Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:44:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525163.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_SRR10525163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:44:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,861,125
Mapped reads	2,592,646 / 90.62%
Unmapped reads	268,479 / 9.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,319 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	123,402 / 4.31%
Duplication rate	3.51%
Clipped reads	2,594,840 / 90.69%

2.2. ACGT Content

Number/percentage of A's	37,668,444 / 25.15%
Number/percentage of C's	28,710,363 / 19.17%
Number/percentage of T's	47,329,795 / 31.6%
Number/percentage of G's	36,069,820 / 24.08%
Number/percentage of N's	3,390 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0484

Standard Deviation	0.4206

2.4. Mapping Quality

Mean Mapping Quality	44.48

2.5. Mismatches and indels

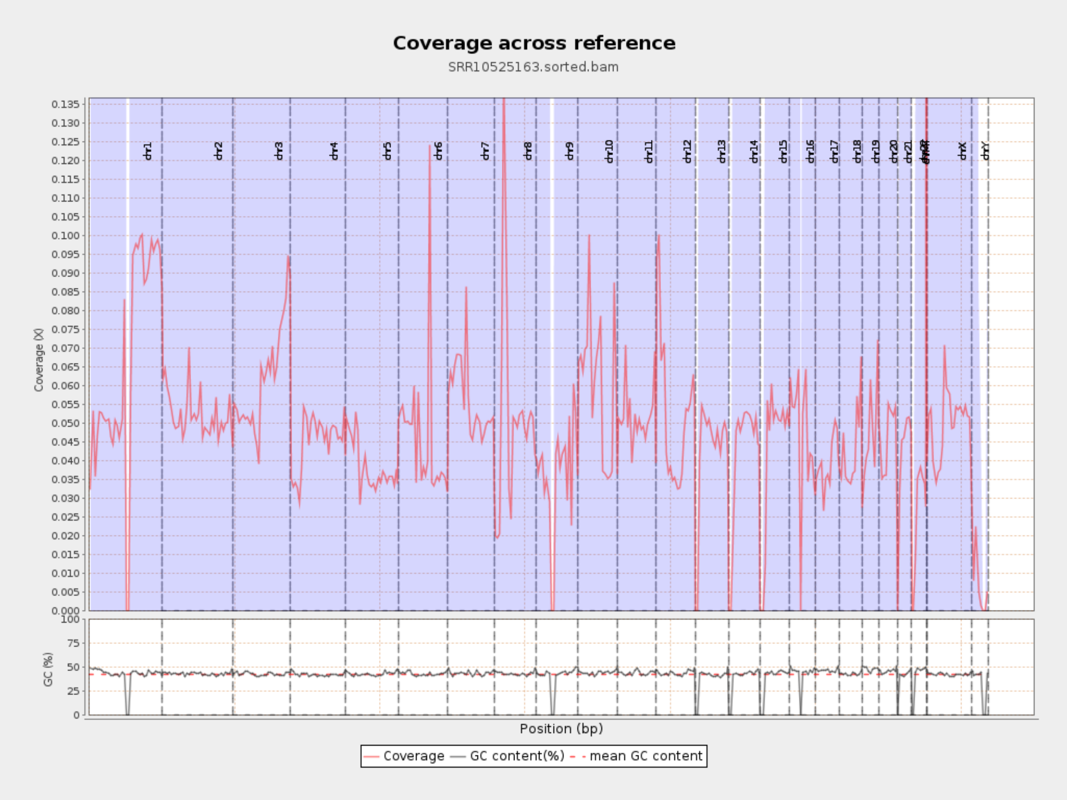
General error rate	0.52%
Mismatches	768,642
Insertions	9,747
Mapped reads with at least one insertion	0.37%
Deletions	29,784
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.04%

2.6. Chromosome stats

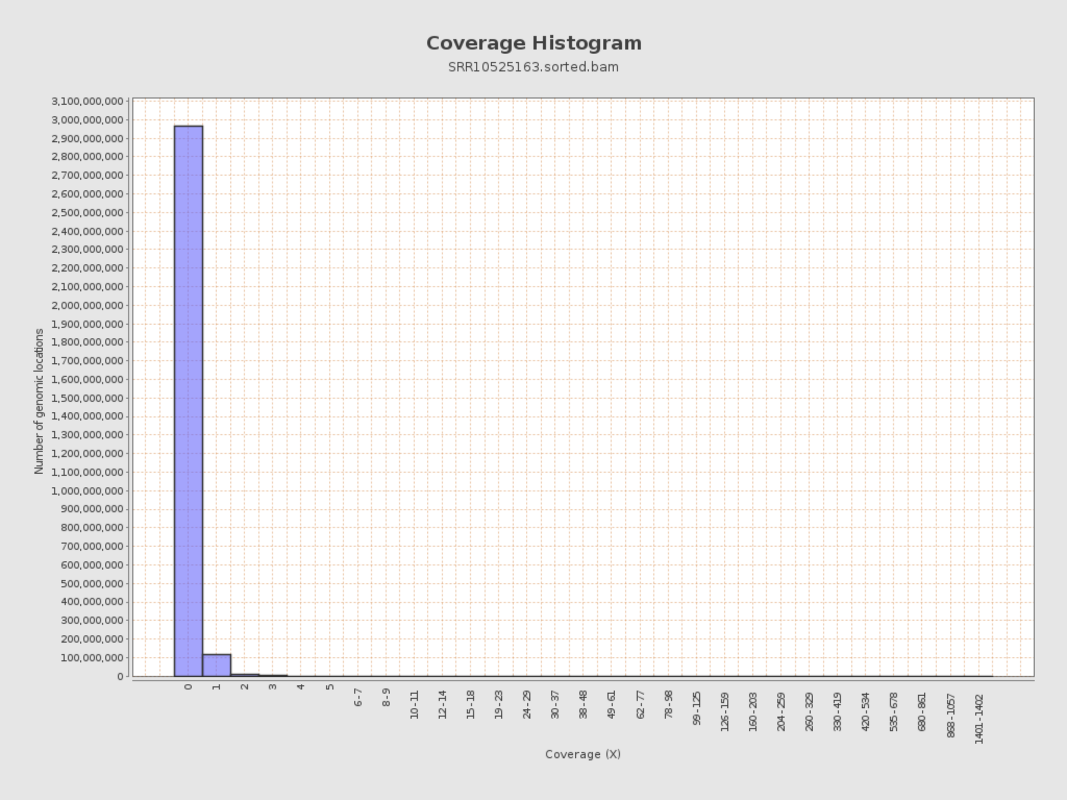
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16387827	0.0657	0.7973
chr2	243199373	12776581	0.0525	0.6196
chr3	198022430	12074171	0.061	0.2858
chr4	191154276	8609448	0.045	0.2614
chr5	180915260	6941029	0.0384	0.2236
chr6	171115067	7957646	0.0465	0.3006
chr7	159138663	8992440	0.0565	0.6295

chr8	146364022	7396674	0.0505	0.3584
chr9	141213431	5040338	0.0357	0.2826
chr10	135534747	8257015	0.0609	0.4503
chr11	135006516	6995946	0.0518	0.3352
chr12	133851895	7019789	0.0524	0.2655
chr13	115169878	4886772	0.0424	0.2391
chr14	107349540	4435372	0.0413	0.2421
chr15	102531392	4309054	0.042	0.2439
chr16	90354753	4169861	0.0461	0.2775
chr17	81195210	3170304	0.039	0.2384
chr18	78077248	3304611	0.0423	0.5649
chr19	59128983	2816610	0.0476	0.5444
chr20	63025520	2871254	0.0456	0.2495
chr21	48129895	1986974	0.0413	0.2483
chr22	51304566	1267775	0.0247	0.1772
chrMT	16571	11637	0.7023	0.9622
chrX	155270560	7730574	0.0498	0.2885
chrY	59373566	419214	0.0071	0.182

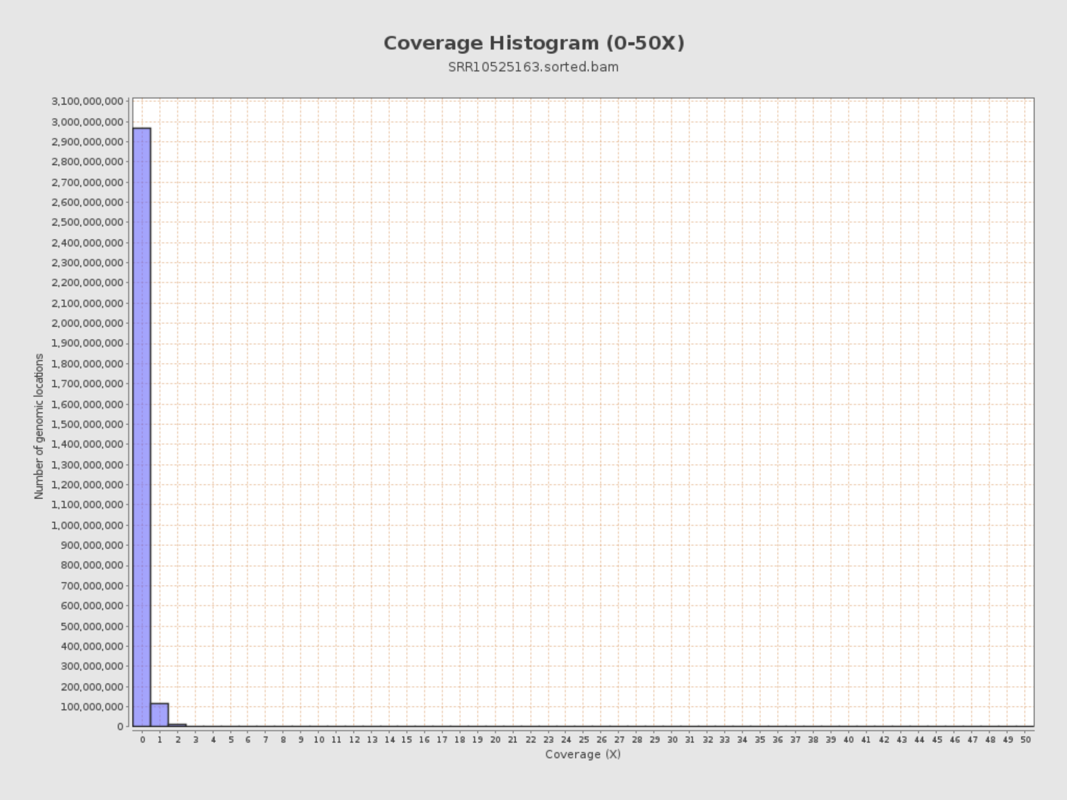
3. Results : Coverage across reference



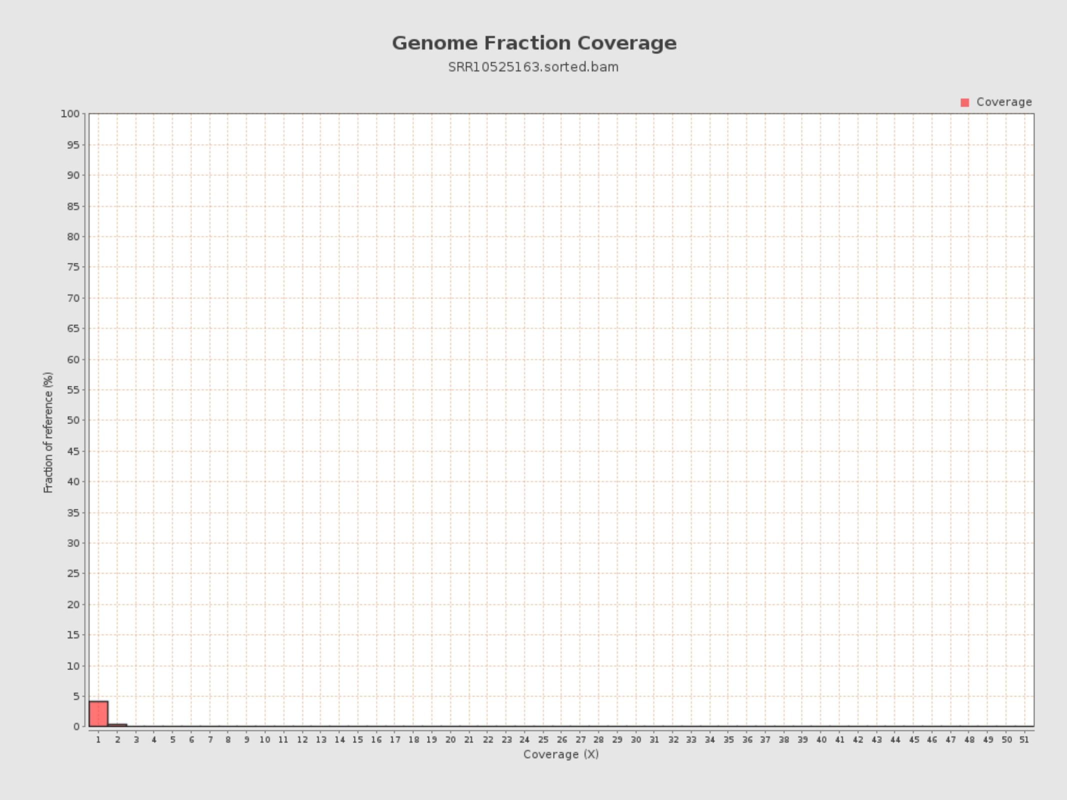
4. Results : Coverage Histogram



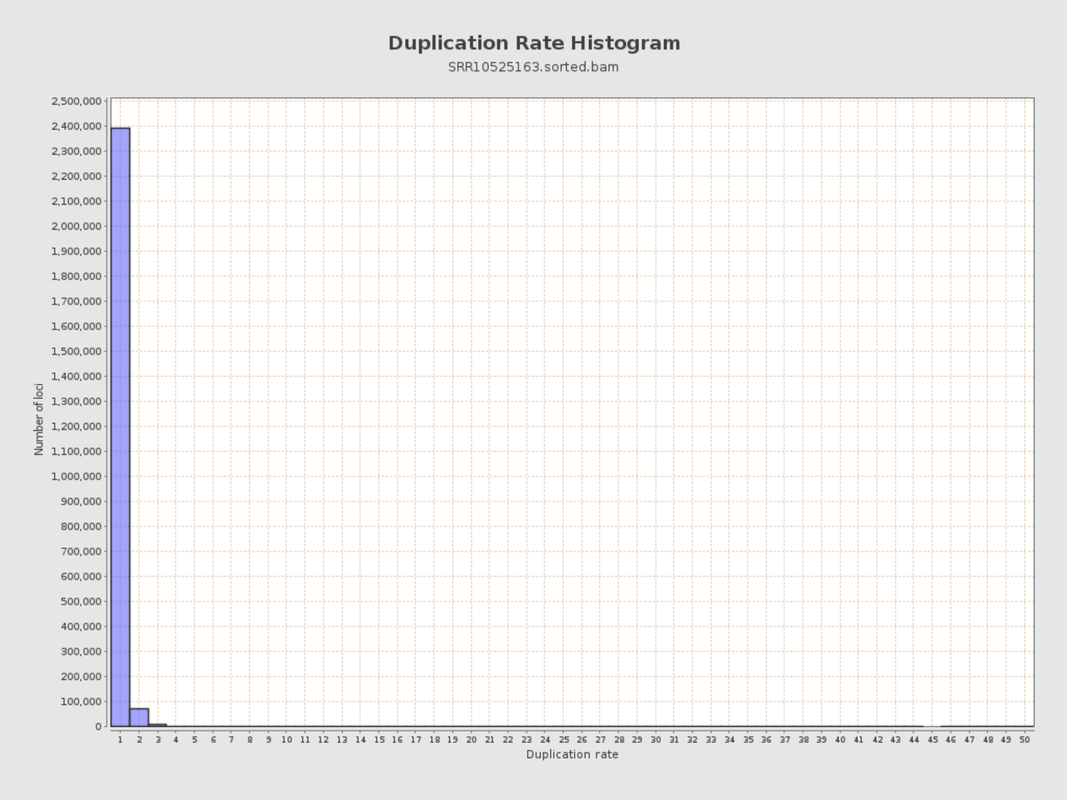
5. Results : Coverage Histogram (0-50X)



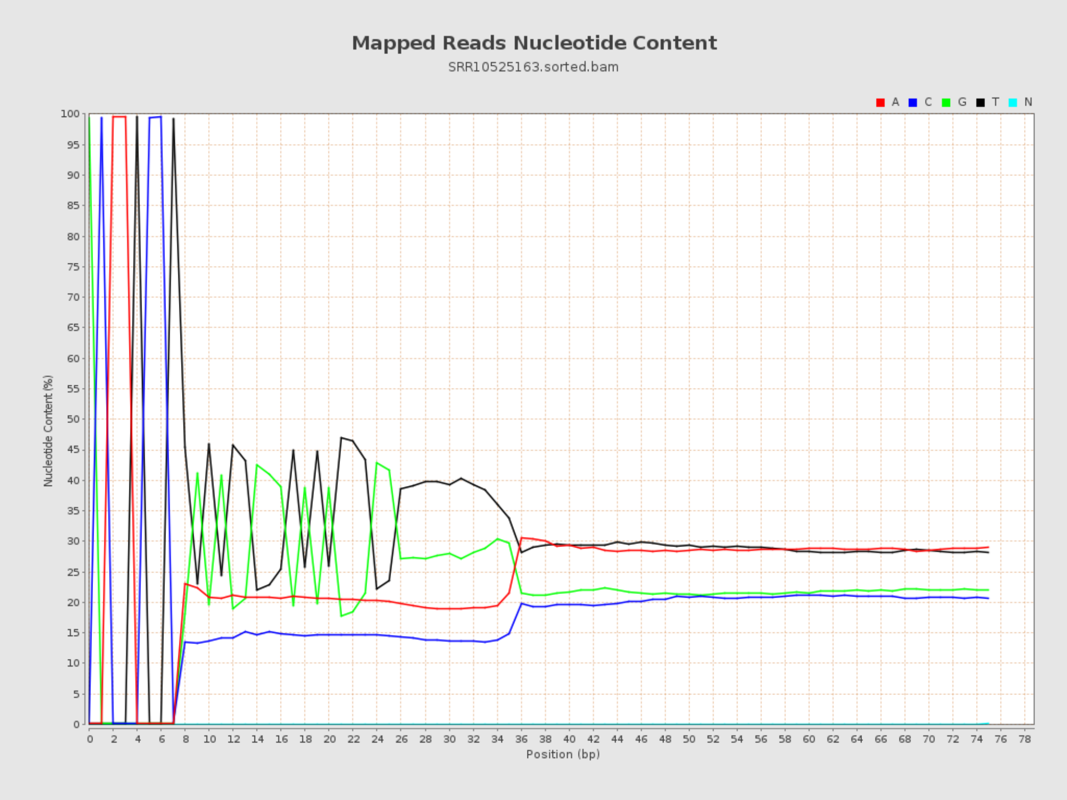
6. Results : Genome Fraction Coverage



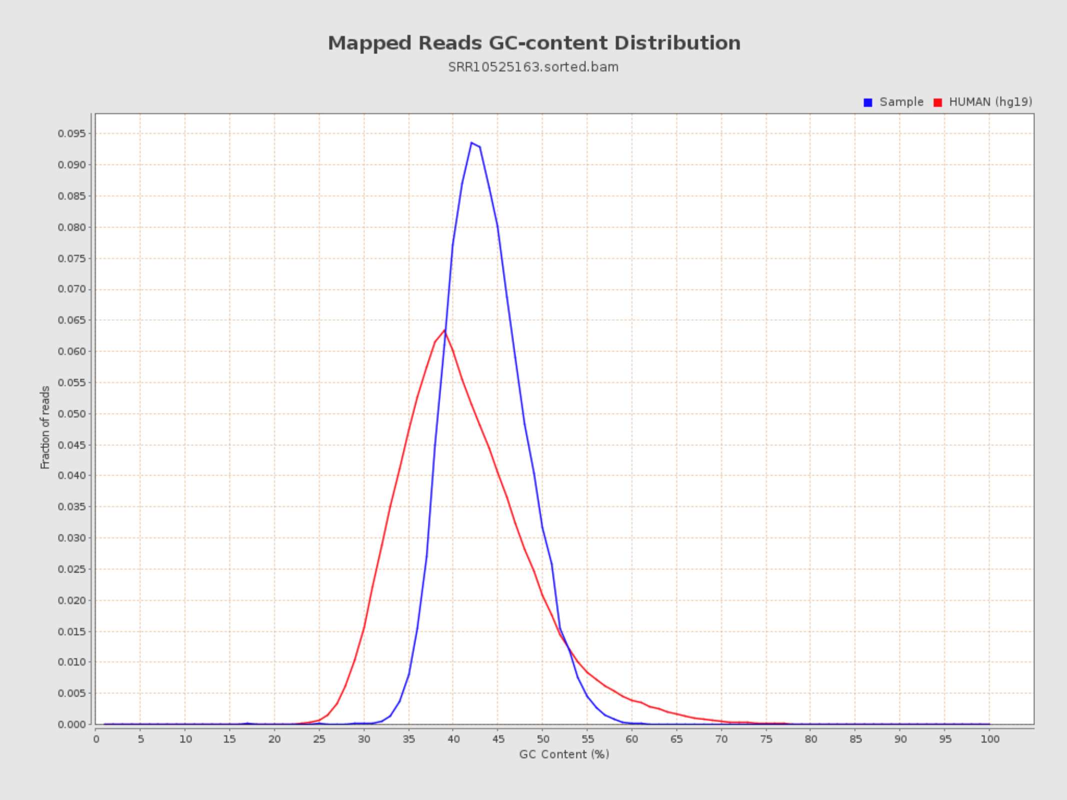
7. Results : Duplication Rate Histogram



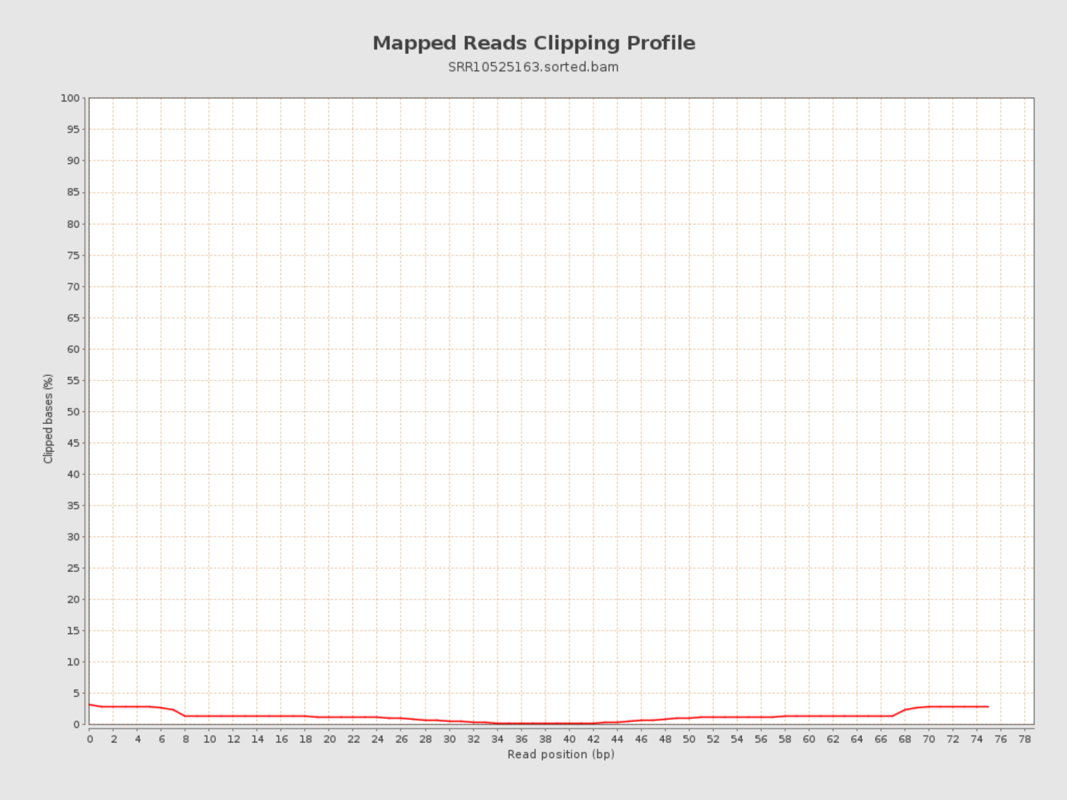
8. Results : Mapped Reads Nucleotide Content



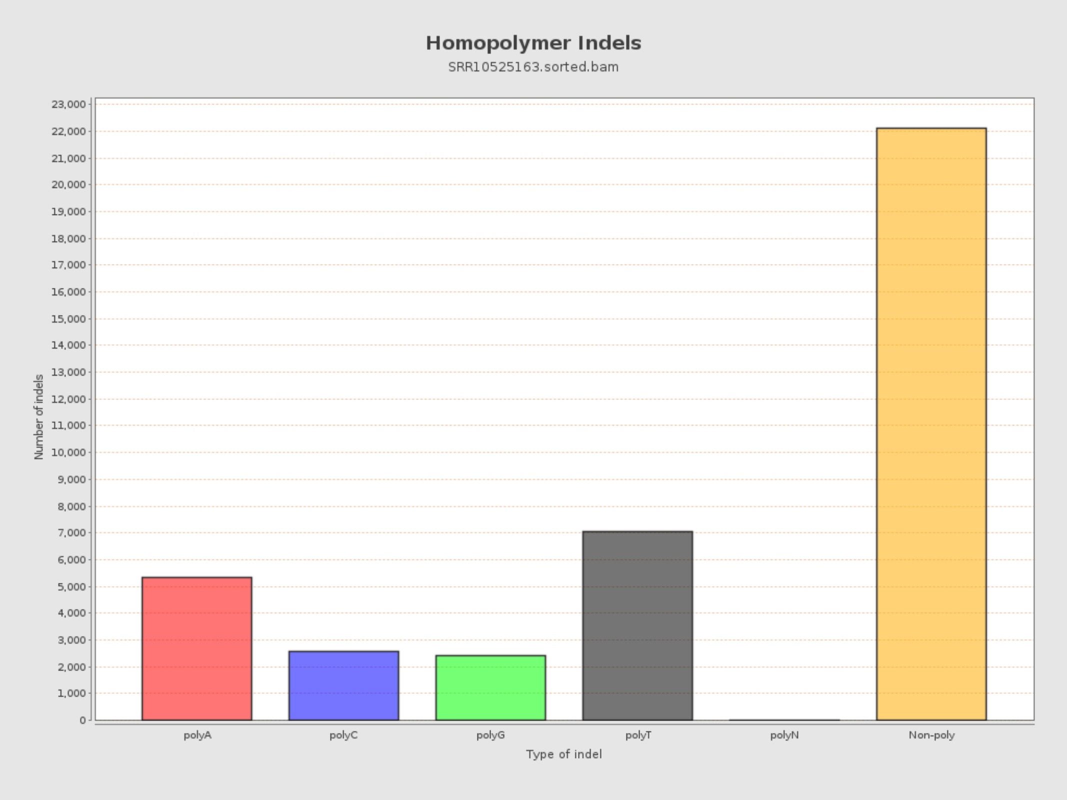
9. Results : Mapped Reads GC-content Distribution



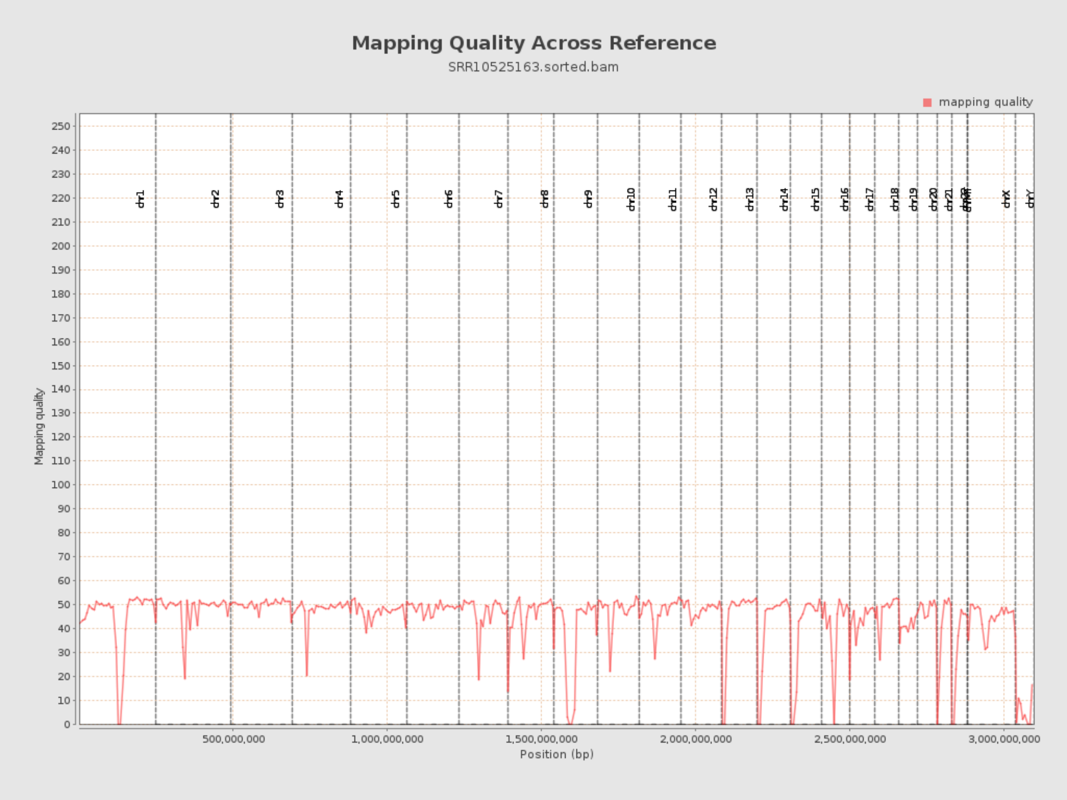
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram