Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 23:08:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524853.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_SRR10524853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 23:08:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,326,987
Mapped reads	1,212,108 / 91.34%
Unmapped reads	114,879 / 8.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,245 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	32,731 / 2.47%
Duplication rate	1.88%
Clipped reads	1,215,686 / 91.61%

2.2. ACGT Content

Number/percentage of A's	18,406,625 / 26.17%
Number/percentage of C's	12,758,844 / 18.14%
Number/percentage of T's	22,855,101 / 32.49%
Number/percentage of G's	16,305,908 / 23.18%
Number/percentage of N's	8,760 / 0.01%
GC Percentage	41.32%

2.3. Coverage

Mean	0.0227

Standard Deviation	0.234

2.4. Mapping Quality

Mean Mapping Quality	44.85

2.5. Mismatches and indels

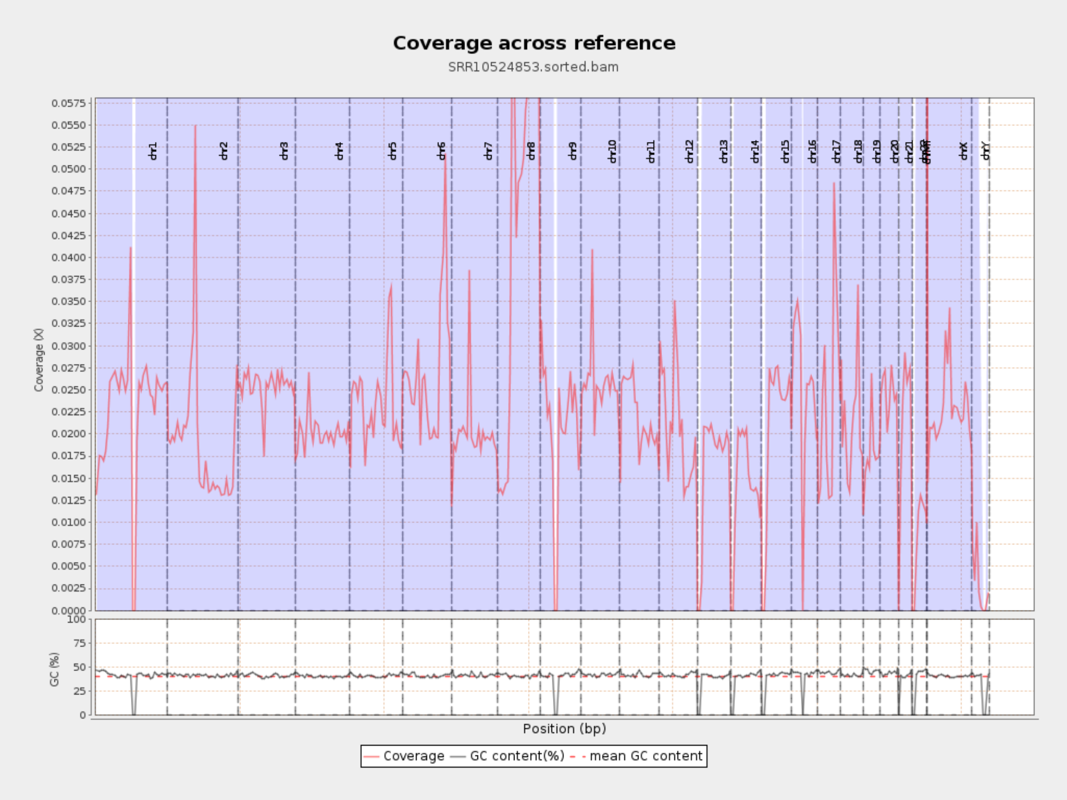
General error rate	0.5%
Mismatches	343,015
Insertions	5,153
Mapped reads with at least one insertion	0.42%
Deletions	13,175
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.06%

2.6. Chromosome stats

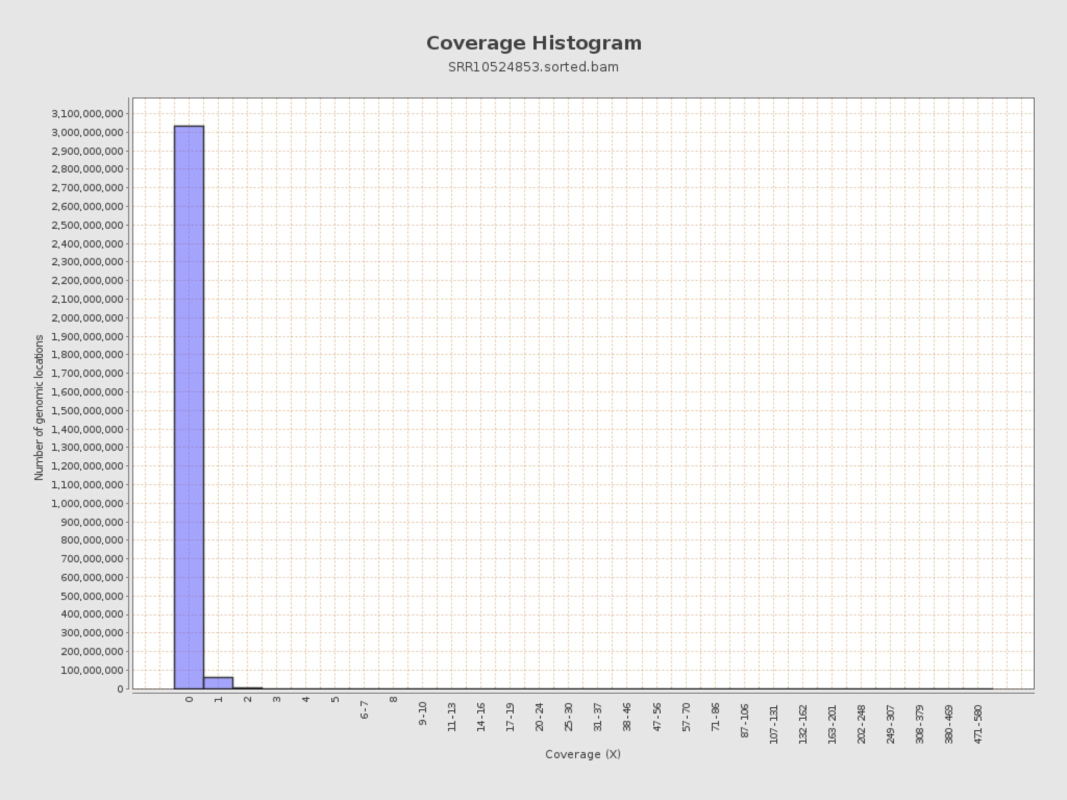
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5685204	0.0228	0.4313
chr2	243199373	4609029	0.019	0.2399
chr3	198022430	5028515	0.0254	0.1678
chr4	191154276	3846133	0.0201	0.1615
chr5	180915260	4290434	0.0237	0.1636
chr6	171115067	4577426	0.0268	0.1868
chr7	159138663	3224361	0.0203	0.3094

chr8	146364022	7685673	0.0525	0.3214
chr9	141213431	2930300	0.0208	0.2028
chr10	135534747	3505555	0.0259	0.2237
chr11	135006516	2996131	0.0222	0.2026
chr12	133851895	2791584	0.0209	0.1556
chr13	115169878	1872471	0.0163	0.1355
chr14	107349540	1498151	0.014	0.134
chr15	102531392	2123930	0.0207	0.1541
chr16	90354753	2234452	0.0247	0.174
chr17	81195210	1965900	0.0242	0.1823
chr18	78077248	1677070	0.0215	0.3369
chr19	59128983	1065421	0.018	0.323
chr20	63025520	1521597	0.0241	0.1659
chr21	48129895	1039560	0.0216	0.1629
chr22	51304566	437640	0.0085	0.097
chrMT	16571	3626	0.2188	0.4989
chrX	155270560	3569304	0.023	0.1789
chrY	59373566	176780	0.003	0.0806

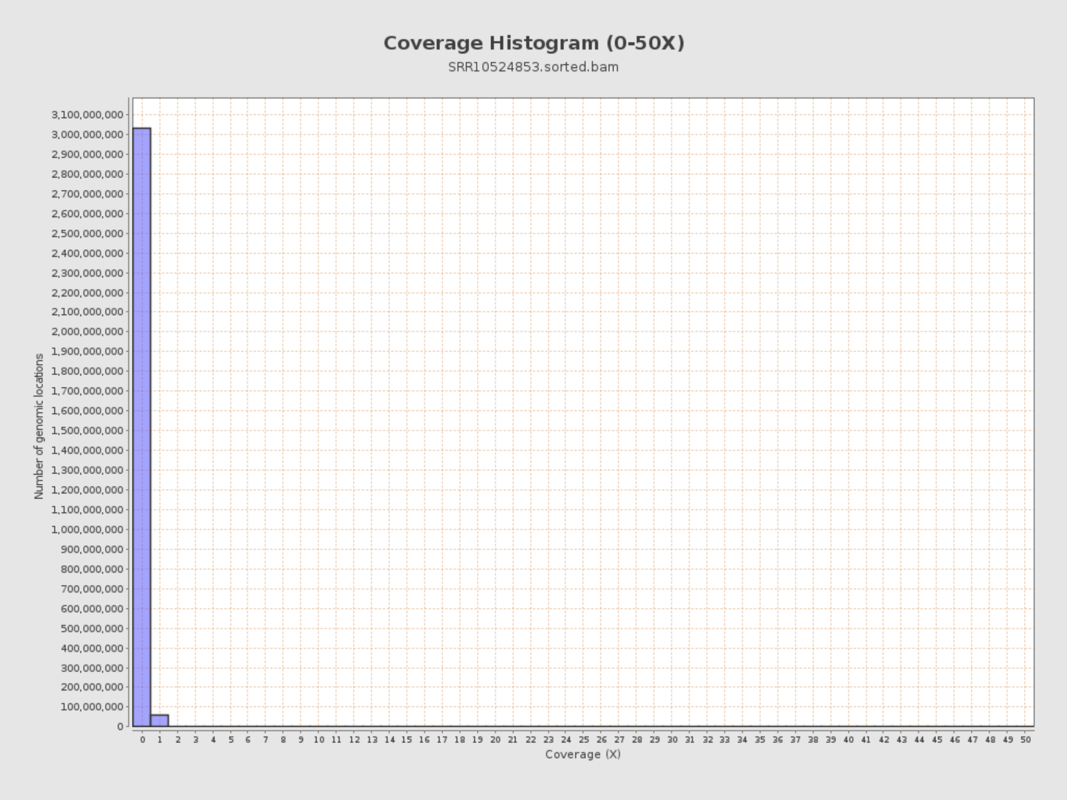
3. Results : Coverage across reference



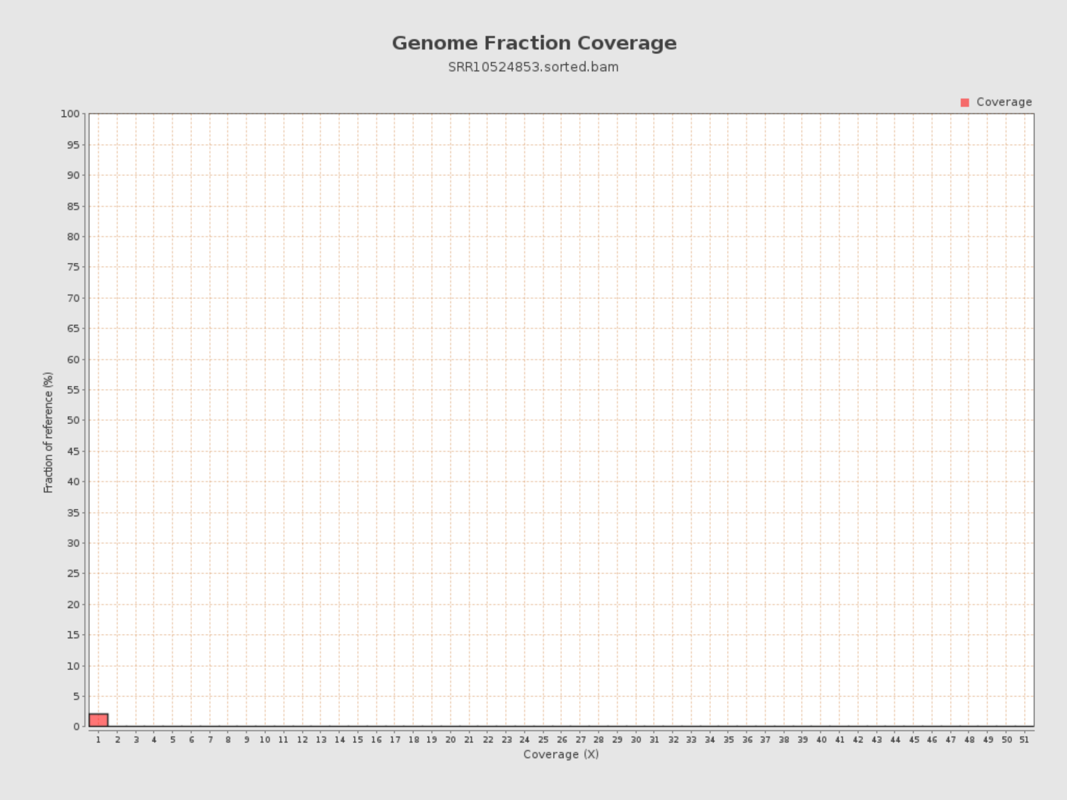
4. Results : Coverage Histogram



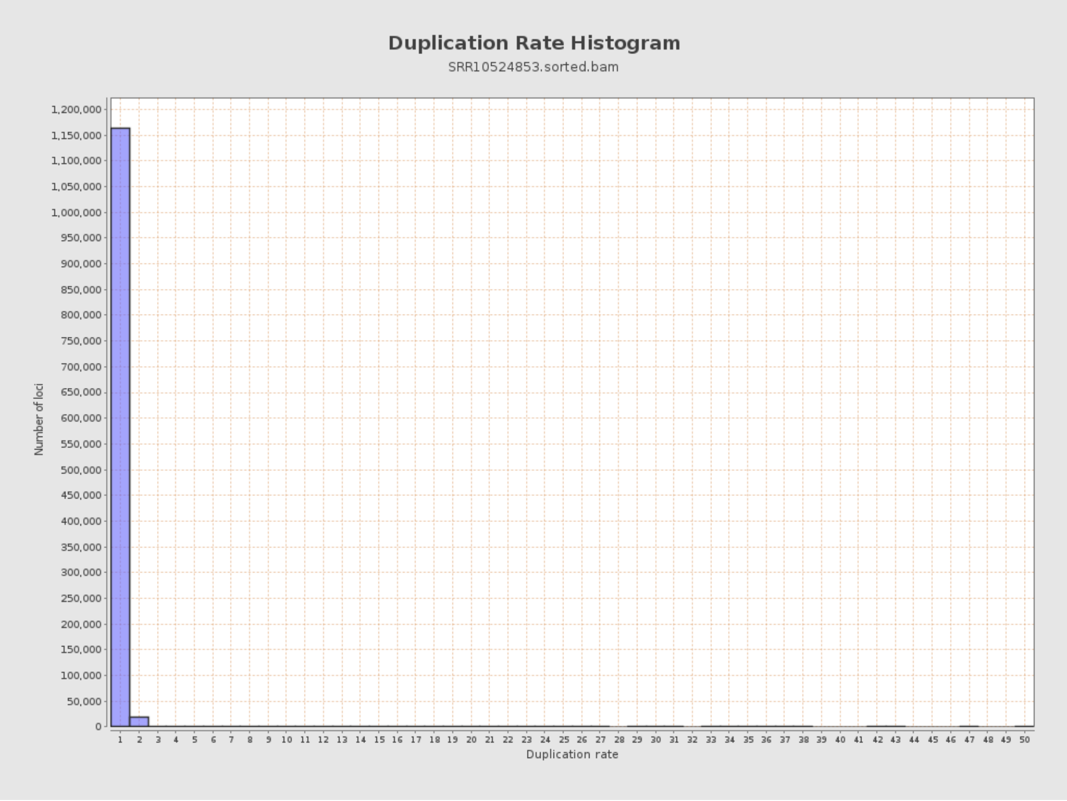
5. Results : Coverage Histogram (0-50X)



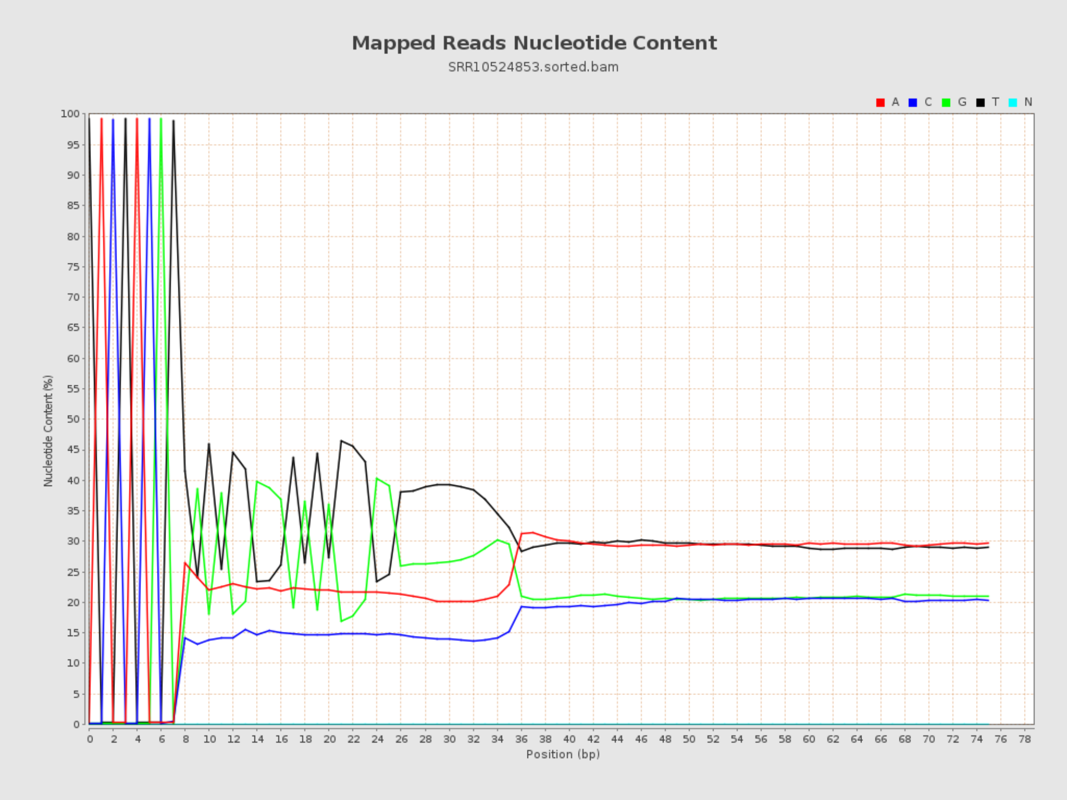
6. Results : Genome Fraction Coverage



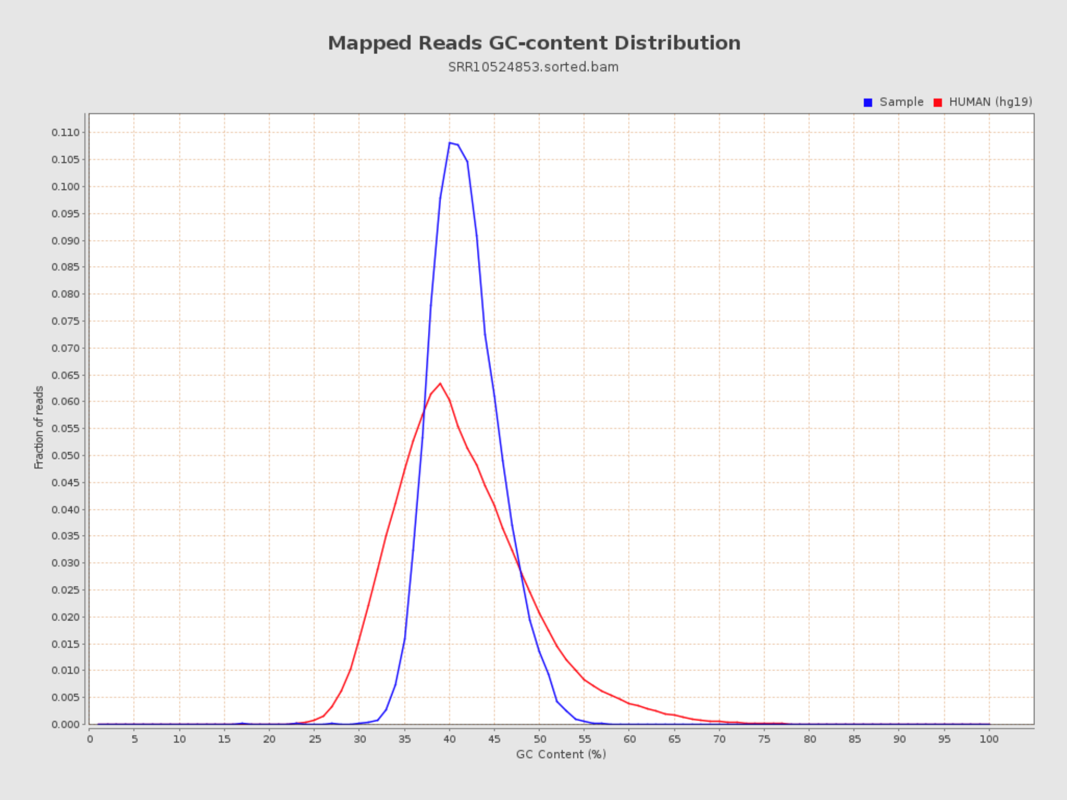
7. Results : Duplication Rate Histogram



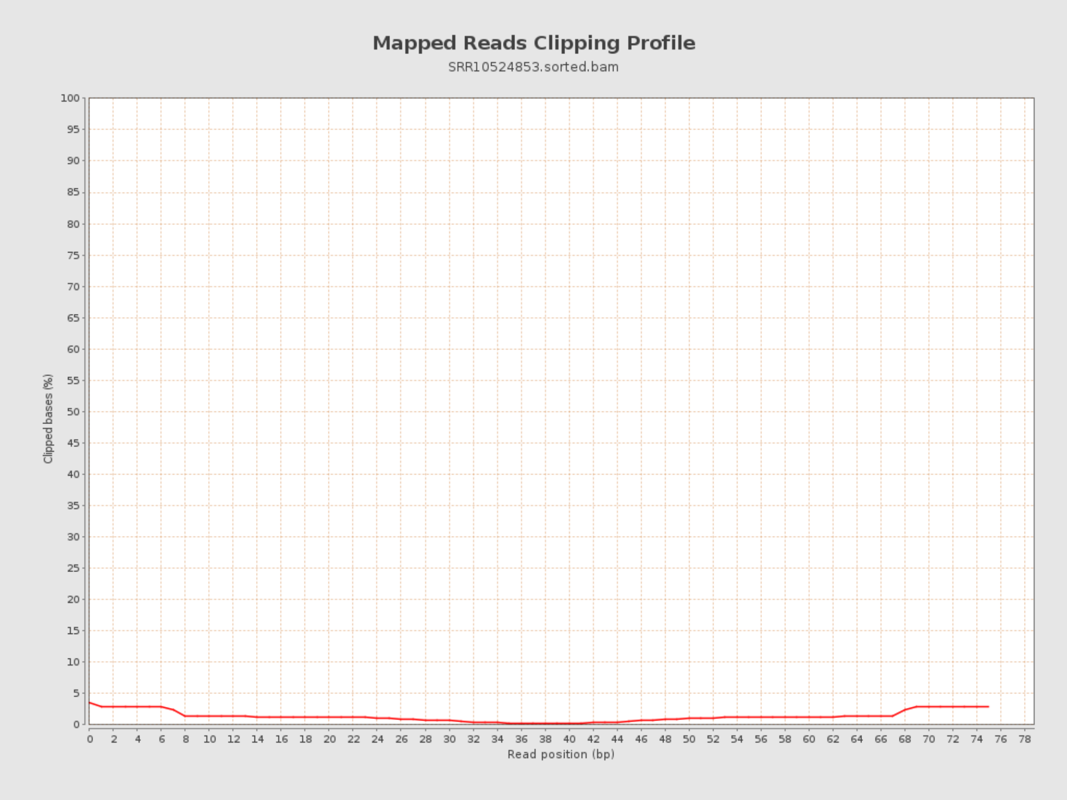
8. Results : Mapped Reads Nucleotide Content



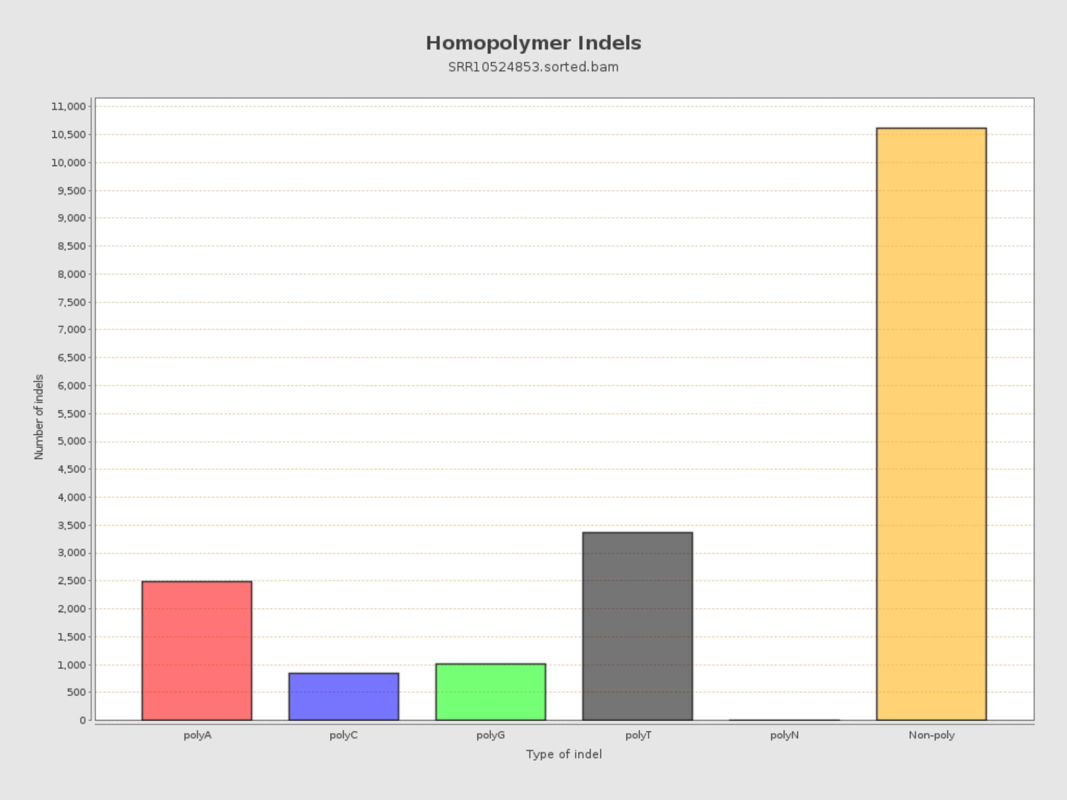
9. Results : Mapped Reads GC-content Distribution



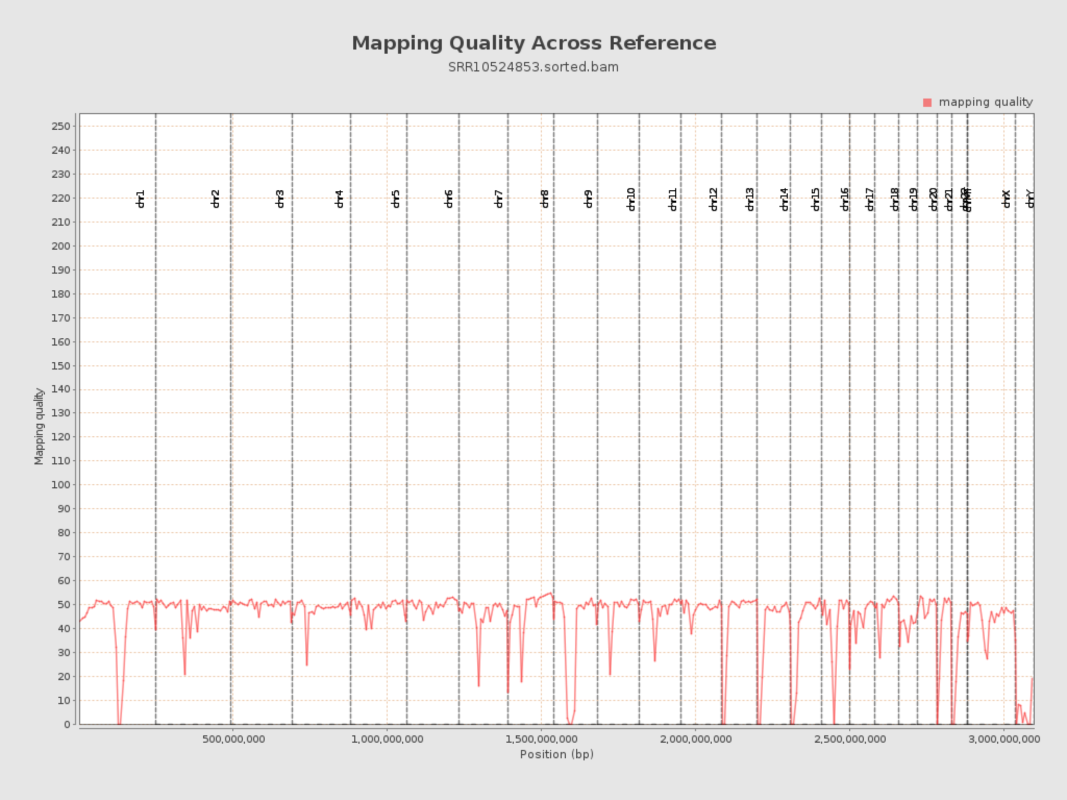
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram