Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:43:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525140.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_SRR10525140 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525140.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:43:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525140.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	671,801
Mapped reads	607,813 / 90.48%
Unmapped reads	63,988 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,048 / 2.54%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	13,226 / 1.97%
Duplication rate	1.29%
Clipped reads	623,638 / 92.83%

2.2. ACGT Content

Number/percentage of A's	12,393,068 / 26.48%
Number/percentage of C's	9,023,050 / 19.28%
Number/percentage of T's	14,540,513 / 31.07%
Number/percentage of G's	10,846,392 / 23.17%
Number/percentage of N's	1,822 / 0%
GC Percentage	42.45%

2.3. Coverage

Mean	0.0151

Standard Deviation	0.1906

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

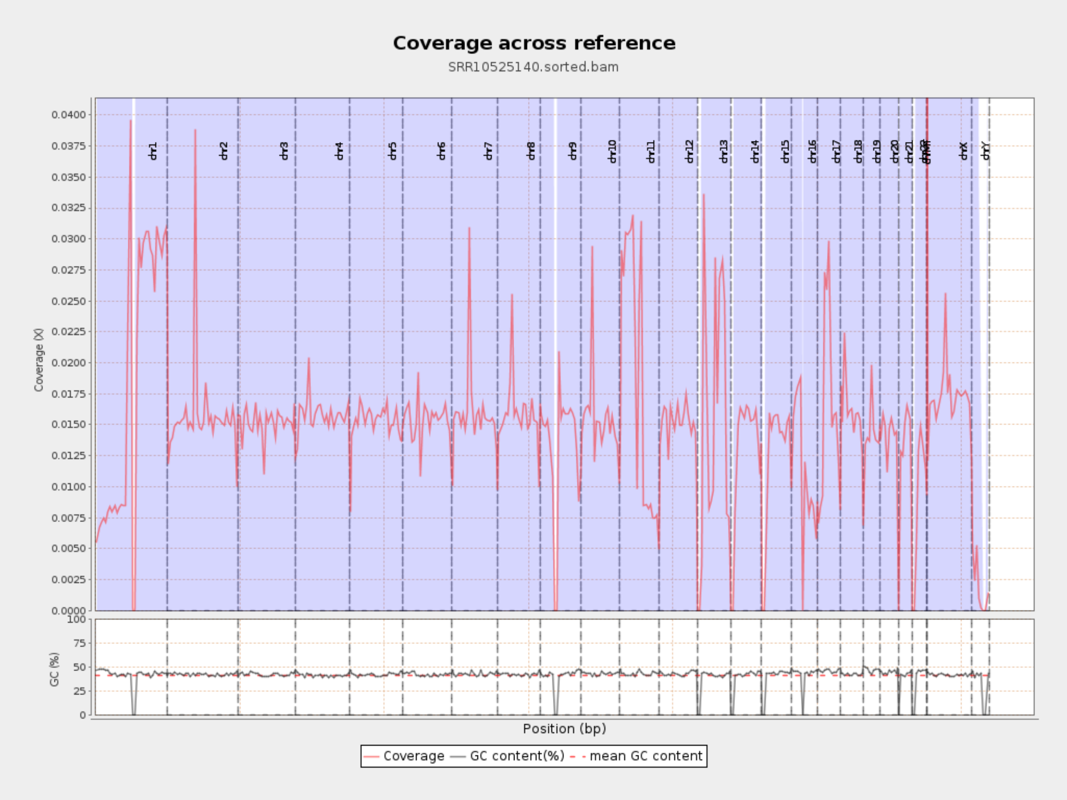
General error rate	0.75%
Mismatches	341,050
Insertions	4,279
Mapped reads with at least one insertion	0.69%
Deletions	11,278
Mapped reads with at least one deletion	1.83%
Homopolymer indels	43.08%

2.6. Chromosome stats

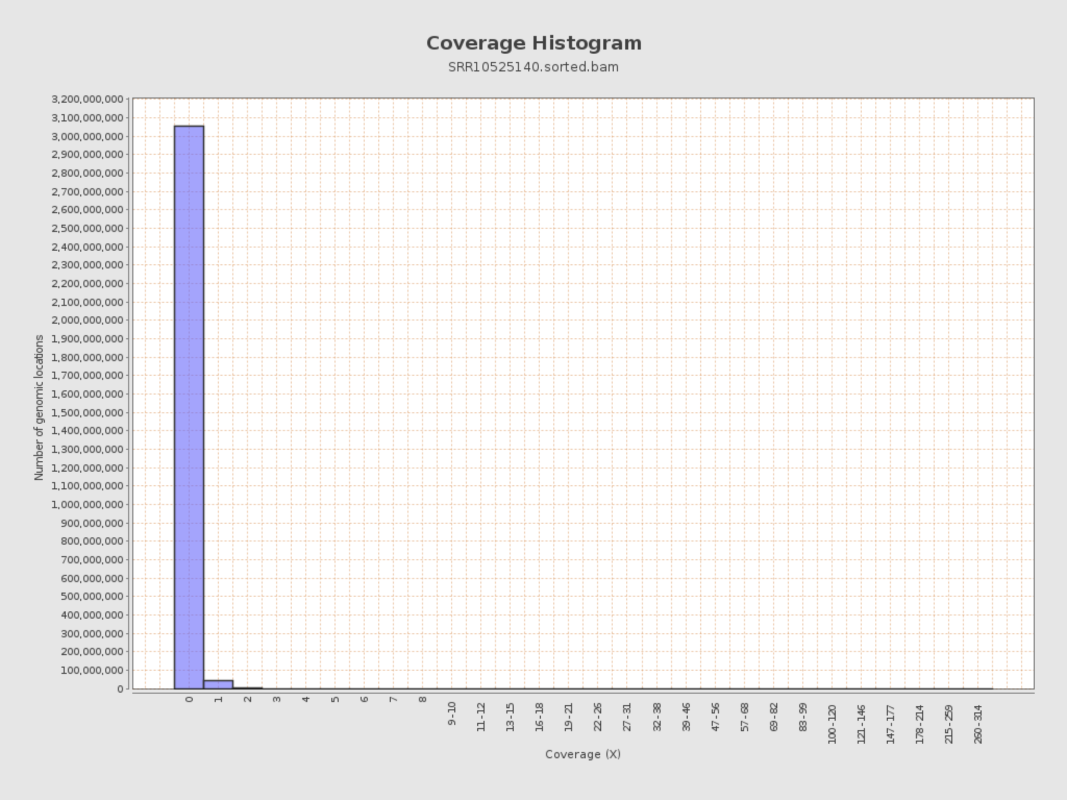
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4496192	0.018	0.3055
chr2	243199373	3853127	0.0158	0.2467
chr3	198022430	2994454	0.0151	0.1287
chr4	191154276	3014238	0.0158	0.1341
chr5	180915260	2790008	0.0154	0.1309
chr6	171115067	2626413	0.0153	0.1395
chr7	159138663	2556502	0.0161	0.2663

chr8	146364022	2336867	0.016	0.2284
chr9	141213431	1882448	0.0133	0.1753
chr10	135534747	2117837	0.0156	0.1987
chr11	135006516	2563656	0.019	0.2125
chr12	133851895	2034490	0.0152	0.1294
chr13	115169878	1727753	0.015	0.1284
chr14	107349540	1373086	0.0128	0.128
chr15	102531392	1256231	0.0123	0.1153
chr16	90354753	1000829	0.0111	0.1179
chr17	81195210	1321419	0.0163	0.1444
chr18	78077248	1268267	0.0162	0.2919
chr19	59128983	845536	0.0143	0.2257
chr20	63025520	883505	0.014	0.1266
chr21	48129895	613144	0.0127	0.1233
chr22	51304566	466908	0.0091	0.0989
chrMT	16571	2751	0.166	0.455
chrX	155270560	2691413	0.0173	0.1654
chrY	59373566	107113	0.0018	0.0546

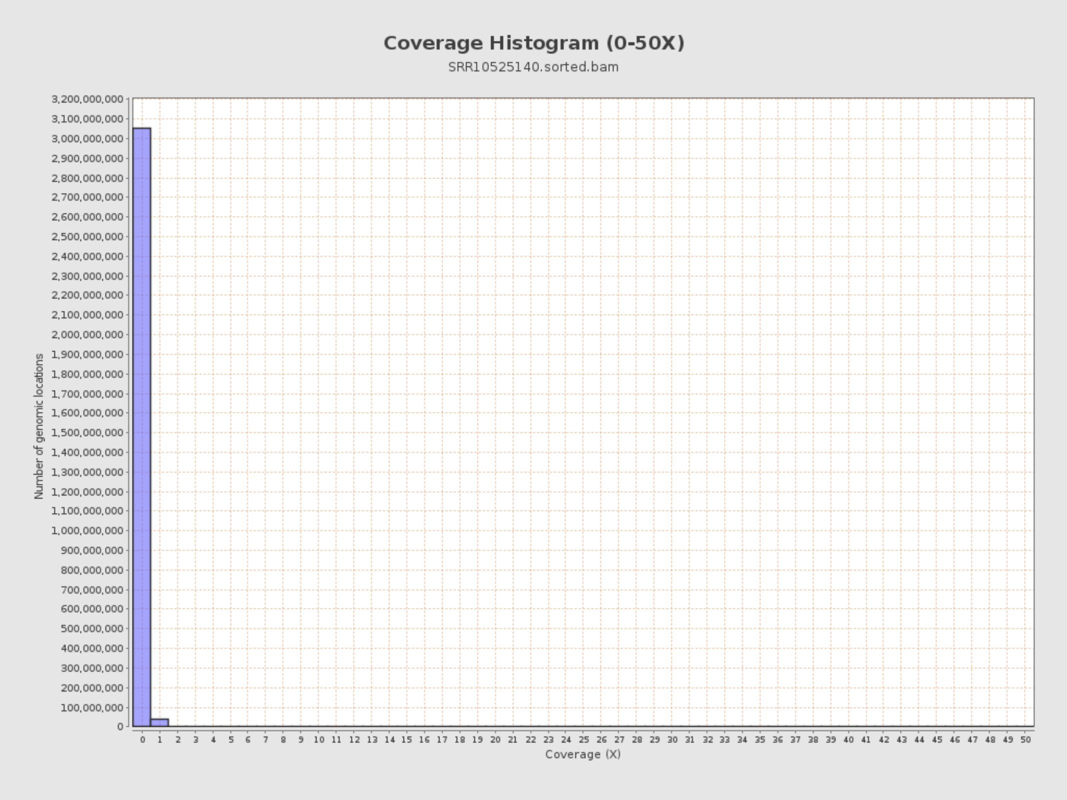
3. Results : Coverage across reference



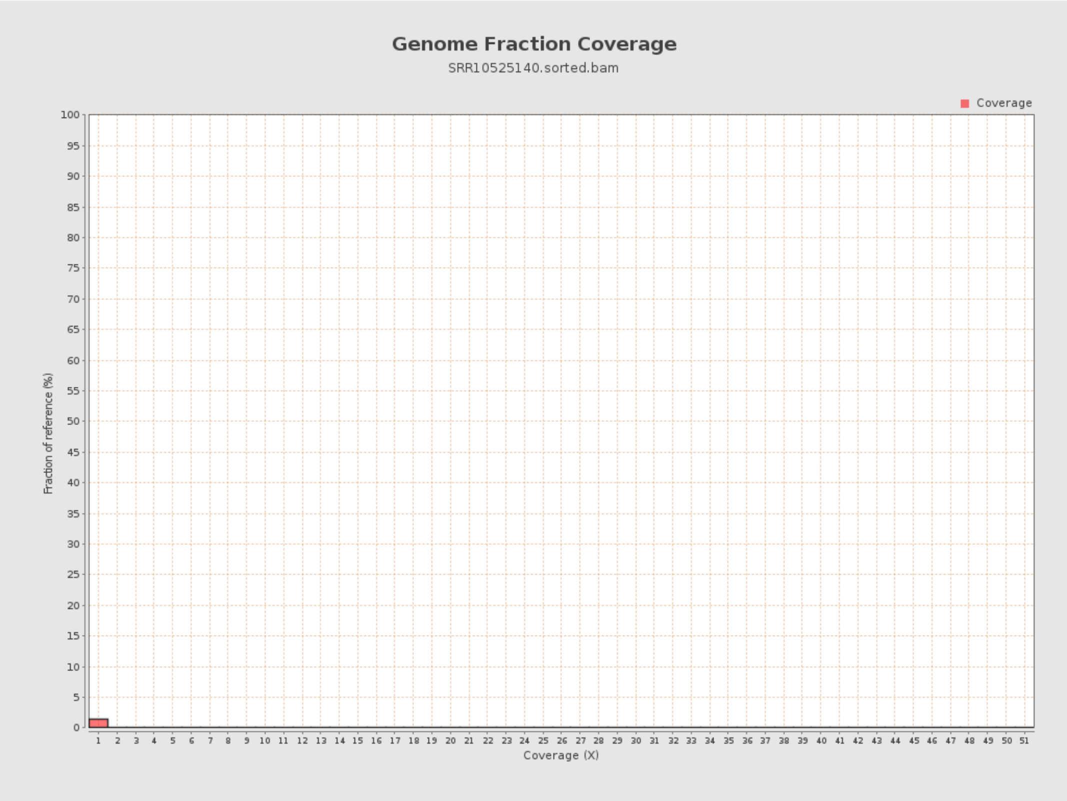
4. Results : Coverage Histogram



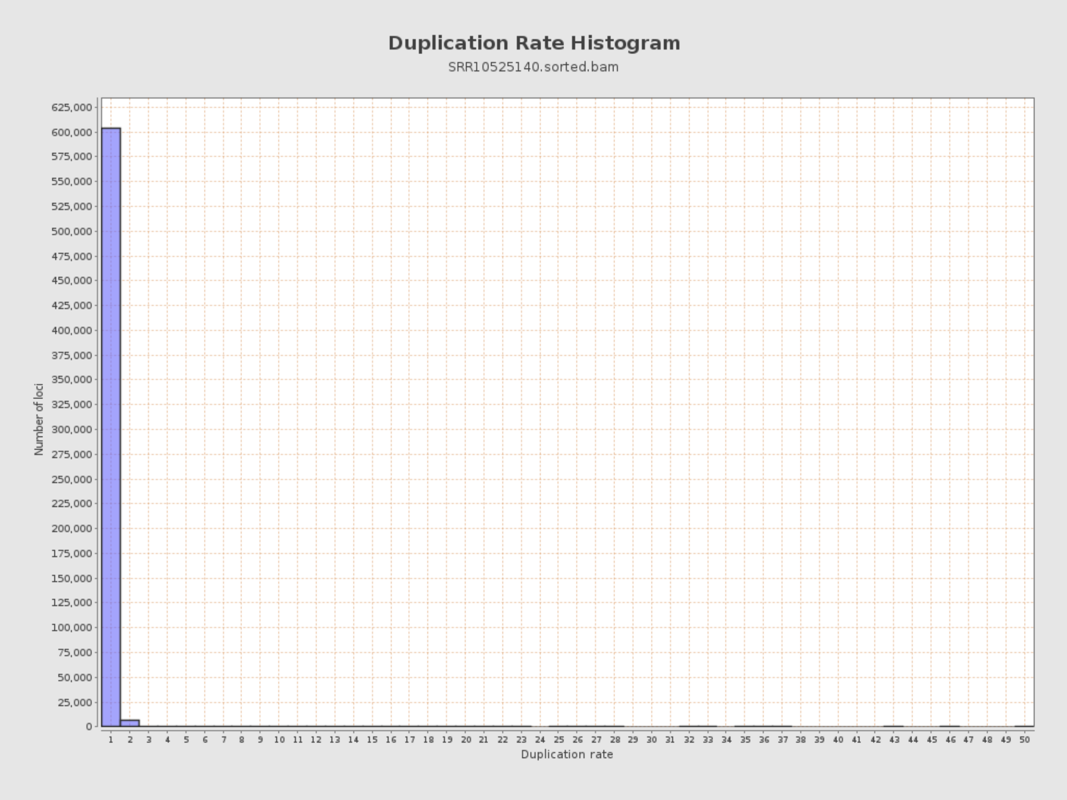
5. Results : Coverage Histogram (0-50X)



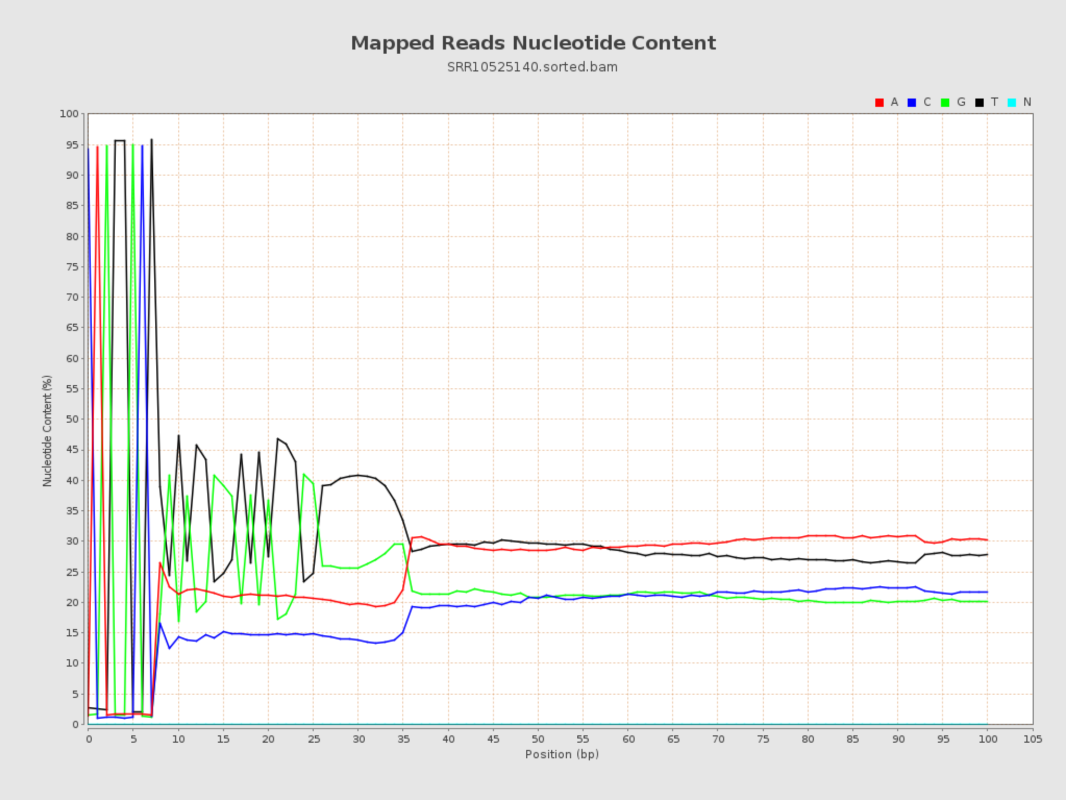
6. Results : Genome Fraction Coverage



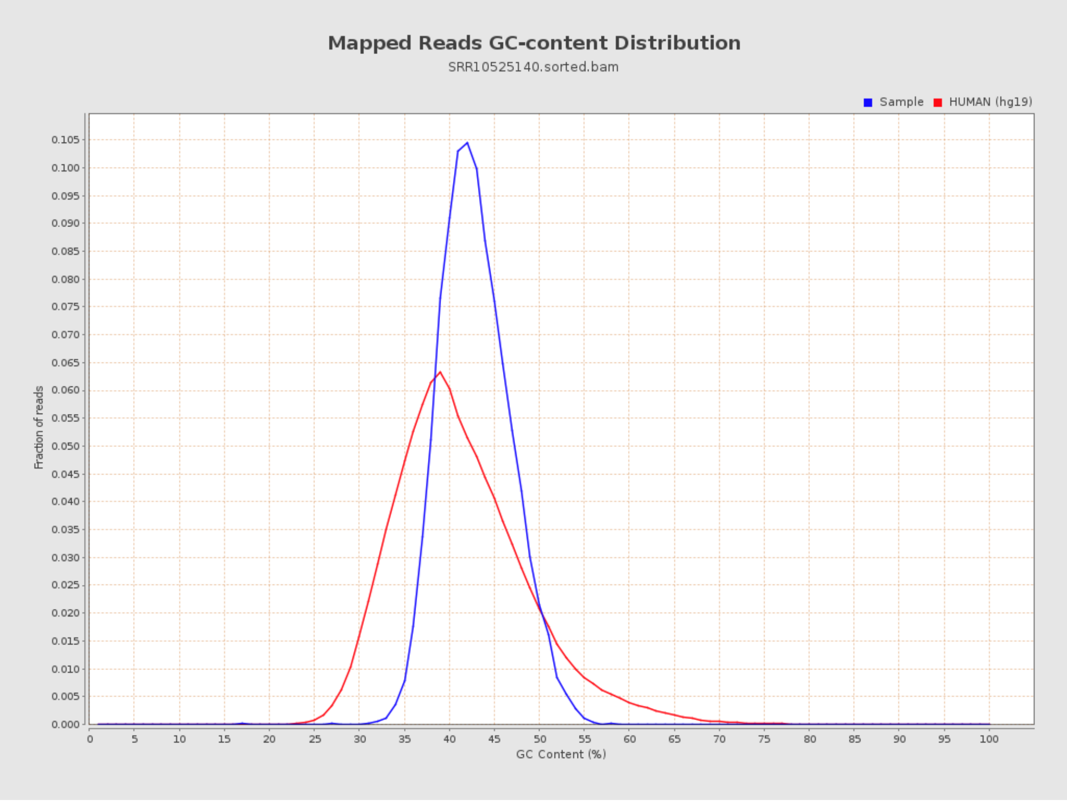
7. Results : Duplication Rate Histogram



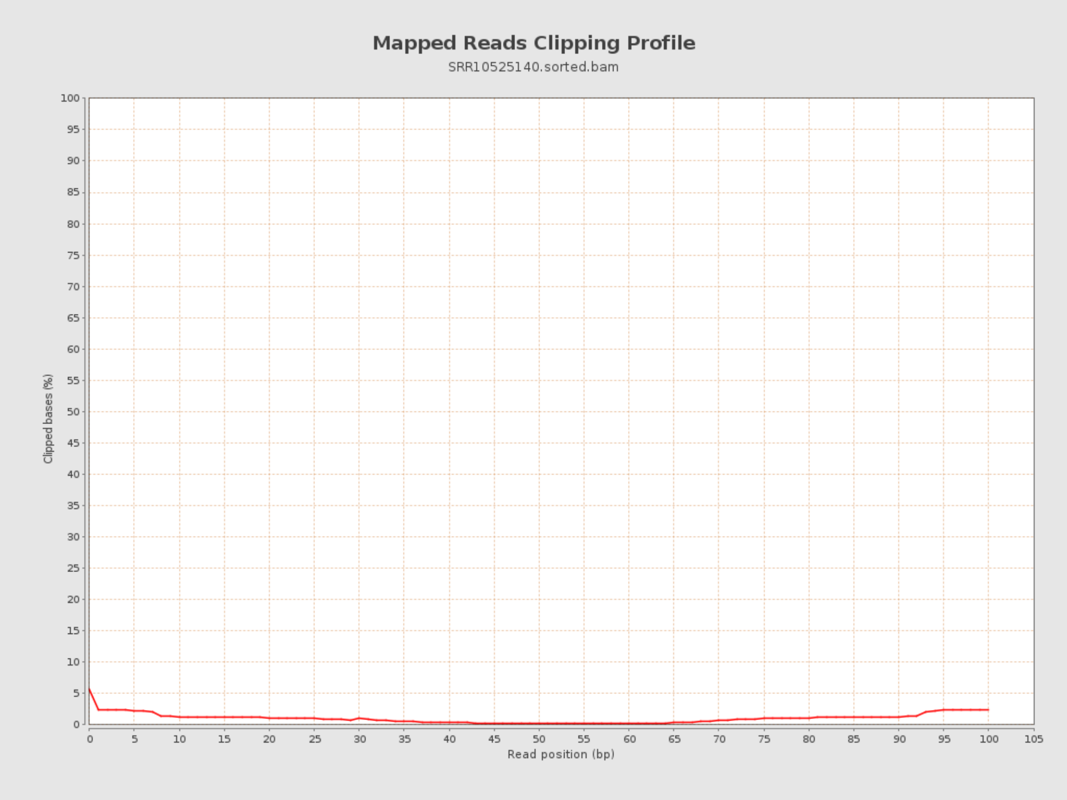
8. Results : Mapped Reads Nucleotide Content



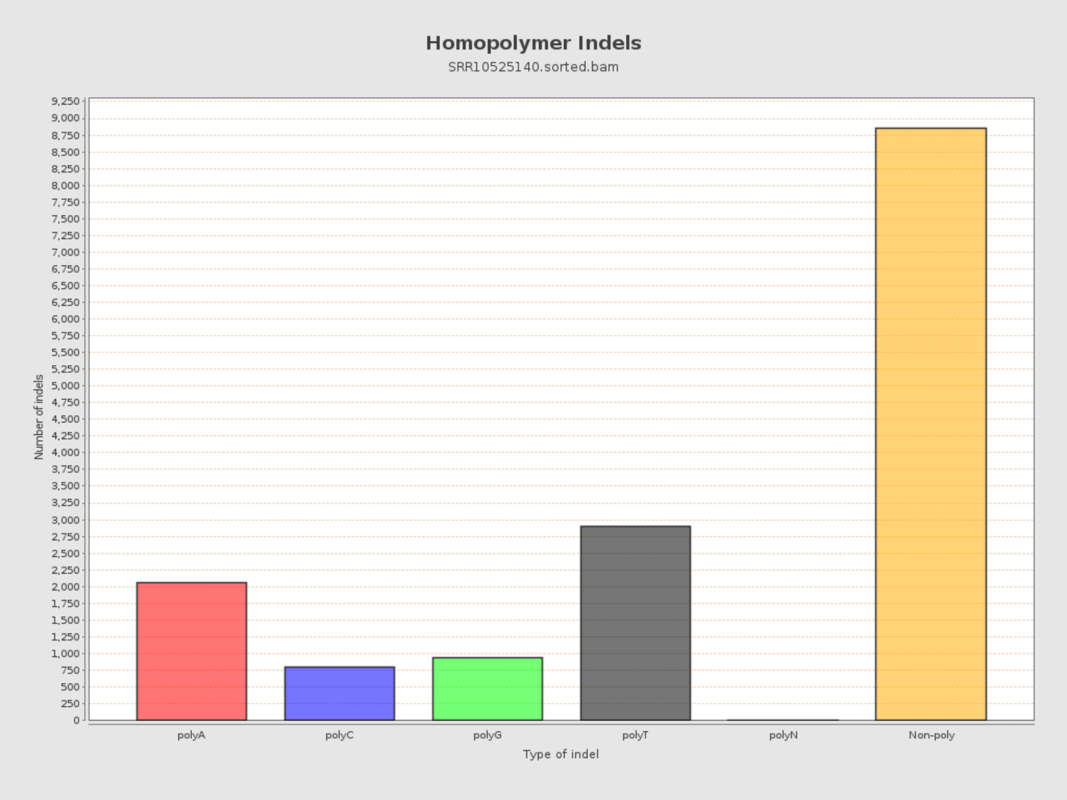
9. Results : Mapped Reads GC-content Distribution



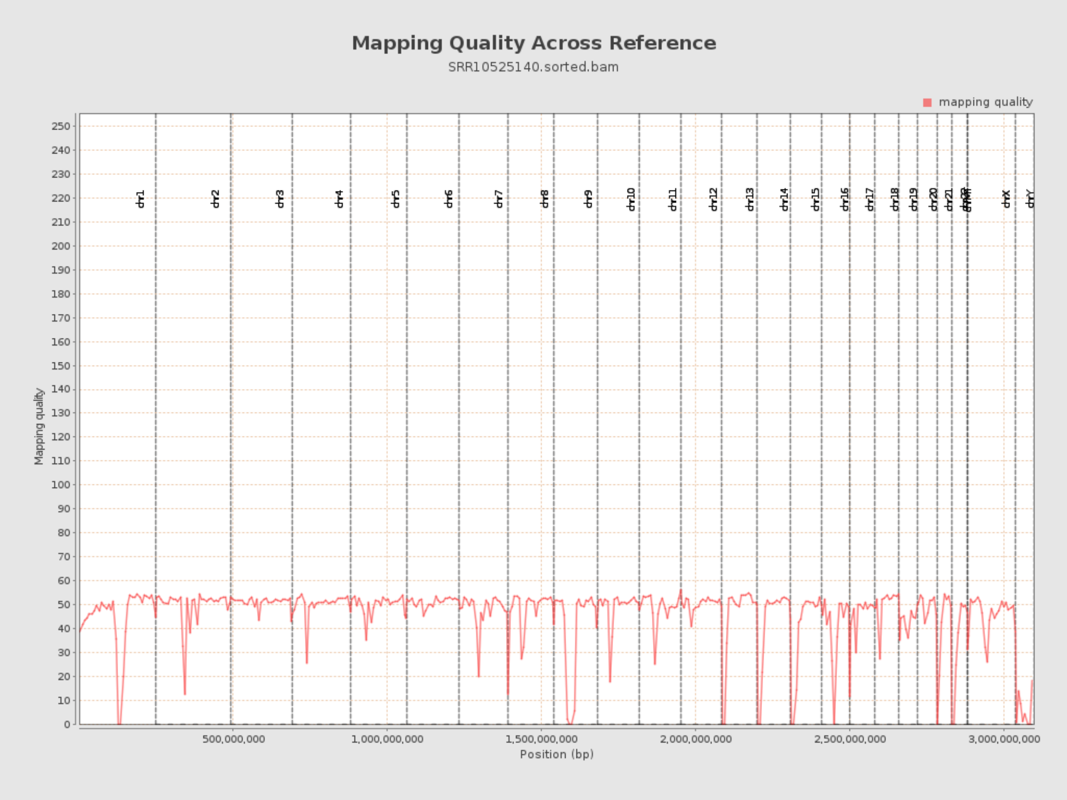
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram