Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:10:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525056.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_SRR10525056 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525056.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:10:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525056.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,536,638
Mapped reads	1,402,040 / 91.24%
Unmapped reads	134,598 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,709 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	47,110 / 3.07%
Duplication rate	2.38%
Clipped reads	1,402,773 / 91.29%

2.2. ACGT Content

Number/percentage of A's	20,094,228 / 25%
Number/percentage of C's	14,635,421 / 18.21%
Number/percentage of T's	26,330,096 / 32.76%
Number/percentage of G's	19,319,727 / 24.04%
Number/percentage of N's	1,465 / 0%
GC Percentage	42.24%

2.3. Coverage

Mean	0.026

Standard Deviation	0.2492

2.4. Mapping Quality

Mean Mapping Quality	44.15

2.5. Mismatches and indels

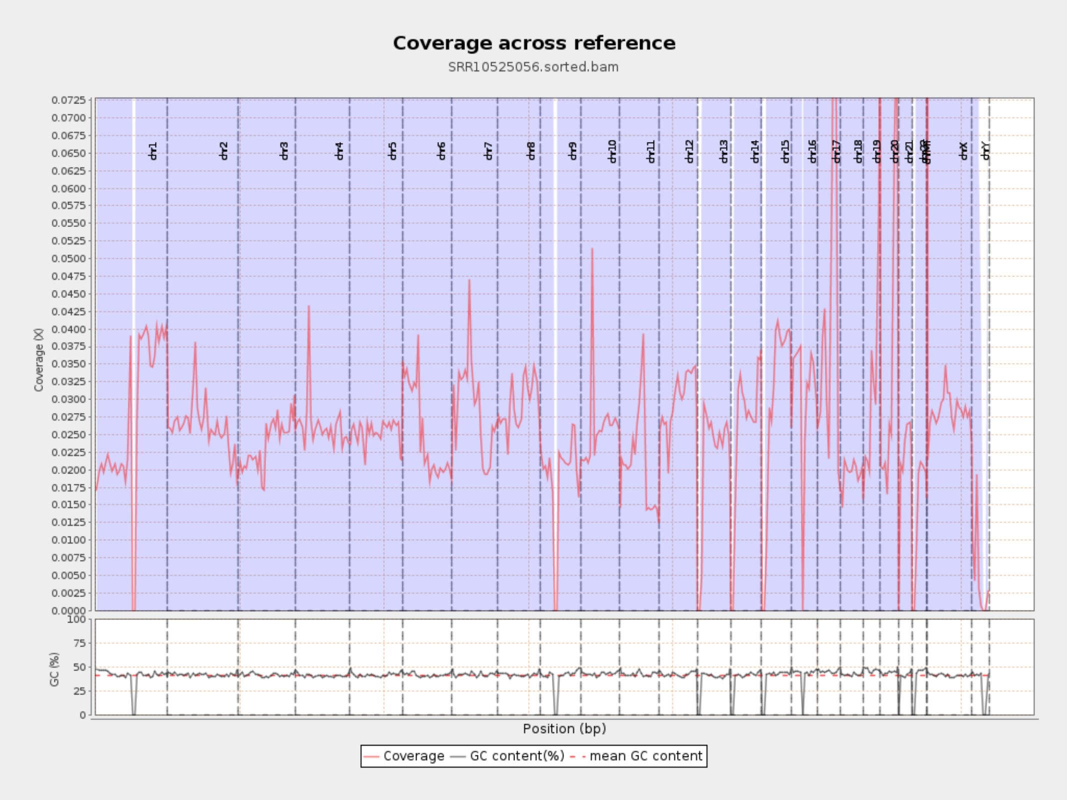
General error rate	0.53%
Mismatches	416,479
Insertions	6,456
Mapped reads with at least one insertion	0.46%
Deletions	16,552
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.36%

2.6. Chromosome stats

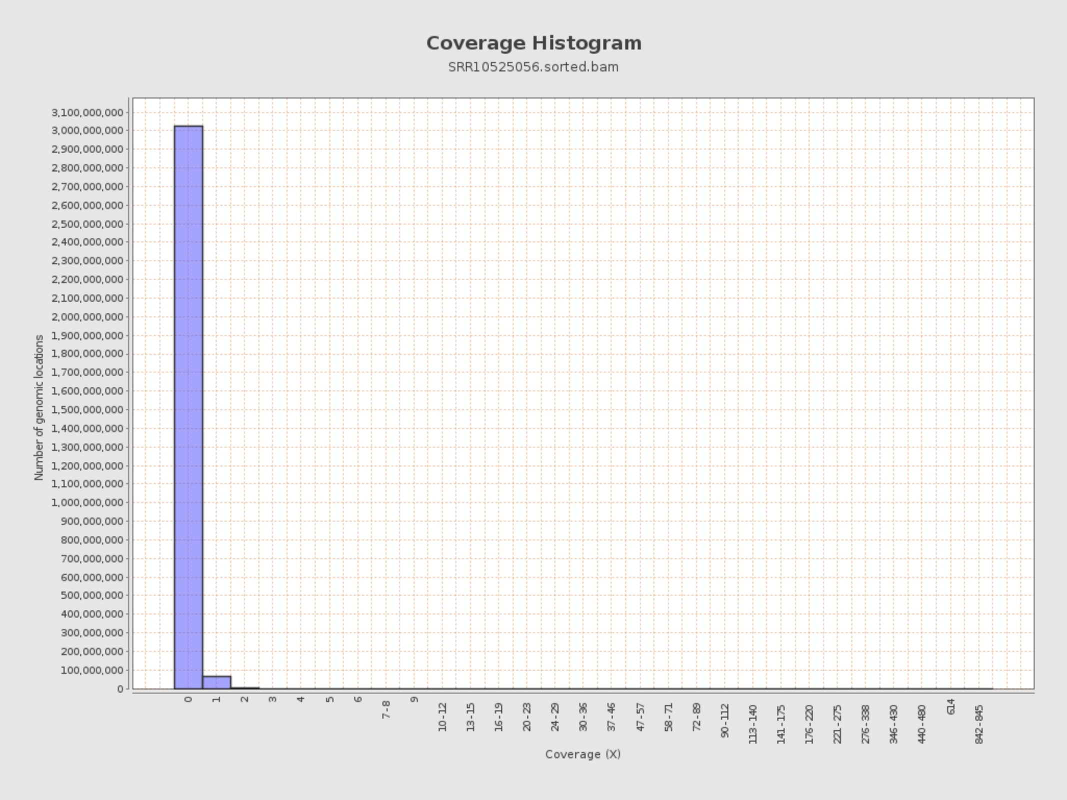
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6785965	0.0272	0.3741
chr2	243199373	6375121	0.0262	0.3803
chr3	198022430	4662503	0.0235	0.1678
chr4	191154276	5039370	0.0264	0.2002
chr5	180915260	4600599	0.0254	0.1711
chr6	171115067	4322437	0.0253	0.1985
chr7	159138663	4598843	0.0289	0.3256

chr8	146364022	4299938	0.0294	0.3037
chr9	141213431	2653843	0.0188	0.1759
chr10	135534747	3554752	0.0262	0.2573
chr11	135006516	2892106	0.0214	0.1954
chr12	133851895	4000365	0.0299	0.1875
chr13	115169878	2457506	0.0213	0.1575
chr14	107349540	2729642	0.0254	0.1743
chr15	102531392	2985315	0.0291	0.1924
chr16	90354753	2738137	0.0303	0.199
chr17	81195210	3475844	0.0428	0.234
chr18	78077248	1516180	0.0194	0.2872
chr19	59128983	1942007	0.0328	0.3069
chr20	63025520	2315679	0.0367	0.2127
chr21	48129895	1029142	0.0214	0.1851
chr22	51304566	723458	0.0141	0.1292
chrMT	16571	17082	1.0308	1.2268
chrX	155270560	4404105	0.0284	0.1959
chrY	59373566	287327	0.0048	0.1833

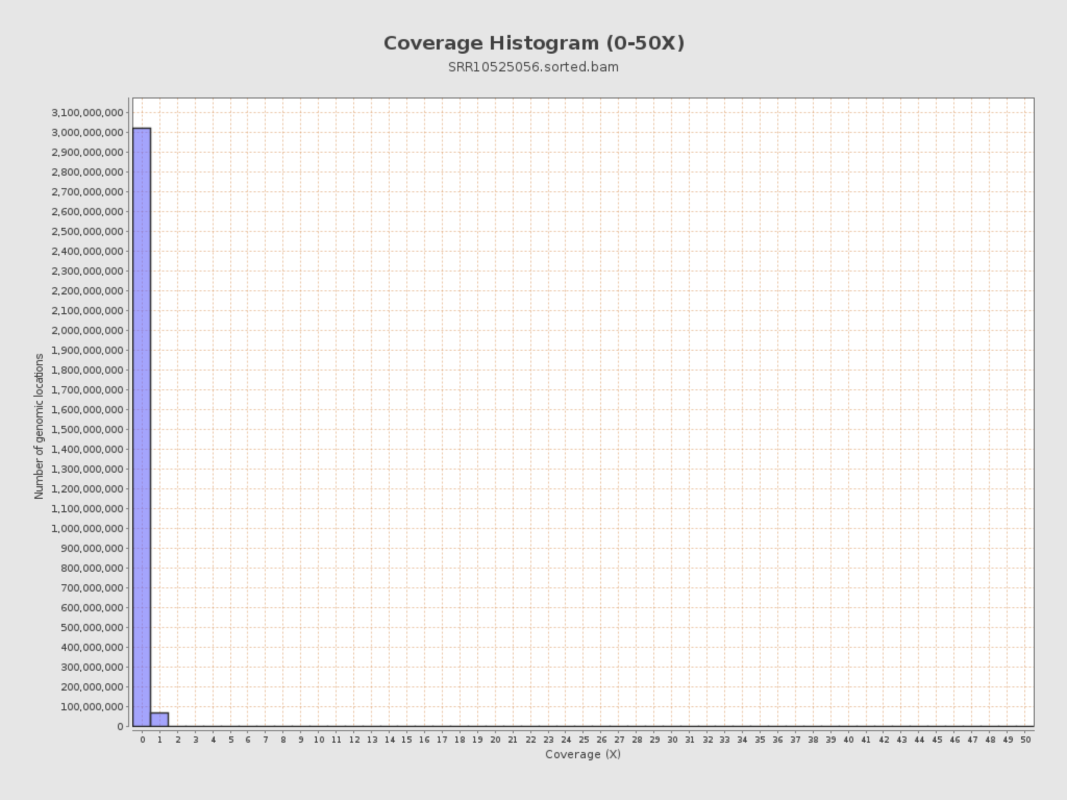
3. Results : Coverage across reference



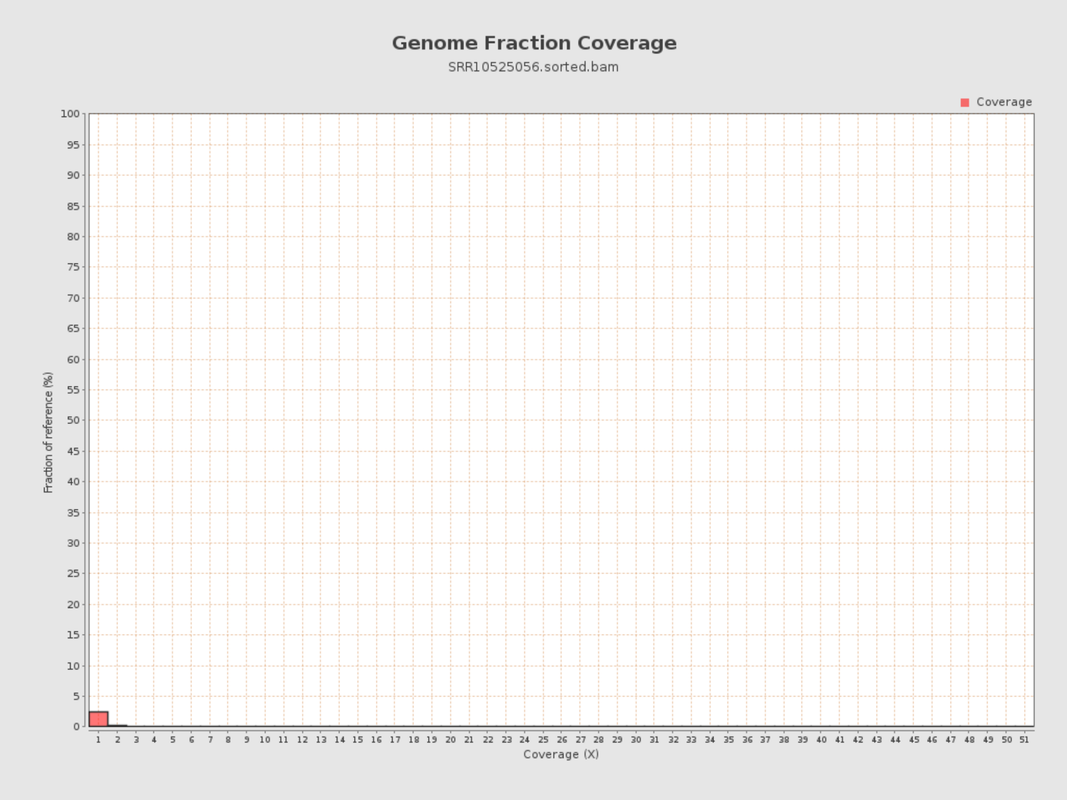
4. Results : Coverage Histogram



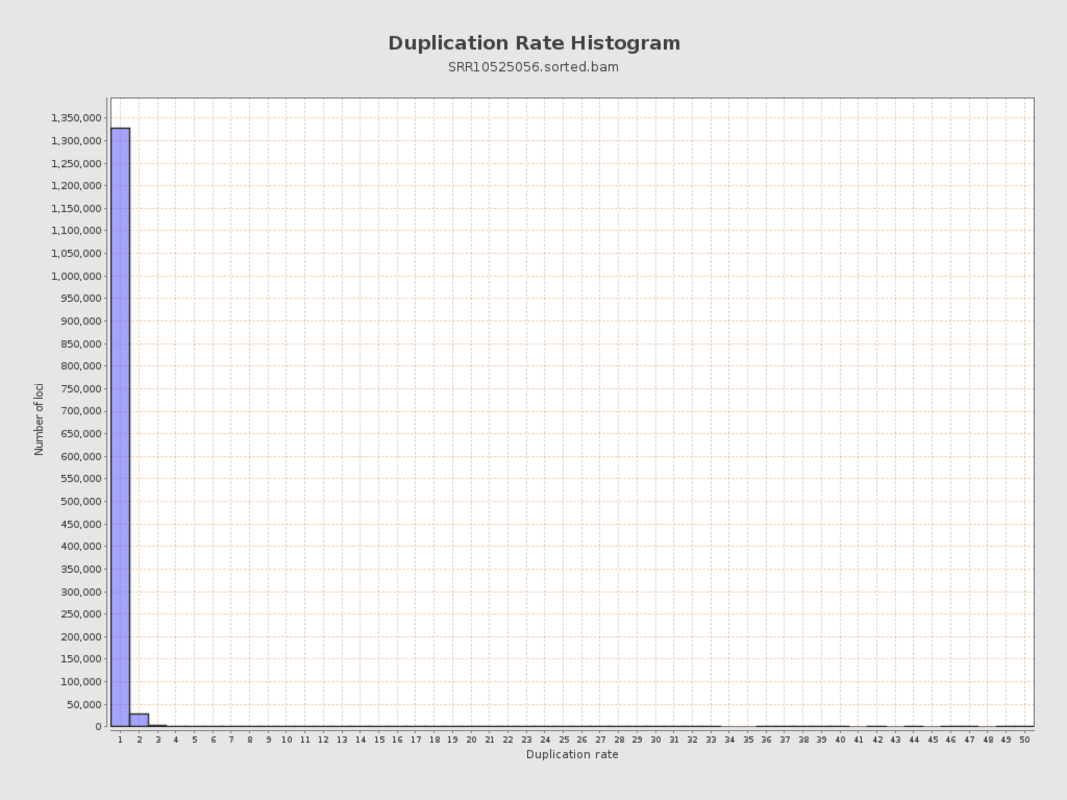
5. Results : Coverage Histogram (0-50X)



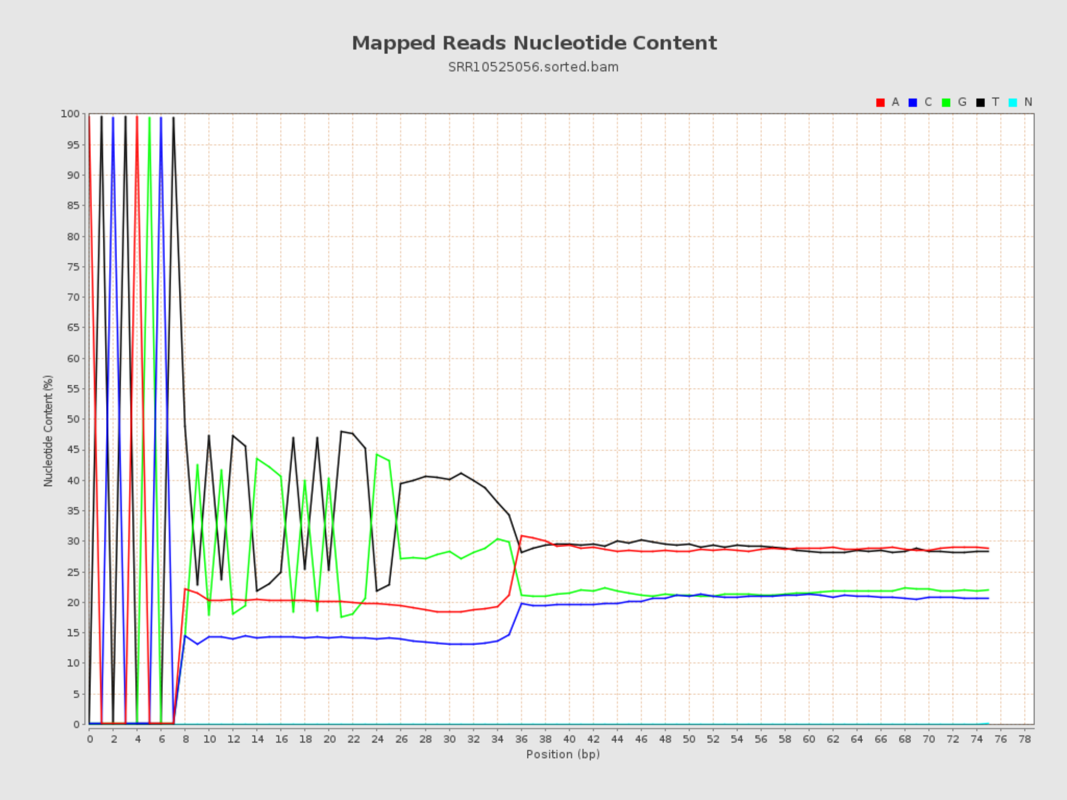
6. Results : Genome Fraction Coverage



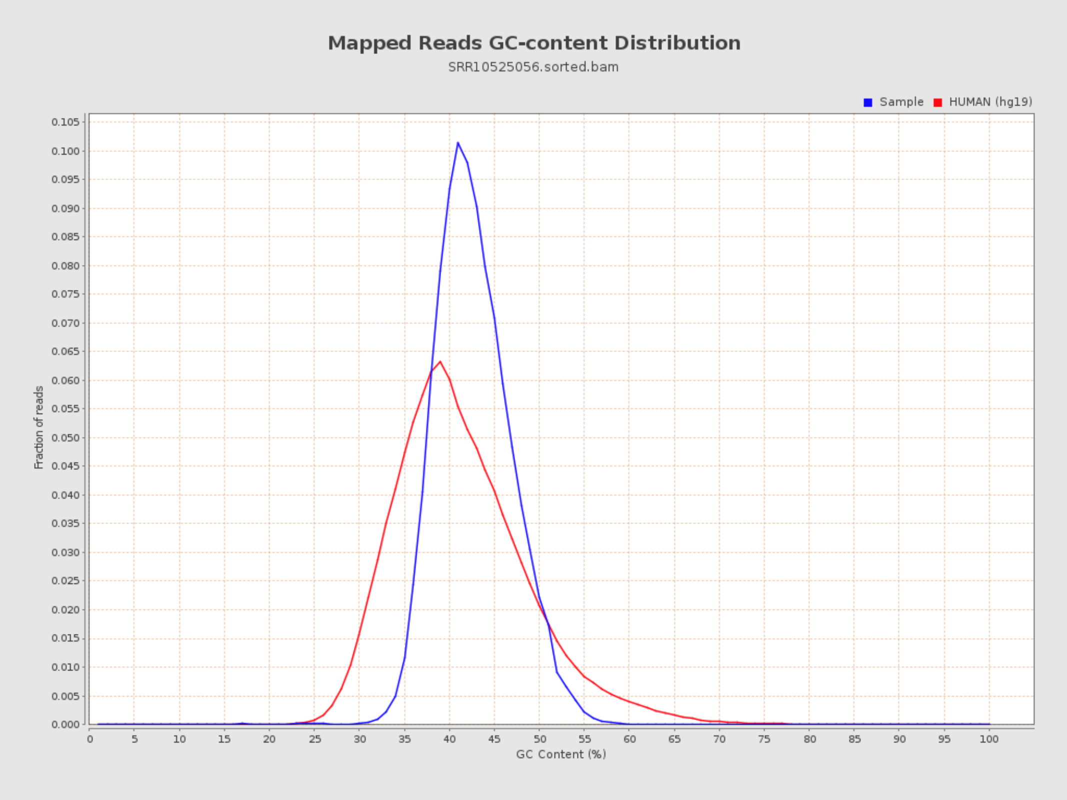
7. Results : Duplication Rate Histogram



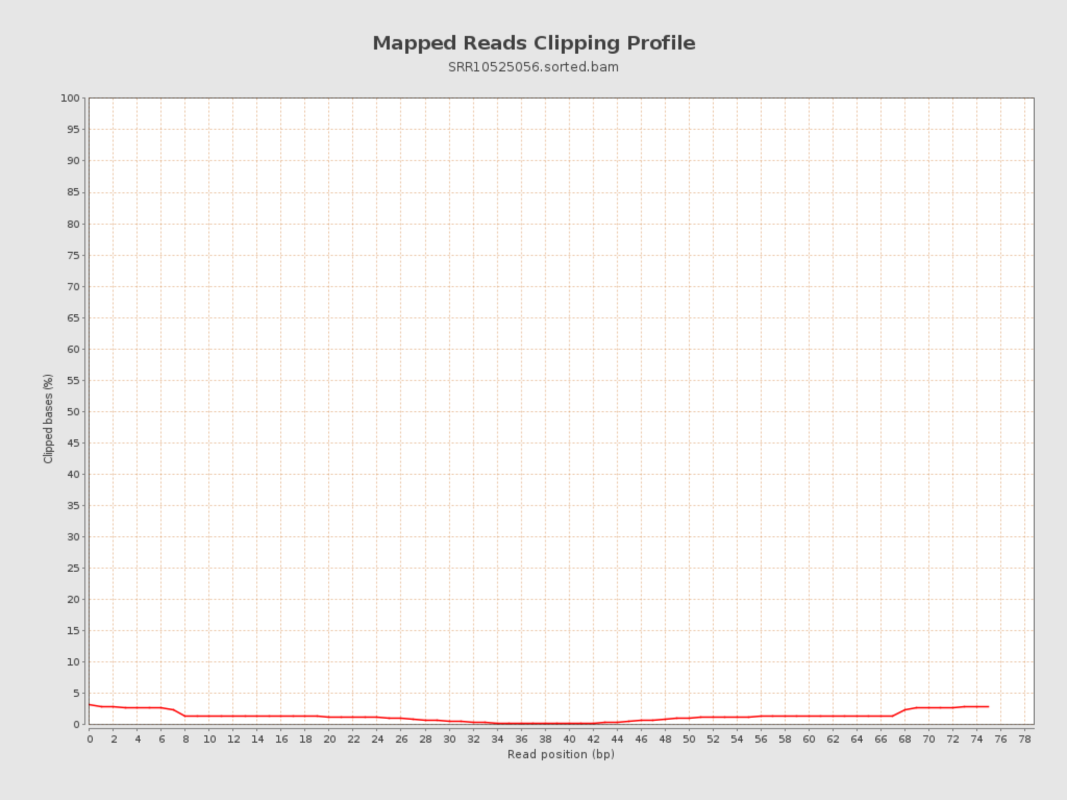
8. Results : Mapped Reads Nucleotide Content



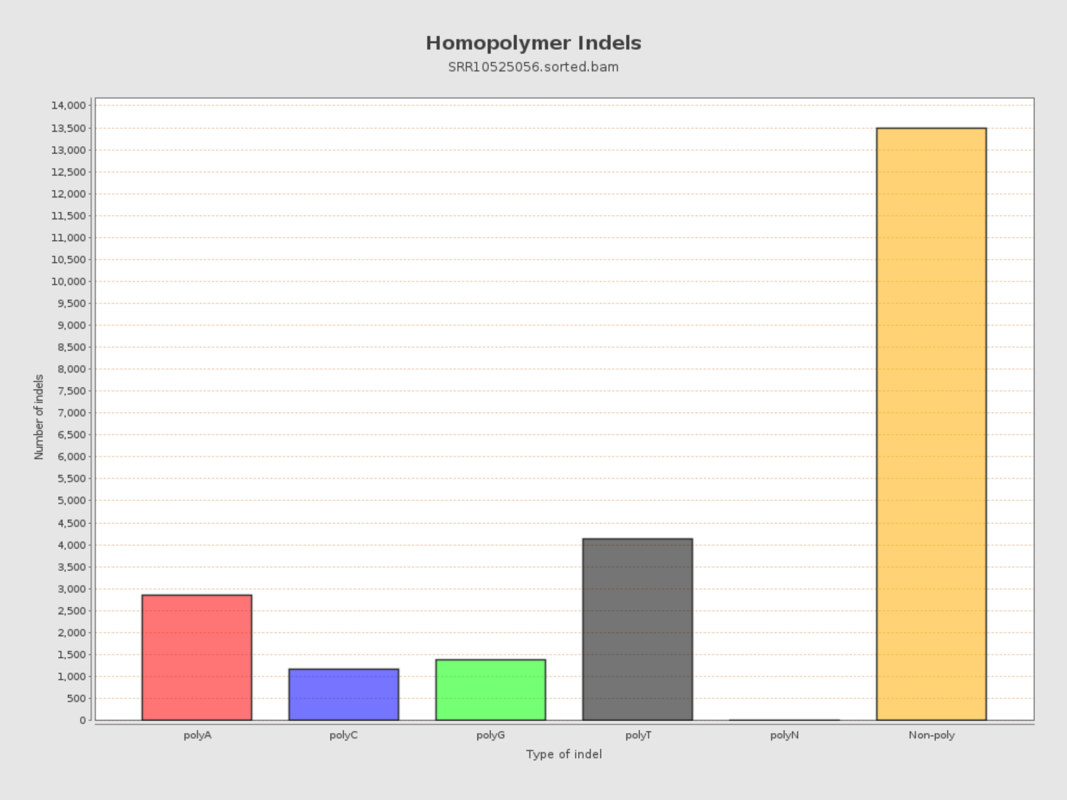
9. Results : Mapped Reads GC-content Distribution



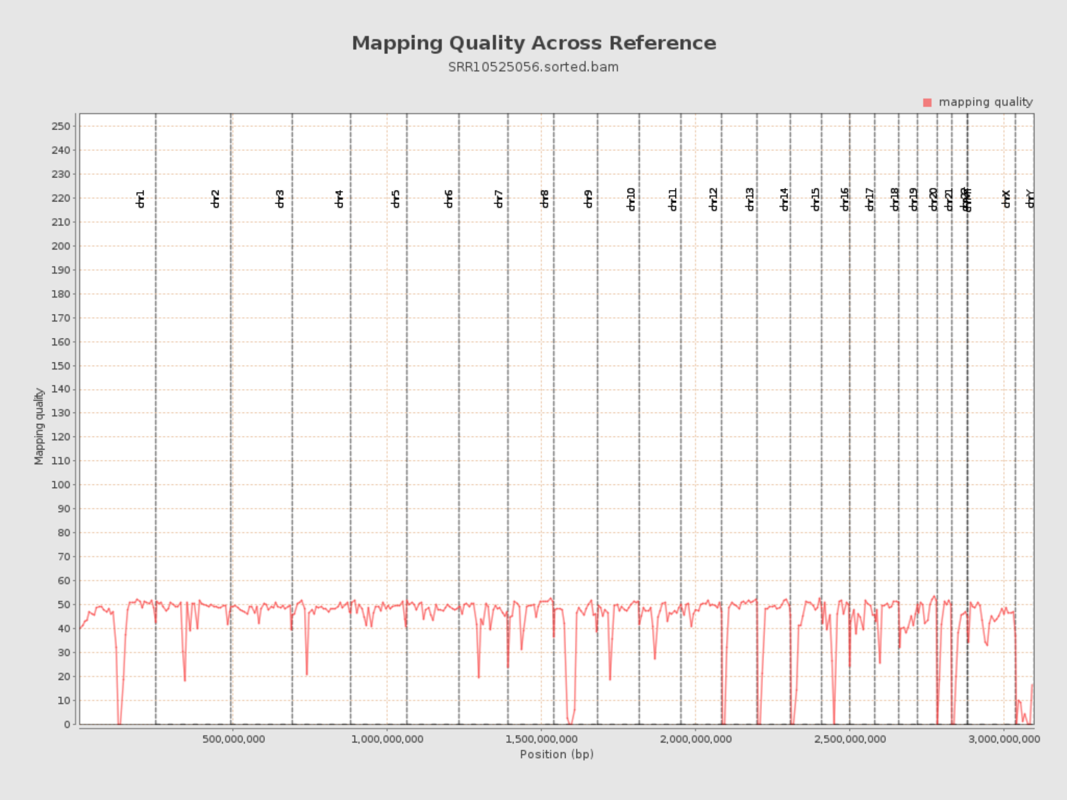
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram