Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:44:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524865.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_SRR10524865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:44:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,129,002
Mapped reads	1,030,758 / 91.3%
Unmapped reads	98,244 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,704 / 0.51%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	24,720 / 2.19%
Duplication rate	1.62%
Clipped reads	1,032,831 / 91.48%

2.2. ACGT Content

Number/percentage of A's	16,244,131 / 27.12%
Number/percentage of C's	10,866,962 / 18.14%
Number/percentage of T's	18,503,208 / 30.89%
Number/percentage of G's	14,285,483 / 23.85%
Number/percentage of N's	7,978 / 0.01%
GC Percentage	41.99%

2.3. Coverage

Mean	0.0194

Standard Deviation	0.2102

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

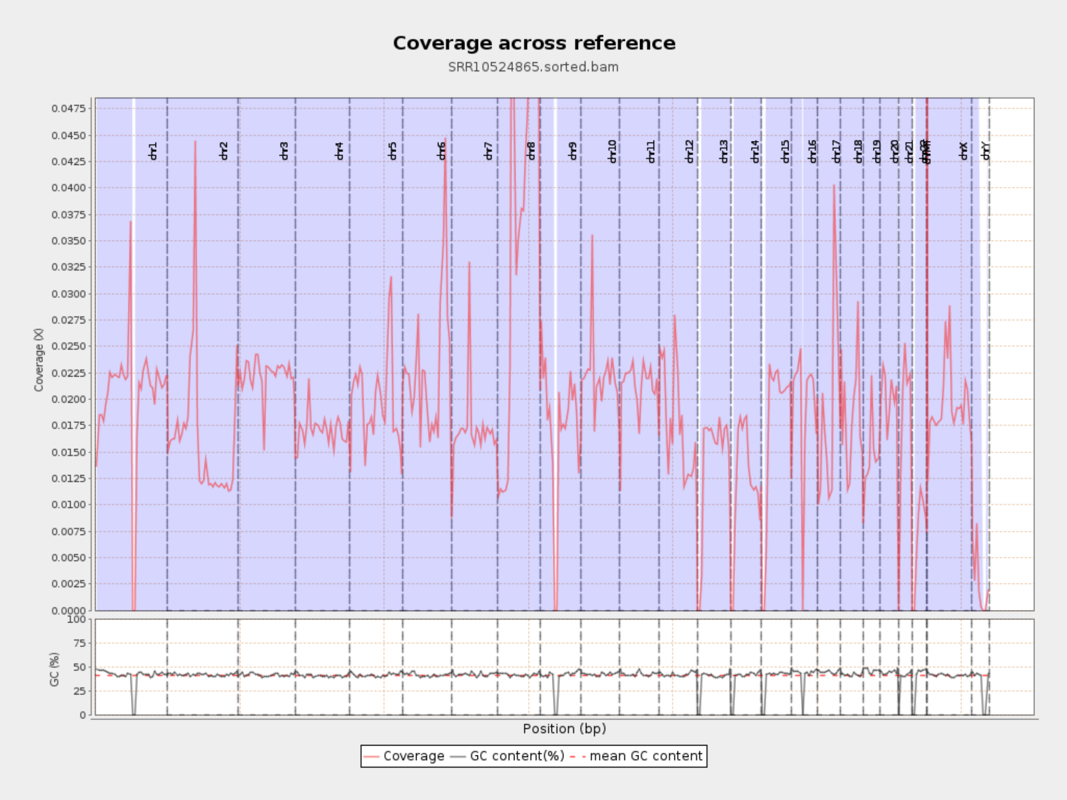
General error rate	0.5%
Mismatches	292,323
Insertions	4,962
Mapped reads with at least one insertion	0.48%
Deletions	11,589
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.47%

2.6. Chromosome stats

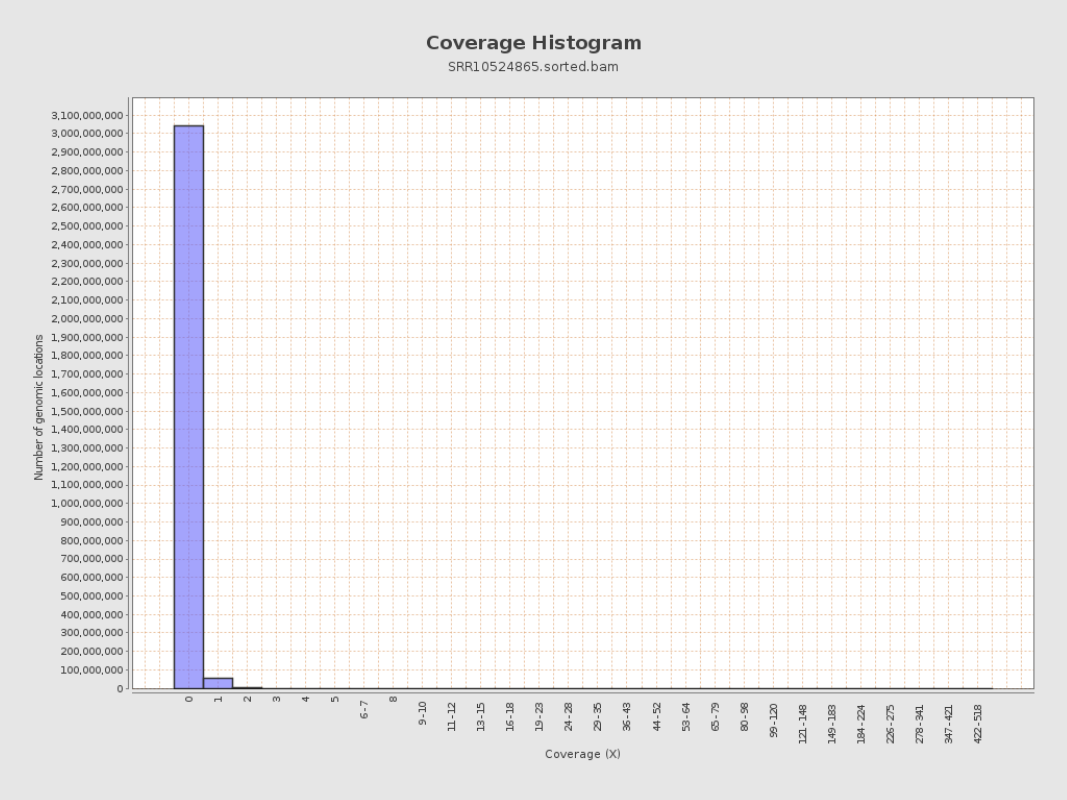
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5041571	0.0202	0.3964
chr2	243199373	3907656	0.0161	0.2075
chr3	198022430	4420897	0.0223	0.1559
chr4	191154276	3259113	0.017	0.1425
chr5	180915260	3642031	0.0201	0.1491
chr6	171115067	3901536	0.0228	0.1709
chr7	159138663	2754879	0.0173	0.2713

chr8	146364022	6265626	0.0428	0.2858
chr9	141213431	2452849	0.0174	0.1789
chr10	135534747	3027168	0.0223	0.202
chr11	135006516	2887311	0.0214	0.1893
chr12	133851895	2359096	0.0176	0.1427
chr13	115169878	1600557	0.0139	0.1229
chr14	107349540	1300137	0.0121	0.1218
chr15	102531392	1790444	0.0175	0.1397
chr16	90354753	1715521	0.019	0.1508
chr17	81195210	1568229	0.0193	0.1573
chr18	78077248	1446946	0.0185	0.3085
chr19	59128983	873482	0.0148	0.2572
chr20	63025520	1253906	0.0199	0.1489
chr21	48129895	873618	0.0182	0.1487
chr22	51304566	365665	0.0071	0.0876
chrMT	16571	2476	0.1494	0.3831
chrX	155270560	3063851	0.0197	0.1625
chrY	59373566	151239	0.0025	0.0748

3. Results : Coverage across reference



4. Results : Coverage Histogram



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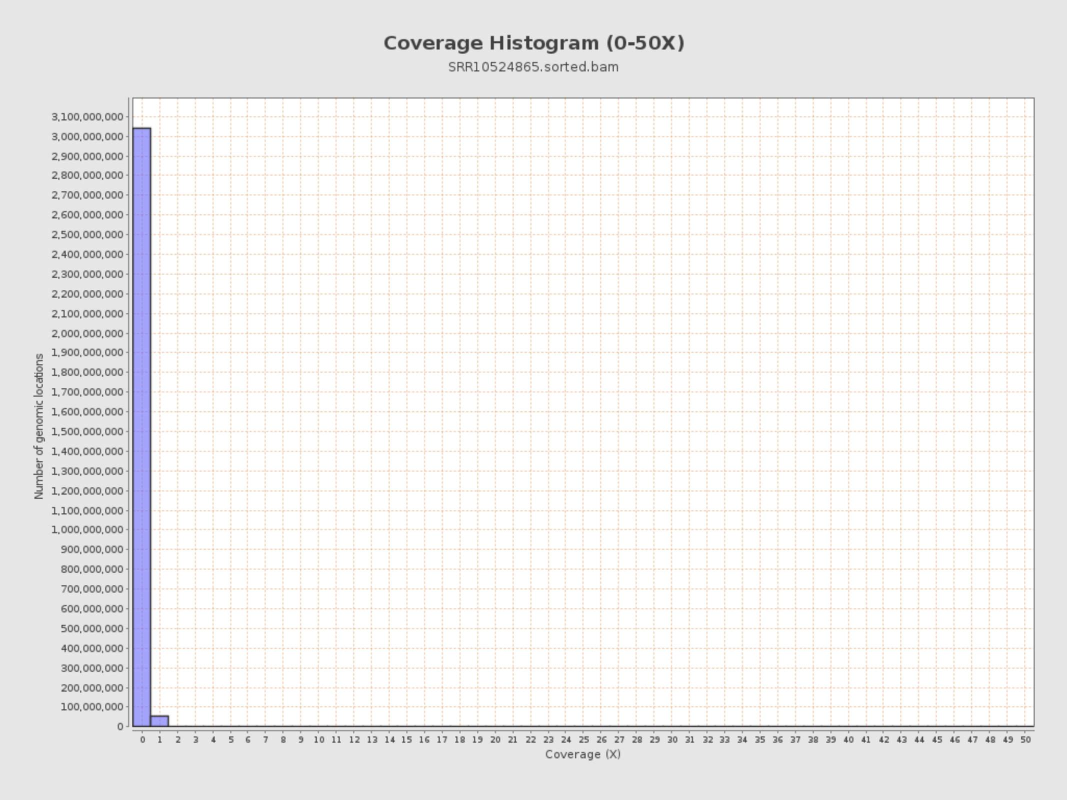
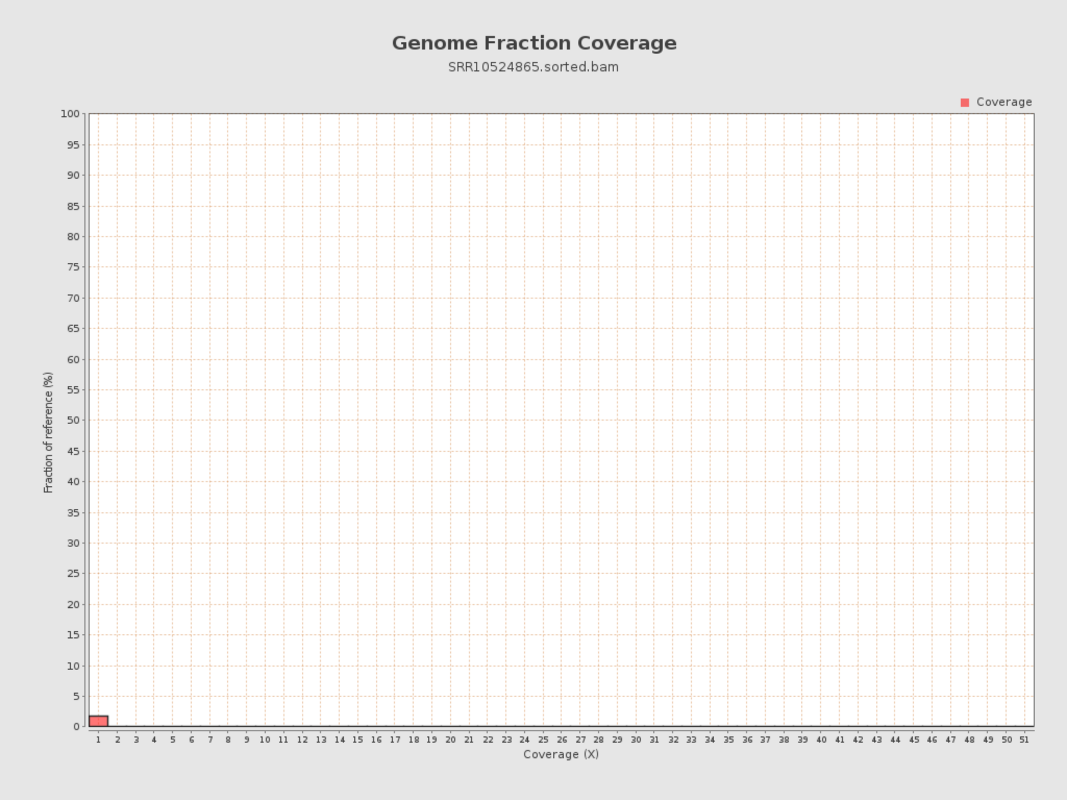
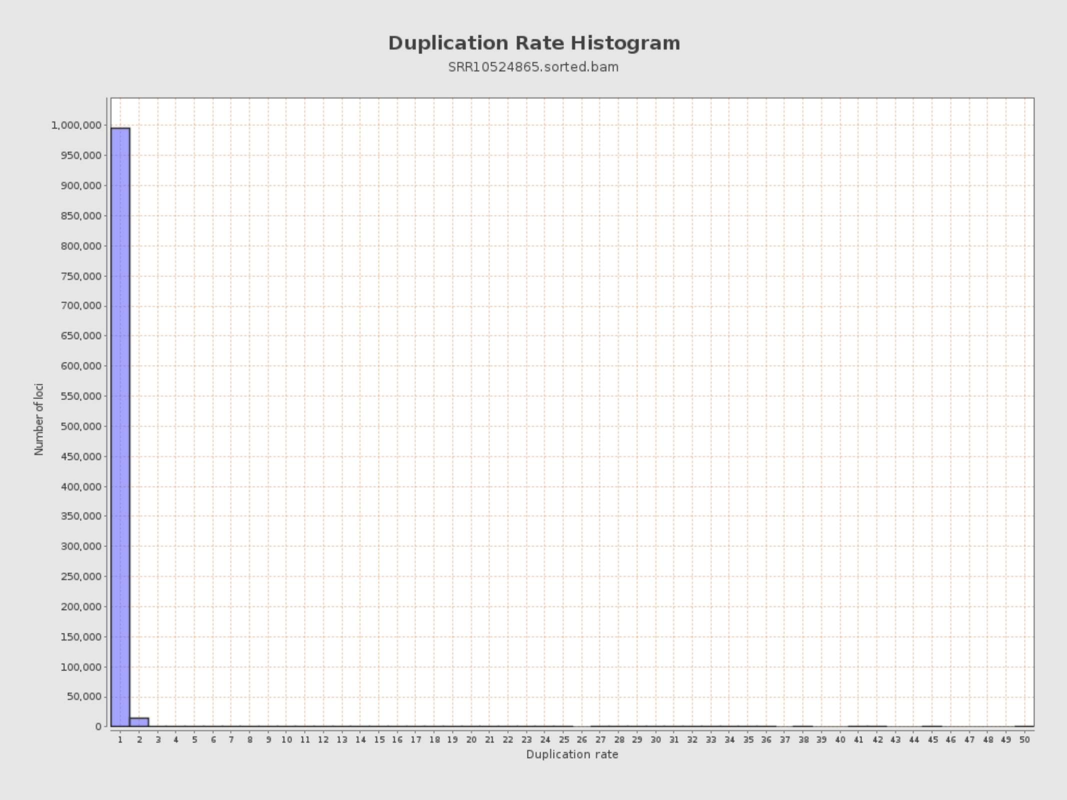
5. Results : Coverage Histogram (0-50X)



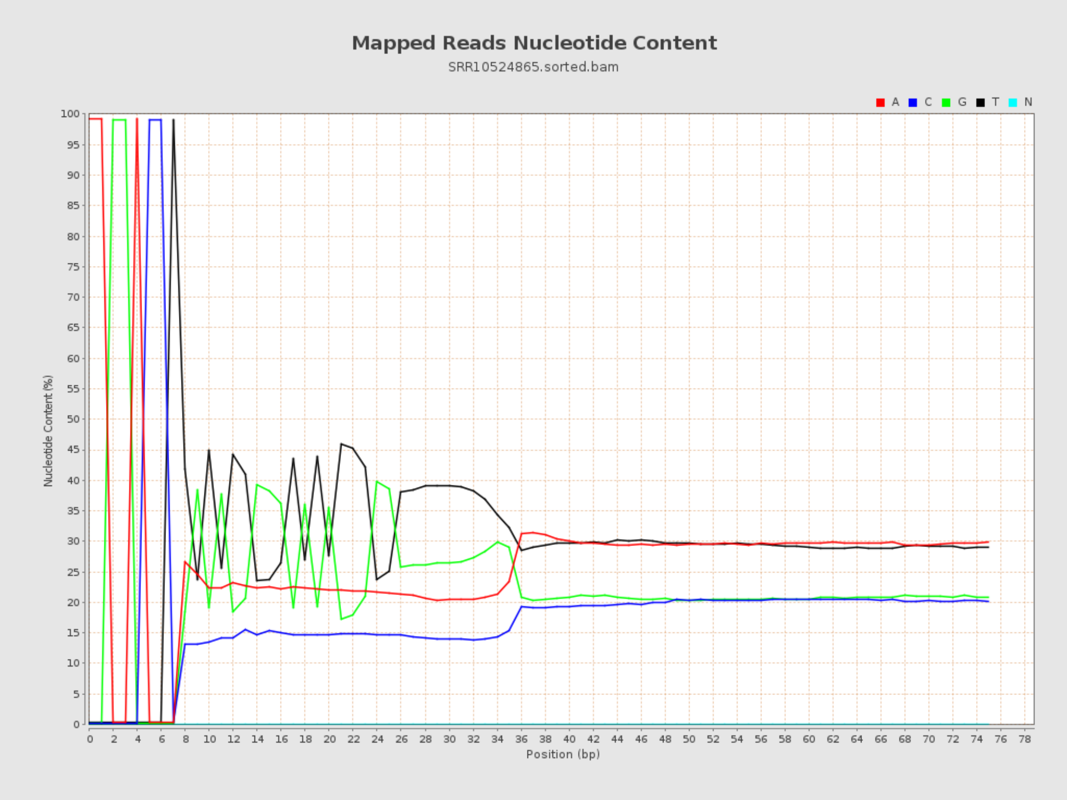
6. Results : Genome Fraction Coverage



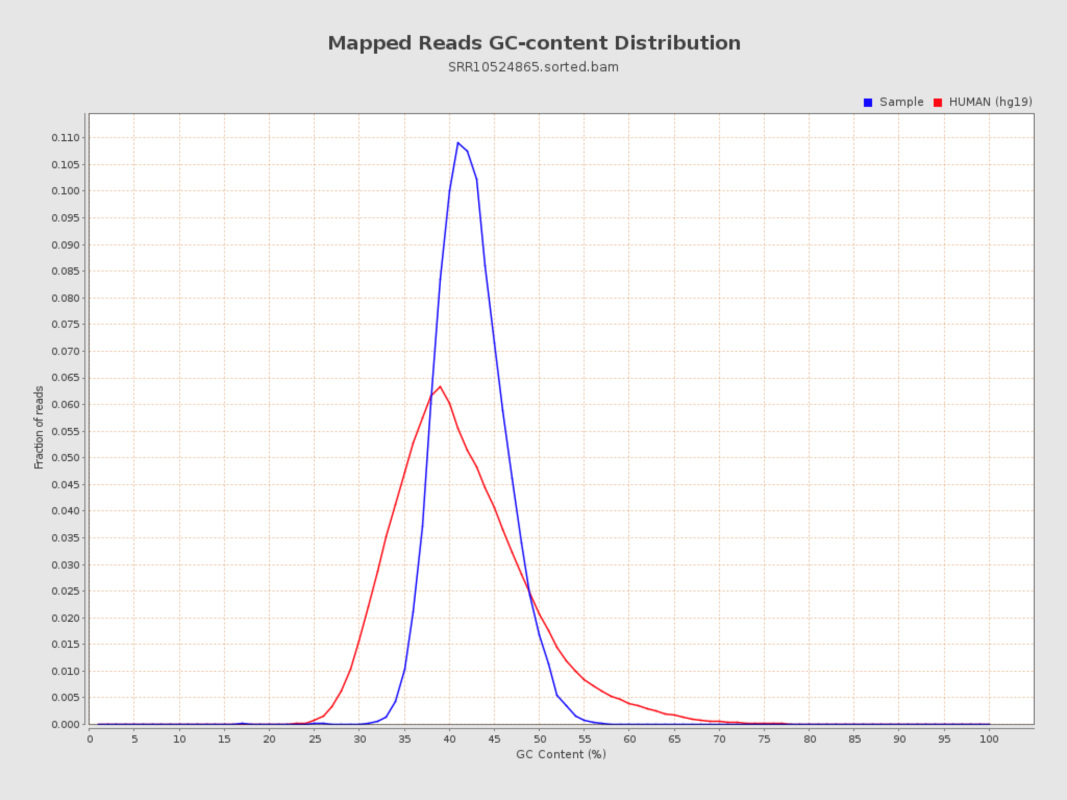
7. Results : Duplication Rate Histogram



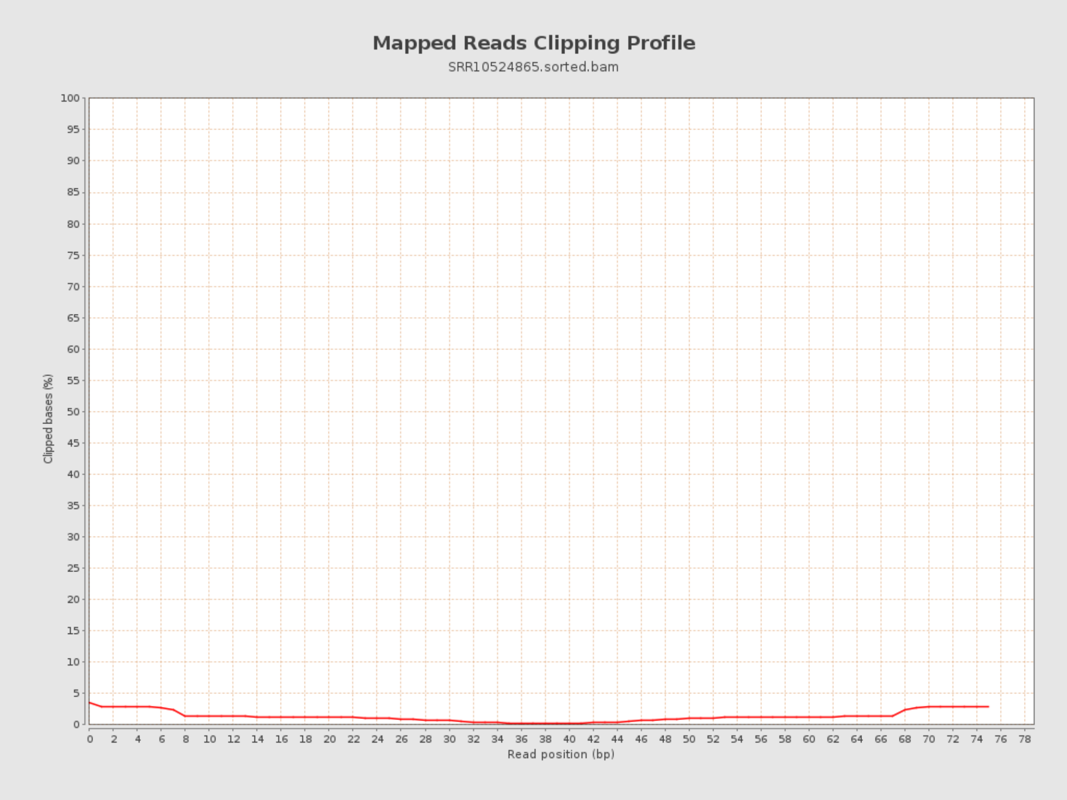
8. Results : Mapped Reads Nucleotide Content



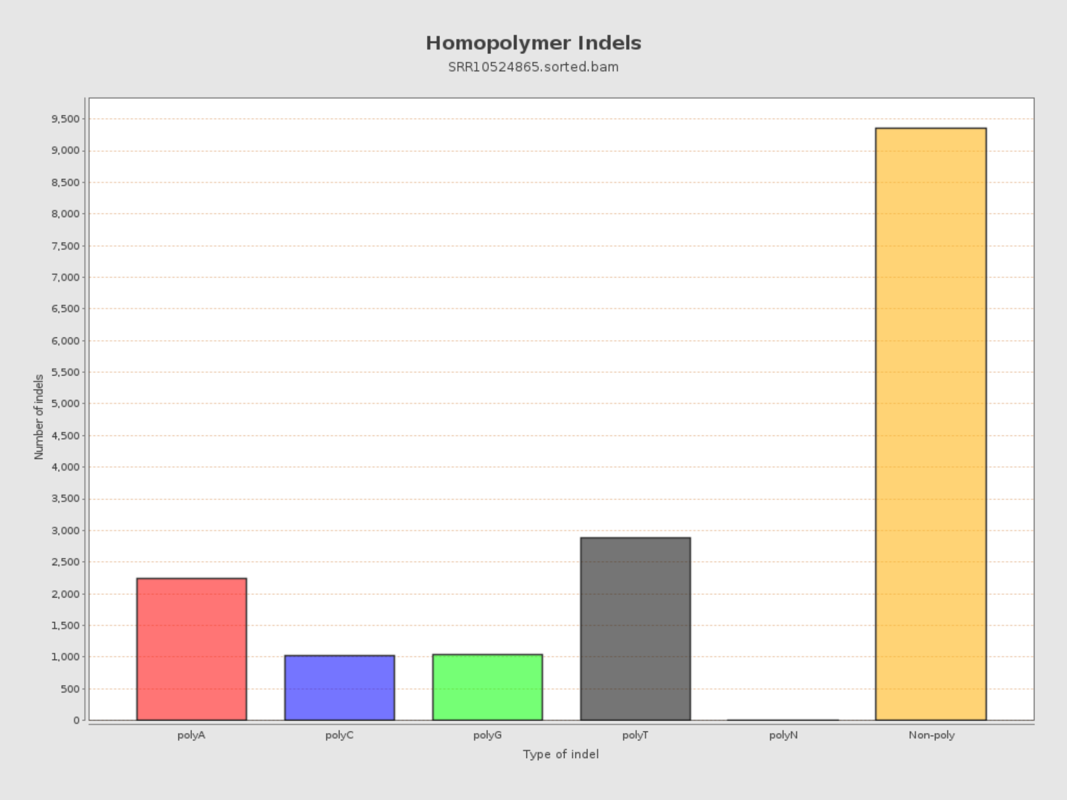
9. Results : Mapped Reads GC-content Distribution



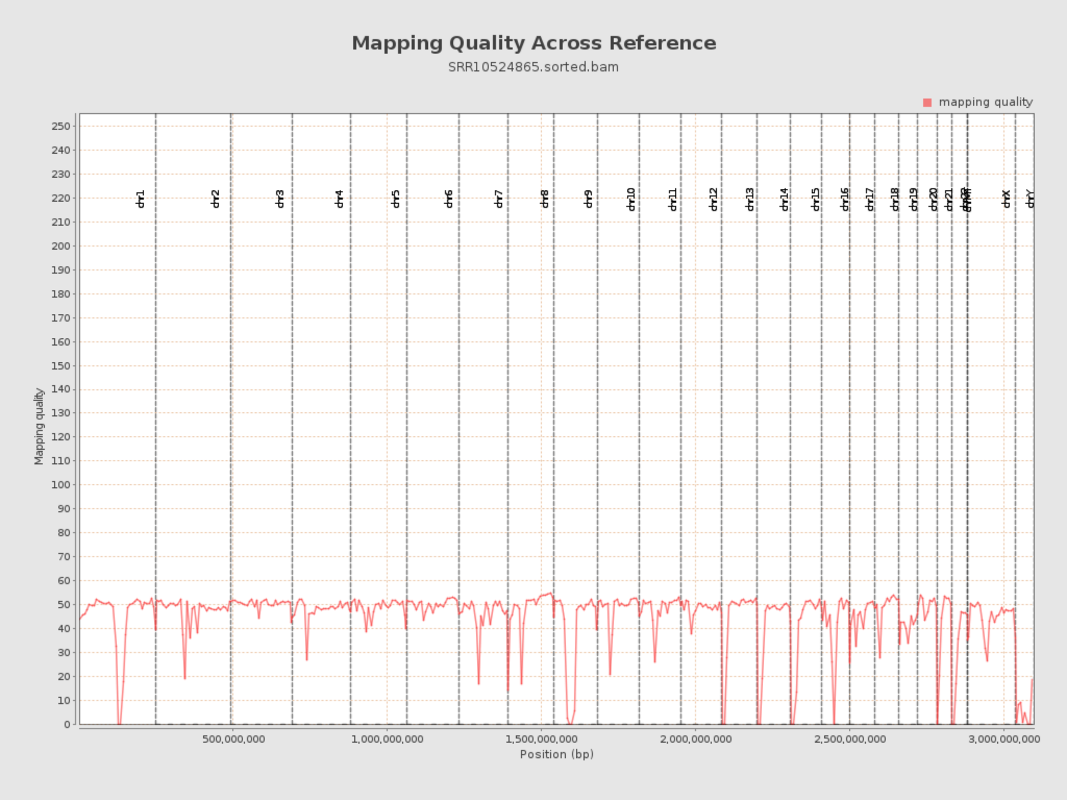
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram