Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:24:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525259.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_SRR10525259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525259.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:24:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525259.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,628,478
Mapped reads	1,465,706 / 90%
Unmapped reads	162,772 / 10%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,774 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	52,406 / 3.22%
Duplication rate	2.59%
Clipped reads	1,466,992 / 90.08%

2.2. ACGT Content

Number/percentage of A's	20,276,675 / 23.75%
Number/percentage of C's	15,196,676 / 17.8%
Number/percentage of T's	28,178,254 / 33%
Number/percentage of G's	21,724,961 / 25.45%
Number/percentage of N's	1,767 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2615

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

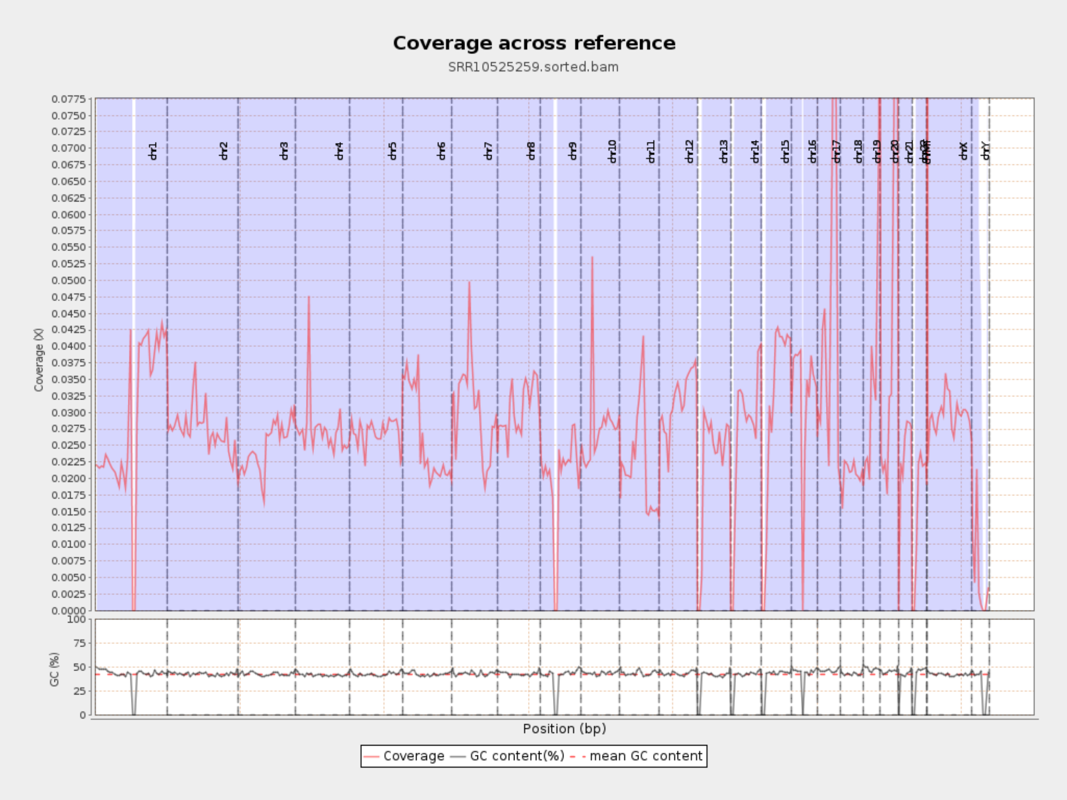
General error rate	0.52%
Mismatches	429,560
Insertions	6,360
Mapped reads with at least one insertion	0.43%
Deletions	17,009
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.69%

2.6. Chromosome stats

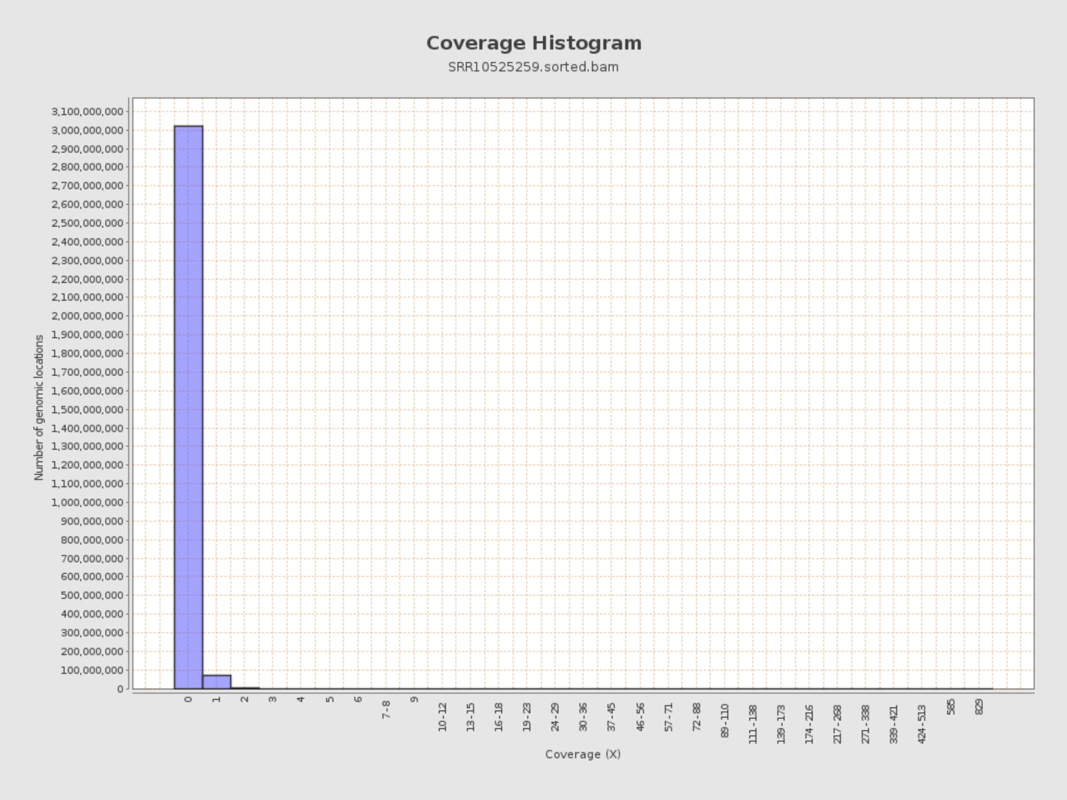
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7178568	0.0288	0.3911
chr2	243199373	6651444	0.0273	0.379
chr3	198022430	4899943	0.0247	0.1704
chr4	191154276	5244176	0.0274	0.2129
chr5	180915260	4891544	0.027	0.1777
chr6	171115067	4503910	0.0263	0.2028
chr7	159138663	4868087	0.0306	0.326

chr8	146364022	4491229	0.0307	0.3552
chr9	141213431	2814820	0.0199	0.1865
chr10	135534747	3778111	0.0279	0.2708
chr11	135006516	3030549	0.0224	0.2017
chr12	133851895	4239432	0.0317	0.1932
chr13	115169878	2546929	0.0221	0.1611
chr14	107349540	2869199	0.0267	0.179
chr15	102531392	3145490	0.0307	0.1909
chr16	90354753	2904264	0.0321	0.201
chr17	81195210	3693358	0.0455	0.2425
chr18	78077248	1604447	0.0205	0.3086
chr19	59128983	2190753	0.0371	0.3215
chr20	63025520	2831411	0.0449	0.2386
chr21	48129895	1113414	0.0231	0.1961
chr22	51304566	807100	0.0157	0.135
chrMT	16571	195506	11.7981	7.5191
chrX	155270560	4602573	0.0296	0.198
chrY	59373566	309828	0.0052	0.2158

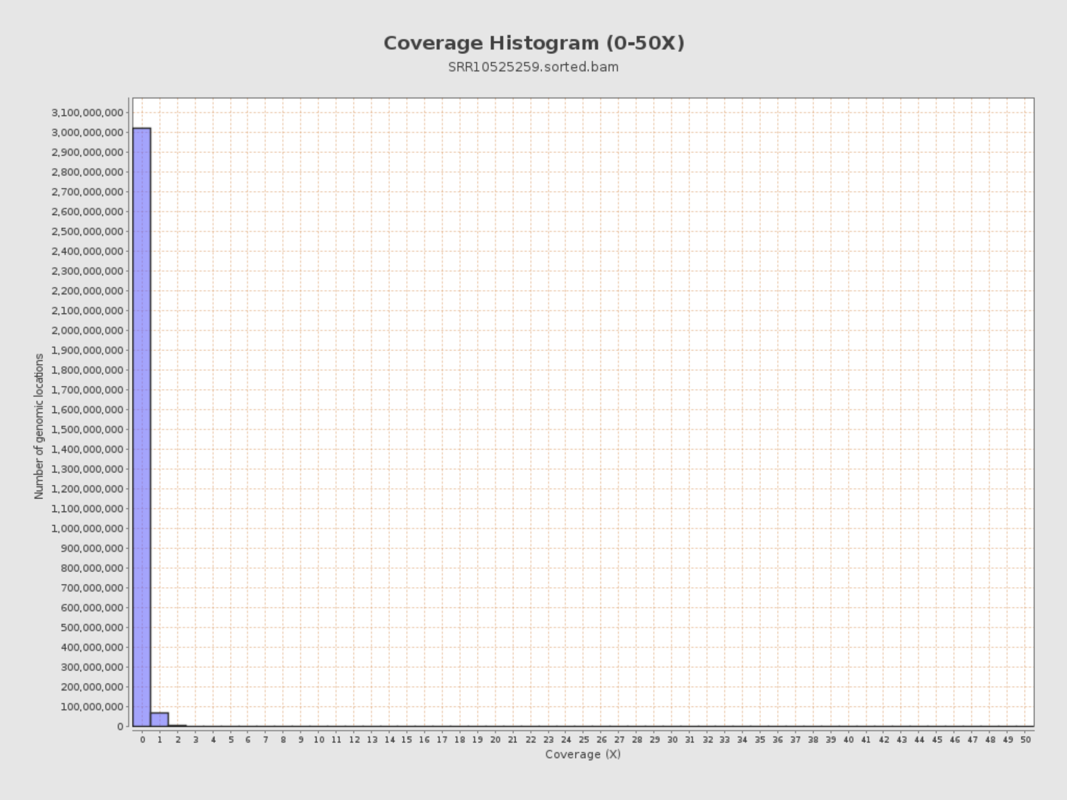
3. Results : Coverage across reference



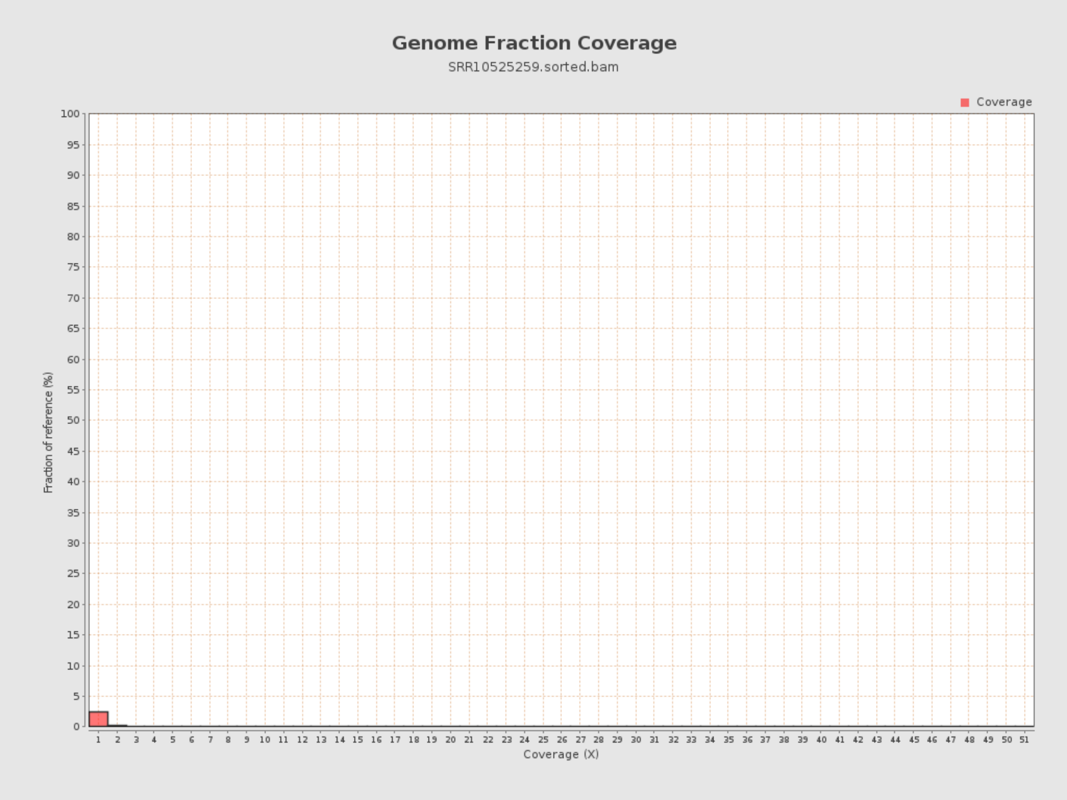
4. Results : Coverage Histogram



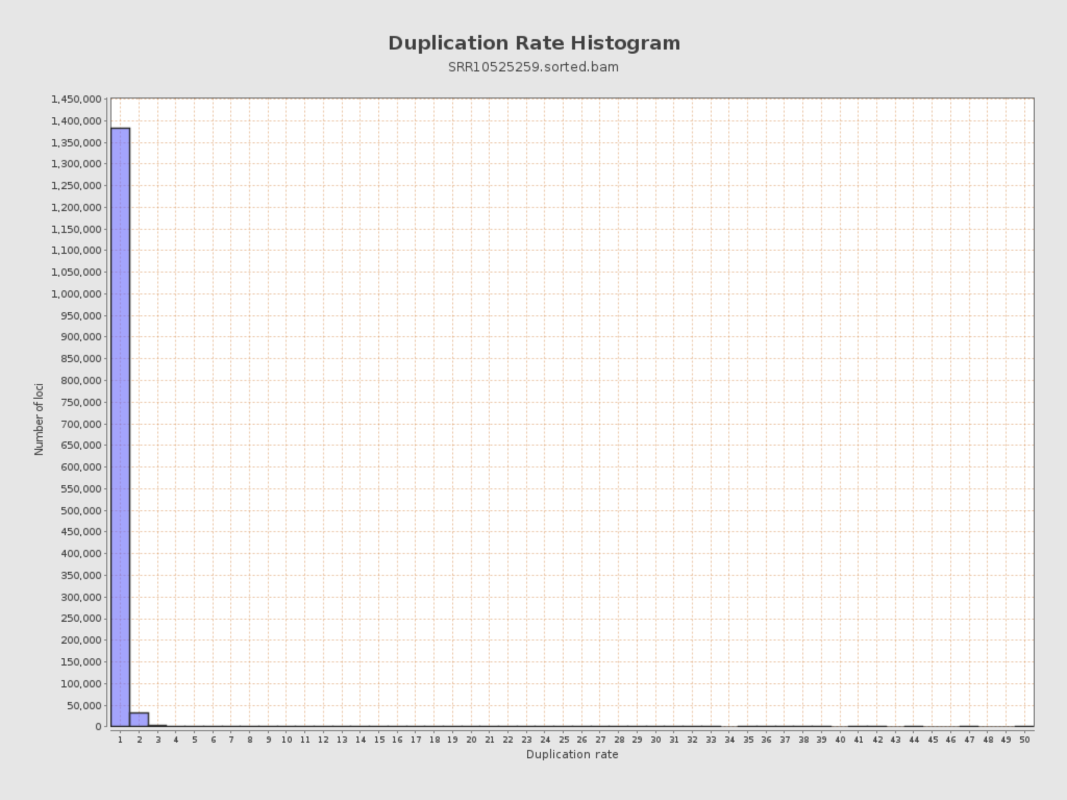
5. Results : Coverage Histogram (0-50X)



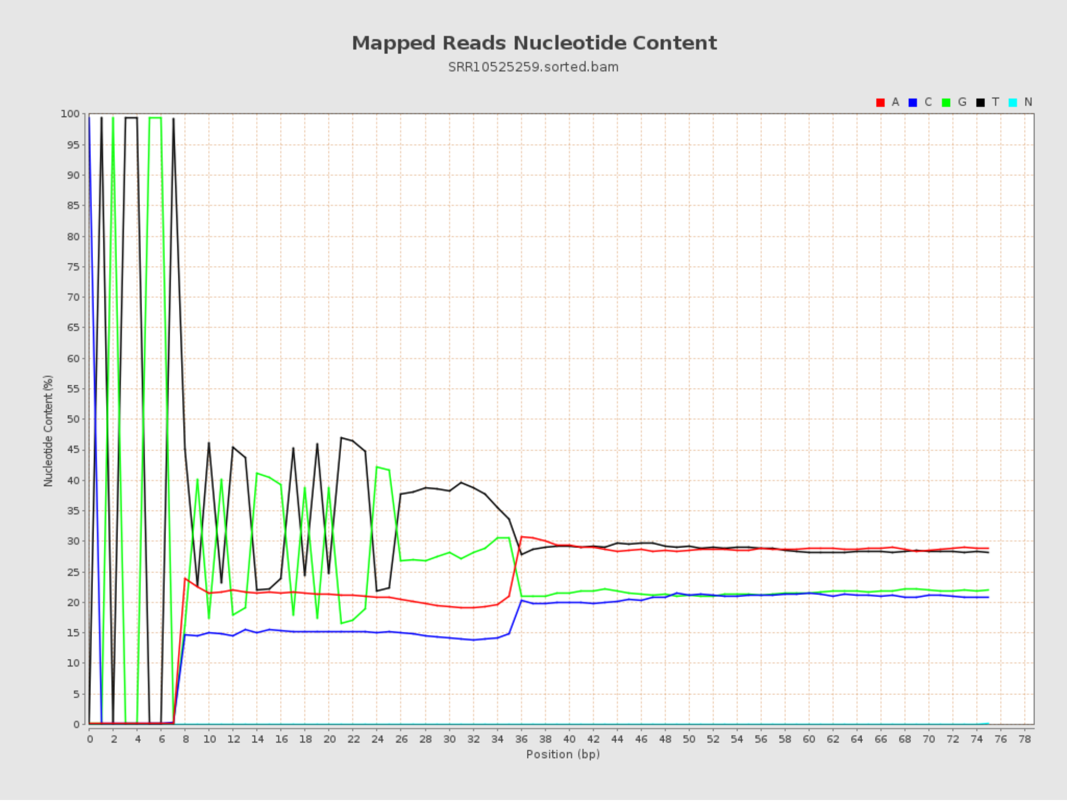
6. Results : Genome Fraction Coverage



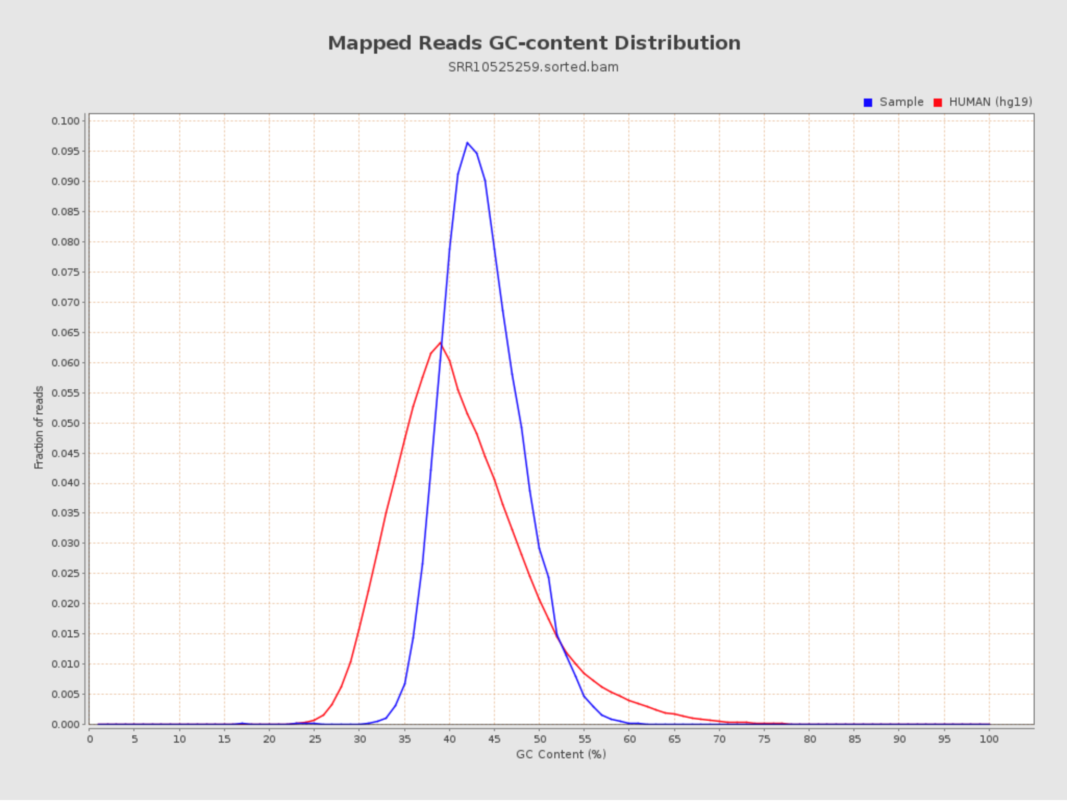
7. Results : Duplication Rate Histogram



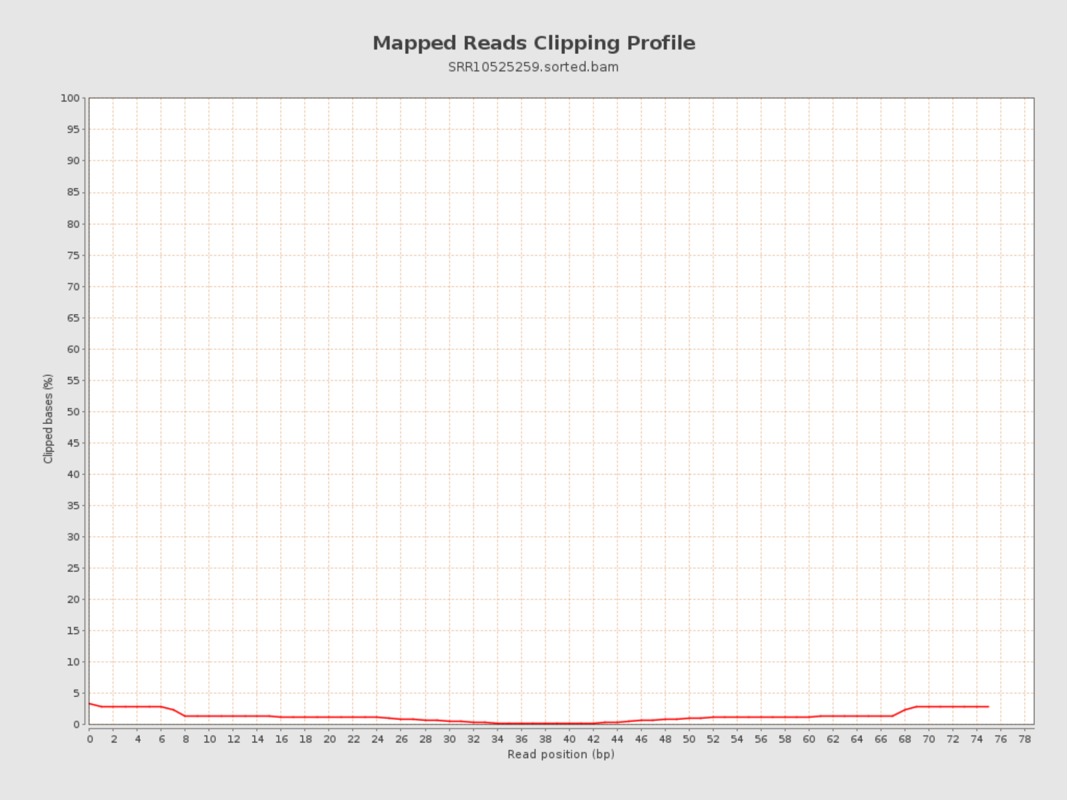
8. Results : Mapped Reads Nucleotide Content



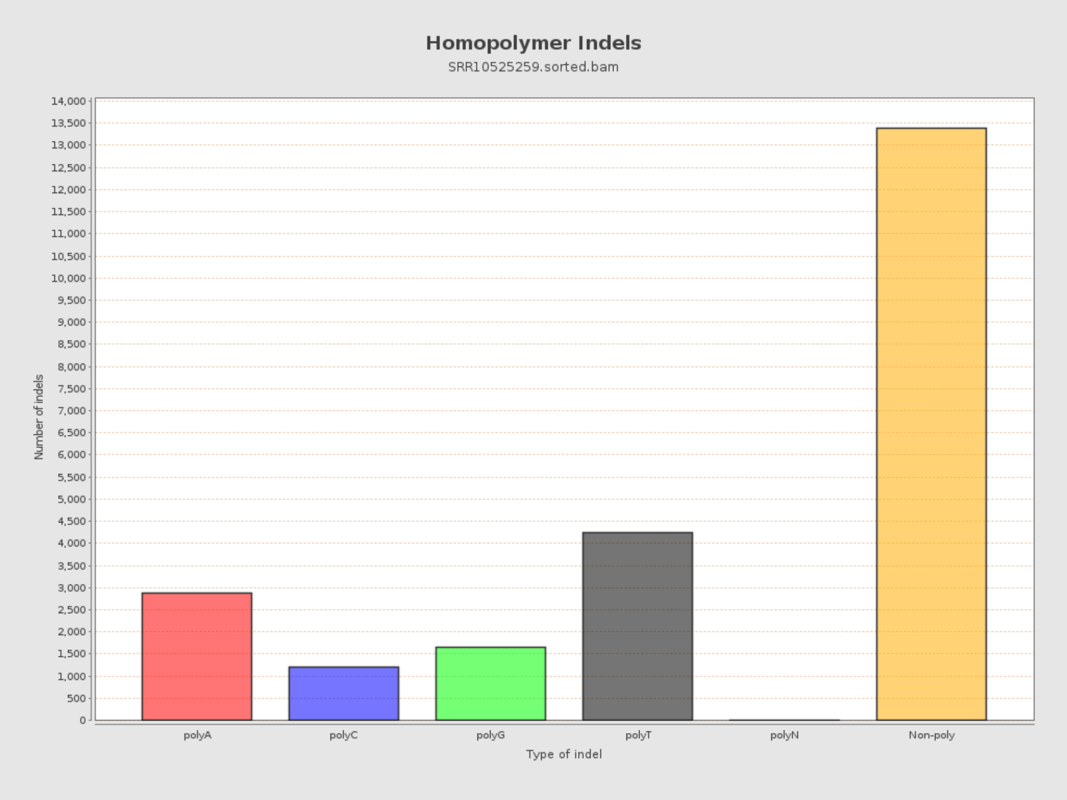
9. Results : Mapped Reads GC-content Distribution



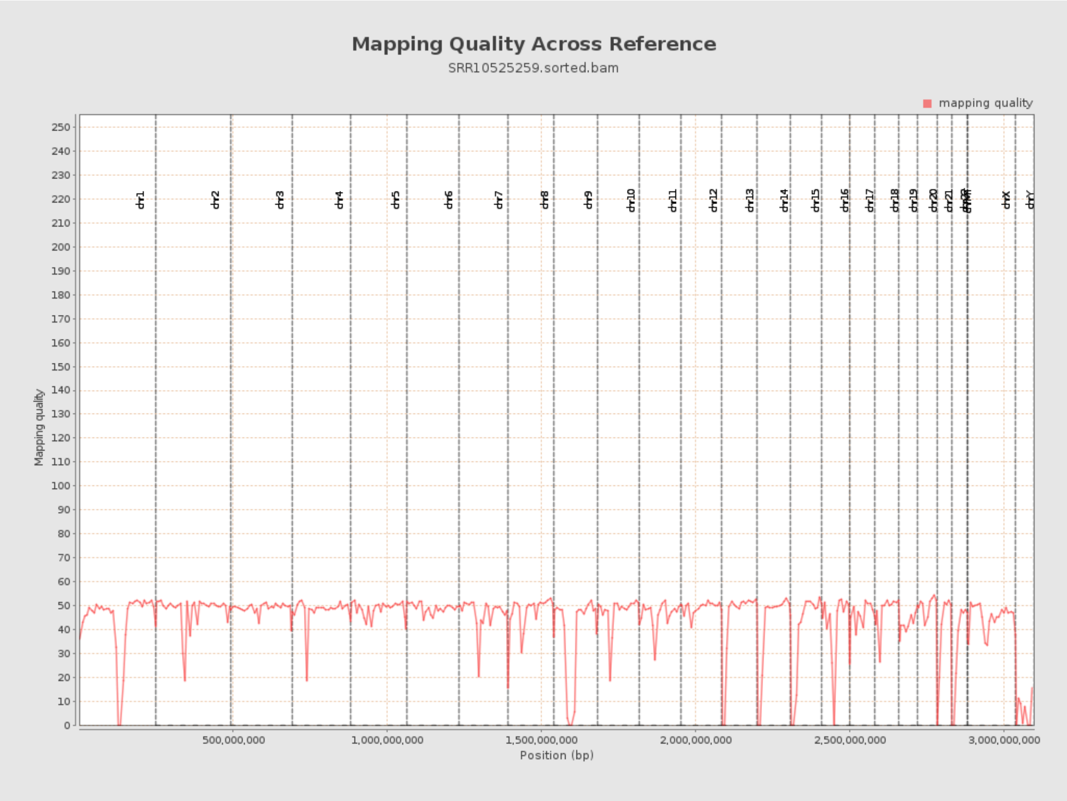
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram