Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 05:55:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054598.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_SRR054598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054598.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 05:55:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054598.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,137,266
Mapped reads	2,481,784 / 79.11%
Unmapped reads	655,482 / 20.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	78 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	301,688 / 9.62%
Duplication rate	10.02%
Clipped reads	318,030 / 10.14%

2.2. ACGT Content

Number/percentage of A's	35,279,976 / 30.35%
Number/percentage of C's	22,983,835 / 19.77%
Number/percentage of T's	34,394,719 / 29.58%
Number/percentage of G's	23,586,782 / 20.29%
Number/percentage of N's	13,468 / 0.01%
GC Percentage	40.06%

2.3. Coverage

Mean	0.0376

Standard Deviation	0.3348

2.4. Mapping Quality

Mean Mapping Quality	44.55

2.5. Mismatches and indels

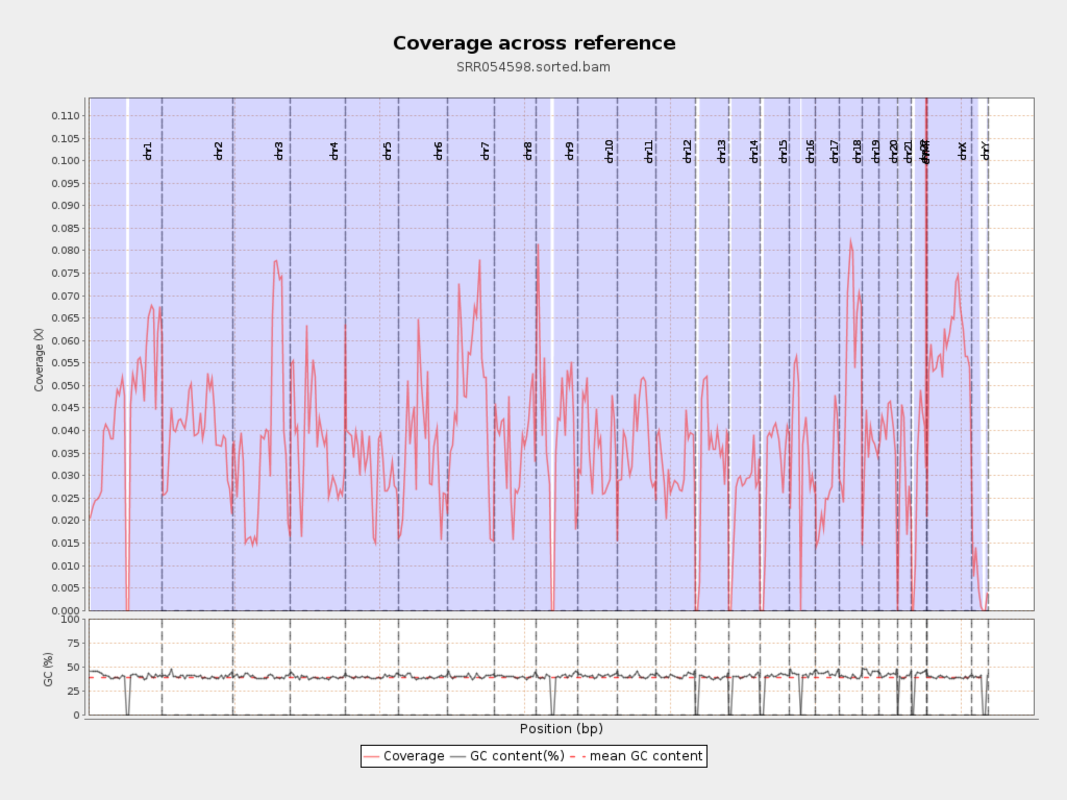
General error rate	0.73%
Mismatches	847,232
Insertions	5,091
Mapped reads with at least one insertion	0.2%
Deletions	16,236
Mapped reads with at least one deletion	0.65%
Homopolymer indels	44.63%

2.6. Chromosome stats

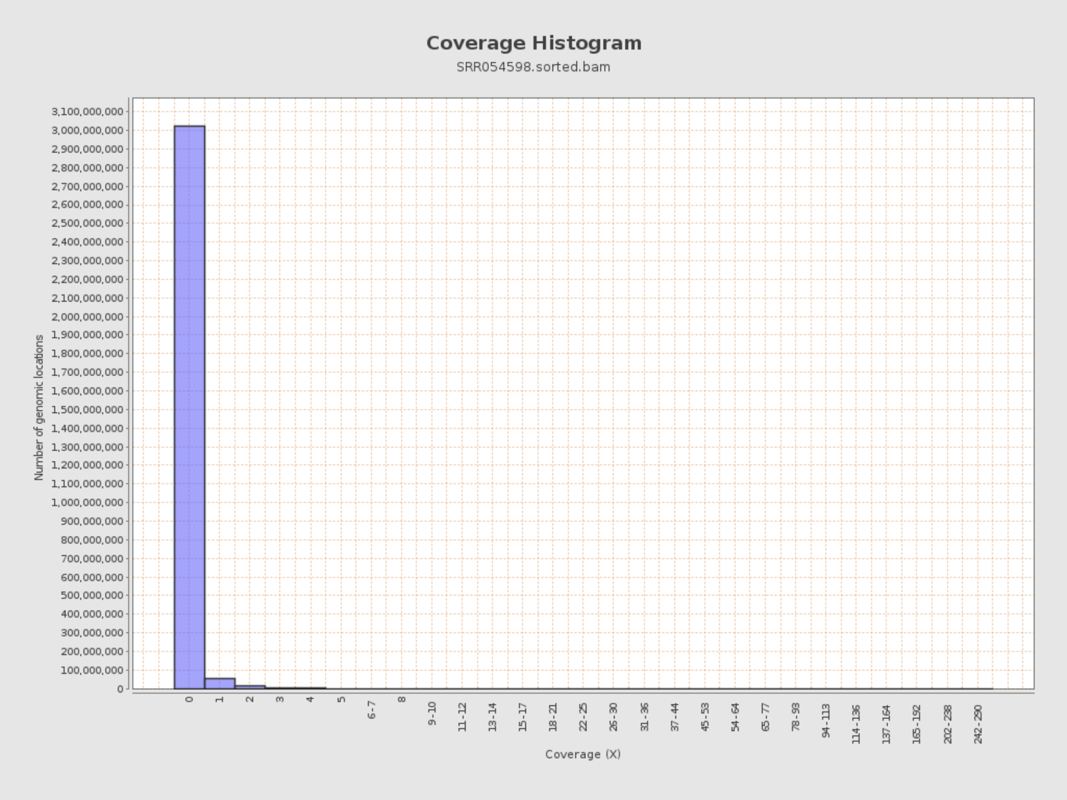
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10749621	0.0431	0.3726
chr2	243199373	9598254	0.0395	0.4024
chr3	198022430	7391072	0.0373	0.3145
chr4	191154276	7144540	0.0374	0.3203
chr5	180915260	5841813	0.0323	0.2801
chr6	171115067	5955736	0.0348	0.3154
chr7	159138663	7856464	0.0494	0.3994

chr8	146364022	5373879	0.0367	0.3297
chr9	141213431	5691219	0.0403	0.3438
chr10	135534747	4968504	0.0367	0.32
chr11	135006516	5090563	0.0377	0.343
chr12	133851895	4310040	0.0322	0.2819
chr13	115169878	3807733	0.0331	0.2864
chr14	107349540	2658797	0.0248	0.2812
chr15	102531392	3100023	0.0302	0.2695
chr16	90354753	3256679	0.036	0.3159
chr17	81195210	2206165	0.0272	0.2536
chr18	78077248	4455624	0.0571	0.4279
chr19	59128983	2126259	0.036	0.3434
chr20	63025520	2511804	0.0399	0.3203
chr21	48129895	1341746	0.0279	0.2945
chr22	51304566	1448395	0.0282	0.2605
chrMT	16571	10986	0.663	1.4579
chrX	155270560	9069322	0.0584	0.4244
chrY	59373566	316991	0.0053	0.1238

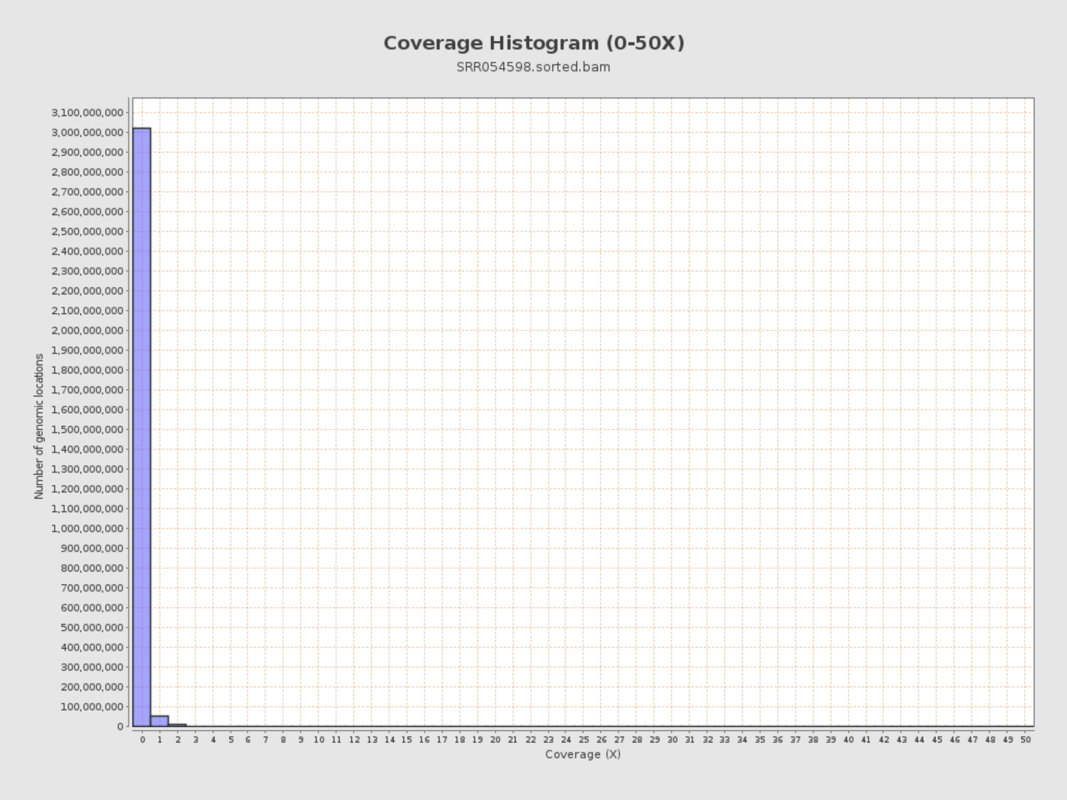
3. Results : Coverage across reference



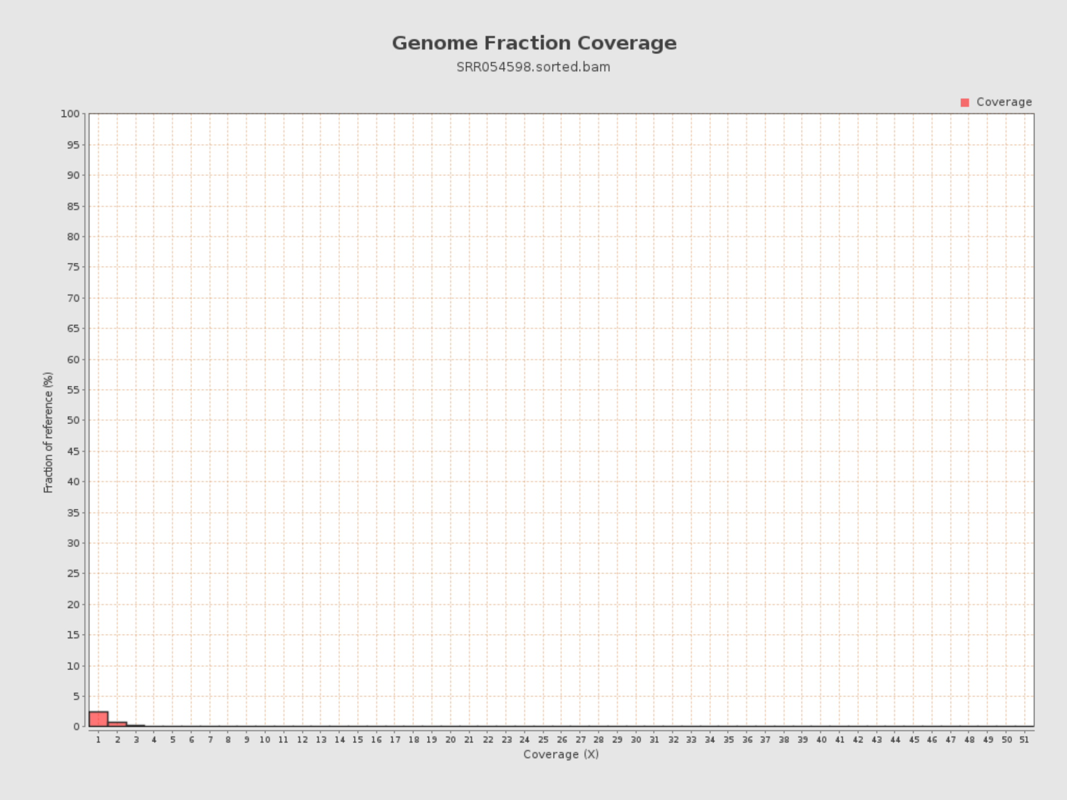
4. Results : Coverage Histogram



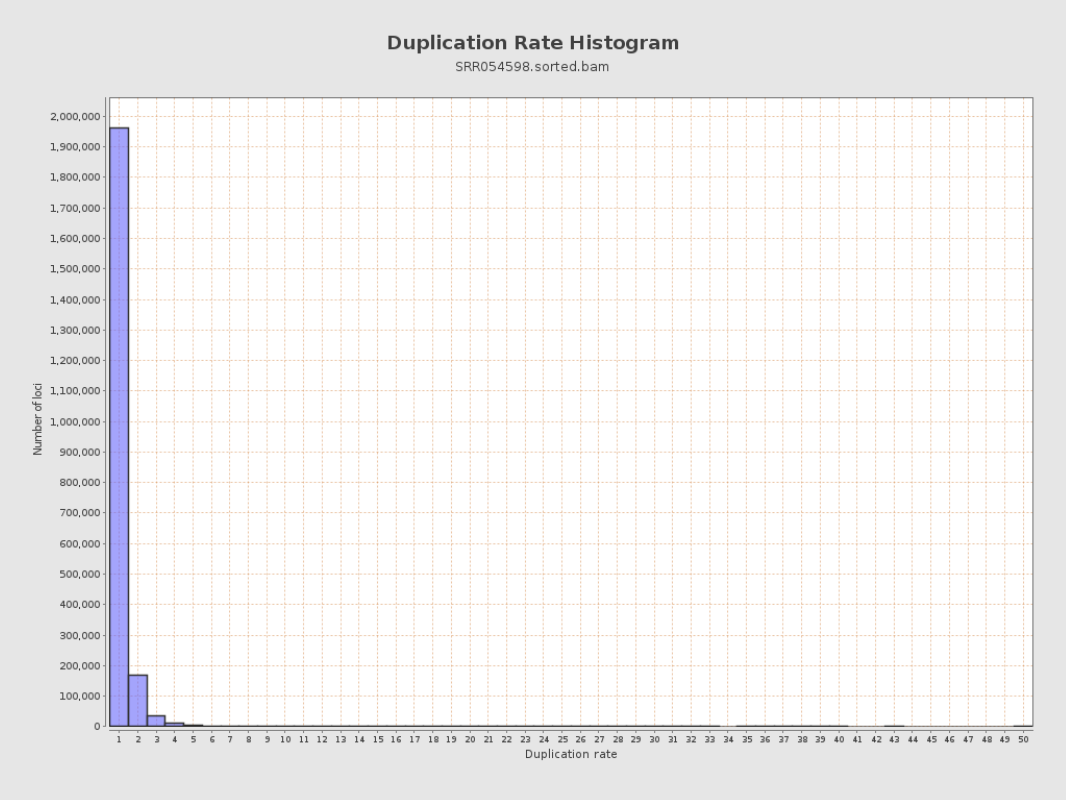
5. Results : Coverage Histogram (0-50X)



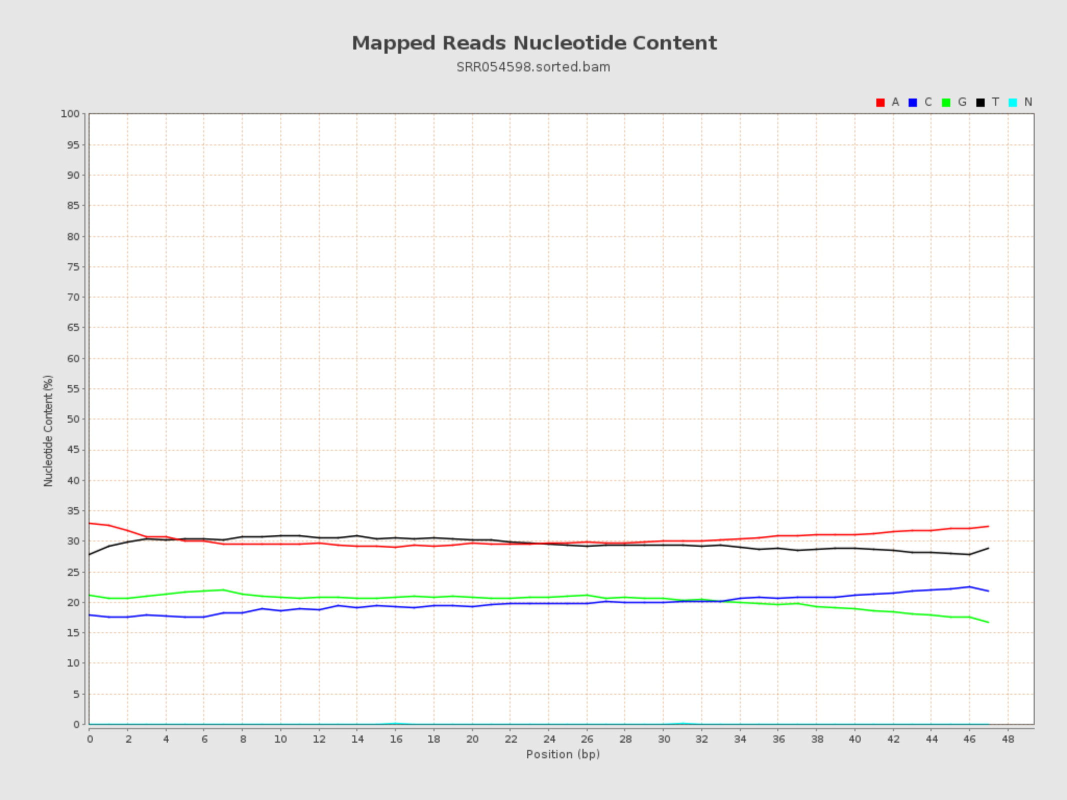
6. Results : Genome Fraction Coverage



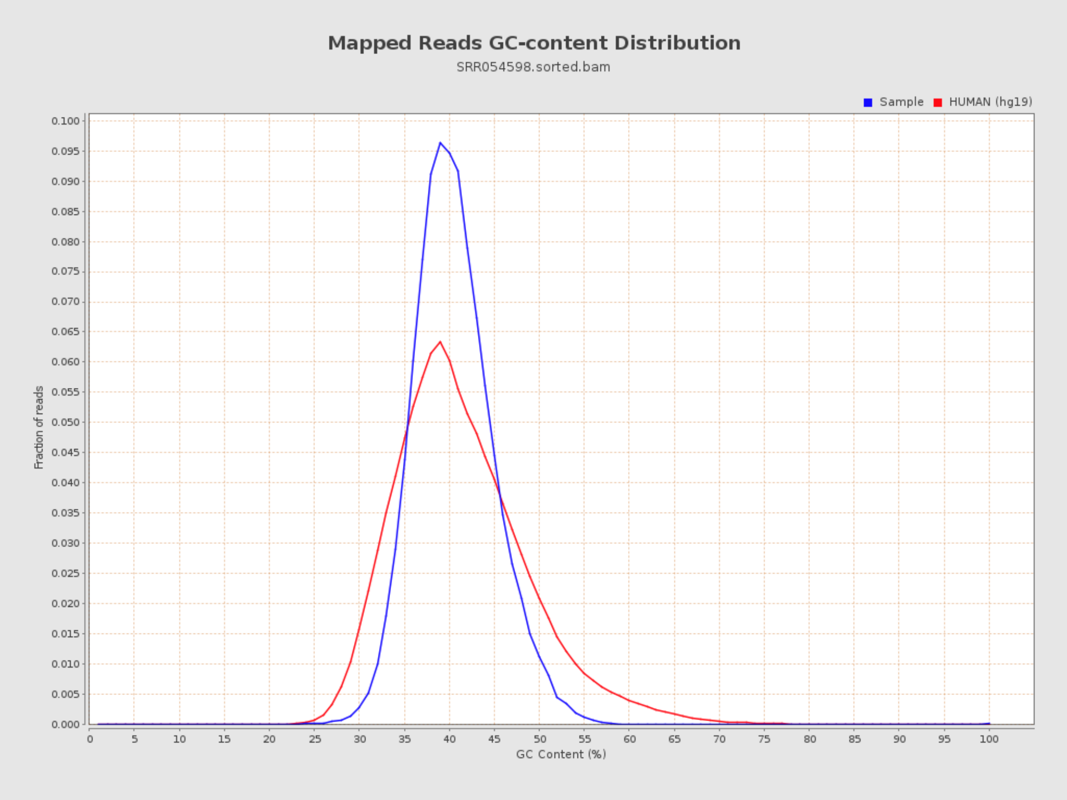
7. Results : Duplication Rate Histogram



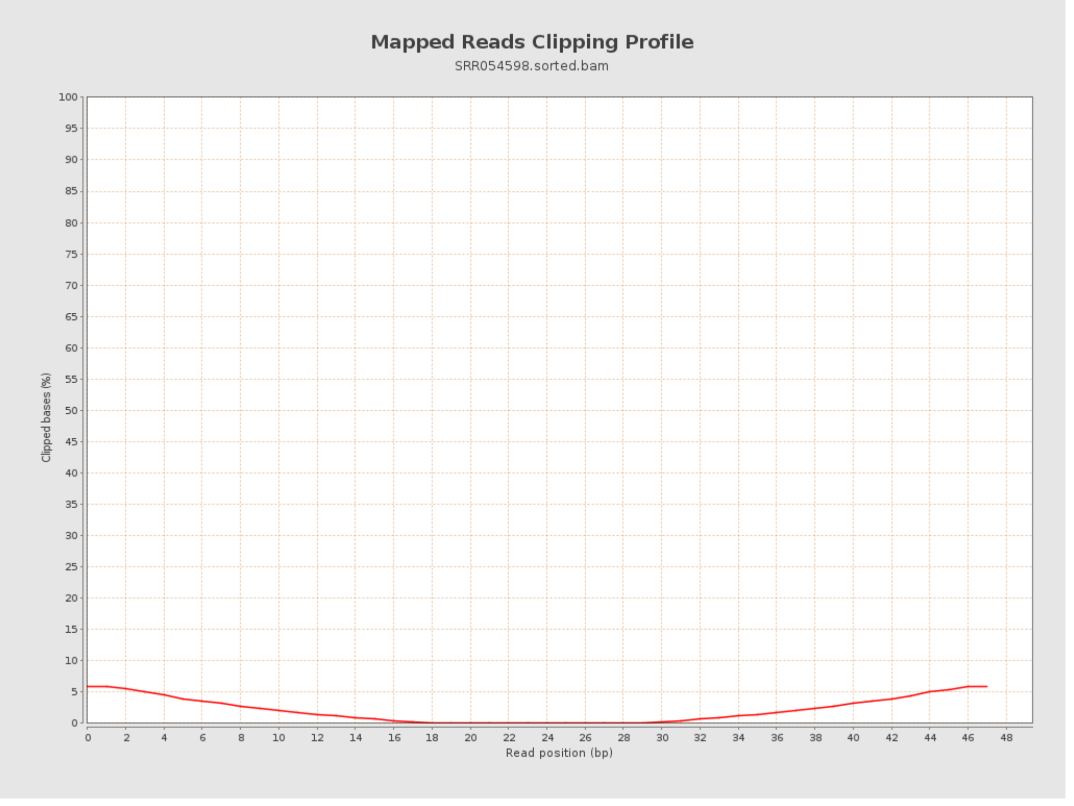
8. Results : Mapped Reads Nucleotide Content



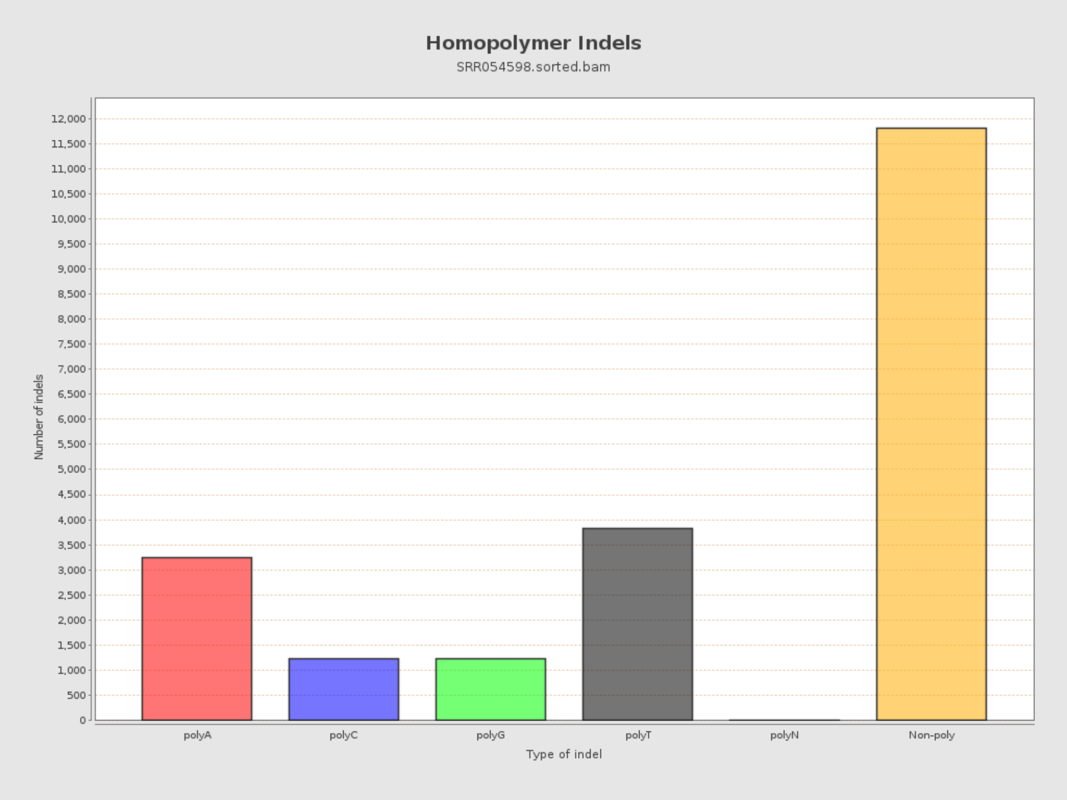
9. Results : Mapped Reads GC-content Distribution



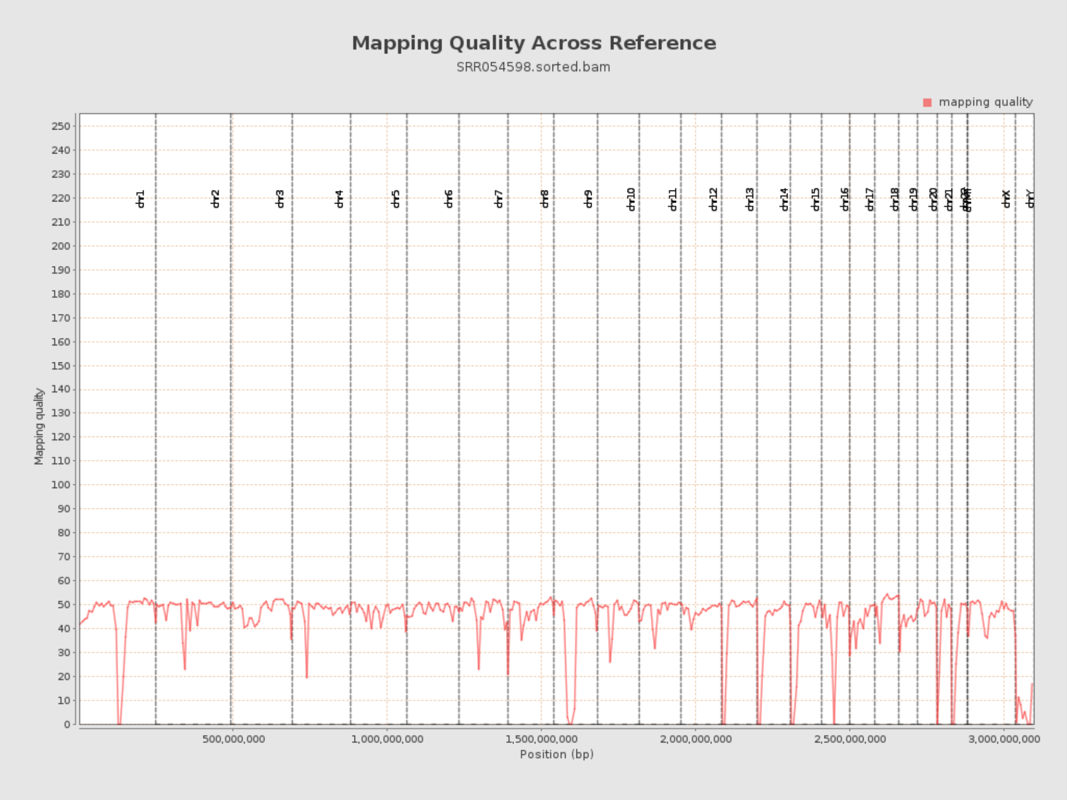
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram