

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 02:24:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716650.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_SRR9716650 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716650.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 02:23:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716650.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,562,620
Mapped reads	1,432,433 / 91.67%
Unmapped reads	130,187 / 8.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,319 / 2.77%
Read min/max/mean length	30 / 101 / 102
Duplicated reads (estimated)	31,735 / 2.03%
Duplication rate	1.43%
Clipped reads	1,475,075 / 94.4%

2.2. ACGT Content

Number/percentage of A's	26,841,064 / 25.06%
Number/percentage of C's	22,733,552 / 21.23%
Number/percentage of T's	31,214,759 / 29.14%
Number/percentage of G's	26,304,071 / 24.56%
Number/percentage of N's	12,626 / 0.01%
GC Percentage	45.78%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.2792
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2.4. Mapping Quality

Mean Mapping Quality	44.7
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2.5. Mismatches and indels

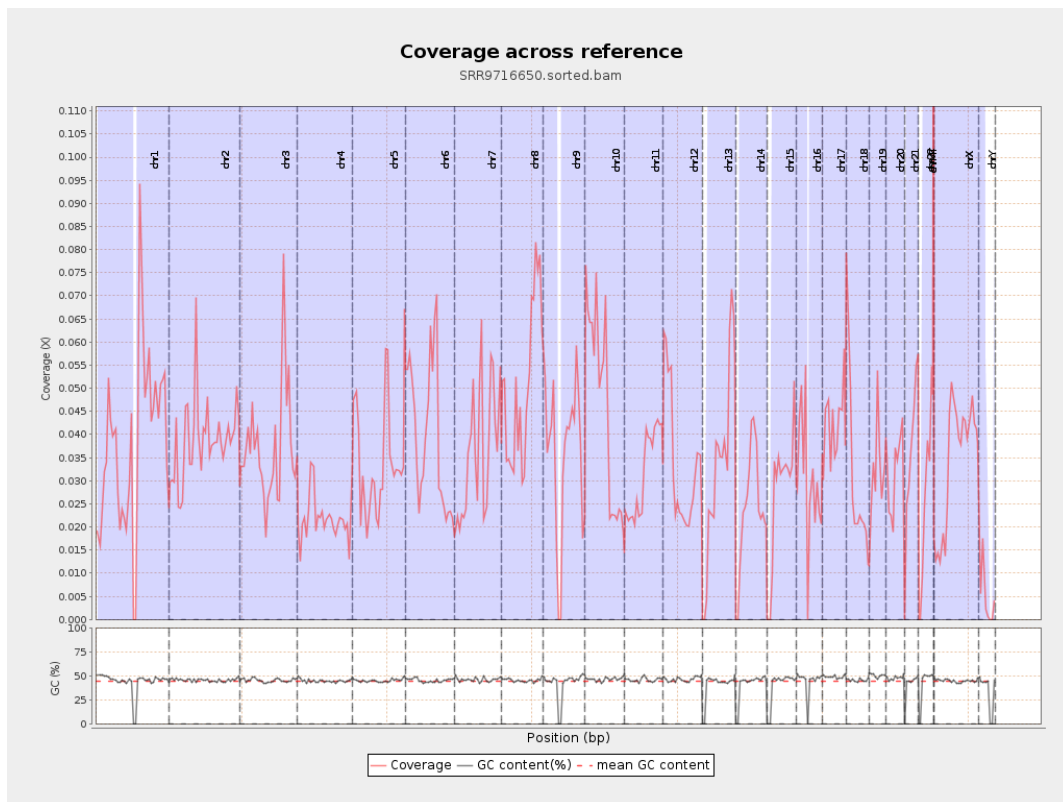
General error rate	0.77%
Mismatches	804,217
Insertions	8,166
Mapped reads with at least one insertion	0.56%
Deletions	22,335
Mapped reads with at least one deletion	1.54%
Homopolymer indels	40.07%

2.6. Chromosome stats

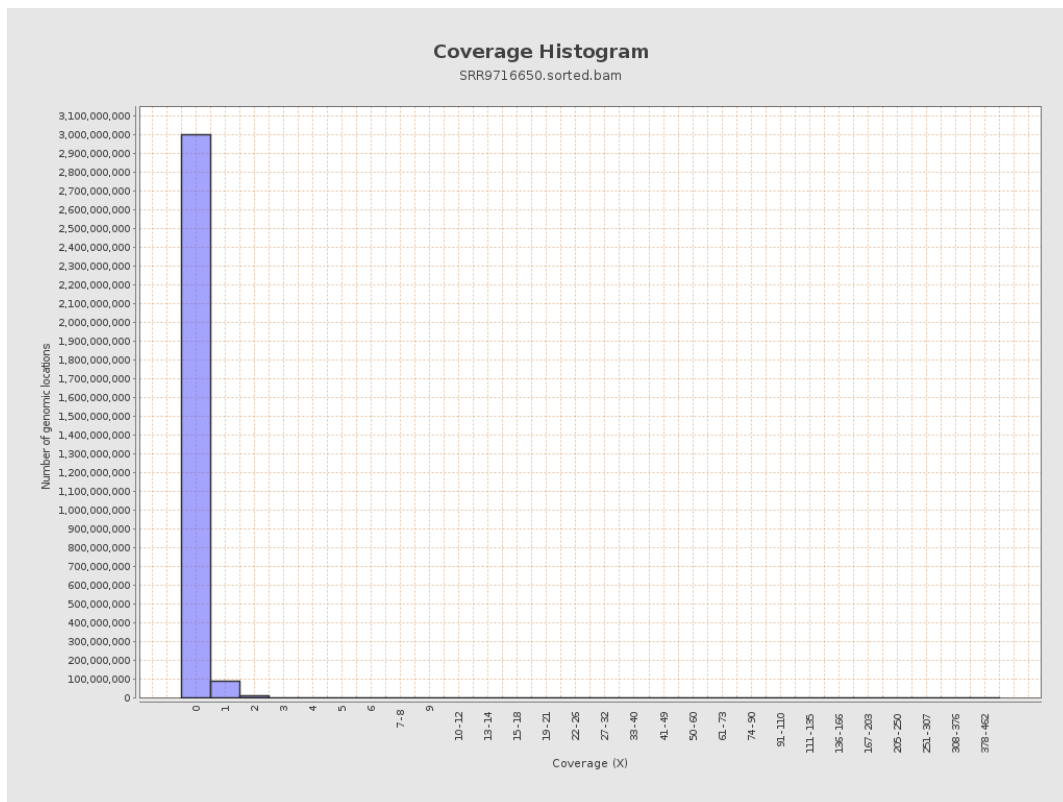
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9442658	0.0379	0.3821
chr2	243199373	9428754	0.0388	0.4035
chr3	198022430	7341095	0.0371	0.2096
chr4	191154276	4122971	0.0216	0.173
chr5	180915260	6048354	0.0334	0.1985
chr6	171115067	6815878	0.0398	0.2275
chr7	159138663	5846157	0.0367	0.3682

chr8	146364022	7449745	0.0509	0.3512
chr9	141213431	5046353	0.0357	0.2688
chr10	135534747	6335936	0.0467	0.3561
chr11	135006516	4251941	0.0315	0.2424
chr12	133851895	4448847	0.0332	0.1988
chr13	115169878	3907419	0.0339	0.2004
chr14	107349540	2593975	0.0242	0.1799
chr15	102531392	2840227	0.0277	0.1819
chr16	90354753	2731404	0.0302	0.204
chr17	81195210	3414824	0.0421	0.2471
chr18	78077248	2408724	0.0309	0.3891
chr19	59128983	1941978	0.0328	0.3223
chr20	63025520	1974469	0.0313	0.1956
chr21	48129895	1751562	0.0364	0.2195
chr22	51304566	1345173	0.0262	0.178
chrMT	16571	3643	0.2198	0.5024
chrX	155270560	5335283	0.0344	0.2272
chrY	59373566	318212	0.0054	0.1796

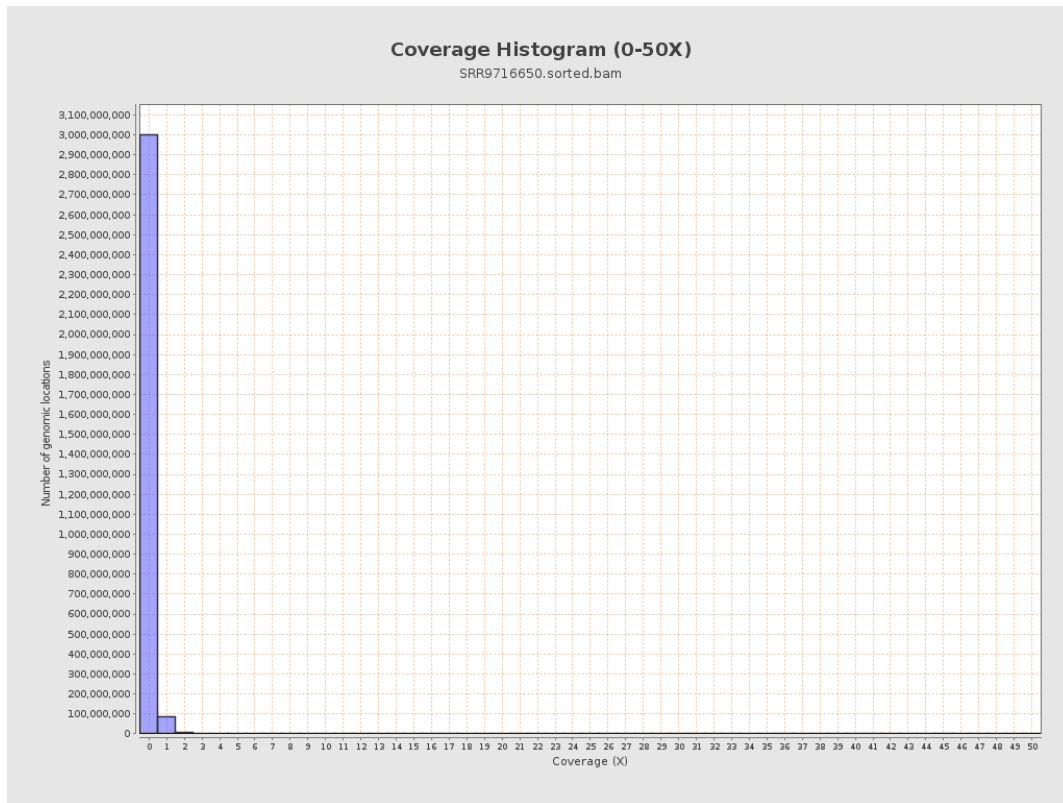
3. Results : Coverage across reference



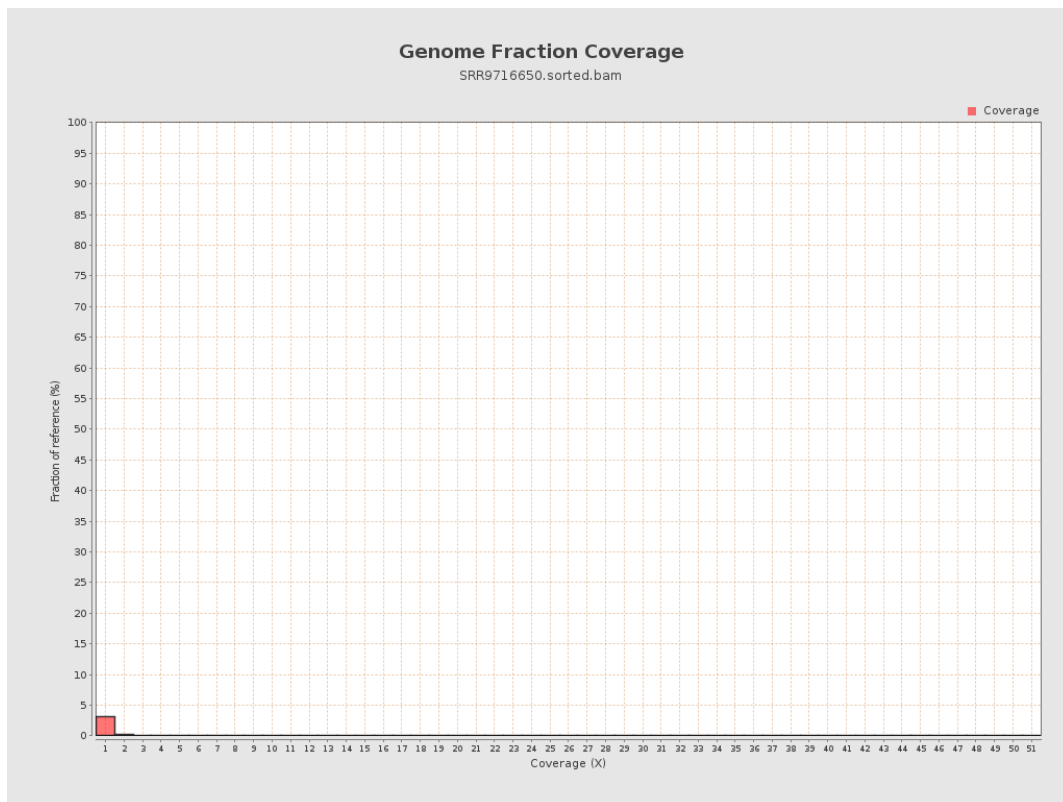
4. Results : Coverage Histogram



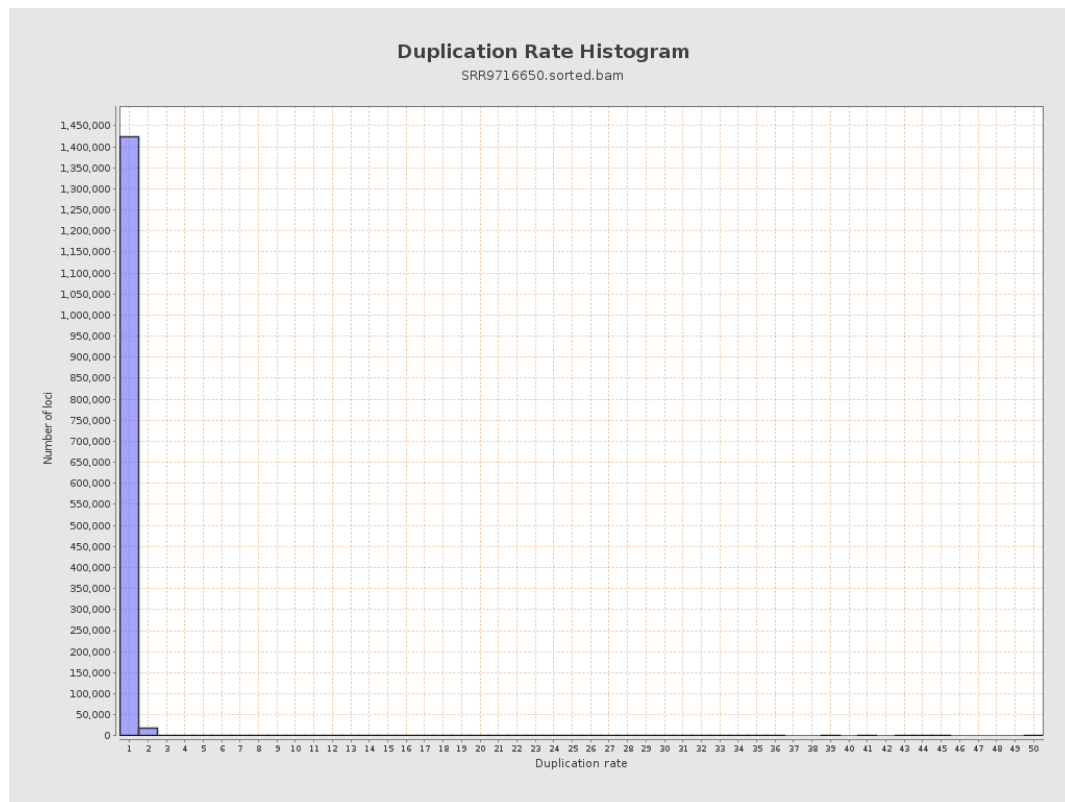
5. Results : Coverage Histogram (0-50X)



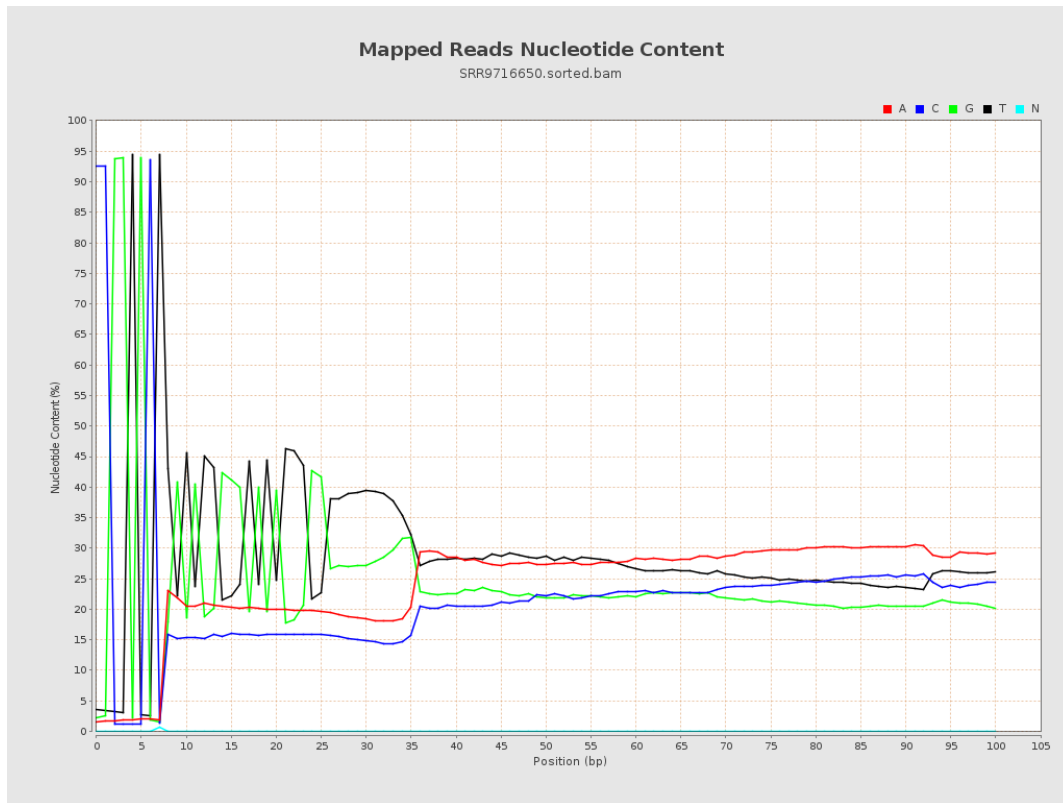
6. Results : Genome Fraction Coverage



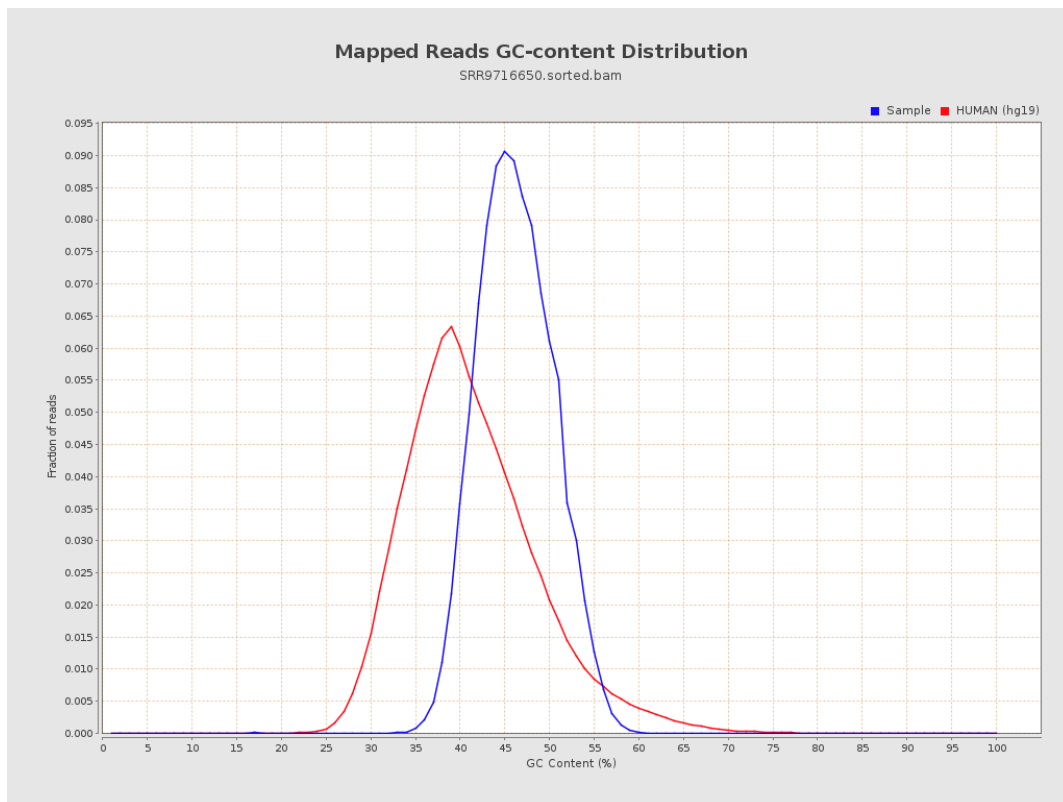
7. Results : Duplication Rate Histogram



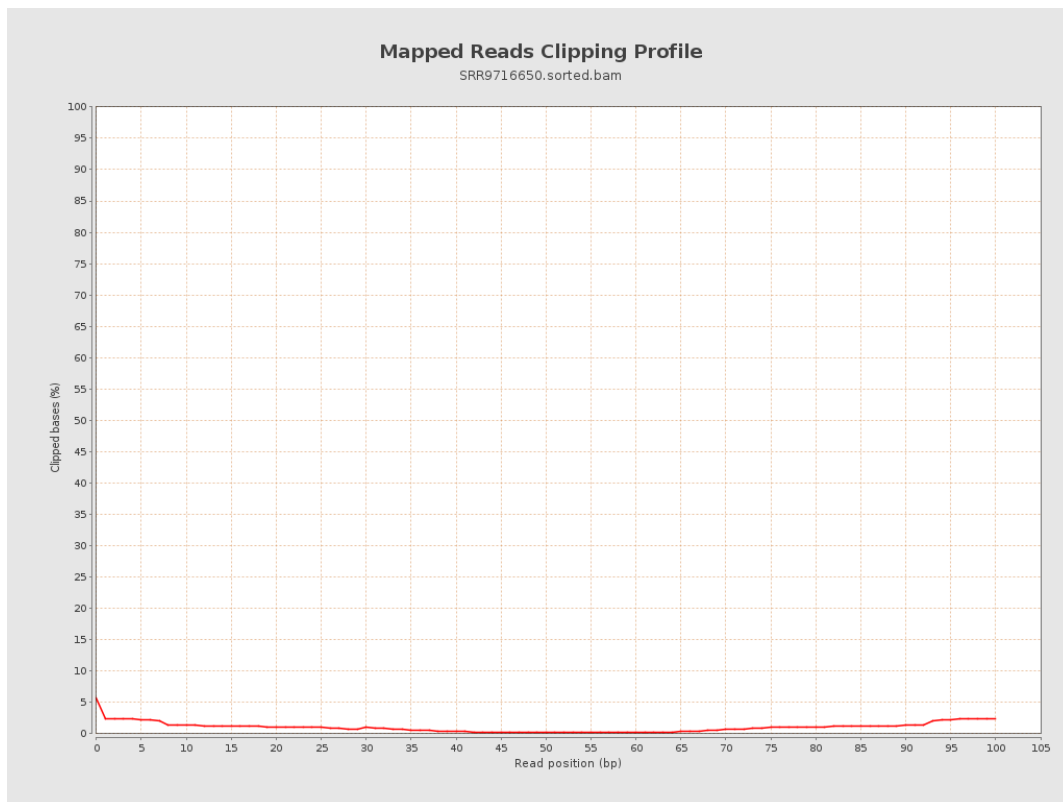
8. Results : Mapped Reads Nucleotide Content



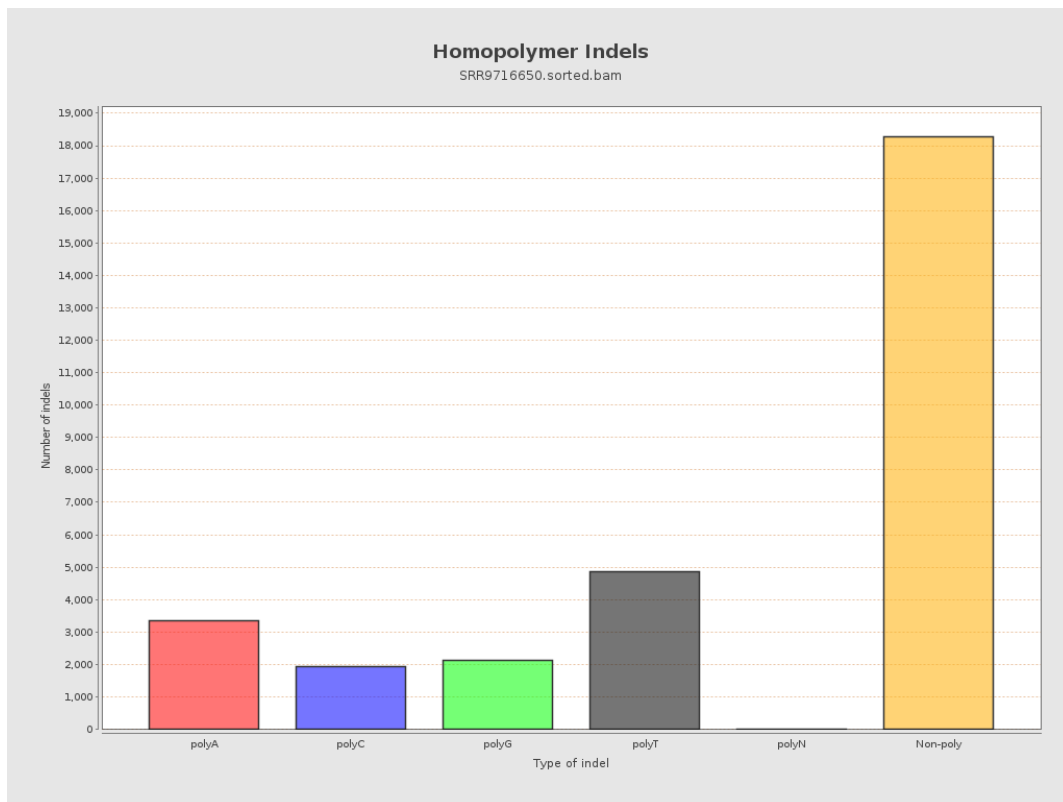
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

