Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:24:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053634.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_SRR053634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:24:47 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,393,961
Mapped reads	11,859,734 / 72.34%
Unmapped reads	4,534,227 / 27.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	364 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,335,511 / 20.35%
Duplication rate	19.9%
Clipped reads	1,251,744 / 7.64%

2.2. ACGT Content

Number/percentage of A's	170,044,719 / 30.5%
Number/percentage of C's	104,870,648 / 18.81%
Number/percentage of T's	169,338,626 / 30.37%
Number/percentage of G's	113,325,665 / 20.32%
Number/percentage of N's	6,309 / 0%
GC Percentage	39.13%

2.3. Coverage

Mean	0.1802

Standard Deviation	1.2769

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

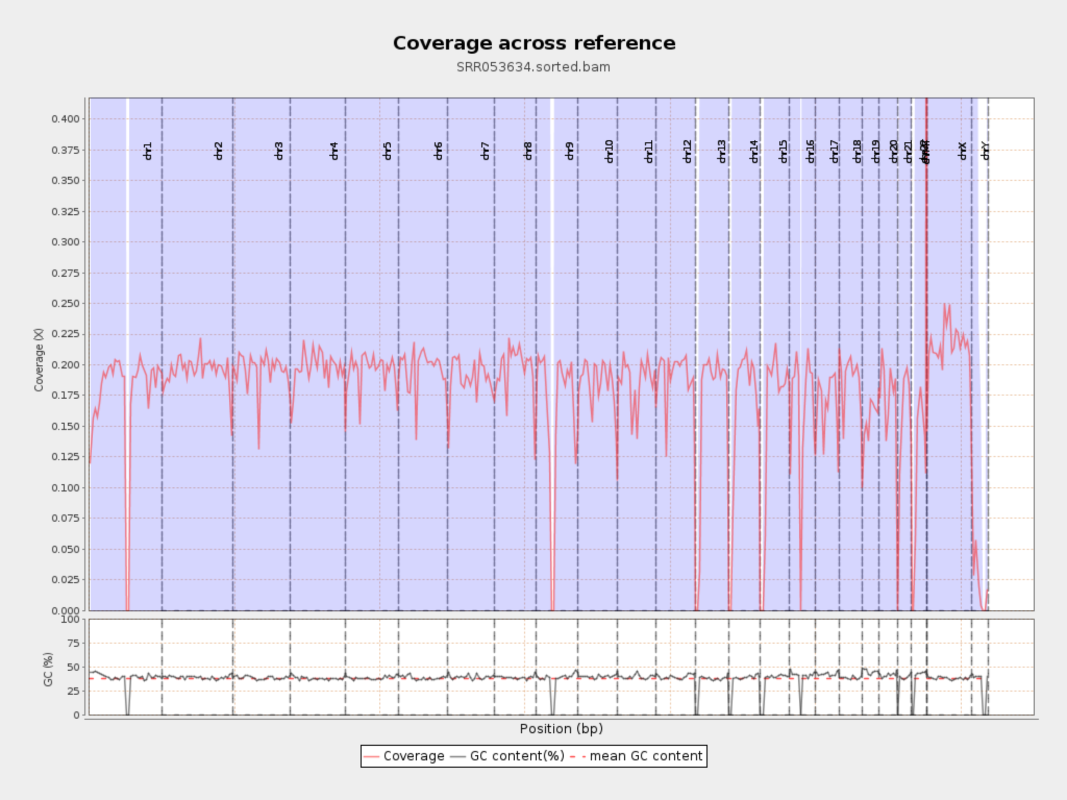
General error rate	0.48%
Mismatches	2,668,130
Insertions	25,218
Mapped reads with at least one insertion	0.21%
Deletions	84,589
Mapped reads with at least one deletion	0.71%
Homopolymer indels	48.47%

2.6. Chromosome stats

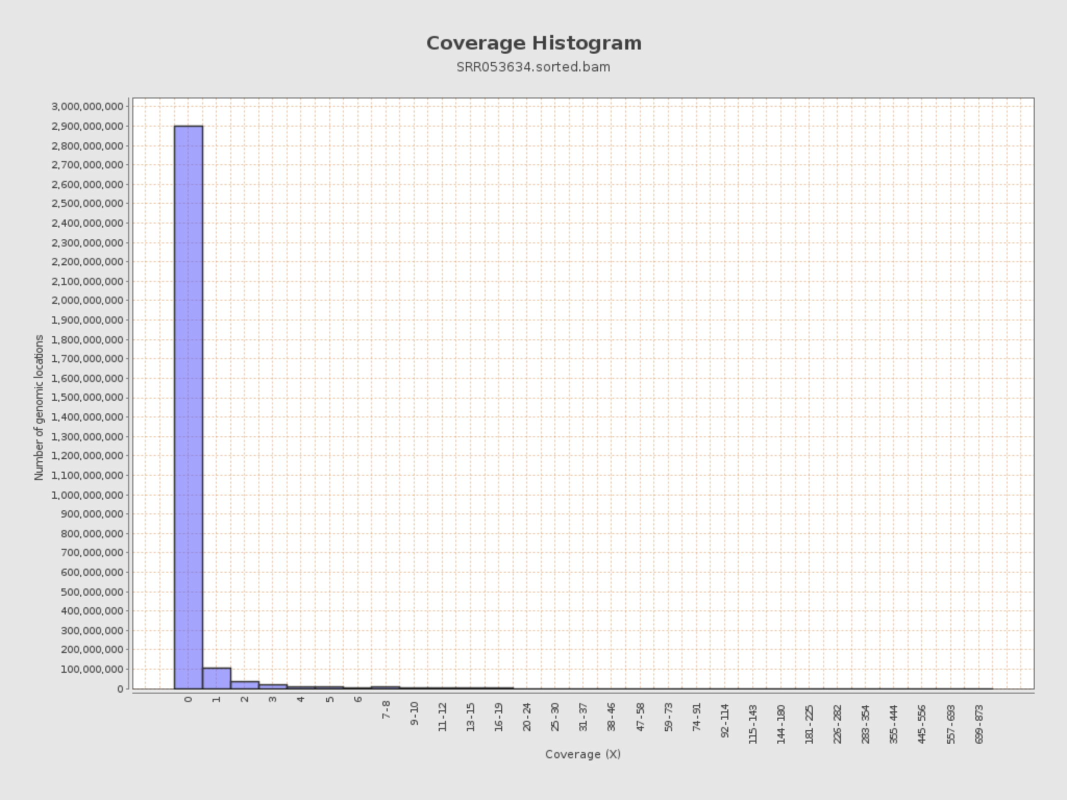
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	43571411	0.1748	1.3563
chr2	243199373	47595765	0.1957	1.3871
chr3	198022430	38861450	0.1962	1.2419
chr4	191154276	37745433	0.1975	1.3333
chr5	180915260	35400363	0.1957	1.2405
chr6	171115067	33685169	0.1969	1.3344
chr7	159138663	30352317	0.1907	1.4006

chr8	146364022	28775811	0.1966	1.418
chr9	141213431	22918063	0.1623	1.1837
chr10	135534747	25331452	0.1869	1.3123
chr11	135006516	25055474	0.1856	1.3211
chr12	133851895	25606028	0.1913	1.2388
chr13	115169878	18631147	0.1618	1.1387
chr14	107349540	17112413	0.1594	1.2155
chr15	102531392	15942838	0.1555	1.1035
chr16	90354753	14856590	0.1644	1.1747
chr17	81195210	13574074	0.1672	1.1136
chr18	78077248	14779145	0.1893	1.422
chr19	59128983	9191596	0.1554	1.2126
chr20	63025520	11111279	0.1763	1.1716
chr21	48129895	7125002	0.148	1.1272
chr22	51304566	5639759	0.1099	0.8844
chrMT	16571	29567	1.7843	3.7788
chrX	155270560	33447265	0.2154	1.4085
chrY	59373566	1372205	0.0231	0.4576

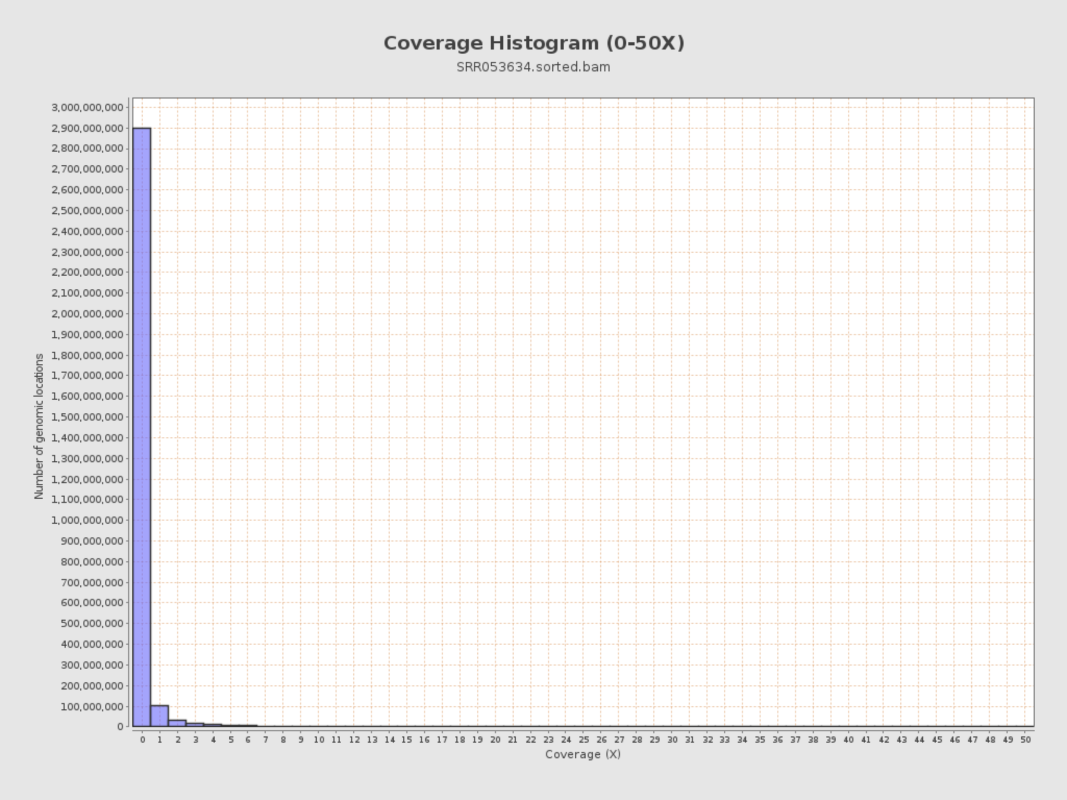
3. Results : Coverage across reference



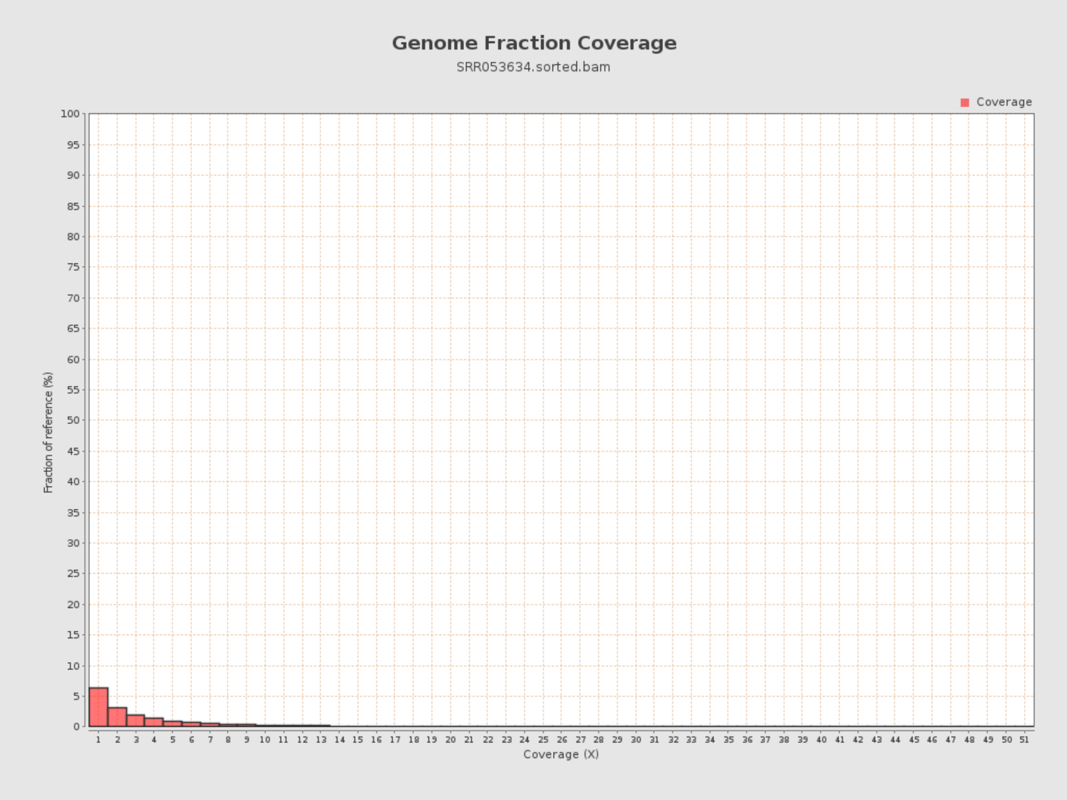
4. Results : Coverage Histogram



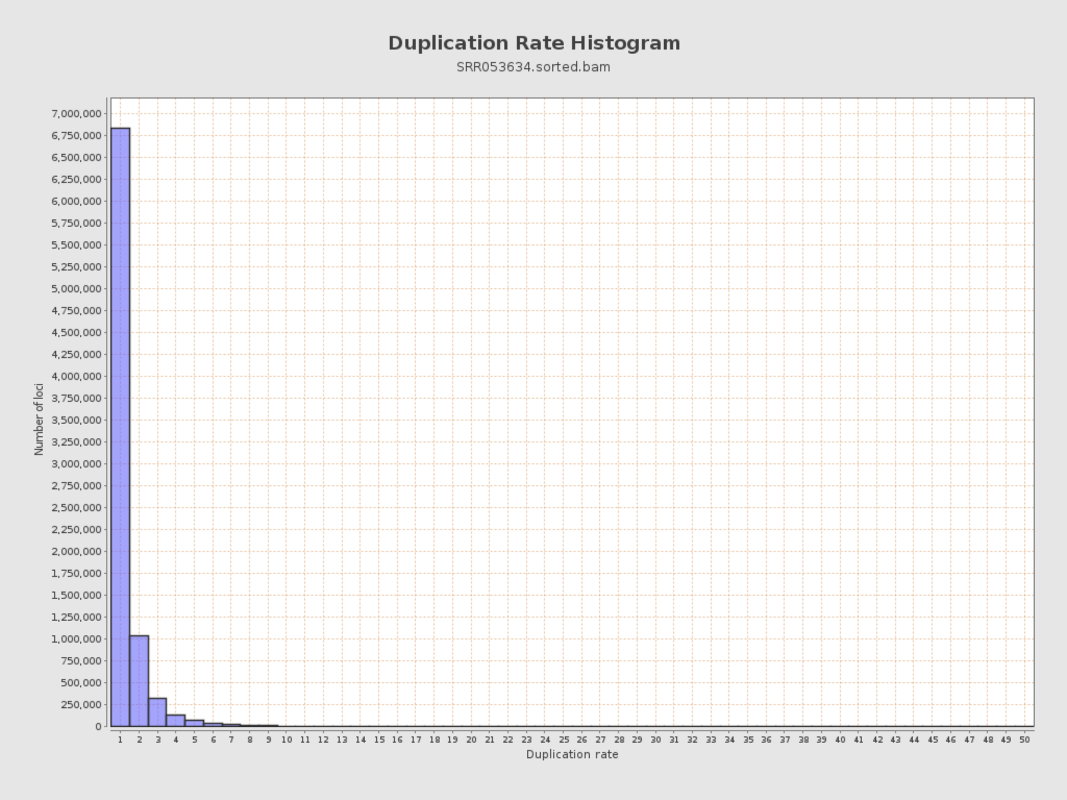
5. Results : Coverage Histogram (0-50X)



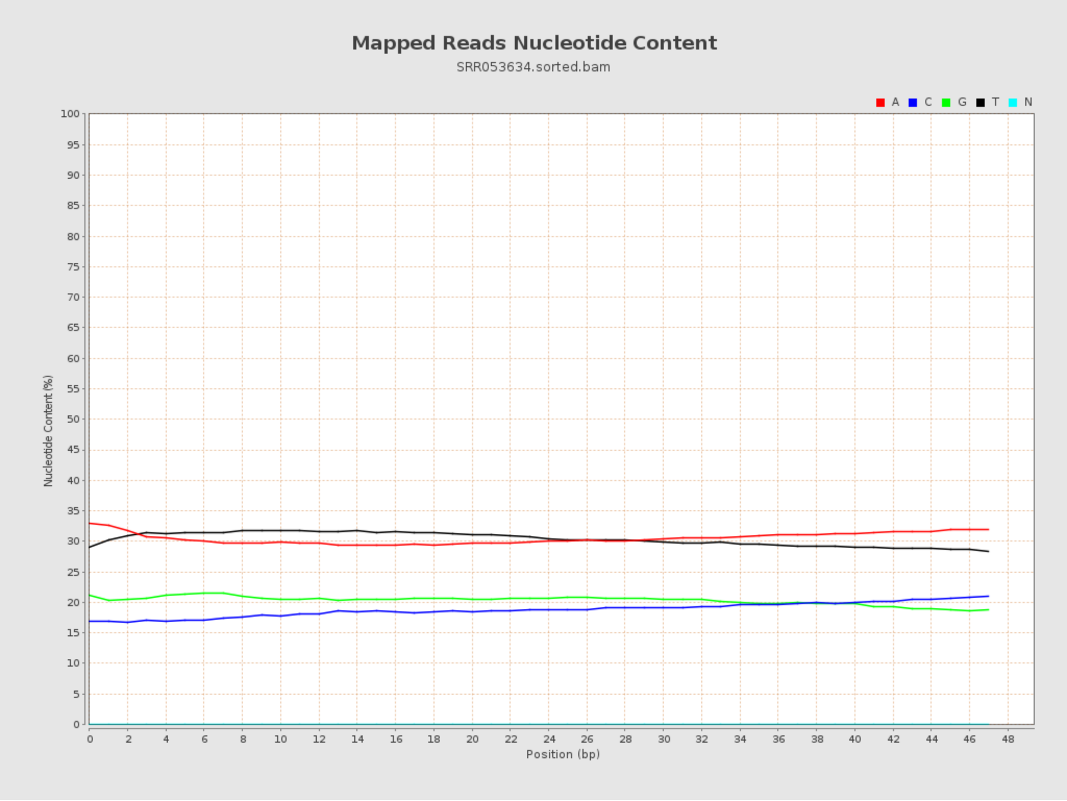
6. Results : Genome Fraction Coverage



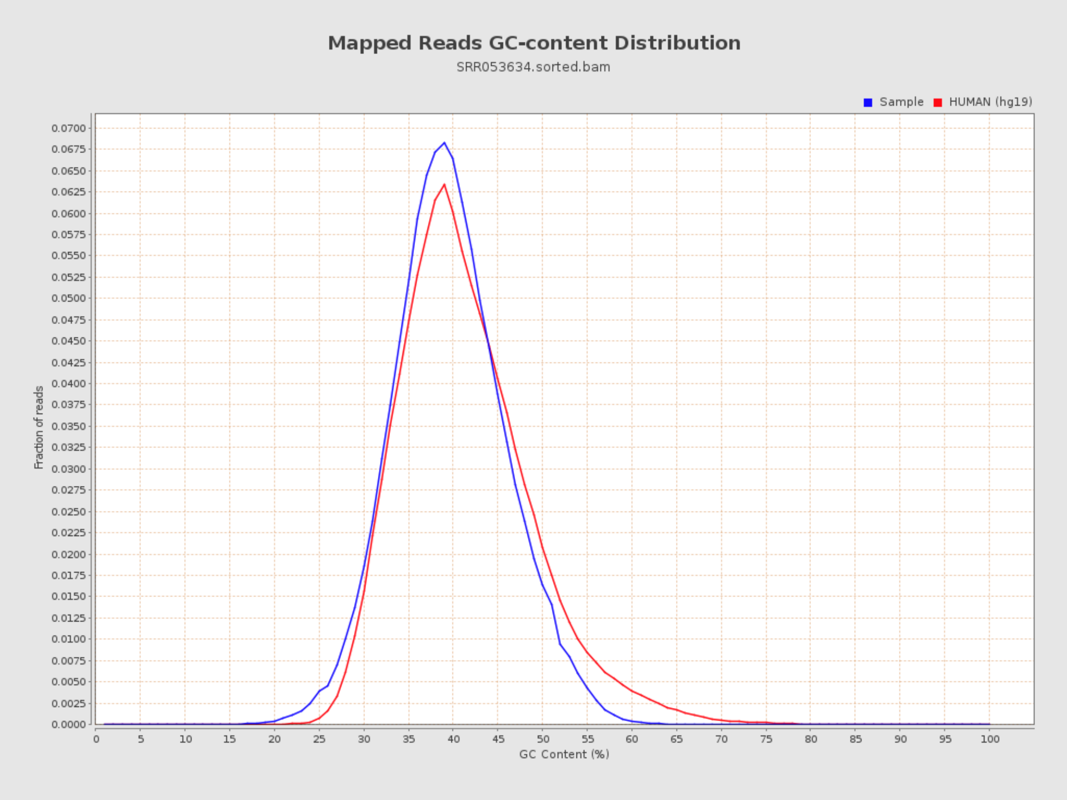
7. Results : Duplication Rate Histogram



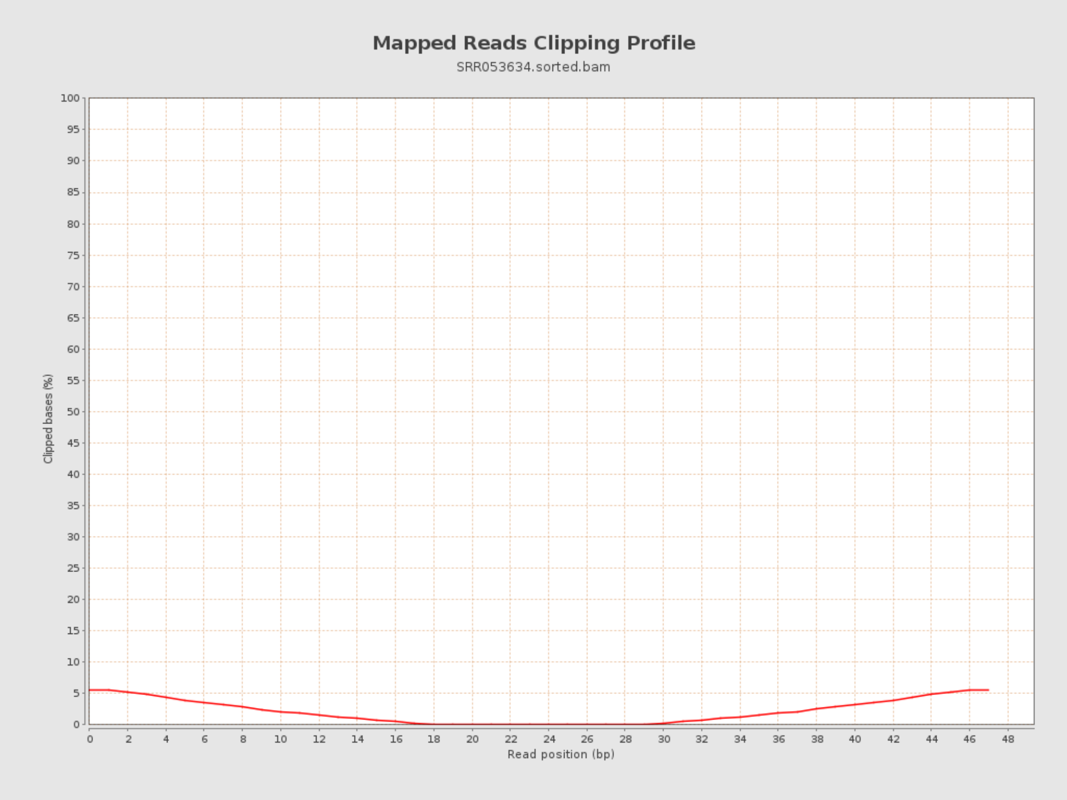
8. Results : Mapped Reads Nucleotide Content



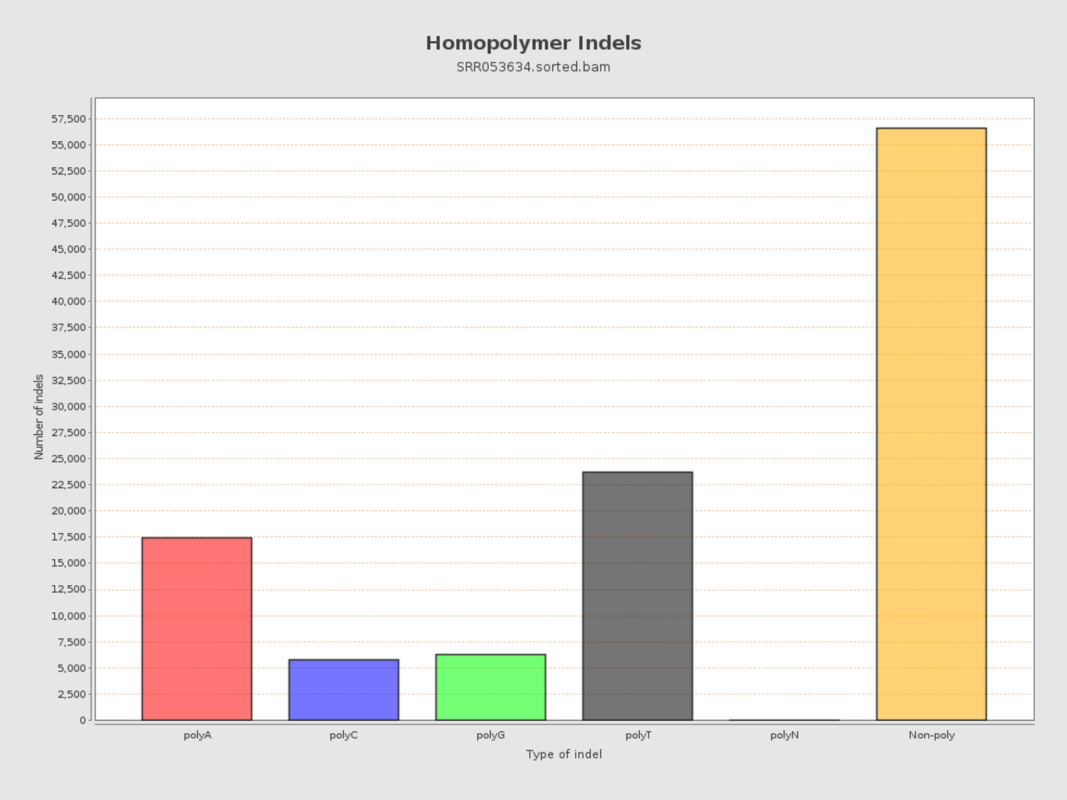
9. Results : Mapped Reads GC-content Distribution



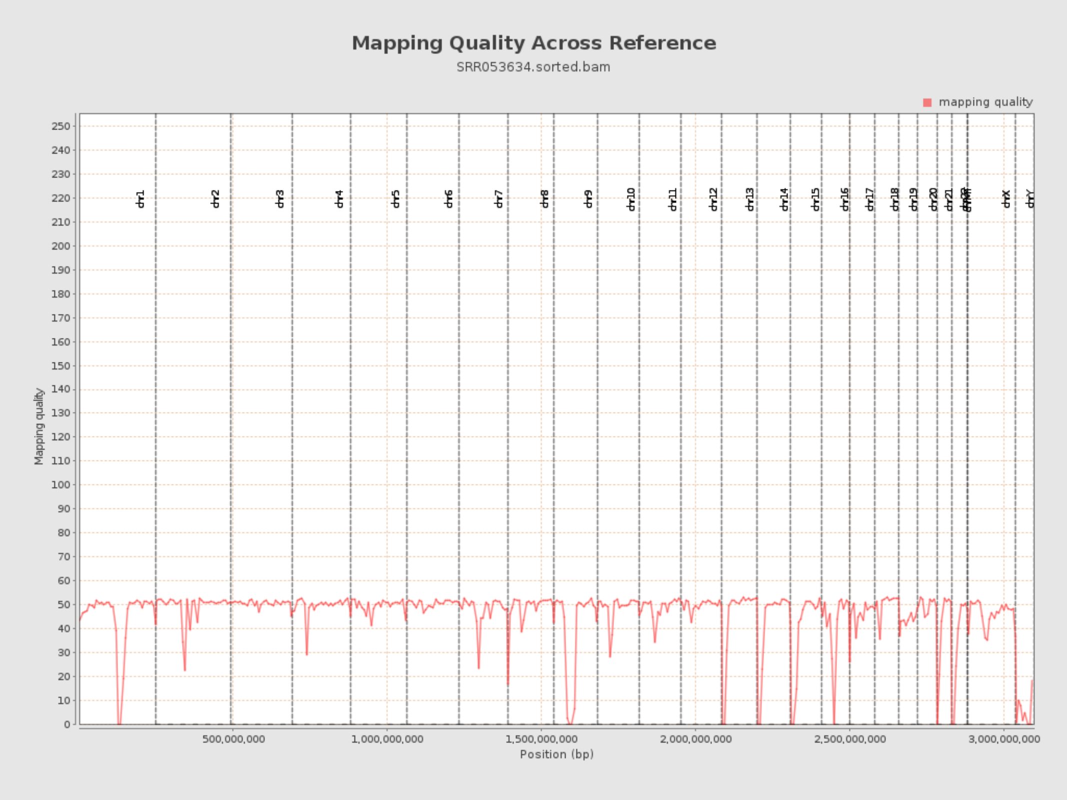
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram