Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:15:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525130.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_SRR10525130 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525130.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:15:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525130.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,829,076
Mapped reads	1,689,337 / 92.36%
Unmapped reads	139,739 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	44,725 / 2.45%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	58,218 / 3.18%
Duplication rate	2.02%
Clipped reads	1,732,935 / 94.74%

2.2. ACGT Content

Number/percentage of A's	35,108,862 / 26.91%
Number/percentage of C's	25,125,950 / 19.26%
Number/percentage of T's	39,260,391 / 30.09%
Number/percentage of G's	30,984,941 / 23.75%
Number/percentage of N's	5,004 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0422

Standard Deviation	0.4599

2.4. Mapping Quality

Mean Mapping Quality	46.13

2.5. Mismatches and indels

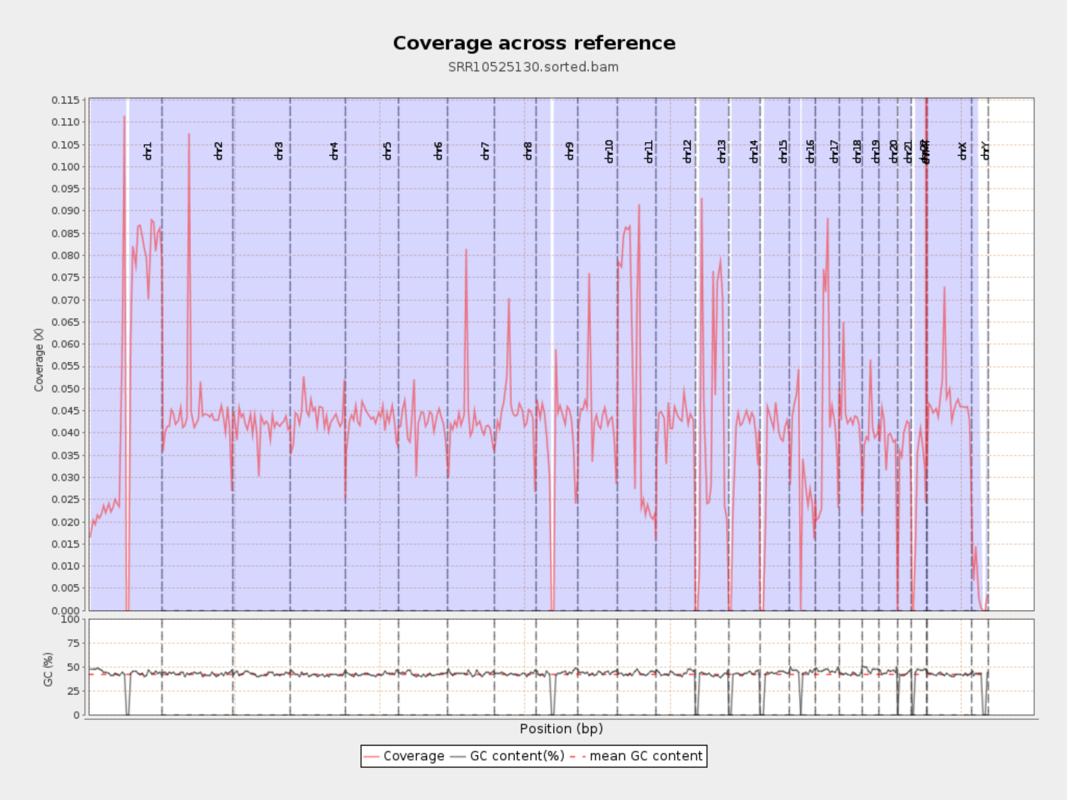
General error rate	0.73%
Mismatches	925,799
Insertions	10,867
Mapped reads with at least one insertion	0.63%
Deletions	30,066
Mapped reads with at least one deletion	1.75%
Homopolymer indels	42.79%

2.6. Chromosome stats

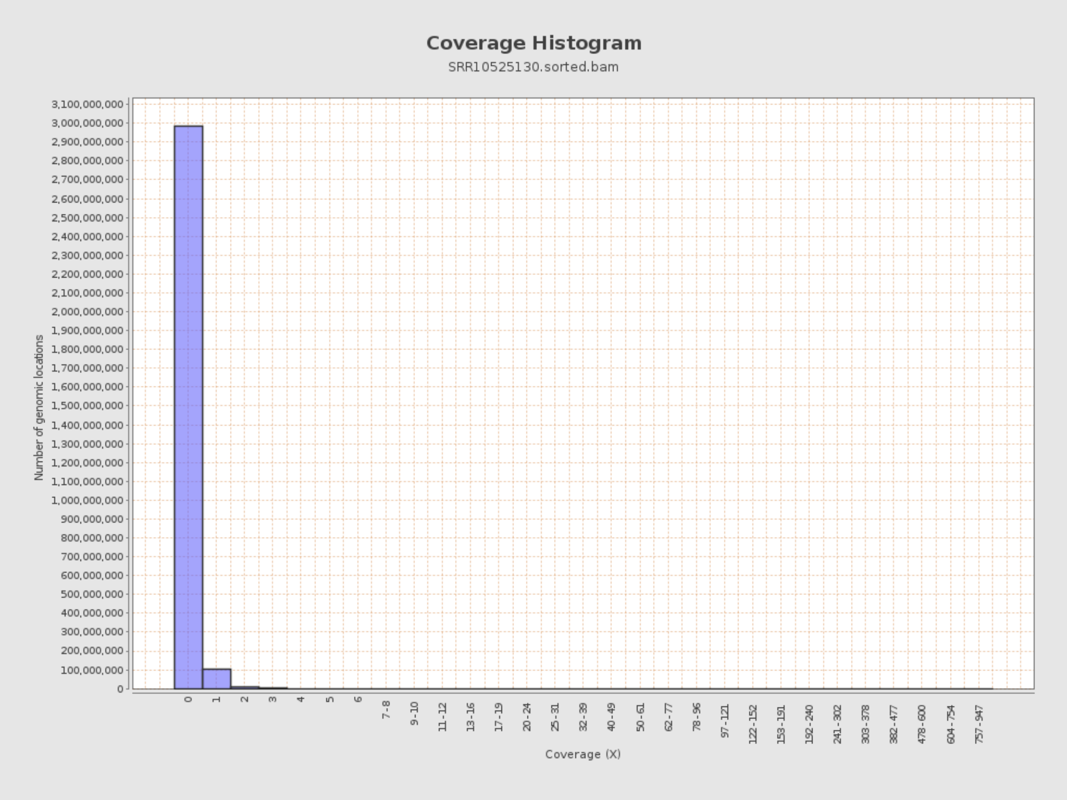
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12657990	0.0508	0.8374
chr2	243199373	10918372	0.0449	0.6247
chr3	198022430	8288223	0.0419	0.2286
chr4	191154276	8385581	0.0439	0.2421
chr5	180915260	7799443	0.0431	0.2354
chr6	171115067	7268471	0.0425	0.2644
chr7	159138663	6894648	0.0433	0.6494

chr8	146364022	6569230	0.0449	0.6017
chr9	141213431	5356464	0.0379	0.4217
chr10	135534747	5996246	0.0442	0.4467
chr11	135006516	7157505	0.053	0.5272
chr12	133851895	5715813	0.0427	0.2321
chr13	115169878	4816636	0.0418	0.2287
chr14	107349540	3787144	0.0353	0.2597
chr15	102531392	3517992	0.0343	0.2052
chr16	90354753	2833144	0.0314	0.2297
chr17	81195210	3690789	0.0455	0.2957
chr18	78077248	3511120	0.045	0.7927
chr19	59128983	2410335	0.0408	0.5693
chr20	63025520	2417428	0.0384	0.2268
chr21	48129895	1650953	0.0343	0.2268
chr22	51304566	1284716	0.025	0.1742
chrMT	16571	51766	3.1239	3.205
chrX	155270560	7270737	0.0468	0.3446
chrY	59373566	286380	0.0048	0.1139

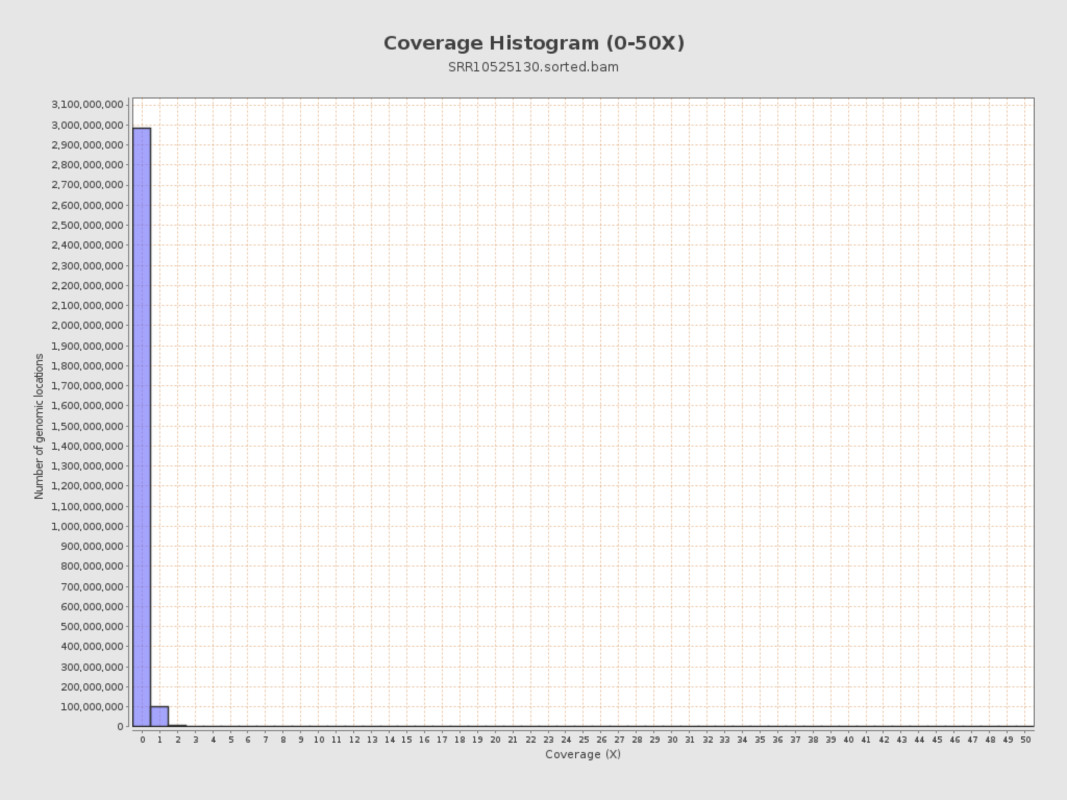
3. Results : Coverage across reference



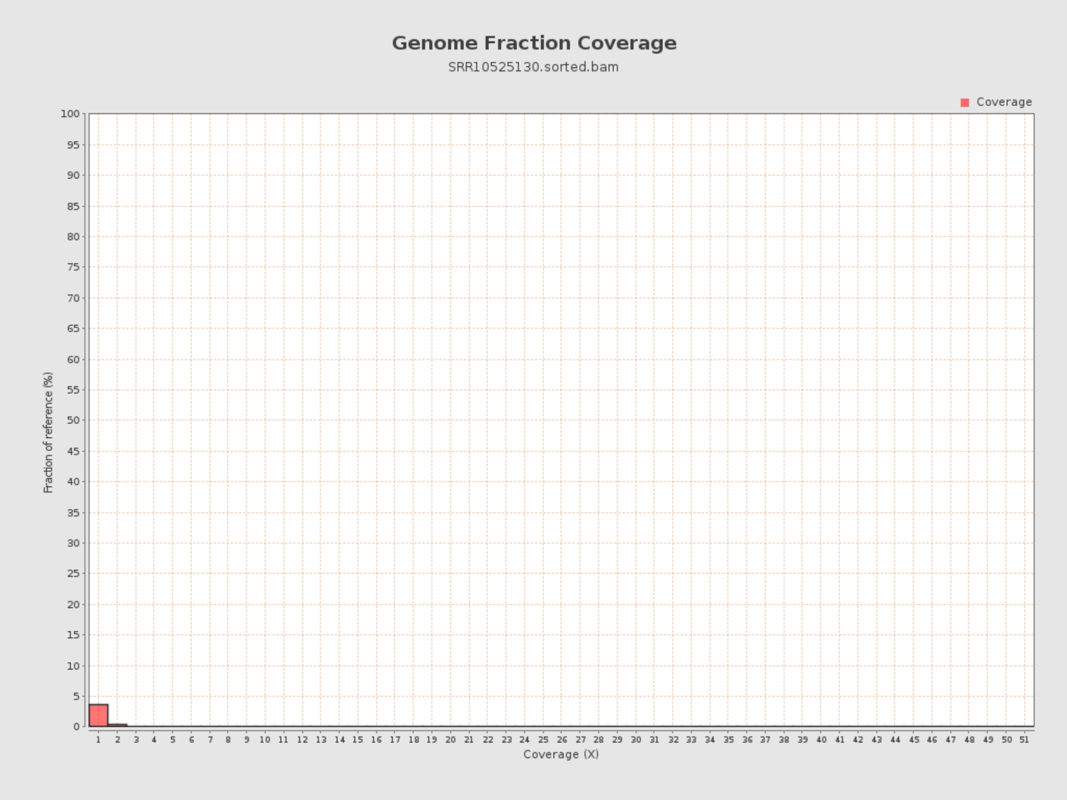
4. Results : Coverage Histogram



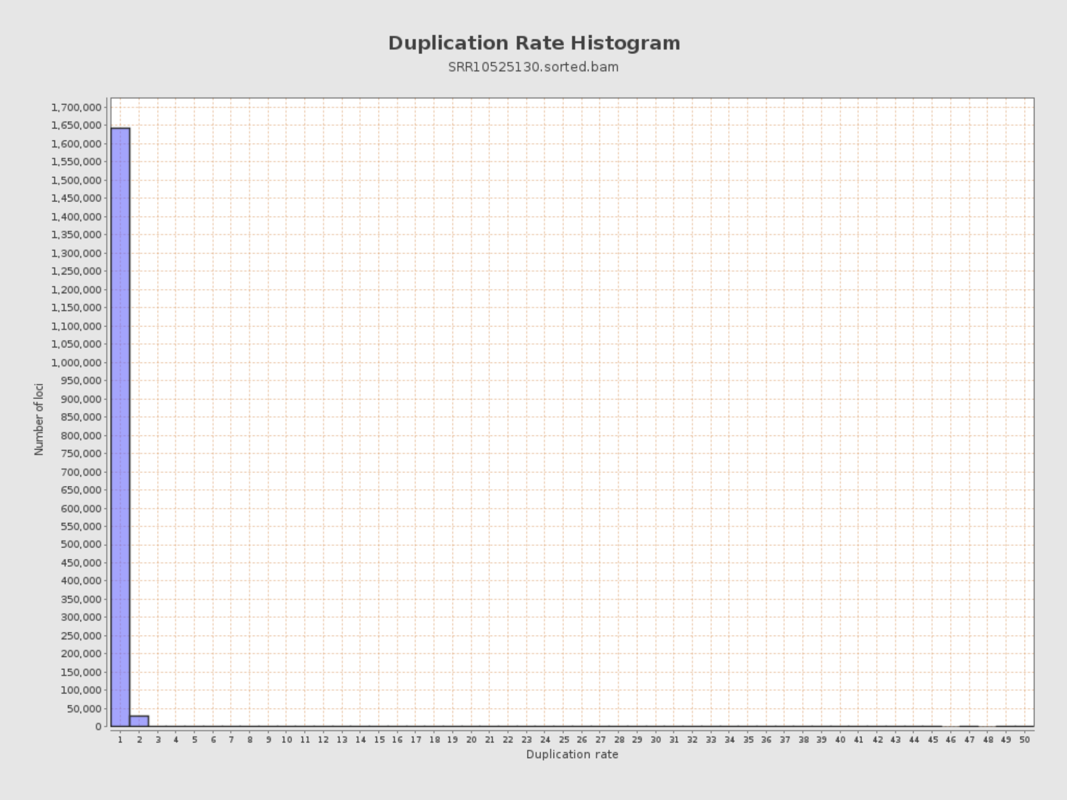
5. Results : Coverage Histogram (0-50X)



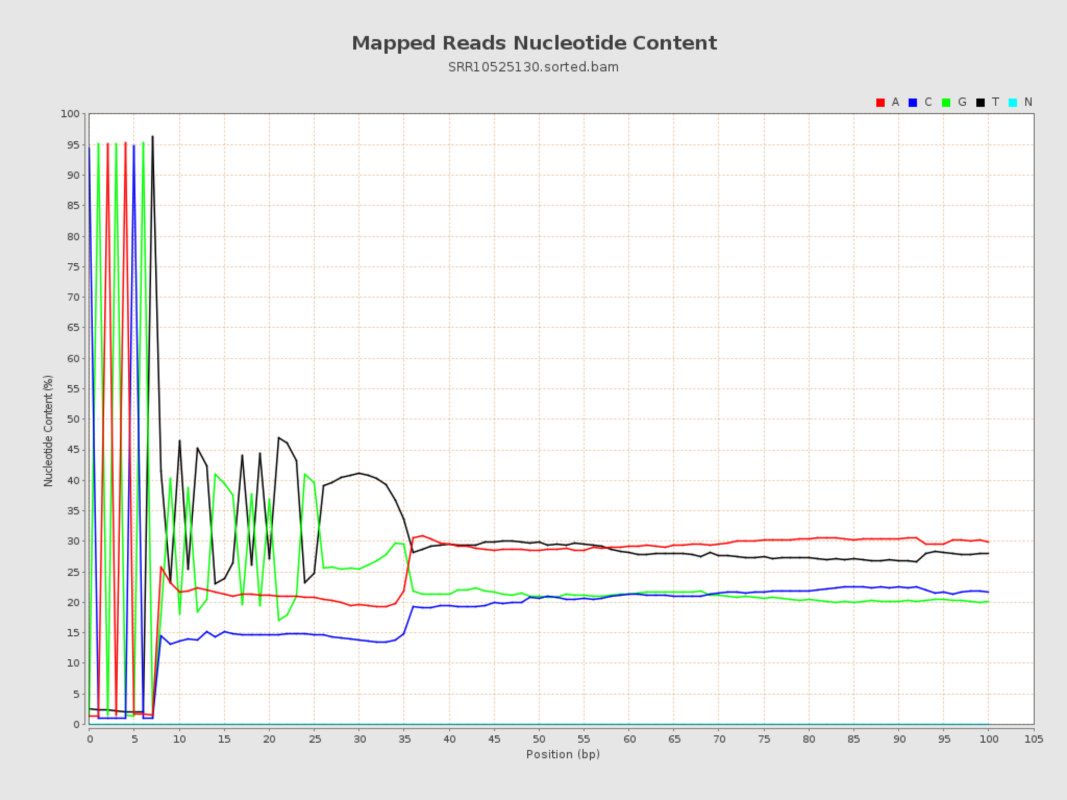
6. Results : Genome Fraction Coverage



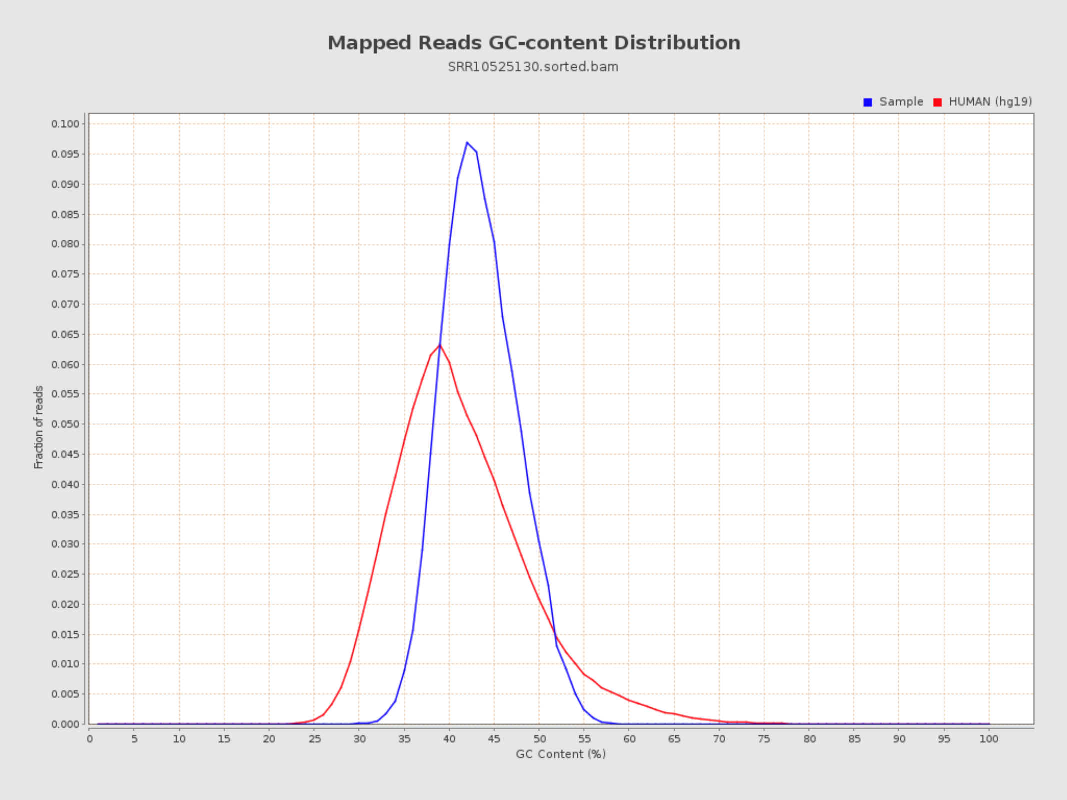
7. Results : Duplication Rate Histogram



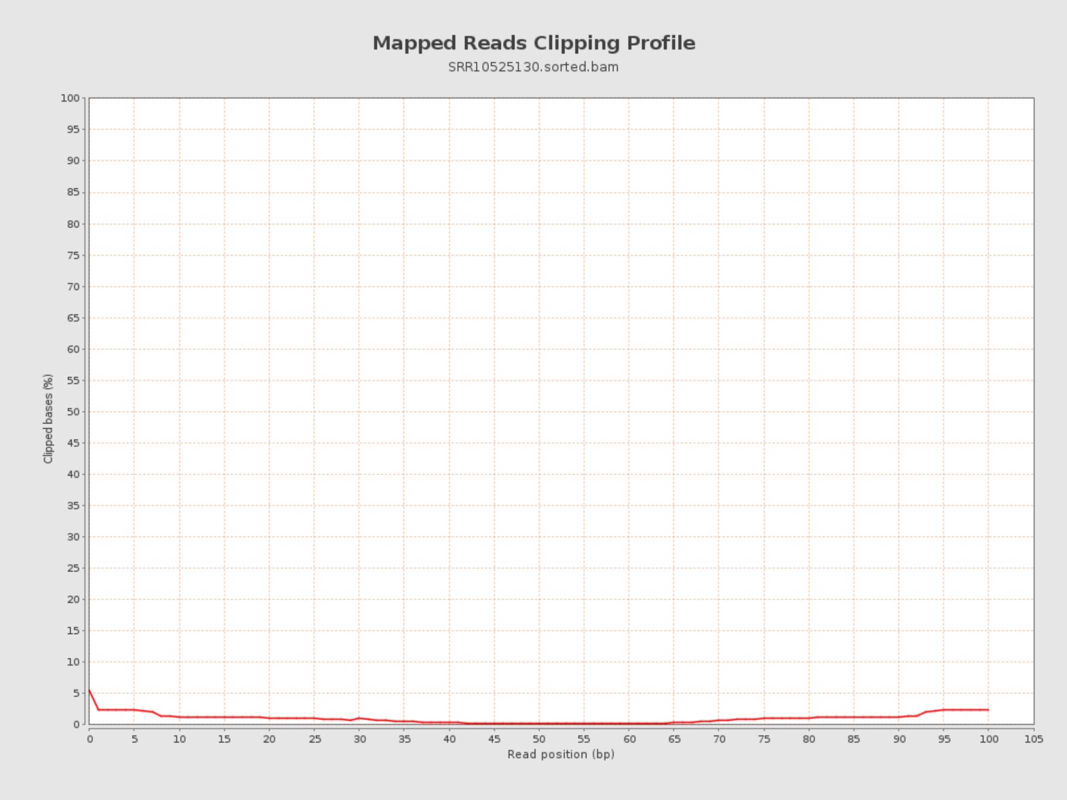
8. Results : Mapped Reads Nucleotide Content



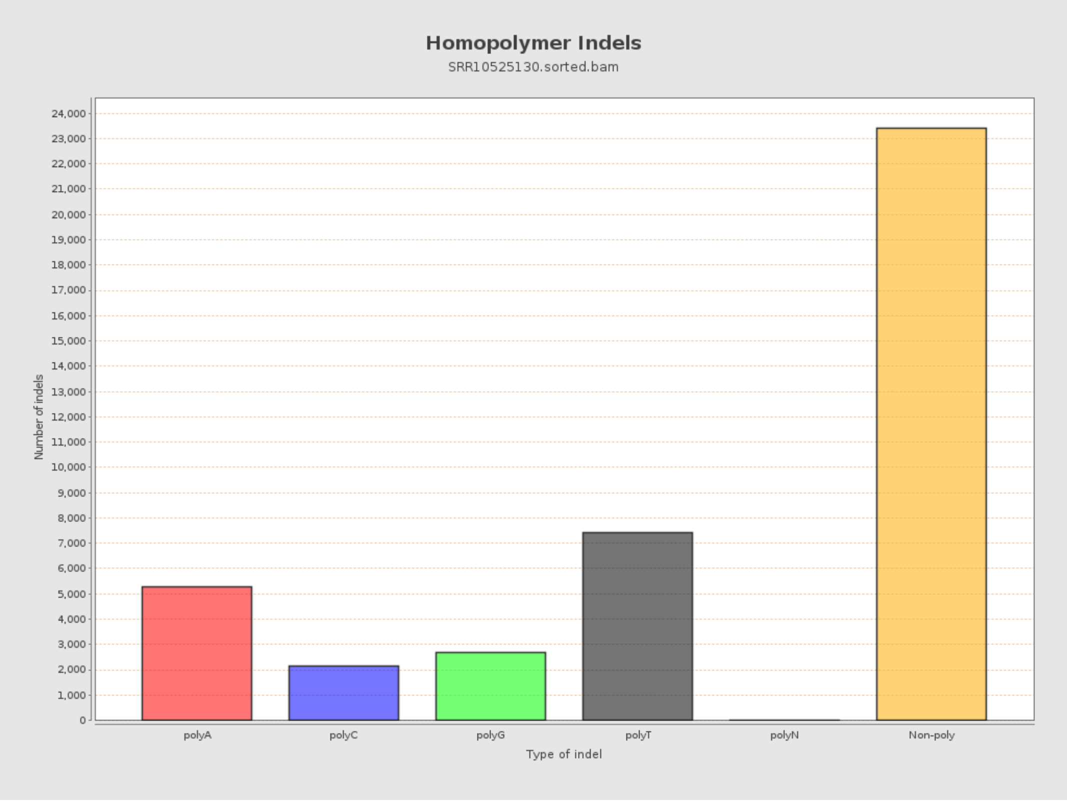
9. Results : Mapped Reads GC-content Distribution



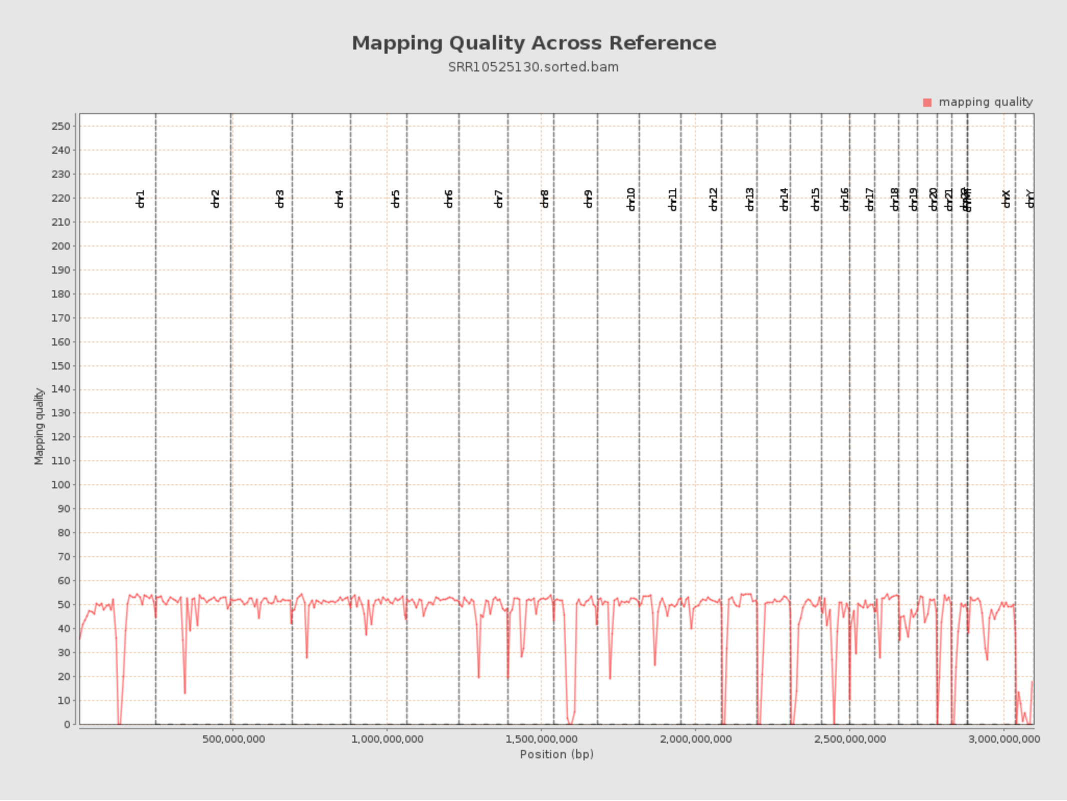
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram