Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 01:54:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053638.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_SRR053638 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053638.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 01:54:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053638.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,865,170
Mapped reads	3,773,204 / 77.56%
Unmapped reads	1,091,966 / 22.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	95 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,125,613 / 23.14%
Duplication rate	19.94%
Clipped reads	695,298 / 14.29%

2.2. ACGT Content

Number/percentage of A's	54,601,006 / 31.25%
Number/percentage of C's	36,686,850 / 21%
Number/percentage of T's	47,246,058 / 27.04%
Number/percentage of G's	36,190,342 / 20.71%
Number/percentage of N's	491 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.0565

Standard Deviation	0.6681

2.4. Mapping Quality

Mean Mapping Quality	43.72

2.5. Mismatches and indels

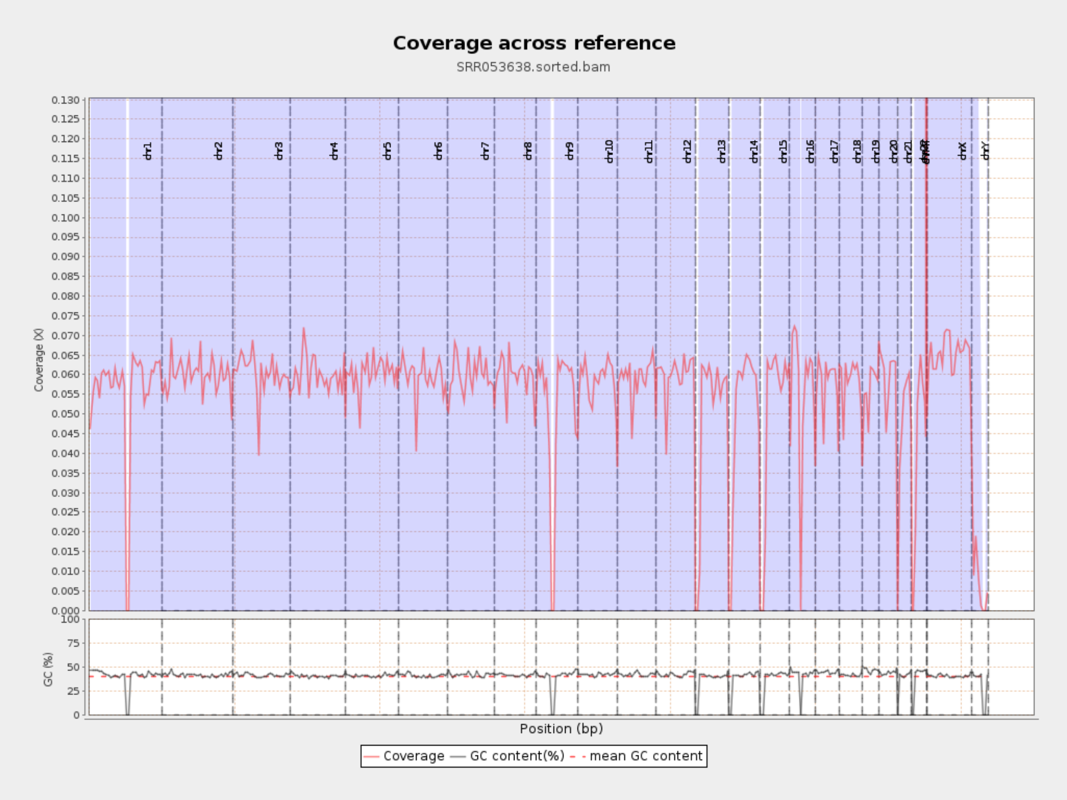
General error rate	0.6%
Mismatches	1,032,813
Insertions	7,821
Mapped reads with at least one insertion	0.21%
Deletions	22,436
Mapped reads with at least one deletion	0.59%
Homopolymer indels	41.52%

2.6. Chromosome stats

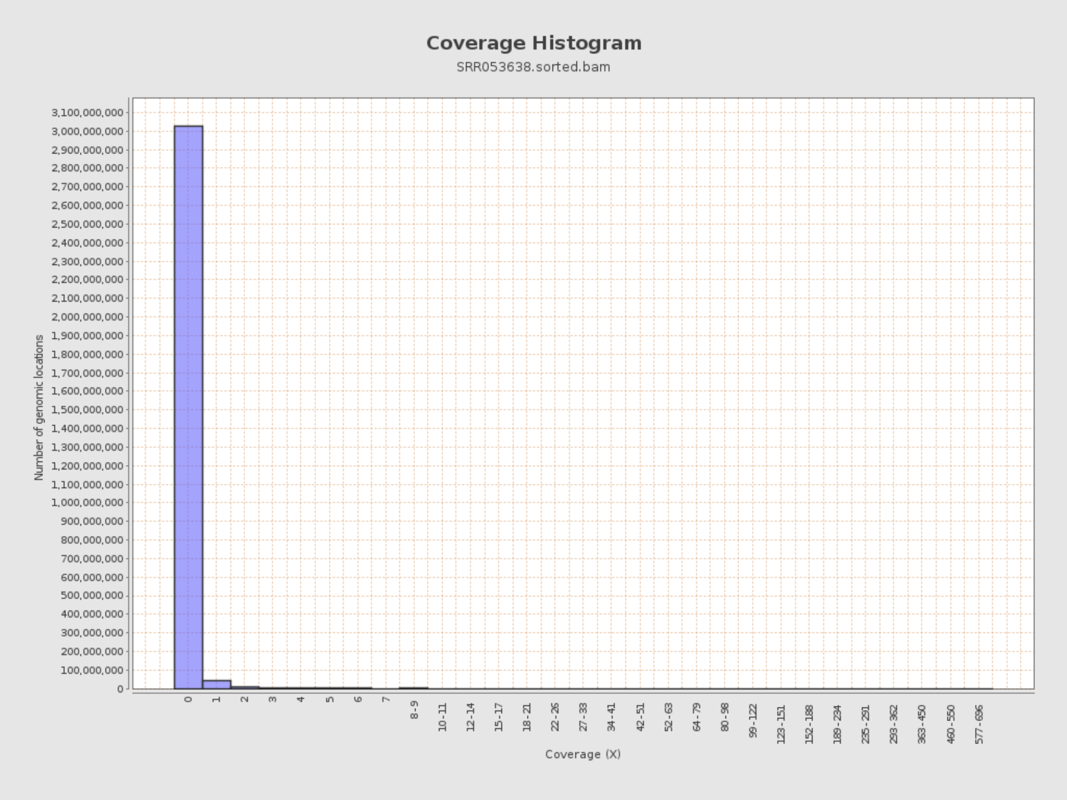
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13783550	0.0553	0.6651
chr2	243199373	14602269	0.06	0.7437
chr3	198022430	11975112	0.0605	0.6499
chr4	191154276	11465983	0.06	0.696
chr5	180915260	10927440	0.0604	0.7333
chr6	171115067	10178798	0.0595	0.7024
chr7	159138663	9594894	0.0603	0.7101

chr8	146364022	8749038	0.0598	0.6747
chr9	141213431	7229241	0.0512	0.6058
chr10	135534747	8010523	0.0591	0.6559
chr11	135006516	7968057	0.059	0.7336
chr12	133851895	7996304	0.0597	0.6537
chr13	115169878	5627439	0.0489	0.599
chr14	107349540	5373651	0.0501	0.6183
chr15	102531392	5054629	0.0493	0.5766
chr16	90354753	5029424	0.0557	0.6424
chr17	81195210	4654115	0.0573	0.6307
chr18	78077248	4593742	0.0588	0.6647
chr19	59128983	3329907	0.0563	0.6656
chr20	63025520	3700426	0.0587	0.6497
chr21	48129895	2216604	0.0461	0.6624
chr22	51304566	2013829	0.0393	0.5741
chrMT	16571	138925	8.3836	16.36
chrX	155270560	10099983	0.065	0.6853
chrY	59373566	444617	0.0075	0.1832

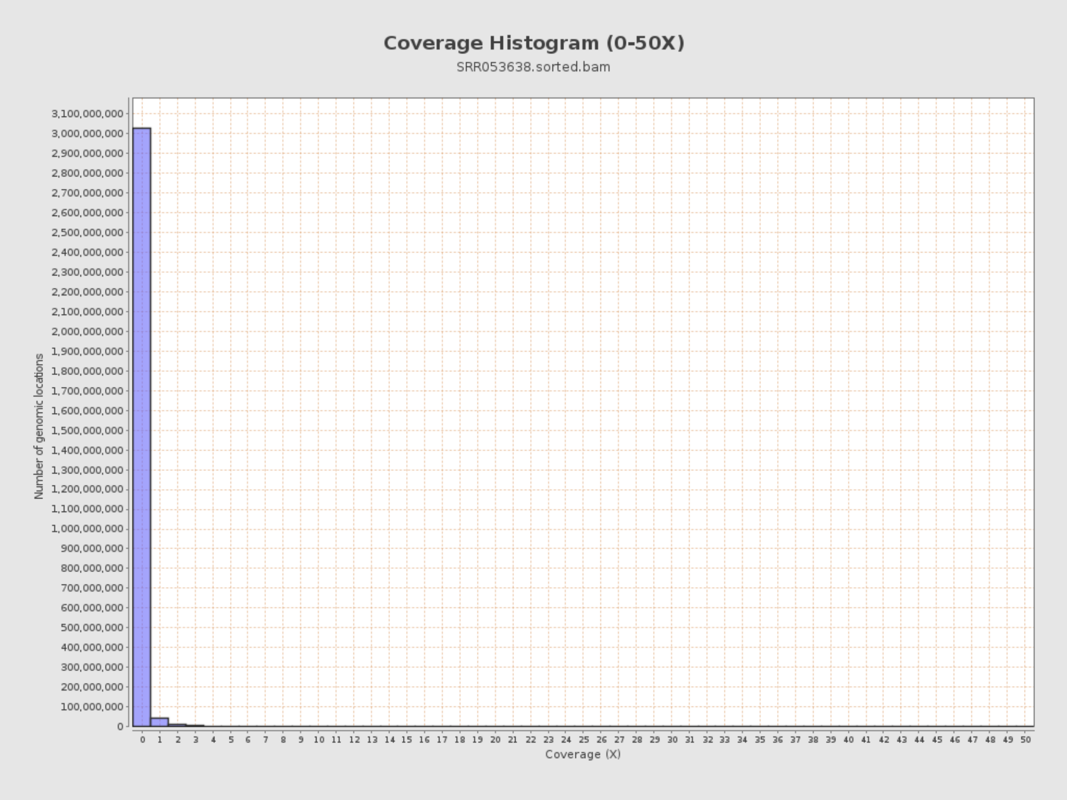
3. Results : Coverage across reference



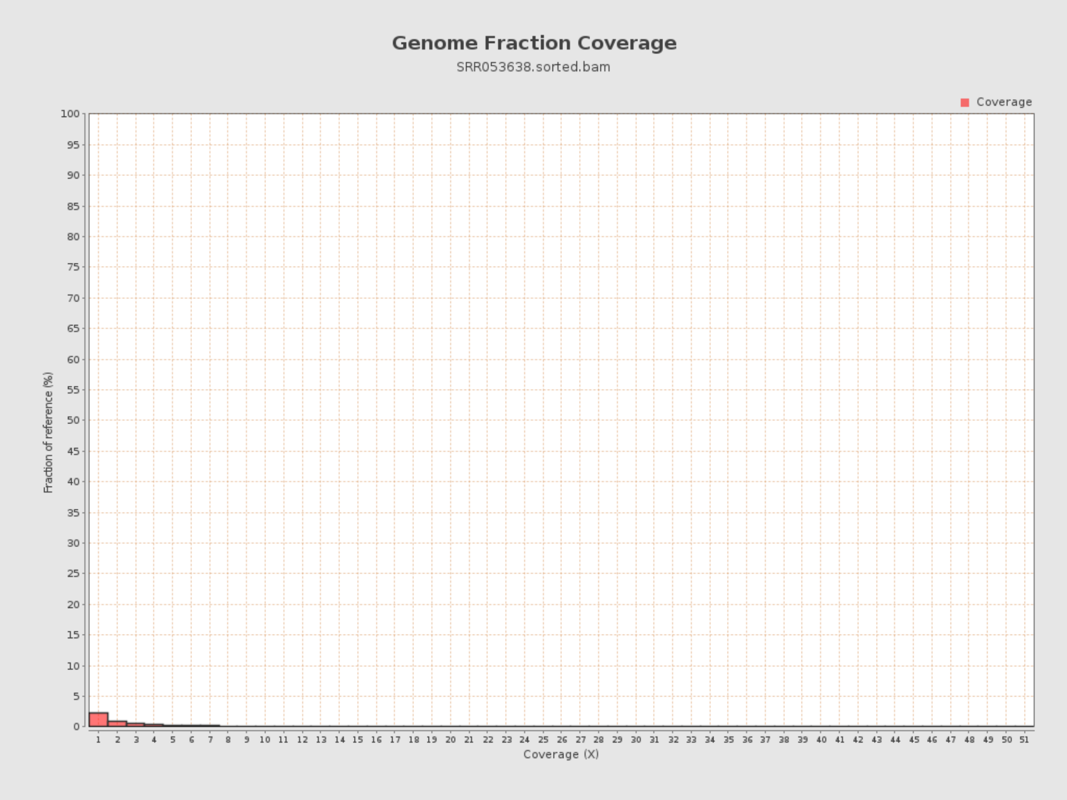
4. Results : Coverage Histogram



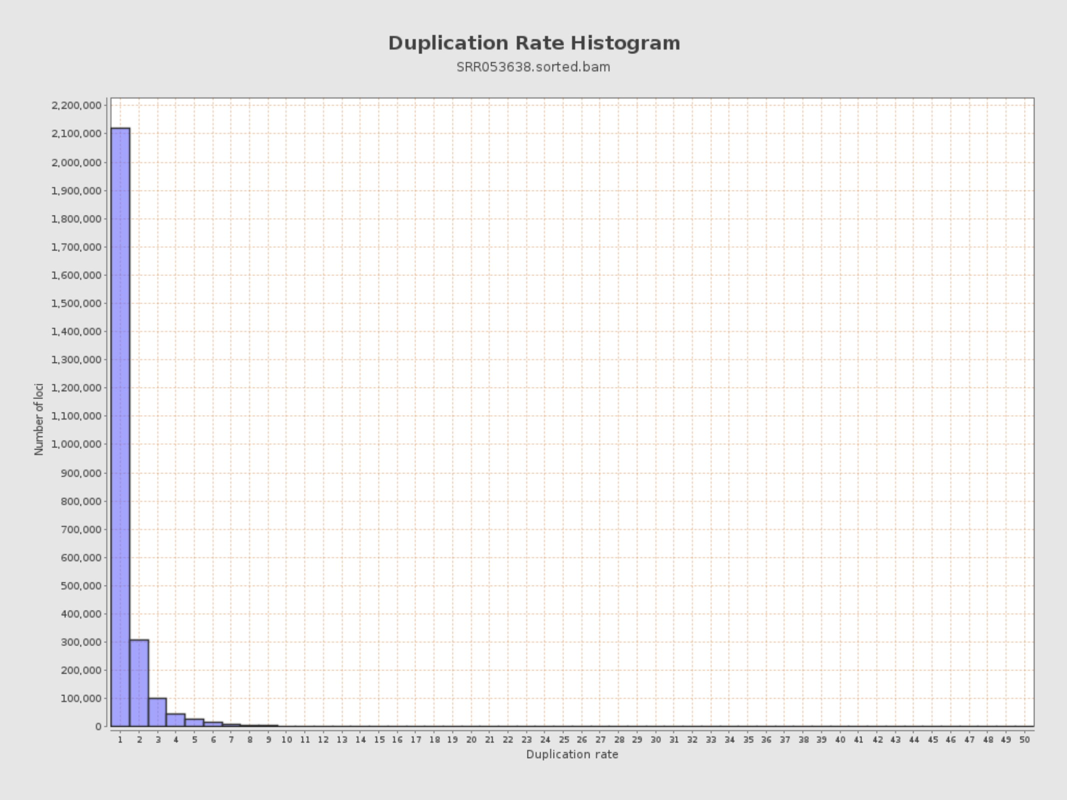
5. Results : Coverage Histogram (0-50X)



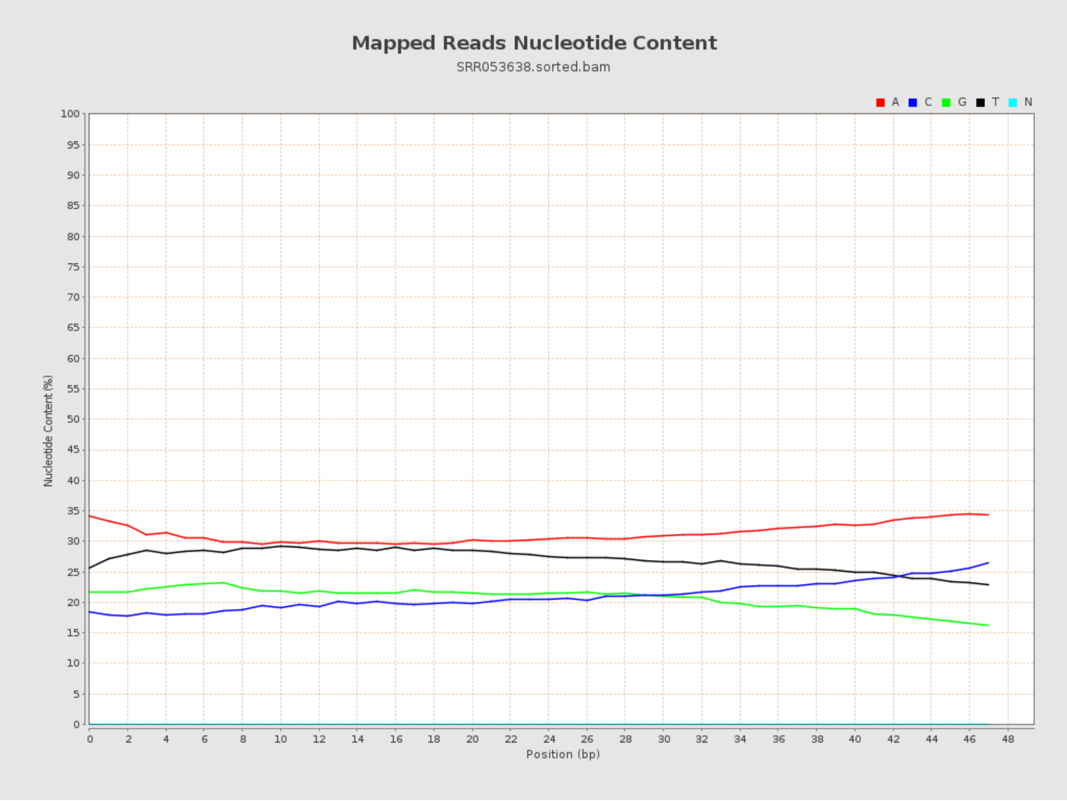
6. Results : Genome Fraction Coverage



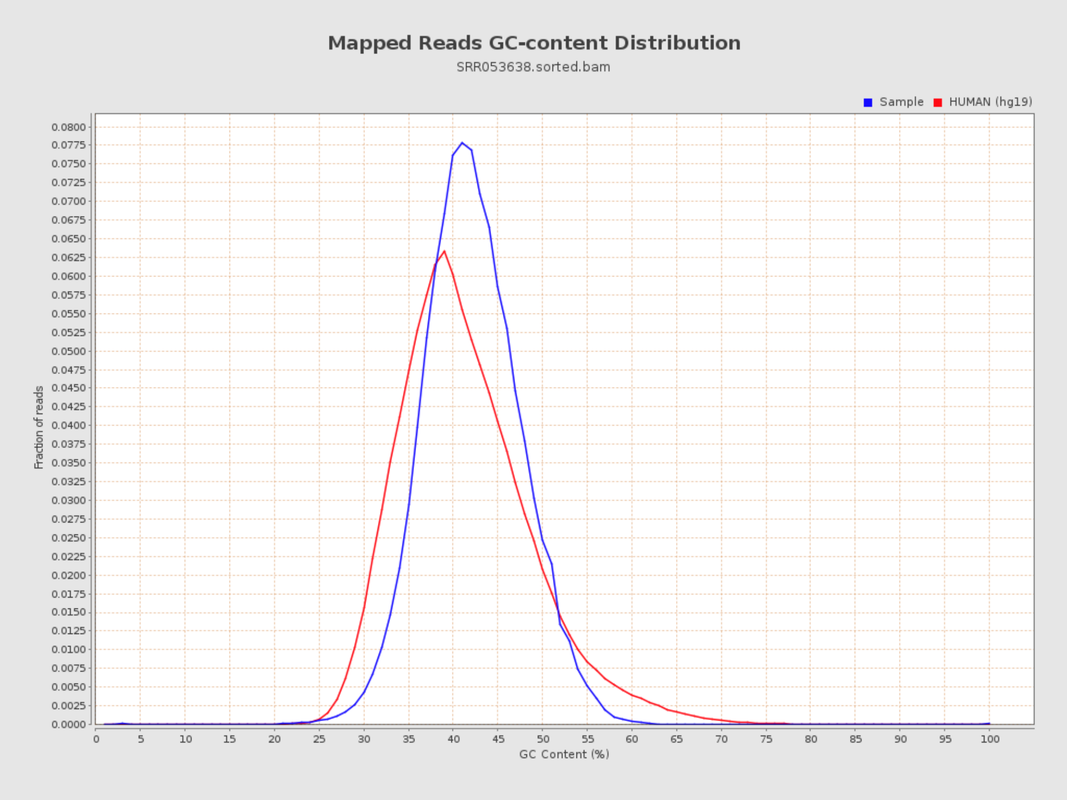
7. Results : Duplication Rate Histogram



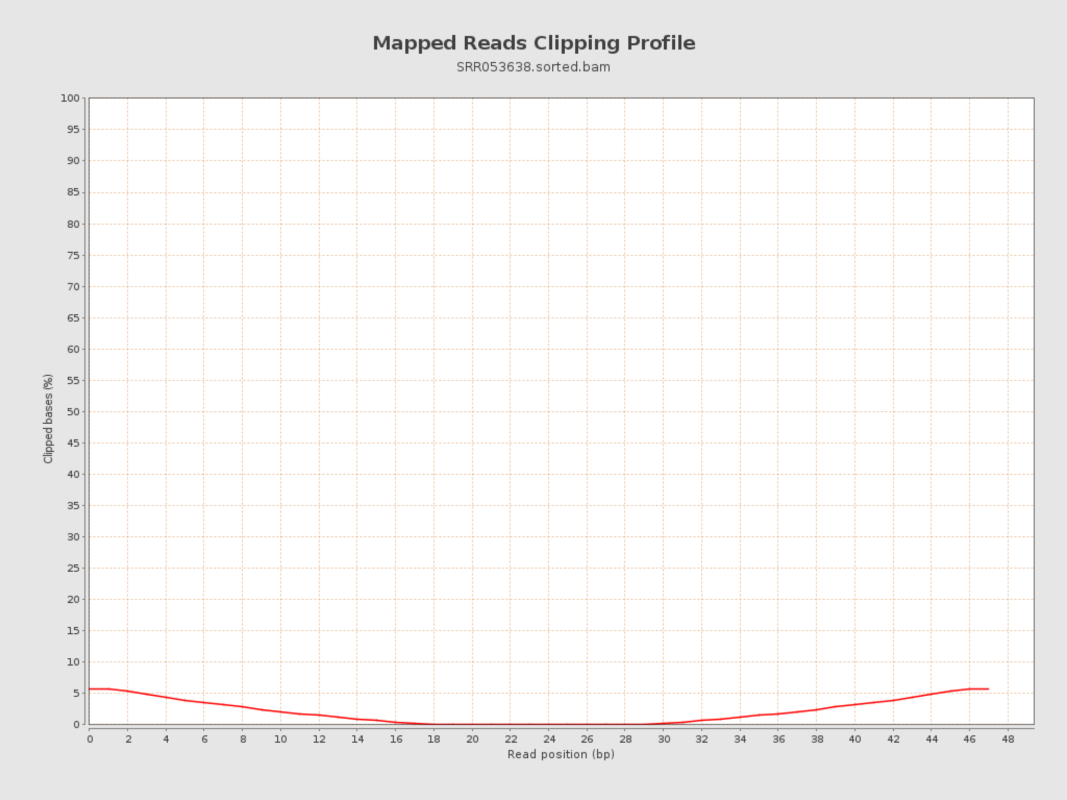
8. Results : Mapped Reads Nucleotide Content



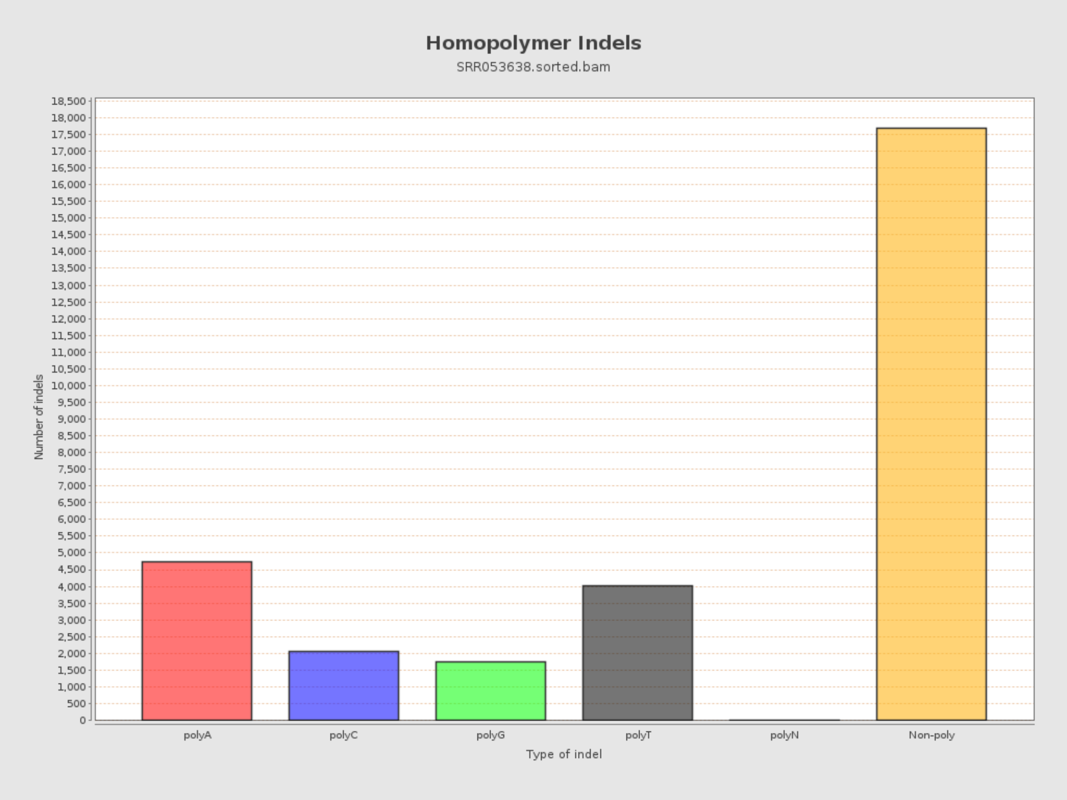
9. Results : Mapped Reads GC-content Distribution



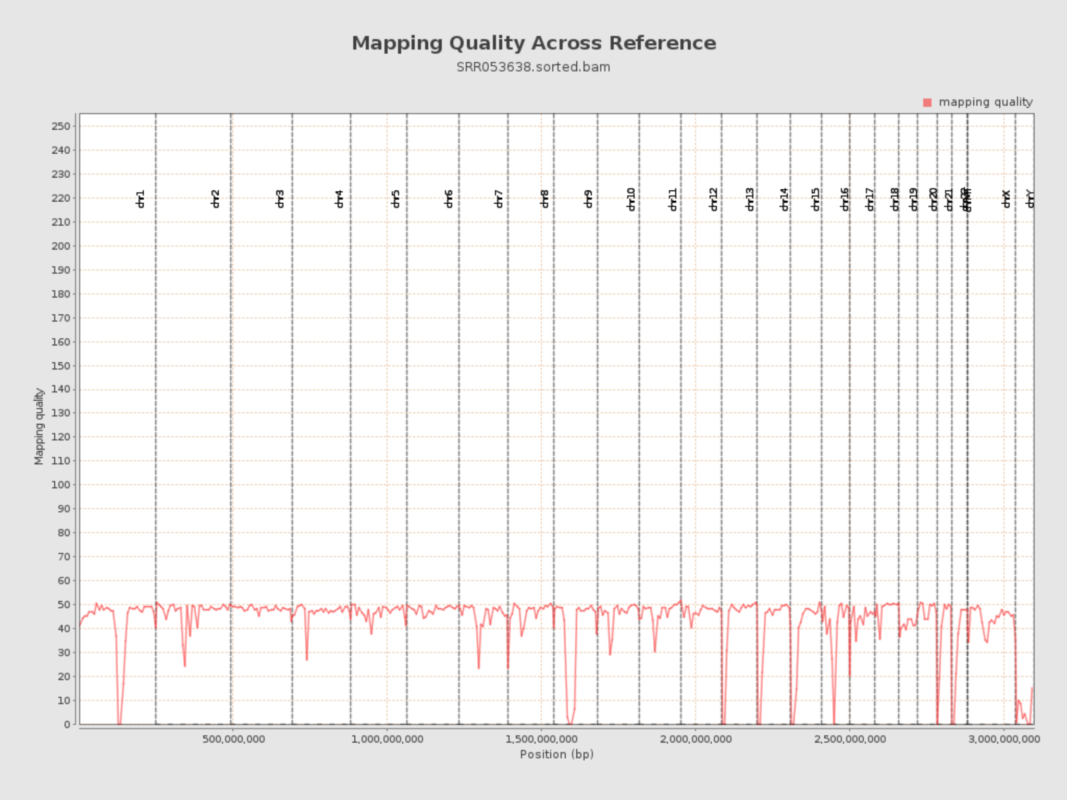
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram