Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 03:42:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006434.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_SRR1006434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006434.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 03:42:11 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006434.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,249,204
Mapped reads	1,050,869 / 84.12%
Unmapped reads	198,335 / 15.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,473 / 0.2%
Read min/max/mean length	30 / 59 / 59.06
Duplicated reads (estimated)	70,035 / 5.61%
Duplication rate	5.96%
Clipped reads	314,237 / 25.15%

2.2. ACGT Content

Number/percentage of A's	16,233,523 / 27.93%
Number/percentage of C's	12,592,878 / 21.67%
Number/percentage of T's	16,581,582 / 28.53%
Number/percentage of G's	12,709,049 / 21.87%
Number/percentage of N's	2,641 / 0%
GC Percentage	43.53%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2481

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

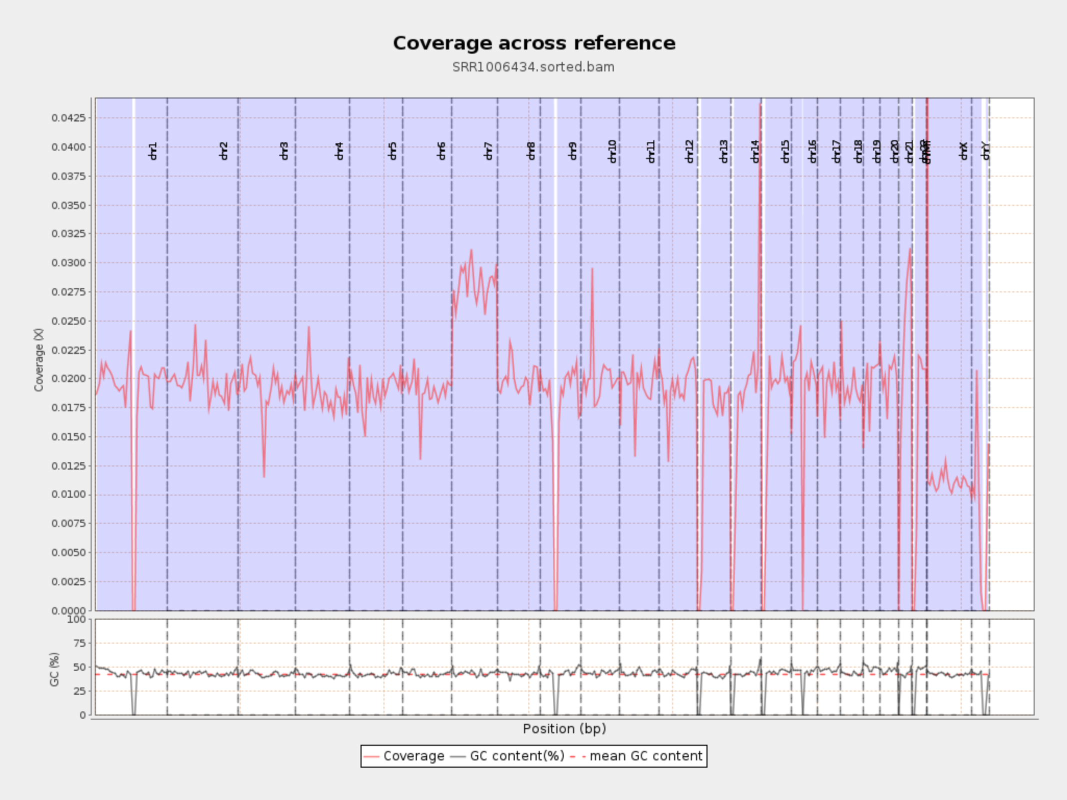
General error rate	0.44%
Mismatches	246,367
Insertions	4,684
Mapped reads with at least one insertion	0.44%
Deletions	10,982
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.93%

2.6. Chromosome stats

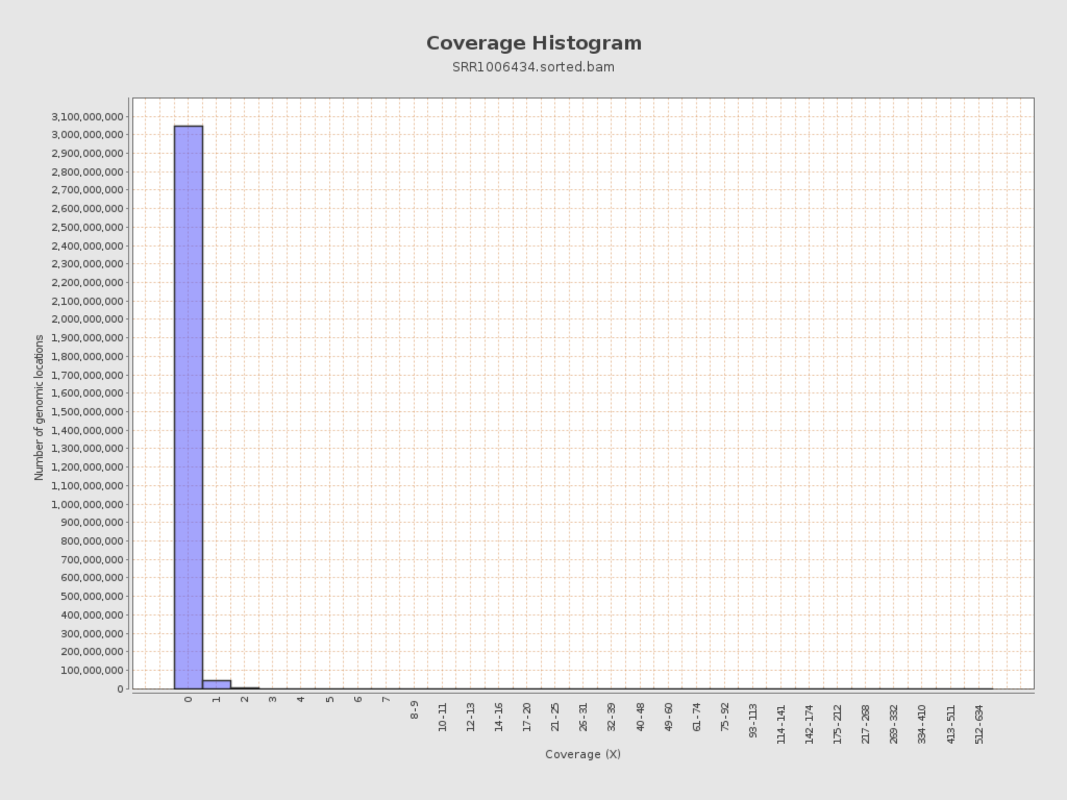
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4663577	0.0187	0.2022
chr2	243199373	4820181	0.0198	0.1718
chr3	198022430	3785846	0.0191	0.1534
chr4	191154276	3616587	0.0189	0.1563
chr5	180915260	3450814	0.0191	0.1528
chr6	171115067	3254643	0.019	0.1843
chr7	159138663	4491831	0.0282	0.219

chr8	146364022	2910114	0.0199	0.3844
chr9	141213431	2397391	0.017	0.1574
chr10	135534747	2744324	0.0202	0.1811
chr11	135006516	2634780	0.0195	0.1651
chr12	133851895	2585348	0.0193	0.1545
chr13	115169878	1795735	0.0156	0.1384
chr14	107349540	1935489	0.018	0.8961
chr15	102531392	1691476	0.0165	0.1424
chr16	90354753	1713594	0.019	0.1627
chr17	81195210	1578847	0.0194	0.1624
chr18	78077248	1514093	0.0194	0.191
chr19	59128983	1176440	0.0199	0.1923
chr20	63025520	1262341	0.02	0.2232
chr21	48129895	1071065	0.0223	0.1741
chr22	51304566	746650	0.0146	0.1502
chrMT	16571	79314	4.7863	4.4639
chrX	155270560	1721332	0.0111	0.1183
chrY	59373566	495622	0.0083	0.1323

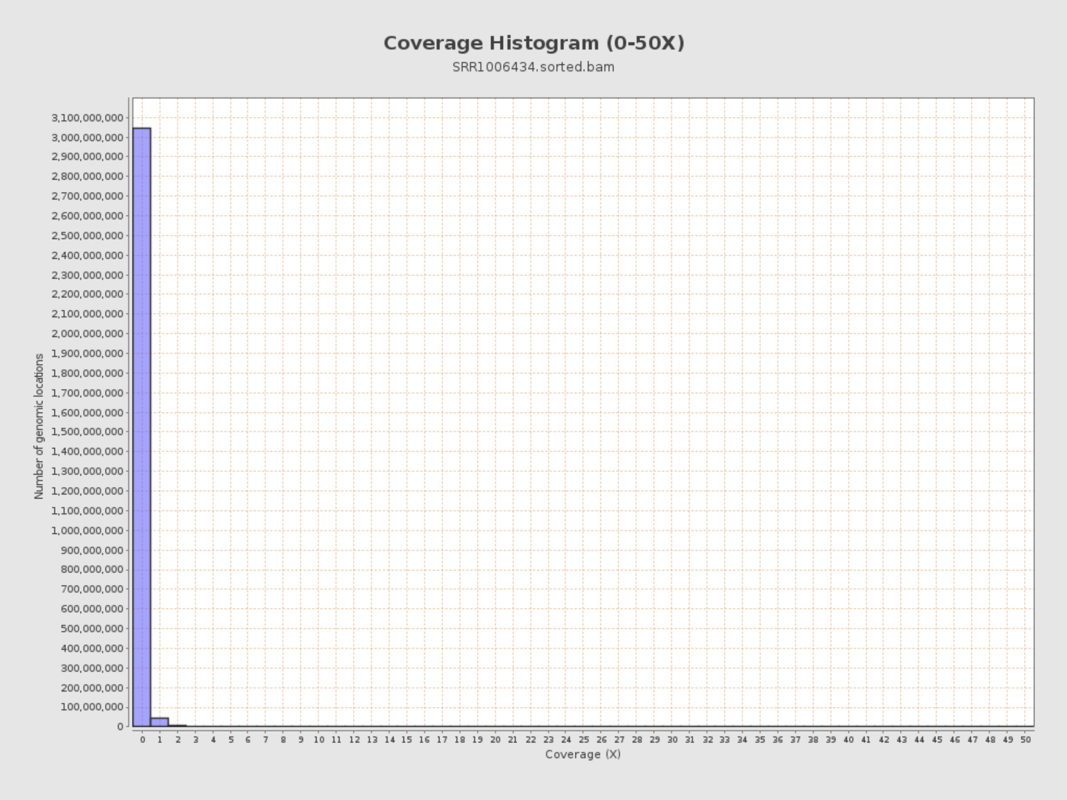
3. Results : Coverage across reference



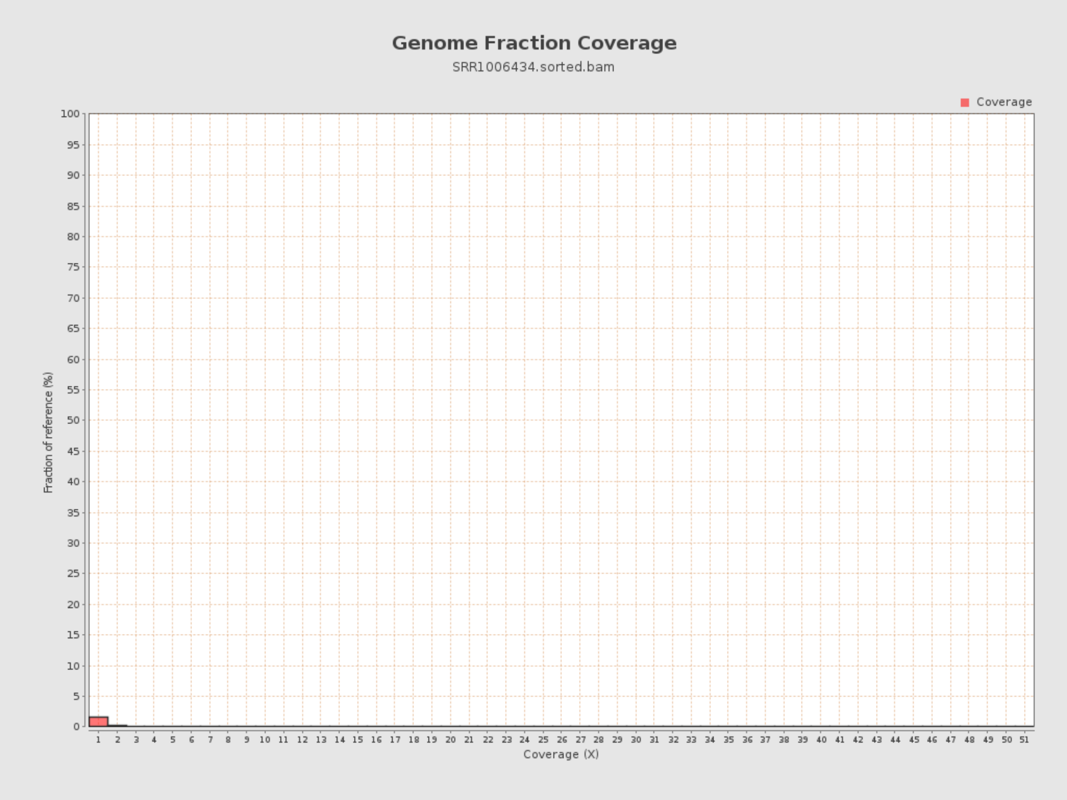
4. Results : Coverage Histogram



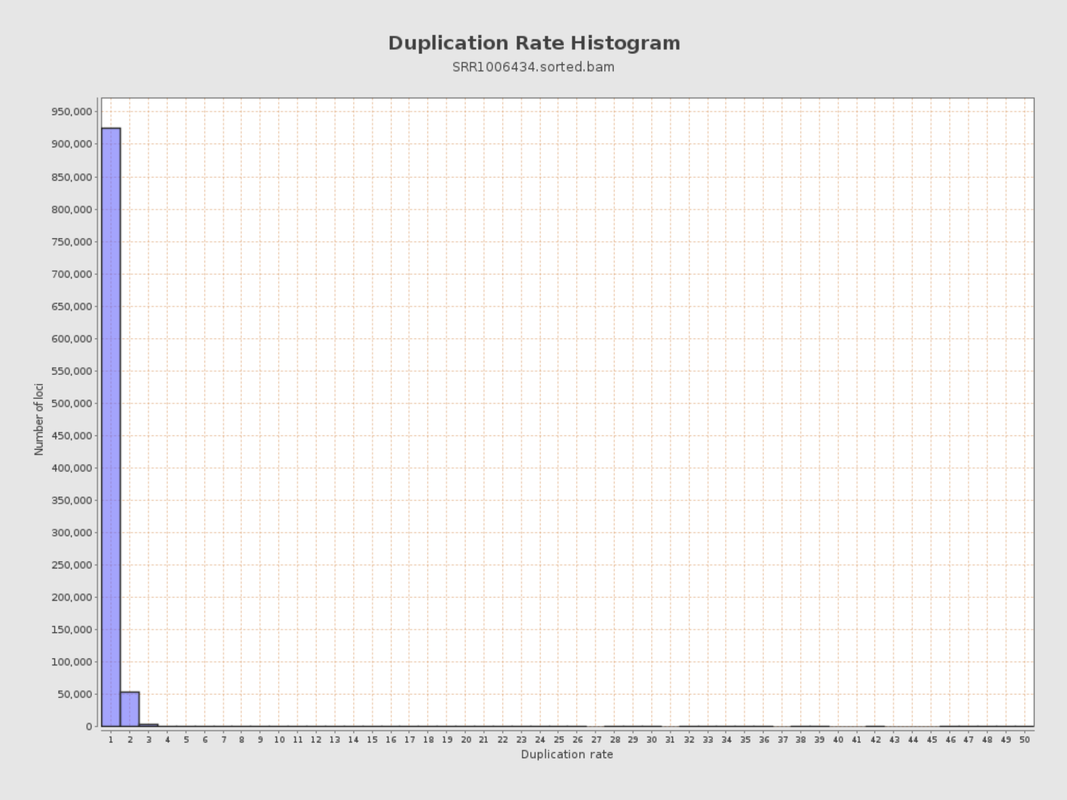
5. Results : Coverage Histogram (0-50X)



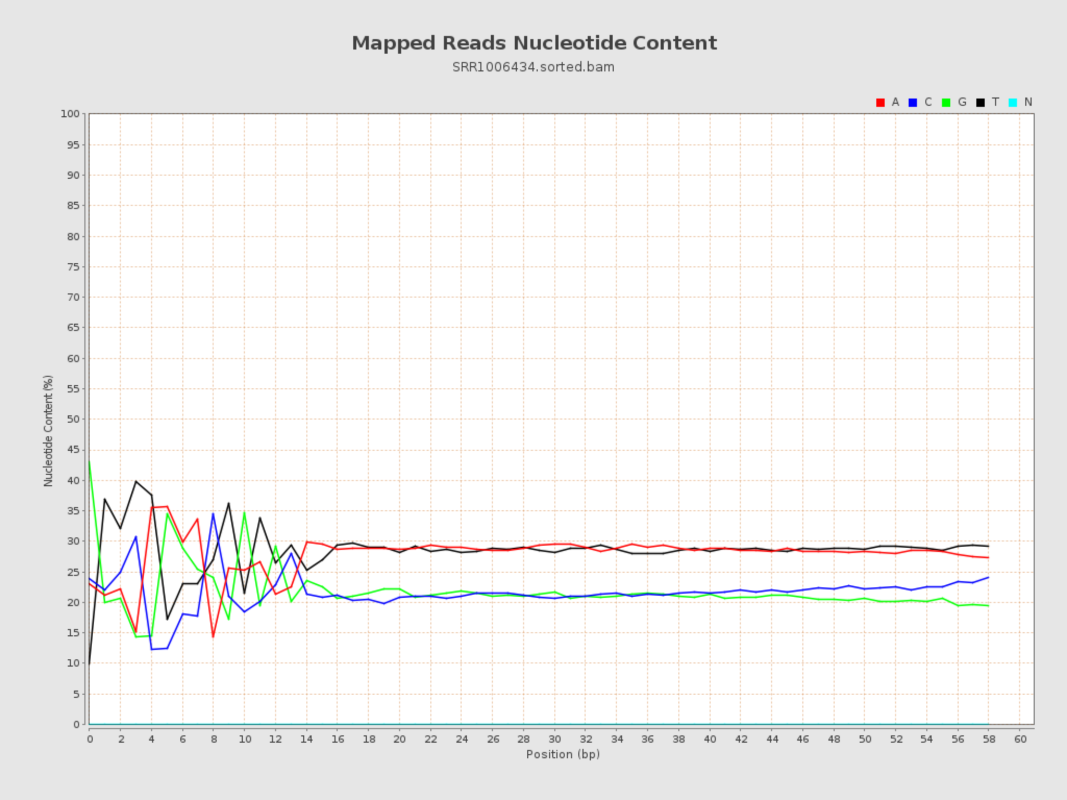
6. Results : Genome Fraction Coverage



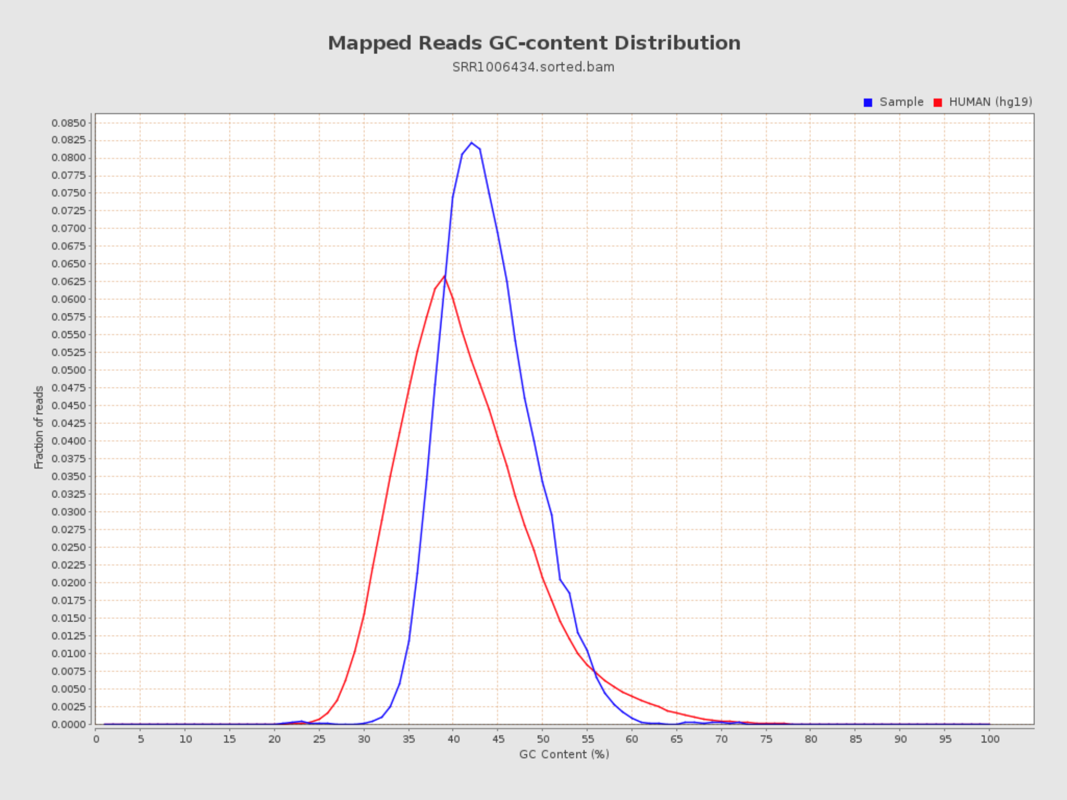
7. Results : Duplication Rate Histogram



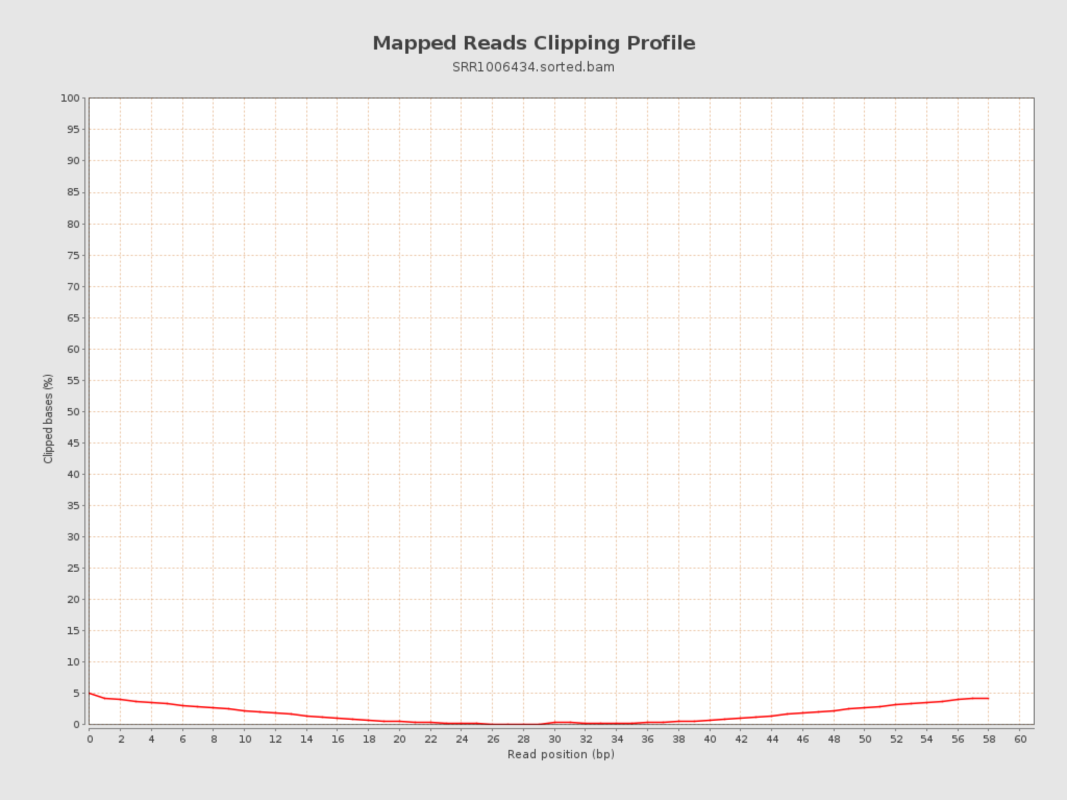
8. Results : Mapped Reads Nucleotide Content



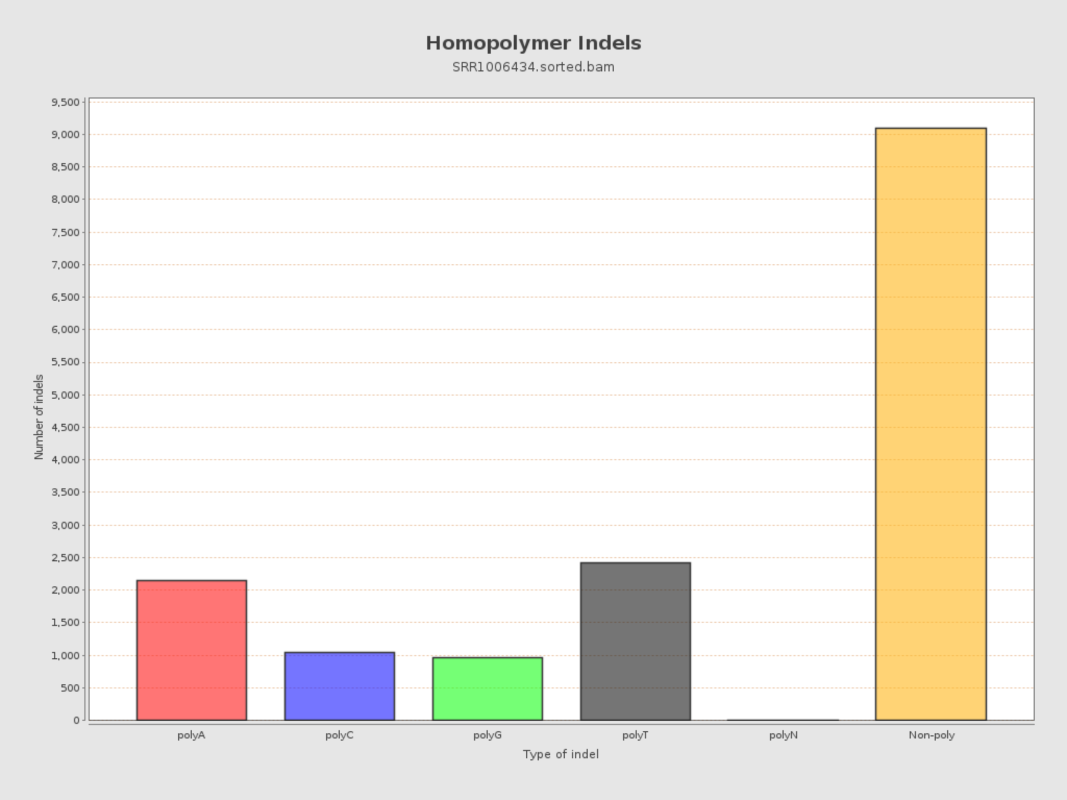
9. Results : Mapped Reads GC-content Distribution



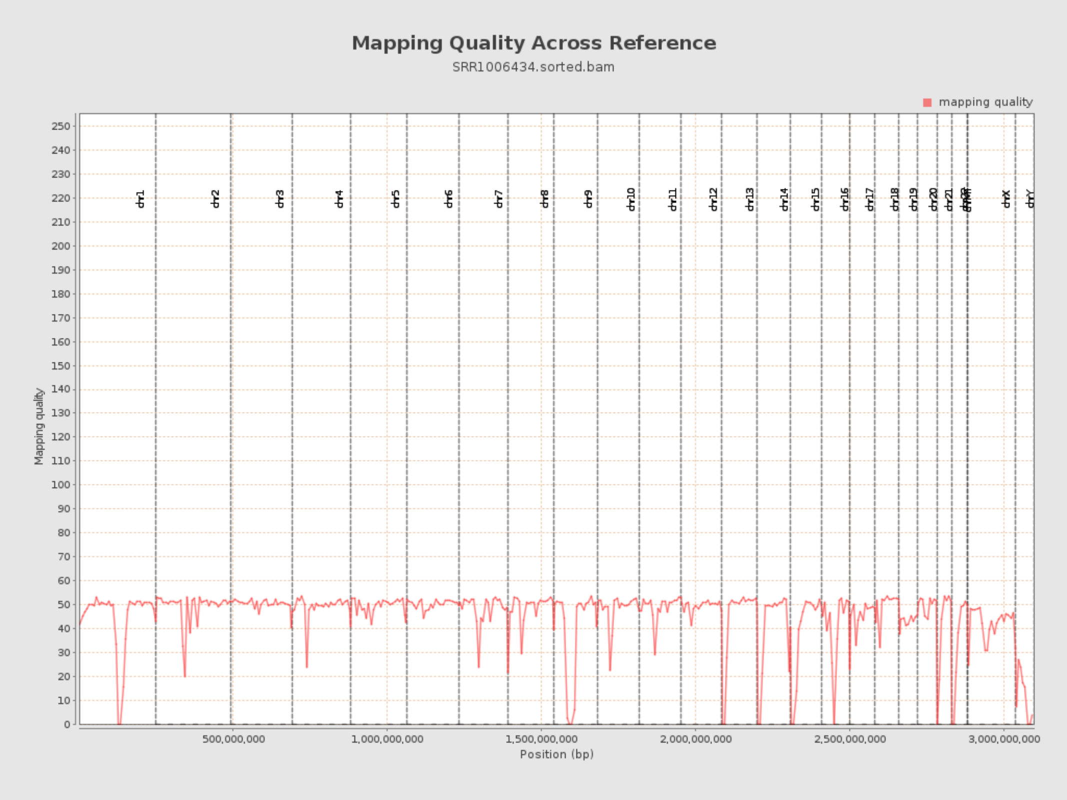
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram