Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:02:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525147.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_SRR10525147 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525147.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:02:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525147.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,806,937
Mapped reads	1,626,884 / 90.04%
Unmapped reads	180,053 / 9.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,953 / 2.16%
Read min/max/mean length	30 / 101 / 101.8
Duplicated reads (estimated)	55,655 / 3.08%
Duplication rate	2.02%
Clipped reads	1,661,354 / 91.94%

2.2. ACGT Content

Number/percentage of A's	33,401,578 / 26.77%
Number/percentage of C's	23,727,584 / 19.01%
Number/percentage of T's	39,141,976 / 31.37%
Number/percentage of G's	28,516,084 / 22.85%
Number/percentage of N's	4,934 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0403

Standard Deviation	0.4351

2.4. Mapping Quality

Mean Mapping Quality	46.17

2.5. Mismatches and indels

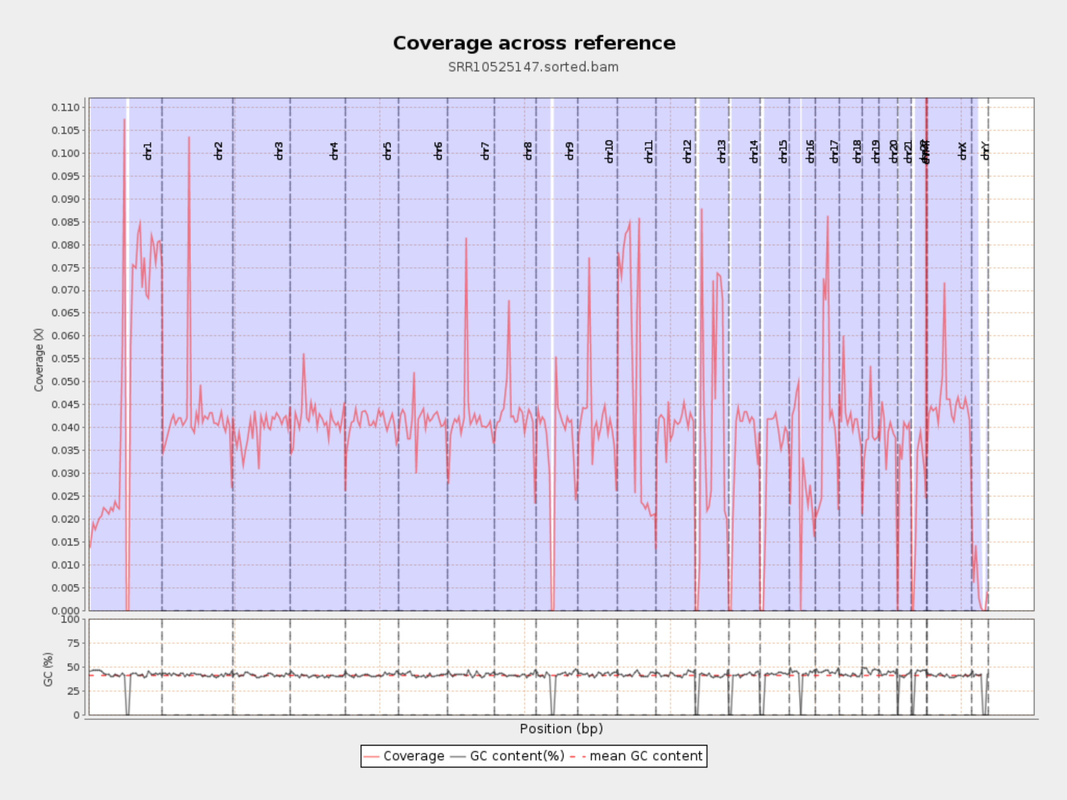
General error rate	0.78%
Mismatches	945,941
Insertions	12,182
Mapped reads with at least one insertion	0.74%
Deletions	28,300
Mapped reads with at least one deletion	1.72%
Homopolymer indels	42.34%

2.6. Chromosome stats

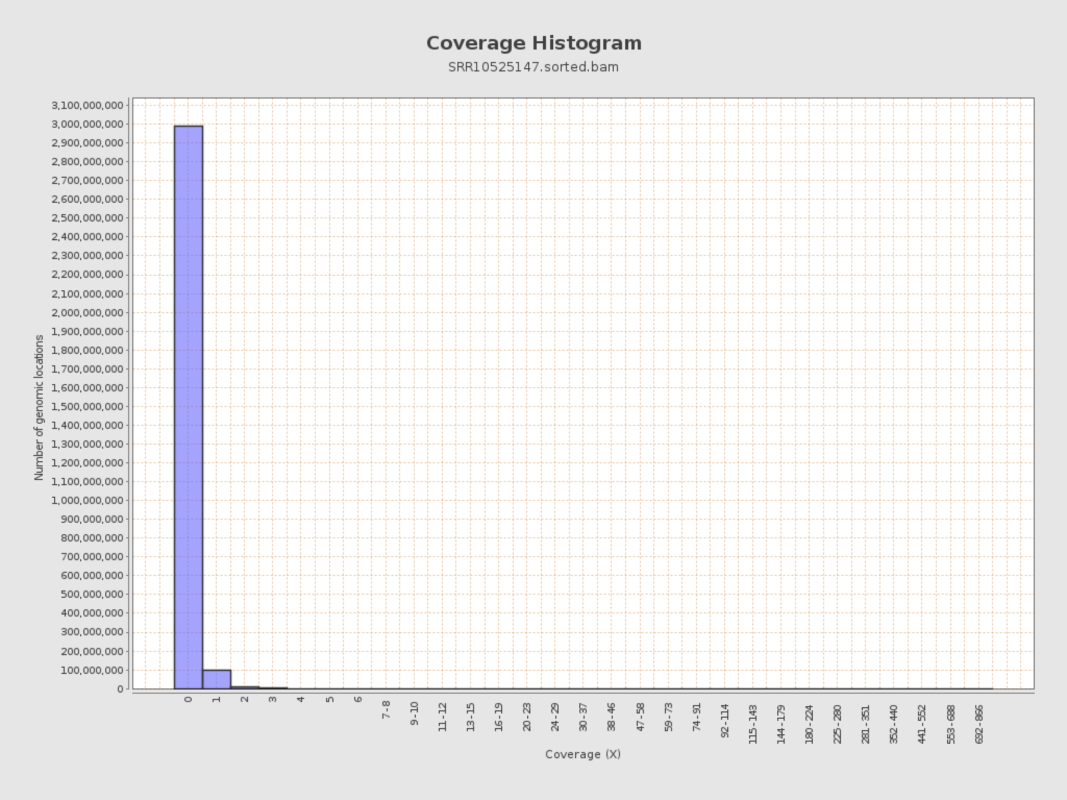
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11844874	0.0475	0.7524
chr2	243199373	10428370	0.0429	0.6164
chr3	198022430	7830292	0.0395	0.2243
chr4	191154276	8030262	0.042	0.2425
chr5	180915260	7422236	0.041	0.2295
chr6	171115067	7070632	0.0413	0.2666
chr7	159138663	6774050	0.0426	0.6401

chr8	146364022	6294478	0.043	0.5485
chr9	141213431	5057638	0.0358	0.3914
chr10	135534747	5698734	0.042	0.4718
chr11	135006516	6867865	0.0509	0.4826
chr12	133851895	5436346	0.0406	0.2273
chr13	115169878	4584009	0.0398	0.2241
chr14	107349540	3670269	0.0342	0.2457
chr15	102531392	3331474	0.0325	0.1988
chr16	90354753	2702347	0.0299	0.2204
chr17	81195210	3584327	0.0441	0.2812
chr18	78077248	3363676	0.0431	0.7037
chr19	59128983	2268190	0.0384	0.5702
chr20	63025520	2406100	0.0382	0.2295
chr21	48129895	1615490	0.0336	0.222
chr22	51304566	1222890	0.0238	0.1691
chrMT	16571	6616	0.3993	1.0013
chrX	155270560	7047556	0.0454	0.3321
chrY	59373566	282124	0.0048	0.1191

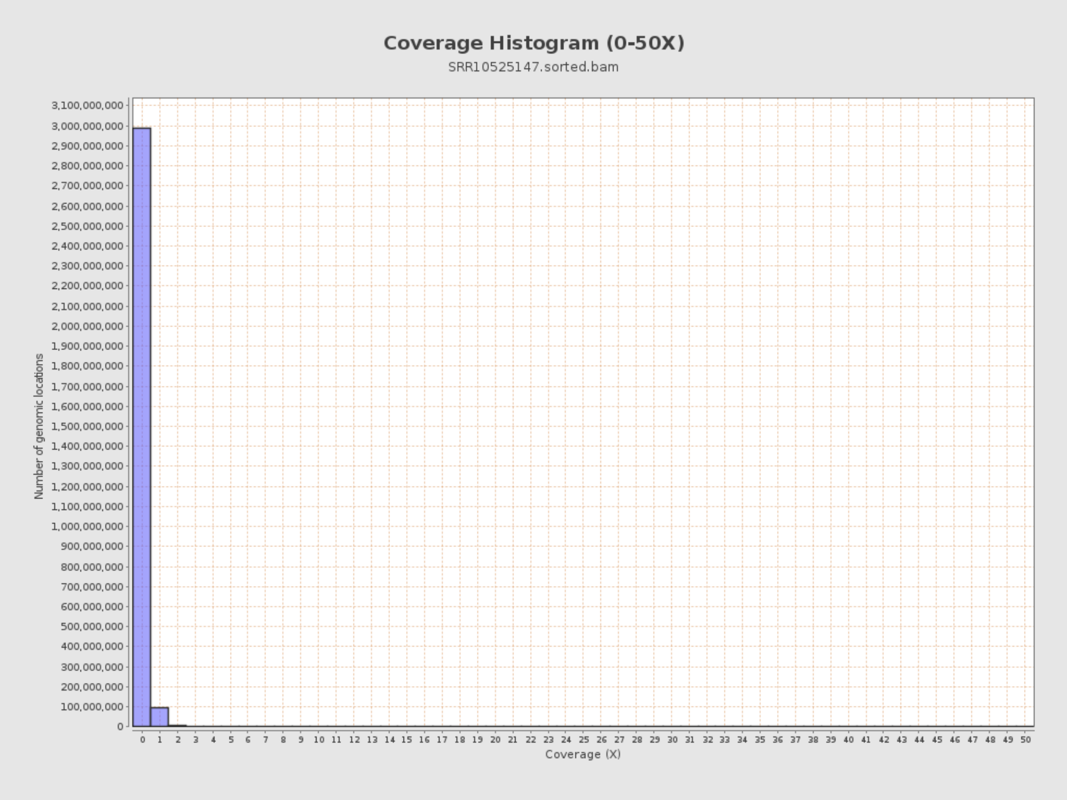
3. Results : Coverage across reference



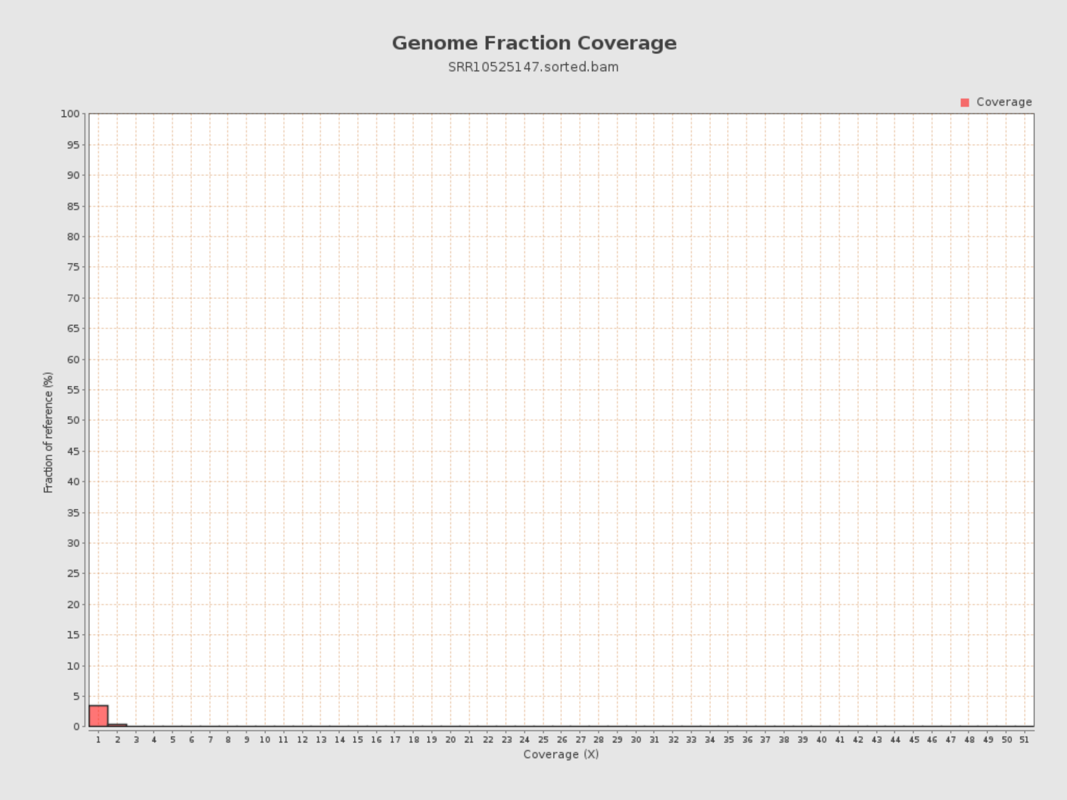
4. Results : Coverage Histogram



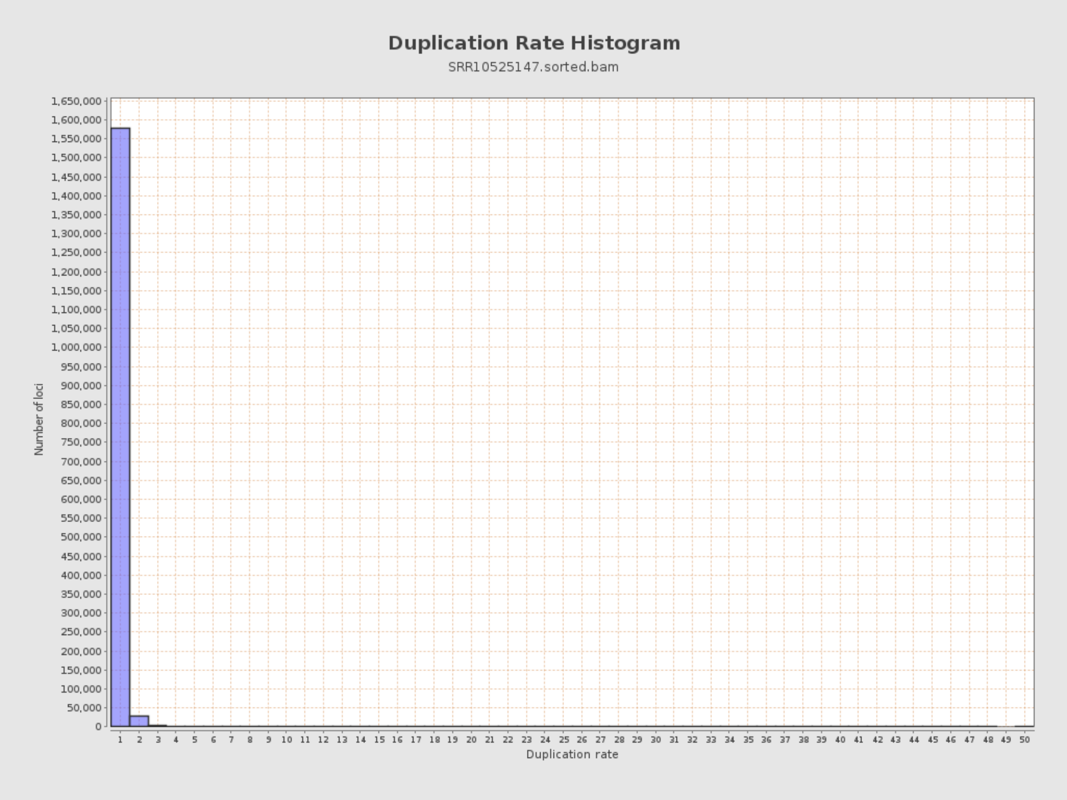
5. Results : Coverage Histogram (0-50X)



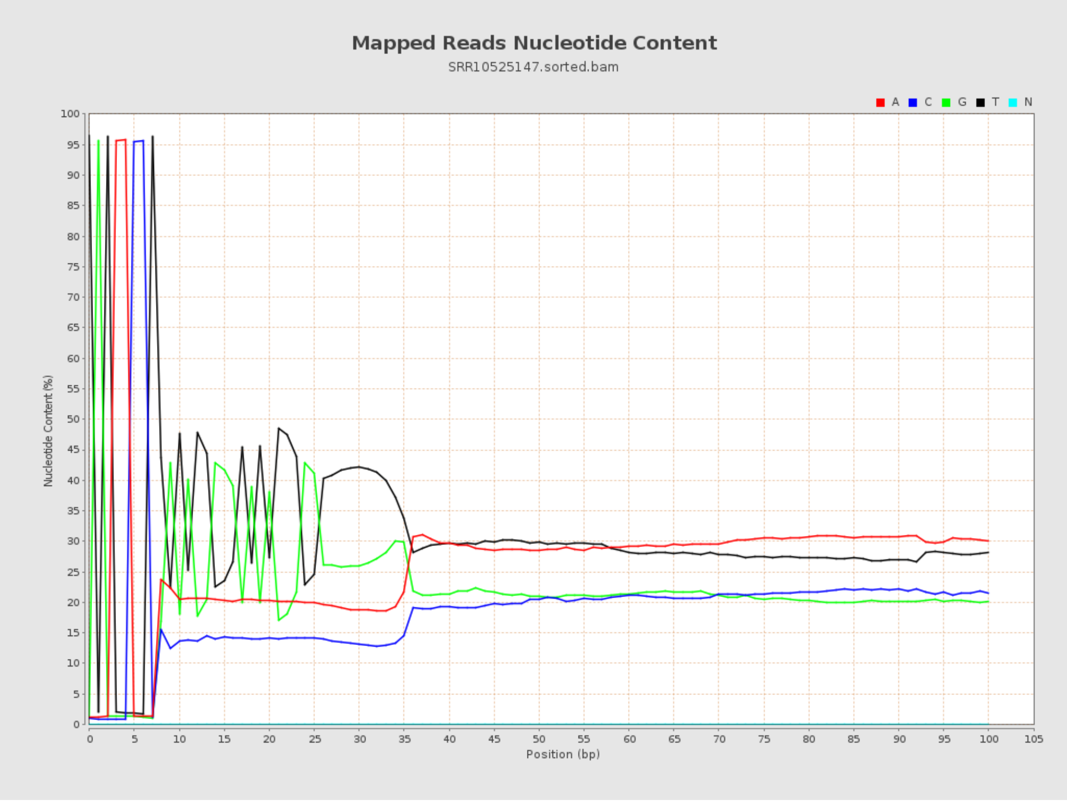
6. Results : Genome Fraction Coverage



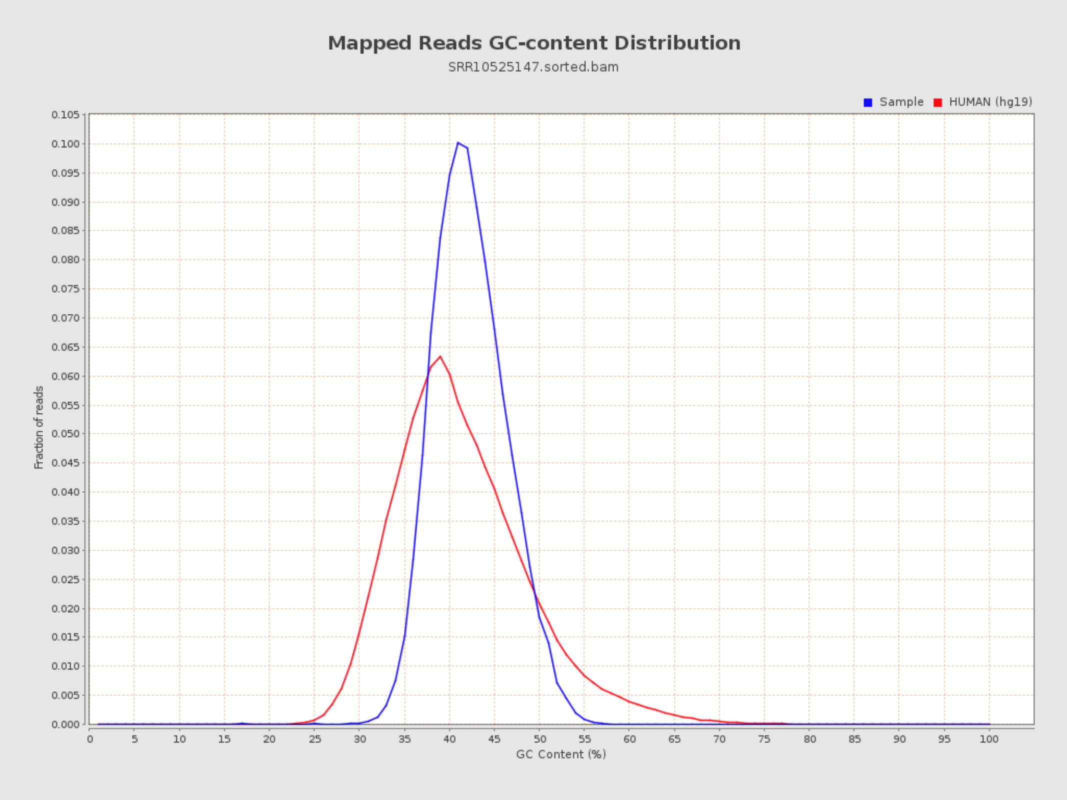
7. Results : Duplication Rate Histogram



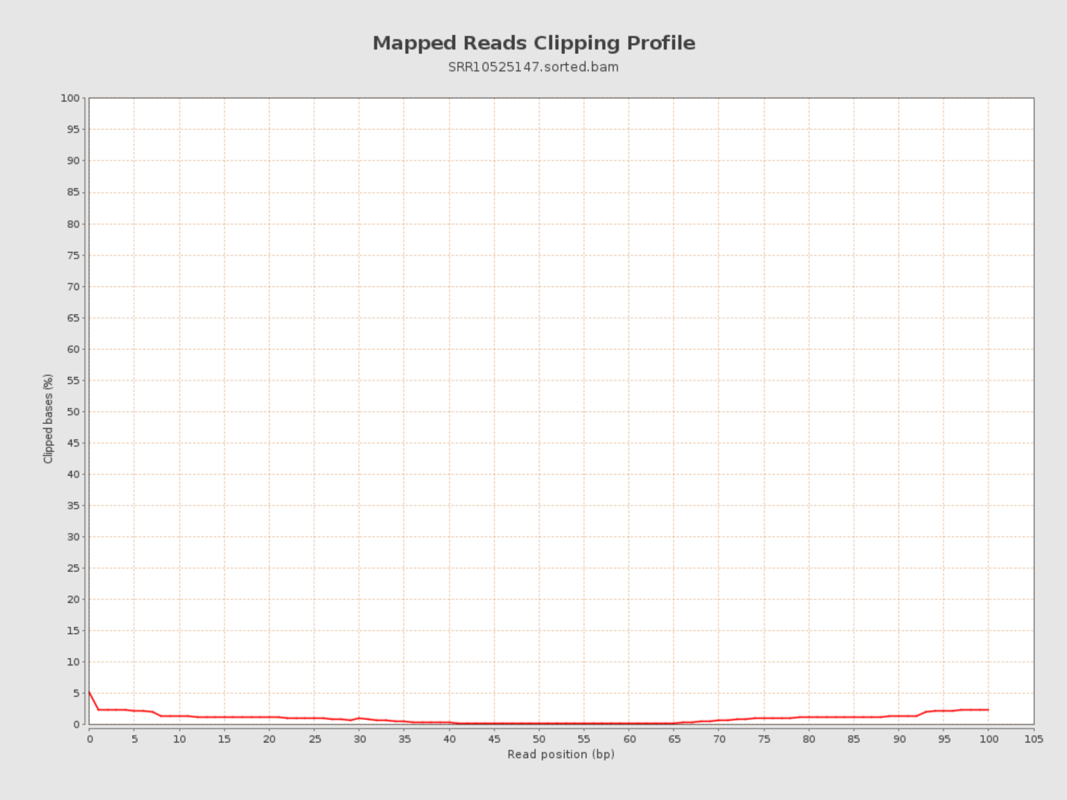
8. Results : Mapped Reads Nucleotide Content



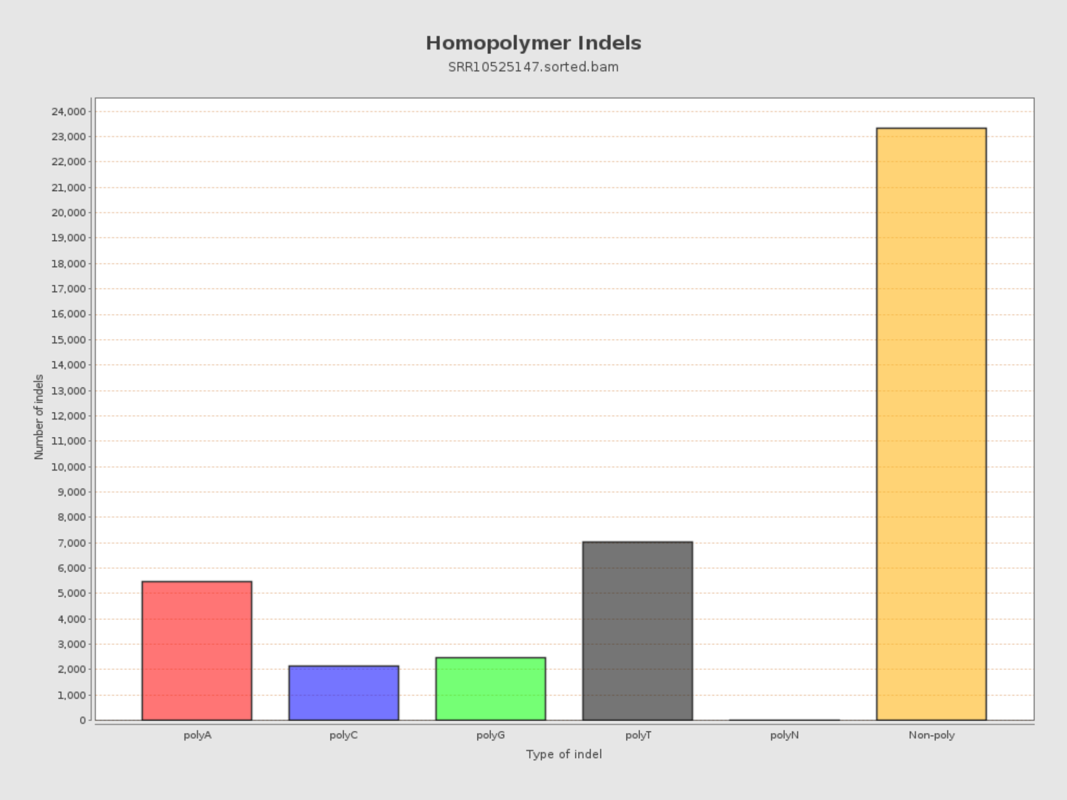
9. Results : Mapped Reads GC-content Distribution



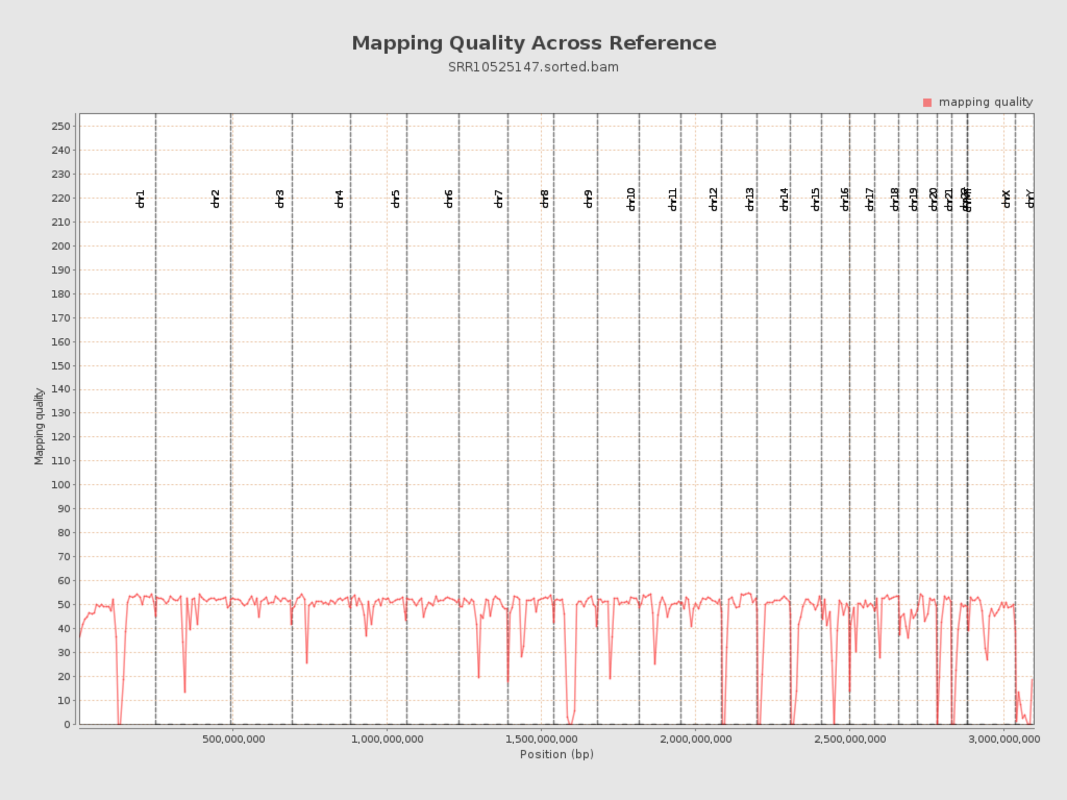
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram