Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:38:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525216.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_SRR10525216 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525216.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:38:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525216.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	420,628
Mapped reads	356,977 / 84.87%
Unmapped reads	63,651 / 15.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,093 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	5,577 / 1.33%
Duplication rate	1.18%
Clipped reads	356,865 / 84.84%

2.2. ACGT Content

Number/percentage of A's	5,553,579 / 26.36%
Number/percentage of C's	3,637,100 / 17.26%
Number/percentage of T's	6,659,245 / 31.61%
Number/percentage of G's	5,216,921 / 24.76%
Number/percentage of N's	445 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0994

2.4. Mapping Quality

Mean Mapping Quality	45.36

2.5. Mismatches and indels

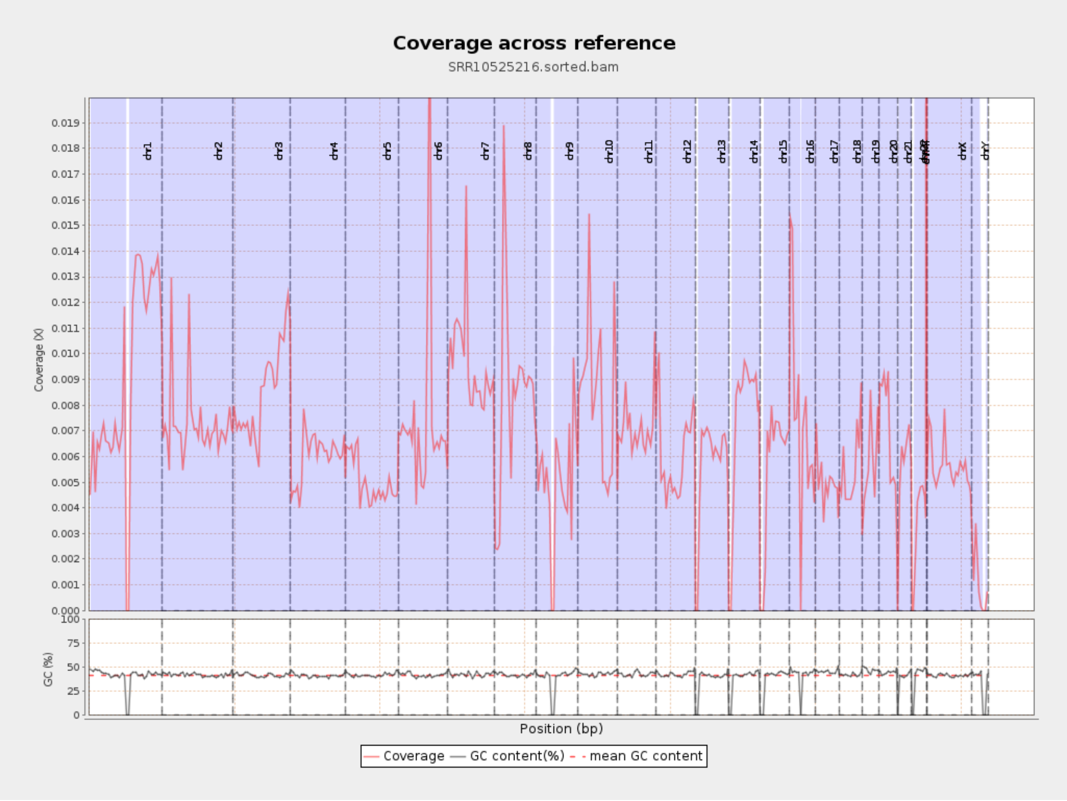
General error rate	0.53%
Mismatches	107,874
Insertions	1,567
Mapped reads with at least one insertion	0.44%
Deletions	4,447
Mapped reads with at least one deletion	1.24%
Homopolymer indels	42.87%

2.6. Chromosome stats

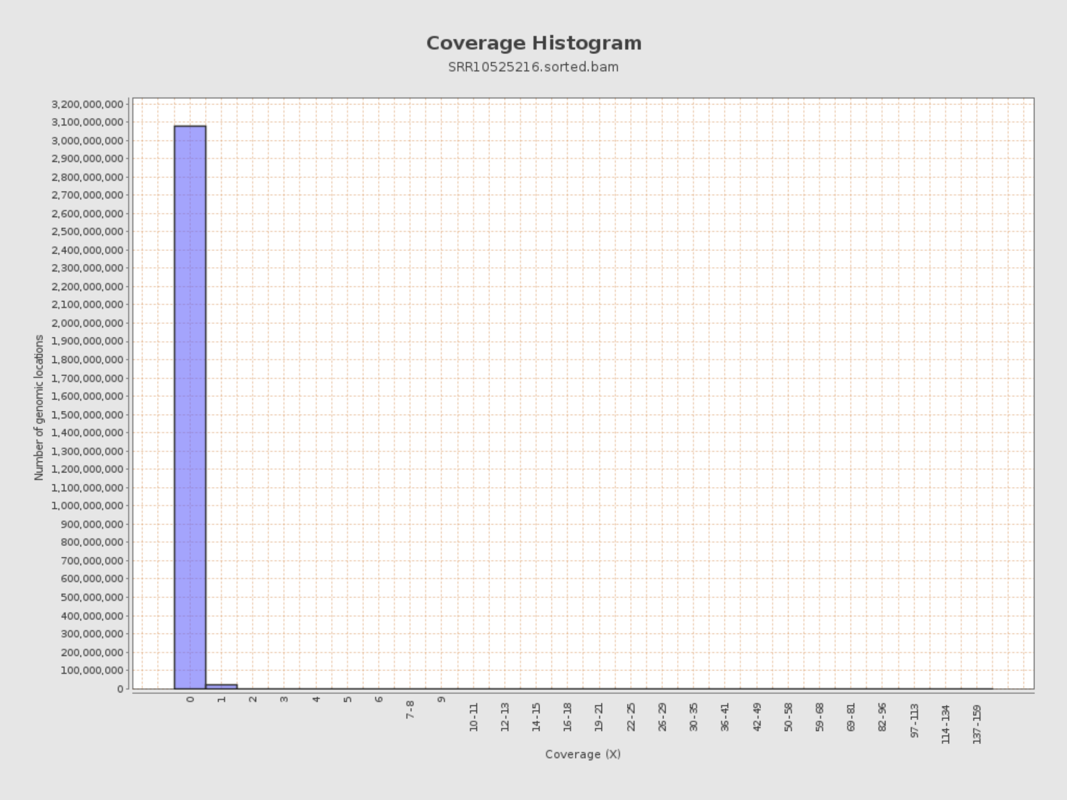
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2226587	0.0089	0.1501
chr2	243199373	1766532	0.0073	0.1149
chr3	198022430	1685536	0.0085	0.0944
chr4	191154276	1144312	0.006	0.0803
chr5	180915260	902542	0.005	0.0723
chr6	171115067	1295512	0.0076	0.0918
chr7	159138663	1539136	0.0097	0.1509

chr8	146364022	1212664	0.0083	0.0991
chr9	141213431	700543	0.005	0.0785
chr10	135534747	1155117	0.0085	0.1104
chr11	135006516	963362	0.0071	0.0916
chr12	133851895	815077	0.0061	0.0799
chr13	115169878	653002	0.0057	0.077
chr14	107349540	789247	0.0074	0.0884
chr15	102531392	568836	0.0055	0.0761
chr16	90354753	653979	0.0072	0.0902
chr17	81195210	404238	0.005	0.0731
chr18	78077248	427212	0.0055	0.1051
chr19	59128983	344319	0.0058	0.1044
chr20	63025520	452761	0.0072	0.0871
chr21	48129895	268103	0.0056	0.0781
chr22	51304566	165078	0.0032	0.0577
chrMT	16571	2189	0.1321	0.3543
chrX	155270560	878483	0.0057	0.0788
chrY	59373566	59918	0.001	0.042

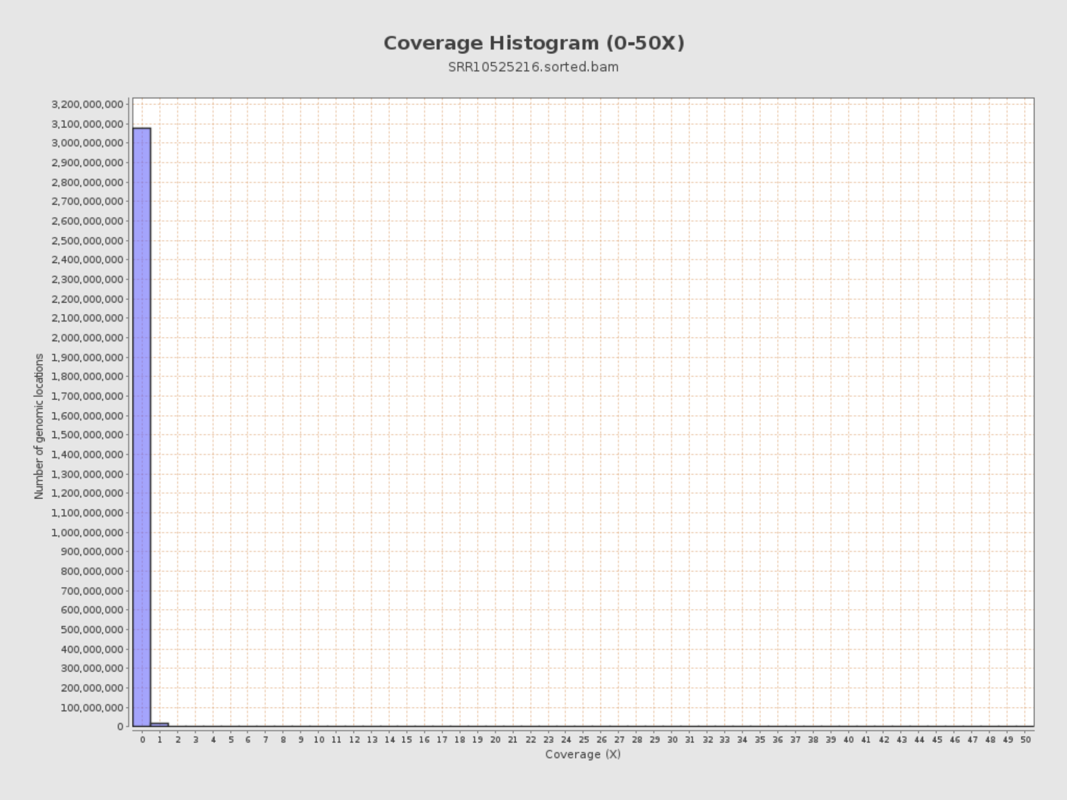
3. Results : Coverage across reference



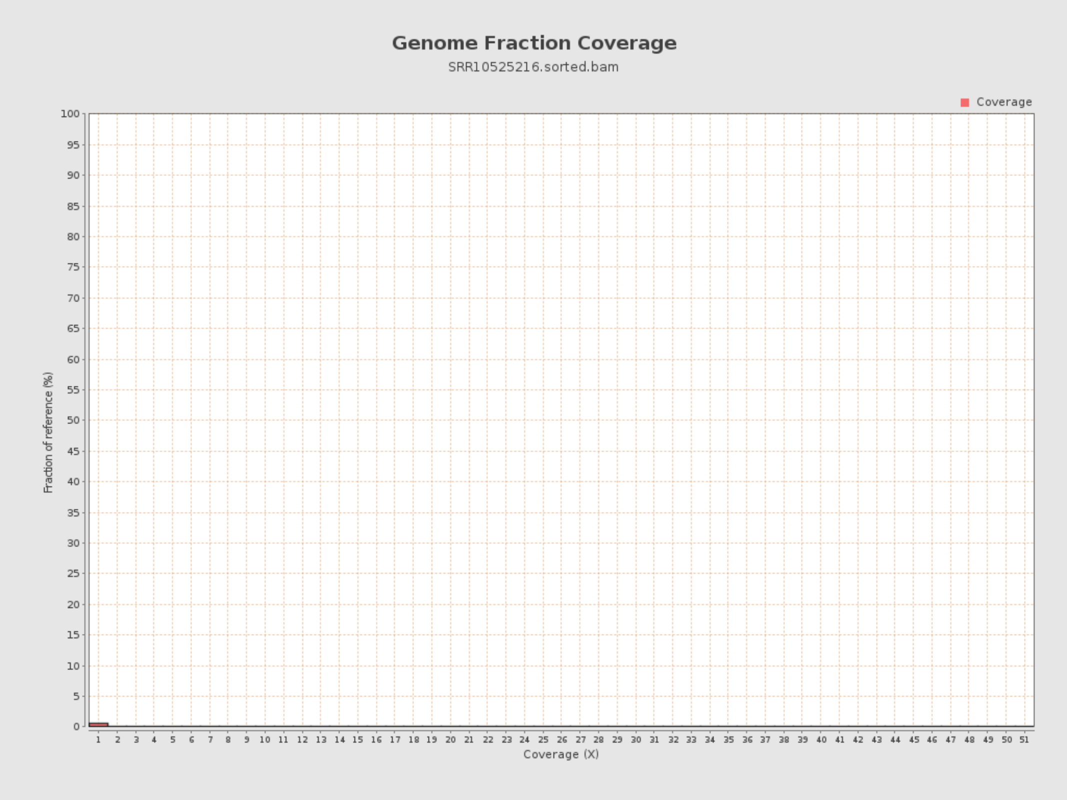
4. Results : Coverage Histogram



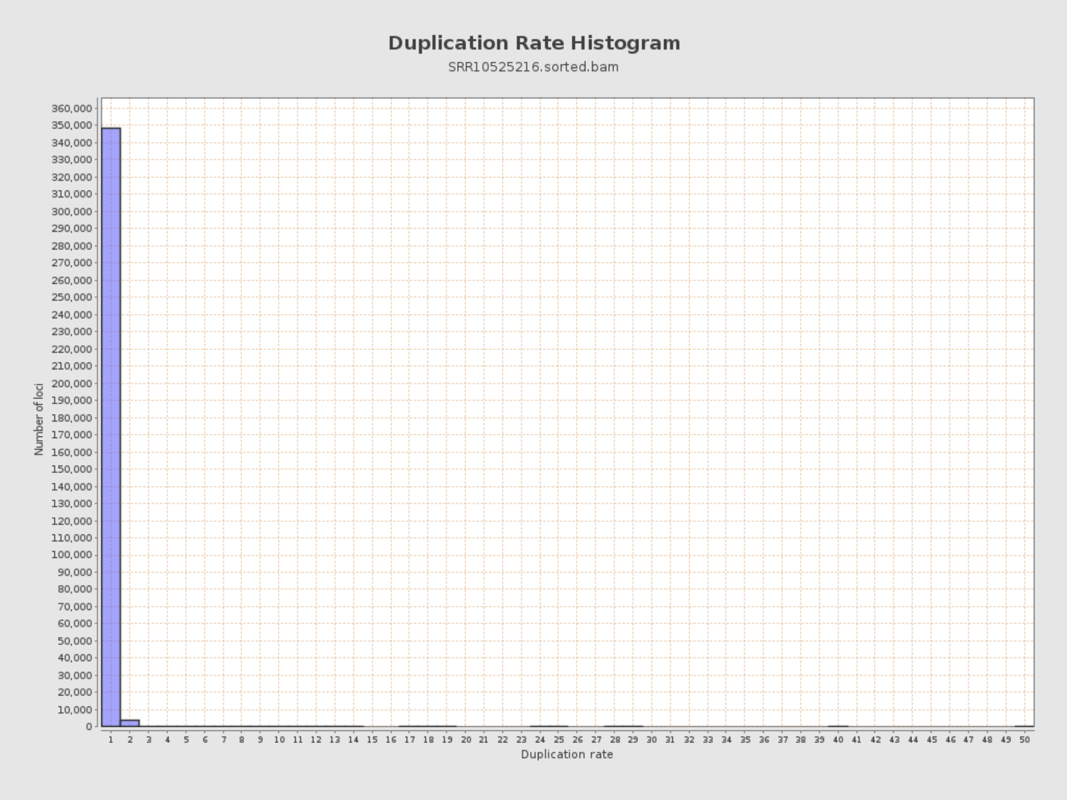
5. Results : Coverage Histogram (0-50X)



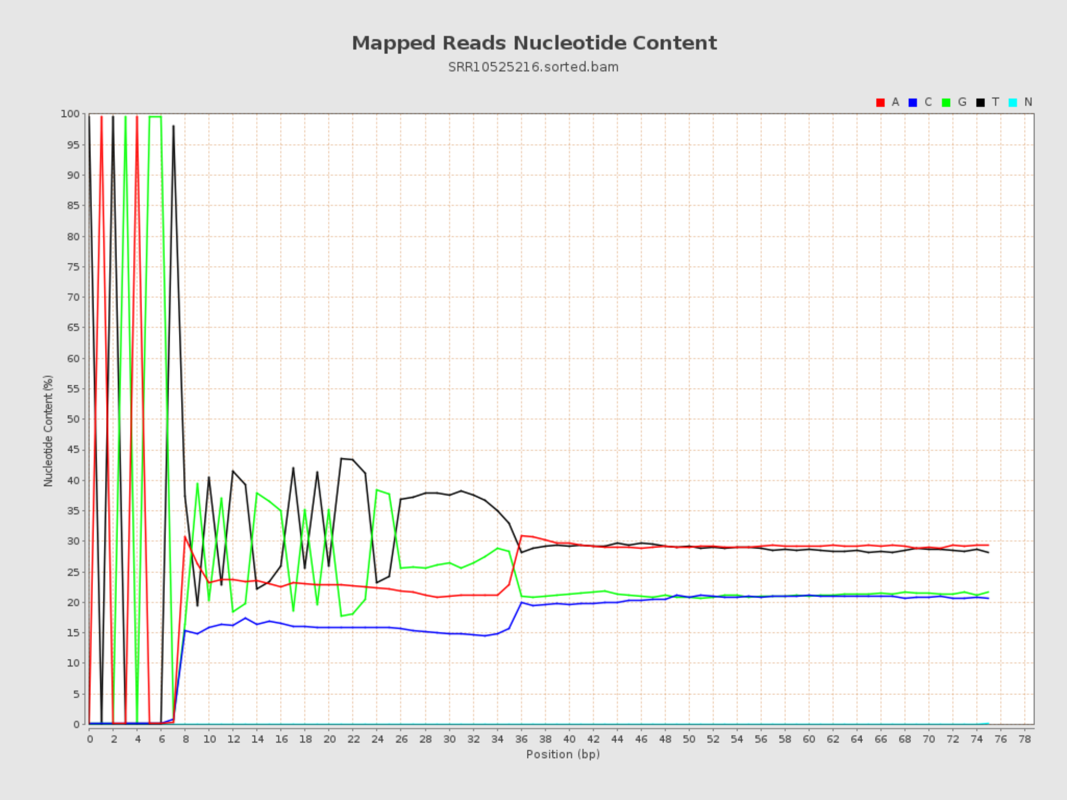
6. Results : Genome Fraction Coverage



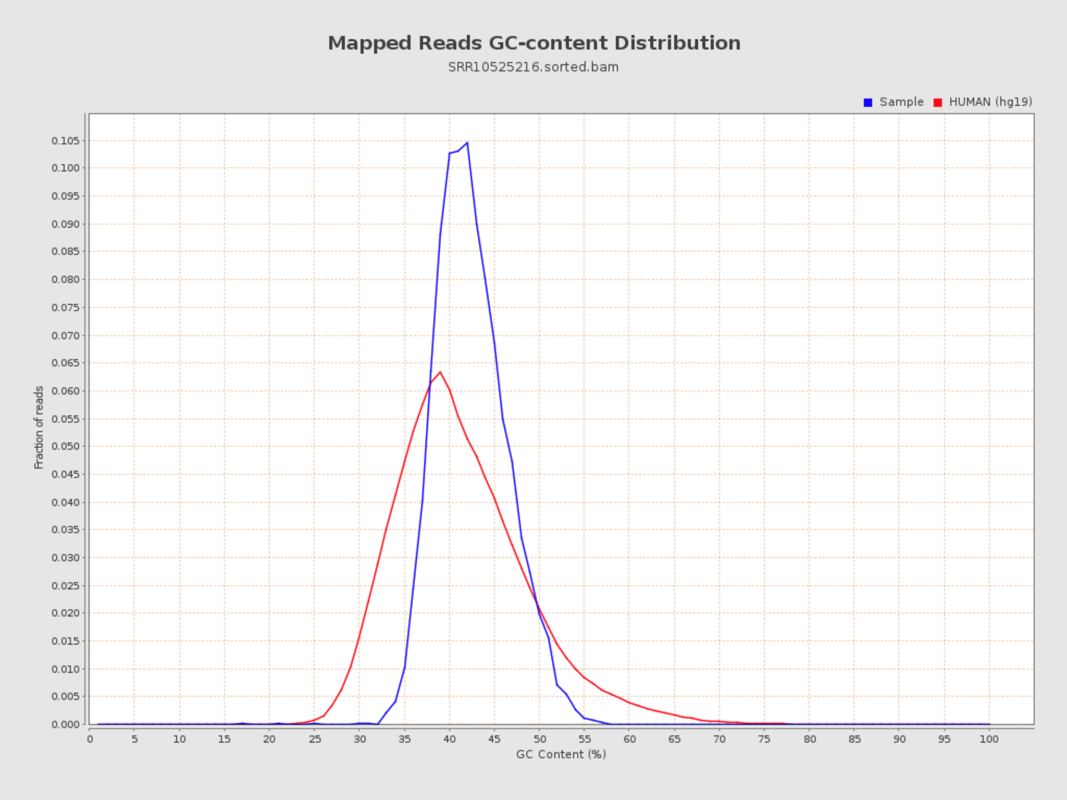
7. Results : Duplication Rate Histogram



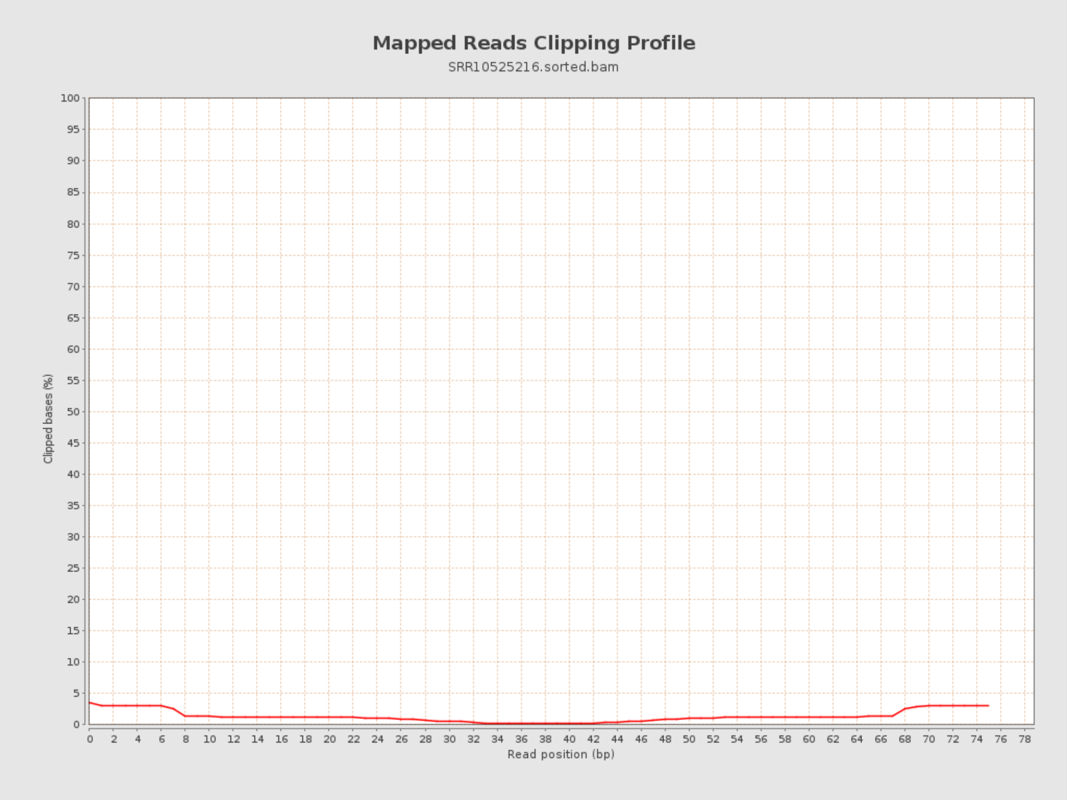
8. Results : Mapped Reads Nucleotide Content



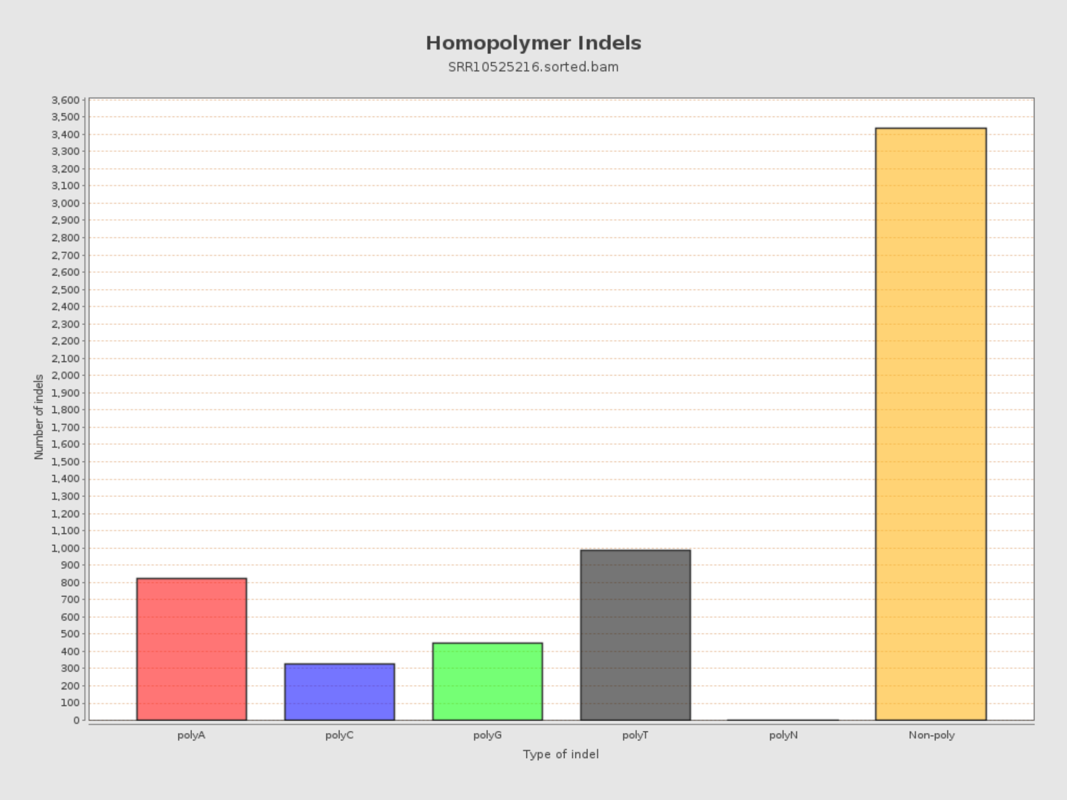
9. Results : Mapped Reads GC-content Distribution



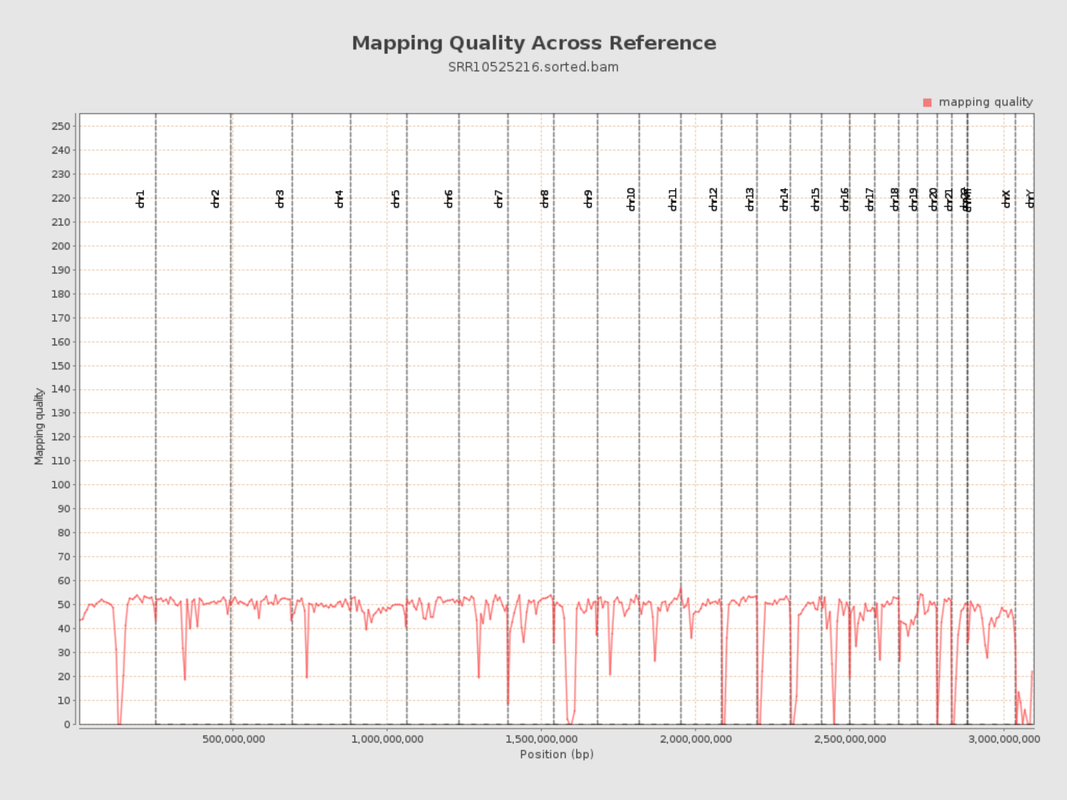
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram