Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:59:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818930.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_SRR1818930 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818930.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:59:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818930.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,142,877
Mapped reads	1,104,220 / 96.62%
Unmapped reads	38,657 / 3.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,453 / 1.35%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	350,414 / 30.66%
Duplication rate	28.8%
Clipped reads	1,109,147 / 97.05%

2.2. ACGT Content

Number/percentage of A's	29,327,654 / 28.7%
Number/percentage of C's	21,200,877 / 20.75%
Number/percentage of T's	29,850,048 / 29.21%
Number/percentage of G's	21,791,690 / 21.33%
Number/percentage of N's	4,203 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.033

Standard Deviation	0.3852

2.4. Mapping Quality

Mean Mapping Quality	49.09

2.5. Mismatches and indels

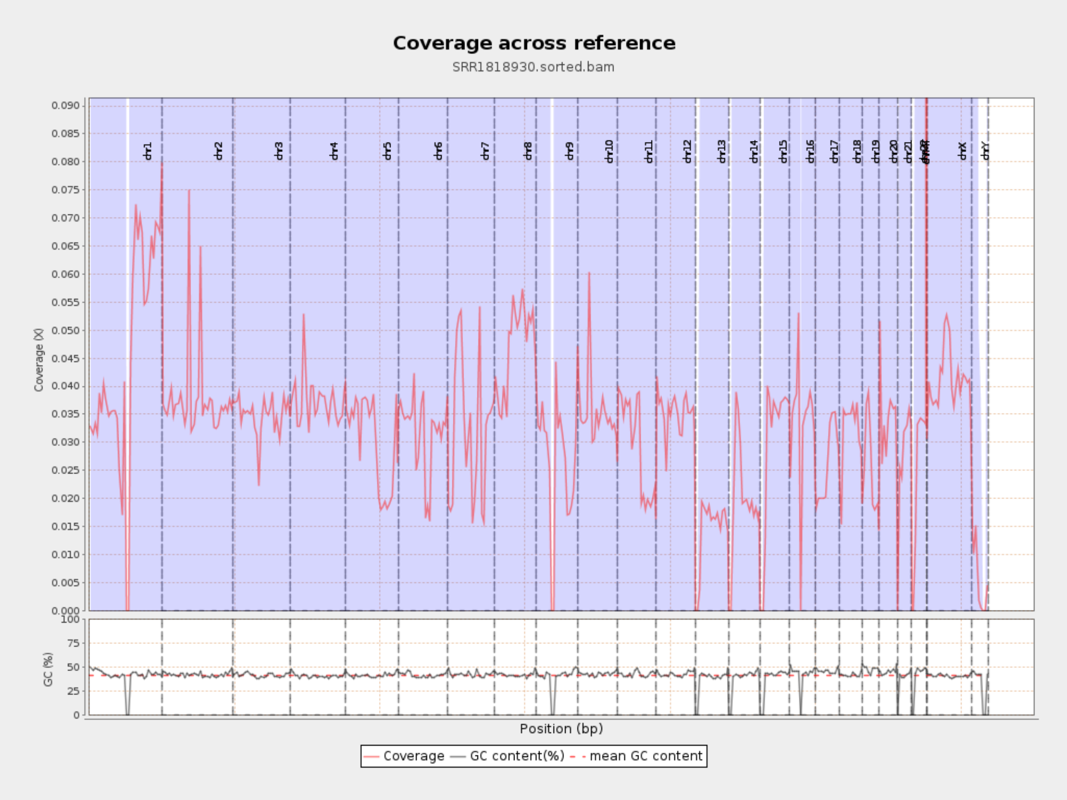
General error rate	0.67%
Mismatches	655,598
Insertions	14,094
Mapped reads with at least one insertion	1.24%
Deletions	31,012
Mapped reads with at least one deletion	2.75%
Homopolymer indels	42.53%

2.6. Chromosome stats

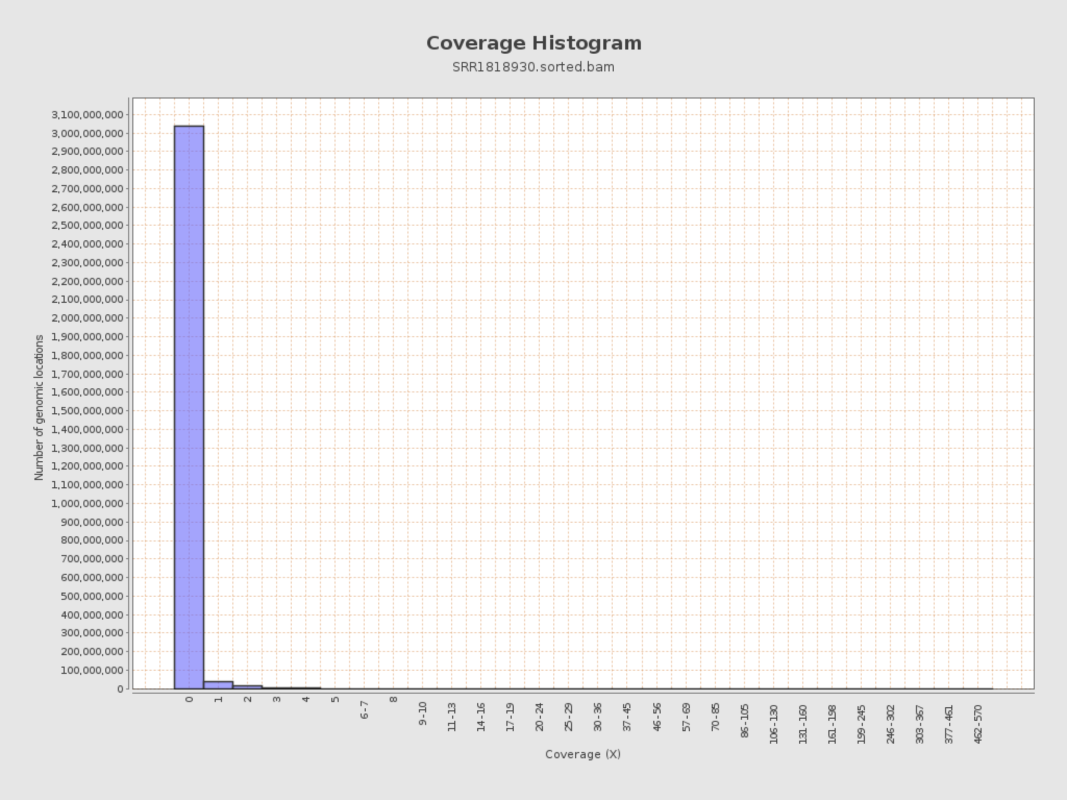
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11130627	0.0447	0.5453
chr2	243199373	9243163	0.038	0.6221
chr3	198022430	6905459	0.0349	0.2827
chr4	191154276	7105720	0.0372	0.3092
chr5	180915260	5473497	0.0303	0.2686
chr6	171115067	5440585	0.0318	0.2844
chr7	159138663	5105546	0.0321	0.3296

chr8	146364022	6920107	0.0473	0.378
chr9	141213431	3688139	0.0261	0.4111
chr10	135534747	4820434	0.0356	0.4334
chr11	135006516	3965555	0.0294	0.2913
chr12	133851895	4733104	0.0354	0.29
chr13	115169878	1655390	0.0144	0.1801
chr14	107349540	2088861	0.0195	0.2463
chr15	102531392	3060563	0.0299	0.2662
chr16	90354753	3041440	0.0337	0.4257
chr17	81195210	2134703	0.0263	0.2602
chr18	78077248	2504849	0.0321	0.5185
chr19	59128983	1539814	0.026	0.4986
chr20	63025520	2165473	0.0344	0.2907
chr21	48129895	1327437	0.0276	0.2665
chr22	51304566	1205372	0.0235	0.2539
chrMT	16571	258231	15.5833	10.6525
chrX	155270560	6396192	0.0412	0.3678
chrY	59373566	320406	0.0054	0.306

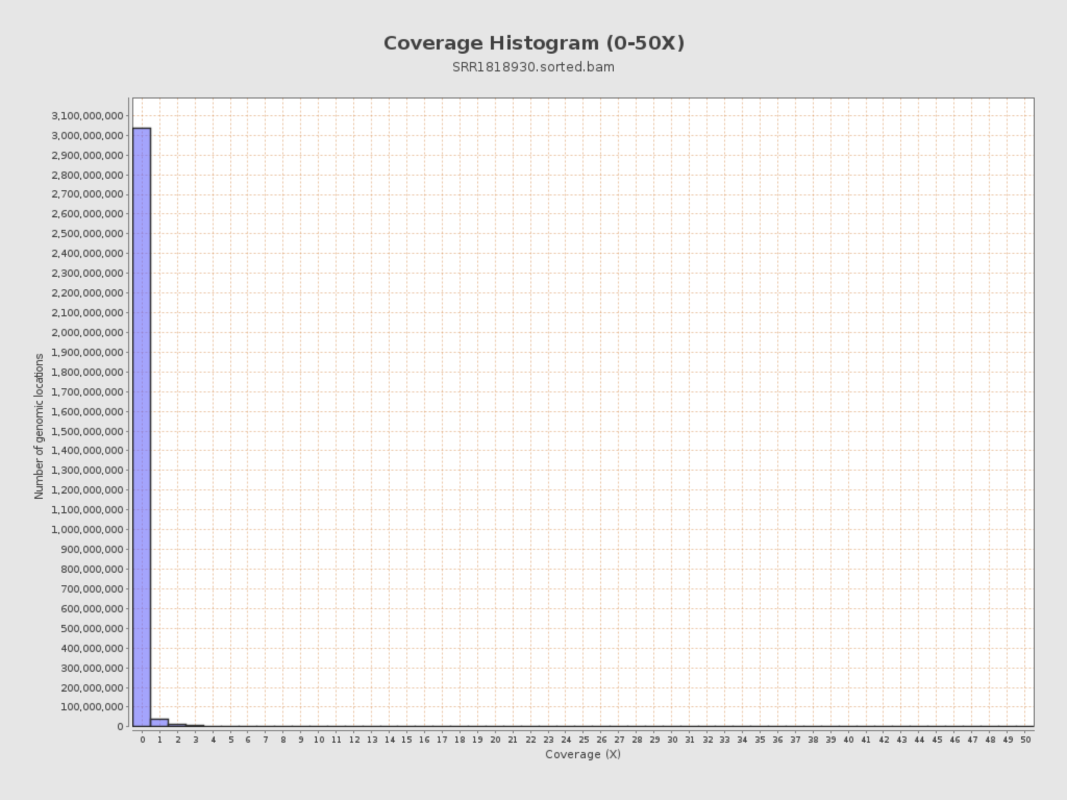
3. Results : Coverage across reference



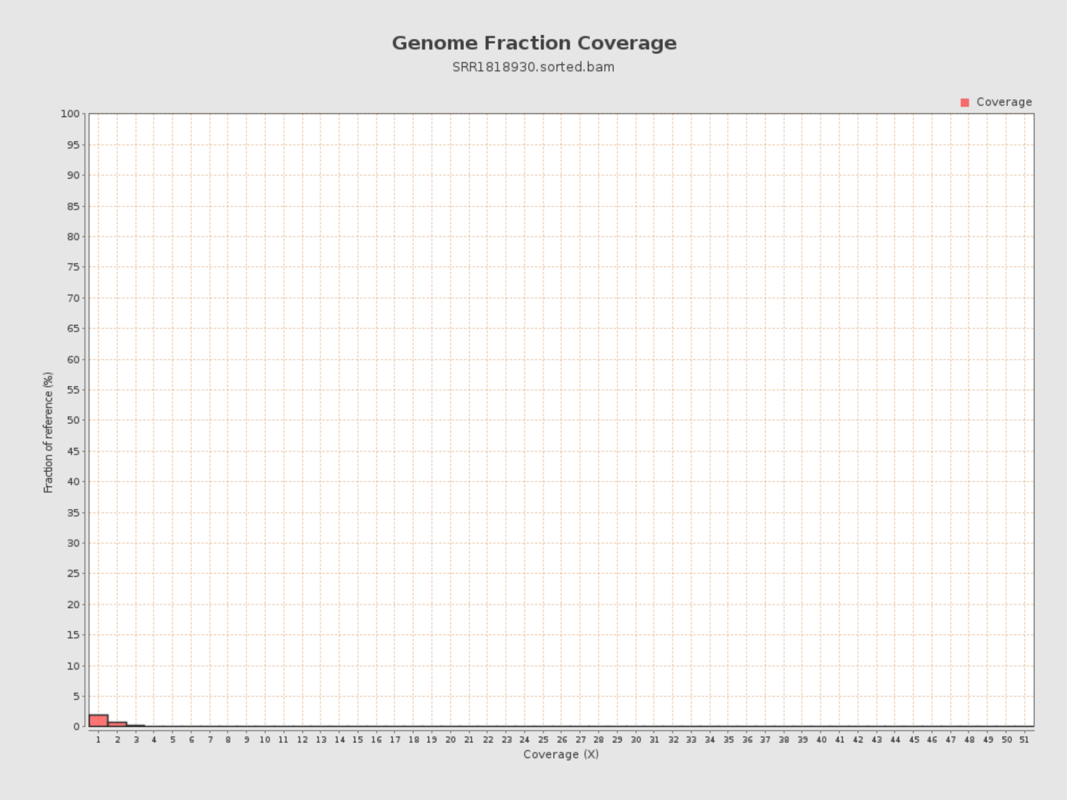
4. Results : Coverage Histogram



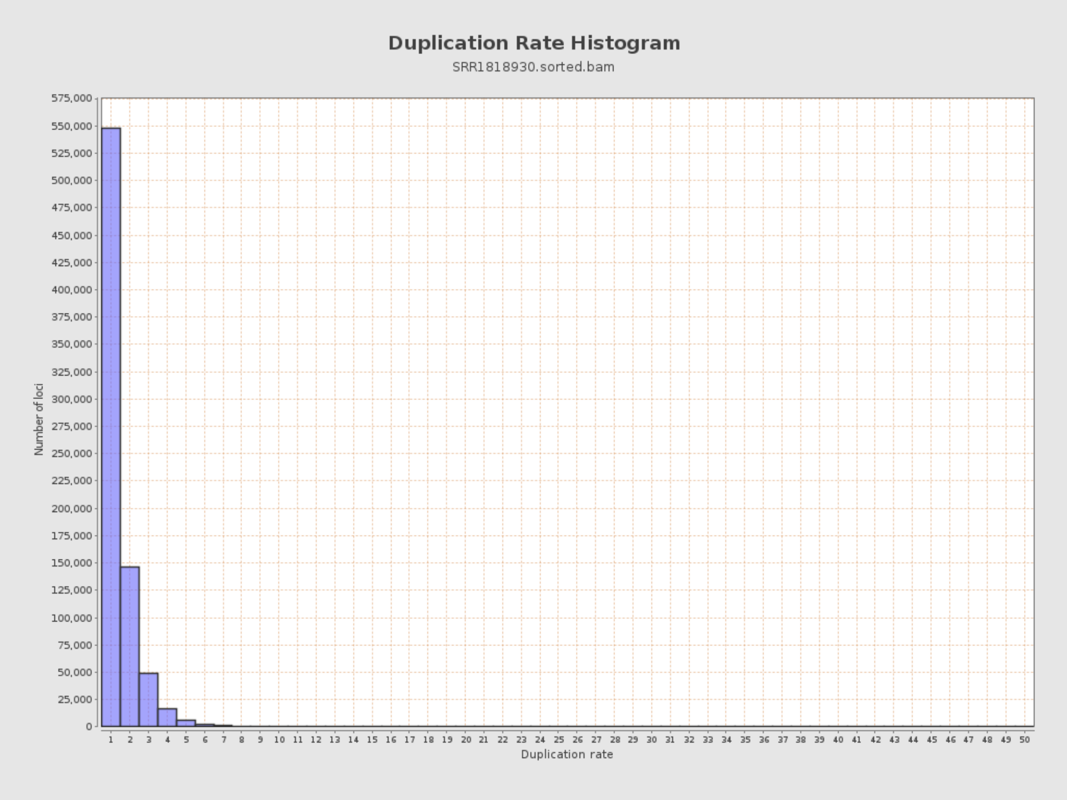
5. Results : Coverage Histogram (0-50X)



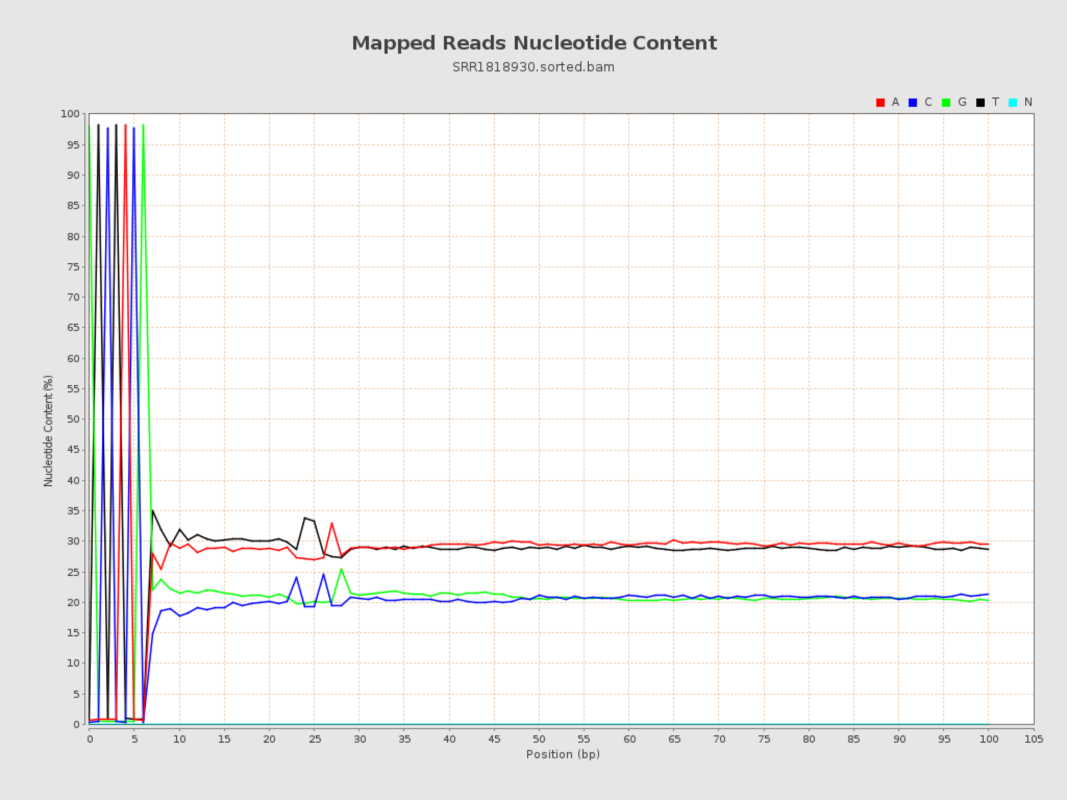
6. Results : Genome Fraction Coverage



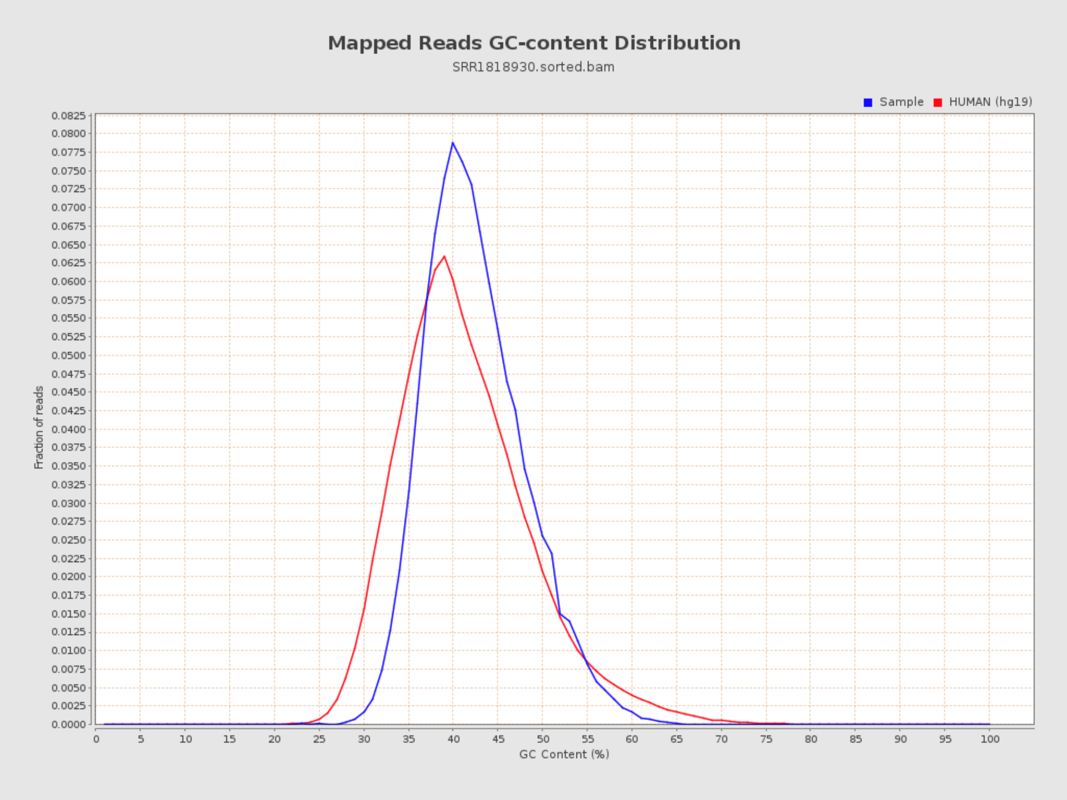
7. Results : Duplication Rate Histogram



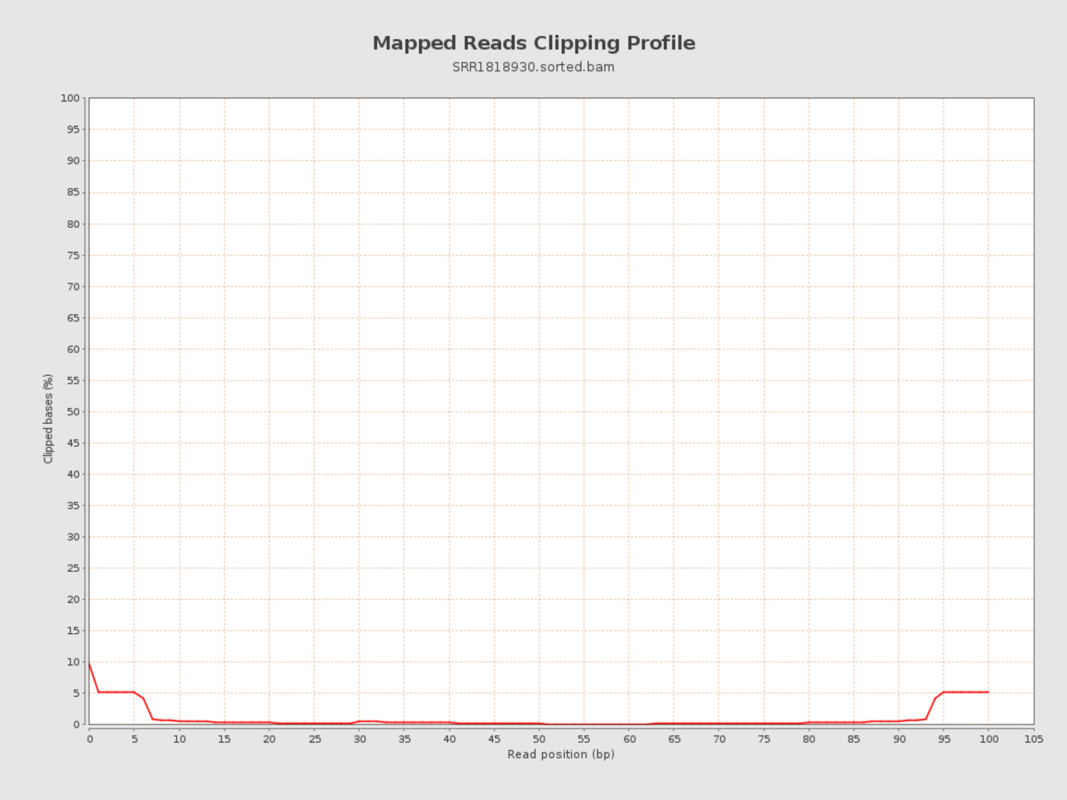
8. Results : Mapped Reads Nucleotide Content



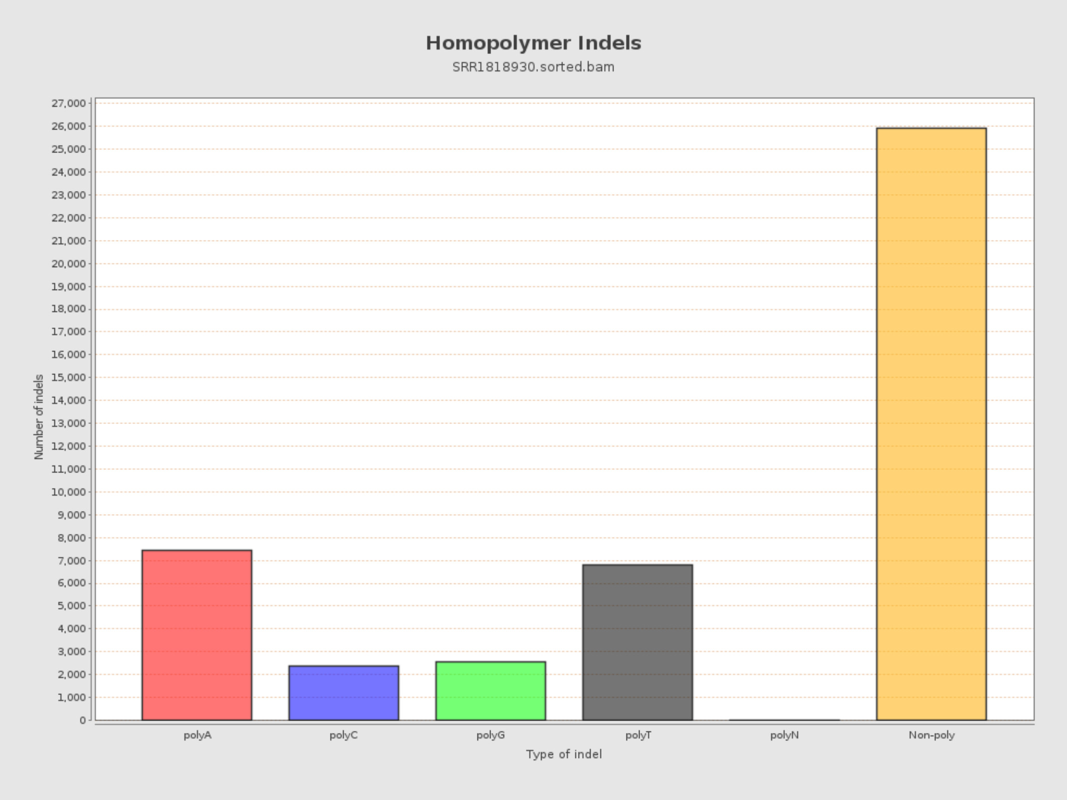
9. Results : Mapped Reads GC-content Distribution



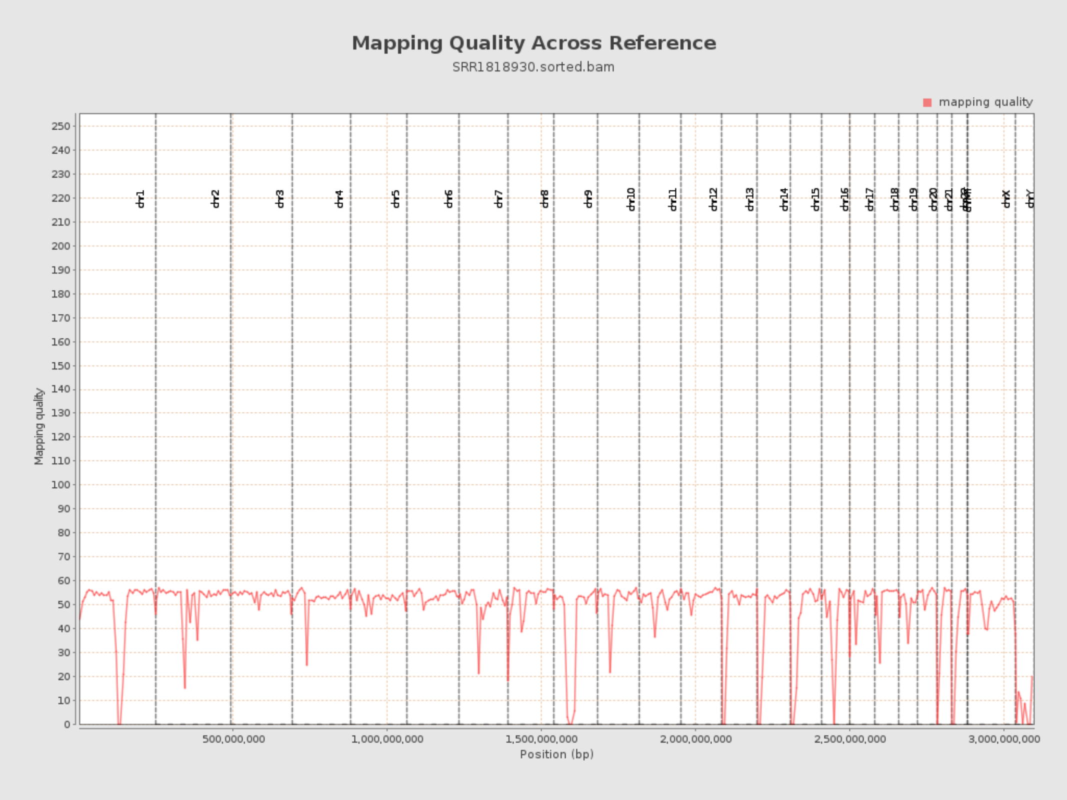
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram