Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 21:08:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524286.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_SRR10524286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524286.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 21:08:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524286.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,887
Mapped reads	1,609,658 / 91.72%
Unmapped reads	145,229 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,962 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	77,366 / 4.41%
Duplication rate	3.61%
Clipped reads	1,610,180 / 91.75%

2.2. ACGT Content

Number/percentage of A's	22,184,860 / 23.92%
Number/percentage of C's	17,630,950 / 19.01%
Number/percentage of T's	31,074,018 / 33.5%
Number/percentage of G's	21,861,672 / 23.57%
Number/percentage of N's	11,032 / 0.01%
GC Percentage	42.57%

2.3. Coverage

Mean	0.03

Standard Deviation	0.3058

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

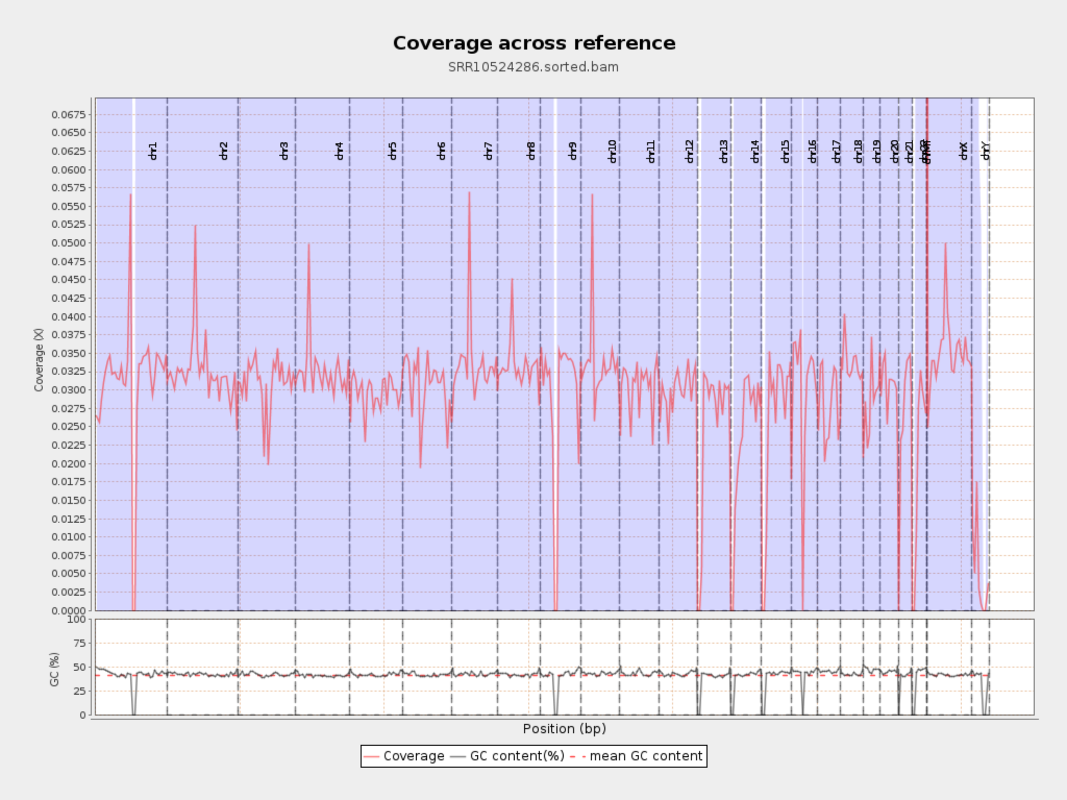
General error rate	0.51%
Mismatches	463,785
Insertions	7,351
Mapped reads with at least one insertion	0.46%
Deletions	17,375
Mapped reads with at least one deletion	1.07%
Homopolymer indels	41.3%

2.6. Chromosome stats

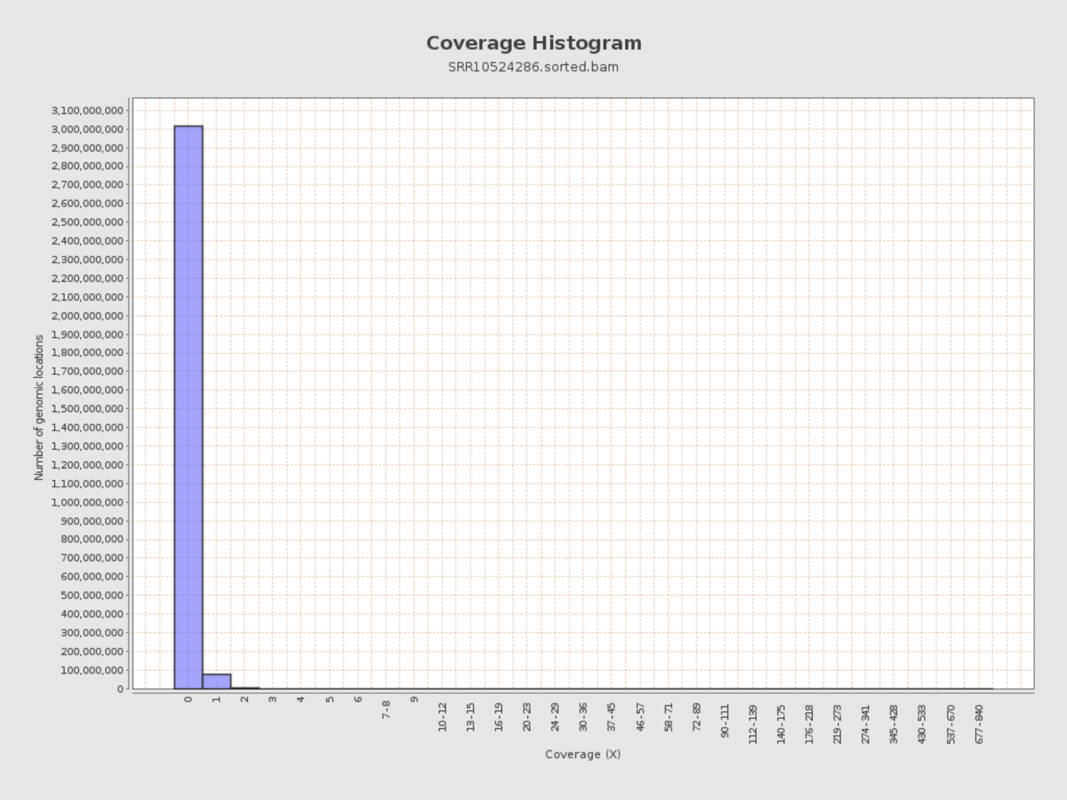
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7711659	0.0309	0.6021
chr2	243199373	7912517	0.0325	0.3276
chr3	198022430	6144580	0.031	0.1928
chr4	191154276	6234895	0.0326	0.2232
chr5	180915260	5383449	0.0298	0.192
chr6	171115067	5225740	0.0305	0.2084
chr7	159138663	5375160	0.0338	0.4221

chr8	146364022	4880471	0.0333	0.2936
chr9	141213431	4049303	0.0287	0.273
chr10	135534747	4562615	0.0337	0.2764
chr11	135006516	4132592	0.0306	0.2849
chr12	133851895	3989874	0.0298	0.199
chr13	115169878	2853673	0.0248	0.1739
chr14	107349540	2490141	0.0232	0.1812
chr15	102531392	2577747	0.0251	0.1745
chr16	90354753	2668129	0.0295	0.2057
chr17	81195210	2249996	0.0277	0.2
chr18	78077248	2625382	0.0336	0.5349
chr19	59128983	1685174	0.0285	0.3822
chr20	63025520	1922935	0.0305	0.1956
chr21	48129895	1290466	0.0268	0.2007
chr22	51304566	1044852	0.0204	0.1577
chrMT	16571	20743	1.2518	1.3542
chrX	155270560	5464466	0.0352	0.2397
chrY	59373566	293250	0.0049	0.132

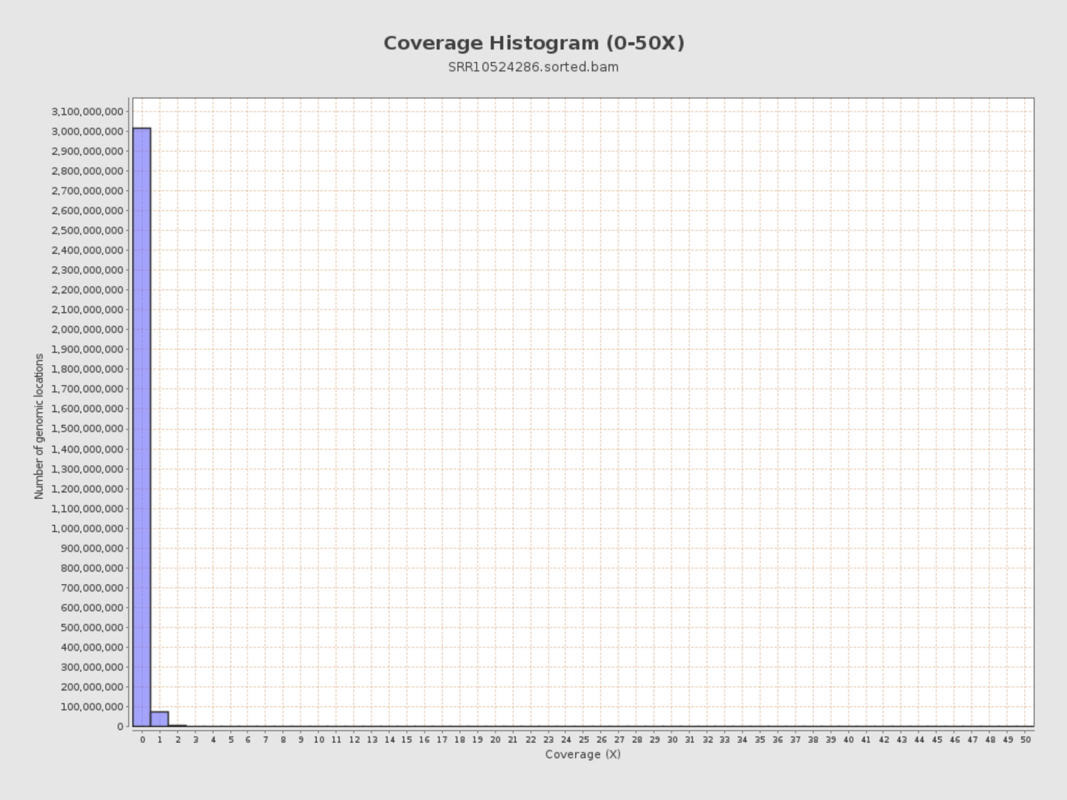
3. Results : Coverage across reference



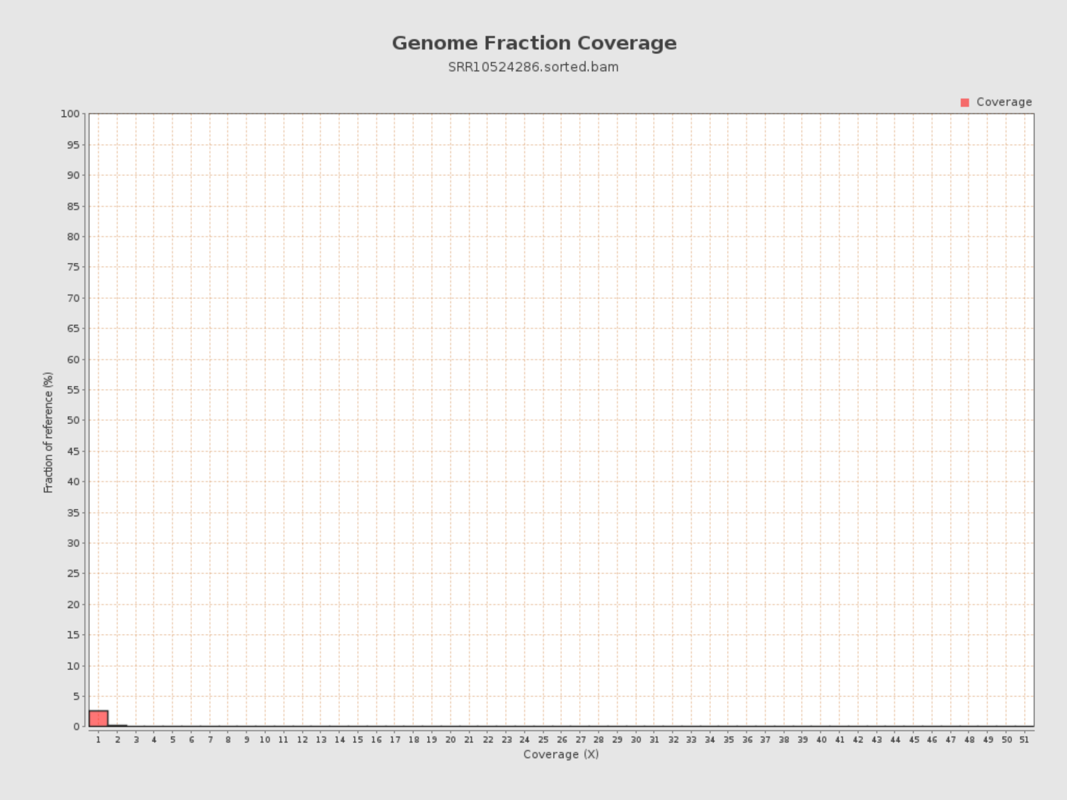
4. Results : Coverage Histogram



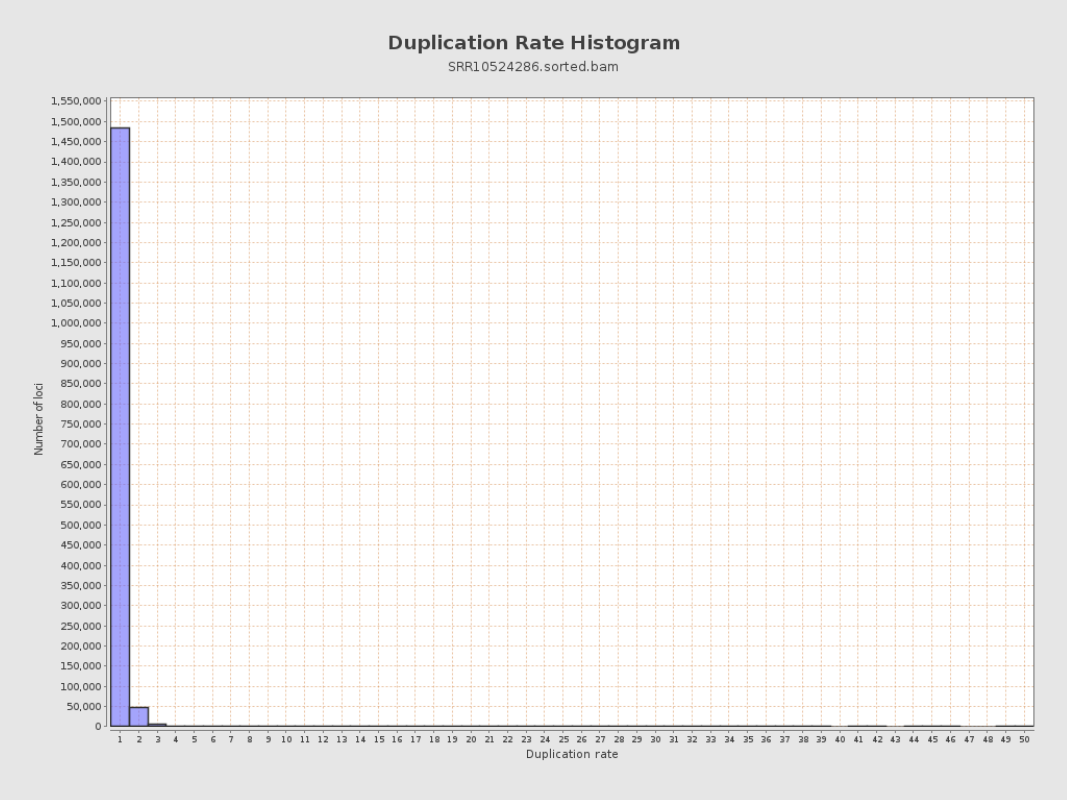
5. Results : Coverage Histogram (0-50X)



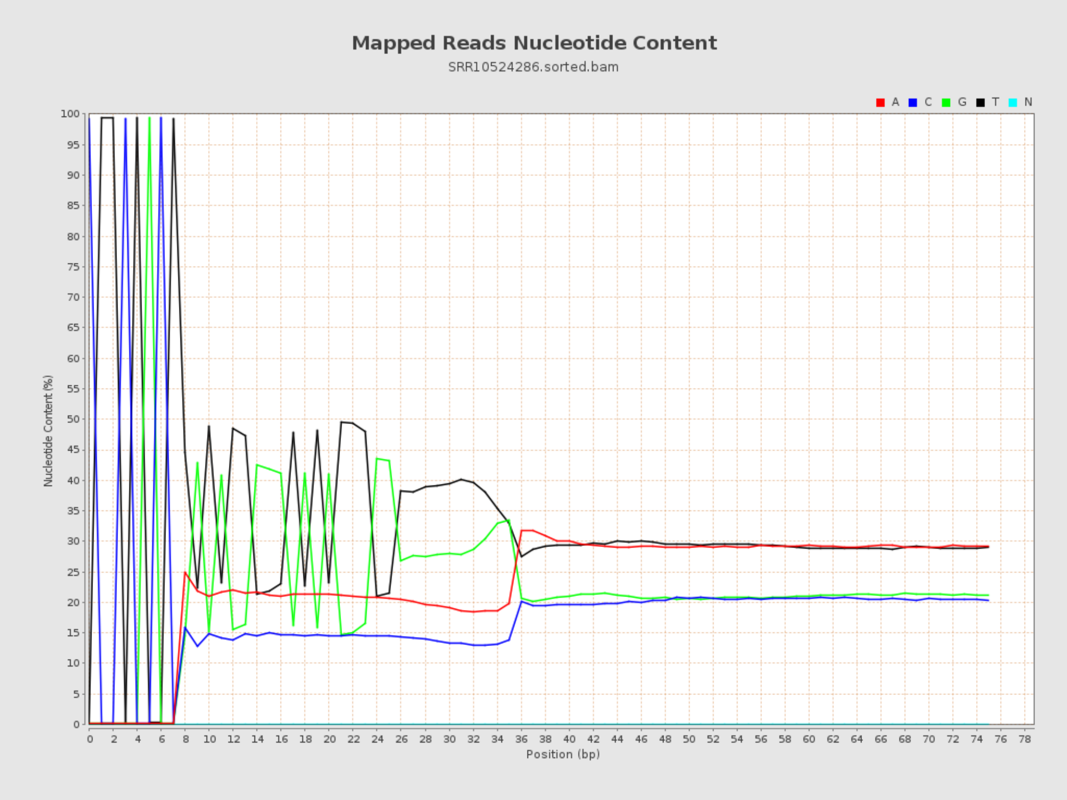
6. Results : Genome Fraction Coverage



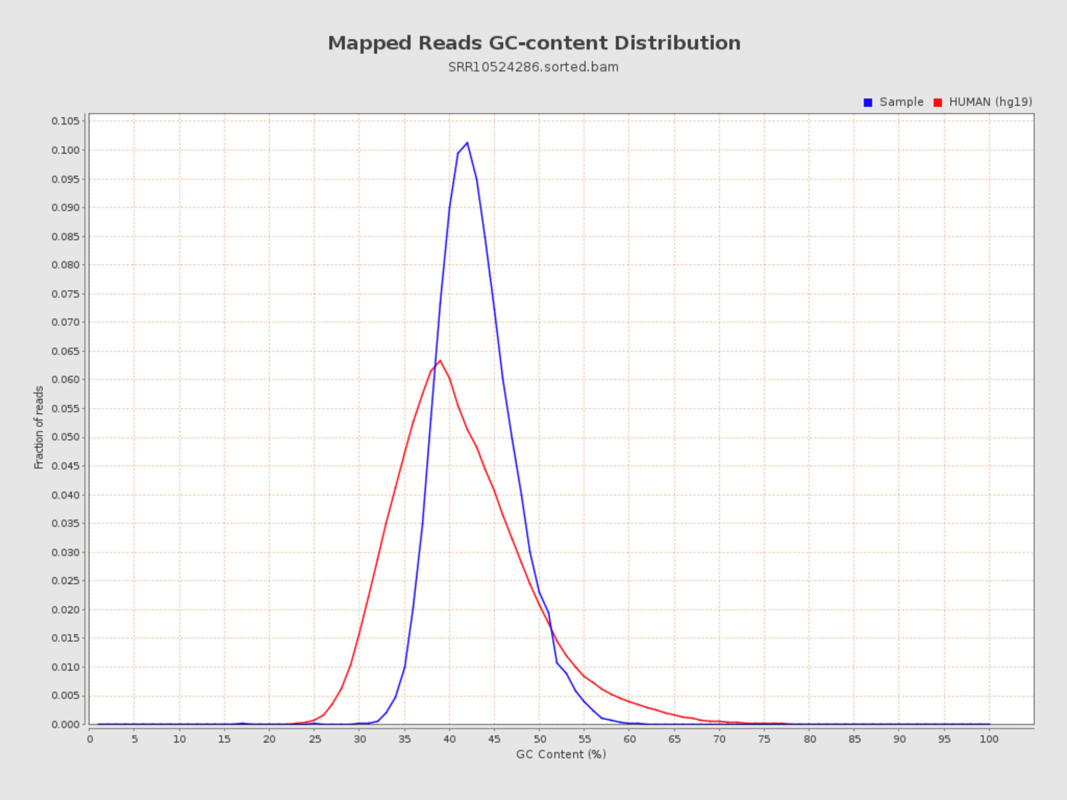
7. Results : Duplication Rate Histogram



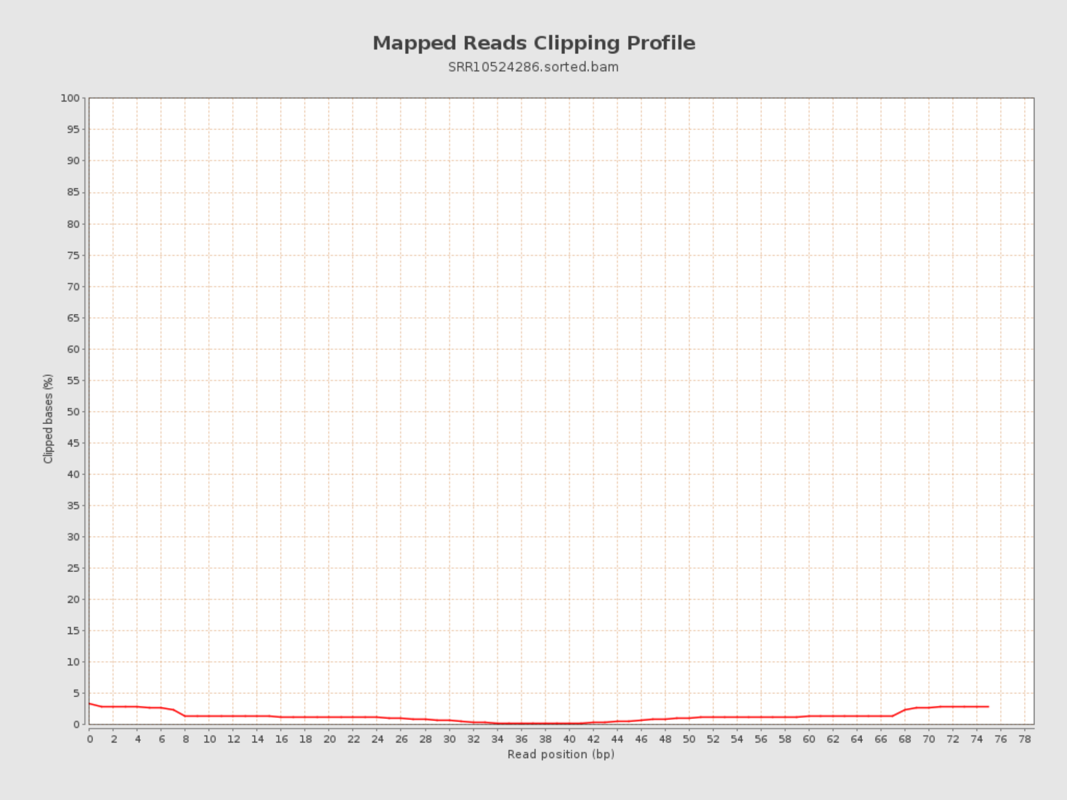
8. Results : Mapped Reads Nucleotide Content



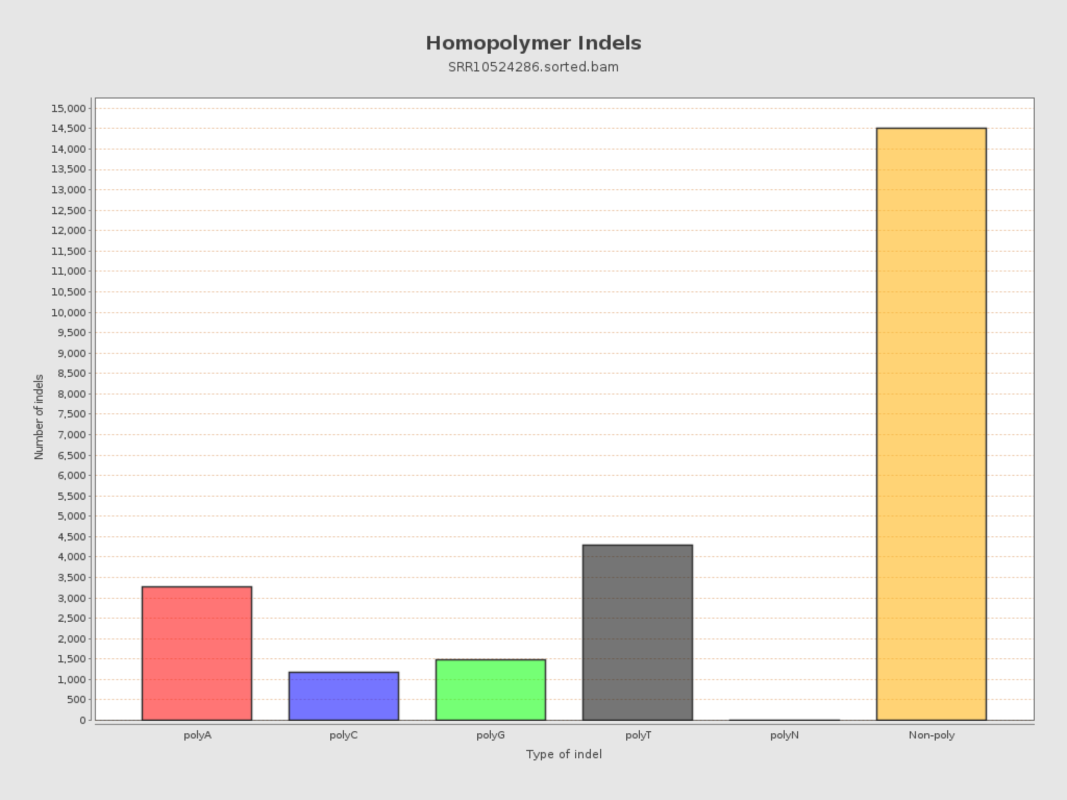
9. Results : Mapped Reads GC-content Distribution



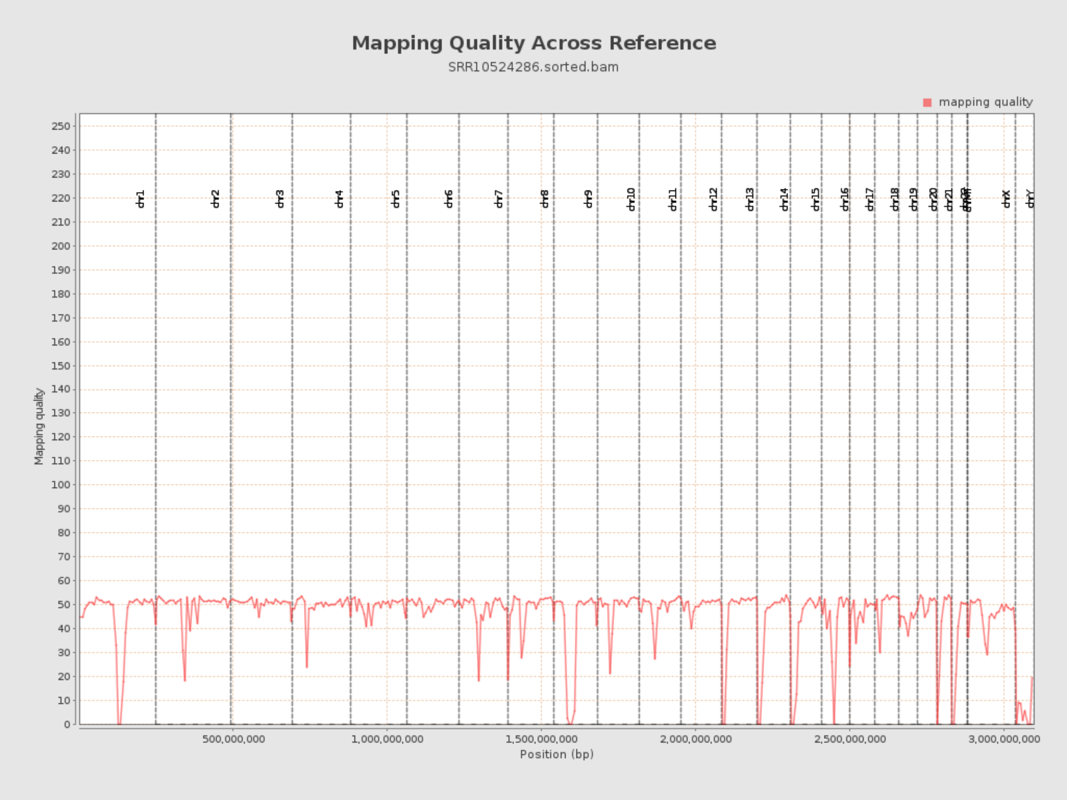
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram