Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:47:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525245.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_SRR10525245 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525245.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:47:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525245.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,150,769
Mapped reads	1,040,833 / 90.45%
Unmapped reads	109,936 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,559 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	28,335 / 2.46%
Duplication rate	1.97%
Clipped reads	1,041,270 / 90.48%

2.2. ACGT Content

Number/percentage of A's	15,990,792 / 26.63%
Number/percentage of C's	10,184,666 / 16.96%
Number/percentage of T's	19,332,402 / 32.19%
Number/percentage of G's	14,545,682 / 24.22%
Number/percentage of N's	1,189 / 0%
GC Percentage	41.18%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2035

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

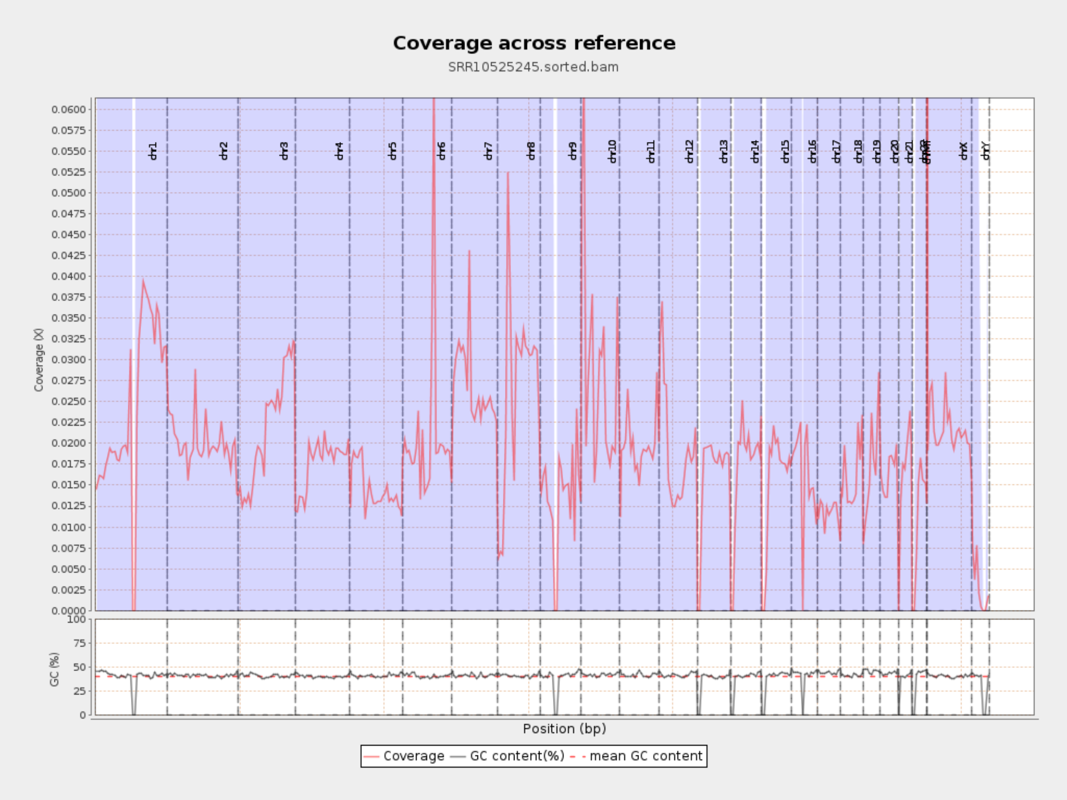
General error rate	0.51%
Mismatches	298,996
Insertions	4,637
Mapped reads with at least one insertion	0.44%
Deletions	12,325
Mapped reads with at least one deletion	1.18%
Homopolymer indels	43.72%

2.6. Chromosome stats

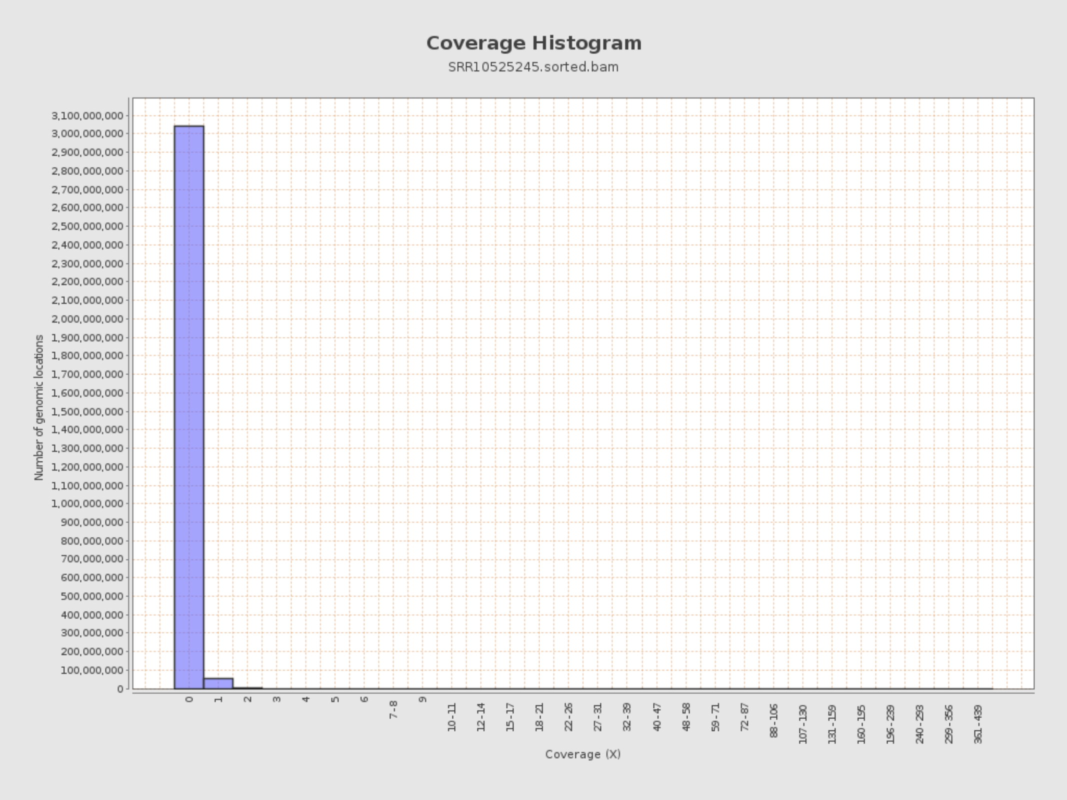
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6043639	0.0242	0.3198
chr2	243199373	4860947	0.02	0.2421
chr3	198022430	4285647	0.0216	0.1567
chr4	191154276	3387508	0.0177	0.1436
chr5	180915260	2652983	0.0147	0.1285
chr6	171115067	3627651	0.0212	0.1667
chr7	159138663	4295046	0.027	0.3514

chr8	146364022	3932730	0.0269	0.2221
chr9	141213431	1910116	0.0135	0.1531
chr10	135534747	3897471	0.0288	0.2346
chr11	135006516	2648804	0.0196	0.1792
chr12	133851895	2592975	0.0194	0.1478
chr13	115169878	1857408	0.0161	0.1366
chr14	107349540	1807062	0.0168	0.1402
chr15	102531392	1550324	0.0151	0.1328
chr16	90354753	1460577	0.0162	0.1454
chr17	81195210	948519	0.0117	0.1173
chr18	78077248	1251113	0.016	0.2926
chr19	59128983	1032545	0.0175	0.2327
chr20	63025520	1027240	0.0163	0.1371
chr21	48129895	805821	0.0167	0.1394
chr22	51304566	573874	0.0112	0.1118
chrMT	16571	81480	4.917	3.5784
chrX	155270560	3379414	0.0218	0.1659
chrY	59373566	163373	0.0028	0.072

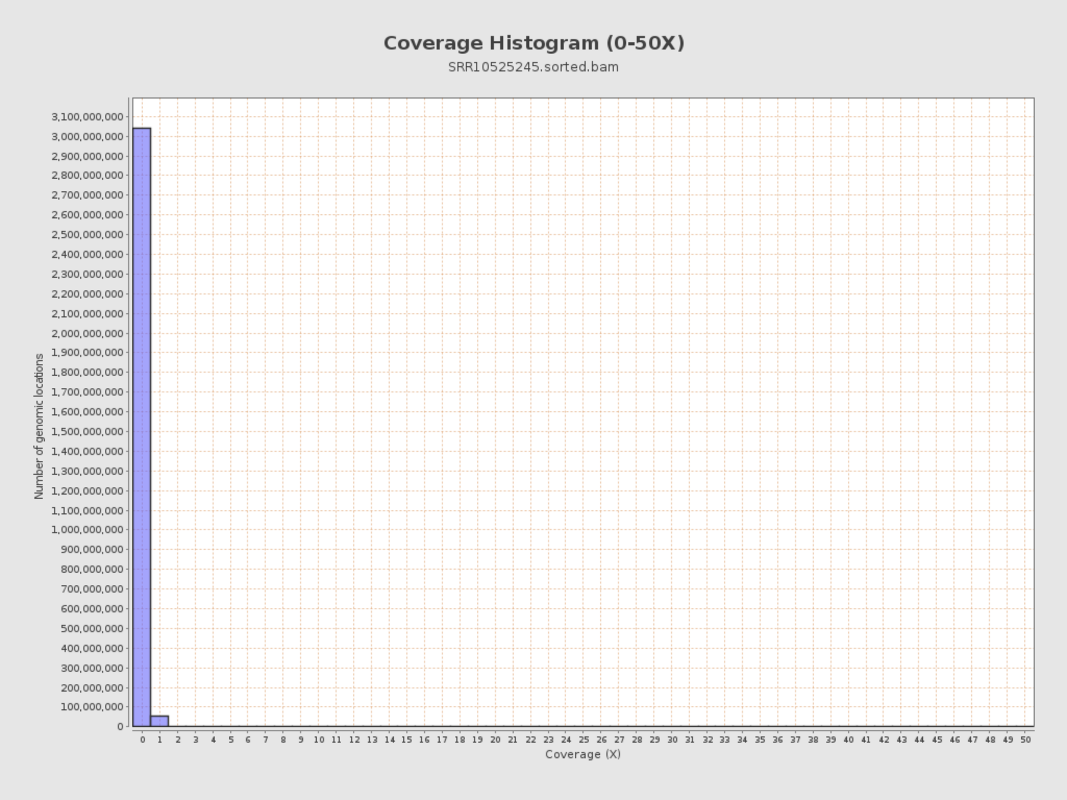
3. Results : Coverage across reference



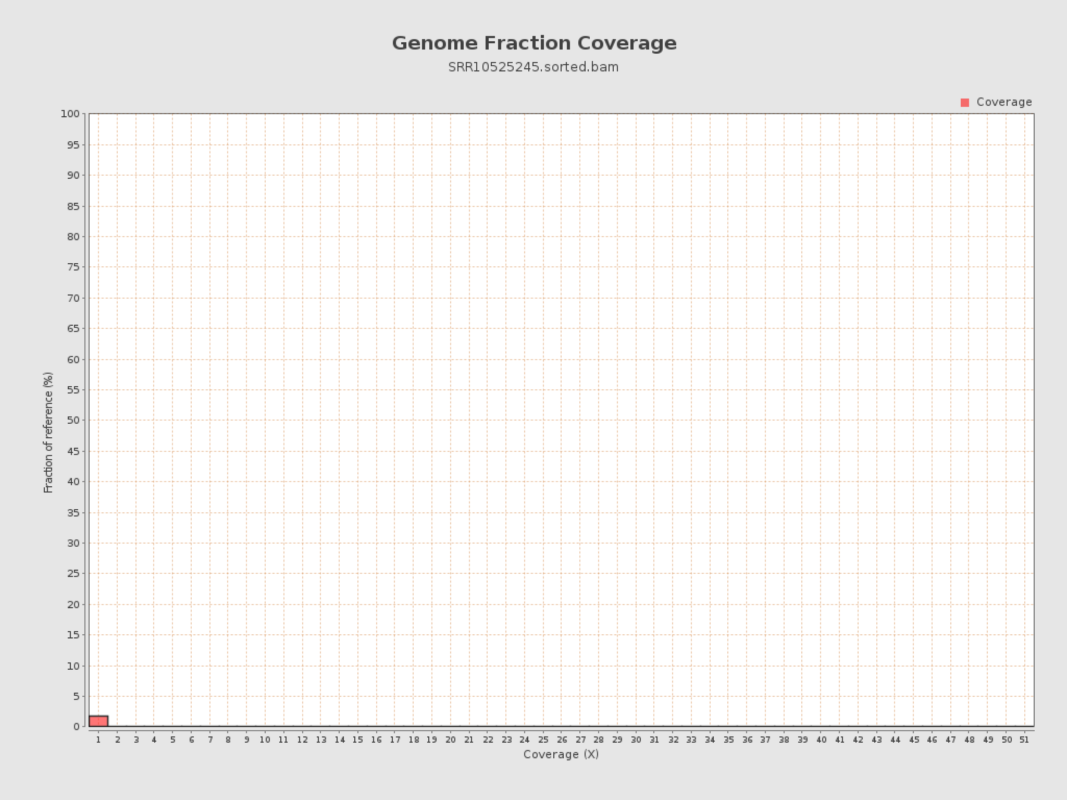
4. Results : Coverage Histogram



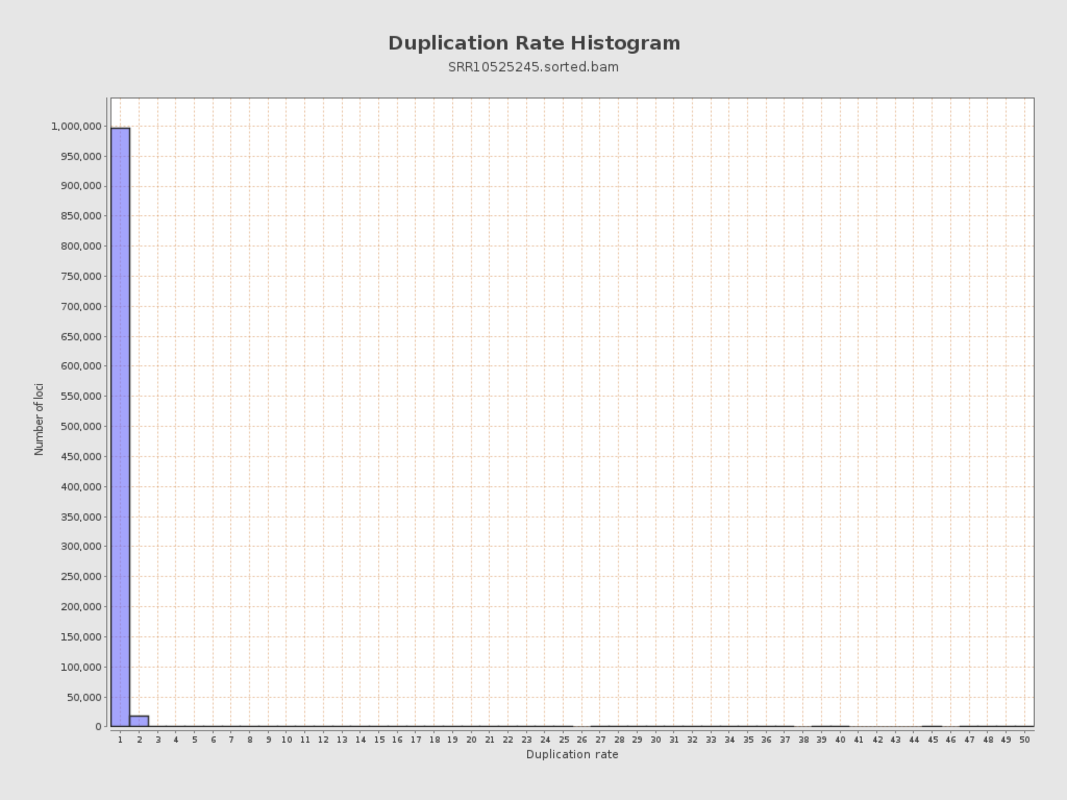
5. Results : Coverage Histogram (0-50X)



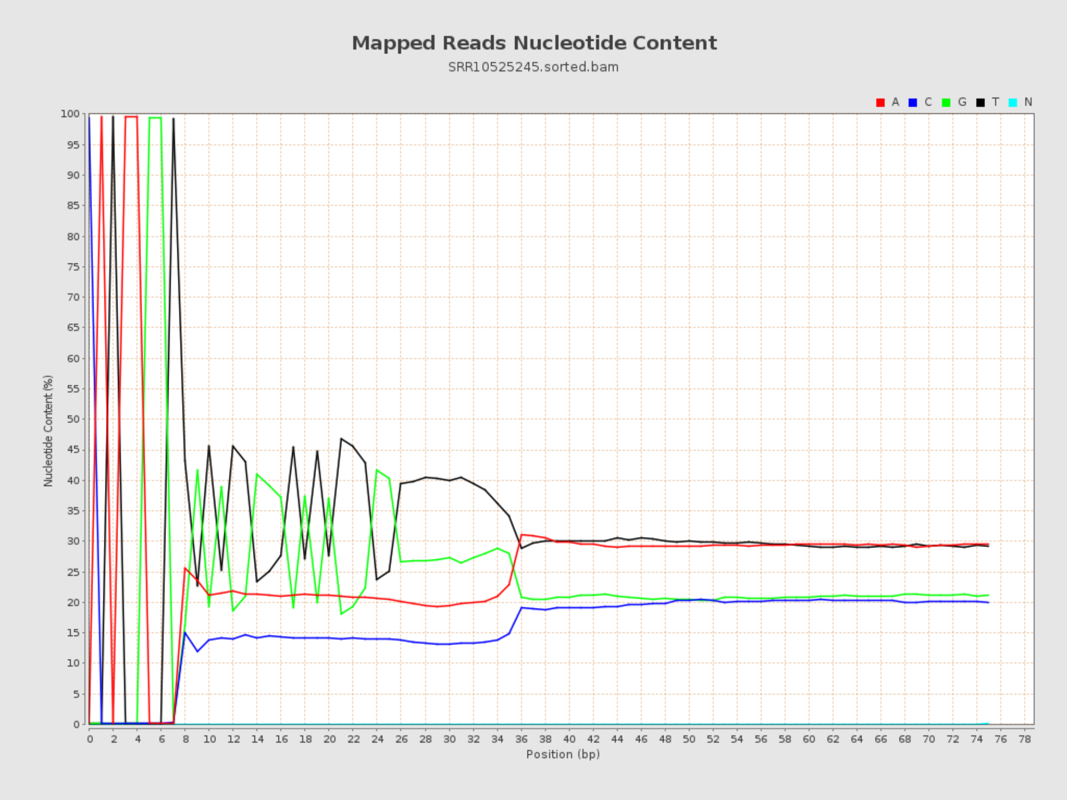
6. Results : Genome Fraction Coverage



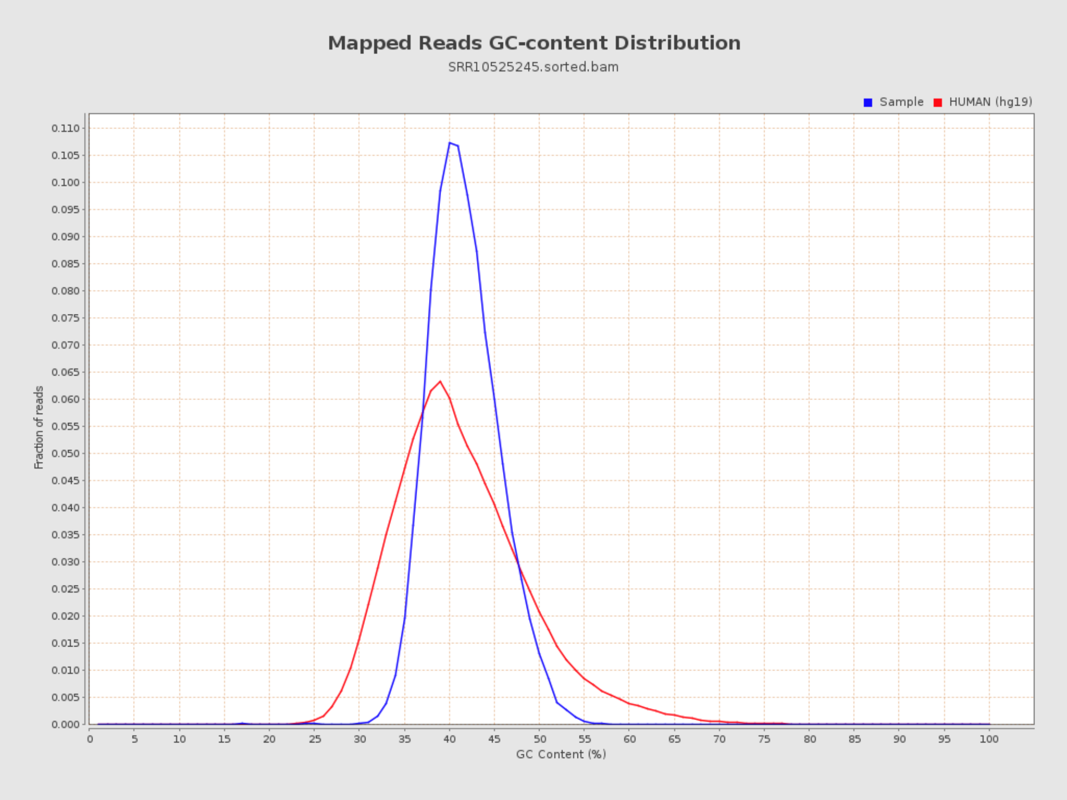
7. Results : Duplication Rate Histogram



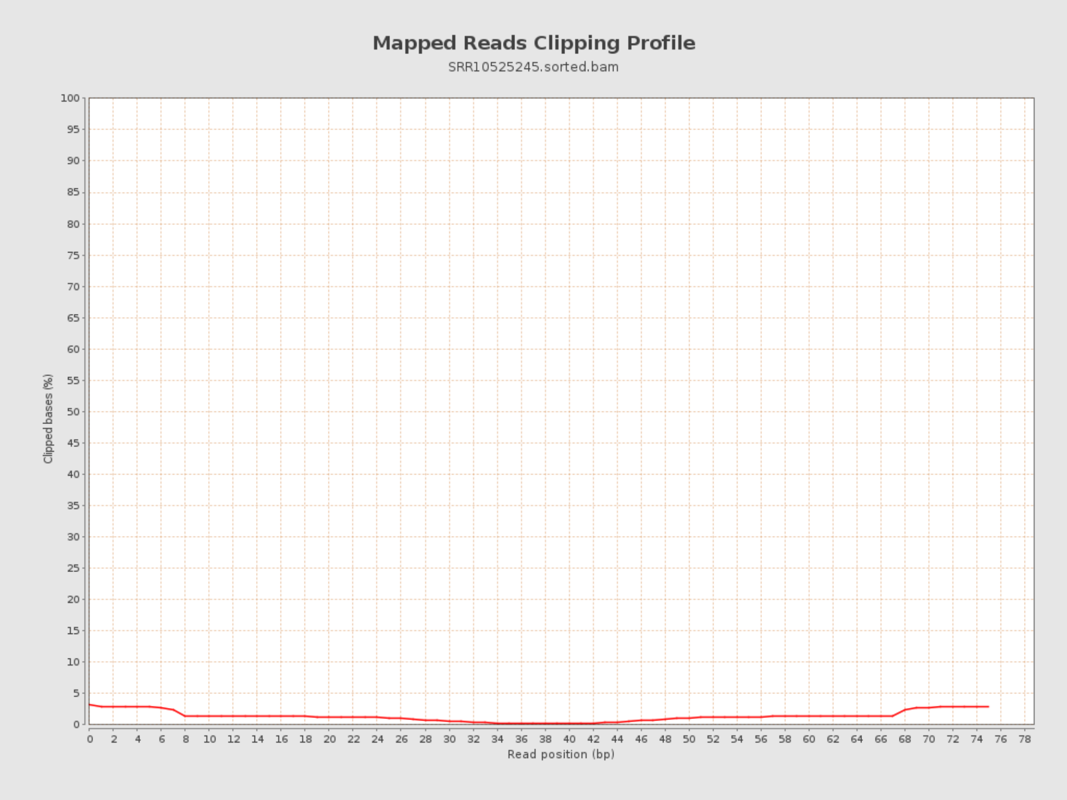
8. Results : Mapped Reads Nucleotide Content



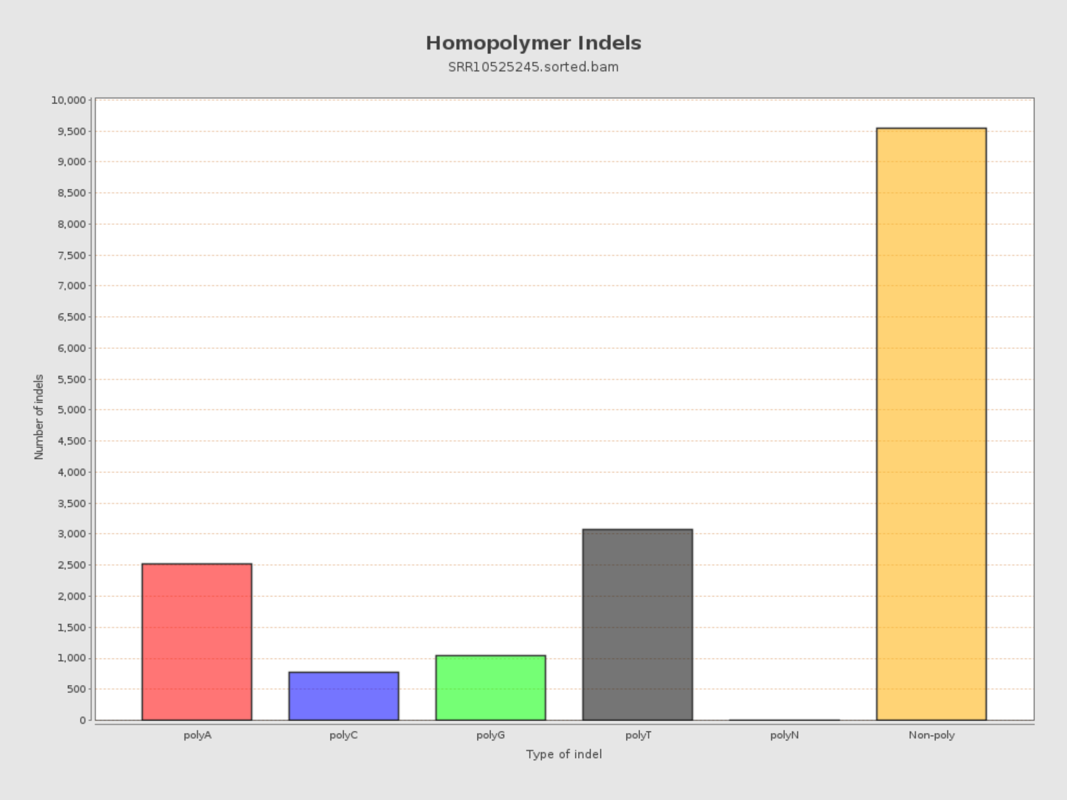
9. Results : Mapped Reads GC-content Distribution



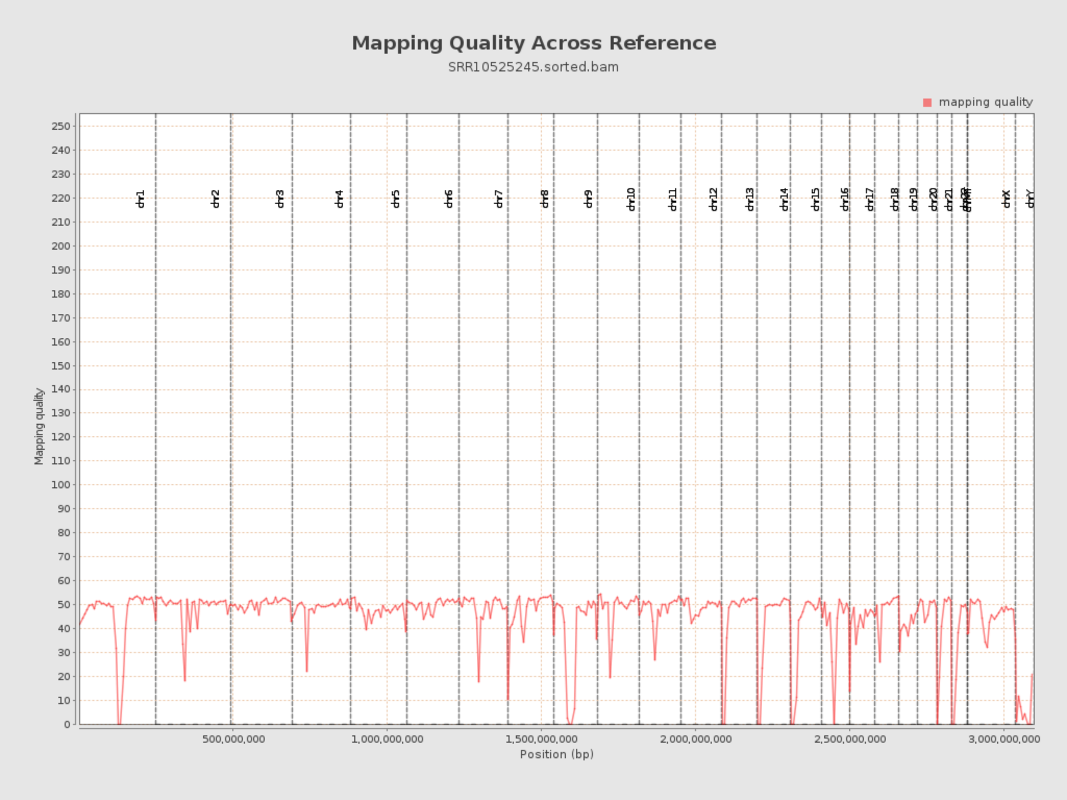
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram