

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:53:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525144.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_SRR10525144 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525144.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:53:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525144.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	938,705
Mapped reads	852,613 / 90.83%
Unmapped reads	86,092 / 9.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,798 / 2.43%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	20,363 / 2.17%
Duplication rate	1.45%
Clipped reads	874,803 / 93.19%

2.2. ACGT Content

Number/percentage of A's	17,361,667 / 26.42%
Number/percentage of C's	12,355,249 / 18.8%
Number/percentage of T's	20,112,934 / 30.61%
Number/percentage of G's	15,874,504 / 24.16%
Number/percentage of N's	2,274 / 0%
GC Percentage	42.96%

2.3. Coverage

Mean	0.0212

Standard Deviation	0.2334
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2.4. Mapping Quality

Mean Mapping Quality	46.48
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2.5. Mismatches and indels

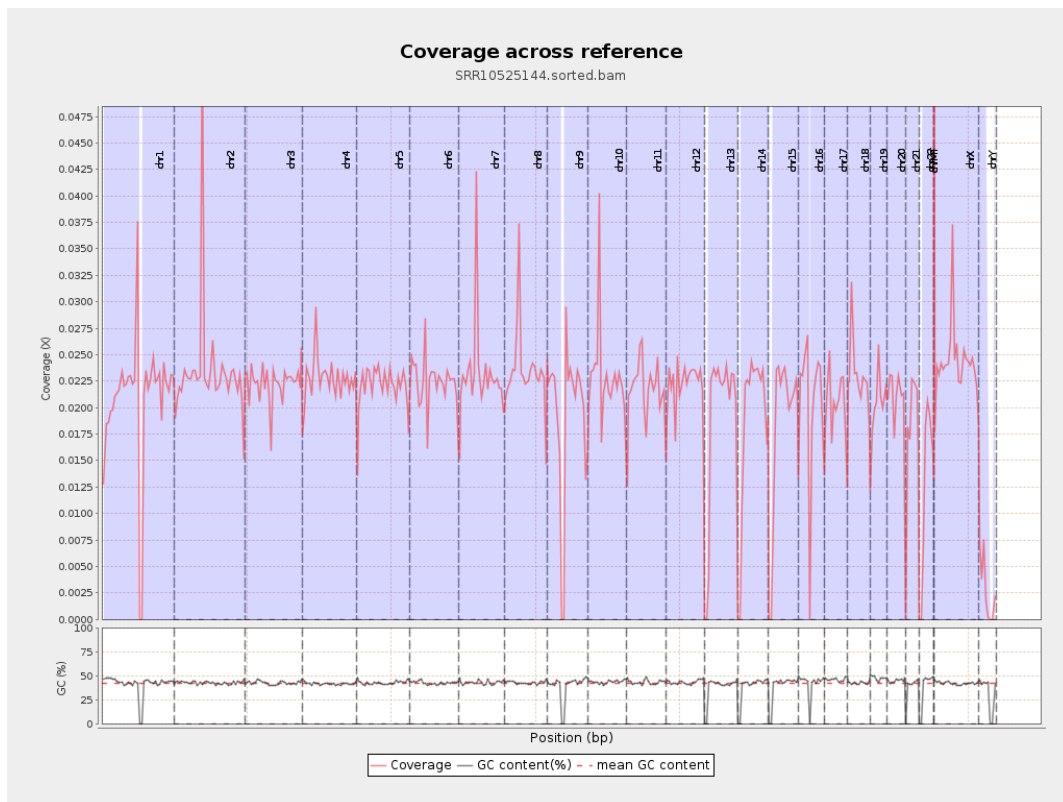
General error rate	0.75%
Mismatches	481,151
Insertions	5,388
Mapped reads with at least one insertion	0.62%
Deletions	15,096
Mapped reads with at least one deletion	1.75%
Homopolymer indels	43.55%

2.6. Chromosome stats

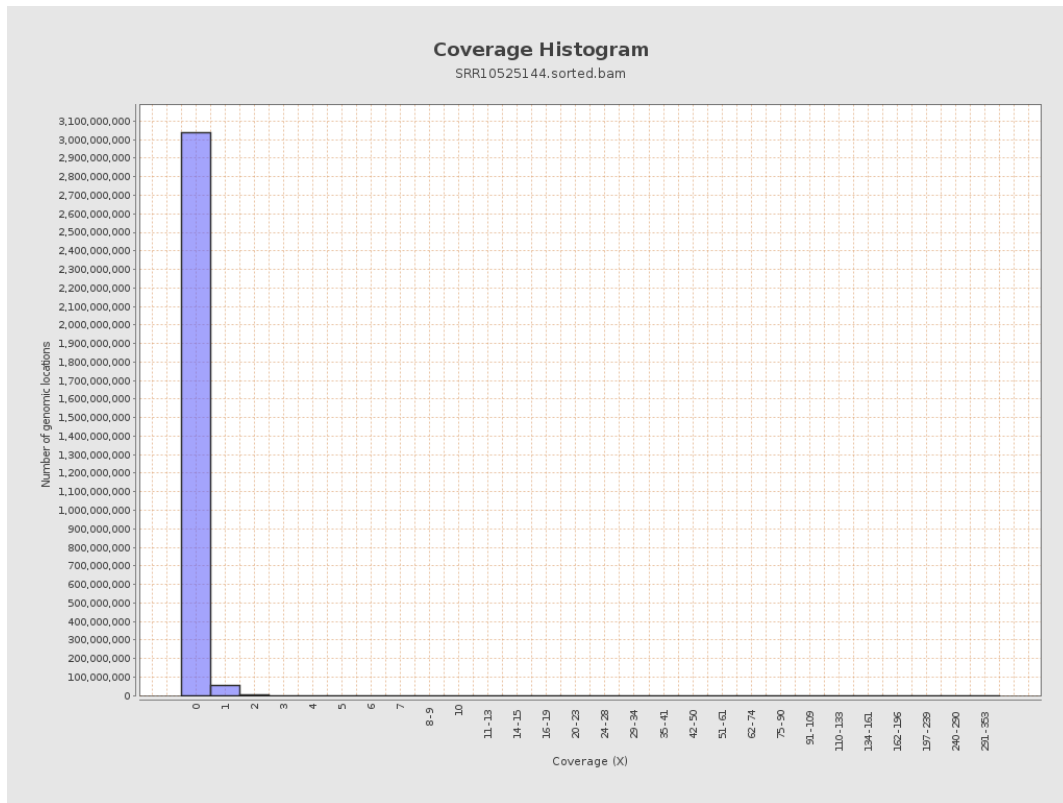
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5181959	0.0208	0.329
chr2	243199373	5716898	0.0235	0.3277
chr3	198022430	4412279	0.0223	0.1584
chr4	191154276	4344891	0.0227	0.1657
chr5	180915260	4028868	0.0223	0.1594
chr6	171115067	3832255	0.0224	0.1771
chr7	159138663	3694700	0.0232	0.3353

chr8	146364022	3449430	0.0236	0.29
chr9	141213431	2731860	0.0193	0.2309
chr10	135534747	3089083	0.0228	0.2511
chr11	135006516	2960736	0.0219	0.24
chr12	133851895	2976653	0.0222	0.1591
chr13	115169878	2160963	0.0188	0.1444
chr14	107349540	2001818	0.0186	0.1611
chr15	102531392	1864593	0.0182	0.1424
chr16	90354753	1811132	0.02	0.1603
chr17	81195210	1653300	0.0204	0.1822
chr18	78077248	1806133	0.0231	0.3785
chr19	59128983	1217171	0.0206	0.2576
chr20	63025520	1313167	0.0208	0.1605
chr21	48129895	869369	0.0181	0.151
chr22	51304566	656826	0.0128	0.1197
chrMT	16571	2099	0.1267	0.3838
chrX	155270560	3795820	0.0244	0.2088
chrY	59373566	160882	0.0027	0.0724

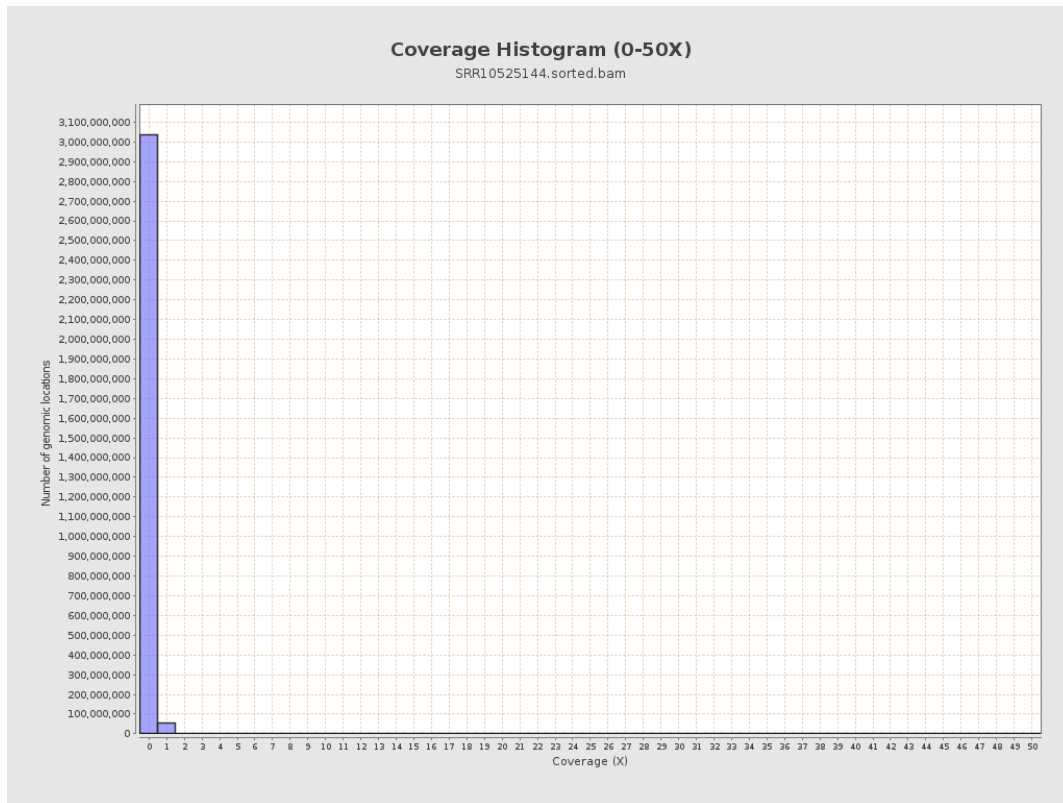
3. Results : Coverage across reference



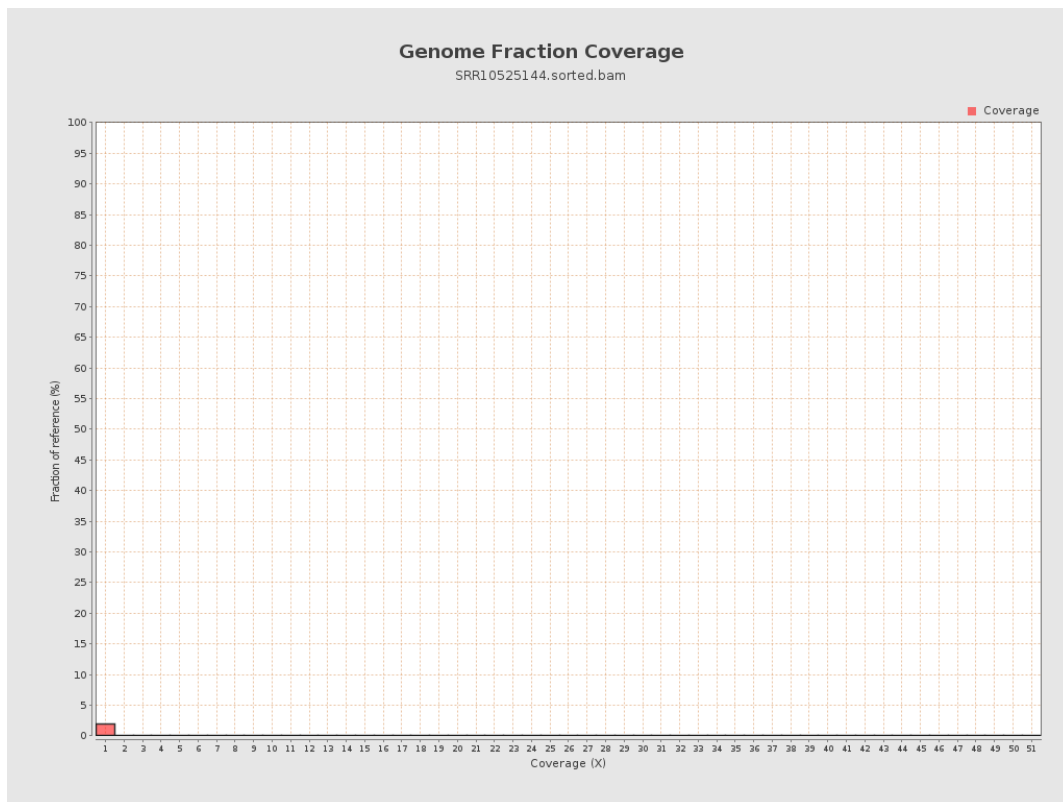
4. Results : Coverage Histogram



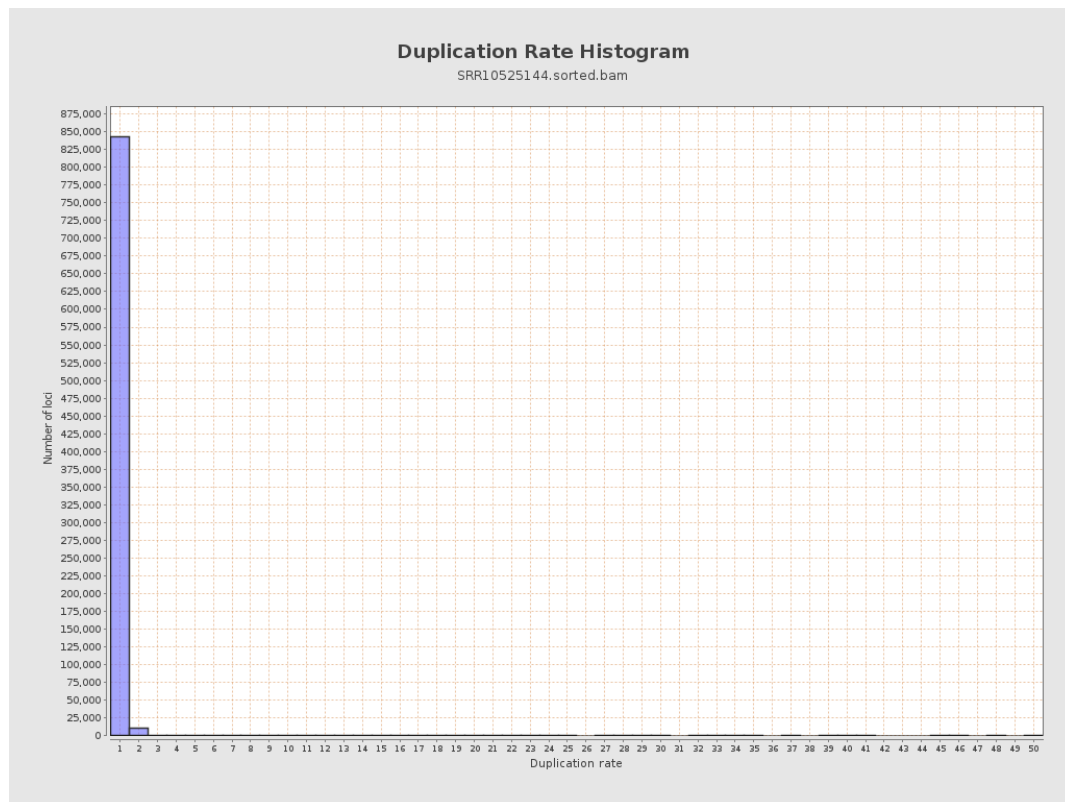
5. Results : Coverage Histogram (0-50X)



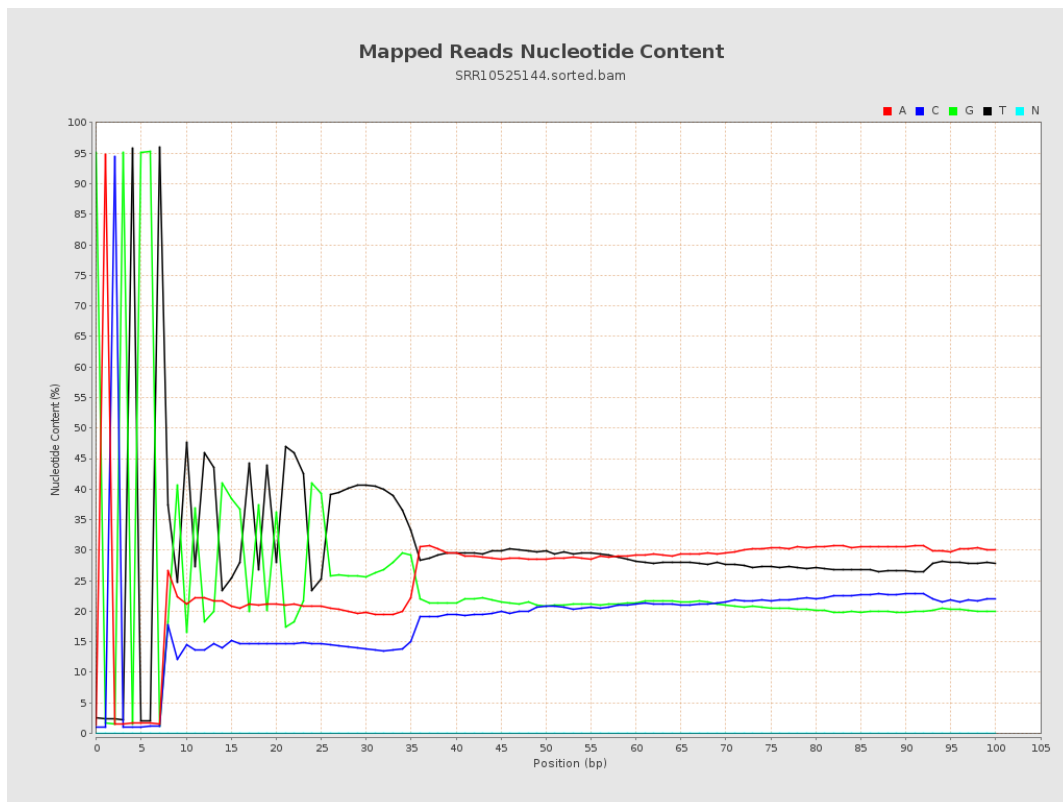
6. Results : Genome Fraction Coverage



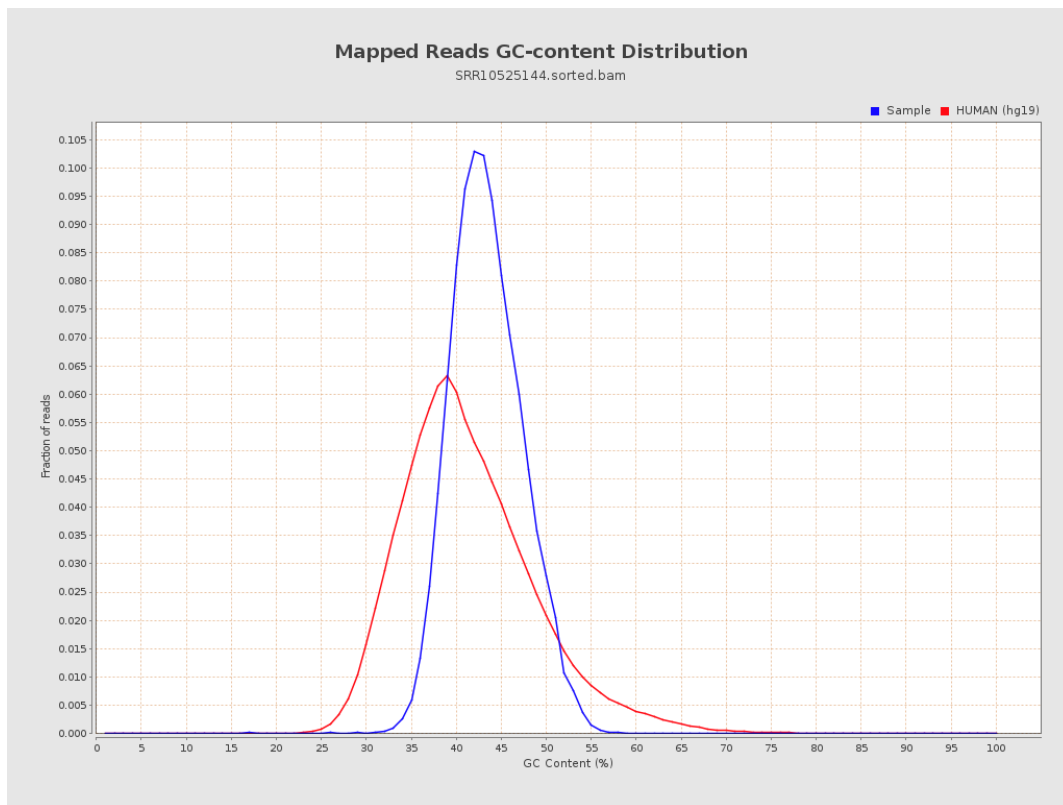
7. Results : Duplication Rate Histogram



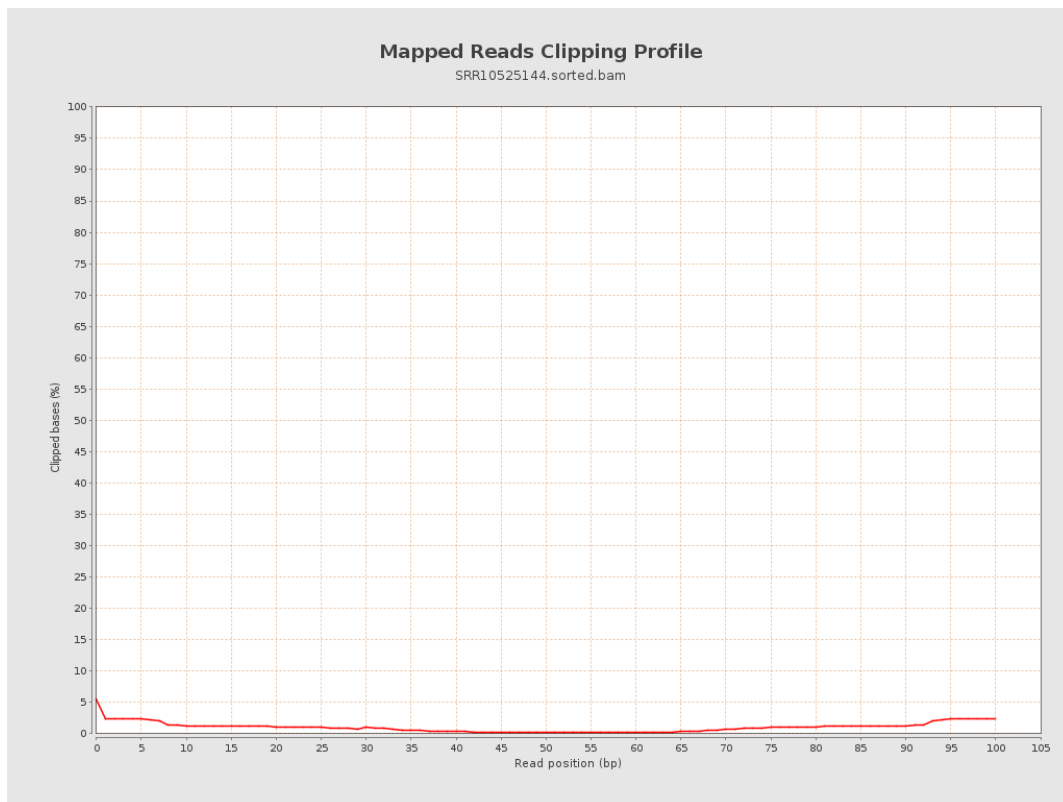
8. Results : Mapped Reads Nucleotide Content



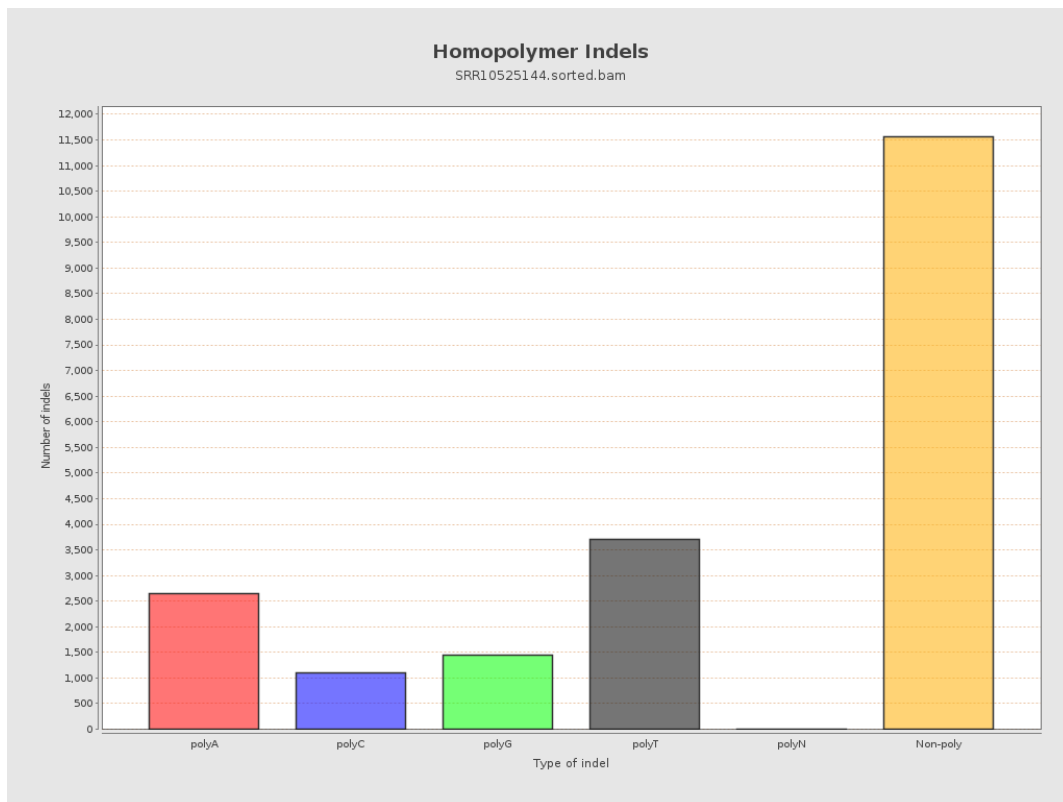
9. Results : Mapped Reads GC-content Distribution



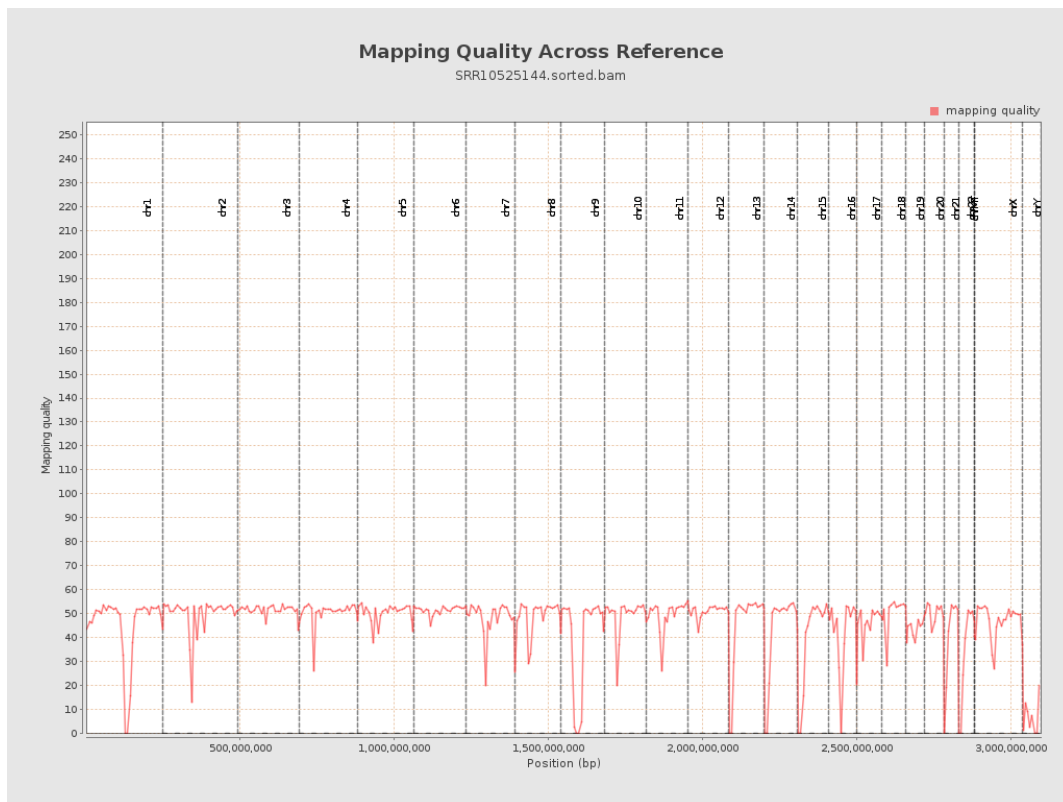
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

