Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:24:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525133.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_SRR10525133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:24:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,778,592
Mapped reads	1,561,456 / 87.79%
Unmapped reads	217,136 / 12.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	43,204 / 2.43%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	49,733 / 2.8%
Duplication rate	1.9%
Clipped reads	1,601,375 / 90.04%

2.2. ACGT Content

Number/percentage of A's	32,084,161 / 26.85%
Number/percentage of C's	22,786,774 / 19.07%
Number/percentage of T's	37,481,782 / 31.36%
Number/percentage of G's	27,154,114 / 22.72%
Number/percentage of N's	4,371 / 0%
GC Percentage	41.79%

2.3. Coverage

Mean	0.0386

Standard Deviation	0.3935

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

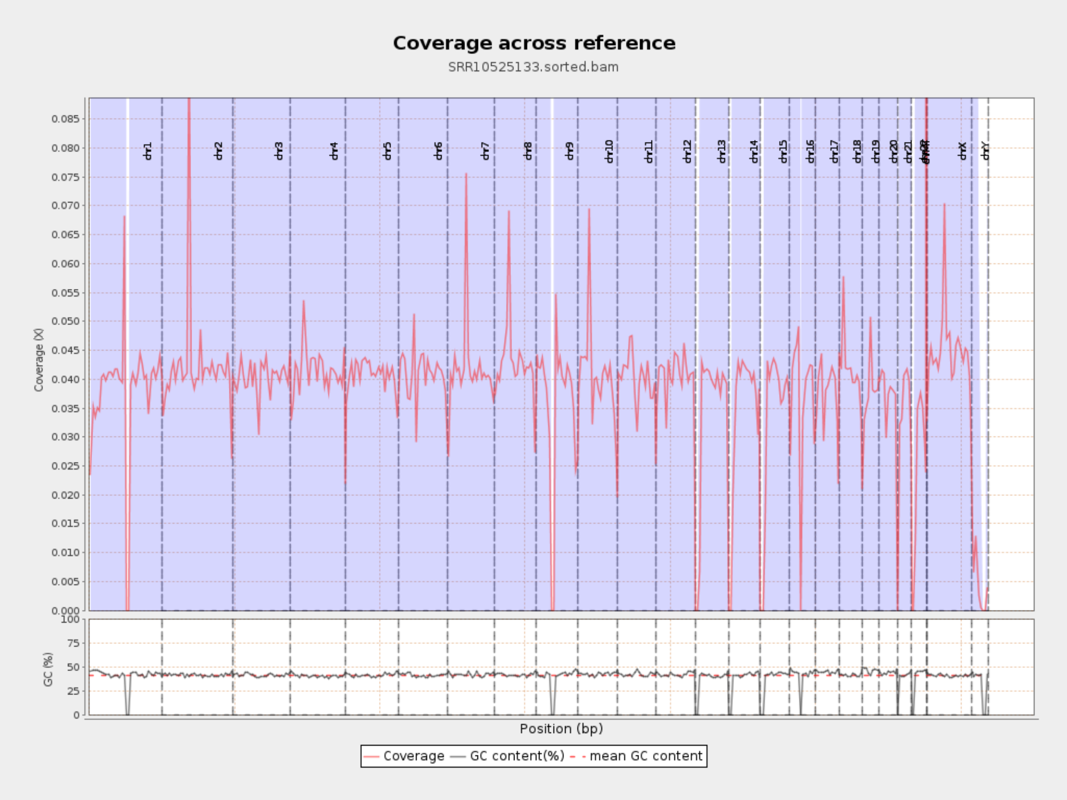
General error rate	0.77%
Mismatches	904,202
Insertions	10,967
Mapped reads with at least one insertion	0.69%
Deletions	28,699
Mapped reads with at least one deletion	1.81%
Homopolymer indels	41.78%

2.6. Chromosome stats

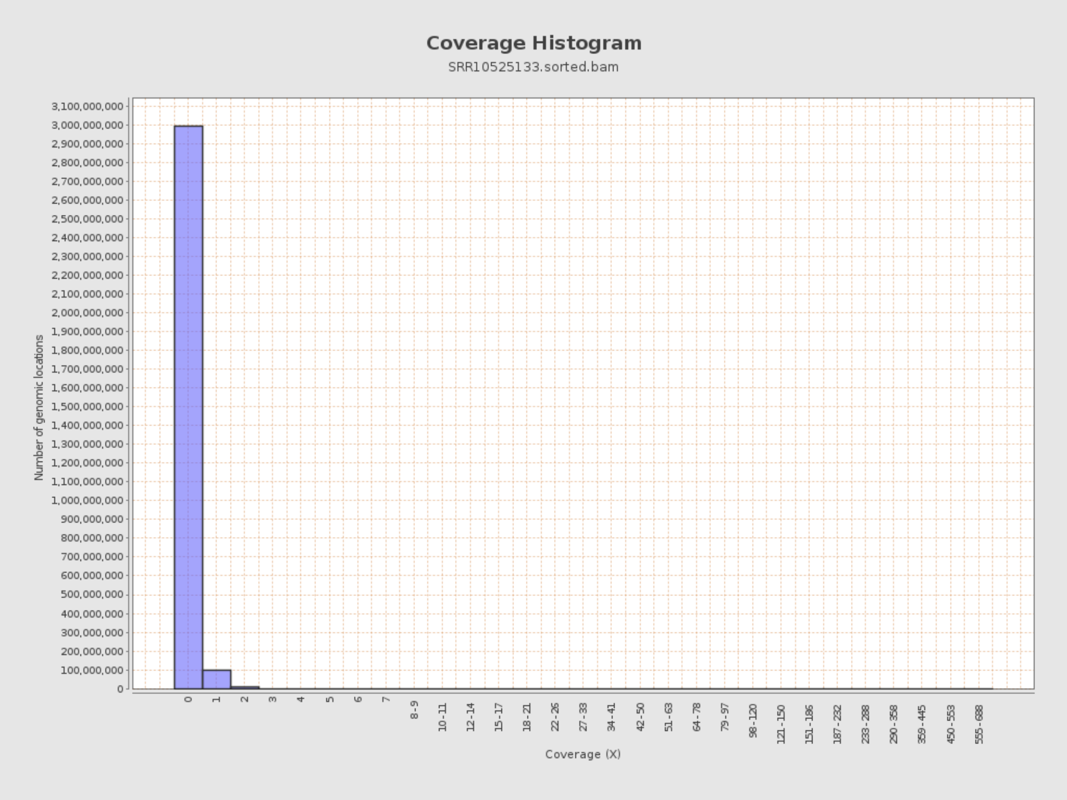
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9416890	0.0378	0.5916
chr2	243199373	10366531	0.0426	0.5987
chr3	198022430	7981724	0.0403	0.2208
chr4	191154276	7924839	0.0415	0.2392
chr5	180915260	7384142	0.0408	0.2269
chr6	171115067	6996553	0.0409	0.2609
chr7	159138663	6703233	0.0421	0.5873

chr8	146364022	6297737	0.043	0.5419
chr9	141213431	5015287	0.0355	0.396
chr10	135534747	5573477	0.0411	0.3939
chr11	135006516	5395097	0.04	0.3706
chr12	133851895	5433782	0.0406	0.2248
chr13	115169878	3837112	0.0333	0.1997
chr14	107349540	3603357	0.0336	0.2448
chr15	102531392	3360936	0.0328	0.1996
chr16	90354753	3314482	0.0367	0.2433
chr17	81195210	3019031	0.0372	0.2656
chr18	78077248	3294838	0.0422	0.6705
chr19	59128983	2231750	0.0377	0.4681
chr20	63025520	2326442	0.0369	0.2173
chr21	48129895	1589080	0.033	0.2174
chr22	51304566	1200279	0.0234	0.1664
chrMT	16571	13046	0.7873	1.0984
chrX	155270560	7008198	0.0451	0.3133
chrY	59373566	272928	0.0046	0.1092

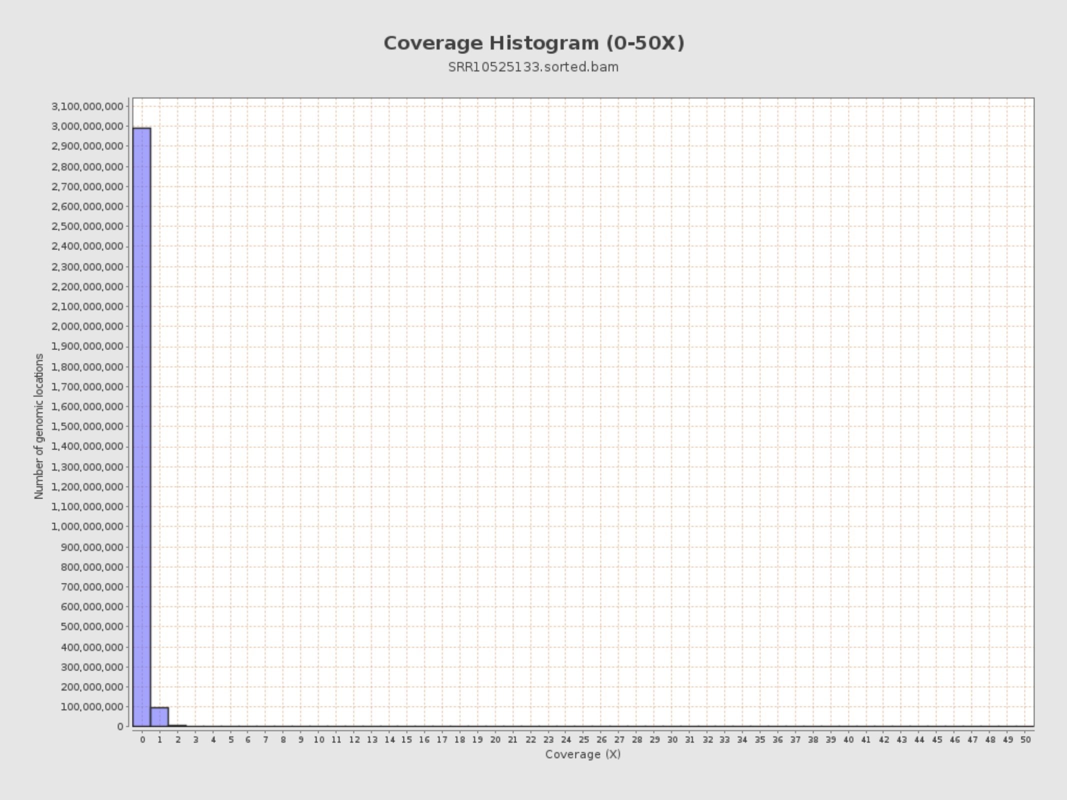
3. Results : Coverage across reference



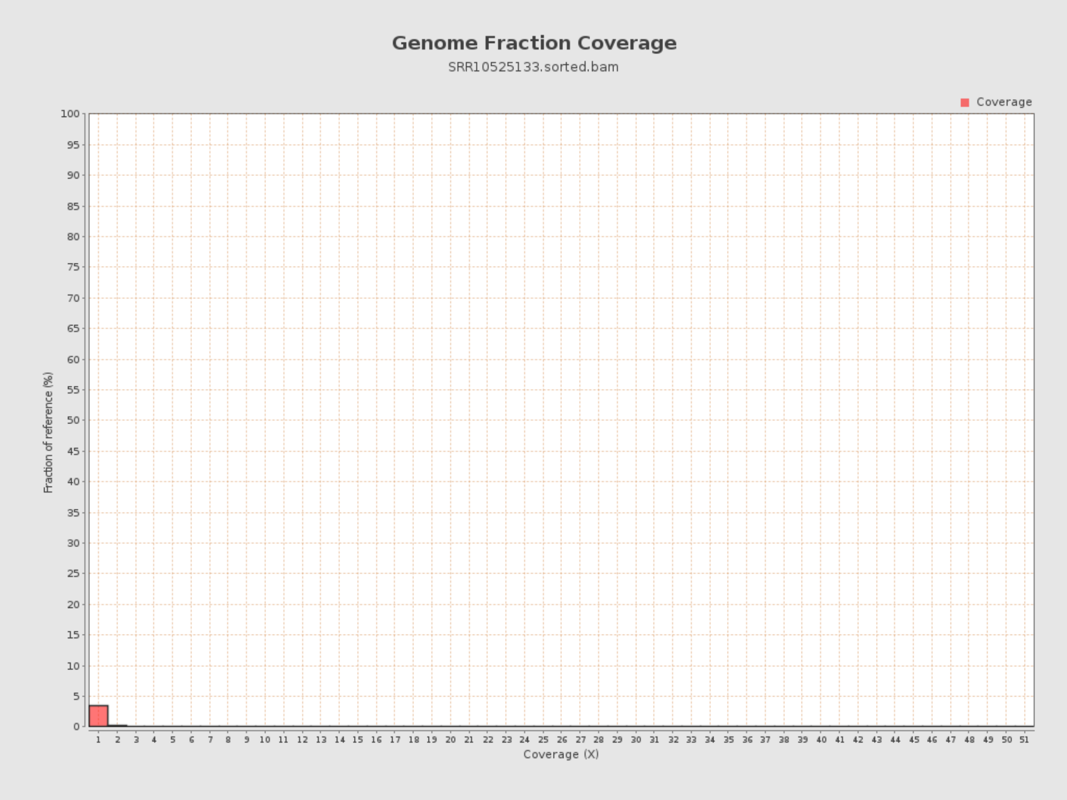
4. Results : Coverage Histogram



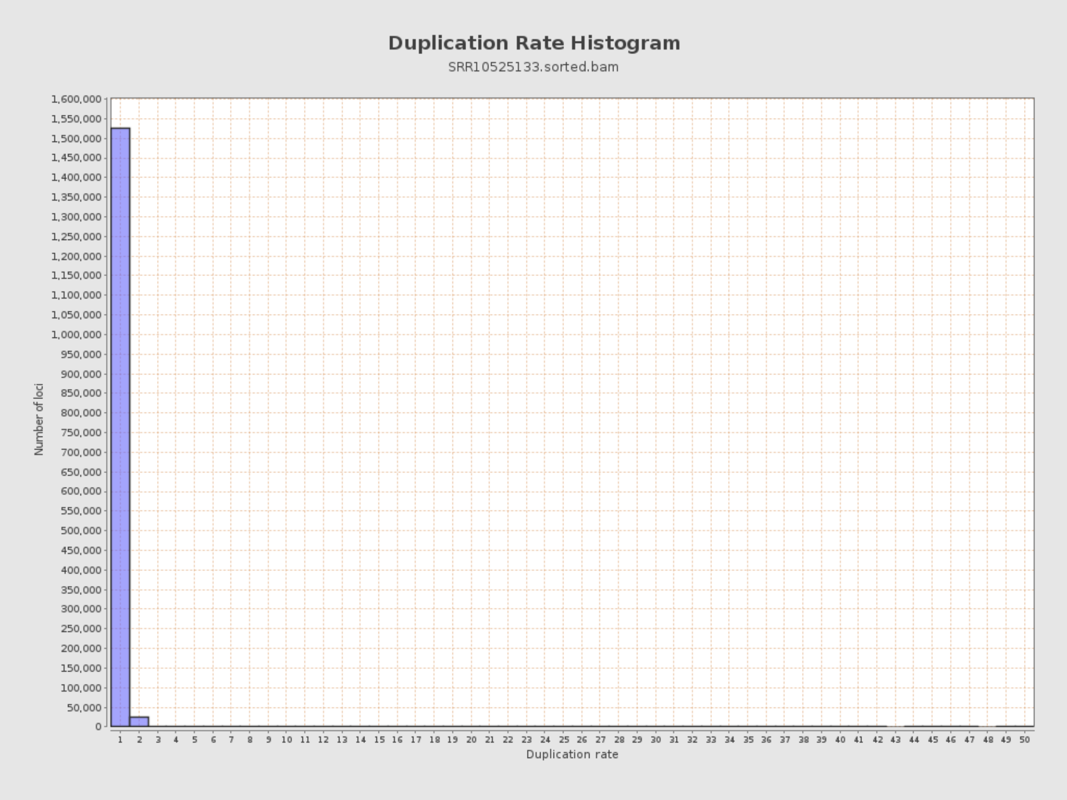
5. Results : Coverage Histogram (0-50X)



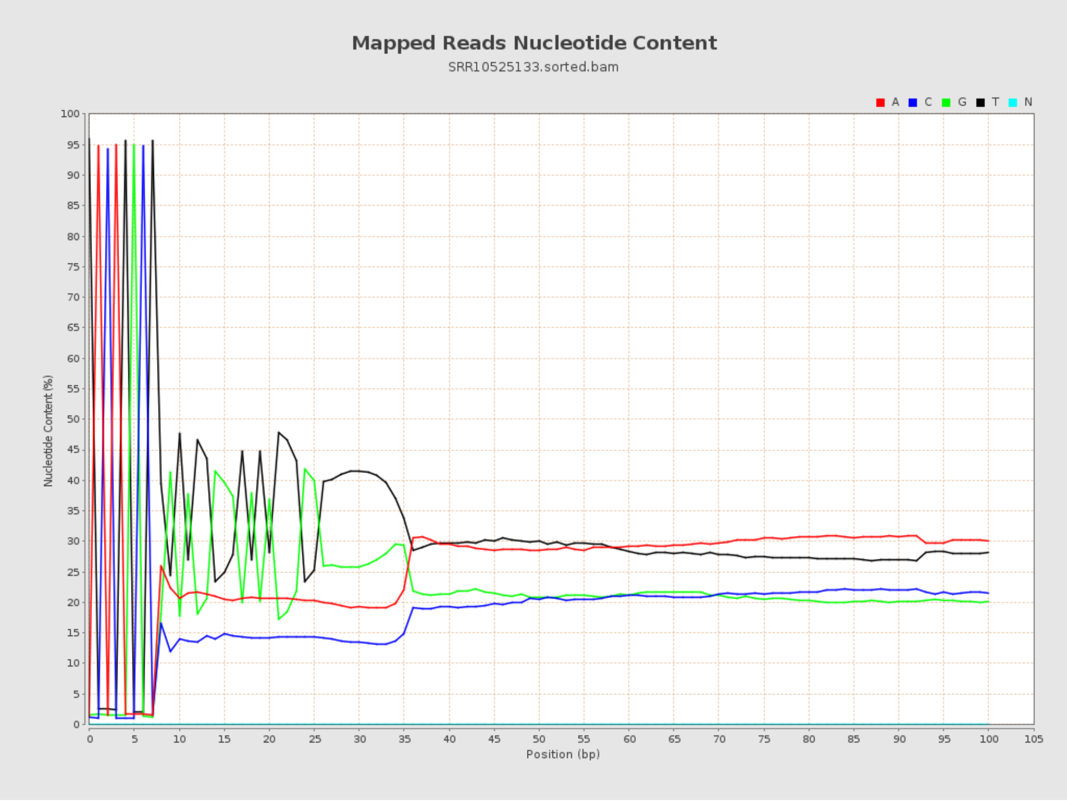
6. Results : Genome Fraction Coverage



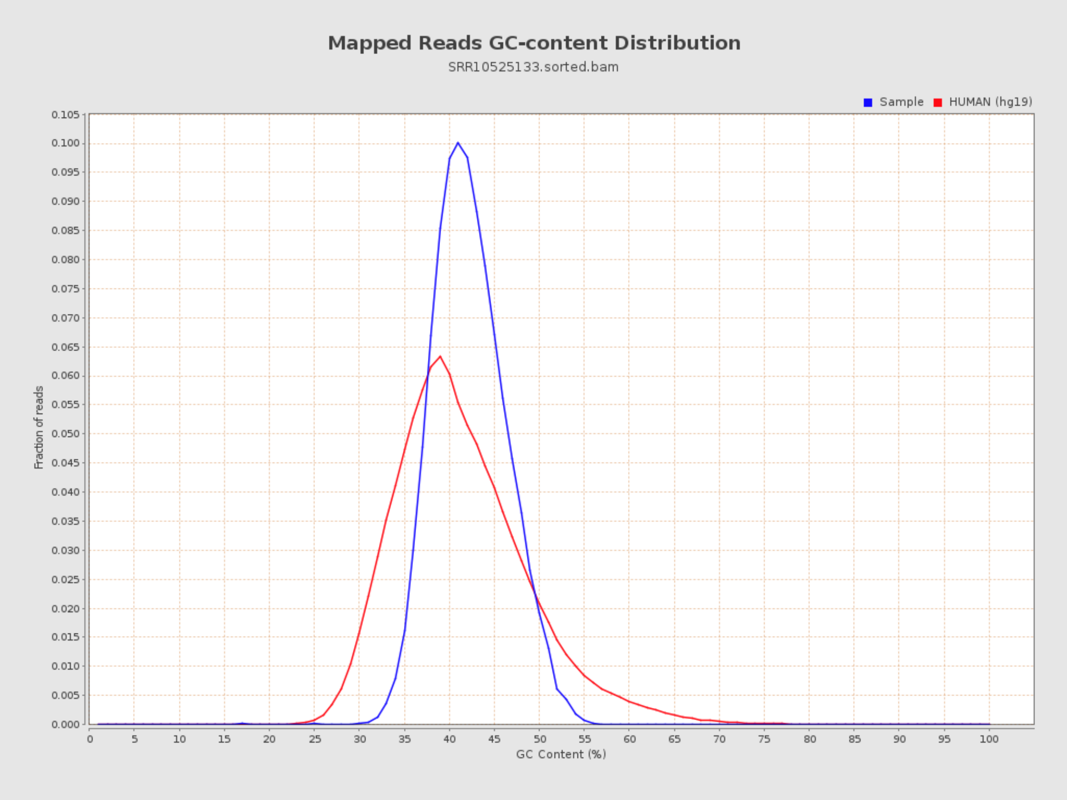
7. Results : Duplication Rate Histogram



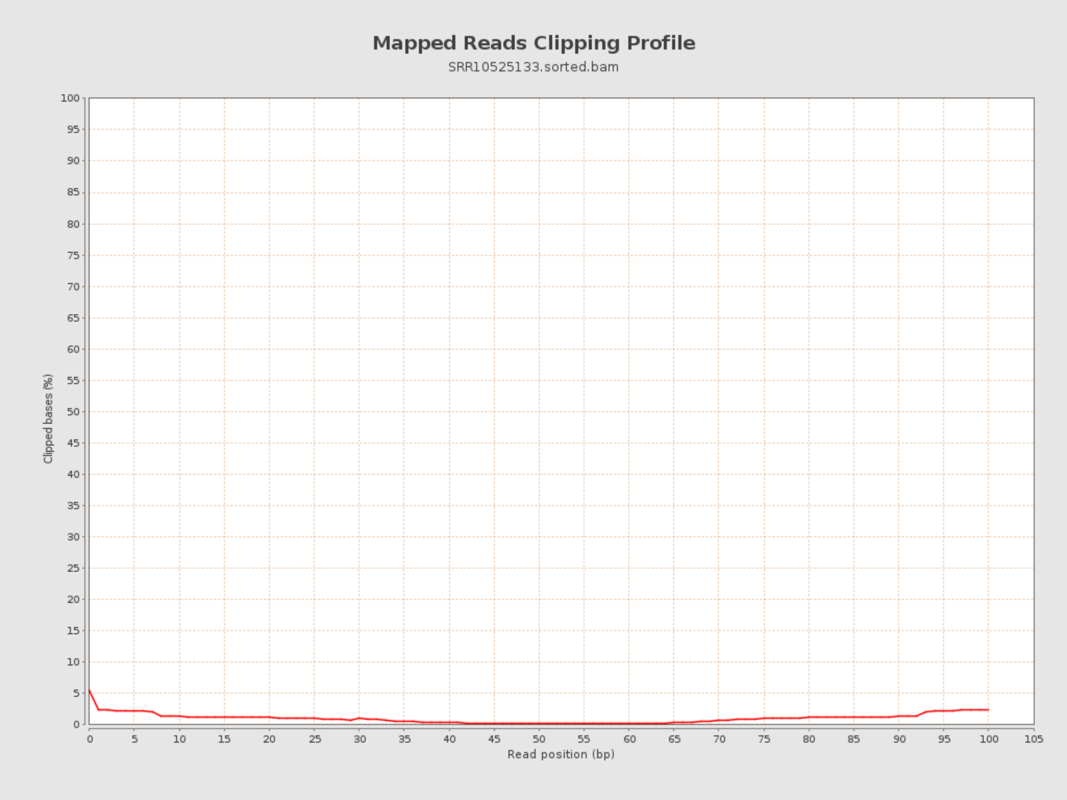
8. Results : Mapped Reads Nucleotide Content



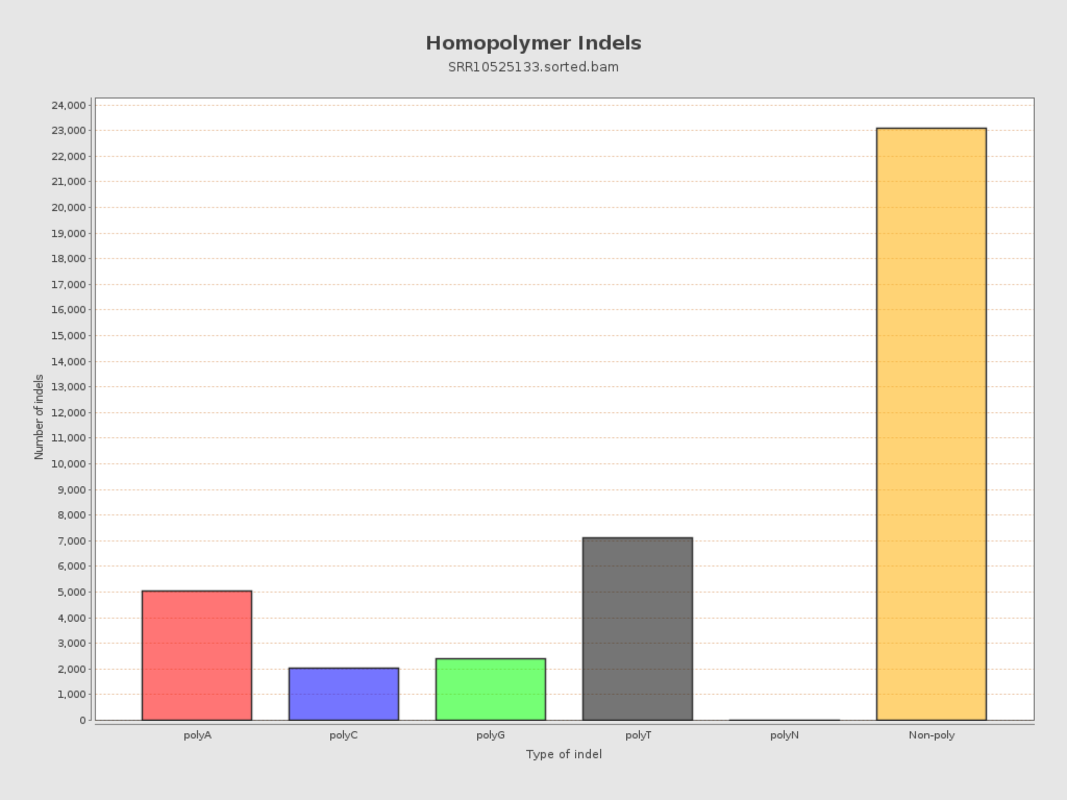
9. Results : Mapped Reads GC-content Distribution



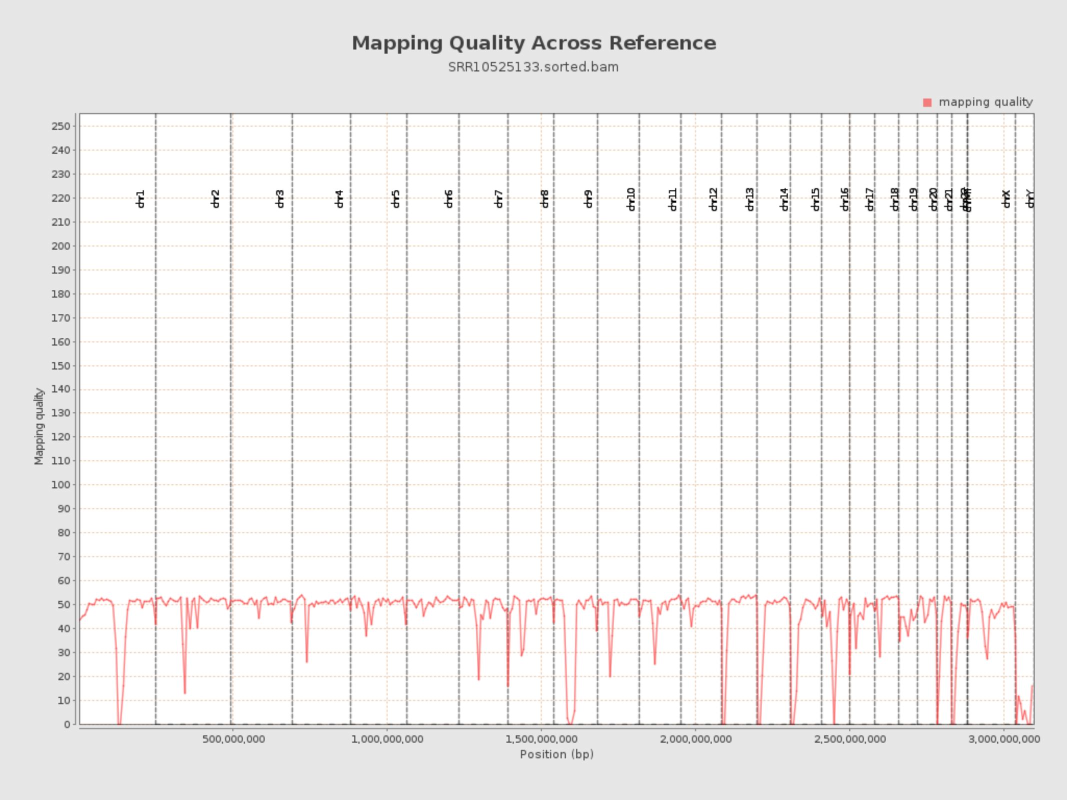
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram