Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:15:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818842.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_SRR1818842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:15:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	802,718
Mapped reads	779,774 / 97.14%
Unmapped reads	22,944 / 2.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,985 / 1.49%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	75,752 / 9.44%
Duplication rate	7.52%
Clipped reads	789,030 / 98.29%

2.2. ACGT Content

Number/percentage of A's	20,689,815 / 28.66%
Number/percentage of C's	15,767,104 / 21.84%
Number/percentage of T's	20,542,576 / 28.46%
Number/percentage of G's	15,190,921 / 21.04%
Number/percentage of N's	974 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.3198

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

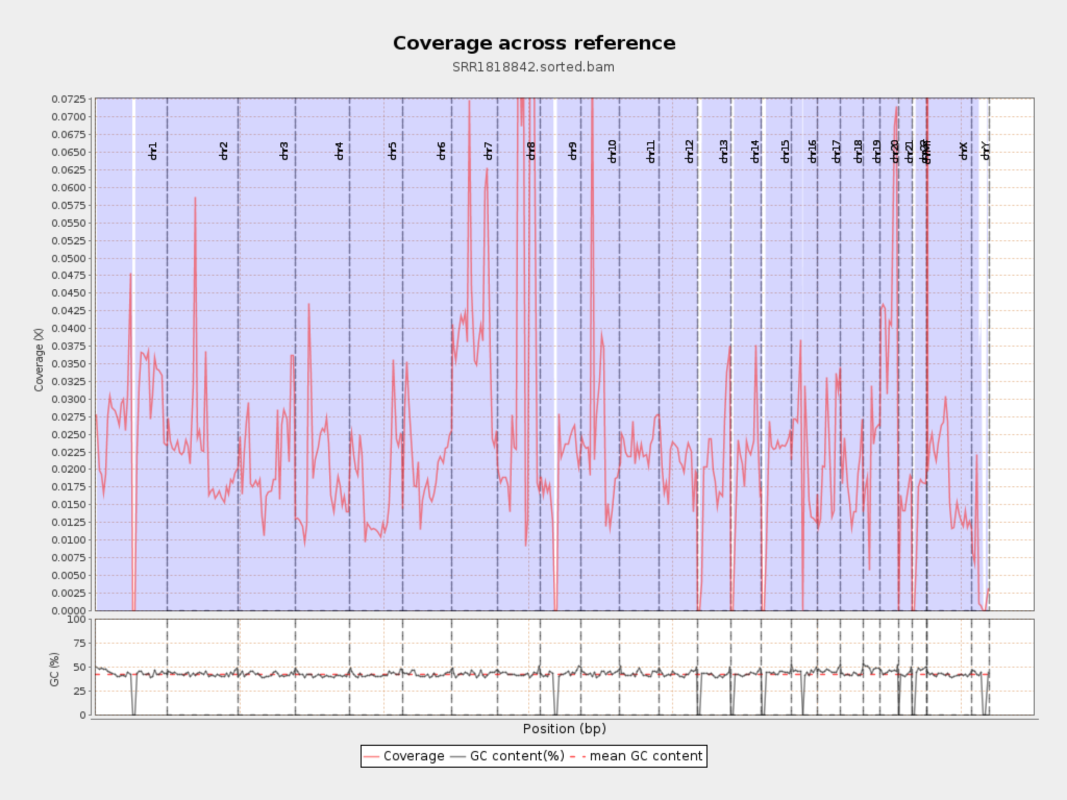
General error rate	0.62%
Mismatches	424,353
Insertions	9,184
Mapped reads with at least one insertion	1.14%
Deletions	20,496
Mapped reads with at least one deletion	2.57%
Homopolymer indels	41.19%

2.6. Chromosome stats

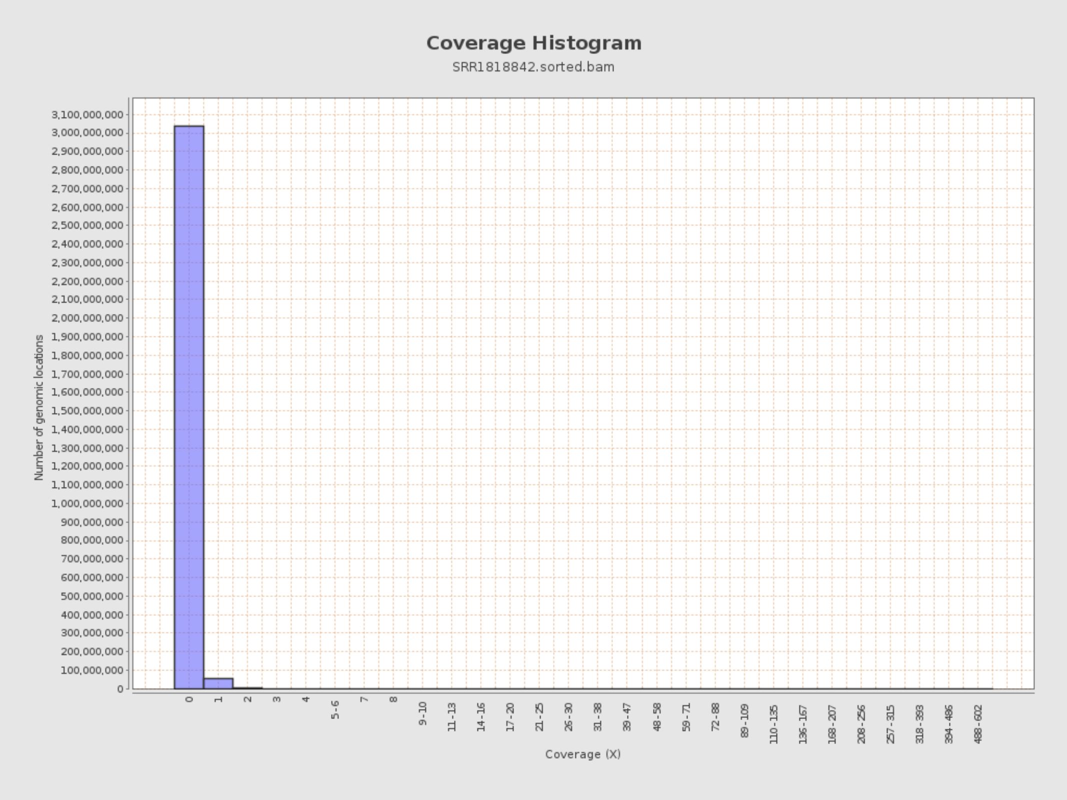
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6822585	0.0274	0.4742
chr2	243199373	5479949	0.0225	0.3686
chr3	198022430	4300508	0.0217	0.1658
chr4	191154276	3709756	0.0194	0.2135
chr5	180915260	3216701	0.0178	0.1519
chr6	171115067	3534635	0.0207	0.1701
chr7	159138663	6471394	0.0407	0.6941

chr8	146364022	6262383	0.0428	0.2904
chr9	141213431	2668845	0.0189	0.2867
chr10	135534747	3519948	0.026	0.5331
chr11	135006516	3168844	0.0235	0.2075
chr12	133851895	2775105	0.0207	0.1611
chr13	115169878	2211285	0.0192	0.1551
chr14	107349540	2080139	0.0194	0.1618
chr15	102531392	1987371	0.0194	0.1544
chr16	90354753	1891899	0.0209	0.2503
chr17	81195210	1815706	0.0224	0.2185
chr18	78077248	1423470	0.0182	0.3277
chr19	59128983	1253236	0.0212	0.4194
chr20	63025520	2965671	0.0471	0.2544
chr21	48129895	710762	0.0148	0.1636
chr22	51304566	658508	0.0128	0.1314
chrMT	16571	93620	5.6496	4.1728
chrX	155270560	2906535	0.0187	0.1812
chrY	59373566	303268	0.0051	0.3463

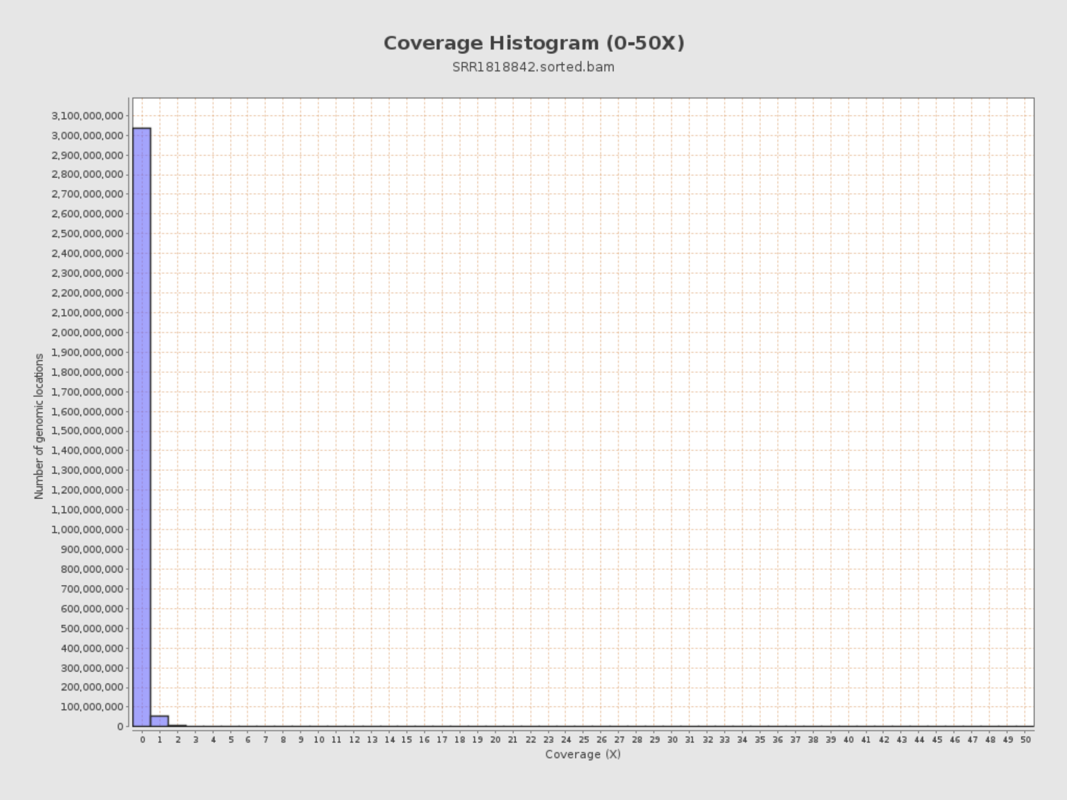
3. Results : Coverage across reference



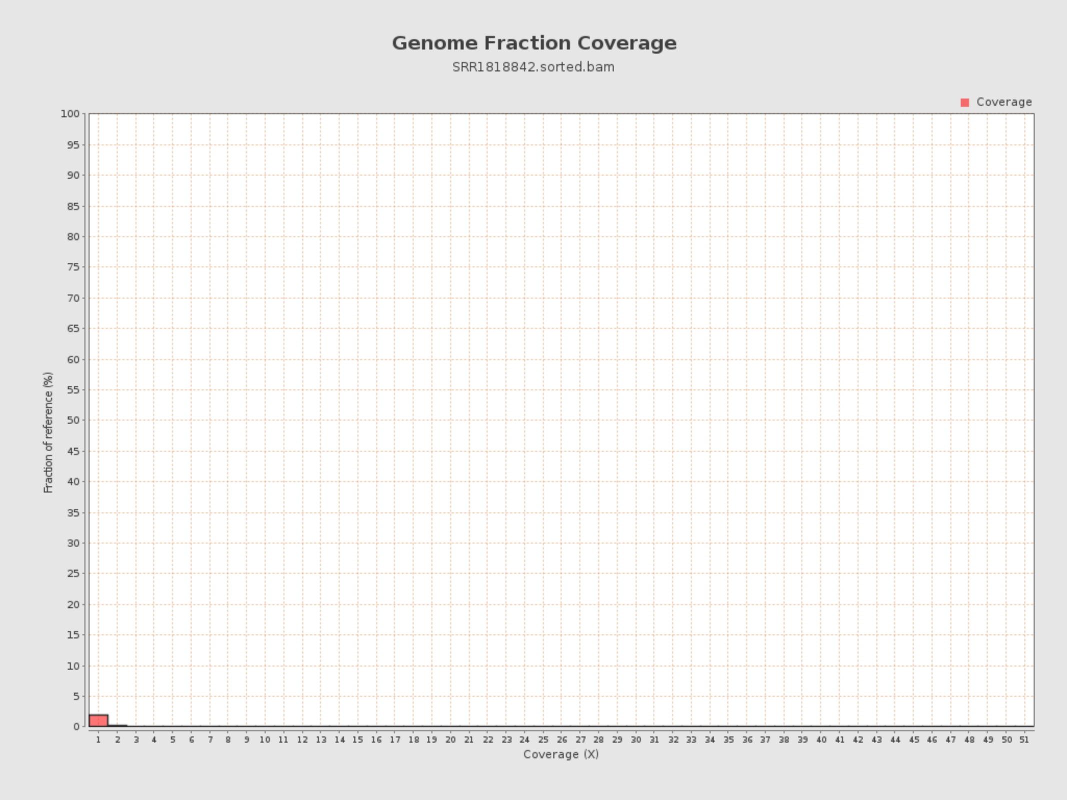
4. Results : Coverage Histogram



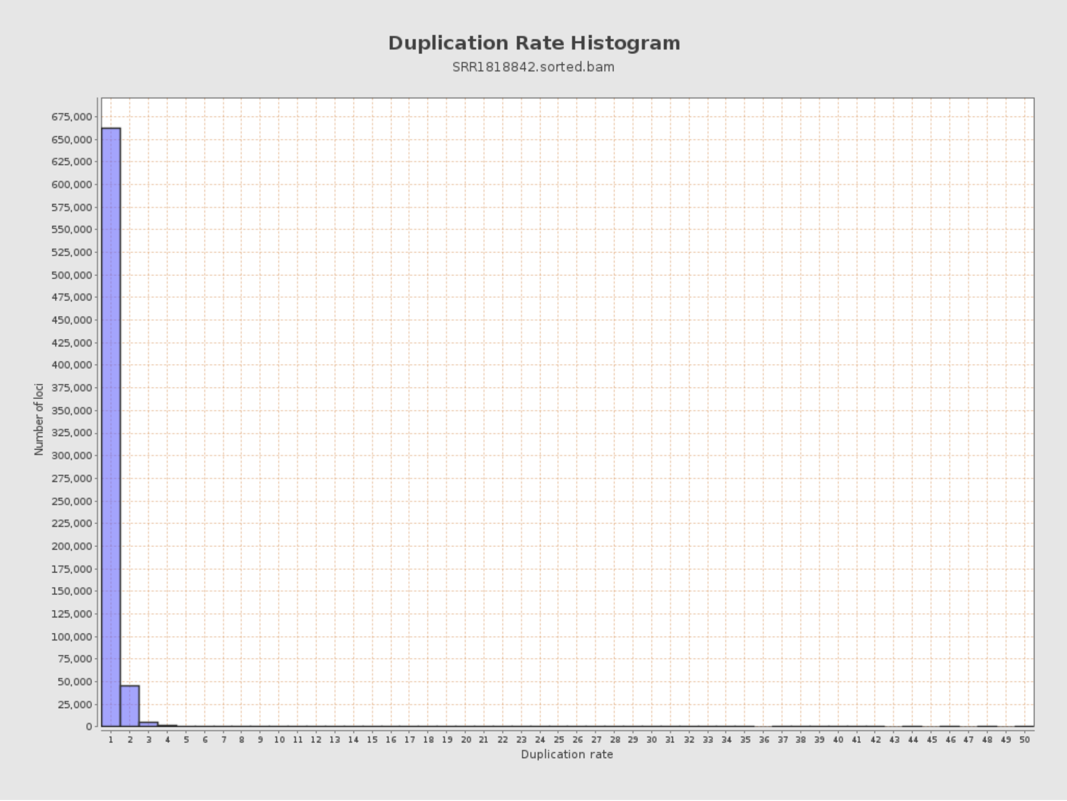
5. Results : Coverage Histogram (0-50X)



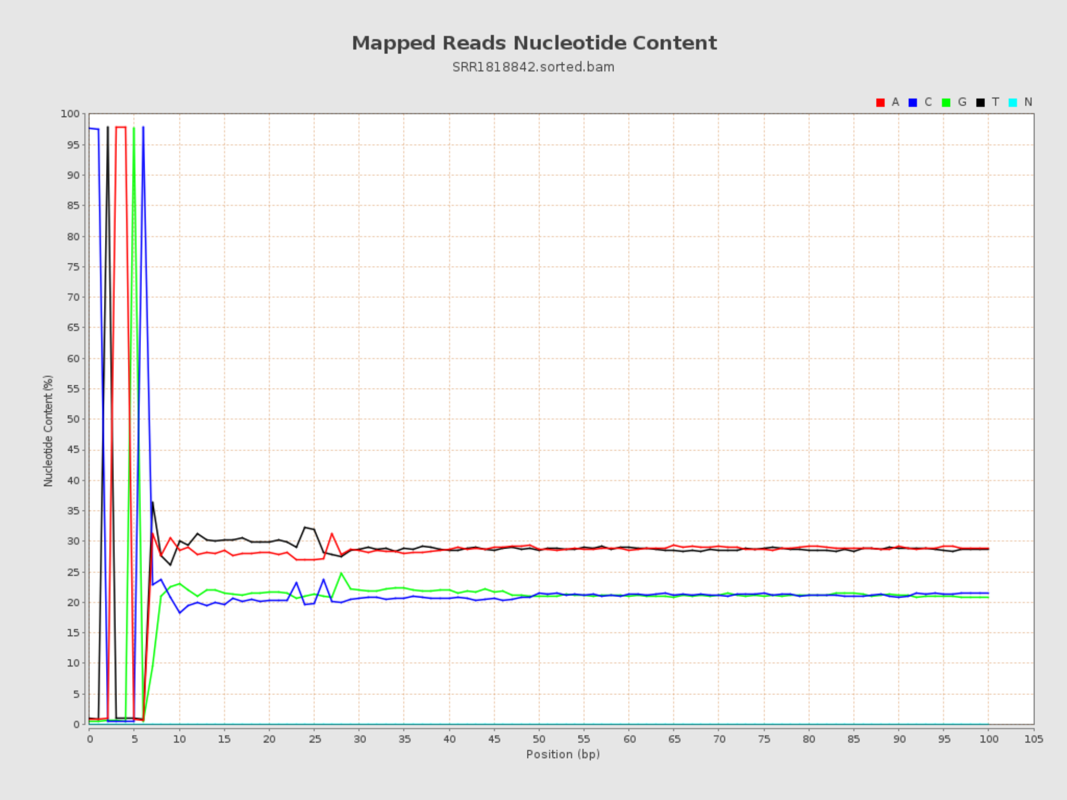
6. Results : Genome Fraction Coverage



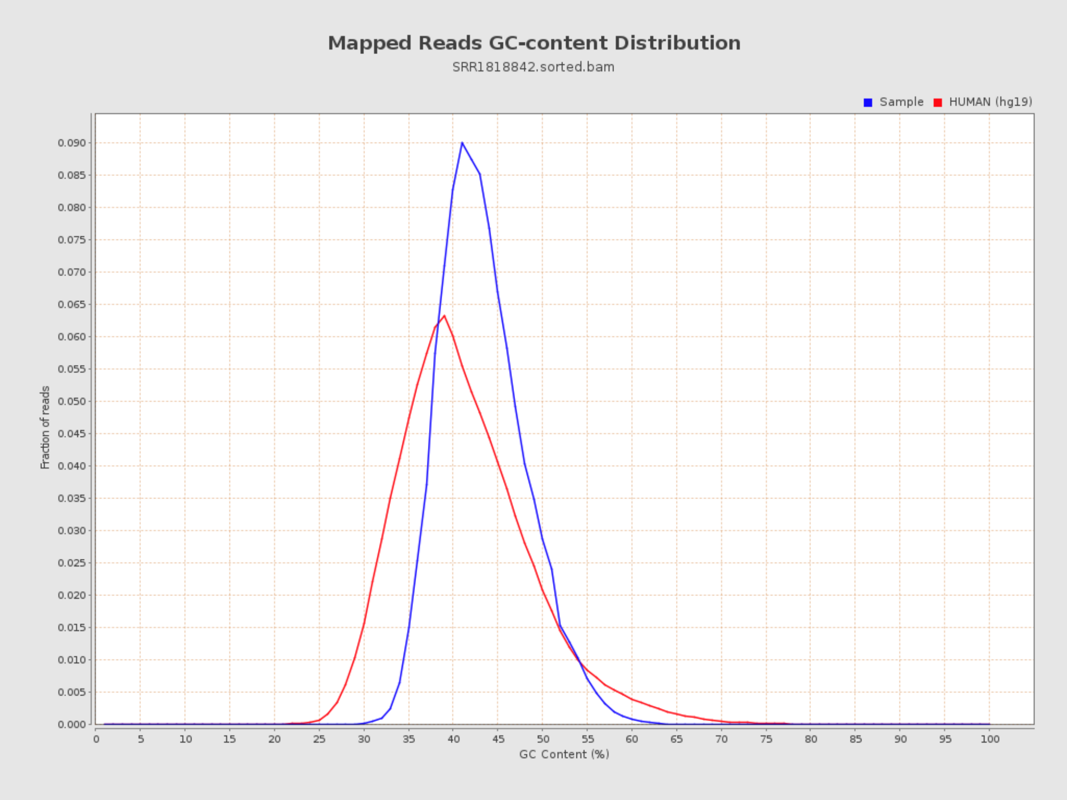
7. Results : Duplication Rate Histogram



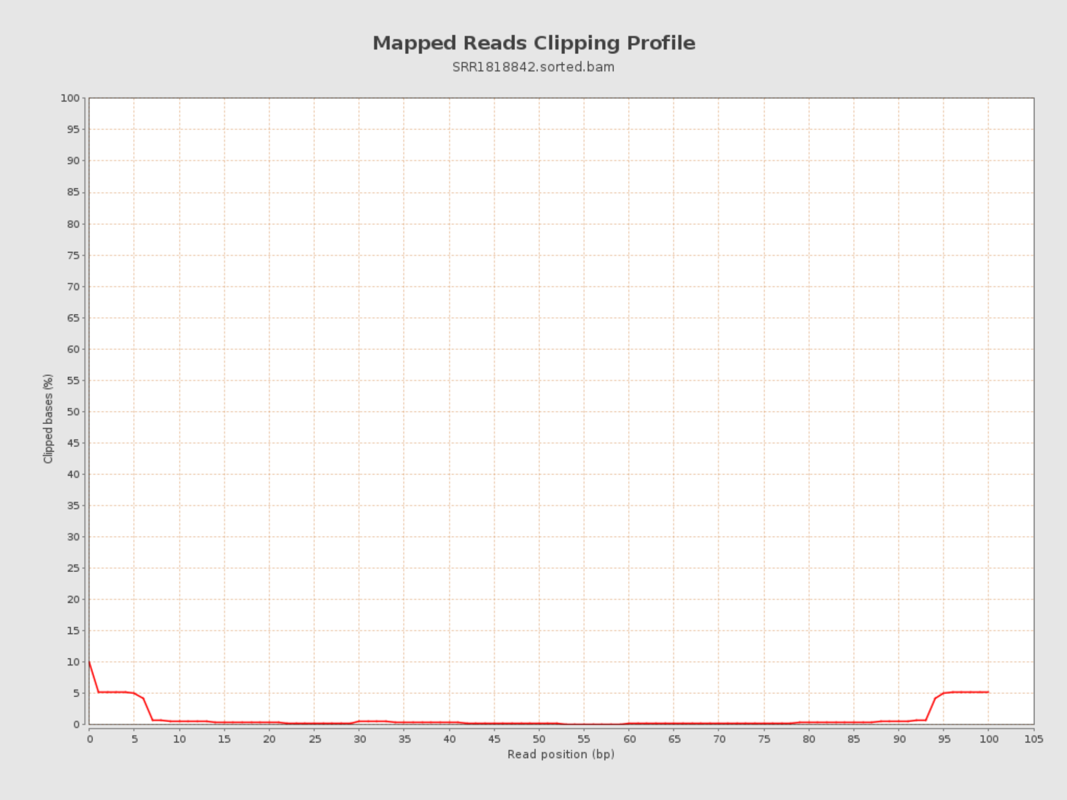
8. Results : Mapped Reads Nucleotide Content



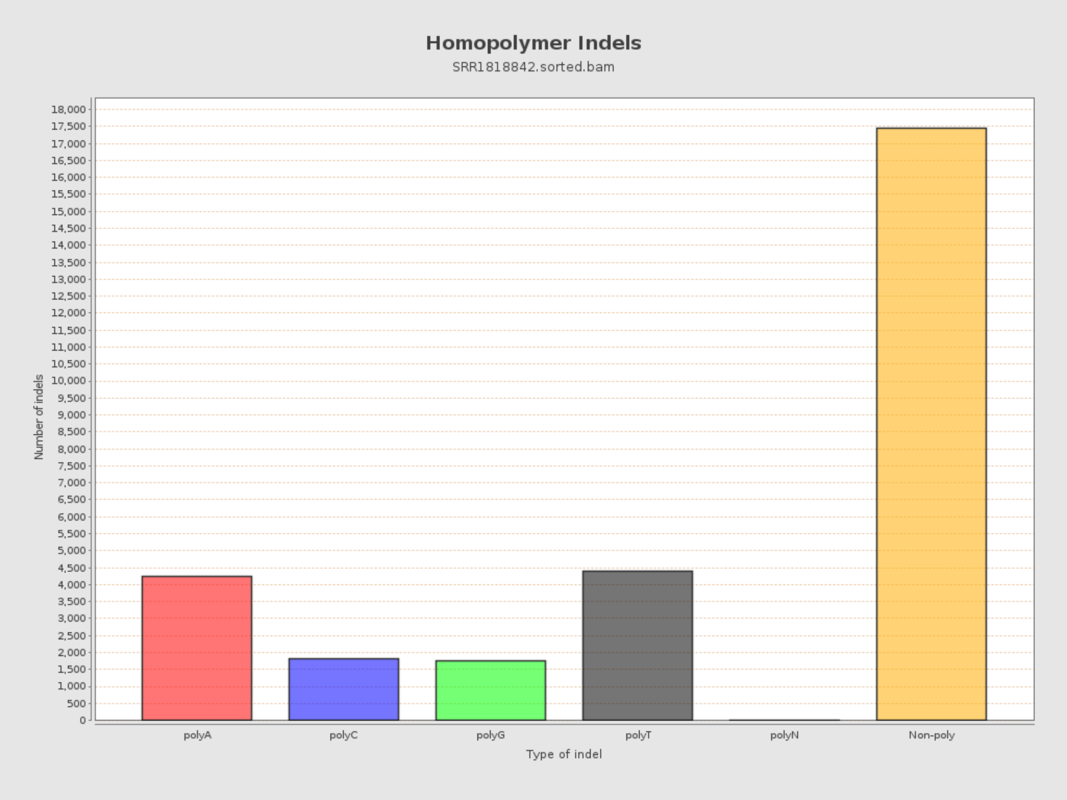
9. Results : Mapped Reads GC-content Distribution



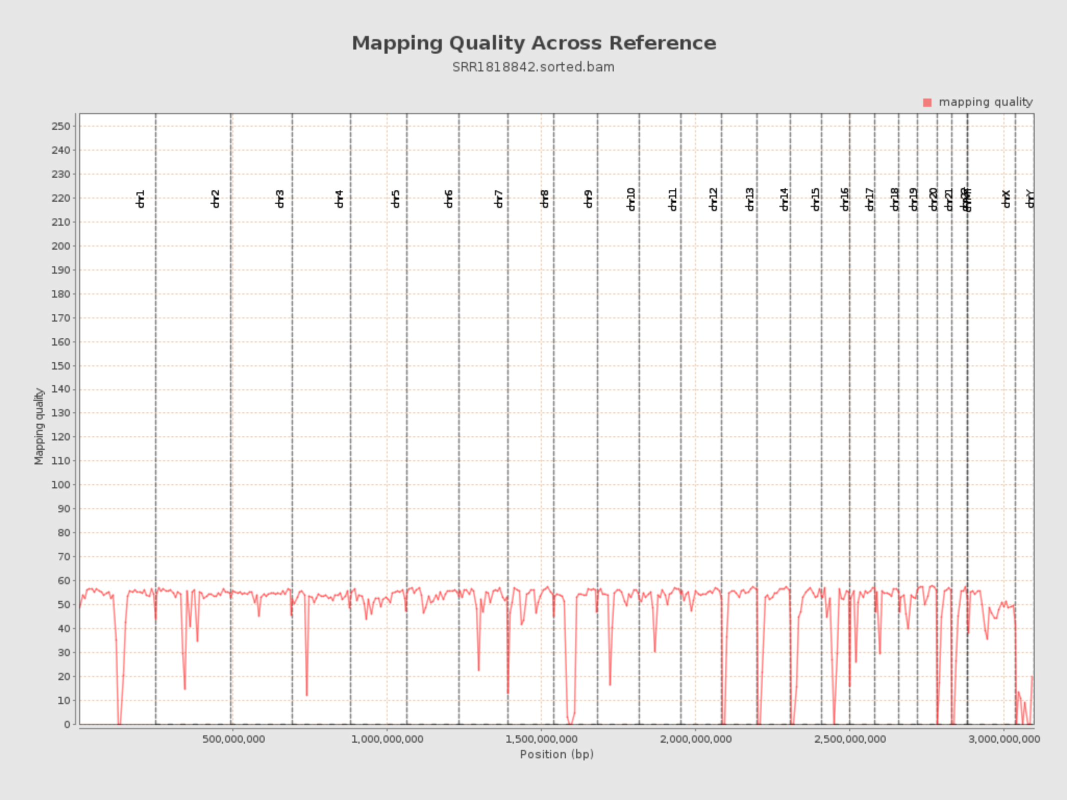
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram