Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:28:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525176.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_SRR10525176 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525176.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:28:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525176.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,865,970
Mapped reads	3,504,838 / 90.66%
Unmapped reads	361,132 / 9.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,024 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	221,298 / 5.72%
Duplication rate	4.7%
Clipped reads	3,508,053 / 90.74%

2.2. ACGT Content

Number/percentage of A's	51,068,024 / 25.27%
Number/percentage of C's	36,737,175 / 18.18%
Number/percentage of T's	65,933,045 / 32.63%
Number/percentage of G's	48,348,235 / 23.92%
Number/percentage of N's	4,641 / 0%
GC Percentage	42.1%

2.3. Coverage

Mean	0.0653

Standard Deviation	0.563

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

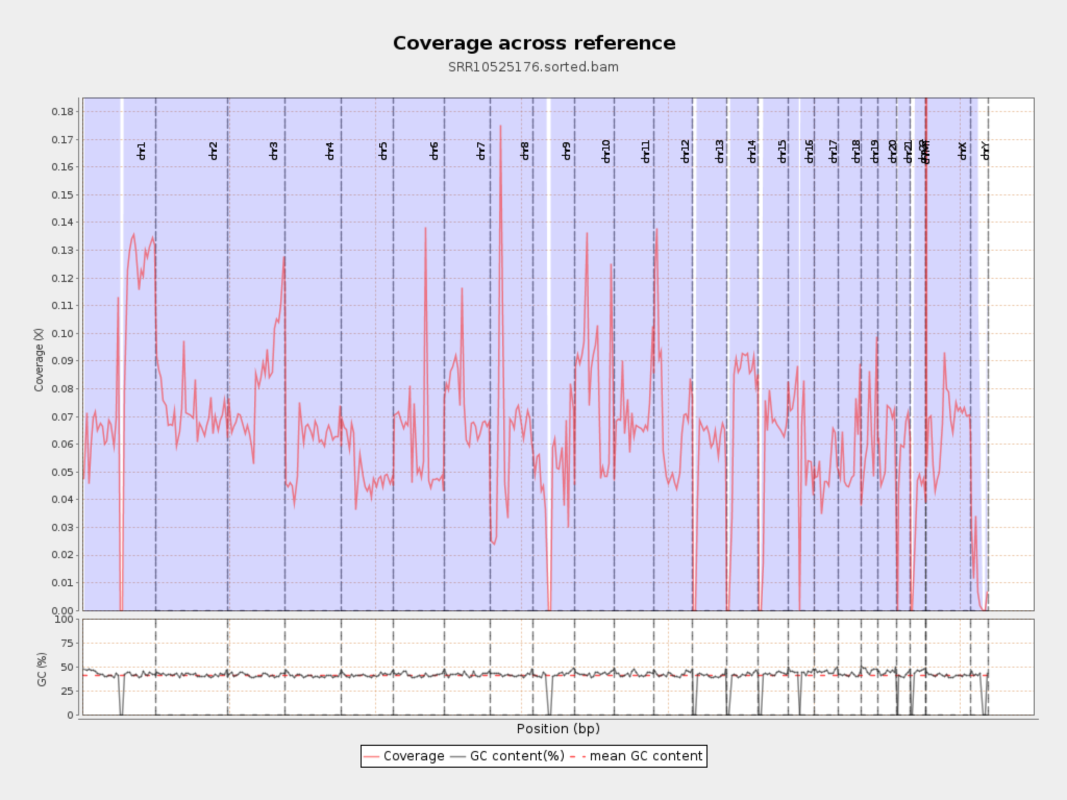
General error rate	0.52%
Mismatches	1,033,046
Insertions	12,970
Mapped reads with at least one insertion	0.37%
Deletions	40,212
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44%

2.6. Chromosome stats

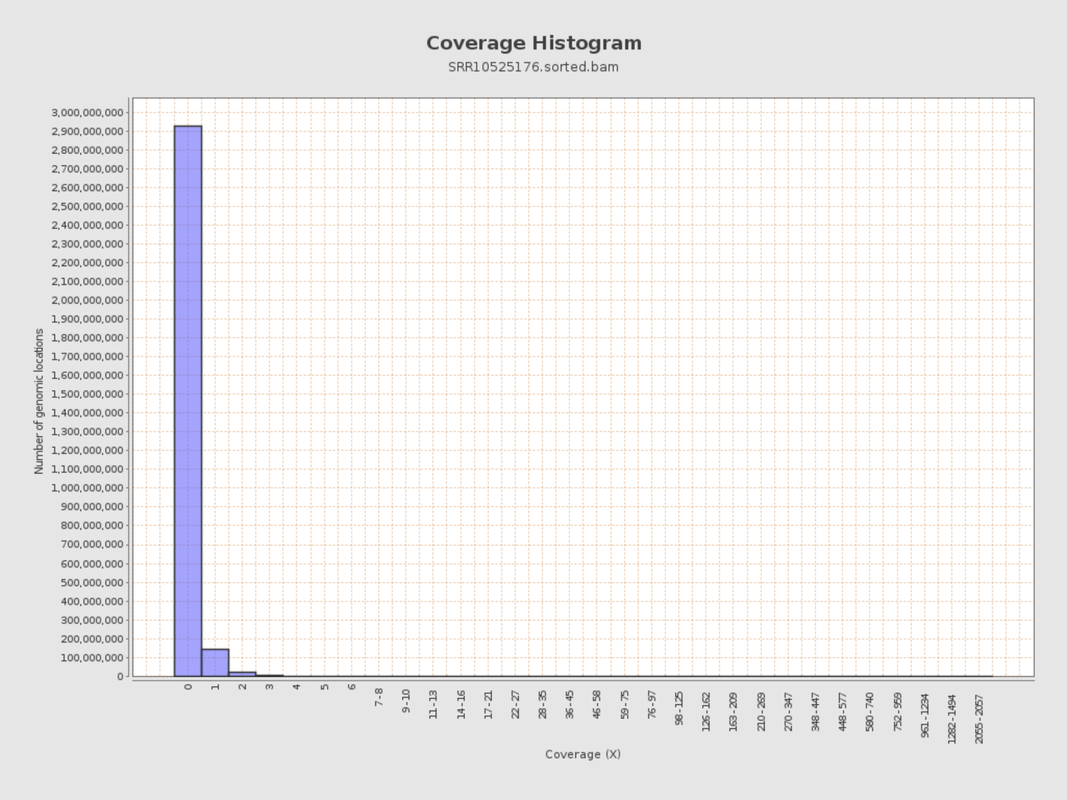
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21918721	0.0879	1.0841
chr2	243199373	17442258	0.0717	0.8767
chr3	198022430	16072294	0.0812	0.3454
chr4	191154276	11527422	0.0603	0.3219
chr5	180915260	9234547	0.051	0.2686
chr6	171115067	10465999	0.0612	0.3696
chr7	159138663	11929479	0.075	0.8239

chr8	146364022	9704925	0.0663	0.5004
chr9	141213431	6748146	0.0478	0.3853
chr10	135534747	11312151	0.0835	0.5777
chr11	135006516	9475334	0.0702	0.4334
chr12	133851895	9362427	0.0699	0.3213
chr13	115169878	6343055	0.0551	0.2857
chr14	107349540	7863278	0.0732	0.3333
chr15	102531392	5633314	0.0549	0.2935
chr16	90354753	5493112	0.0608	0.3473
chr17	81195210	4133487	0.0509	0.2863
chr18	78077248	4367418	0.0559	0.8143
chr19	59128983	3779892	0.0639	0.748
chr20	63025520	3843118	0.061	0.3016
chr21	48129895	2648123	0.055	0.3055
chr22	51304566	1679460	0.0327	0.2147
chrMT	16571	116363	7.0221	5.0433
chrX	155270560	10441722	0.0672	0.361
chrY	59373566	618835	0.0104	0.265

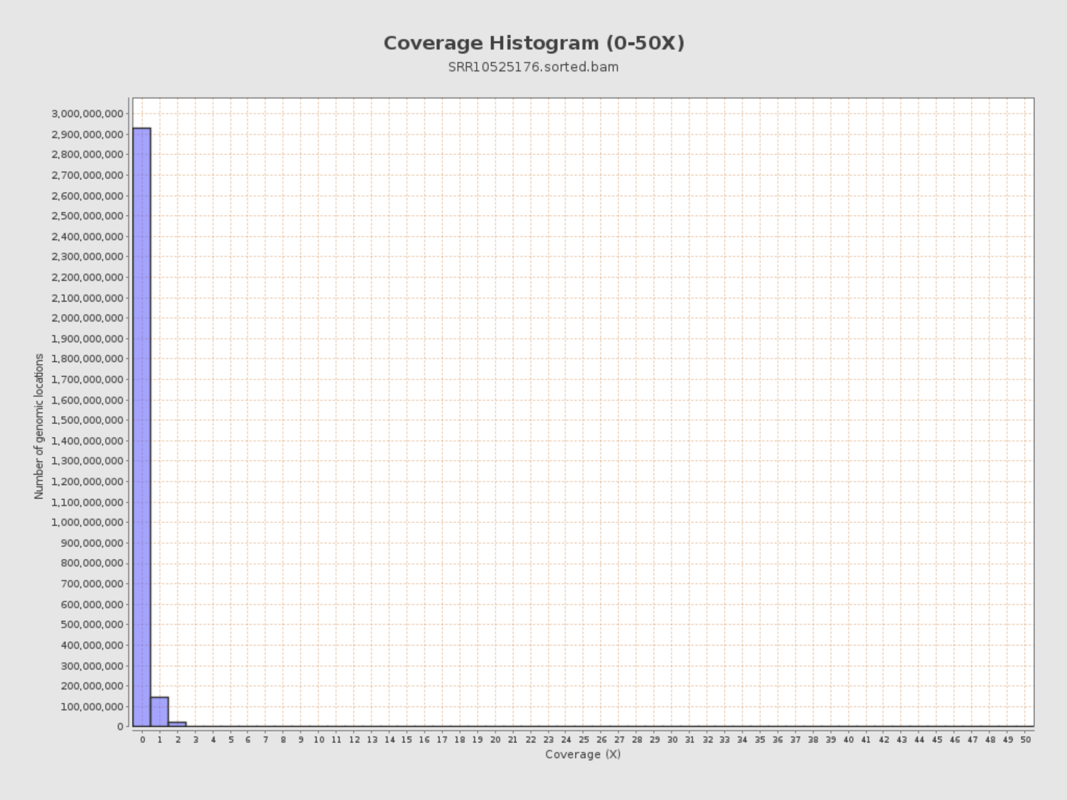
3. Results : Coverage across reference



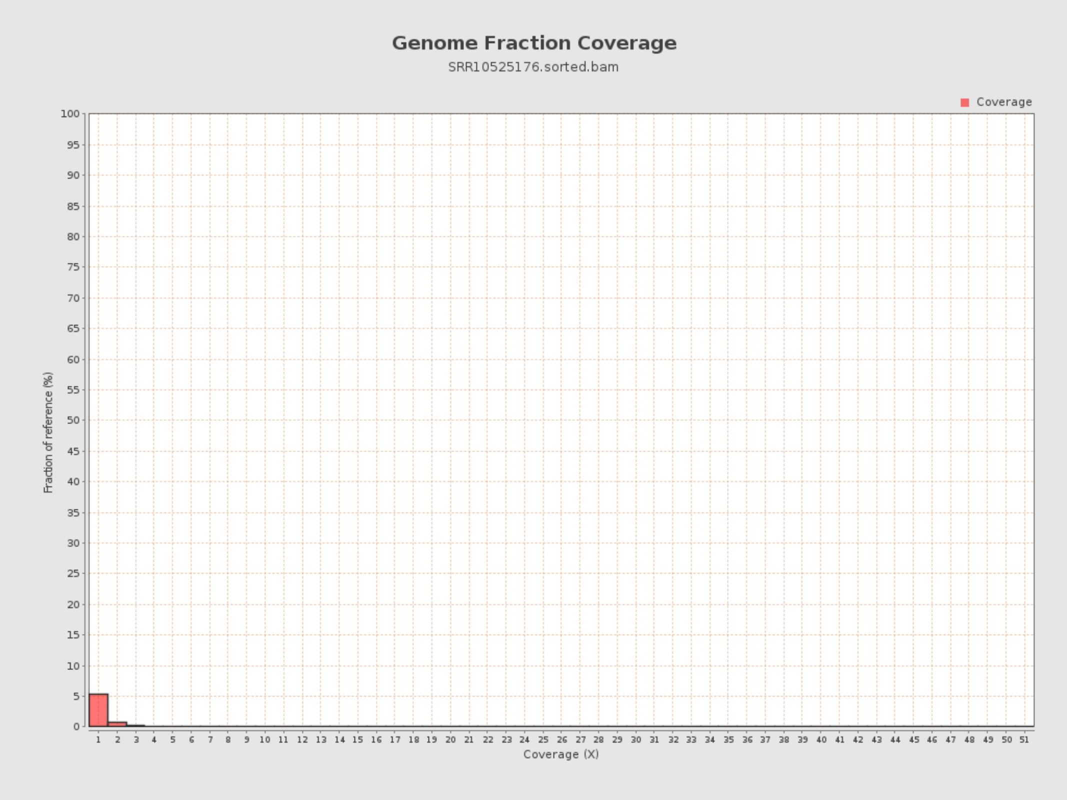
4. Results : Coverage Histogram



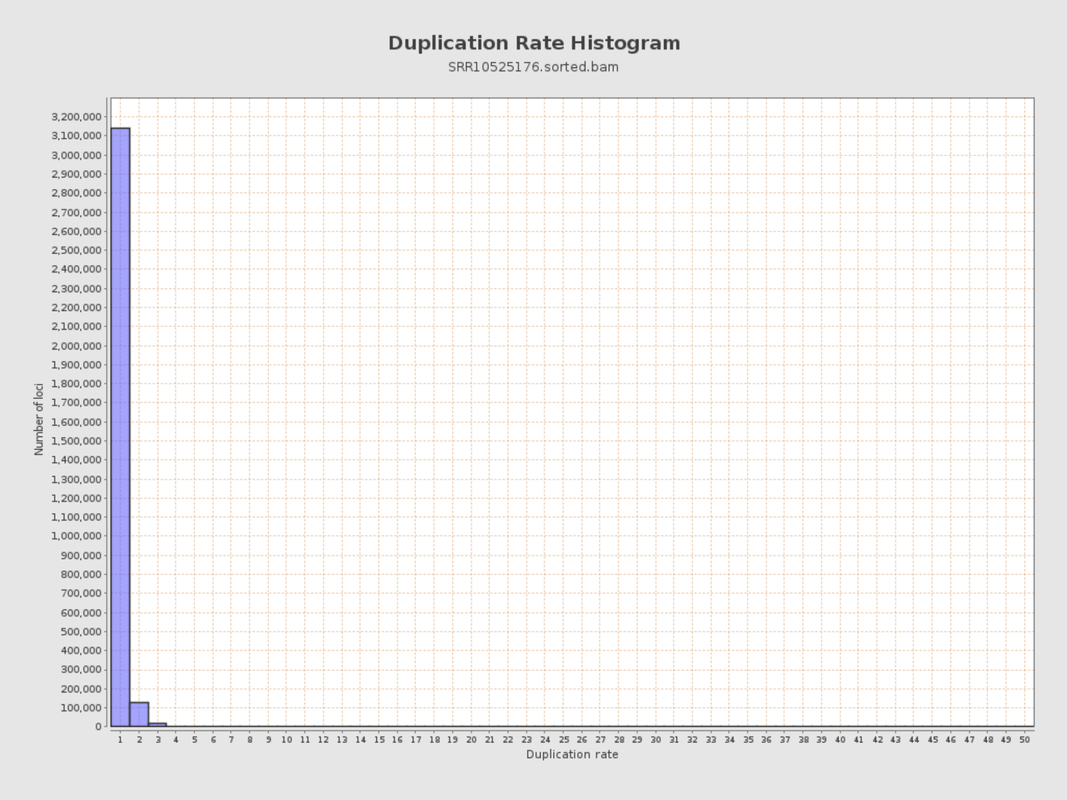
5. Results : Coverage Histogram (0-50X)



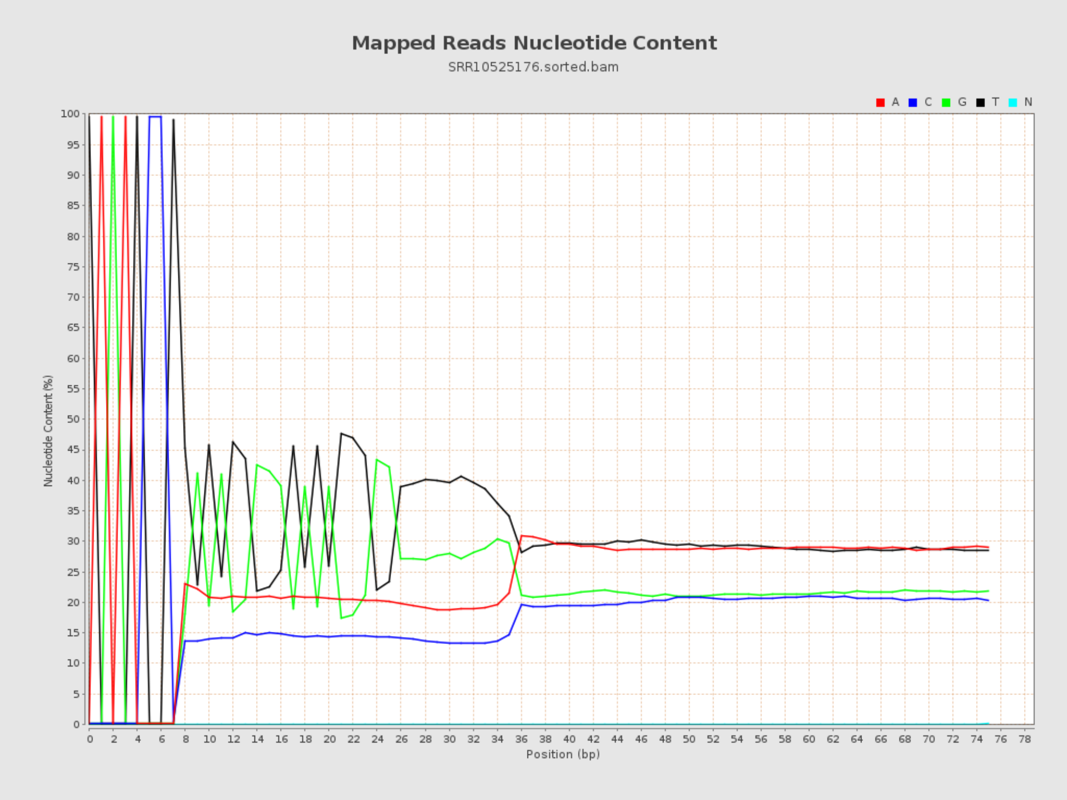
6. Results : Genome Fraction Coverage



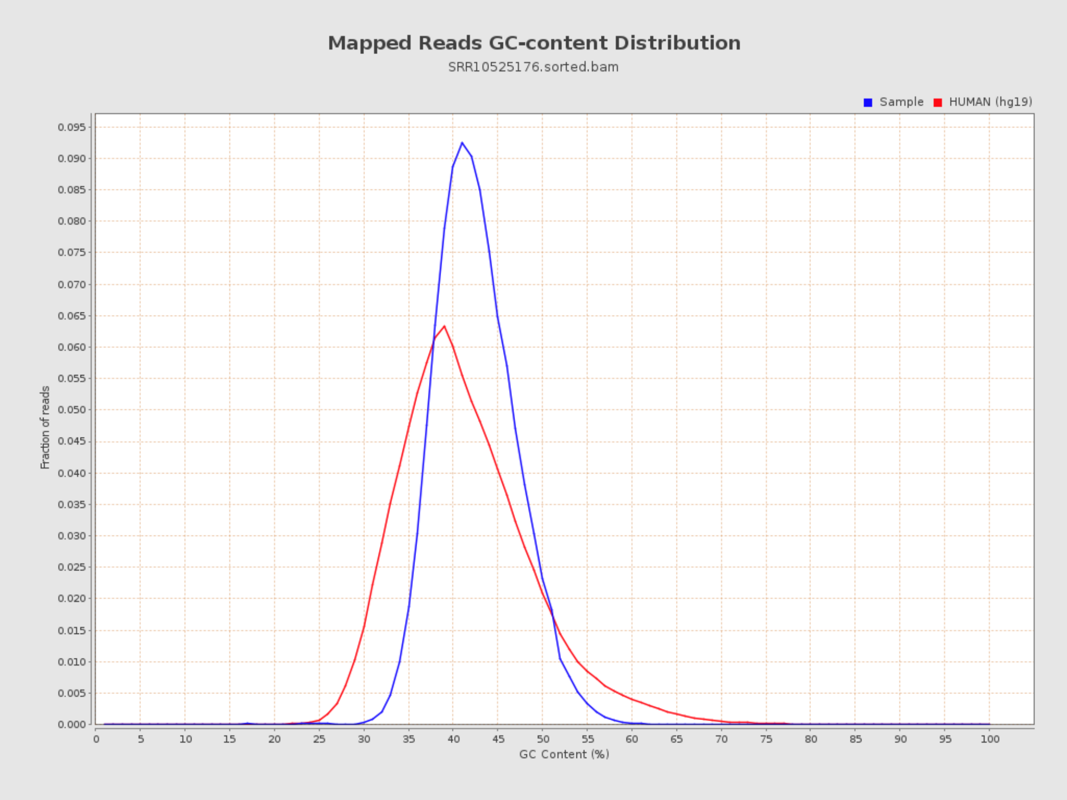
7. Results : Duplication Rate Histogram



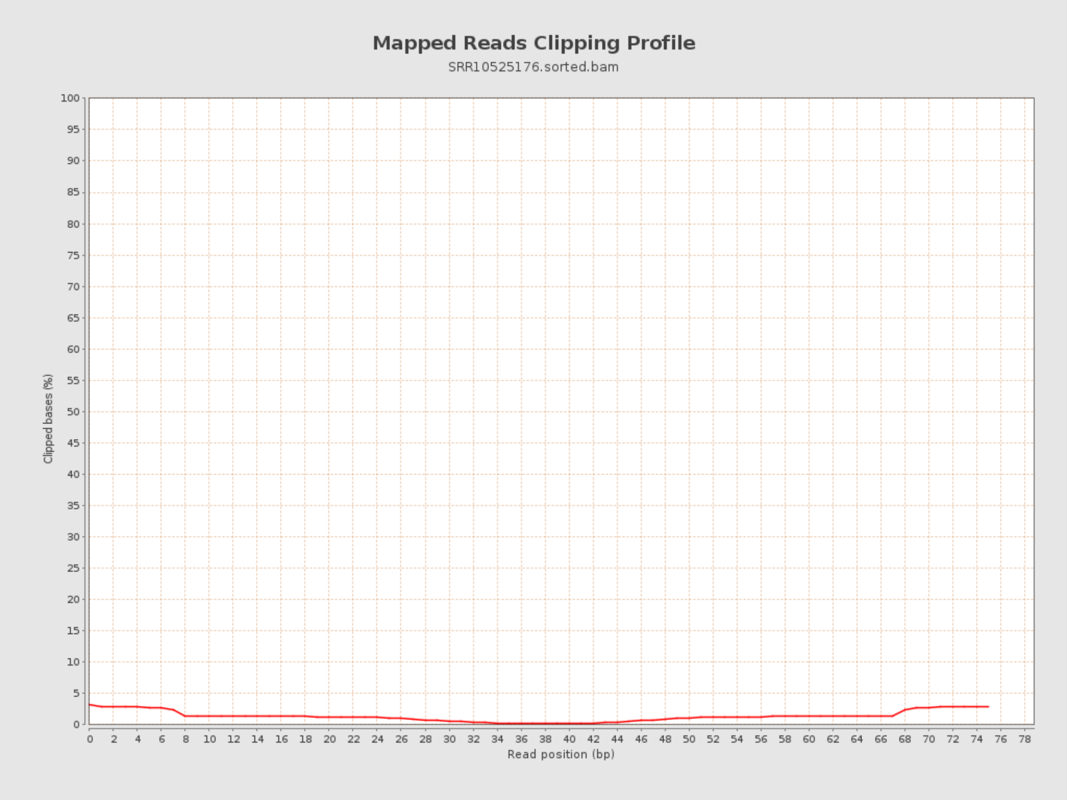
8. Results : Mapped Reads Nucleotide Content



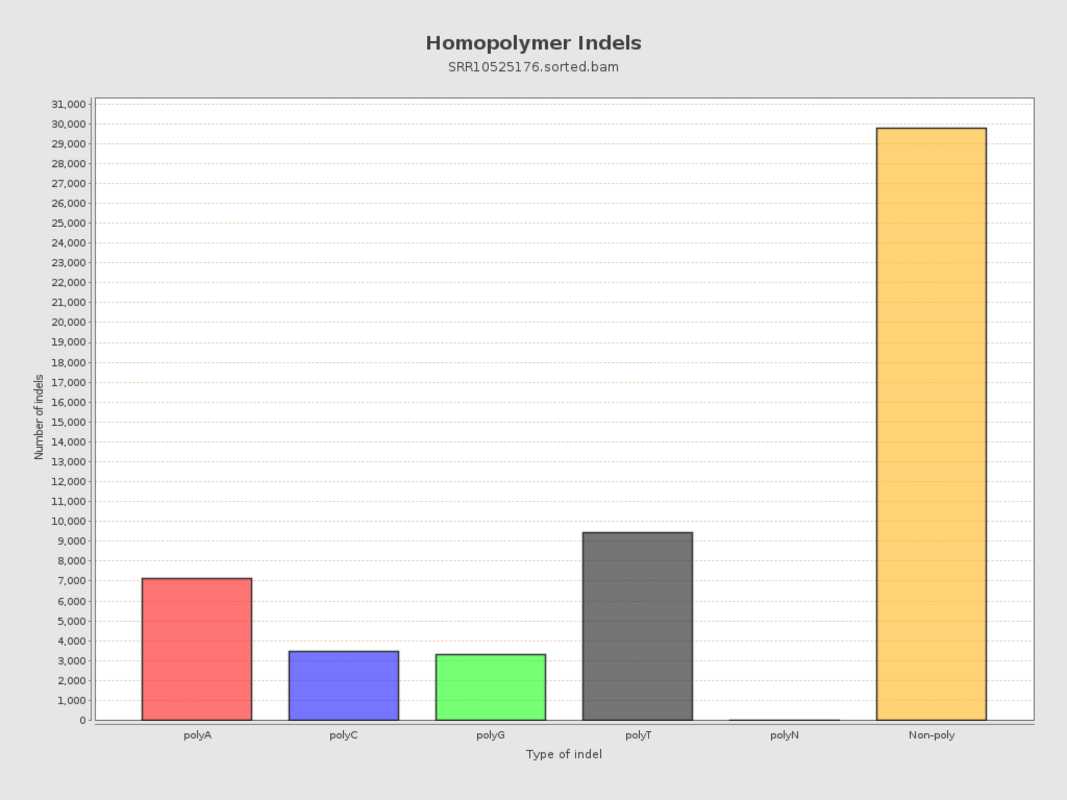
9. Results : Mapped Reads GC-content Distribution



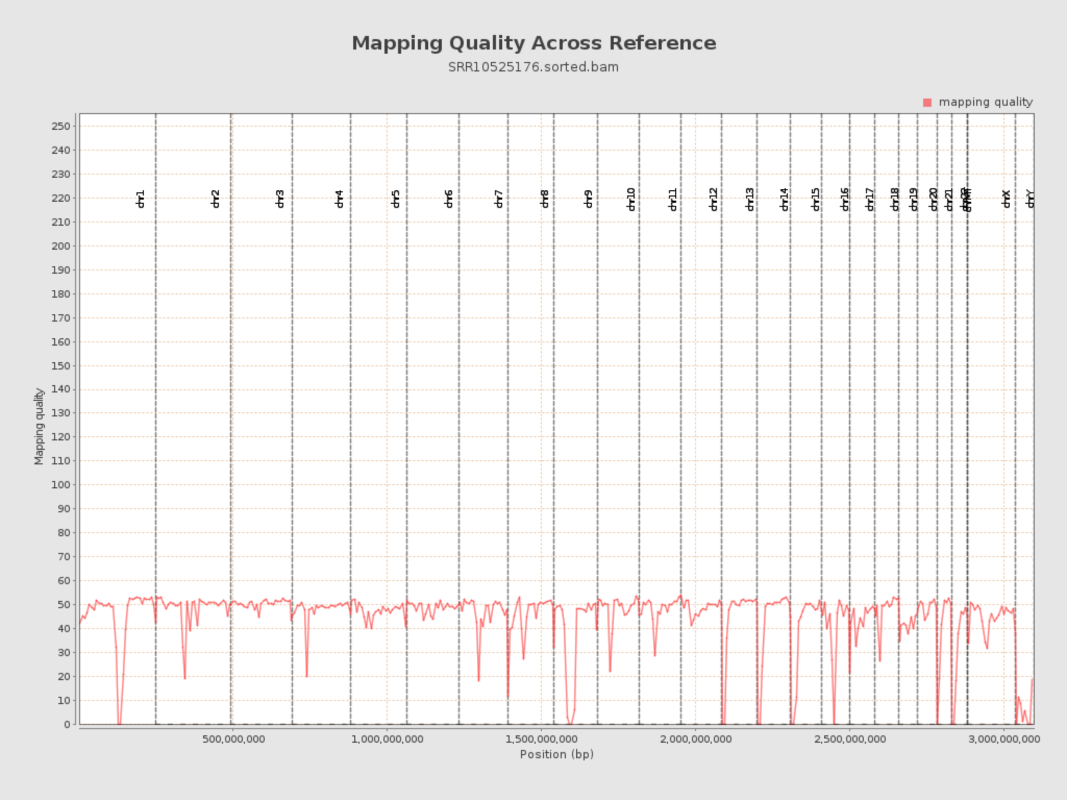
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram