Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:39:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525116.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_SRR10525116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:39:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	617,101
Mapped reads	559,935 / 90.74%
Unmapped reads	57,166 / 9.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,044 / 2.6%
Read min/max/mean length	30 / 101 / 101.96
Duplicated reads (estimated)	10,711 / 1.74%
Duplication rate	1.19%
Clipped reads	575,614 / 93.28%

2.2. ACGT Content

Number/percentage of A's	11,572,105 / 26.67%
Number/percentage of C's	8,831,566 / 20.36%
Number/percentage of T's	13,040,283 / 30.06%
Number/percentage of G's	9,937,030 / 22.91%
Number/percentage of N's	1,666 / 0%
GC Percentage	43.26%

2.3. Coverage

Mean	0.014

Standard Deviation	0.1697

2.4. Mapping Quality

Mean Mapping Quality	46.4

2.5. Mismatches and indels

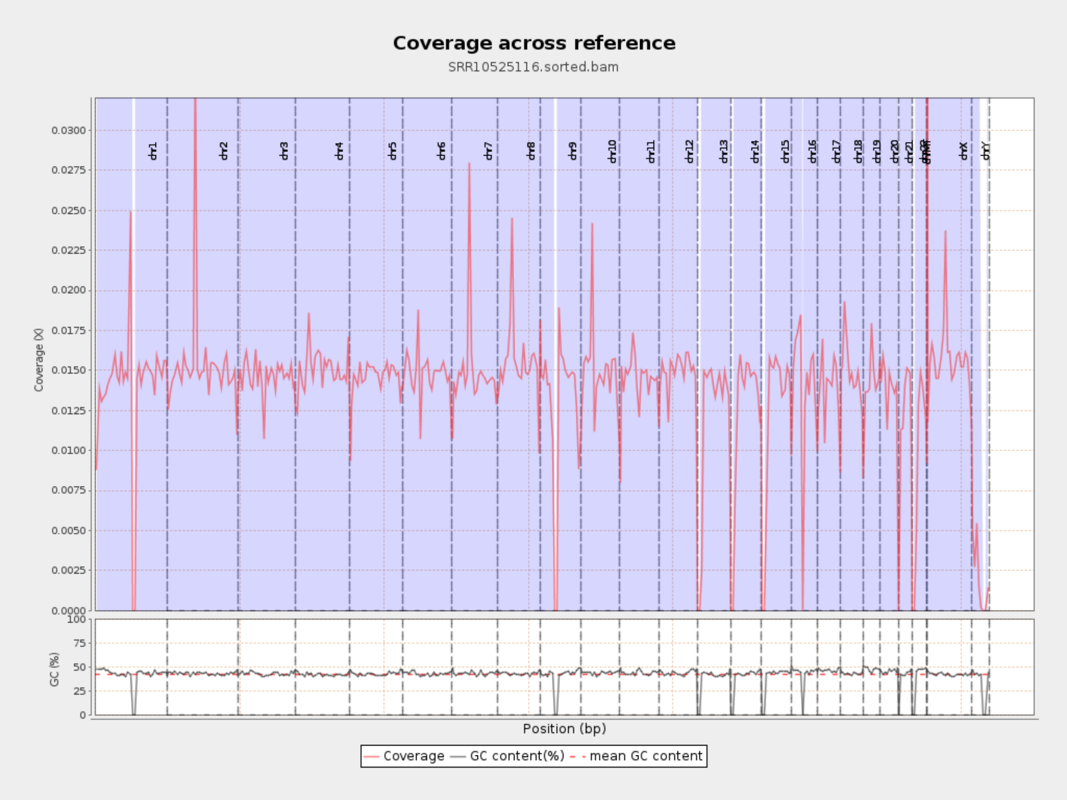
General error rate	0.72%
Mismatches	306,864
Insertions	3,525
Mapped reads with at least one insertion	0.62%
Deletions	9,956
Mapped reads with at least one deletion	1.75%
Homopolymer indels	44.02%

2.6. Chromosome stats

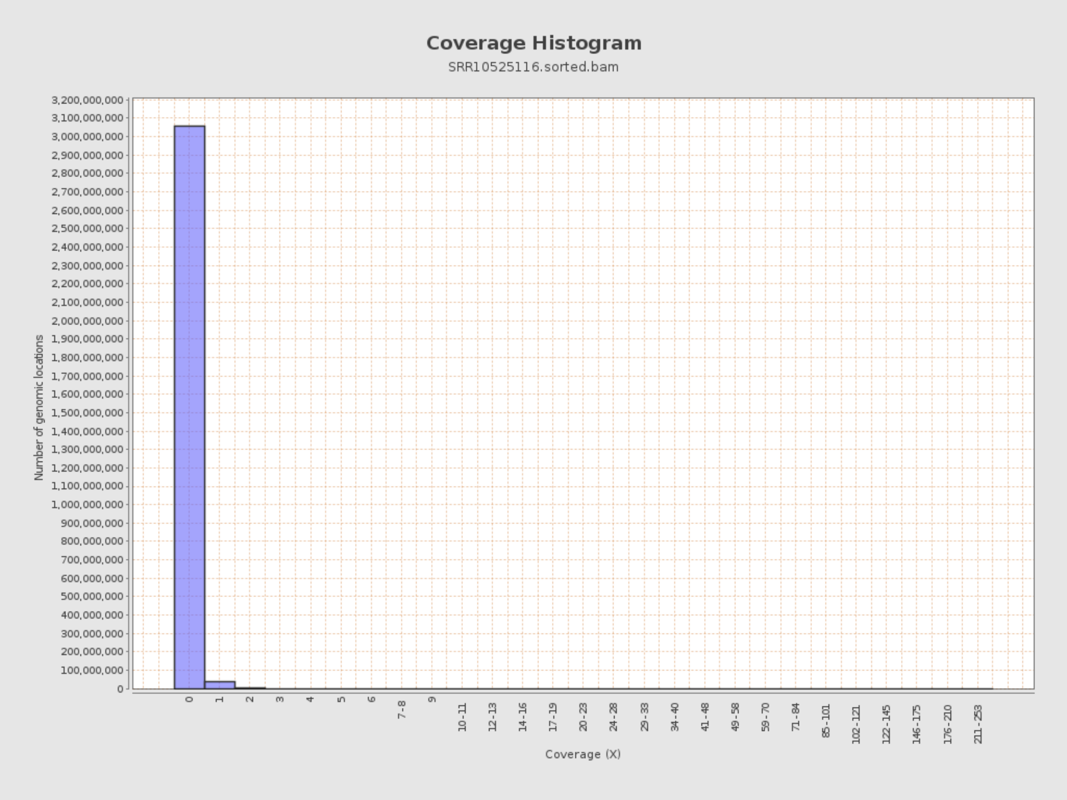
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3469372	0.0139	0.2415
chr2	243199373	3748362	0.0154	0.2261
chr3	198022430	2896922	0.0146	0.1254
chr4	191154276	2879556	0.0151	0.1306
chr5	180915260	2654127	0.0147	0.127
chr6	171115067	2529920	0.0148	0.1363
chr7	159138663	2384415	0.015	0.2373

chr8	146364022	2281038	0.0156	0.2267
chr9	141213431	1807780	0.0128	0.1638
chr10	135534747	2024935	0.0149	0.1684
chr11	135006516	1962171	0.0145	0.1645
chr12	133851895	1997915	0.0149	0.1271
chr13	115169878	1366256	0.0119	0.1126
chr14	107349540	1300985	0.0121	0.1204
chr15	102531392	1246381	0.0122	0.114
chr16	90354753	1228792	0.0136	0.1259
chr17	81195210	1128256	0.0139	0.1368
chr18	78077248	1168552	0.015	0.2396
chr19	59128983	848939	0.0144	0.1912
chr20	63025520	867374	0.0138	0.124
chr21	48129895	568202	0.0118	0.1162
chr22	51304566	472647	0.0092	0.0991
chrMT	16571	4067	0.2454	0.4823
chrX	155270560	2449063	0.0158	0.15
chrY	59373566	114156	0.0019	0.0562

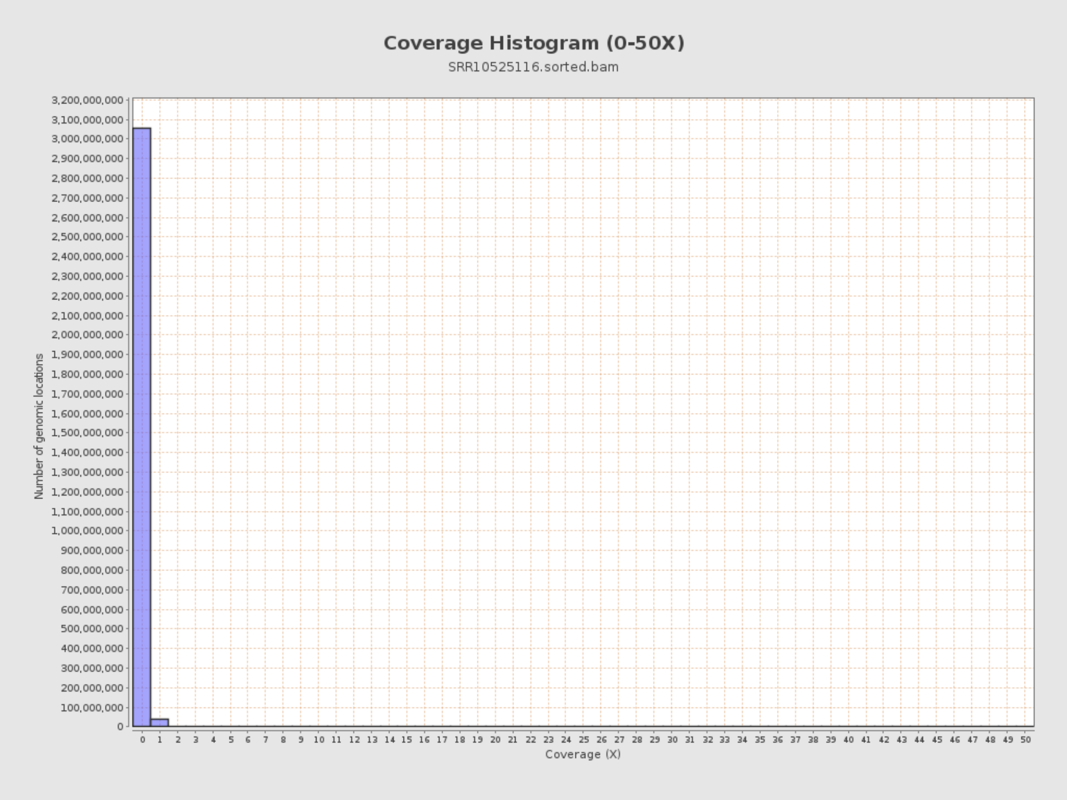
3. Results : Coverage across reference



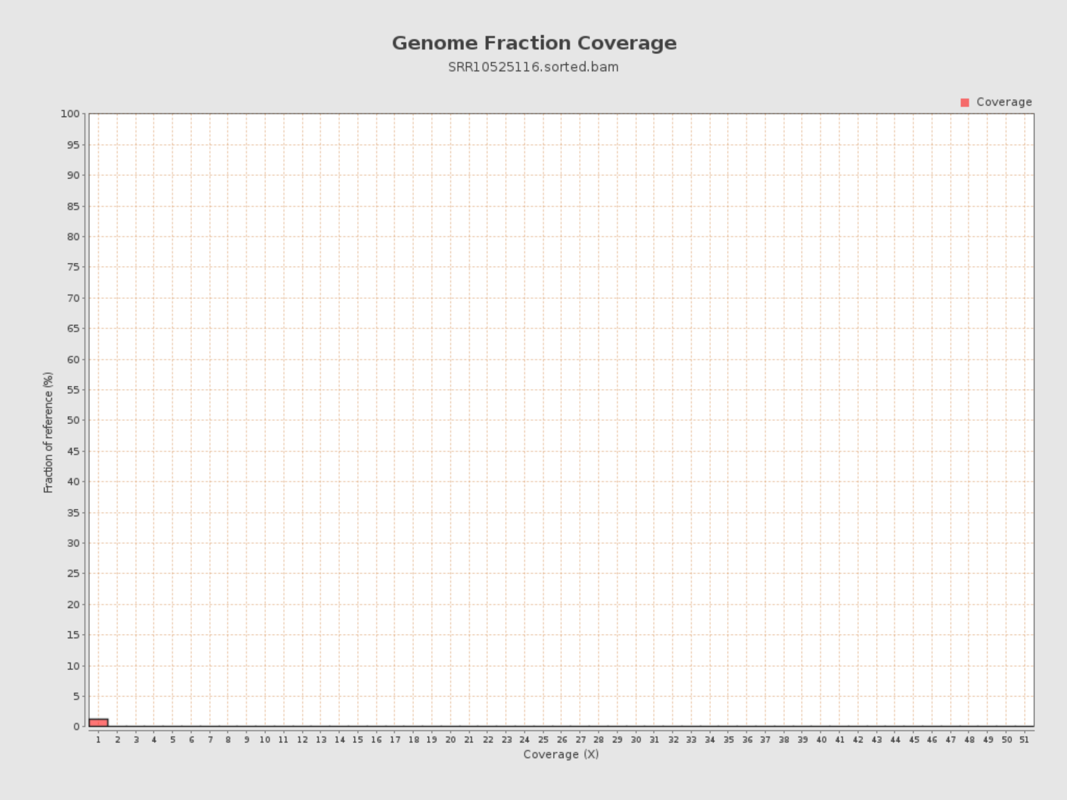
4. Results : Coverage Histogram



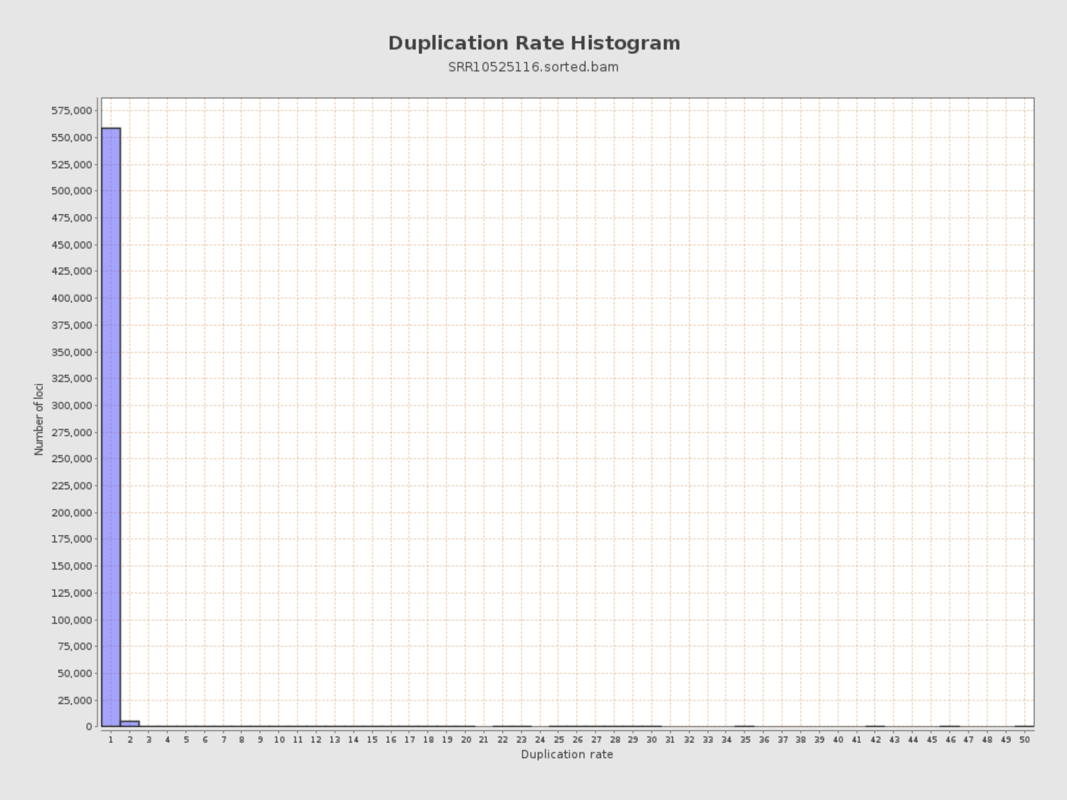
5. Results : Coverage Histogram (0-50X)



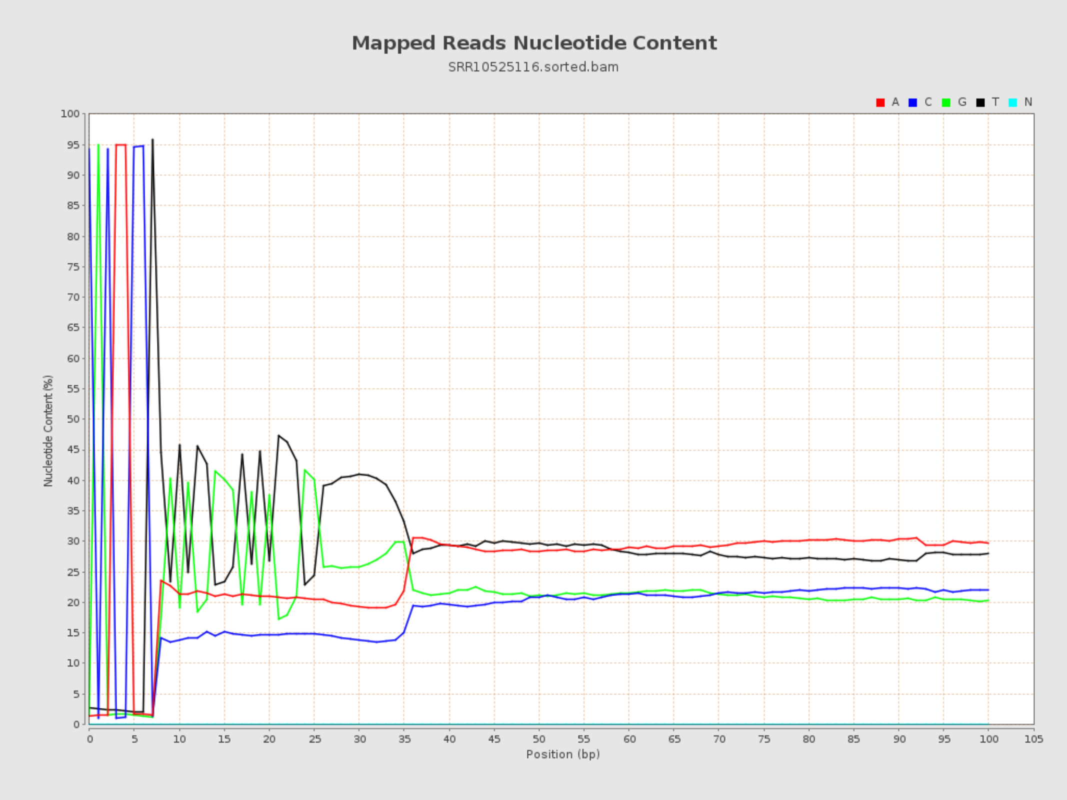
6. Results : Genome Fraction Coverage



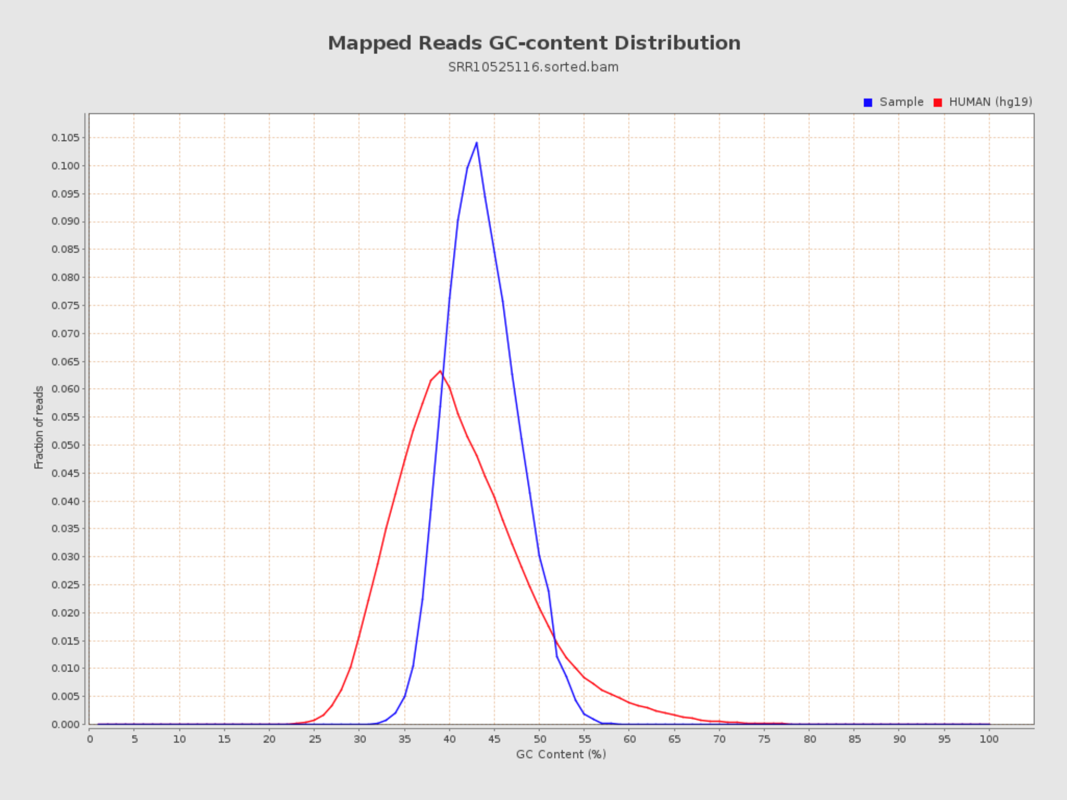
7. Results : Duplication Rate Histogram



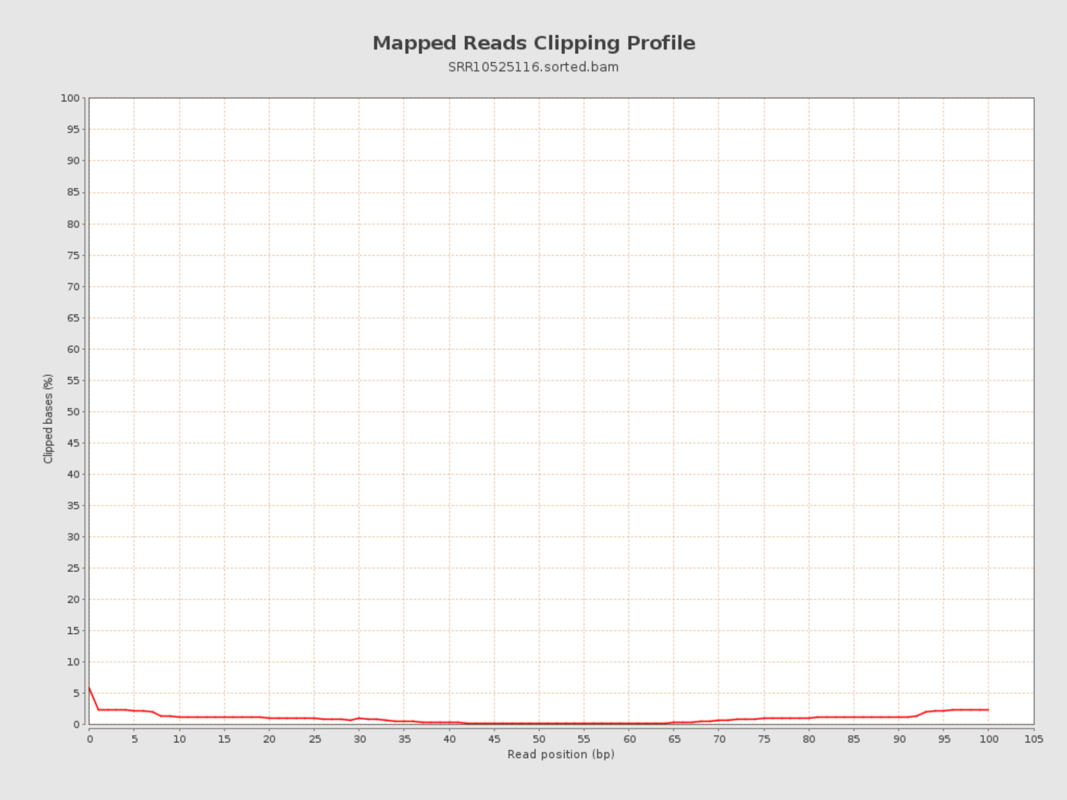
8. Results : Mapped Reads Nucleotide Content



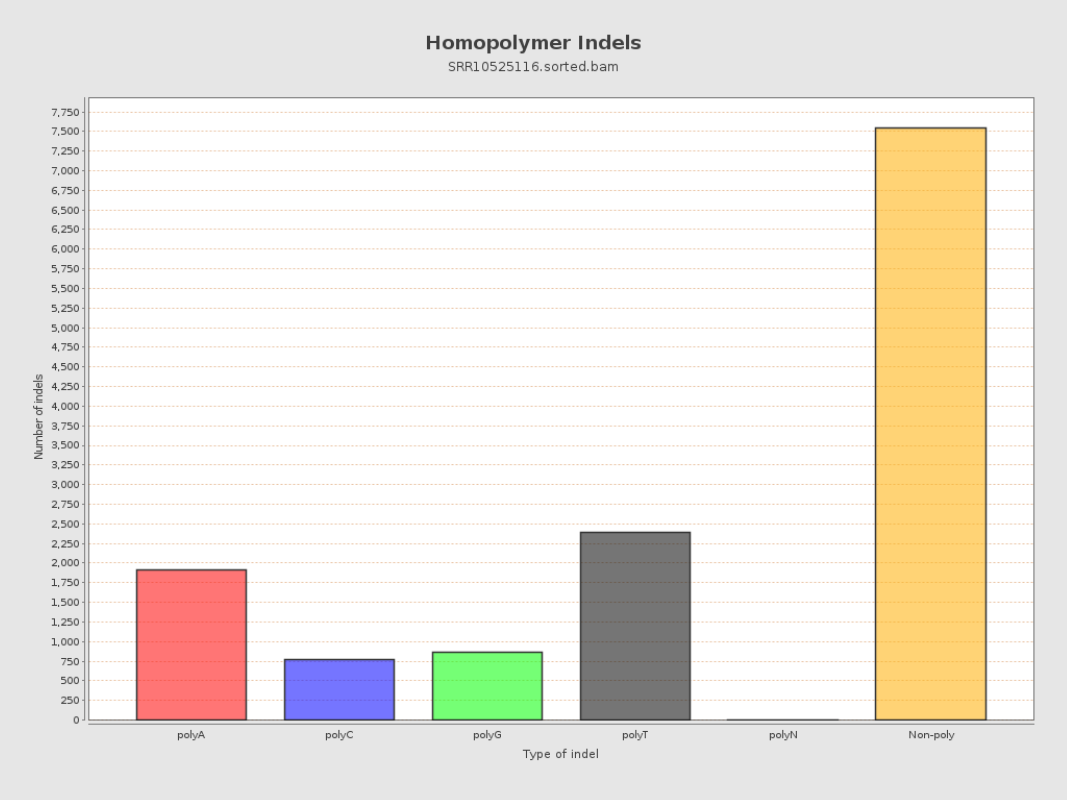
9. Results : Mapped Reads GC-content Distribution



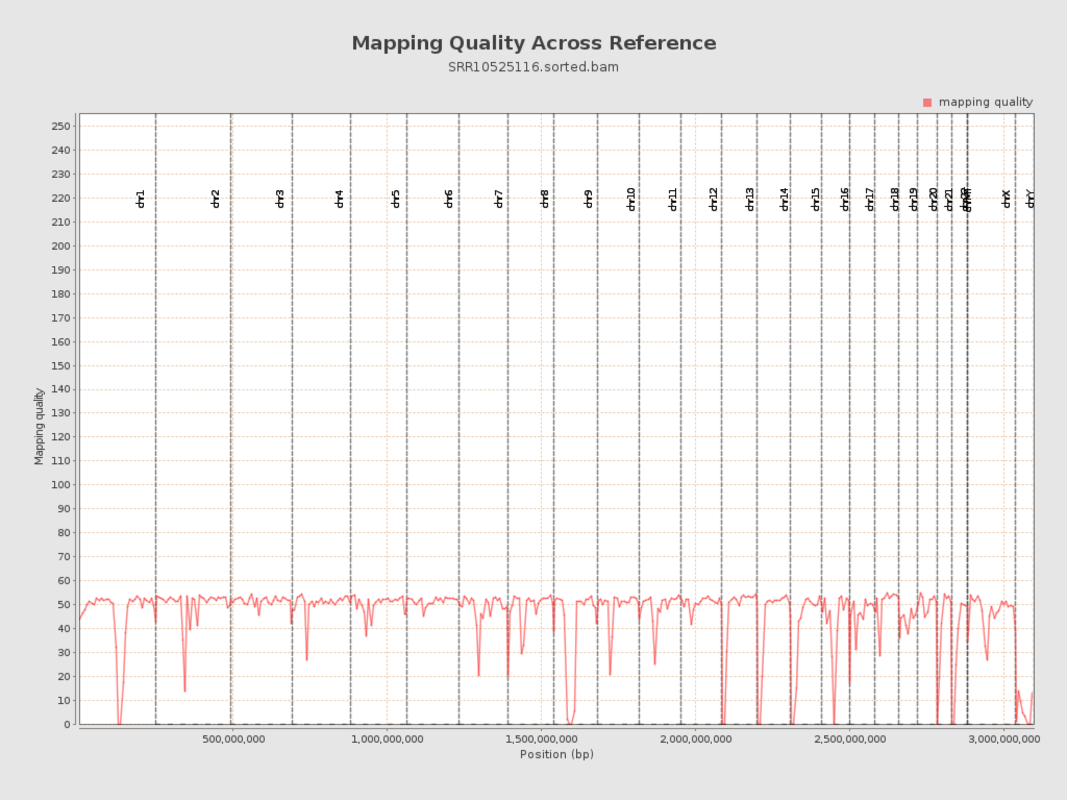
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram