Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 03:33:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053680.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_SRR053680 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053680.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 03:33:34 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053680.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,182,848
Mapped reads	5,933,742 / 82.61%
Unmapped reads	1,249,106 / 17.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	256 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,200,061 / 16.71%
Duplication rate	15.29%
Clipped reads	586,257 / 8.16%

2.2. ACGT Content

Number/percentage of A's	80,400,723 / 28.78%
Number/percentage of C's	55,483,048 / 19.86%
Number/percentage of T's	81,898,291 / 29.32%
Number/percentage of G's	61,531,704 / 22.03%
Number/percentage of N's	11,243 / 0%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0902

Standard Deviation	0.6845

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

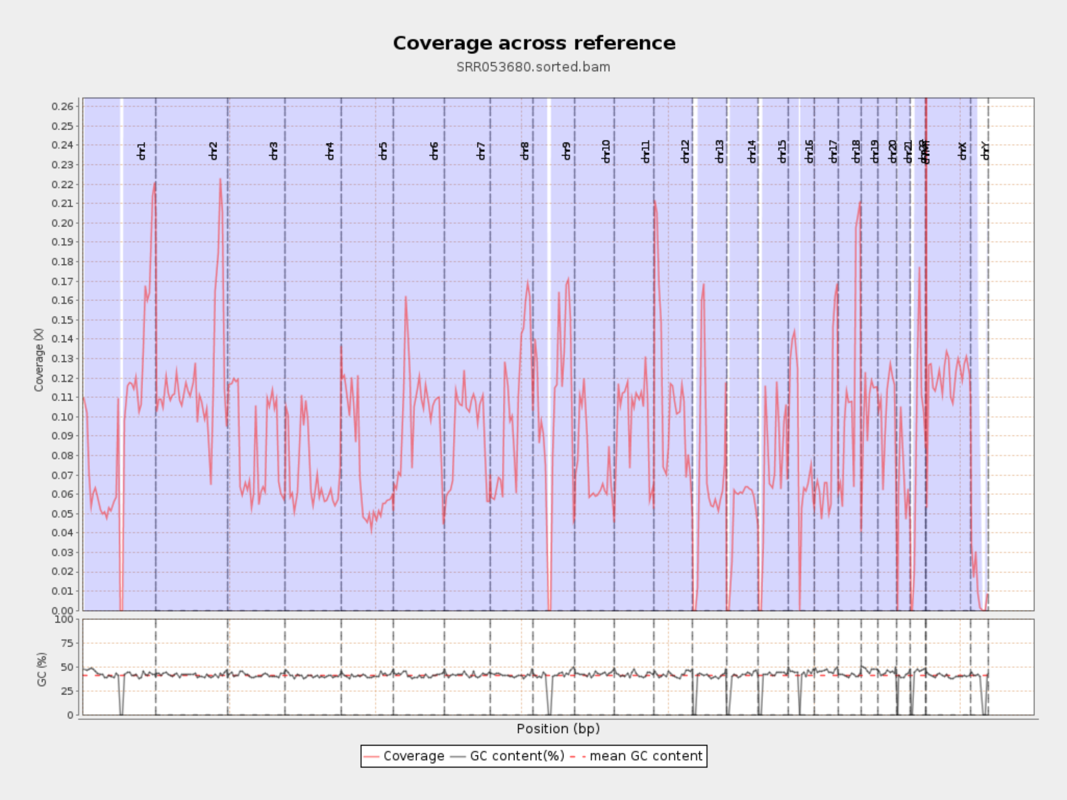
General error rate	0.48%
Mismatches	1,330,729
Insertions	11,171
Mapped reads with at least one insertion	0.19%
Deletions	38,725
Mapped reads with at least one deletion	0.65%
Homopolymer indels	46.29%

2.6. Chromosome stats

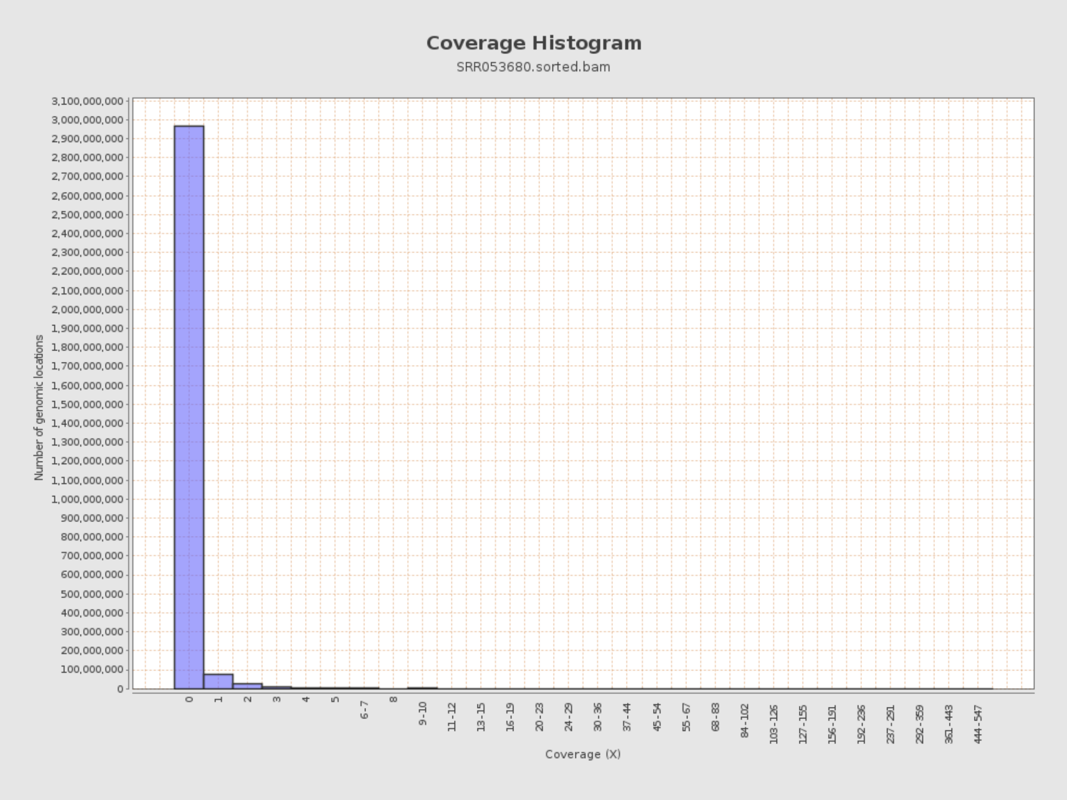
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23552119	0.0945	0.7914
chr2	243199373	28898478	0.1188	0.8408
chr3	198022430	16618360	0.0839	0.6028
chr4	191154276	13548718	0.0709	0.5593
chr5	180915260	13148812	0.0727	0.5476
chr6	171115067	17445814	0.102	0.7177
chr7	159138663	14544631	0.0914	0.7104

chr8	146364022	15160659	0.1036	0.7173
chr9	141213431	14695390	0.1041	0.7149
chr10	135534747	10023111	0.074	0.6402
chr11	135006516	13590728	0.1007	0.7089
chr12	133851895	15096502	0.1128	0.7291
chr13	115169878	7639603	0.0663	0.5694
chr14	107349540	5407648	0.0504	0.5266
chr15	102531392	7344442	0.0716	0.5622
chr16	90354753	7494296	0.0829	0.6444
chr17	81195210	6747383	0.0831	0.608
chr18	78077248	9078120	0.1163	0.8171
chr19	59128983	6248558	0.1057	0.7857
chr20	63025520	6578916	0.1044	0.7048
chr21	48129895	2919967	0.0607	0.6334
chr22	51304566	4341264	0.0846	0.618
chrMT	16571	16602	1.0019	2.1247
chrX	155270560	18553023	0.1195	0.7796
chrY	59373566	691085	0.0116	0.268

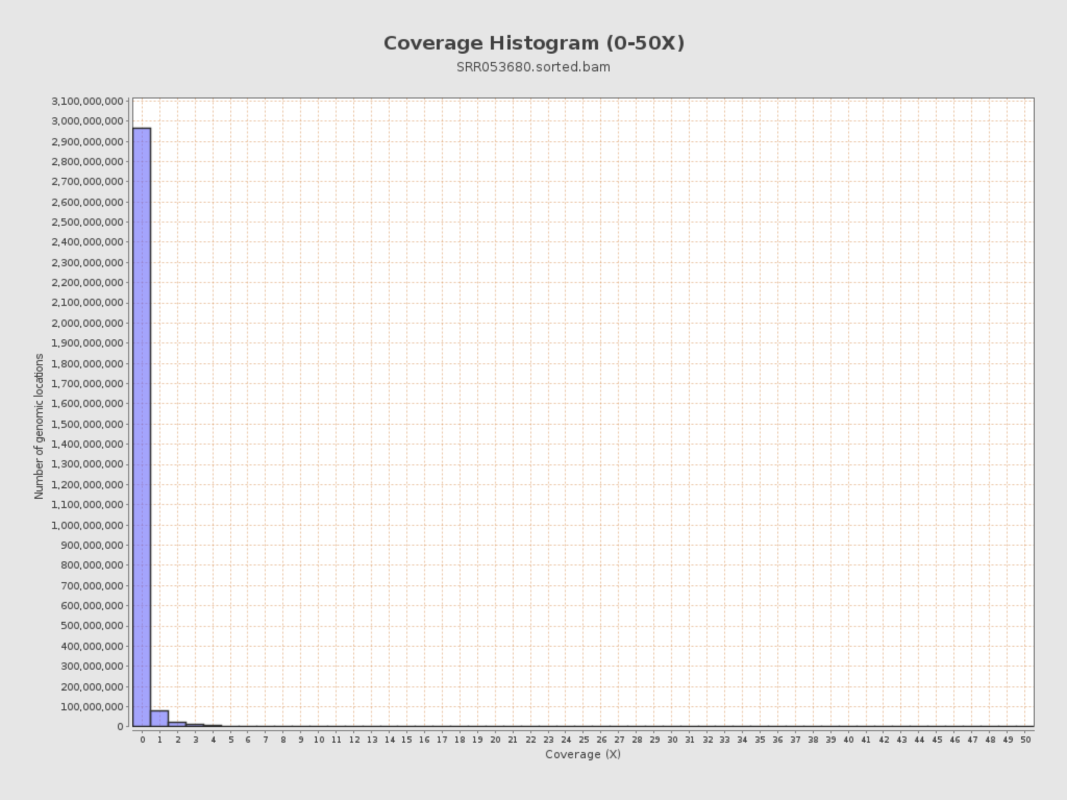
3. Results : Coverage across reference



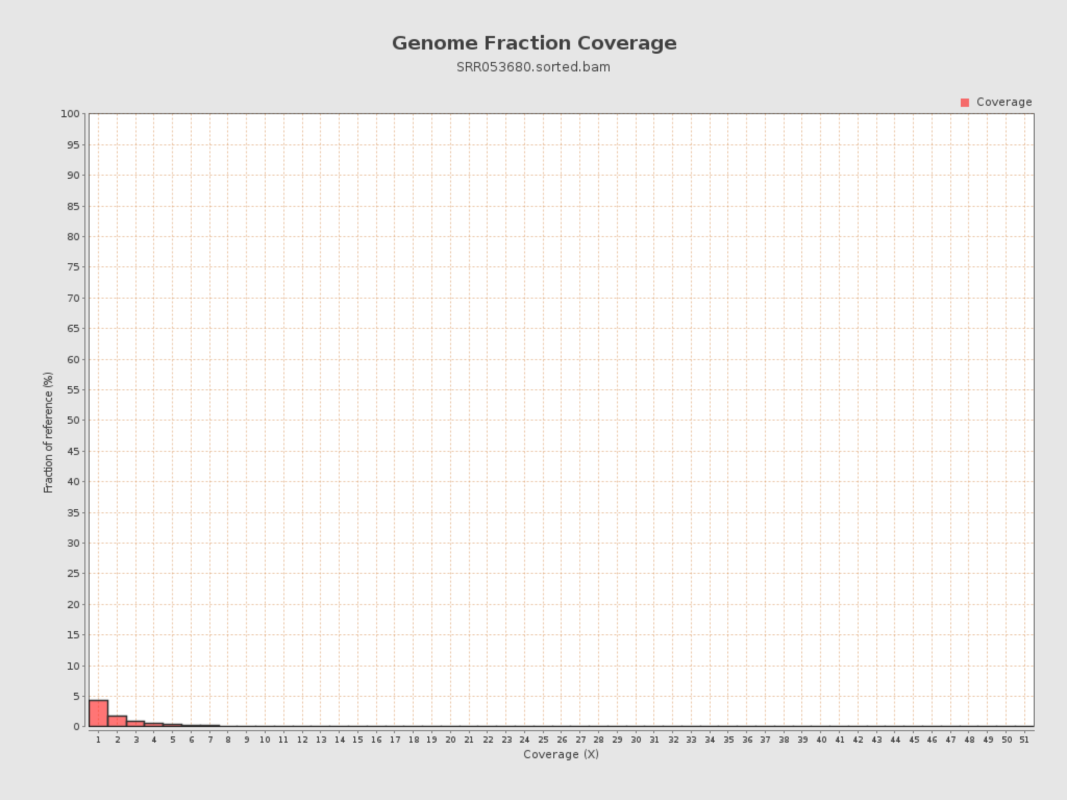
4. Results : Coverage Histogram



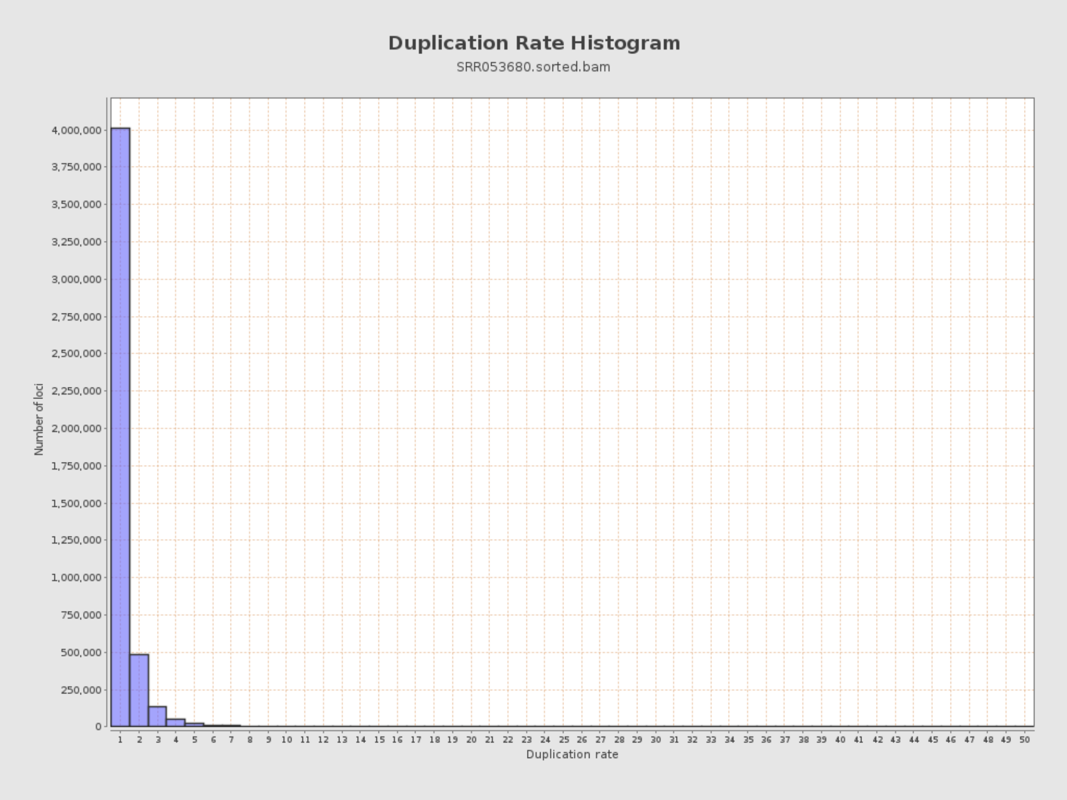
5. Results : Coverage Histogram (0-50X)



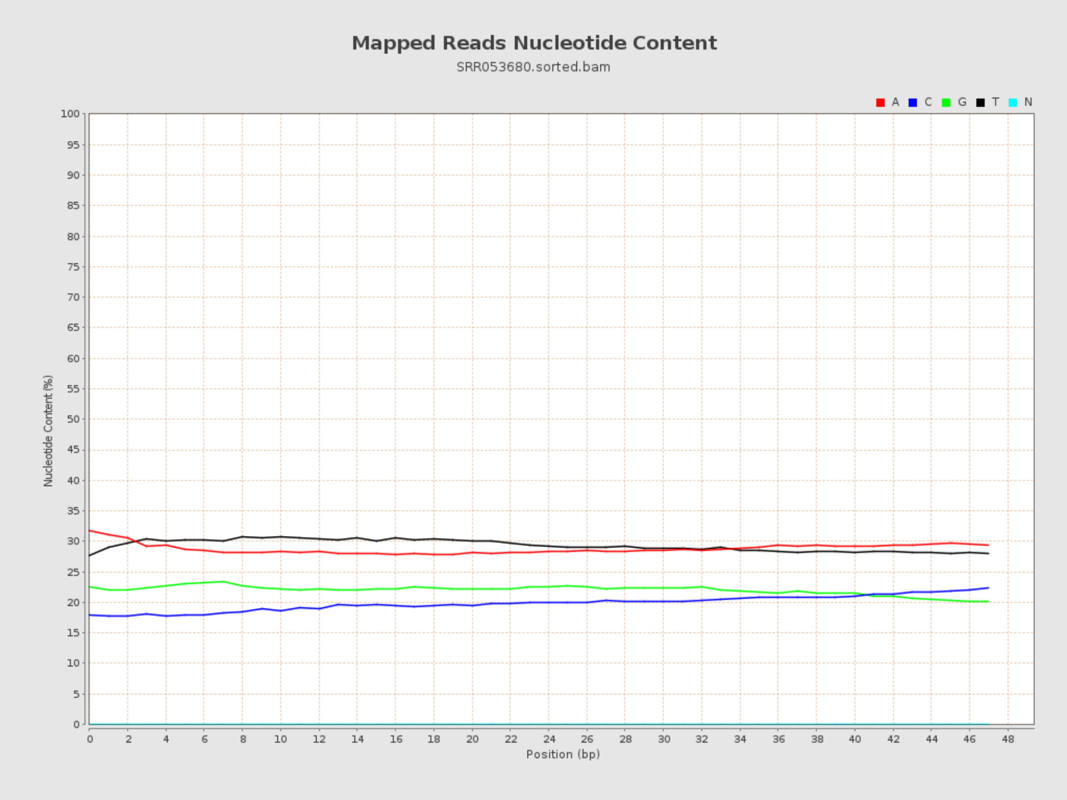
6. Results : Genome Fraction Coverage



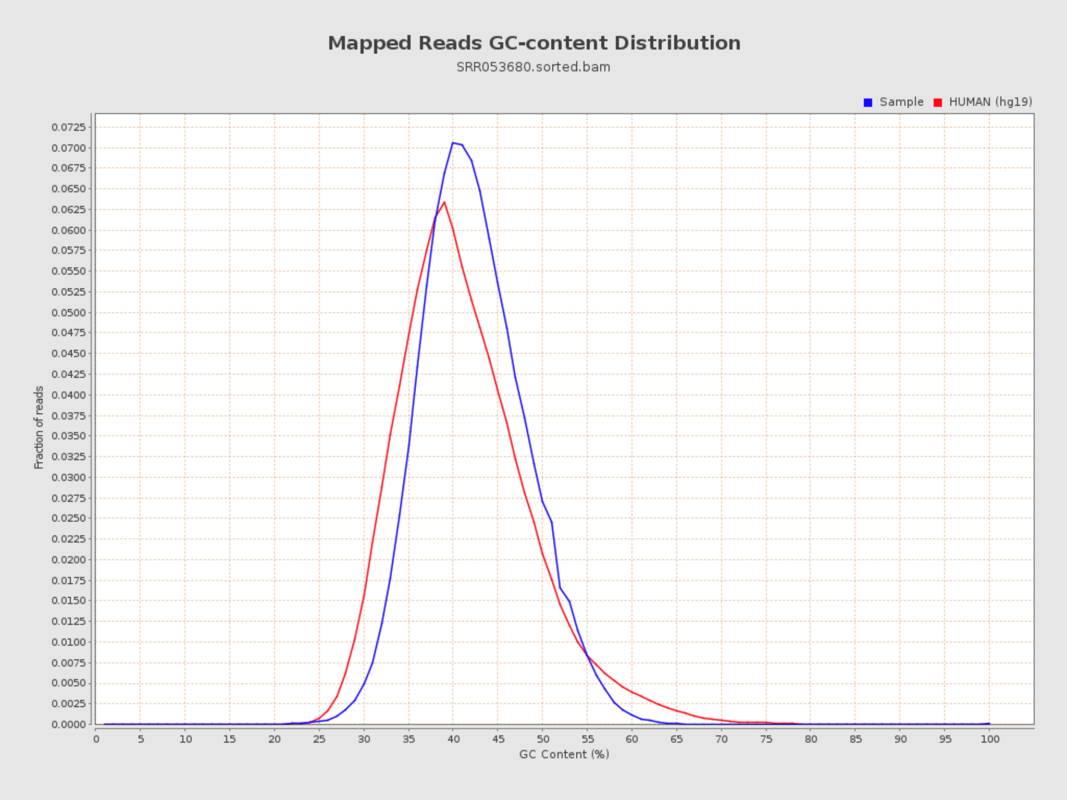
7. Results : Duplication Rate Histogram



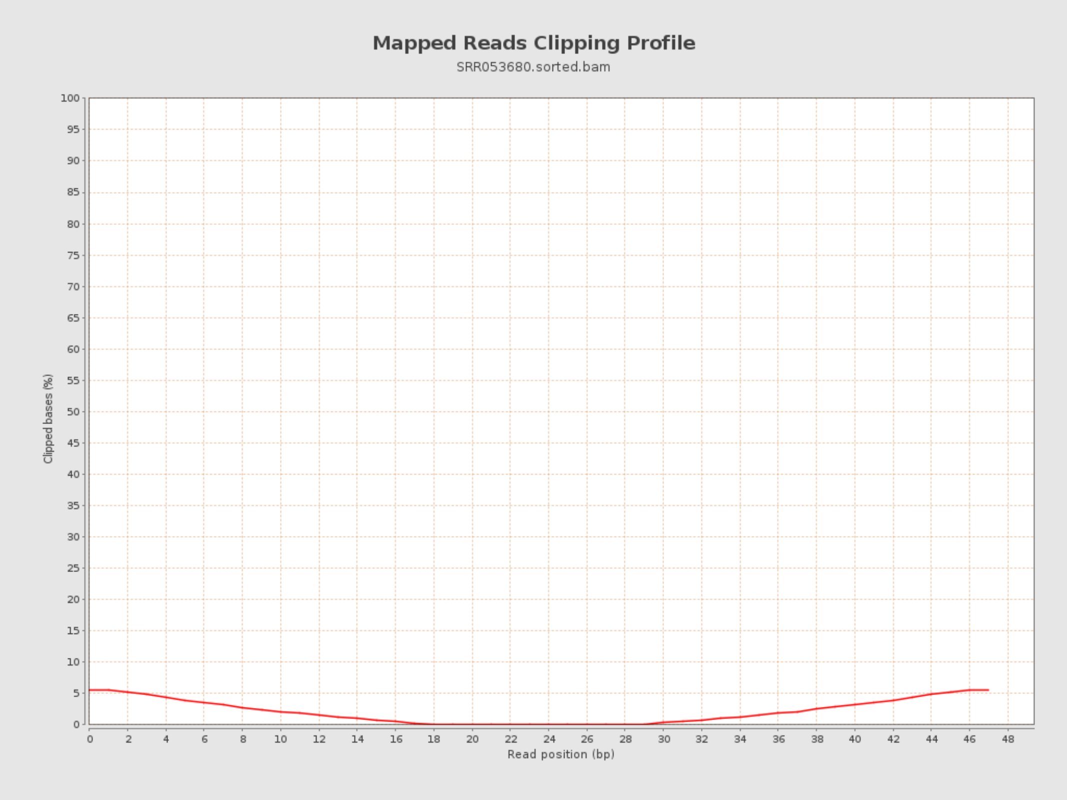
8. Results : Mapped Reads Nucleotide Content



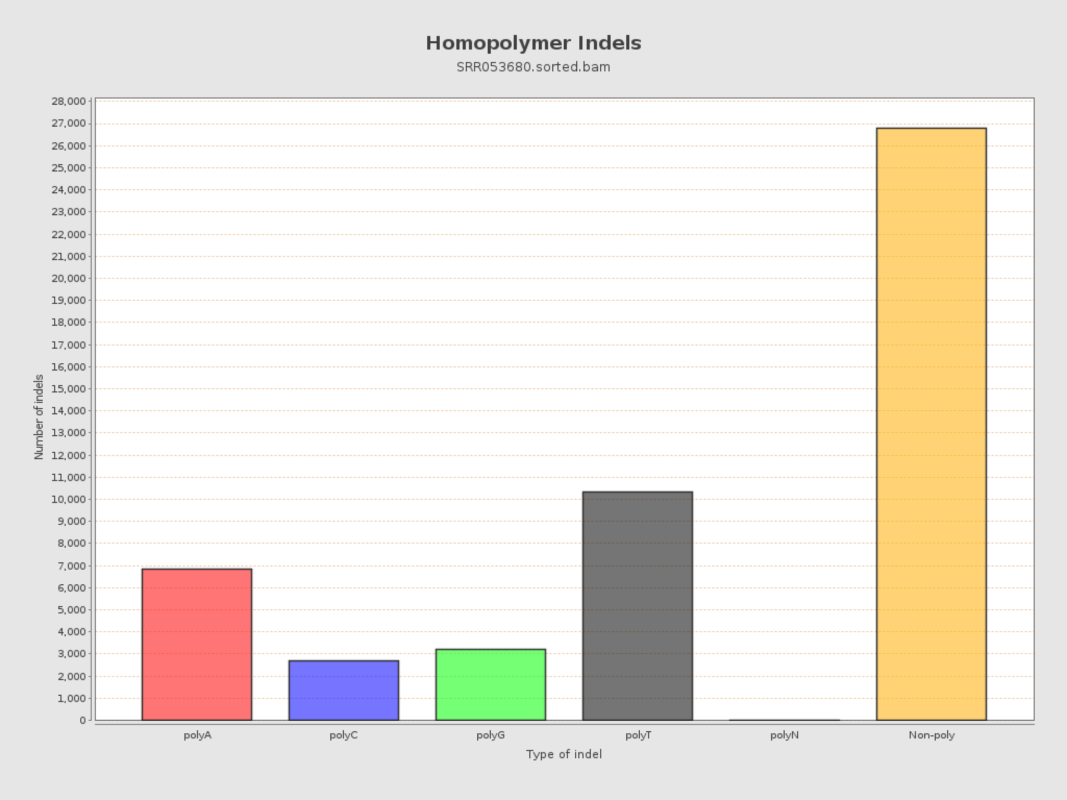
9. Results : Mapped Reads GC-content Distribution



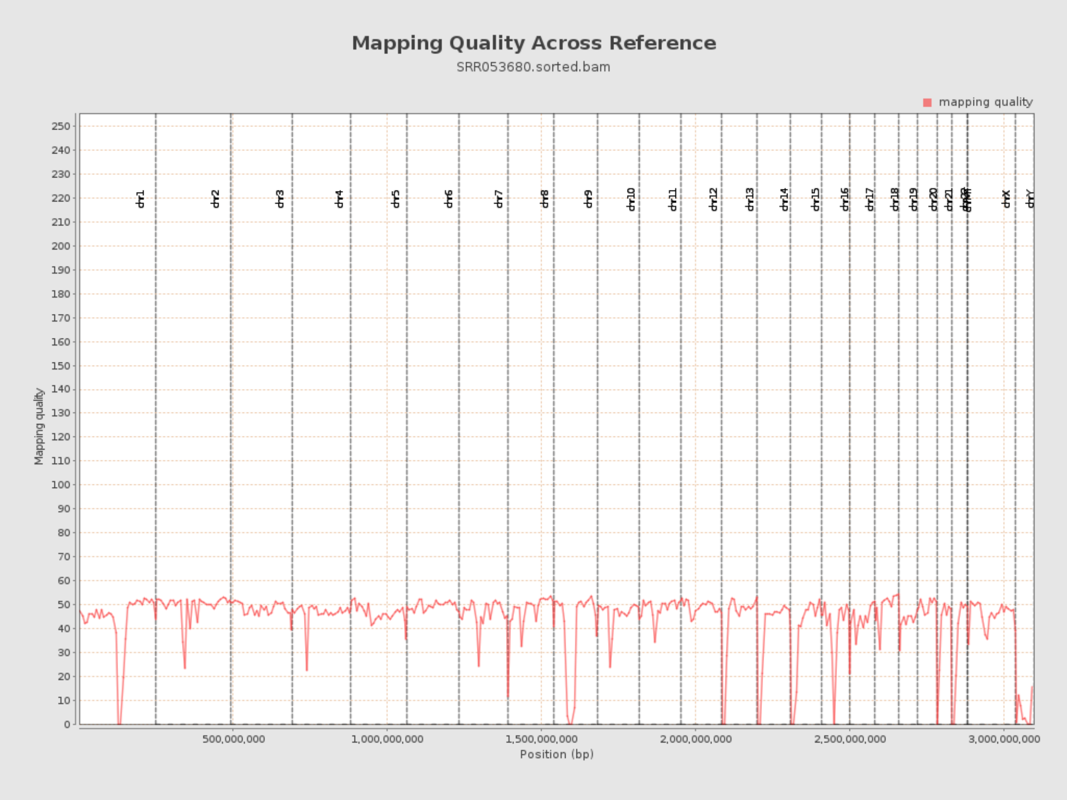
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram