Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:25:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525156.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_SRR10525156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:25:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,081,800
Mapped reads	979,784 / 90.57%
Unmapped reads	102,016 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,196 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	22,707 / 2.1%
Duplication rate	1.64%
Clipped reads	979,977 / 90.59%

2.2. ACGT Content

Number/percentage of A's	14,570,939 / 24.74%
Number/percentage of C's	10,889,599 / 18.49%
Number/percentage of T's	18,805,877 / 31.93%
Number/percentage of G's	14,637,558 / 24.85%
Number/percentage of N's	1,384 / 0%
GC Percentage	43.34%

2.3. Coverage

Mean	0.019

Standard Deviation	0.201

2.4. Mapping Quality

Mean Mapping Quality	45.3

2.5. Mismatches and indels

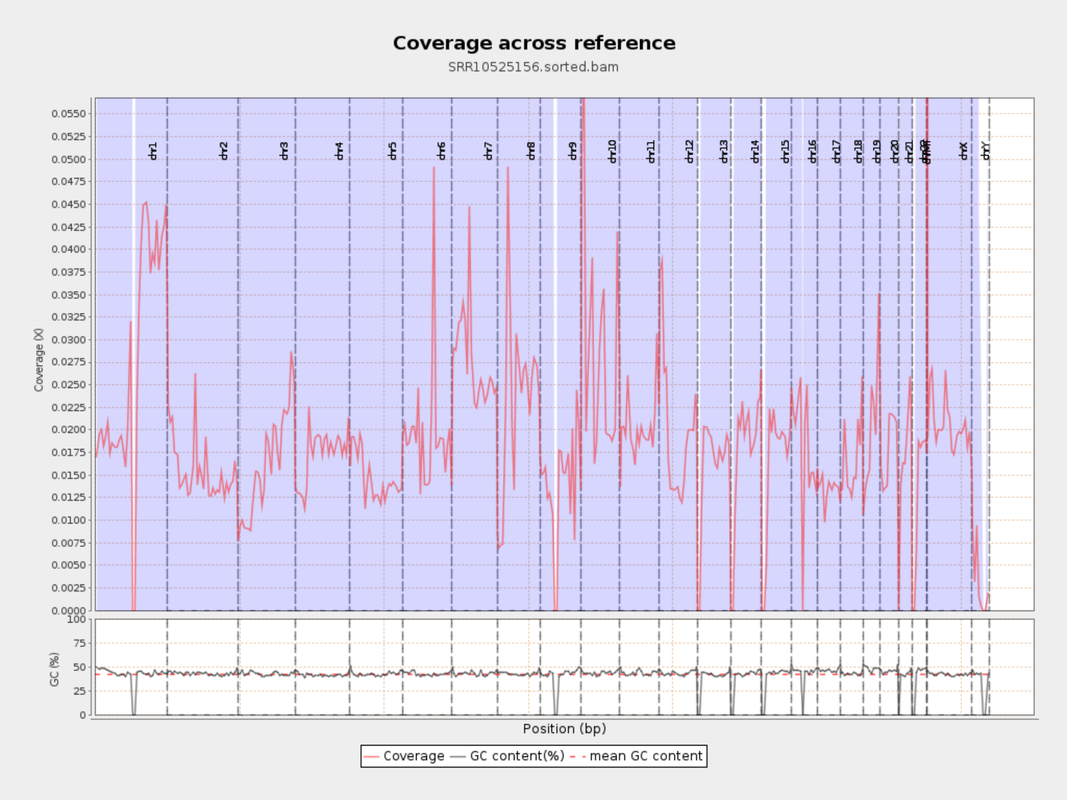
General error rate	0.51%
Mismatches	290,300
Insertions	4,017
Mapped reads with at least one insertion	0.41%
Deletions	11,590
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.85%

