Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:44:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525179.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_SRR10525179 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525179.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:44:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525179.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,102,758
Mapped reads	3,734,584 / 91.03%
Unmapped reads	368,174 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,721 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	243,394 / 5.93%
Duplication rate	4.76%
Clipped reads	3,743,858 / 91.25%

2.2. ACGT Content

Number/percentage of A's	54,365,801 / 25.2%
Number/percentage of C's	41,268,140 / 19.13%
Number/percentage of T's	68,522,595 / 31.76%
Number/percentage of G's	51,604,118 / 23.92%
Number/percentage of N's	5,225 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0697

Standard Deviation	0.6261

2.4. Mapping Quality

Mean Mapping Quality	44.57

2.5. Mismatches and indels

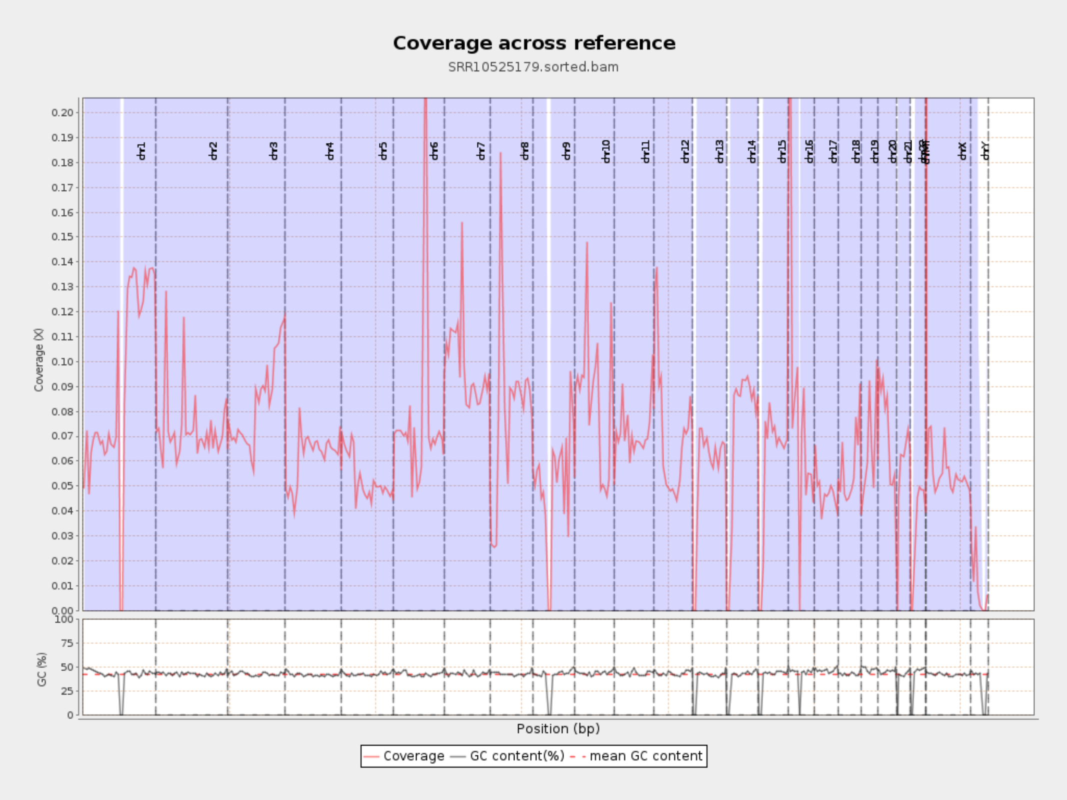
General error rate	0.53%
Mismatches	1,115,678
Insertions	12,450
Mapped reads with at least one insertion	0.33%
Deletions	42,555
Mapped reads with at least one deletion	1.13%
Homopolymer indels	44.32%

2.6. Chromosome stats

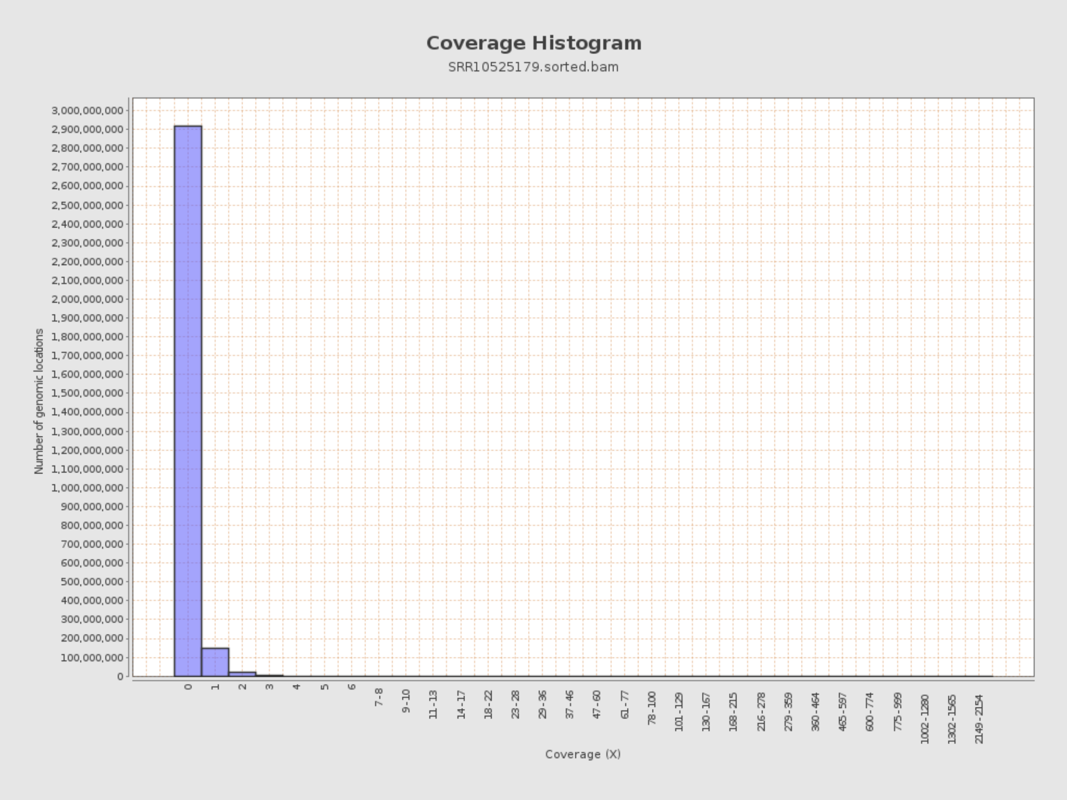
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22589259	0.0906	1.1575
chr2	243199373	17796776	0.0732	0.9541
chr3	198022430	16435477	0.083	0.3503
chr4	191154276	11916944	0.0623	0.3326
chr5	180915260	9576548	0.0529	0.2771
chr6	171115067	13415639	0.0784	0.403
chr7	159138663	15710890	0.0987	1.1573

chr8	146364022	12075168	0.0825	0.5254
chr9	141213431	7148720	0.0506	0.4251
chr10	135534747	11408056	0.0842	0.6393
chr11	135006516	9677289	0.0717	0.4578
chr12	133851895	9557563	0.0714	0.3279
chr13	115169878	6510556	0.0565	0.2926
chr14	107349540	7851871	0.0731	0.341
chr15	102531392	5841607	0.057	0.3024
chr16	90354753	7562715	0.0837	0.4123
chr17	81195210	3909893	0.0482	0.2865
chr18	78077248	4484901	0.0574	0.8348
chr19	59128983	3850006	0.0651	0.8289
chr20	63025520	4566721	0.0725	0.3343
chr21	48129895	2718643	0.0565	0.3072
chr22	51304566	1710527	0.0333	0.2161
chrMT	16571	316793	19.1173	11.3008
chrX	155270560	8600125	0.0554	0.3386
chrY	59373566	601210	0.0101	0.2661

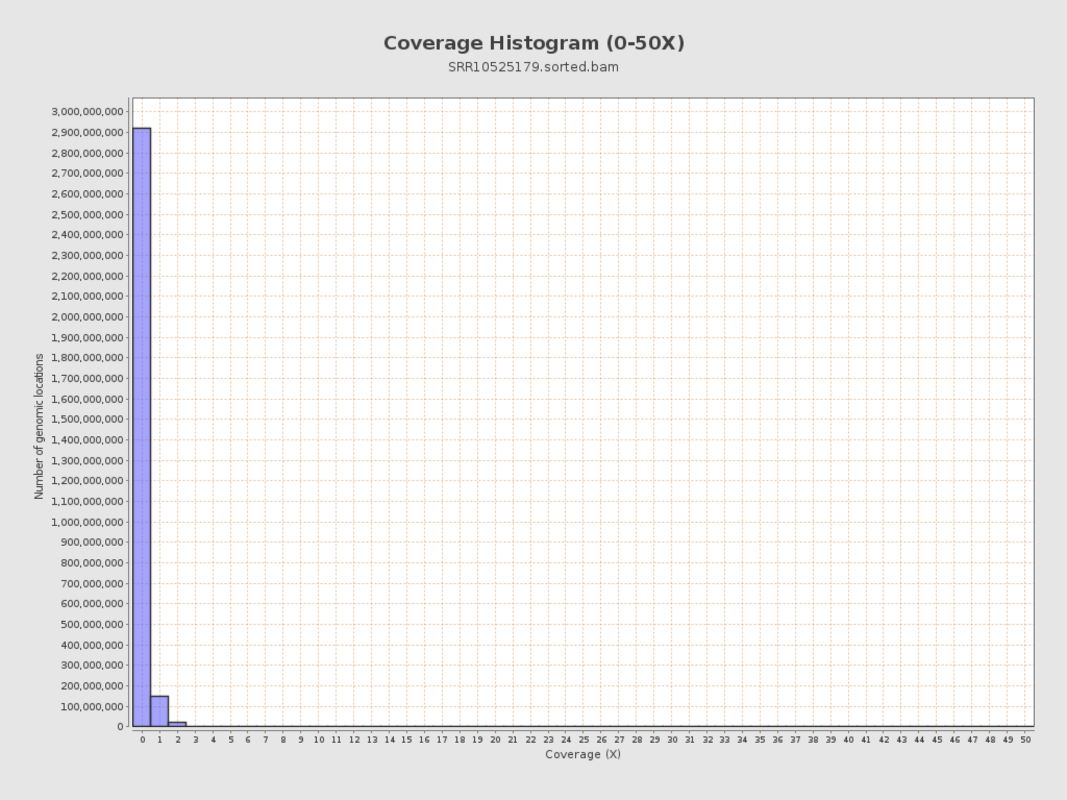
3. Results : Coverage across reference



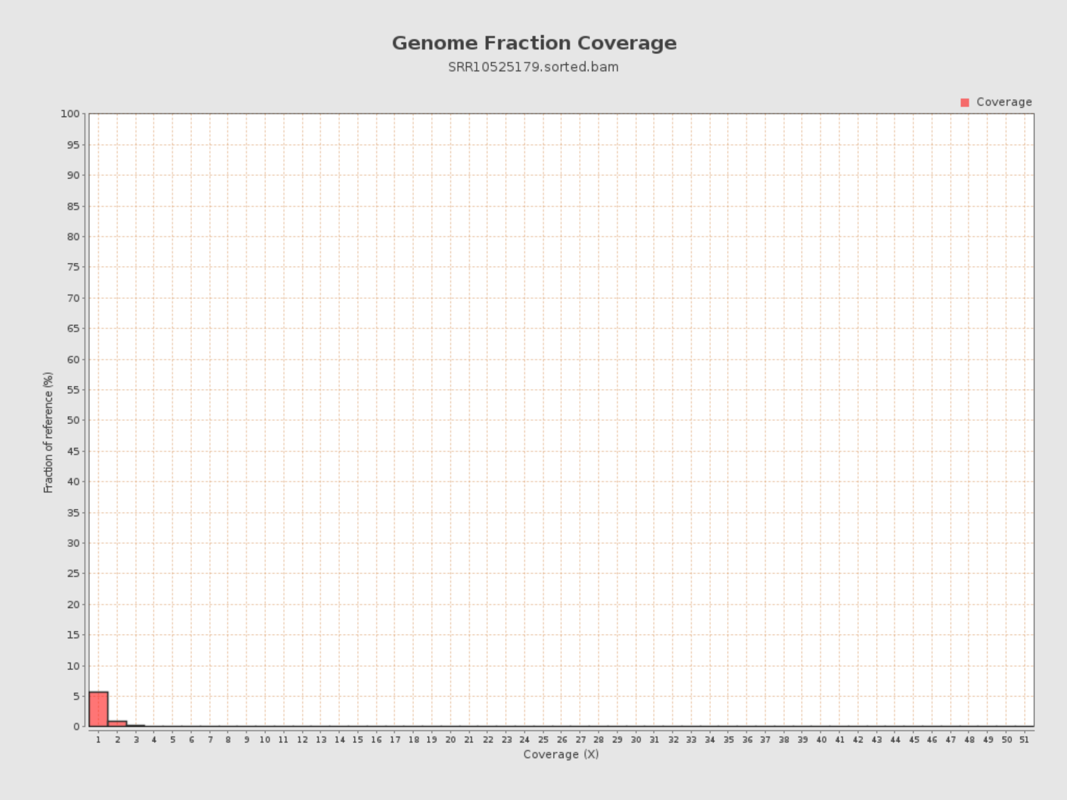
4. Results : Coverage Histogram



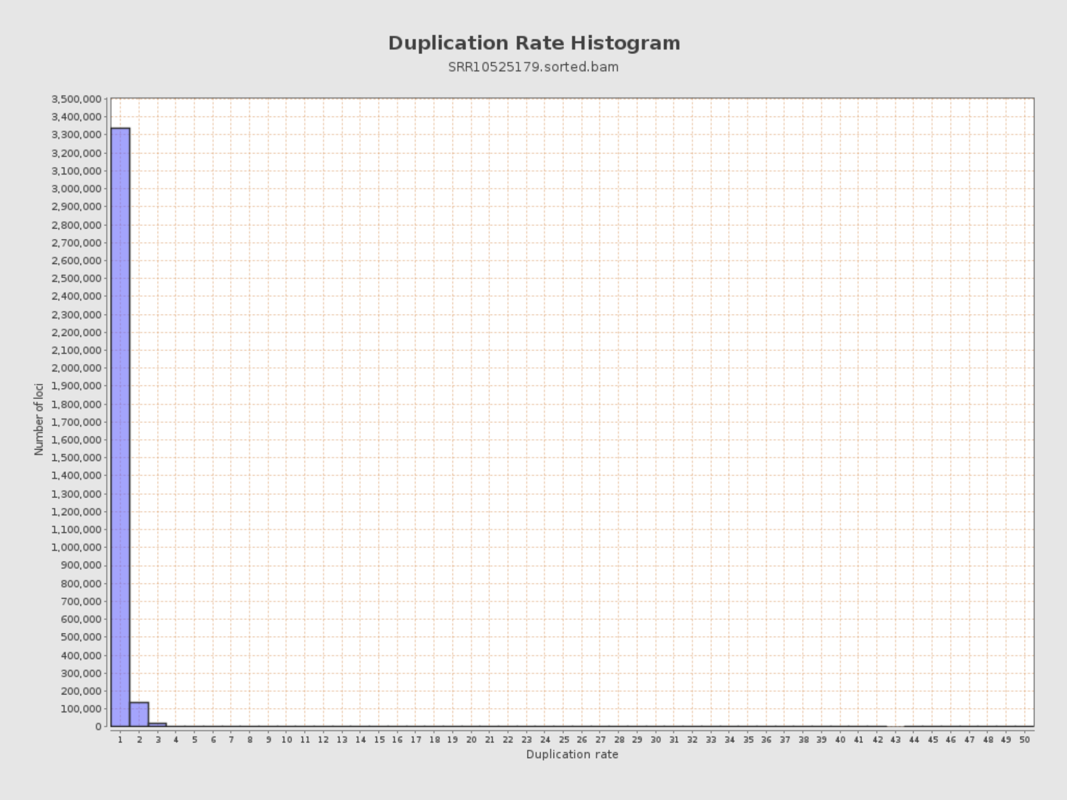
5. Results : Coverage Histogram (0-50X)



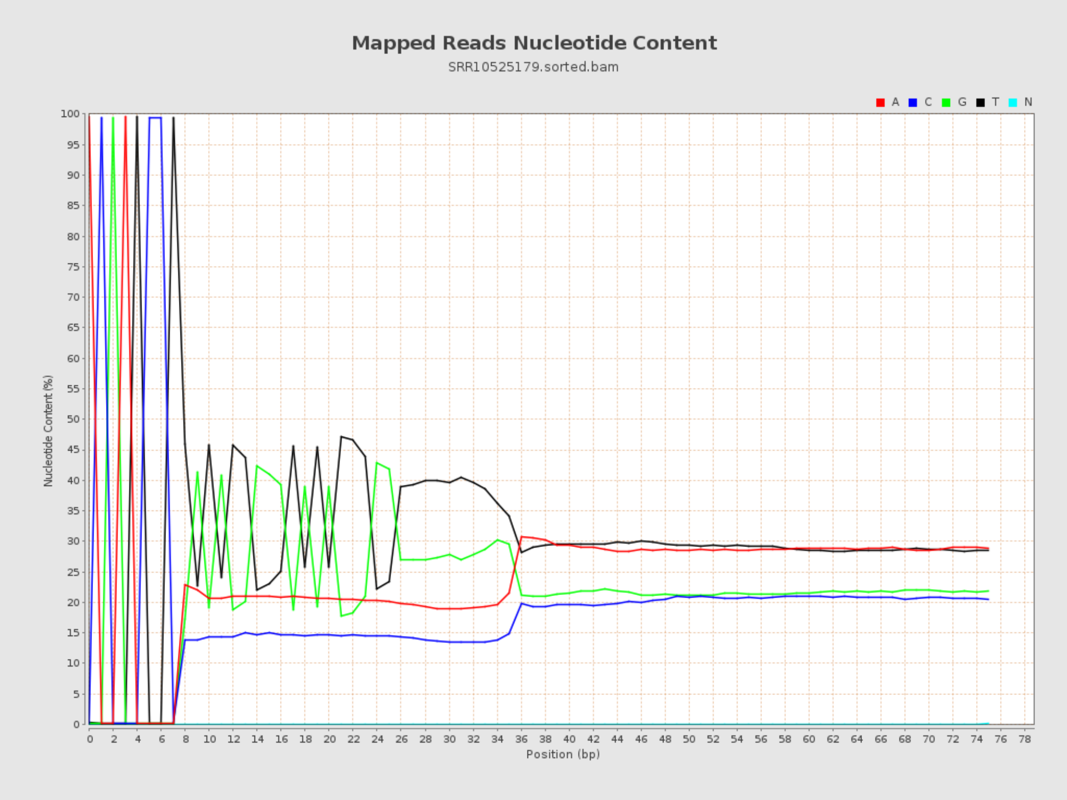
6. Results : Genome Fraction Coverage



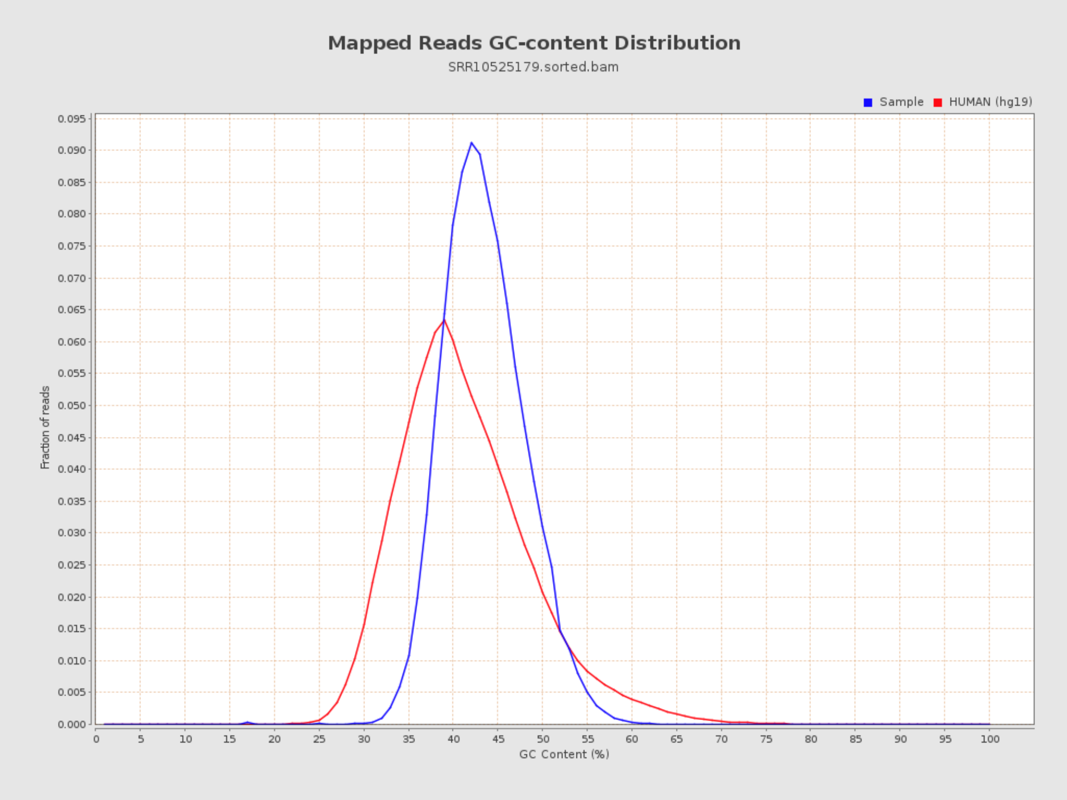
7. Results : Duplication Rate Histogram



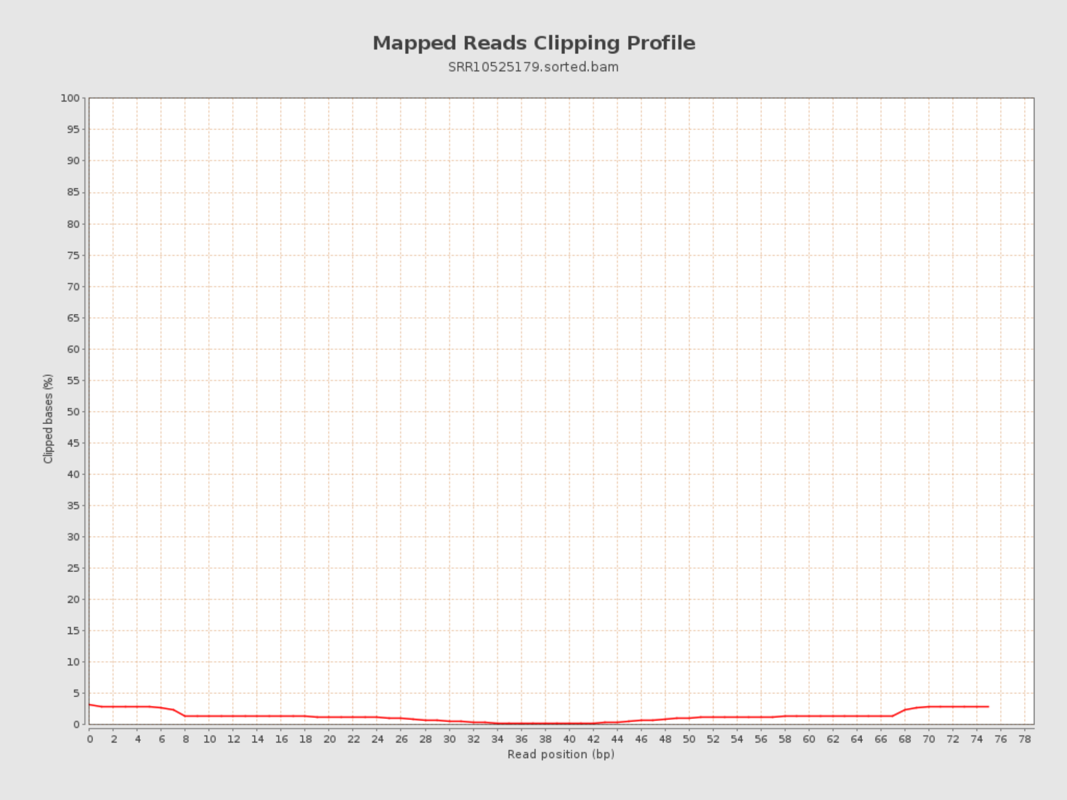
8. Results : Mapped Reads Nucleotide Content



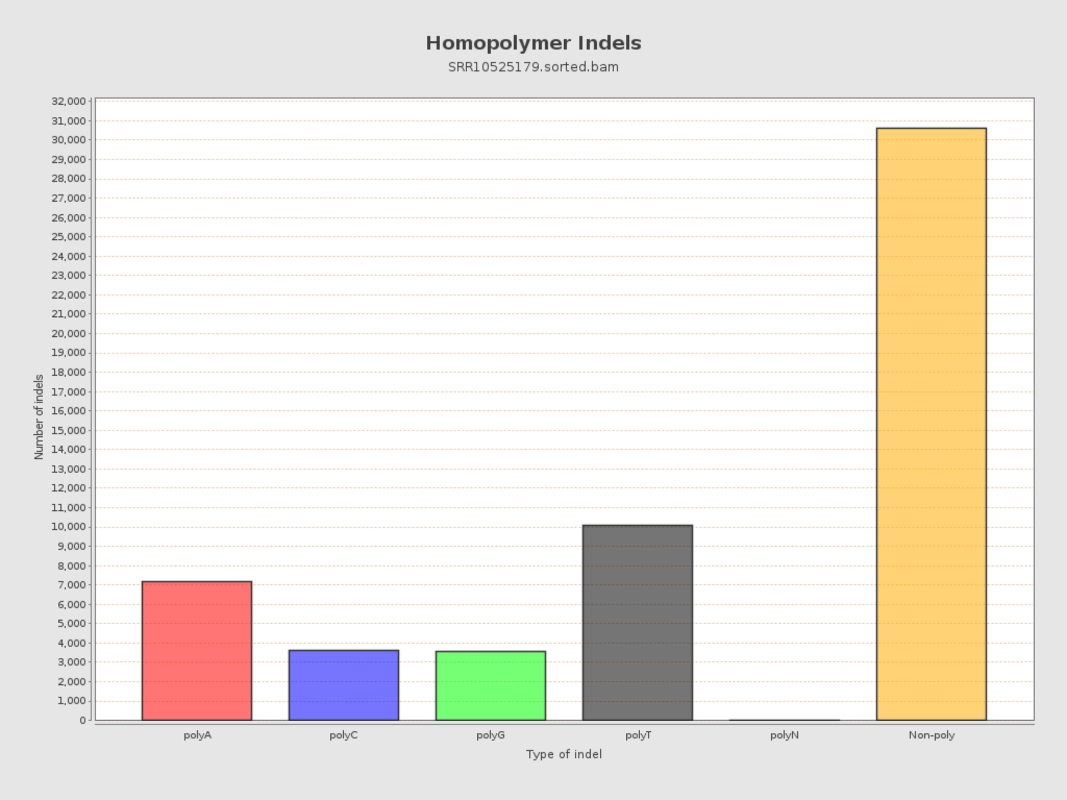
9. Results : Mapped Reads GC-content Distribution



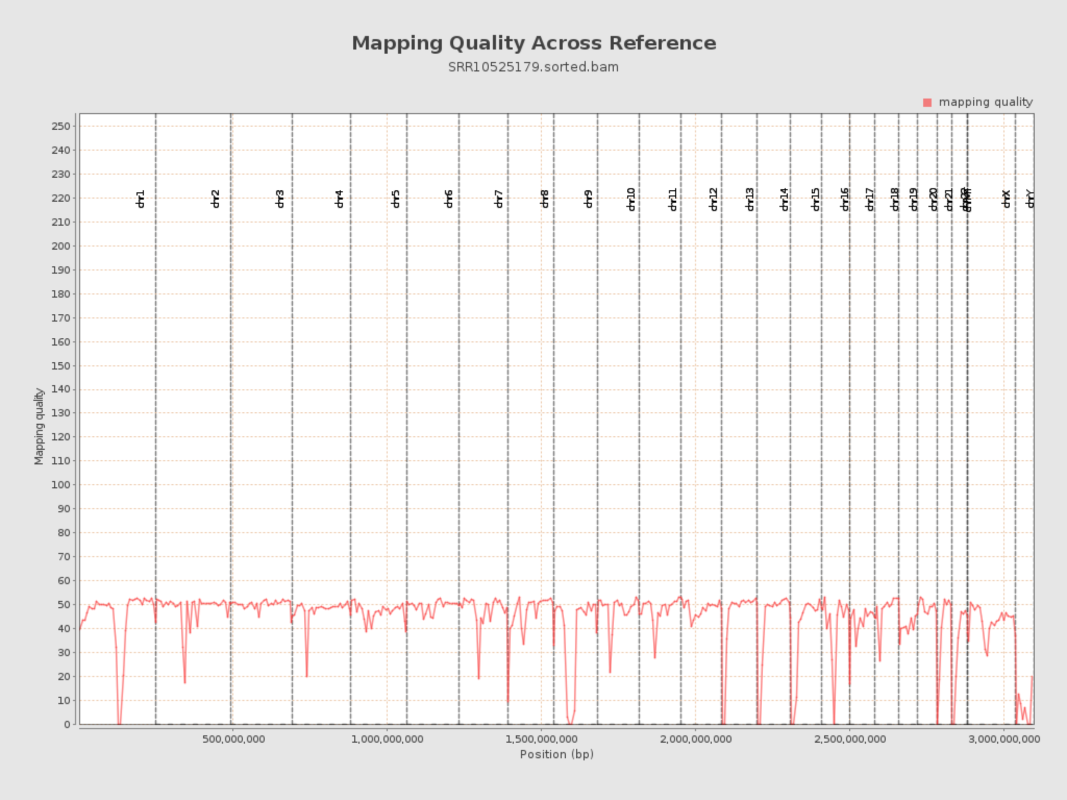
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram