Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 07:22:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR054611.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_SRR054611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 07:22:43 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR054611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,350,656
Mapped reads	13,119,903 / 75.62%
Unmapped reads	4,230,753 / 24.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	344 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,882,277 / 22.38%
Duplication rate	20.55%
Clipped reads	874,883 / 5.04%

2.2. ACGT Content

Number/percentage of A's	186,687,983 / 30.02%
Number/percentage of C's	113,256,400 / 18.21%
Number/percentage of T's	195,019,596 / 31.36%
Number/percentage of G's	126,902,114 / 20.41%
Number/percentage of N's	2,966 / 0%
GC Percentage	38.62%

2.3. Coverage

Mean	0.2009

Standard Deviation	1.5678

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

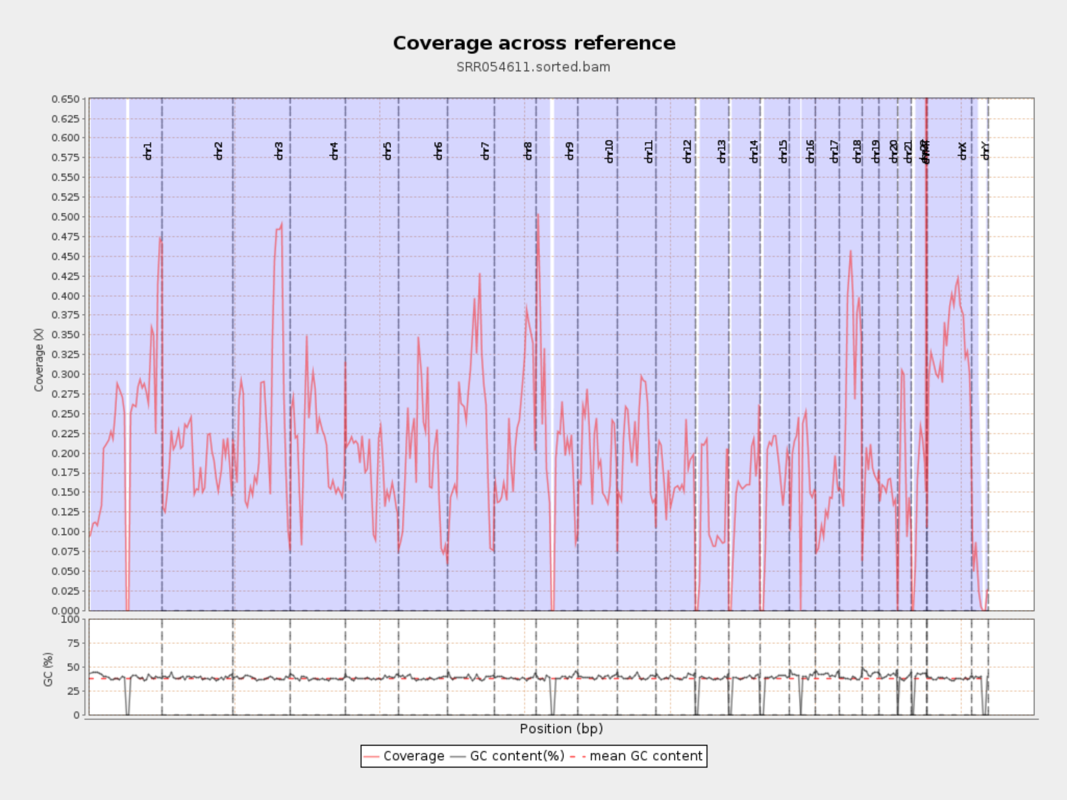
General error rate	0.52%
Mismatches	3,185,923
Insertions	25,022
Mapped reads with at least one insertion	0.19%
Deletions	85,857
Mapped reads with at least one deletion	0.65%
Homopolymer indels	49.56%

2.6. Chromosome stats

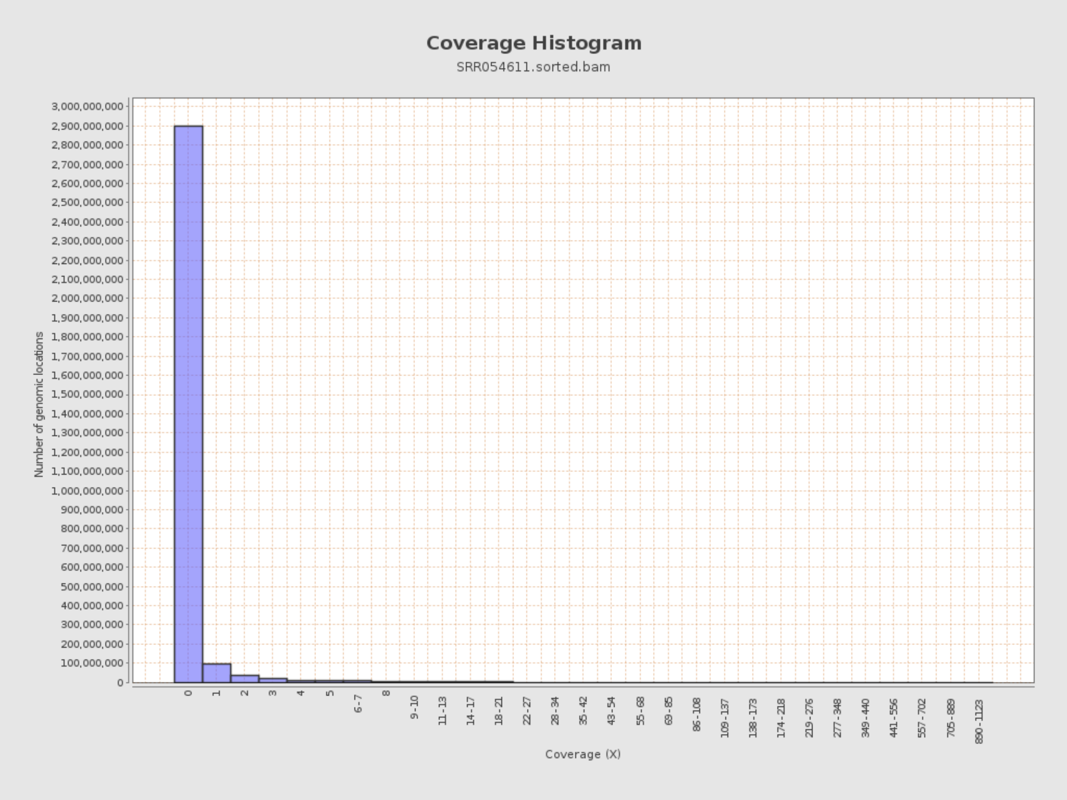
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	57885583	0.2322	1.7814
chr2	243199373	46401681	0.1908	1.6828
chr3	198022430	49304270	0.249	1.6578
chr4	191154276	39951122	0.209	1.5394
chr5	180915260	32364052	0.1789	1.3211
chr6	171115067	31336409	0.1831	1.4318
chr7	159138663	38562117	0.2423	1.7353

chr8	146364022	33935989	0.2319	1.698
chr9	141213431	29745918	0.2106	1.6037
chr10	135534747	27028054	0.1994	1.6366
chr11	135006516	28752449	0.213	1.5673
chr12	133851895	22926082	0.1713	1.277
chr13	115169878	12675735	0.1101	1.0052
chr14	107349540	15456010	0.144	1.354
chr15	102531392	16039921	0.1564	1.2103
chr16	90354753	16231819	0.1796	1.4874
chr17	81195210	10231519	0.126	1.0325
chr18	78077248	24148978	0.3093	2.2441
chr19	59128983	10257978	0.1735	1.4809
chr20	63025520	9347554	0.1483	1.2545
chr21	48129895	8354075	0.1736	1.533
chr22	51304566	6969883	0.1359	1.1183
chrMT	16571	68489	4.1331	9.822
chrX	155270560	52095458	0.3355	2.1164
chrY	59373566	1925418	0.0324	0.7463

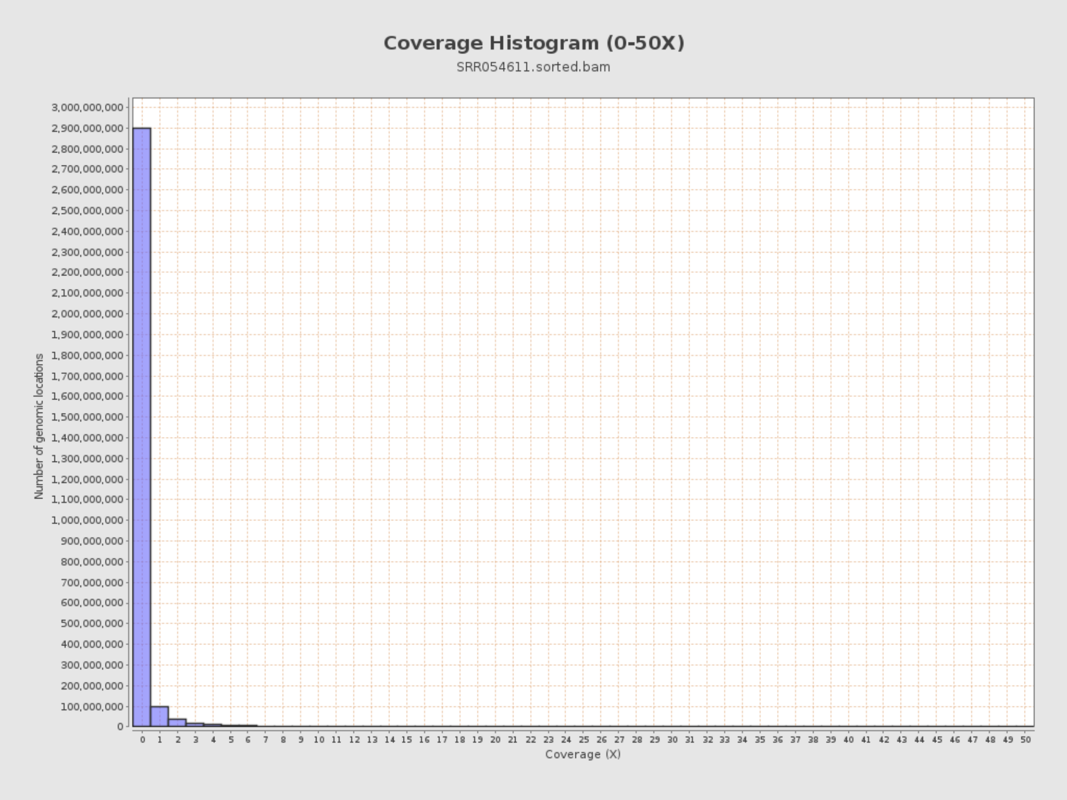
3. Results : Coverage across reference



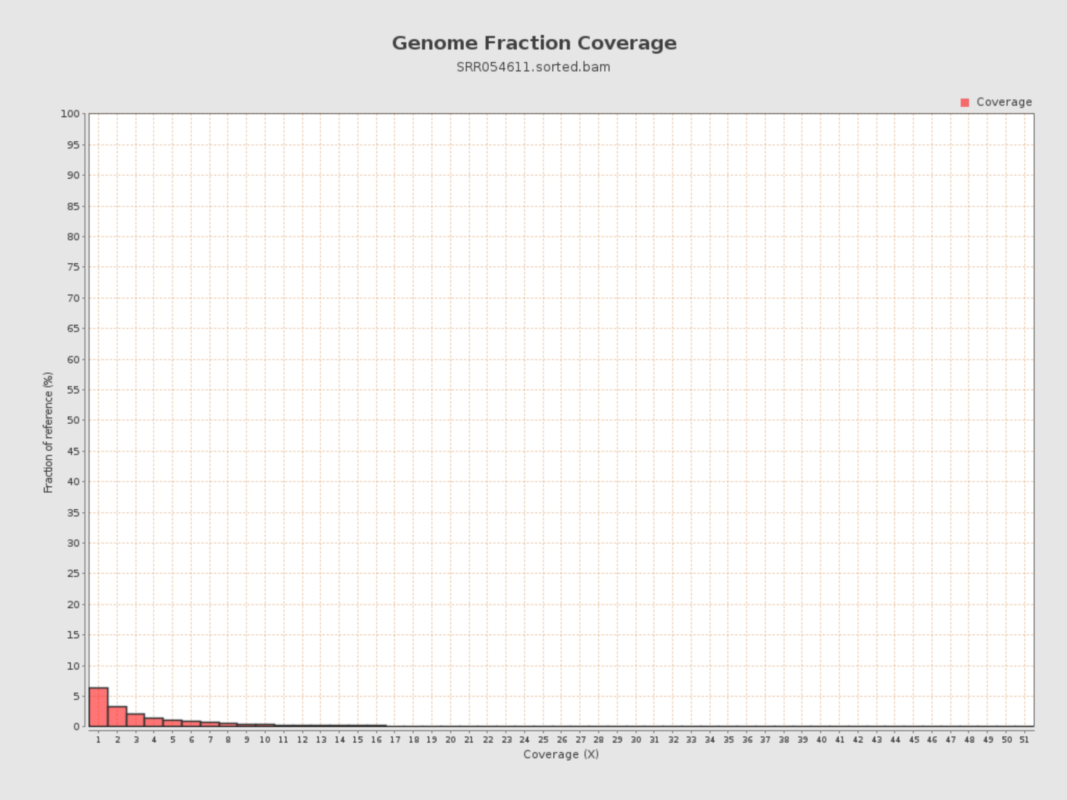
4. Results : Coverage Histogram



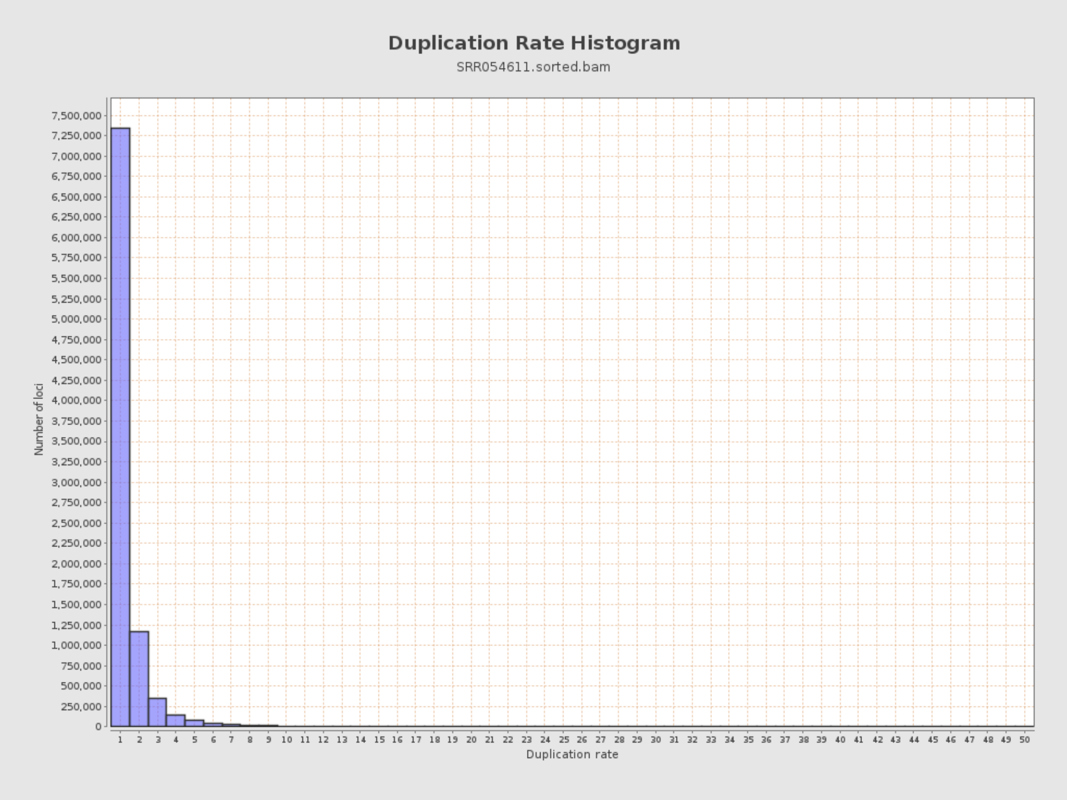
5. Results : Coverage Histogram (0-50X)



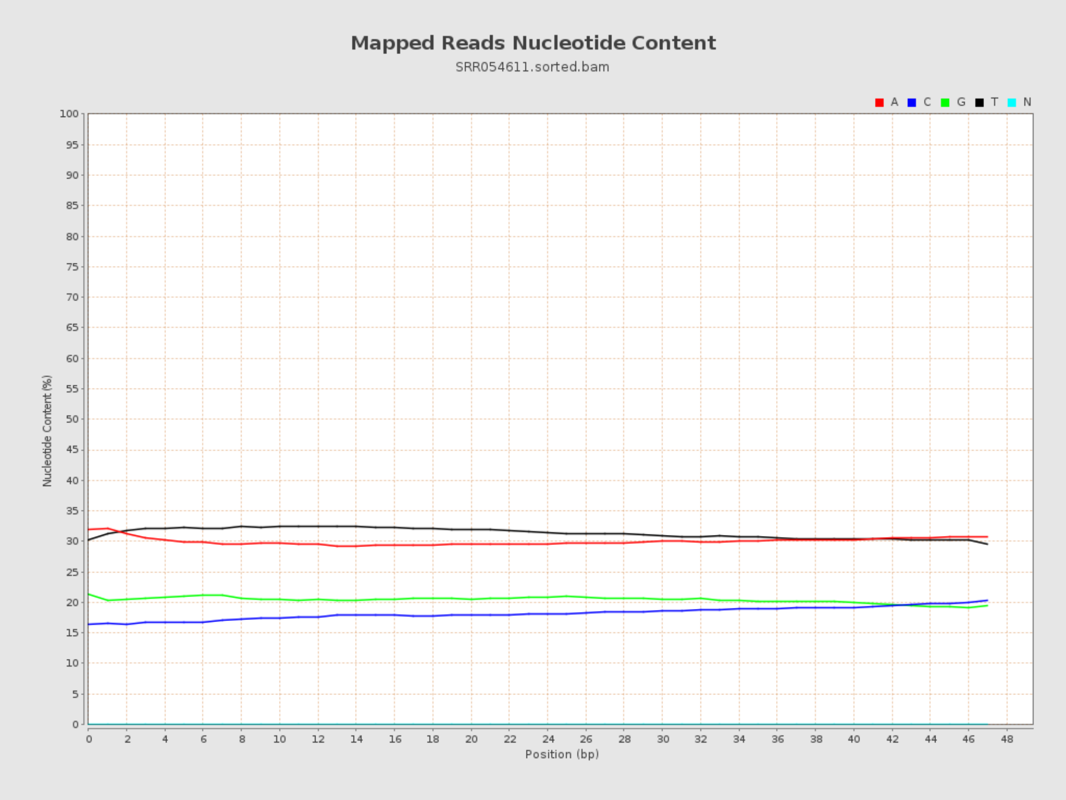
6. Results : Genome Fraction Coverage



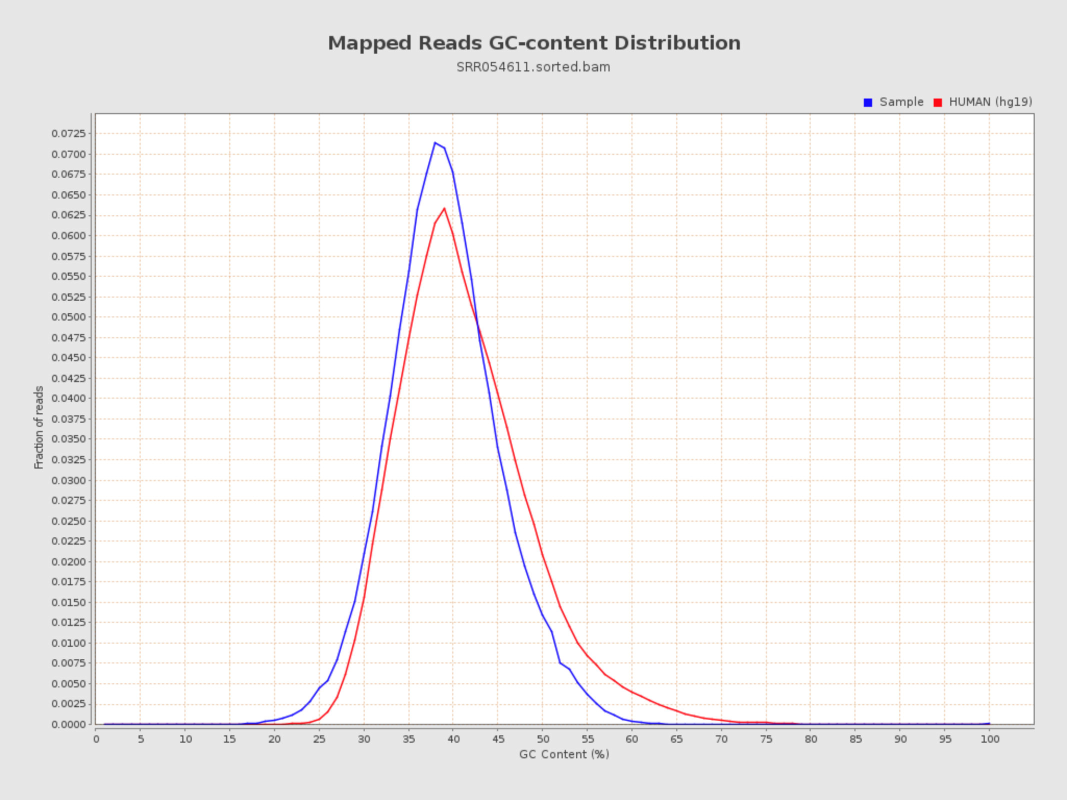
7. Results : Duplication Rate Histogram



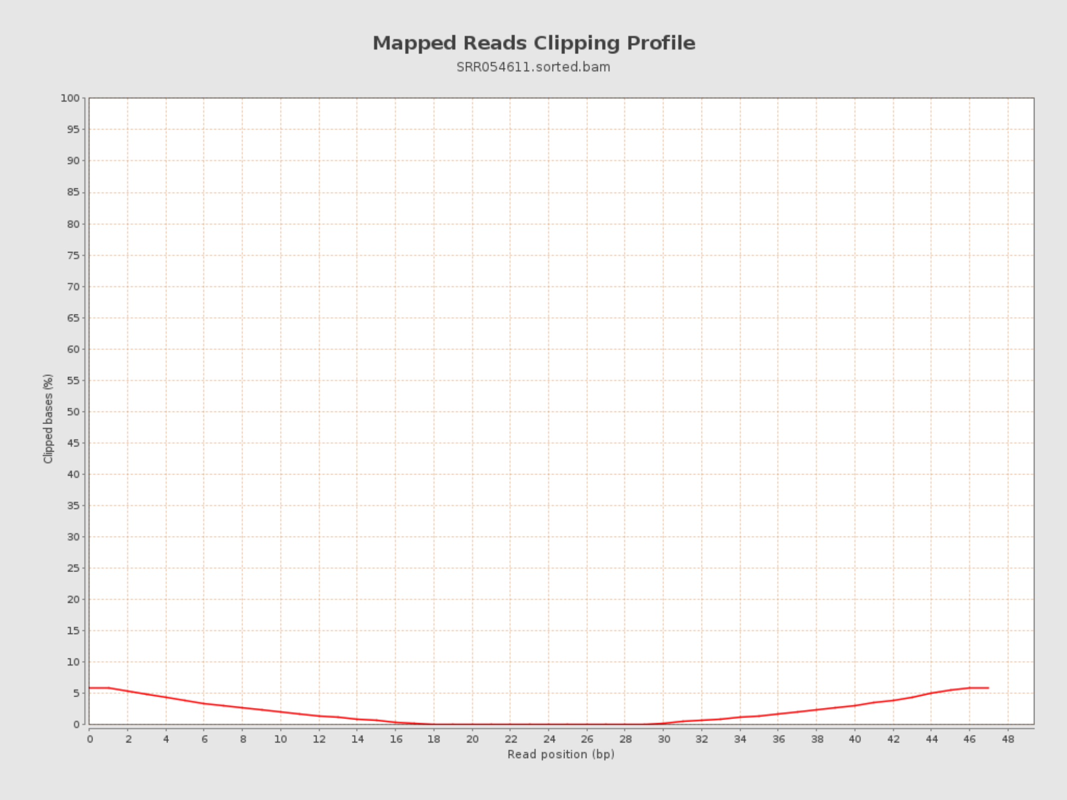
8. Results : Mapped Reads Nucleotide Content



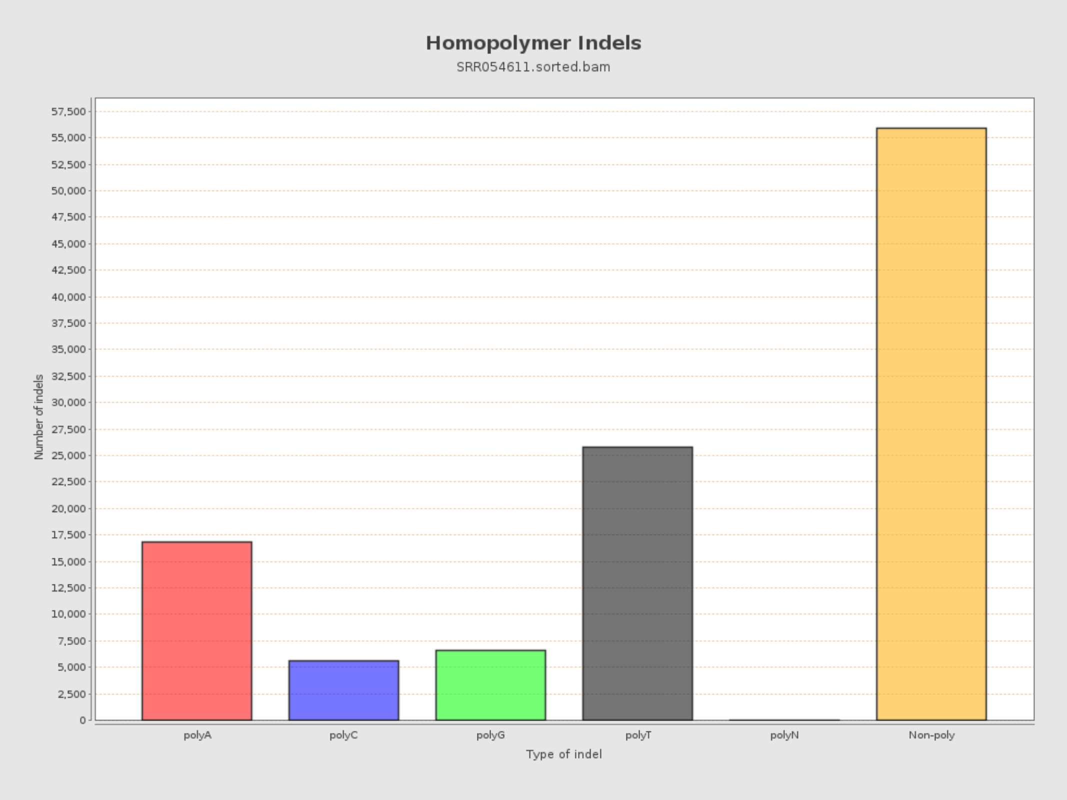
9. Results : Mapped Reads GC-content Distribution



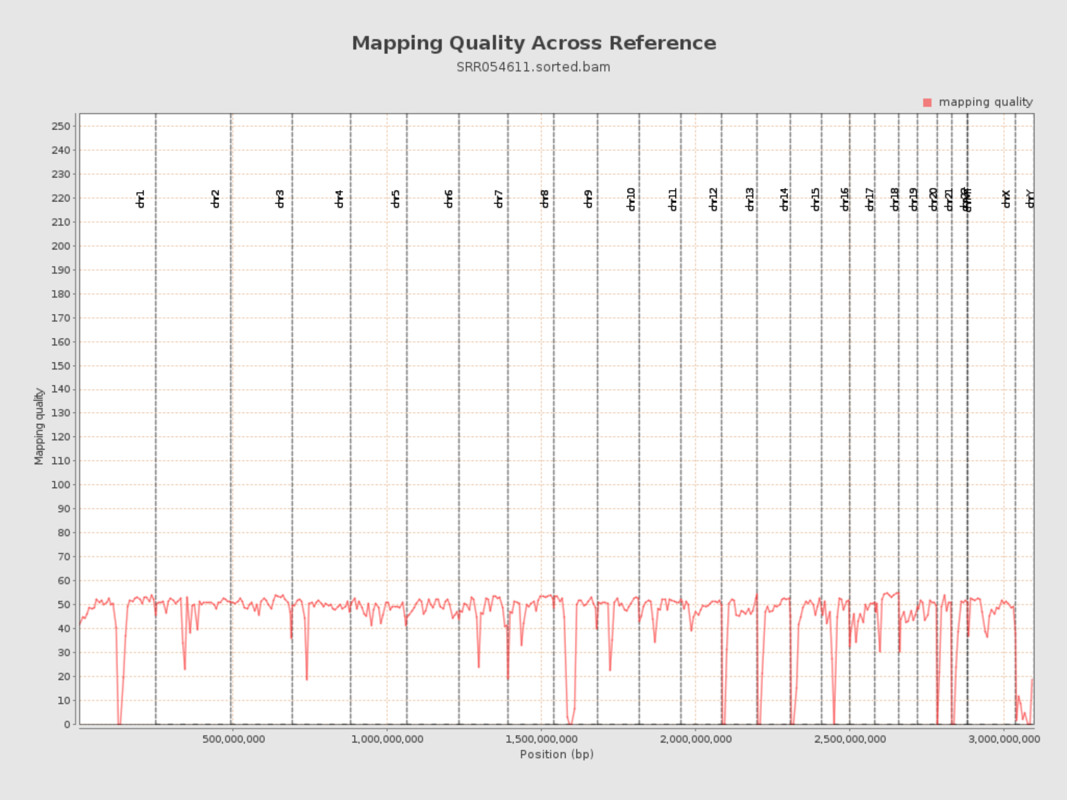
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram