Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:14:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524333.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_SRR10524333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524333.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:14:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524333.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	580,860
Mapped reads	523,748 / 90.17%
Unmapped reads	57,112 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,933 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	11,889 / 2.05%
Duplication rate	1.74%
Clipped reads	524,302 / 90.26%

2.2. ACGT Content

Number/percentage of A's	7,703,380 / 25.64%
Number/percentage of C's	5,387,089 / 17.93%
Number/percentage of T's	9,926,097 / 33.04%
Number/percentage of G's	7,022,525 / 23.38%
Number/percentage of N's	657 / 0%
GC Percentage	41.31%

2.3. Coverage

Mean	0.0097

Standard Deviation	0.1256

2.4. Mapping Quality

Mean Mapping Quality	45.34

2.5. Mismatches and indels

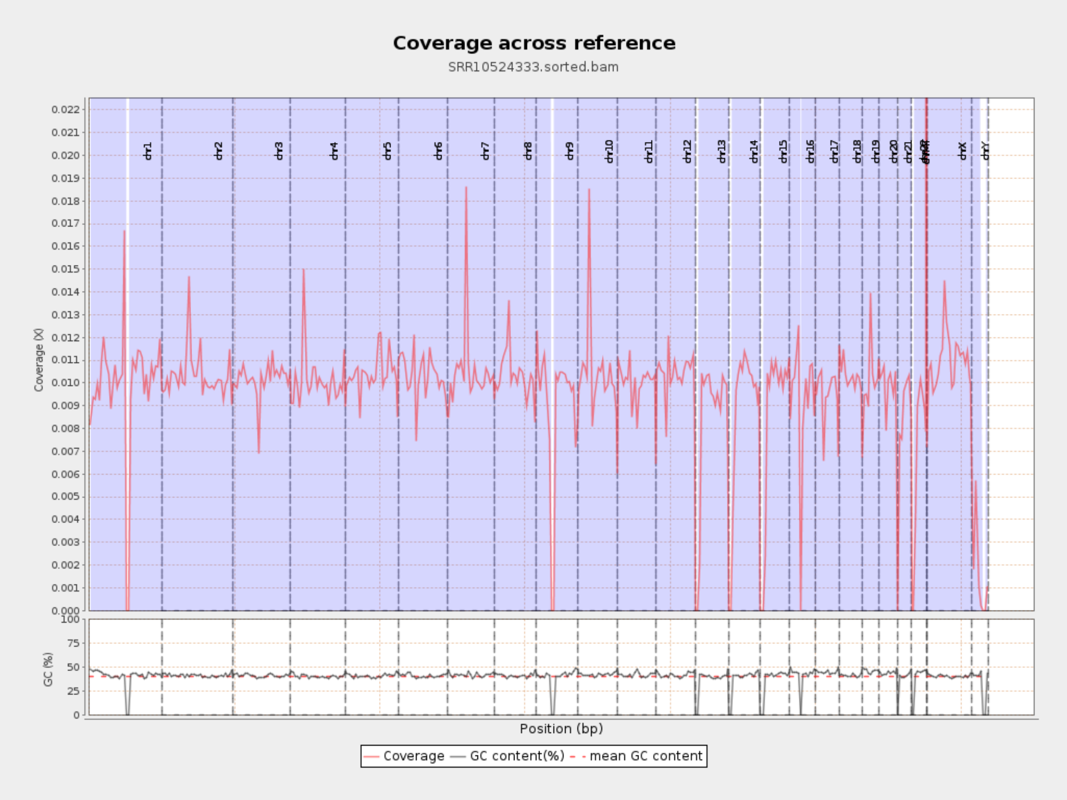
General error rate	0.53%
Mismatches	156,602
Insertions	2,038
Mapped reads with at least one insertion	0.39%
Deletions	6,399
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.05%

2.6. Chromosome stats

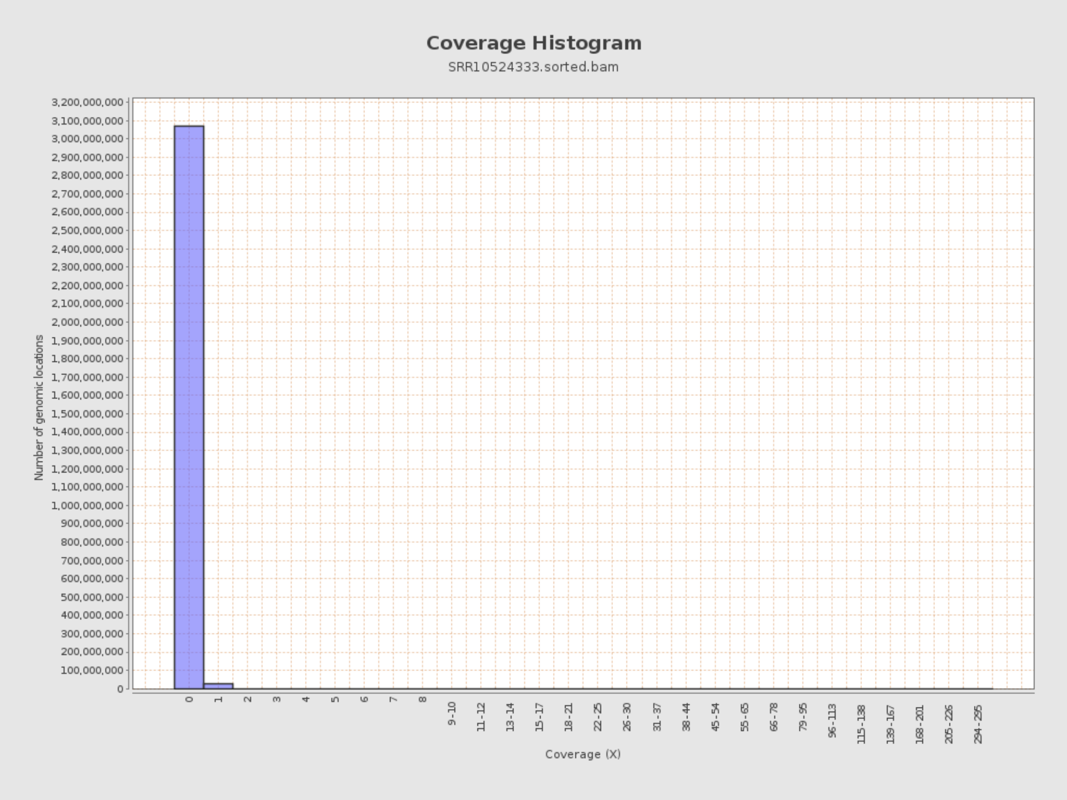
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2455470	0.0099	0.1844
chr2	243199373	2520820	0.0104	0.1601
chr3	198022430	2014267	0.0102	0.1045
chr4	191154276	1930945	0.0101	0.107
chr5	180915260	1881006	0.0104	0.1059
chr6	171115067	1770886	0.0103	0.1104
chr7	159138663	1684241	0.0106	0.1591

chr8	146364022	1512974	0.0103	0.1382
chr9	141213431	1243683	0.0088	0.1113
chr10	135534747	1428139	0.0105	0.1254
chr11	135006516	1346250	0.01	0.1105
chr12	133851895	1397195	0.0104	0.1064
chr13	115169878	940262	0.0082	0.0937
chr14	107349540	922126	0.0086	0.0972
chr15	102531392	853385	0.0083	0.096
chr16	90354753	829724	0.0092	0.1026
chr17	81195210	762511	0.0094	0.1024
chr18	78077248	808413	0.0104	0.1576
chr19	59128983	601878	0.0102	0.1568
chr20	63025520	618099	0.0098	0.1035
chr21	48129895	393190	0.0082	0.0958
chr22	51304566	334095	0.0065	0.0836
chrMT	16571	6900	0.4164	0.6848
chrX	155270560	1698791	0.0109	0.1127
chrY	59373566	94706	0.0016	0.0575

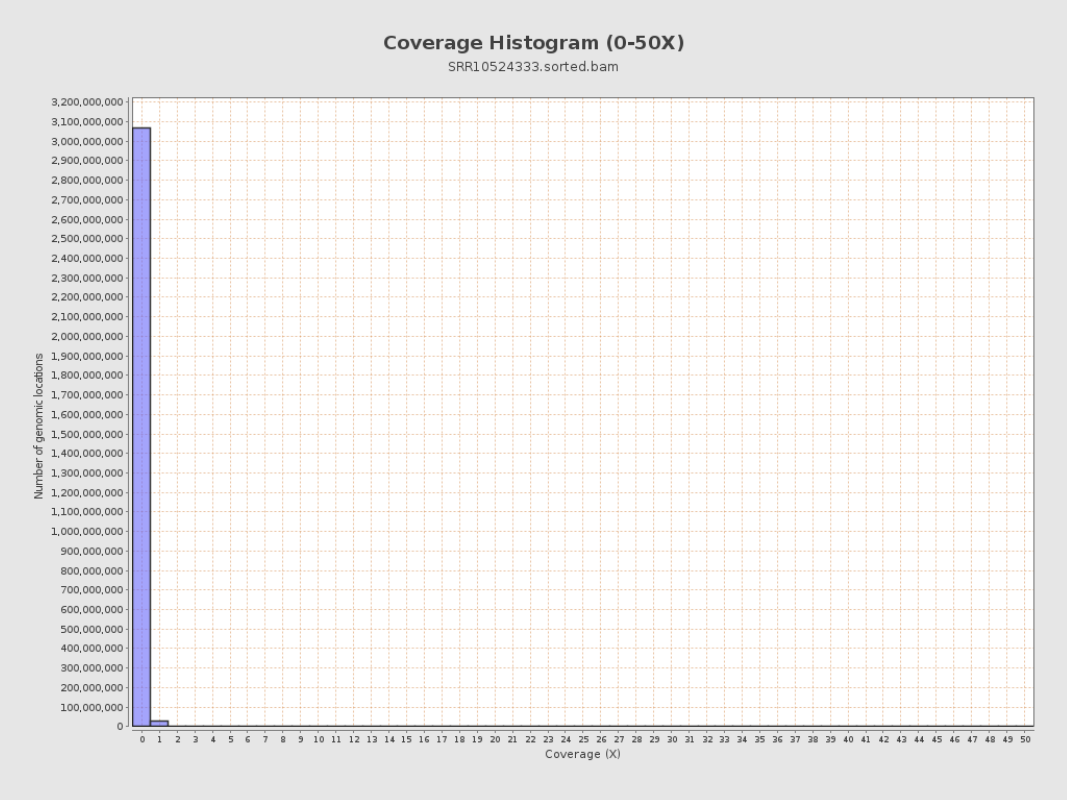
3. Results : Coverage across reference



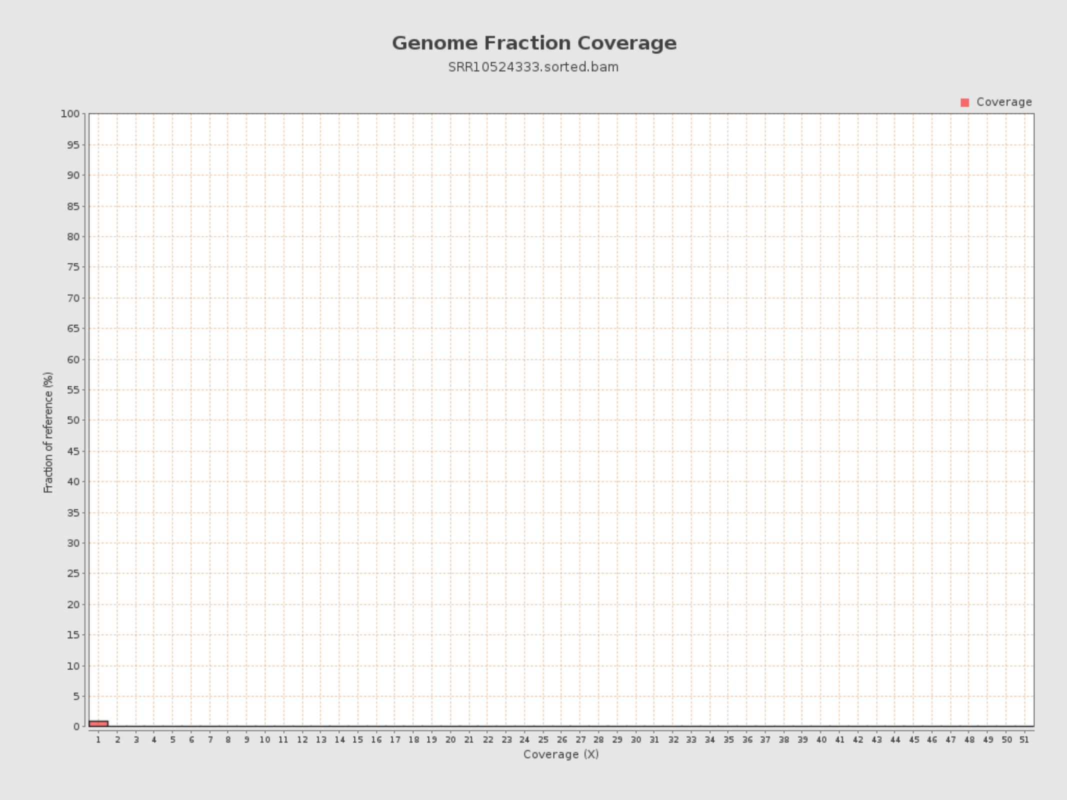
4. Results : Coverage Histogram



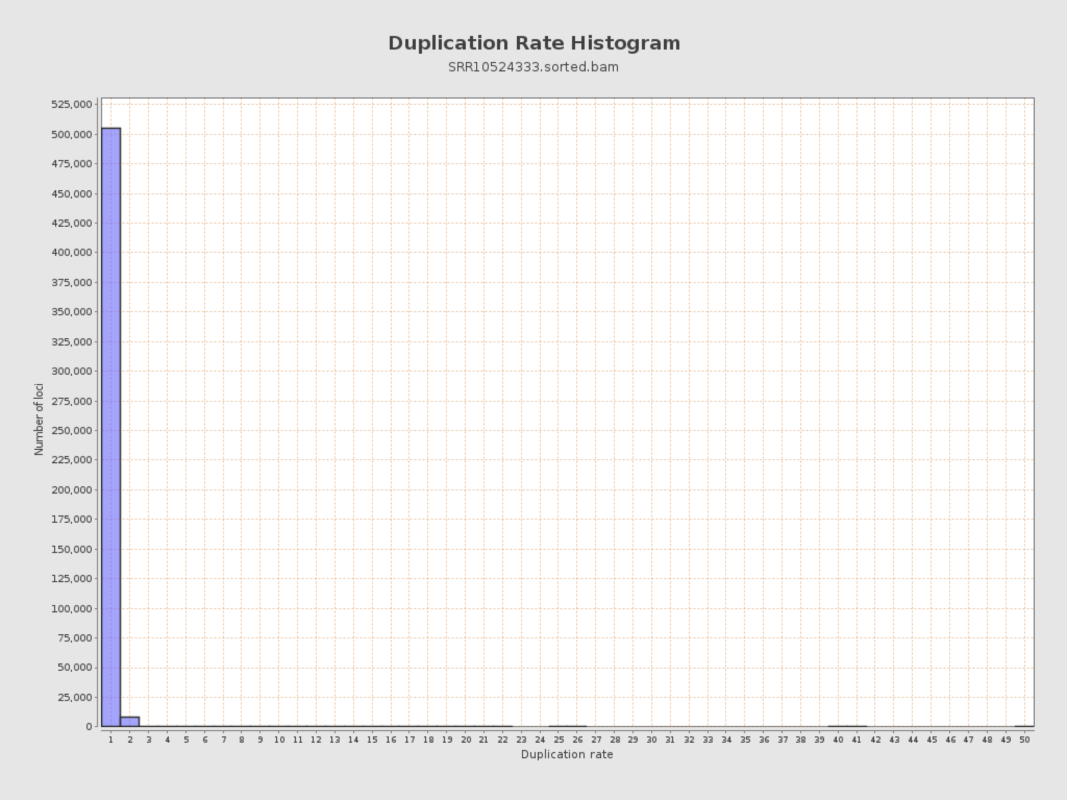
5. Results : Coverage Histogram (0-50X)



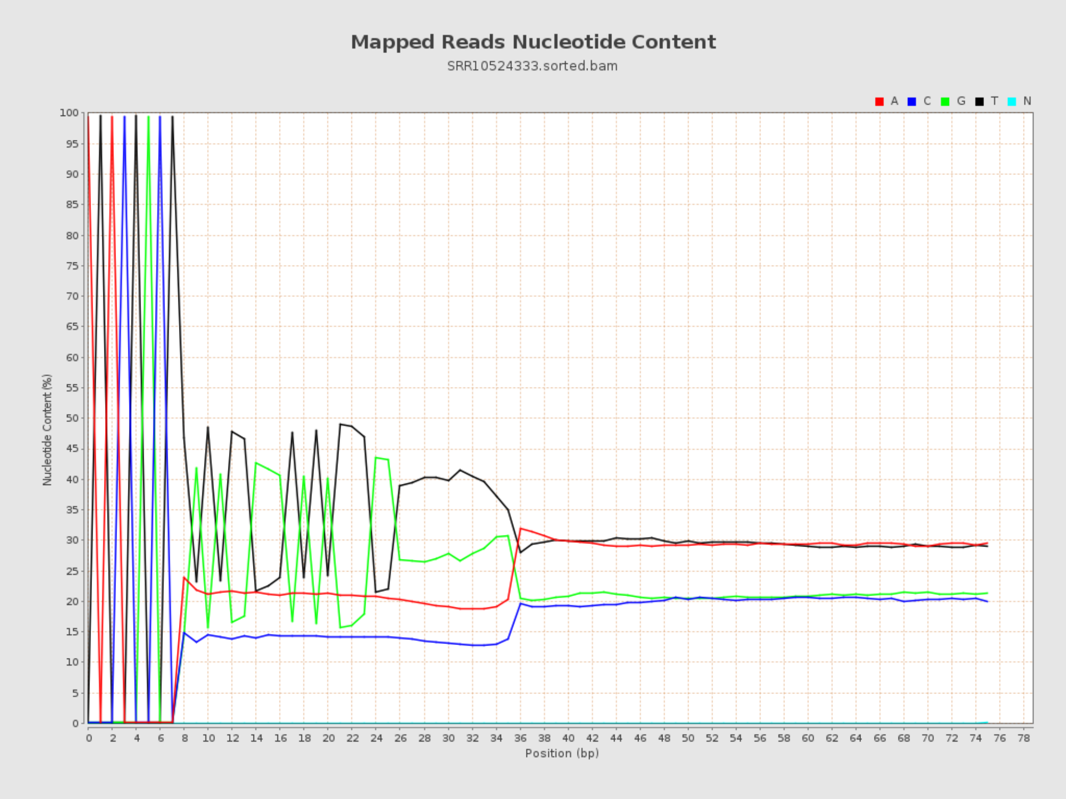
6. Results : Genome Fraction Coverage



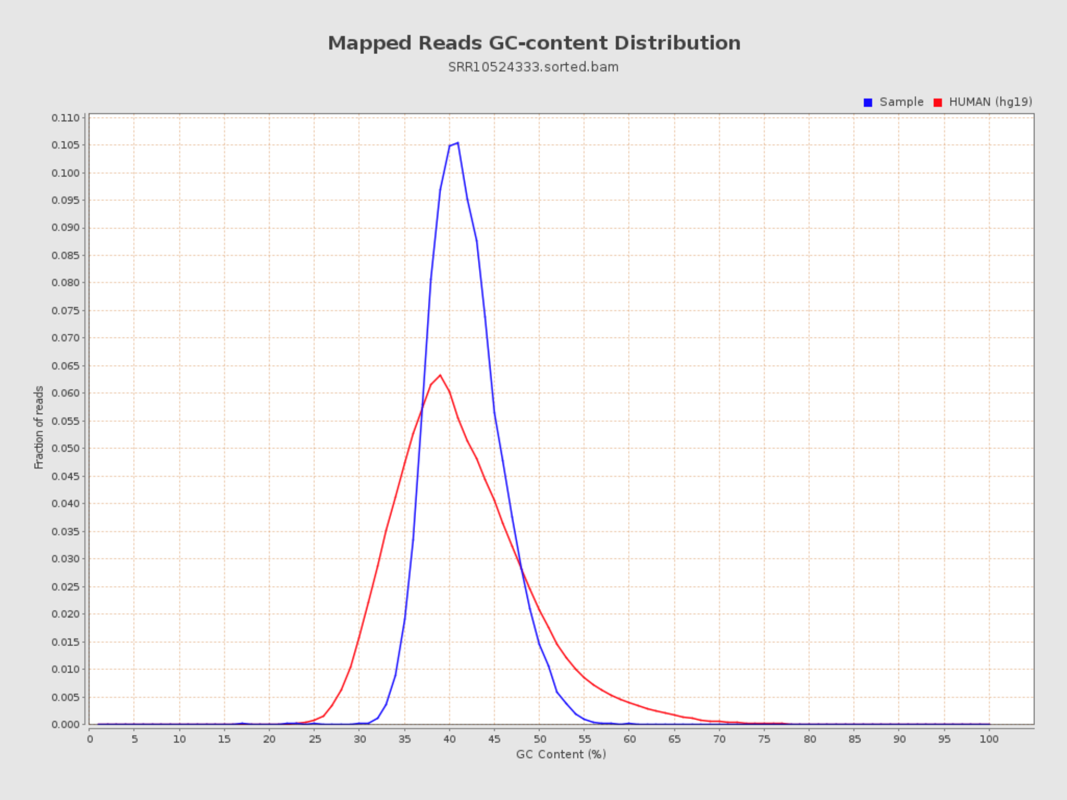
7. Results : Duplication Rate Histogram



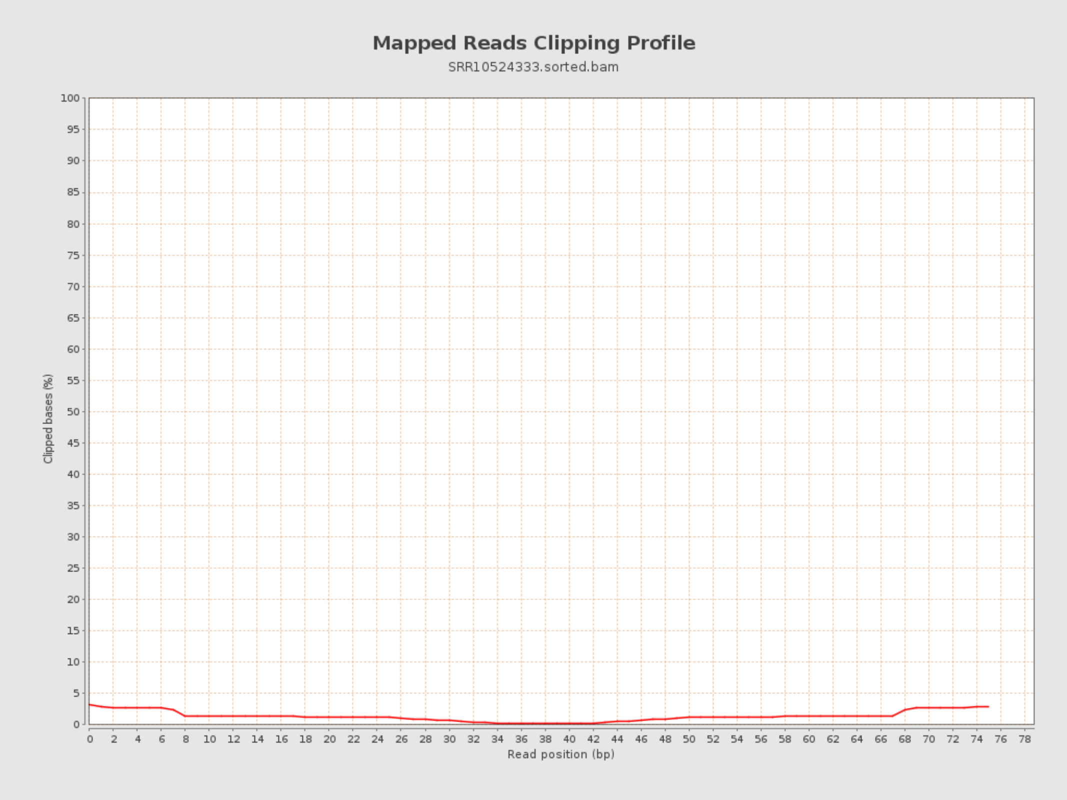
8. Results : Mapped Reads Nucleotide Content



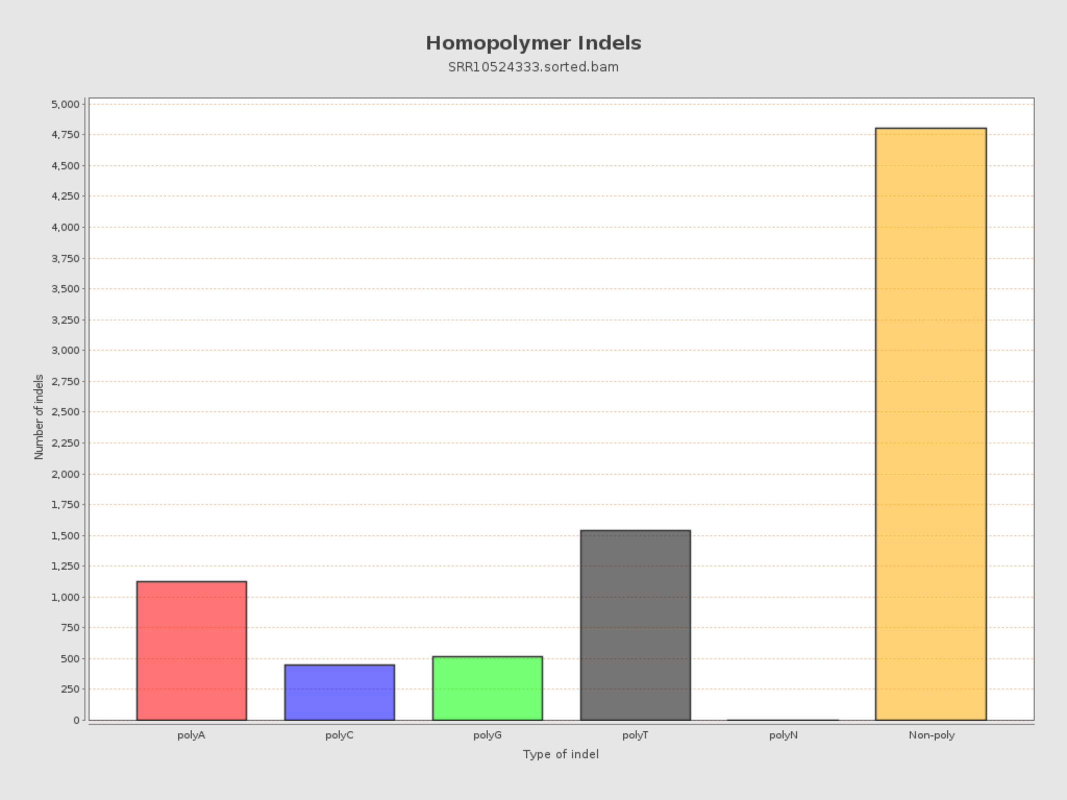
9. Results : Mapped Reads GC-content Distribution



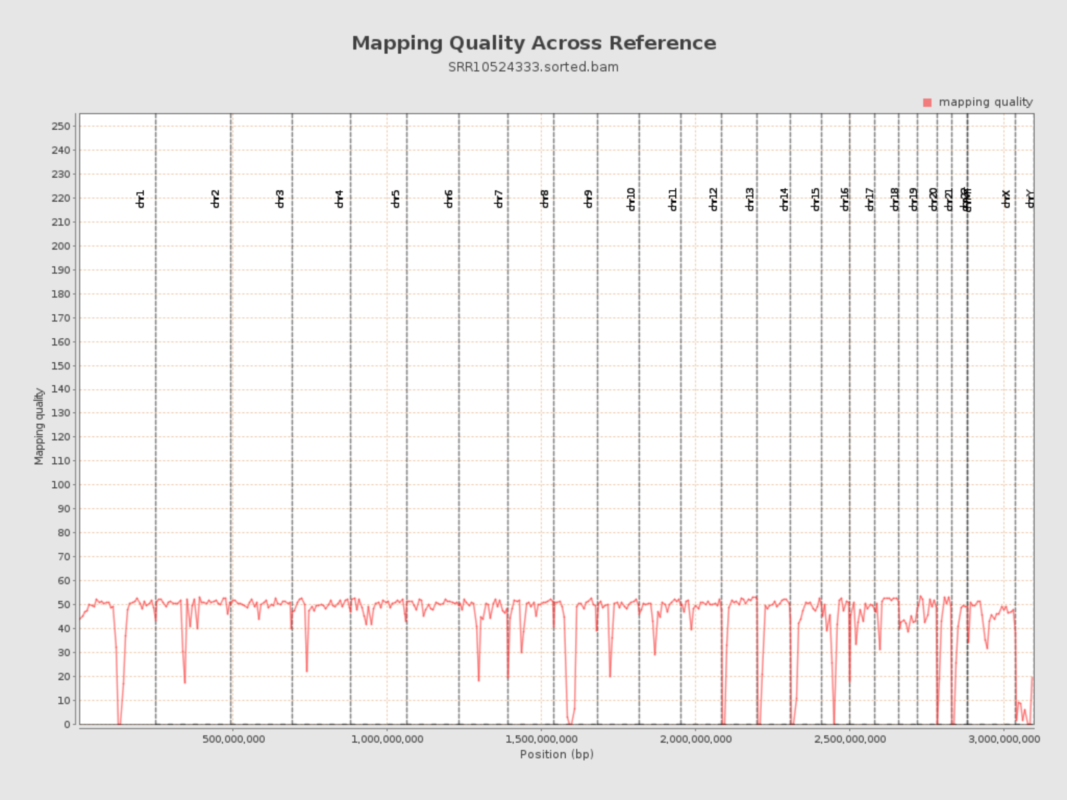
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram