

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:04:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054573.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_SRR054573 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054573.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:04:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054573.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,814,259
Mapped reads	7,116,760 / 72.51%
Unmapped reads	2,697,499 / 27.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	204 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,022,007 / 20.6%
Duplication rate	21.13%
Clipped reads	527,799 / 5.38%

2.2. ACGT Content

Number/percentage of A's	98,678,169 / 29.29%
Number/percentage of C's	65,244,899 / 19.37%
Number/percentage of T's	100,963,262 / 29.97%
Number/percentage of G's	71,817,593 / 21.32%
Number/percentage of N's	144,945 / 0.04%
GC Percentage	40.69%

2.3. Coverage

Mean	0.1088

Standard Deviation	0.8859
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2.4. Mapping Quality

Mean Mapping Quality	44.76
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2.5. Mismatches and indels

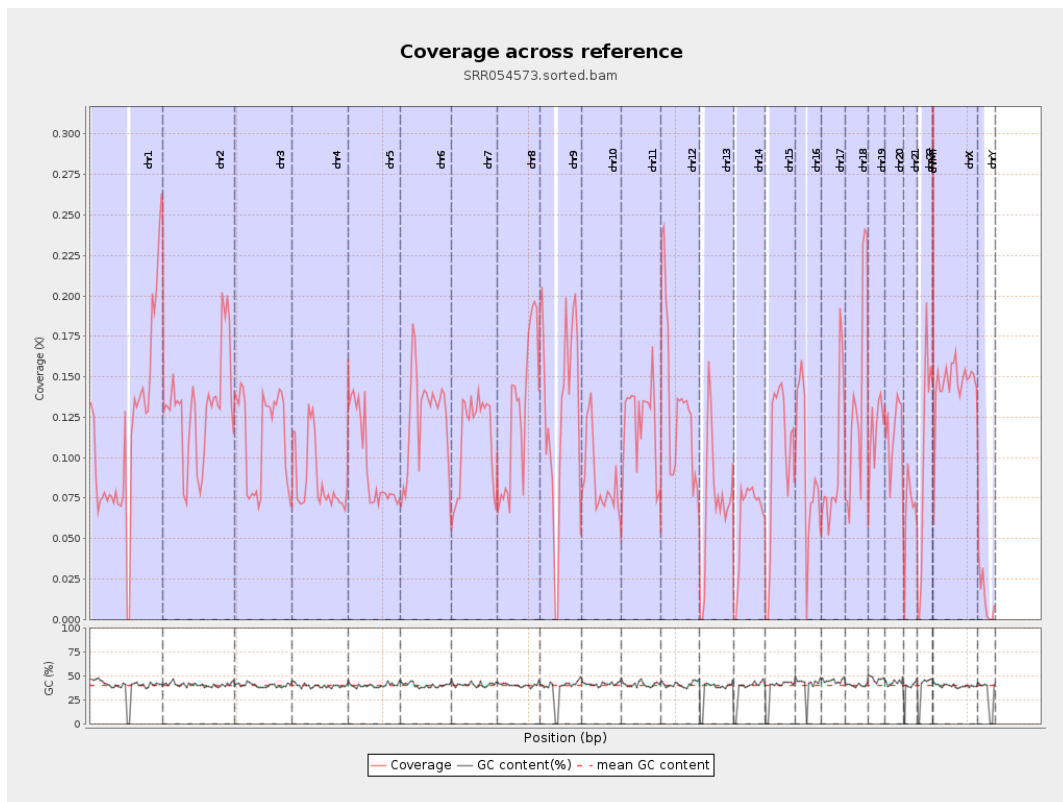
General error rate	0.62%
Mismatches	2,056,831
Insertions	14,168
Mapped reads with at least one insertion	0.2%
Deletions	45,617
Mapped reads with at least one deletion	0.64%
Homopolymer indels	47.8%

2.6. Chromosome stats

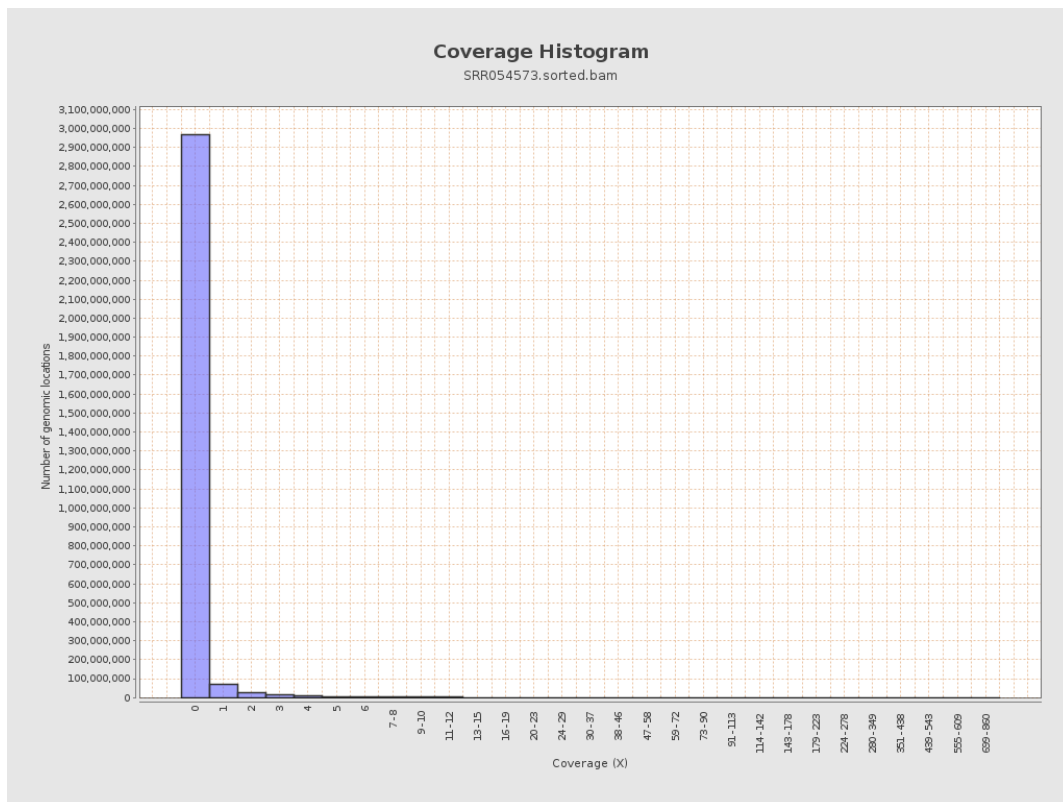
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	28863658	0.1158	0.9819
chr2	243199373	31939619	0.1313	1.1445
chr3	198022430	22278949	0.1125	0.8486
chr4	191154276	16525459	0.0865	0.7254
chr5	180915260	17276026	0.0955	0.7653
chr6	171115067	21550280	0.1259	0.9432
chr7	159138663	17548288	0.1103	0.9071

chr8	146364022	18653169	0.1274	0.942
chr9	141213431	17880786	0.1266	0.9454
chr10	135534747	11716838	0.0864	0.7843
chr11	135006516	16467985	0.122	0.9304
chr12	133851895	17945845	0.1341	0.9398
chr13	115169878	8354045	0.0725	0.6689
chr14	107349540	6755830	0.0629	0.6831
chr15	102531392	10187520	0.0994	0.7772
chr16	90354753	8292817	0.0918	0.7539
chr17	81195210	7847183	0.0966	0.7605
chr18	78077248	10613726	0.1359	1.0491
chr19	59128983	6990730	0.1182	0.9311
chr20	63025520	7292140	0.1157	0.8323
chr21	48129895	3201111	0.0665	0.6539
chr22	51304566	5355641	0.1044	0.8044
chrMT	16571	12098	0.7301	1.8445
chrX	155270560	22581714	0.1454	1.021
chrY	59373566	786313	0.0132	0.2443

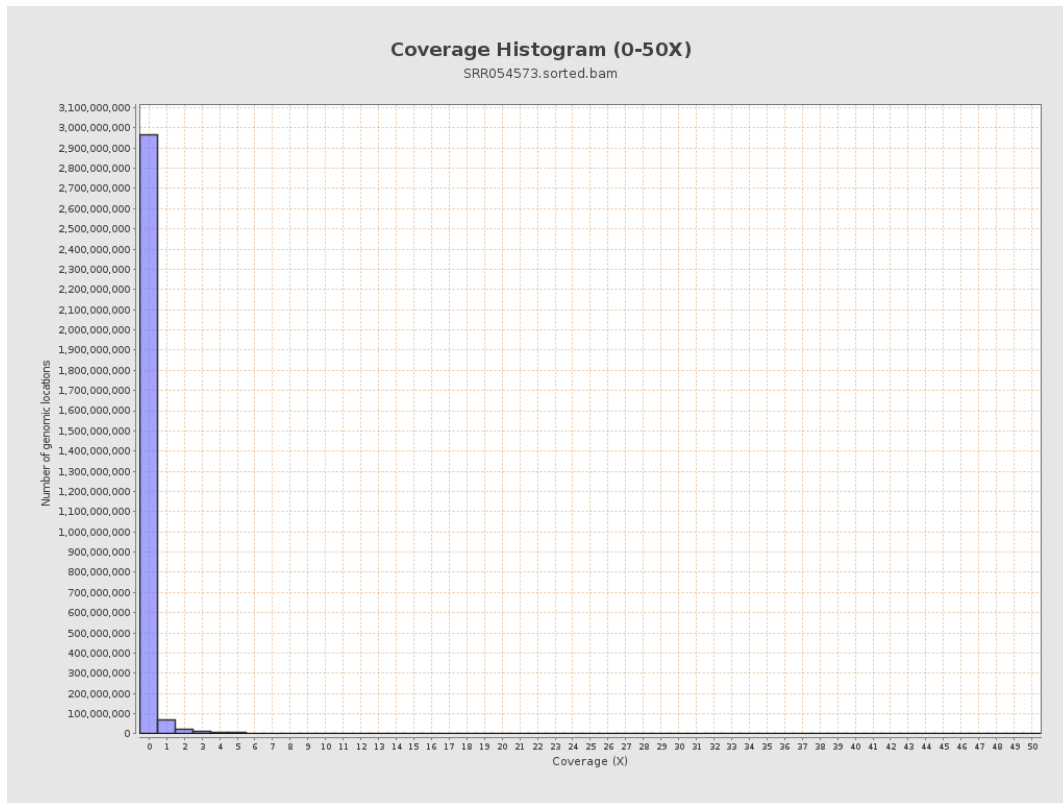
3. Results : Coverage across reference



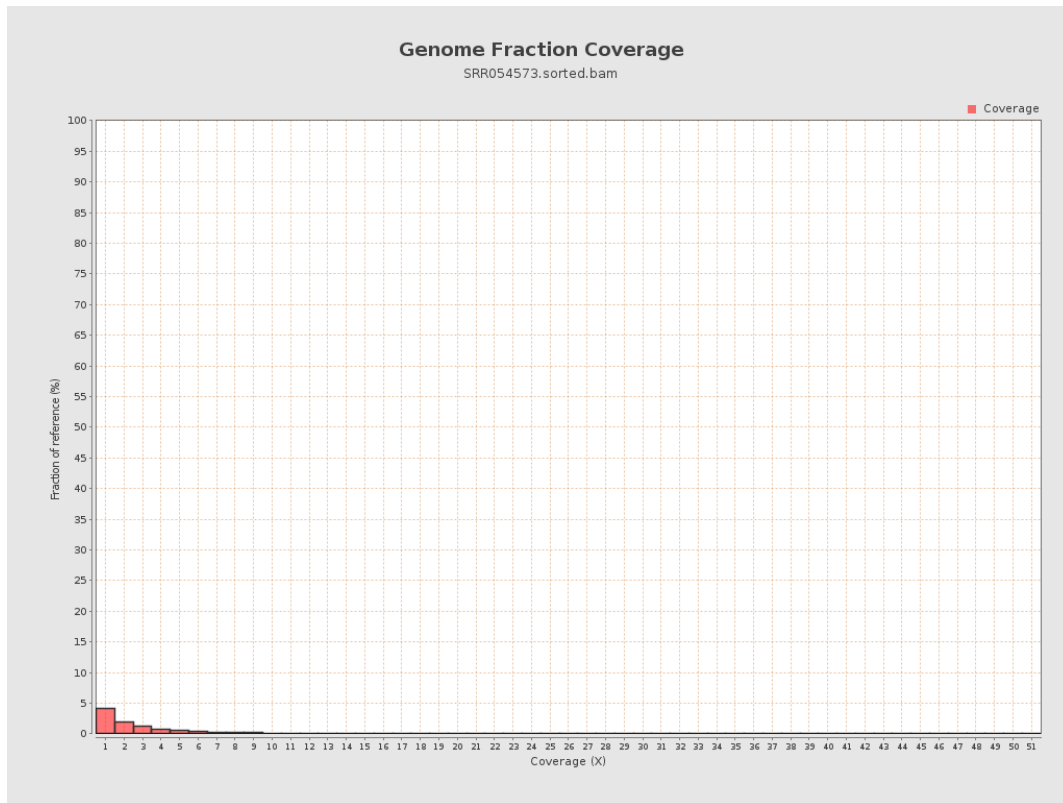
4. Results : Coverage Histogram



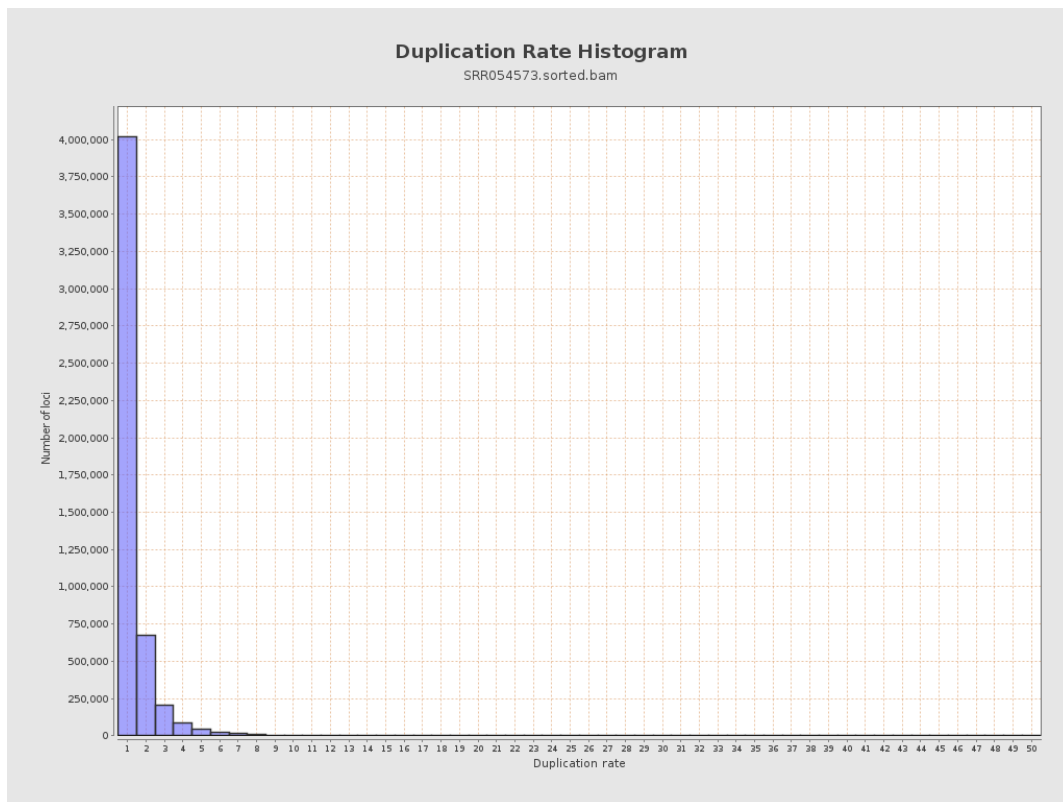
5. Results : Coverage Histogram (0-50X)



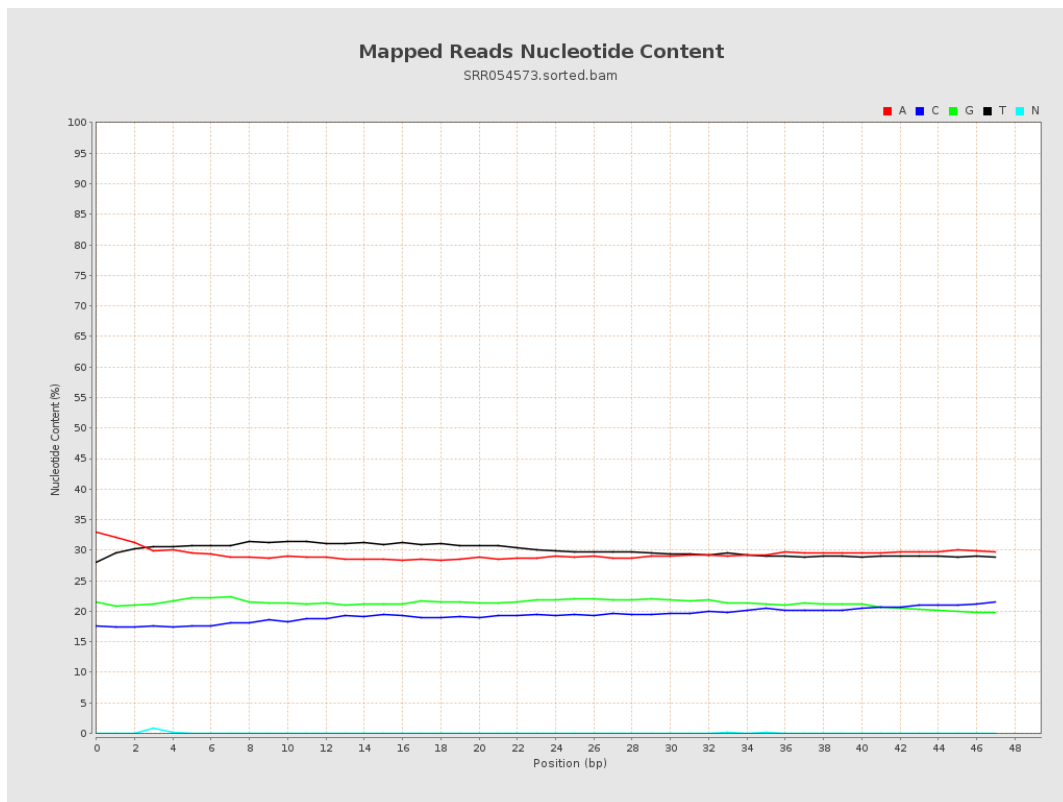
6. Results : Genome Fraction Coverage



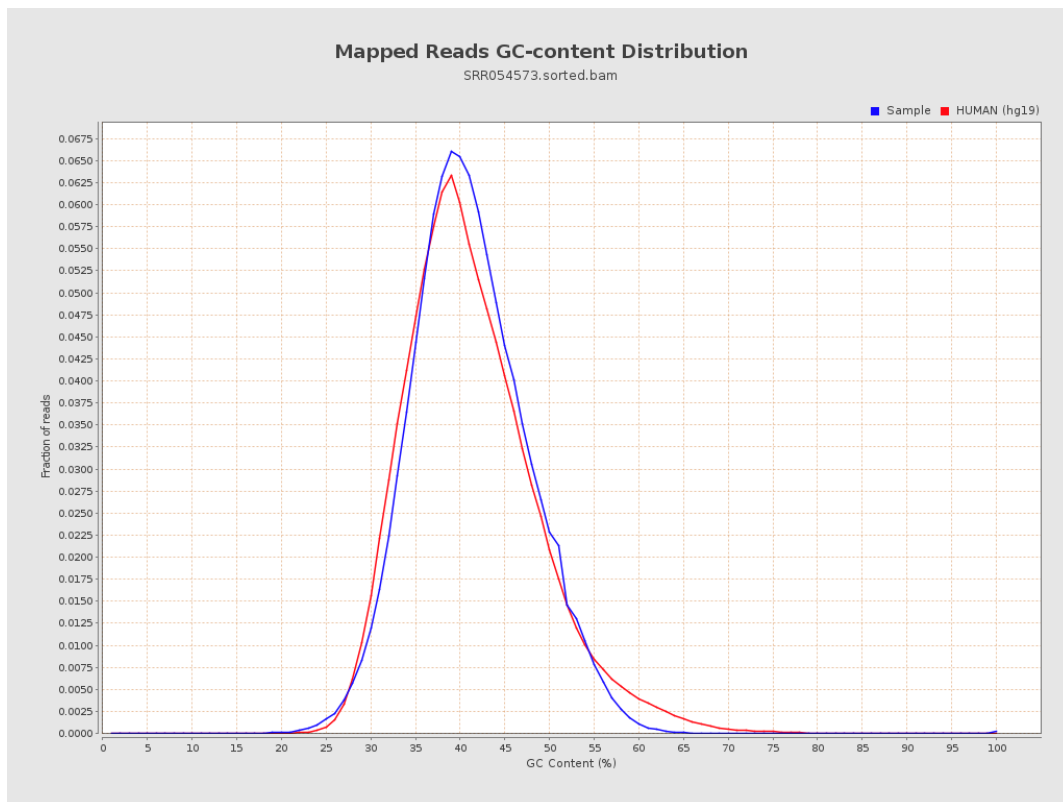
7. Results : Duplication Rate Histogram



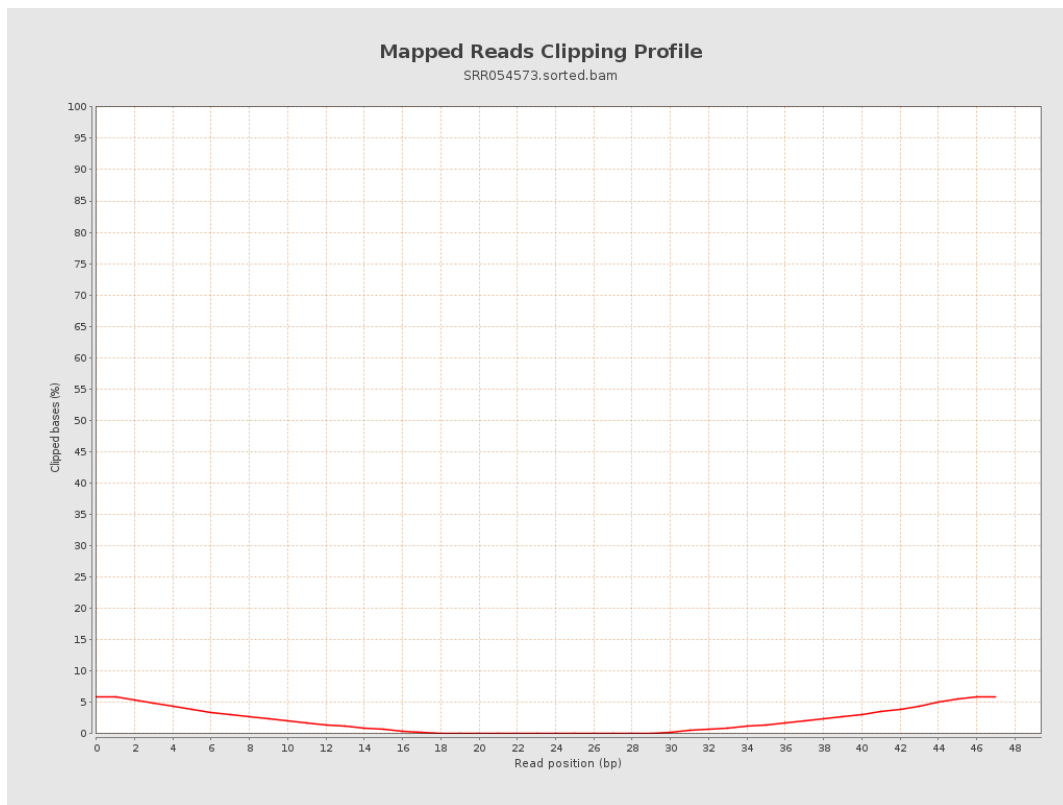
8. Results : Mapped Reads Nucleotide Content



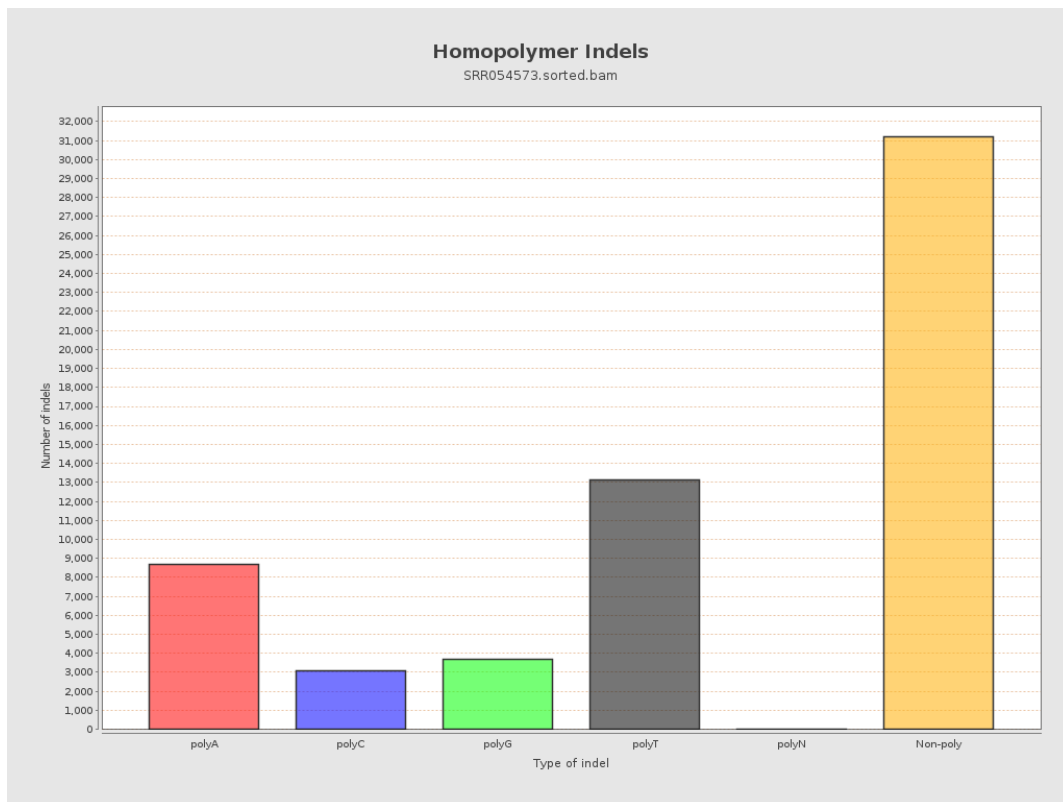
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

