Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053632.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_SRR053632 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053632.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:04:39 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053632.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,193,445
Mapped reads	10,246,402 / 77.66%
Unmapped reads	2,947,043 / 22.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	273 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,590,985 / 19.64%
Duplication rate	17.59%
Clipped reads	760,050 / 5.76%

2.2. ACGT Content

Number/percentage of A's	141,924,739 / 29.27%
Number/percentage of C's	93,812,451 / 19.35%
Number/percentage of T's	143,479,603 / 29.59%
Number/percentage of G's	105,687,628 / 21.8%
Number/percentage of N's	6,140 / 0%
GC Percentage	41.14%

2.3. Coverage

Mean	0.1567

Standard Deviation	1.1413

2.4. Mapping Quality

Mean Mapping Quality	45.6

2.5. Mismatches and indels

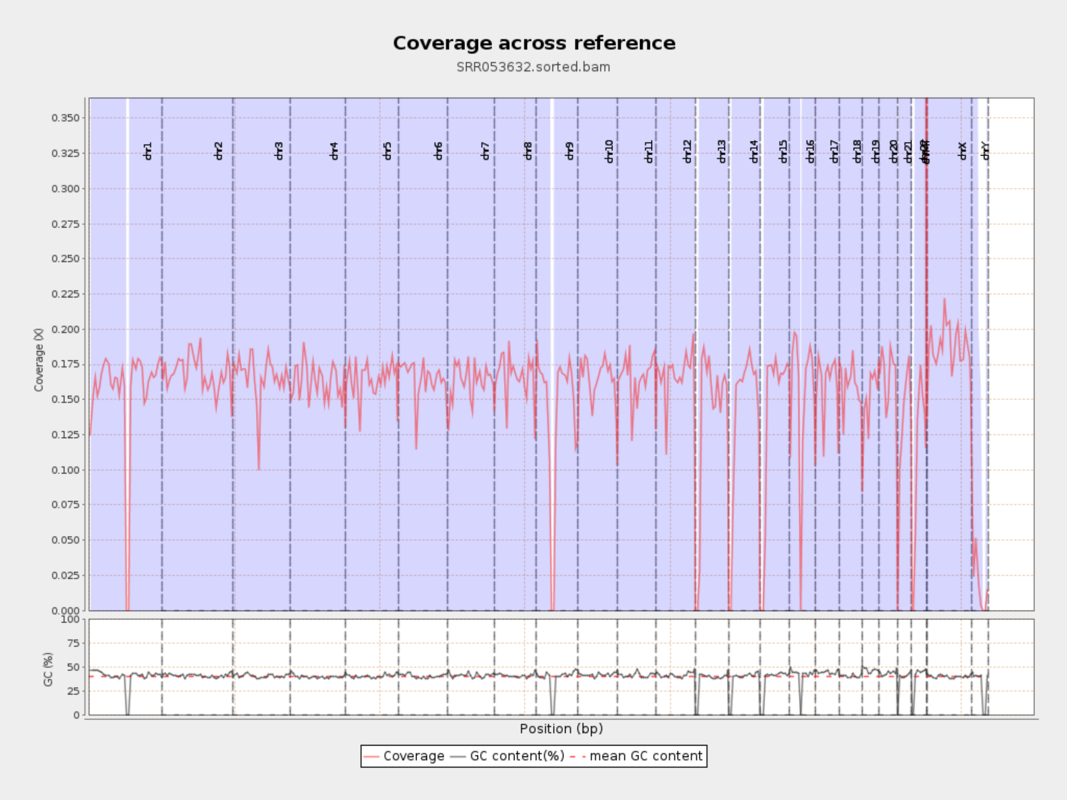
General error rate	0.52%
Mismatches	2,493,192
Insertions	18,860
Mapped reads with at least one insertion	0.18%
Deletions	61,773
Mapped reads with at least one deletion	0.6%
Homopolymer indels	48.03%

2.6. Chromosome stats

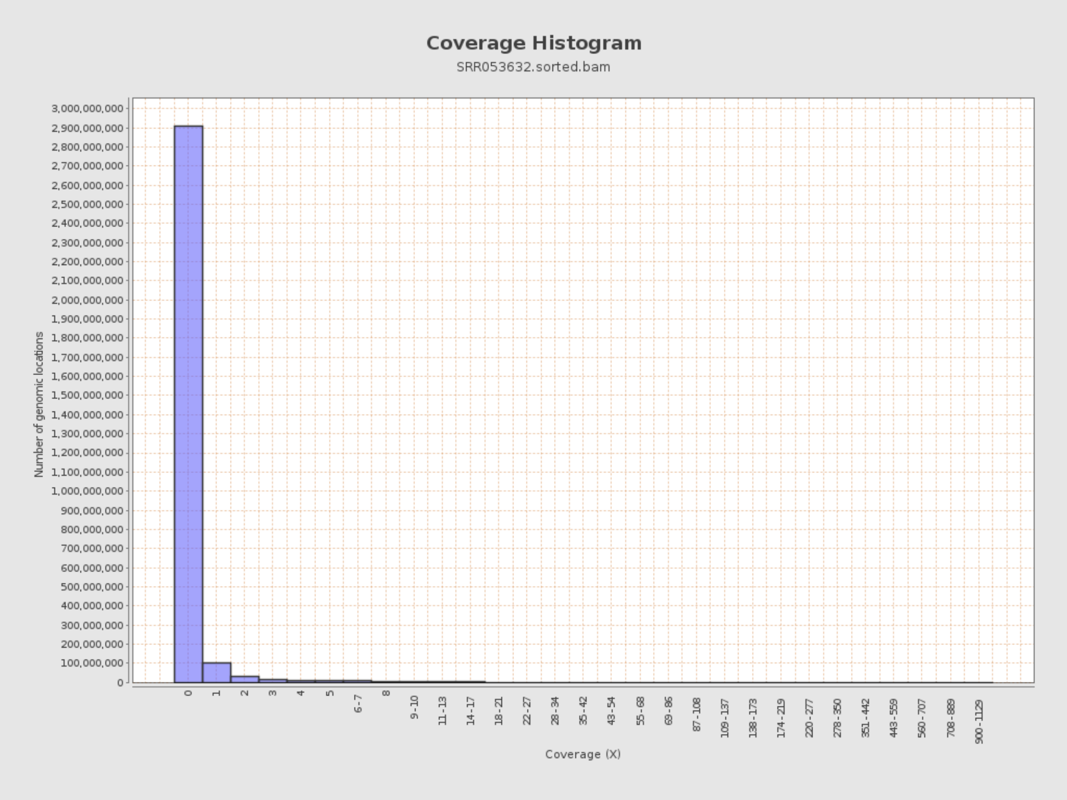
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	38535517	0.1546	1.1769
chr2	243199373	41044741	0.1688	1.3505
chr3	198022430	32966181	0.1665	1.0558
chr4	191154276	31125047	0.1628	1.1016
chr5	180915260	29754825	0.1645	1.0591
chr6	171115067	28250272	0.1651	1.1332
chr7	159138663	26045136	0.1637	1.3702

chr8	146364022	24390923	0.1666	1.1449
chr9	141213431	19843102	0.1405	1.1031
chr10	135534747	22566042	0.1665	1.1784
chr11	135006516	22328093	0.1654	1.2107
chr12	133851895	22466499	0.1678	1.0893
chr13	115169878	15656955	0.1359	0.9758
chr14	107349540	14929615	0.1391	1.1162
chr15	102531392	14171616	0.1382	0.9839
chr16	90354753	13962472	0.1545	1.0324
chr17	81195210	12983511	0.1599	1.0668
chr18	78077248	12574062	0.161	1.2301
chr19	59128983	8953123	0.1514	1.1698
chr20	63025520	10512722	0.1668	1.1215
chr21	48129895	6237363	0.1296	1.0602
chr22	51304566	5317960	0.1037	0.8116
chrMT	16571	93237	5.6265	10.2786
chrX	155270560	29107807	0.1875	1.2694
chrY	59373566	1185186	0.02	0.3926

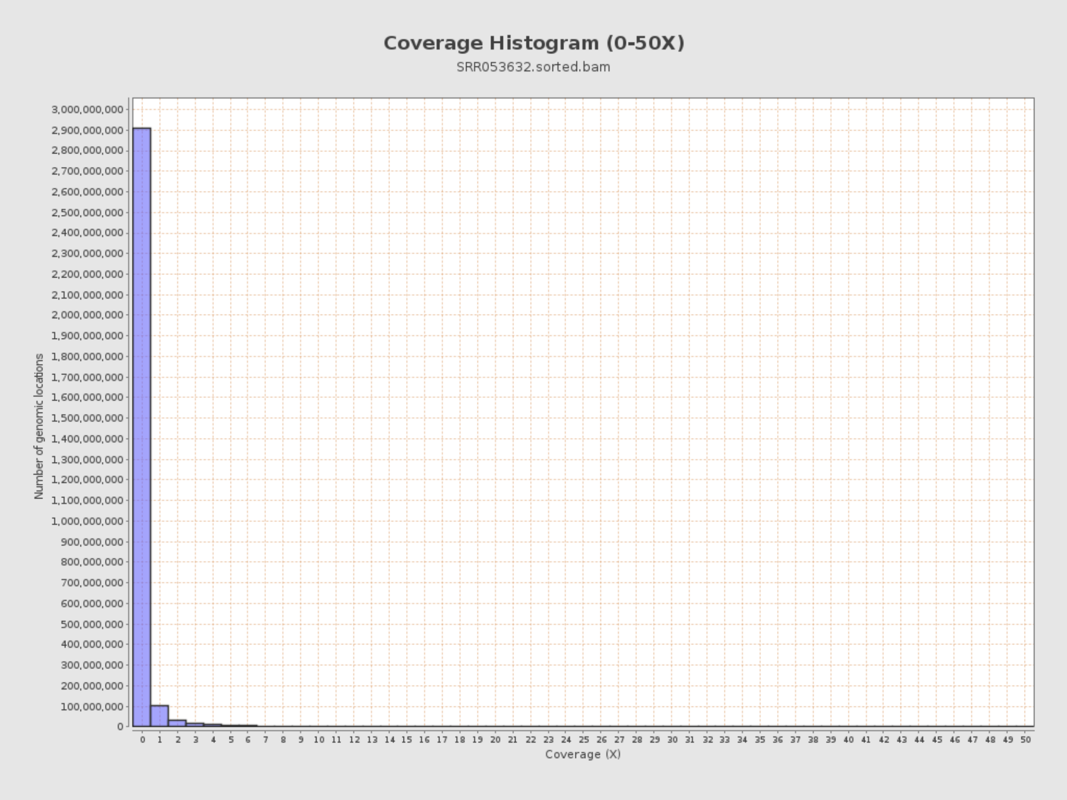
3. Results : Coverage across reference



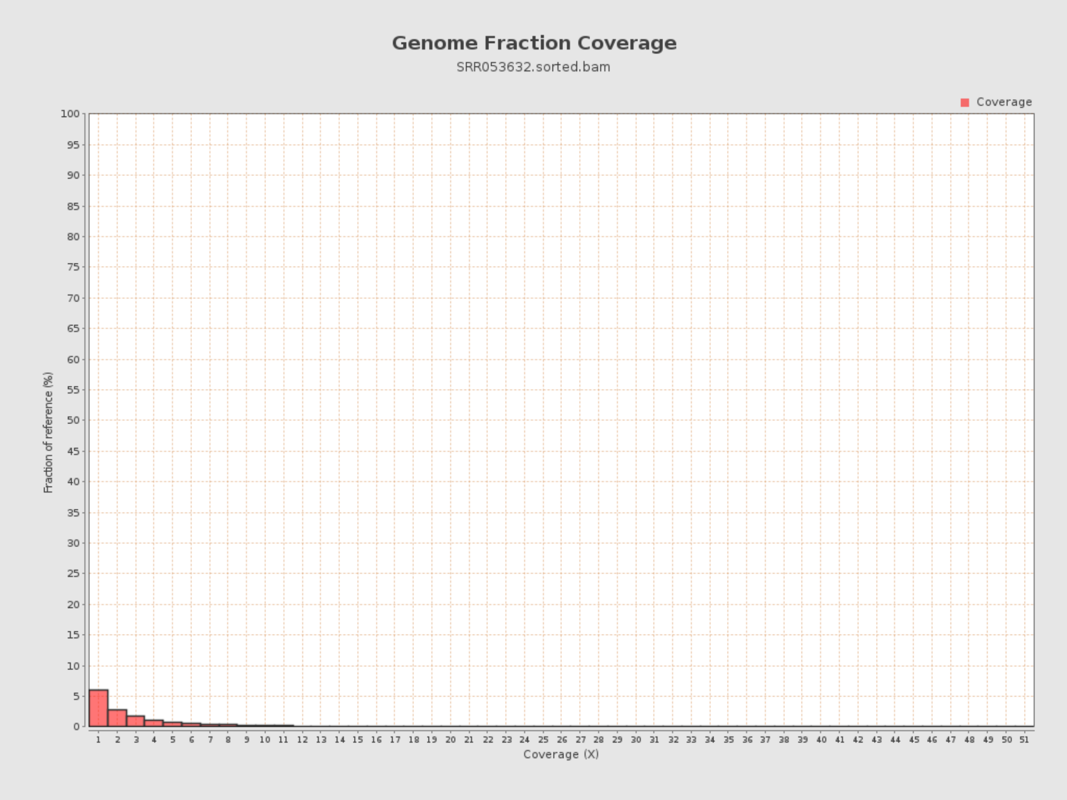
4. Results : Coverage Histogram



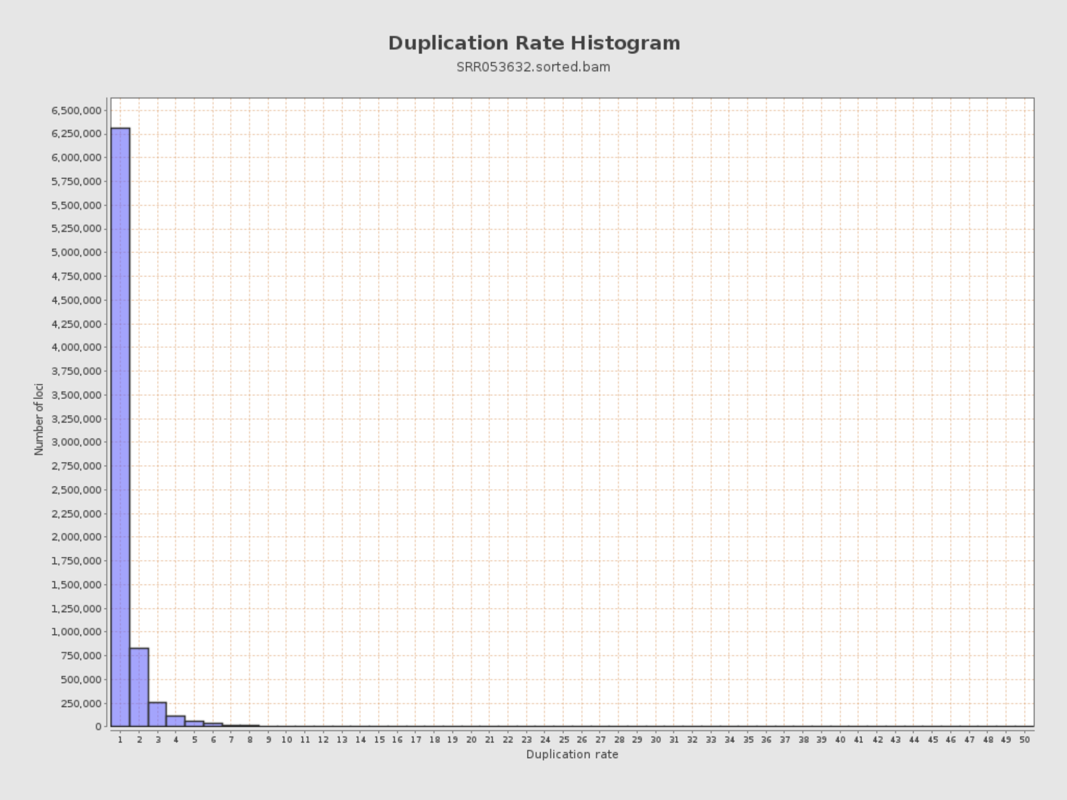
5. Results : Coverage Histogram (0-50X)



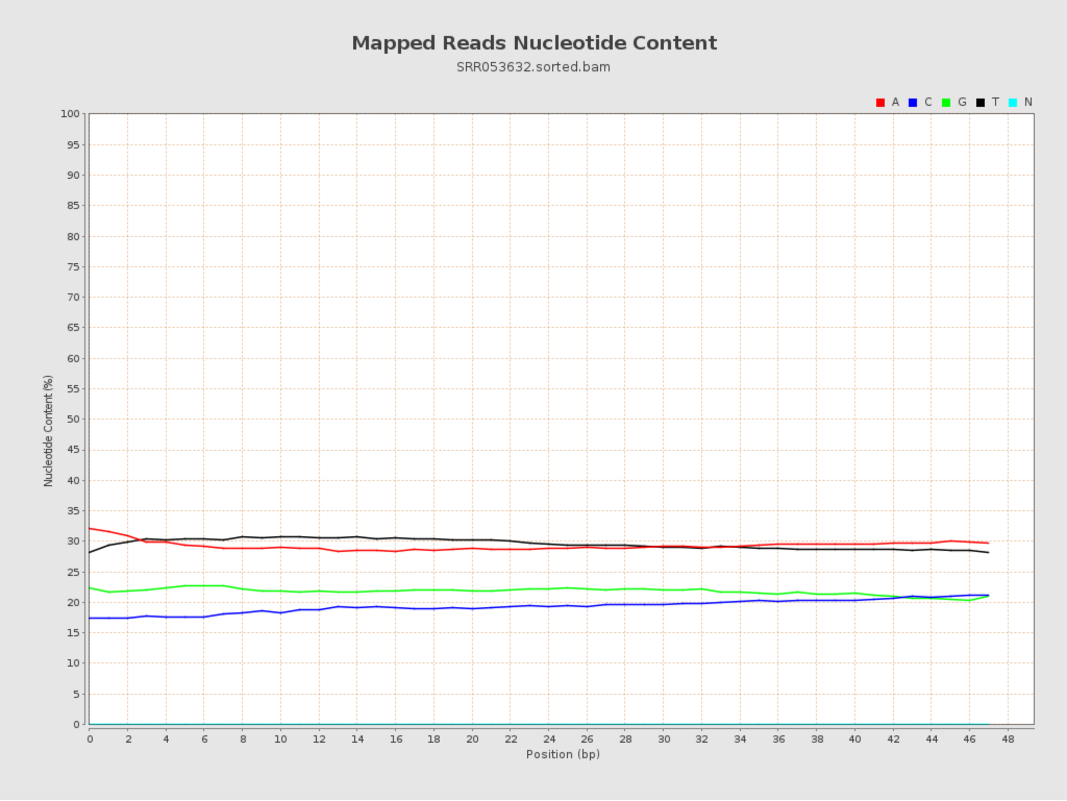
6. Results : Genome Fraction Coverage



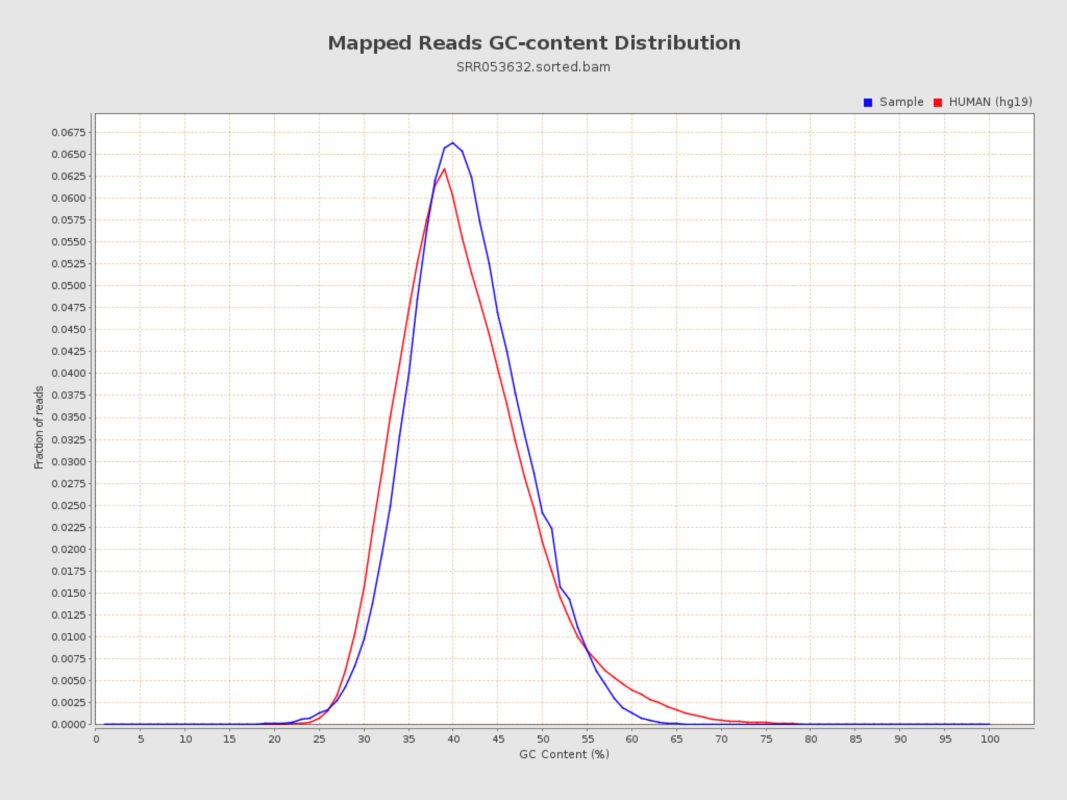
7. Results : Duplication Rate Histogram



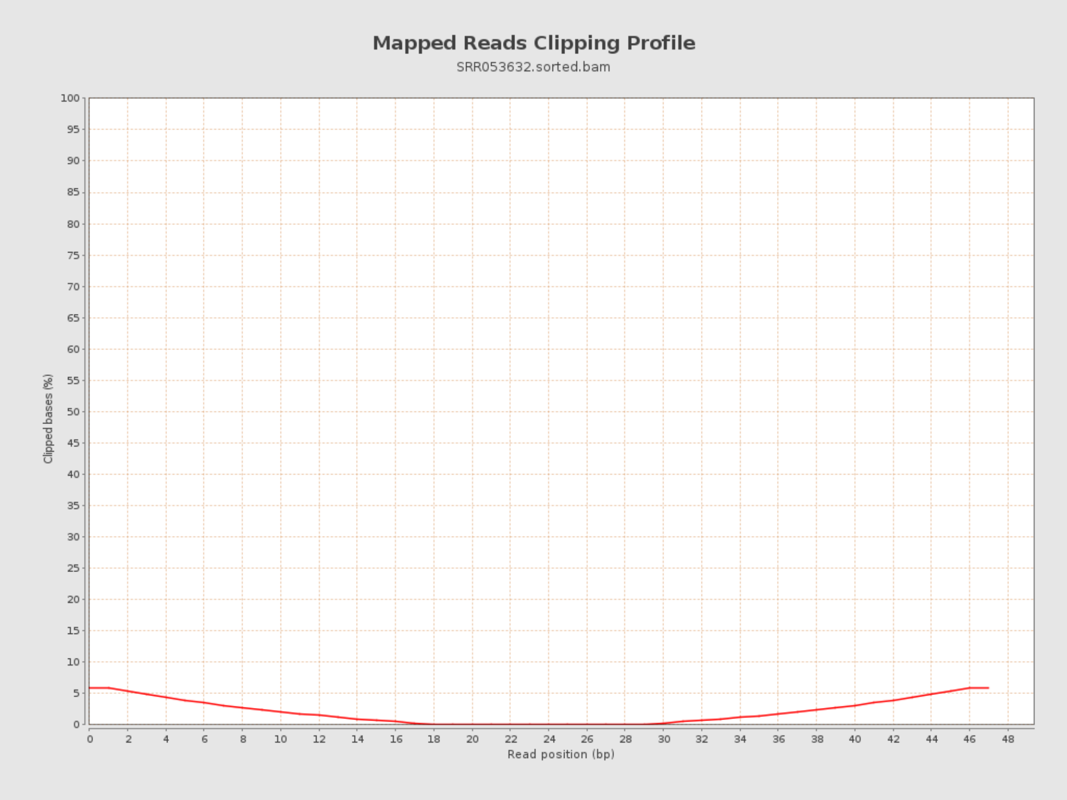
8. Results : Mapped Reads Nucleotide Content



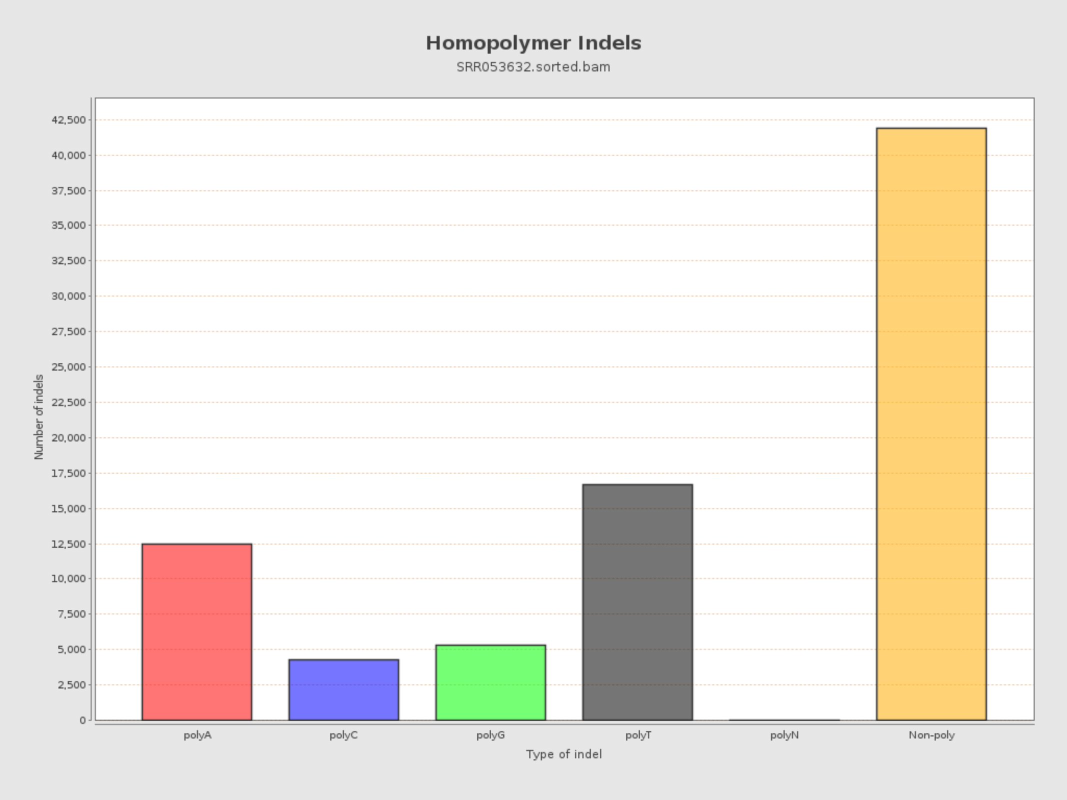
9. Results : Mapped Reads GC-content Distribution



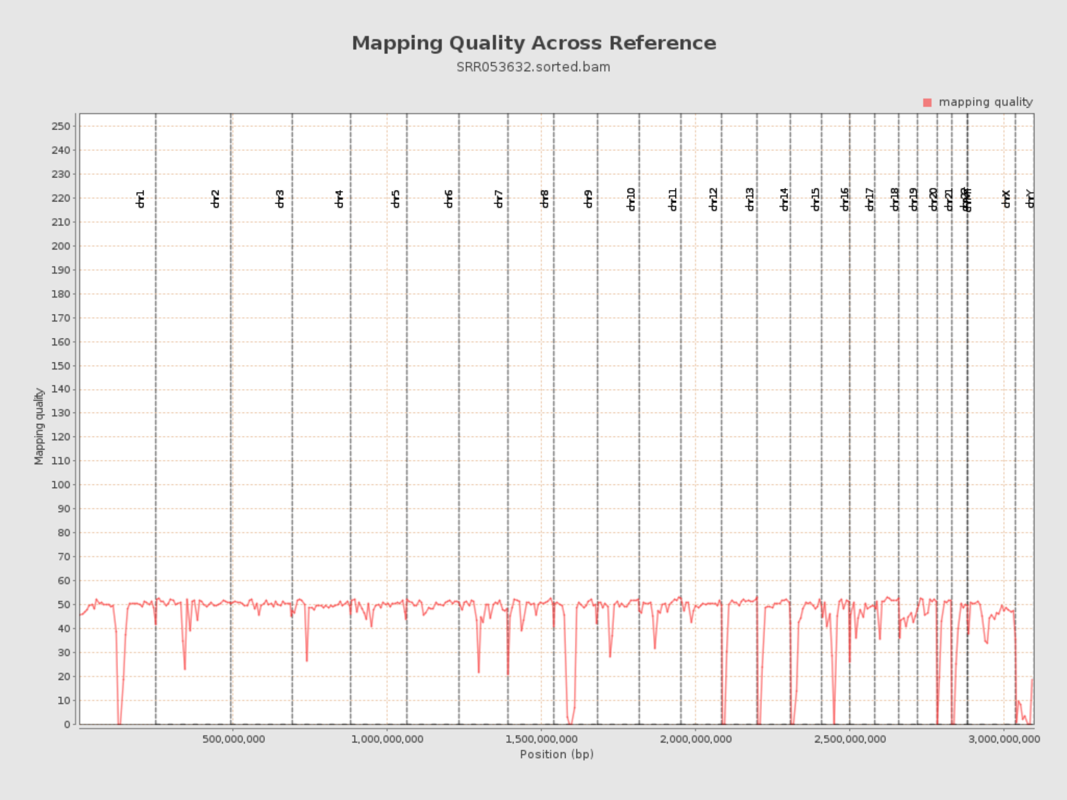
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram