Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:08:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525170.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_SRR10525170 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525170.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:08:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525170.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,510,025
Mapped reads	1,357,252 / 89.88%
Unmapped reads	152,773 / 10.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,653 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	34,668 / 2.3%
Duplication rate	1.8%
Clipped reads	1,359,664 / 90.04%

2.2. ACGT Content

Number/percentage of A's	20,571,157 / 26.06%
Number/percentage of C's	14,571,485 / 18.46%
Number/percentage of T's	25,299,802 / 32.04%
Number/percentage of G's	18,506,476 / 23.44%
Number/percentage of N's	2,487 / 0%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0255

Standard Deviation	0.2409

2.4. Mapping Quality

Mean Mapping Quality	45.71

2.5. Mismatches and indels

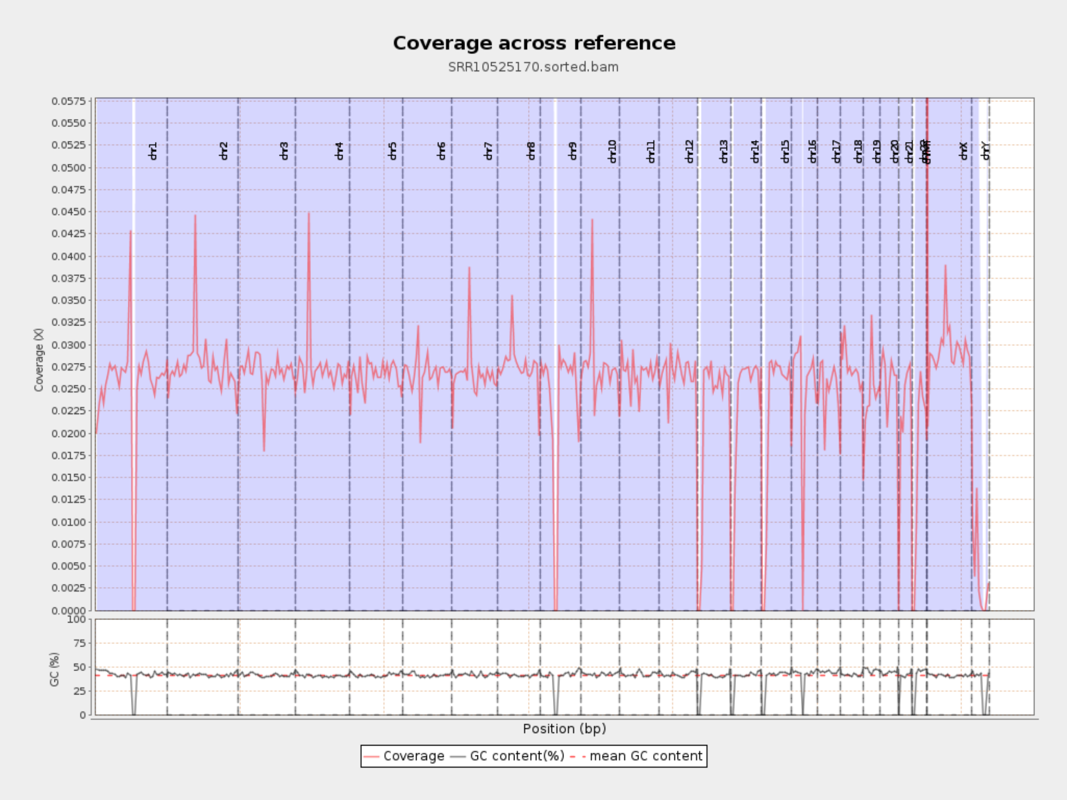
General error rate	0.49%
Mismatches	379,205
Insertions	4,908
Mapped reads with at least one insertion	0.36%
Deletions	12,695
Mapped reads with at least one deletion	0.93%
Homopolymer indels	42.06%

2.6. Chromosome stats

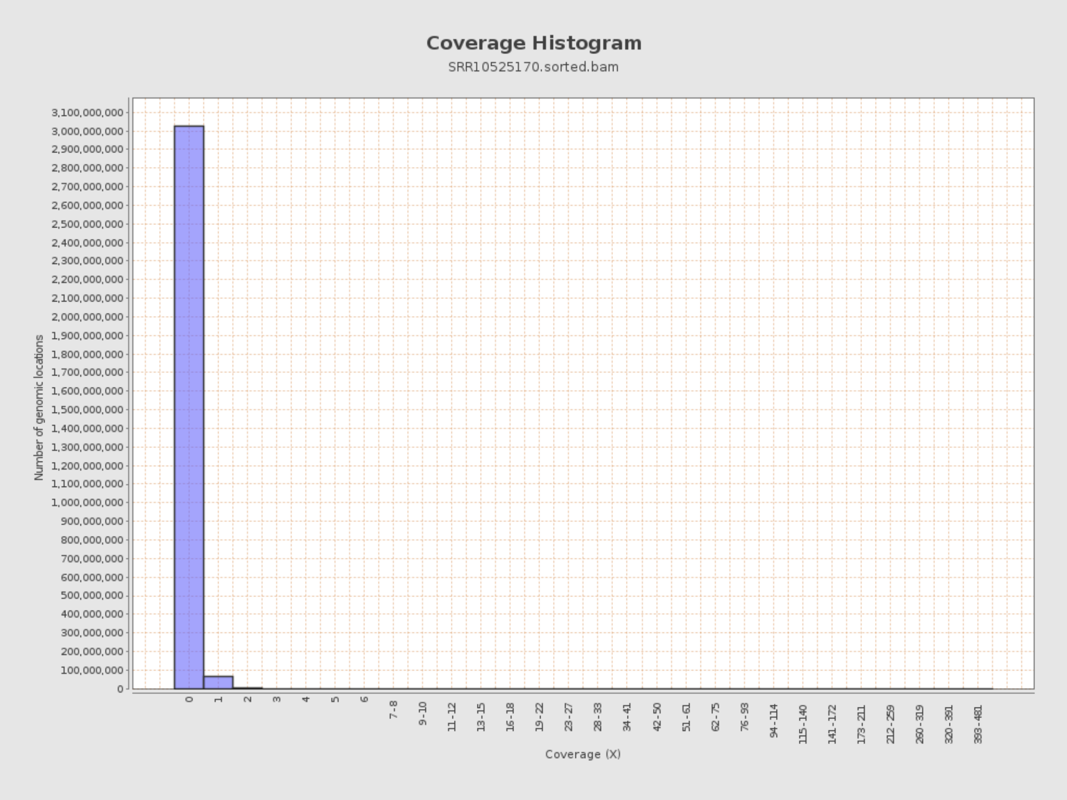
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6269858	0.0252	0.4321
chr2	243199373	6757134	0.0278	0.2507
chr3	198022430	5335703	0.0269	0.1755
chr4	191154276	5264327	0.0275	0.1949
chr5	180915260	4834935	0.0267	0.1763
chr6	171115067	4583027	0.0268	0.1871
chr7	159138663	4263324	0.0268	0.2655

chr8	146364022	4046794	0.0276	0.2812
chr9	141213431	3311206	0.0234	0.2286
chr10	135534747	3746660	0.0276	0.2326
chr11	135006516	3625416	0.0269	0.2296
chr12	133851895	3588363	0.0268	0.1787
chr13	115169878	2525880	0.0219	0.1573
chr14	107349540	2401523	0.0224	0.1761
chr15	102531392	2244136	0.0219	0.1581
chr16	90354753	2205426	0.0244	0.1774
chr17	81195210	2017487	0.0248	0.1766
chr18	78077248	2150015	0.0275	0.3983
chr19	59128983	1452470	0.0246	0.3108
chr20	63025520	1630916	0.0259	0.176
chr21	48129895	1053493	0.0219	0.1781
chr22	51304566	863456	0.0168	0.1385
chrMT	16571	6964	0.4203	0.7214
chrX	155270560	4562420	0.0294	0.2046
chrY	59373566	231586	0.0039	0.1097

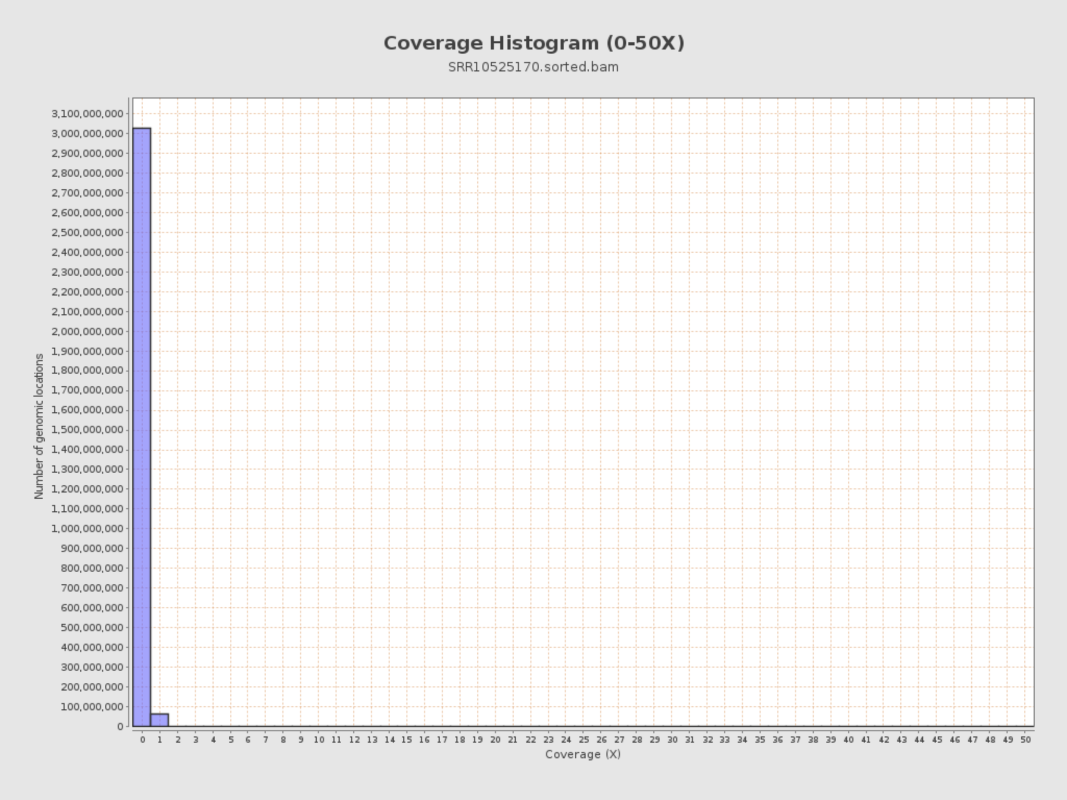
3. Results : Coverage across reference



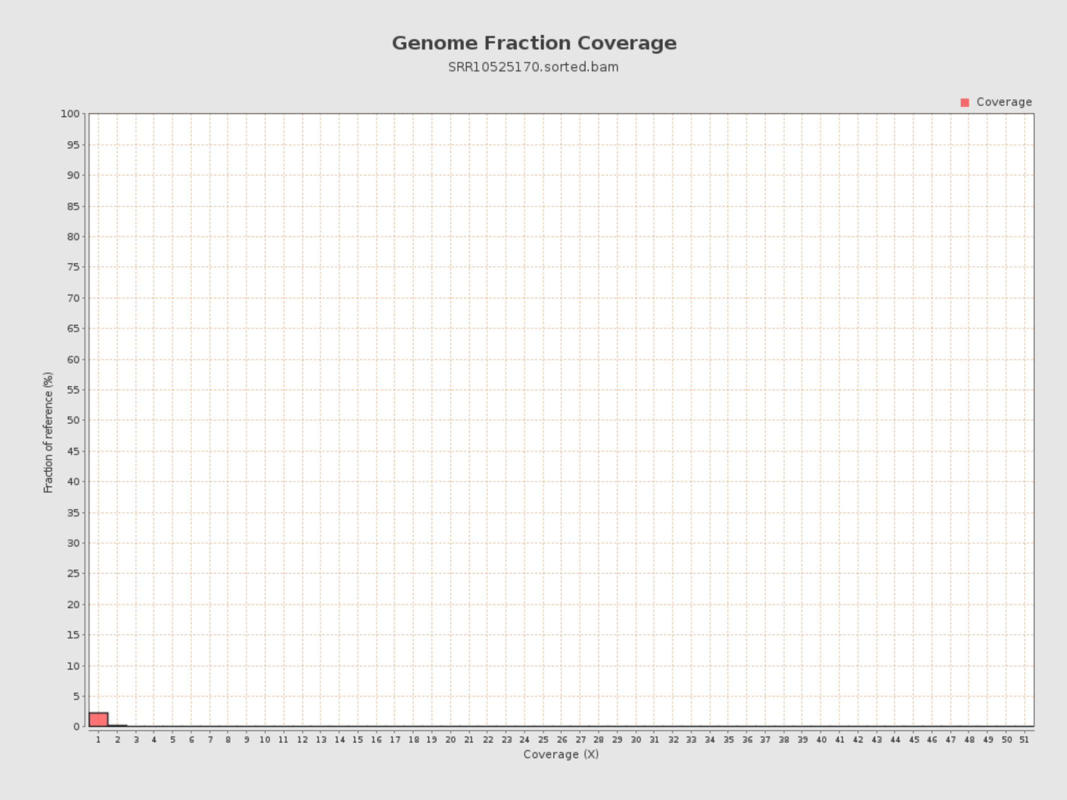
4. Results : Coverage Histogram



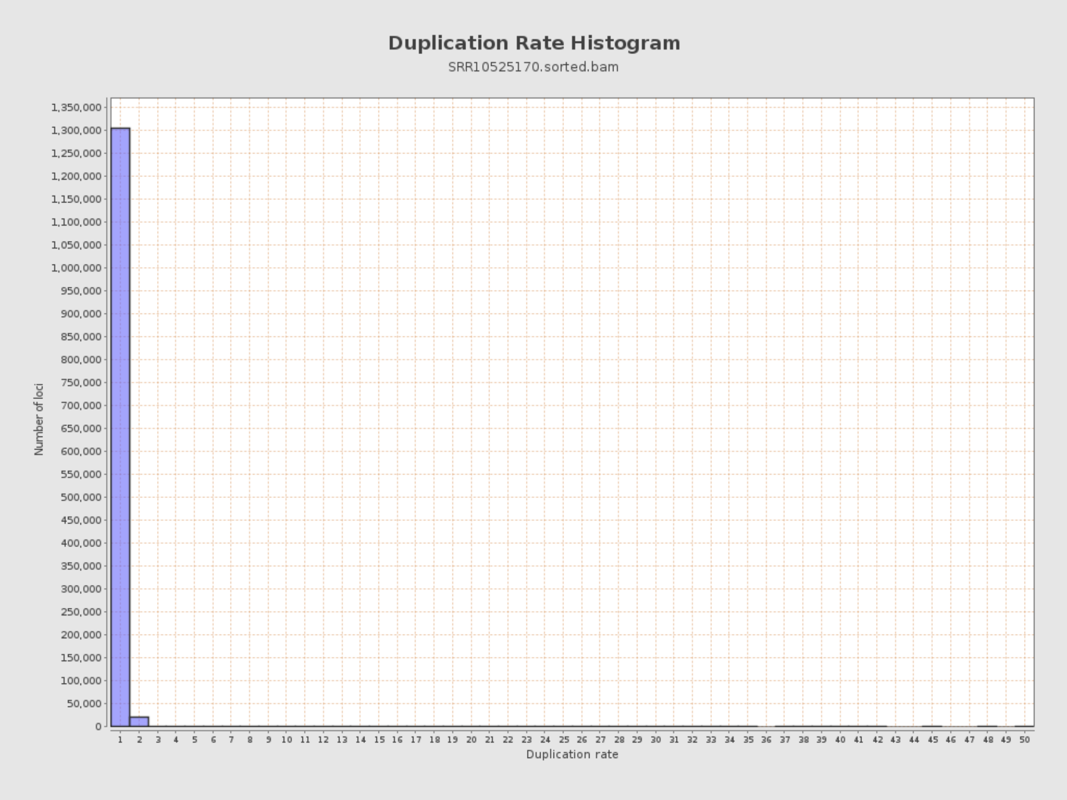
5. Results : Coverage Histogram (0-50X)



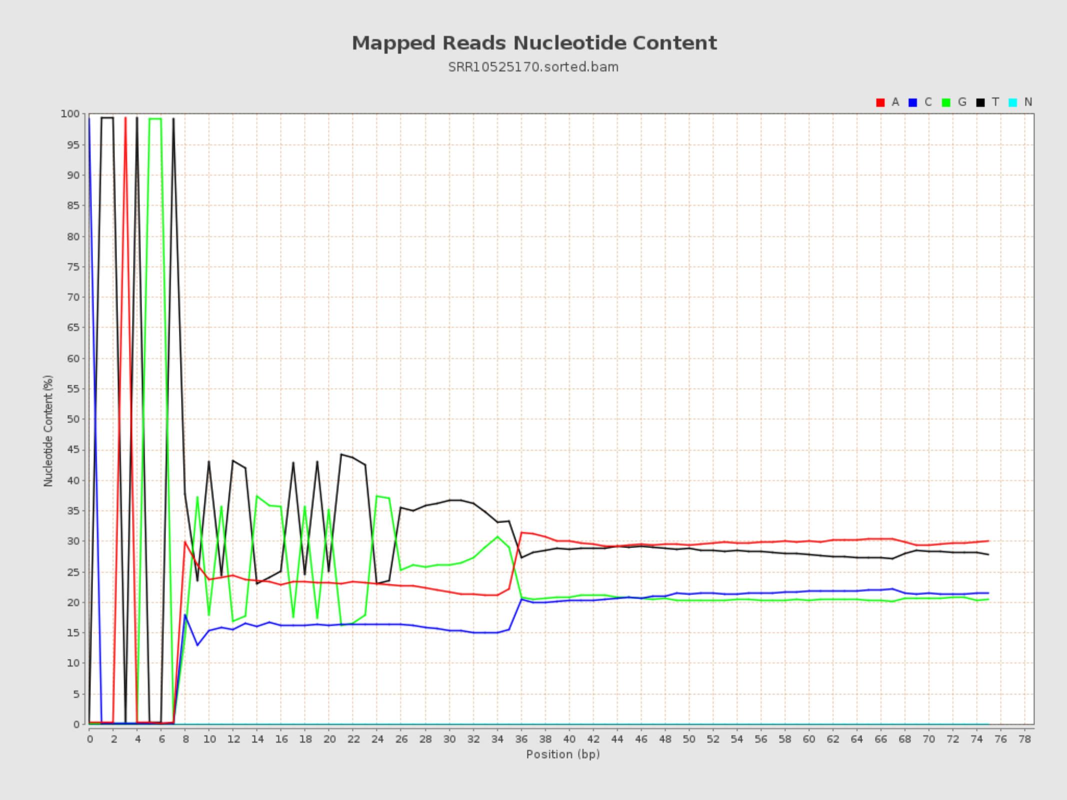
6. Results : Genome Fraction Coverage



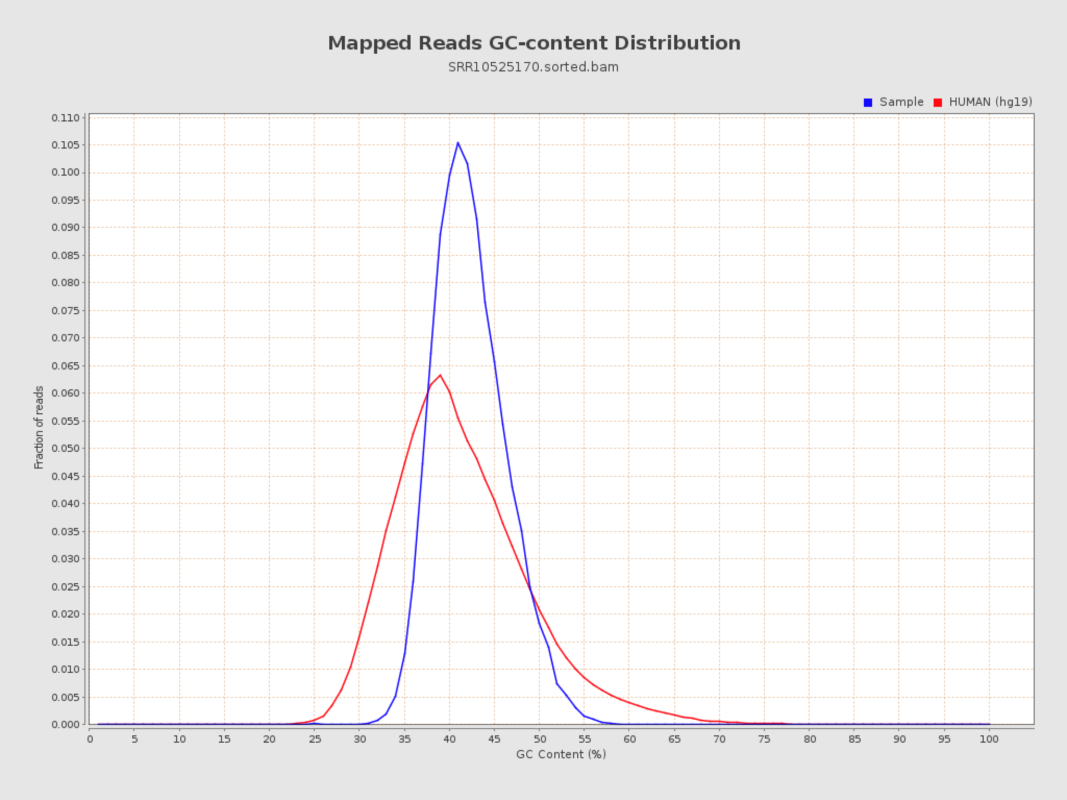
7. Results : Duplication Rate Histogram



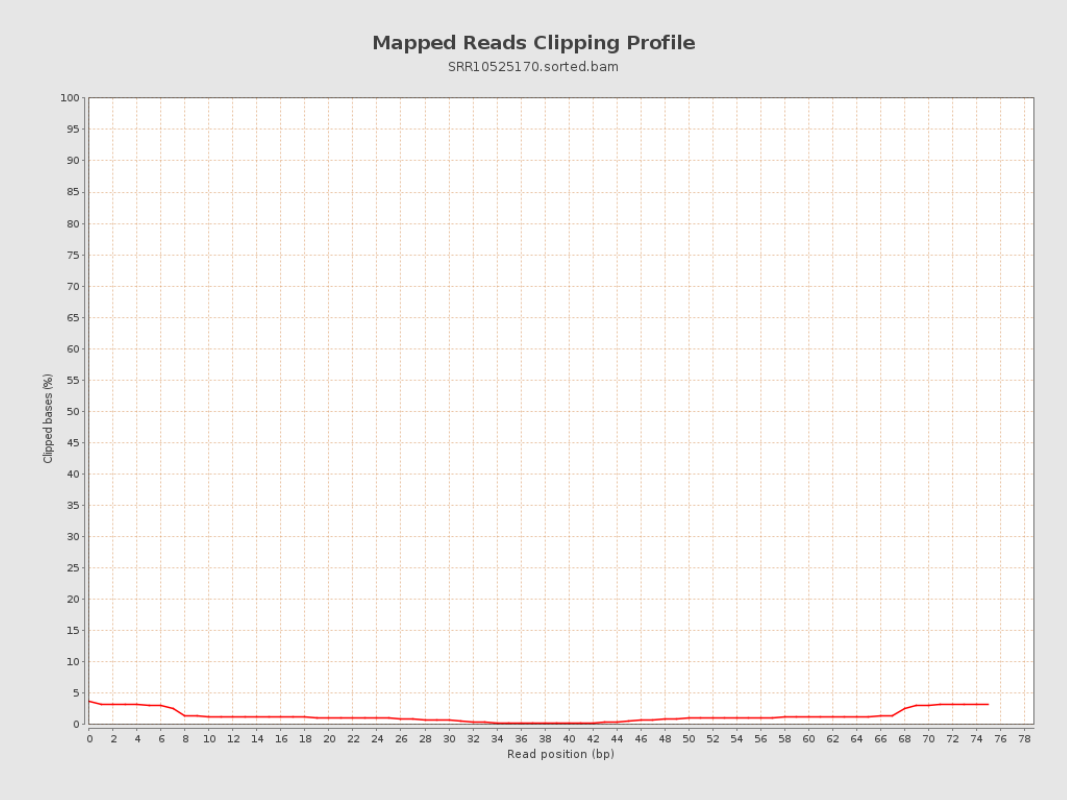
8. Results : Mapped Reads Nucleotide Content



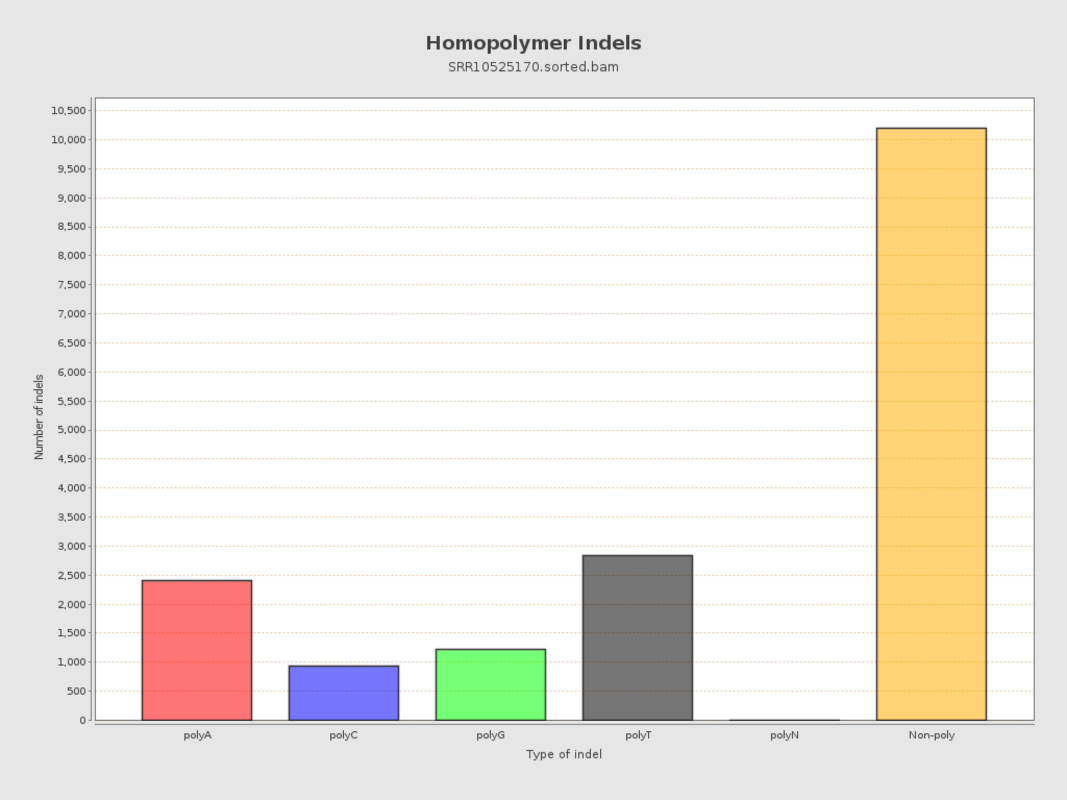
9. Results : Mapped Reads GC-content Distribution



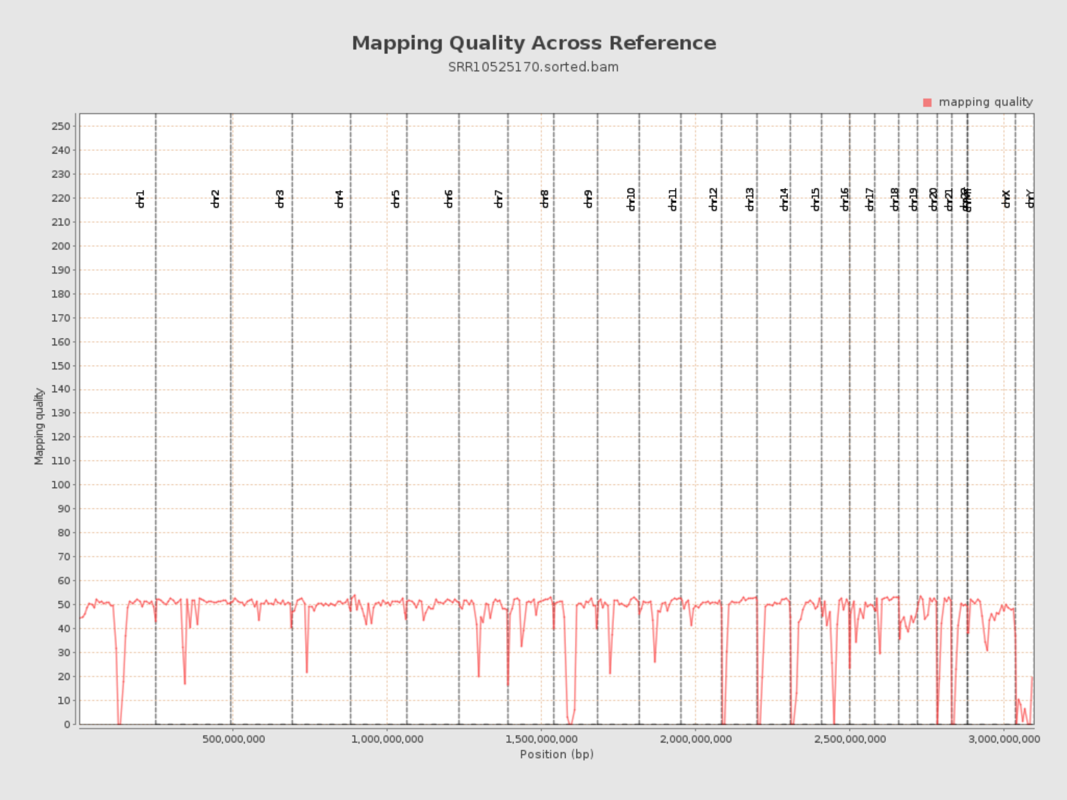
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram