Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:11:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054574.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_SRR054574 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054574.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:11:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054574.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,079,505
Mapped reads	7,586,461 / 75.27%
Unmapped reads	2,493,044 / 24.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	255 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,938,869 / 19.24%
Duplication rate	19.03%
Clipped reads	558,079 / 5.54%

2.2. ACGT Content

Number/percentage of A's	104,311,881 / 29.04%
Number/percentage of C's	70,810,715 / 19.72%
Number/percentage of T's	105,702,424 / 29.43%
Number/percentage of G's	78,226,326 / 21.78%
Number/percentage of N's	111,370 / 0.03%
GC Percentage	41.5%

2.3. Coverage

Mean	0.116

Standard Deviation	0.9023

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

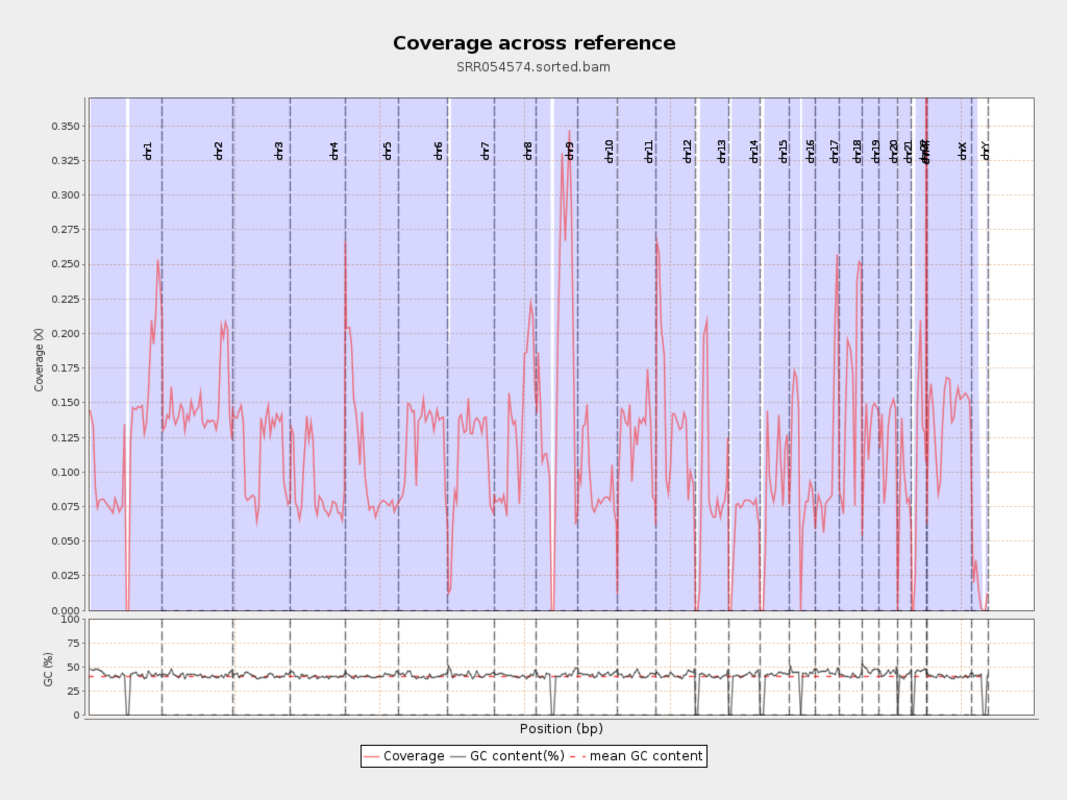
General error rate	0.53%
Mismatches	1,873,069
Insertions	14,426
Mapped reads with at least one insertion	0.19%
Deletions	46,522
Mapped reads with at least one deletion	0.61%
Homopolymer indels	48.03%

2.6. Chromosome stats

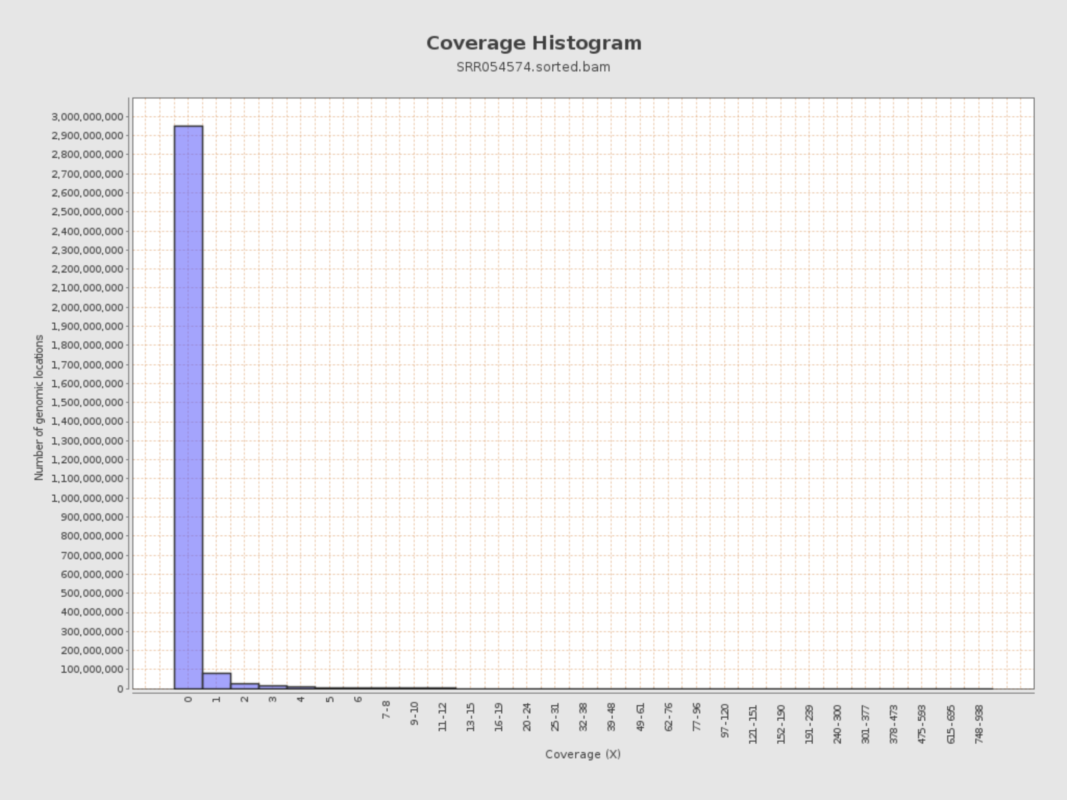
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29756715	0.1194	0.9529
chr2	243199373	36045143	0.1482	1.2258
chr3	198022430	22839702	0.1153	0.8281
chr4	191154276	16908437	0.0885	0.7212
chr5	180915260	19196286	0.1061	0.7819
chr6	171115067	21525125	0.1258	0.9138
chr7	159138663	17552377	0.1103	0.8857

chr8	146364022	19539916	0.1335	0.9532
chr9	141213431	24328259	0.1723	1.1491
chr10	135534747	12530449	0.0925	0.7677
chr11	135006516	16835929	0.1247	0.9054
chr12	133851895	18818262	0.1406	0.9339
chr13	115169878	9530436	0.0828	0.7049
chr14	107349540	6827360	0.0636	0.7137
chr15	102531392	8760063	0.0854	0.6822
chr16	90354753	9063496	0.1003	0.7894
chr17	81195210	9139473	0.1126	0.8256
chr18	78077248	12439660	0.1593	1.1022
chr19	59128983	7788593	0.1317	0.9794
chr20	63025520	7858131	0.1247	0.8861
chr21	48129895	4003470	0.0832	0.744
chr22	51304566	5216022	0.1017	0.8043
chrMT	16571	25683	1.5499	2.9905
chrX	155270560	21843143	0.1407	0.9754
chrY	59373566	860804	0.0145	0.3098

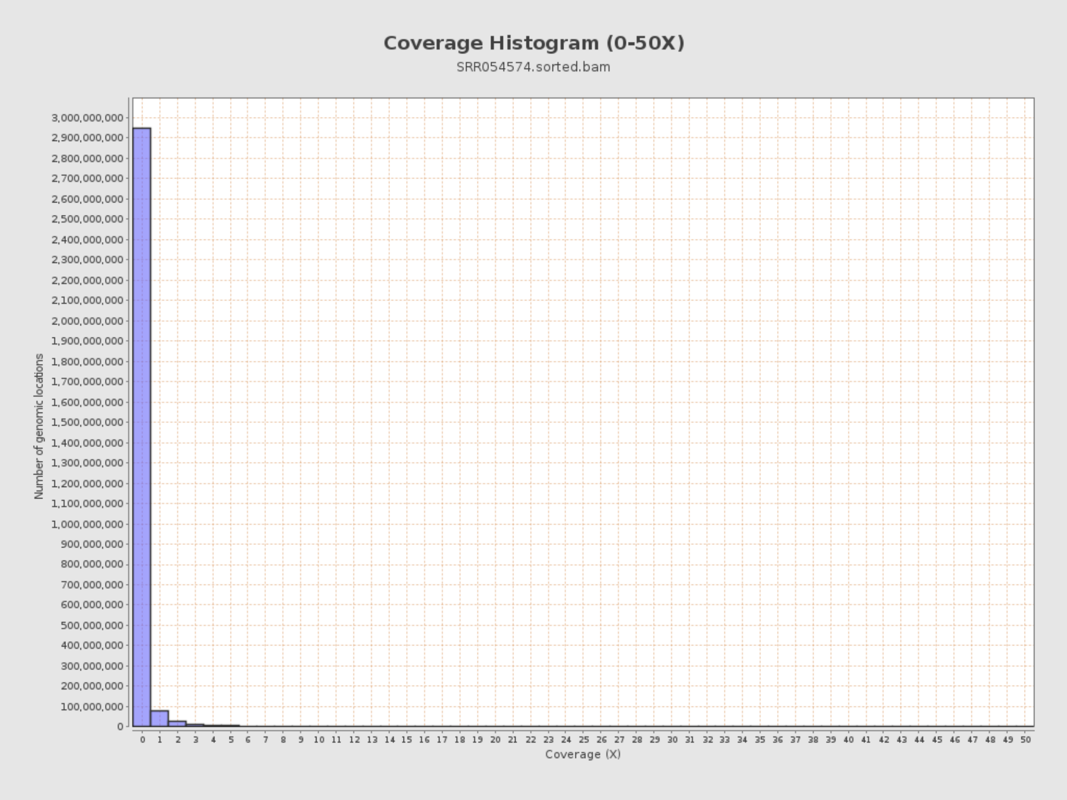
3. Results : Coverage across reference



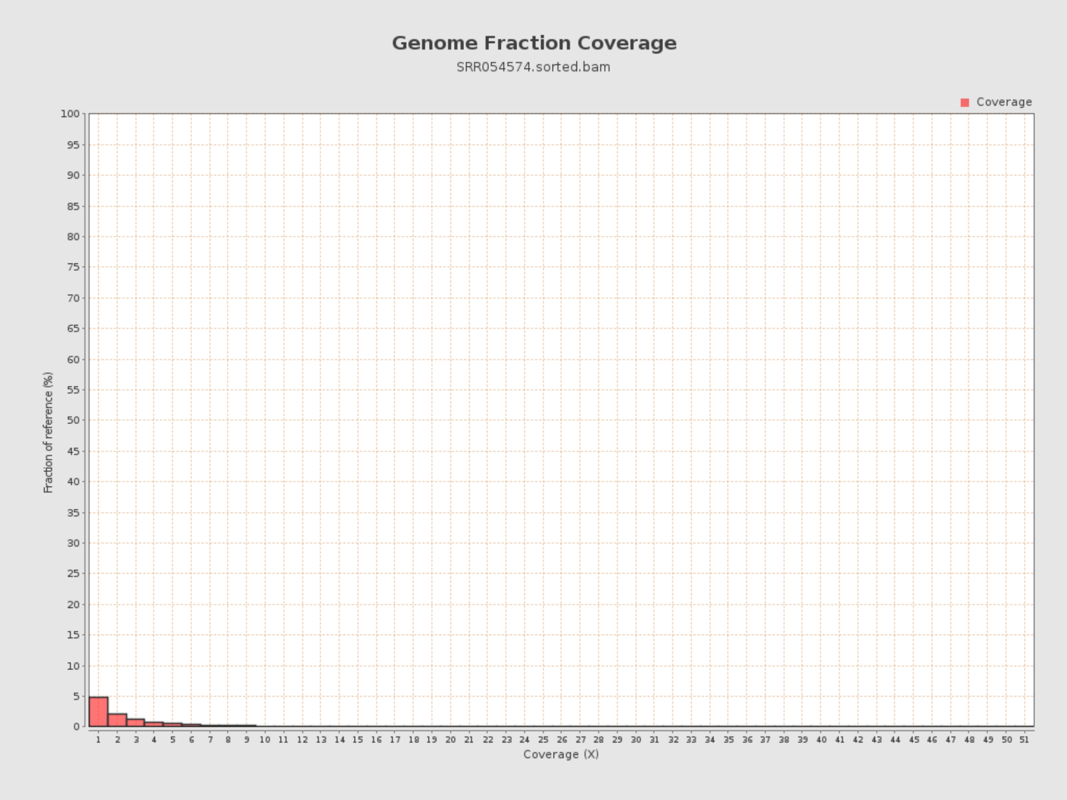
4. Results : Coverage Histogram



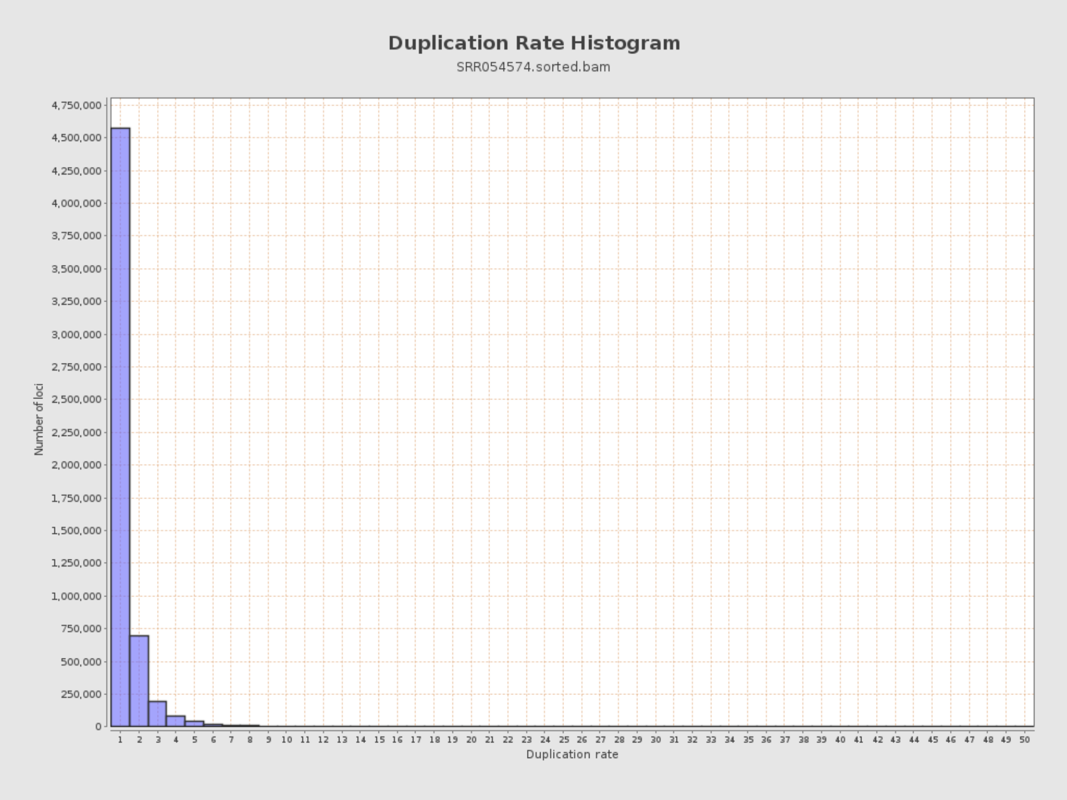
5. Results : Coverage Histogram (0-50X)



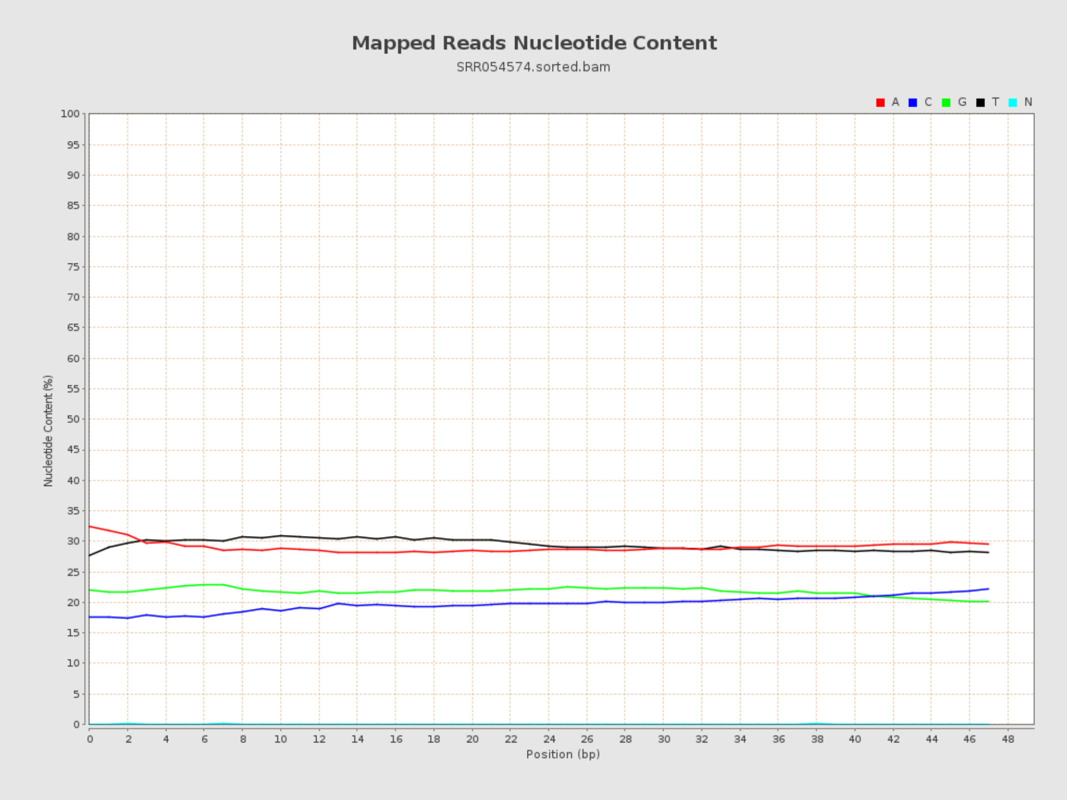
6. Results : Genome Fraction Coverage



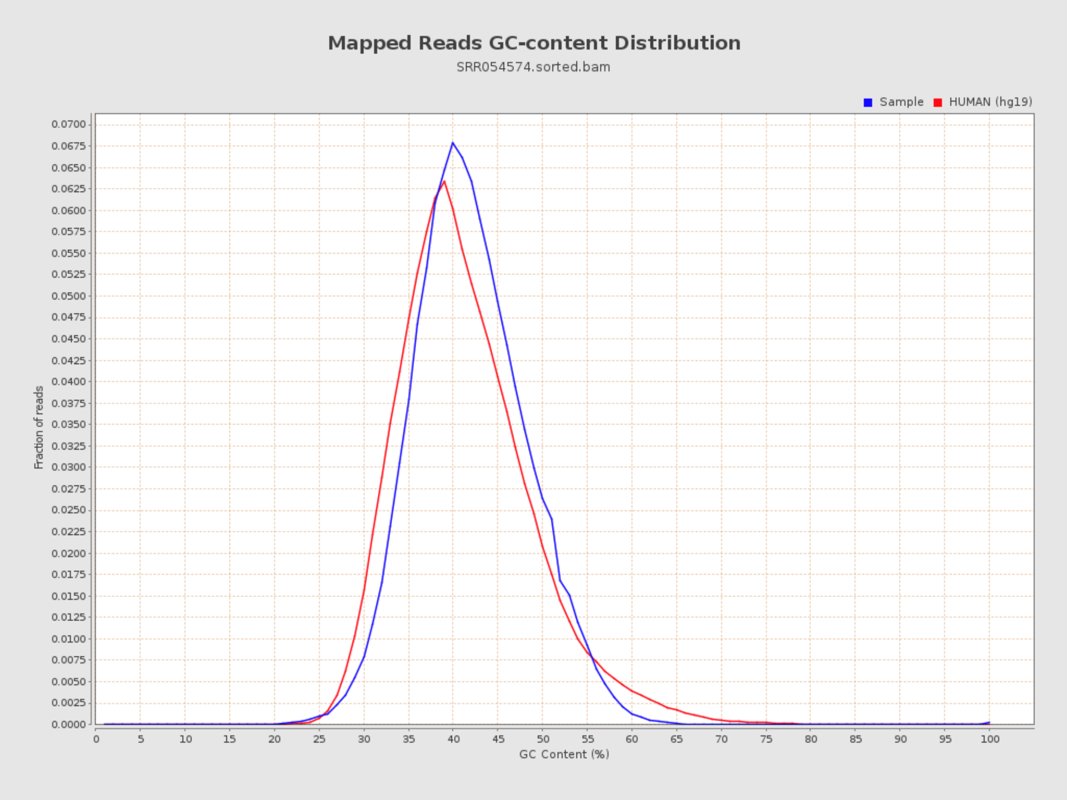
7. Results : Duplication Rate Histogram



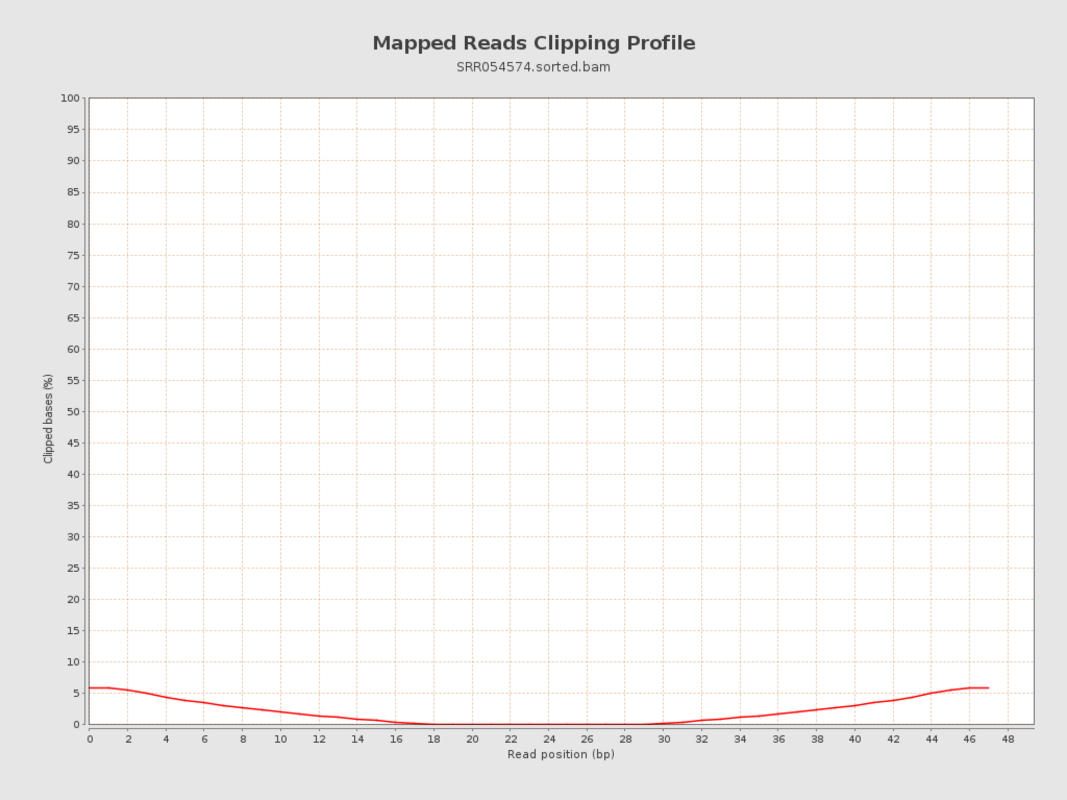
8. Results : Mapped Reads Nucleotide Content



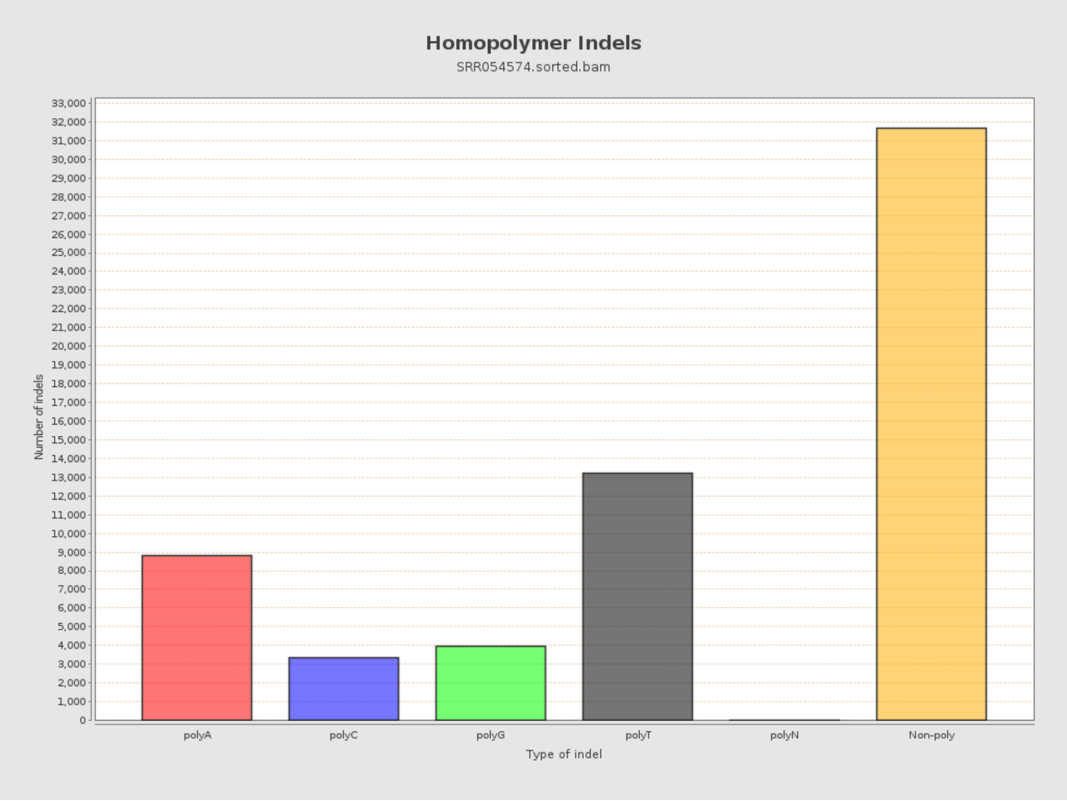
9. Results : Mapped Reads GC-content Distribution



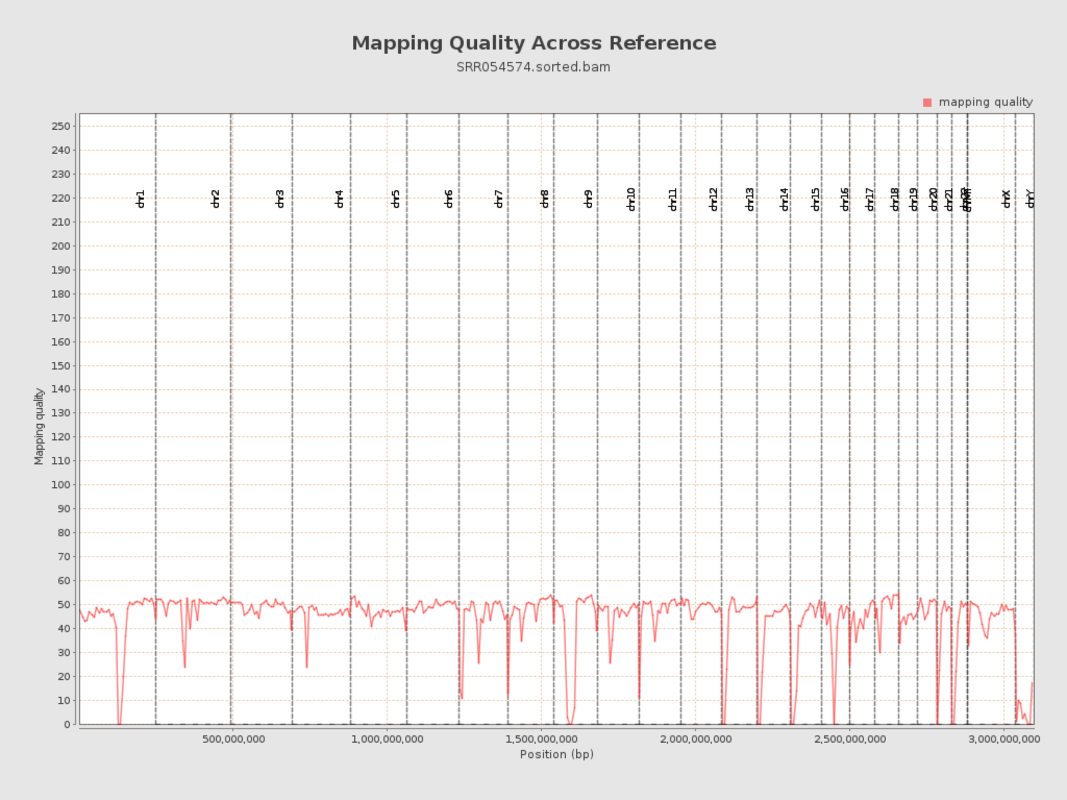
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram