

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 08:59:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054633.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_SRR054633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 08:59:06 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,798,958
Mapped reads	5,507,929 / 70.62%
Unmapped reads	2,291,029 / 29.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	144 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,159,733 / 14.87%
Duplication rate	15.75%
Clipped reads	652,121 / 8.36%

2.2. ACGT Content

Number/percentage of A's	79,004,734 / 30.57%
Number/percentage of C's	49,664,932 / 19.22%
Number/percentage of T's	77,217,259 / 29.88%
Number/percentage of G's	52,479,444 / 20.31%
Number/percentage of N's	51,456 / 0.02%
GC Percentage	39.53%

2.3. Coverage

Mean	0.0835

Standard Deviation	0.6854
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2.4. Mapping Quality

Mean Mapping Quality	45.35
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2.5. Mismatches and indels

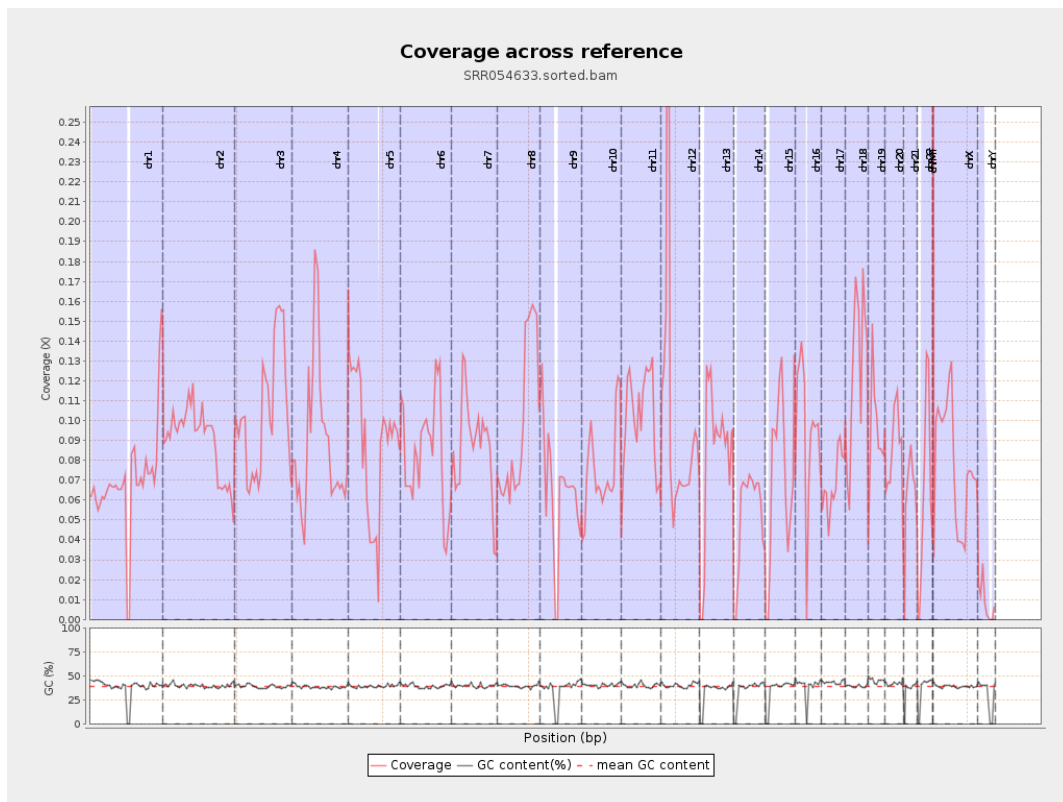
General error rate	0.65%
Mismatches	1,666,240
Insertions	12,028
Mapped reads with at least one insertion	0.22%
Deletions	37,089
Mapped reads with at least one deletion	0.67%
Homopolymer indels	46.68%

2.6. Chromosome stats

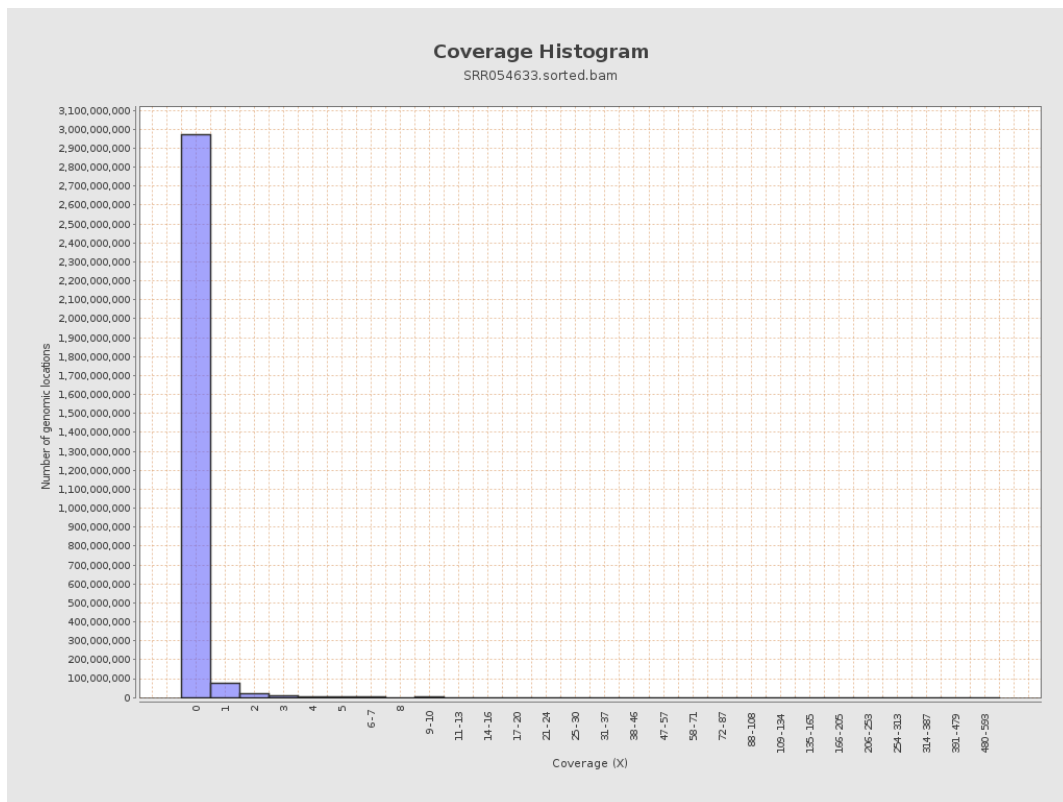
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17406248	0.0698	0.6608
chr2	243199373	21956761	0.0903	0.8128
chr3	198022430	20506627	0.1036	0.7066
chr4	191154276	16772129	0.0877	0.6718
chr5	180915260	15885504	0.0878	0.6619
chr6	171115067	14288900	0.0835	0.6751
chr7	159138663	13683698	0.086	0.7156

chr8	146364022	14480311	0.0989	0.7422
chr9	141213431	9063001	0.0642	0.5702
chr10	135534747	10173882	0.0751	0.6132
chr11	135006516	13836684	0.1025	0.7762
chr12	133851895	14043113	0.1049	0.8467
chr13	115169878	9542925	0.0829	0.6335
chr14	107349540	5757537	0.0536	0.5371
chr15	102531392	7220527	0.0704	0.5622
chr16	90354753	8444131	0.0935	0.7026
chr17	81195210	5576169	0.0687	0.5359
chr18	78077248	9763406	0.125	0.852
chr19	59128983	5728912	0.0969	0.7796
chr20	63025520	5373962	0.0853	0.625
chr21	48129895	2972047	0.0618	0.5666
chr22	51304566	3388552	0.066	0.539
chrMT	16571	20513	1.2379	3.0107
chrX	155270560	12061496	0.0777	0.7035
chrY	59373566	525139	0.0088	0.2181

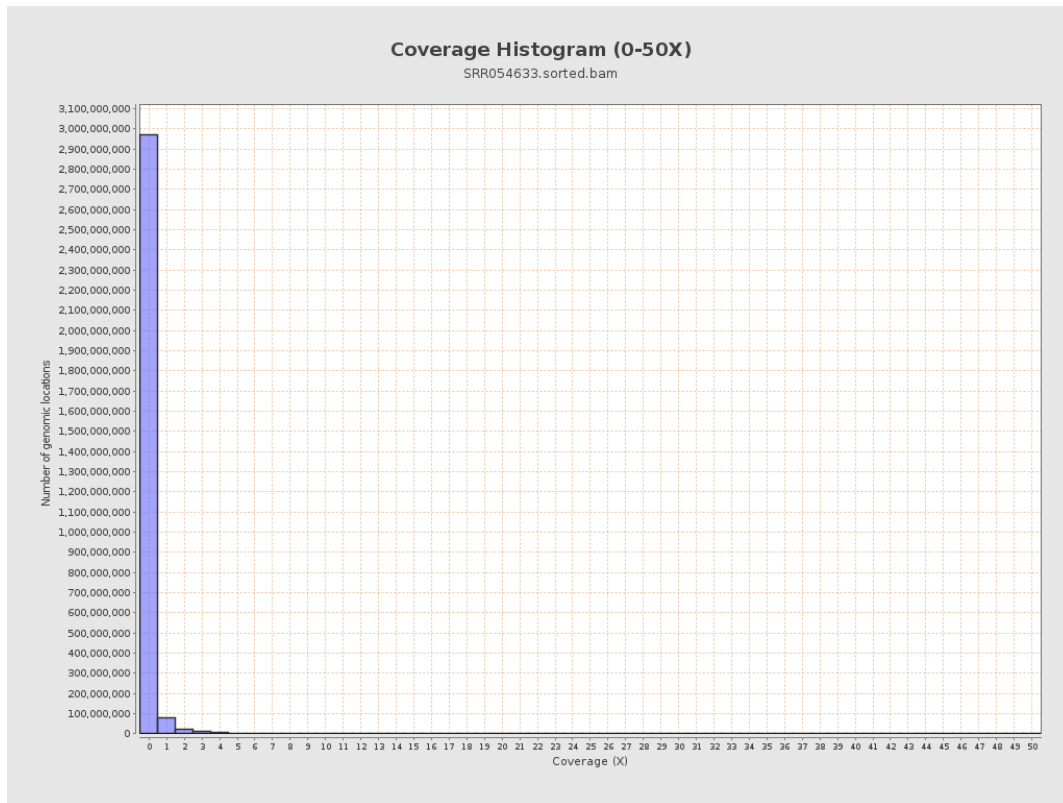
3. Results : Coverage across reference



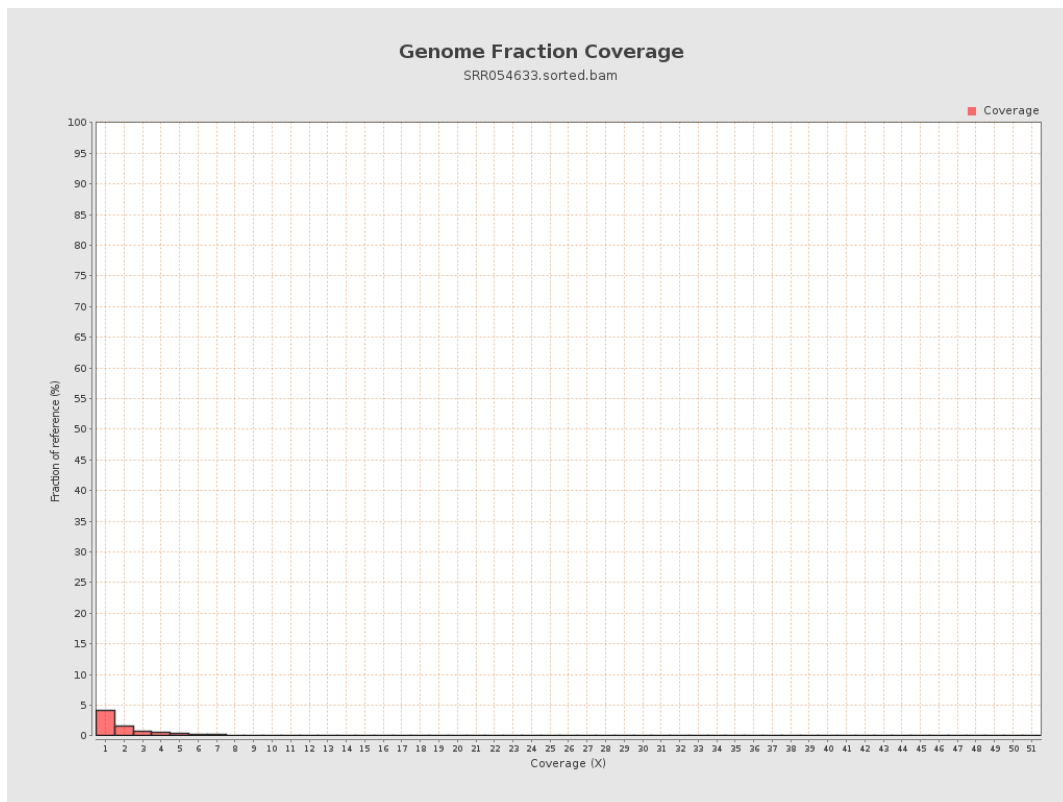
4. Results : Coverage Histogram



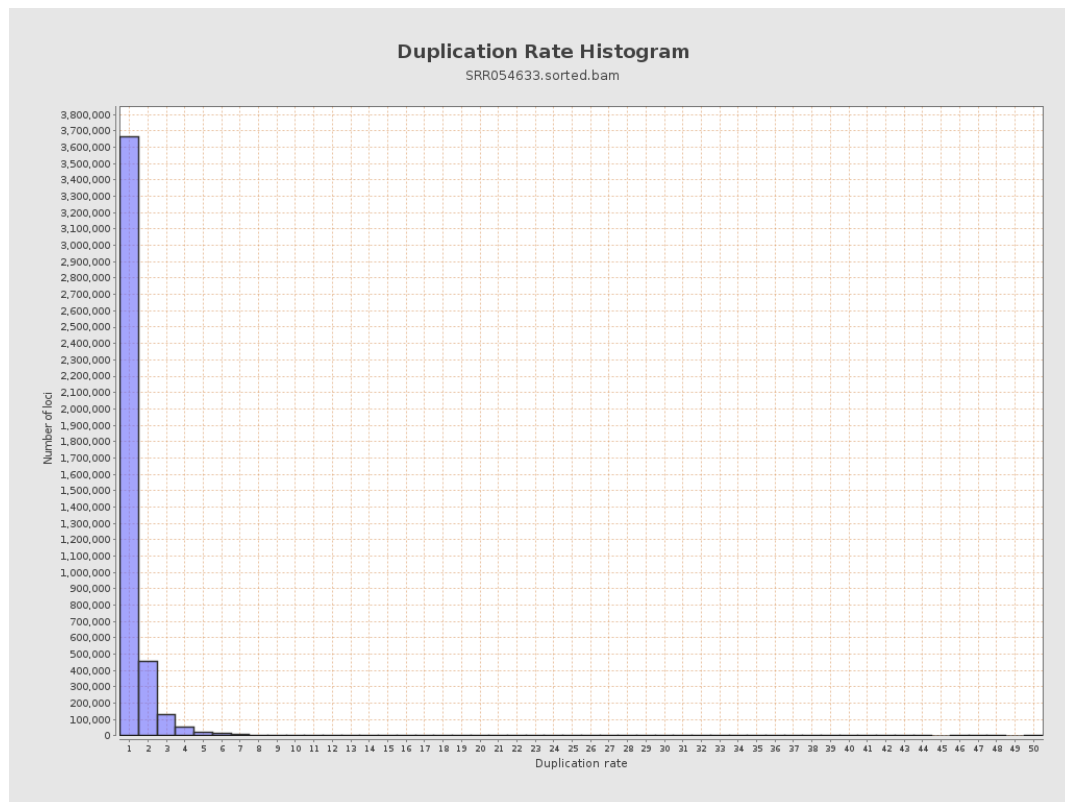
5. Results : Coverage Histogram (0-50X)



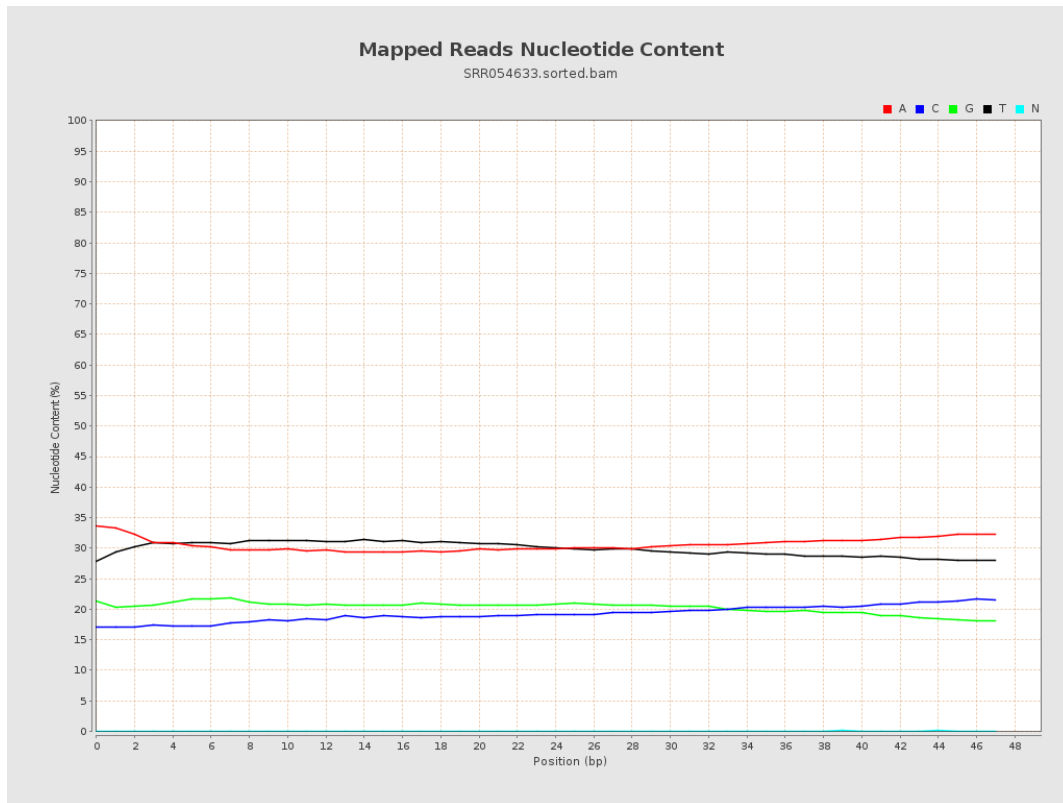
6. Results : Genome Fraction Coverage



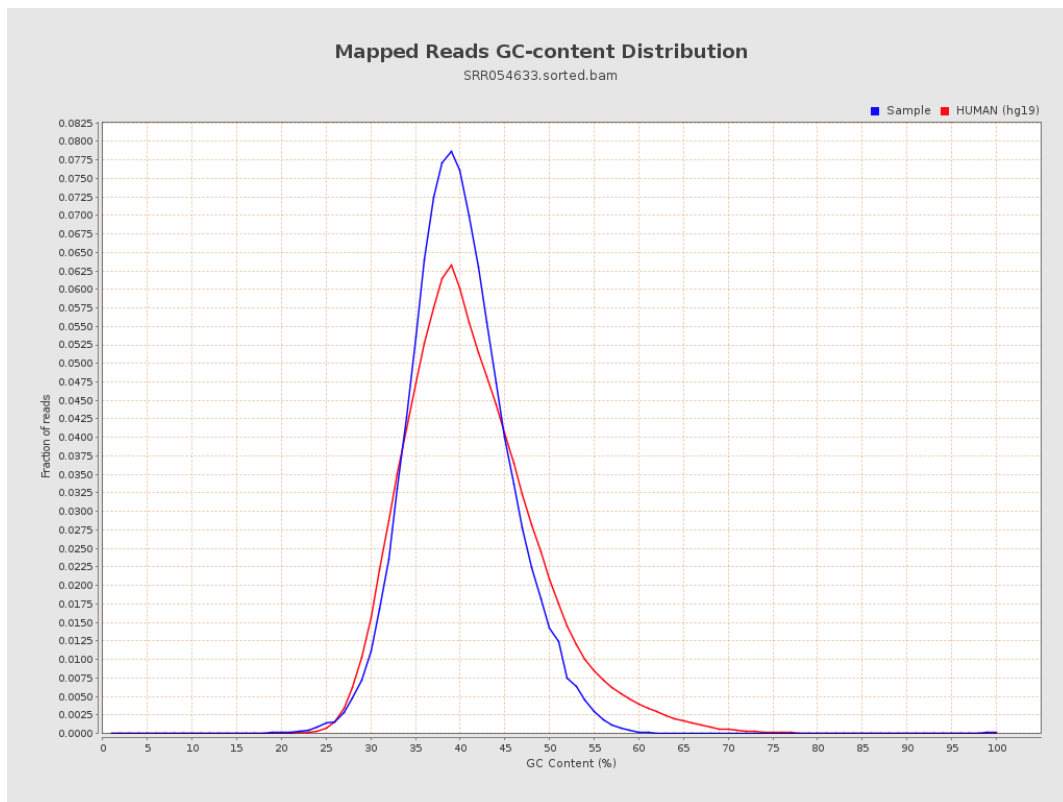
7. Results : Duplication Rate Histogram



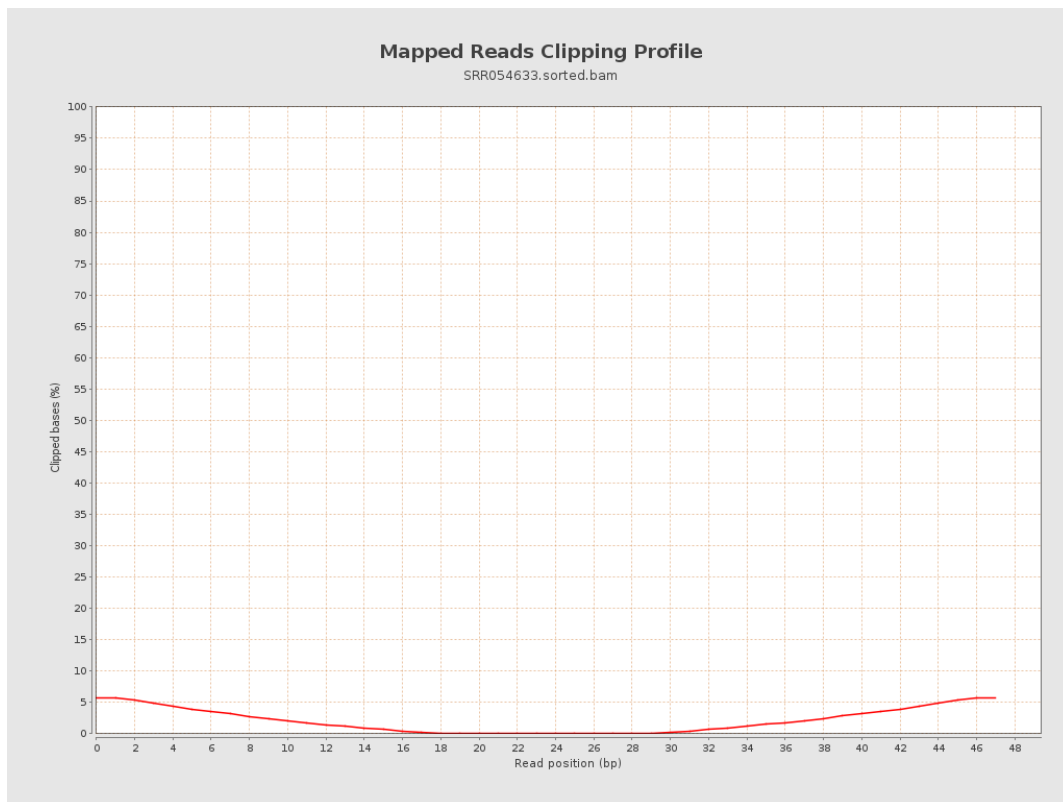
8. Results : Mapped Reads Nucleotide Content



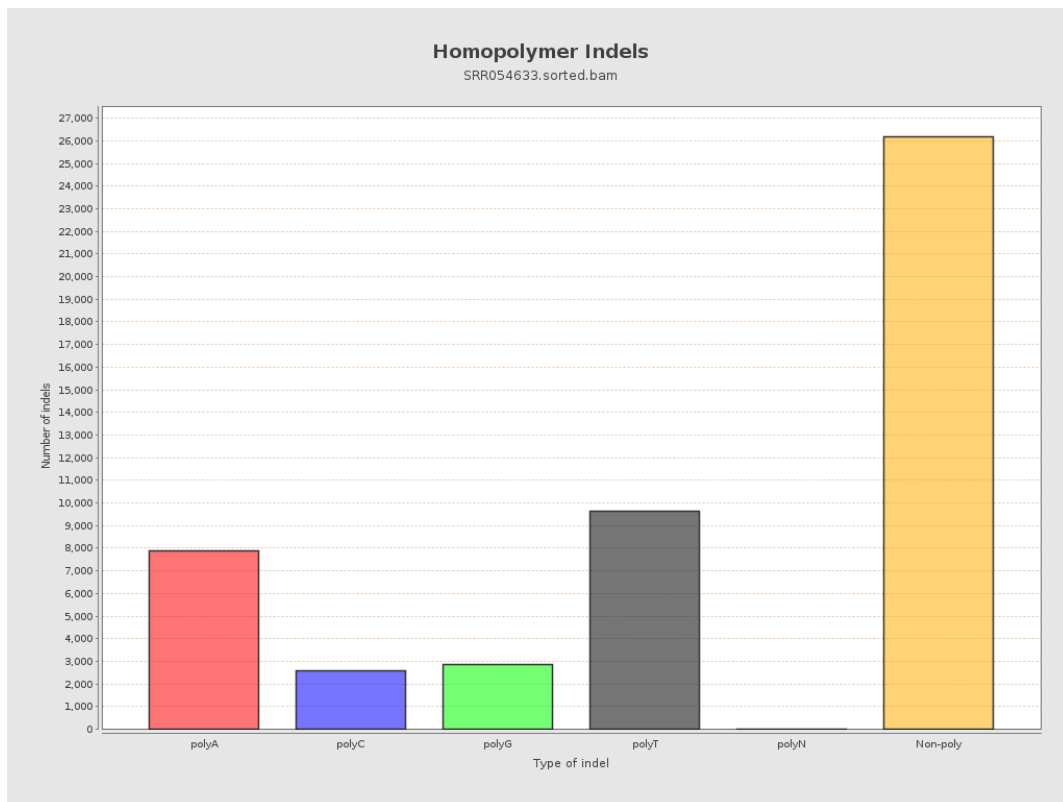
9. Results : Mapped Reads GC-content Distribution



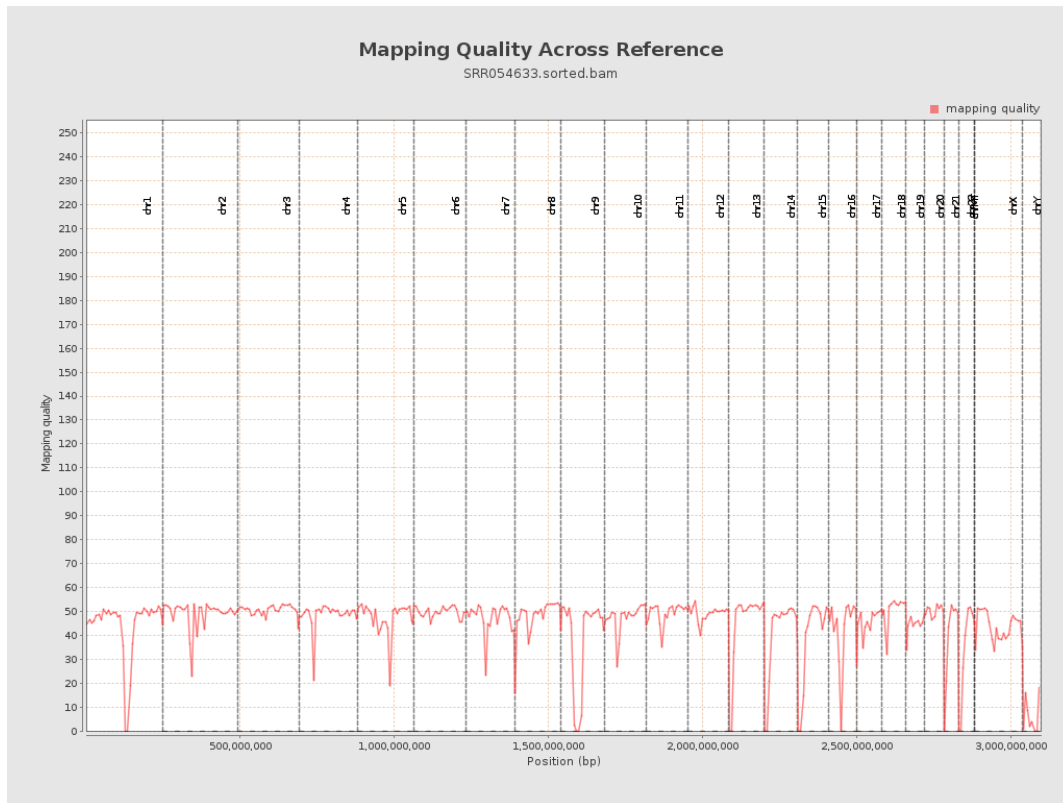
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