2.6. Chromosome stats

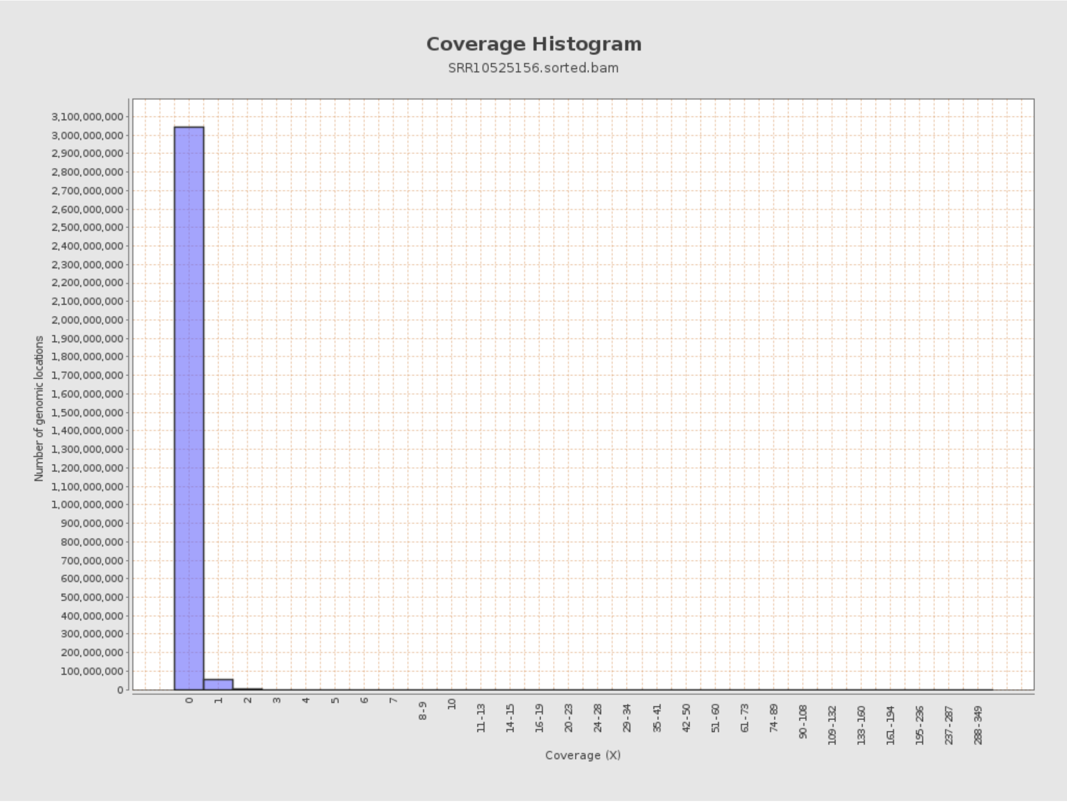
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6772208	0.0272	0.3363
chr2	243199373	3758822	0.0155	0.212
chr3	198022430	3218224	0.0163	0.1356
chr4	191154276	3312341	0.0173	0.1436
chr5	180915260	2661874	0.0147	0.1274
chr6	171115067	3390573	0.0198	0.162
chr7	159138663	4410966	0.0277	0.3622

chr8	146364022	3468978	0.0237	0.1846
chr9	141213431	1959855	0.0139	0.1524
chr10	135534747	3980027	0.0294	0.2293
chr11	135006516	2729796	0.0202	0.1718
chr12	133851895	2678009	0.02	0.1489
chr13	115169878	1820036	0.0158	0.133
chr14	107349540	1881013	0.0175	0.1437
chr15	102531392	1624531	0.0158	0.1328
chr16	90354753	1631218	0.0181	0.154
chr17	81195210	1088518	0.0134	0.125
chr18	78077248	1284905	0.0165	0.303
chr19	59128983	1217321	0.0206	0.2444
chr20	63025520	1116461	0.0177	0.1419
chr21	48129895	822932	0.0171	0.1415
chr22	51304566	661416	0.0129	0.1191
chrMT	16571	44090	2.6607	2.0985
chrX	155270560	3213804	0.0207	0.1587
chrY	59373566	176262	0.003	0.0881

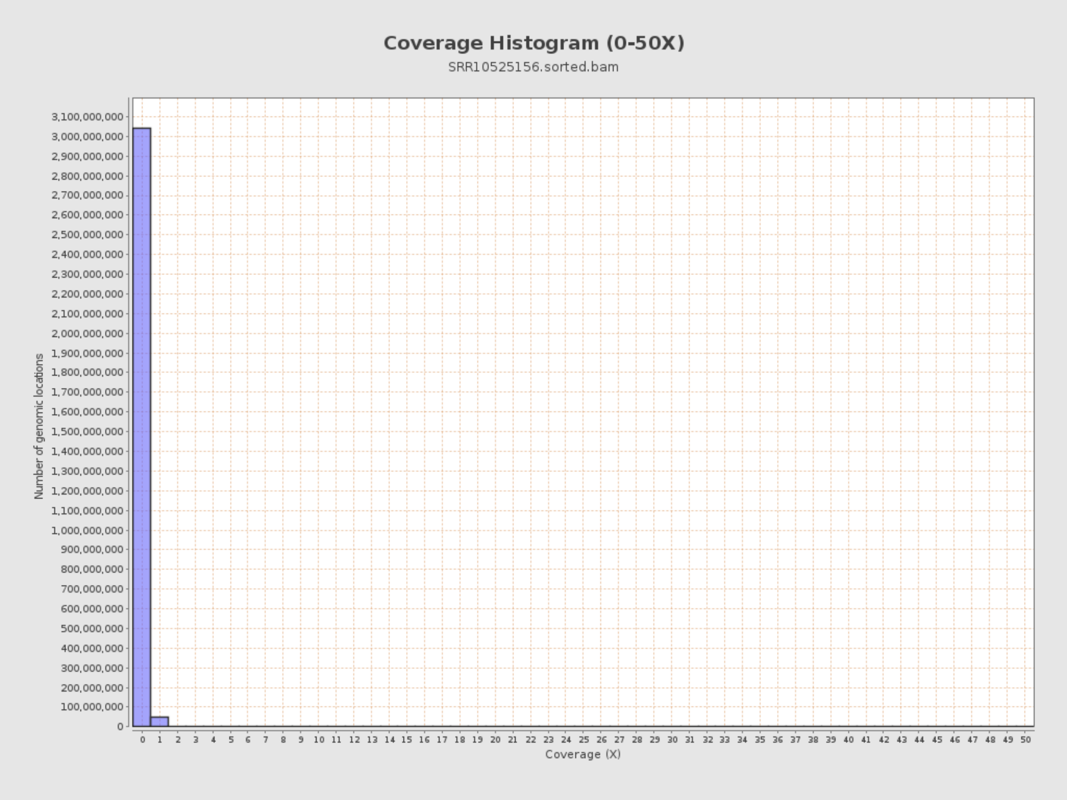
3. Results : Coverage across reference



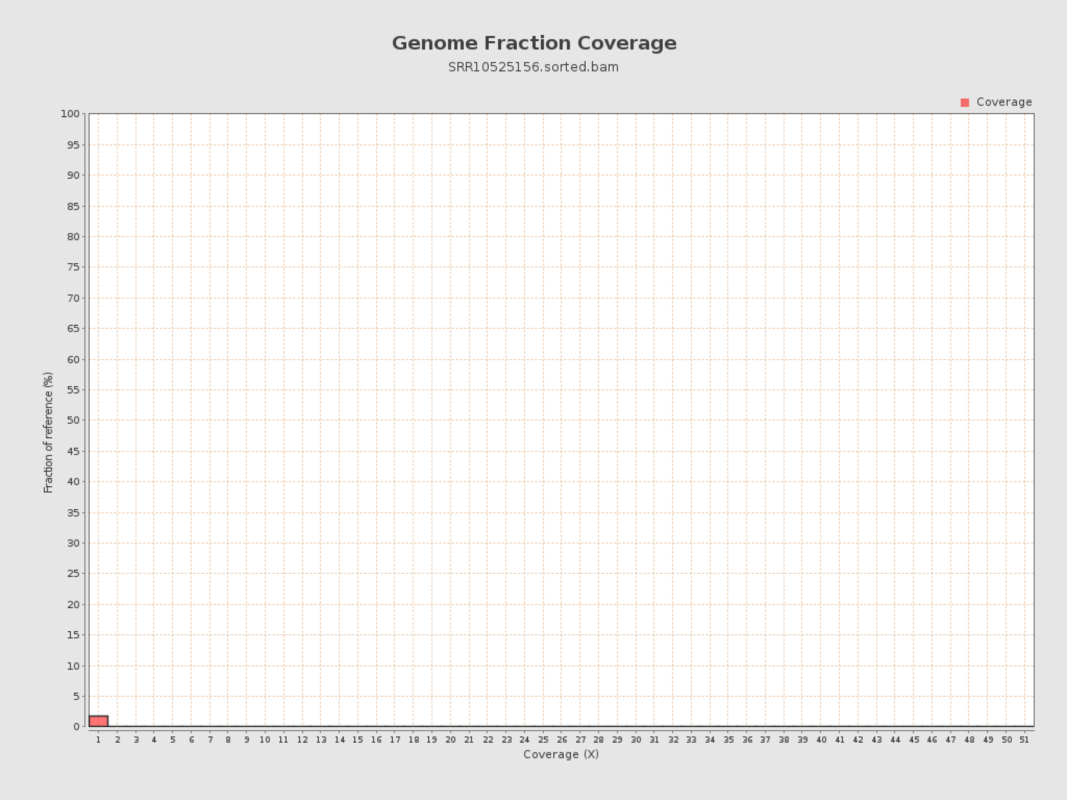
4. Results : Coverage Histogram



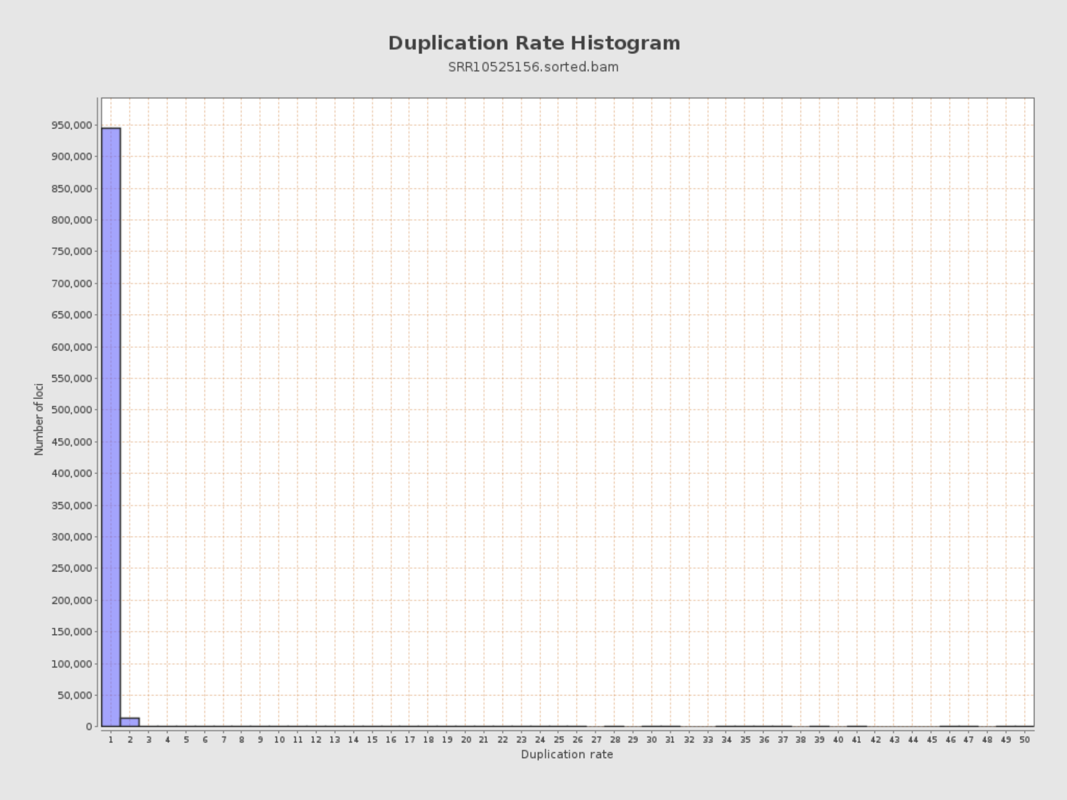
5. Results : Coverage Histogram (0-50X)



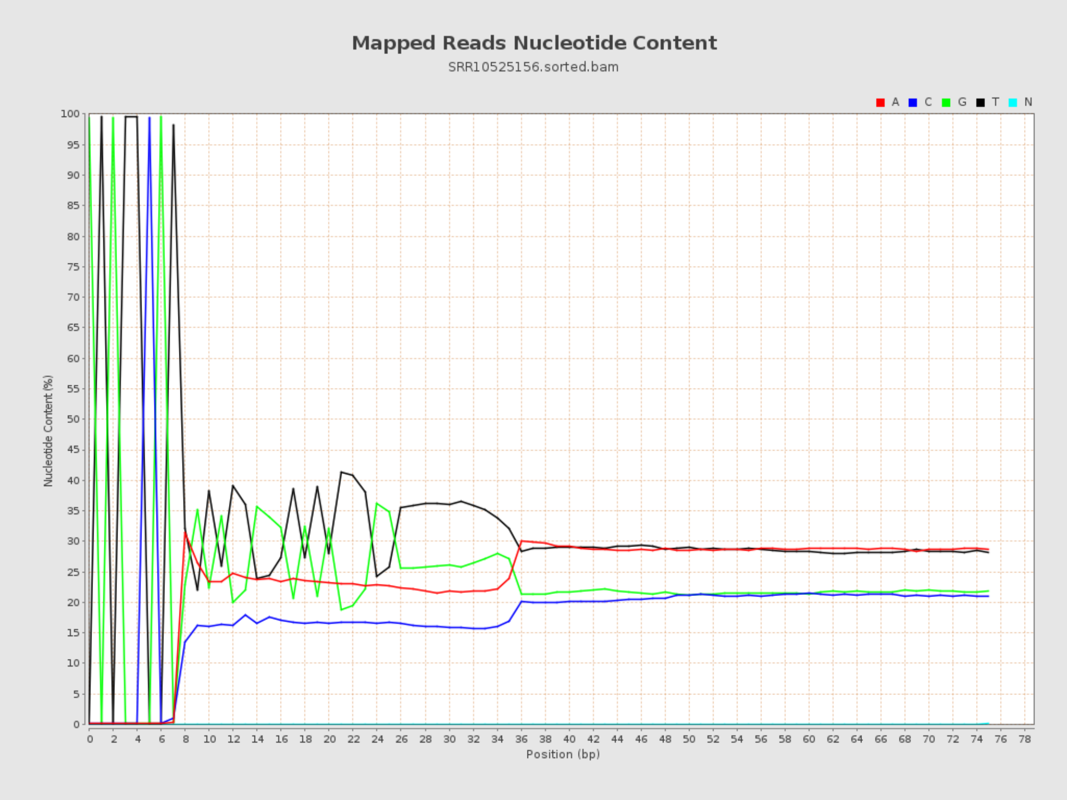
6. Results : Genome Fraction Coverage



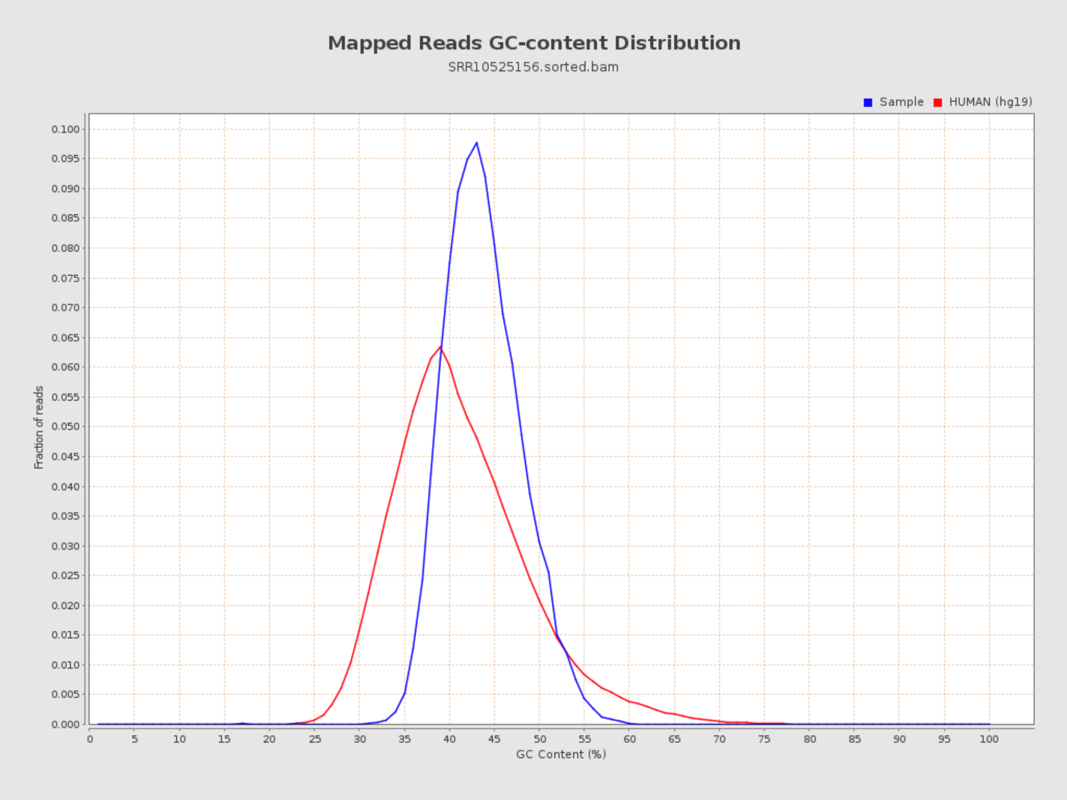
7. Results : Duplication Rate Histogram



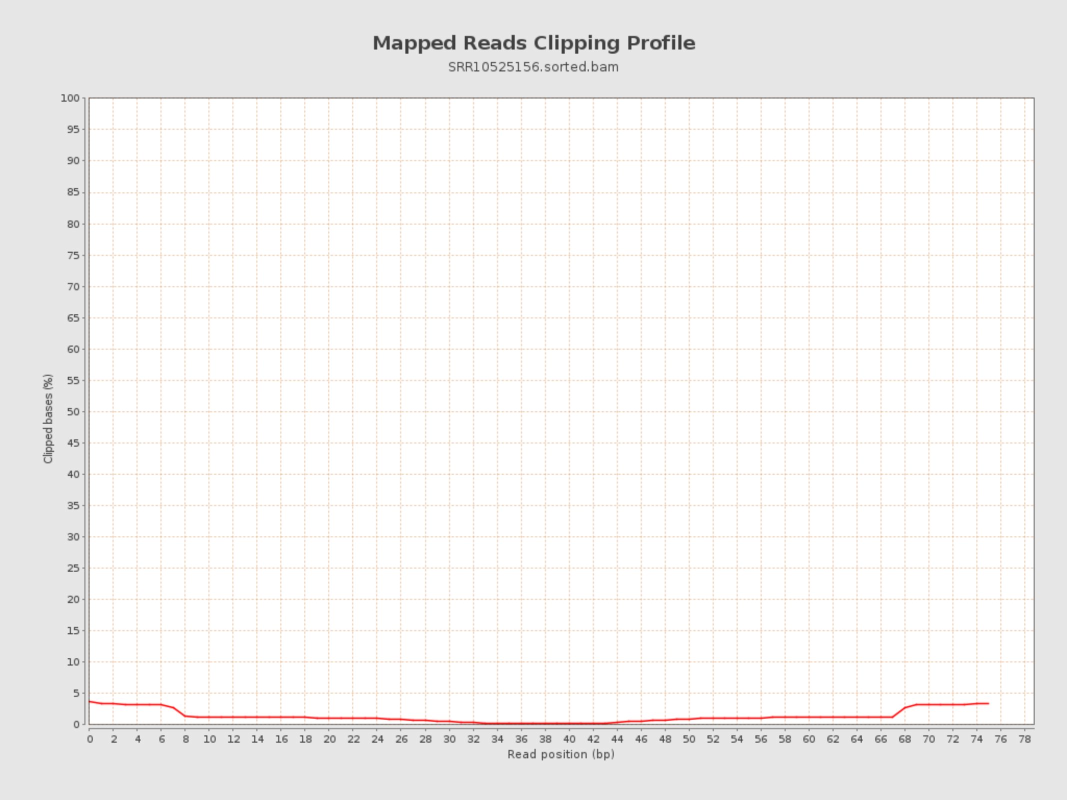
8. Results : Mapped Reads Nucleotide Content



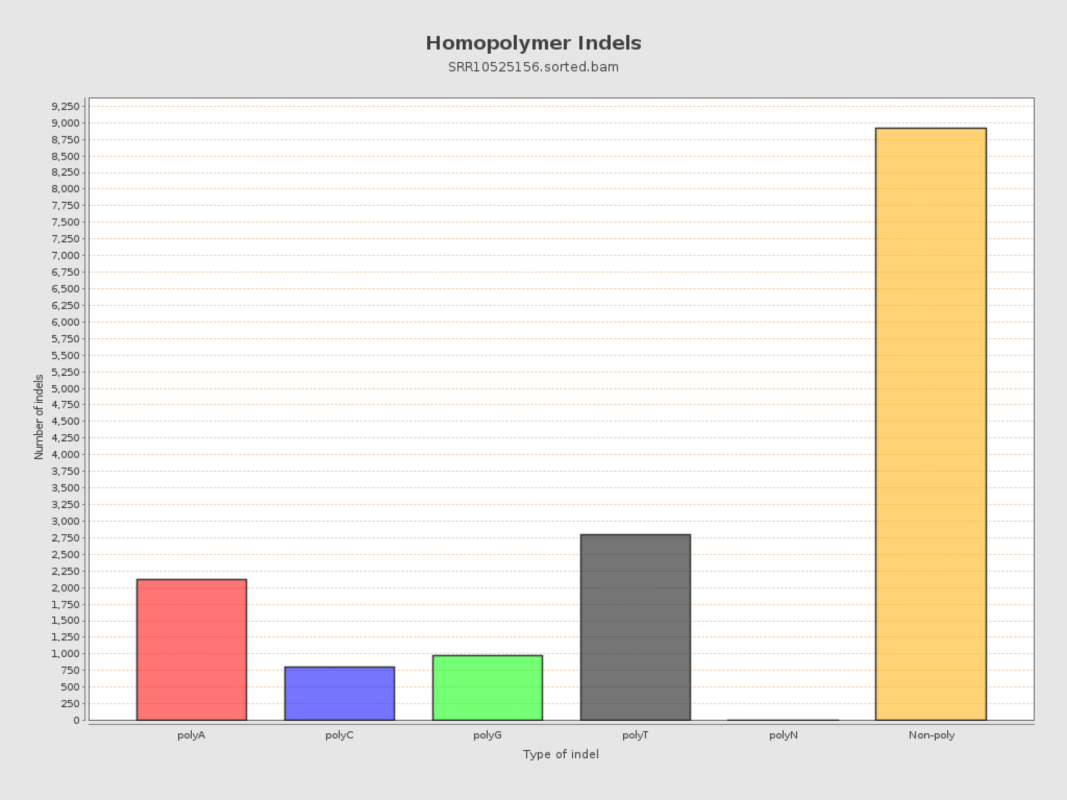
9. Results : Mapped Reads GC-content Distribution



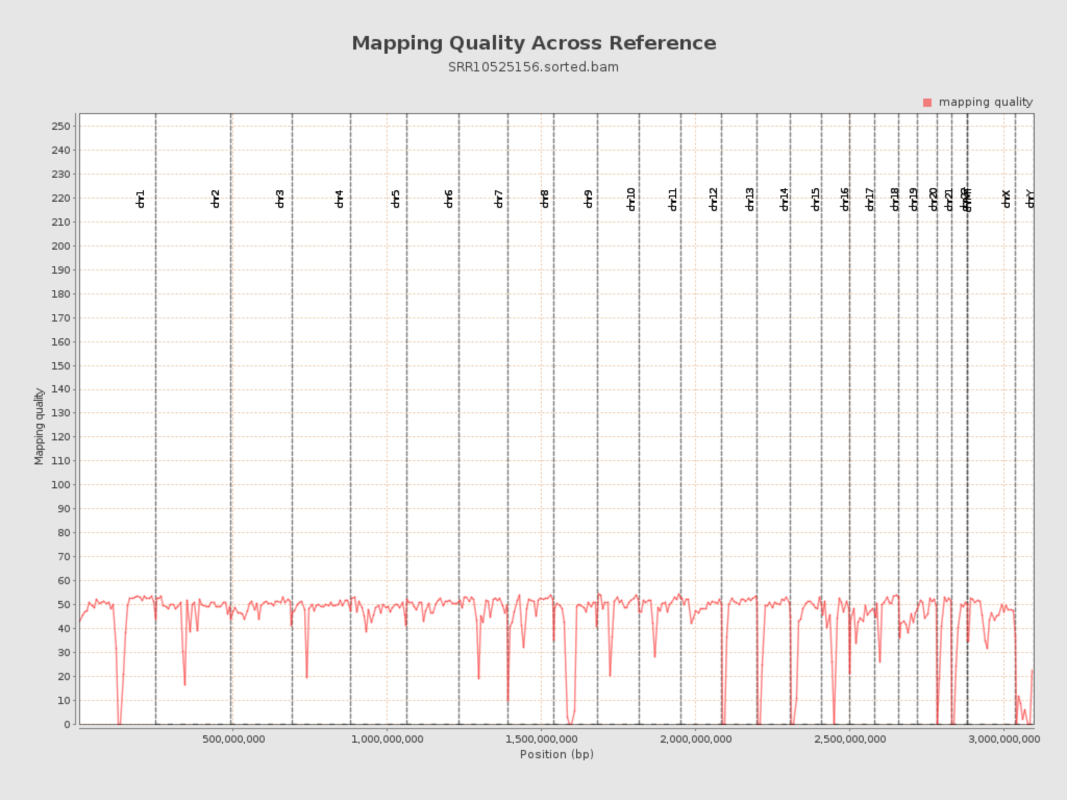
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram