Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 23:21:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524335.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_SRR10524335 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524335.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 23:21:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524335.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,021,312
Mapped reads	2,758,486 / 91.3%
Unmapped reads	262,826 / 8.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,779 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	122,050 / 4.04%
Duplication rate	3.14%
Clipped reads	2,767,528 / 91.6%

2.2. ACGT Content

Number/percentage of A's	37,863,091 / 23.53%
Number/percentage of C's	30,849,761 / 19.17%
Number/percentage of T's	51,045,595 / 31.72%
Number/percentage of G's	41,121,346 / 25.56%
Number/percentage of N's	21,550 / 0.01%
GC Percentage	44.73%

2.3. Coverage

Mean	0.052

Standard Deviation	0.4384

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

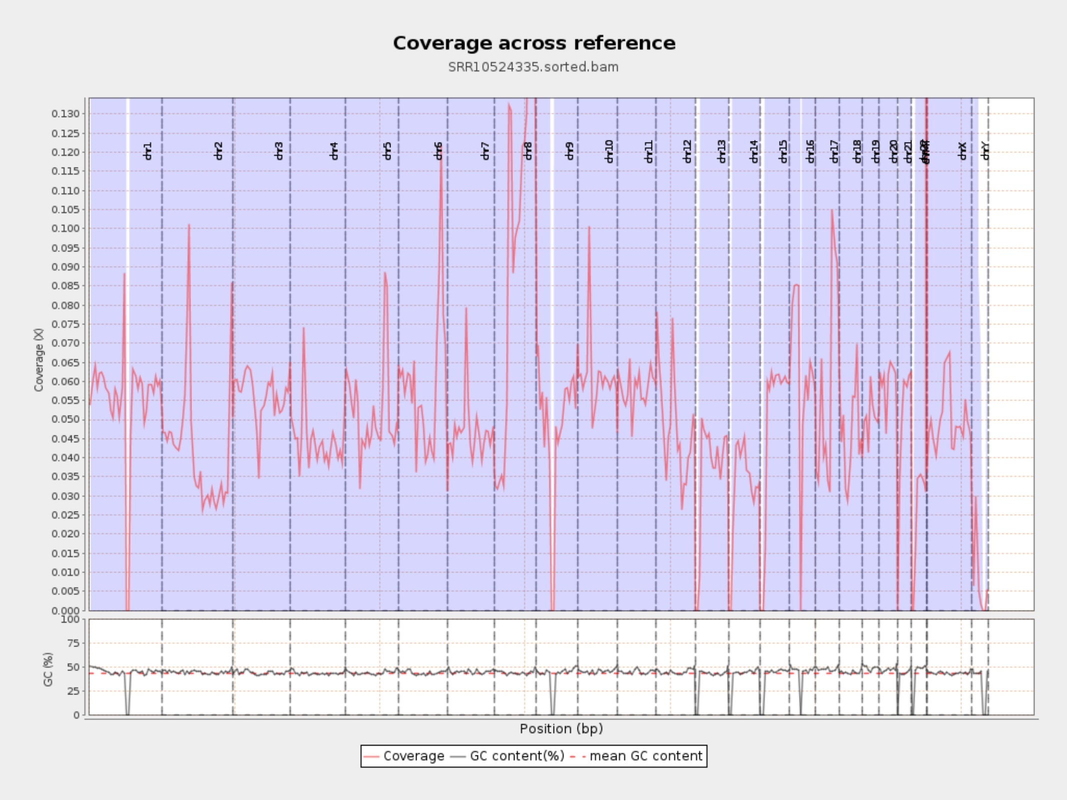
General error rate	0.51%
Mismatches	810,816
Insertions	8,932
Mapped reads with at least one insertion	0.32%
Deletions	25,620
Mapped reads with at least one deletion	0.92%
Homopolymer indels	42%

2.6. Chromosome stats

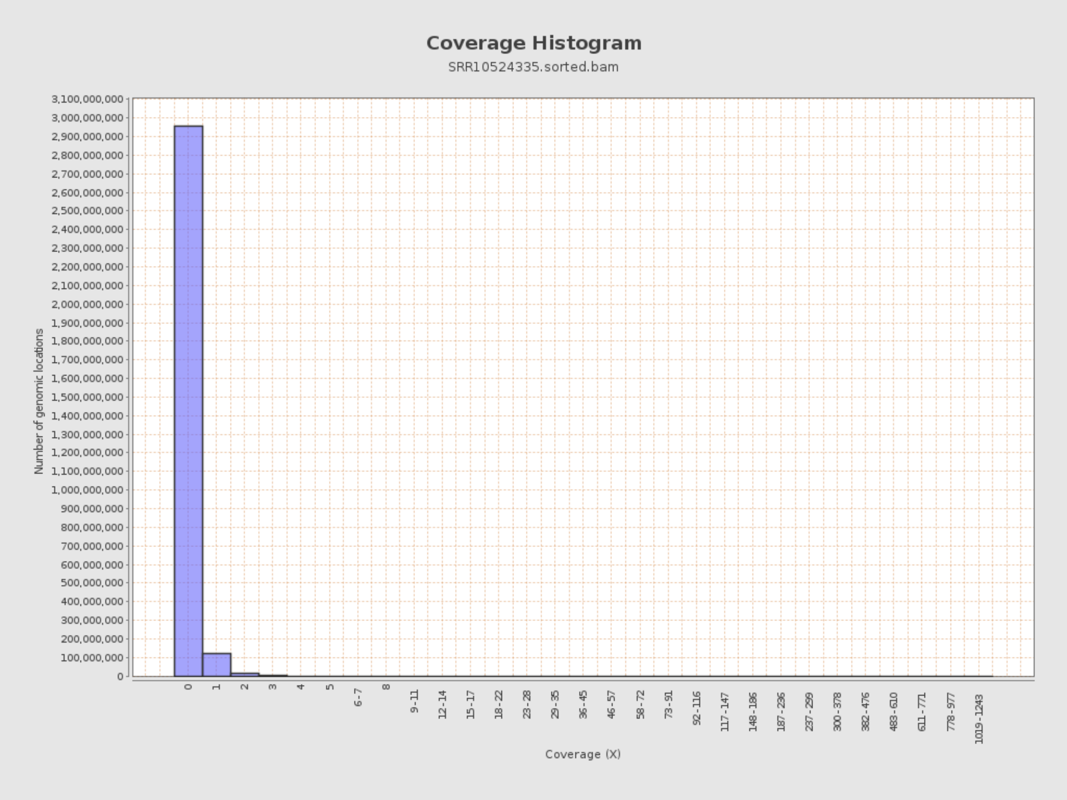
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13702435	0.055	0.8664
chr2	243199373	10276631	0.0423	0.5735
chr3	198022430	11122217	0.0562	0.2719
chr4	191154276	8482632	0.0444	0.2876
chr5	180915260	9484220	0.0524	0.2602
chr6	171115067	10140977	0.0593	0.3139
chr7	159138663	7502056	0.0471	0.5579

chr8	146364022	15758529	0.1077	0.5207
chr9	141213431	6710207	0.0475	0.323
chr10	135534747	8313519	0.0613	0.4425
chr11	135006516	7814743	0.0579	0.3579
chr12	133851895	6441761	0.0481	0.254
chr13	115169878	4118373	0.0358	0.2153
chr14	107349540	3395381	0.0316	0.2187
chr15	102531392	4965452	0.0484	0.2504
chr16	90354753	5667904	0.0627	0.31
chr17	81195210	4786794	0.059	0.3169
chr18	78077248	3683570	0.0472	0.616
chr19	59128983	2990031	0.0506	0.5838
chr20	63025520	3768866	0.0598	0.2853
chr21	48129895	2354270	0.0489	0.2878
chr22	51304566	1238975	0.0241	0.1756
chrMT	16571	31403	1.8951	1.8356
chrX	155270560	7719564	0.0497	0.2959
chrY	59373566	472610	0.008	0.2333

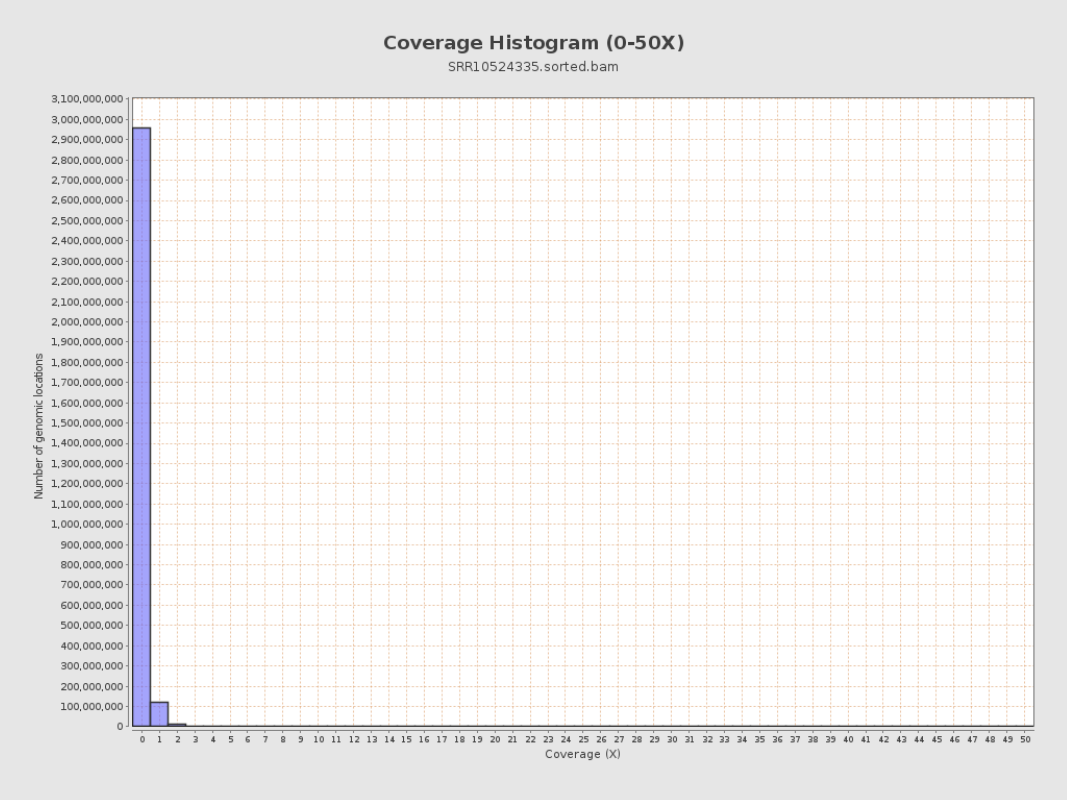
3. Results : Coverage across reference



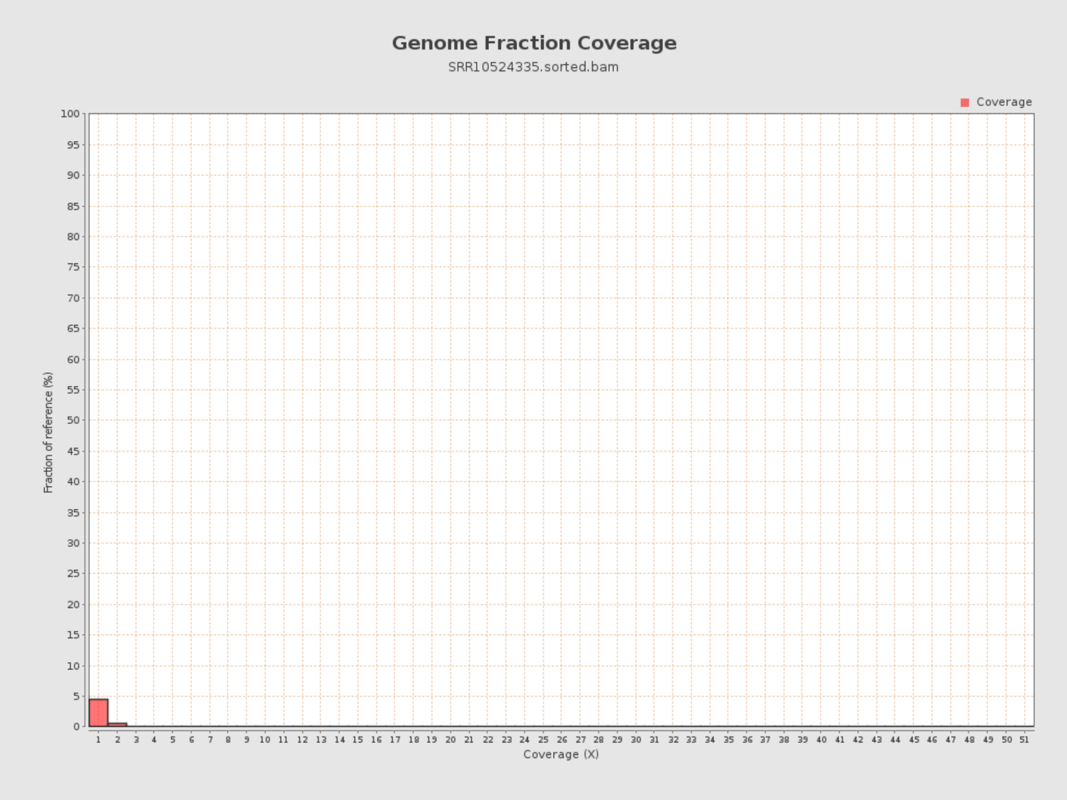
4. Results : Coverage Histogram



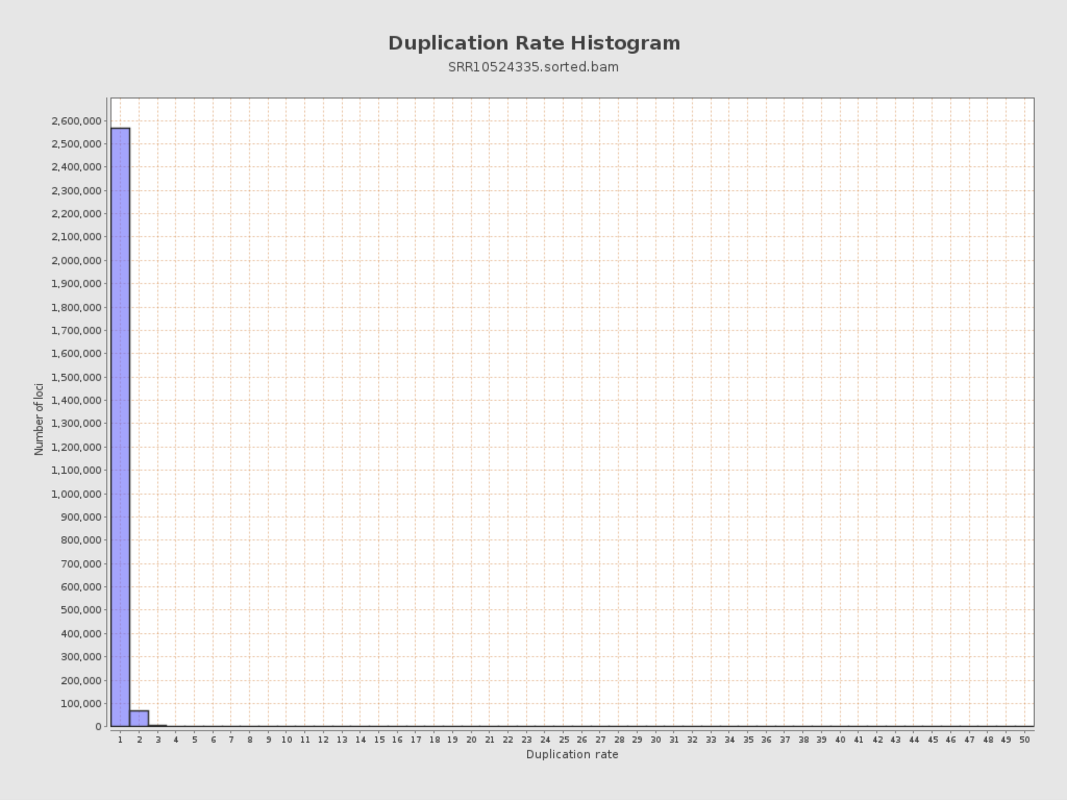
5. Results : Coverage Histogram (0-50X)



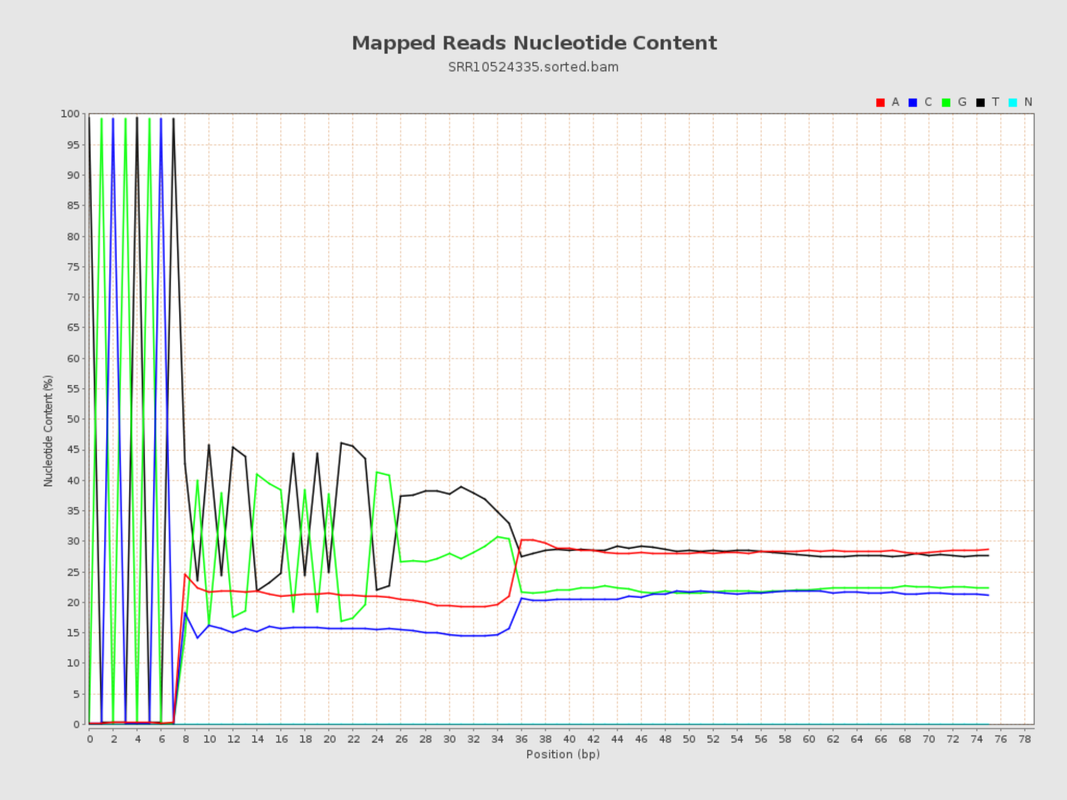
6. Results : Genome Fraction Coverage



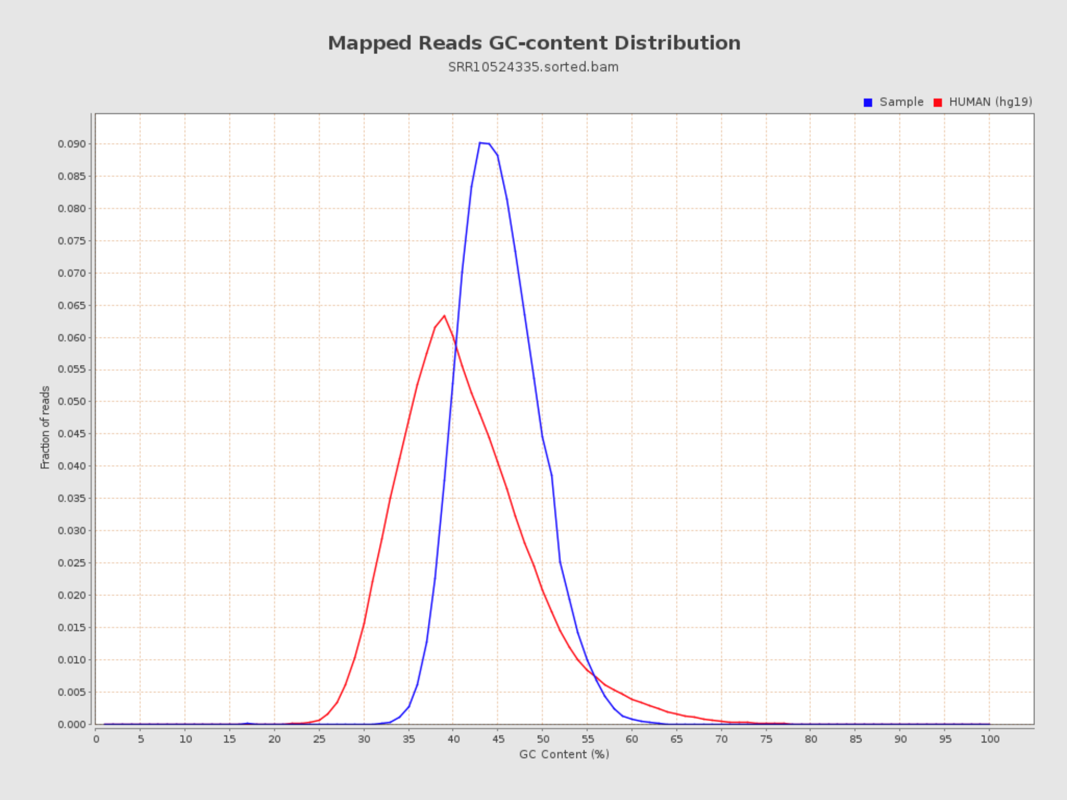
7. Results : Duplication Rate Histogram



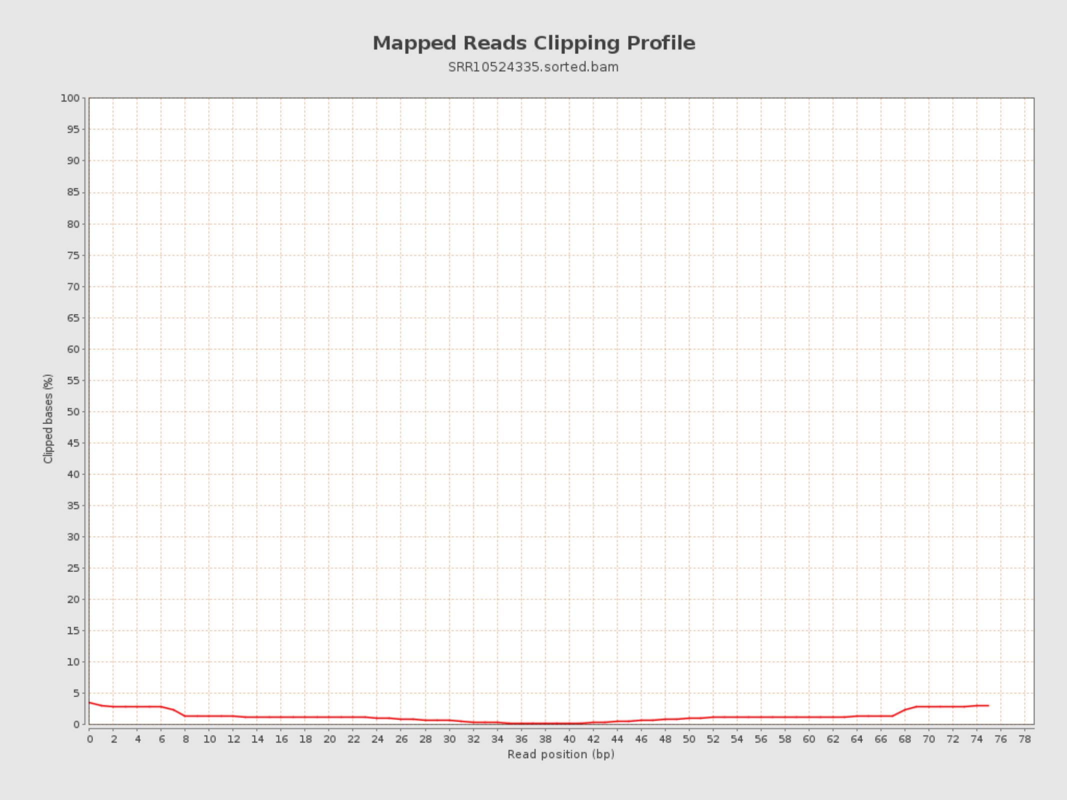
8. Results : Mapped Reads Nucleotide Content



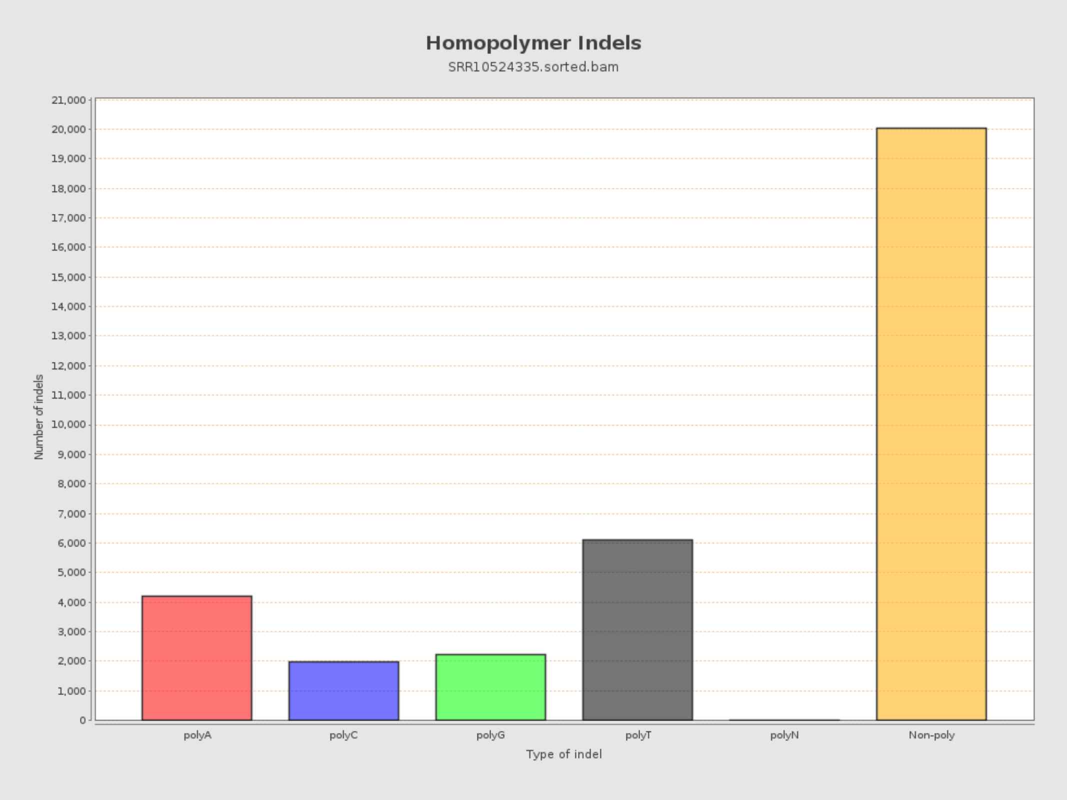
9. Results : Mapped Reads GC-content Distribution



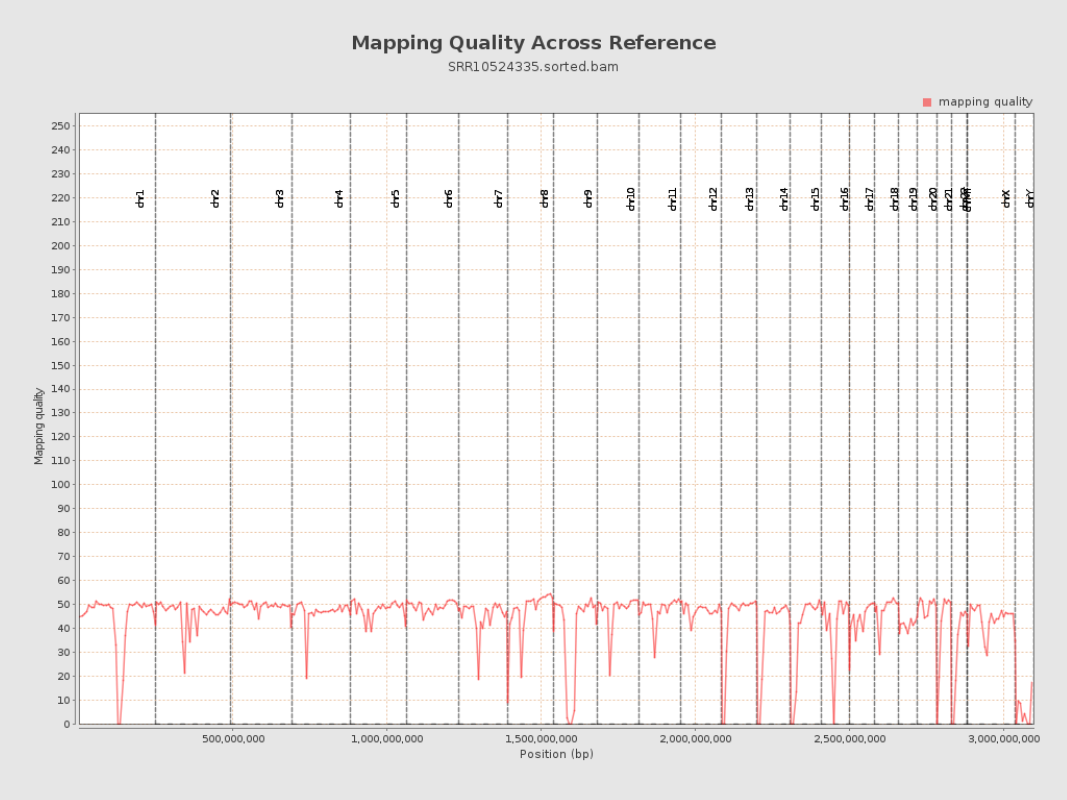
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram