Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:06:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525228.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_SRR10525228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:06:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	546,565
Mapped reads	498,312 / 91.17%
Unmapped reads	48,253 / 8.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,975 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,770 / 1.42%
Duplication rate	1.1%
Clipped reads	497,512 / 91.03%

2.2. ACGT Content

Number/percentage of A's	8,650,250 / 27.19%
Number/percentage of C's	6,828,220 / 21.47%
Number/percentage of T's	9,633,185 / 30.28%
Number/percentage of G's	6,697,152 / 21.05%
Number/percentage of N's	805 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0103

Standard Deviation	0.1316

2.4. Mapping Quality

Mean Mapping Quality	46.99

2.5. Mismatches and indels

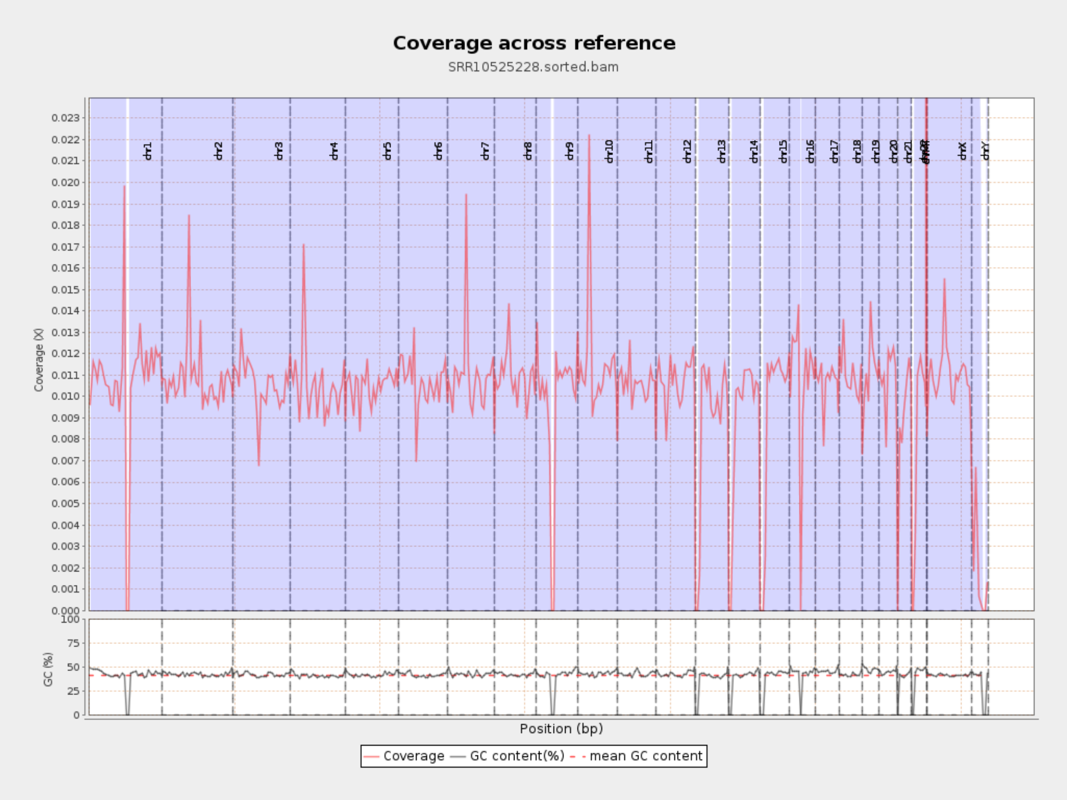
General error rate	0.5%
Mismatches	153,589
Insertions	2,378
Mapped reads with at least one insertion	0.47%
Deletions	7,148
Mapped reads with at least one deletion	1.42%
Homopolymer indels	43.07%

2.6. Chromosome stats

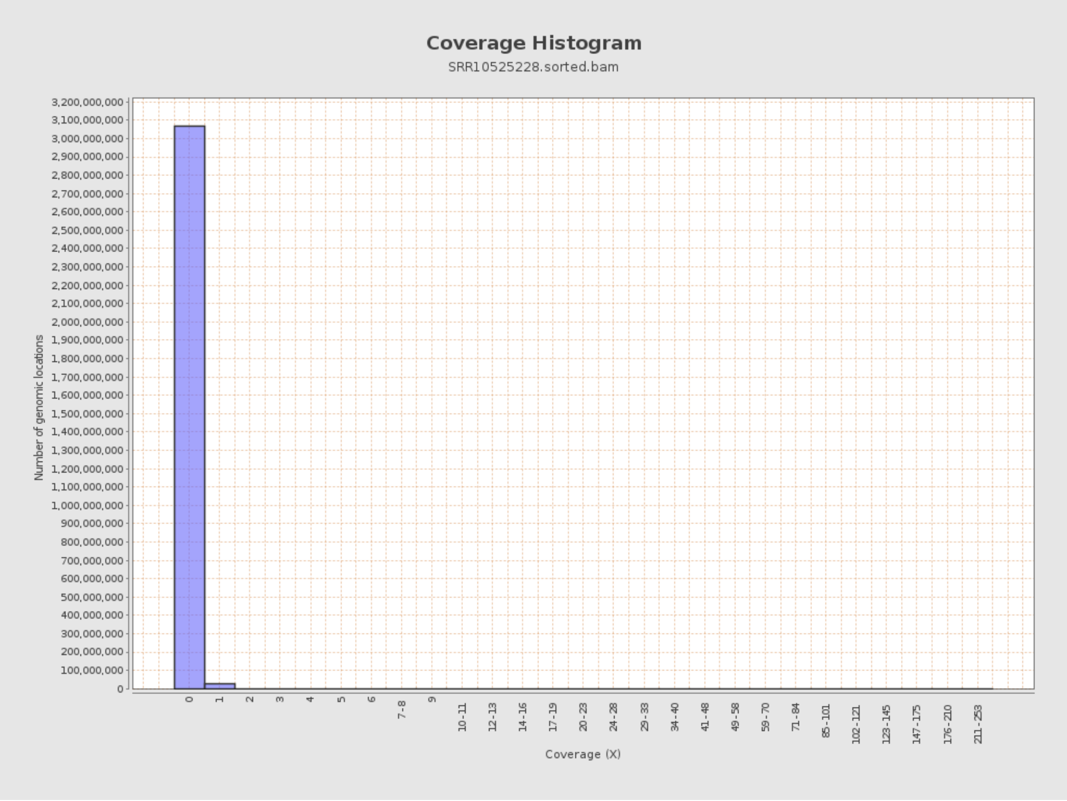
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2668177	0.0107	0.2208
chr2	243199373	2652351	0.0109	0.1332
chr3	198022430	2091718	0.0106	0.106
chr4	191154276	2005828	0.0105	0.1104
chr5	180915260	1897300	0.0105	0.1056
chr6	171115067	1831275	0.0107	0.1123
chr7	159138663	1754924	0.011	0.1685

chr8	146364022	1596599	0.0109	0.1268
chr9	141213431	1343811	0.0095	0.1166
chr10	135534747	1553812	0.0115	0.1399
chr11	135006516	1429398	0.0106	0.1162
chr12	133851895	1439068	0.0108	0.1072
chr13	115169878	988365	0.0086	0.0953
chr14	107349540	946765	0.0088	0.0986
chr15	102531392	923182	0.009	0.0978
chr16	90354753	970050	0.0107	0.1124
chr17	81195210	861238	0.0106	0.1092
chr18	78077248	862371	0.011	0.1835
chr19	59128983	665088	0.0112	0.175
chr20	63025520	684327	0.0109	0.1081
chr21	48129895	426758	0.0089	0.1053
chr22	51304566	391877	0.0076	0.09
chrMT	16571	16953	1.0231	1.1168
chrX	155270560	1715628	0.011	0.1117
chrY	59373566	104520	0.0018	0.0695

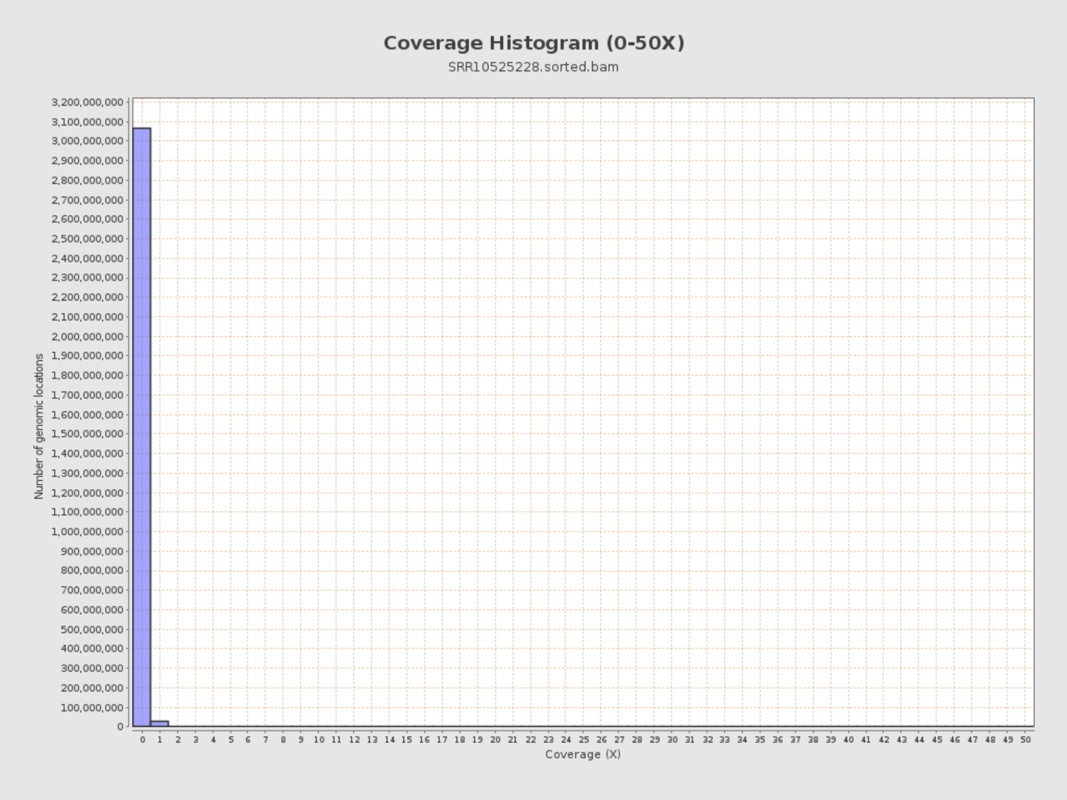
3. Results : Coverage across reference



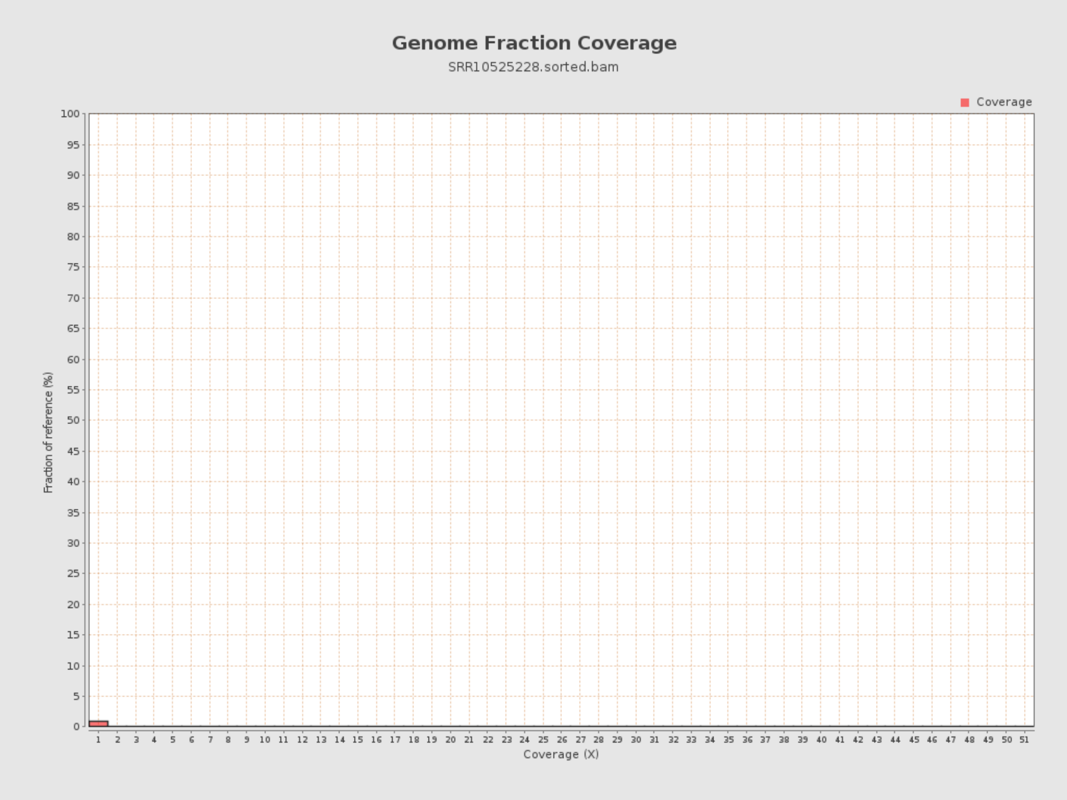
4. Results : Coverage Histogram



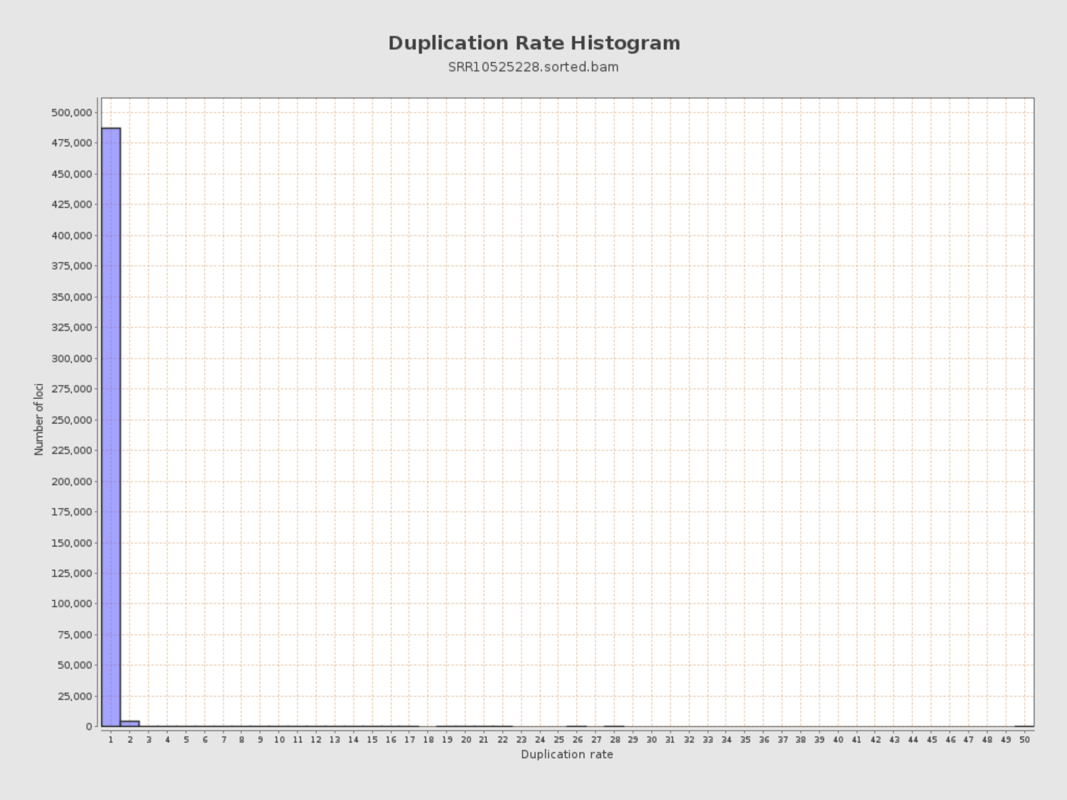
5. Results : Coverage Histogram (0-50X)



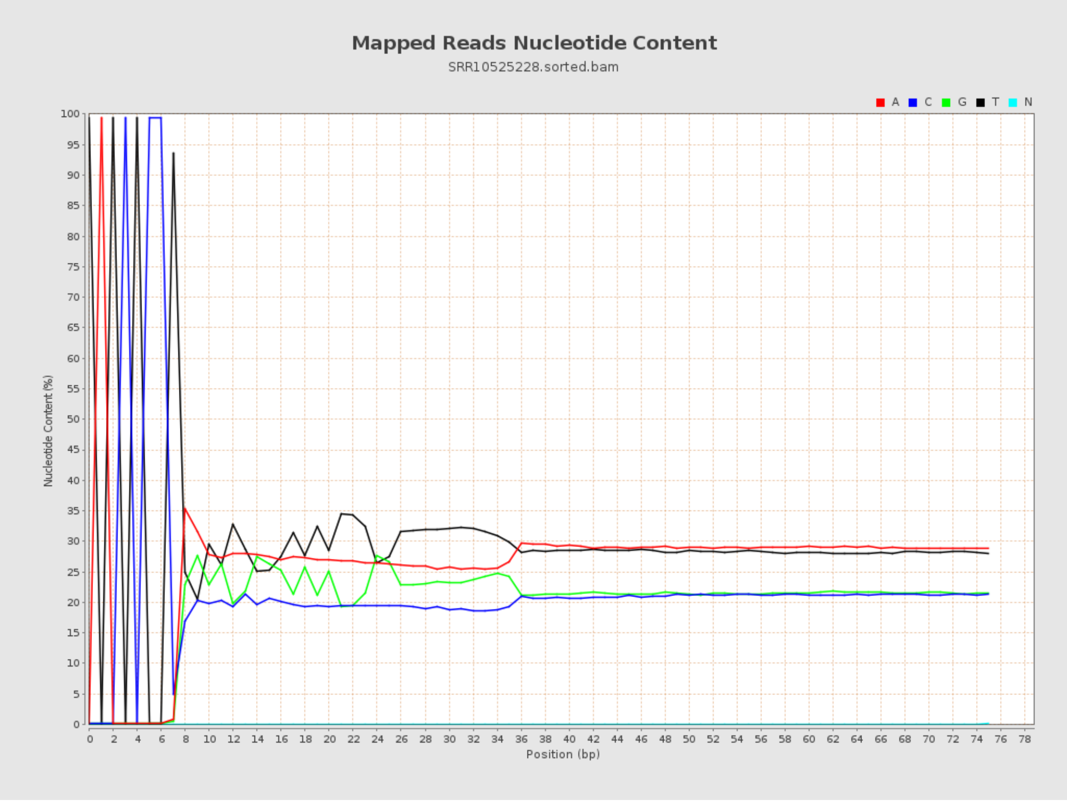
6. Results : Genome Fraction Coverage



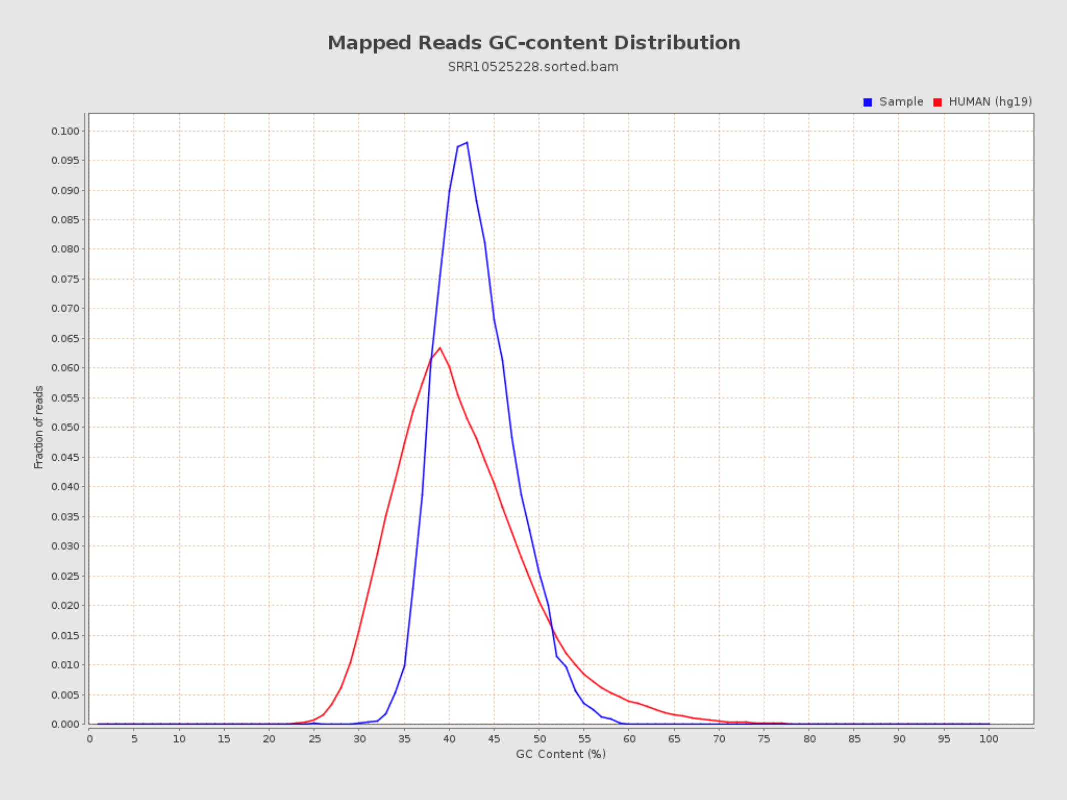
7. Results : Duplication Rate Histogram



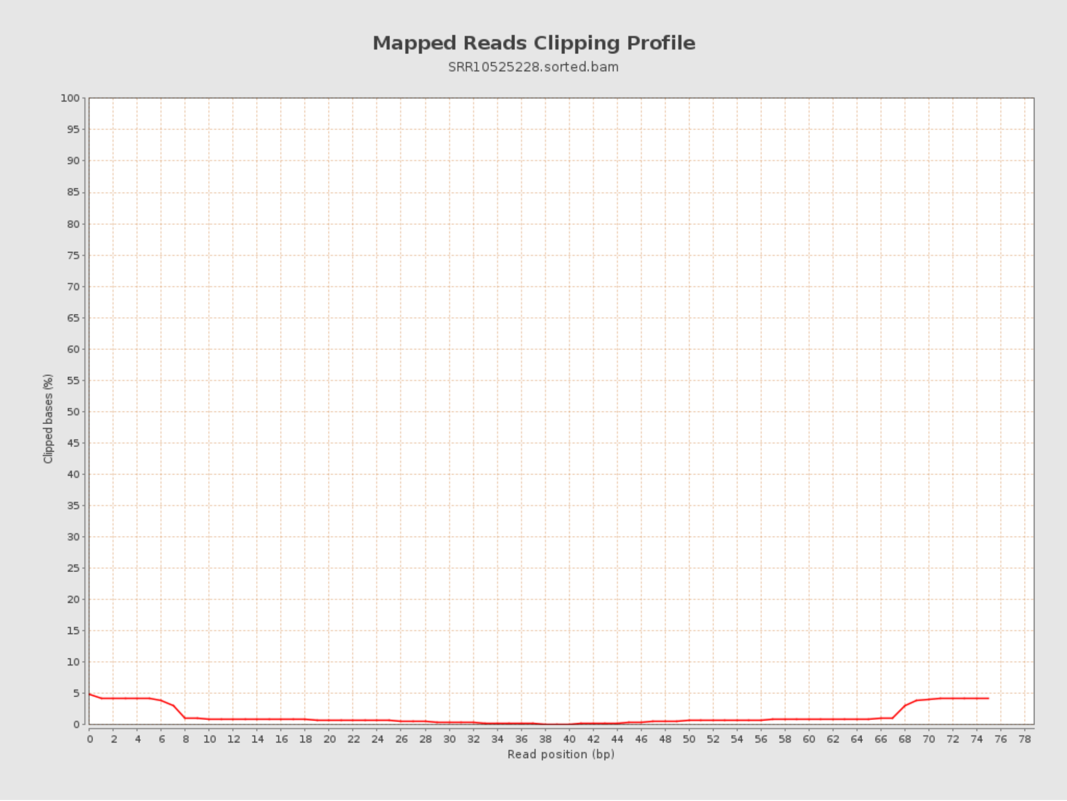
8. Results : Mapped Reads Nucleotide Content



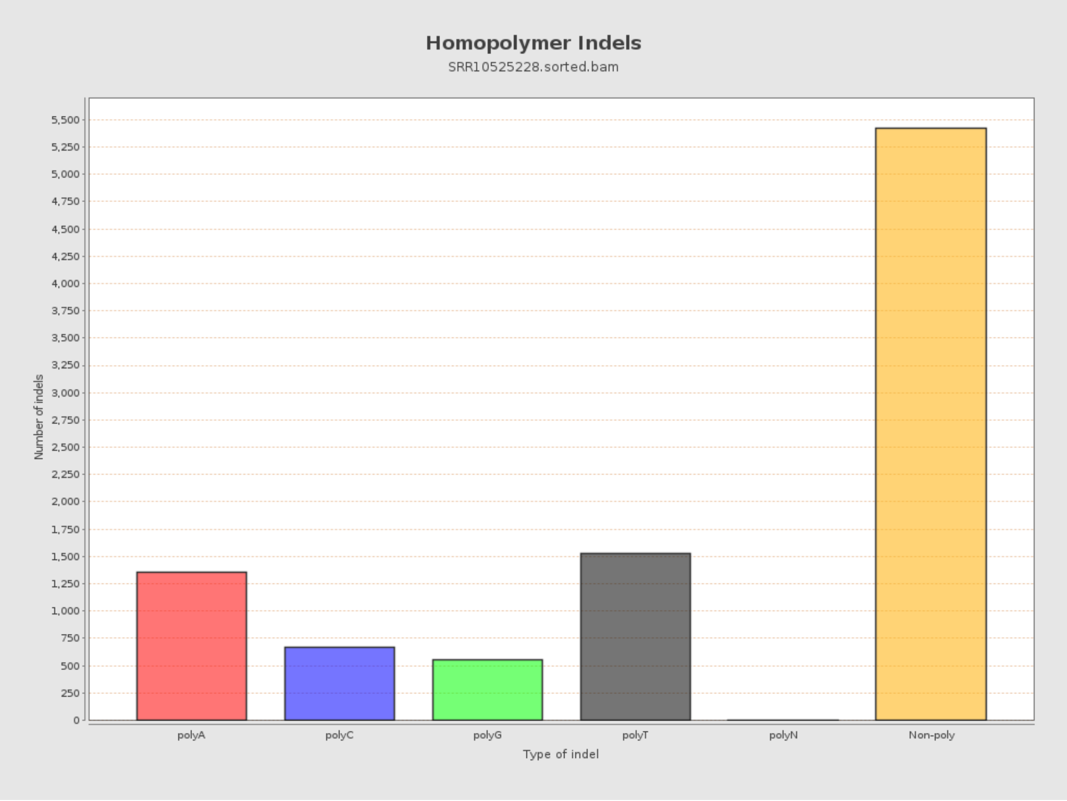
9. Results : Mapped Reads GC-content Distribution



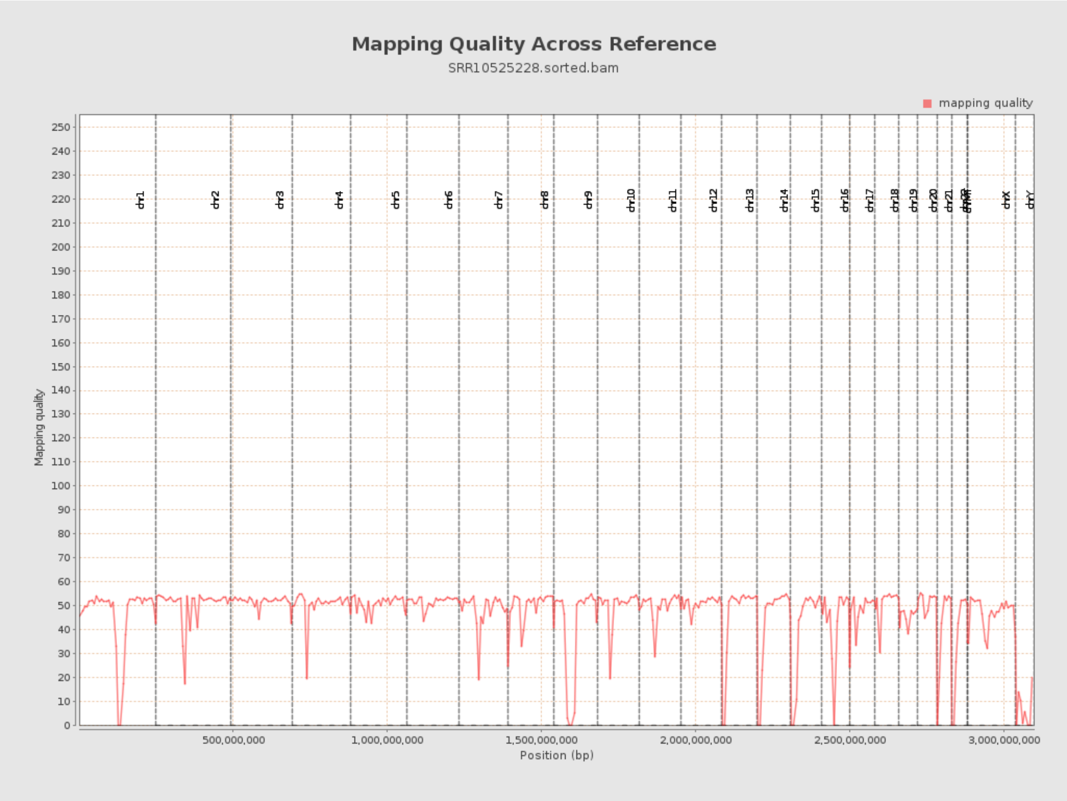
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram