Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:56:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524725.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_SRR10524725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524725.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:56:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,381,340
Mapped reads	1,257,820 / 91.06%
Unmapped reads	123,520 / 8.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,627 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	51,887 / 3.76%
Duplication rate	3.17%
Clipped reads	1,259,379 / 91.17%

2.2. ACGT Content

Number/percentage of A's	17,191,001 / 24.06%
Number/percentage of C's	12,993,657 / 18.18%
Number/percentage of T's	23,424,259 / 32.78%
Number/percentage of G's	17,848,206 / 24.97%
Number/percentage of N's	8,272 / 0.01%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2239

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

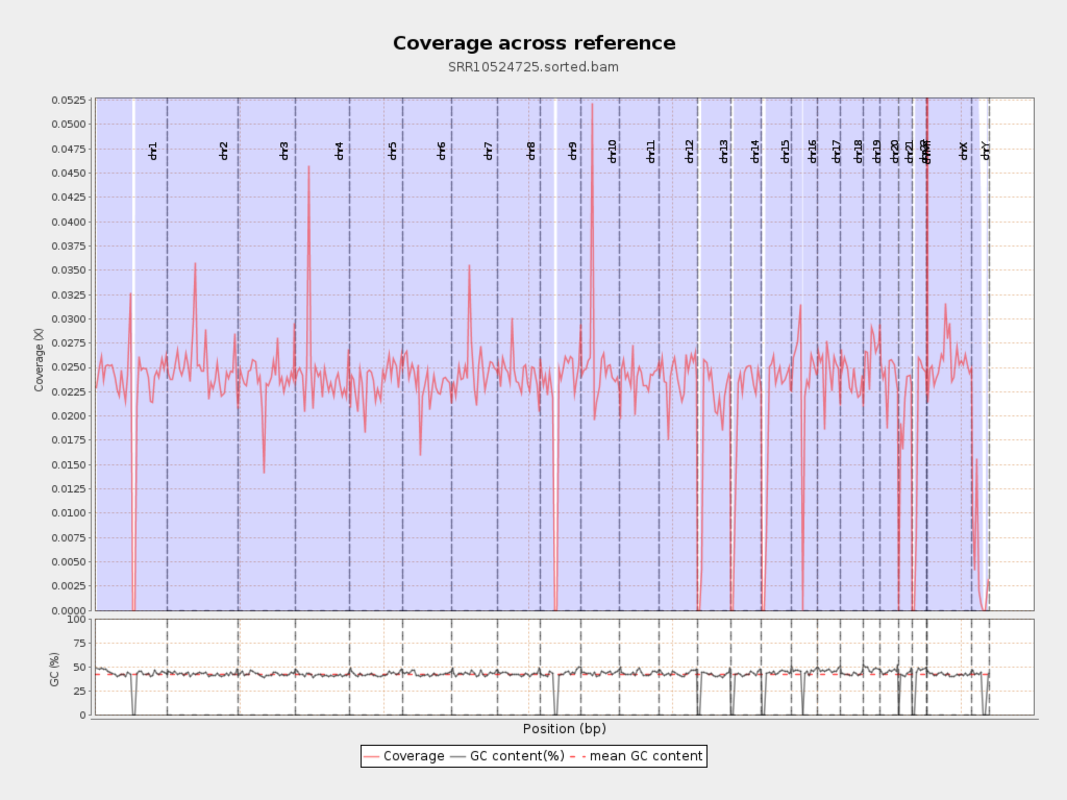
General error rate	0.53%
Mismatches	364,928
Insertions	5,678
Mapped reads with at least one insertion	0.45%
Deletions	14,258
Mapped reads with at least one deletion	1.13%
Homopolymer indels	40.51%

2.6. Chromosome stats

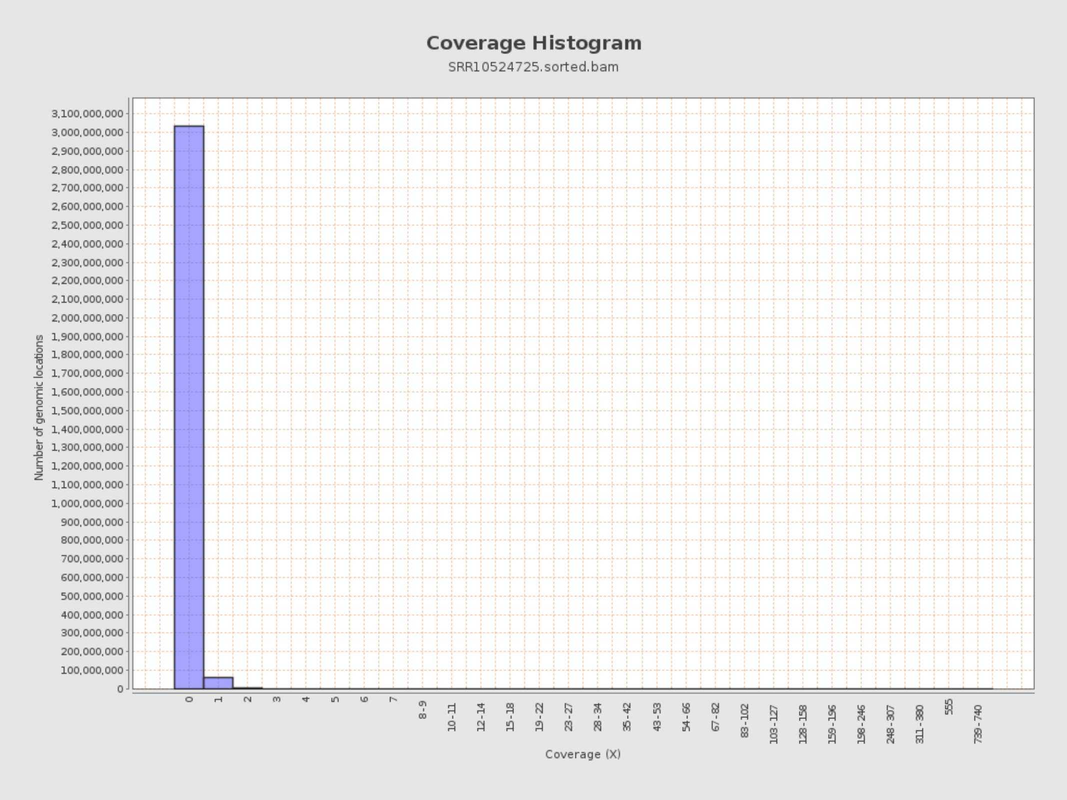
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5702967	0.0229	0.3113
chr2	243199373	6092079	0.025	0.3575
chr3	198022430	4691939	0.0237	0.1721
chr4	191154276	4676401	0.0245	0.197
chr5	180915260	4282635	0.0237	0.1683
chr6	171115067	3998502	0.0234	0.183
chr7	159138663	3959124	0.0249	0.2493

chr8	146364022	3555405	0.0243	0.2093
chr9	141213431	3065212	0.0217	0.1913
chr10	135534747	3493087	0.0258	0.2778
chr11	135006516	3241925	0.024	0.197
chr12	133851895	3228923	0.0241	0.1724
chr13	115169878	2193124	0.019	0.1517
chr14	107349540	2144663	0.02	0.1581
chr15	102531392	2027935	0.0198	0.1562
chr16	90354753	2106295	0.0233	0.1819
chr17	81195210	2010997	0.0248	0.1781
chr18	78077248	1863602	0.0239	0.2911
chr19	59128983	1572673	0.0266	0.2485
chr20	63025520	1513146	0.024	0.1795
chr21	48129895	933907	0.0194	0.17
chr22	51304566	891611	0.0174	0.1458
chrMT	16571	16240	0.98	1.2572
chrX	155270560	3973924	0.0256	0.1863
chrY	59373566	251920	0.0042	0.1338

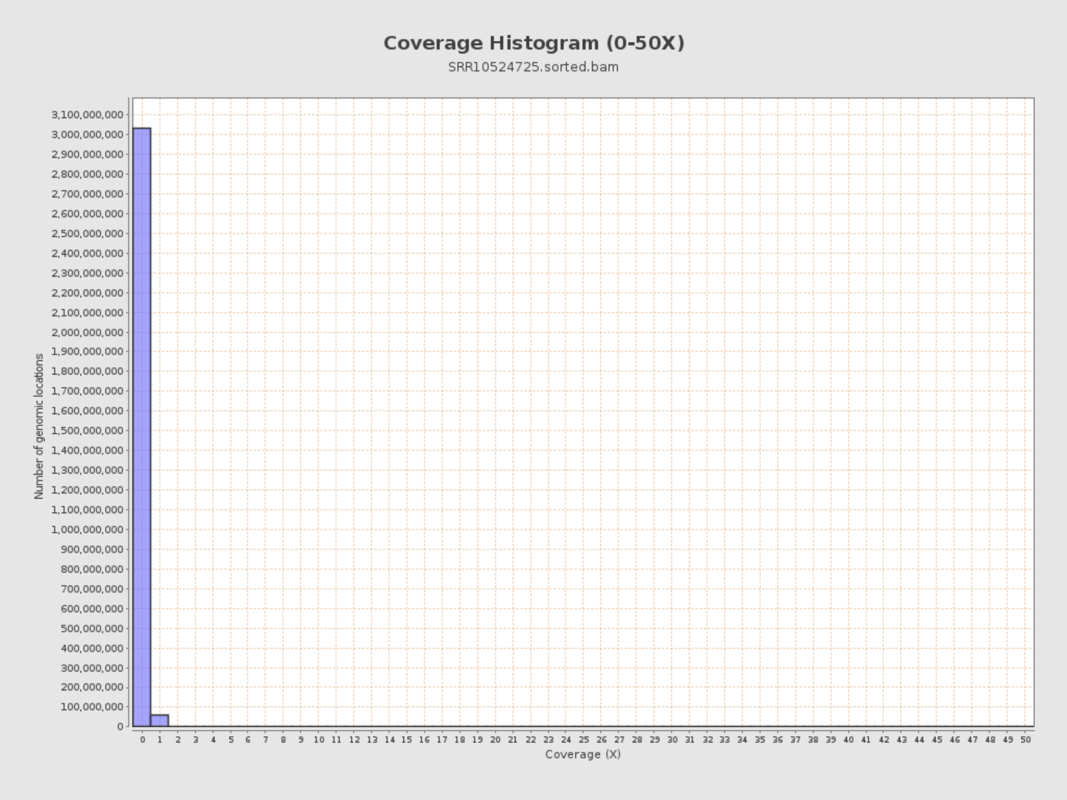
3. Results : Coverage across reference



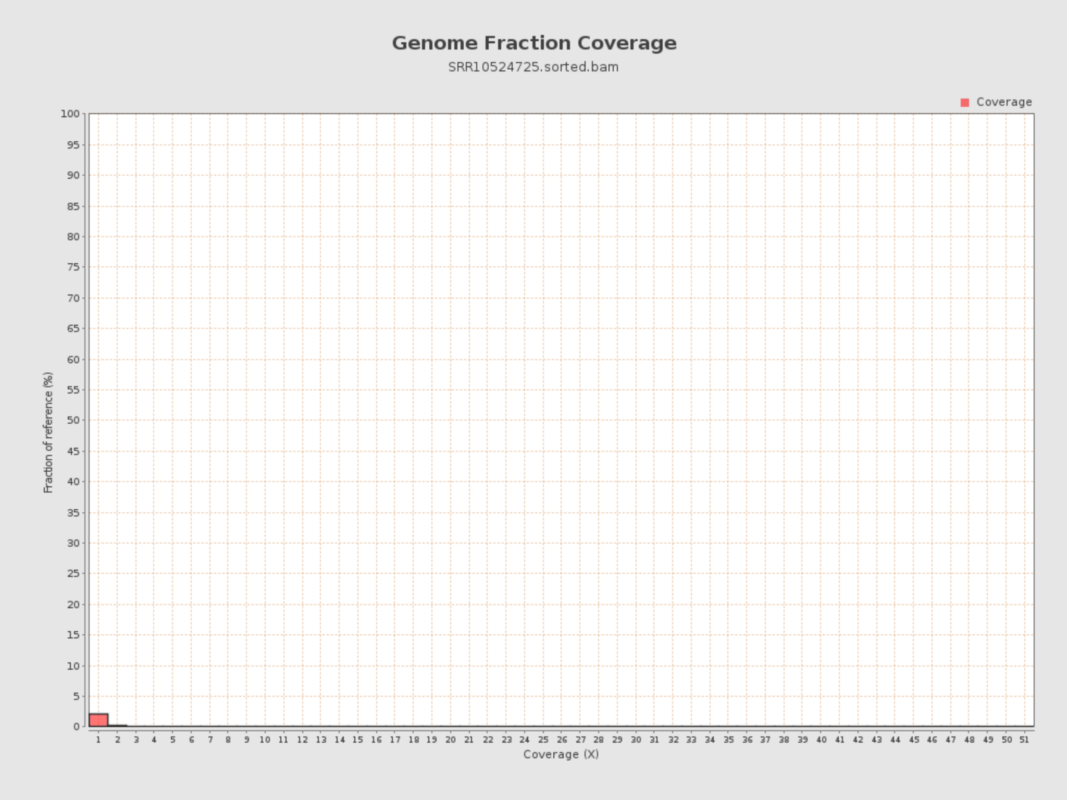
4. Results : Coverage Histogram



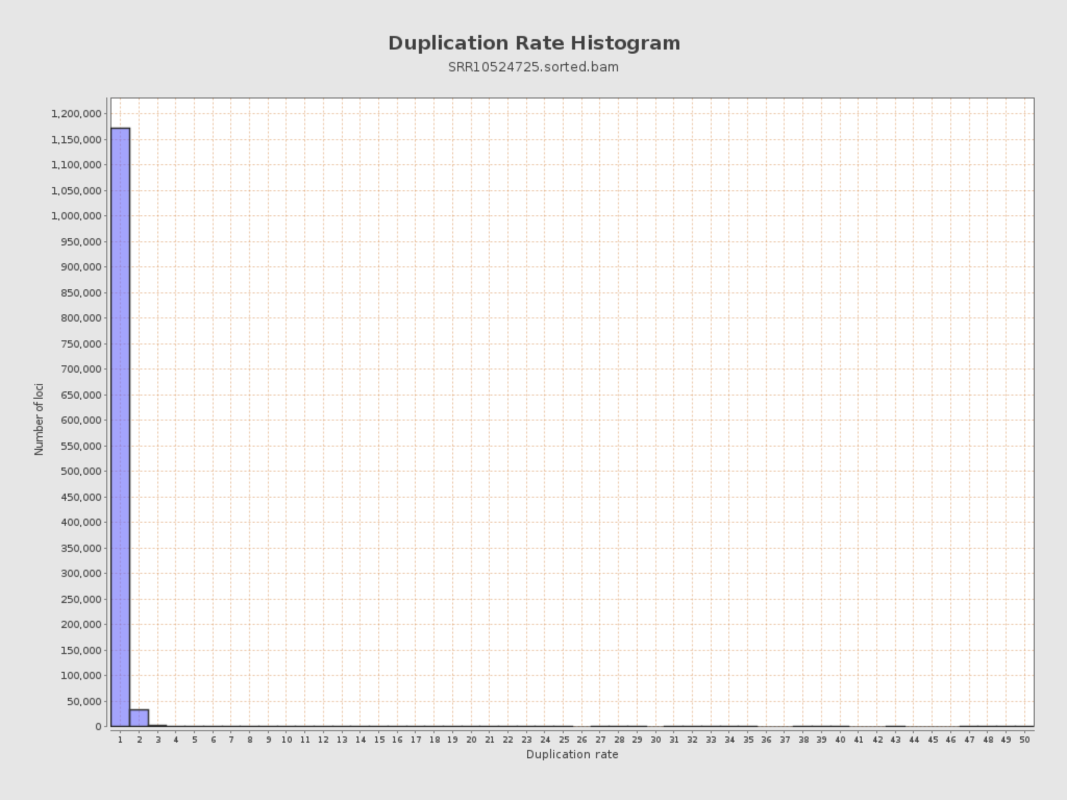
5. Results : Coverage Histogram (0-50X)



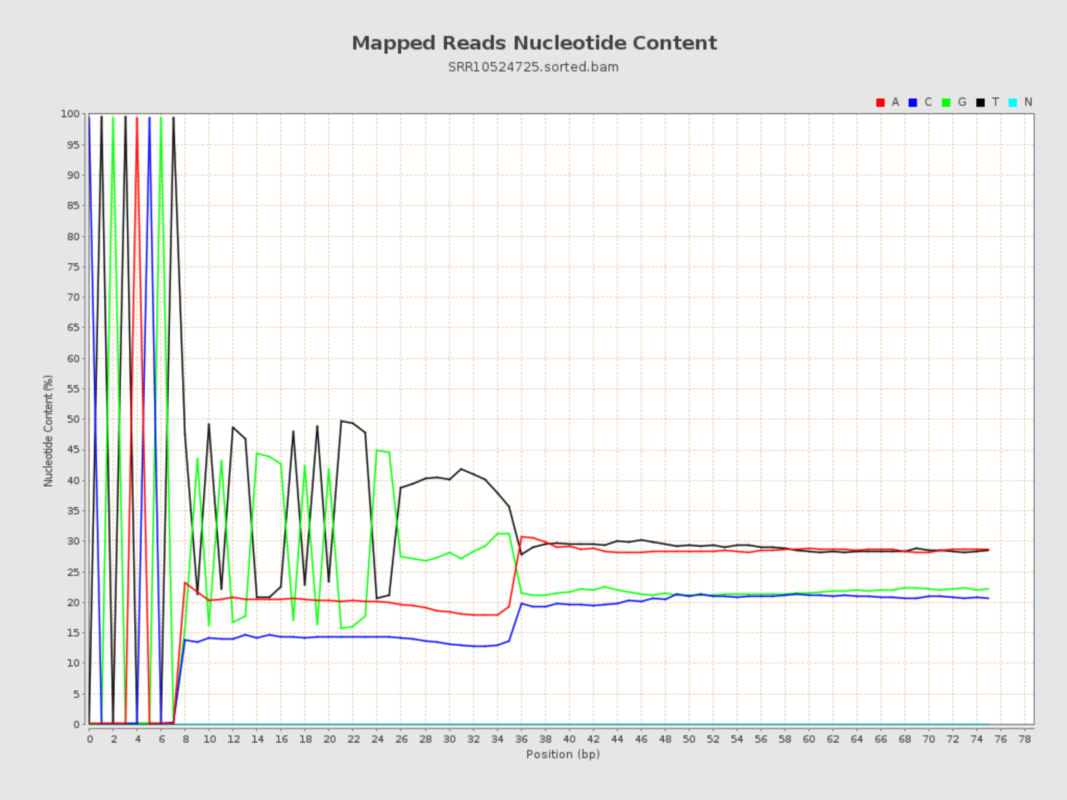
6. Results : Genome Fraction Coverage



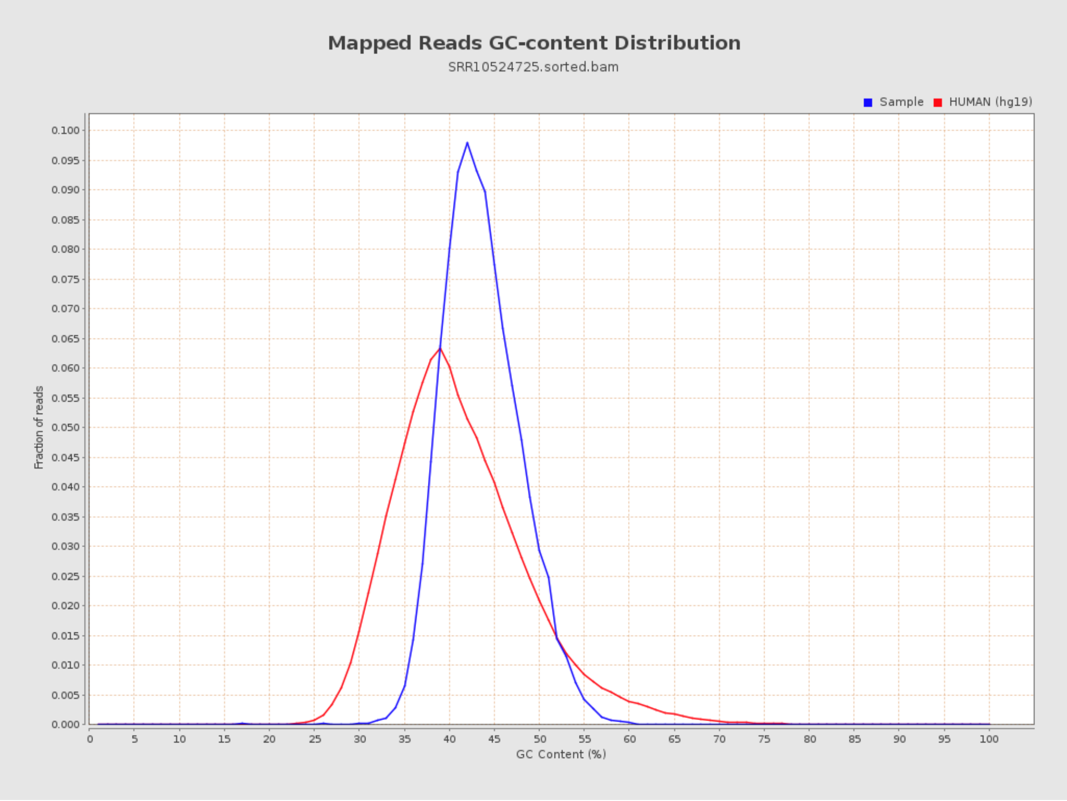
7. Results : Duplication Rate Histogram



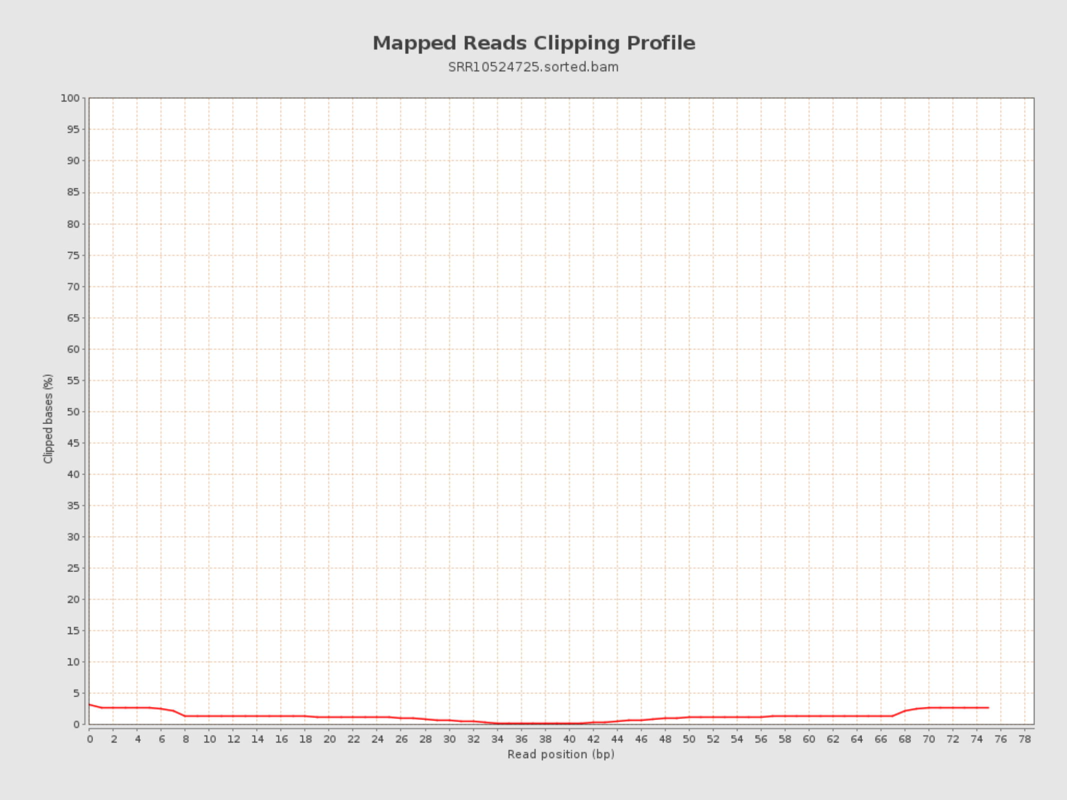
8. Results : Mapped Reads Nucleotide Content



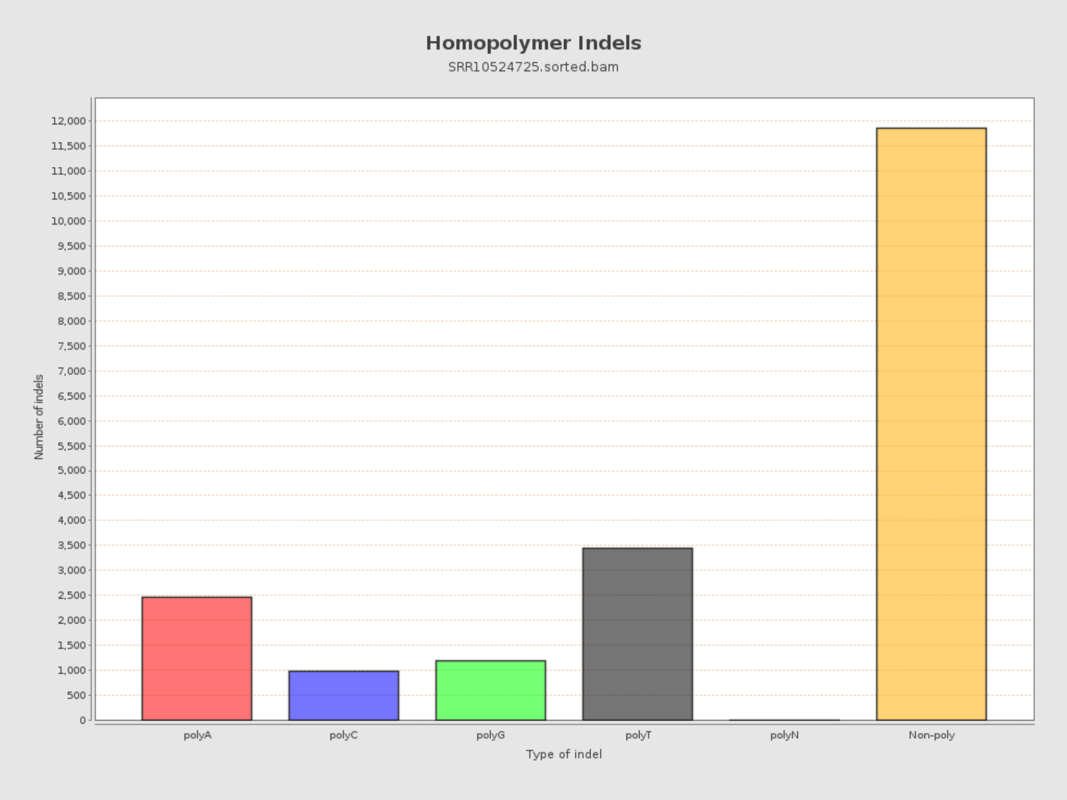
9. Results : Mapped Reads GC-content Distribution



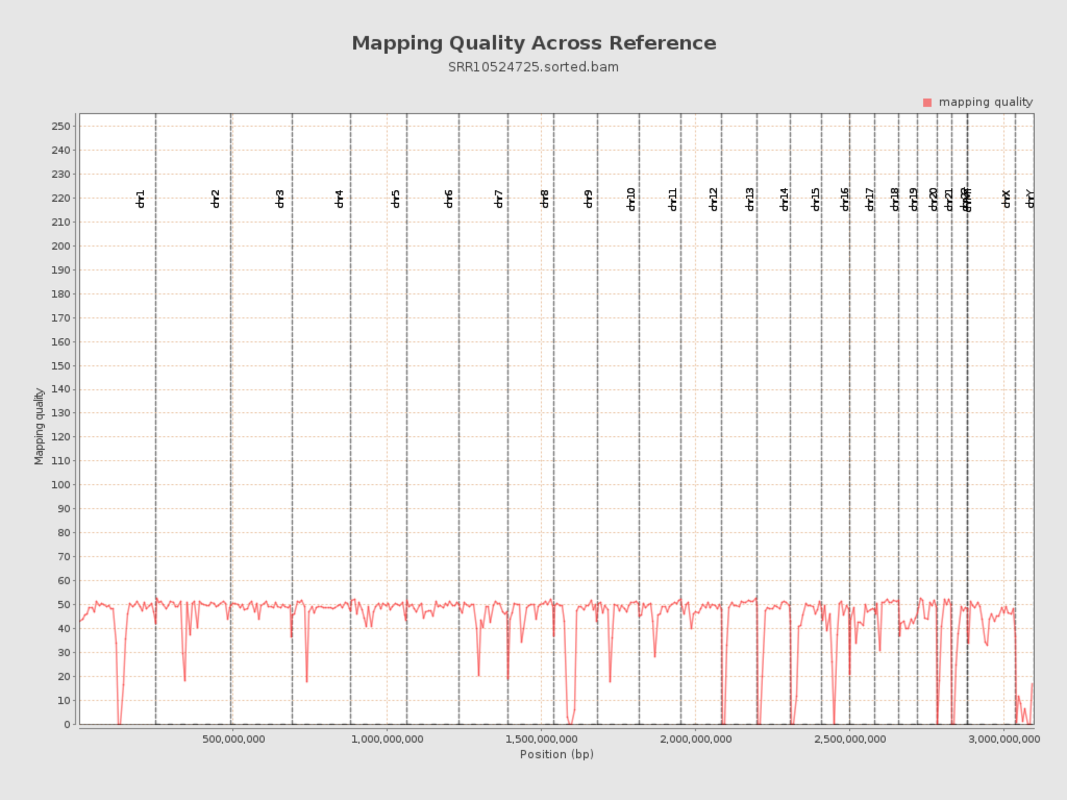
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram