Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:23:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525036.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_SRR10525036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:23:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,419,415
Mapped reads	1,305,404 / 91.97%
Unmapped reads	114,011 / 8.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,188 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	42,375 / 2.99%
Duplication rate	2.4%
Clipped reads	1,308,208 / 92.17%

2.2. ACGT Content

Number/percentage of A's	19,002,443 / 24.92%
Number/percentage of C's	14,315,173 / 18.77%
Number/percentage of T's	24,384,254 / 31.97%
Number/percentage of G's	18,563,014 / 24.34%
Number/percentage of N's	759 / 0%
GC Percentage	43.11%

2.3. Coverage

Mean	0.0246

Standard Deviation	0.2297

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

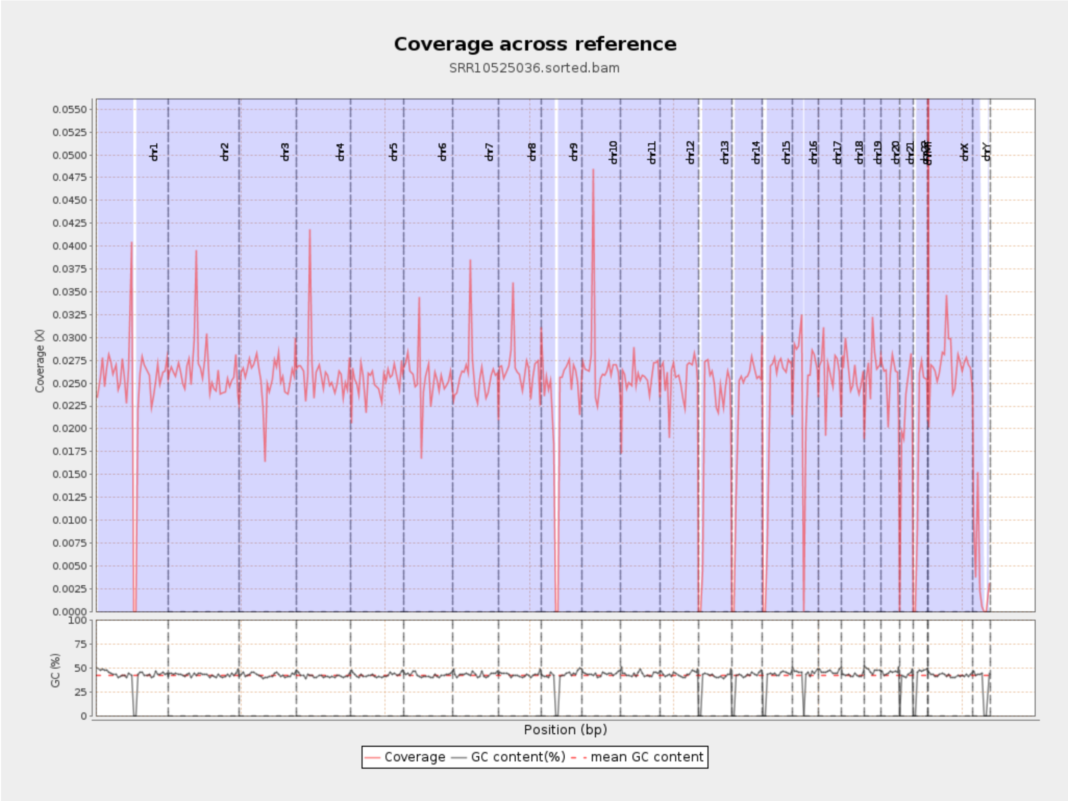
General error rate	0.51%
Mismatches	377,790
Insertions	5,184
Mapped reads with at least one insertion	0.4%
Deletions	15,321
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.94%

2.6. Chromosome stats

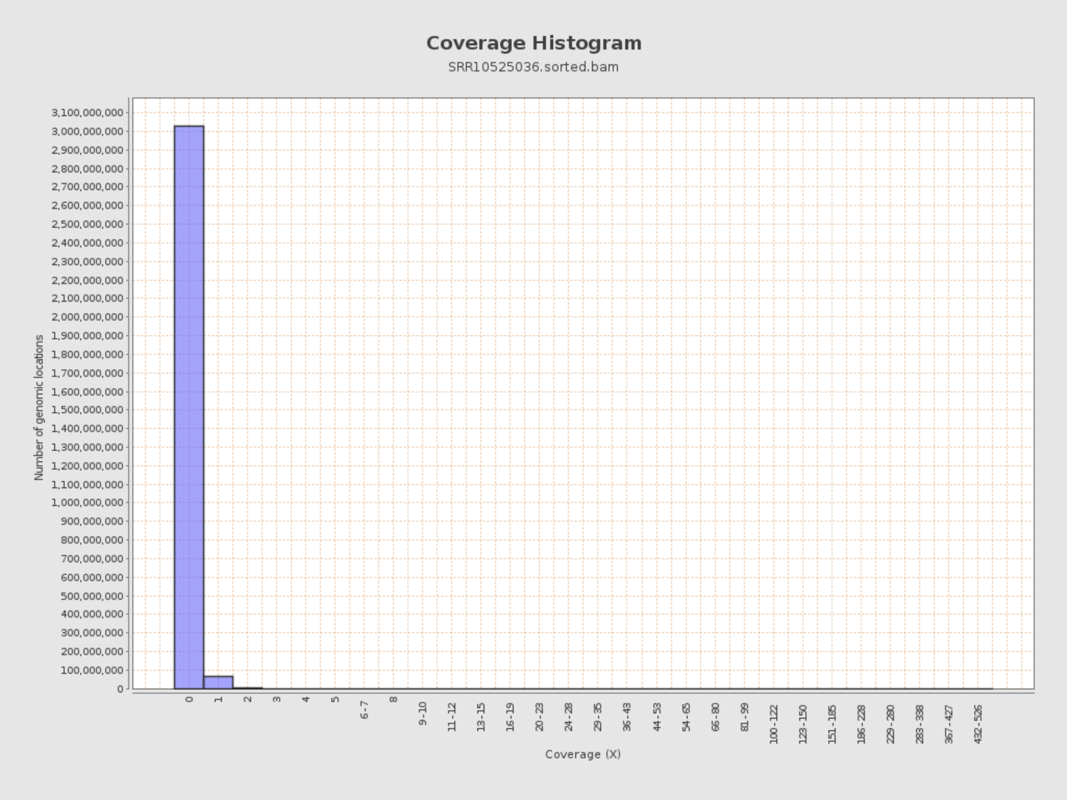
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6139135	0.0246	0.3984
chr2	243199373	6404394	0.0263	0.2589
chr3	198022430	5057829	0.0255	0.1716
chr4	191154276	5006569	0.0262	0.1945
chr5	180915260	4592673	0.0254	0.1714
chr6	171115067	4357260	0.0255	0.2063
chr7	159138663	4127480	0.0259	0.2628

chr8	146364022	3899848	0.0266	0.2476
chr9	141213431	3167059	0.0224	0.1961
chr10	135534747	3697245	0.0273	0.25
chr11	135006516	3467273	0.0257	0.213
chr12	133851895	3427895	0.0256	0.1737
chr13	115169878	2398957	0.0208	0.1554
chr14	107349540	2330657	0.0217	0.1626
chr15	102531392	2231125	0.0218	0.1628
chr16	90354753	2236870	0.0248	0.1781
chr17	81195210	2128941	0.0262	0.1906
chr18	78077248	2026552	0.026	0.3173
chr19	59128983	1584582	0.0268	0.2796
chr20	63025520	1611027	0.0256	0.174
chr21	48129895	1020677	0.0212	0.176
chr22	51304566	921171	0.018	0.1431
chrMT	16571	2628	0.1586	0.4081
chrX	155270560	4209226	0.0271	0.1901
chrY	59373566	244279	0.0041	0.1317

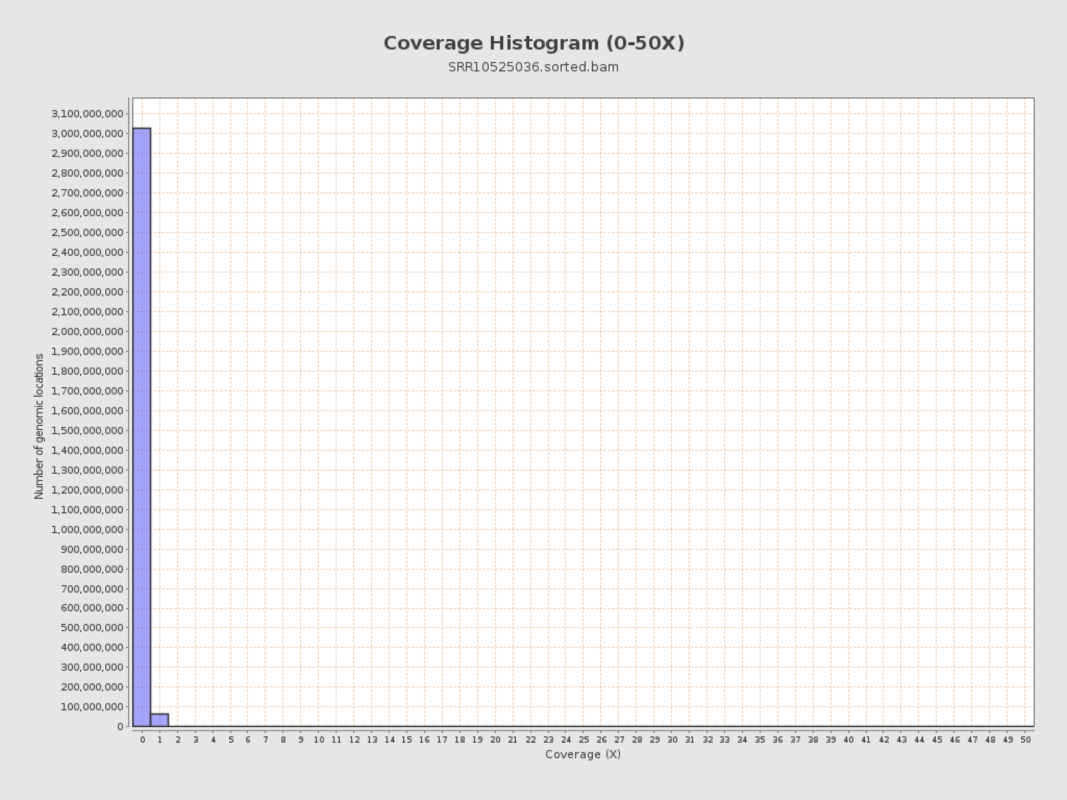
3. Results : Coverage across reference



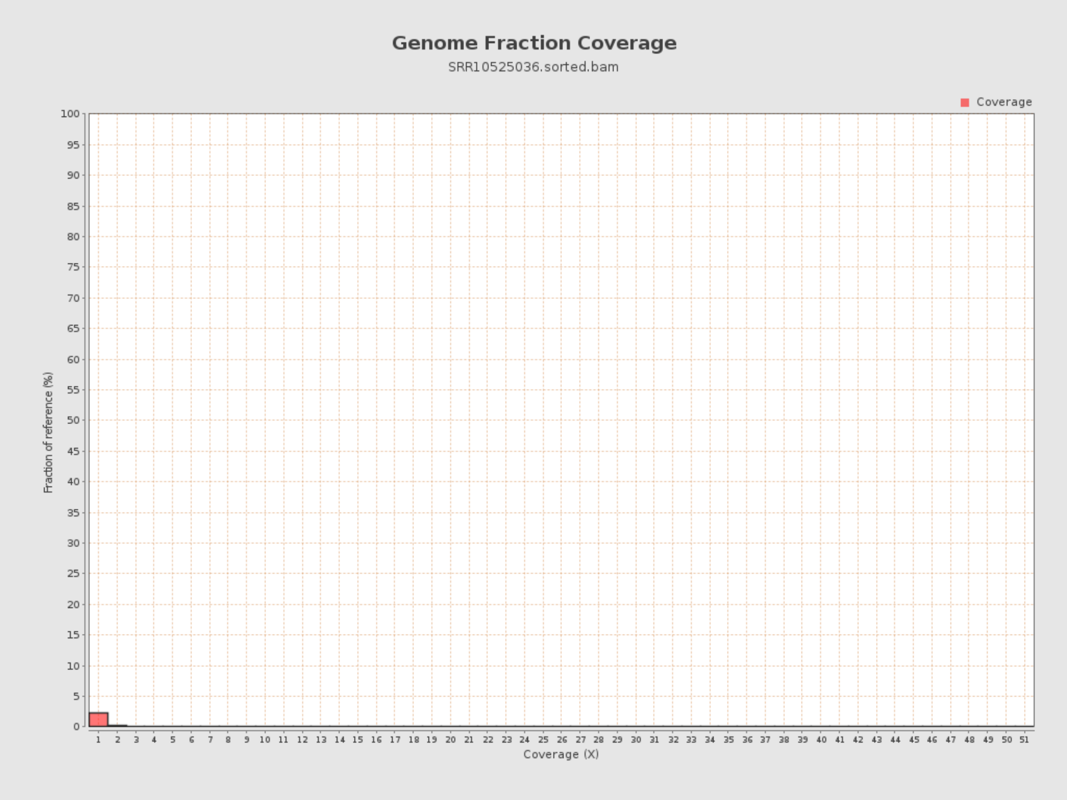
4. Results : Coverage Histogram



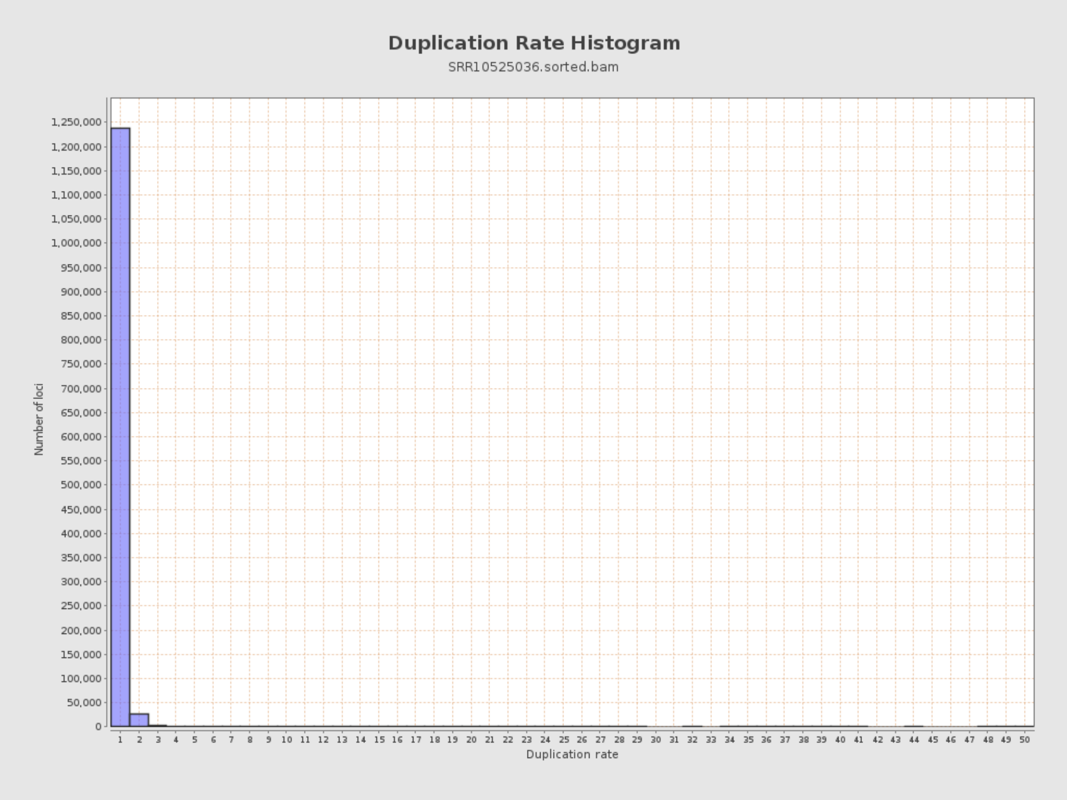
5. Results : Coverage Histogram (0-50X)



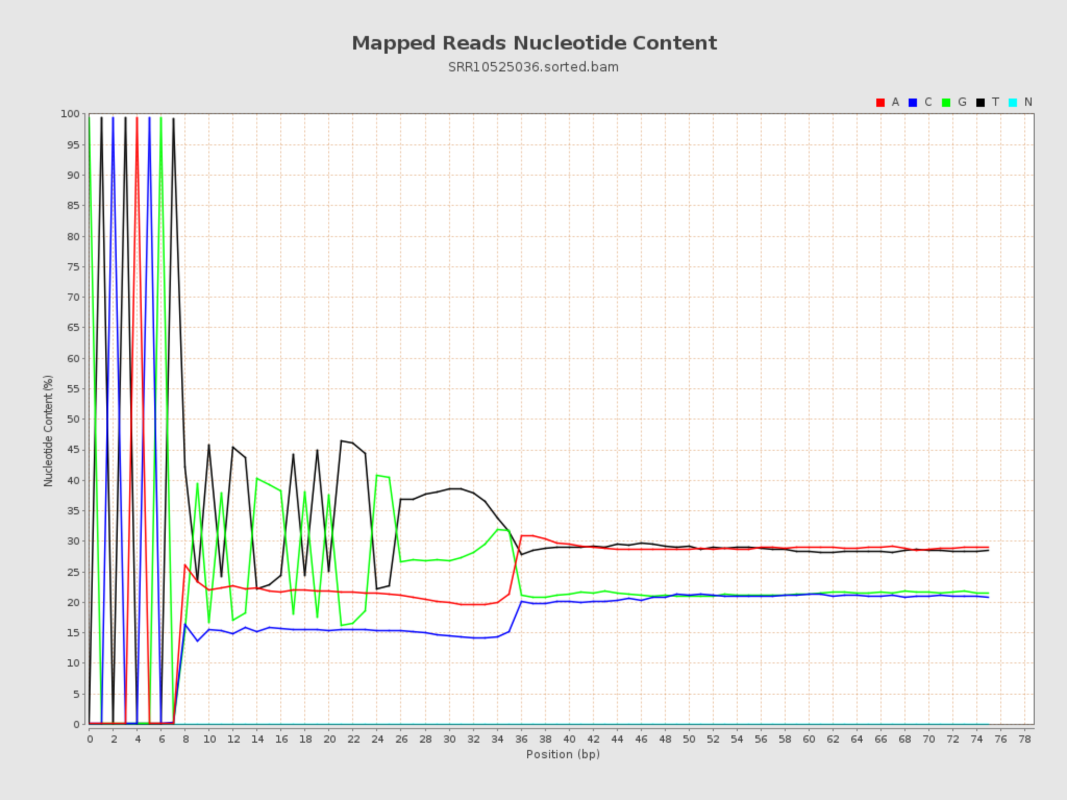
6. Results : Genome Fraction Coverage



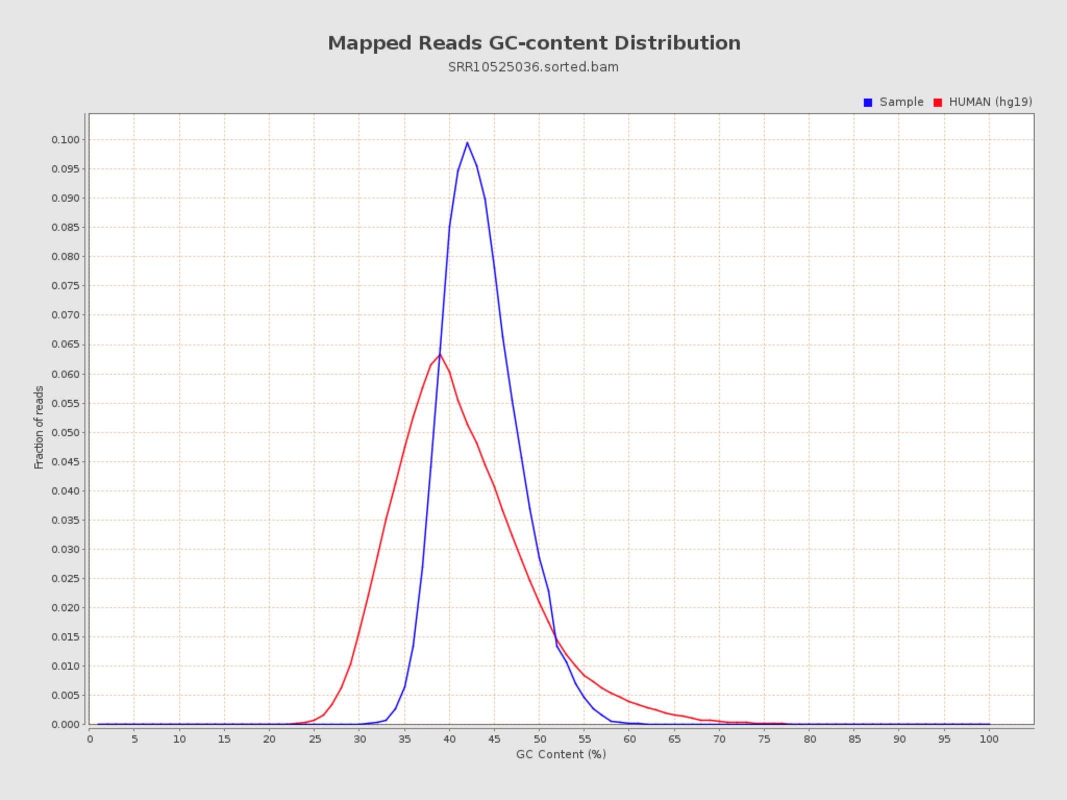
7. Results : Duplication Rate Histogram



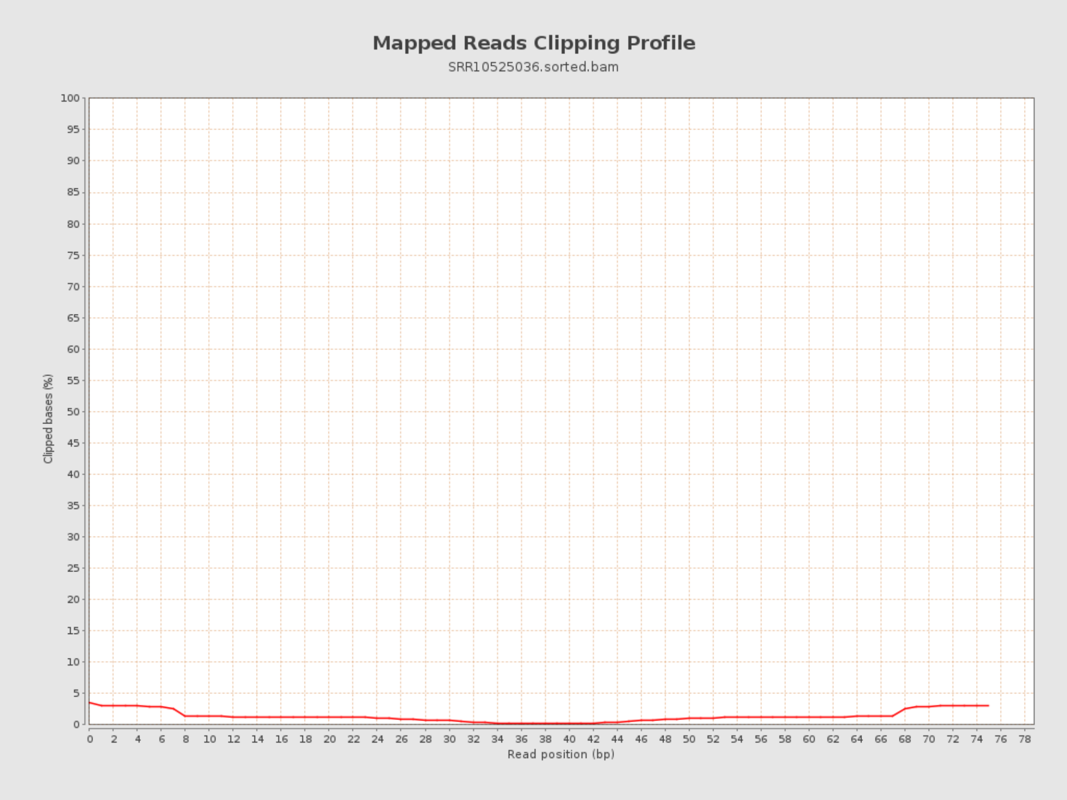
8. Results : Mapped Reads Nucleotide Content



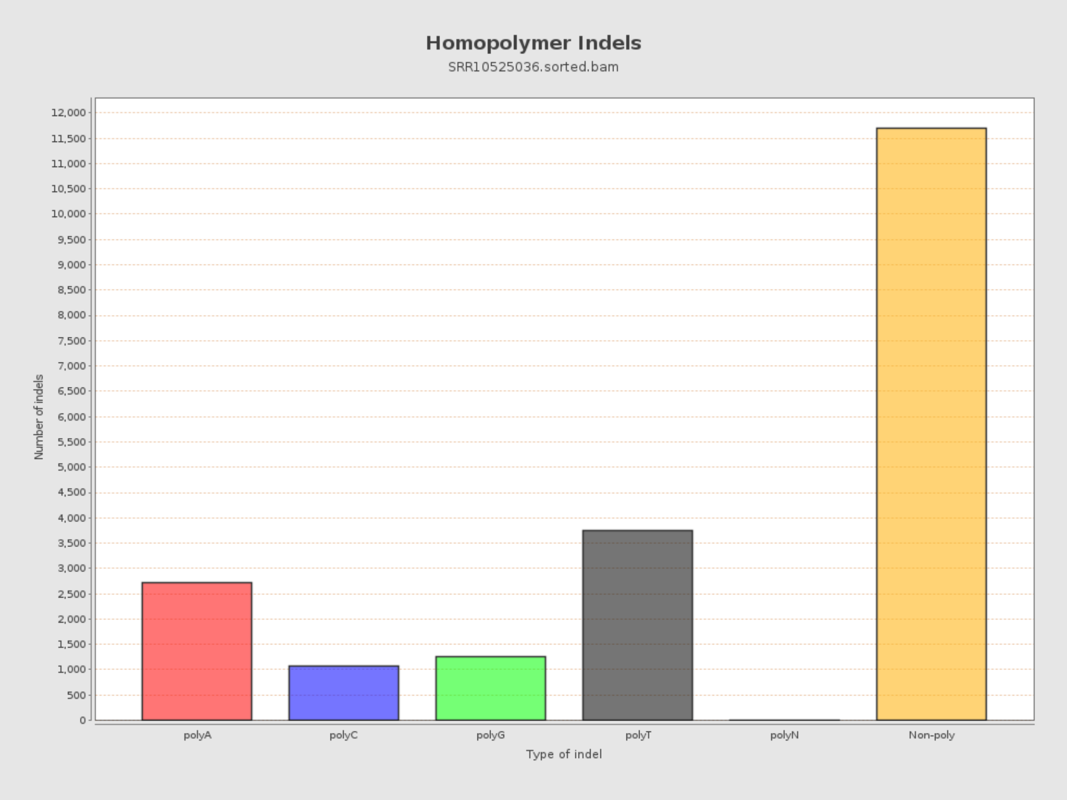
9. Results : Mapped Reads GC-content Distribution



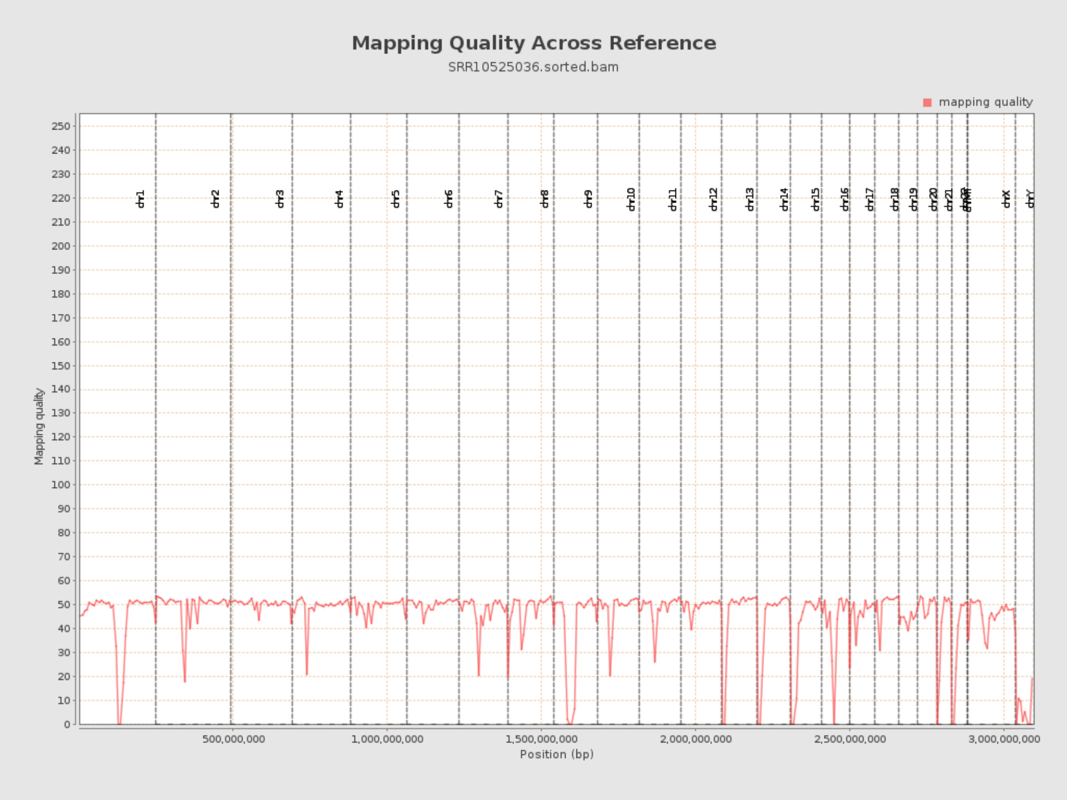
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram