Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:04:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525126.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_SRR10525126 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525126.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:04:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525126.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,384,910
Mapped reads	1,278,549 / 92.32%
Unmapped reads	106,361 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,780 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	32,921 / 2.38%
Duplication rate	1.96%
Clipped reads	1,280,809 / 92.48%

2.2. ACGT Content

Number/percentage of A's	20,126,895 / 26.88%
Number/percentage of C's	14,467,902 / 19.32%
Number/percentage of T's	23,481,661 / 31.36%
Number/percentage of G's	16,803,953 / 22.44%
Number/percentage of N's	2,181 / 0%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2261

2.4. Mapping Quality

Mean Mapping Quality	46.09

2.5. Mismatches and indels

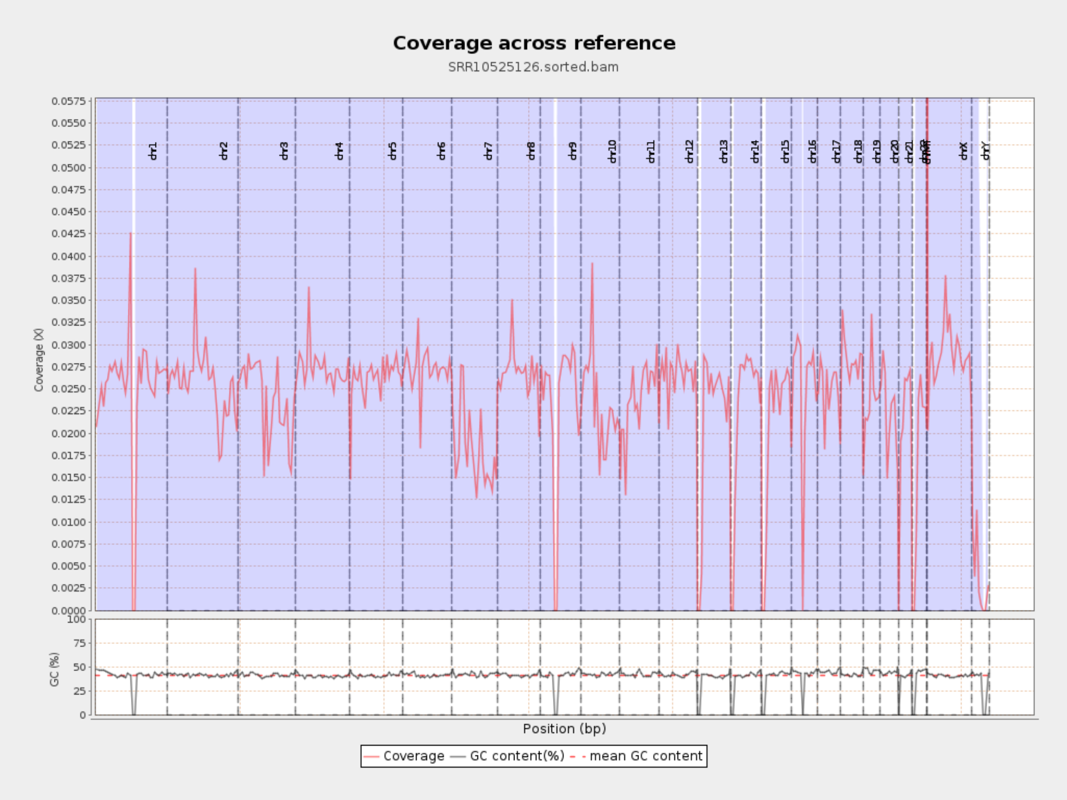
General error rate	0.48%
Mismatches	351,826
Insertions	4,929
Mapped reads with at least one insertion	0.38%
Deletions	12,061
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.46%

2.6. Chromosome stats

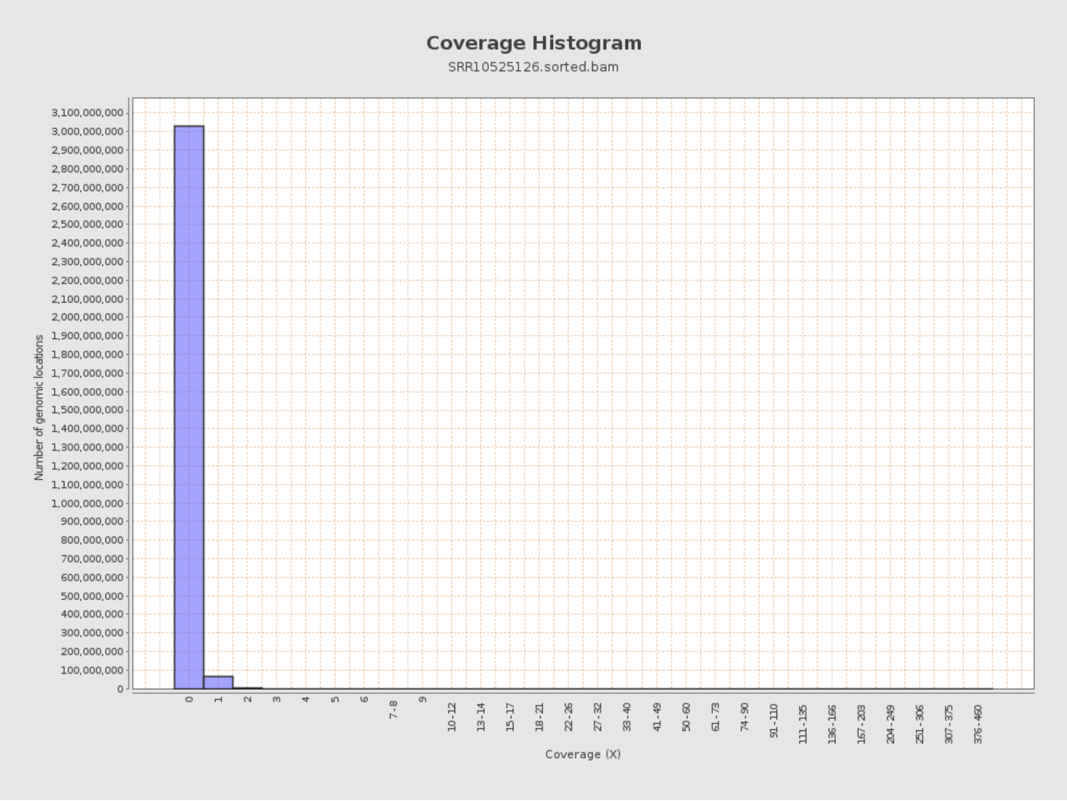
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6236470	0.025	0.4259
chr2	243199373	6252405	0.0257	0.2106
chr3	198022430	4723802	0.0239	0.1654
chr4	191154276	5229954	0.0274	0.1884
chr5	180915260	4802330	0.0265	0.1755
chr6	171115067	4665440	0.0273	0.1904
chr7	159138663	2884885	0.0181	0.1834

chr8	146364022	3946180	0.027	0.2764
chr9	141213431	3288025	0.0233	0.2008
chr10	135534747	3178078	0.0234	0.2062
chr11	135006516	3218968	0.0238	0.2002
chr12	133851895	3578427	0.0267	0.1788
chr13	115169878	2454585	0.0213	0.1567
chr14	107349540	2411731	0.0225	0.1674
chr15	102531392	2099850	0.0205	0.1543
chr16	90354753	2230706	0.0247	0.1762
chr17	81195210	2019855	0.0249	0.1775
chr18	78077248	2224372	0.0285	0.3656
chr19	59128983	1426397	0.0241	0.3126
chr20	63025520	1406760	0.0223	0.1655
chr21	48129895	1026082	0.0213	0.1661
chr22	51304566	857237	0.0167	0.1385
chrMT	16571	25267	1.5248	1.5104
chrX	155270560	4504757	0.029	0.1992
chrY	59373566	209835	0.0035	0.0894

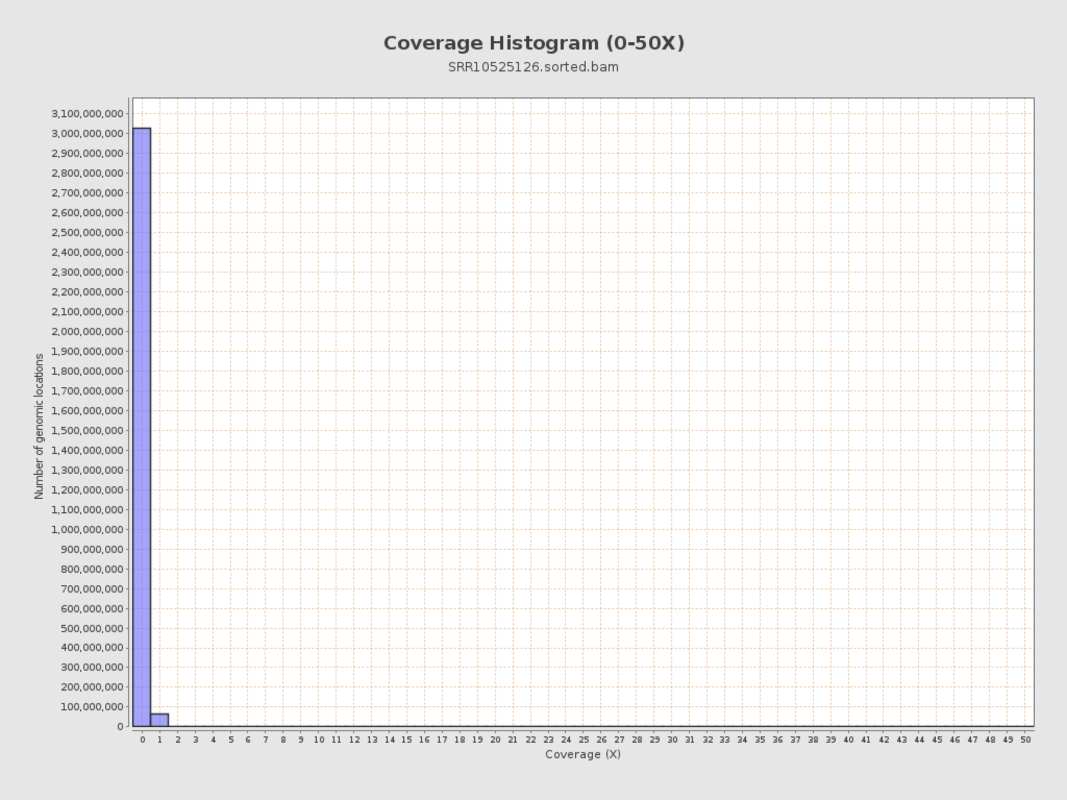
3. Results : Coverage across reference



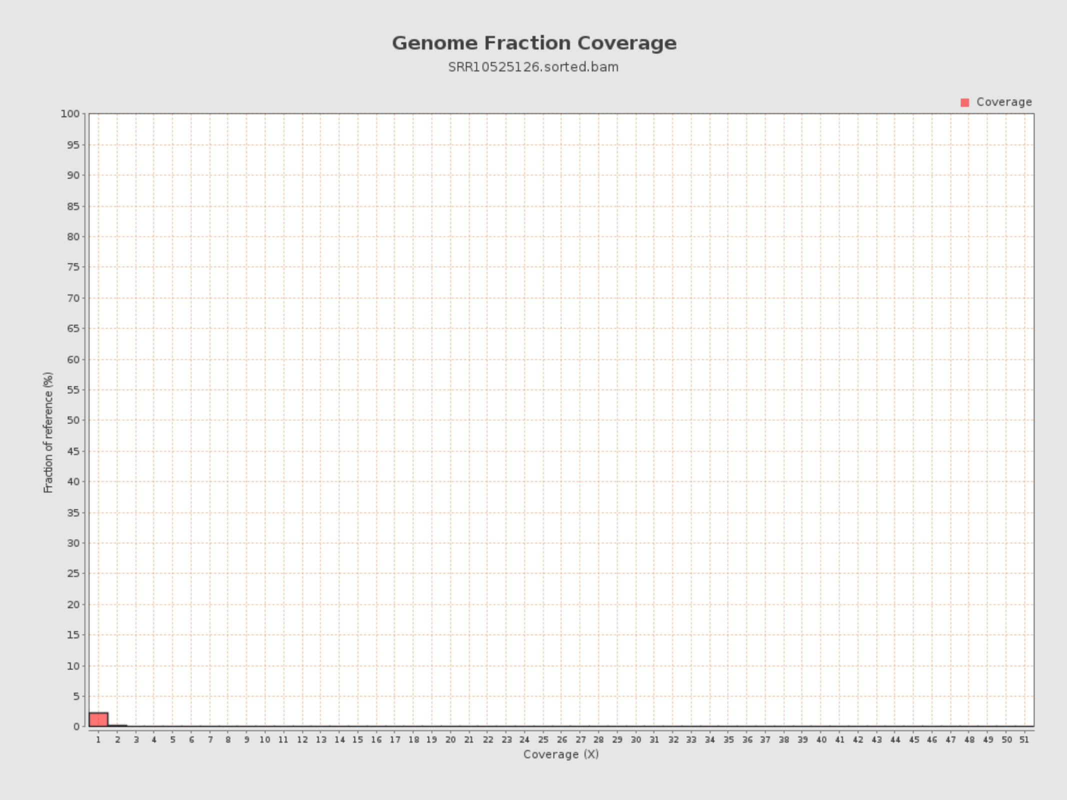
4. Results : Coverage Histogram



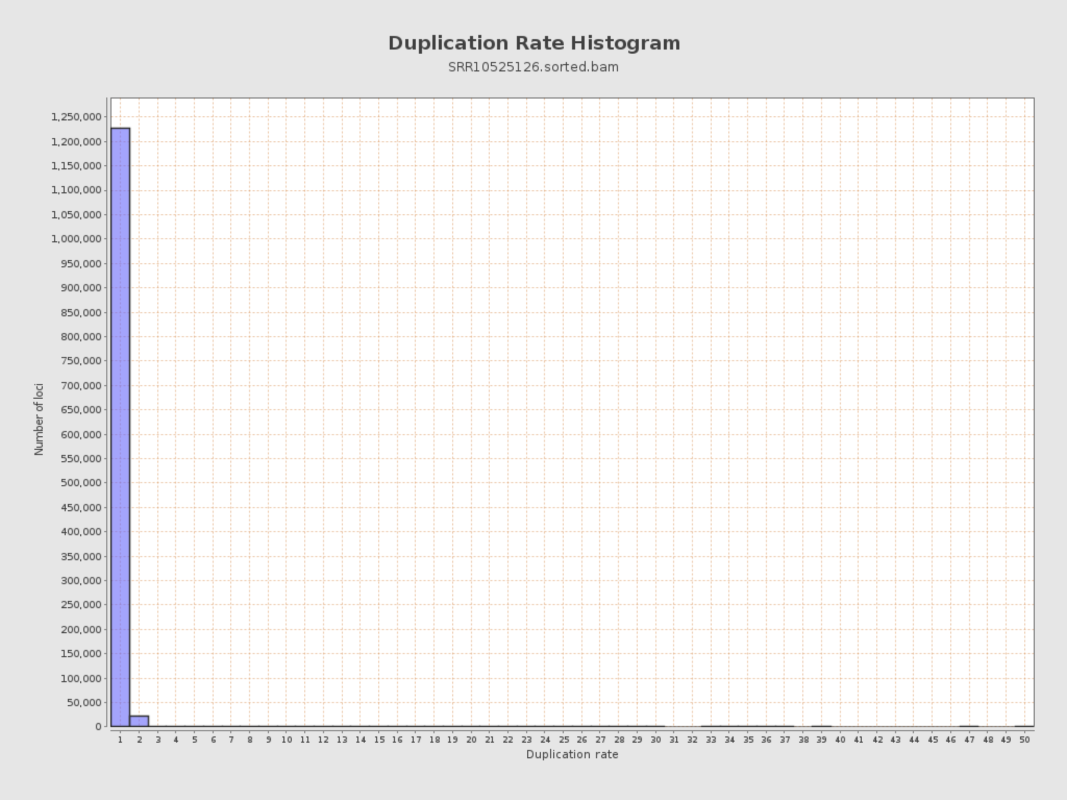
5. Results : Coverage Histogram (0-50X)



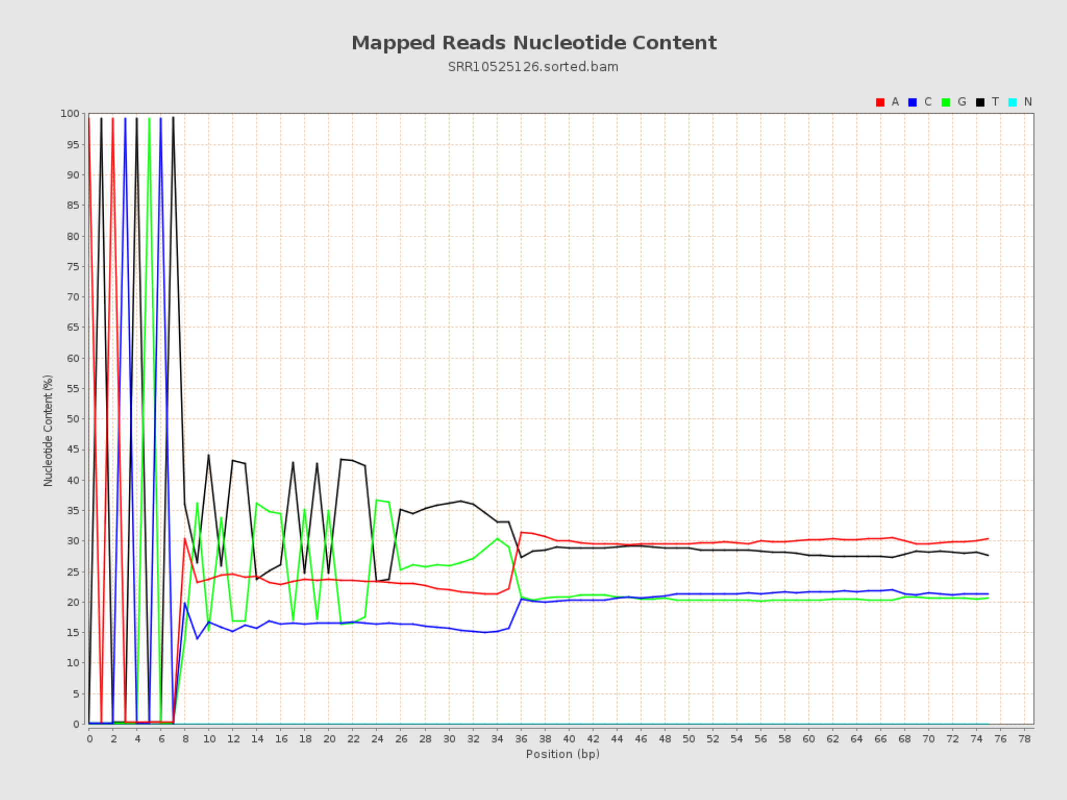
6. Results : Genome Fraction Coverage



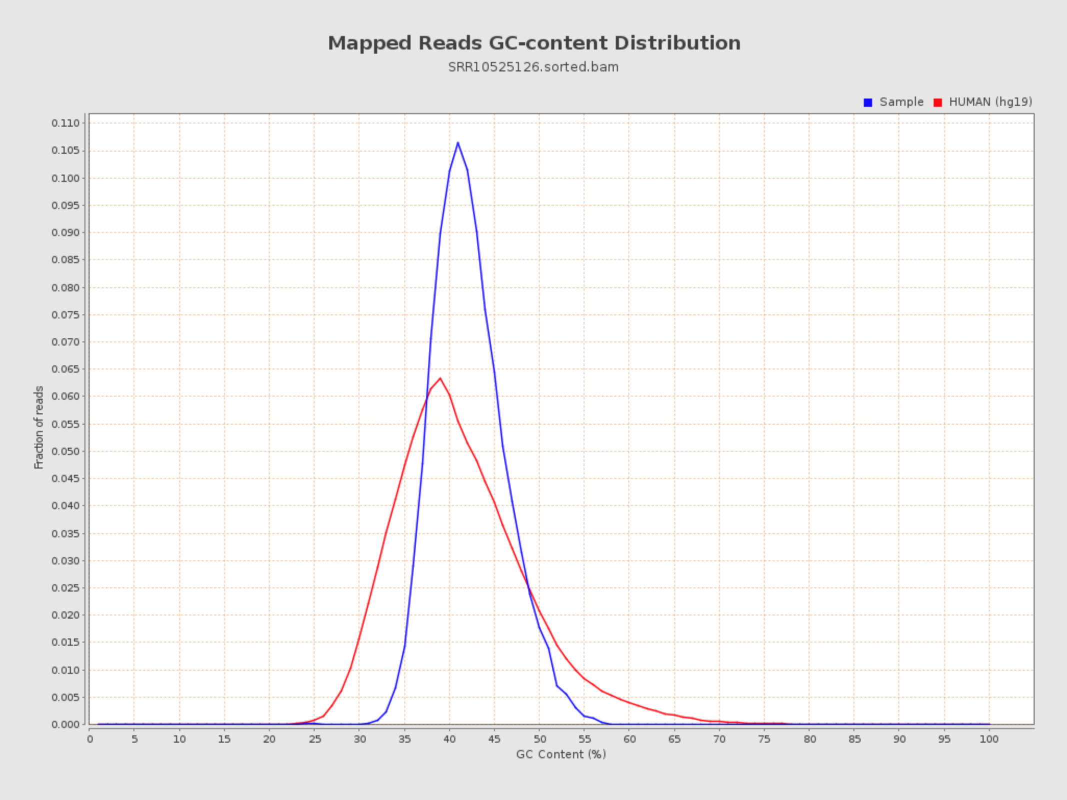
7. Results : Duplication Rate Histogram



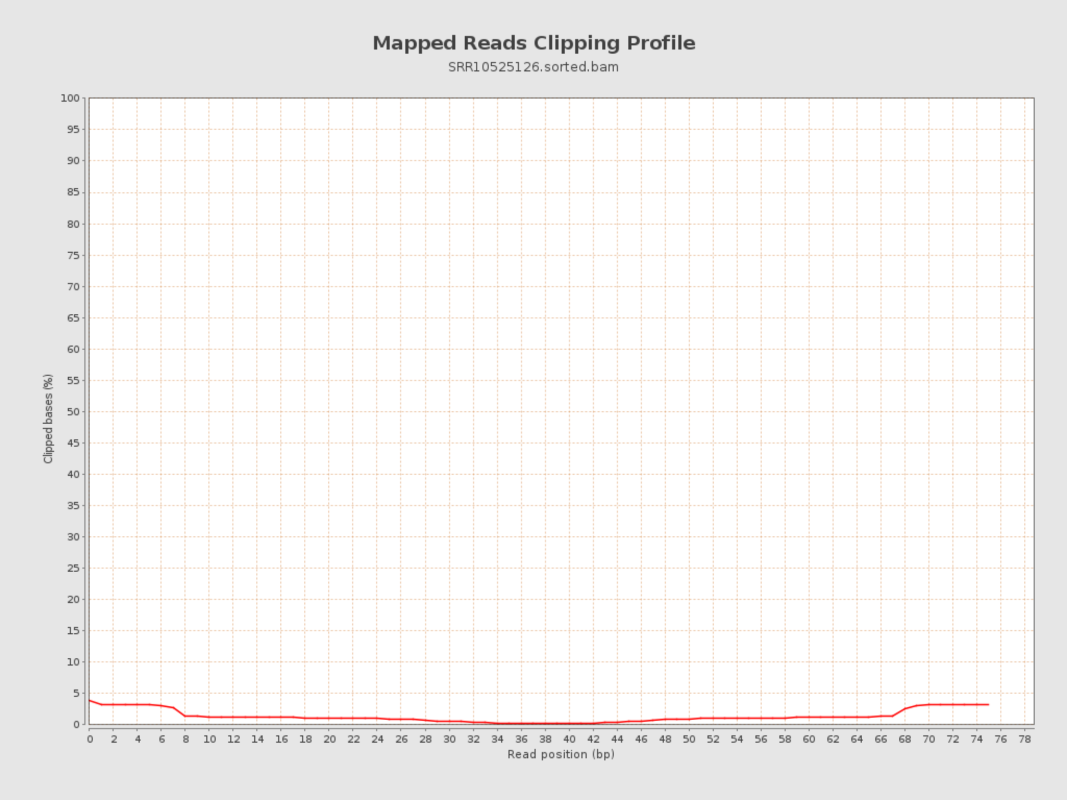
8. Results : Mapped Reads Nucleotide Content



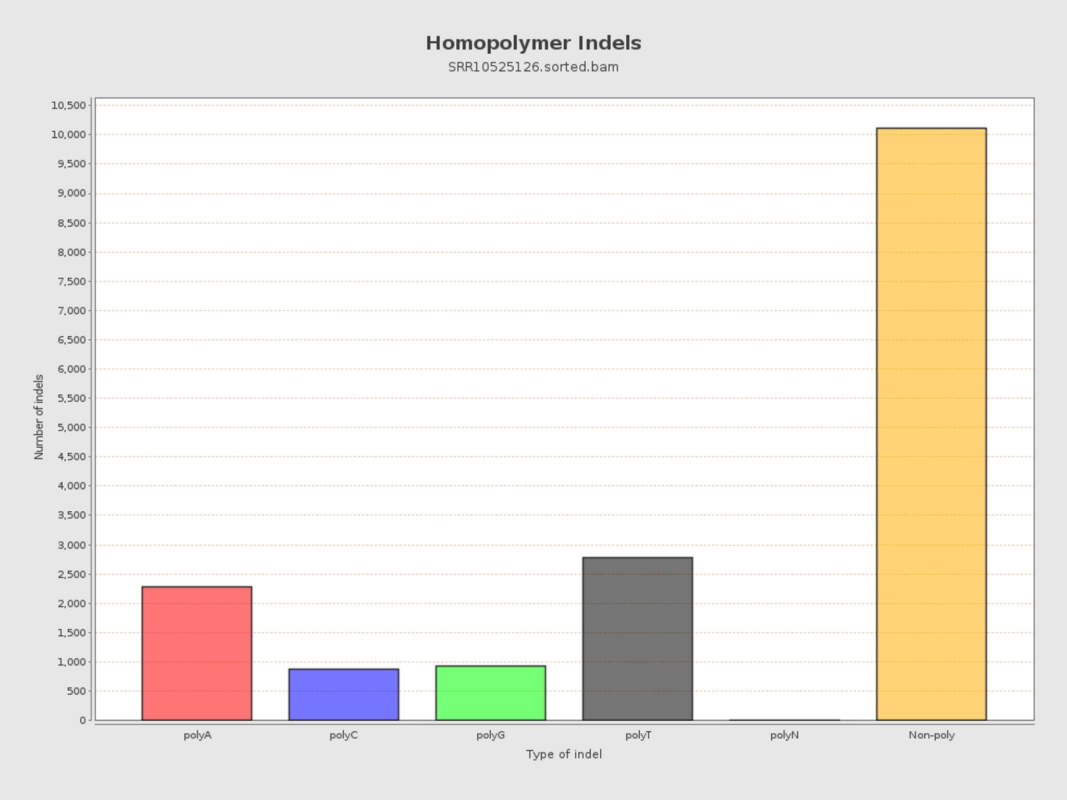
9. Results : Mapped Reads GC-content Distribution



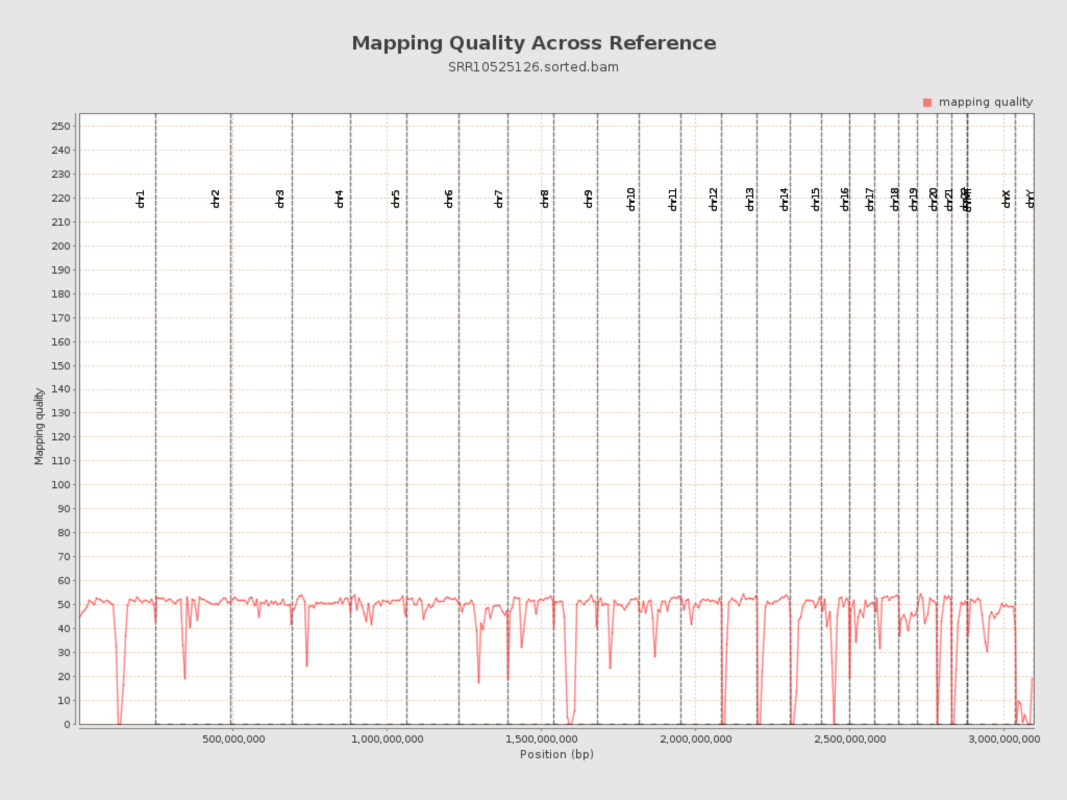
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram