Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:50:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525221.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_SRR10525221 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525221.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:50:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525221.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,180,047
Mapped reads	1,088,937 / 92.28%
Unmapped reads	91,110 / 7.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,289 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	29,648 / 2.51%
Duplication rate	1.98%
Clipped reads	1,089,140 / 92.3%

2.2. ACGT Content

Number/percentage of A's	15,599,241 / 24.64%
Number/percentage of C's	11,119,828 / 17.56%
Number/percentage of T's	20,958,892 / 33.1%
Number/percentage of G's	15,634,662 / 24.69%
Number/percentage of N's	1,528 / 0%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0205

Standard Deviation	0.2077

2.4. Mapping Quality

Mean Mapping Quality	44.69

2.5. Mismatches and indels

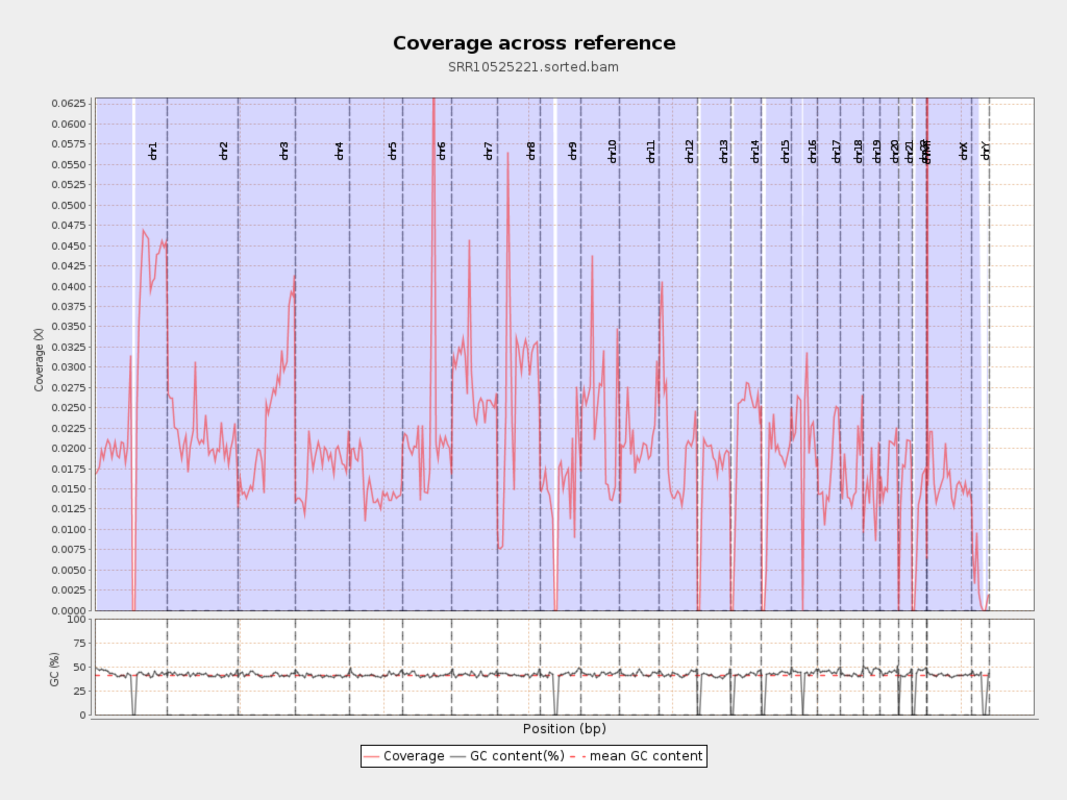
General error rate	0.51%
Mismatches	316,619
Insertions	4,679
Mapped reads with at least one insertion	0.43%
Deletions	12,009
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.16%

2.6. Chromosome stats

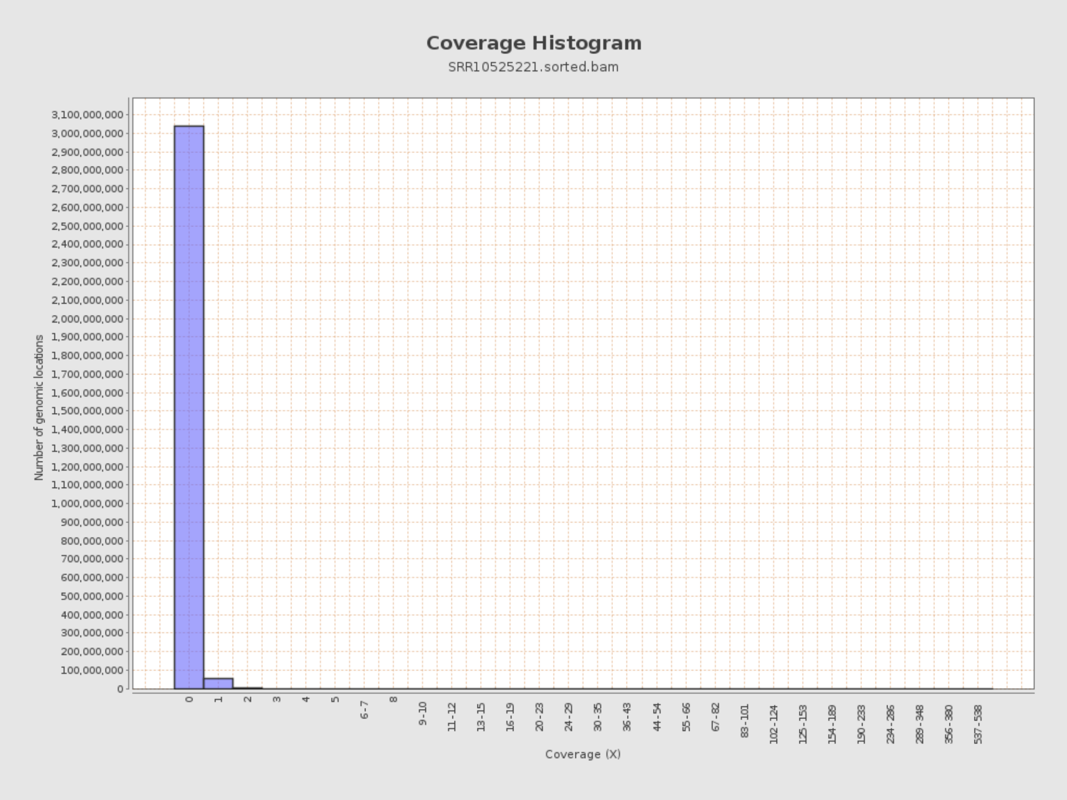
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7107861	0.0285	0.3143
chr2	243199373	5185780	0.0213	0.2699
chr3	198022430	4667957	0.0236	0.1662
chr4	191154276	3429547	0.0179	0.1466
chr5	180915260	2792624	0.0154	0.1317
chr6	171115067	3932276	0.023	0.1733
chr7	159138663	4529498	0.0285	0.3728

chr8	146364022	4049254	0.0277	0.208
chr9	141213431	2075595	0.0147	0.1546
chr10	135534747	3313813	0.0244	0.2341
chr11	135006516	2825390	0.0209	0.1786
chr12	133851895	2788302	0.0208	0.1538
chr13	115169878	1918073	0.0167	0.1386
chr14	107349540	2309079	0.0215	0.159
chr15	102531392	1671393	0.0163	0.1353
chr16	90354753	1959547	0.0217	0.1668
chr17	81195210	1425751	0.0176	0.1429
chr18	78077248	1300134	0.0167	0.2697
chr19	59128983	876030	0.0148	0.2296
chr20	63025520	1132496	0.018	0.1435
chr21	48129895	789852	0.0164	0.1413
chr22	51304566	534178	0.0104	0.1077
chrMT	16571	49418	2.9822	2.2299
chrX	155270560	2495527	0.0161	0.1432
chrY	59373566	174056	0.0029	0.0846

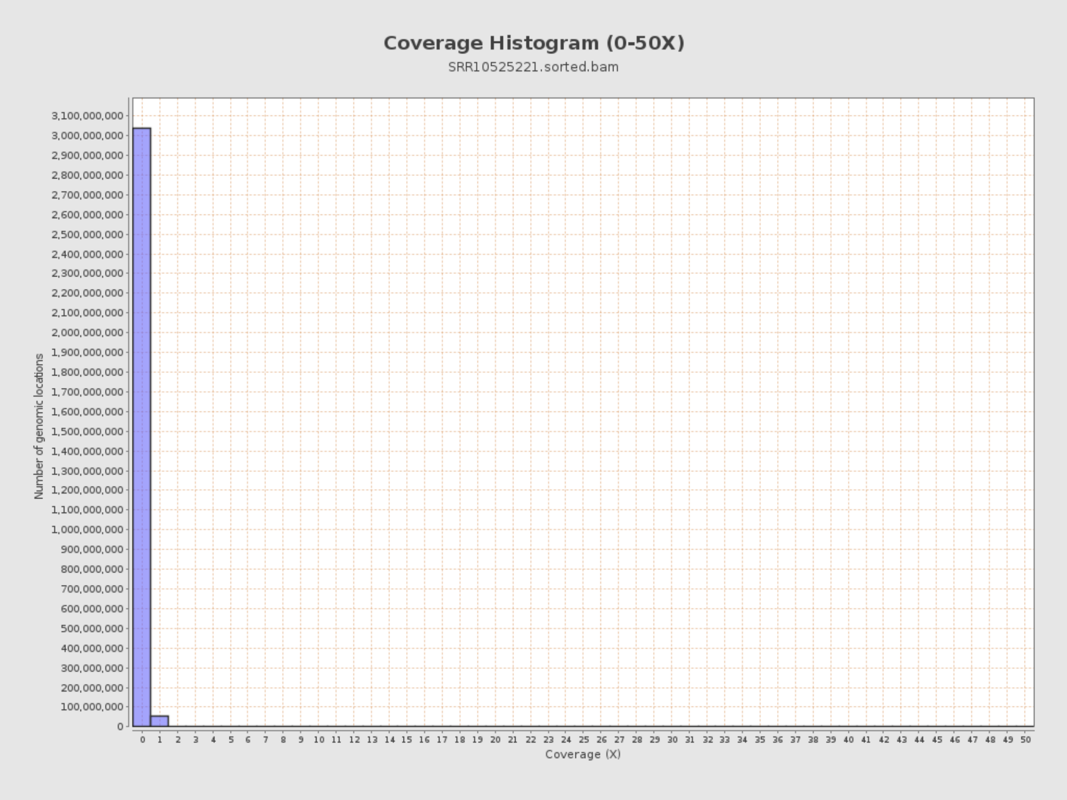
3. Results : Coverage across reference



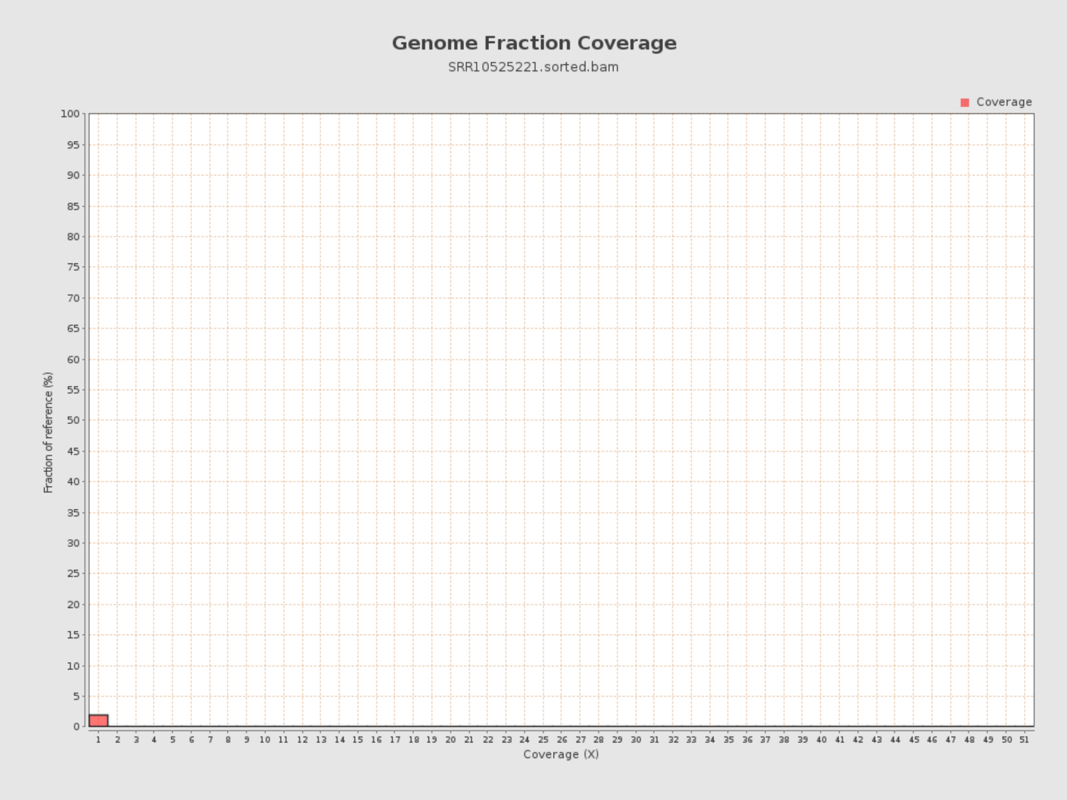
4. Results : Coverage Histogram



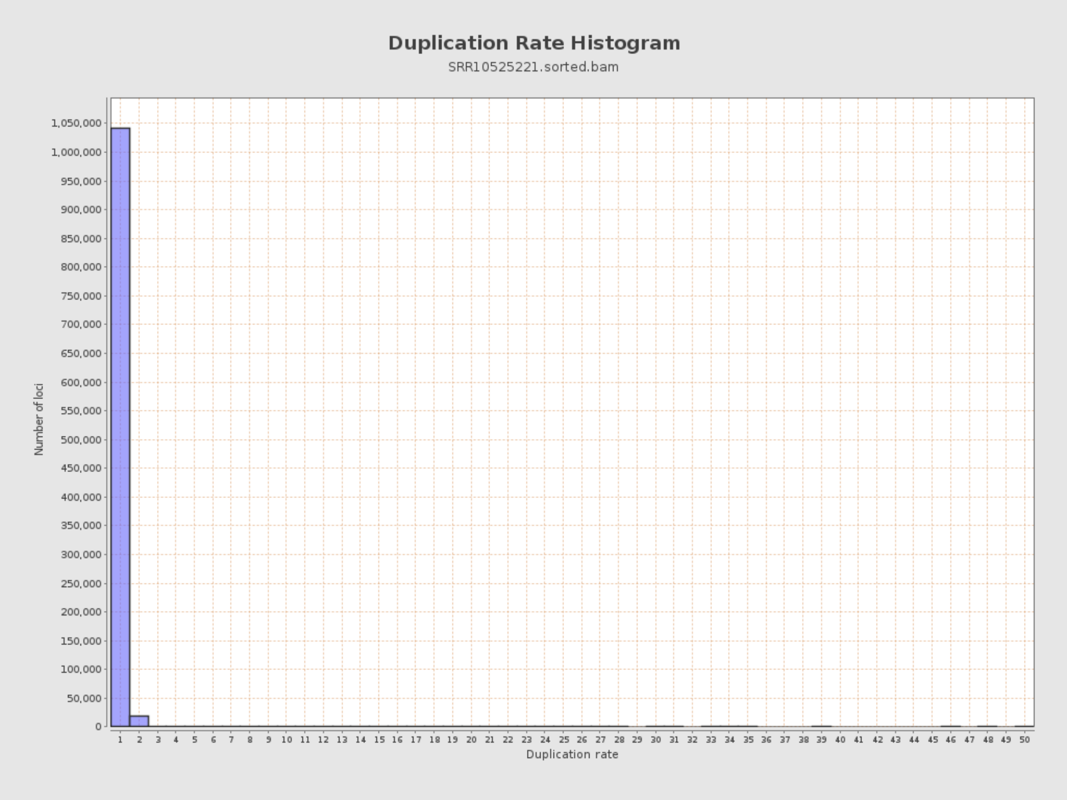
5. Results : Coverage Histogram (0-50X)



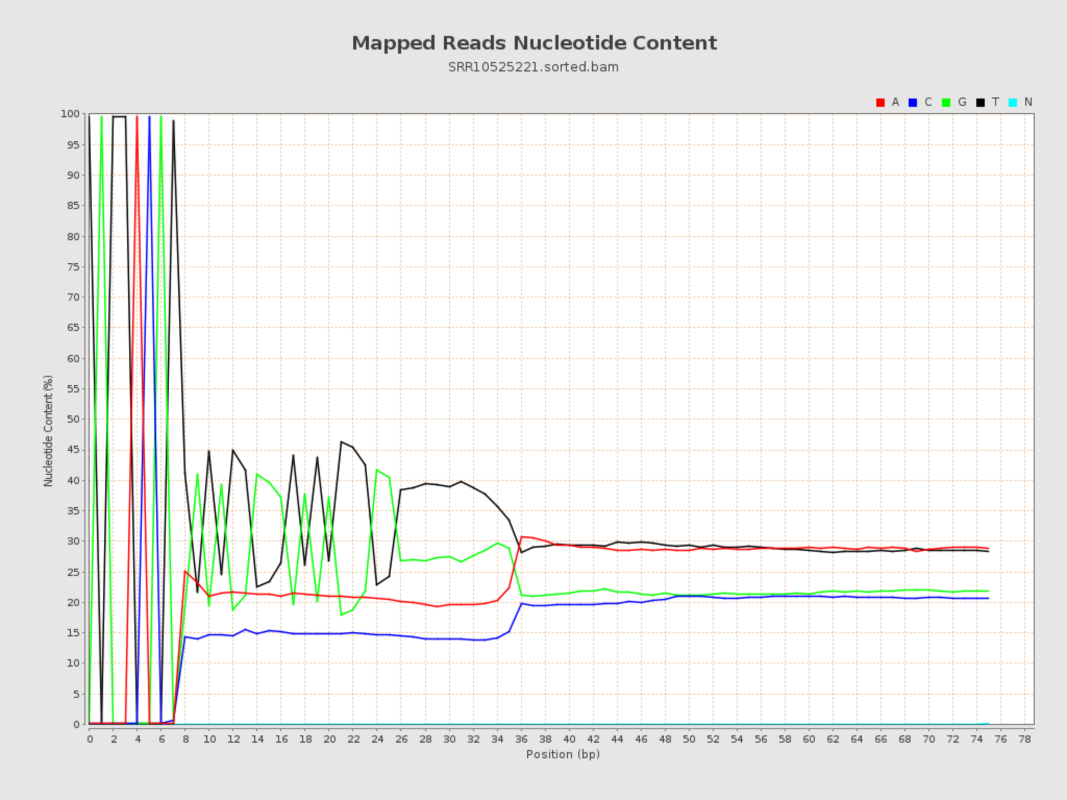
6. Results : Genome Fraction Coverage



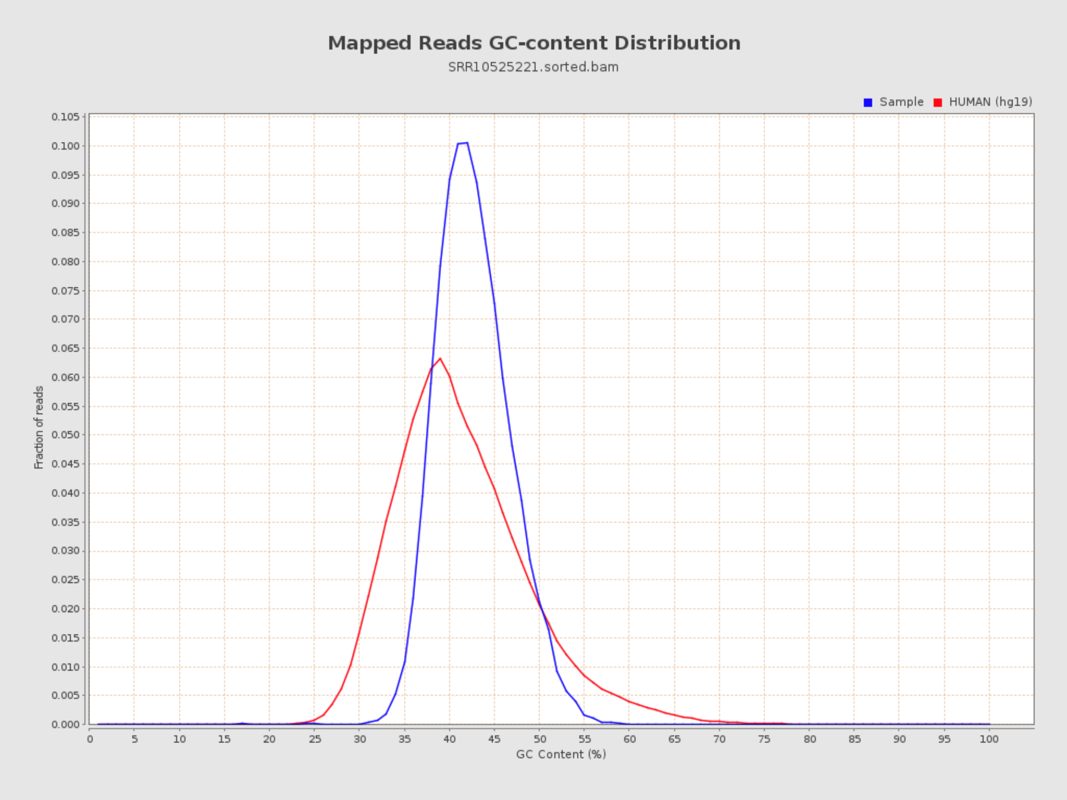
7. Results : Duplication Rate Histogram



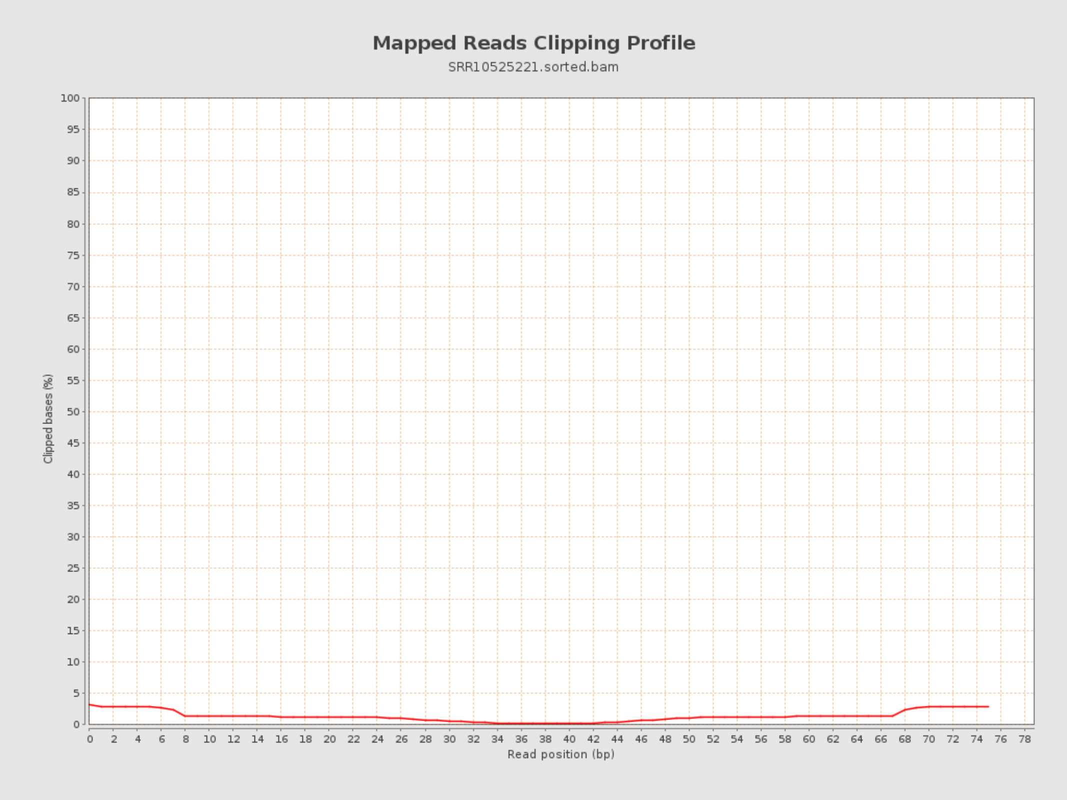
8. Results : Mapped Reads Nucleotide Content



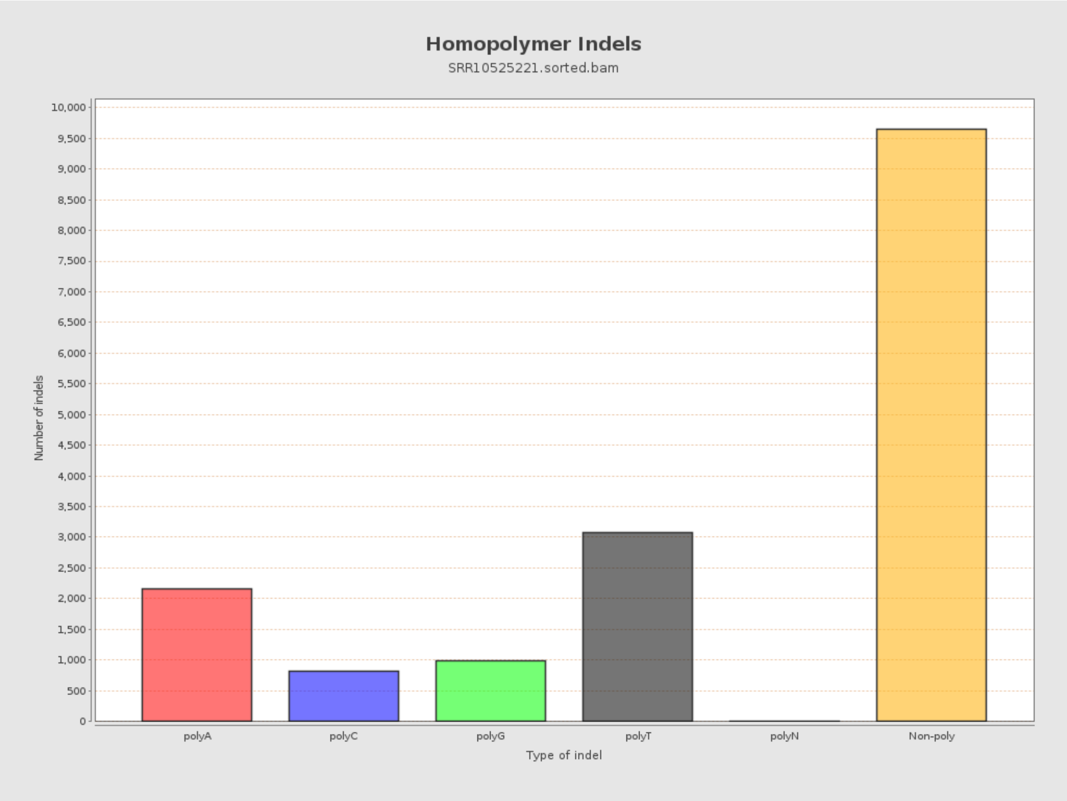
9. Results : Mapped Reads GC-content Distribution



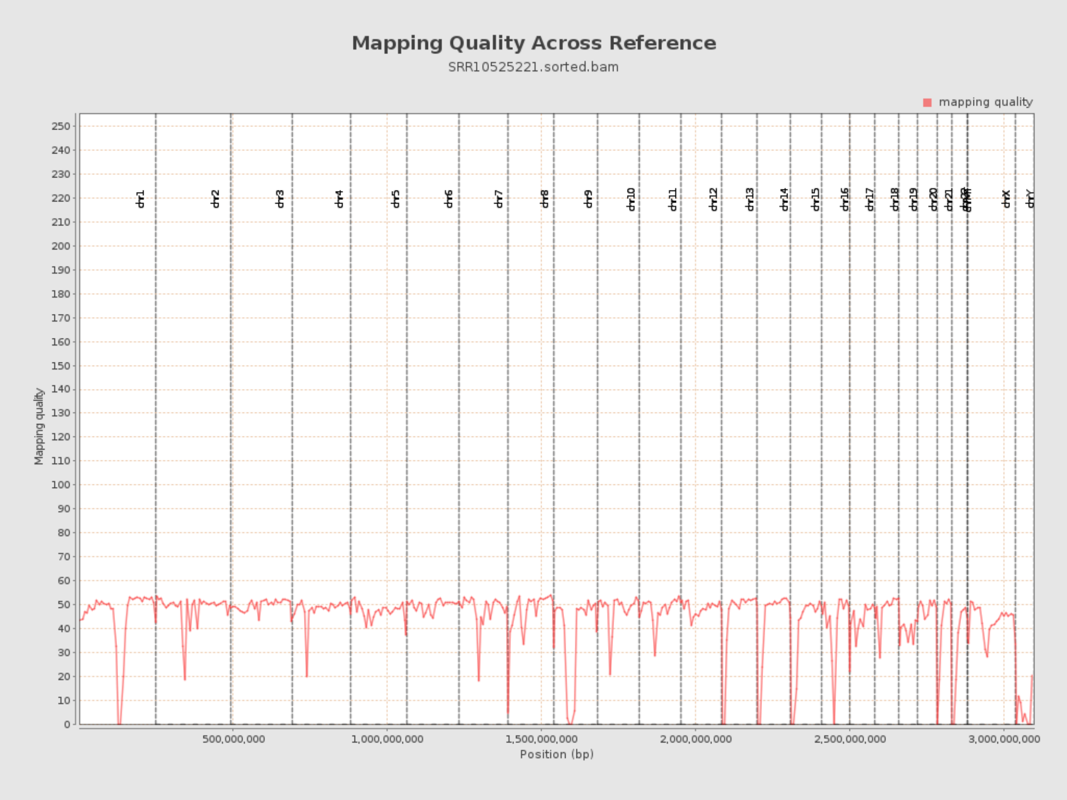
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram