Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 02:10:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525270.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_SRR10525270 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525270.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 02:10:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525270.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,520,368
Mapped reads	1,331,913 / 87.6%
Unmapped reads	188,455 / 12.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,682 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	42,097 / 2.77%
Duplication rate	2.19%
Clipped reads	1,333,093 / 87.68%

2.2. ACGT Content

Number/percentage of A's	18,106,810 / 23.53%
Number/percentage of C's	14,178,664 / 18.43%
Number/percentage of T's	24,969,121 / 32.45%
Number/percentage of G's	19,695,259 / 25.59%
Number/percentage of N's	1,498 / 0%
GC Percentage	44.02%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2446

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

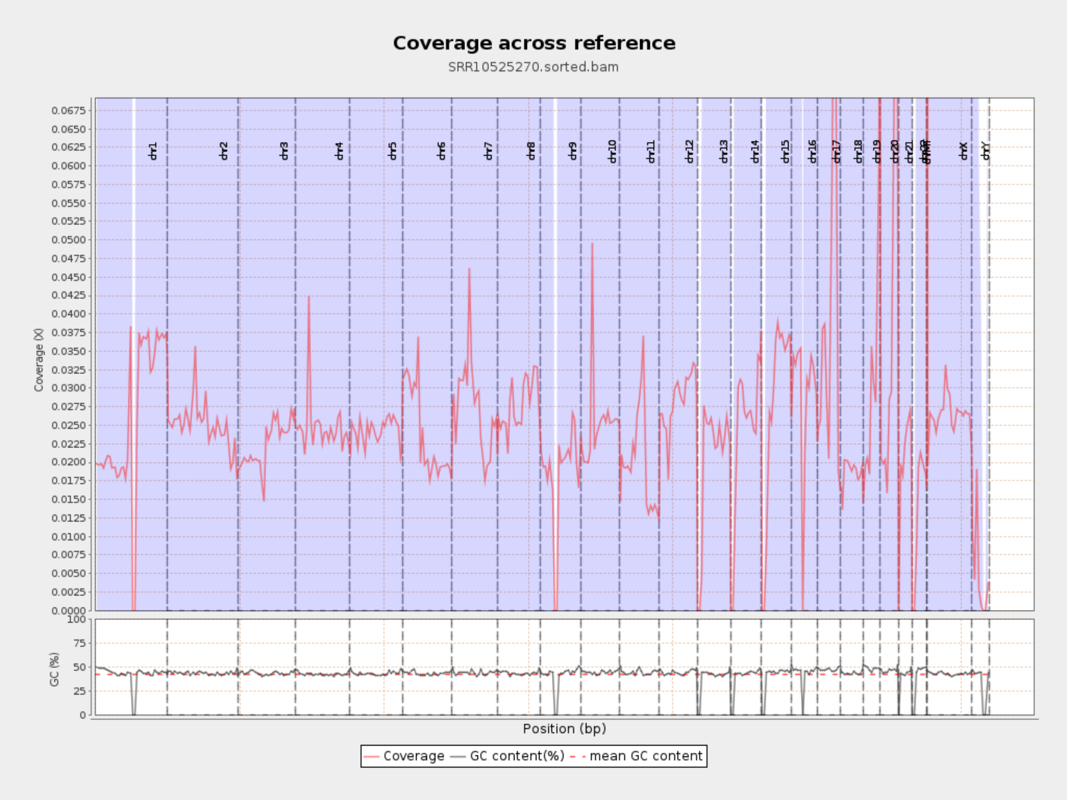
General error rate	0.53%
Mismatches	401,979
Insertions	5,184
Mapped reads with at least one insertion	0.39%
Deletions	16,486
Mapped reads with at least one deletion	1.23%
Homopolymer indels	42.64%

2.6. Chromosome stats

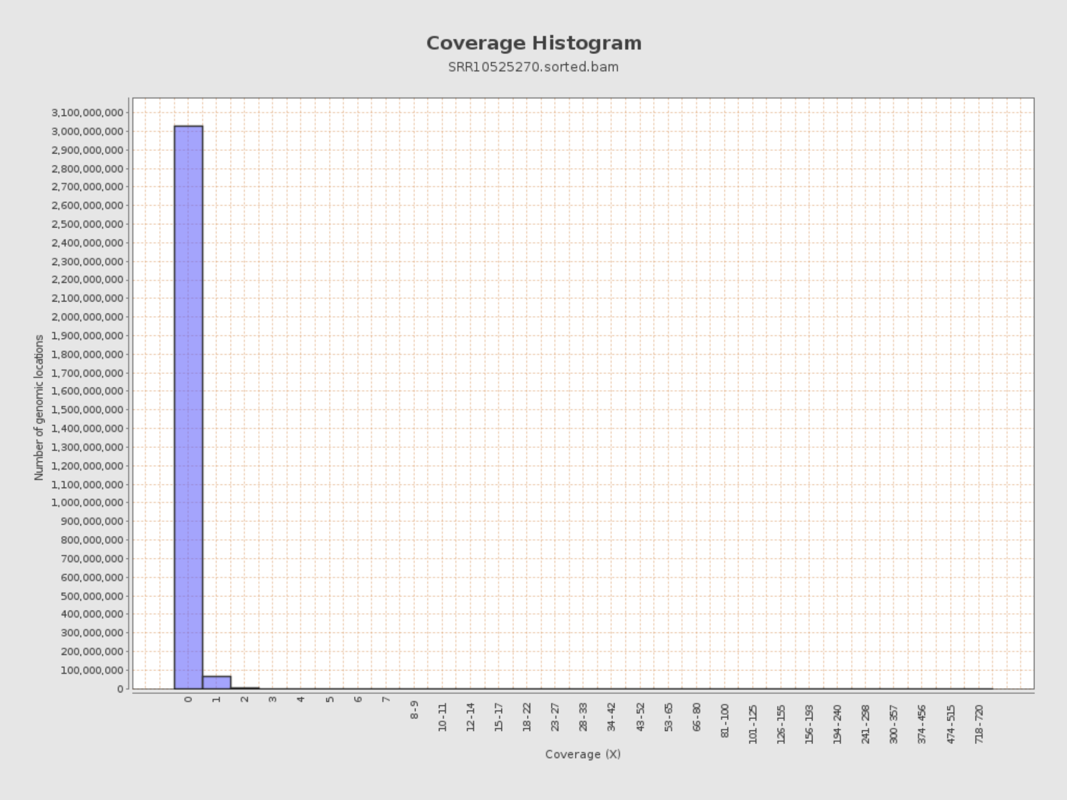
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6444485	0.0259	0.3827
chr2	243199373	6097773	0.0251	0.338
chr3	198022430	4425570	0.0223	0.1612
chr4	191154276	4742358	0.0248	0.1957
chr5	180915260	4410775	0.0244	0.1672
chr6	171115067	4098602	0.024	0.1955
chr7	159138663	4396572	0.0276	0.3169

chr8	146364022	4075872	0.0278	0.3133
chr9	141213431	2583444	0.0183	0.1728
chr10	135534747	3438381	0.0254	0.2525
chr11	135006516	2737275	0.0203	0.1883
chr12	133851895	3789557	0.0283	0.1817
chr13	115169878	2341760	0.0203	0.1558
chr14	107349540	2571784	0.024	0.1689
chr15	102531392	2805142	0.0274	0.18
chr16	90354753	2589998	0.0287	0.1891
chr17	81195210	3269352	0.0403	0.2235
chr18	78077248	1445924	0.0185	0.2736
chr19	59128983	1904847	0.0322	0.2994
chr20	63025520	2499412	0.0397	0.2205
chr21	48129895	987978	0.0205	0.1741
chr22	51304566	703587	0.0137	0.1254
chrMT	16571	204255	12.3261	7.9186
chrX	155270560	4123043	0.0266	0.1886
chrY	59373566	289925	0.0049	0.1979

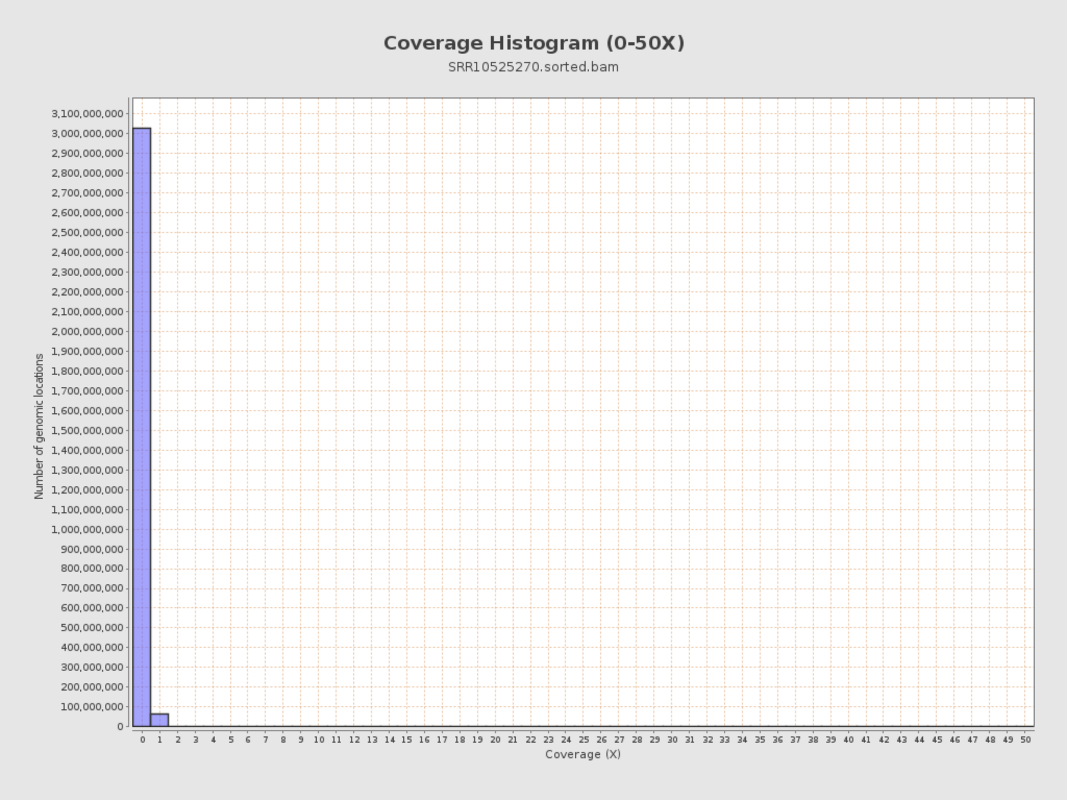
3. Results : Coverage across reference



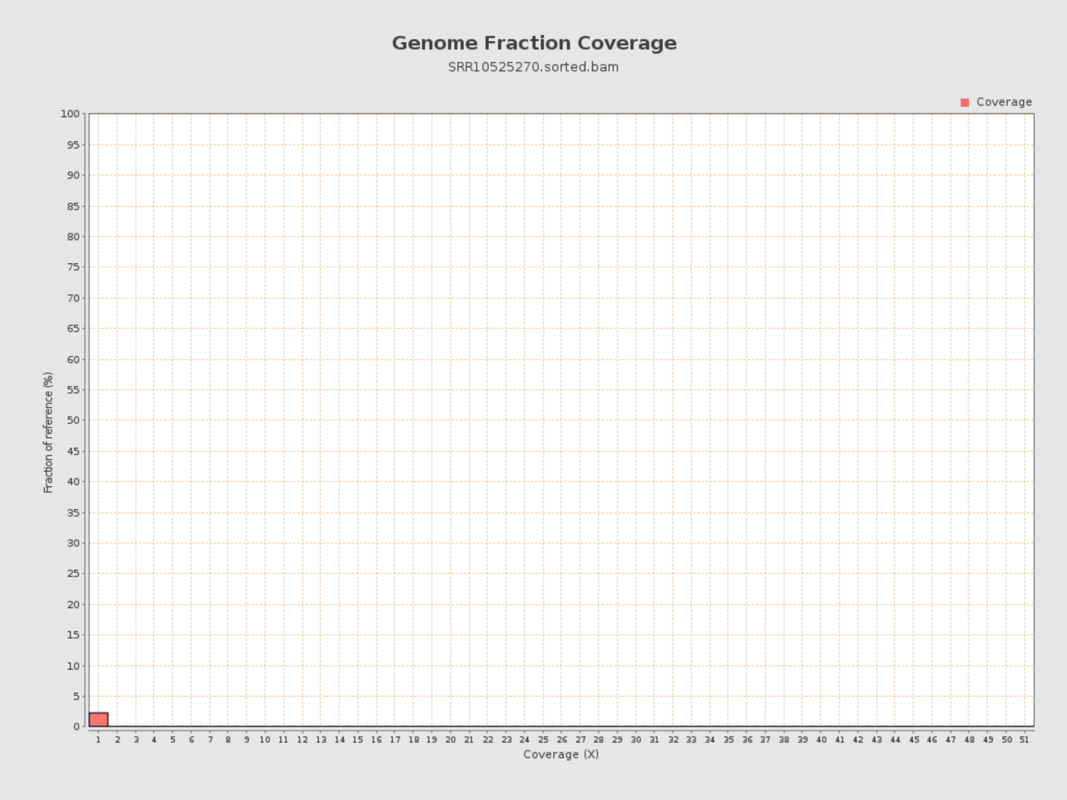
4. Results : Coverage Histogram



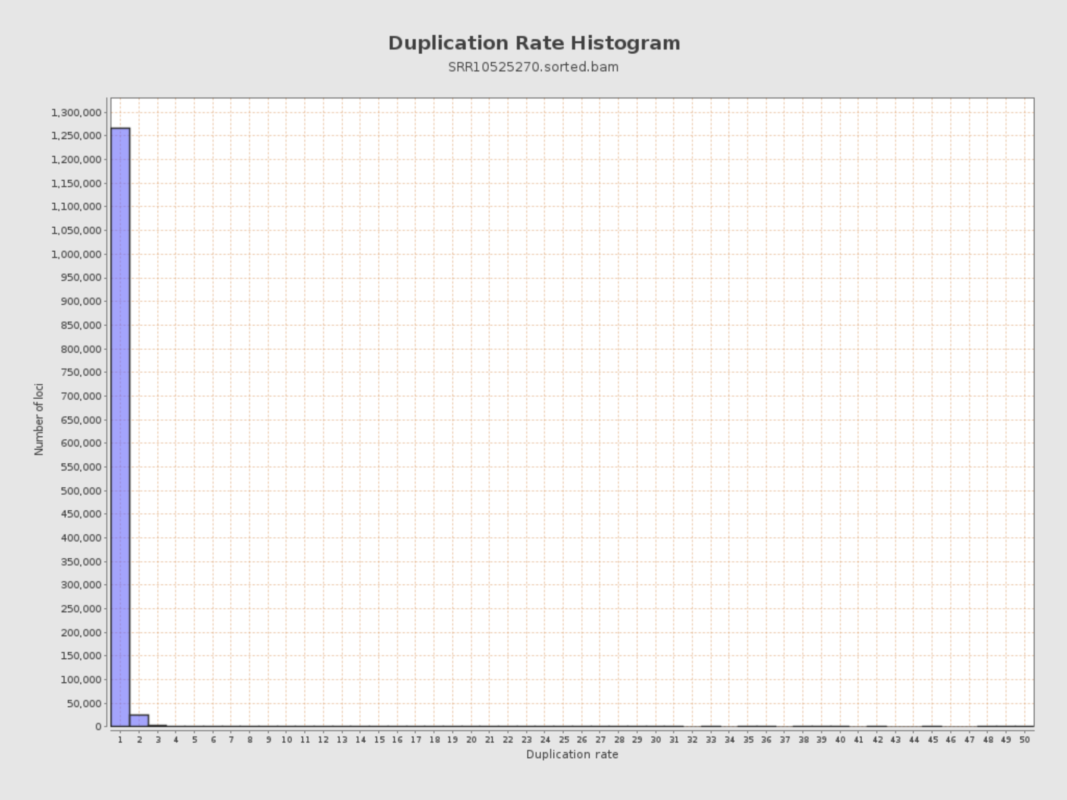
5. Results : Coverage Histogram (0-50X)



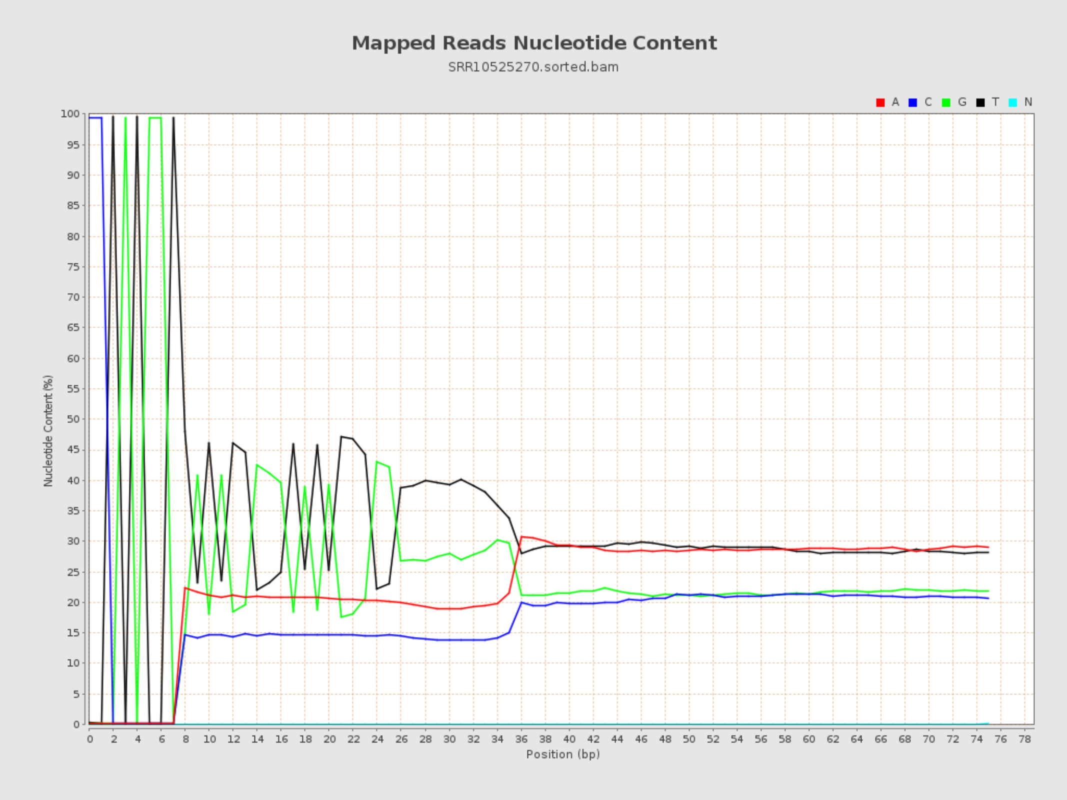
6. Results : Genome Fraction Coverage



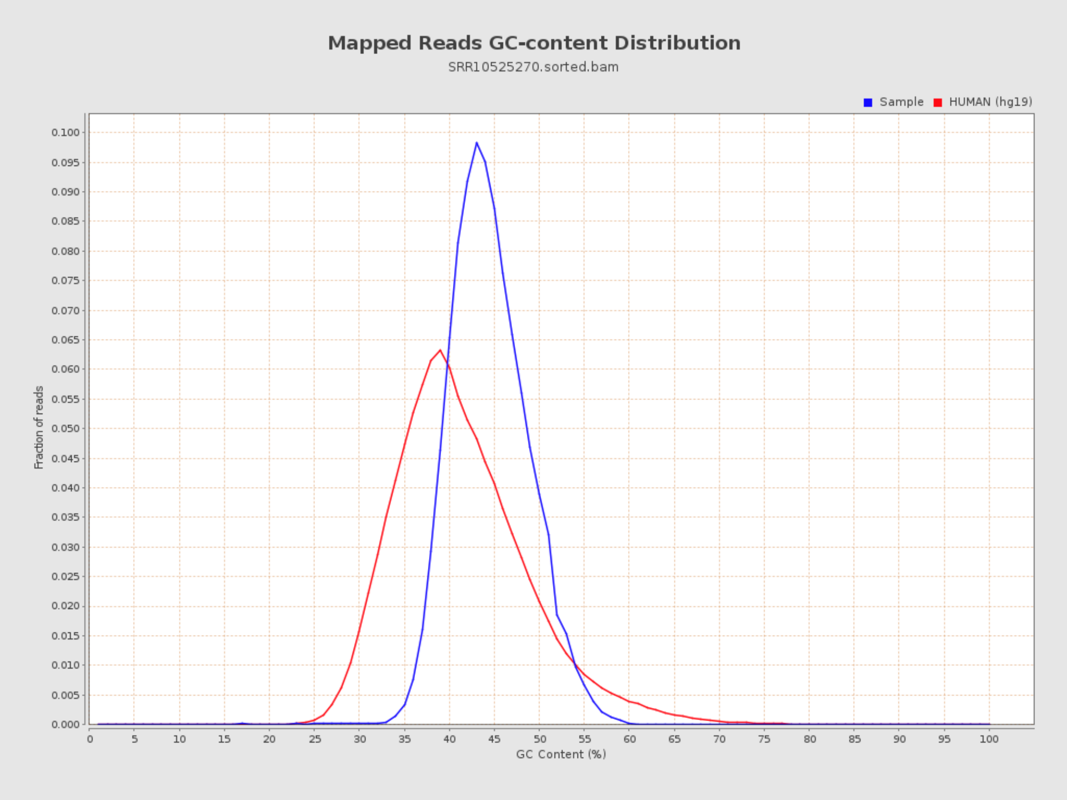
7. Results : Duplication Rate Histogram



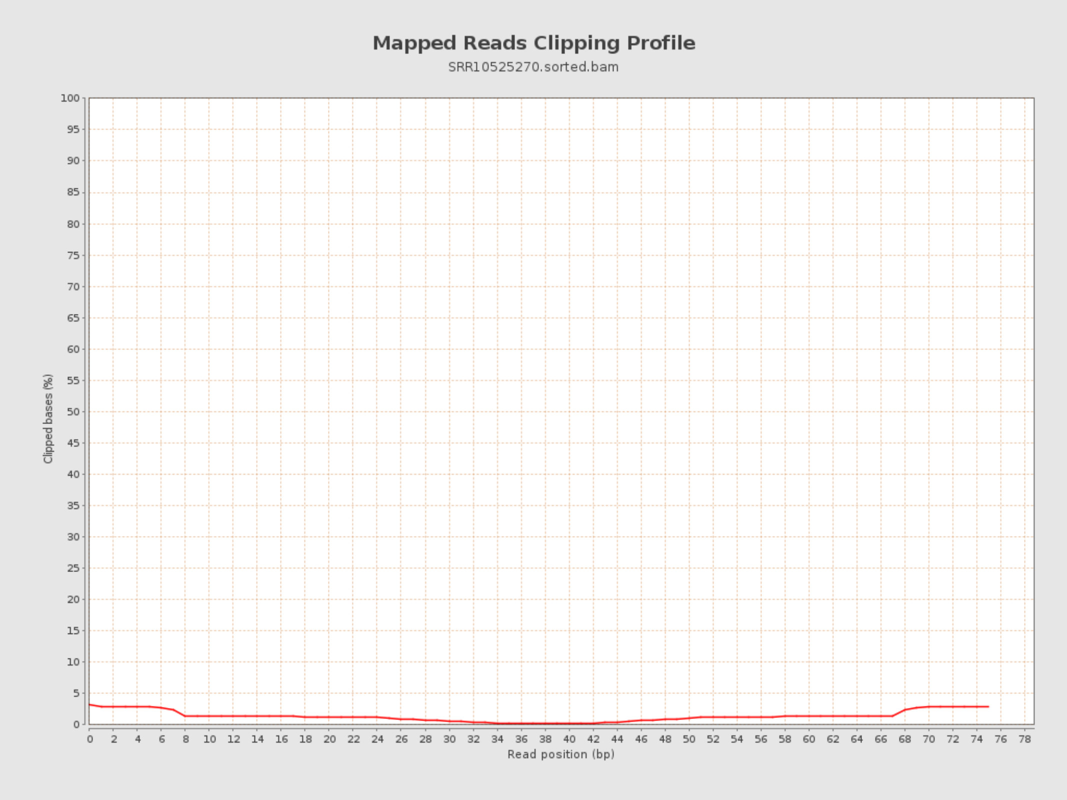
8. Results : Mapped Reads Nucleotide Content



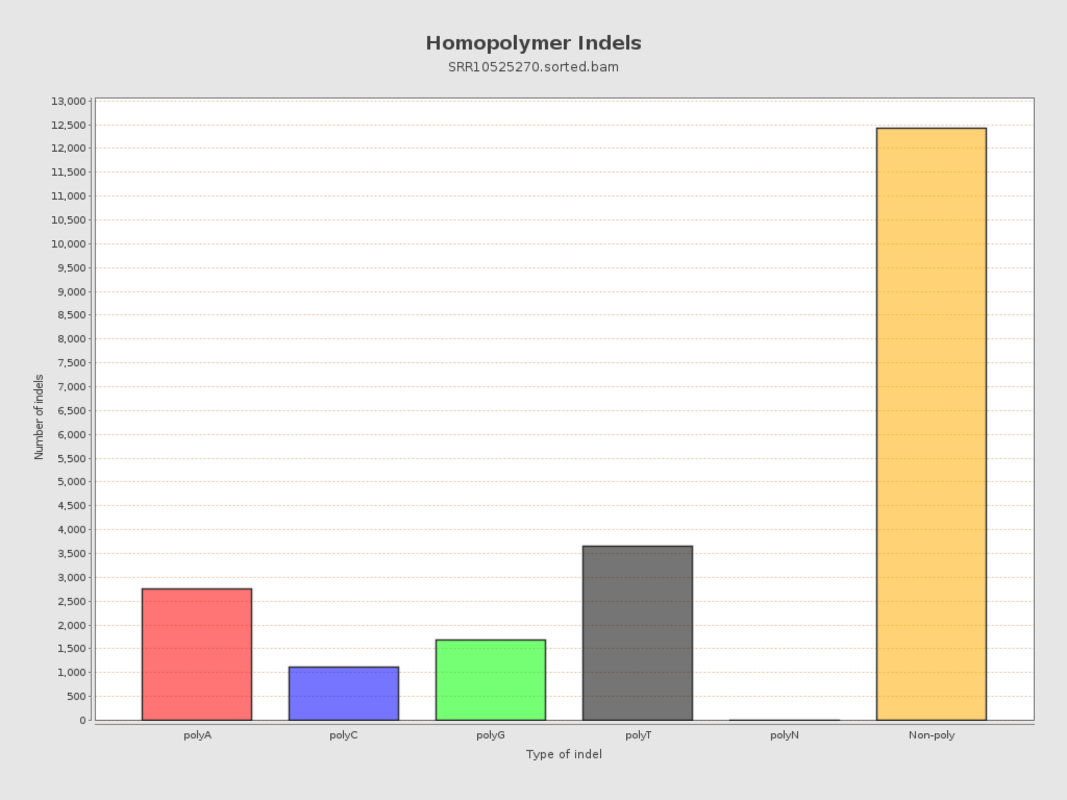
9. Results : Mapped Reads GC-content Distribution



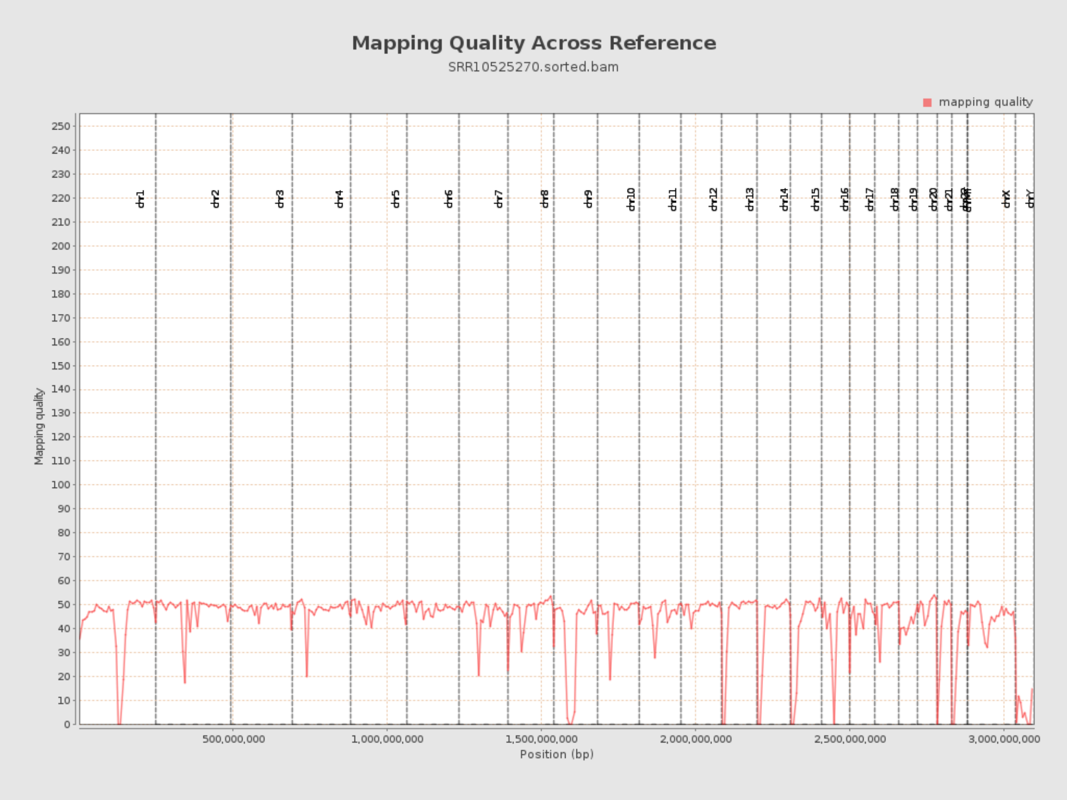
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram