Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 21:11:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525171.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_SRR10525171 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525171.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 21:11:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525171.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,259,923
Mapped reads	2,087,314 / 92.36%
Unmapped reads	172,609 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,210 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	94,916 / 4.2%
Duplication rate	3.28%
Clipped reads	2,091,481 / 92.55%

2.2. ACGT Content

Number/percentage of A's	28,938,291 / 23.71%
Number/percentage of C's	22,987,978 / 18.84%
Number/percentage of T's	39,135,654 / 32.07%
Number/percentage of G's	30,976,300 / 25.38%
Number/percentage of N's	2,480 / 0%
GC Percentage	44.22%

2.3. Coverage

Mean	0.0394

Standard Deviation	0.3496

2.4. Mapping Quality

Mean Mapping Quality	44.79

2.5. Mismatches and indels

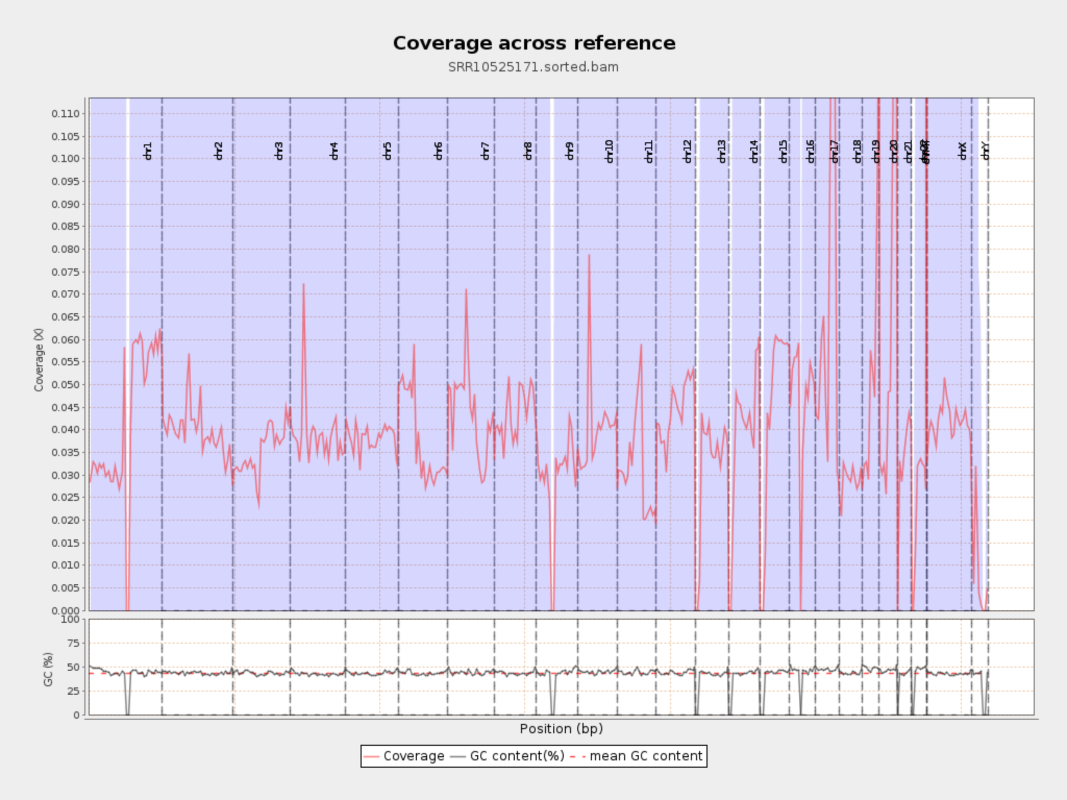
General error rate	0.52%
Mismatches	618,131
Insertions	8,599
Mapped reads with at least one insertion	0.41%
Deletions	23,667
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.88%

2.6. Chromosome stats

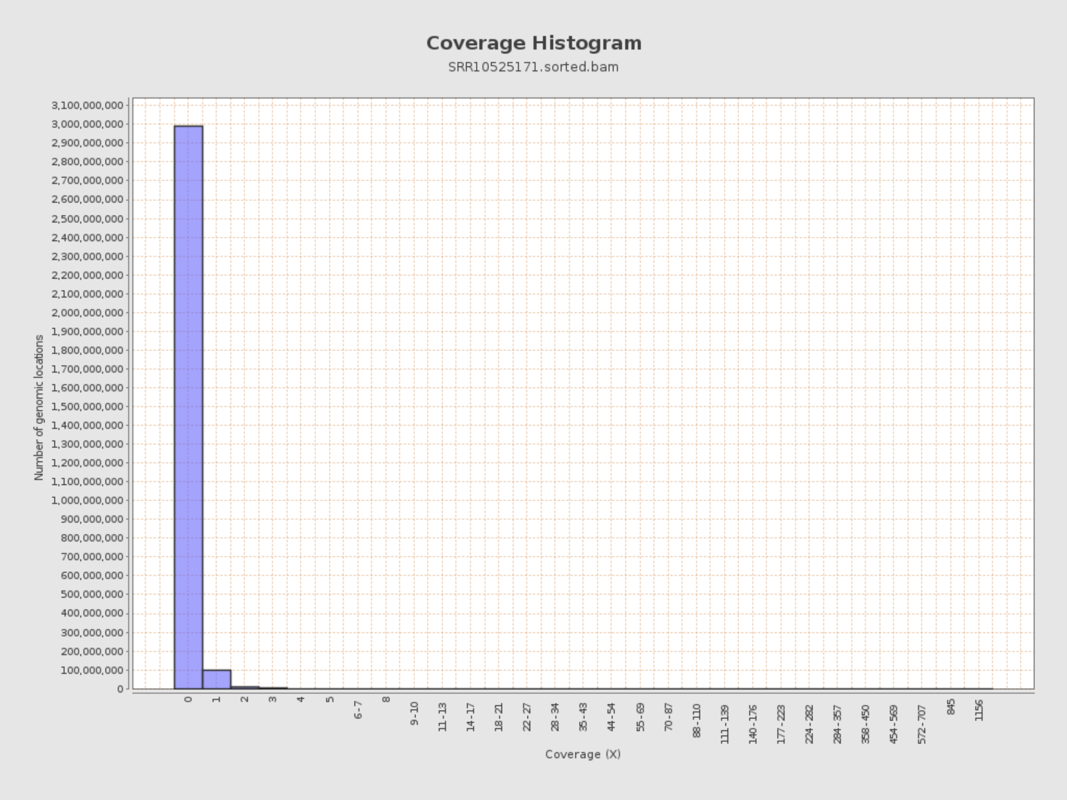
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10252976	0.0411	0.549
chr2	243199373	9721810	0.04	0.527
chr3	198022430	6989374	0.0353	0.2103
chr4	191154276	7428692	0.0389	0.2784
chr5	180915260	6906612	0.0382	0.2171
chr6	171115067	6501554	0.038	0.2642
chr7	159138663	7012448	0.0441	0.4612

chr8	146364022	6387863	0.0436	0.4653
chr9	141213431	4067542	0.0288	0.2443
chr10	135534747	5449367	0.0402	0.3774
chr11	135006516	4335577	0.0321	0.2638
chr12	133851895	5961126	0.0445	0.2379
chr13	115169878	3617750	0.0314	0.1986
chr14	107349540	4079108	0.038	0.2228
chr15	102531392	4501759	0.0439	0.2347
chr16	90354753	4222102	0.0467	0.257
chr17	81195210	5377495	0.0662	0.3054
chr18	78077248	2253325	0.0289	0.4212
chr19	59128983	3198323	0.0541	0.437
chr20	63025520	4081946	0.0648	0.2987
chr21	48129895	1593902	0.0331	0.2679
chr22	51304566	1155376	0.0225	0.1672
chrMT	16571	6213	0.3749	0.7058
chrX	155270560	6521584	0.042	0.2493
chrY	59373566	455397	0.0077	0.3354

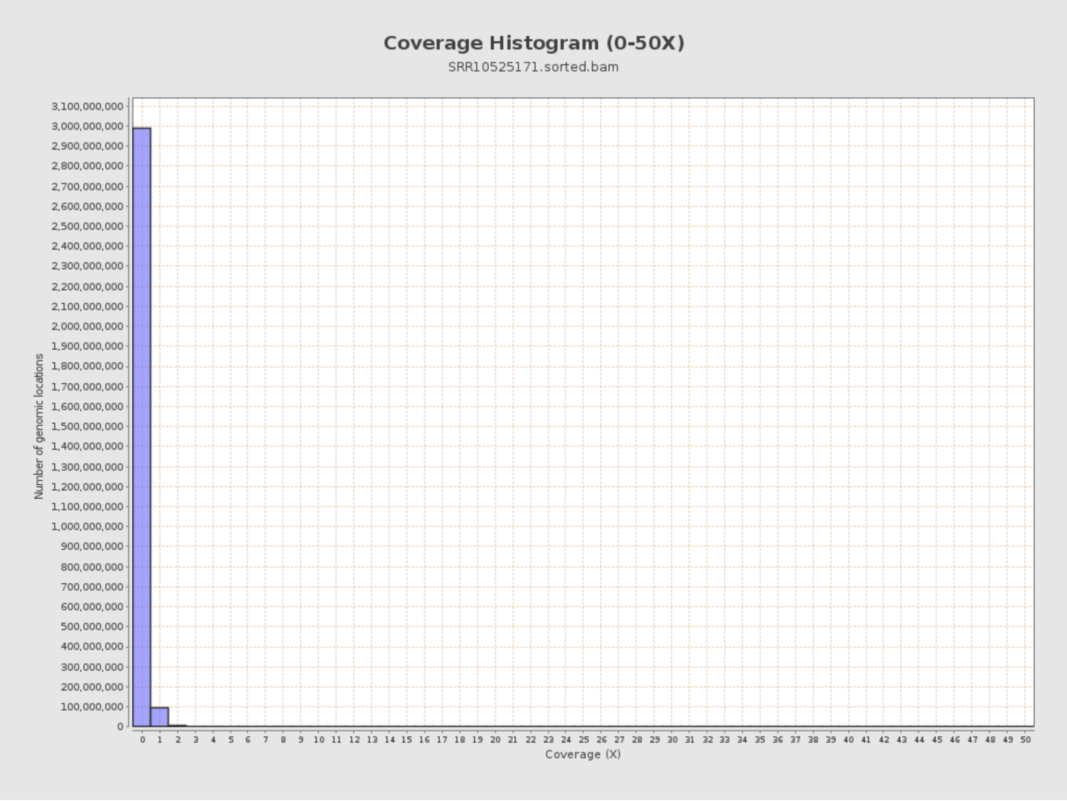
3. Results : Coverage across reference



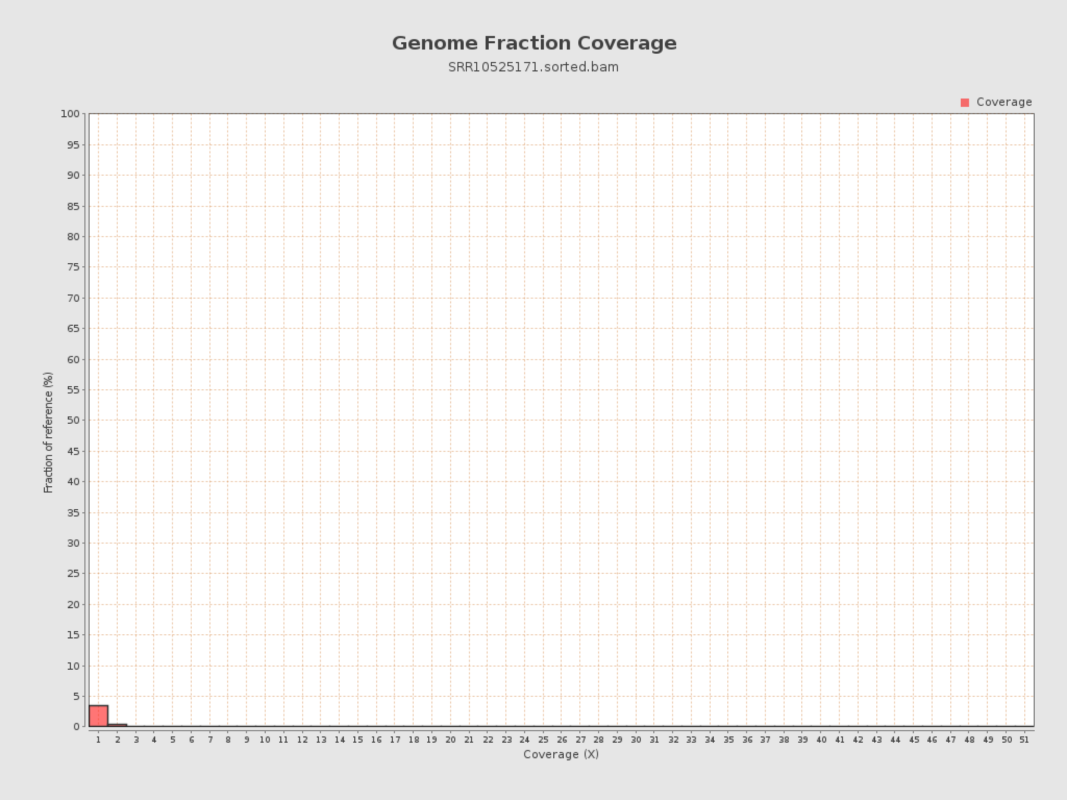
4. Results : Coverage Histogram



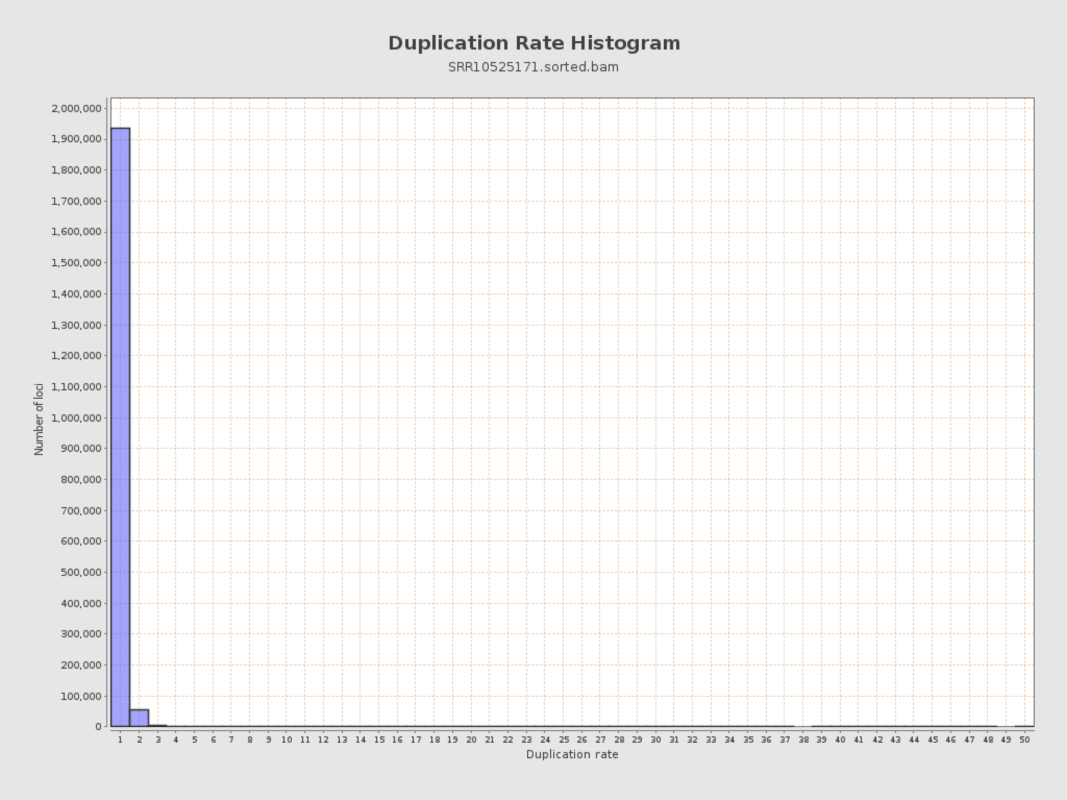
5. Results : Coverage Histogram (0-50X)



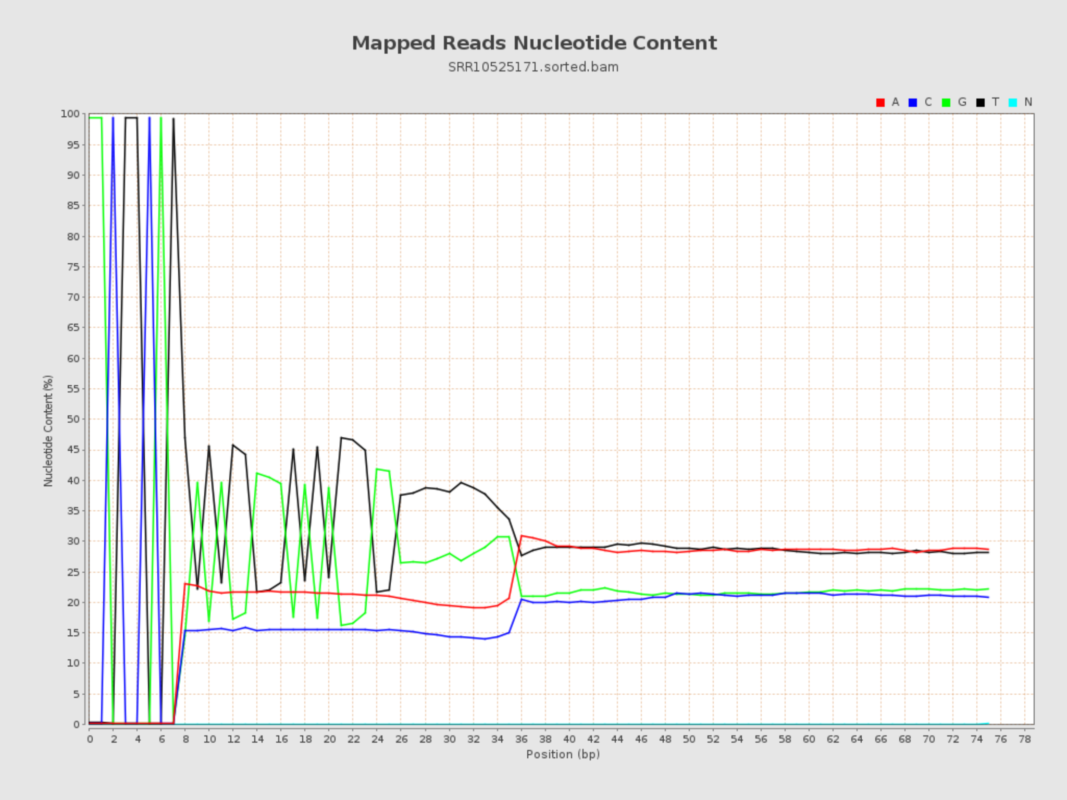
6. Results : Genome Fraction Coverage



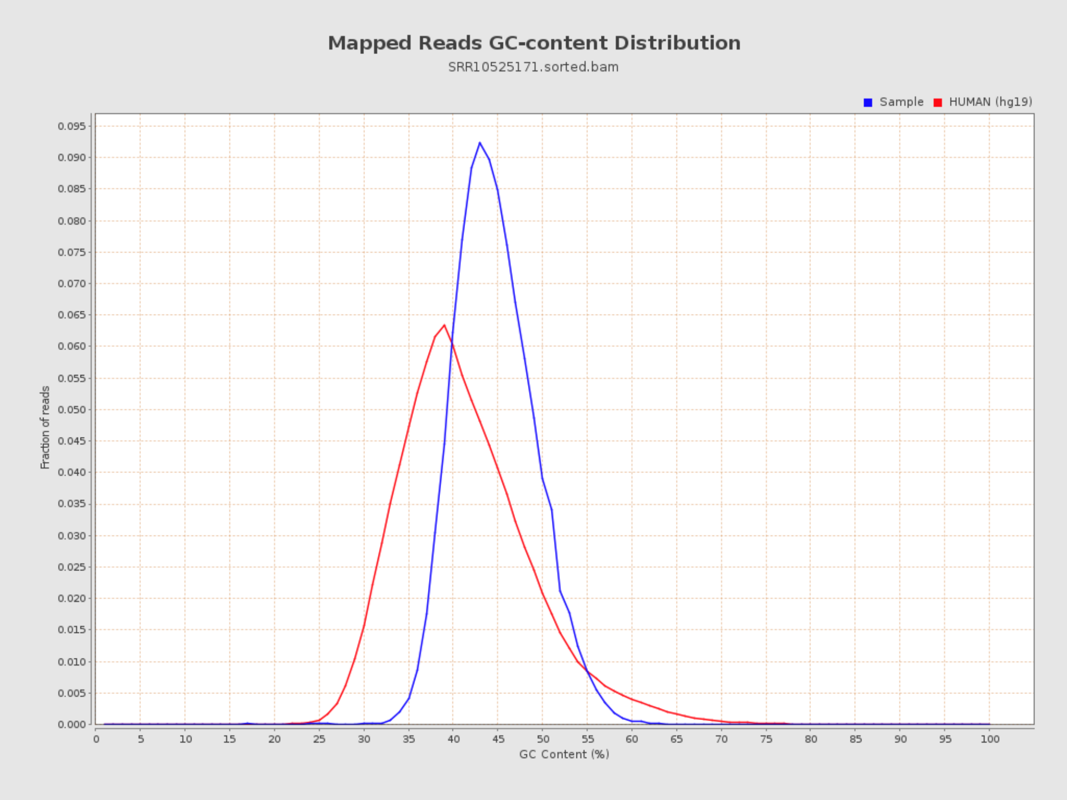
7. Results : Duplication Rate Histogram



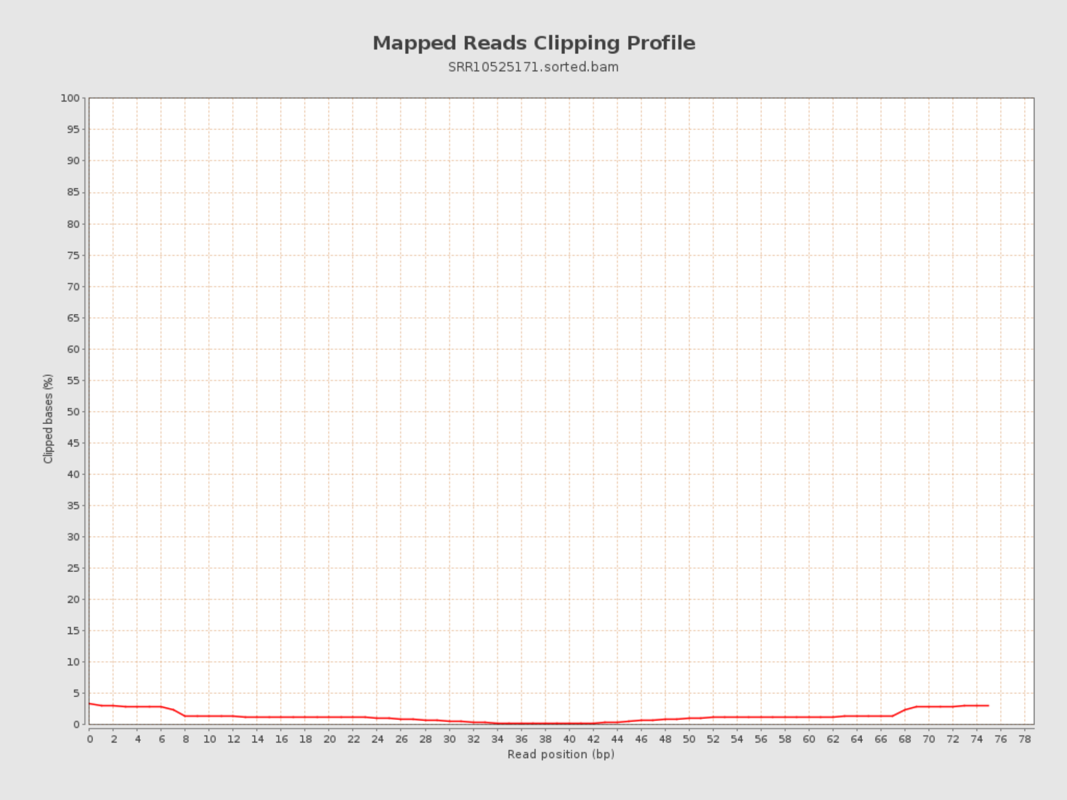
8. Results : Mapped Reads Nucleotide Content



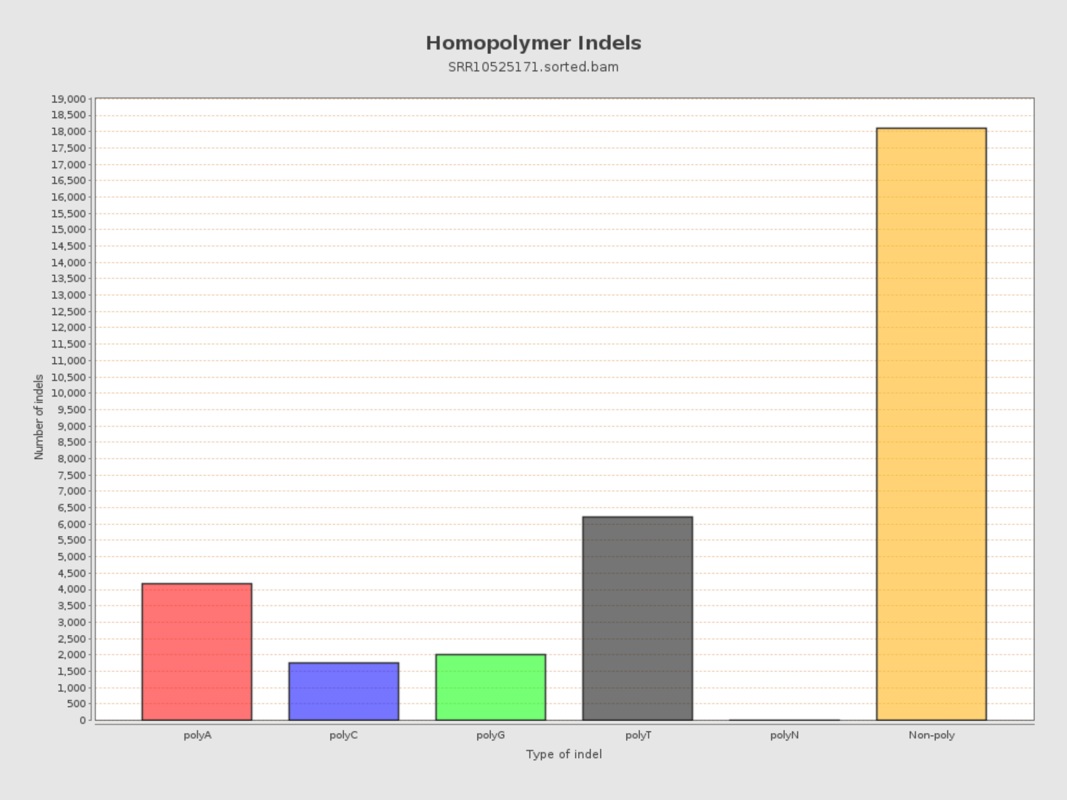
9. Results : Mapped Reads GC-content Distribution



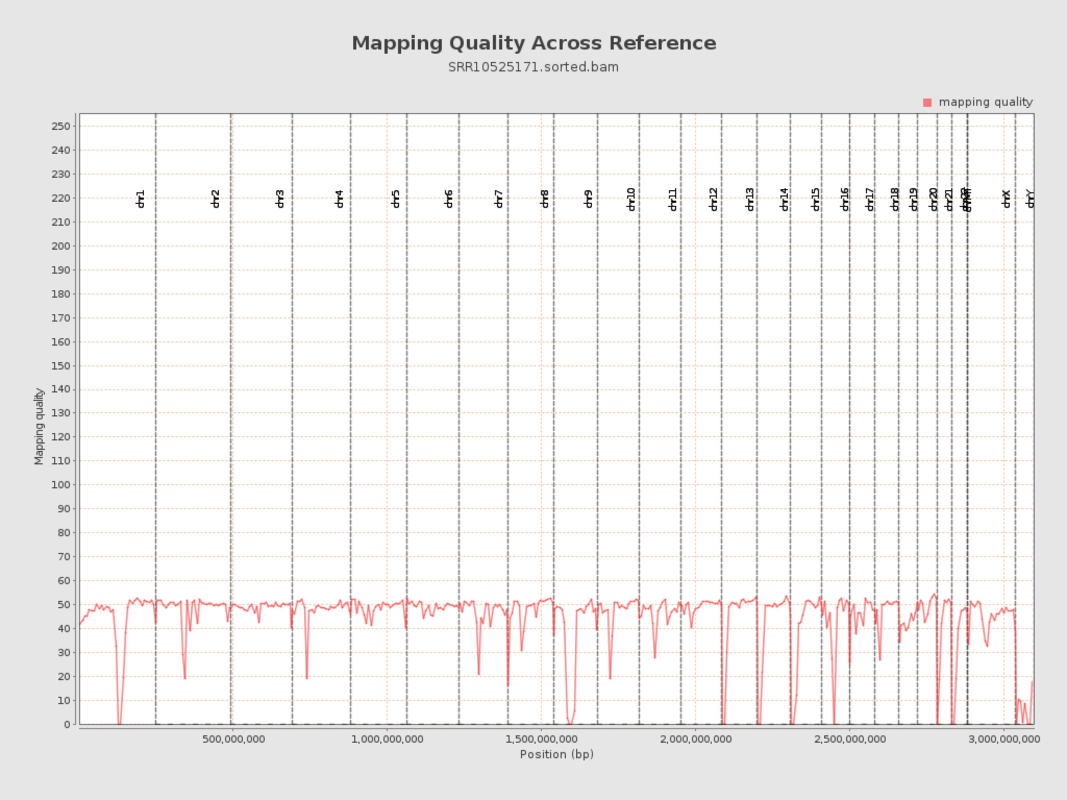
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram