Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 08:45:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524522.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_SRR10524522 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524522.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 08:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524522.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,468,436
Mapped reads	2,267,786 / 91.87%
Unmapped reads	200,650 / 8.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,296 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	94,304 / 3.82%
Duplication rate	3.18%
Clipped reads	2,273,606 / 92.11%

2.2. ACGT Content

Number/percentage of A's	32,937,355 / 25.1%
Number/percentage of C's	25,902,296 / 19.74%
Number/percentage of T's	40,512,552 / 30.87%
Number/percentage of G's	31,881,449 / 24.29%
Number/percentage of N's	3,932 / 0%
GC Percentage	44.03%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.3377

2.4. Mapping Quality

Mean Mapping Quality	45.37

2.5. Mismatches and indels

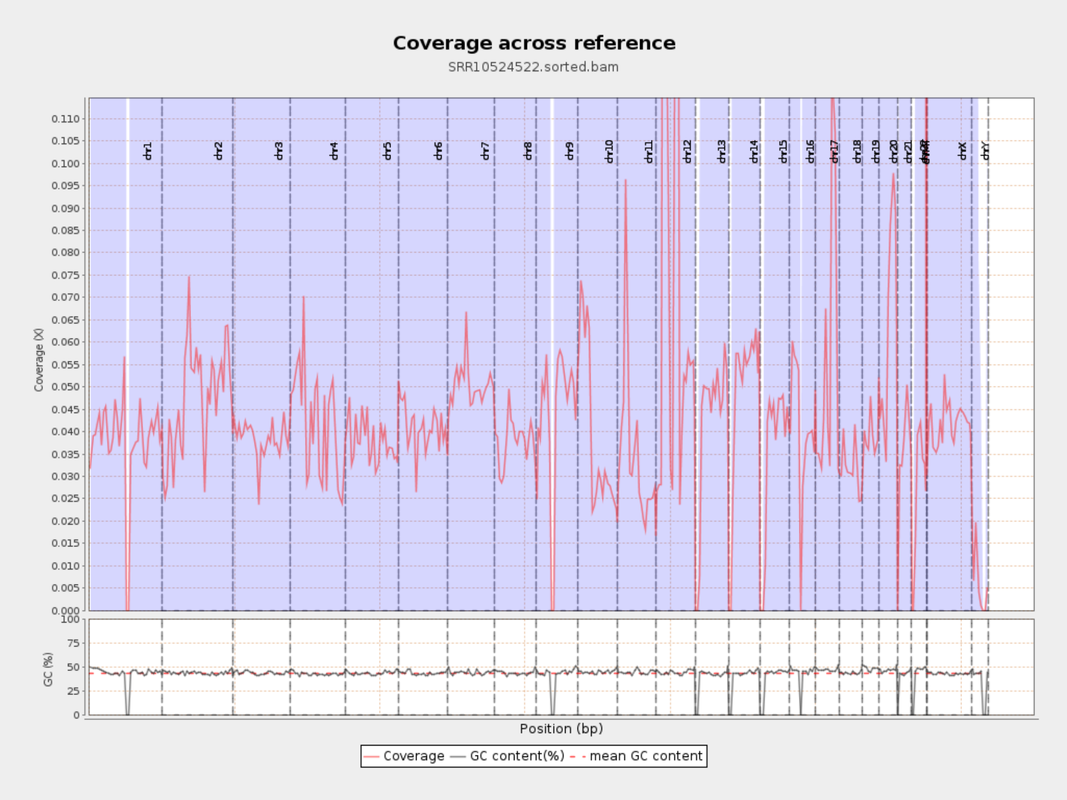
General error rate	0.48%
Mismatches	619,456
Insertions	7,914
Mapped reads with at least one insertion	0.35%
Deletions	20,250
Mapped reads with at least one deletion	0.89%
Homopolymer indels	42.51%

2.6. Chromosome stats

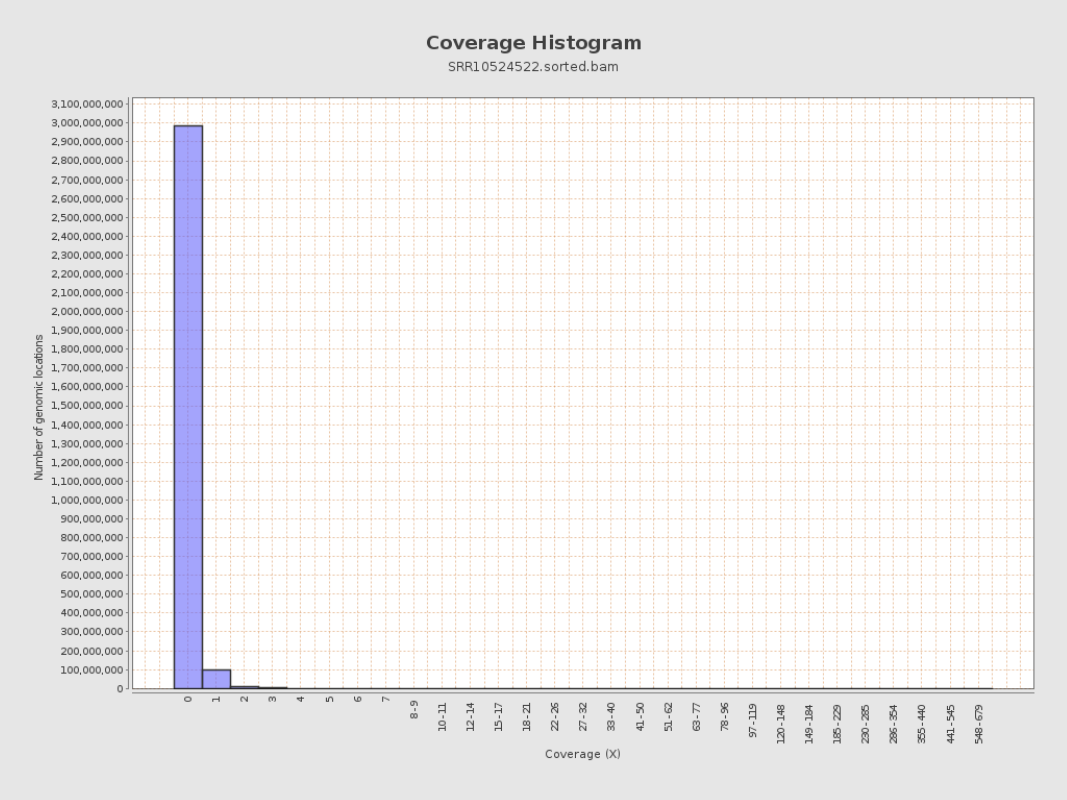
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9415112	0.0378	0.5662
chr2	243199373	11562190	0.0475	0.3553
chr3	198022430	7616138	0.0385	0.219
chr4	191154276	8017811	0.0419	0.2677
chr5	180915260	6854986	0.0379	0.2213
chr6	171115067	6994449	0.0409	0.2419
chr7	159138663	8046732	0.0506	0.4348

chr8	146364022	5562879	0.038	0.3489
chr9	141213431	6188254	0.0438	0.3389
chr10	135534747	5400299	0.0398	0.339
chr11	135006516	4774405	0.0354	0.2882
chr12	133851895	10399725	0.0777	0.3709
chr13	115169878	4774696	0.0415	0.2289
chr14	107349540	5102249	0.0475	0.2691
chr15	102531392	3632330	0.0354	0.2099
chr16	90354753	3672333	0.0406	0.2429
chr17	81195210	4515220	0.0556	0.2801
chr18	78077248	2507209	0.0321	0.5909
chr19	59128983	2309271	0.0391	0.427
chr20	63025520	4045944	0.0642	0.2987
chr21	48129895	1689382	0.0351	0.2418
chr22	51304566	1315854	0.0256	0.1778
chrMT	16571	41491	2.5038	2.3981
chrX	155270560	6472951	0.0417	0.2671
chrY	59373566	359329	0.0061	0.1429

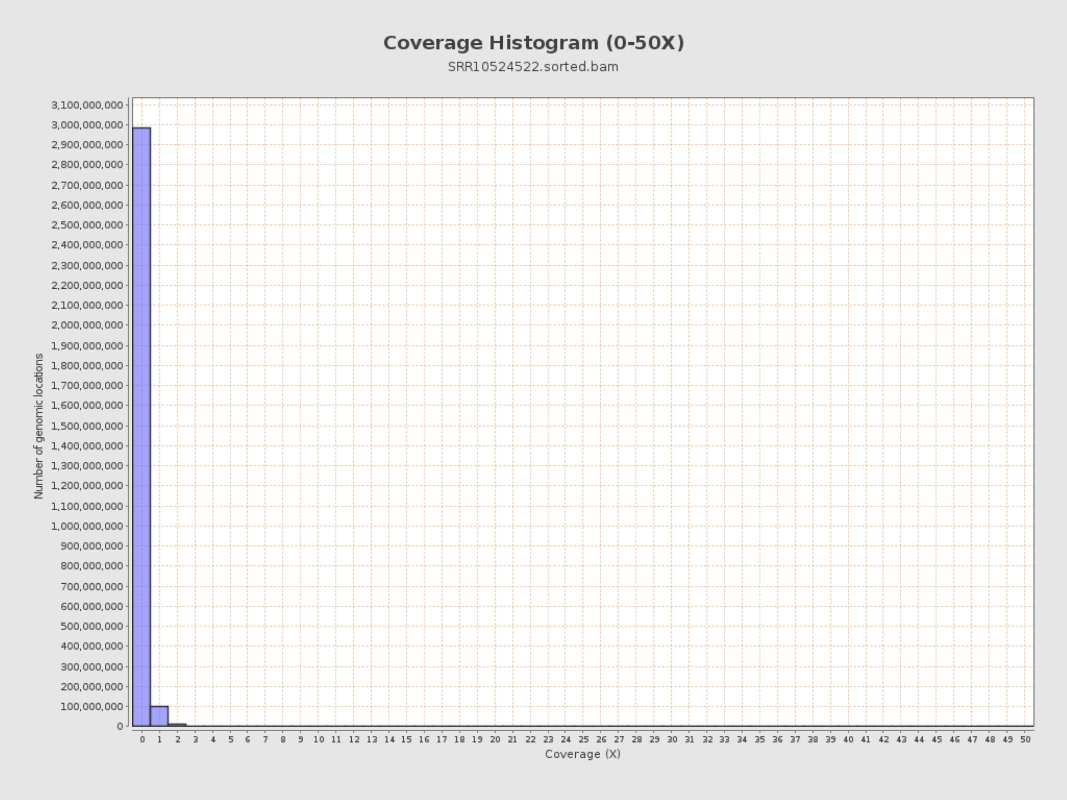
3. Results : Coverage across reference



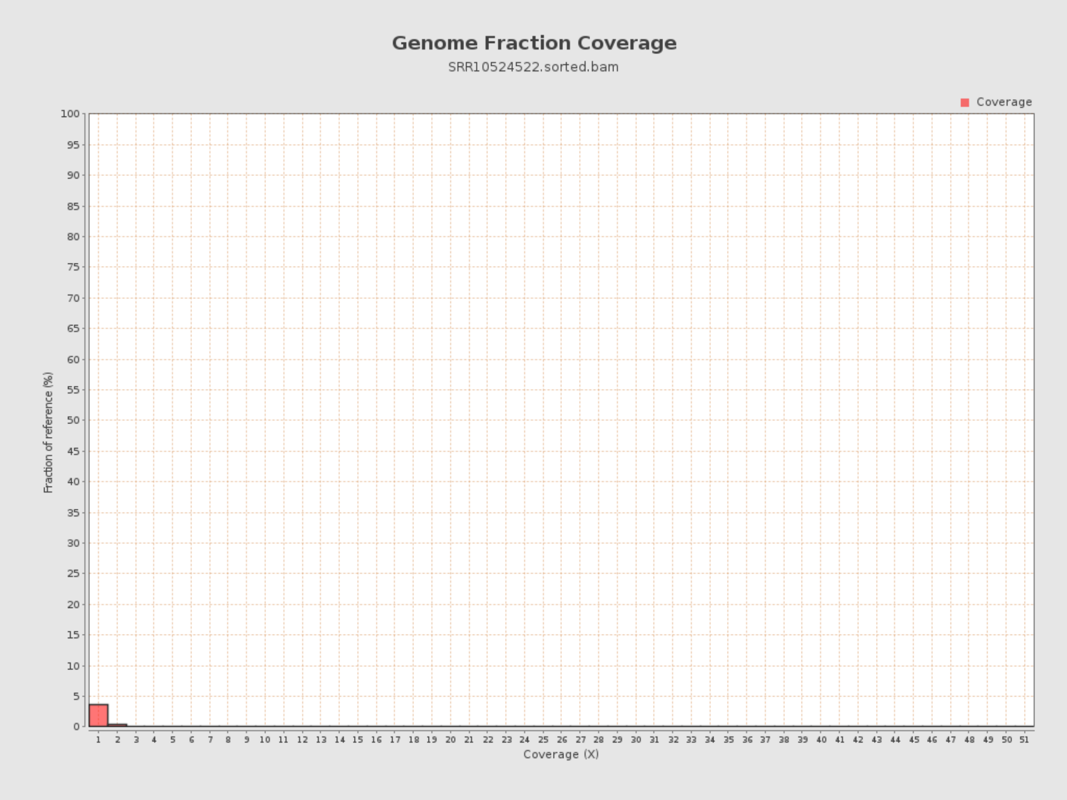
4. Results : Coverage Histogram



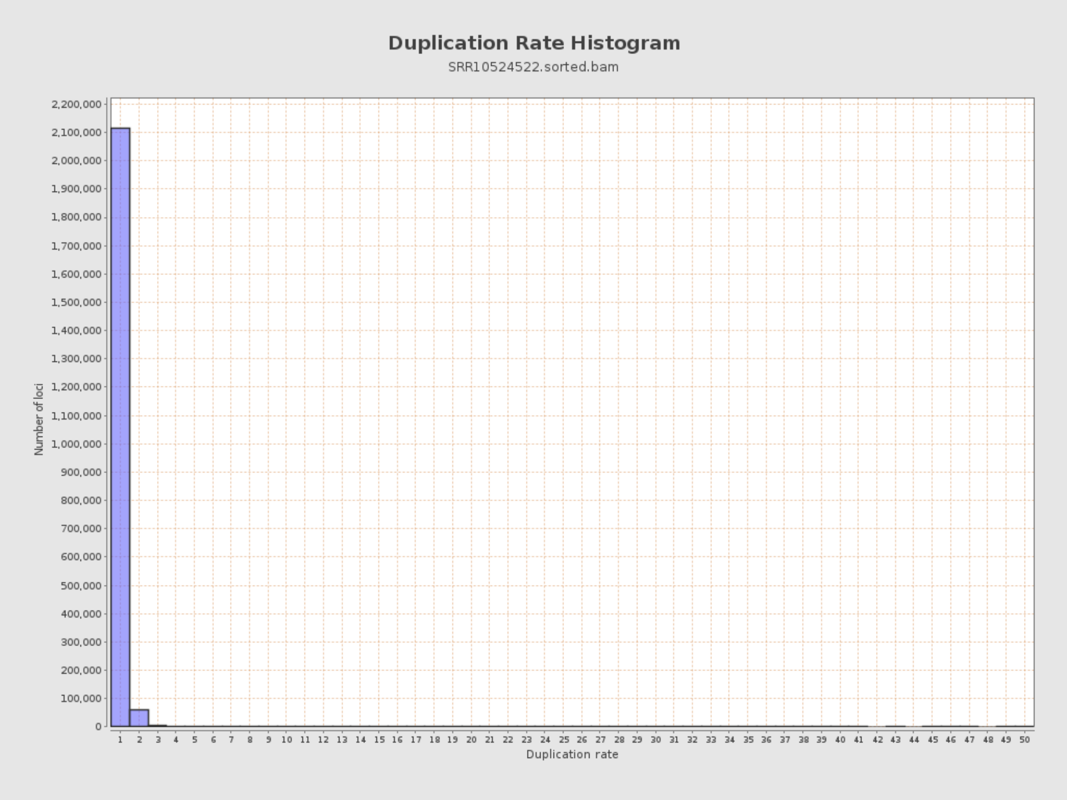
5. Results : Coverage Histogram (0-50X)



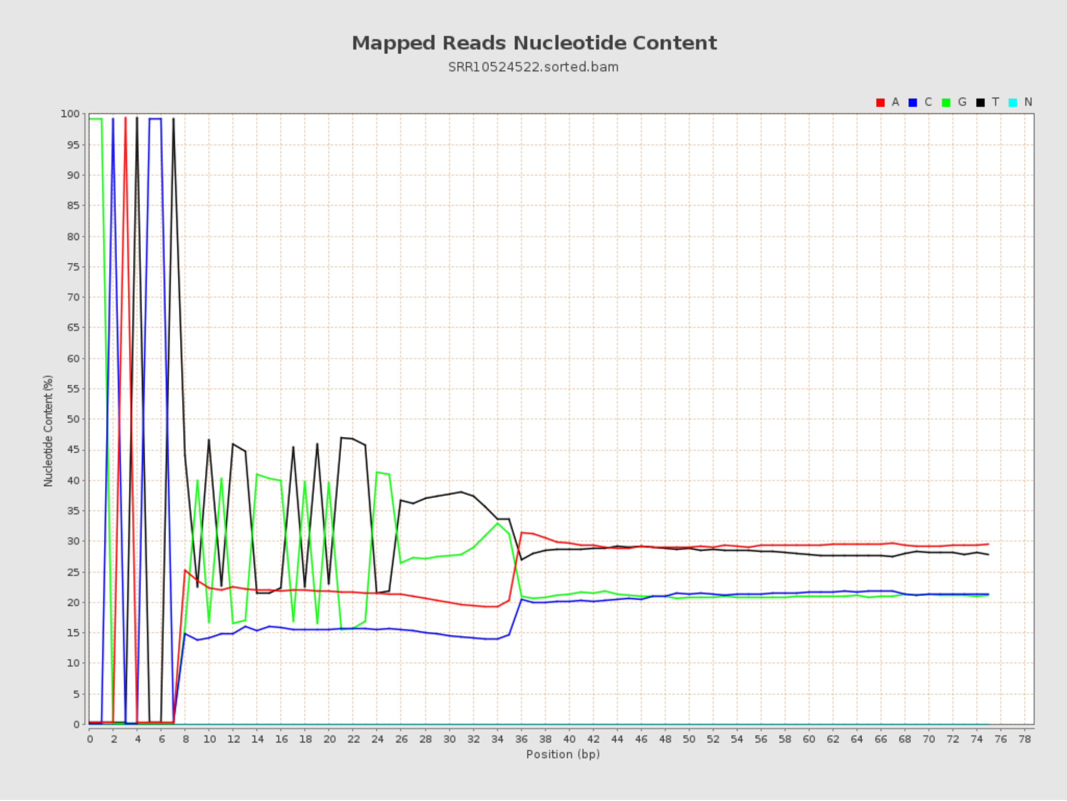
6. Results : Genome Fraction Coverage



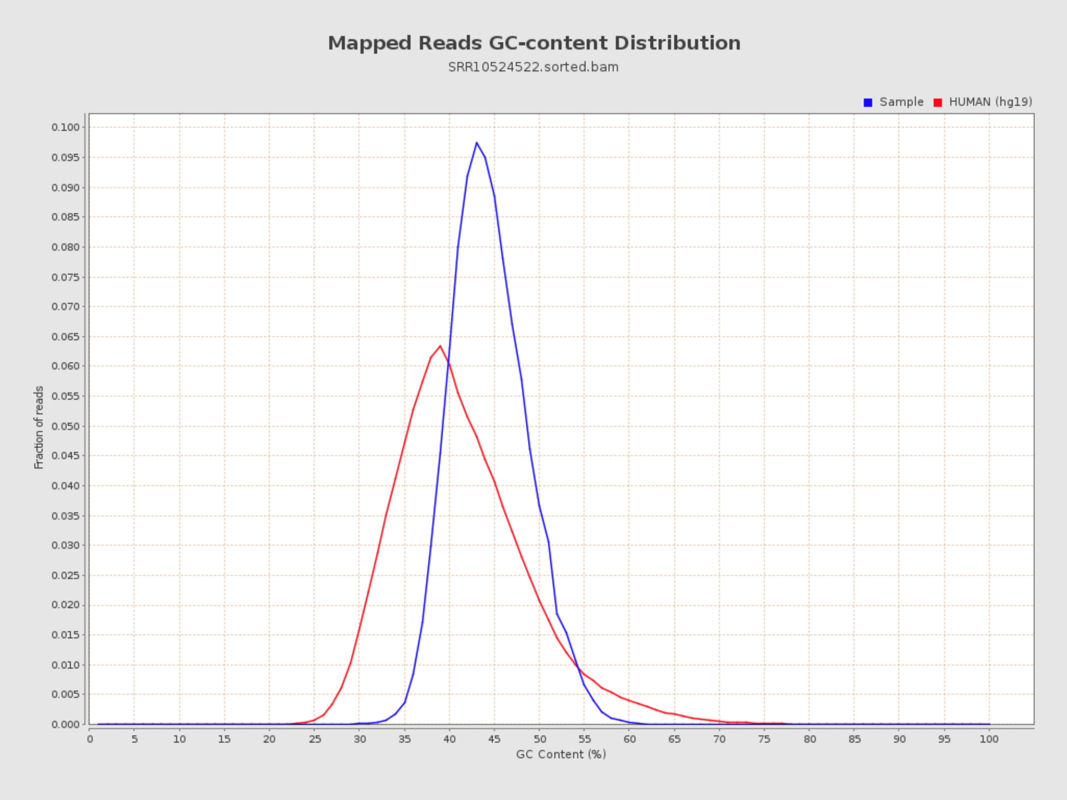
7. Results : Duplication Rate Histogram



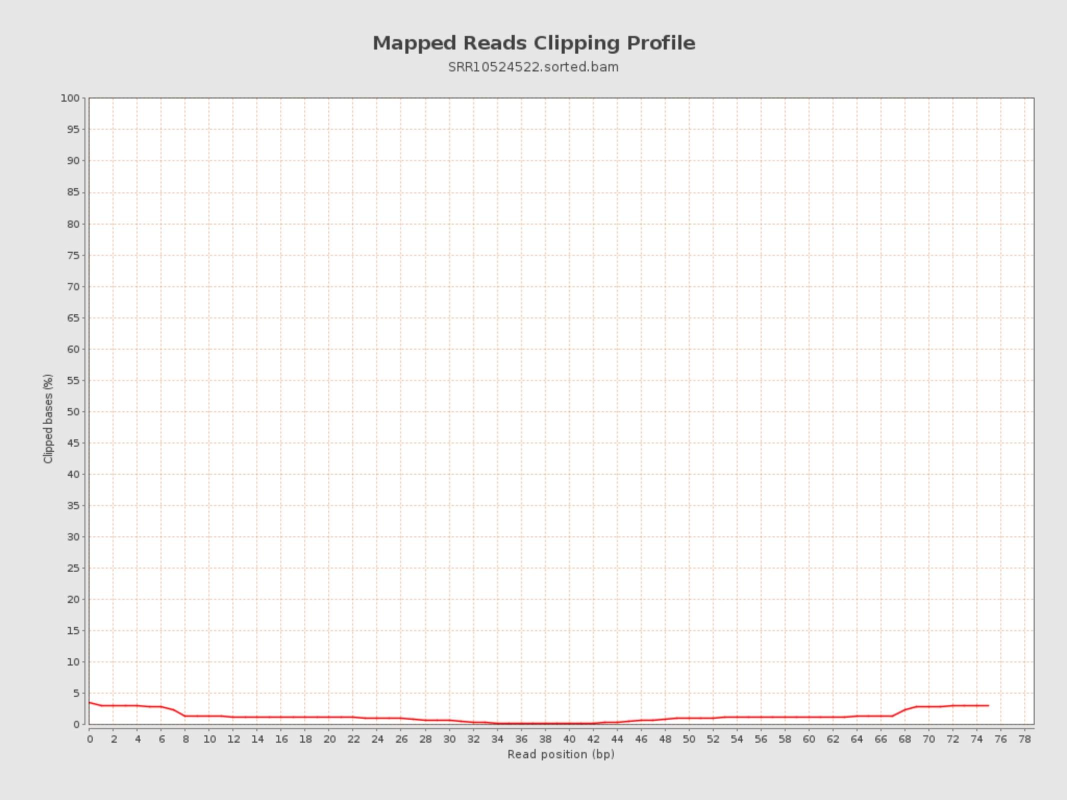
8. Results : Mapped Reads Nucleotide Content



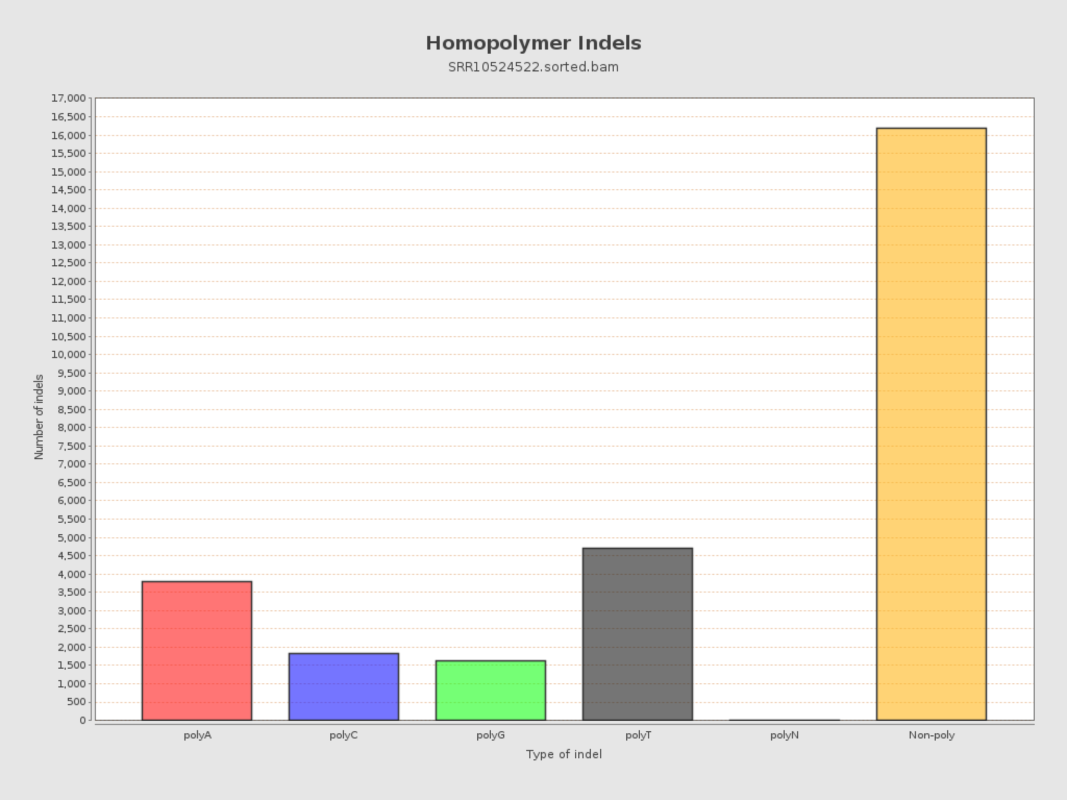
9. Results : Mapped Reads GC-content Distribution



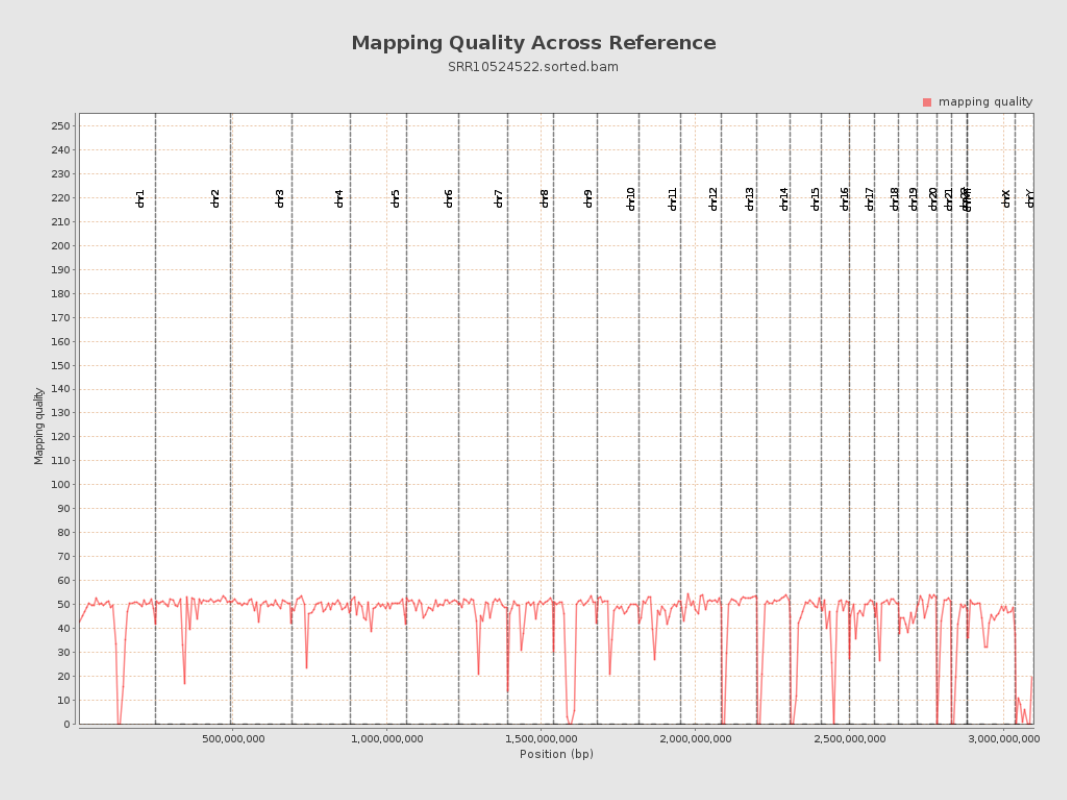
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram