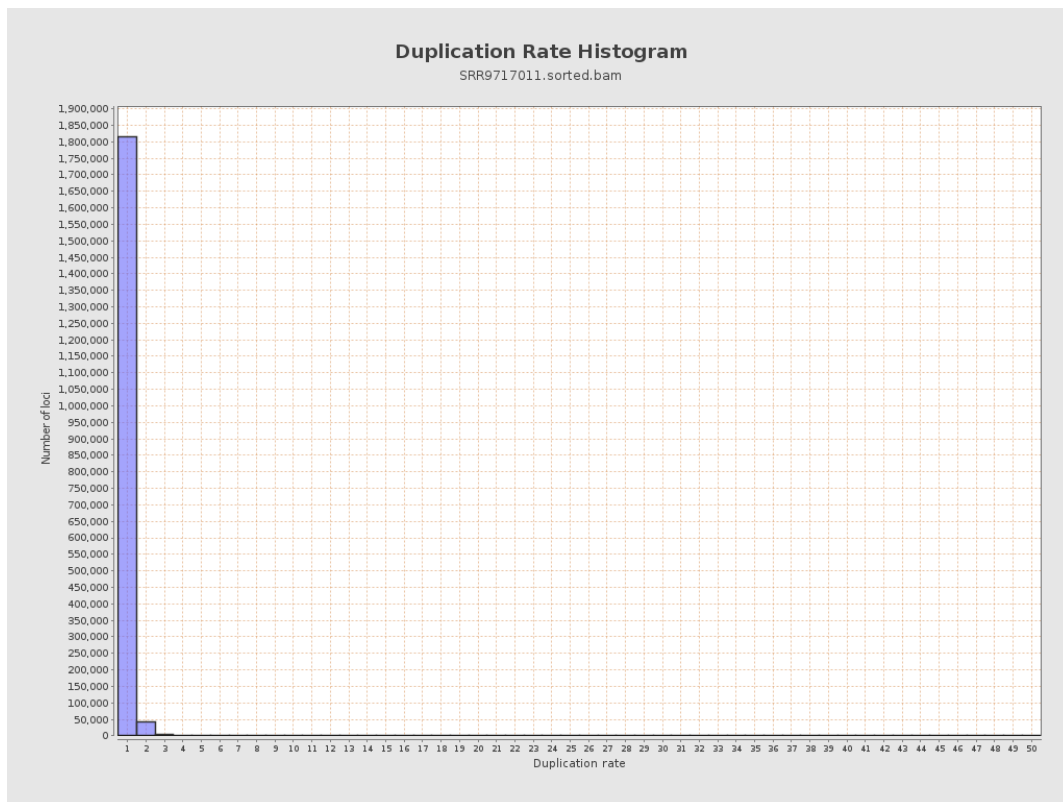
5. Results : Coverage Histogram (0-50X)



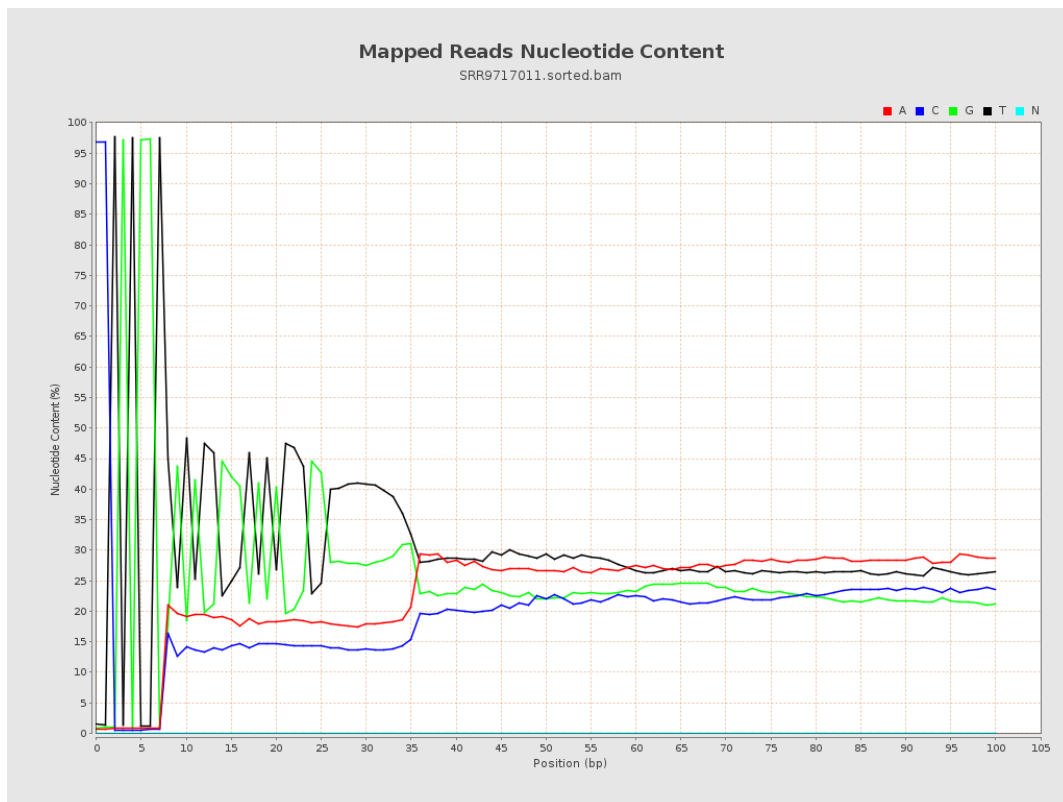
6. Results : Genome Fraction Coverage



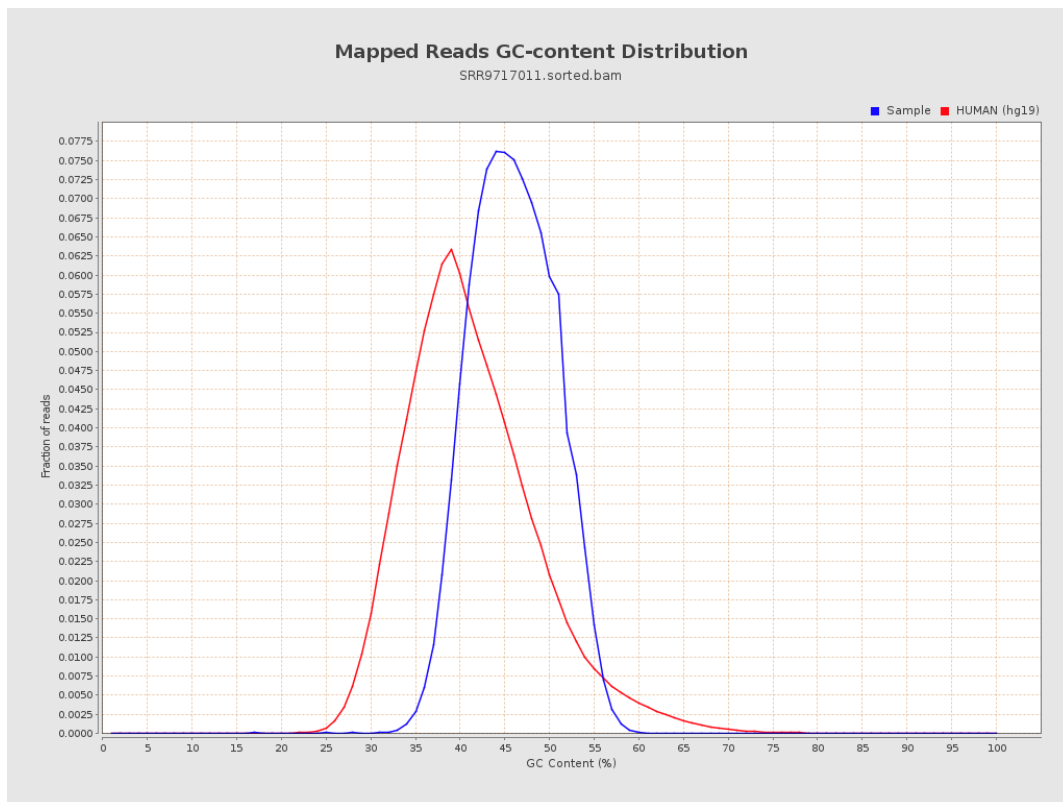
7. Results : Duplication Rate Histogram



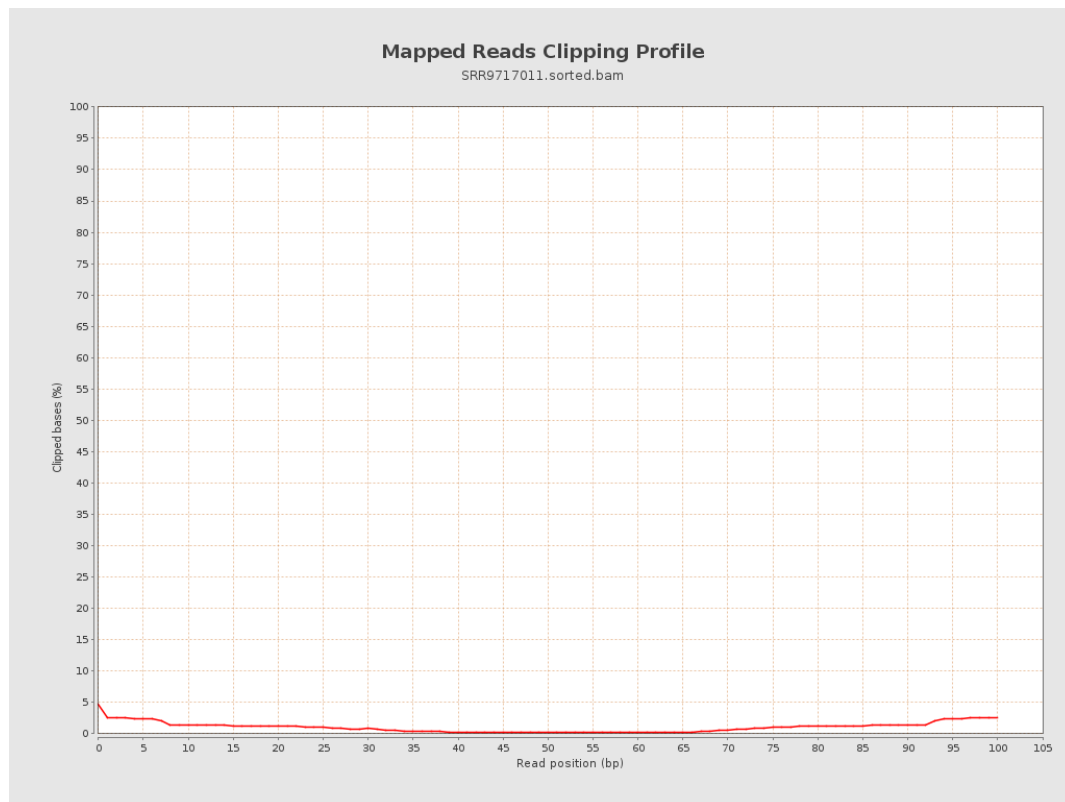
8. Results : Mapped Reads Nucleotide Content



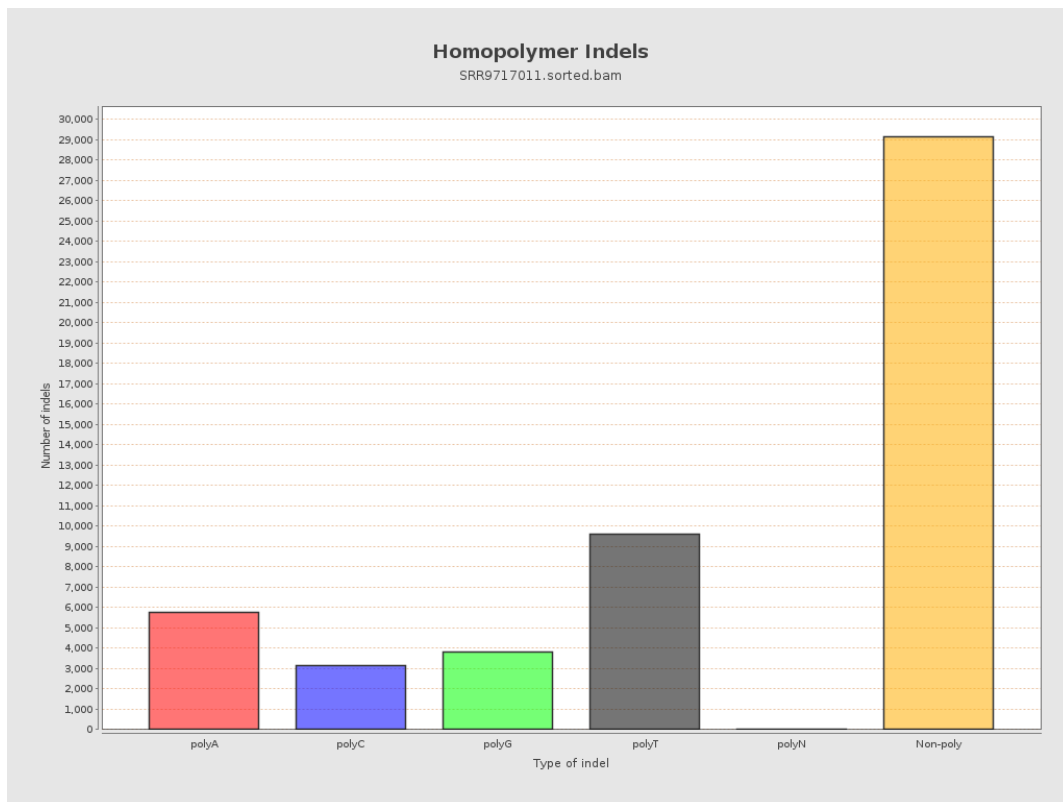
9. Results : Mapped Reads GC-content Distribution



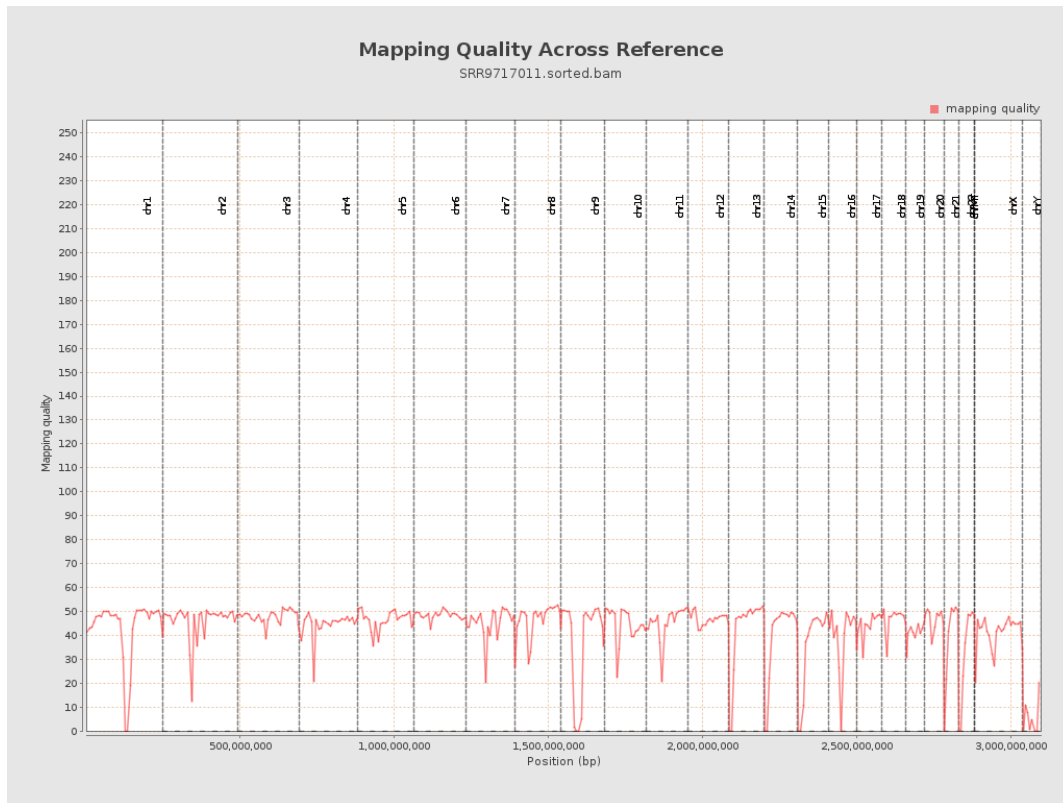
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

