Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:21:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525132.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_SRR10525132 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525132.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:21:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525132.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	597,027
Mapped reads	534,378 / 89.51%
Unmapped reads	62,649 / 10.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,081 / 2.36%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	10,845 / 1.82%
Duplication rate	1.24%
Clipped reads	547,485 / 91.7%

2.2. ACGT Content

Number/percentage of A's	11,083,303 / 26.98%
Number/percentage of C's	8,115,479 / 19.75%
Number/percentage of T's	12,575,688 / 30.61%
Number/percentage of G's	9,306,366 / 22.65%
Number/percentage of N's	1,482 / 0%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0133

Standard Deviation	0.1717

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

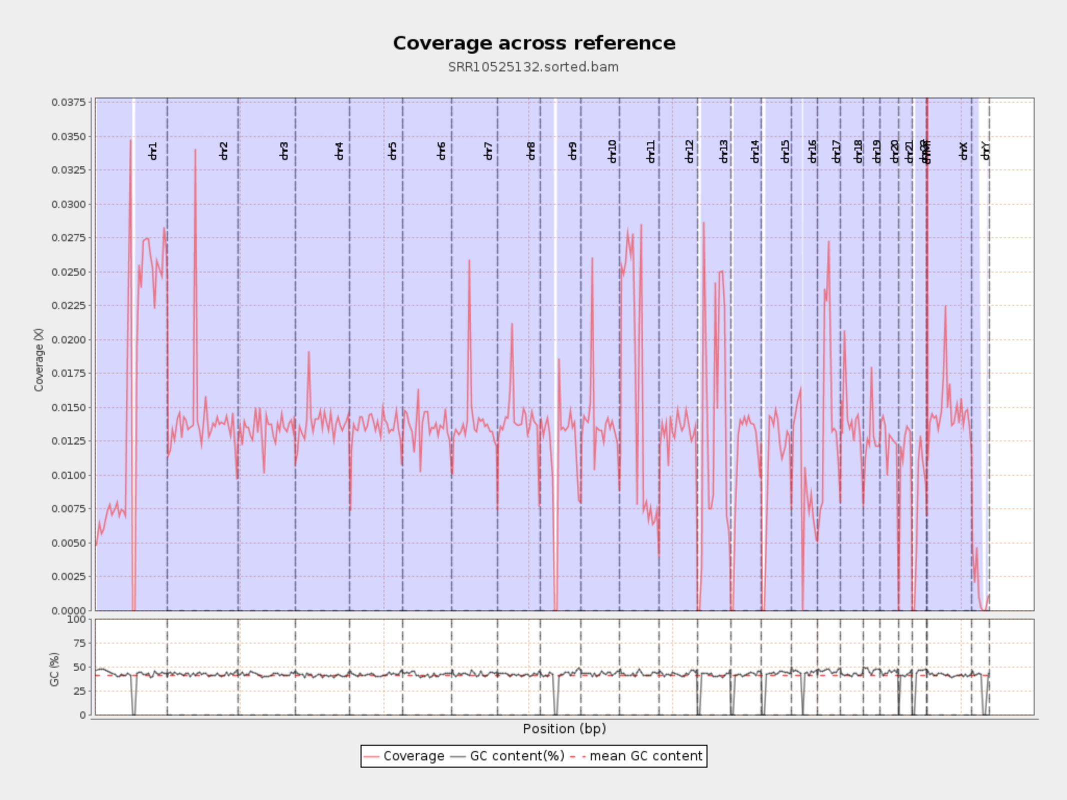
General error rate	0.74%
Mismatches	298,503
Insertions	3,682
Mapped reads with at least one insertion	0.68%
Deletions	9,646
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.68%

2.6. Chromosome stats

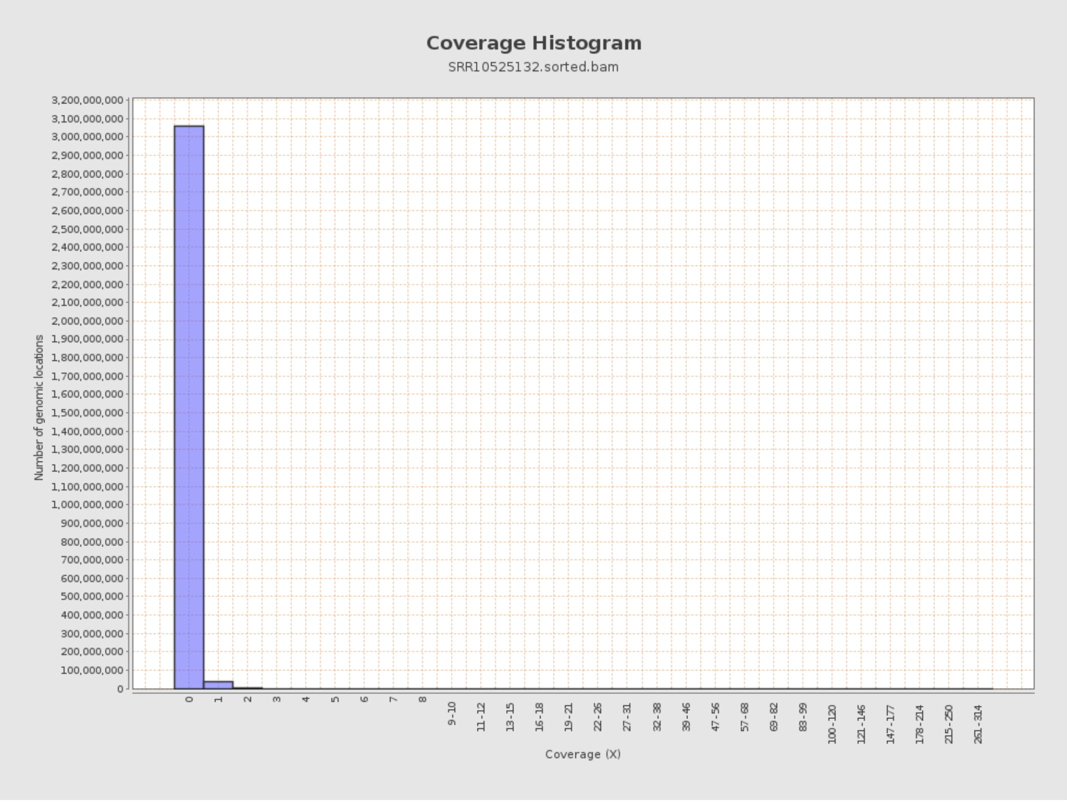
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3955791	0.0159	0.2802
chr2	243199373	3434377	0.0141	0.2111
chr3	198022430	2649742	0.0134	0.1204
chr4	191154276	2640648	0.0138	0.1257
chr5	180915260	2459382	0.0136	0.1223
chr6	171115067	2315014	0.0135	0.1299
chr7	159138663	2221917	0.014	0.2273

chr8	146364022	2056852	0.0141	0.2067
chr9	141213431	1656479	0.0117	0.1573
chr10	135534747	1891929	0.014	0.1806
chr11	135006516	2241031	0.0166	0.1956
chr12	133851895	1772708	0.0132	0.1196
chr13	115169878	1520449	0.0132	0.1197
chr14	107349540	1191466	0.0111	0.1176
chr15	102531392	1100378	0.0107	0.1068
chr16	90354753	866666	0.0096	0.1068
chr17	81195210	1163265	0.0143	0.1361
chr18	78077248	1102672	0.0141	0.2576
chr19	59128983	753592	0.0127	0.2027
chr20	63025520	782160	0.0124	0.117
chr21	48129895	533397	0.0111	0.1134
chr22	51304566	390343	0.0076	0.0906
chrMT	16571	2219	0.1339	0.3605
chrX	155270560	2303102	0.0148	0.1482
chrY	59373566	93260	0.0016	0.048

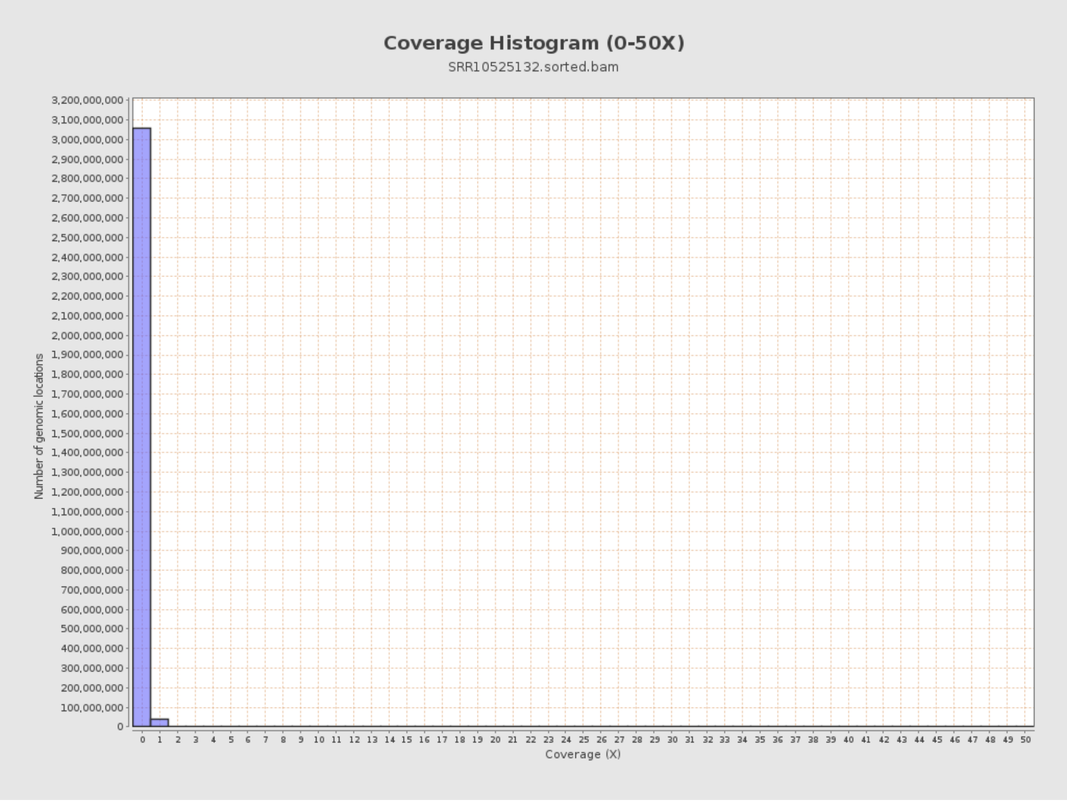
3. Results : Coverage across reference



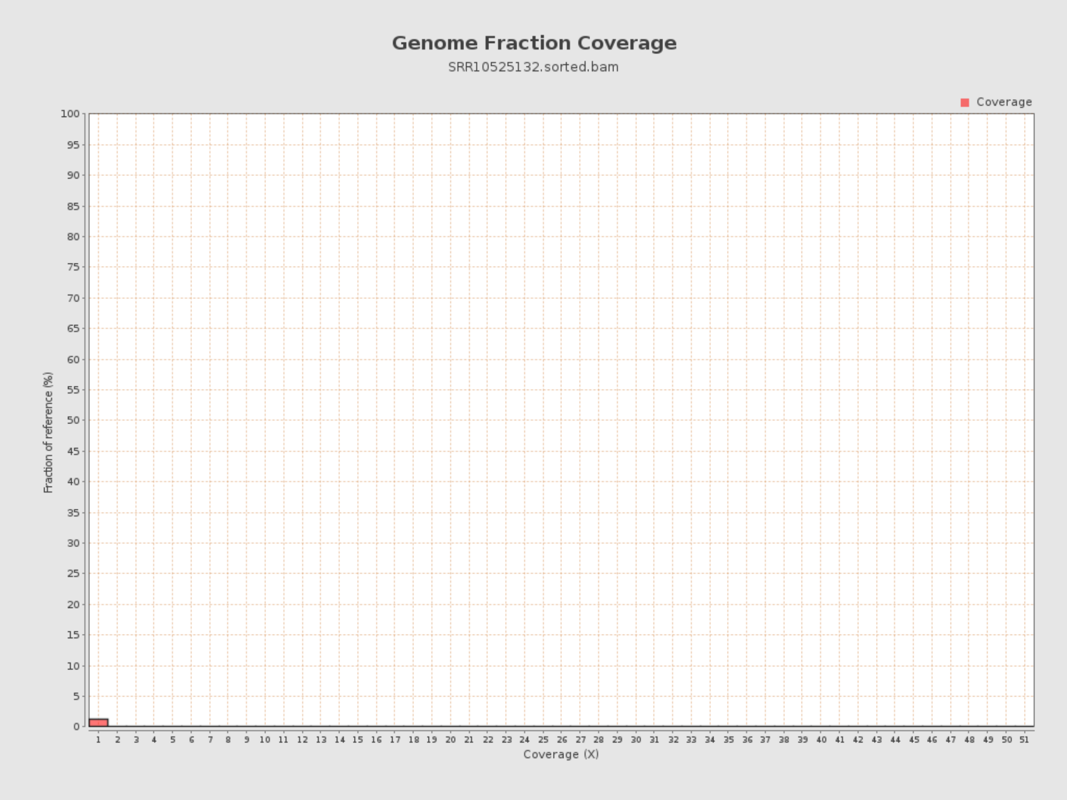
4. Results : Coverage Histogram



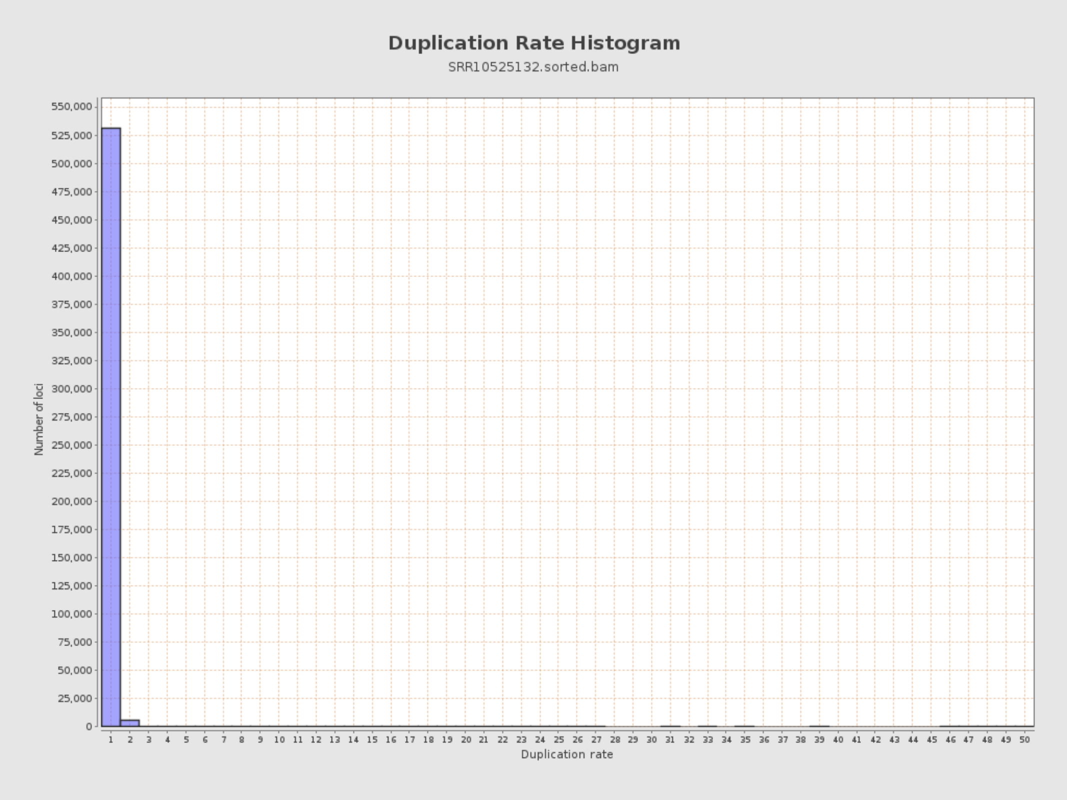
5. Results : Coverage Histogram (0-50X)



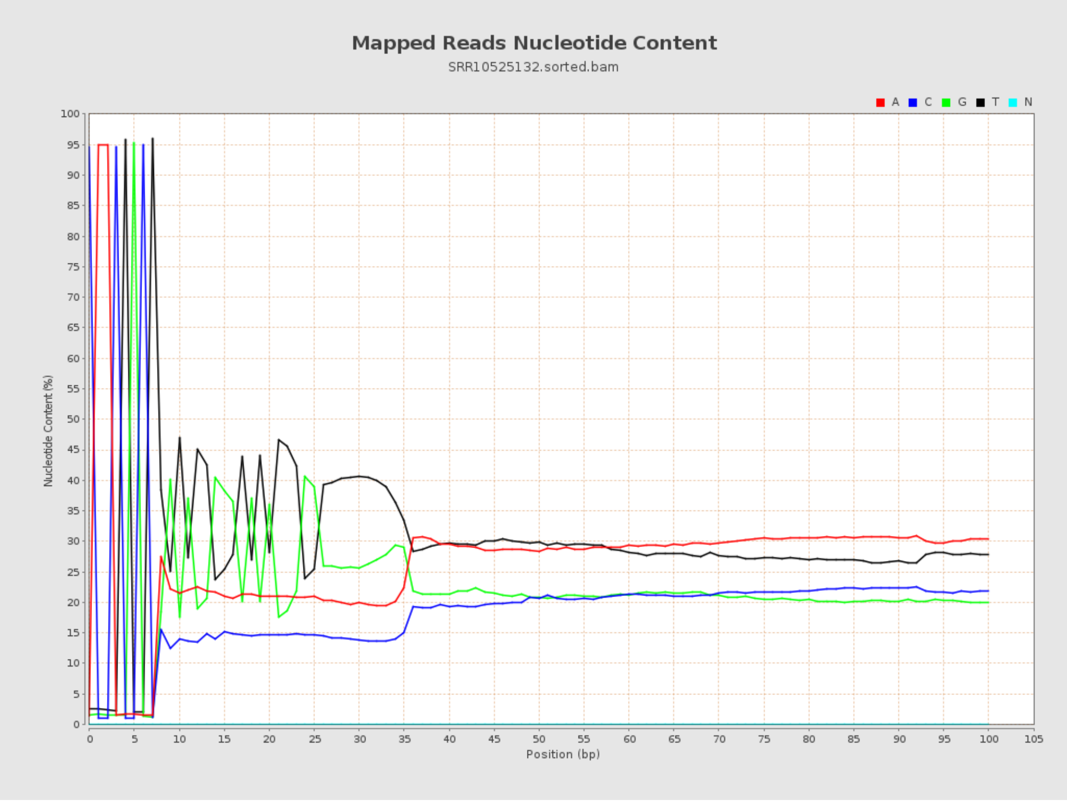
6. Results : Genome Fraction Coverage



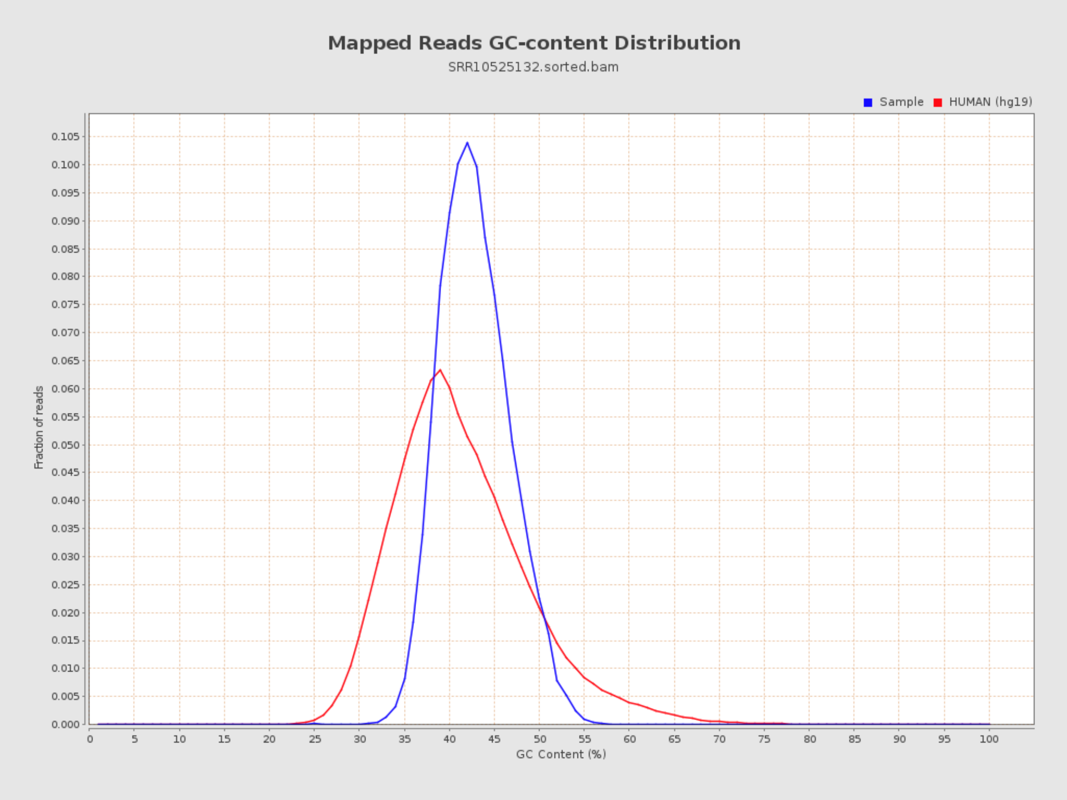
7. Results : Duplication Rate Histogram



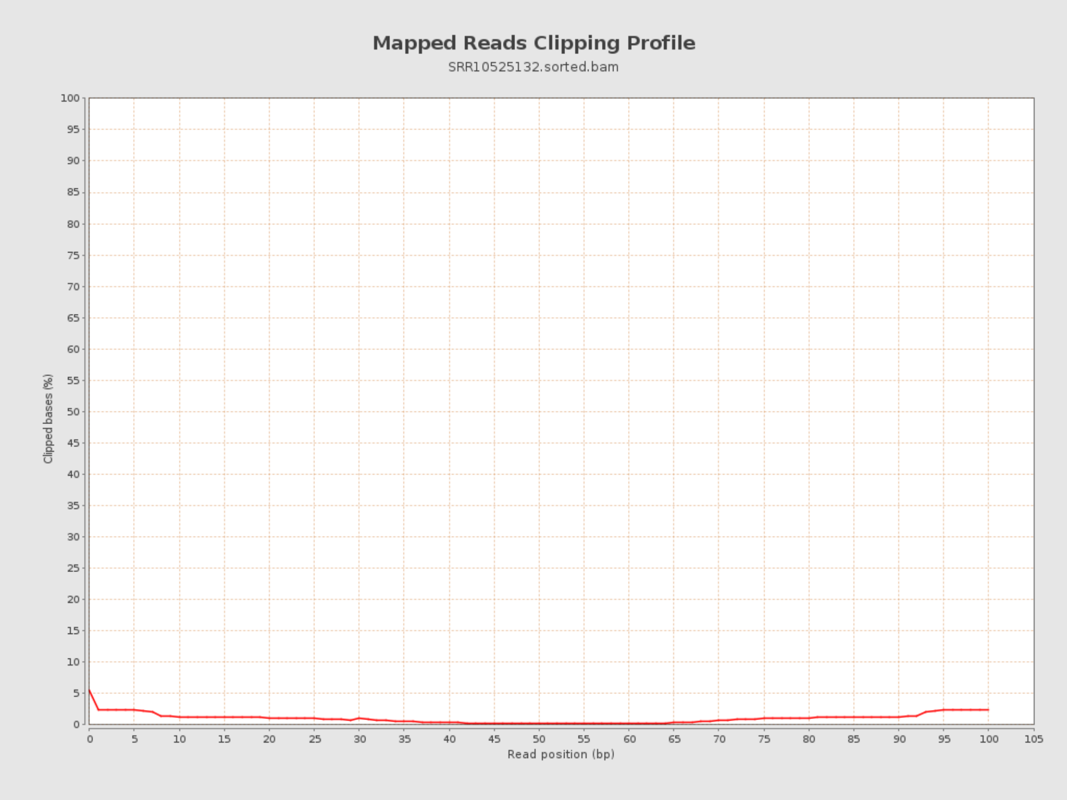
8. Results : Mapped Reads Nucleotide Content



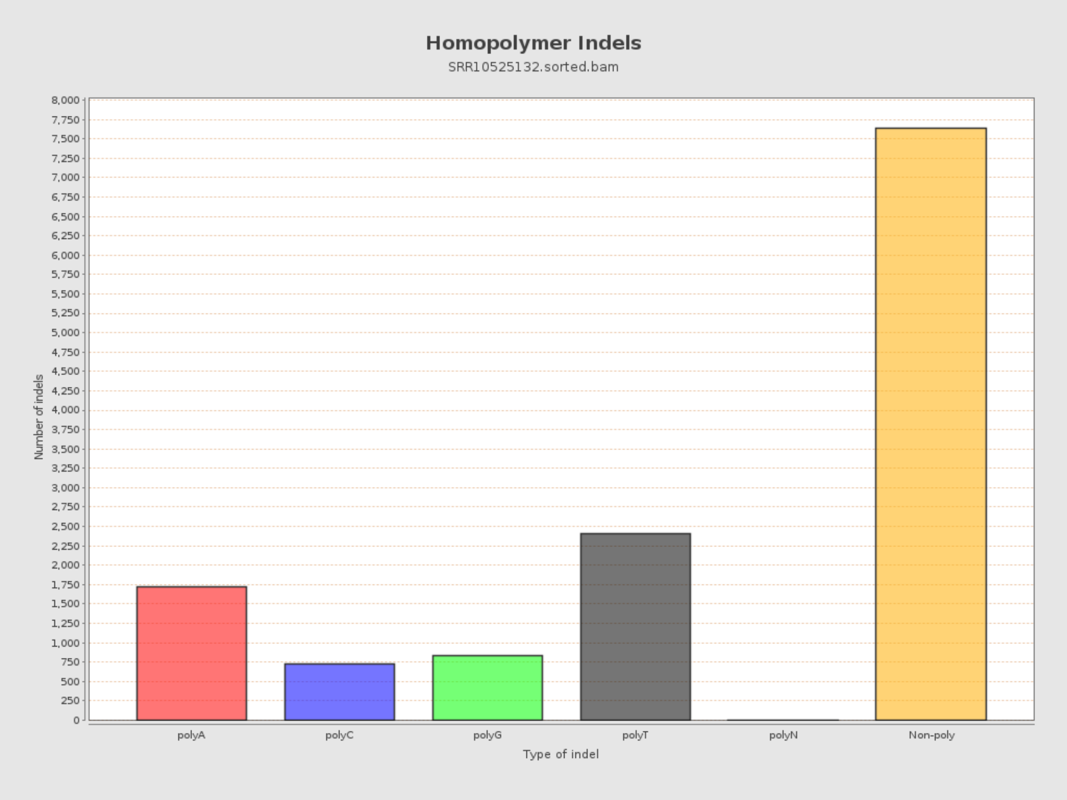
9. Results : Mapped Reads GC-content Distribution



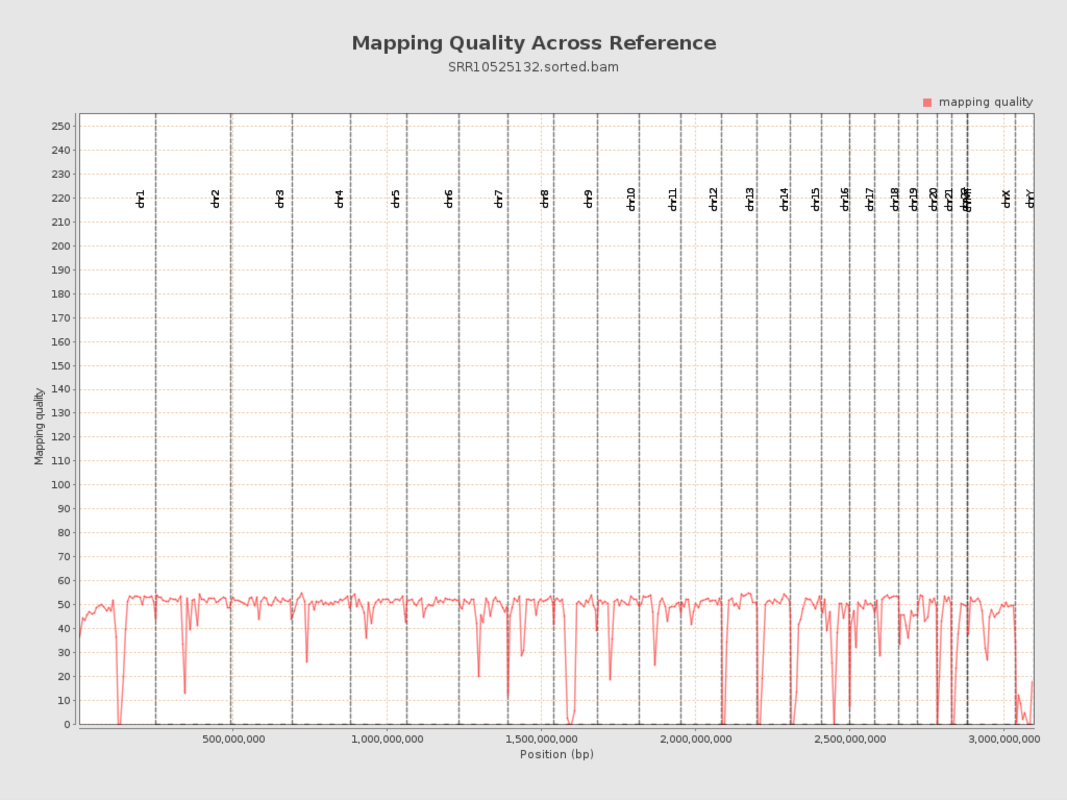
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram