Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:09:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525039.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_SRR10525039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525039.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:09:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525039.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,106,667
Mapped reads	1,013,084 / 91.54%
Unmapped reads	93,583 / 8.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,274 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	29,875 / 2.7%
Duplication rate	2.2%
Clipped reads	1,014,581 / 91.68%

2.2. ACGT Content

Number/percentage of A's	15,557,882 / 26.38%
Number/percentage of C's	10,546,290 / 17.88%
Number/percentage of T's	18,397,939 / 31.19%
Number/percentage of G's	14,481,462 / 24.55%
Number/percentage of N's	534 / 0%
GC Percentage	42.43%

2.3. Coverage

Mean	0.0191

Standard Deviation	0.1905

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

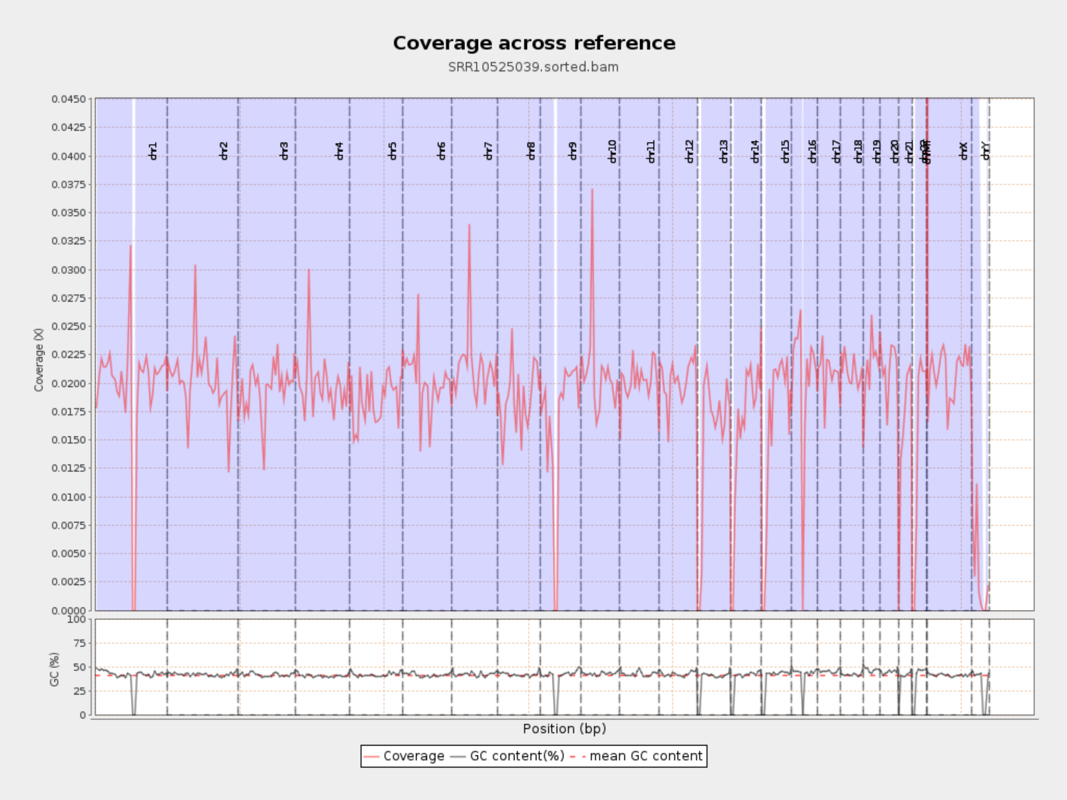
General error rate	0.51%
Mismatches	291,419
Insertions	4,085
Mapped reads with at least one insertion	0.4%
Deletions	11,410
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.17%

2.6. Chromosome stats

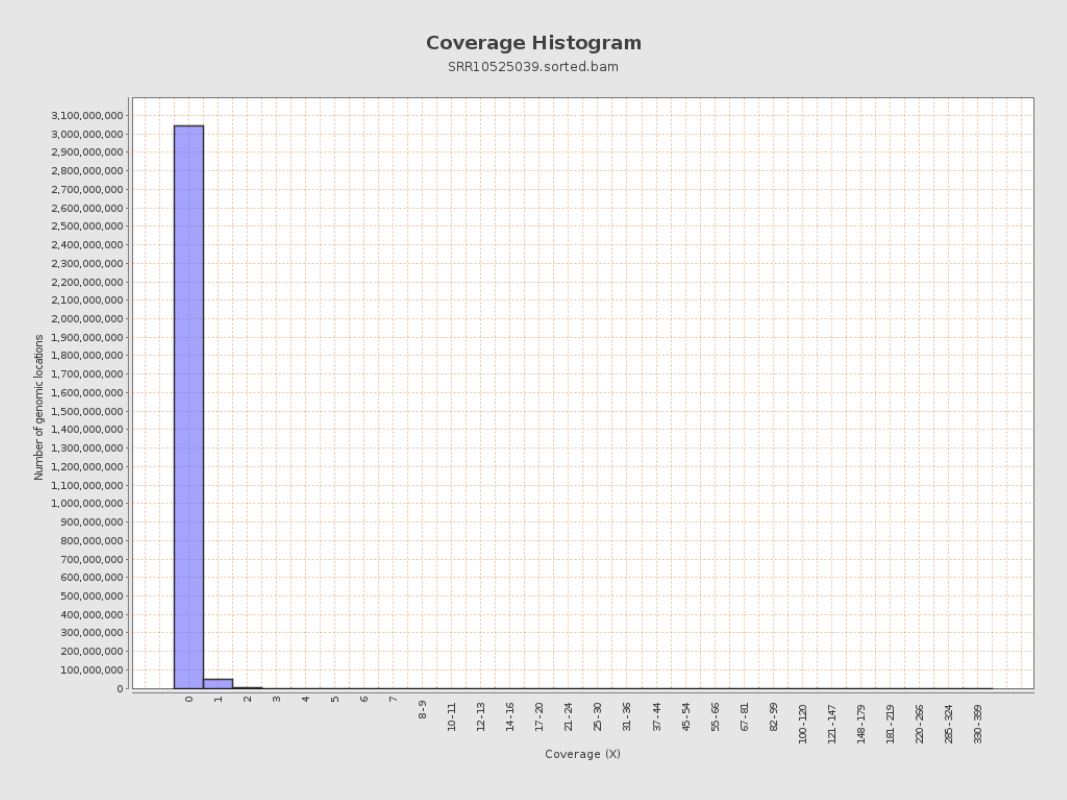
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4898881	0.0197	0.3146
chr2	243199373	4961140	0.0204	0.2129
chr3	198022430	3848512	0.0194	0.1485
chr4	191154276	3829174	0.02	0.1622
chr5	180915260	3358658	0.0186	0.1455
chr6	171115067	3445058	0.0201	0.1771
chr7	159138663	3432275	0.0216	0.2324

chr8	146364022	2726924	0.0186	0.1914
chr9	141213431	2347255	0.0166	0.1605
chr10	135534747	2859731	0.0211	0.1994
chr11	135006516	2751684	0.0204	0.1849
chr12	133851895	2706683	0.0202	0.1528
chr13	115169878	1745340	0.0152	0.1311
chr14	107349540	1704877	0.0159	0.1368
chr15	102531392	1638547	0.016	0.1356
chr16	90354753	1812875	0.0201	0.1587
chr17	81195210	1697737	0.0209	0.1659
chr18	78077248	1643120	0.021	0.263
chr19	59128983	1284190	0.0217	0.2314
chr20	63025520	1334290	0.0212	0.1577
chr21	48129895	787013	0.0164	0.1471
chr22	51304566	751979	0.0147	0.1282
chrMT	16571	9765	0.5893	0.8517
chrX	155270560	3242330	0.0209	0.1661
chrY	59373566	185407	0.0031	0.1009

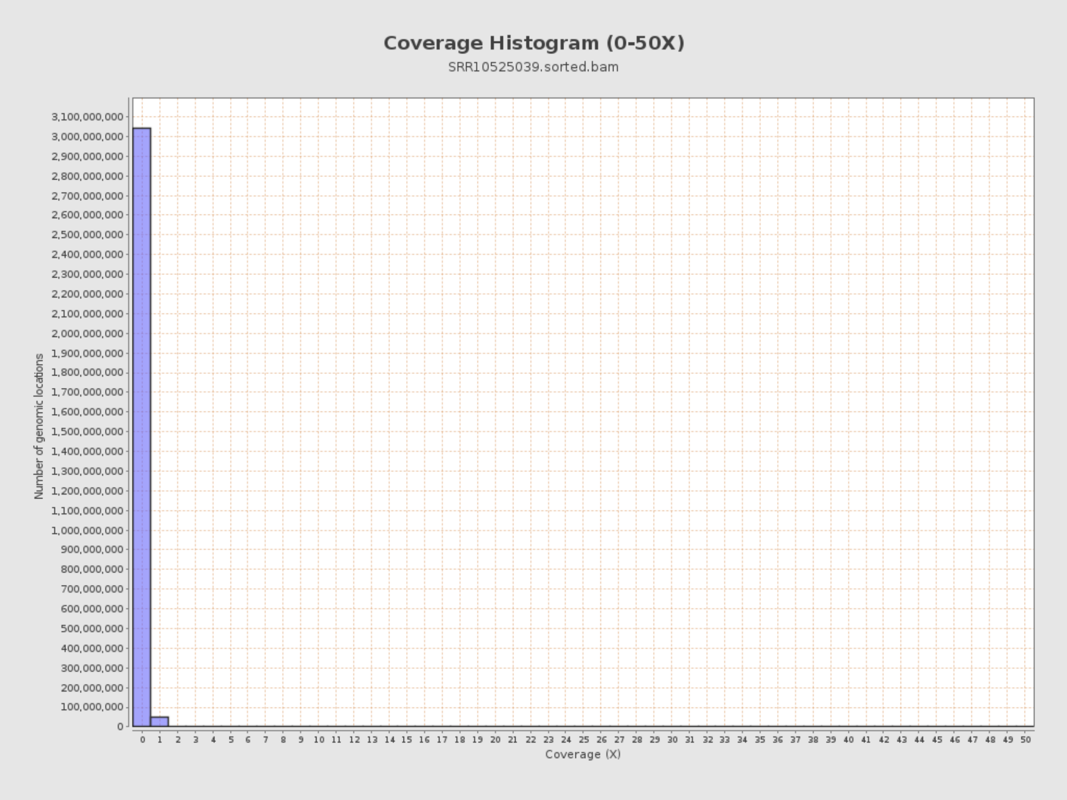
3. Results : Coverage across reference



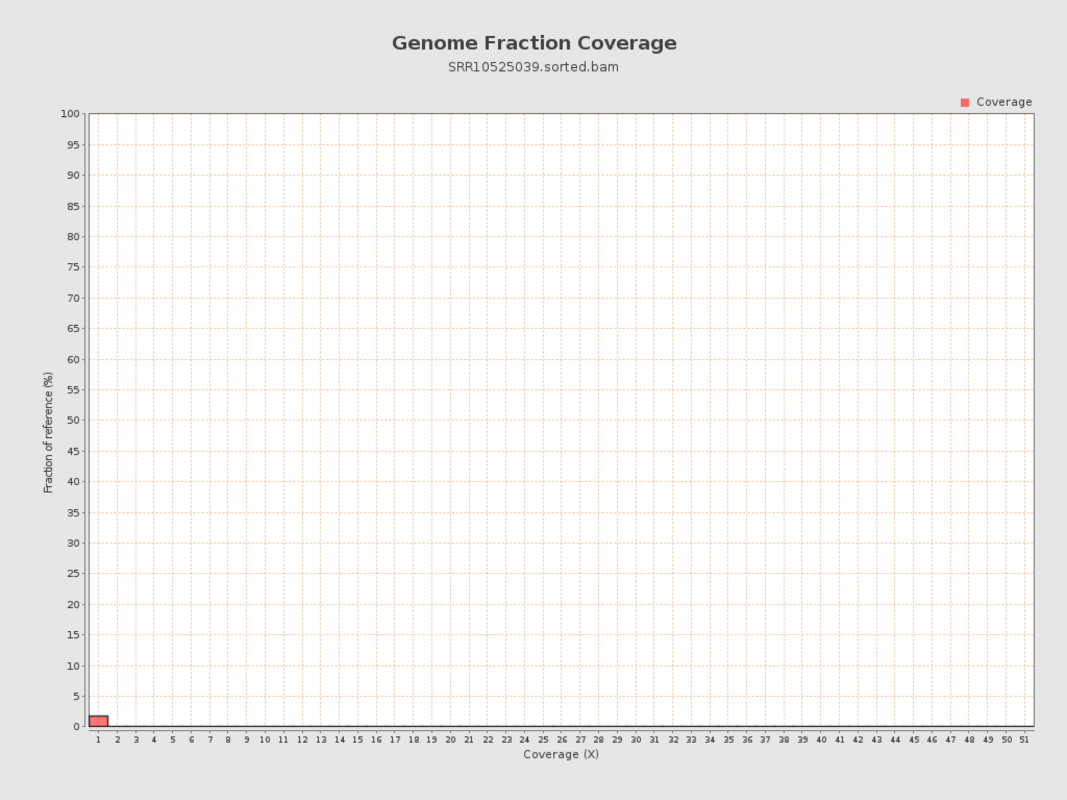
4. Results : Coverage Histogram



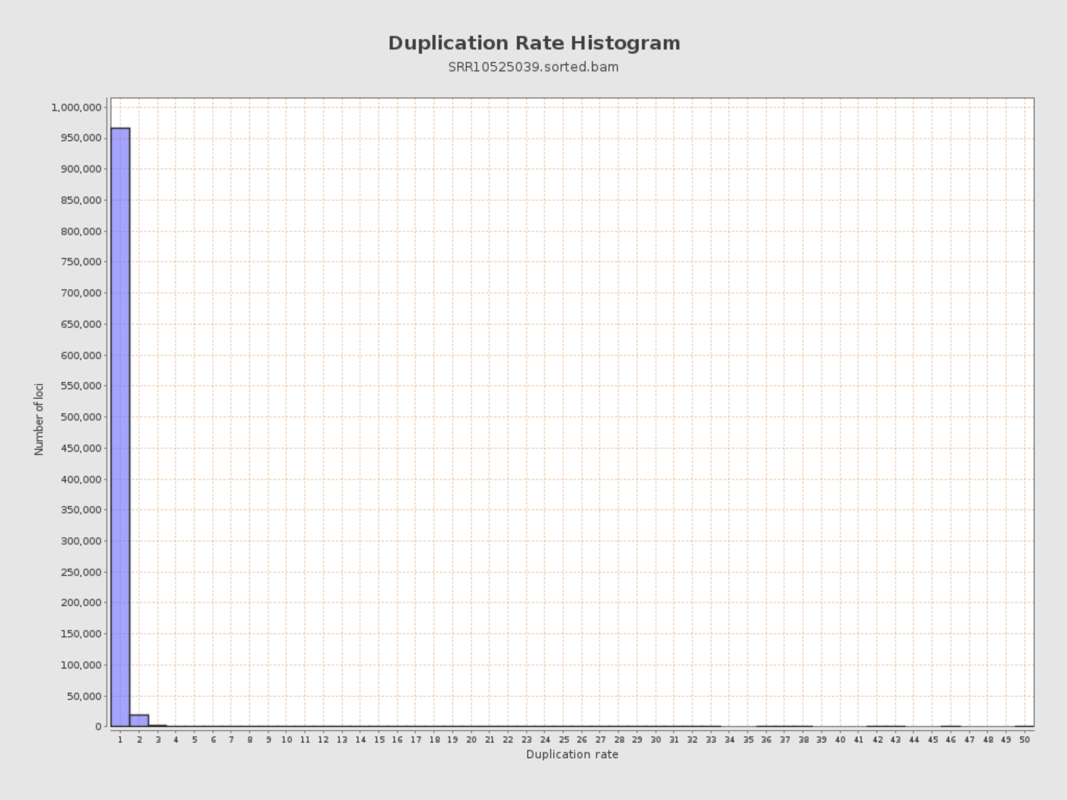
5. Results : Coverage Histogram (0-50X)



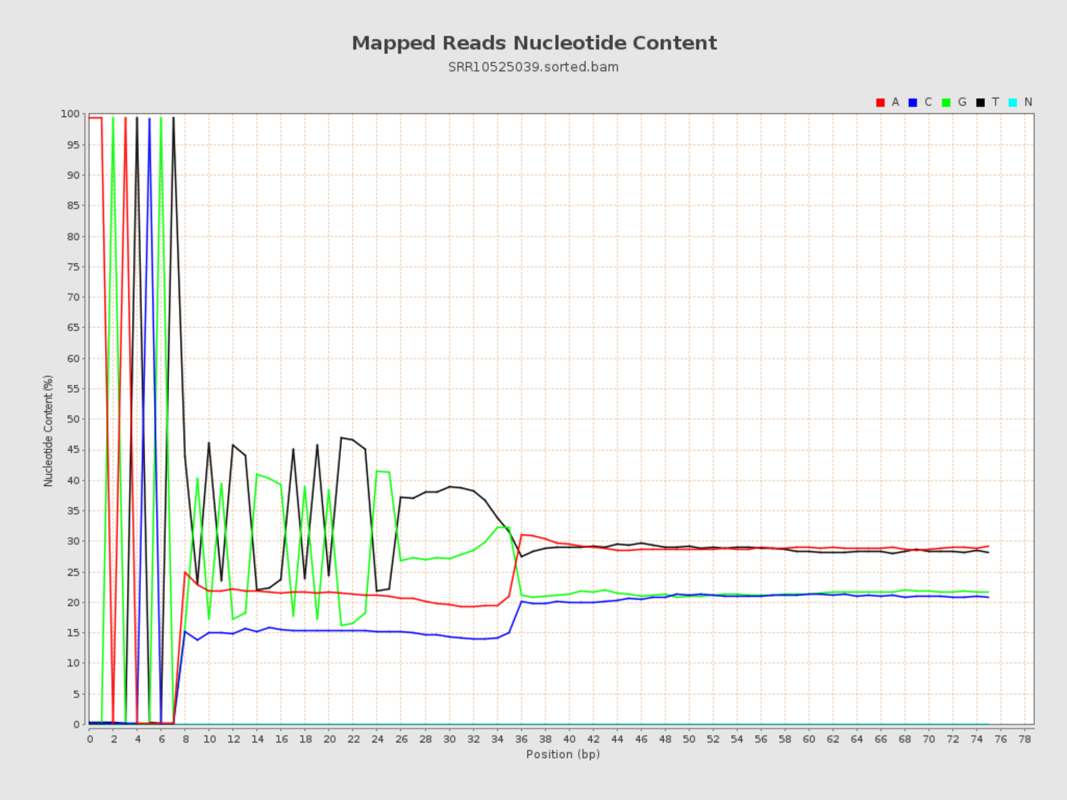
6. Results : Genome Fraction Coverage



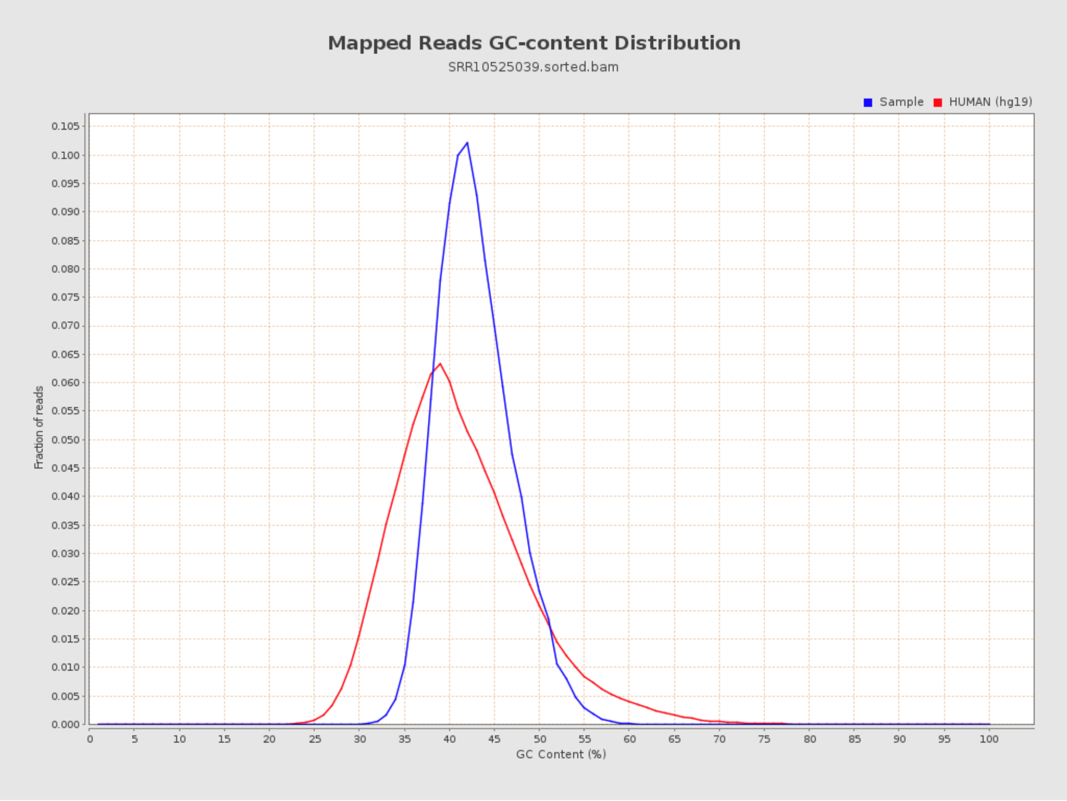
7. Results : Duplication Rate Histogram



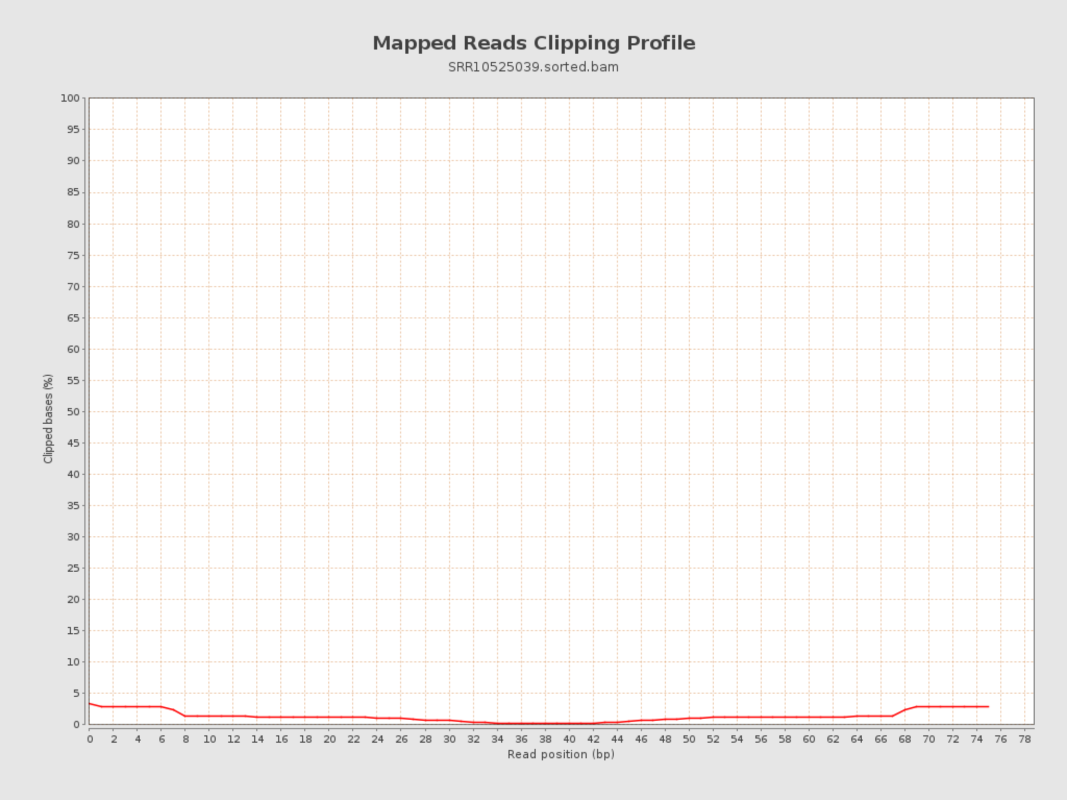
8. Results : Mapped Reads Nucleotide Content



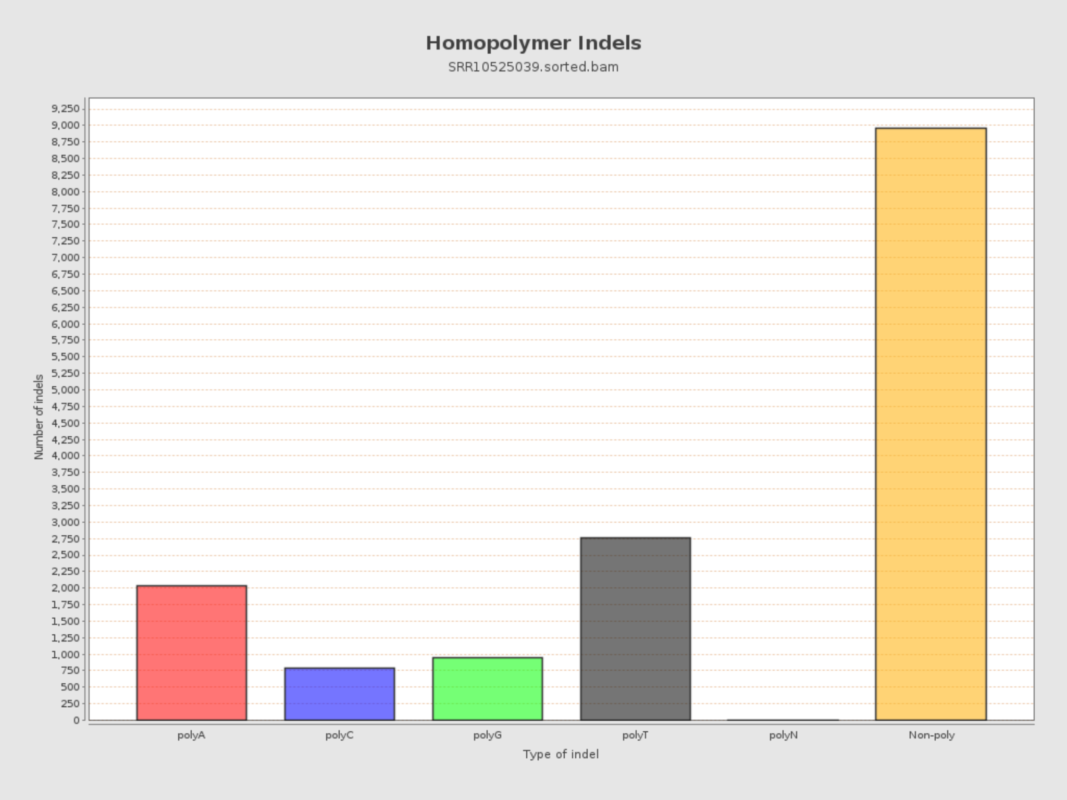
9. Results : Mapped Reads GC-content Distribution



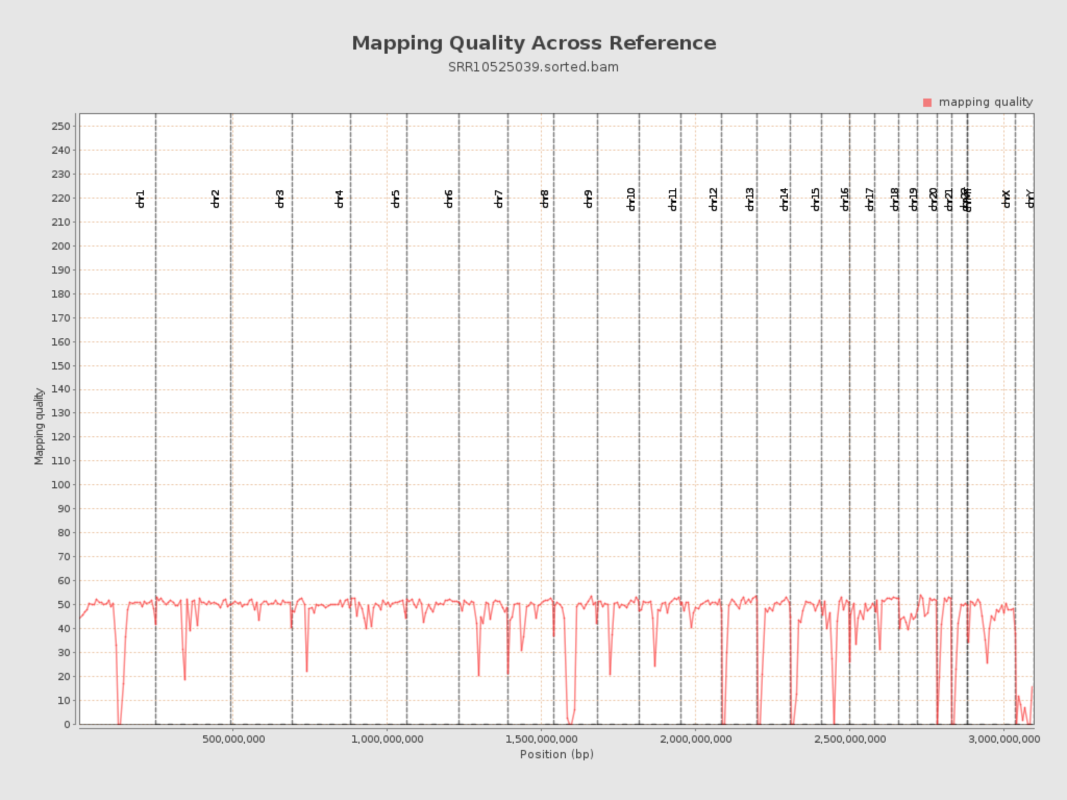
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram