Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 00:47:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053630.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_SRR053630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053630.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 00:47:46 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,568,573
Mapped reads	6,615,809 / 77.21%
Unmapped reads	1,952,764 / 22.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	166 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,528,007 / 17.83%
Duplication rate	16.22%
Clipped reads	677,265 / 7.9%

2.2. ACGT Content

Number/percentage of A's	93,065,885 / 29.88%
Number/percentage of C's	61,966,980 / 19.89%
Number/percentage of T's	90,256,882 / 28.97%
Number/percentage of G's	66,213,599 / 21.26%
Number/percentage of N's	6,389 / 0%
GC Percentage	41.15%

2.3. Coverage

Mean	0.1006

Standard Deviation	0.837

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

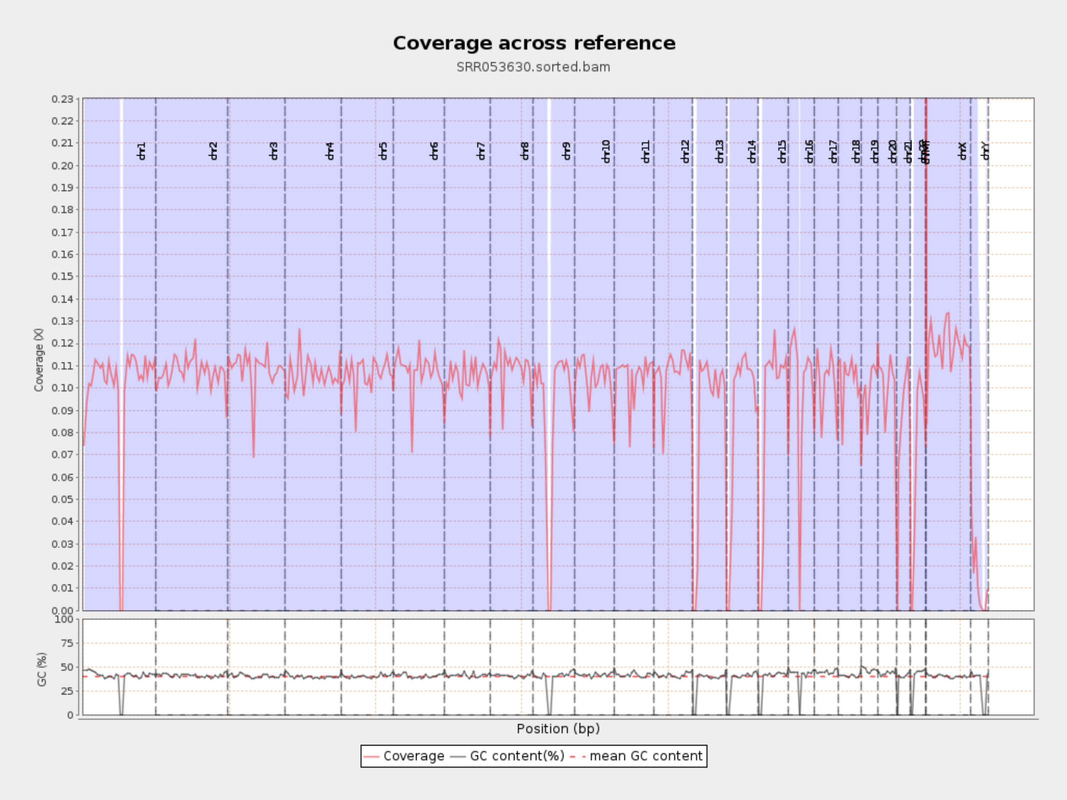
General error rate	0.67%
Mismatches	2,056,504
Insertions	12,977
Mapped reads with at least one insertion	0.2%
Deletions	42,018
Mapped reads with at least one deletion	0.63%
Homopolymer indels	45.67%

2.6. Chromosome stats

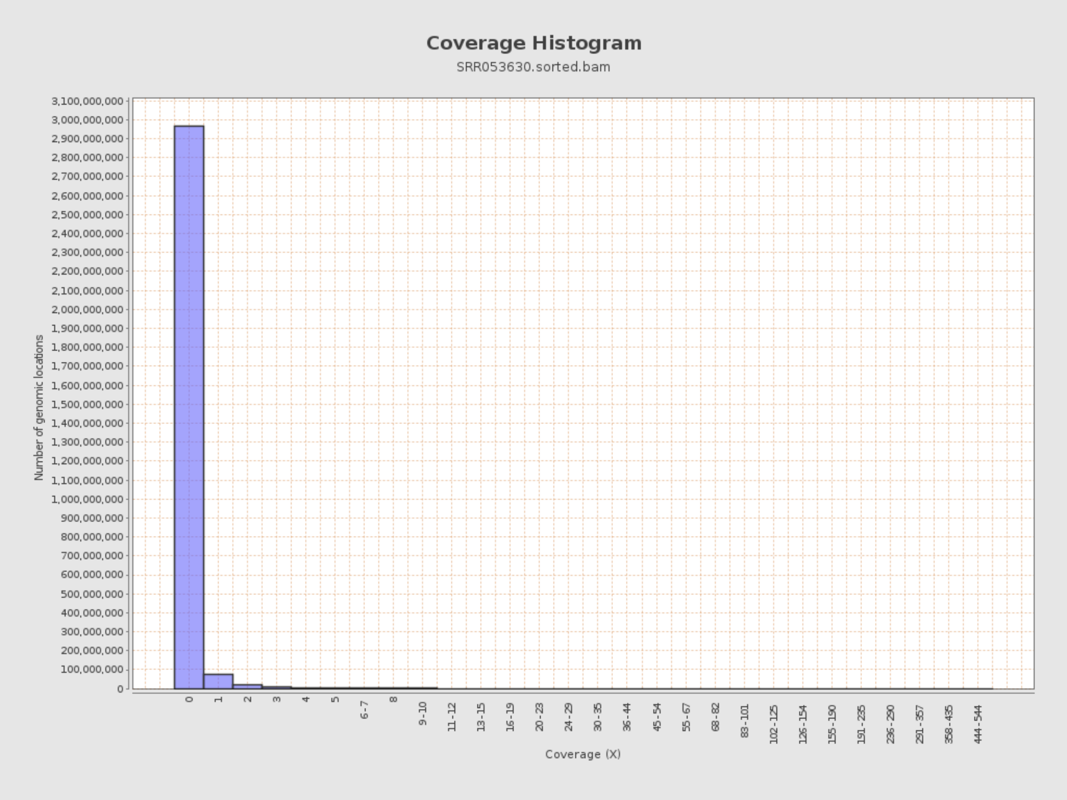
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24823416	0.0996	0.8539
chr2	243199373	26138077	0.1075	0.9047
chr3	198022430	21476997	0.1085	0.832
chr4	191154276	20337573	0.1064	0.8607
chr5	180915260	19162003	0.1059	0.8191
chr6	171115067	18431921	0.1077	0.8806
chr7	159138663	16711976	0.105	0.8705

chr8	146364022	15880144	0.1085	0.872
chr9	141213431	12741624	0.0902	0.7656
chr10	135534747	14292924	0.1055	0.8619
chr11	135006516	14155852	0.1049	0.8743
chr12	133851895	14394523	0.1075	0.8501
chr13	115169878	10033167	0.0871	0.7464
chr14	107349540	9513169	0.0886	0.8183
chr15	102531392	9123327	0.089	0.7574
chr16	90354753	8832231	0.0978	0.8272
chr17	81195210	8394532	0.1034	0.8142
chr18	78077248	8124641	0.1041	0.87
chr19	59128983	5835586	0.0987	0.8487
chr20	63025520	6365890	0.101	0.803
chr21	48129895	4011744	0.0834	0.824
chr22	51304566	3494775	0.0681	0.6209
chrMT	16571	60356	3.6423	8.0021
chrX	155270560	18454440	0.1189	0.9078
chrY	59373566	781321	0.0132	0.2859

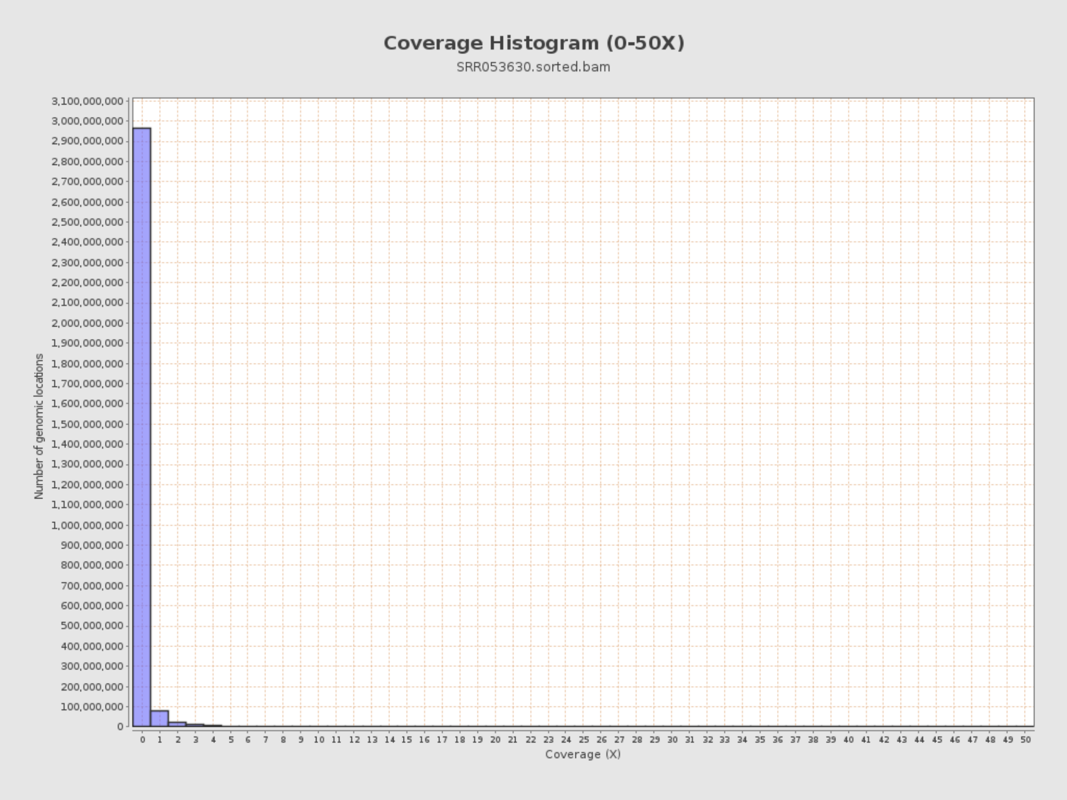
3. Results : Coverage across reference



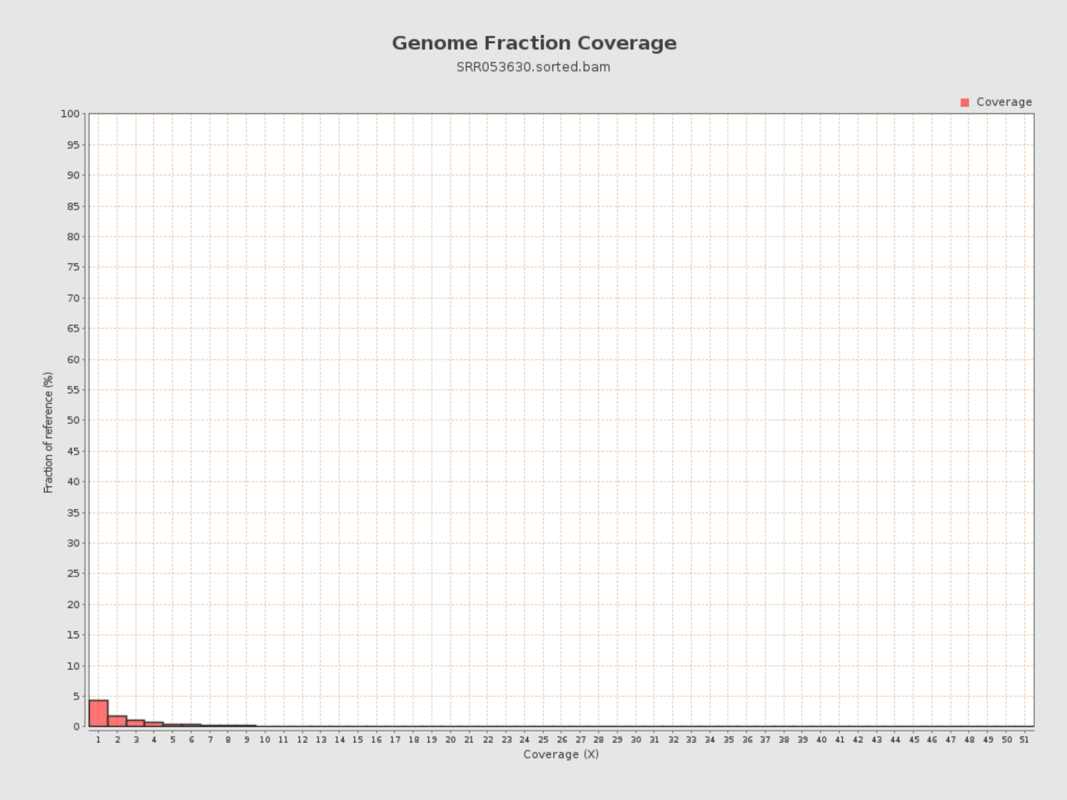
4. Results : Coverage Histogram



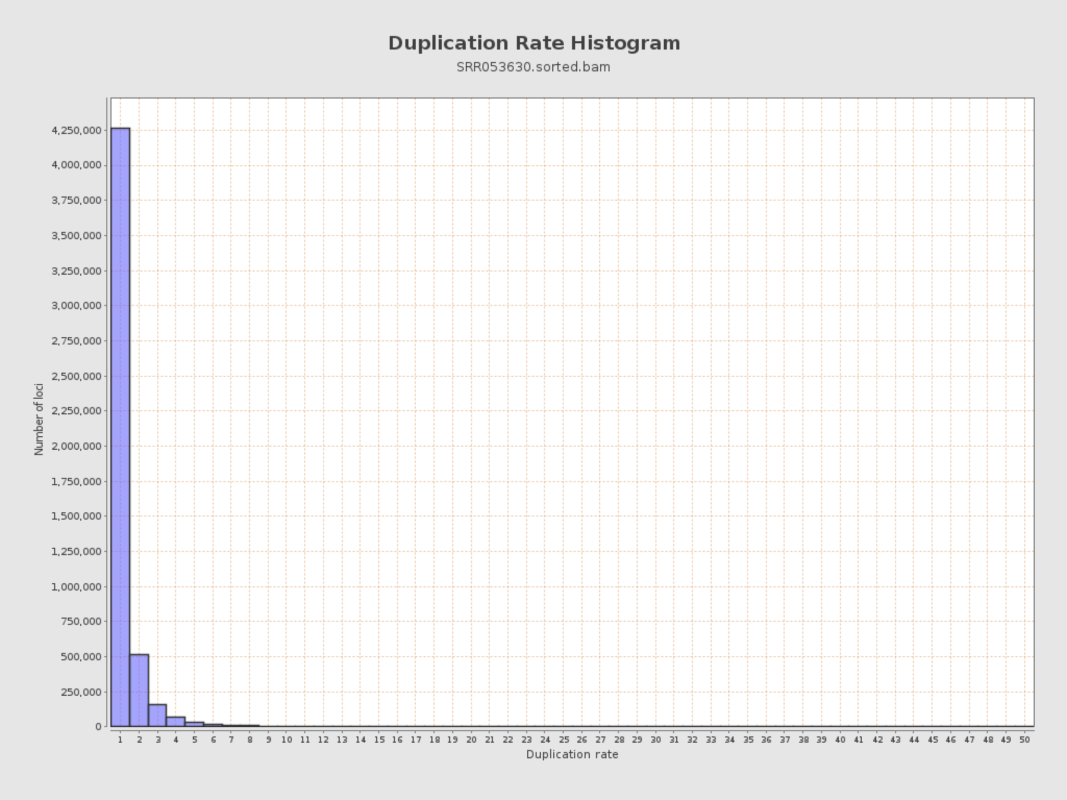
5. Results : Coverage Histogram (0-50X)



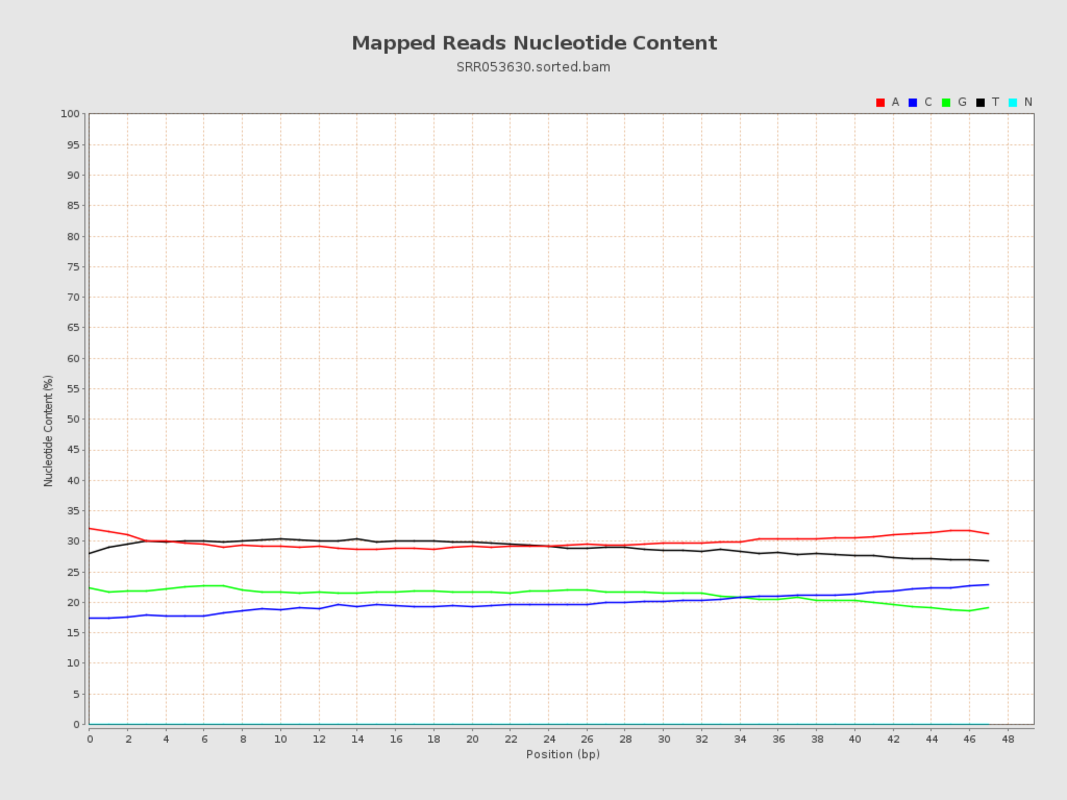
6. Results : Genome Fraction Coverage



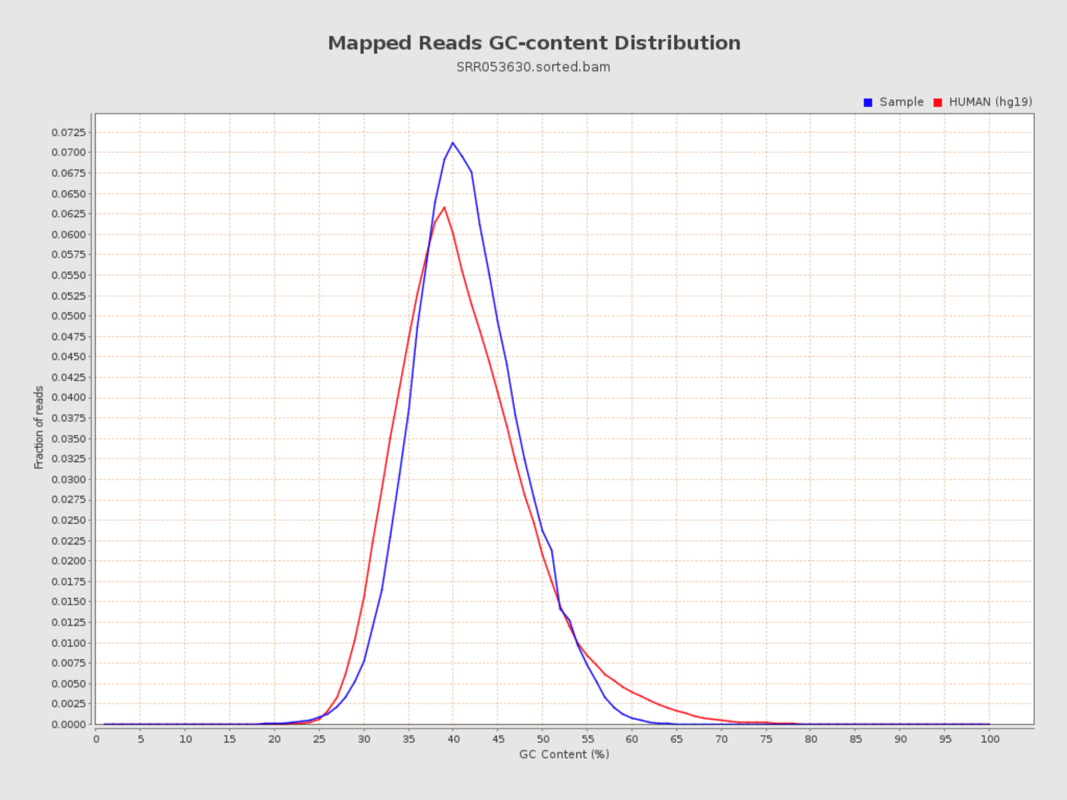
7. Results : Duplication Rate Histogram



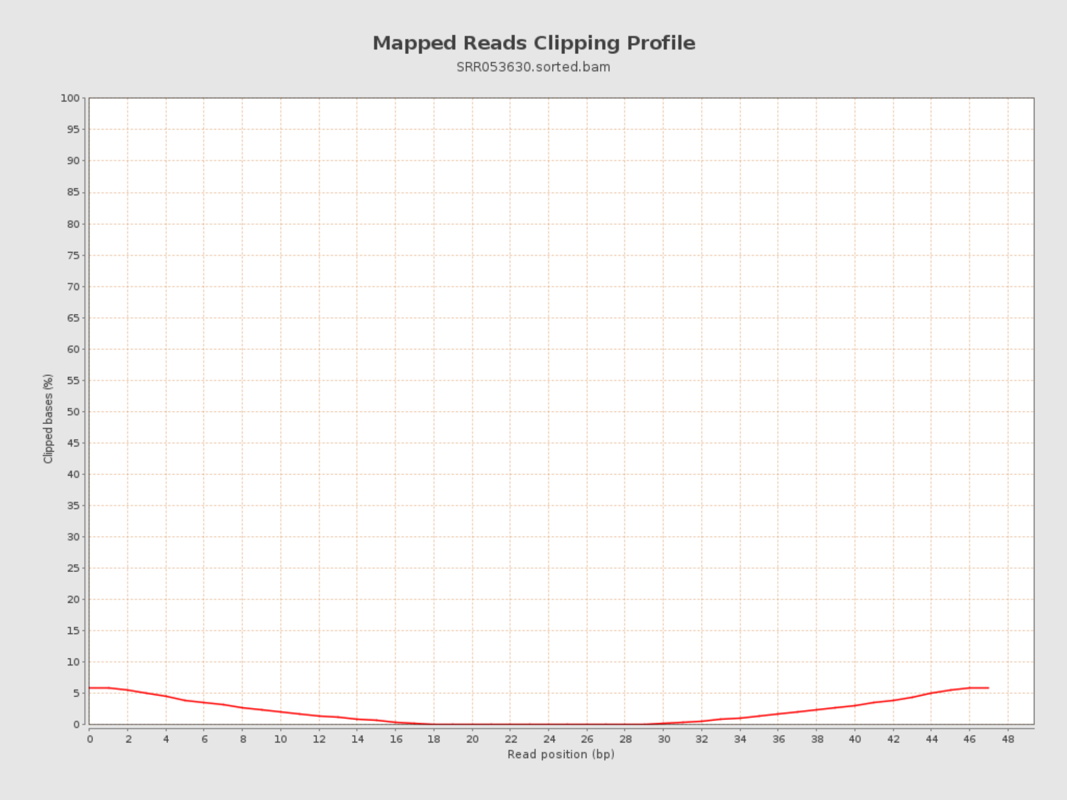
8. Results : Mapped Reads Nucleotide Content



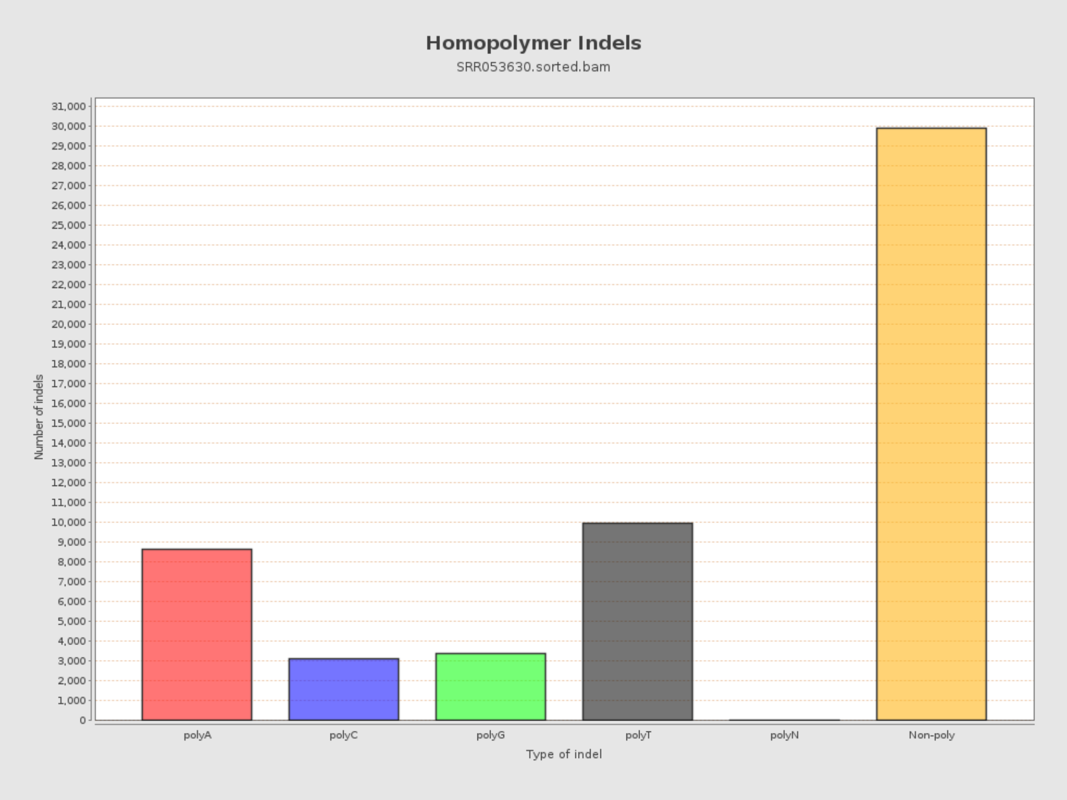
9. Results : Mapped Reads GC-content Distribution



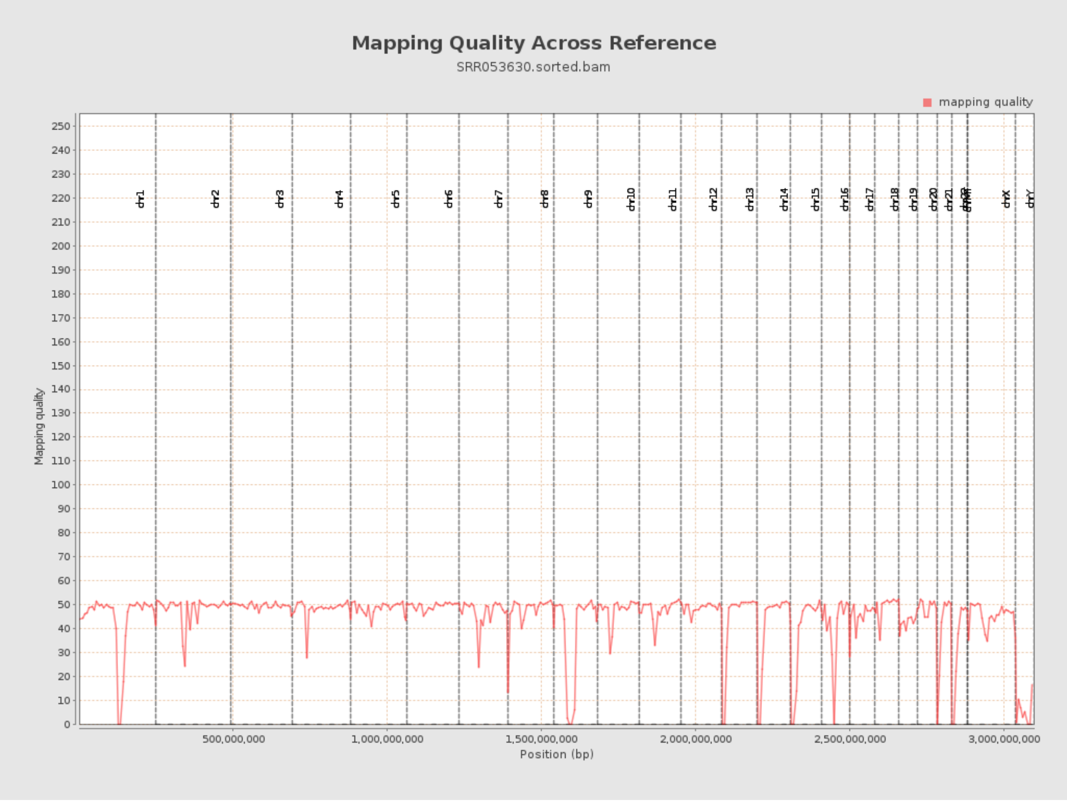
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram