Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:20:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524626.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_SRR10524626 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524626.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:20:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524626.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,788,639
Mapped reads	1,659,692 / 92.79%
Unmapped reads	128,947 / 7.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,586 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	80,008 / 4.47%
Duplication rate	3.74%
Clipped reads	1,658,714 / 92.74%

2.2. ACGT Content

Number/percentage of A's	25,000,855 / 25.78%
Number/percentage of C's	18,656,122 / 19.24%
Number/percentage of T's	30,569,182 / 31.53%
Number/percentage of G's	22,739,338 / 23.45%
Number/percentage of N's	639 / 0%
GC Percentage	42.69%

2.3. Coverage

Mean	0.0313

Standard Deviation	0.2813

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

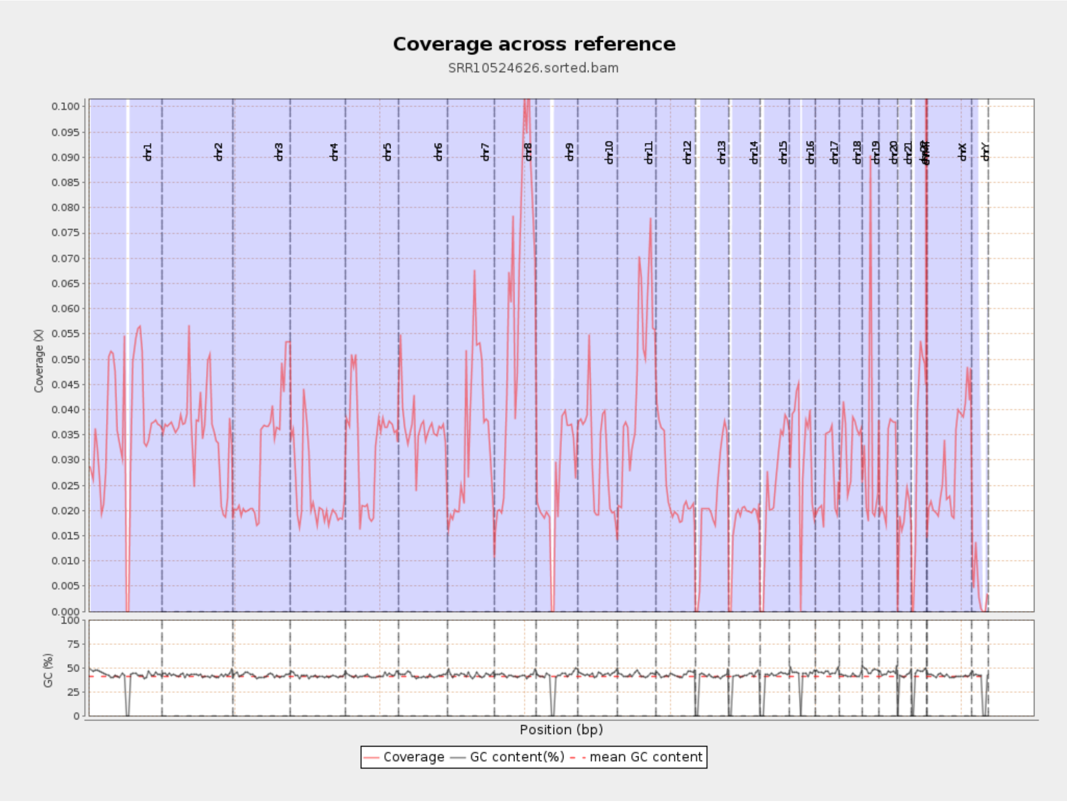
General error rate	0.49%
Mismatches	461,903
Insertions	6,788
Mapped reads with at least one insertion	0.41%
Deletions	18,199
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.62%

2.6. Chromosome stats

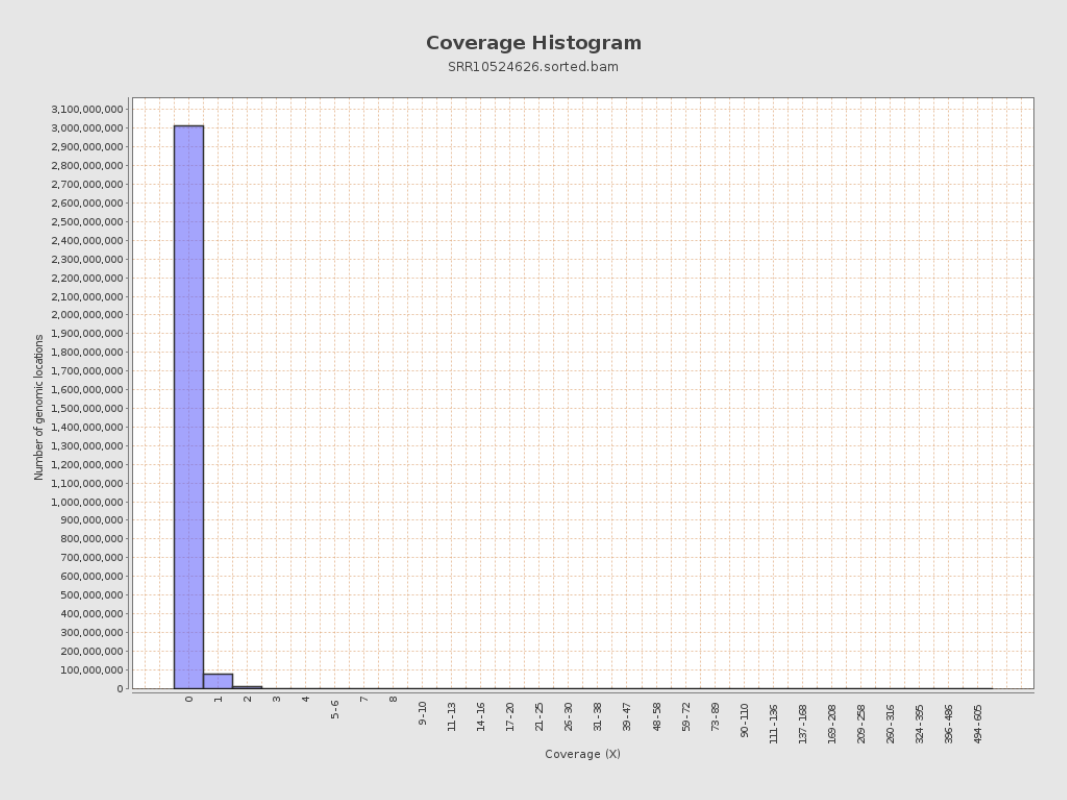
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9021724	0.0362	0.4897
chr2	243199373	8726607	0.0359	0.3261
chr3	198022430	6072618	0.0307	0.1962
chr4	191154276	4389901	0.023	0.1924
chr5	180915260	5980544	0.0331	0.2046
chr6	171115067	6257582	0.0366	0.2301
chr7	159138663	5508473	0.0346	0.3695

chr8	146364022	8711489	0.0595	0.381
chr9	141213431	3503521	0.0248	0.2455
chr10	135534747	4166340	0.0307	0.2696
chr11	135006516	6156739	0.0456	0.2957
chr12	133851895	3251714	0.0243	0.1818
chr13	115169878	2423418	0.021	0.1636
chr14	107349540	1822092	0.017	0.152
chr15	102531392	2489841	0.0243	0.1809
chr16	90354753	2841816	0.0315	0.2102
chr17	81195210	2116292	0.0261	0.1871
chr18	78077248	2635923	0.0338	0.4043
chr19	59128983	1884458	0.0319	0.3621
chr20	63025520	1788552	0.0284	0.1925
chr21	48129895	856565	0.0178	0.1626
chr22	51304566	1674366	0.0326	0.202
chrMT	16571	16679	1.0065	1.2255
chrX	155270560	4465559	0.0288	0.2175
chrY	59373566	234204	0.0039	0.1145

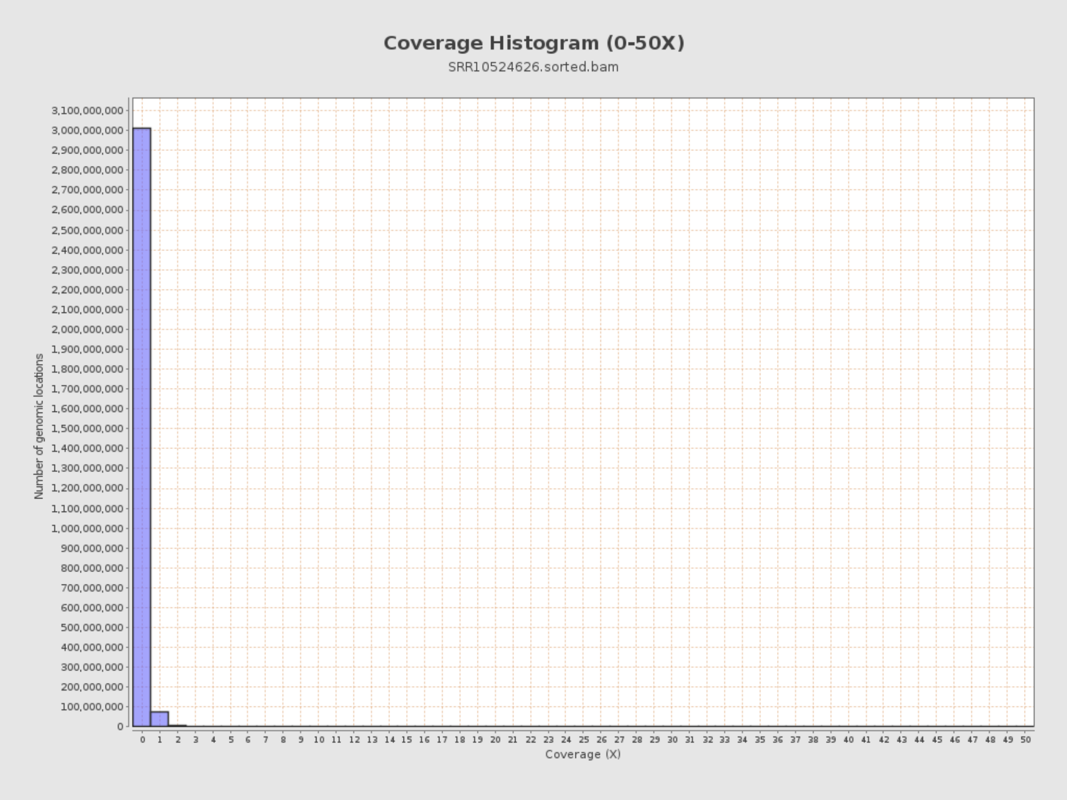
3. Results : Coverage across reference



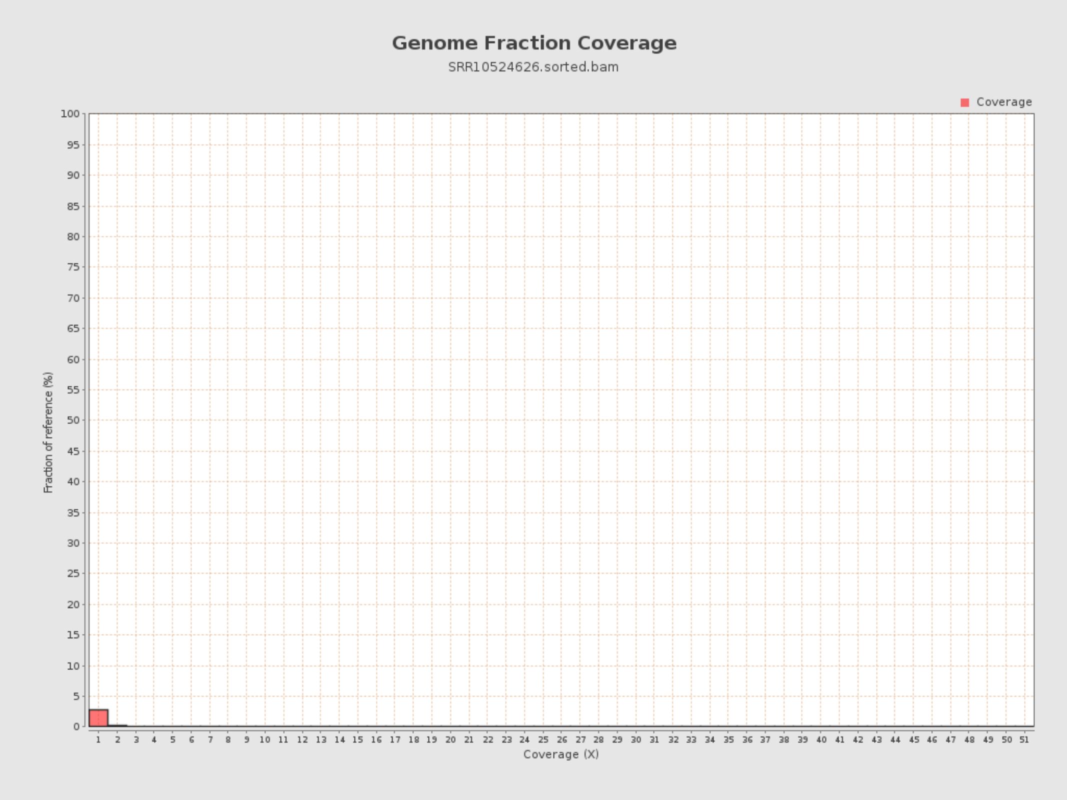
4. Results : Coverage Histogram



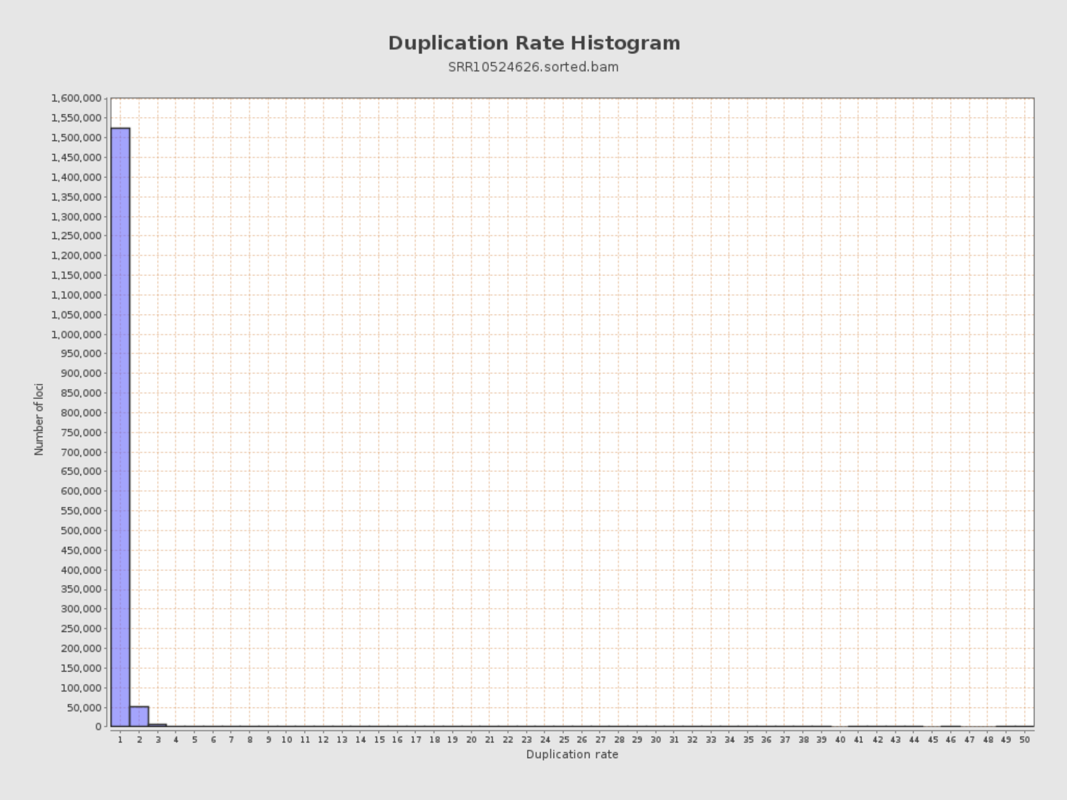
5. Results : Coverage Histogram (0-50X)



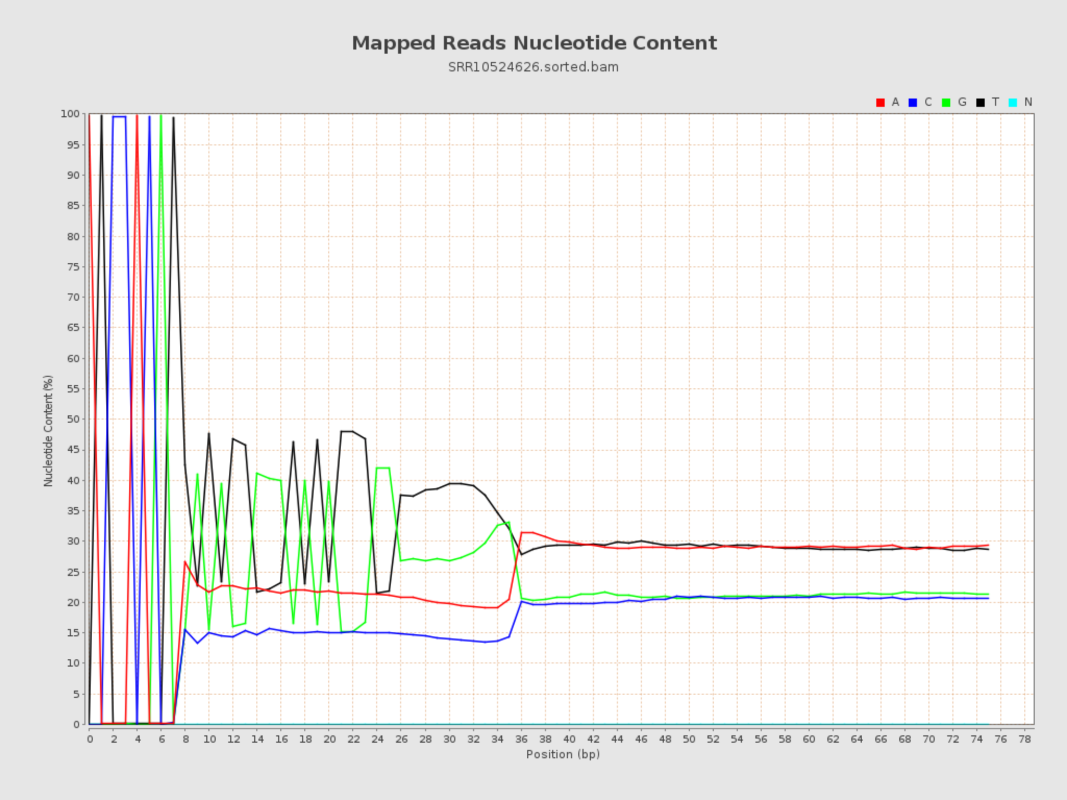
6. Results : Genome Fraction Coverage



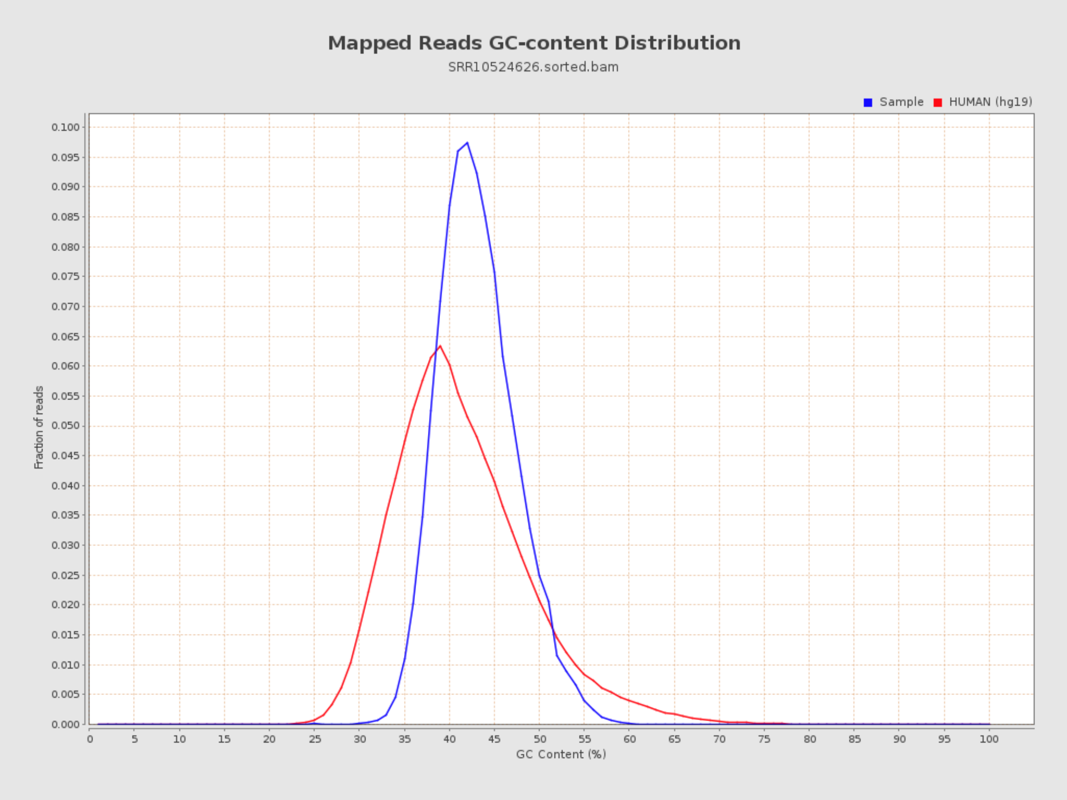
7. Results : Duplication Rate Histogram



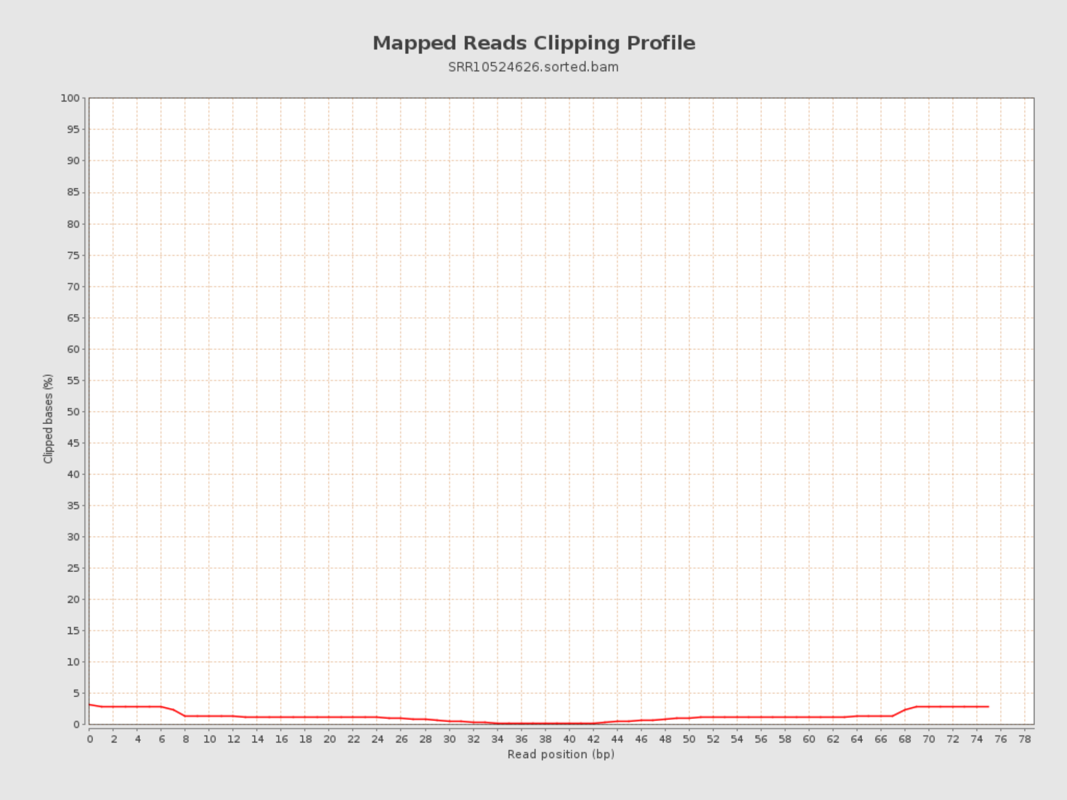
8. Results : Mapped Reads Nucleotide Content



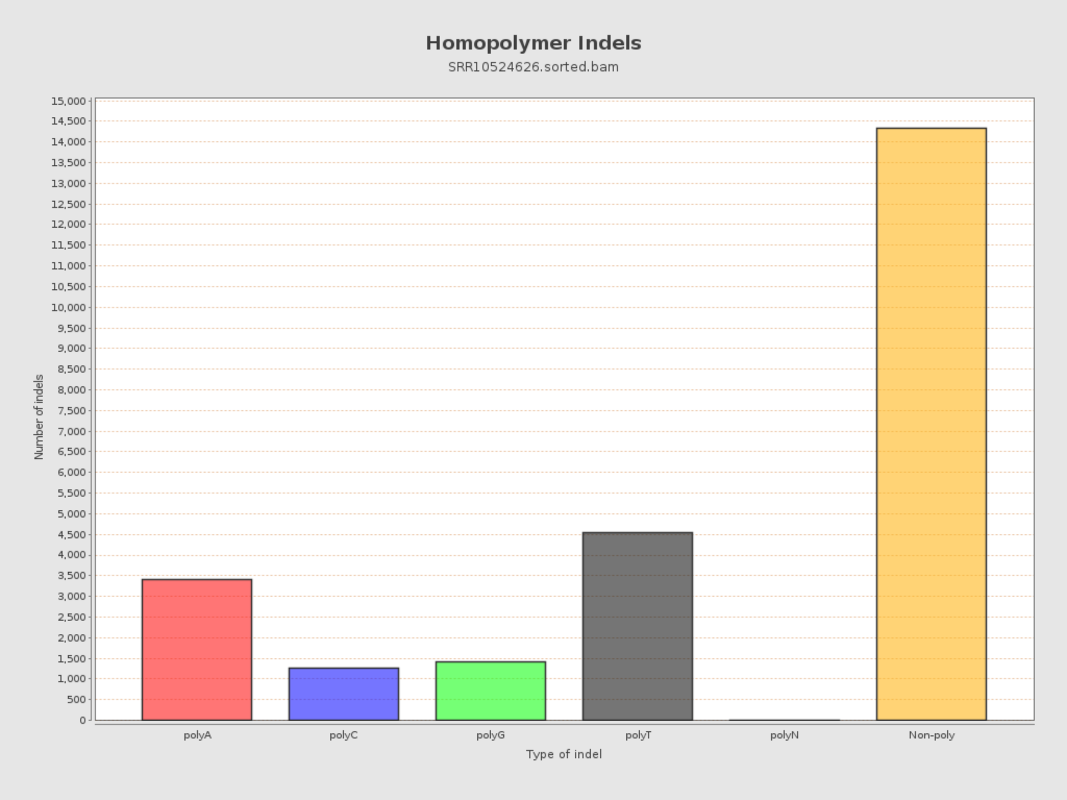
9. Results : Mapped Reads GC-content Distribution



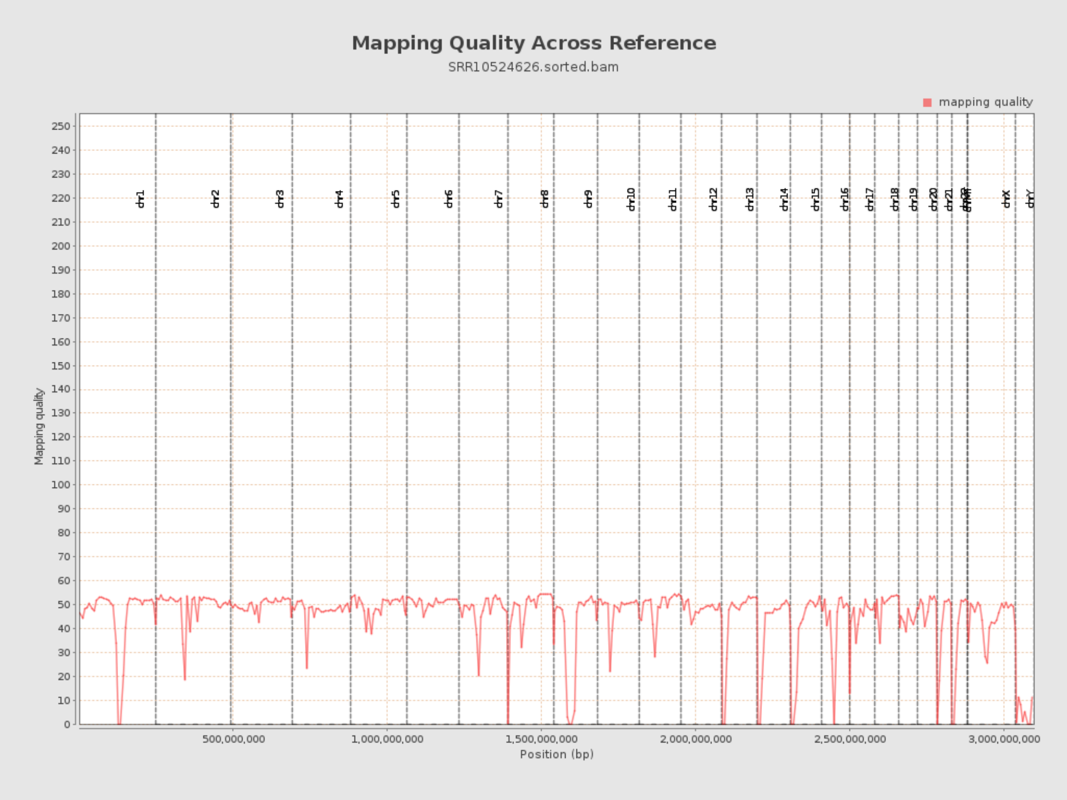
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram