Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:57:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751226.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_SRR8751226 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751226.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:57:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751226.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,480,297
Mapped reads	5,013,849 / 91.49%
Unmapped reads	466,448 / 8.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	183,872 / 3.36%
Read min/max/mean length	30 / 101 / 102.39
Duplicated reads (estimated)	168,512 / 3.07%
Duplication rate	1.86%
Clipped reads	1,024,895 / 18.7%

2.2. ACGT Content

Number/percentage of A's	143,537,185 / 29.21%
Number/percentage of C's	102,159,066 / 20.79%
Number/percentage of T's	144,253,637 / 29.36%
Number/percentage of G's	101,386,793 / 20.63%
Number/percentage of N's	2,662 / 0%
GC Percentage	41.43%

2.3. Coverage

Mean	0.1588

Standard Deviation	1.4837

2.4. Mapping Quality

Mean Mapping Quality	51.17

2.5. Mismatches and indels

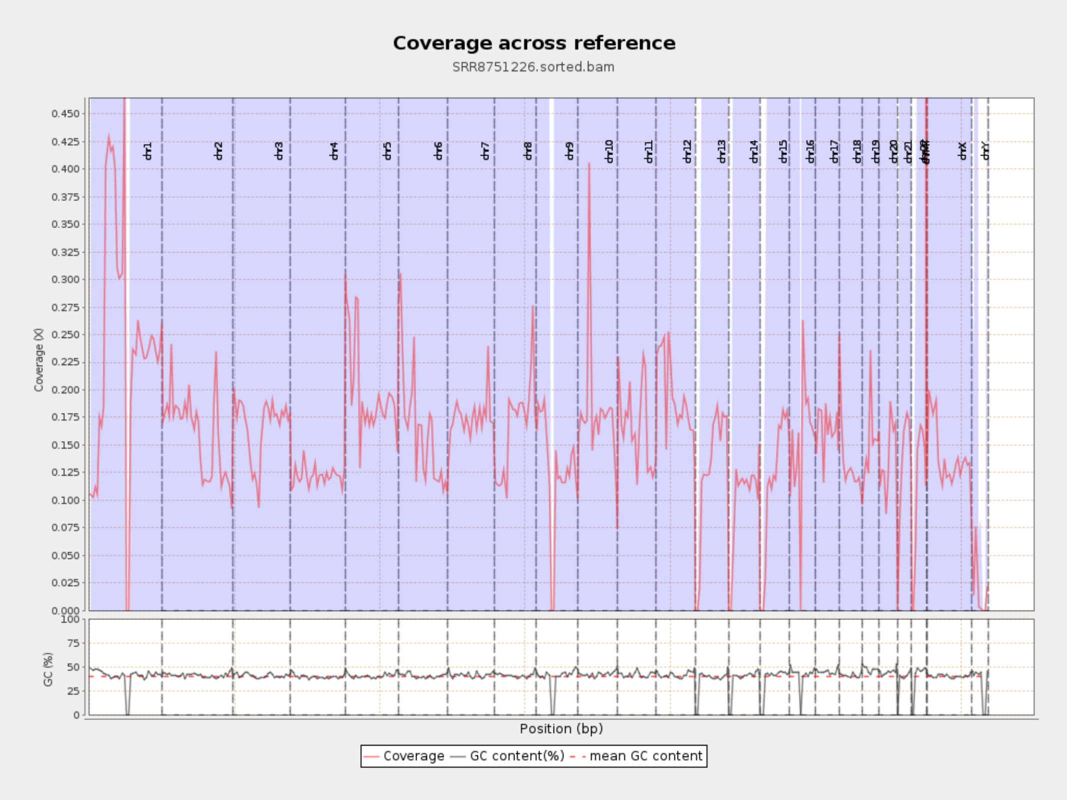
General error rate	0.41%
Mismatches	1,835,180
Insertions	128,391
Mapped reads with at least one insertion	2.51%
Deletions	65,810
Mapped reads with at least one deletion	1.29%
Homopolymer indels	49.14%

2.6. Chromosome stats

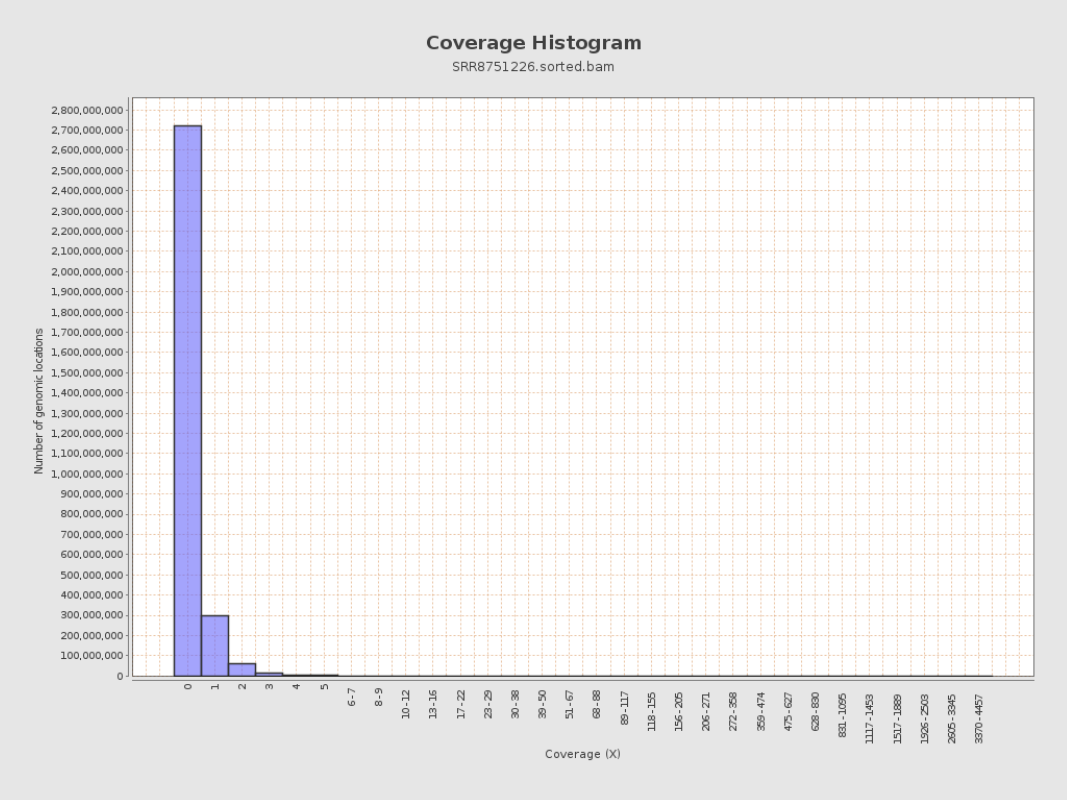
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	60083707	0.2411	4.1379
chr2	243199373	38955475	0.1602	0.6371
chr3	198022430	33080392	0.1671	0.5657
chr4	191154276	23259682	0.1217	0.5006
chr5	180915260	35540088	0.1964	0.5351
chr6	171115067	28331687	0.1656	0.923
chr7	159138663	27964290	0.1757	0.8335

chr8	146364022	24582920	0.168	0.5894
chr9	141213431	18015220	0.1276	0.7421
chr10	135534747	24729718	0.1825	2.1953
chr11	135006516	22466752	0.1664	0.7715
chr12	133851895	26342455	0.1968	0.5402
chr13	115169878	14600232	0.1268	0.4268
chr14	107349540	10459290	0.0974	0.4013
chr15	102531392	11925844	0.1163	0.4078
chr16	90354753	13752488	0.1522	0.9764
chr17	81195210	13275201	0.1635	0.7565
chr18	78077248	10391286	0.1331	1.4549
chr19	59128983	8987786	0.152	2.8899
chr20	63025520	8626705	0.1369	0.4575
chr21	48129895	6278170	0.1304	0.4869
chr22	51304566	5438270	0.106	0.3953
chrMT	16571	1582554	95.5014	36.1342
chrX	155270560	21684677	0.1397	0.5153
chrY	59373566	1127836	0.019	0.7062

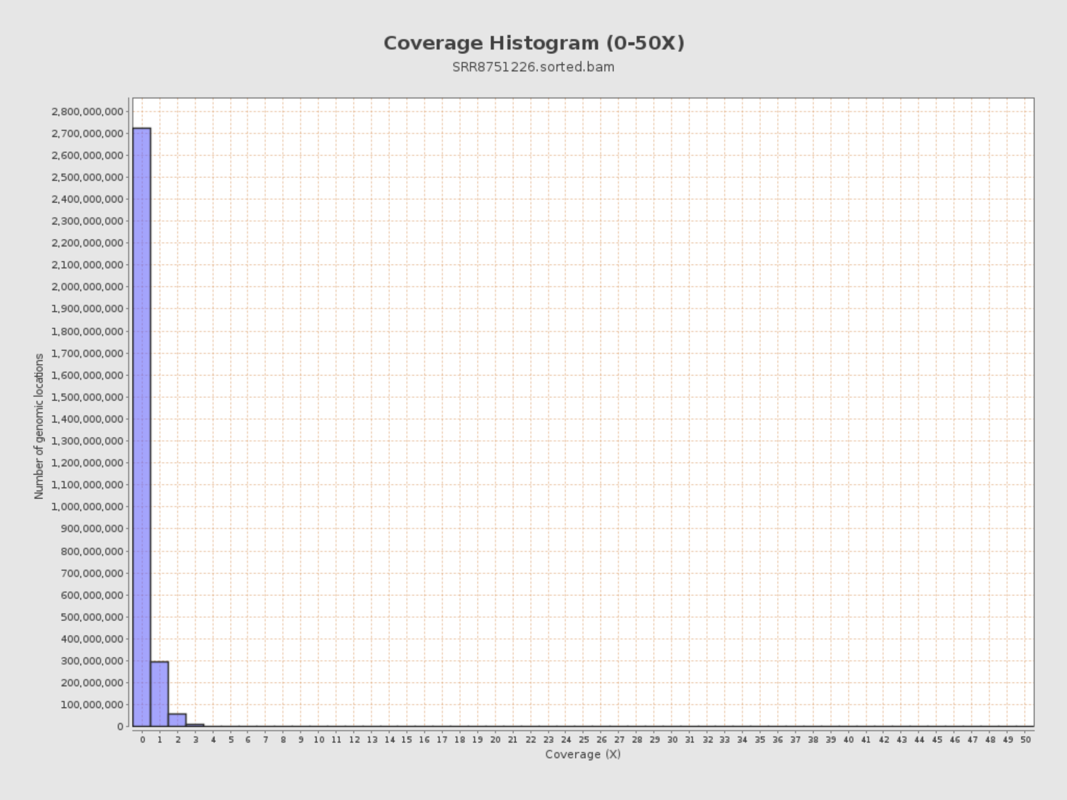
3. Results : Coverage across reference



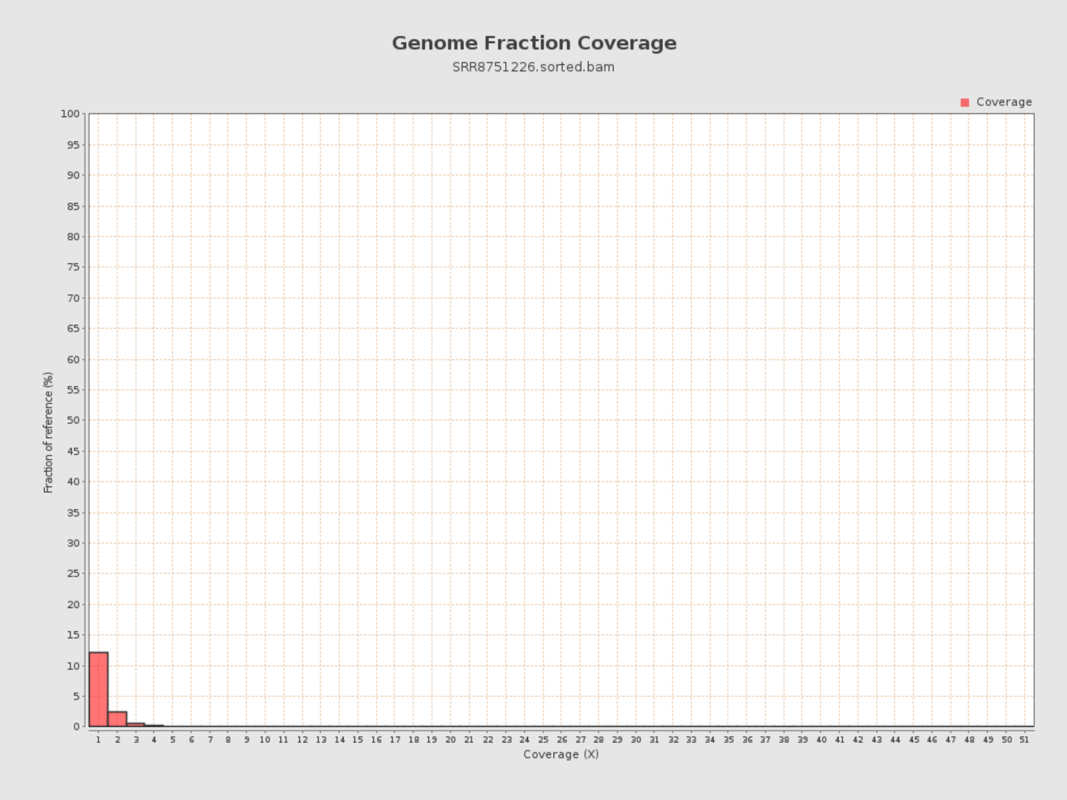
4. Results : Coverage Histogram



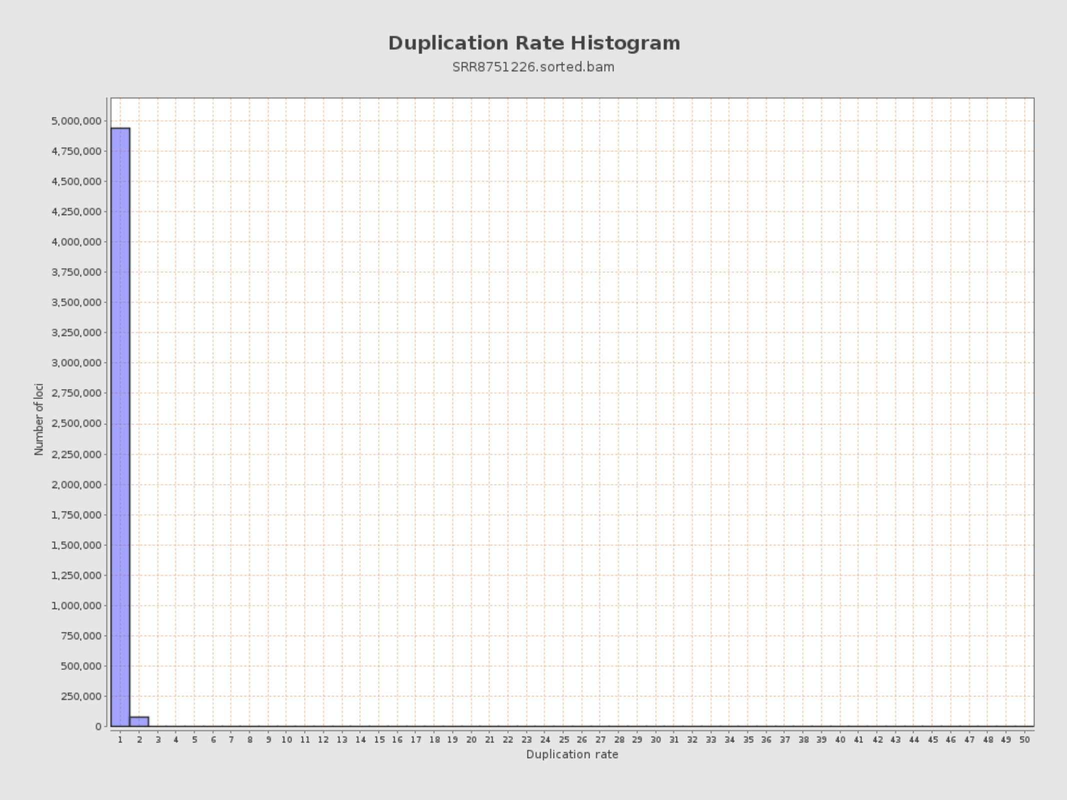
5. Results : Coverage Histogram (0-50X)



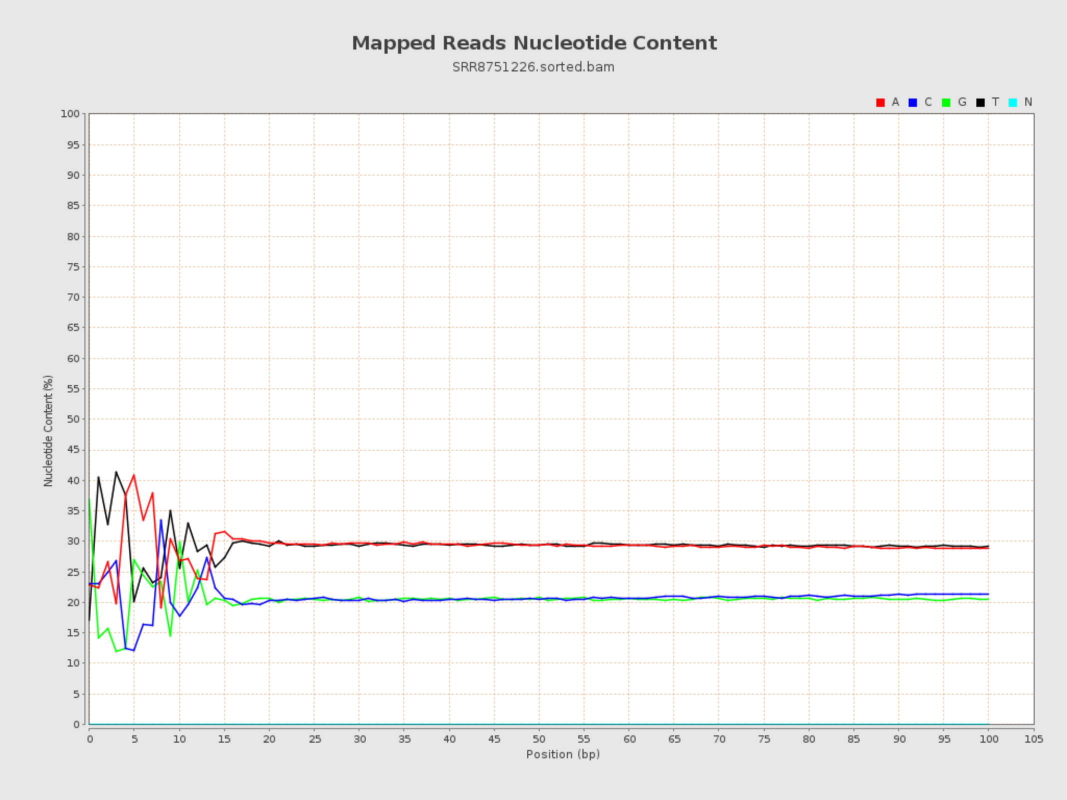
6. Results : Genome Fraction Coverage



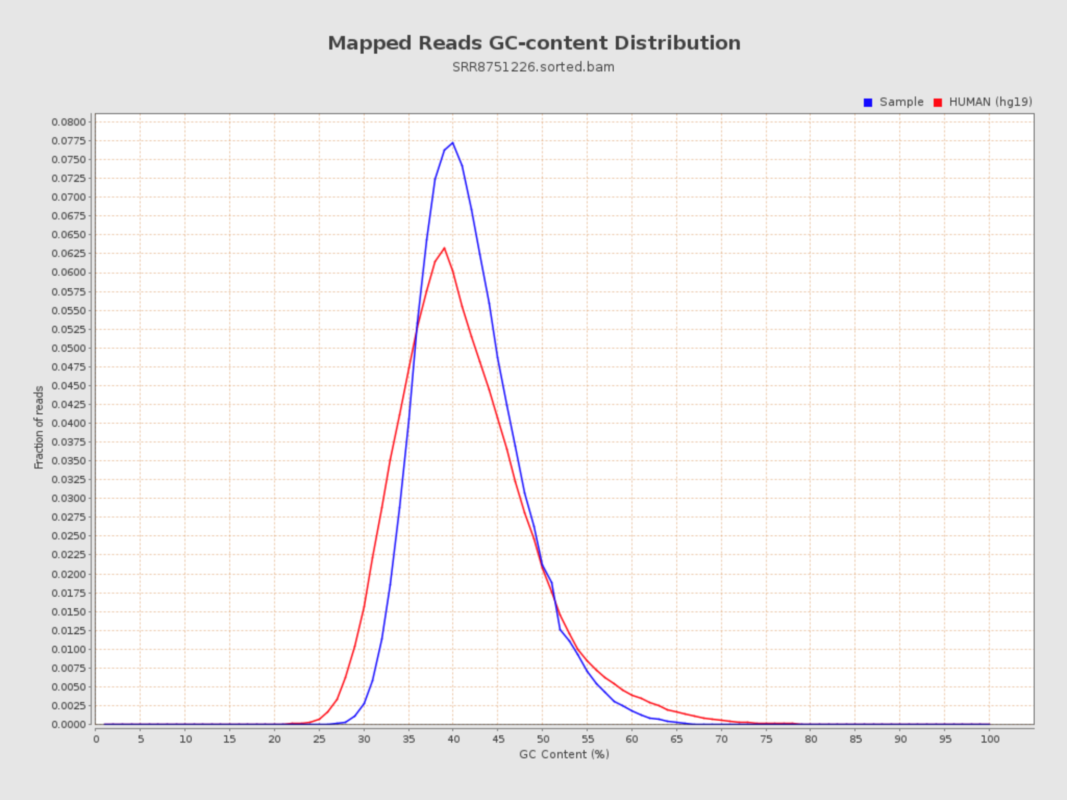
7. Results : Duplication Rate Histogram



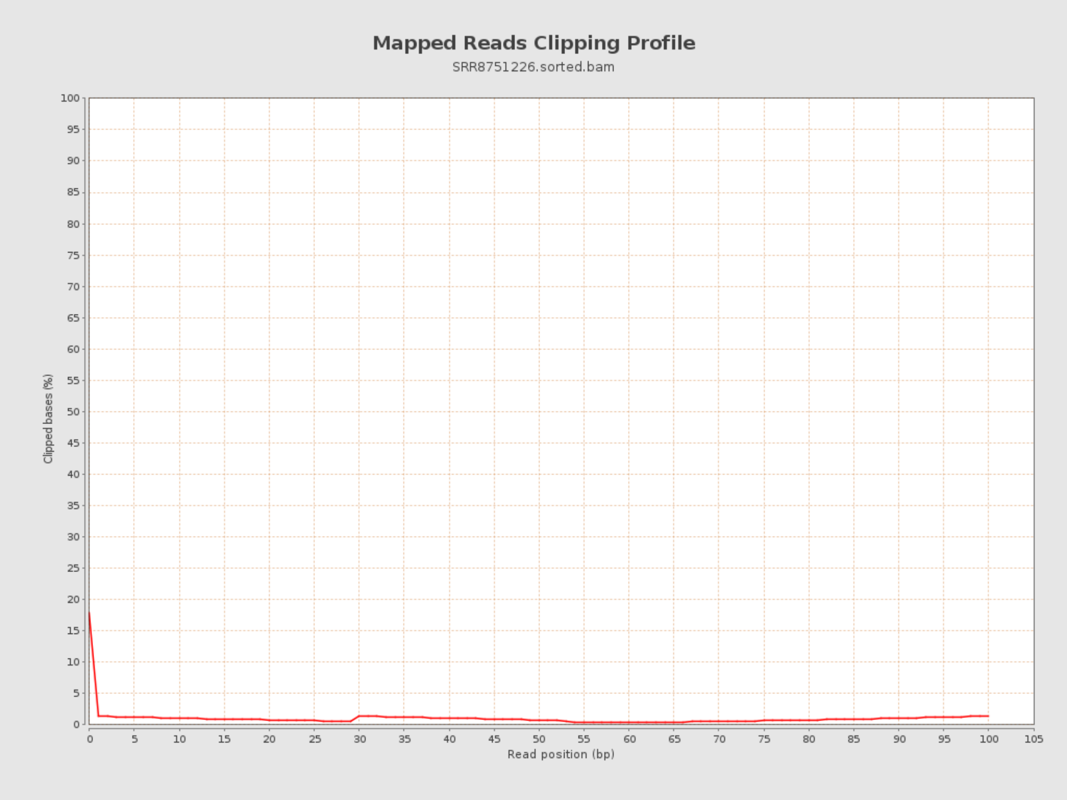
8. Results : Mapped Reads Nucleotide Content



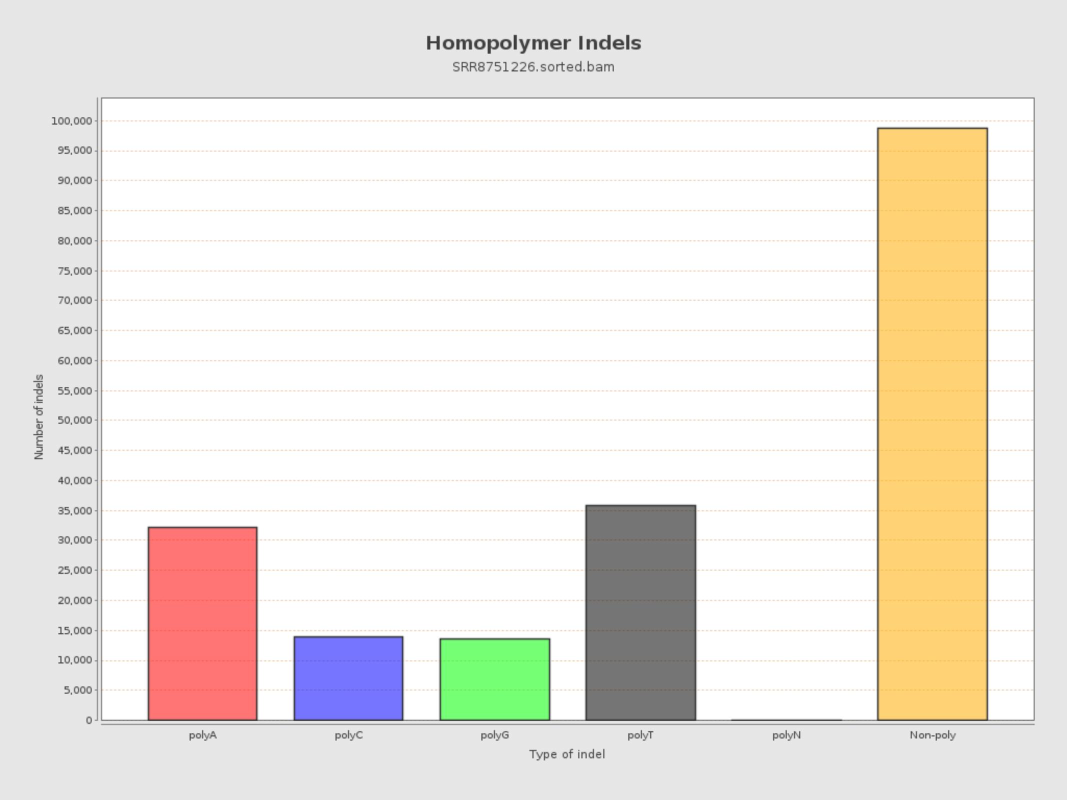
9. Results : Mapped Reads GC-content Distribution



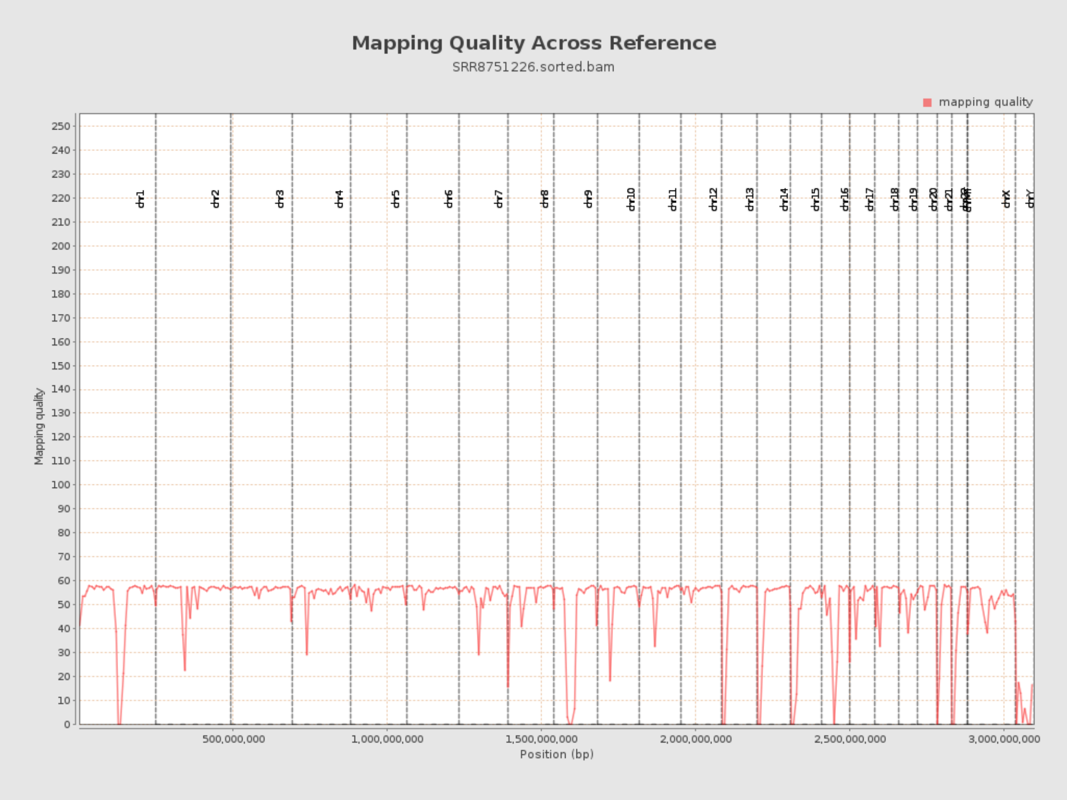
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram