Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:52:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525247.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_SRR10525247 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525247.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:52:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525247.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	891,723
Mapped reads	810,661 / 90.91%
Unmapped reads	81,062 / 9.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,745 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	23,944 / 2.69%
Duplication rate	2.19%
Clipped reads	811,255 / 90.98%

2.2. ACGT Content

Number/percentage of A's	11,557,982 / 24.77%
Number/percentage of C's	7,619,738 / 16.33%
Number/percentage of T's	15,343,819 / 32.88%
Number/percentage of G's	12,139,200 / 26.02%
Number/percentage of N's	908 / 0%
GC Percentage	42.35%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1714

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

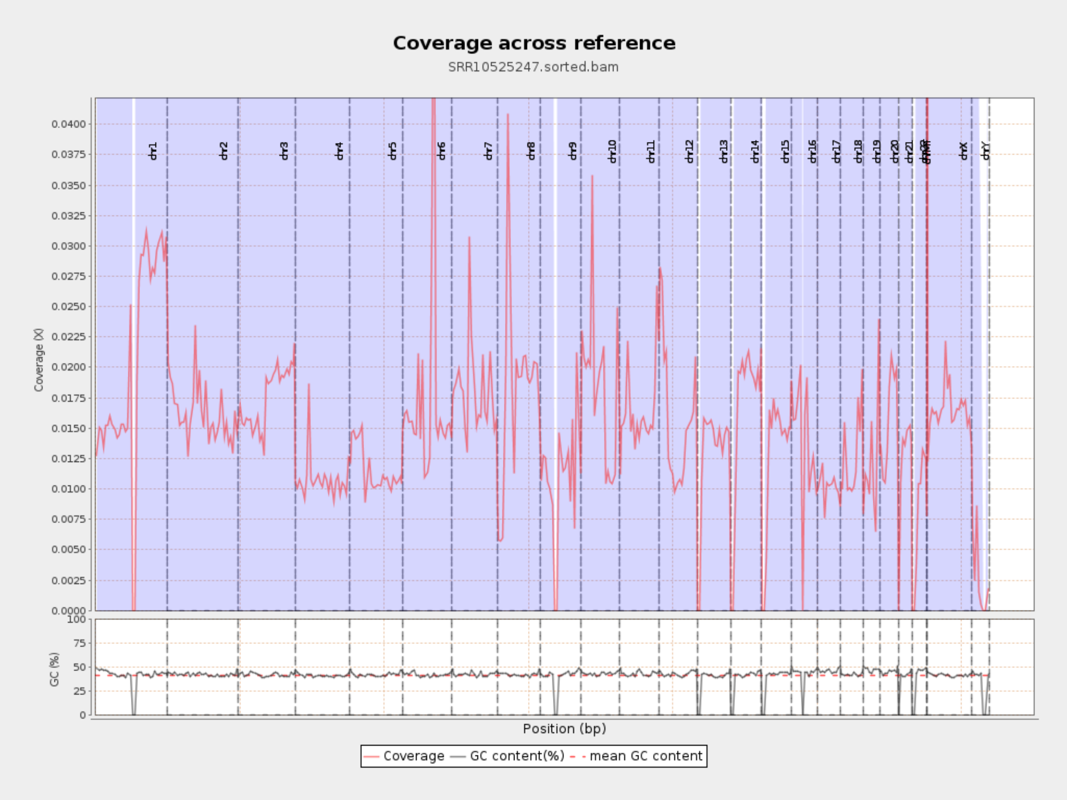
General error rate	0.52%
Mismatches	235,928
Insertions	3,342
Mapped reads with at least one insertion	0.41%
Deletions	9,027
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.1%

2.6. Chromosome stats

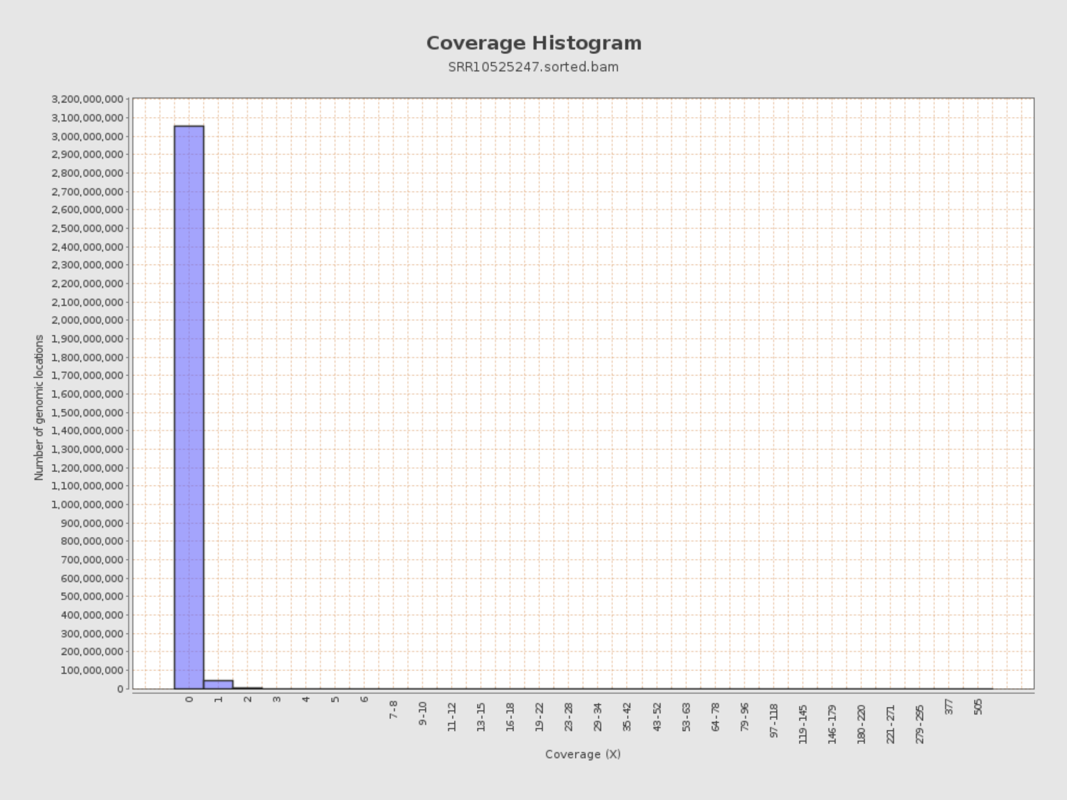
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5042180	0.0202	0.2587
chr2	243199373	3941635	0.0162	0.243
chr3	198022430	3451523	0.0174	0.1425
chr4	191154276	2063462	0.0108	0.1165
chr5	180915260	2102358	0.0116	0.114
chr6	171115067	3066639	0.0179	0.1552
chr7	159138663	2881180	0.0181	0.2308

chr8	146364022	2715263	0.0186	0.1844
chr9	141213431	1555647	0.011	0.1326
chr10	135534747	2500891	0.0185	0.2042
chr11	135006516	2199781	0.0163	0.1517
chr12	133851895	2107659	0.0157	0.1342
chr13	115169878	1469519	0.0128	0.12
chr14	107349540	1756048	0.0164	0.1366
chr15	102531392	1279757	0.0125	0.1195
chr16	90354753	1239771	0.0137	0.1357
chr17	81195210	829954	0.0102	0.1094
chr18	78077248	979492	0.0125	0.2121
chr19	59128983	722669	0.0122	0.1937
chr20	63025520	990888	0.0157	0.1337
chr21	48129895	598282	0.0124	0.1242
chr22	51304566	406252	0.0079	0.0937
chrMT	16571	42904	2.5891	2.0667
chrX	155270560	2581692	0.0166	0.144
chrY	59373566	150509	0.0025	0.0908

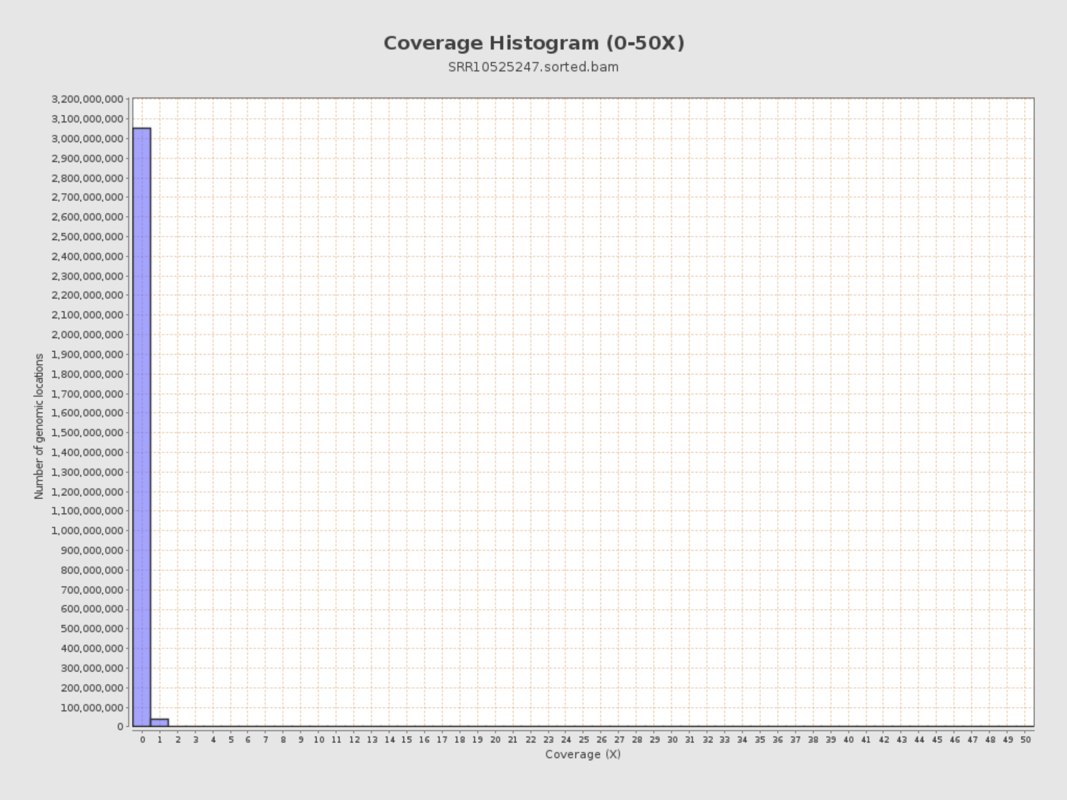
3. Results : Coverage across reference



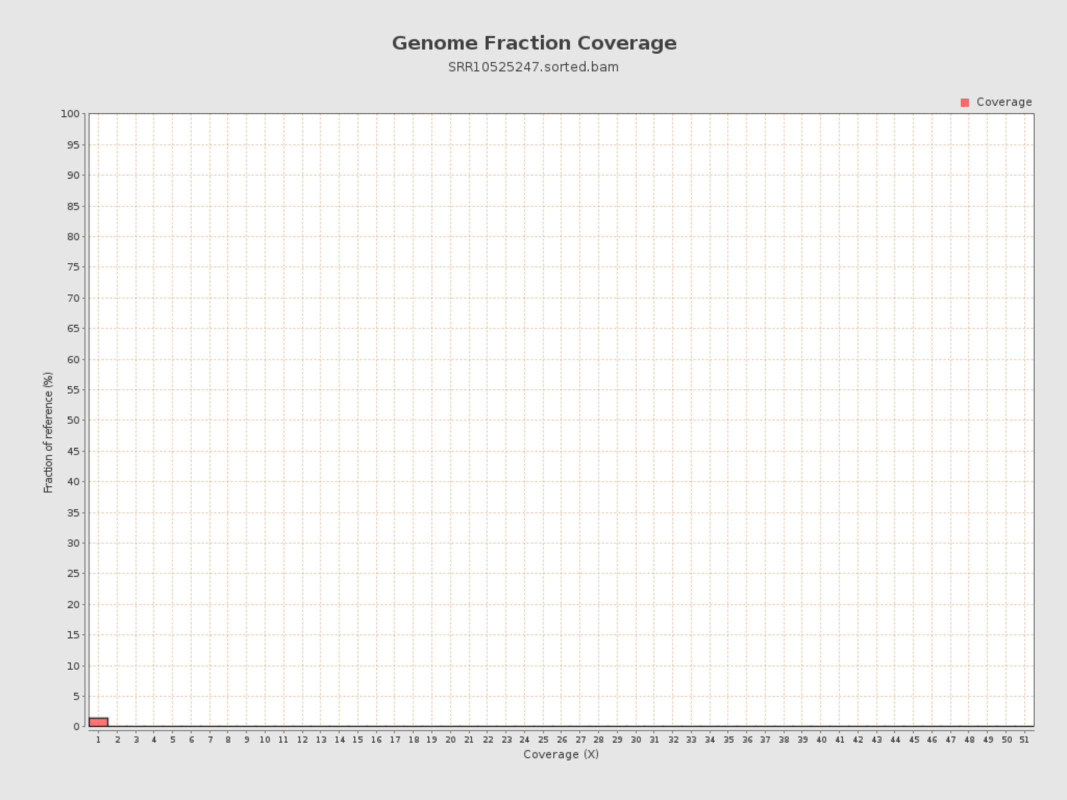
4. Results : Coverage Histogram



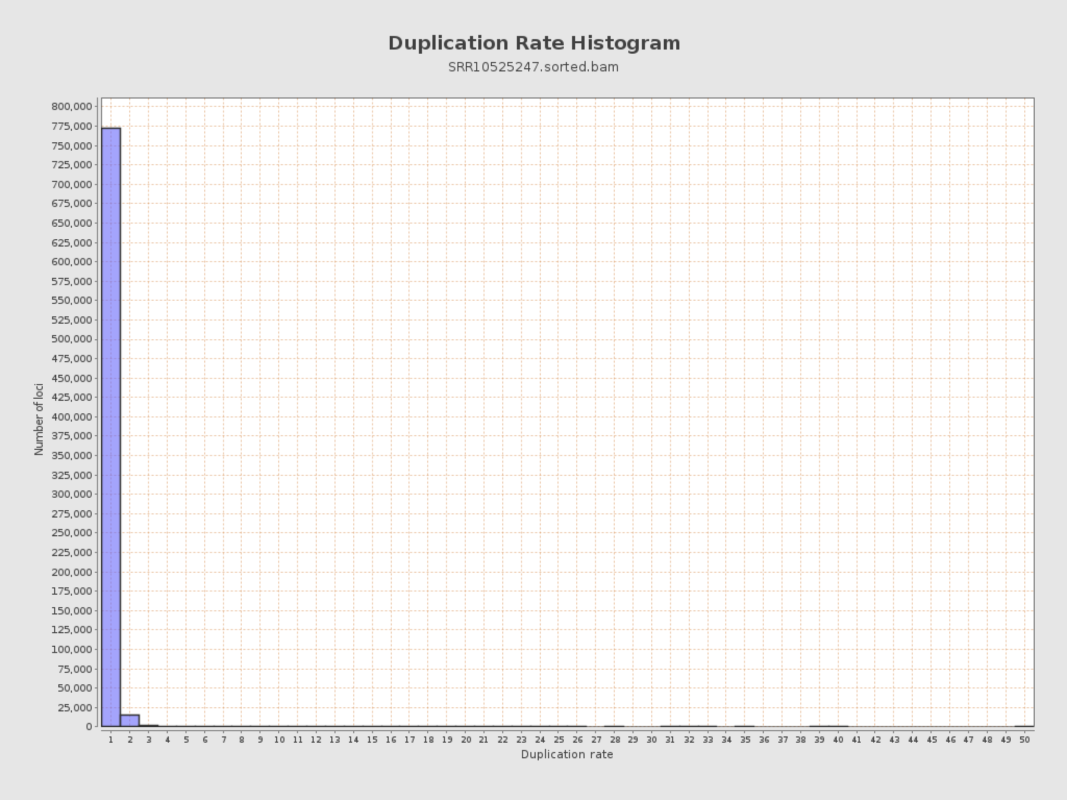
5. Results : Coverage Histogram (0-50X)



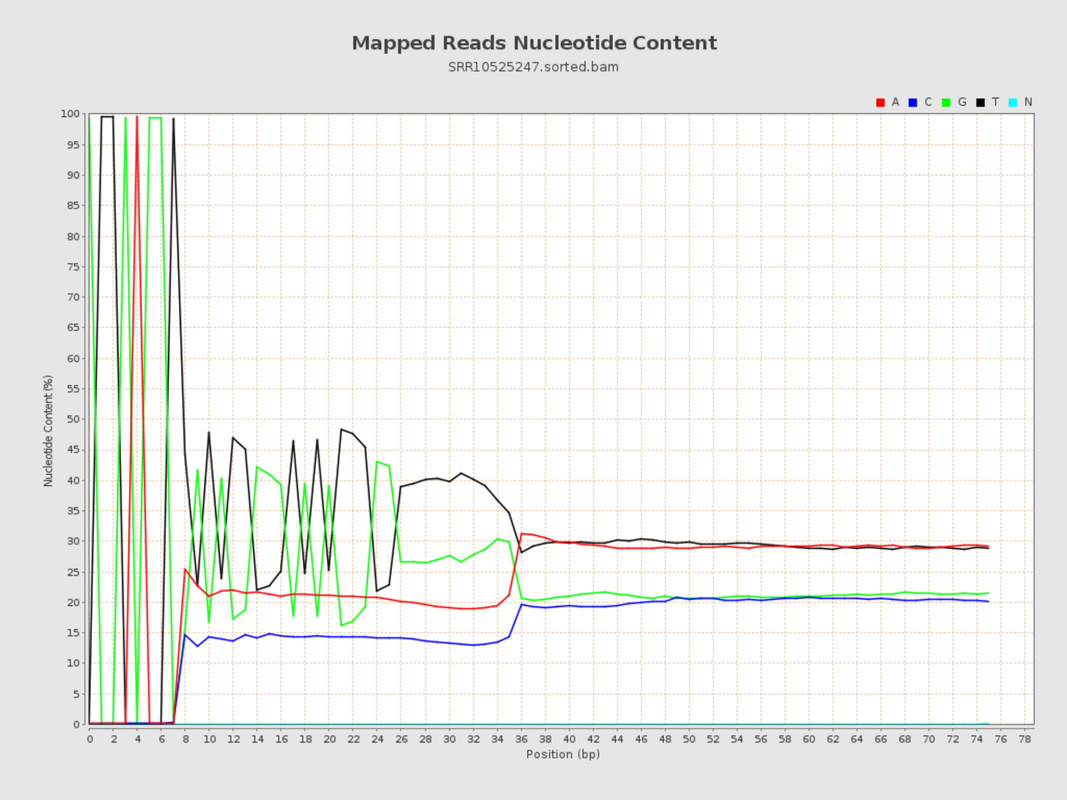
6. Results : Genome Fraction Coverage



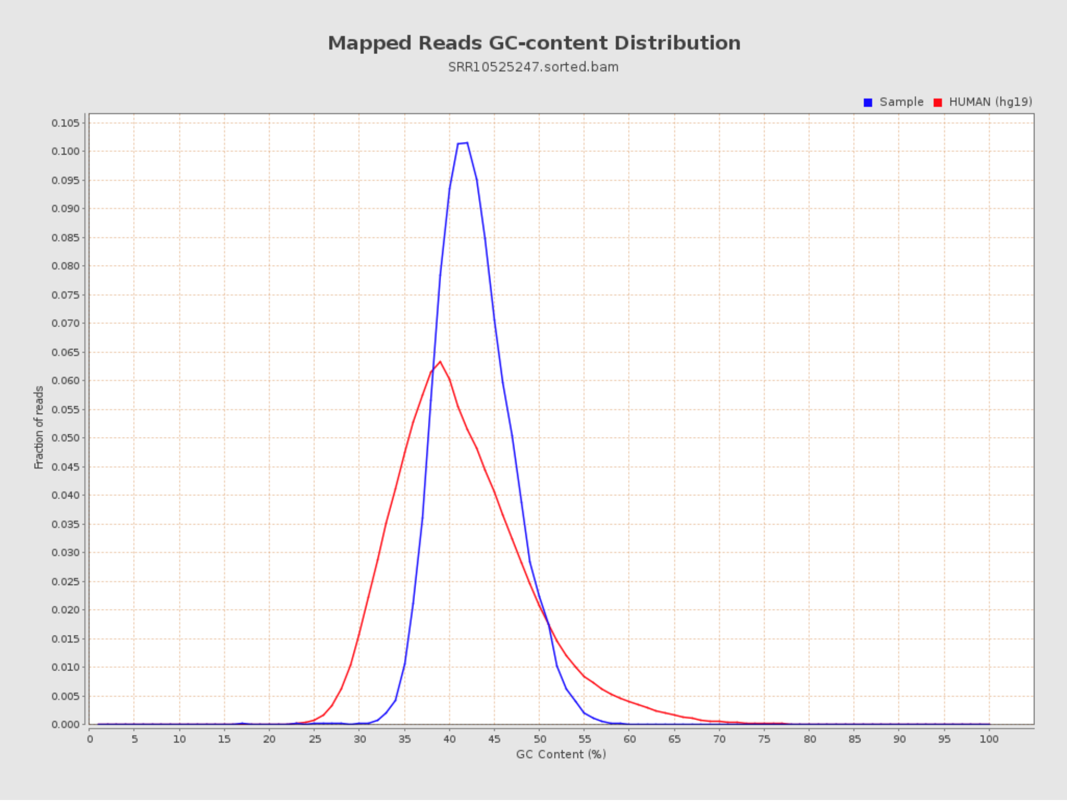
7. Results : Duplication Rate Histogram



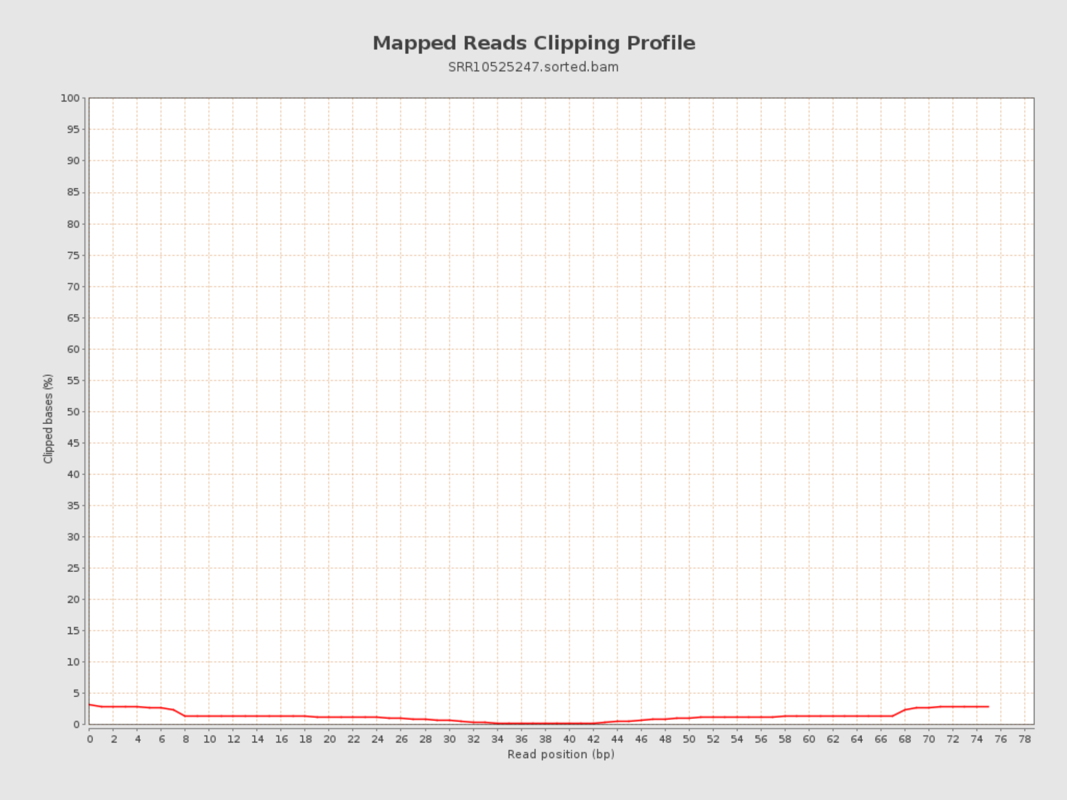
8. Results : Mapped Reads Nucleotide Content



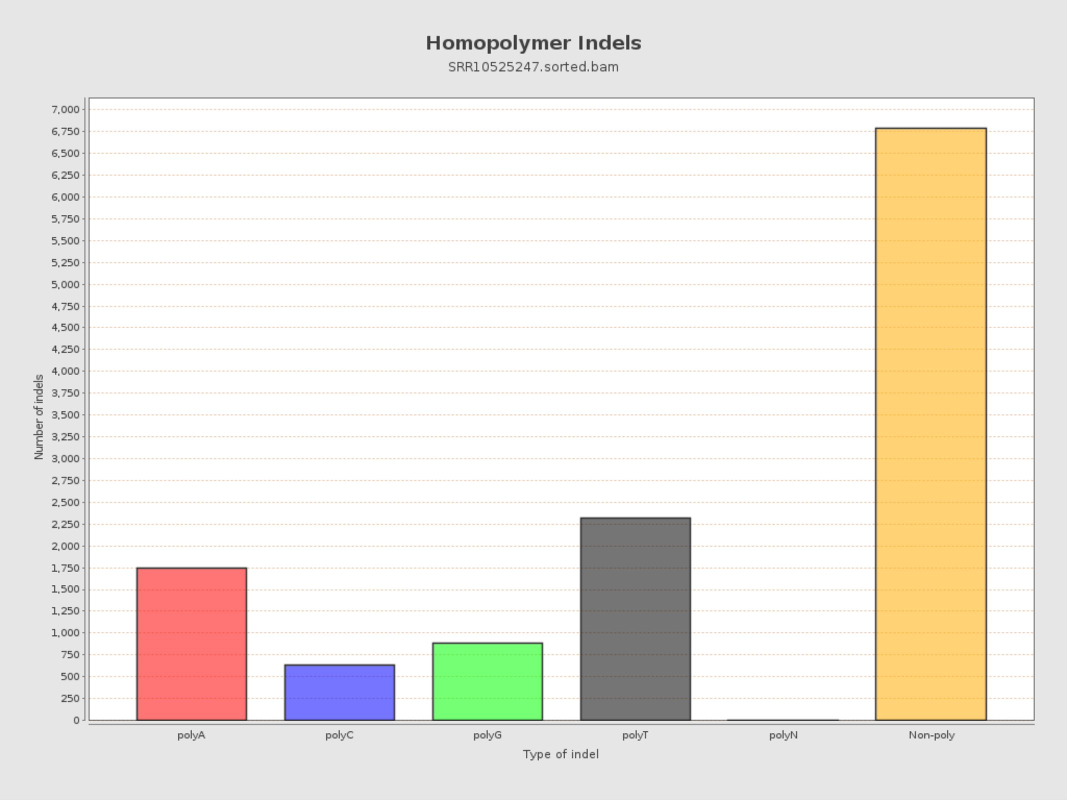
9. Results : Mapped Reads GC-content Distribution



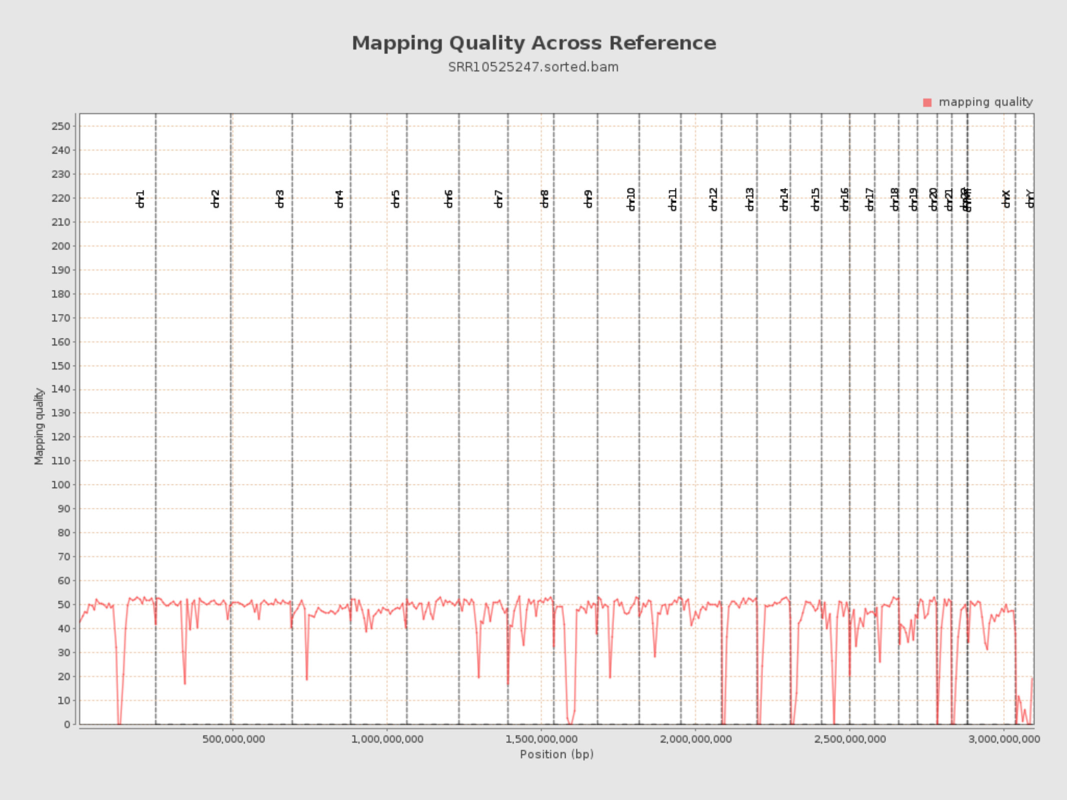
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram