Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/19 23:30:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR089710.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_SRR089710 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR089710.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 19 23:30:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR089710.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,012,166
Mapped reads	14,769,916 / 82%
Unmapped reads	3,242,250 / 18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	593 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	3,157,654 / 17.53%
Duplication rate	12.67%
Clipped reads	1,127,909 / 6.26%

2.2. ACGT Content

Number/percentage of A's	202,940,511 / 29.06%
Number/percentage of C's	142,176,574 / 20.36%
Number/percentage of T's	205,159,376 / 29.38%
Number/percentage of G's	148,087,453 / 21.2%
Number/percentage of N's	32,684 / 0%
GC Percentage	41.56%

2.3. Coverage

Mean	0.2256

Standard Deviation	1.5684

2.4. Mapping Quality

Mean Mapping Quality	44.61

2.5. Mismatches and indels

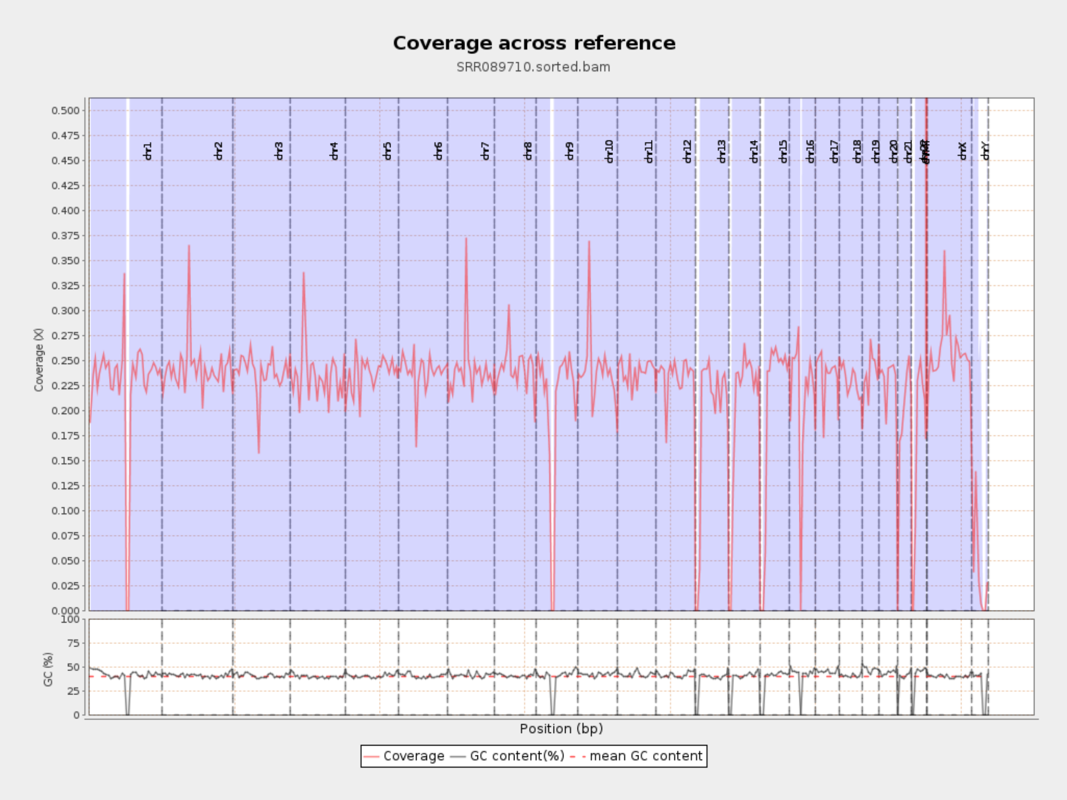
General error rate	0.53%
Mismatches	3,621,853
Insertions	33,350
Mapped reads with at least one insertion	0.23%
Deletions	93,918
Mapped reads with at least one deletion	0.63%
Homopolymer indels	47.63%

2.6. Chromosome stats

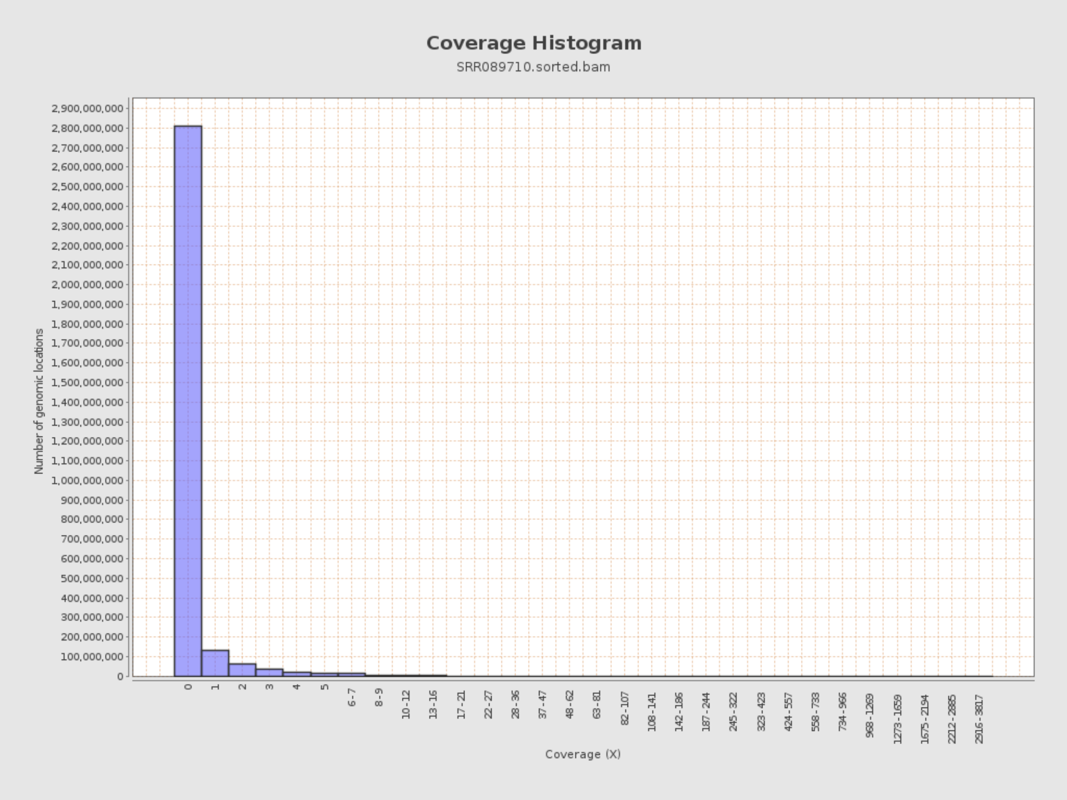
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	56288860	0.2258	2.733
chr2	243199373	59055502	0.2428	1.5377
chr3	198022430	47122958	0.238	0.9905
chr4	191154276	44850817	0.2346	1.1278
chr5	180915260	43020504	0.2378	0.9997
chr6	171115067	40827768	0.2386	1.1006
chr7	159138663	38283025	0.2406	2.1657

chr8	146364022	35344316	0.2415	2.1587
chr9	141213431	28997878	0.2053	1.38
chr10	135534747	32691521	0.2412	1.5477
chr11	135006516	32083469	0.2376	1.4624
chr12	133851895	31326429	0.234	1.0552
chr13	115169878	21786639	0.1892	0.8826
chr14	107349540	21376621	0.1991	0.9803
chr15	102531392	20560406	0.2005	0.9098
chr16	90354753	19327879	0.2139	1.0464
chr17	81195210	19048724	0.2346	1.1564
chr18	78077248	18037545	0.231	2.9941
chr19	59128983	14036122	0.2374	1.9649
chr20	63025520	14496051	0.23	1.0885
chr21	48129895	9131352	0.1897	1.1137
chr22	51304566	8086492	0.1576	0.8011
chrMT	16571	400208	24.1511	15.988
chrX	155270560	39993417	0.2576	1.2151
chrY	59373566	2366847	0.0399	1.0549

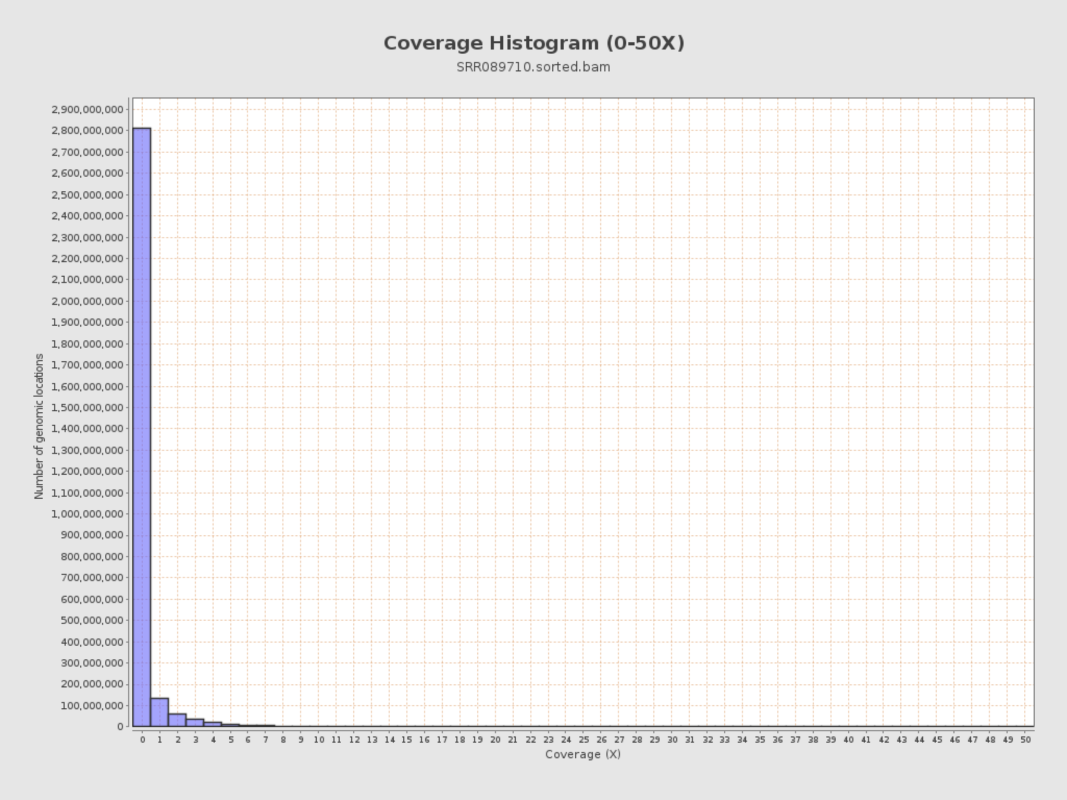
3. Results : Coverage across reference



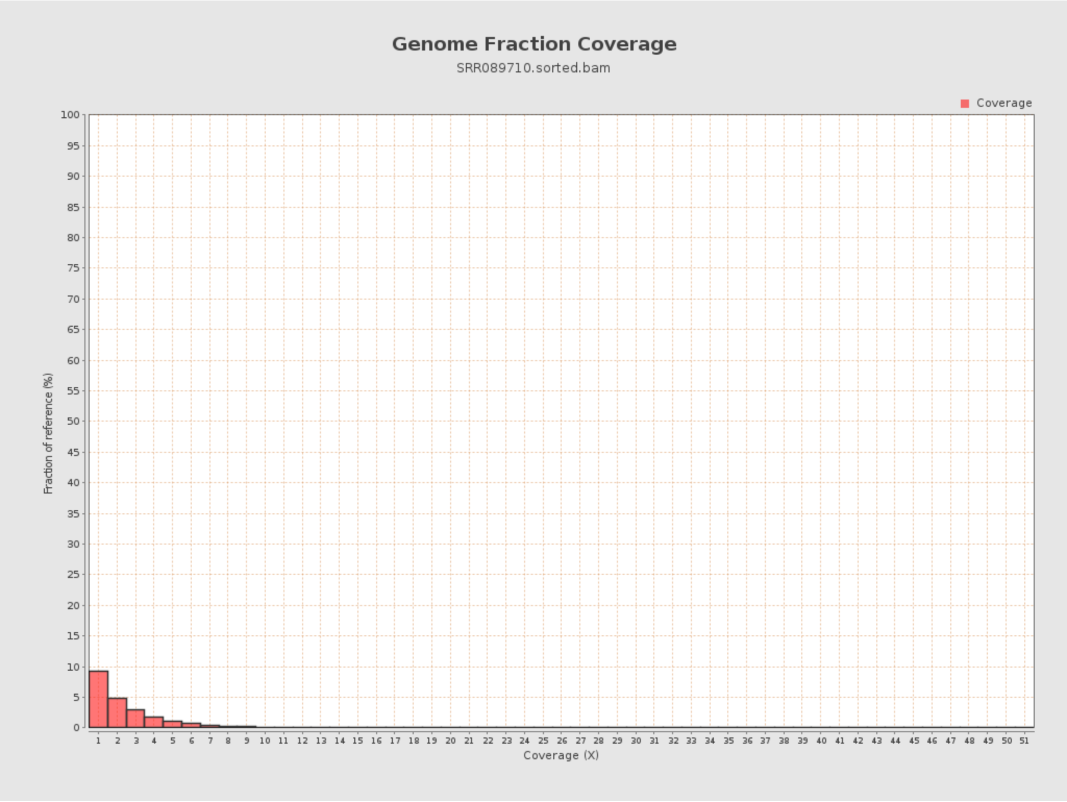
4. Results : Coverage Histogram



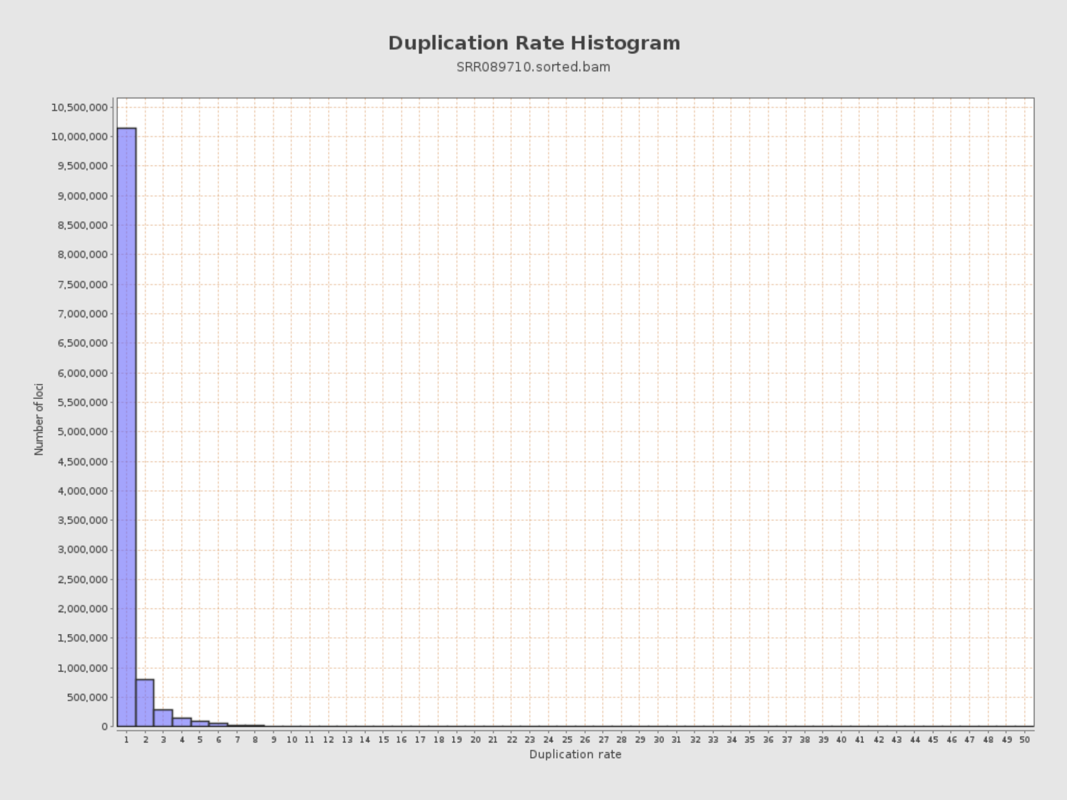
5. Results : Coverage Histogram (0-50X)



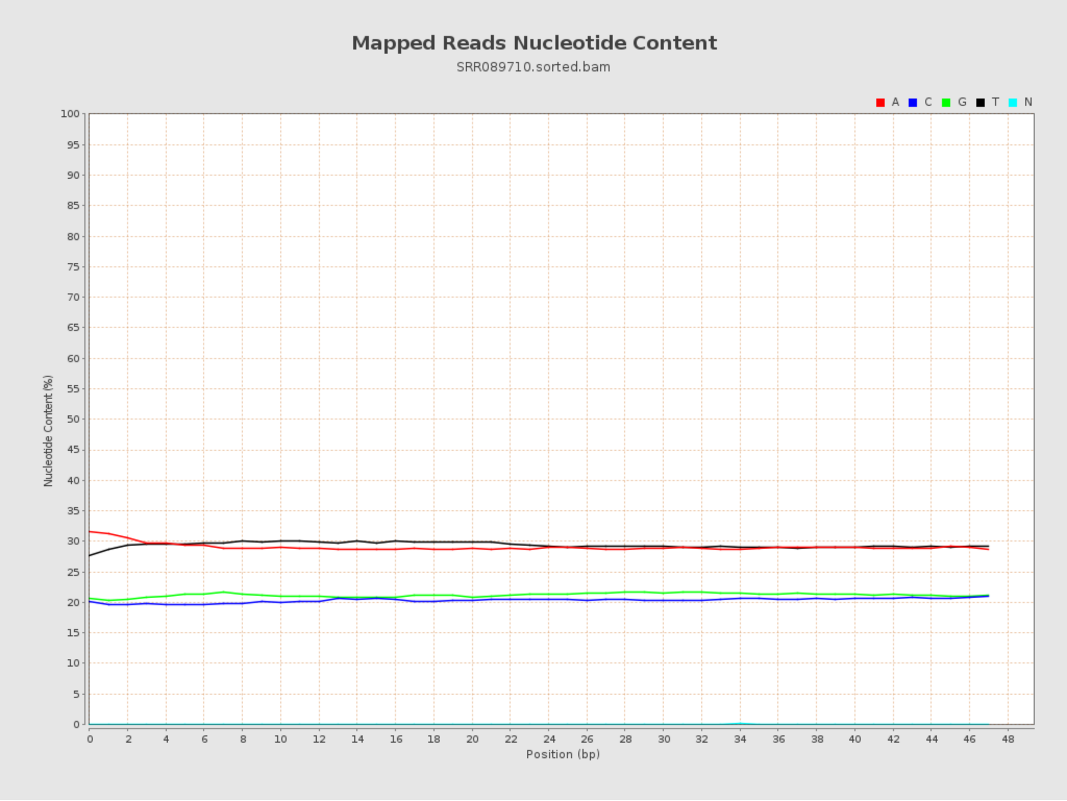
6. Results : Genome Fraction Coverage



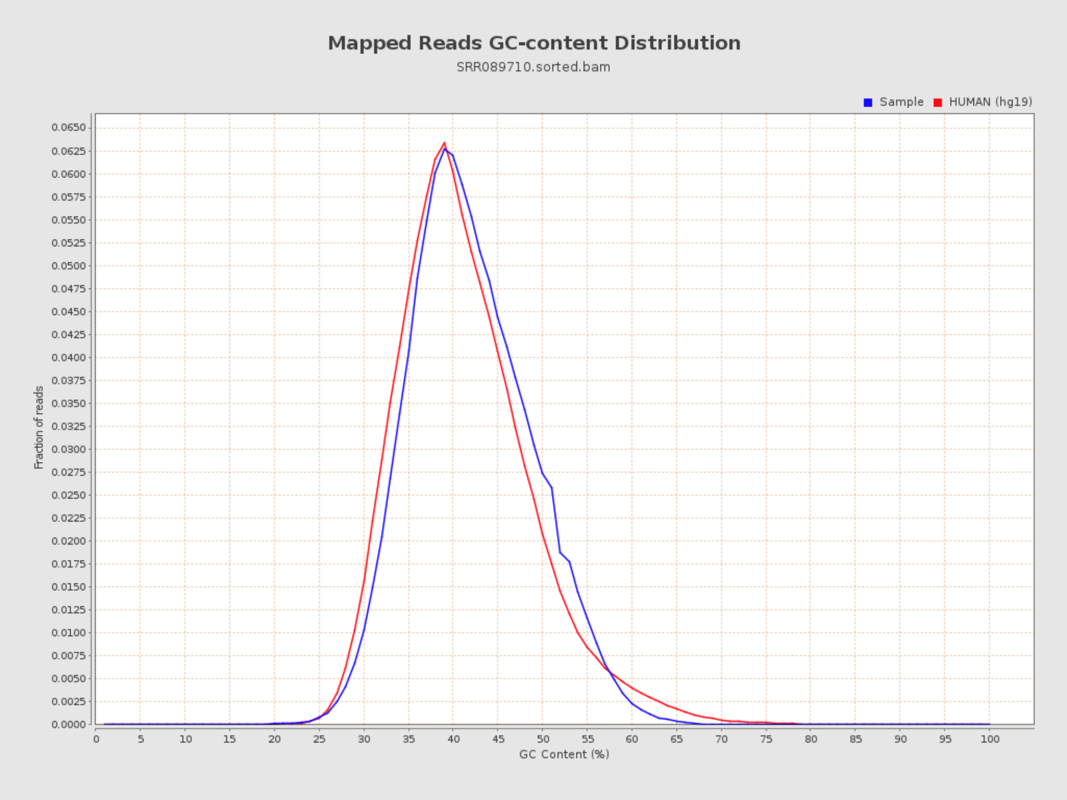
7. Results : Duplication Rate Histogram



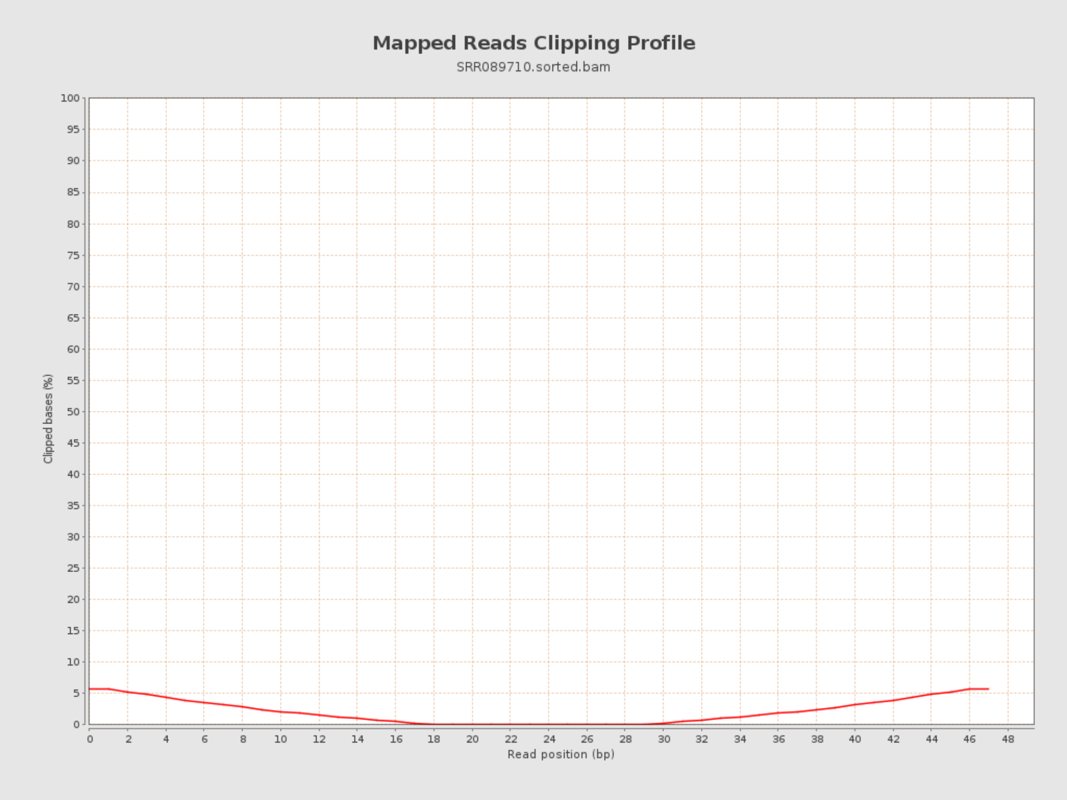
8. Results : Mapped Reads Nucleotide Content



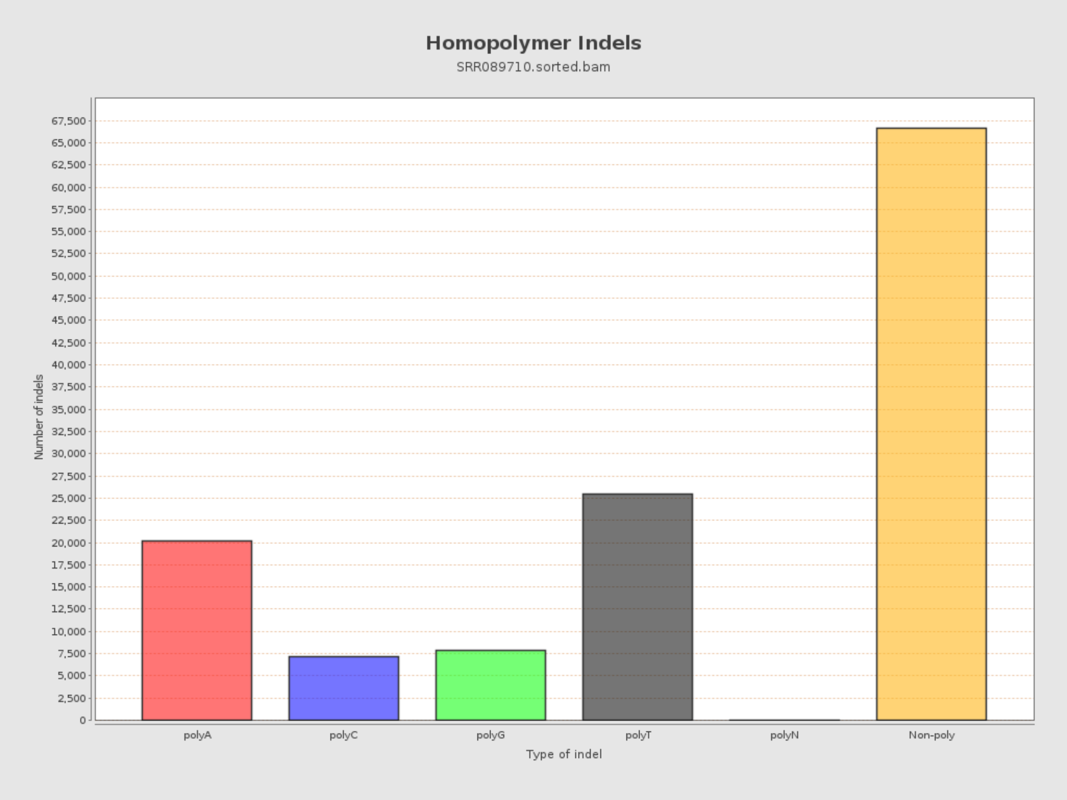
9. Results : Mapped Reads GC-content Distribution



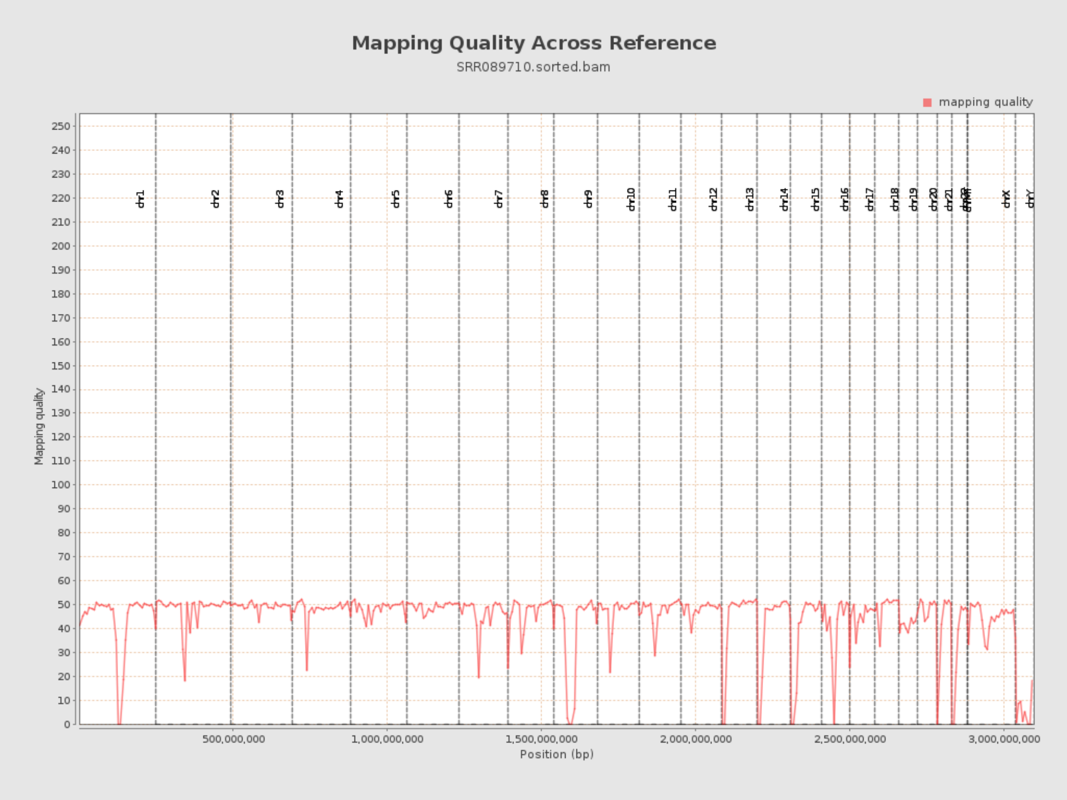
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram