Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:14:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053633.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_SRR053633 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053633.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:14:21 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053633.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,100,758
Mapped reads	12,241,969 / 81.07%
Unmapped reads	2,858,789 / 18.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	357 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,836,378 / 18.78%
Duplication rate	16.78%
Clipped reads	847,766 / 5.61%

2.2. ACGT Content

Number/percentage of A's	170,443,919 / 29.39%
Number/percentage of C's	109,876,529 / 18.95%
Number/percentage of T's	172,893,795 / 29.82%
Number/percentage of G's	126,622,215 / 21.84%
Number/percentage of N's	5,644 / 0%
GC Percentage	40.79%

2.3. Coverage

Mean	0.1873

Standard Deviation	1.2207

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

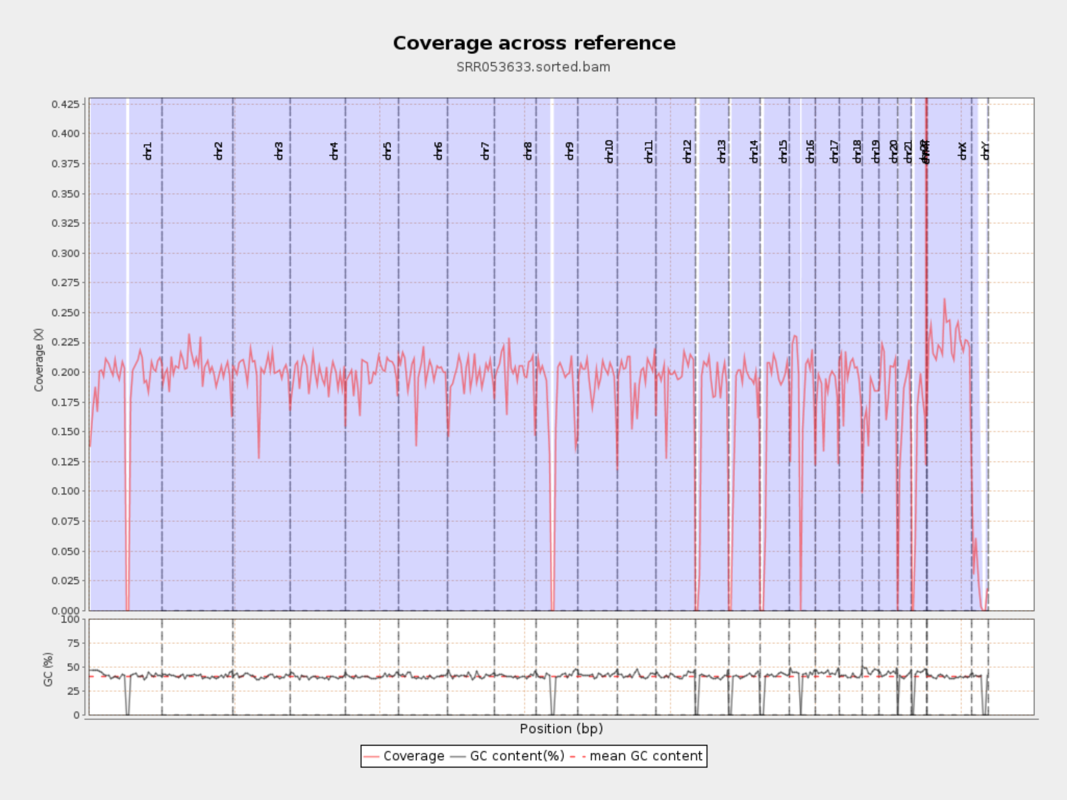
General error rate	0.46%
Mismatches	2,631,742
Insertions	23,120
Mapped reads with at least one insertion	0.19%
Deletions	76,685
Mapped reads with at least one deletion	0.62%
Homopolymer indels	48.57%

2.6. Chromosome stats

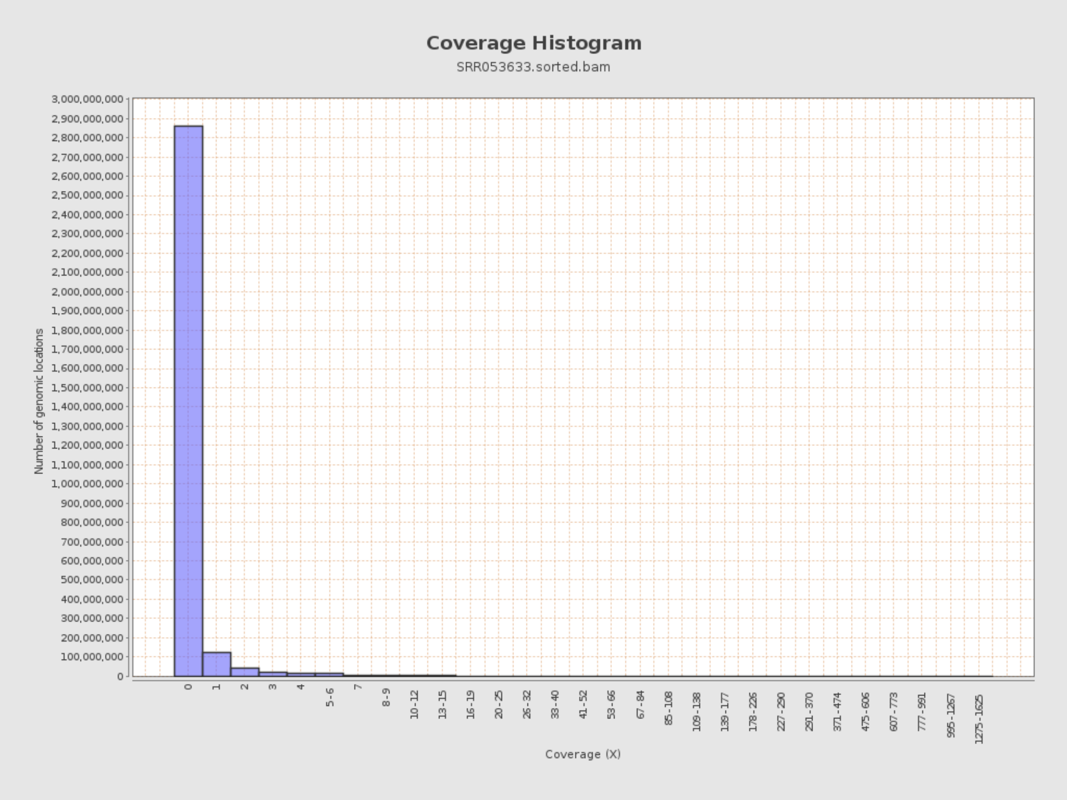
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46195579	0.1853	1.2491
chr2	243199373	49509141	0.2036	1.5298
chr3	198022430	39836769	0.2012	1.0823
chr4	191154276	37776120	0.1976	1.1201
chr5	180915260	35998055	0.199	1.0871
chr6	171115067	34255880	0.2002	1.2039
chr7	159138663	31443845	0.1976	1.6338

chr8	146364022	29480189	0.2014	1.2156
chr9	141213431	23837652	0.1688	1.2555
chr10	135534747	26683092	0.1969	1.2132
chr11	135006516	26495064	0.1963	1.3369
chr12	133851895	26389808	0.1972	1.0846
chr13	115169878	18773833	0.163	0.9745
chr14	107349540	17473720	0.1628	1.1958
chr15	102531392	16673646	0.1626	0.9873
chr16	90354753	16469352	0.1823	1.0785
chr17	81195210	14740490	0.1815	1.0428
chr18	78077248	15556086	0.1992	1.3904
chr19	59128983	10119758	0.1711	1.2117
chr20	63025520	12298699	0.1951	1.1234
chr21	48129895	7413297	0.154	1.0642
chr22	51304566	6229813	0.1214	0.8255
chrMT	16571	91978	5.5505	9.5915
chrX	155270560	34786748	0.224	1.3418
chrY	59373566	1427765	0.024	0.4515

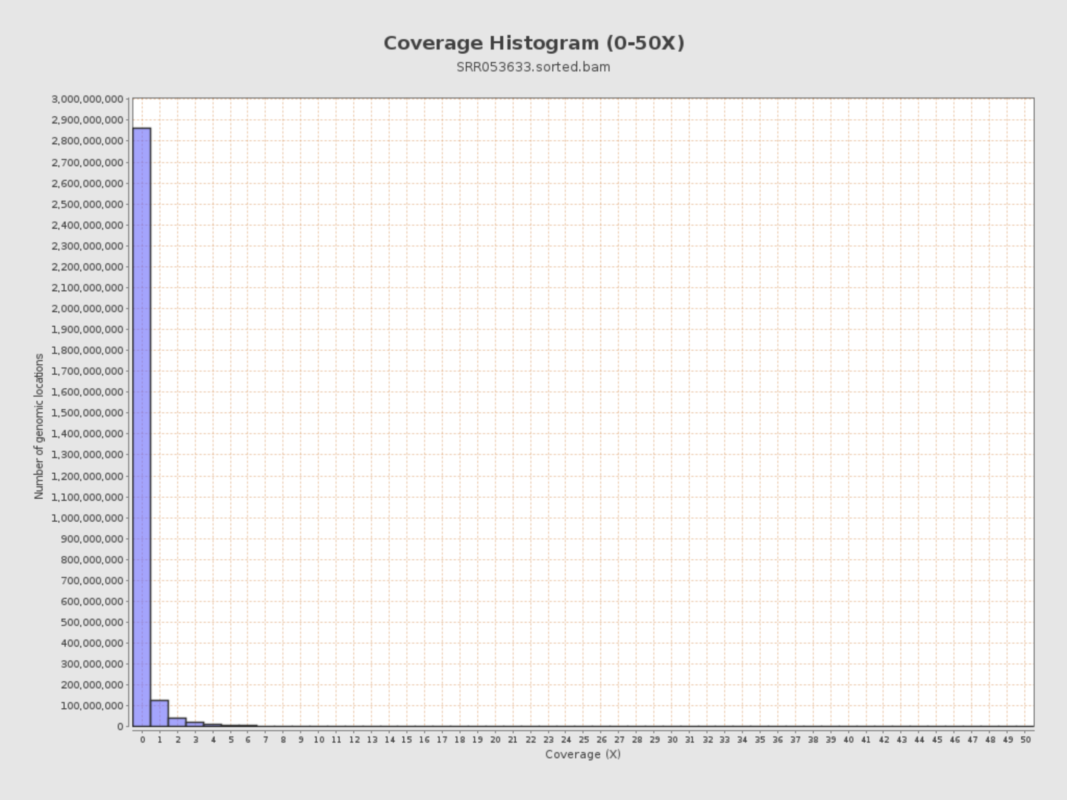
3. Results : Coverage across reference



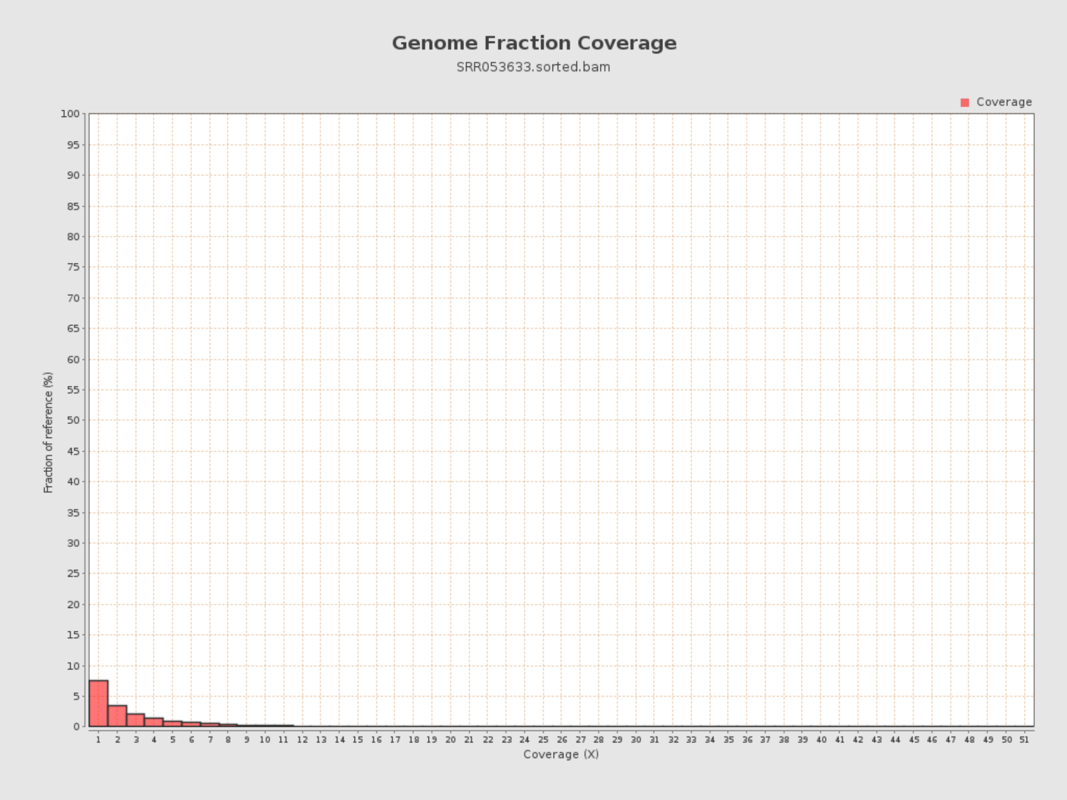
4. Results : Coverage Histogram



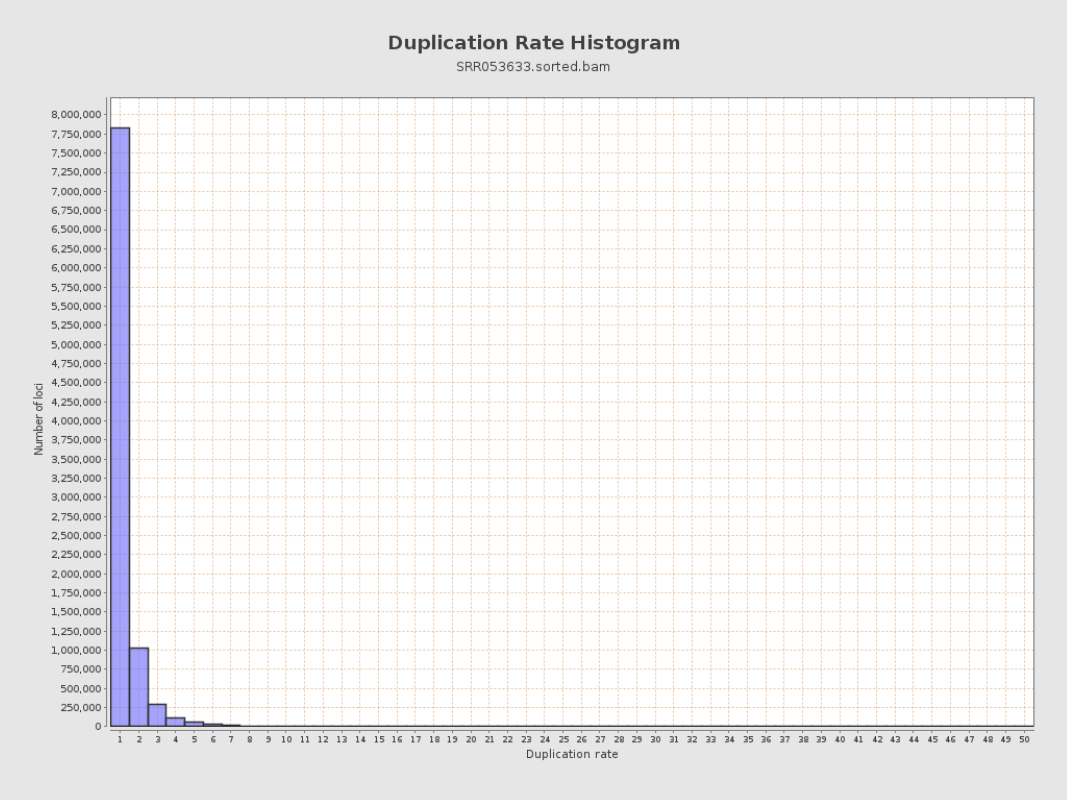
5. Results : Coverage Histogram (0-50X)



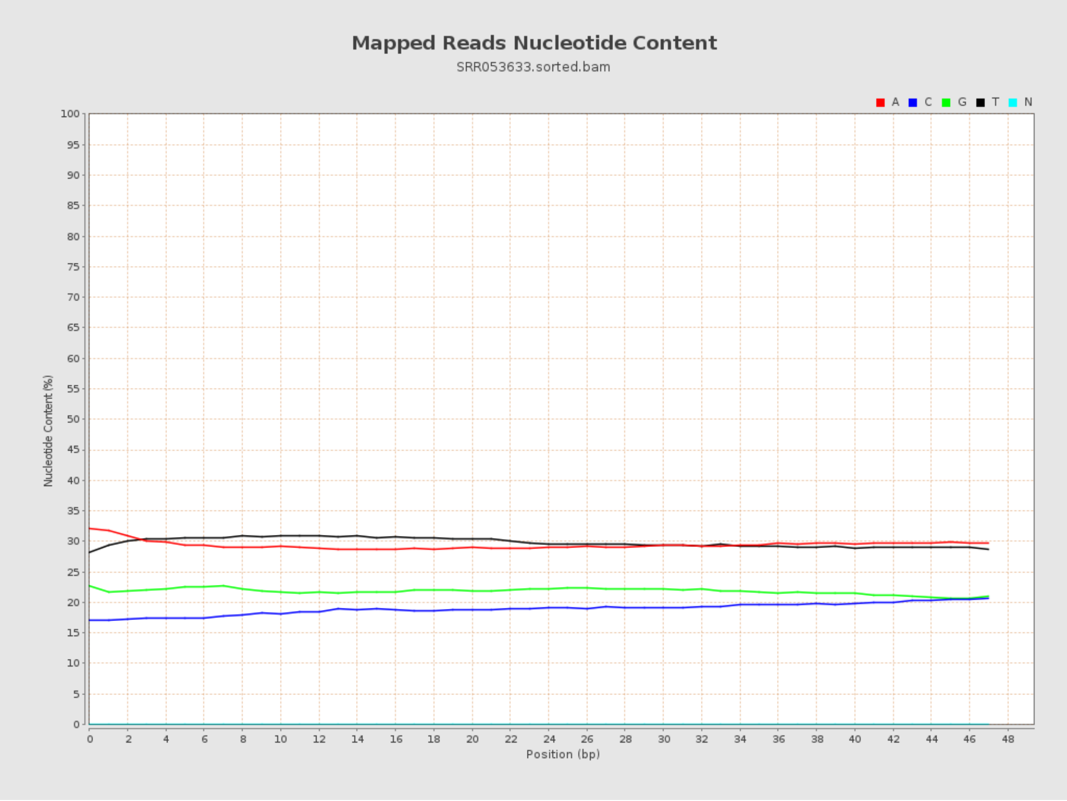
6. Results : Genome Fraction Coverage



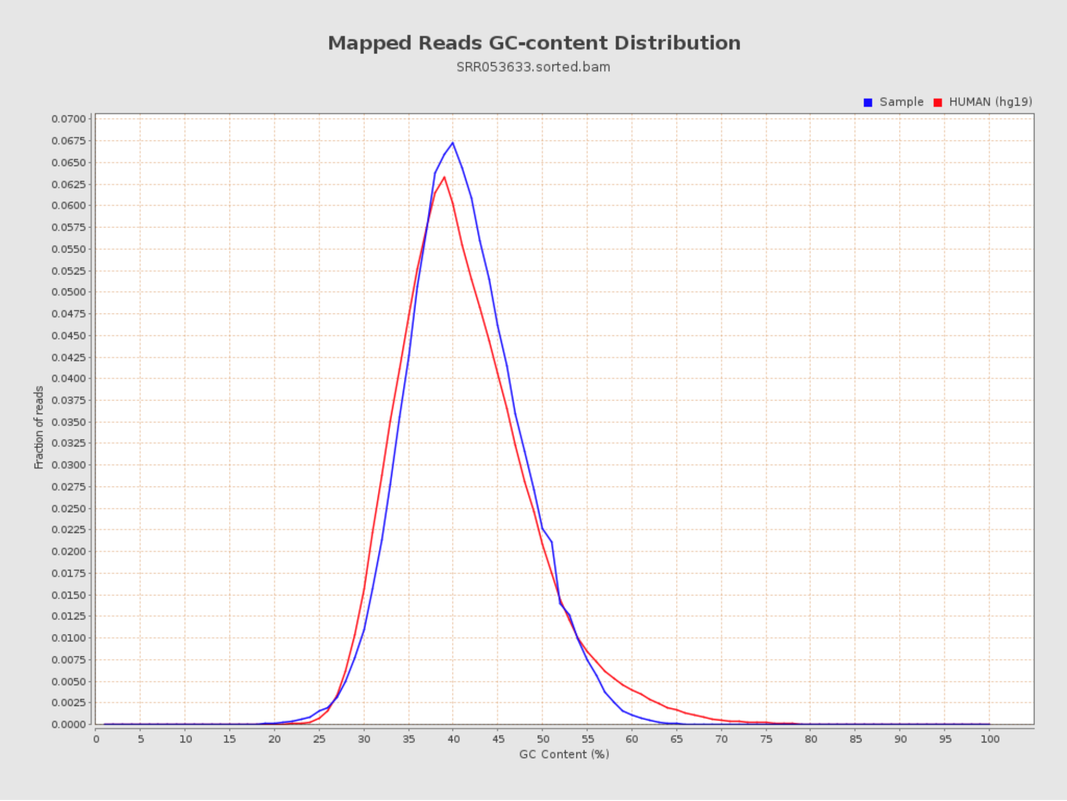
7. Results : Duplication Rate Histogram



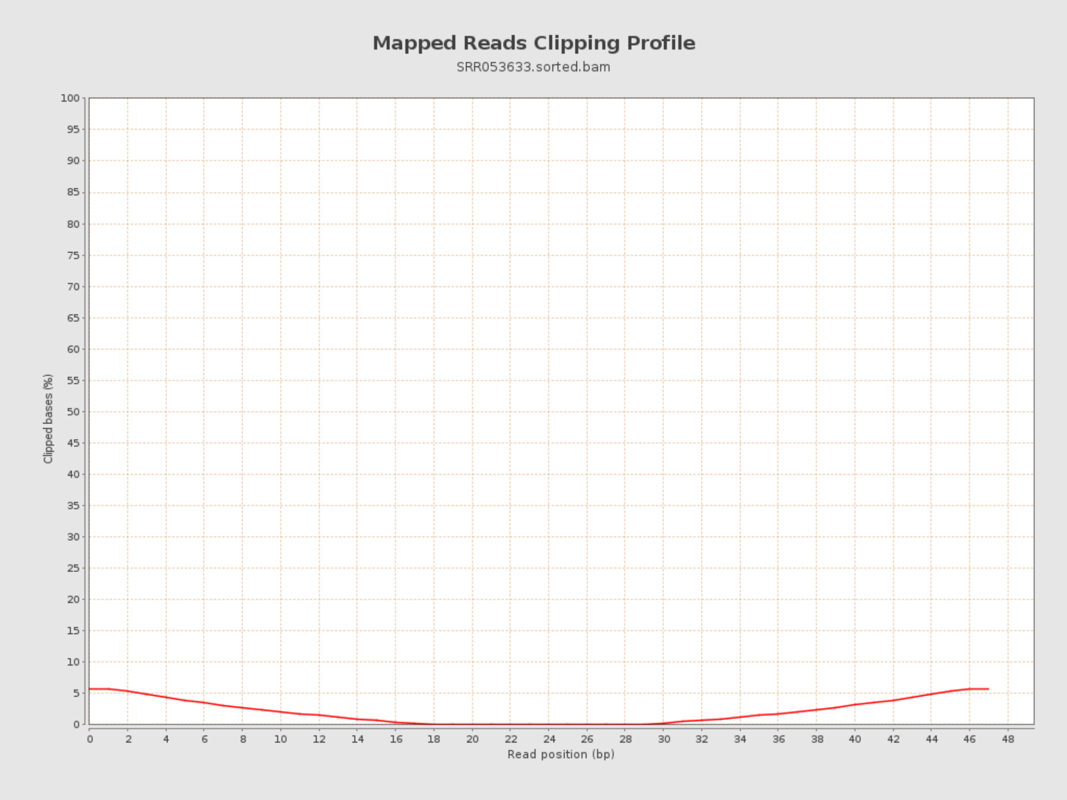
8. Results : Mapped Reads Nucleotide Content



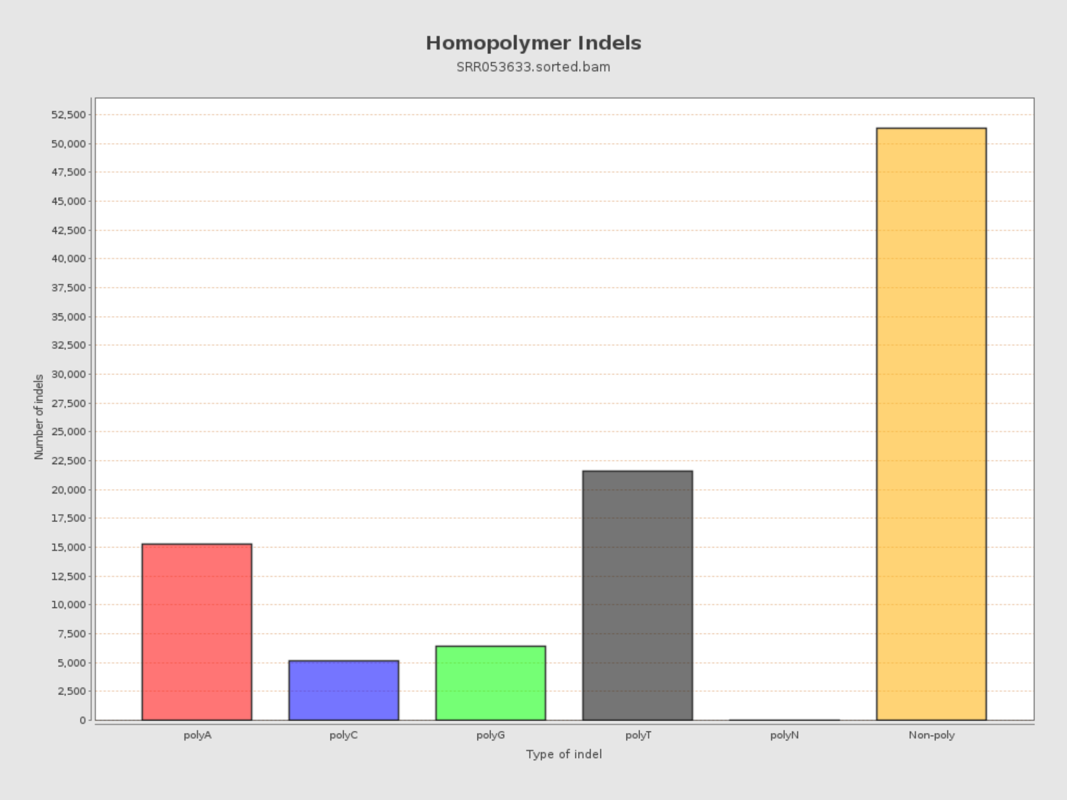
9. Results : Mapped Reads GC-content Distribution



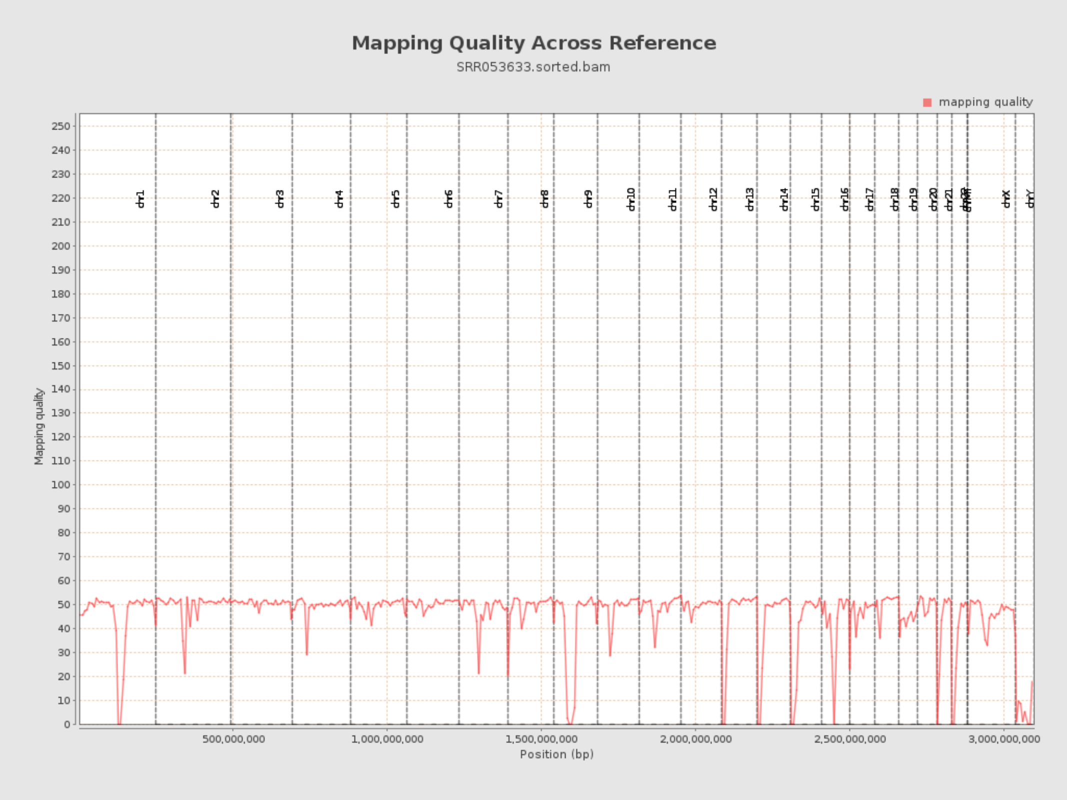
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram