Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 18:49:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524459.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_SRR10524459 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524459.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 18:49:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524459.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,517,531
Mapped reads	4,169,931 / 92.31%
Unmapped reads	347,600 / 7.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,063 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	395,556 / 8.76%
Duplication rate	6.98%
Clipped reads	4,170,866 / 92.33%

2.2. ACGT Content

Number/percentage of A's	57,789,552 / 23.82%
Number/percentage of C's	45,028,532 / 18.56%
Number/percentage of T's	78,073,410 / 32.18%
Number/percentage of G's	61,683,642 / 25.43%
Number/percentage of N's	4,547 / 0%
GC Percentage	43.99%

2.3. Coverage

Mean	0.0784

Standard Deviation	0.6372

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

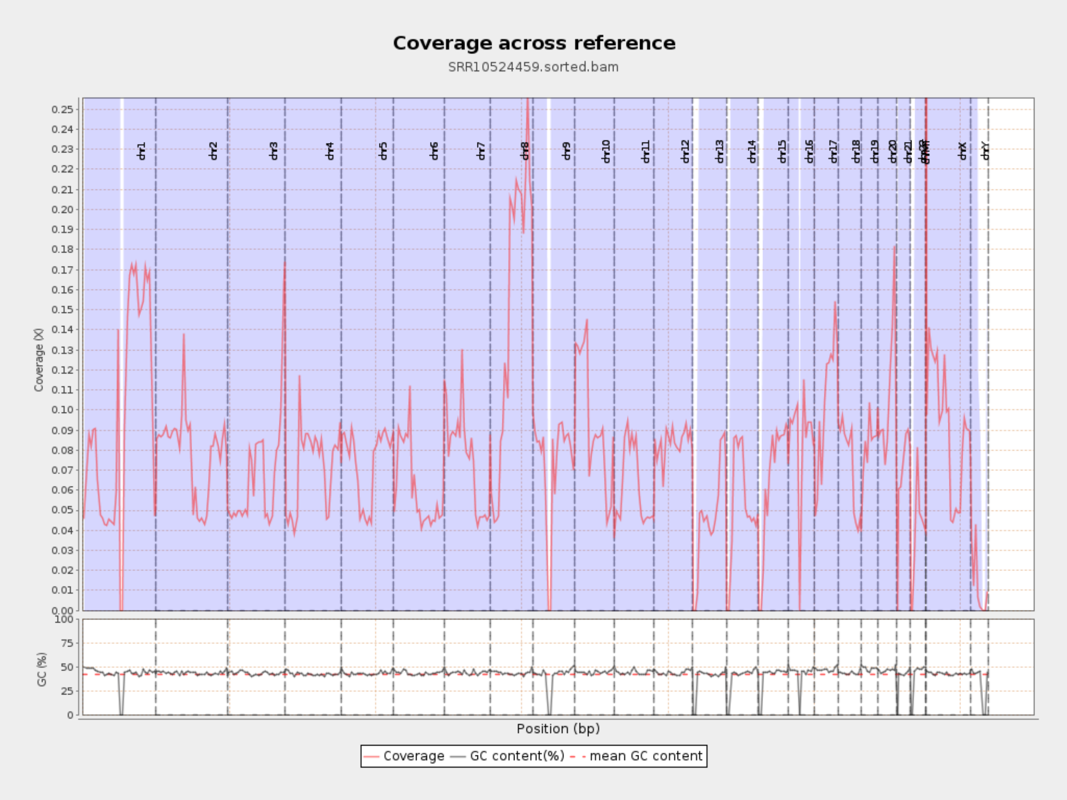
General error rate	0.48%
Mismatches	1,131,692
Insertions	14,845
Mapped reads with at least one insertion	0.35%
Deletions	43,226
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.33%

2.6. Chromosome stats

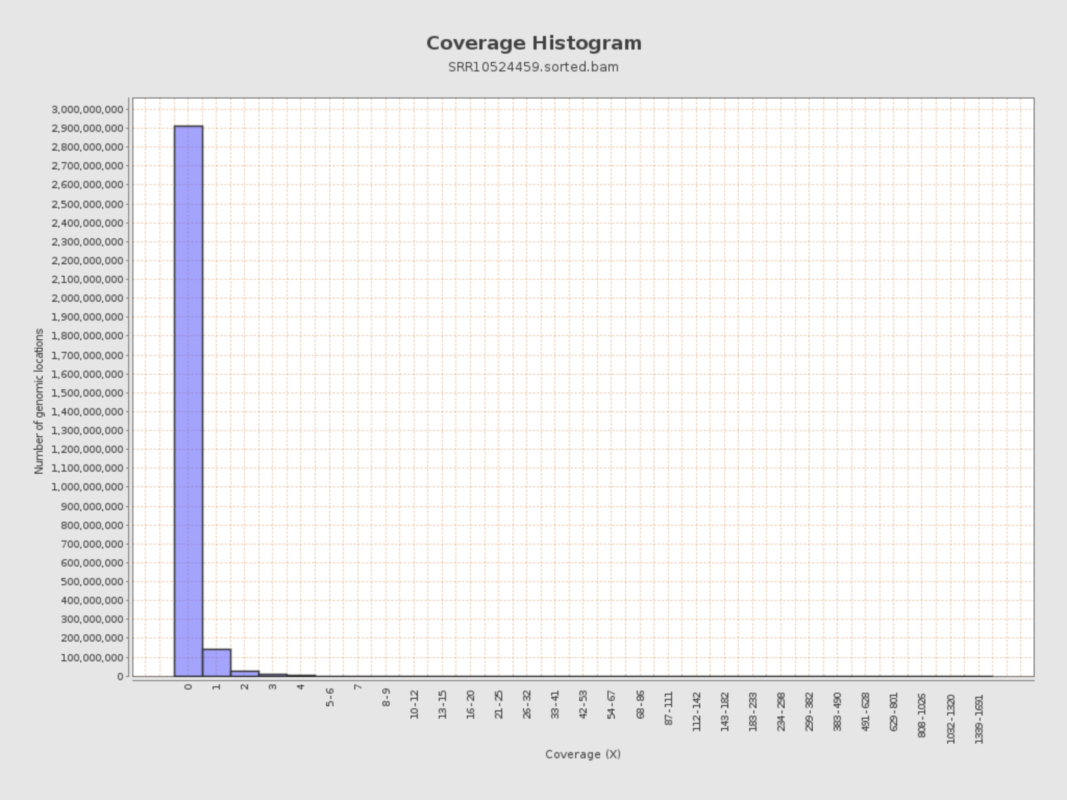
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23799926	0.0955	1.2818
chr2	243199373	19308441	0.0794	0.7316
chr3	198022430	13304803	0.0672	0.336
chr4	191154276	13705492	0.0717	0.4336
chr5	180915260	13363160	0.0739	0.3513
chr6	171115067	10444184	0.061	0.4738
chr7	159138663	12037950	0.0756	0.8336

chr8	146364022	22372721	0.1529	0.6449
chr9	141213431	10281692	0.0728	0.5375
chr10	135534747	12663509	0.0934	0.6268
chr11	135006516	8334212	0.0617	0.6241
chr12	133851895	11231668	0.0839	0.3758
chr13	115169878	5416987	0.047	0.2856
chr14	107349540	5767207	0.0537	0.3104
chr15	102531392	6461090	0.063	0.343
chr16	90354753	7563279	0.0837	0.4172
chr17	81195210	8413539	0.1036	0.4542
chr18	78077248	5705496	0.0731	1.0394
chr19	59128983	4891904	0.0827	0.8547
chr20	63025520	6946580	0.1102	0.4395
chr21	48129895	3333533	0.0693	0.386
chr22	51304566	1969229	0.0384	0.2504
chrMT	16571	160216	9.6685	7.1522
chrX	155270560	14426253	0.0929	0.4882
chrY	59373566	751515	0.0127	0.3071

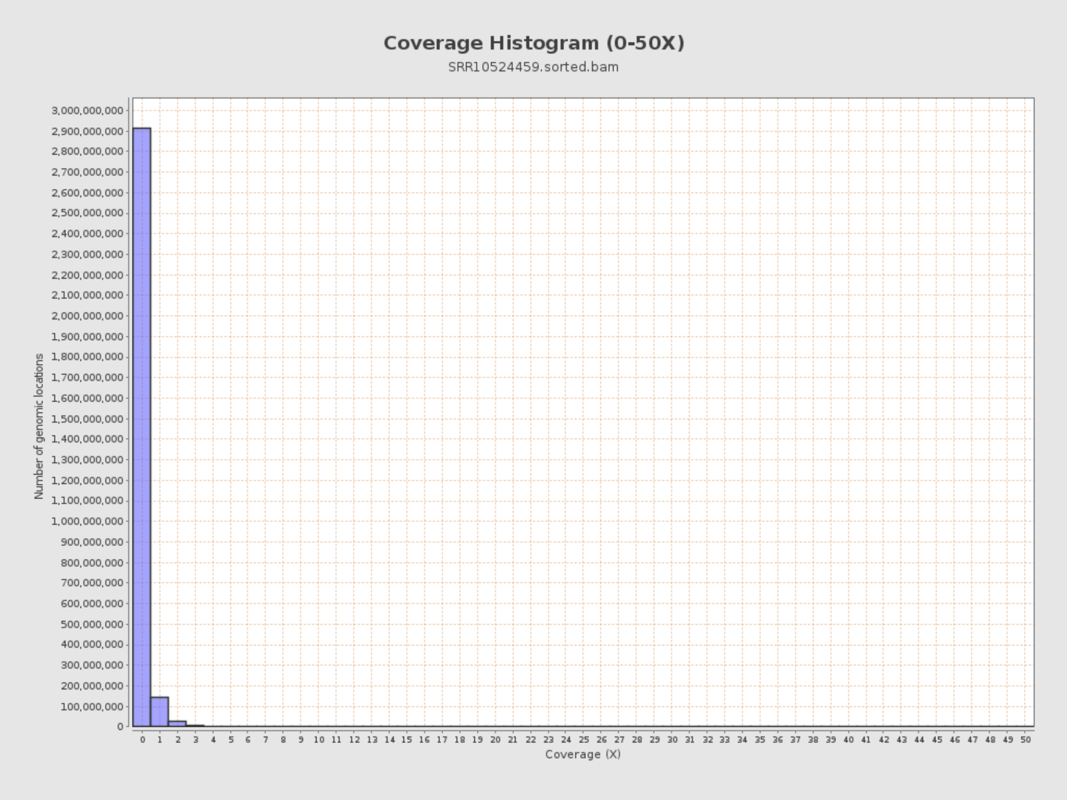
3. Results : Coverage across reference



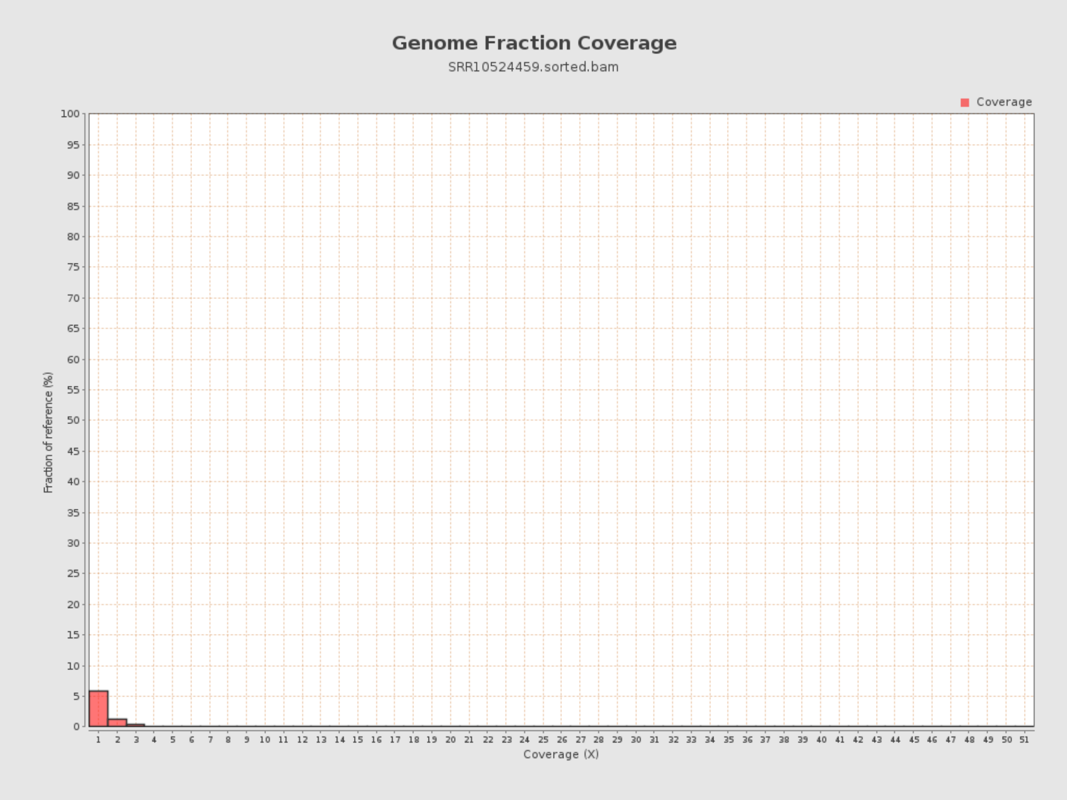
4. Results : Coverage Histogram



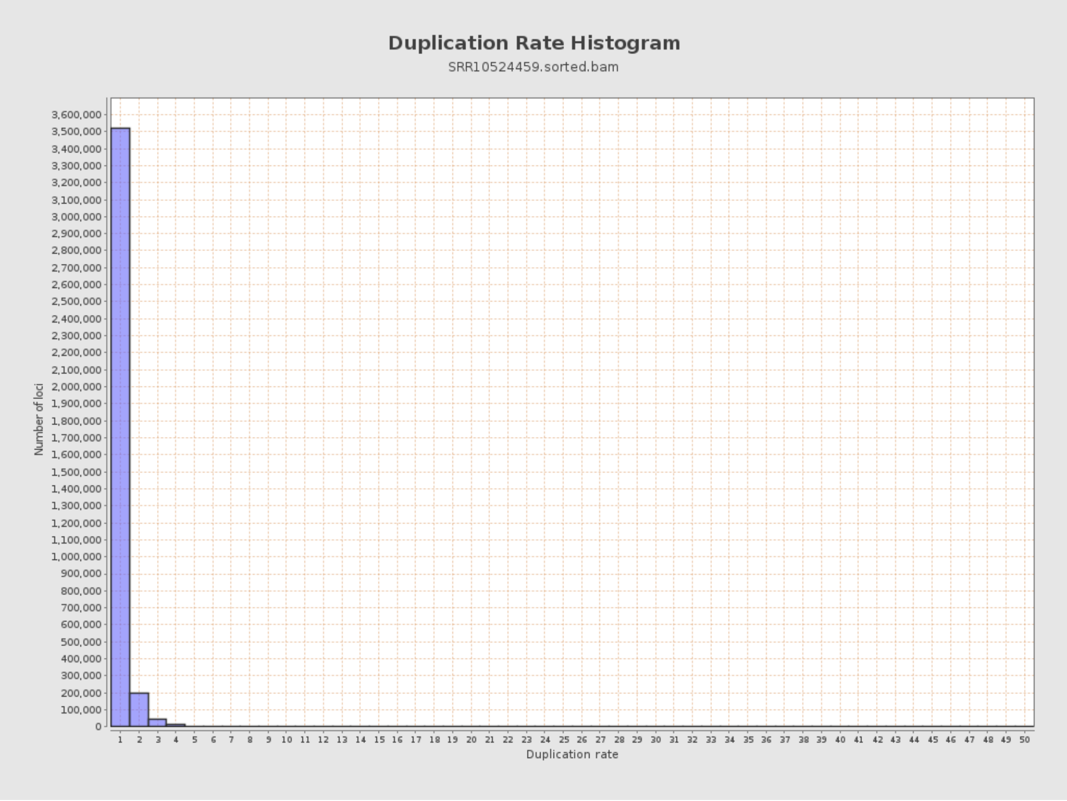
5. Results : Coverage Histogram (0-50X)



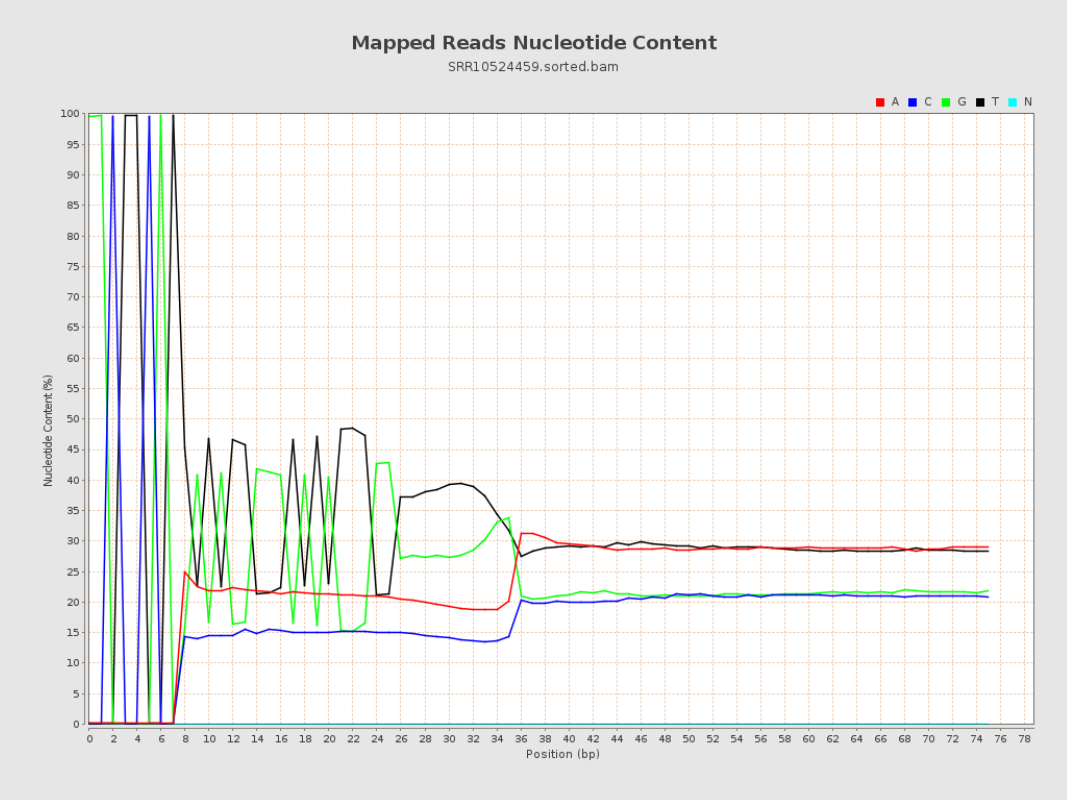
6. Results : Genome Fraction Coverage



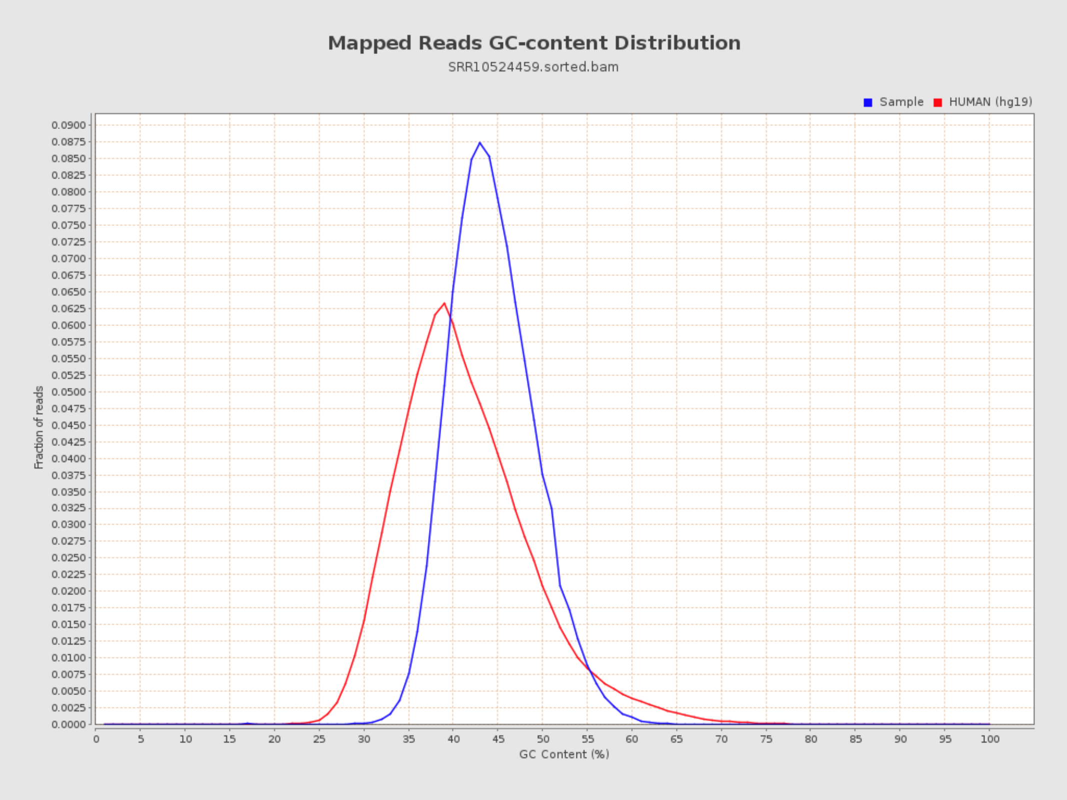
7. Results : Duplication Rate Histogram



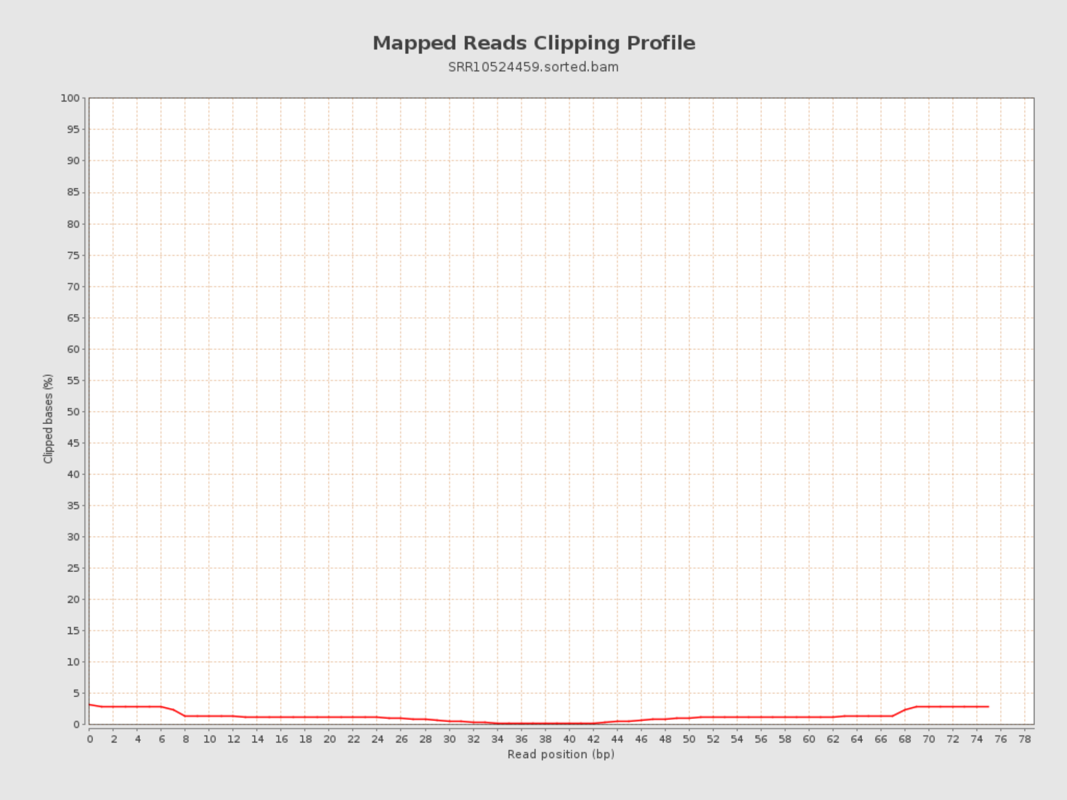
8. Results : Mapped Reads Nucleotide Content



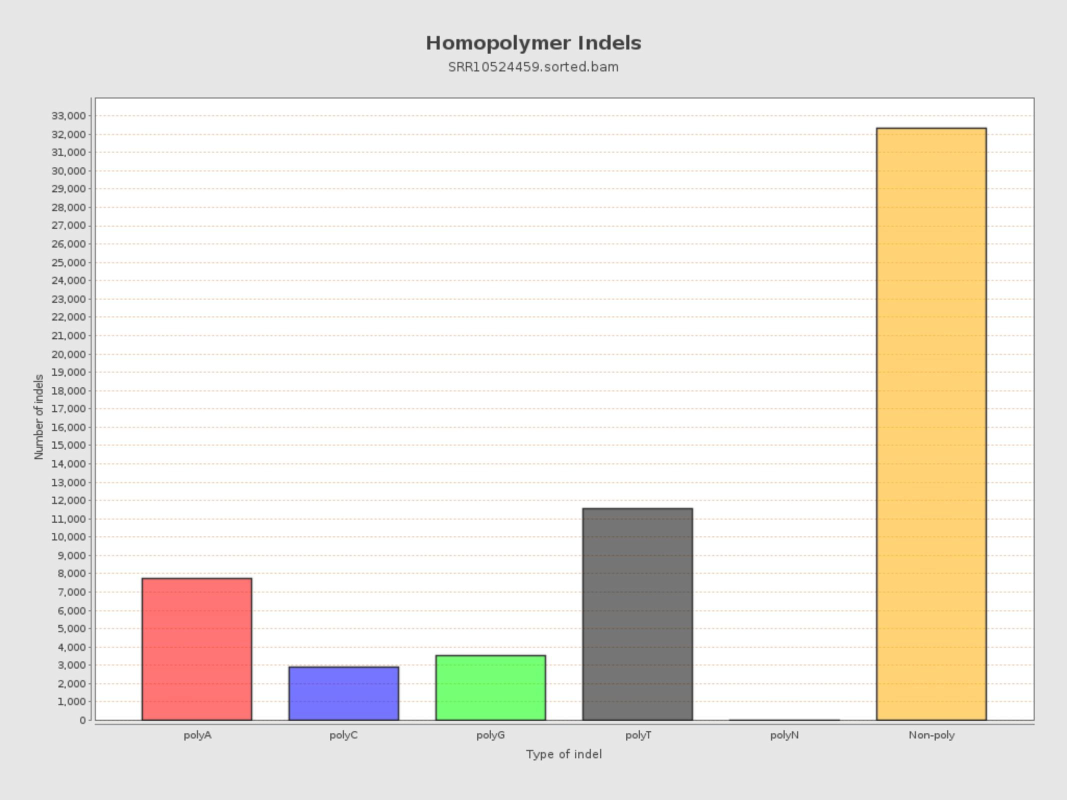
9. Results : Mapped Reads GC-content Distribution



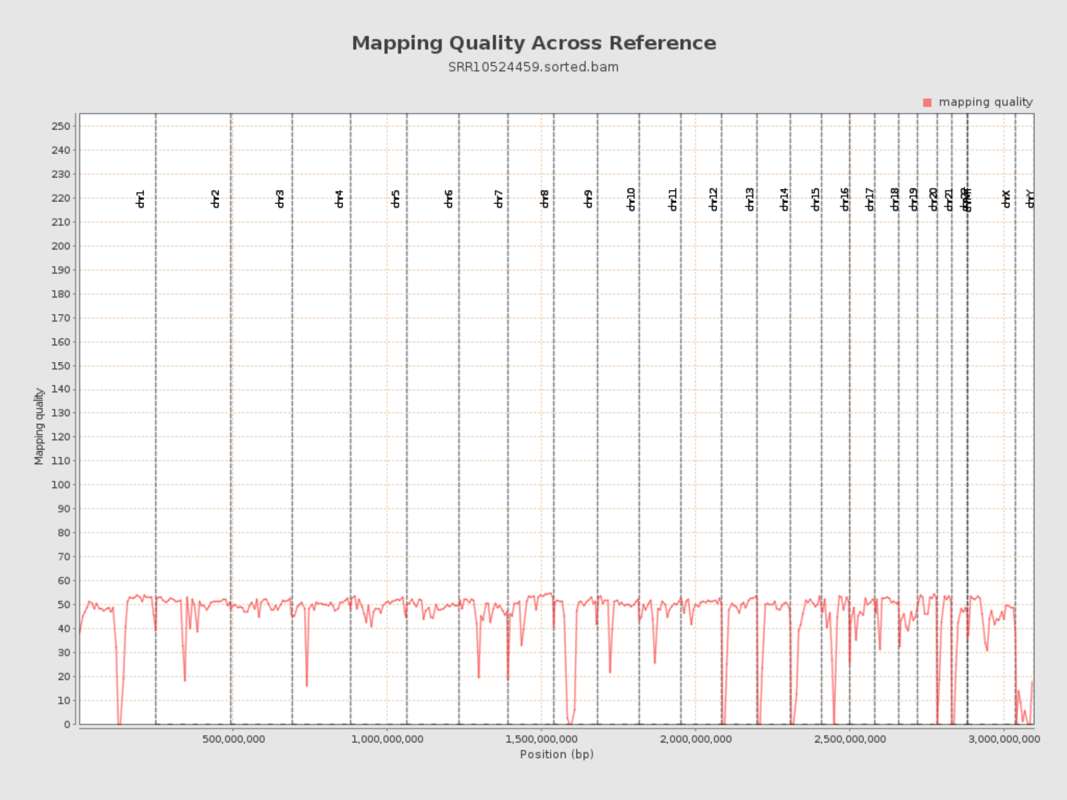
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram