

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 05:50:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549128.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_SRR1549128 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549128.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 05:50:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549128.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,431,556
Mapped reads	13,603,186 / 88.15%
Unmapped reads	1,828,370 / 11.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	635,472 / 4.12%
Duplication rate	3.47%
Clipped reads	711,686 / 4.61%

2.2. ACGT Content

Number/percentage of A's	160,499,457 / 29.73%
Number/percentage of C's	108,671,131 / 20.13%
Number/percentage of T's	162,010,432 / 30.01%
Number/percentage of G's	108,567,738 / 20.11%
Number/percentage of N's	124,864 / 0.02%
GC Percentage	40.24%

2.3. Coverage

Mean	0.1744
Standard Deviation	1.0268

2.4. Mapping Quality

Mean Mapping Quality	43.7
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2.5. Mismatches and indels

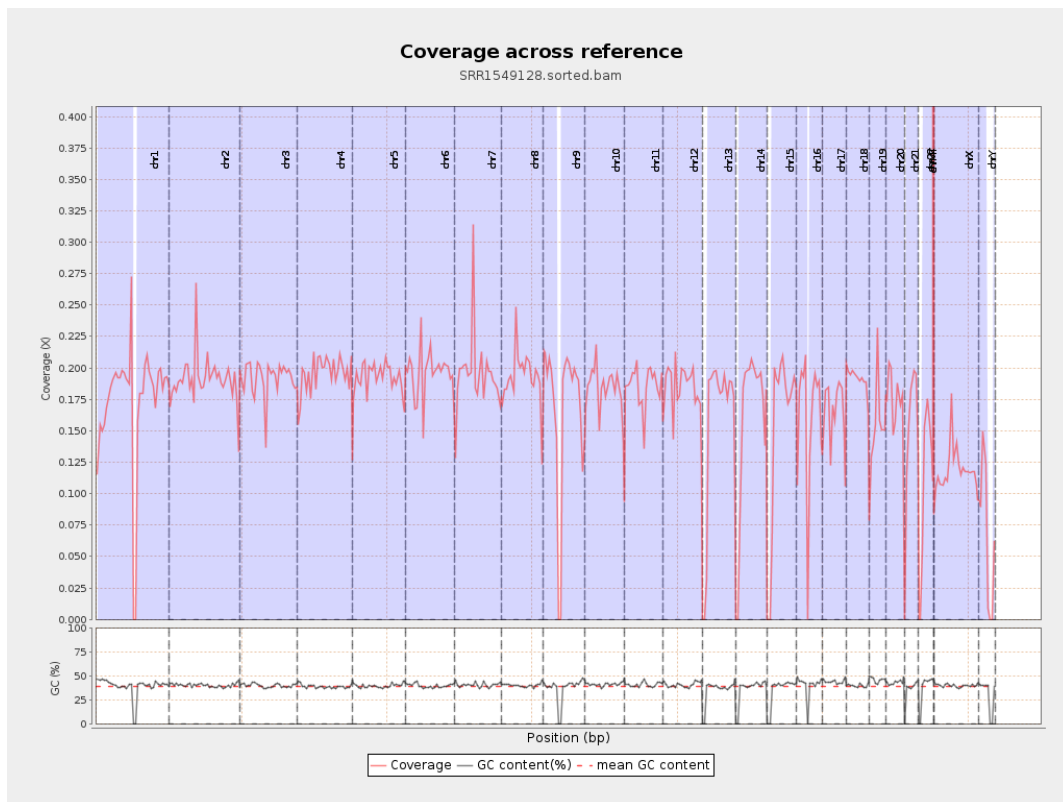
General error rate	0.33%
Mismatches	1,748,163
Insertions	14,110
Mapped reads with at least one insertion	0.1%
Deletions	42,027
Mapped reads with at least one deletion	0.31%
Homopolymer indels	46.98%

2.6. Chromosome stats

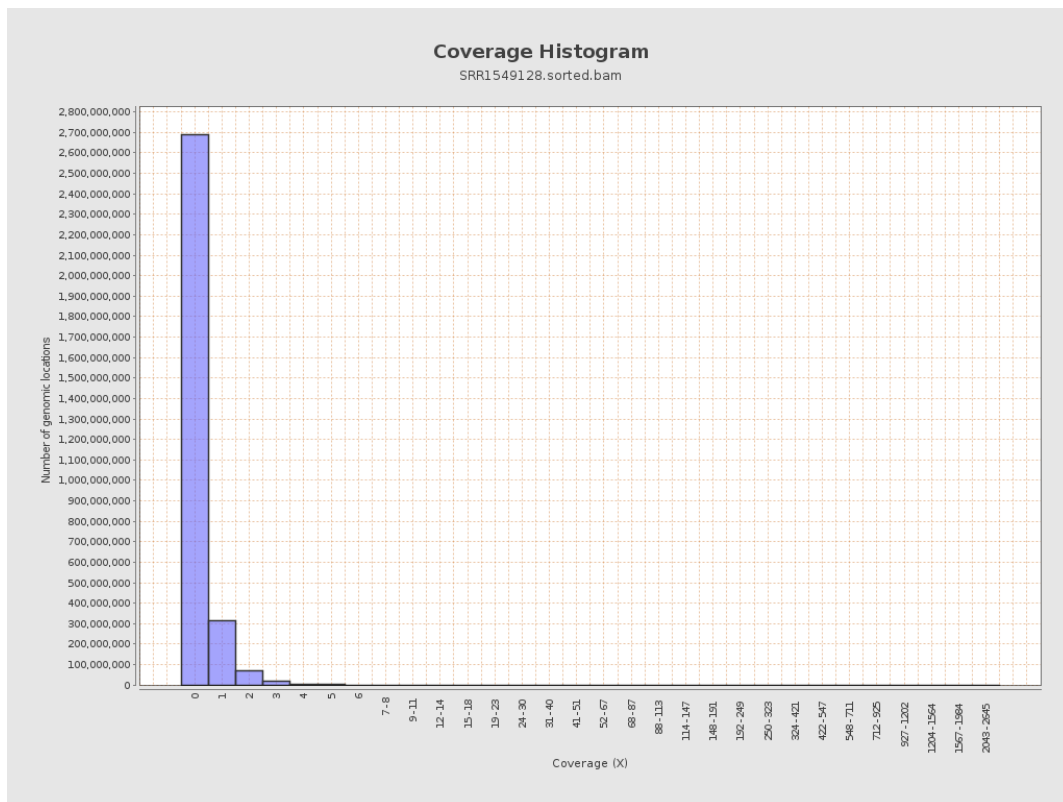
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	43344981	0.1739	2.0379
chr2	243199373	46458656	0.191	0.9549
chr3	198022430	38030031	0.192	0.5549
chr4	191154276	37369023	0.1955	0.5621
chr5	180915260	34832856	0.1925	0.5793
chr6	171115067	33599161	0.1964	0.7289
chr7	159138663	31281224	0.1966	1.6491
chr8	146364022	28194238	0.1926	0.9428

chr9	141213431	23538318	0.1667	0.9258
chr10	135534747	25062461	0.1849	0.8421
chr11	135006516	24874500	0.1842	0.865
chr12	133851895	24727551	0.1847	0.594
chr13	115169878	17875035	0.1552	0.4826
chr14	107349540	16947663	0.1579	0.7845
chr15	102531392	15811187	0.1542	0.4873
chr16	90354753	14551038	0.161	0.6061
chr17	81195210	13272008	0.1635	0.5967
chr18	78077248	14968874	0.1917	2.0471
chr19	59128983	9230423	0.1561	1.6968
chr20	63025520	10930636	0.1734	0.5782
chr21	48129895	7203122	0.1497	0.616
chr22	51304566	5446869	0.1062	0.4779
chrMT	16571	100705	6.0772	8.0357
chrX	155270560	18423974	0.1187	0.6465
chrY	59373566	3851579	0.0649	0.3934

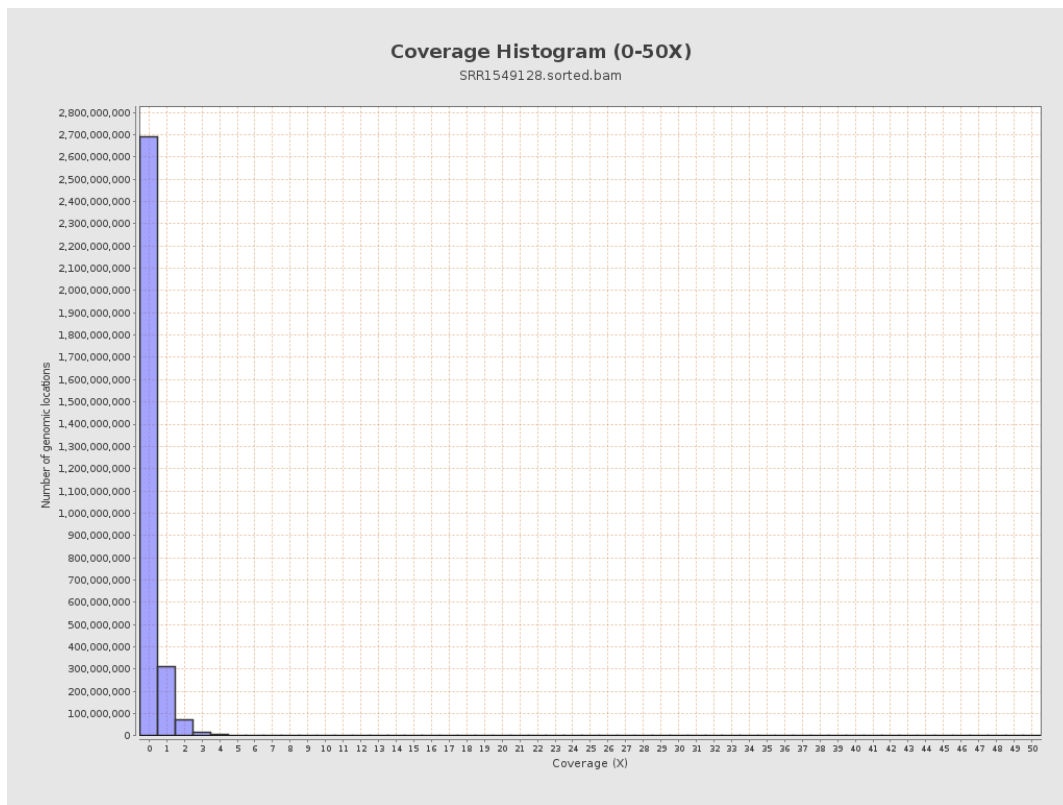
3. Results : Coverage across reference



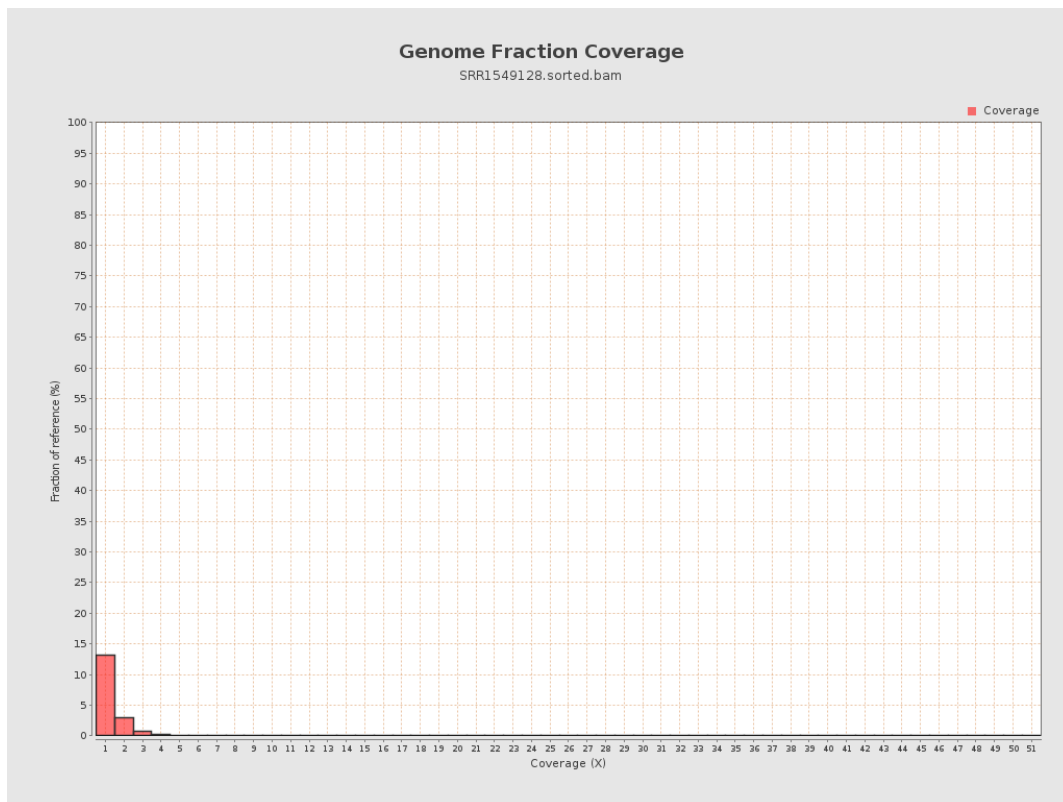
4. Results : Coverage Histogram



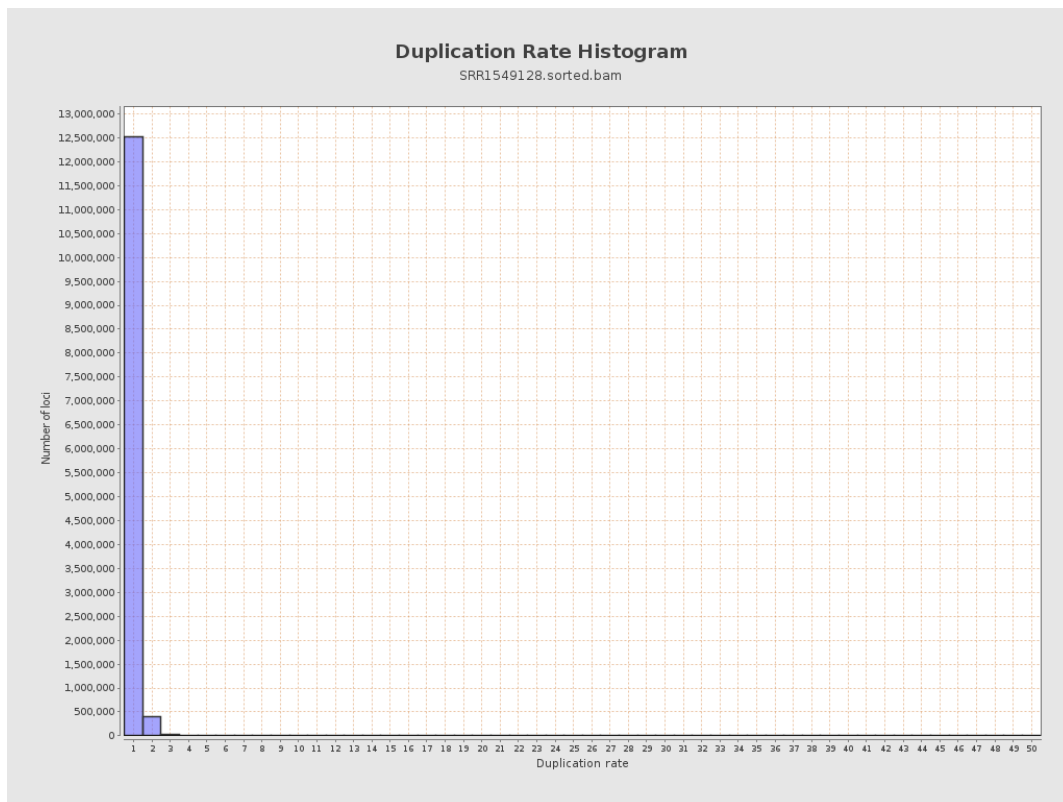
5. Results : Coverage Histogram (0-50X)



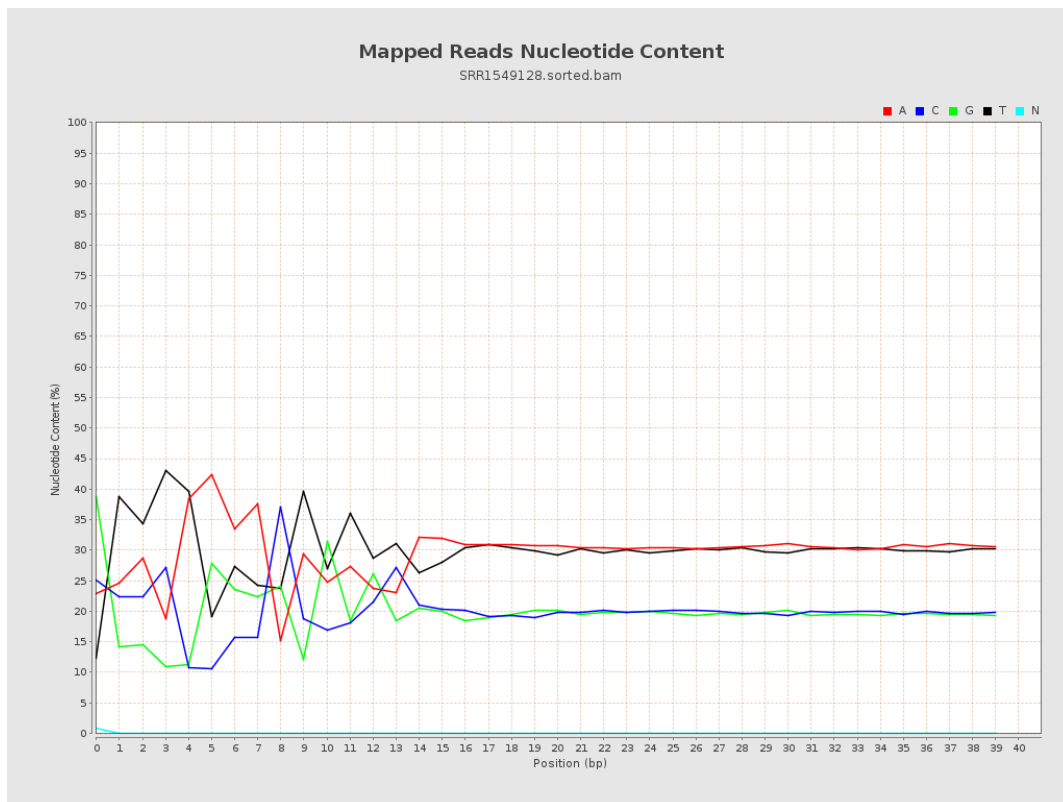
6. Results : Genome Fraction Coverage



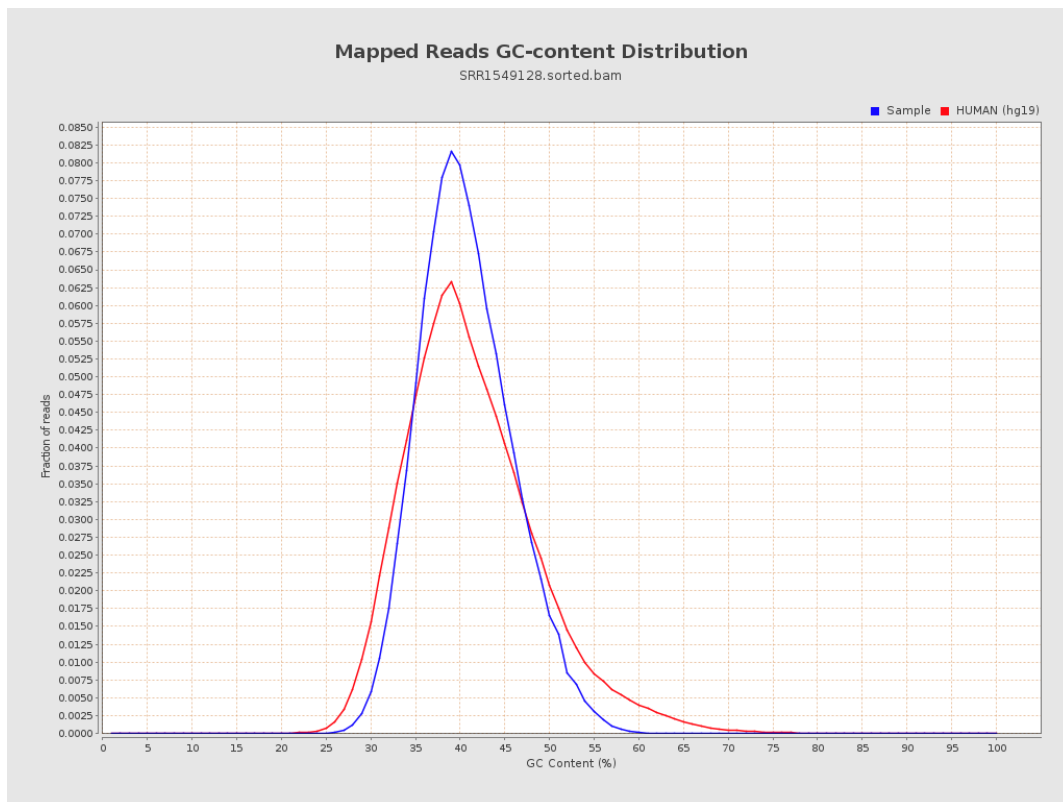
7. Results : Duplication Rate Histogram



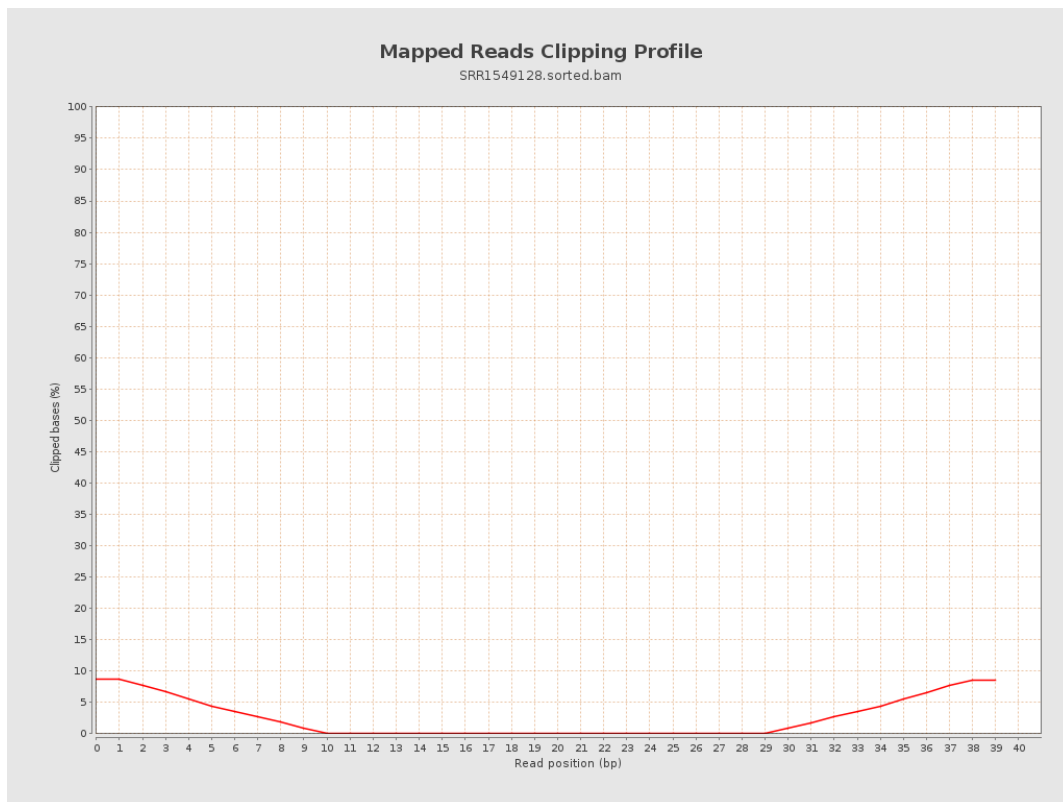
8. Results : Mapped Reads Nucleotide Content



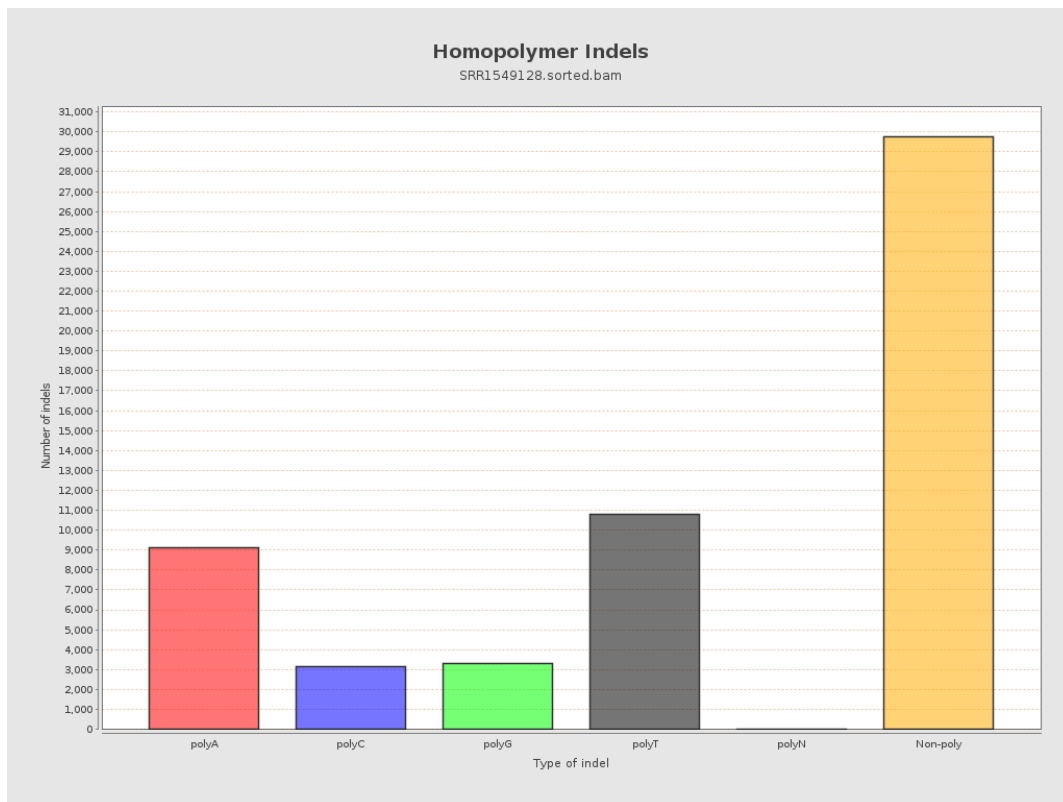
9. Results : Mapped Reads GC-content Distribution



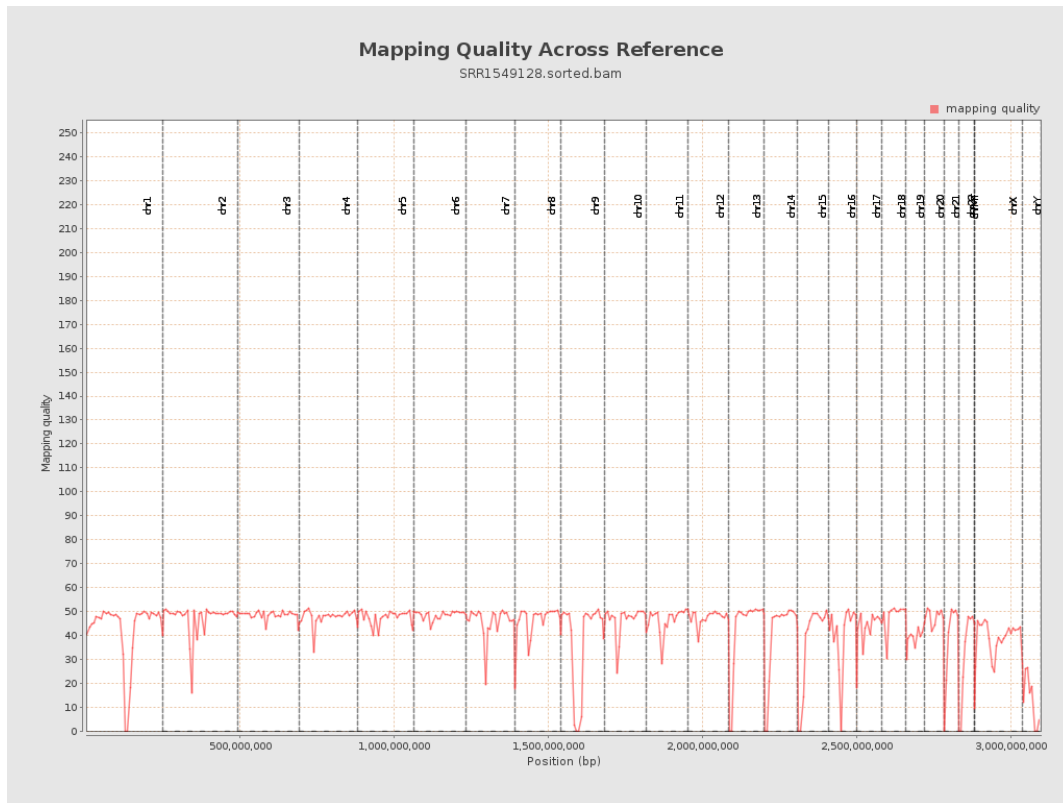
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

