Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:43:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524979.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_SRR10524979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524979.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:43:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,657,828
Mapped reads	1,540,430 / 92.92%
Unmapped reads	117,398 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,795 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	63,664 / 3.84%
Duplication rate	3.2%
Clipped reads	1,542,666 / 93.05%

2.2. ACGT Content

Number/percentage of A's	22,974,842 / 25.61%
Number/percentage of C's	17,356,758 / 19.35%
Number/percentage of T's	28,098,426 / 31.33%
Number/percentage of G's	21,265,621 / 23.71%
Number/percentage of N's	1,017 / 0%
GC Percentage	43.06%

2.3. Coverage

Mean	0.029

Standard Deviation	0.2544

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

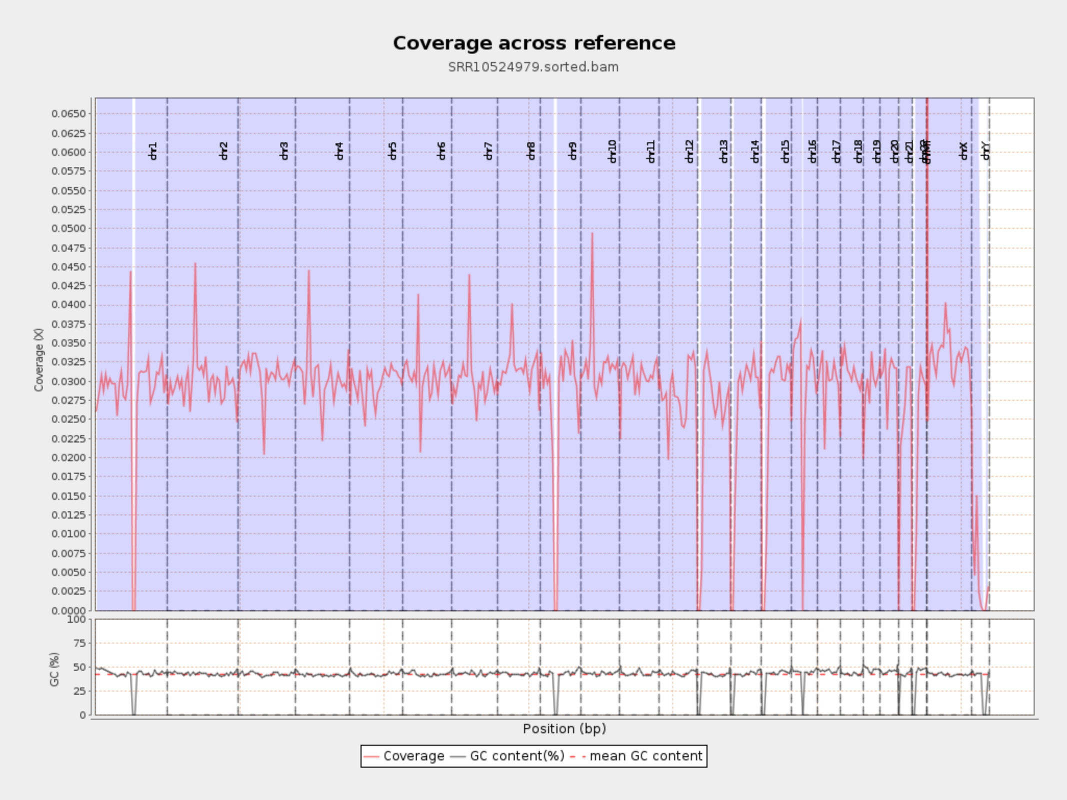
General error rate	0.49%
Mismatches	426,172
Insertions	5,011
Mapped reads with at least one insertion	0.32%
Deletions	15,601
Mapped reads with at least one deletion	1.01%
Homopolymer indels	44.82%

2.6. Chromosome stats

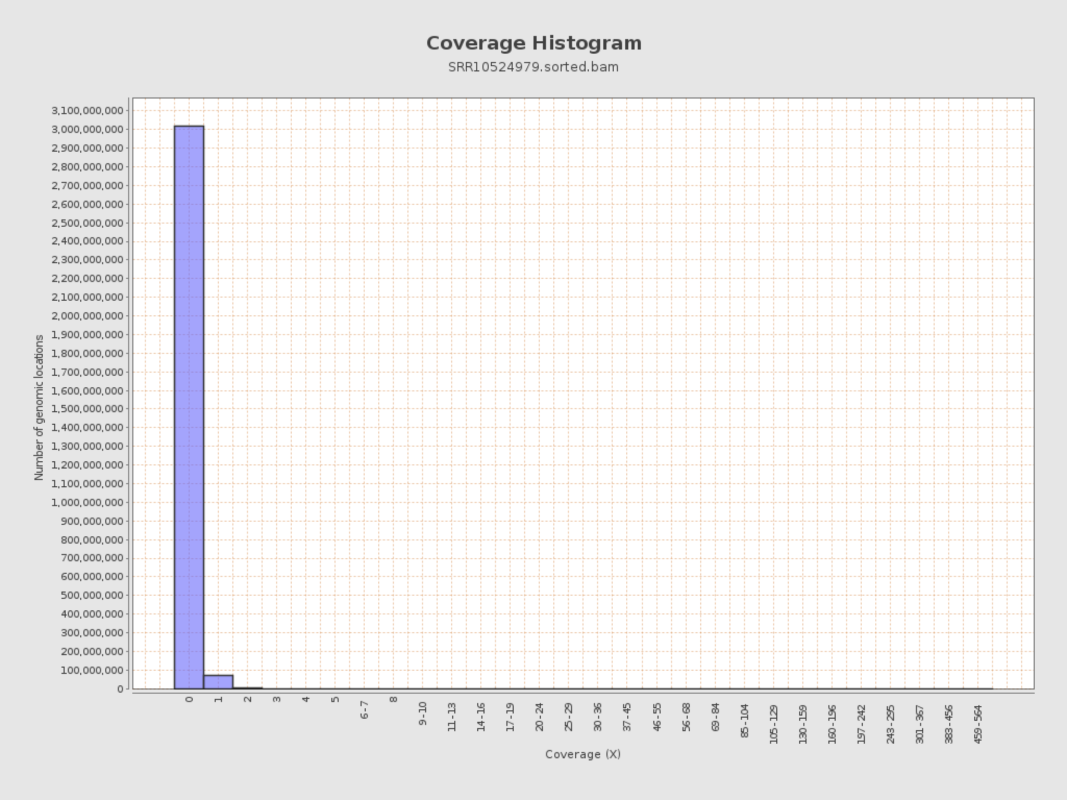
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7051020	0.0283	0.4181
chr2	243199373	7349101	0.0302	0.2962
chr3	198022430	6126367	0.0309	0.1934
chr4	191154276	5830743	0.0305	0.213
chr5	180915260	5406576	0.0299	0.1909
chr6	171115067	5246852	0.0307	0.232
chr7	159138663	4821117	0.0303	0.2979

chr8	146364022	4640882	0.0317	0.2678
chr9	141213431	3816106	0.027	0.2276
chr10	135534747	4386155	0.0324	0.2622
chr11	135006516	4179911	0.031	0.2535
chr12	133851895	3786424	0.0283	0.1874
chr13	115169878	2743091	0.0238	0.1714
chr14	107349540	2741060	0.0255	0.1797
chr15	102531392	2609908	0.0255	0.1853
chr16	90354753	2662917	0.0295	0.1998
chr17	81195210	2430081	0.0299	0.2091
chr18	78077248	2440596	0.0313	0.3799
chr19	59128983	1753219	0.0297	0.3031
chr20	63025520	1926872	0.0306	0.1959
chr21	48129895	1183106	0.0246	0.1892
chr22	51304566	1061045	0.0207	0.1571
chrMT	16571	100441	6.0613	4.0547
chrX	155270560	5172624	0.0333	0.2182
chrY	59373566	257308	0.0043	0.1242

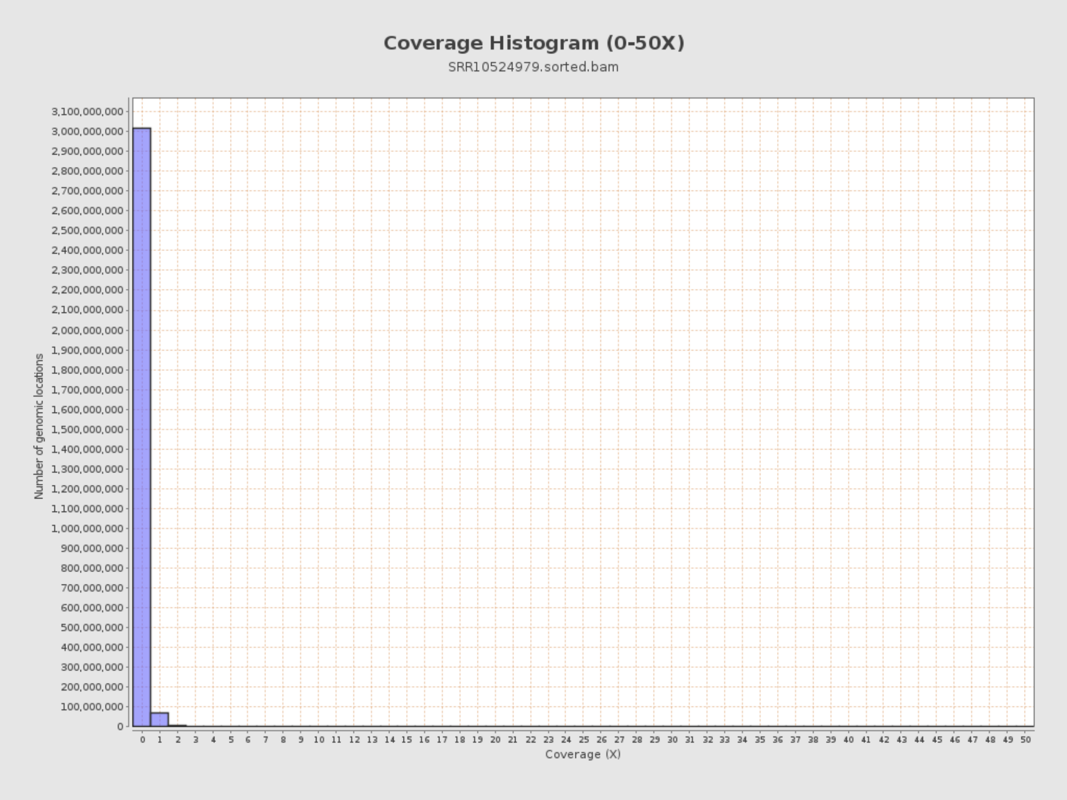
3. Results : Coverage across reference



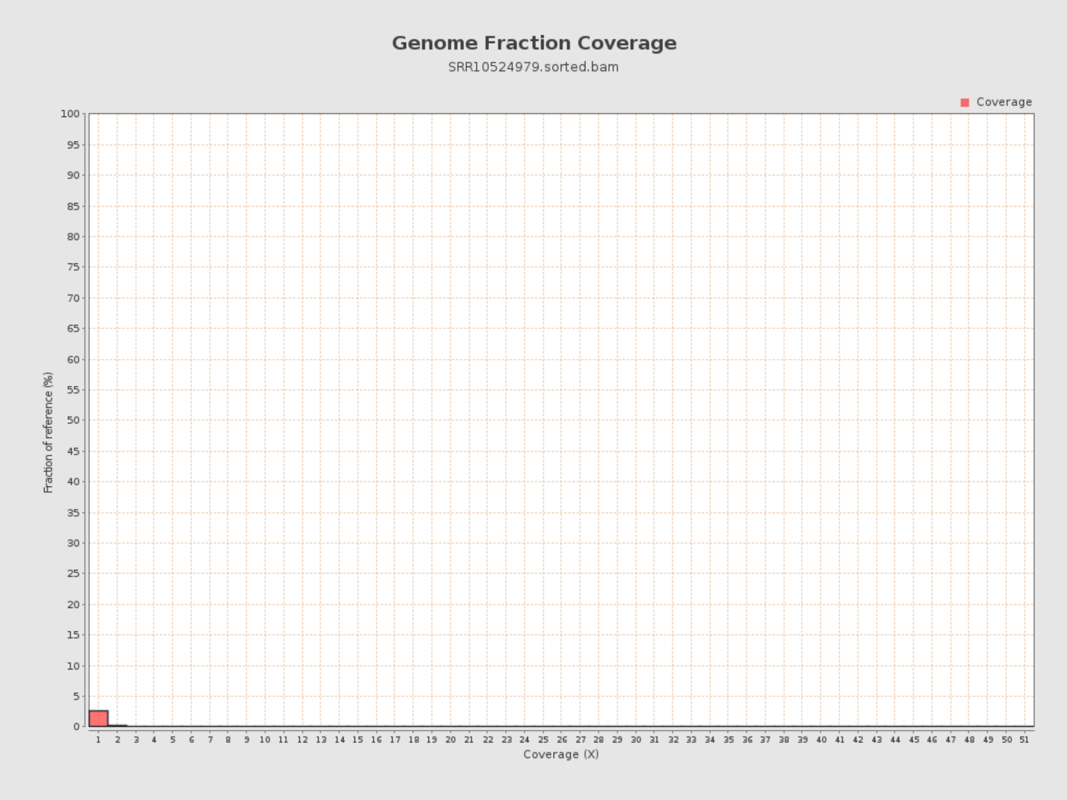
4. Results : Coverage Histogram



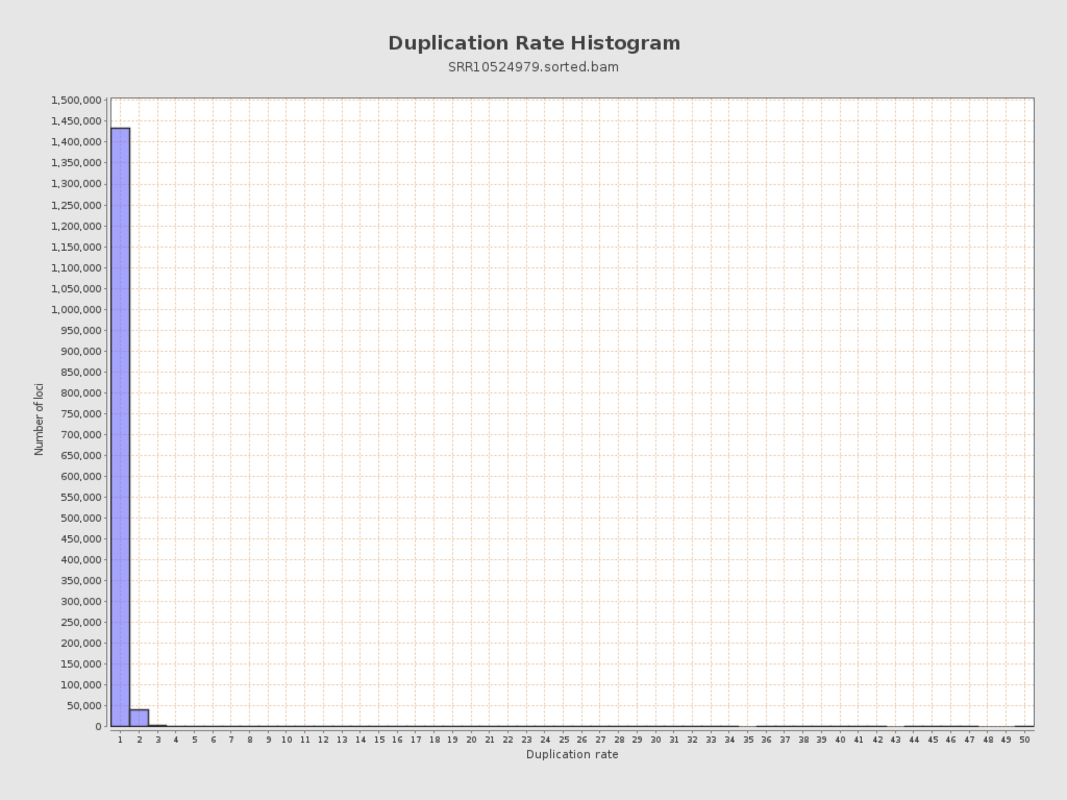
5. Results : Coverage Histogram (0-50X)



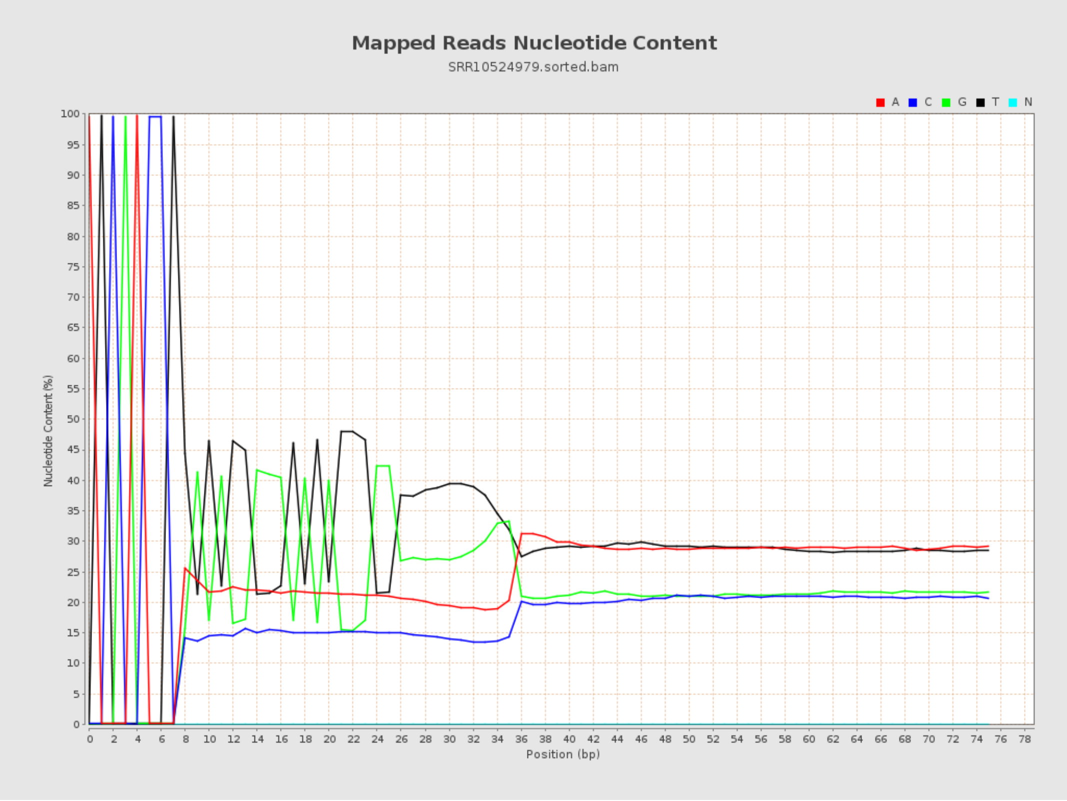
6. Results : Genome Fraction Coverage



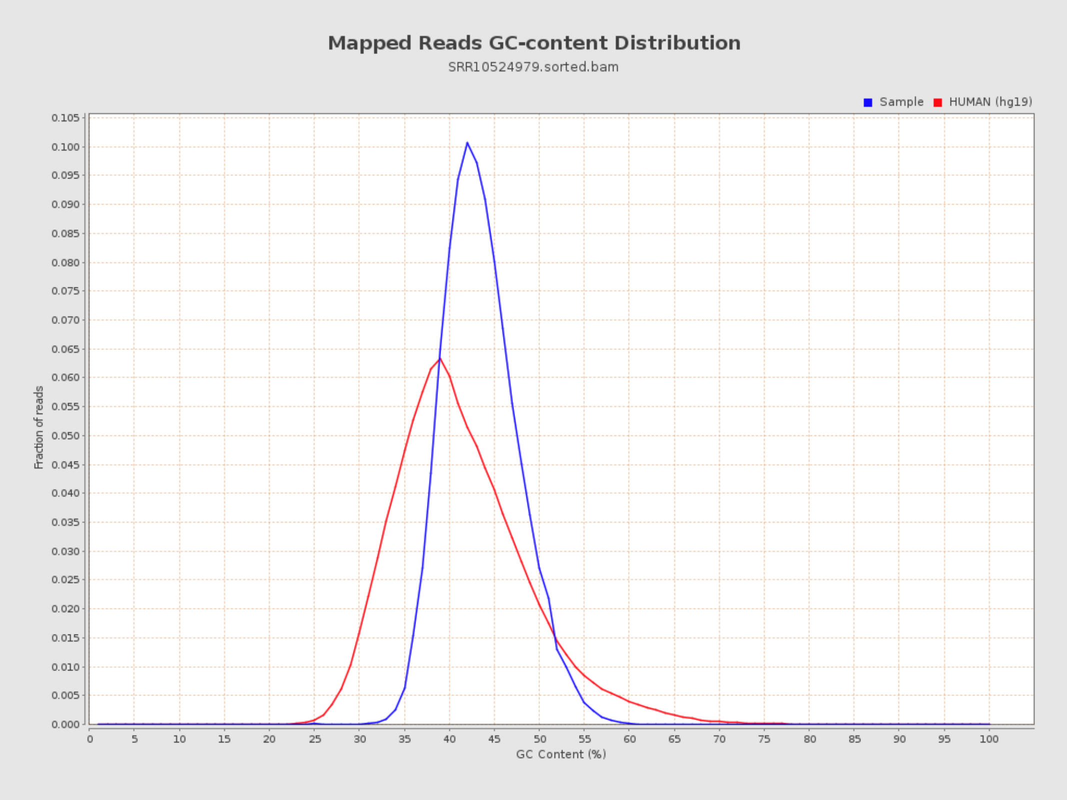
7. Results : Duplication Rate Histogram



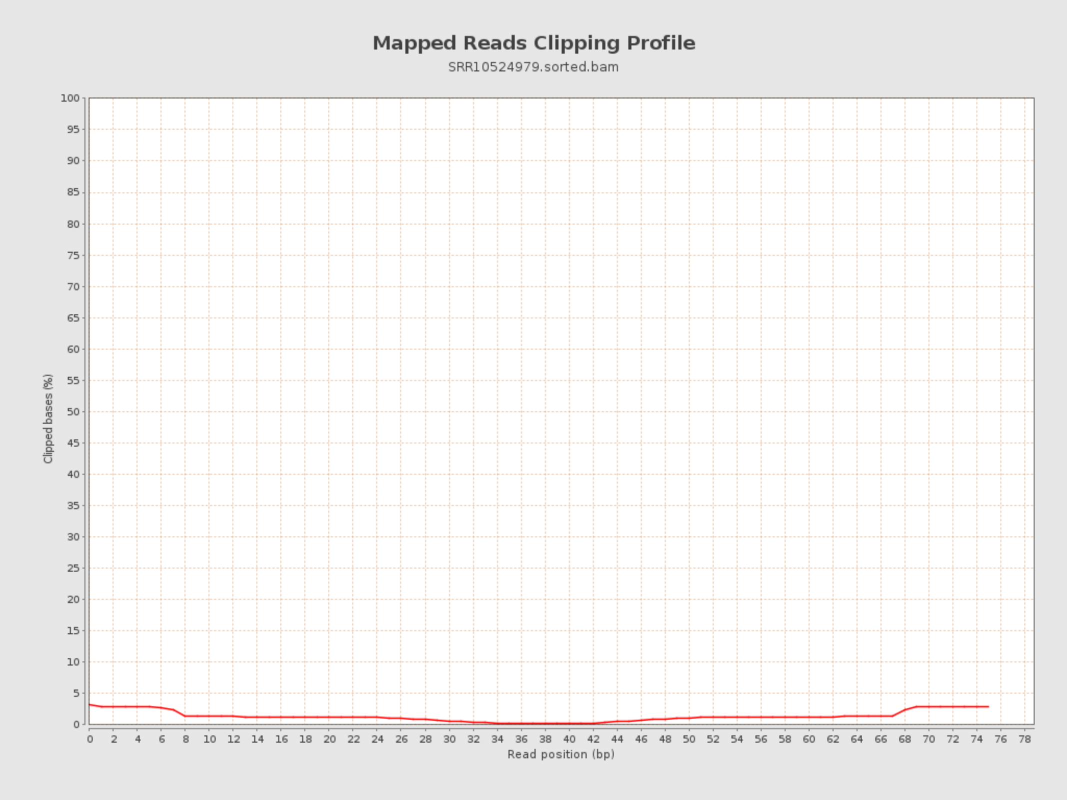
8. Results : Mapped Reads Nucleotide Content



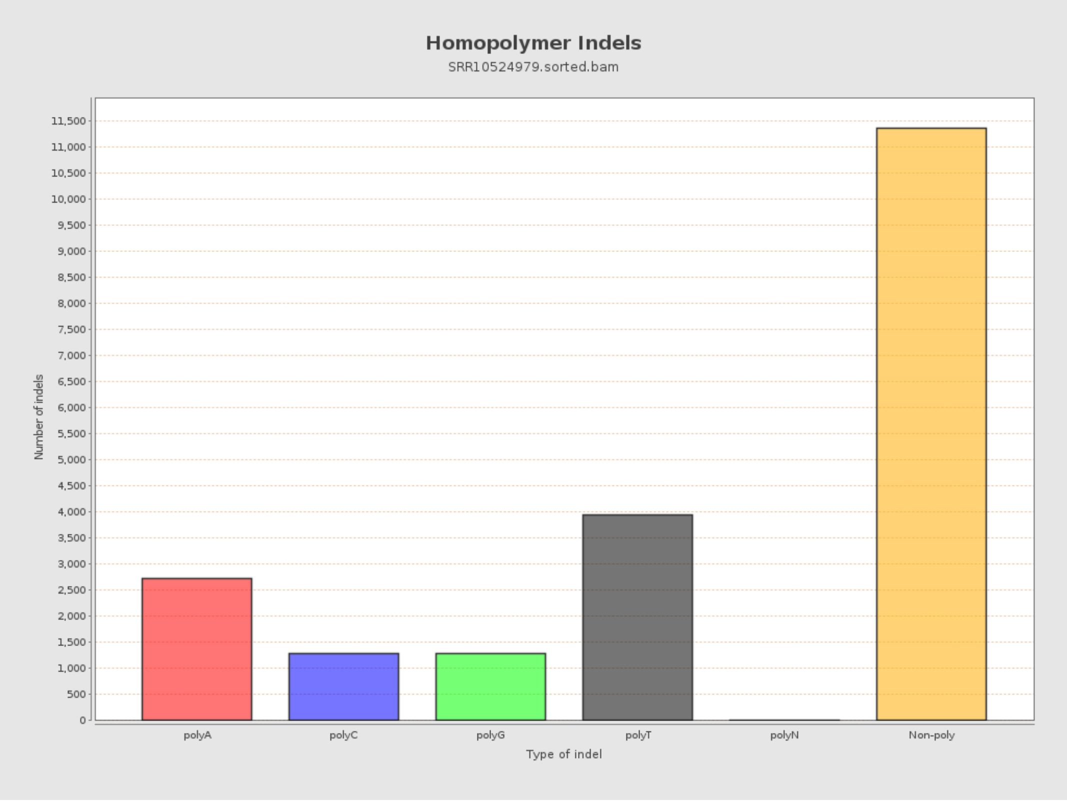
9. Results : Mapped Reads GC-content Distribution



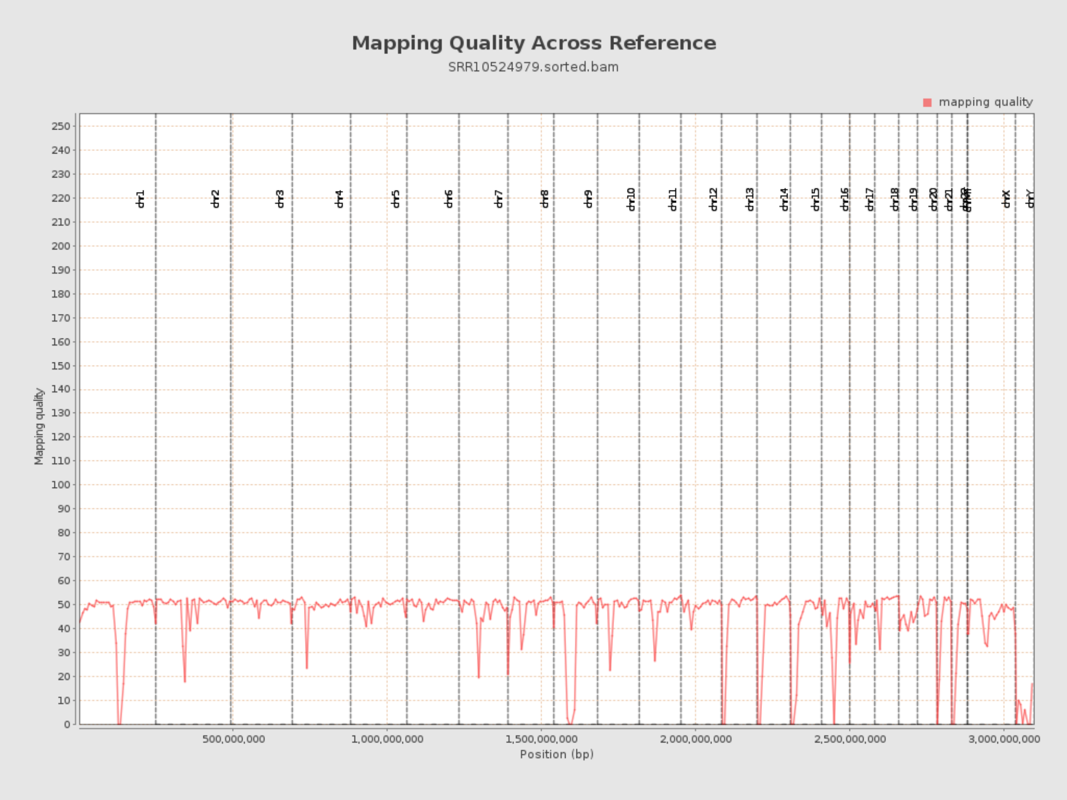
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram