Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:58:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525249.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_SRR10525249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525249.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:58:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525249.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,101,836
Mapped reads	1,005,742 / 91.28%
Unmapped reads	96,094 / 8.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,943 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	28,543 / 2.59%
Duplication rate	2.07%
Clipped reads	1,006,735 / 91.37%

2.2. ACGT Content

Number/percentage of A's	15,441,270 / 26.54%
Number/percentage of C's	10,532,854 / 18.1%
Number/percentage of T's	18,143,041 / 31.18%
Number/percentage of G's	14,071,751 / 24.18%
Number/percentage of N's	1,240 / 0%
GC Percentage	42.28%

2.3. Coverage

Mean	0.0188

Standard Deviation	0.2034

2.4. Mapping Quality

Mean Mapping Quality	45.19

2.5. Mismatches and indels

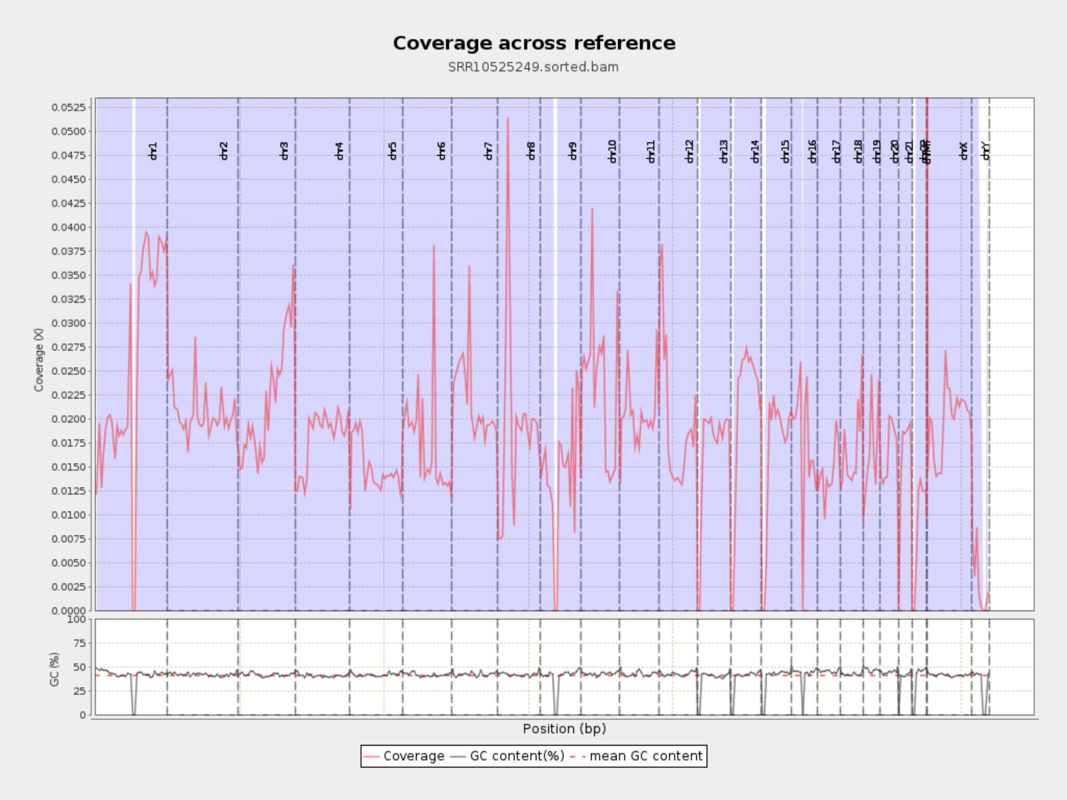
General error rate	0.52%
Mismatches	296,161
Insertions	4,640
Mapped reads with at least one insertion	0.46%
Deletions	11,788
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.51%

2.6. Chromosome stats

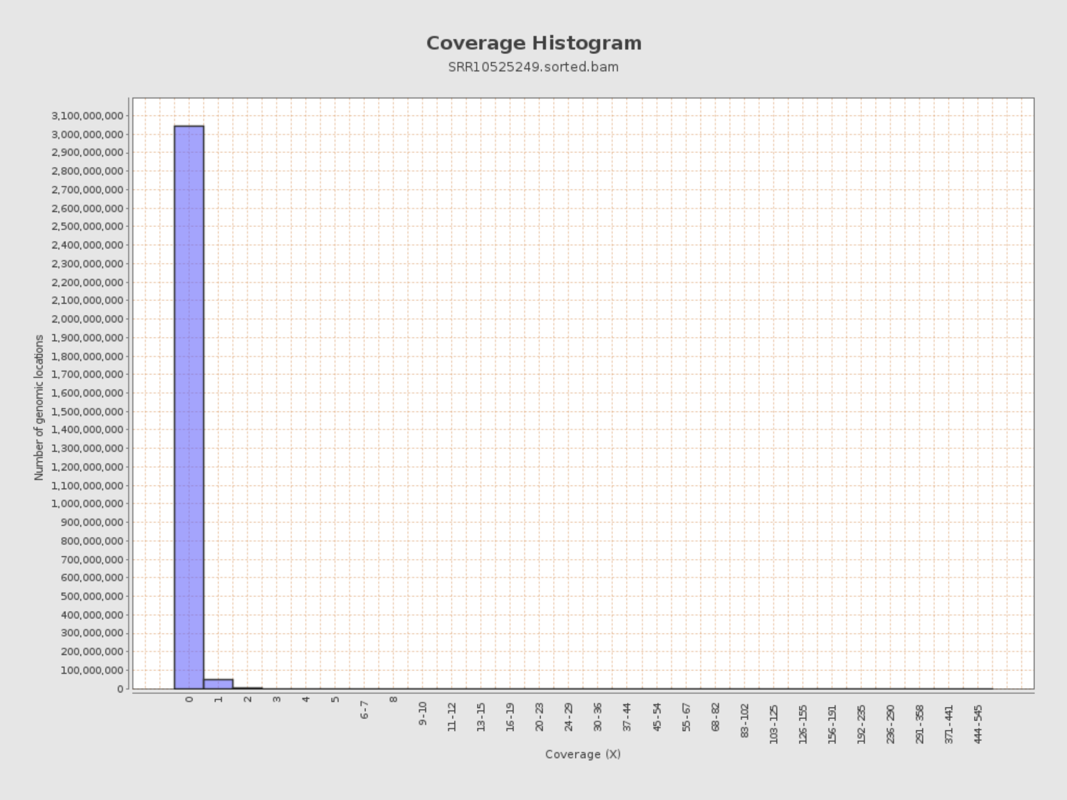
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6287924	0.0252	0.3583
chr2	243199373	5020054	0.0206	0.2658
chr3	198022430	4336667	0.0219	0.1582
chr4	191154276	3468319	0.0181	0.1473
chr5	180915260	2737673	0.0151	0.1301
chr6	171115067	3011010	0.0176	0.1535
chr7	159138663	3511962	0.0221	0.2925

chr8	146364022	2849779	0.0195	0.2022
chr9	141213431	2003872	0.0142	0.1477
chr10	135534747	3221390	0.0238	0.2293
chr11	135006516	2761571	0.0205	0.1757
chr12	133851895	2645552	0.0198	0.1498
chr13	115169878	1908205	0.0166	0.138
chr14	107349540	2231435	0.0208	0.1546
chr15	102531392	1651140	0.0161	0.1356
chr16	90354753	1585117	0.0175	0.1543
chr17	81195210	1173326	0.0145	0.1296
chr18	78077248	1287397	0.0165	0.244
chr19	59128983	998905	0.0169	0.2579
chr20	63025520	1035684	0.0164	0.1366
chr21	48129895	767944	0.016	0.1372
chr22	51304566	454832	0.0089	0.0989
chrMT	16571	2343	0.1414	0.4066
chrX	155270560	3090083	0.0199	0.16
chrY	59373566	166665	0.0028	0.0809

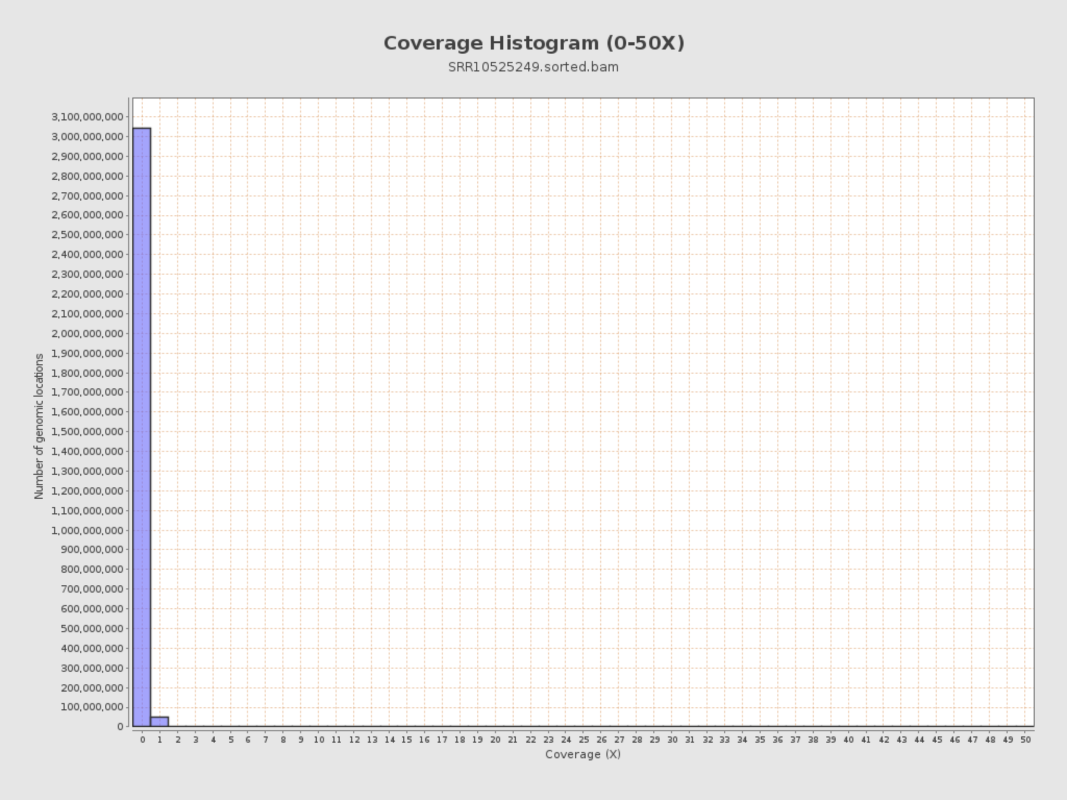
3. Results : Coverage across reference



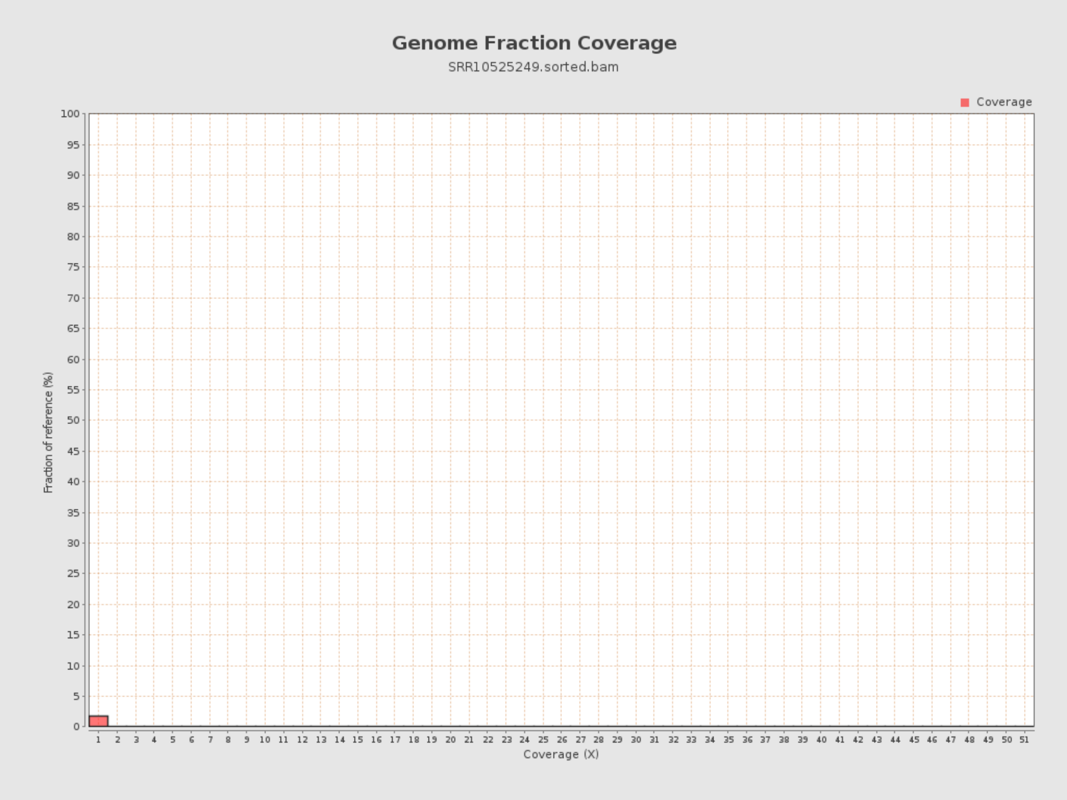
4. Results : Coverage Histogram



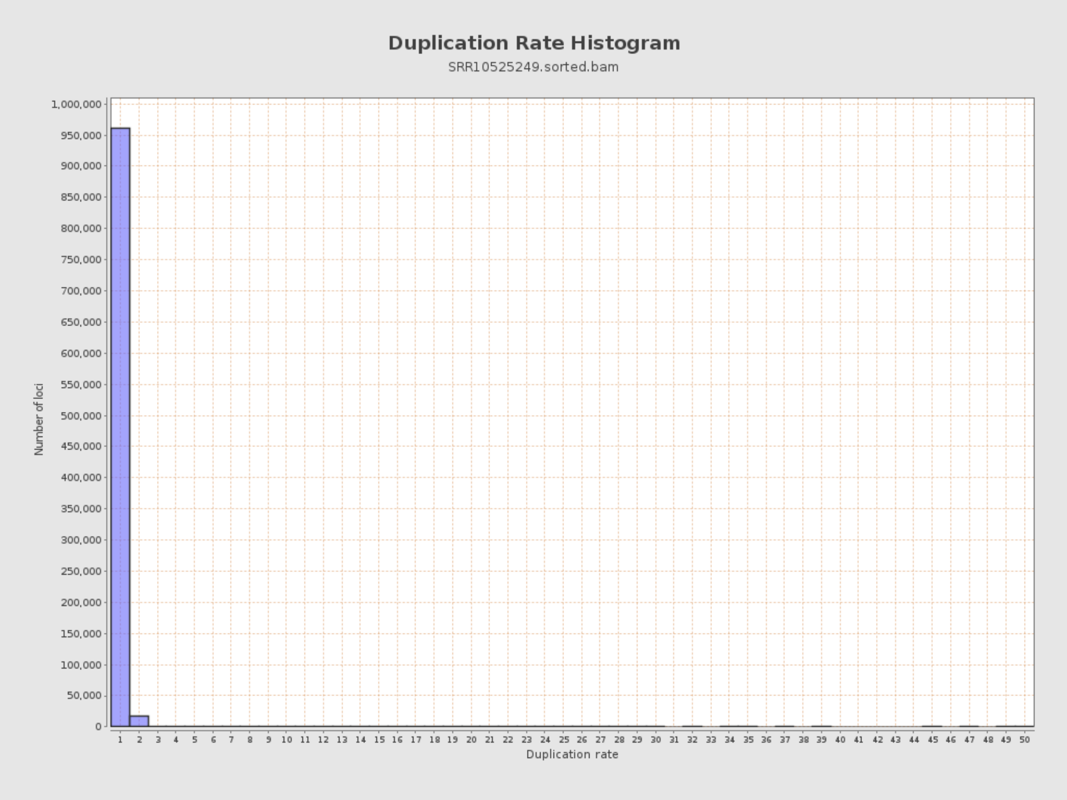
5. Results : Coverage Histogram (0-50X)



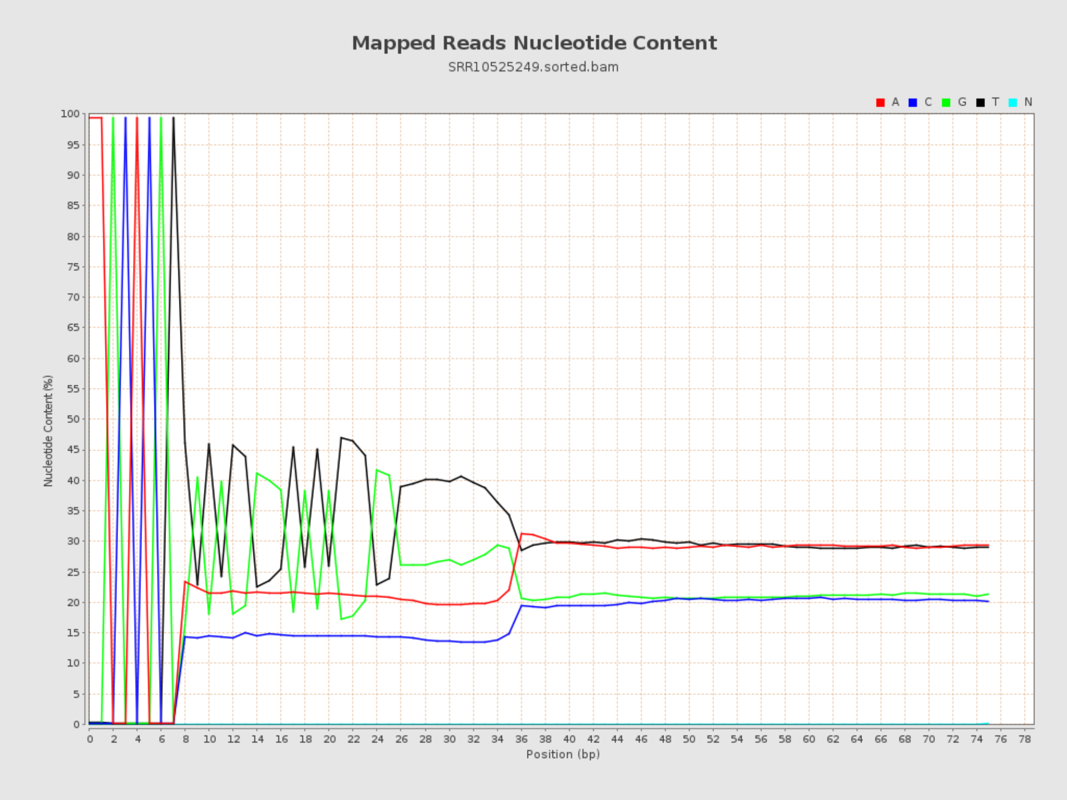
6. Results : Genome Fraction Coverage



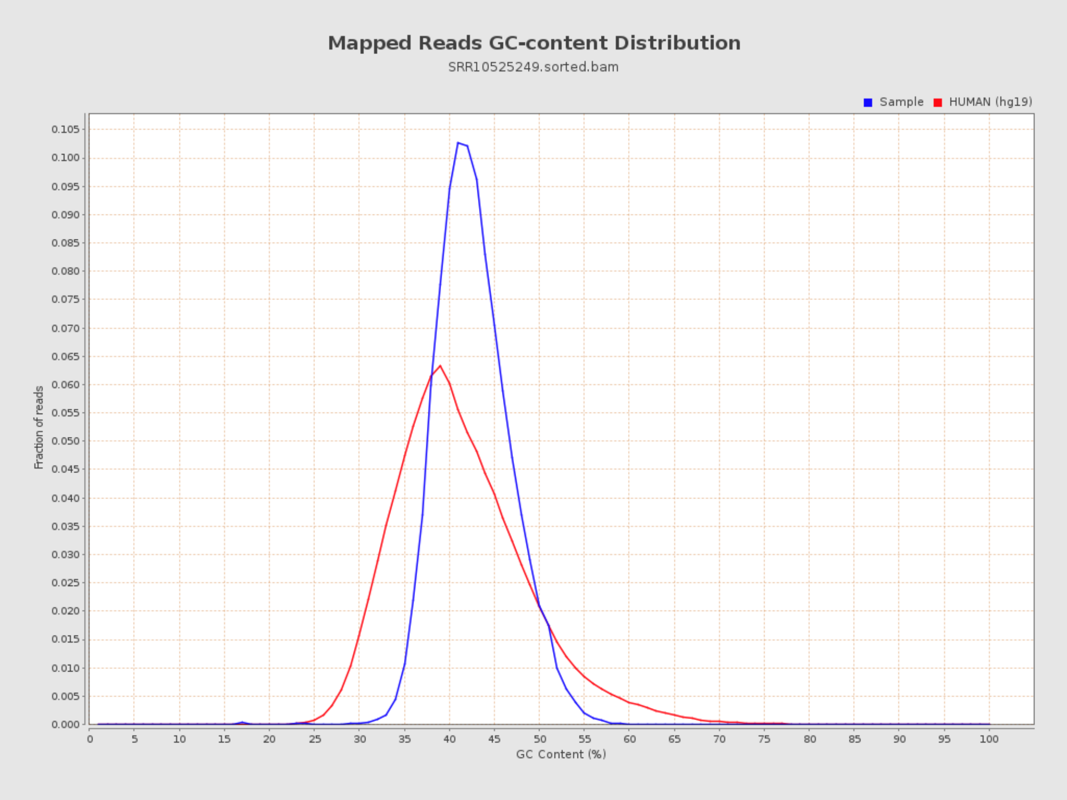
7. Results : Duplication Rate Histogram



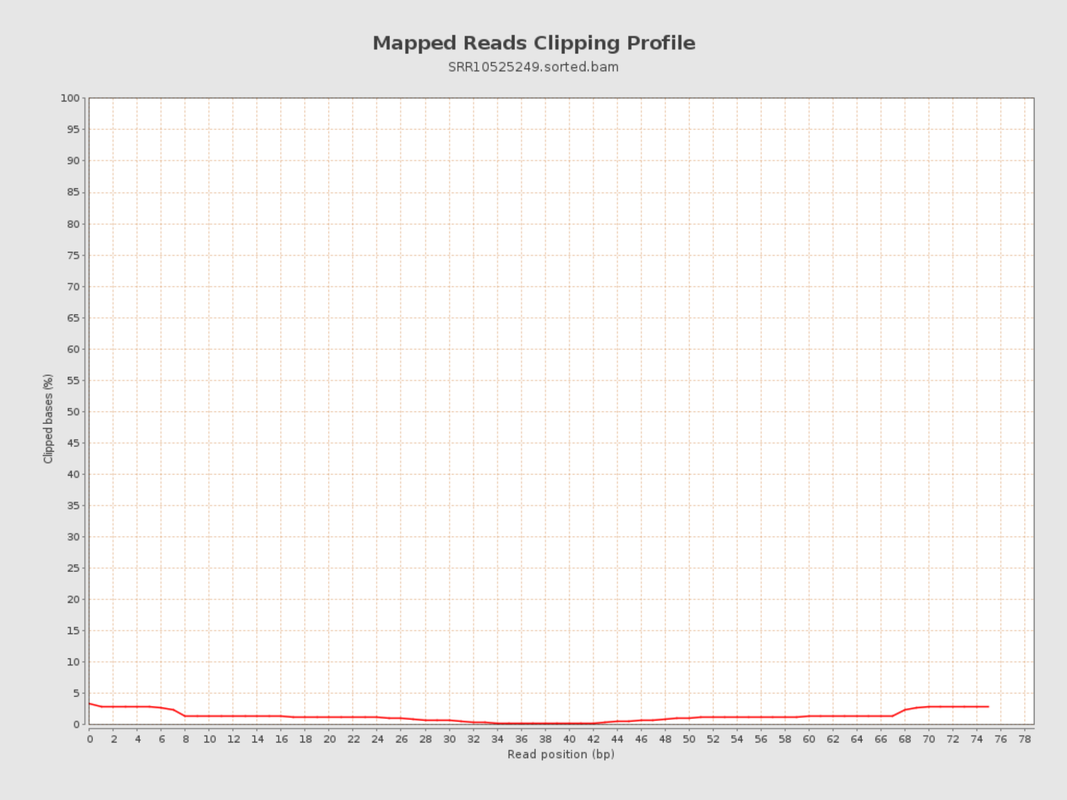
8. Results : Mapped Reads Nucleotide Content



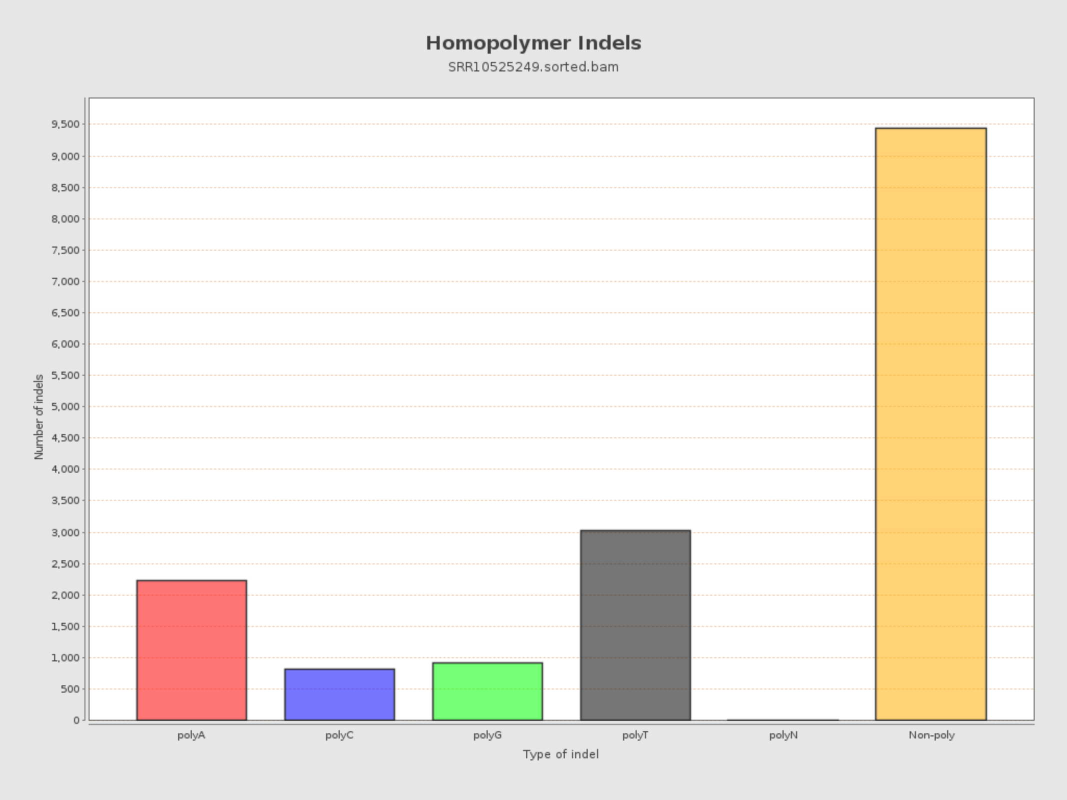
9. Results : Mapped Reads GC-content Distribution



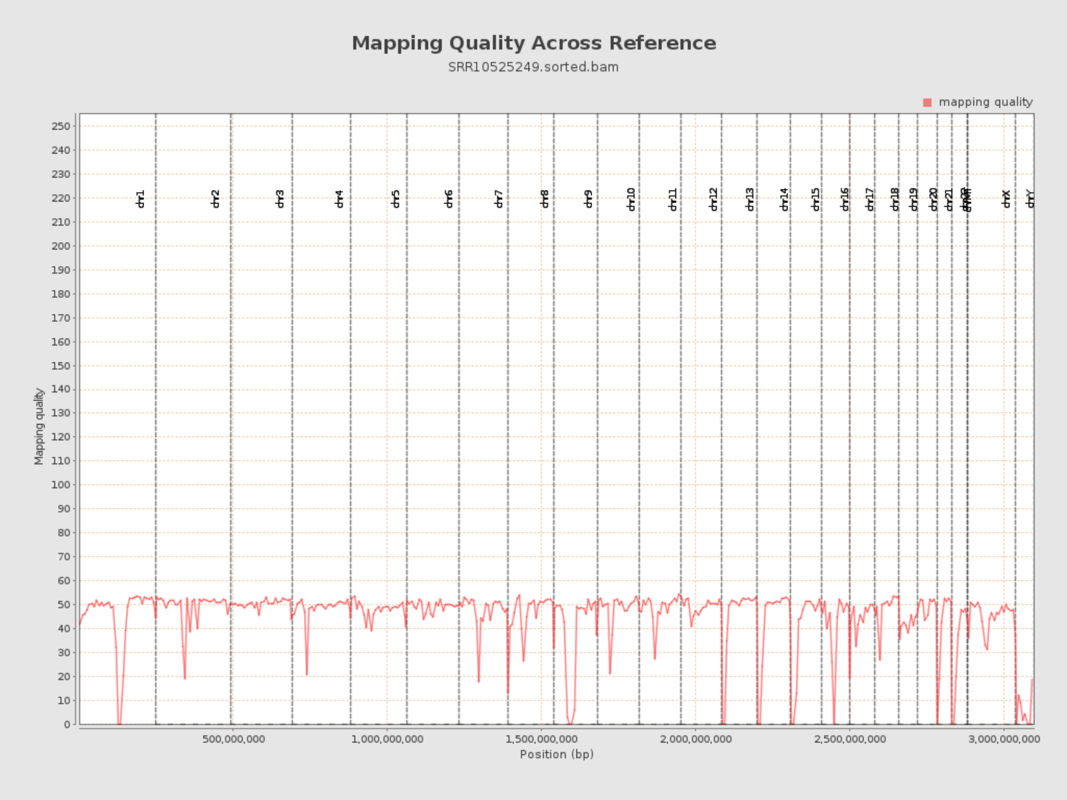
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram