Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:05:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525227.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_SRR10525227 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525227.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:05:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525227.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	492,072
Mapped reads	460,893 / 93.66%
Unmapped reads	31,179 / 6.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,912 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	7,218 / 1.47%
Duplication rate	1.14%
Clipped reads	460,898 / 93.66%

2.2. ACGT Content

Number/percentage of A's	8,066,009 / 27.79%
Number/percentage of C's	5,901,622 / 20.33%
Number/percentage of T's	8,699,372 / 29.97%
Number/percentage of G's	6,358,321 / 21.91%
Number/percentage of N's	723 / 0%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0094

Standard Deviation	0.1225

2.4. Mapping Quality

Mean Mapping Quality	46.77

2.5. Mismatches and indels

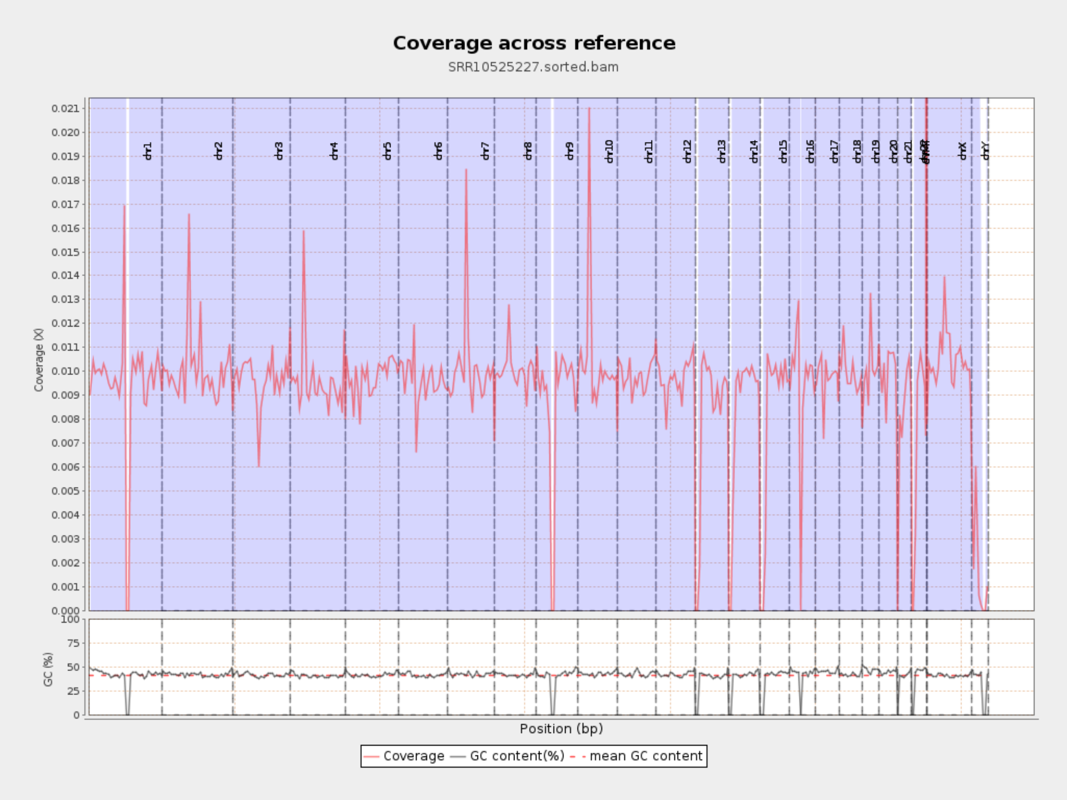
General error rate	0.5%
Mismatches	140,250
Insertions	2,246
Mapped reads with at least one insertion	0.48%
Deletions	6,226
Mapped reads with at least one deletion	1.34%
Homopolymer indels	41.77%

2.6. Chromosome stats

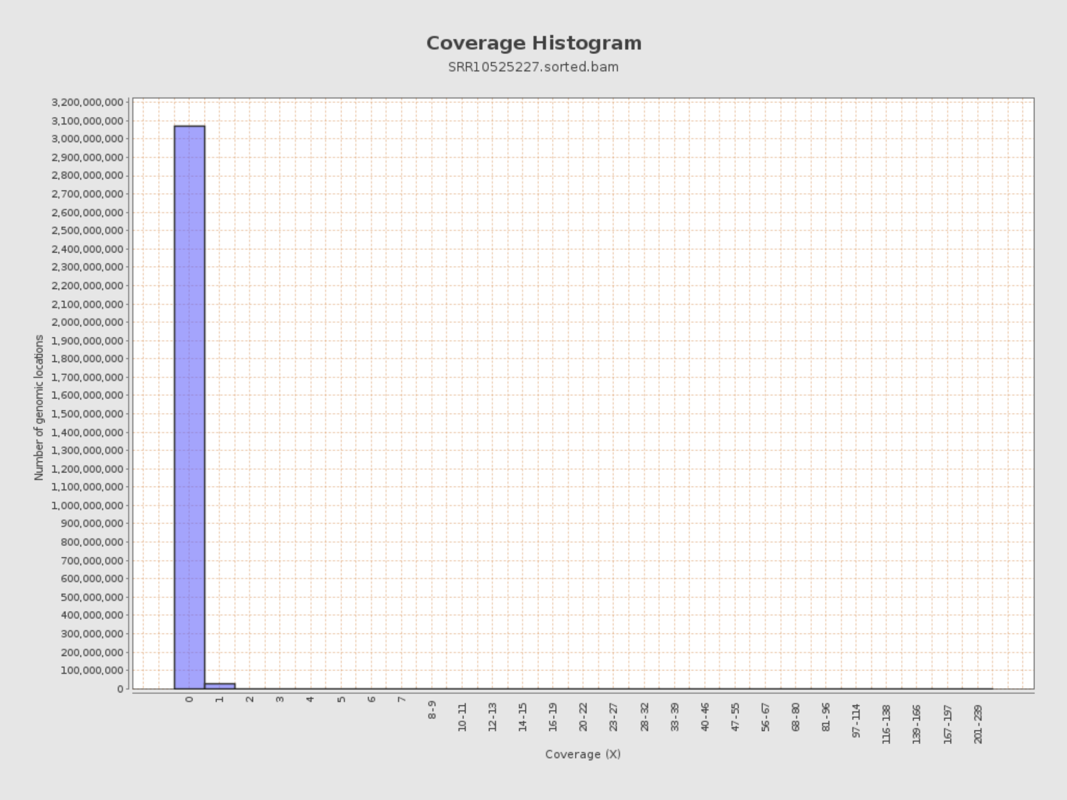
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2351469	0.0094	0.1987
chr2	243199373	2456600	0.0101	0.1237
chr3	198022430	1907290	0.0096	0.1017
chr4	191154276	1830227	0.0096	0.1058
chr5	180915260	1765246	0.0098	0.102
chr6	171115067	1651918	0.0097	0.106
chr7	159138663	1622208	0.0102	0.1558

chr8	146364022	1469132	0.01	0.1132
chr9	141213431	1214644	0.0086	0.1108
chr10	135534747	1411738	0.0104	0.1339
chr11	135006516	1320448	0.0098	0.1091
chr12	133851895	1300874	0.0097	0.102
chr13	115169878	916329	0.008	0.0915
chr14	107349540	879402	0.0082	0.0938
chr15	102531392	821996	0.008	0.092
chr16	90354753	852604	0.0094	0.1072
chr17	81195210	784697	0.0097	0.1044
chr18	78077248	780793	0.01	0.1711
chr19	59128983	599846	0.0101	0.1562
chr20	63025520	625365	0.0099	0.1035
chr21	48129895	389192	0.0081	0.0993
chr22	51304566	348180	0.0068	0.0848
chrMT	16571	14579	0.8798	0.9923
chrX	155270560	1628279	0.0105	0.1078
chrY	59373566	93263	0.0016	0.0635

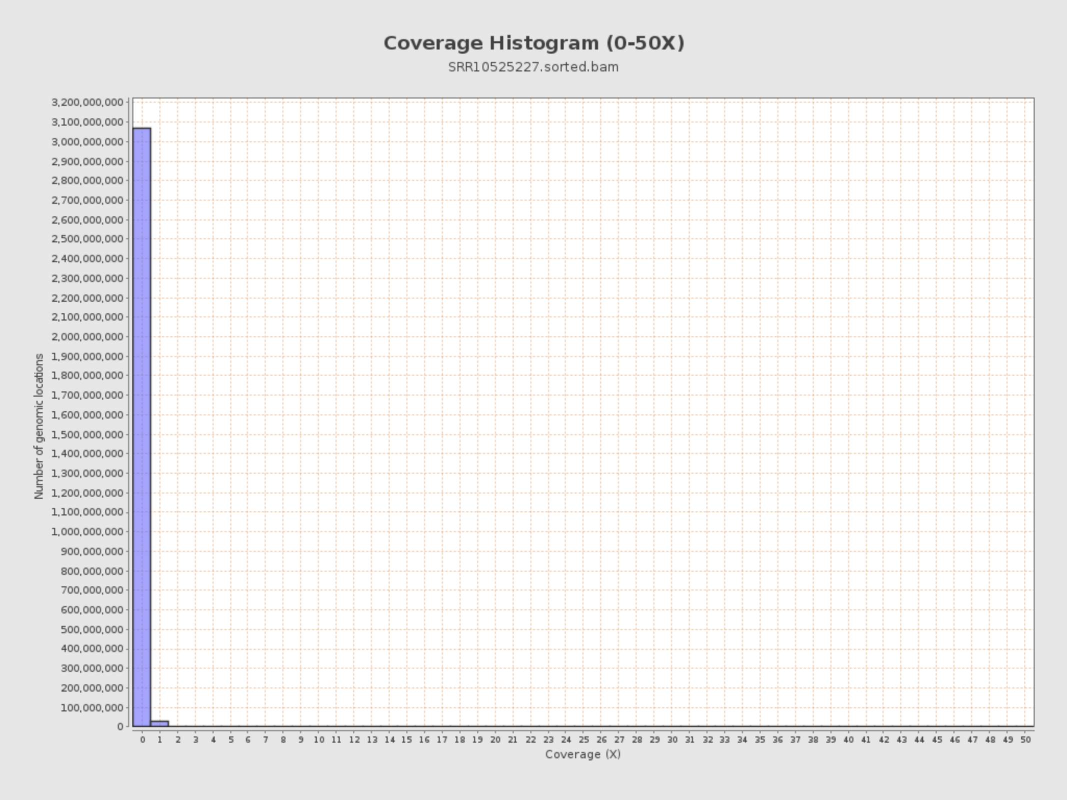
3. Results : Coverage across reference



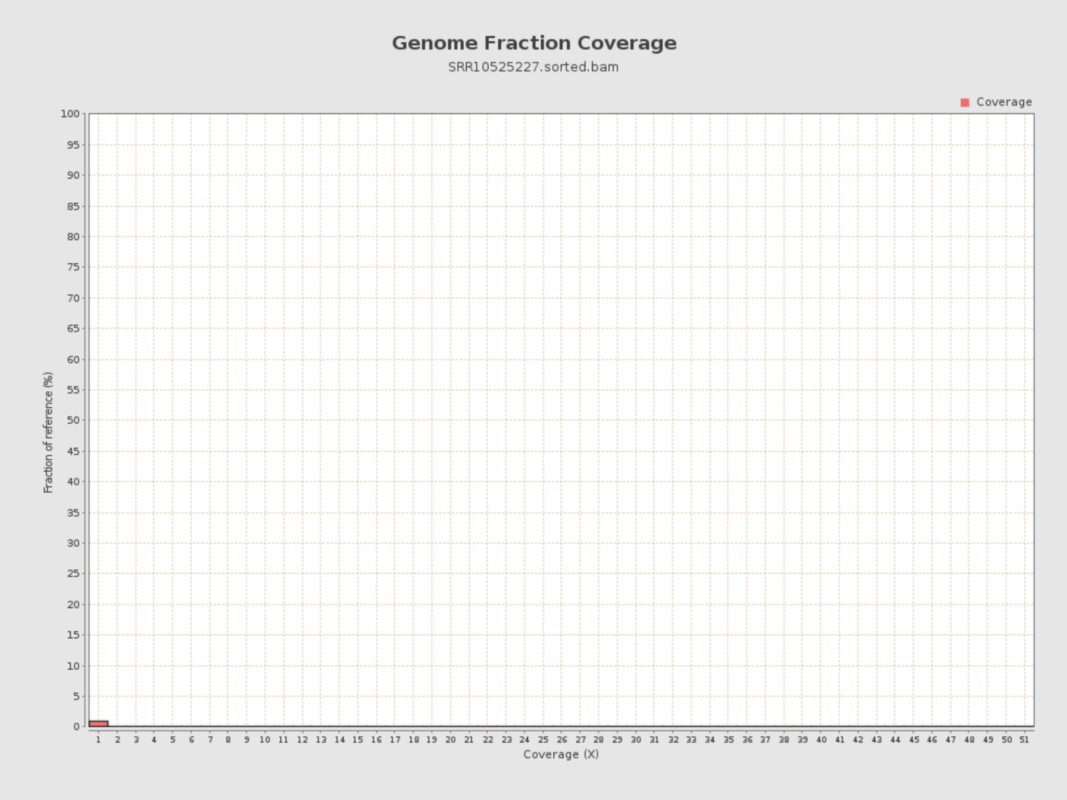
4. Results : Coverage Histogram



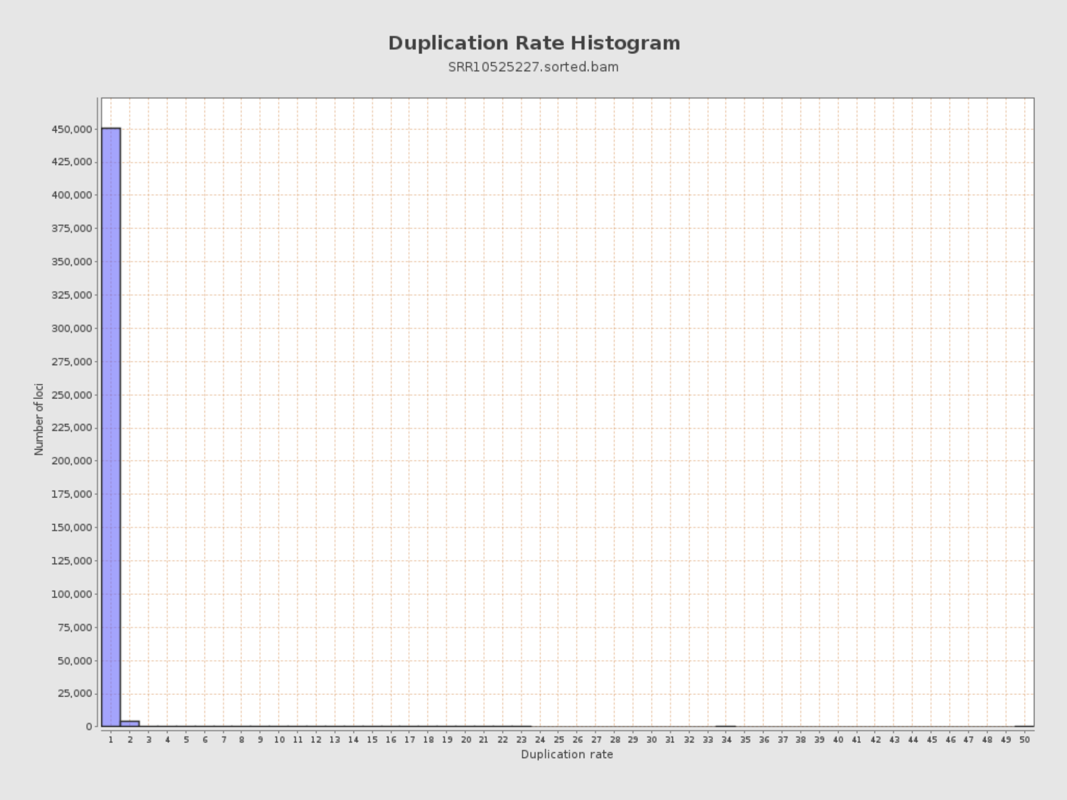
5. Results : Coverage Histogram (0-50X)



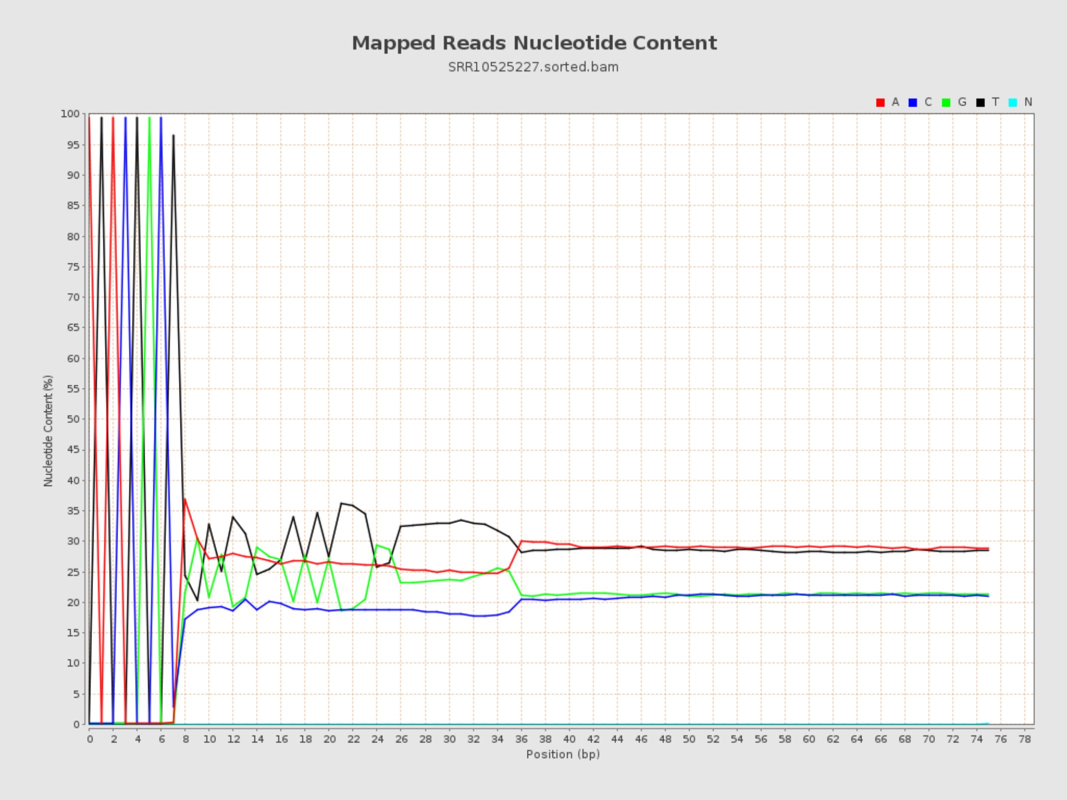
6. Results : Genome Fraction Coverage



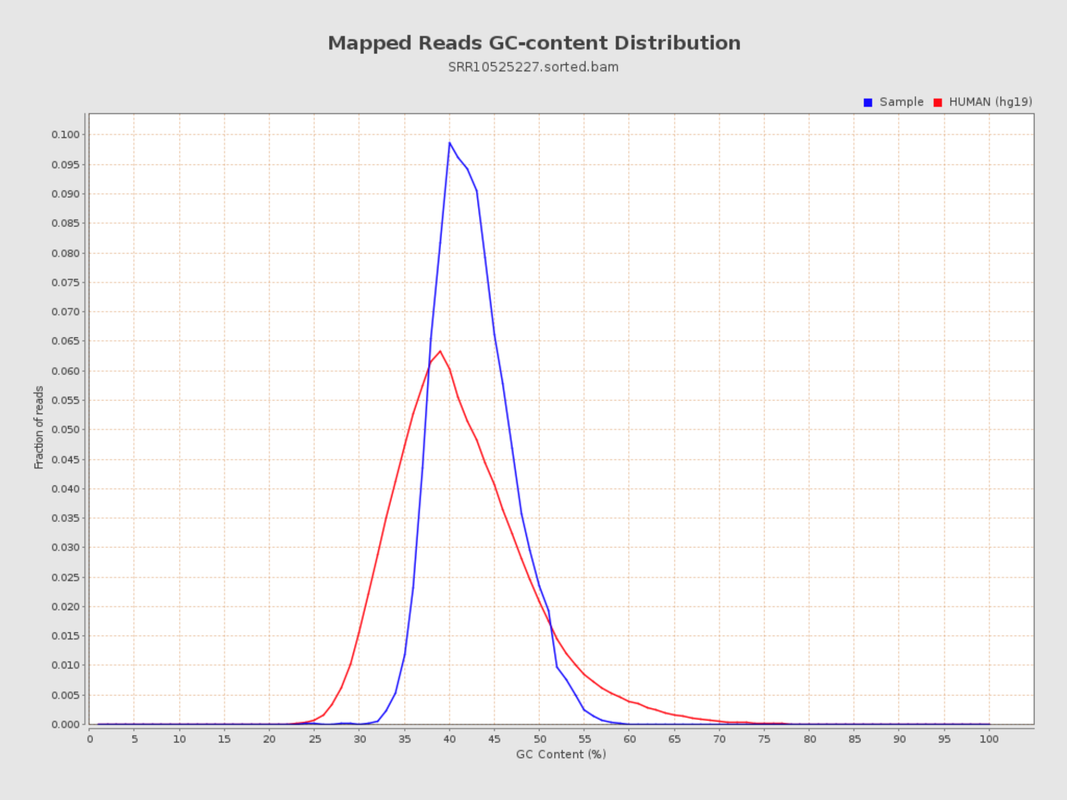
7. Results : Duplication Rate Histogram



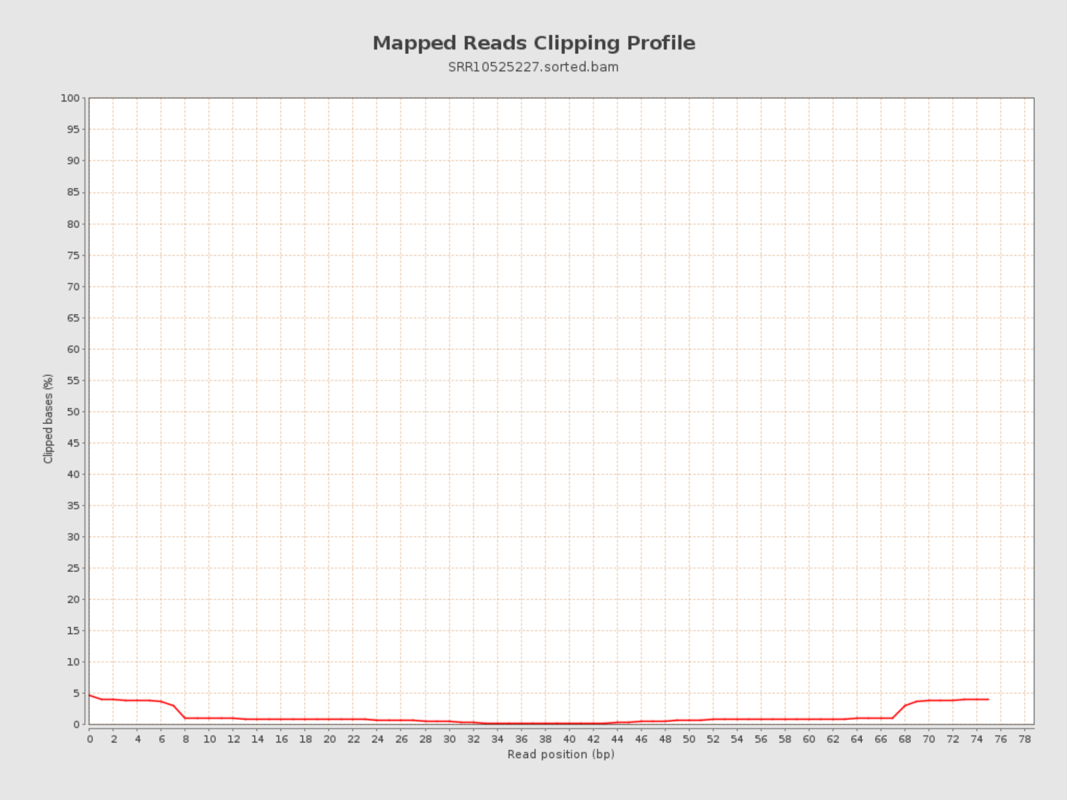
8. Results : Mapped Reads Nucleotide Content



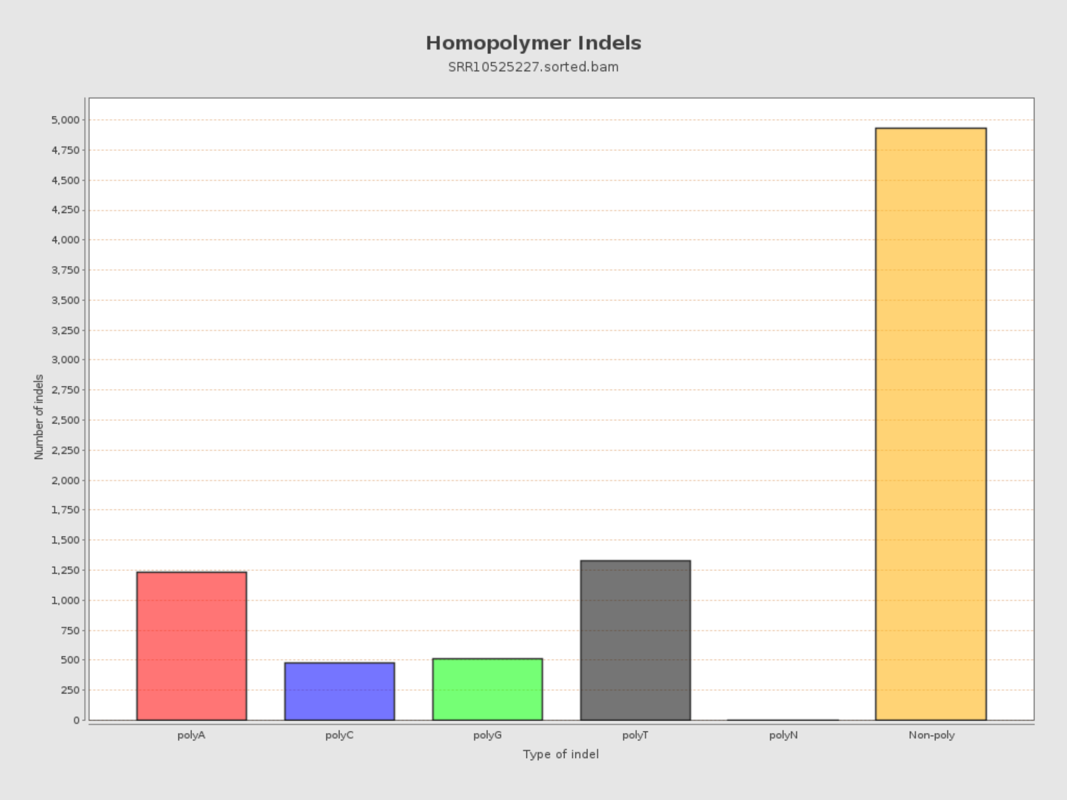
9. Results : Mapped Reads GC-content Distribution



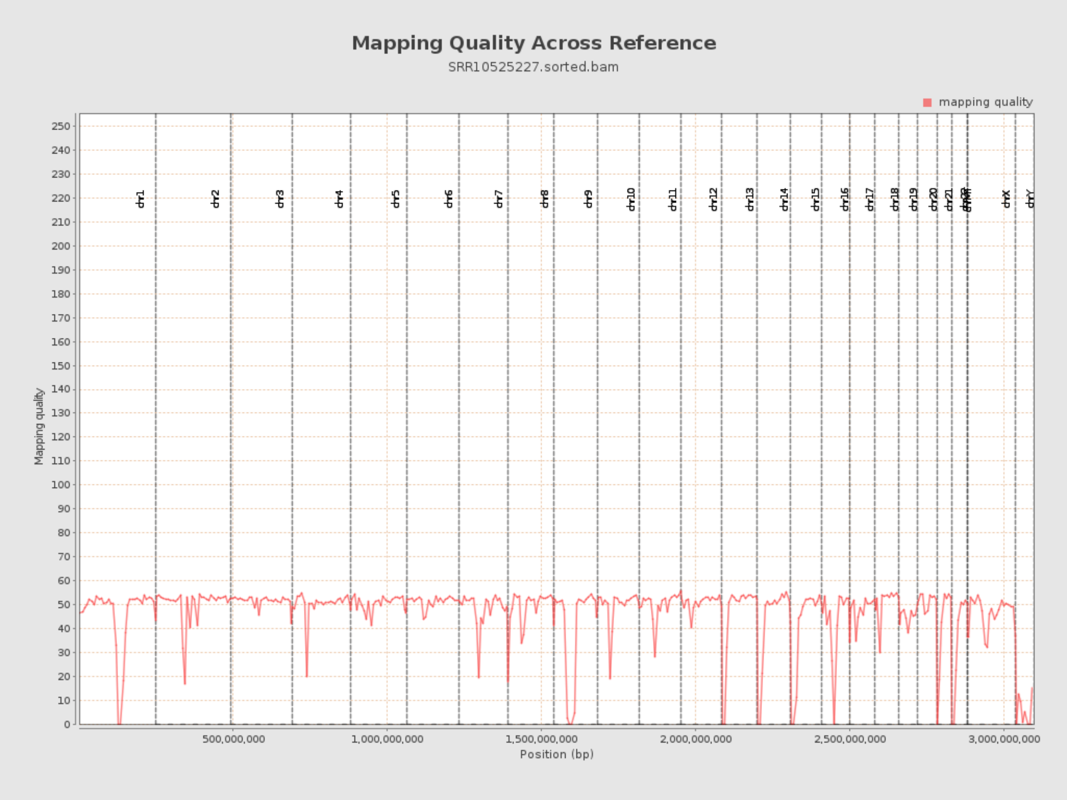
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram