Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 02:10:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053666.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_SRR053666 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053666.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 02:10:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053666.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,450,119
Mapped reads	11,189,187 / 77.43%
Unmapped reads	3,260,932 / 22.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	364 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,282,844 / 22.72%
Duplication rate	20.02%
Clipped reads	787,368 / 5.45%

2.2. ACGT Content

Number/percentage of A's	159,656,472 / 30.12%
Number/percentage of C's	98,303,998 / 18.55%
Number/percentage of T's	163,063,363 / 30.76%
Number/percentage of G's	108,594,937 / 20.49%
Number/percentage of N's	422,979 / 0.08%
GC Percentage	39.03%

2.3. Coverage

Mean	0.1713

Standard Deviation	1.2652

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

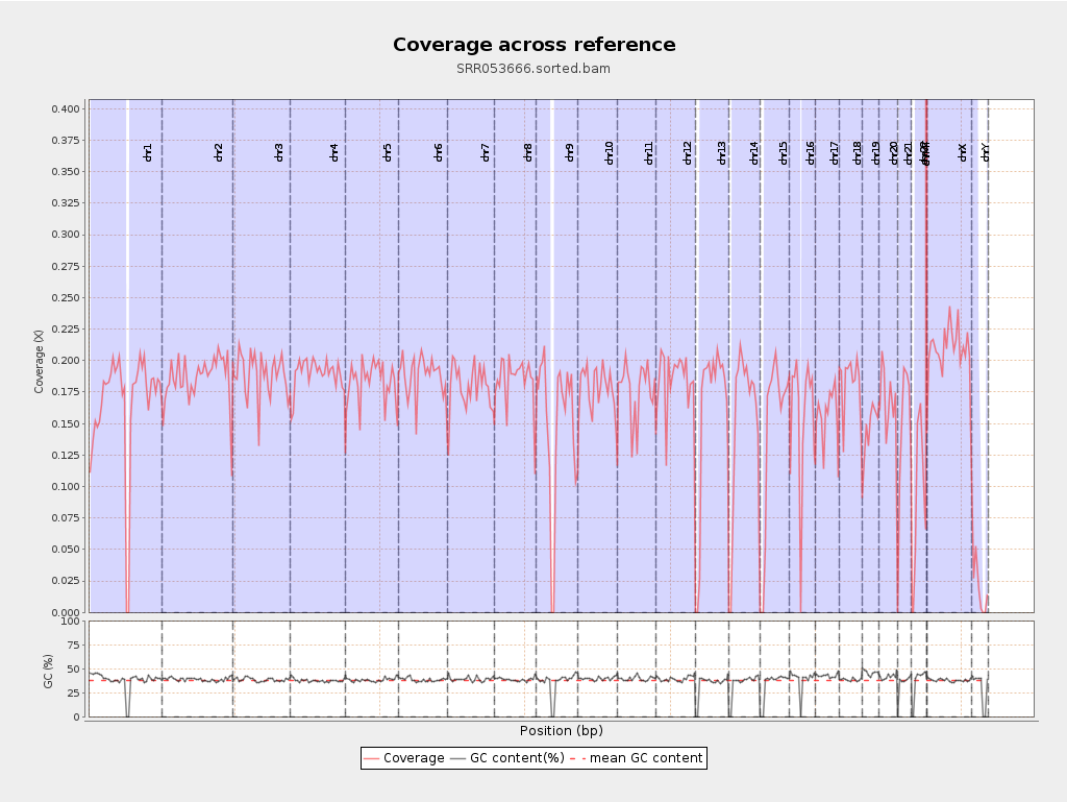
General error rate	0.6%
Mismatches	3,156,067
Insertions	23,153
Mapped reads with at least one insertion	0.21%
Deletions	72,733
Mapped reads with at least one deletion	0.65%
Homopolymer indels	49.18%

2.6. Chromosome stats

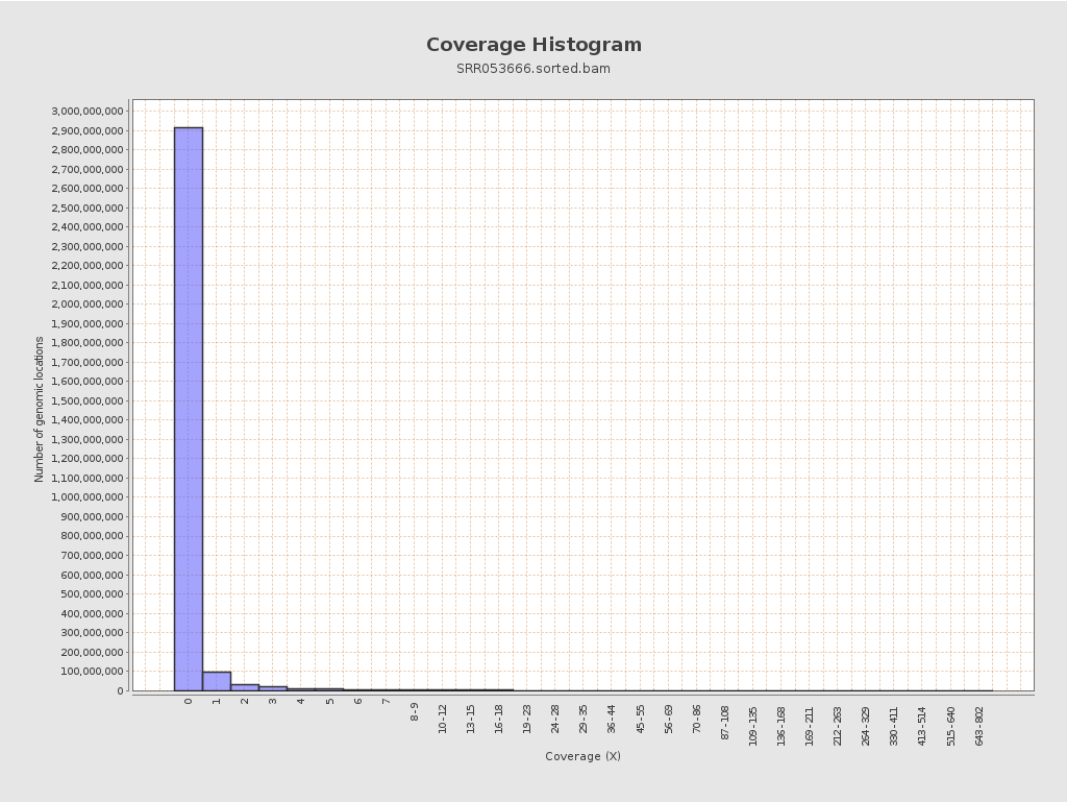
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	41393822	0.1661	1.3316
chr2	243199373	45355109	0.1865	1.4006
chr3	198022430	37429379	0.189	1.2709
chr4	191154276	36255759	0.1897	1.3539
chr5	180915260	33127646	0.1831	1.2342
chr6	171115067	32136935	0.1878	1.2995
chr7	159138663	28729162	0.1805	1.2968

chr8	146364022	27003404	0.1845	1.3482
chr9	141213431	21109945	0.1495	1.148
chr10	135534747	24319297	0.1794	1.2969
chr11	135006516	23816402	0.1764	1.3195
chr12	133851895	24603819	0.1838	1.2354
chr13	115169878	18170587	0.1578	1.2234
chr14	107349540	16335973	0.1522	1.2425
chr15	102531392	14900570	0.1453	1.0709
chr16	90354753	14139209	0.1565	1.1472
chr17	81195210	12681003	0.1562	1.1008
chr18	78077248	14246125	0.1825	1.3908
chr19	59128983	8671664	0.1467	1.1644
chr20	63025520	10523710	0.167	1.1618
chr21	48129895	6925793	0.1439	1.1571
chr22	51304566	4540868	0.0885	0.8002
chrMT	16571	64658	3.9019	11.4394
chrX	155270560	32423520	0.2088	1.4168
chrY	59373566	1245550	0.021	0.4327

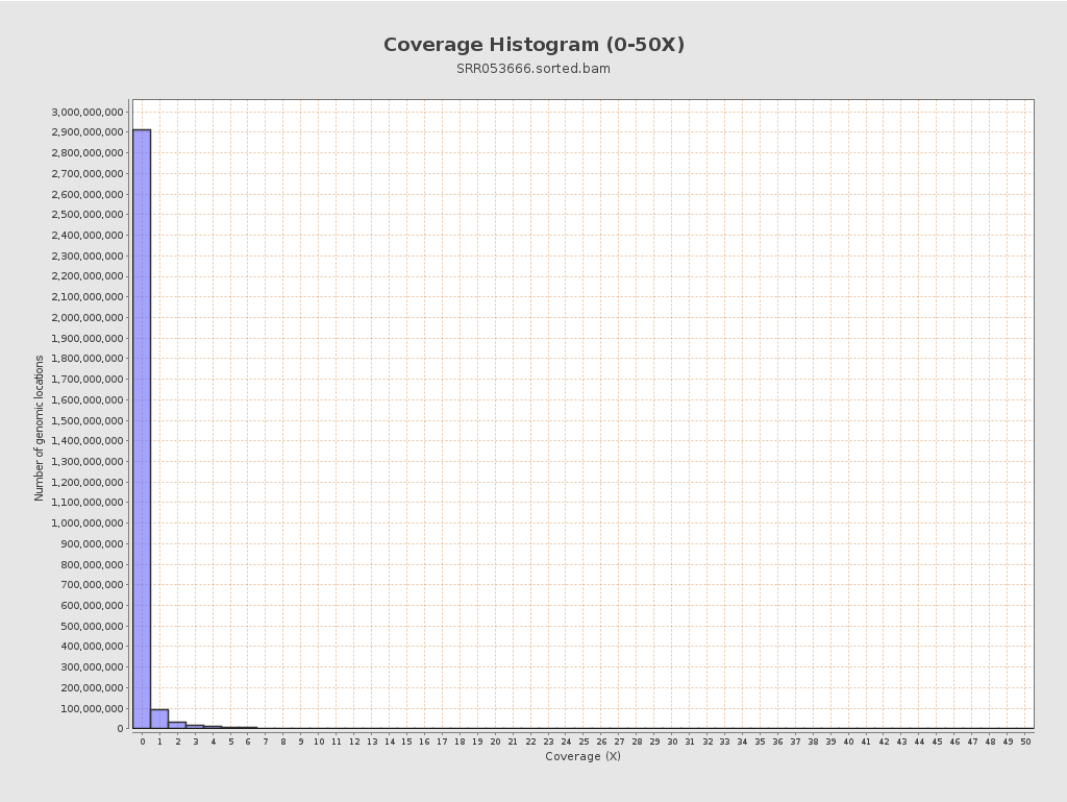
3. Results : Coverage across reference



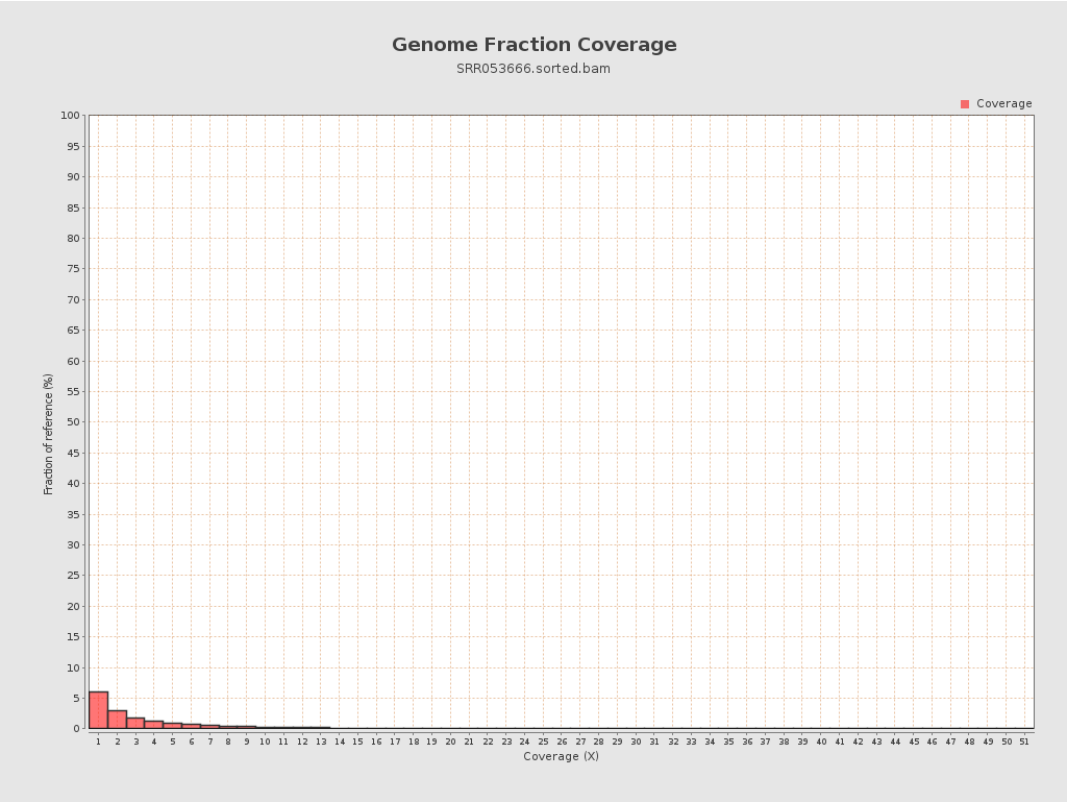
4. Results : Coverage Histogram



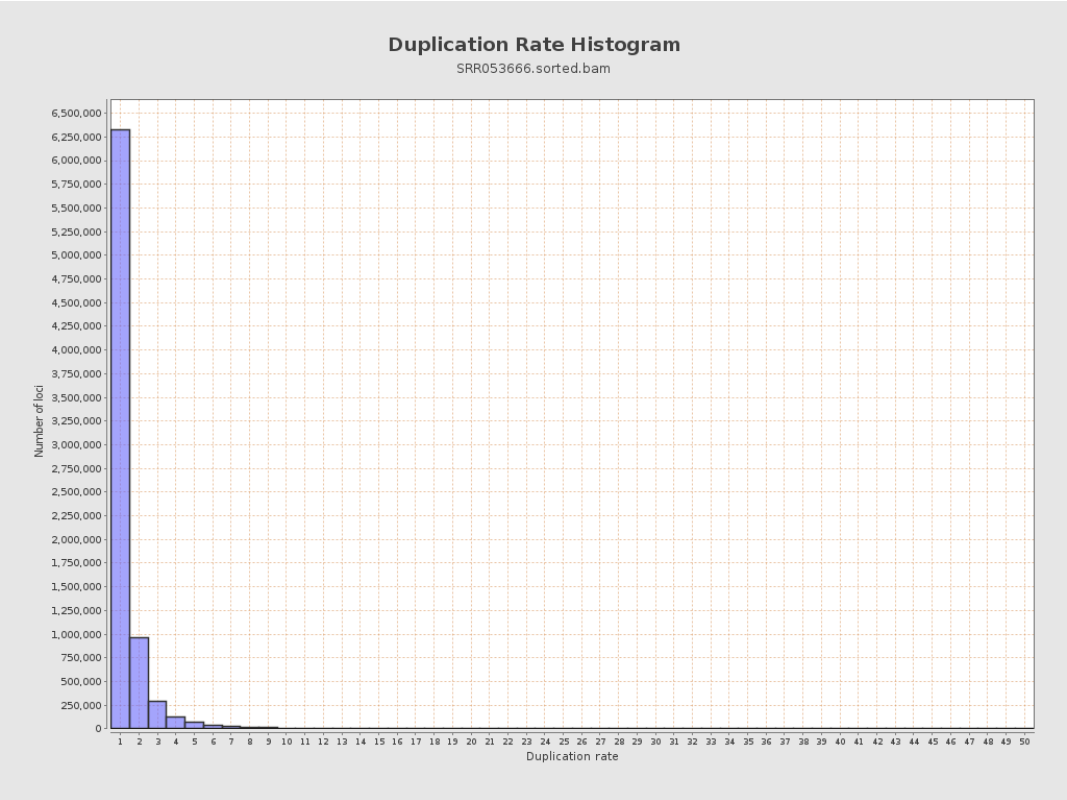
5. Results : Coverage Histogram (0-50X)



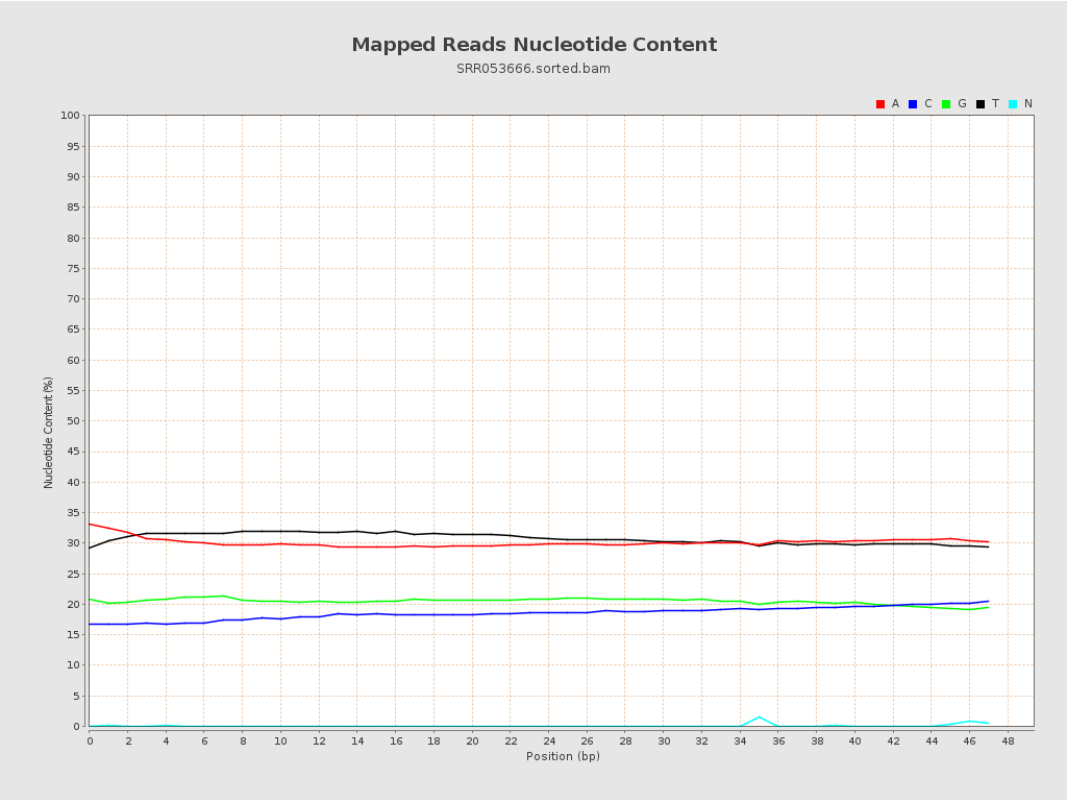
6. Results : Genome Fraction Coverage



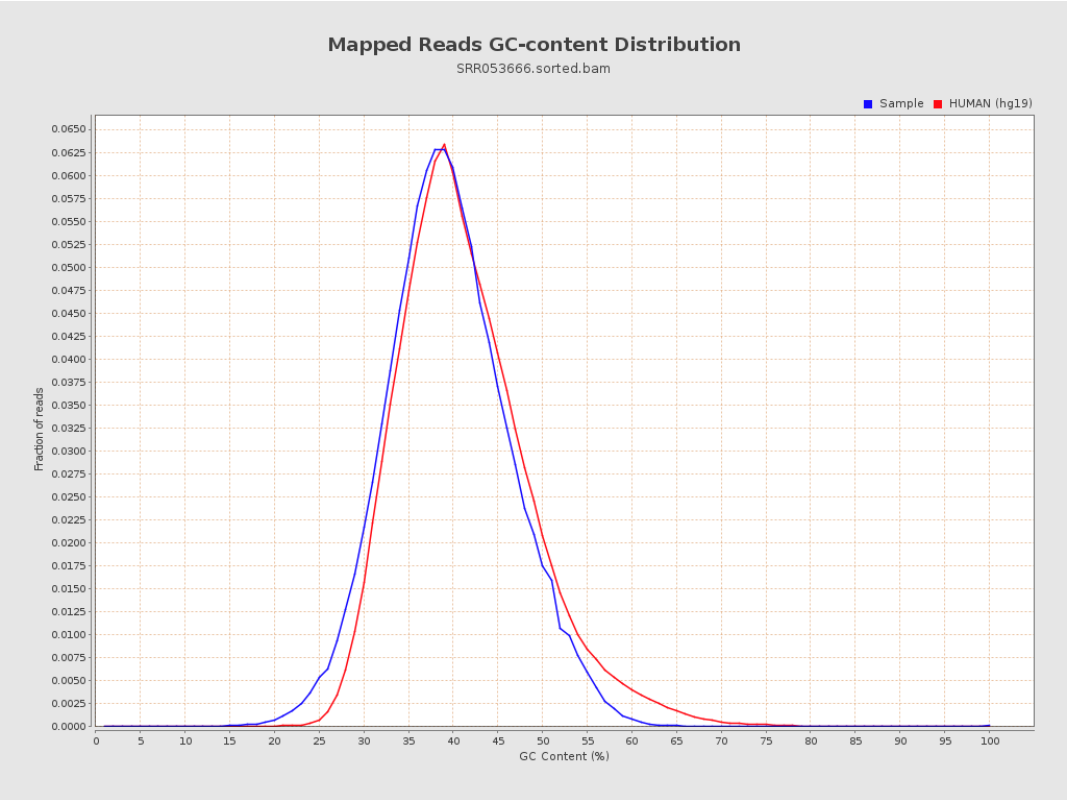
7. Results : Duplication Rate Histogram



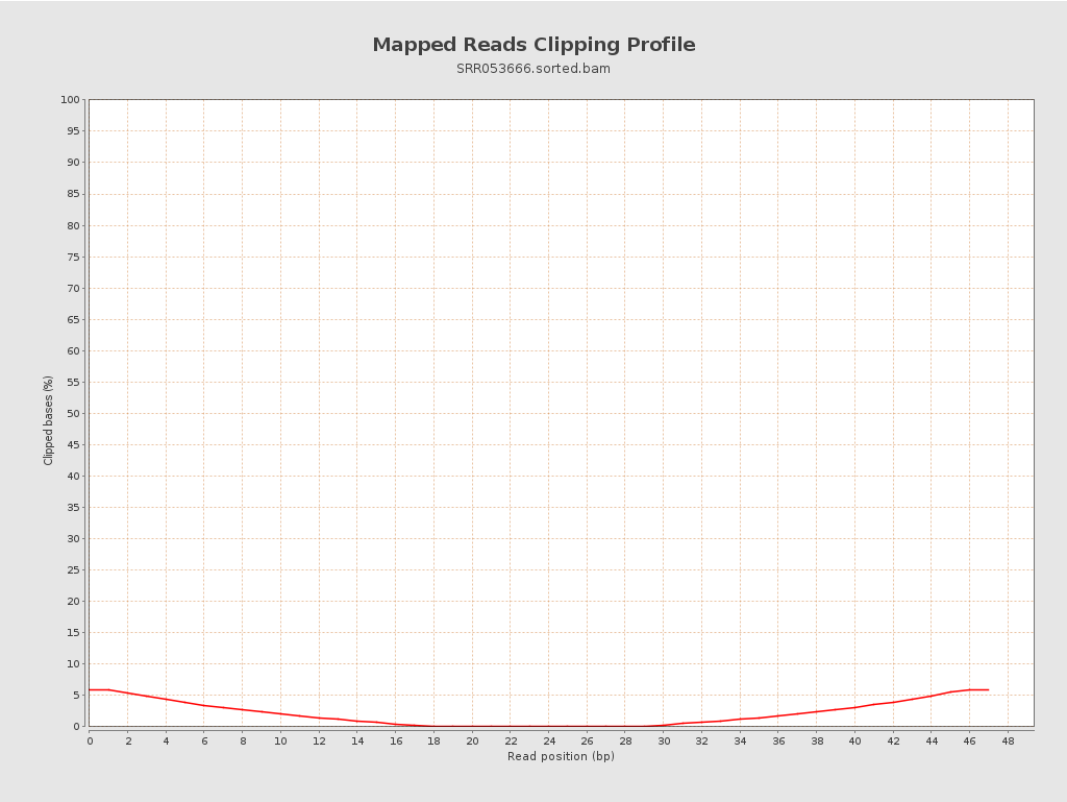
8. Results : Mapped Reads Nucleotide Content



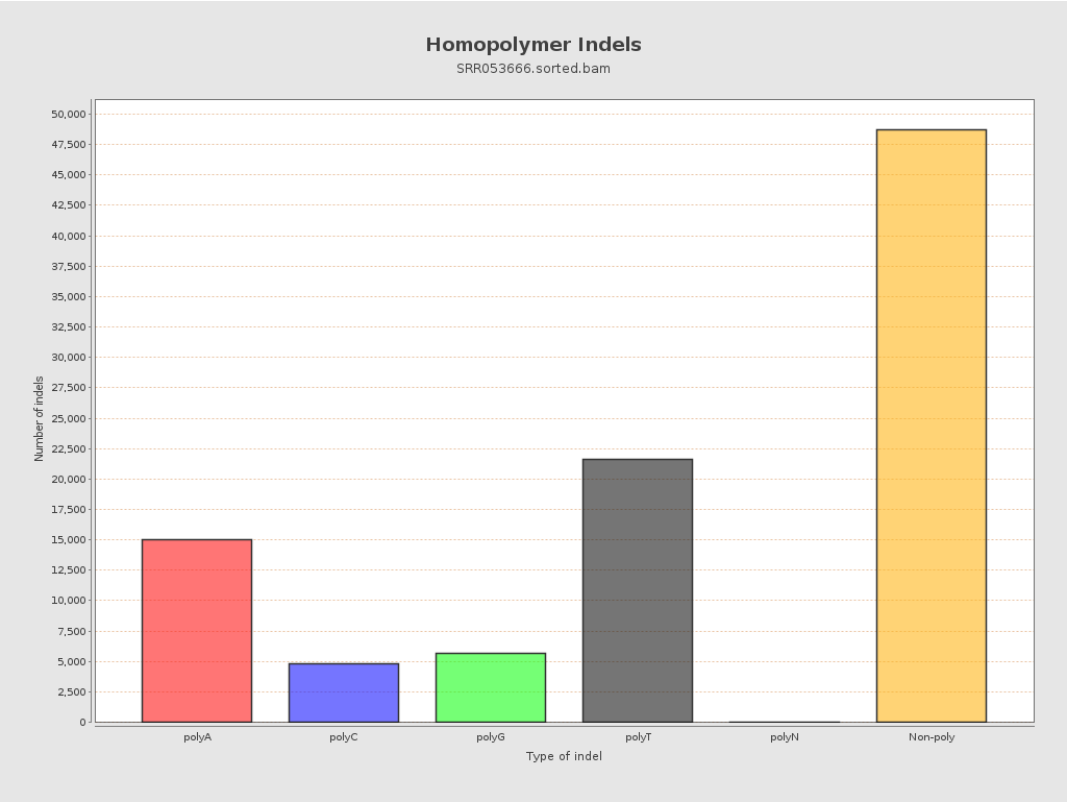
9. Results : Mapped Reads GC-content Distribution



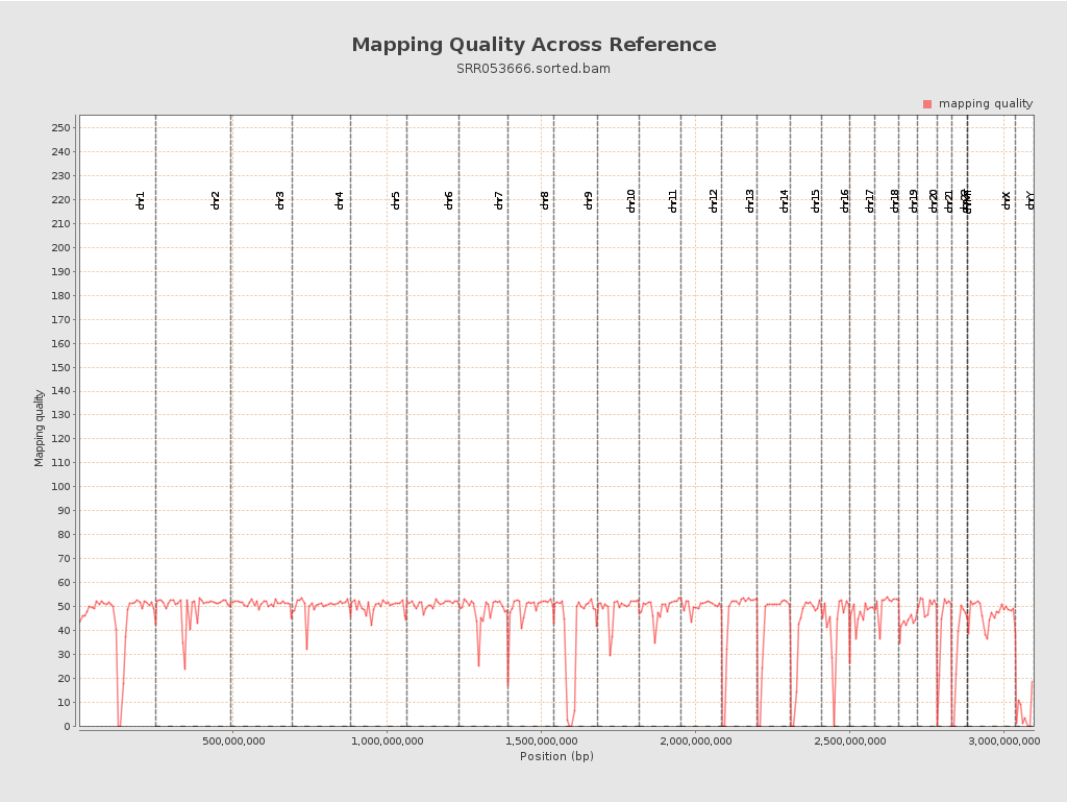
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram