Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 12:39:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525000.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_SRR10525000 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525000.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 12:39:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525000.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,379,395
Mapped reads	1,251,732 / 90.75%
Unmapped reads	127,663 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,837 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	31,435 / 2.28%
Duplication rate	1.7%
Clipped reads	1,253,625 / 90.88%

2.2. ACGT Content

Number/percentage of A's	18,449,676 / 25.76%
Number/percentage of C's	13,876,057 / 19.37%
Number/percentage of T's	22,509,903 / 31.42%
Number/percentage of G's	16,795,783 / 23.45%
Number/percentage of N's	2,204 / 0%
GC Percentage	42.82%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2278

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

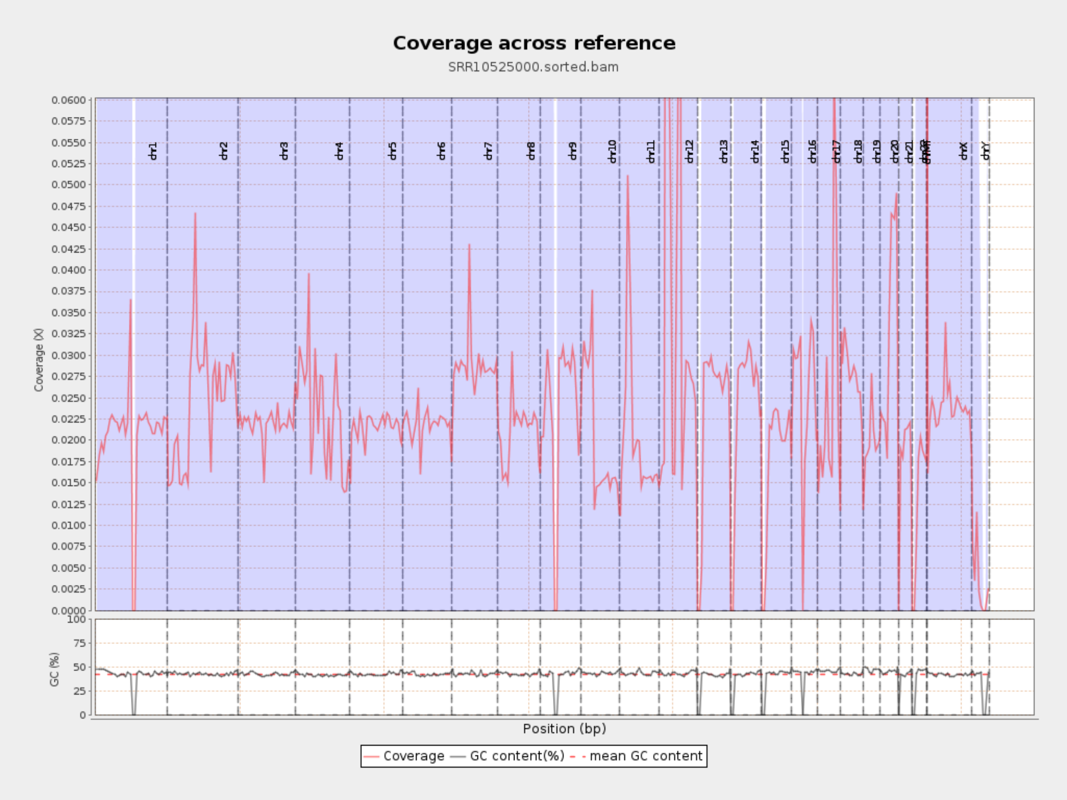
General error rate	0.49%
Mismatches	344,250
Insertions	4,378
Mapped reads with at least one insertion	0.35%
Deletions	11,581
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42.63%

2.6. Chromosome stats

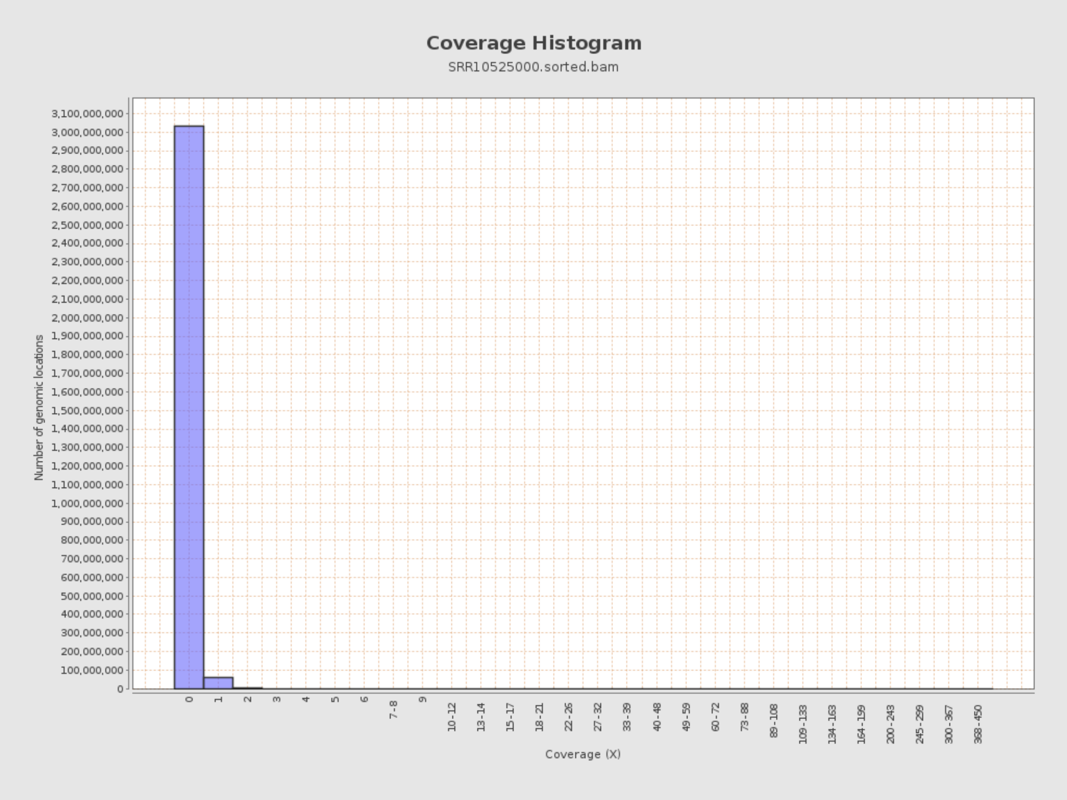
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5111654	0.0205	0.3789
chr2	243199373	5997905	0.0247	0.2441
chr3	198022430	4345737	0.0219	0.1564
chr4	191154276	4464262	0.0234	0.1768
chr5	180915260	3932160	0.0217	0.1575
chr6	171115067	3743954	0.0219	0.1685
chr7	159138663	4602122	0.0289	0.3042

chr8	146364022	3105212	0.0212	0.2129
chr9	141213431	3319248	0.0235	0.2327
chr10	135534747	2737419	0.0202	0.2183
chr11	135006516	2749652	0.0204	0.1988
chr12	133851895	5237065	0.0391	0.2296
chr13	115169878	2681913	0.0233	0.1611
chr14	107349540	2543700	0.0237	0.1741
chr15	102531392	1810508	0.0177	0.1414
chr16	90354753	2235036	0.0247	0.1763
chr17	81195210	2111743	0.026	0.176
chr18	78077248	2189826	0.028	0.4207
chr19	59128983	1184007	0.02	0.274
chr20	63025520	2084001	0.0331	0.1976
chr21	48129895	866332	0.018	0.1589
chr22	51304566	677523	0.0132	0.121
chrMT	16571	4177	0.2521	0.5268
chrX	155270560	3718317	0.0239	0.1884
chrY	59373566	199361	0.0034	0.0895

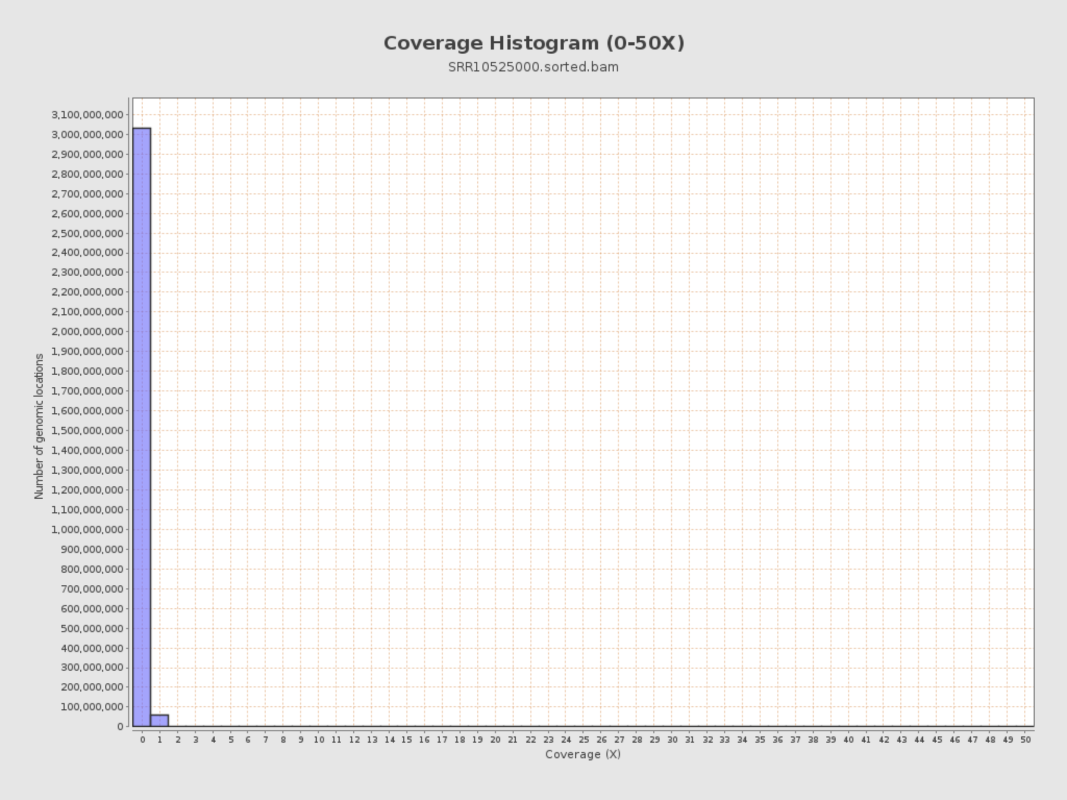
3. Results : Coverage across reference



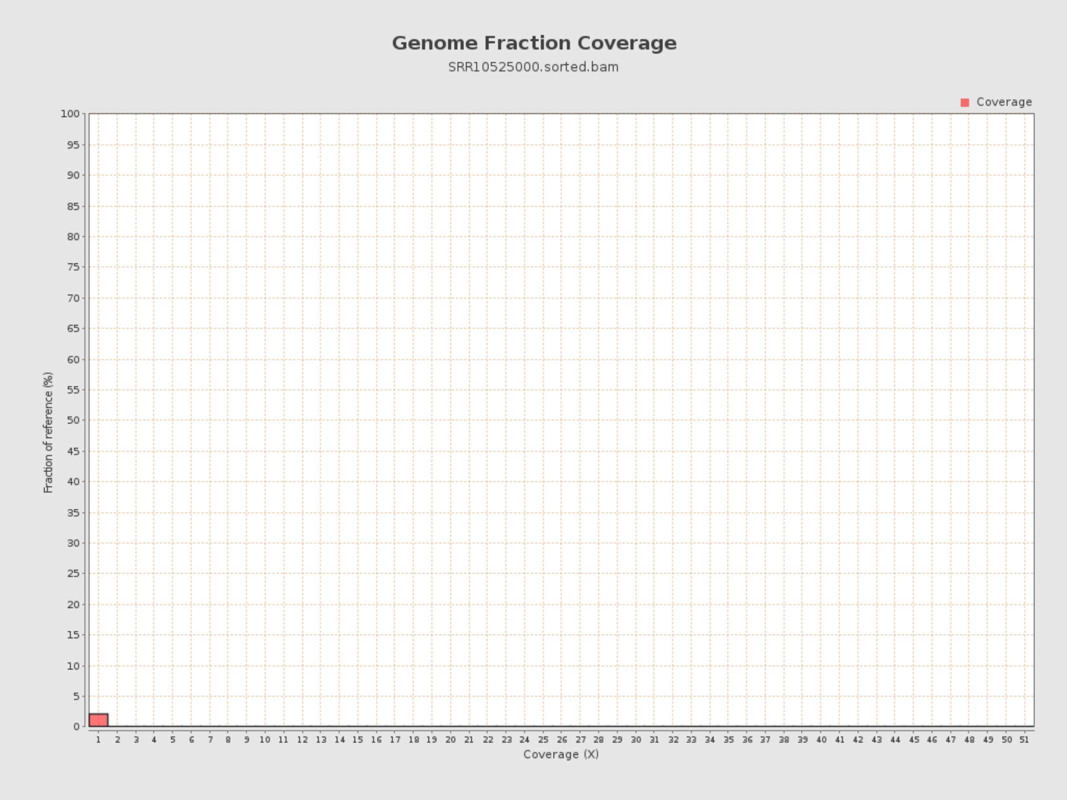
4. Results : Coverage Histogram



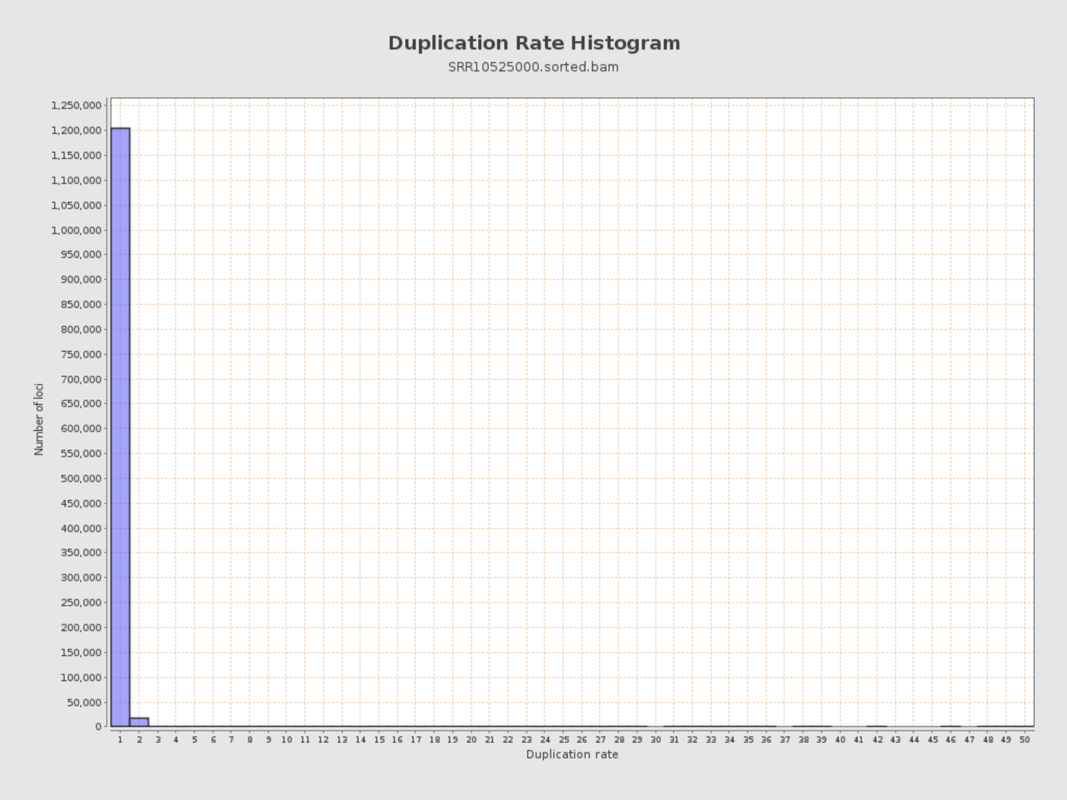
5. Results : Coverage Histogram (0-50X)



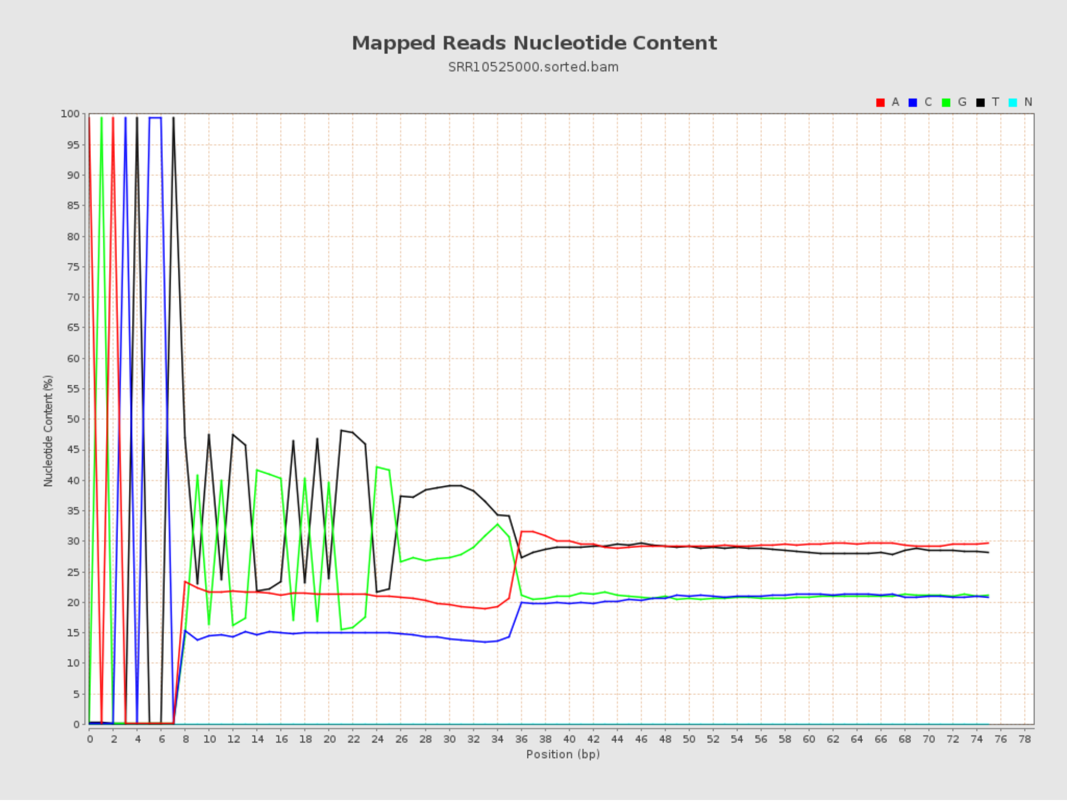
6. Results : Genome Fraction Coverage



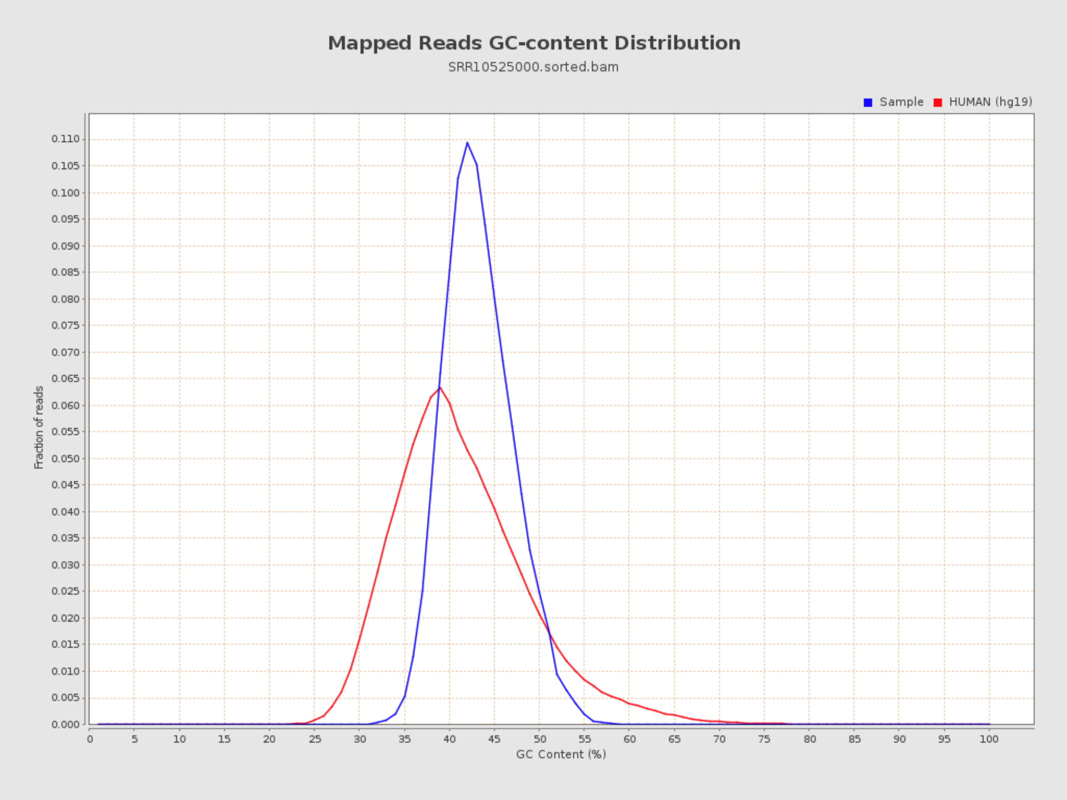
7. Results : Duplication Rate Histogram



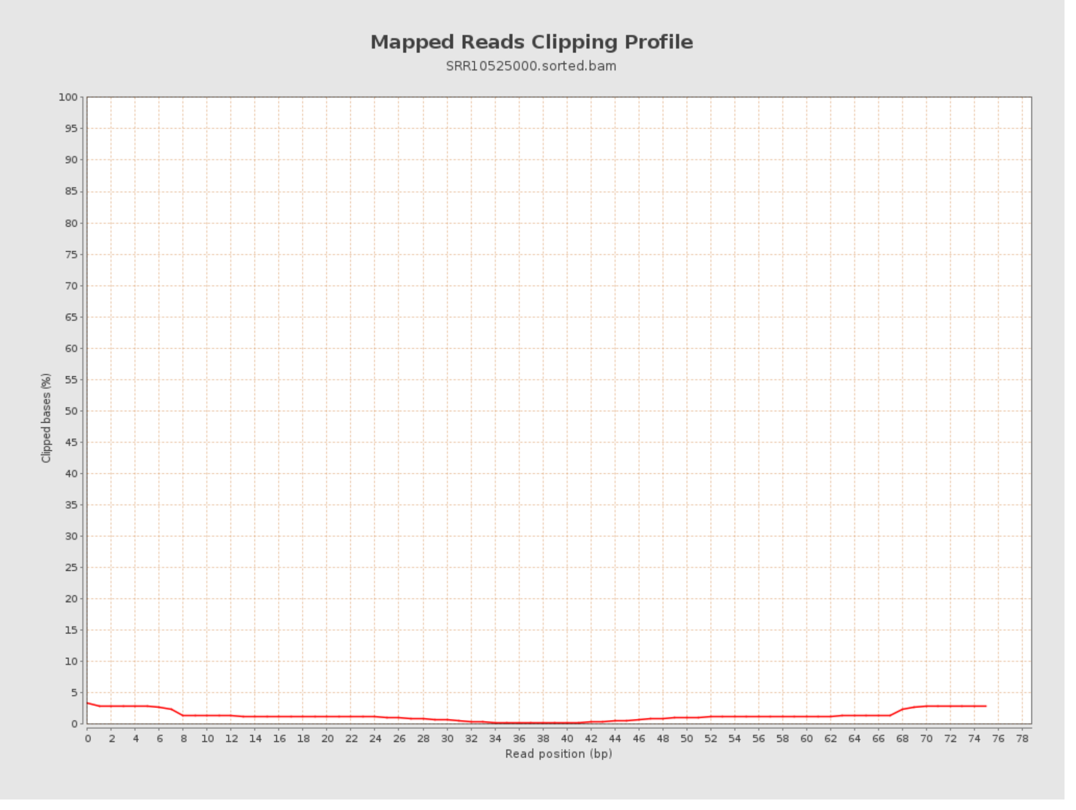
8. Results : Mapped Reads Nucleotide Content



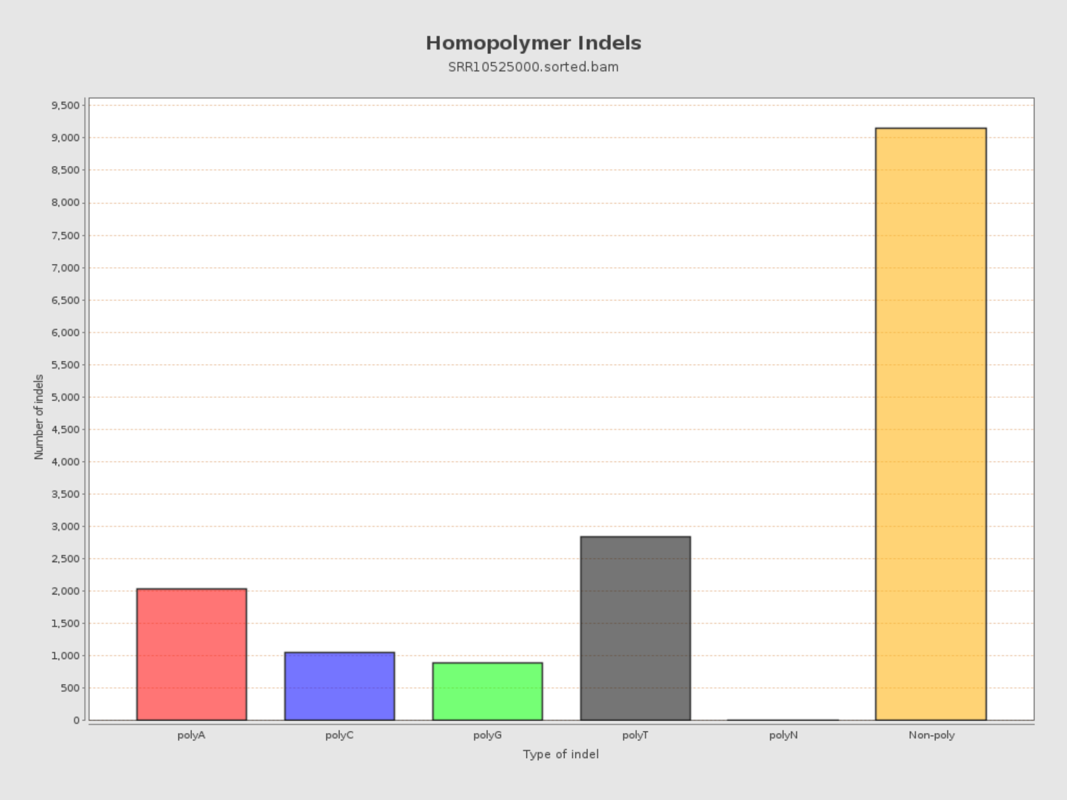
9. Results : Mapped Reads GC-content Distribution



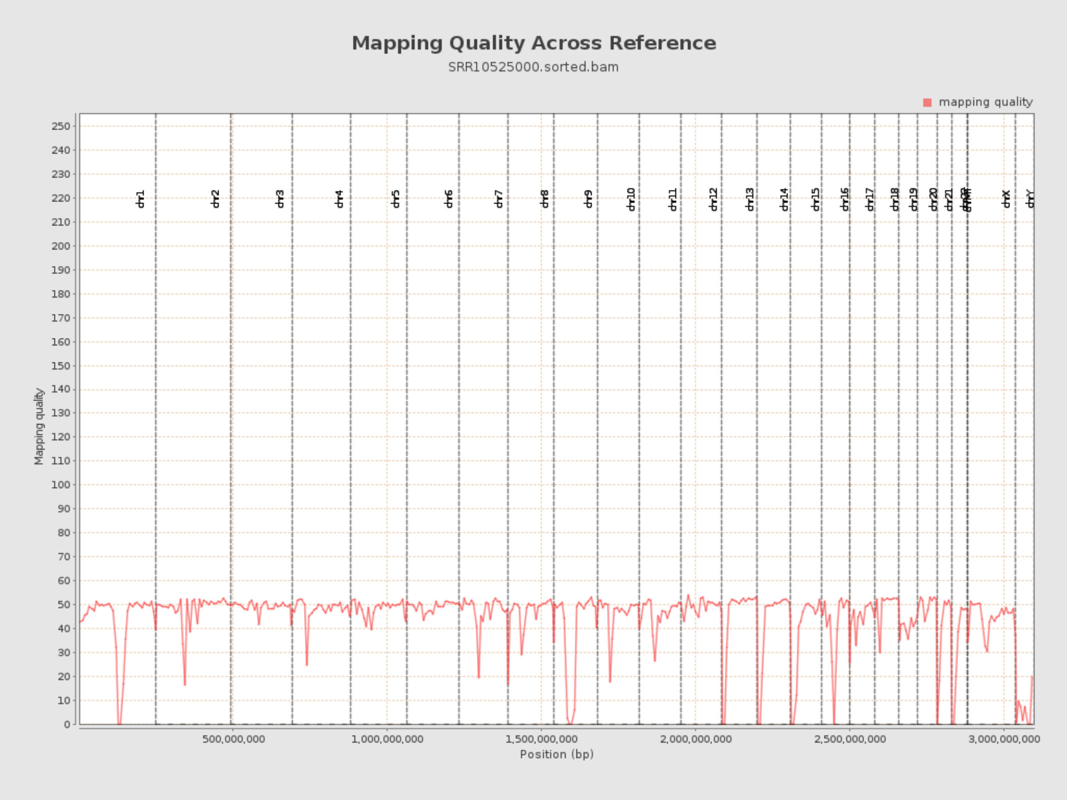
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram