

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 11:32:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549154.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_SRR1549154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 11:31:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,894,191
Mapped reads	13,544,458 / 85.22%
Unmapped reads	2,349,733 / 14.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	944,228 / 5.94%
Duplication rate	5.62%
Clipped reads	729,563 / 4.59%

2.2. ACGT Content

Number/percentage of A's	158,259,848 / 29.45%
Number/percentage of C's	108,684,831 / 20.22%
Number/percentage of T's	160,633,894 / 29.89%
Number/percentage of G's	109,704,501 / 20.41%
Number/percentage of N's	113,549 / 0.02%
GC Percentage	40.64%

2.3. Coverage

Mean	0.1736
Standard Deviation	1.6486

2.4. Mapping Quality

Mean Mapping Quality	43.9
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2.5. Mismatches and indels

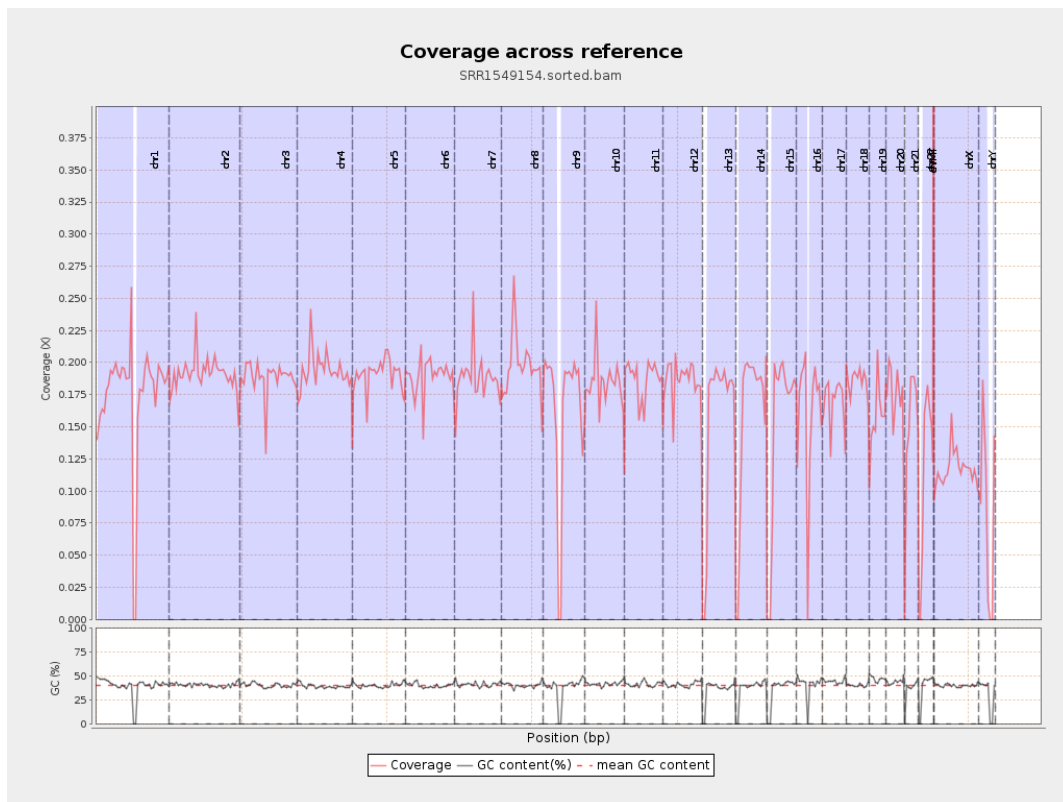
General error rate	0.32%
Mismatches	1,700,007
Insertions	13,651
Mapped reads with at least one insertion	0.1%
Deletions	42,644
Mapped reads with at least one deletion	0.31%
Homopolymer indels	44.09%

2.6. Chromosome stats

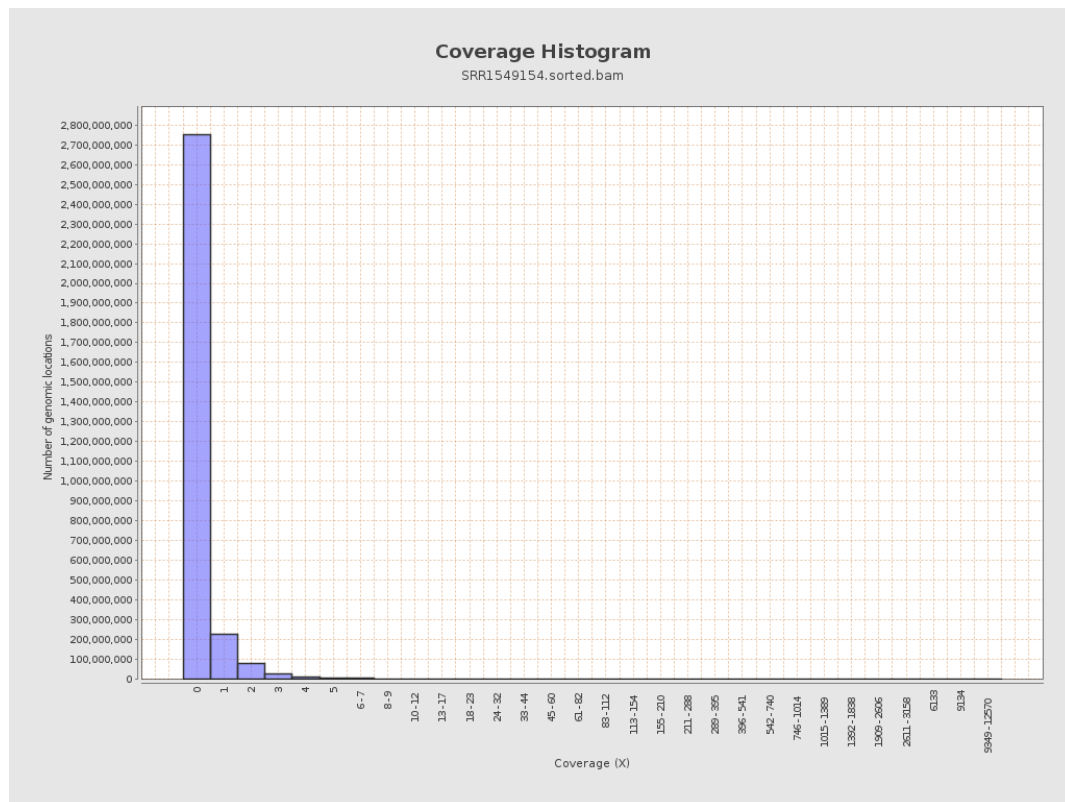
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	43506721	0.1746	1.9875
chr2	243199373	46534657	0.1913	0.9031
chr3	198022430	37312062	0.1884	0.6203
chr4	191154276	37001286	0.1936	0.7221
chr5	180915260	34499261	0.1907	0.6376
chr6	171115067	32441655	0.1896	0.6938
chr7	159138663	30073746	0.189	1.3221
chr8	146364022	28795791	0.1967	6.1553

chr9	141213431	22956288	0.1626	0.8362
chr10	135534747	25094033	0.1851	0.9721
chr11	135006516	25085415	0.1858	0.8061
chr12	133851895	24893708	0.186	0.6488
chr13	115169878	17853522	0.155	0.5573
chr14	107349540	16809995	0.1566	0.7463
chr15	102531392	15592763	0.1521	0.5544
chr16	90354753	14487740	0.1603	0.6338
chr17	81195210	13602970	0.1675	0.6472
chr18	78077248	14543103	0.1863	1.6253
chr19	59128983	9477696	0.1603	1.5456
chr20	63025520	11023455	0.1749	0.6609
chr21	48129895	7138189	0.1483	0.6882
chr22	51304566	5765571	0.1124	0.5236
chrMT	16571	15110	0.9118	1.536
chrX	155270560	18168907	0.117	0.6076
chrY	59373566	4777223	0.0805	0.7798

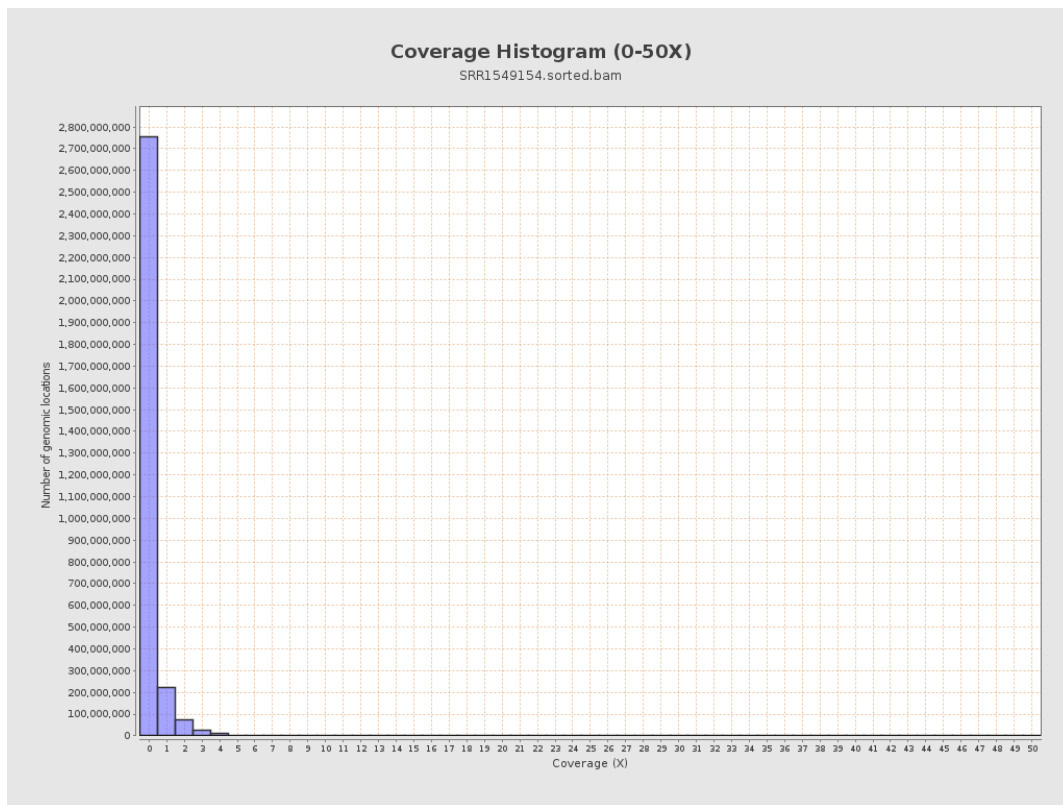
3. Results : Coverage across reference



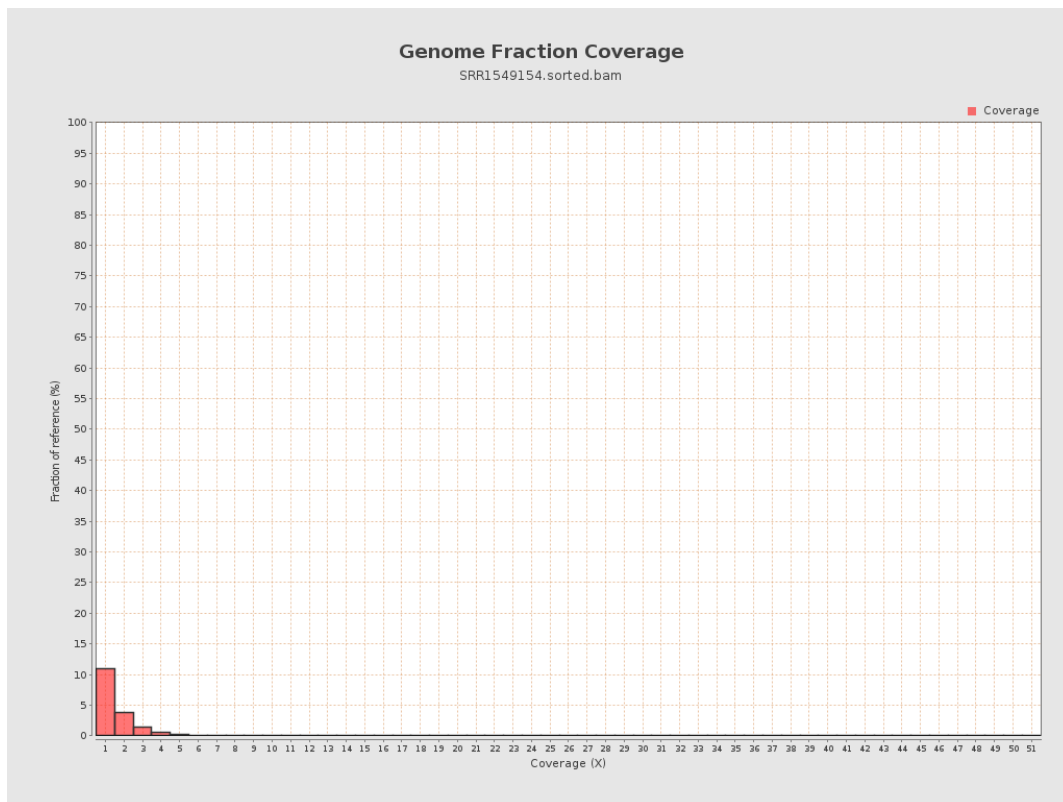
4. Results : Coverage Histogram



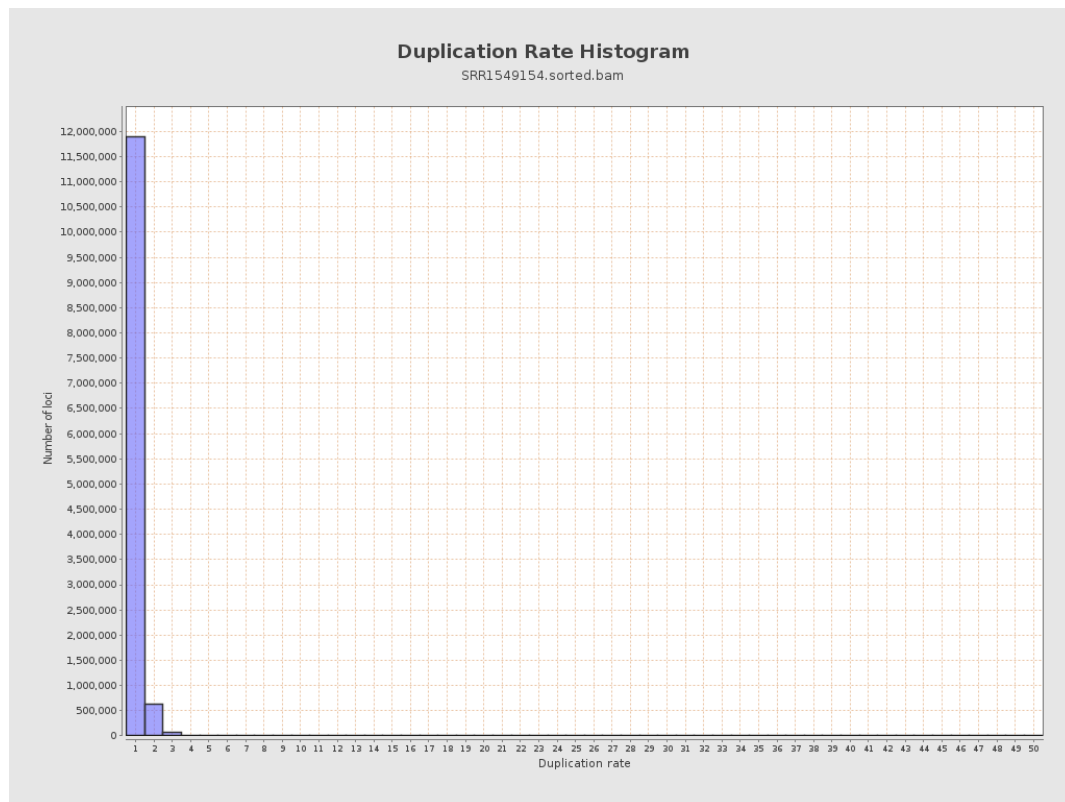
5. Results : Coverage Histogram (0-50X)



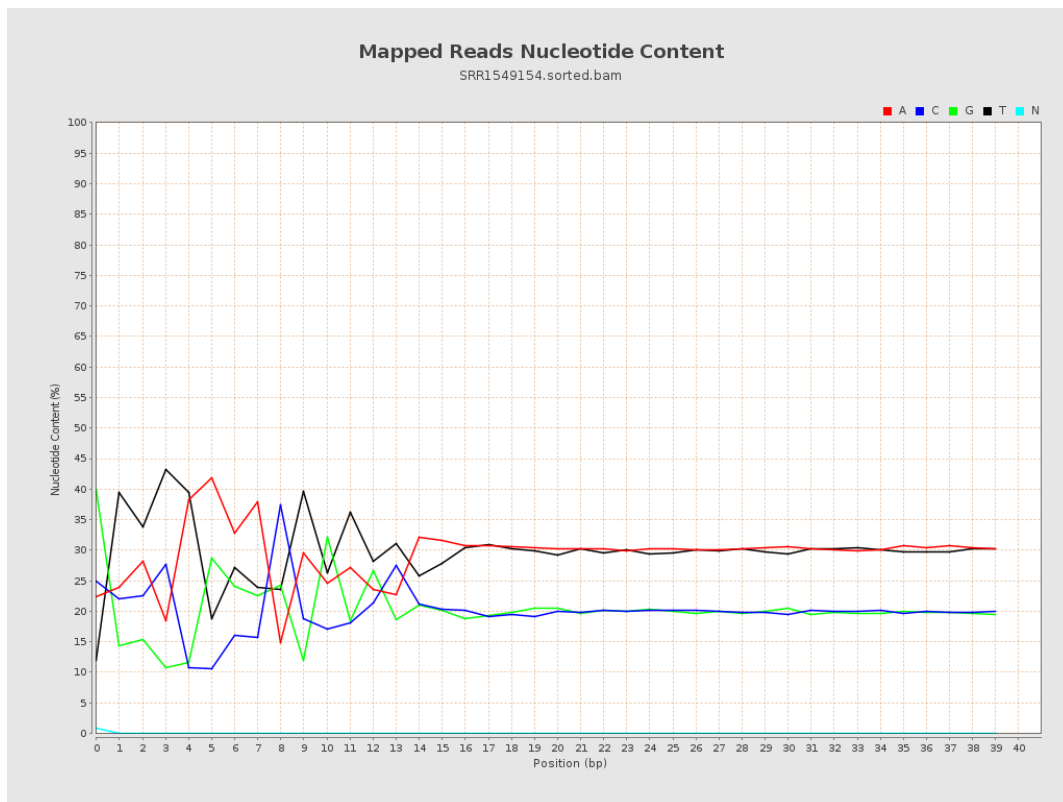
6. Results : Genome Fraction Coverage



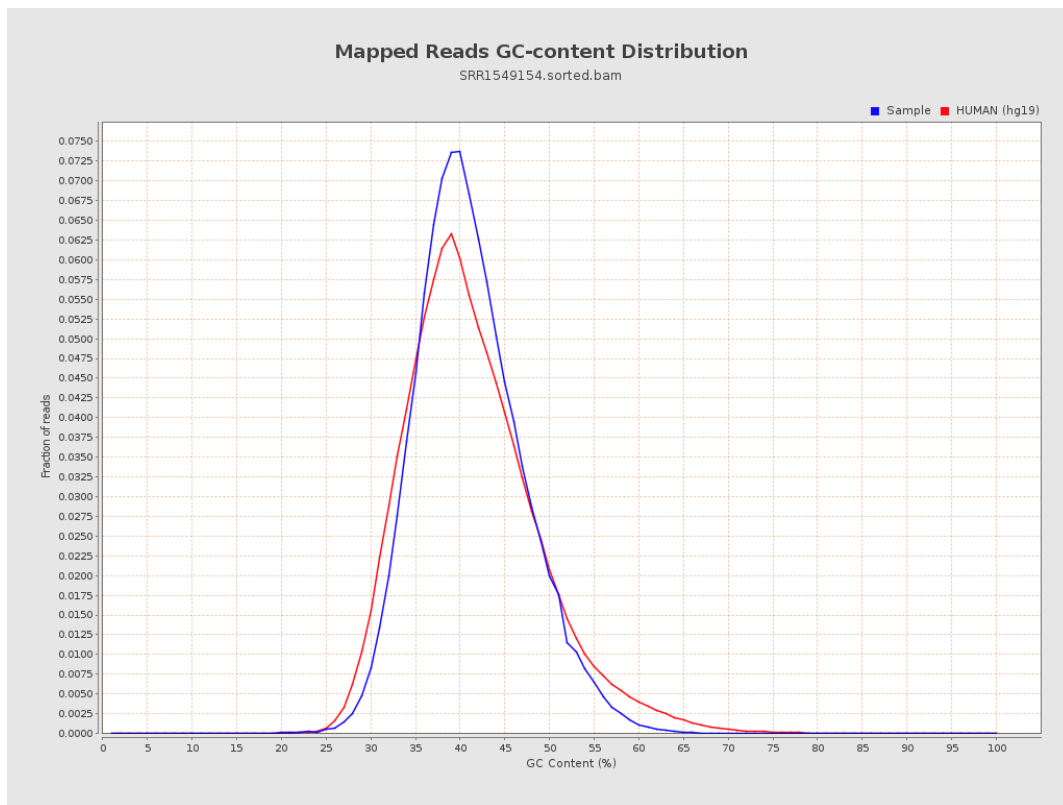
7. Results : Duplication Rate Histogram



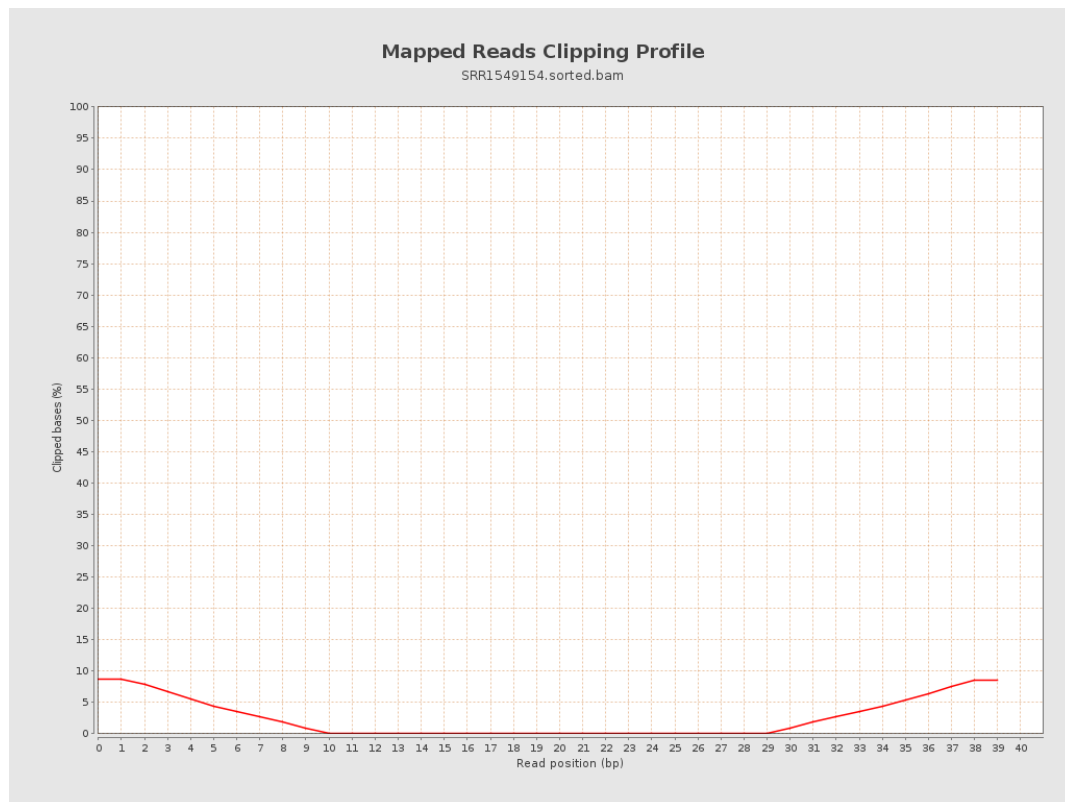
8. Results : Mapped Reads Nucleotide Content



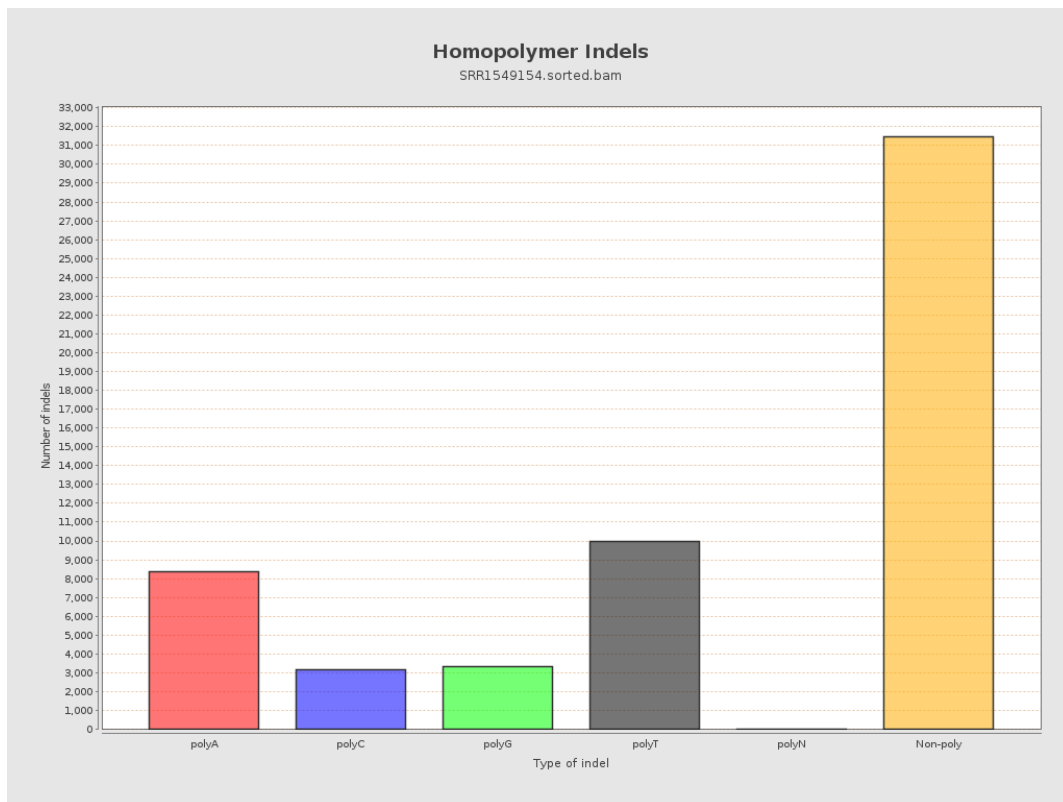
9. Results : Mapped Reads GC-content Distribution



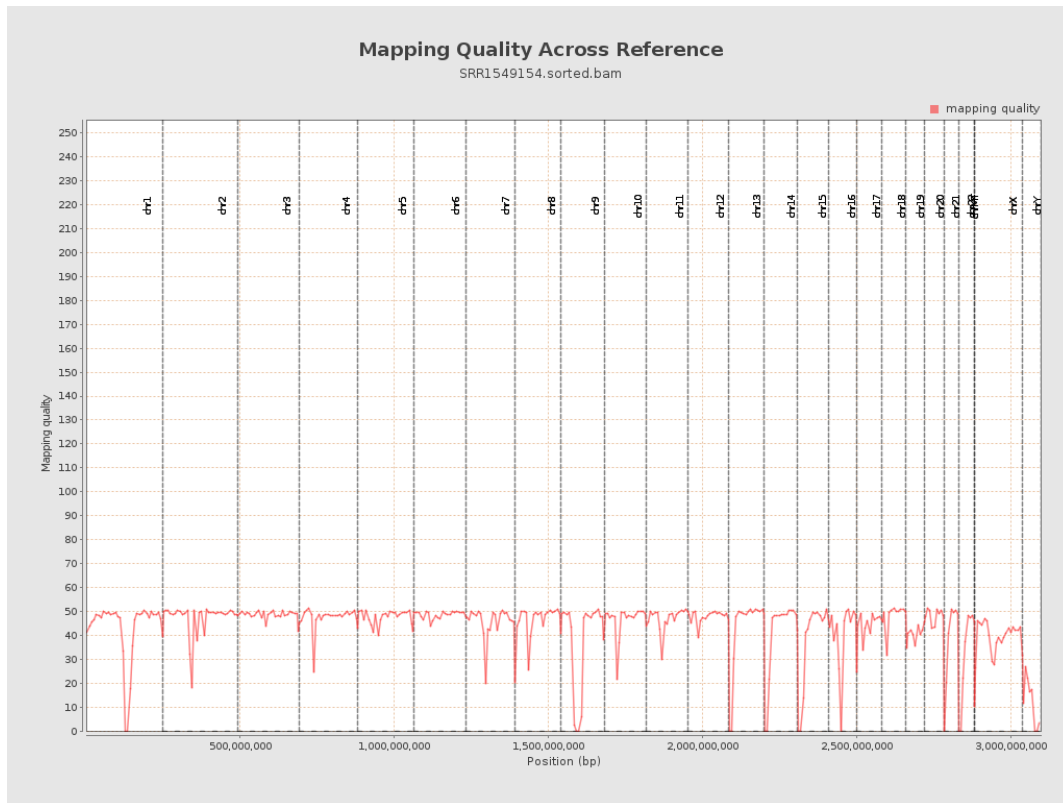
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

