Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:05:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524823.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_SRR10524823 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524823.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:05:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524823.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,526,159
Mapped reads	1,378,494 / 90.32%
Unmapped reads	147,665 / 9.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,452 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	51,023 / 3.34%
Duplication rate	2.84%
Clipped reads	1,378,114 / 90.3%

2.2. ACGT Content

Number/percentage of A's	17,609,791 / 22.7%
Number/percentage of C's	14,830,991 / 19.12%
Number/percentage of T's	25,966,716 / 33.48%
Number/percentage of G's	19,154,176 / 24.69%
Number/percentage of N's	8,745 / 0.01%
GC Percentage	43.81%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2239

2.4. Mapping Quality

Mean Mapping Quality	44.37

2.5. Mismatches and indels

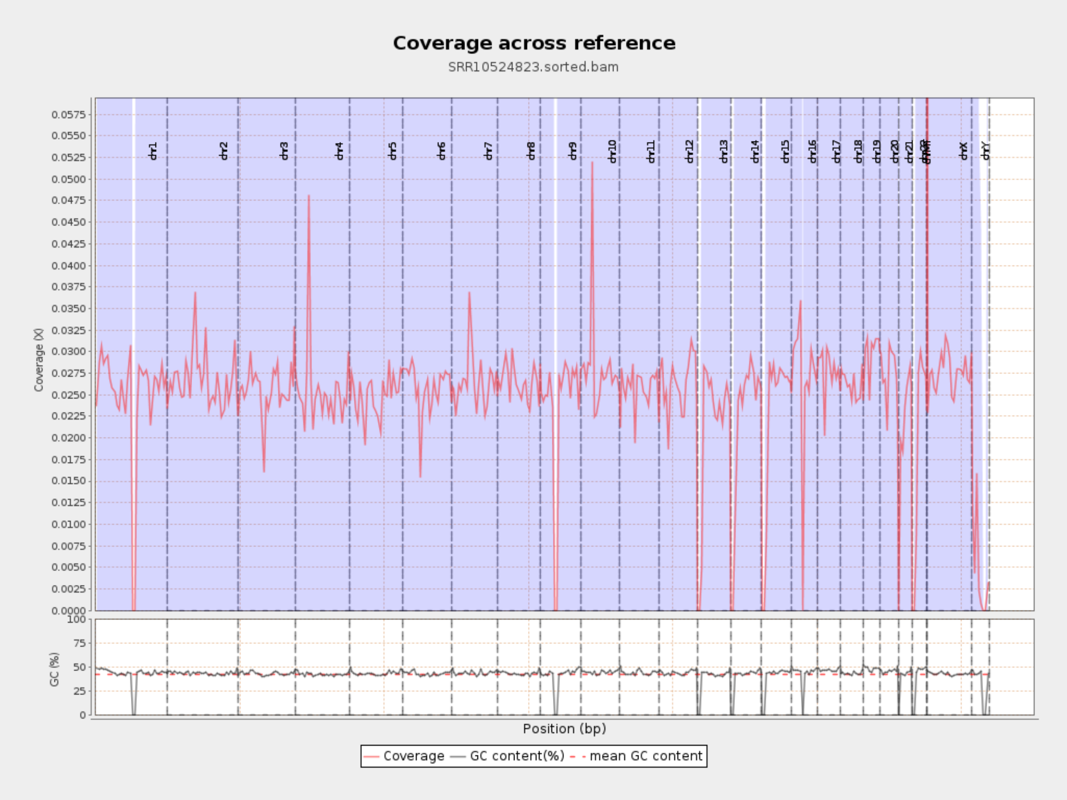
General error rate	0.52%
Mismatches	394,686
Insertions	5,978
Mapped reads with at least one insertion	0.43%
Deletions	14,801
Mapped reads with at least one deletion	1.07%
Homopolymer indels	40.54%

2.6. Chromosome stats

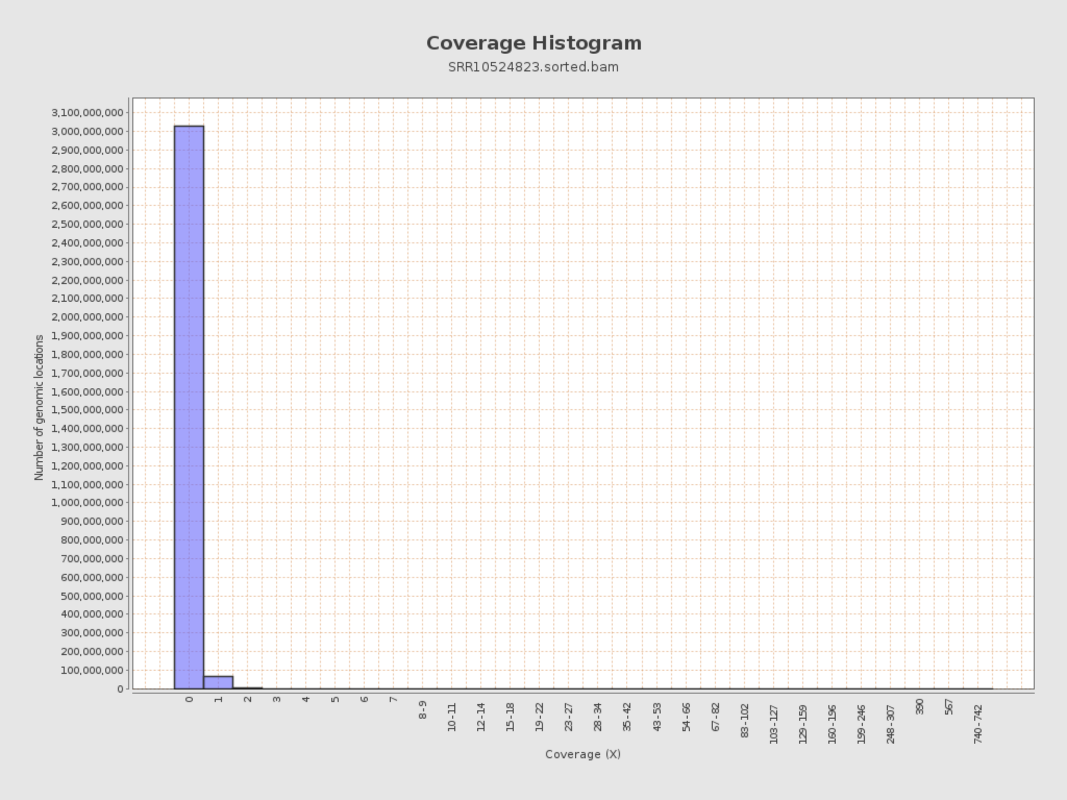
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6190849	0.0248	0.2643
chr2	243199373	6518188	0.0268	0.3664
chr3	198022430	5053117	0.0255	0.1787
chr4	191154276	4895859	0.0256	0.2044
chr5	180915260	4520884	0.025	0.1726
chr6	171115067	4411046	0.0258	0.1886
chr7	159138663	4236750	0.0266	0.2604

chr8	146364022	3863222	0.0264	0.1991
chr9	141213431	3294144	0.0233	0.2044
chr10	135534747	3832375	0.0283	0.2708
chr11	135006516	3504668	0.026	0.2051
chr12	133851895	3527903	0.0264	0.1795
chr13	115169878	2396154	0.0208	0.1583
chr14	107349540	2342230	0.0218	0.1638
chr15	102531392	2258948	0.022	0.1642
chr16	90354753	2396001	0.0265	0.1961
chr17	81195210	2257583	0.0278	0.1917
chr18	78077248	2033474	0.026	0.2862
chr19	59128983	1763869	0.0298	0.238
chr20	63025520	1719660	0.0273	0.19
chr21	48129895	1028373	0.0214	0.1778
chr22	51304566	989340	0.0193	0.1531
chrMT	16571	11616	0.701	0.9865
chrX	155270560	4281269	0.0276	0.1974
chrY	59373566	266726	0.0045	0.1337

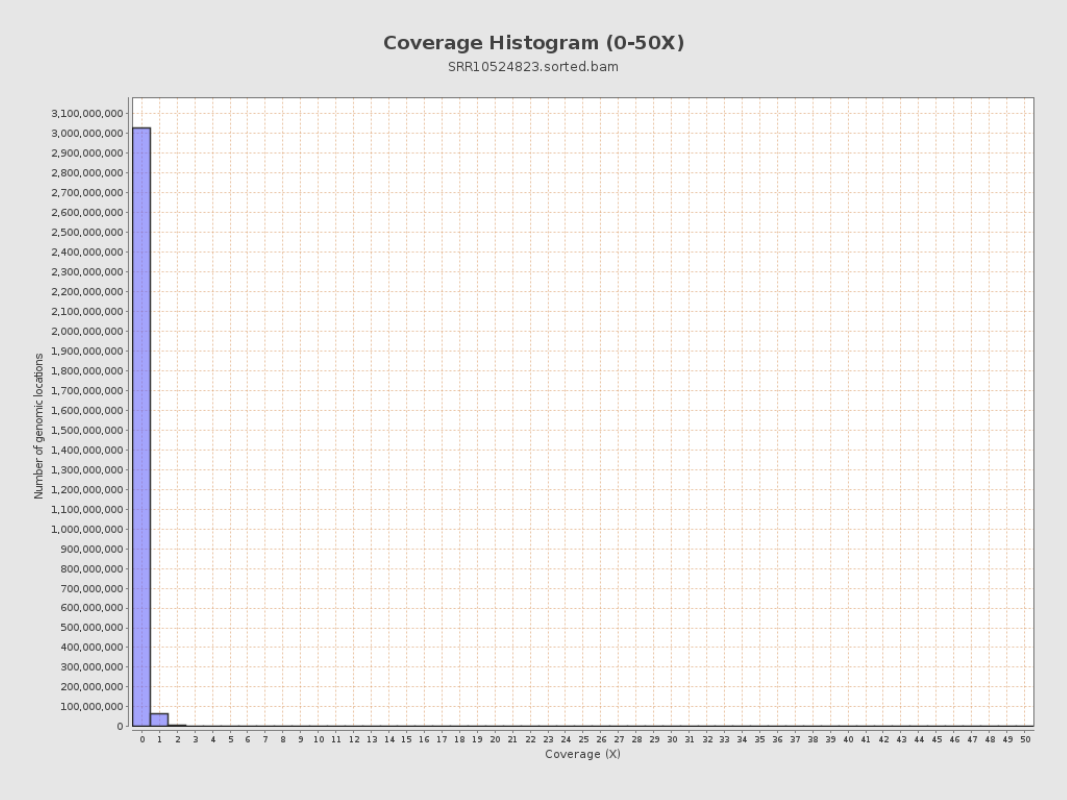
3. Results : Coverage across reference



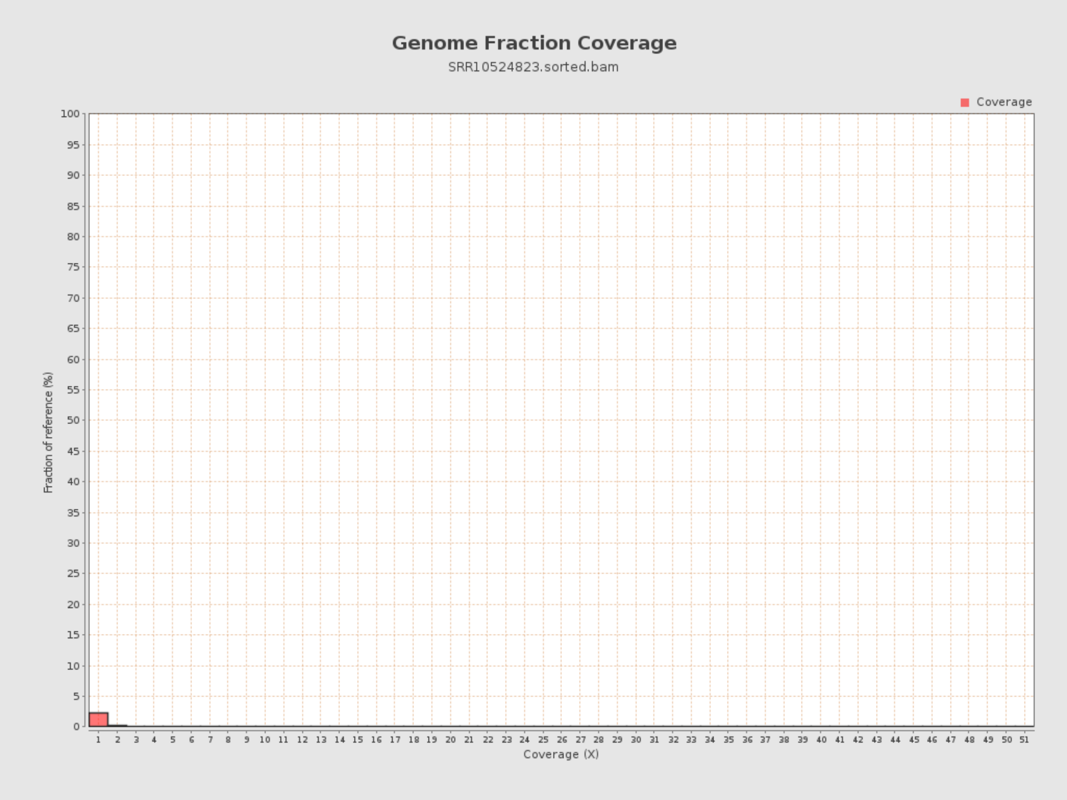
4. Results : Coverage Histogram



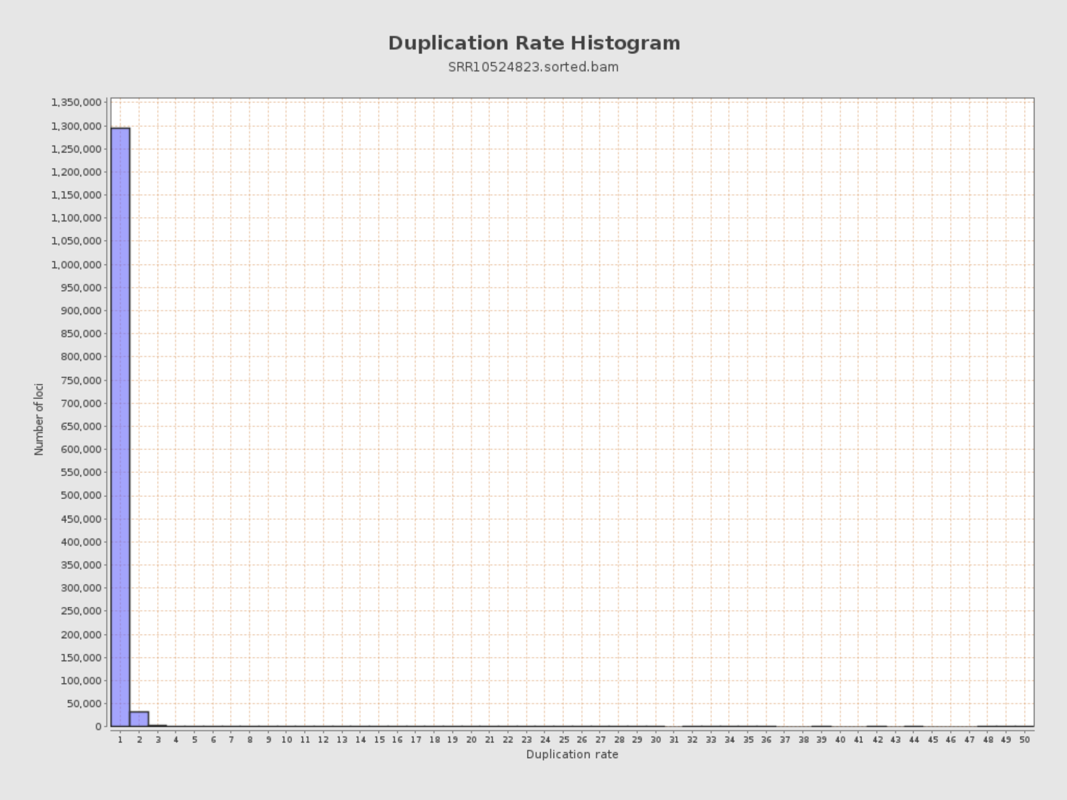
5. Results : Coverage Histogram (0-50X)



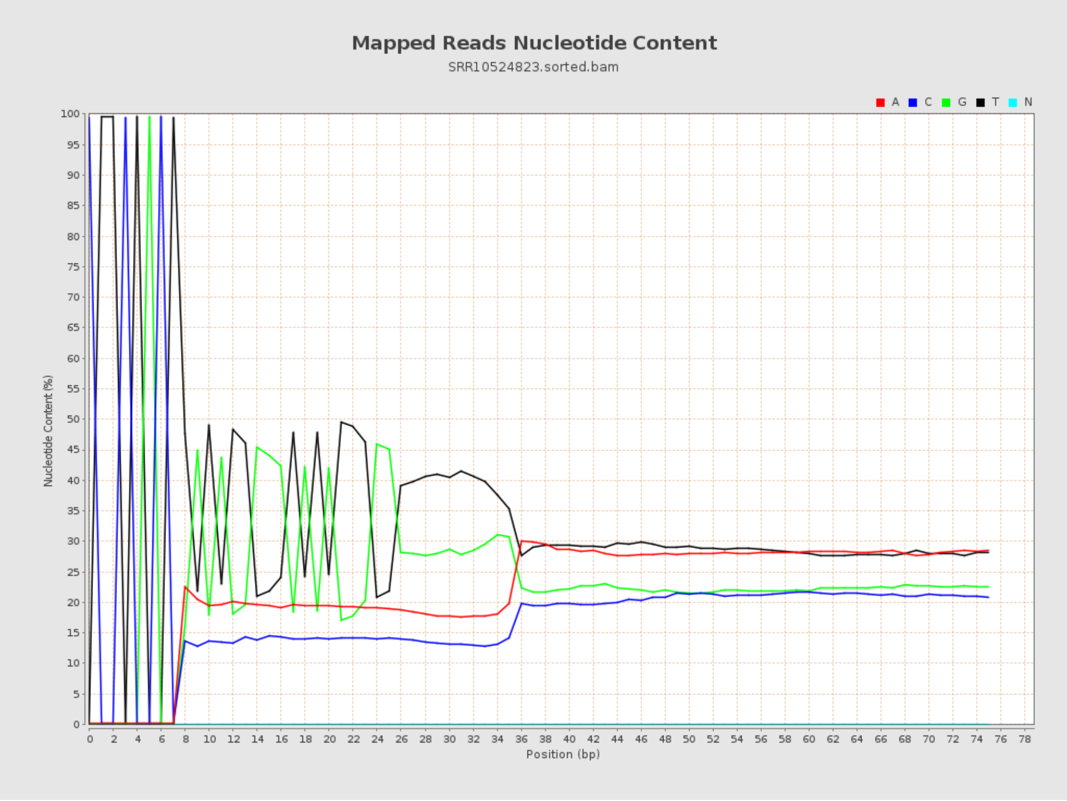
6. Results : Genome Fraction Coverage



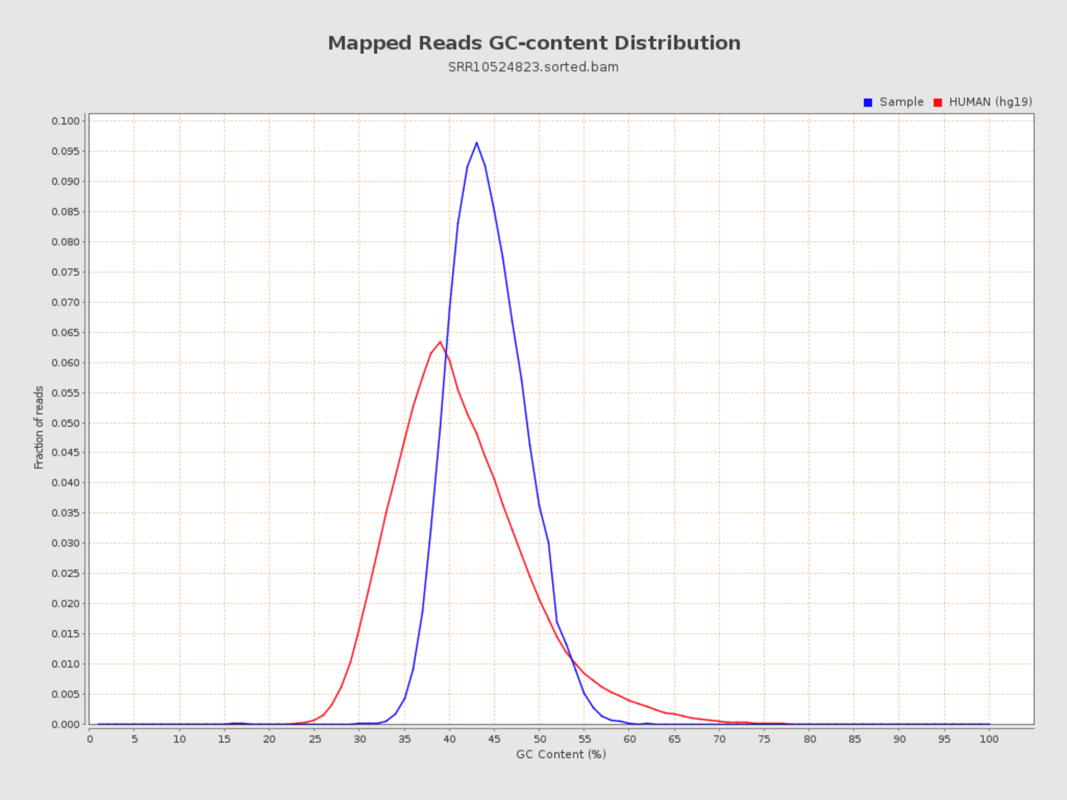
7. Results : Duplication Rate Histogram



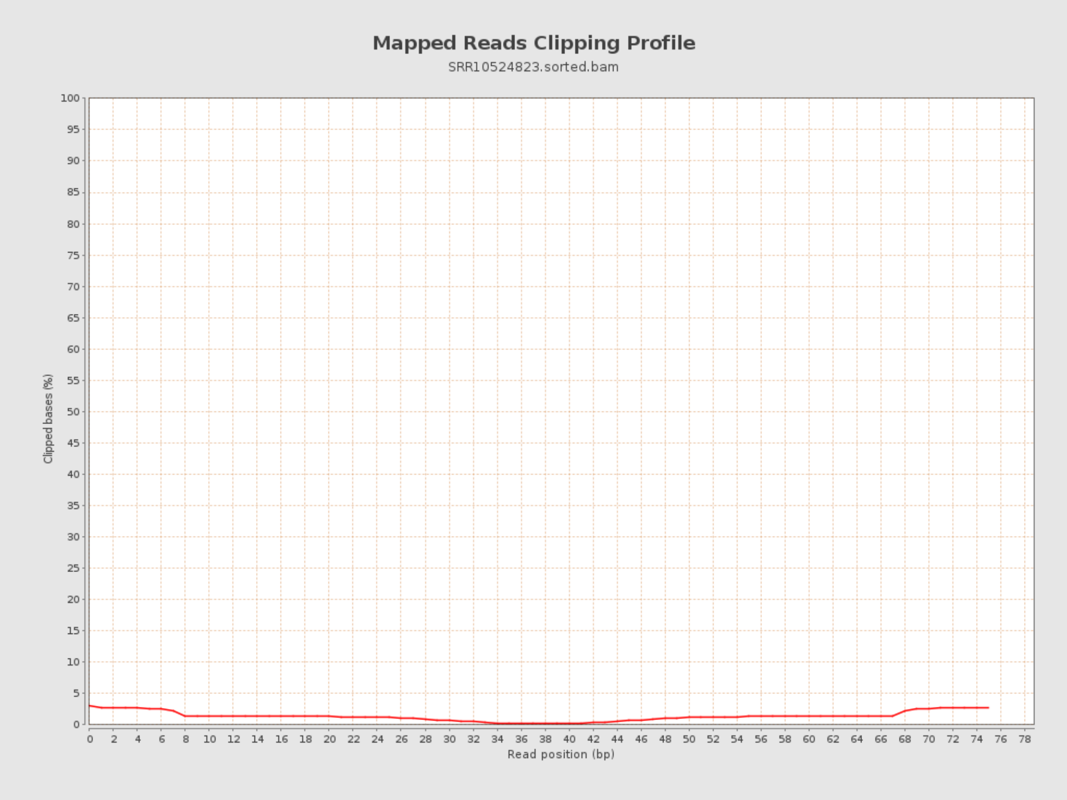
8. Results : Mapped Reads Nucleotide Content



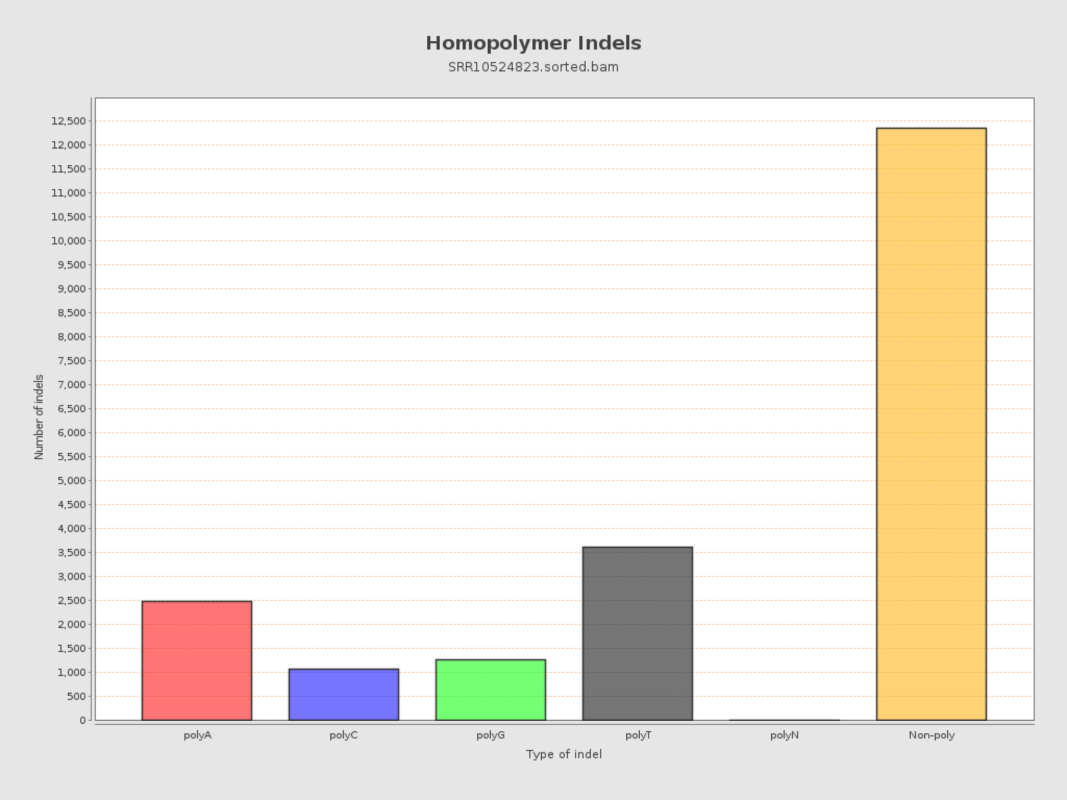
9. Results : Mapped Reads GC-content Distribution



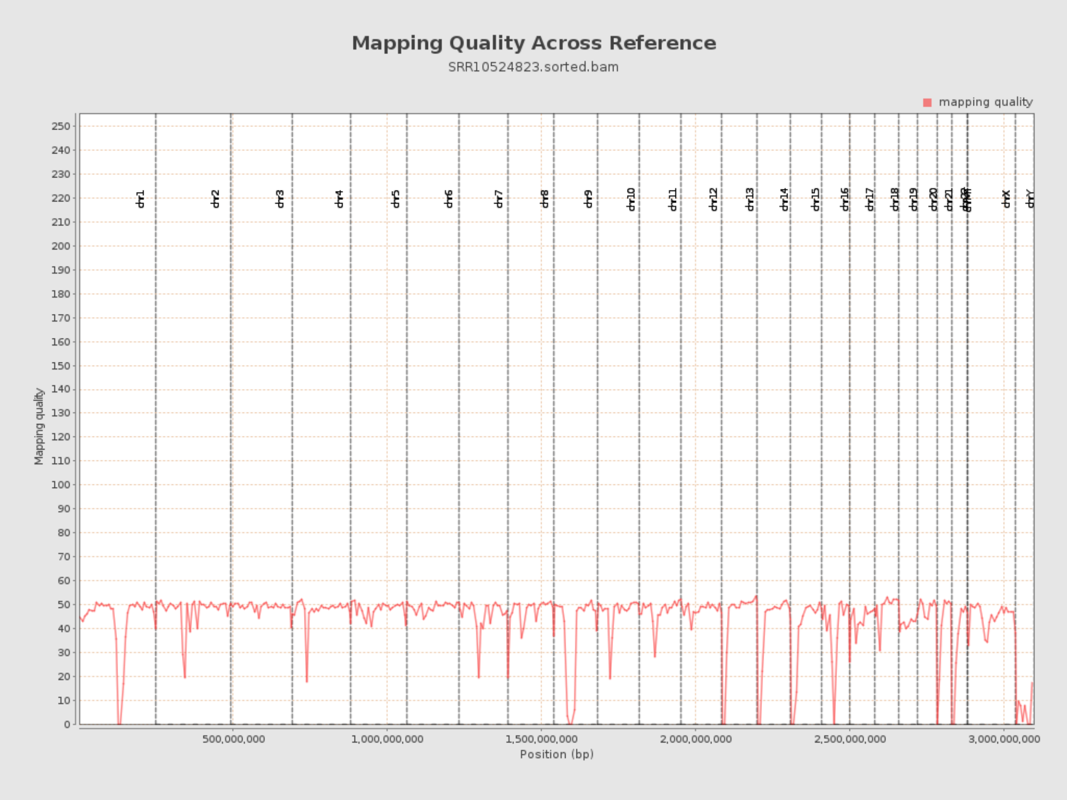
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram