Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 09:06:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054634.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_SRR054634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 09:06:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,243,310
Mapped reads	10,738,044 / 81.08%
Unmapped reads	2,505,266 / 18.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	291 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,443,015 / 18.45%
Duplication rate	16.5%
Clipped reads	829,079 / 6.26%

2.2. ACGT Content

Number/percentage of A's	150,429,895 / 29.62%
Number/percentage of C's	95,998,351 / 18.9%
Number/percentage of T's	154,448,920 / 30.42%
Number/percentage of G's	106,833,389 / 21.04%
Number/percentage of N's	87,385 / 0.02%
GC Percentage	39.94%

2.3. Coverage

Mean	0.1641

Standard Deviation	1.2474

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

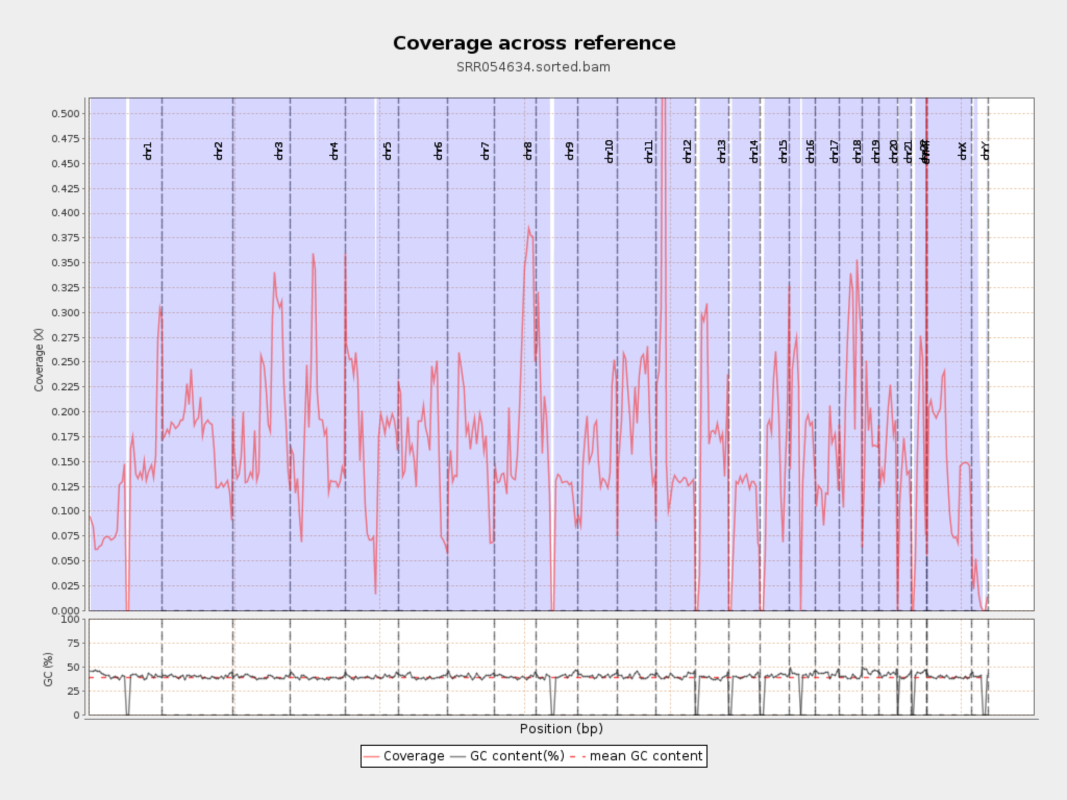
General error rate	0.47%
Mismatches	2,349,742
Insertions	20,638
Mapped reads with at least one insertion	0.19%
Deletions	73,361
Mapped reads with at least one deletion	0.68%
Homopolymer indels	49.05%

2.6. Chromosome stats

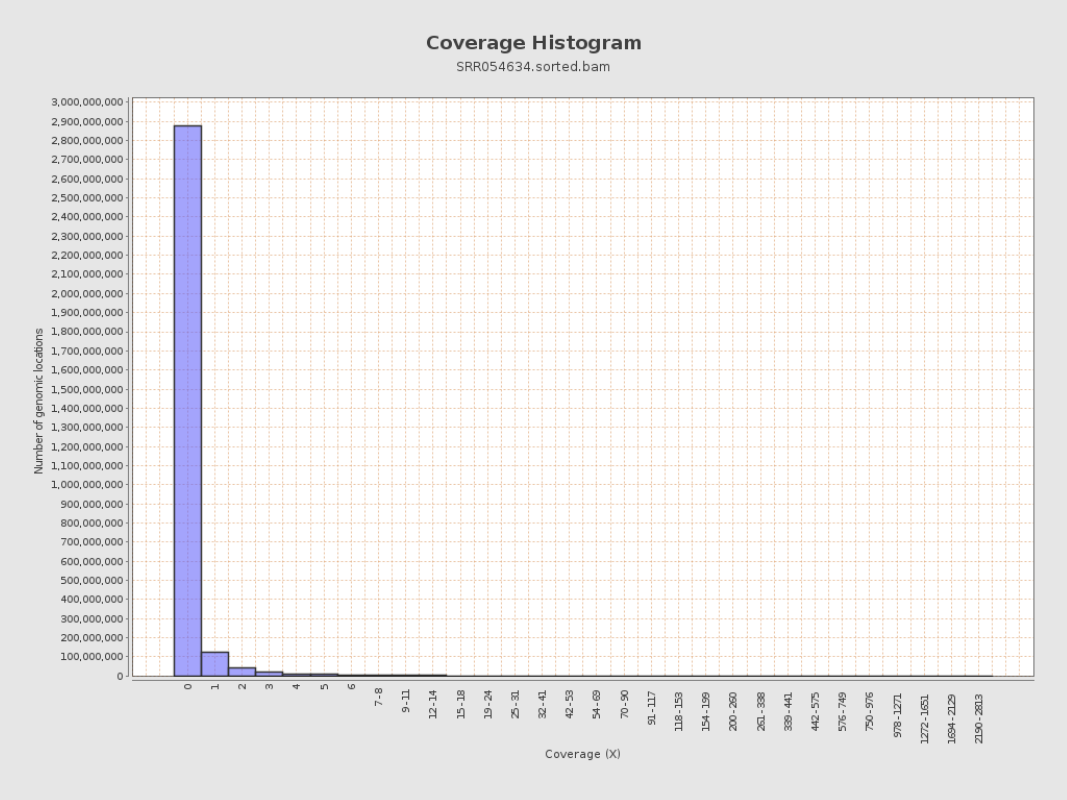
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28875678	0.1158	1.1138
chr2	243199373	42619036	0.1752	1.1496
chr3	198022430	39410029	0.199	1.6023
chr4	191154276	32697726	0.1711	1.2408
chr5	180915260	31223158	0.1726	1.0031
chr6	171115067	28479374	0.1664	1.0854
chr7	159138663	26499832	0.1665	1.1058

chr8	146364022	31818726	0.2174	1.2688
chr9	141213431	19622554	0.139	1.7768
chr10	135534747	21680938	0.16	1.1215
chr11	135006516	27482565	0.2036	1.2942
chr12	133851895	26175965	0.1956	1.3494
chr13	115169878	19912748	0.1729	1.2976
chr14	107349540	11053430	0.103	0.8154
chr15	102531392	15103450	0.1473	0.9184
chr16	90354753	16597736	0.1837	1.1744
chr17	81195210	11080547	0.1365	2.1805
chr18	78077248	19332283	0.2476	1.4518
chr19	59128983	10347140	0.175	1.2622
chr20	63025520	10627378	0.1686	1.0183
chr21	48129895	5889628	0.1224	0.9252
chr22	51304566	6765874	0.1319	0.8574
chrMT	16571	19683	1.1878	2.9684
chrX	155270560	23604636	0.152	1.1435
chrY	59373566	987375	0.0166	0.429

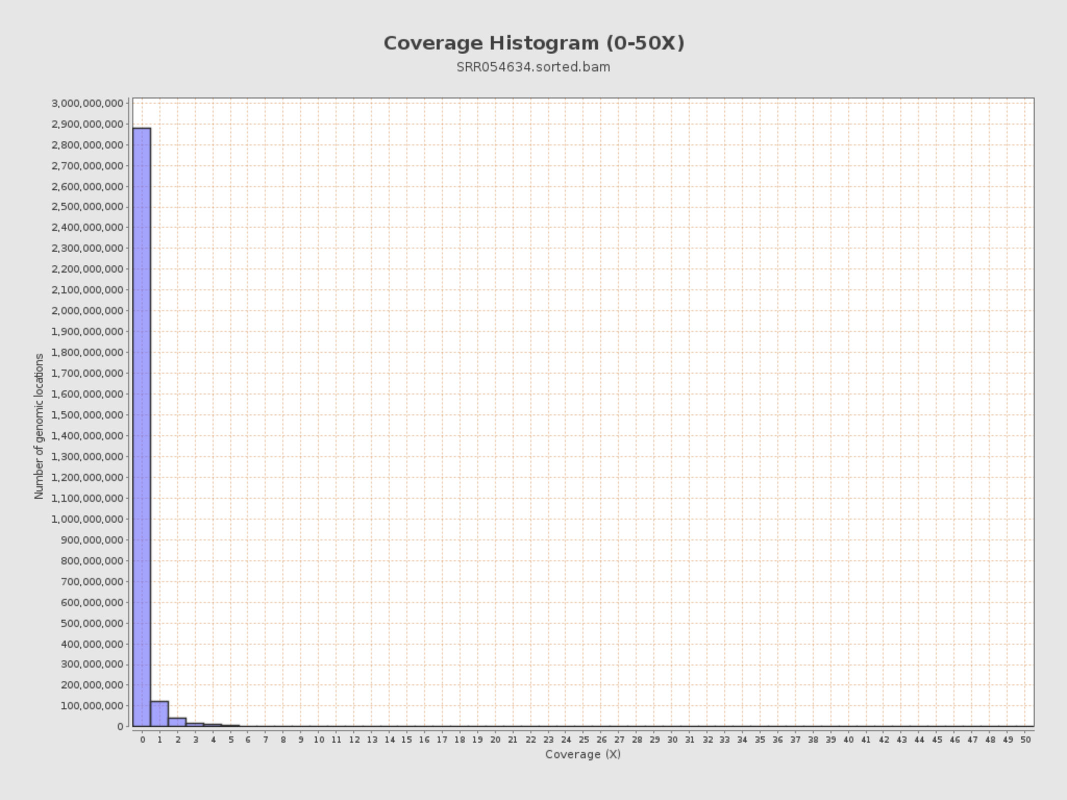
3. Results : Coverage across reference



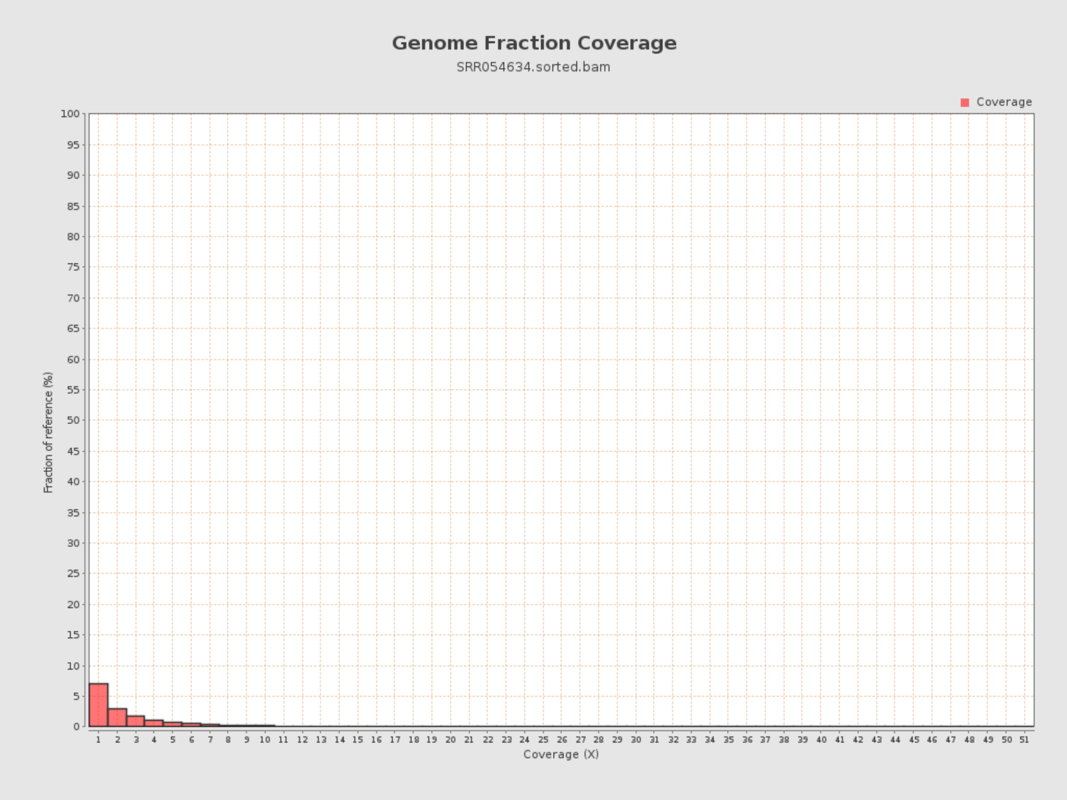
4. Results : Coverage Histogram



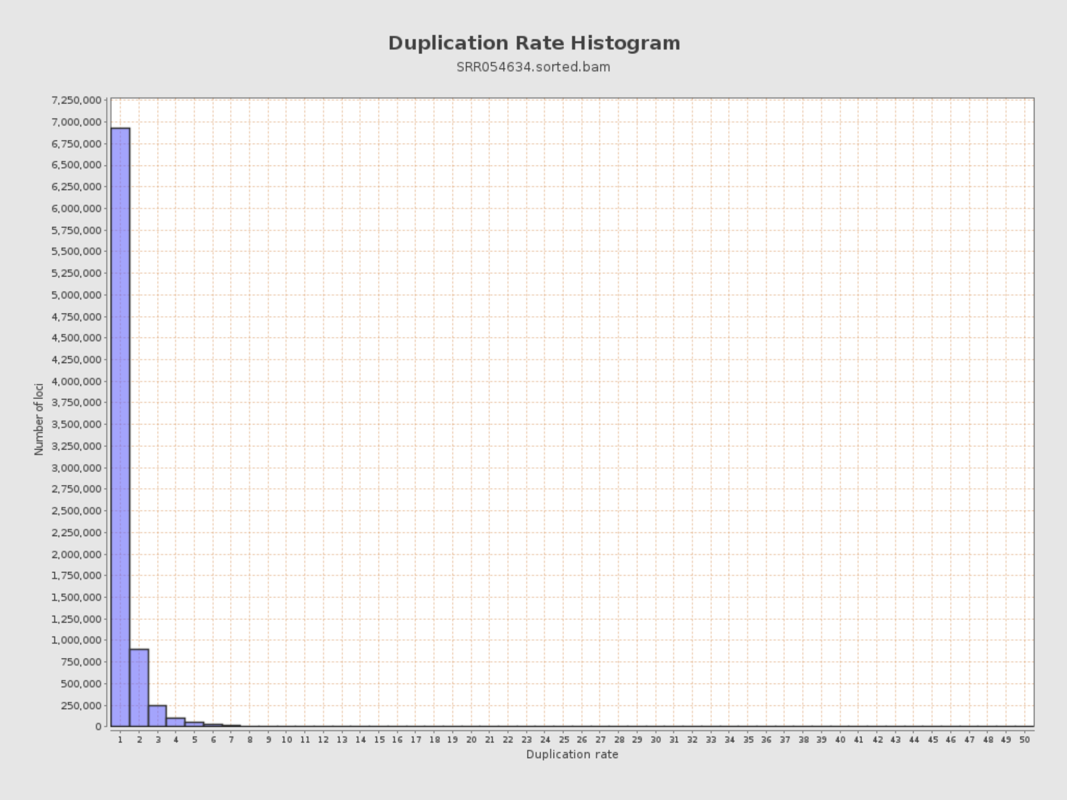
5. Results : Coverage Histogram (0-50X)



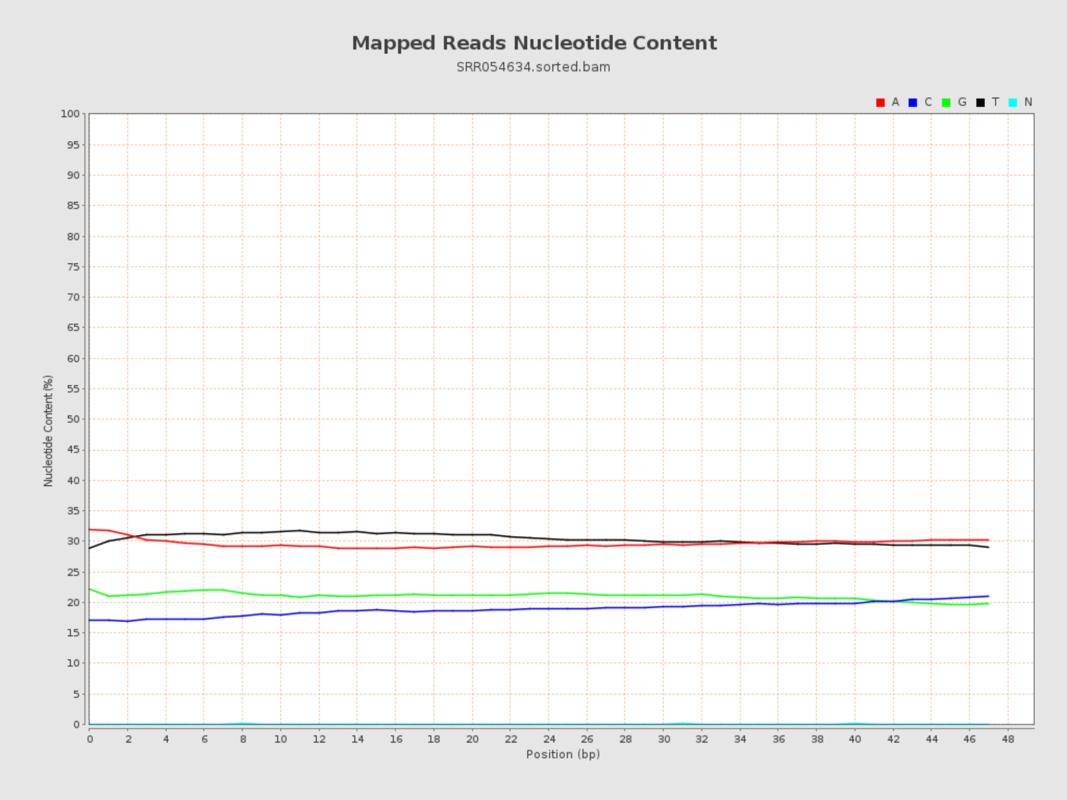
6. Results : Genome Fraction Coverage



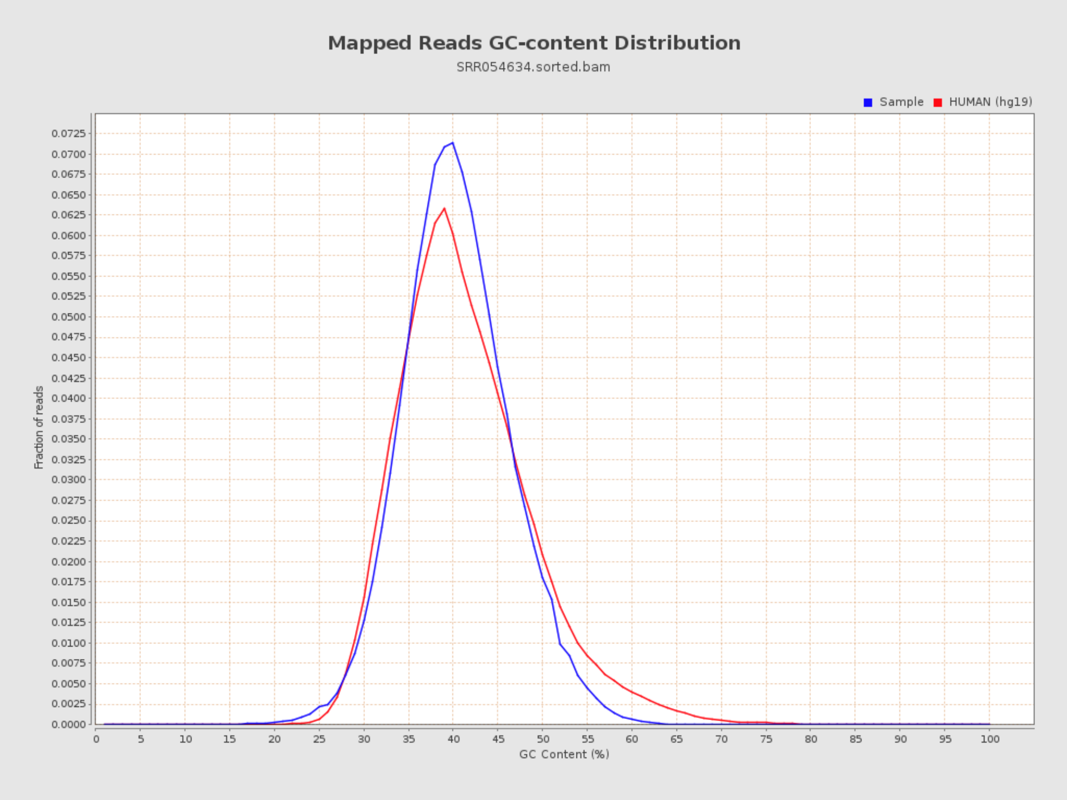
7. Results : Duplication Rate Histogram



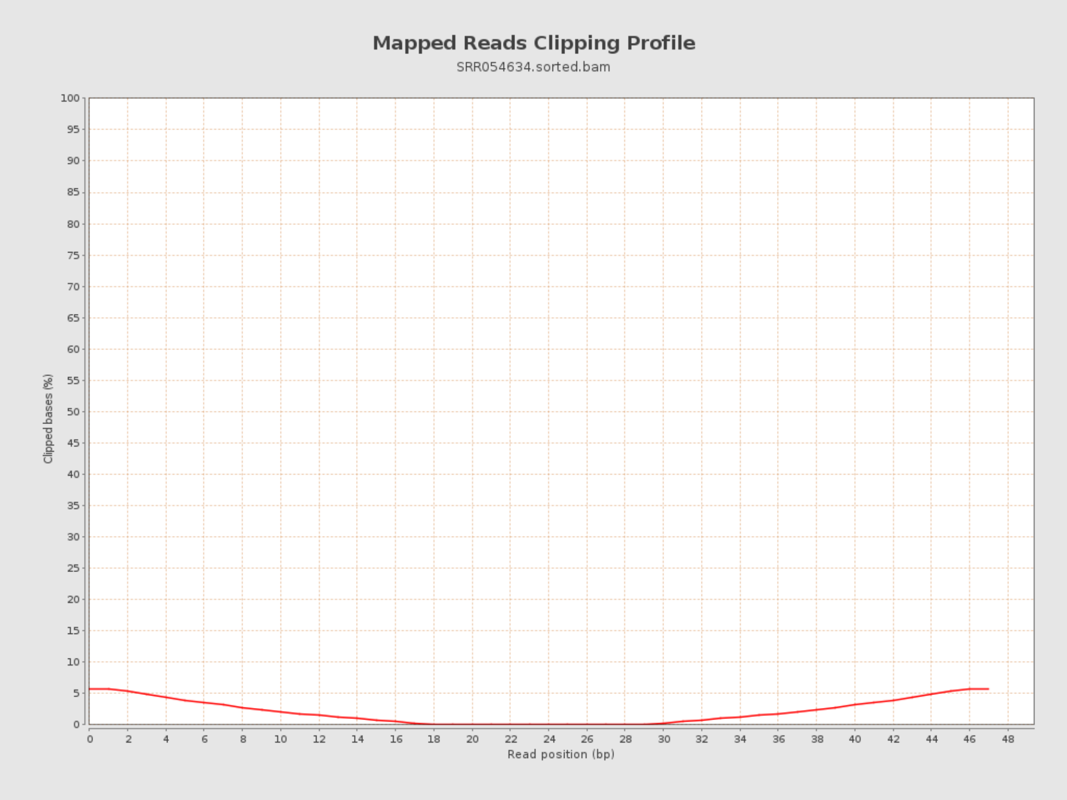
8. Results : Mapped Reads Nucleotide Content



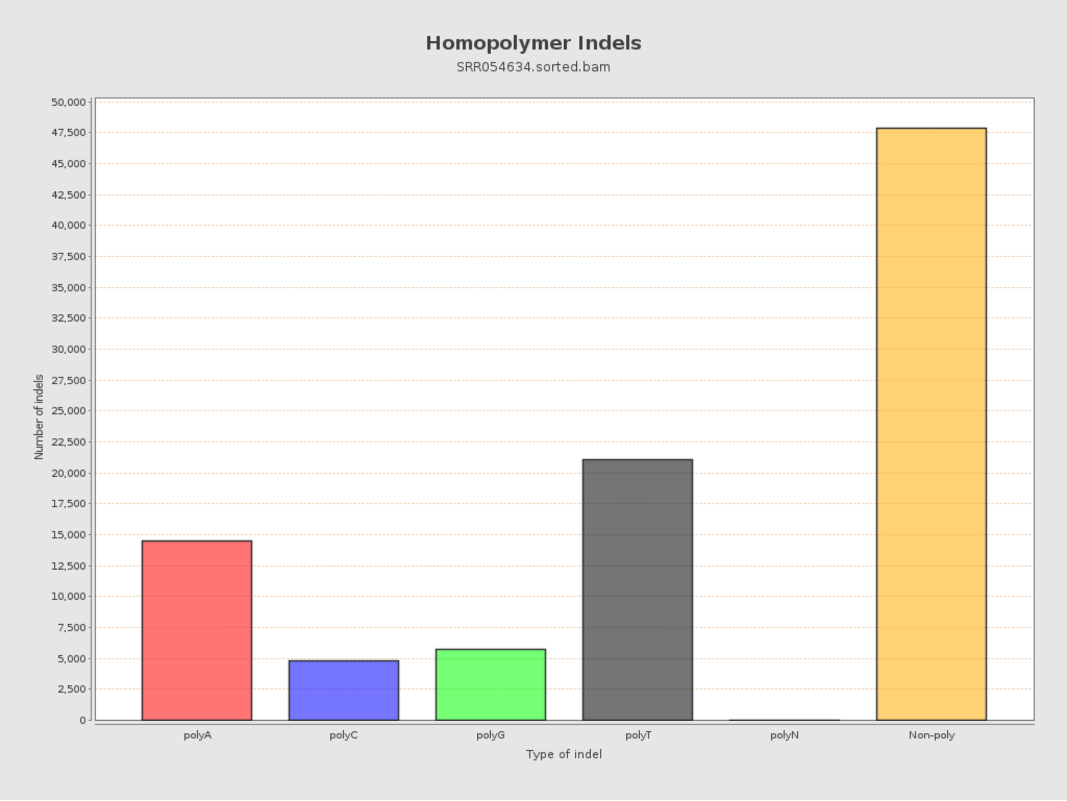
9. Results : Mapped Reads GC-content Distribution



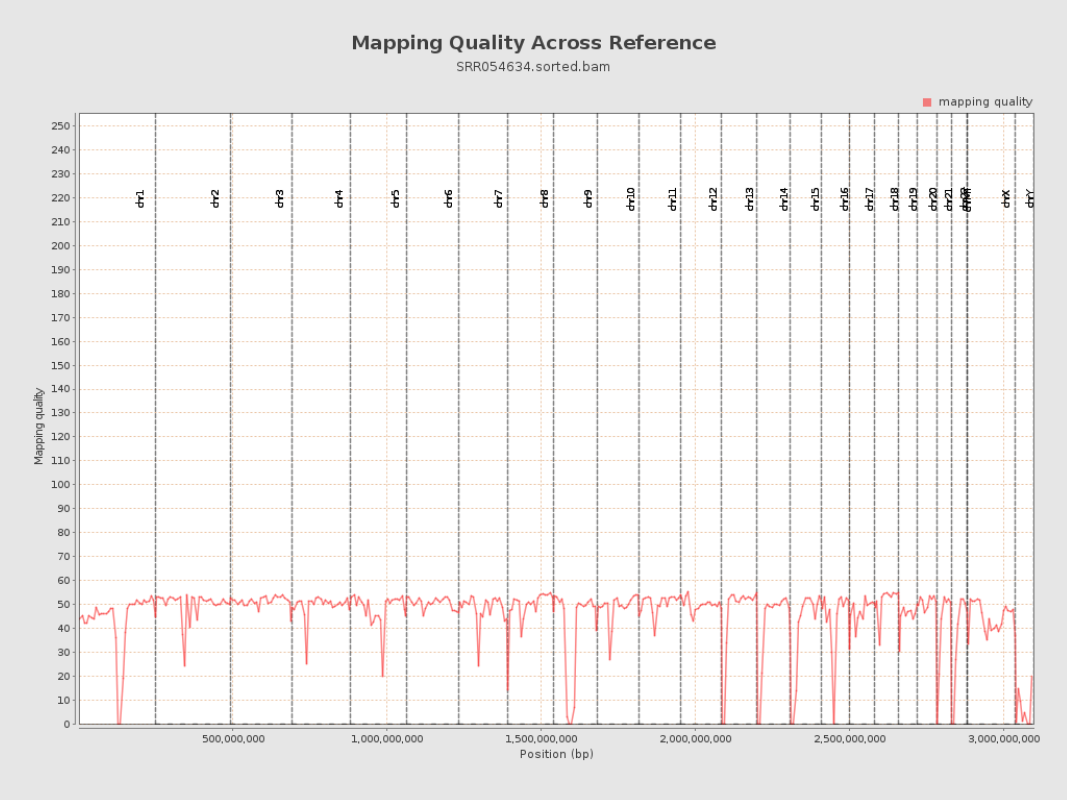
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram