Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:45:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525244.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_SRR10525244 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525244.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:45:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525244.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,406,697
Mapped reads	1,294,951 / 92.06%
Unmapped reads	111,746 / 7.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,328 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	41,388 / 2.94%
Duplication rate	2.37%
Clipped reads	1,295,903 / 92.12%

2.2. ACGT Content

Number/percentage of A's	18,182,833 / 24.11%
Number/percentage of C's	13,164,715 / 17.45%
Number/percentage of T's	25,235,381 / 33.46%
Number/percentage of G's	18,838,613 / 24.98%
Number/percentage of N's	1,565 / 0%
GC Percentage	42.43%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.242

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

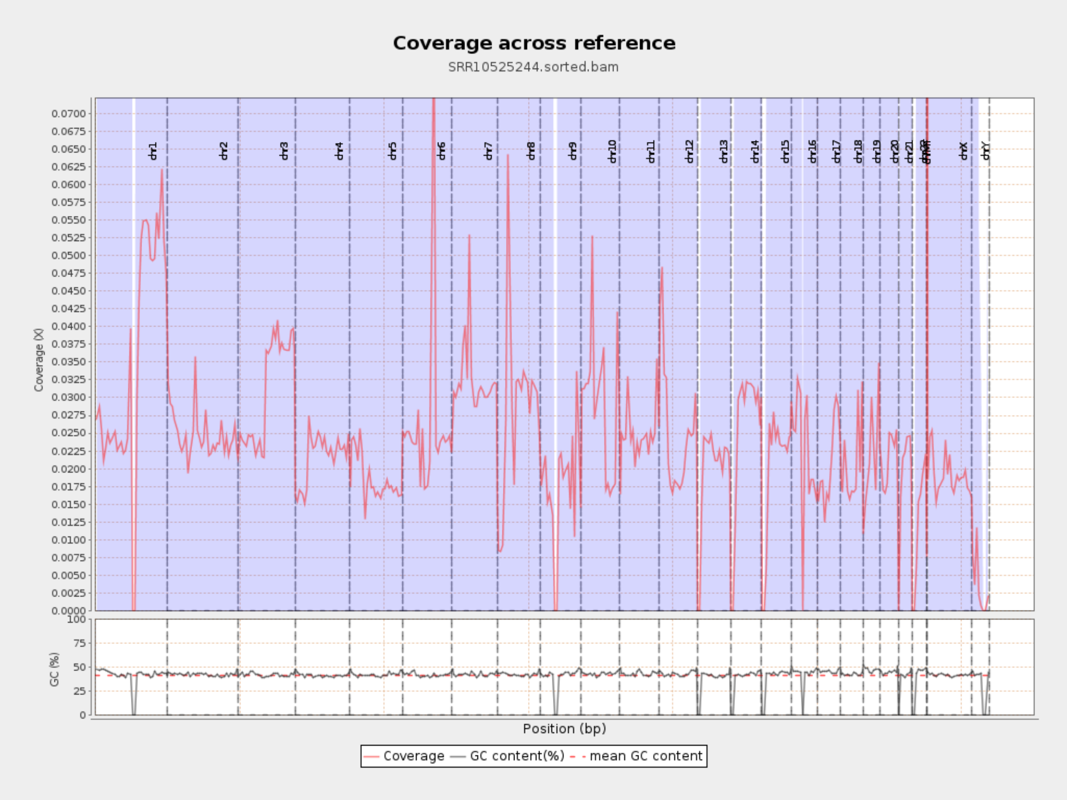
General error rate	0.51%
Mismatches	377,210
Insertions	5,224
Mapped reads with at least one insertion	0.4%
Deletions	15,204
Mapped reads with at least one deletion	1.17%
Homopolymer indels	44.01%

2.6. Chromosome stats

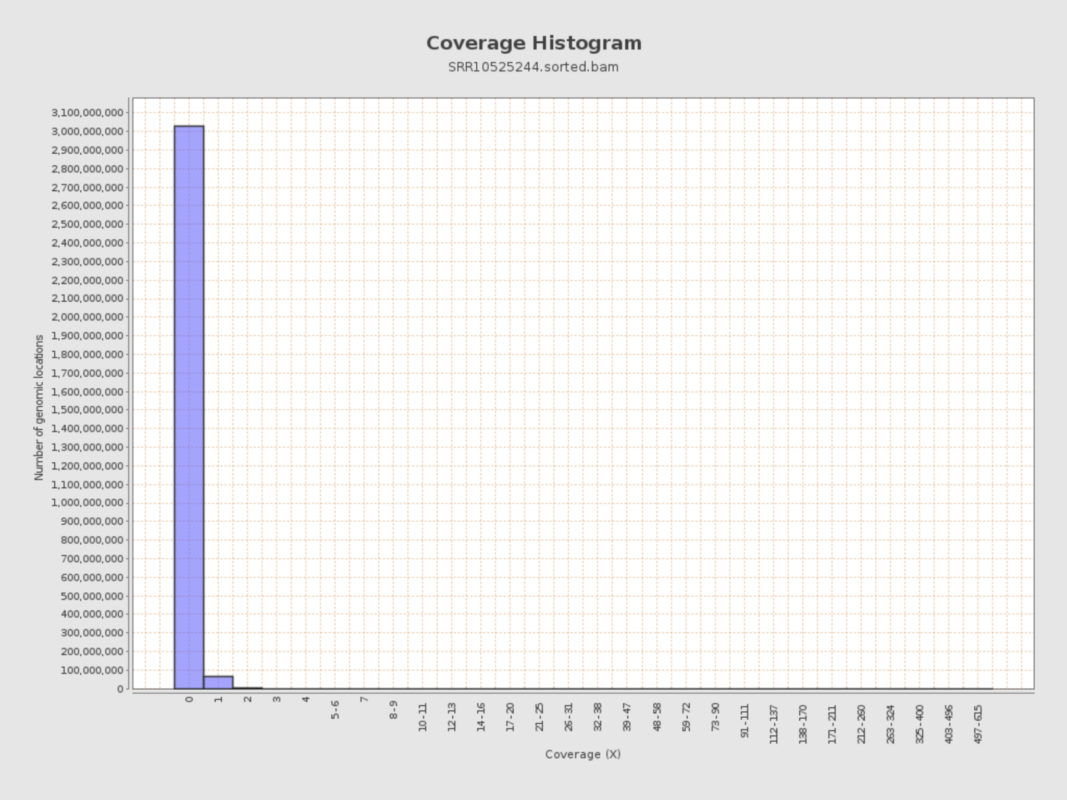
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8656336	0.0347	0.4112
chr2	243199373	6014254	0.0247	0.3051
chr3	198022430	6121497	0.0309	0.1905
chr4	191154276	4152175	0.0217	0.1657
chr5	180915260	3371955	0.0186	0.146
chr6	171115067	4667035	0.0273	0.1944
chr7	159138663	5205462	0.0327	0.4077

chr8	146364022	4250000	0.029	0.2357
chr9	141213431	2472637	0.0175	0.1767
chr10	135534747	3988876	0.0294	0.2687
chr11	135006516	3359600	0.0249	0.198
chr12	133851895	3393866	0.0254	0.1721
chr13	115169878	2257484	0.0196	0.1513
chr14	107349540	2717262	0.0253	0.1747
chr15	102531392	2010598	0.0196	0.1535
chr16	90354753	2011708	0.0223	0.1703
chr17	81195210	1689375	0.0208	0.1575
chr18	78077248	1570332	0.0201	0.3263
chr19	59128983	1308425	0.0221	0.2794
chr20	63025520	1336385	0.0212	0.158
chr21	48129895	944025	0.0196	0.1581
chr22	51304566	628187	0.0122	0.1181
chrMT	16571	142390	8.5927	5.122
chrX	155270560	2980248	0.0192	0.1604
chrY	59373566	197306	0.0033	0.1038

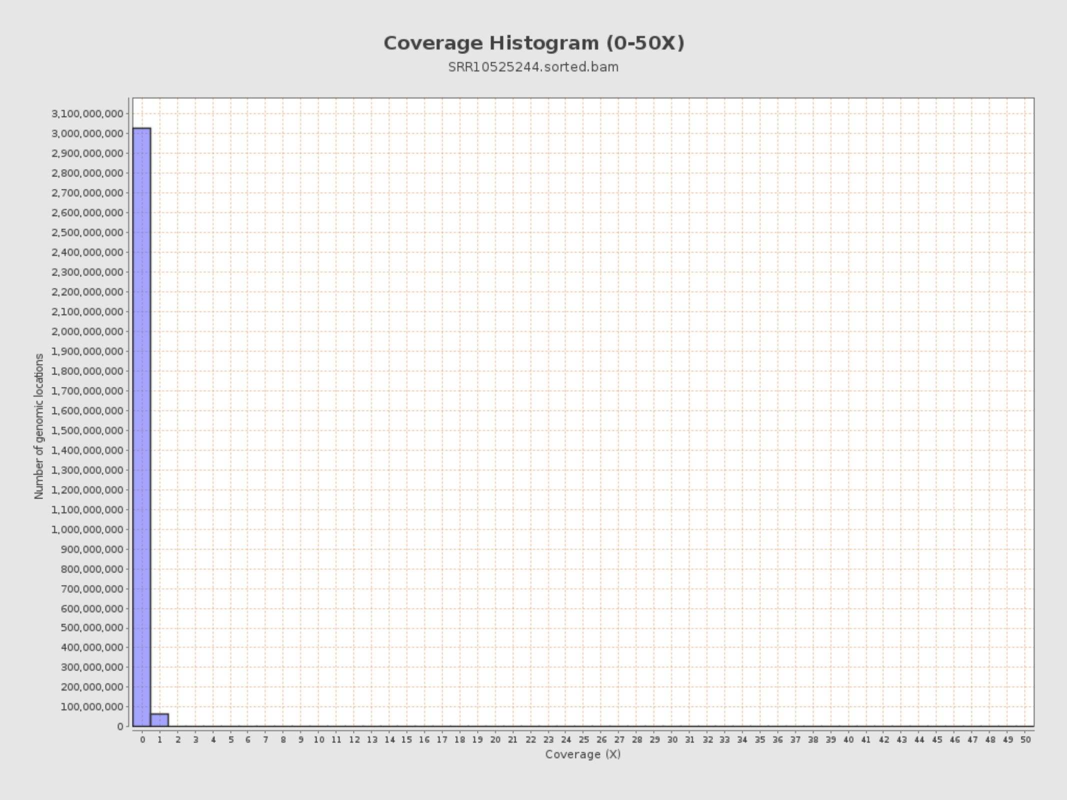
3. Results : Coverage across reference



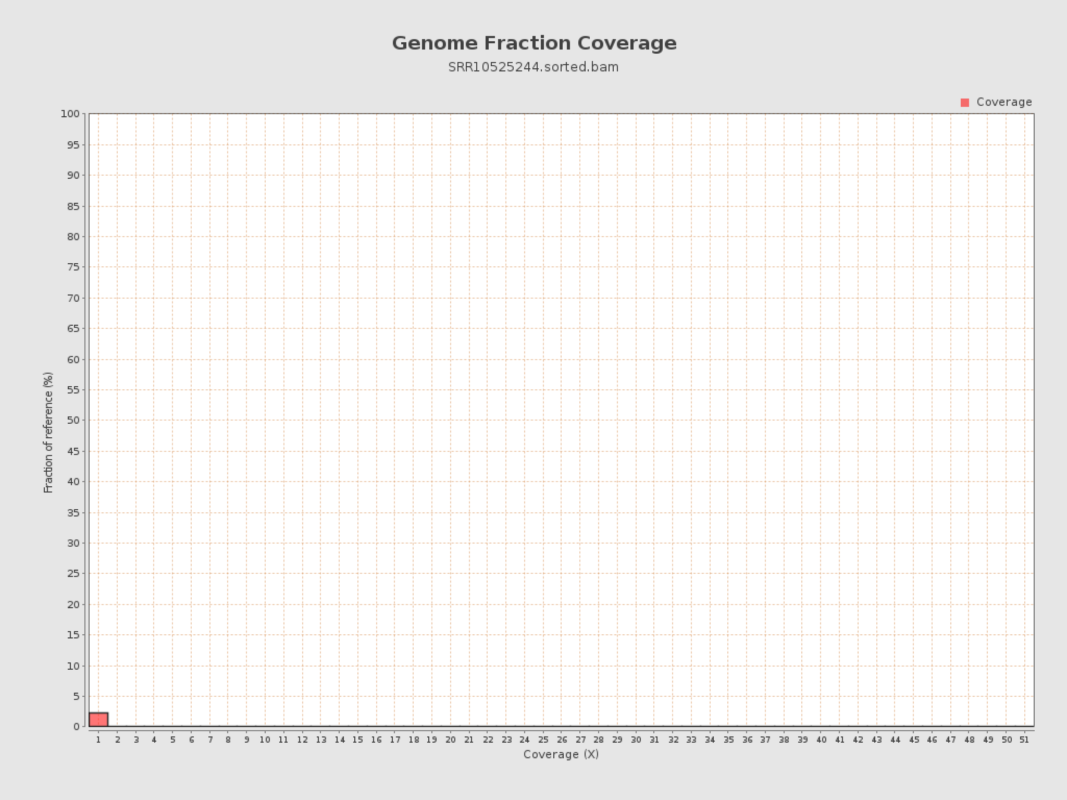
4. Results : Coverage Histogram



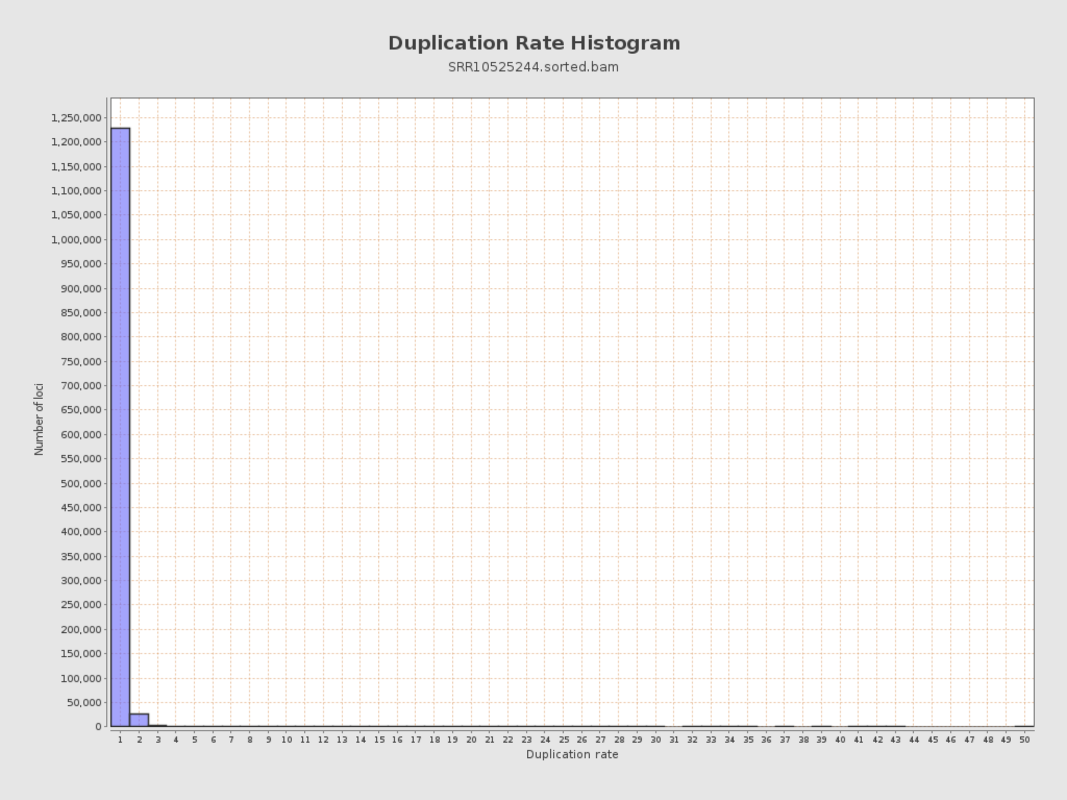
5. Results : Coverage Histogram (0-50X)



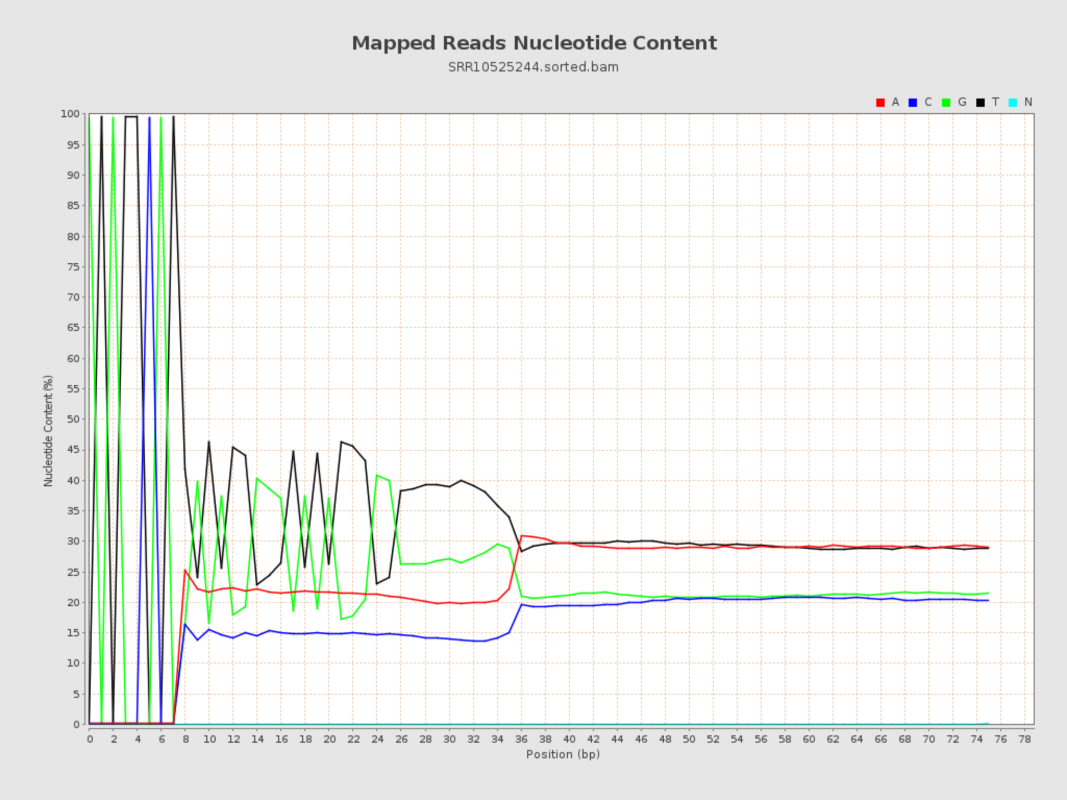
6. Results : Genome Fraction Coverage



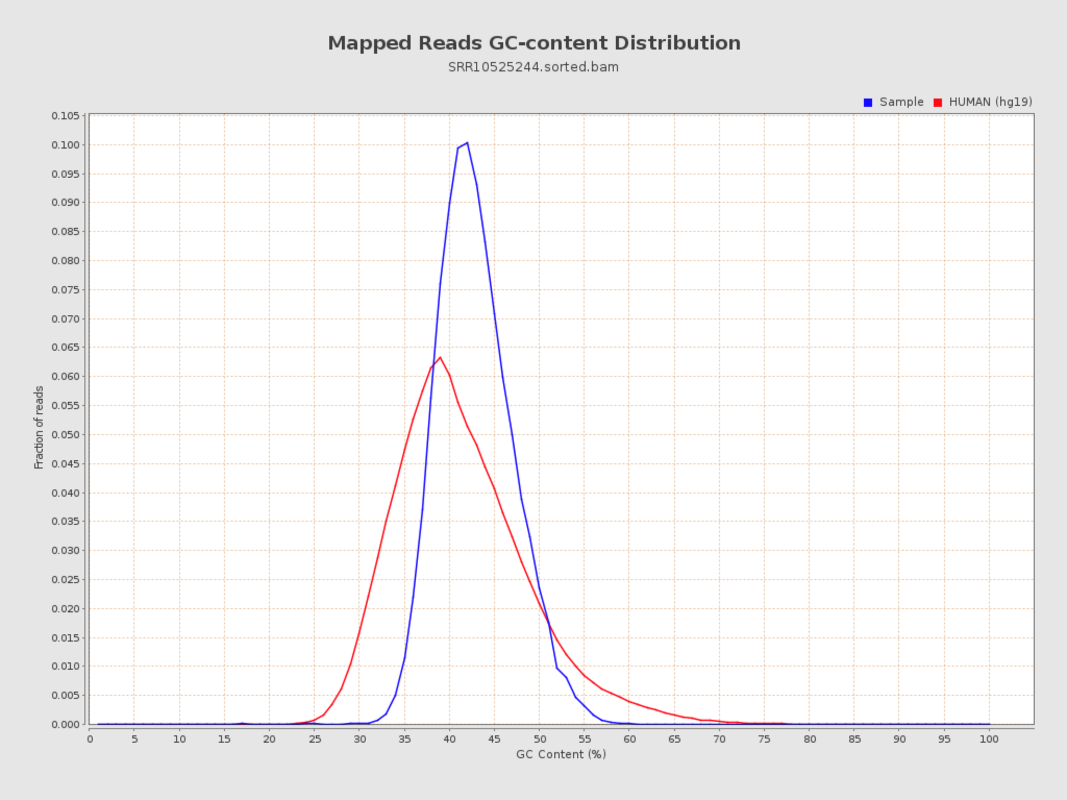
7. Results : Duplication Rate Histogram



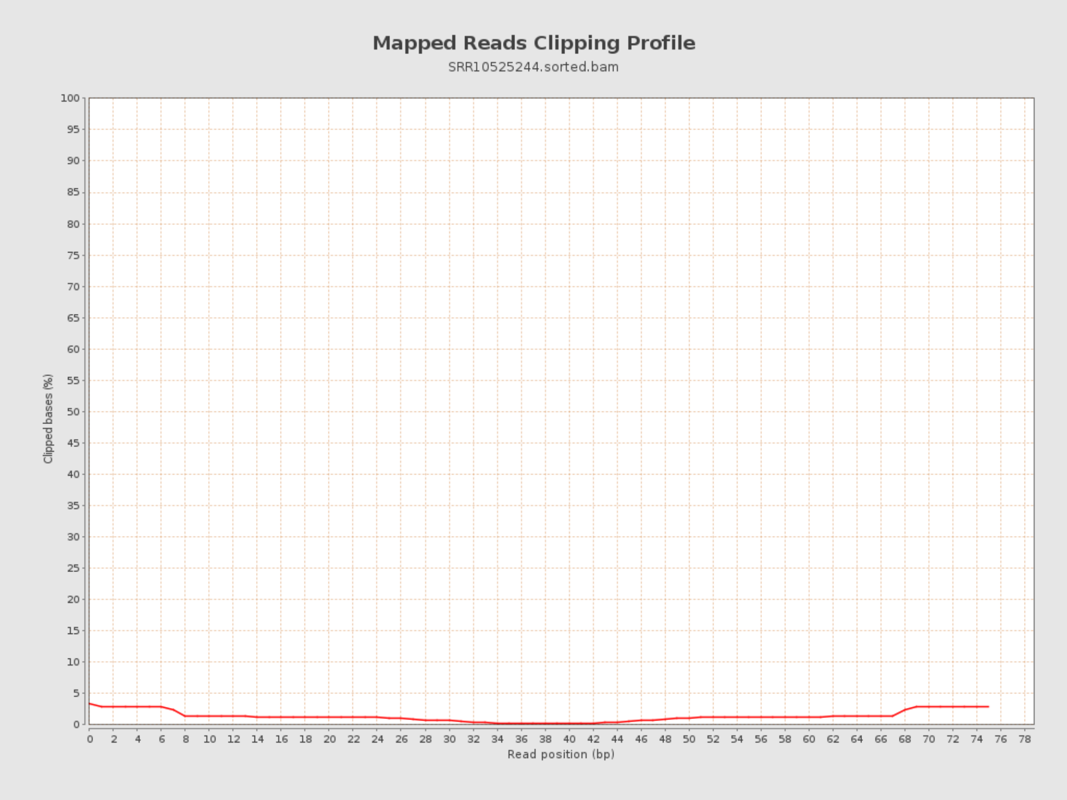
8. Results : Mapped Reads Nucleotide Content



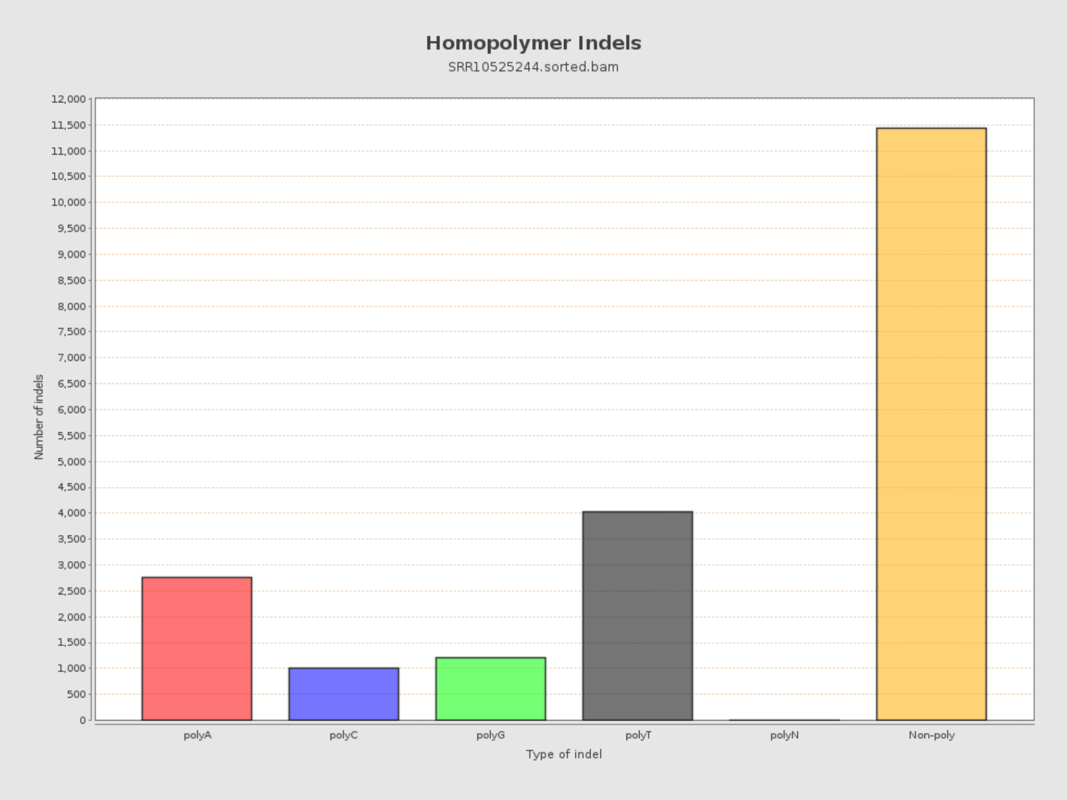
9. Results : Mapped Reads GC-content Distribution



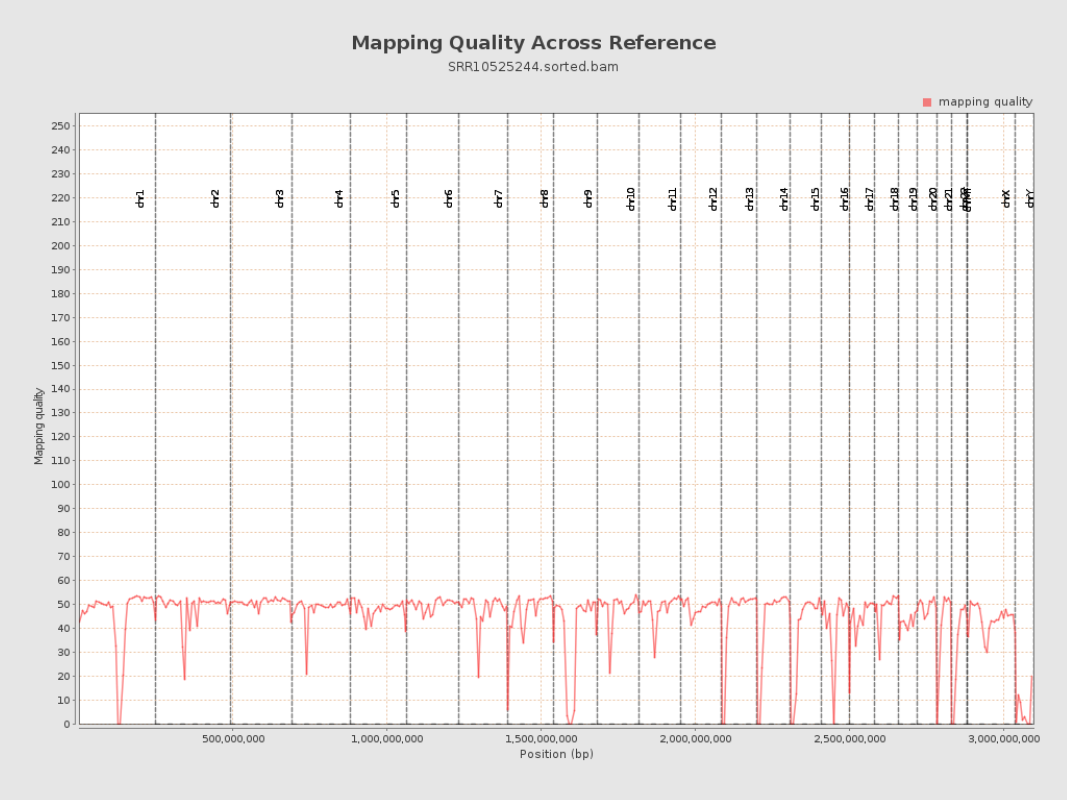
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram