Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:23:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525091.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_SRR10525091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525091.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:23:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525091.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,702,324
Mapped reads	3,357,502 / 90.69%
Unmapped reads	344,822 / 9.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,817 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	304,267 / 8.22%
Duplication rate	6.94%
Clipped reads	3,356,709 / 90.66%

2.2. ACGT Content

Number/percentage of A's	50,973,030 / 25.87%
Number/percentage of C's	36,864,380 / 18.71%
Number/percentage of T's	63,117,356 / 32.04%
Number/percentage of G's	46,043,696 / 23.37%
Number/percentage of N's	18,900 / 0.01%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0637

Standard Deviation	0.5313

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

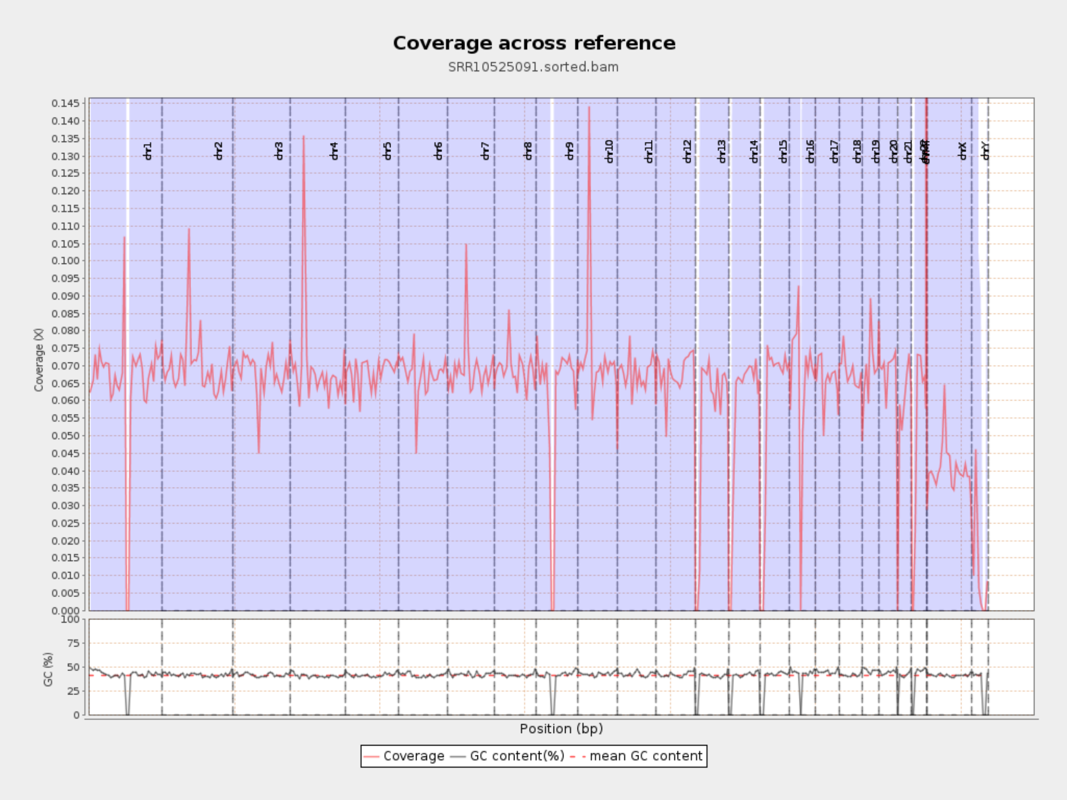
General error rate	0.5%
Mismatches	943,542
Insertions	16,702
Mapped reads with at least one insertion	0.49%
Deletions	38,506
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.93%

2.6. Chromosome stats

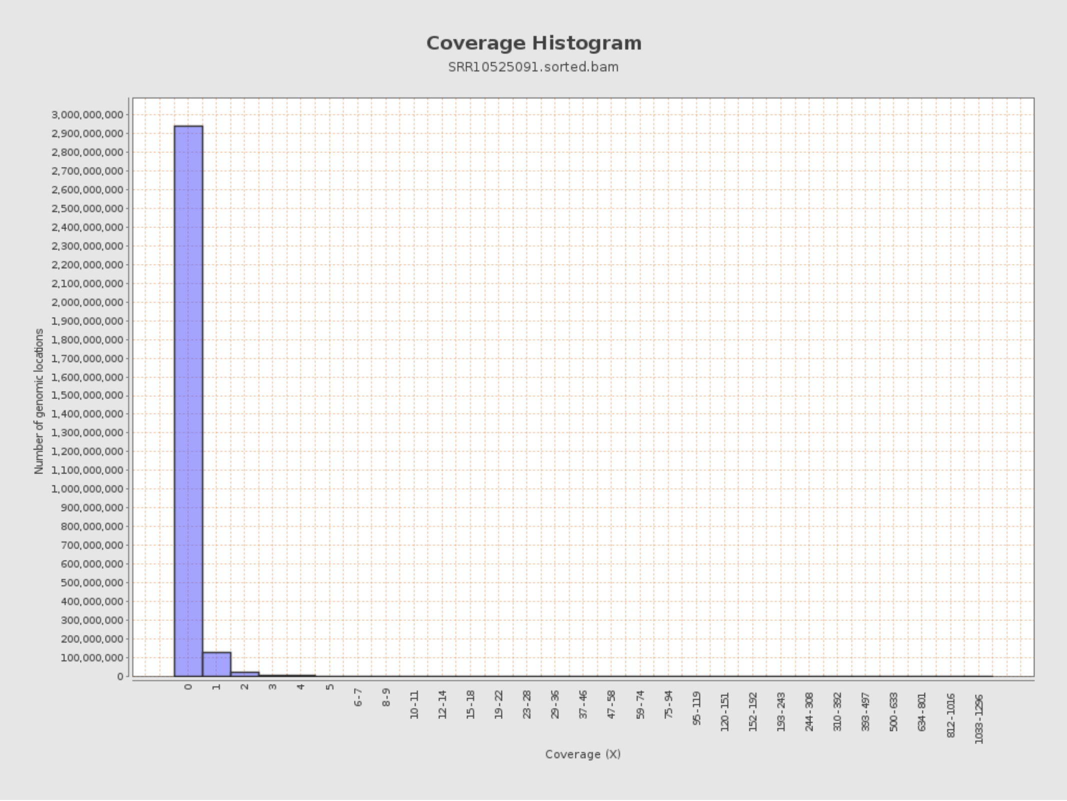
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16203704	0.065	0.9913
chr2	243199373	17042832	0.0701	0.7167
chr3	198022430	13466967	0.068	0.3268
chr4	191154276	13229422	0.0692	0.4316
chr5	180915260	12311615	0.0681	0.3241
chr6	171115067	11573373	0.0676	0.3696
chr7	159138663	11048079	0.0694	0.634

chr8	146364022	10108067	0.0691	0.5569
chr9	141213431	8492362	0.0601	0.4236
chr10	135534747	9865127	0.0728	0.6445
chr11	135006516	9141562	0.0677	0.4251
chr12	133851895	9111906	0.0681	0.3333
chr13	115169878	6281156	0.0545	0.2897
chr14	107349540	6027102	0.0561	0.3045
chr15	102531392	5912285	0.0577	0.2991
chr16	90354753	5960498	0.066	0.3654
chr17	81195210	5319426	0.0655	0.355
chr18	78077248	5338709	0.0684	0.7981
chr19	59128983	4134296	0.0699	0.7182
chr20	63025520	4331619	0.0687	0.347
chr21	48129895	2712228	0.0564	0.3813
chr22	51304566	2455919	0.0479	0.273
chrMT	16571	35845	2.1631	2.0428
chrX	155270560	6324224	0.0407	0.3148
chrY	59373566	651102	0.011	0.3869

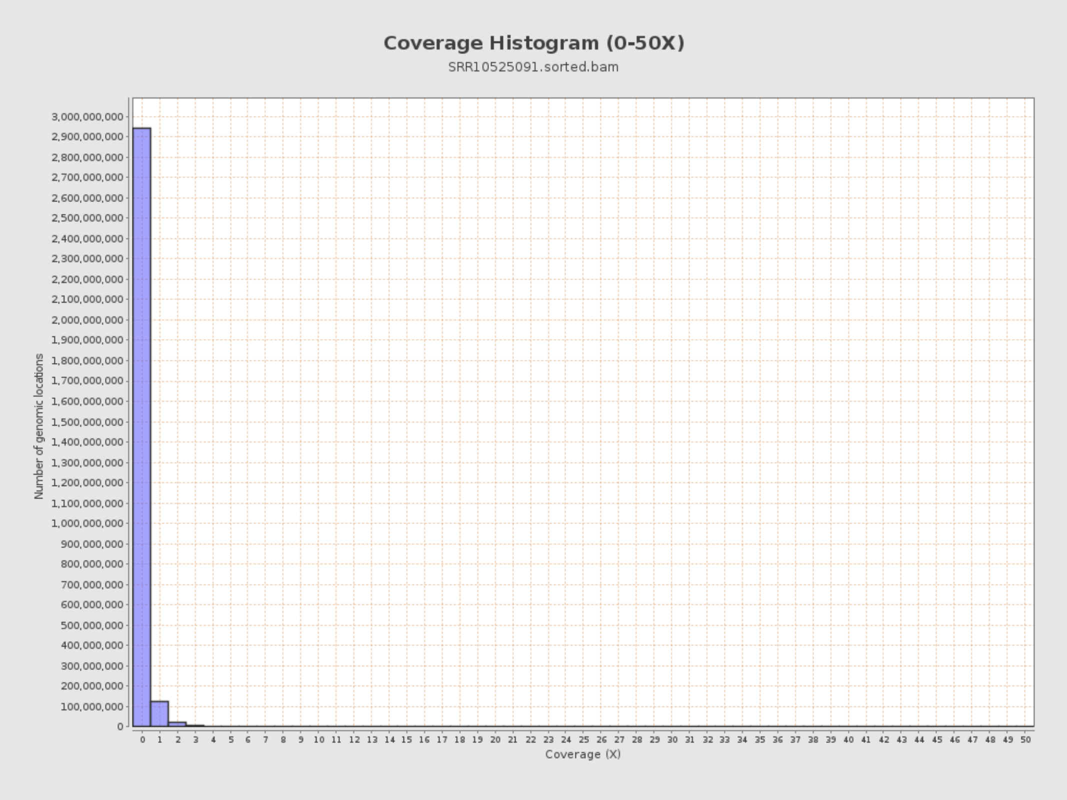
3. Results : Coverage across reference



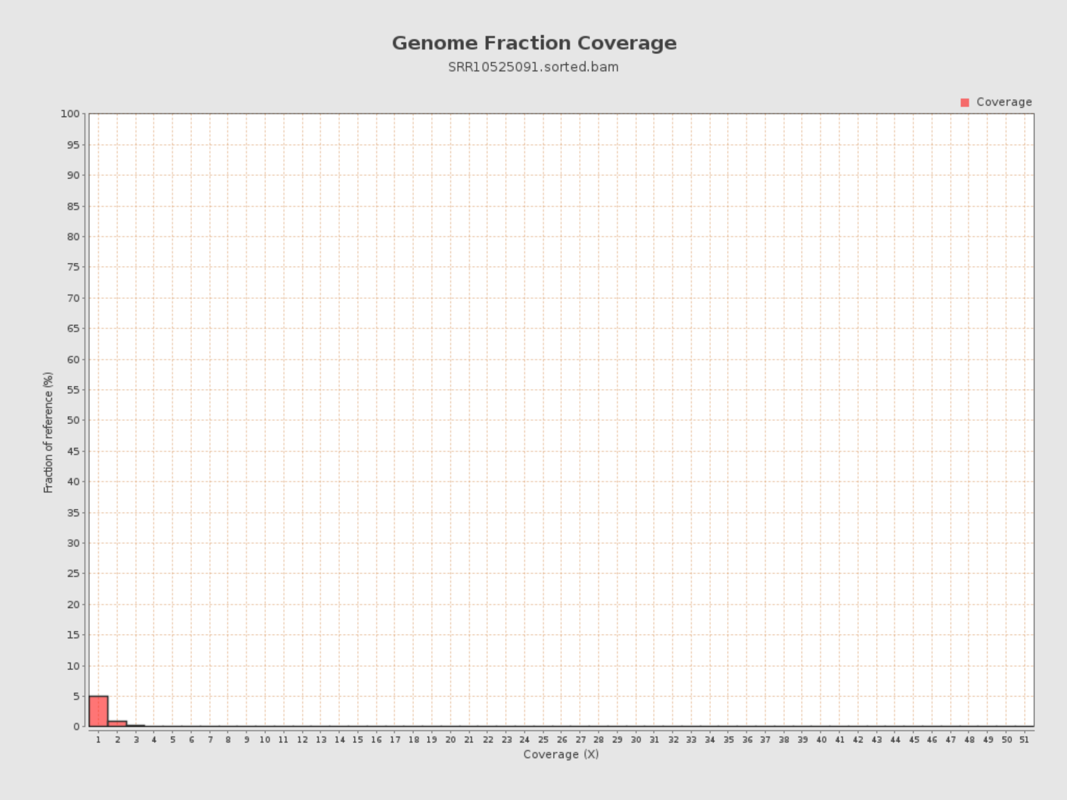
4. Results : Coverage Histogram



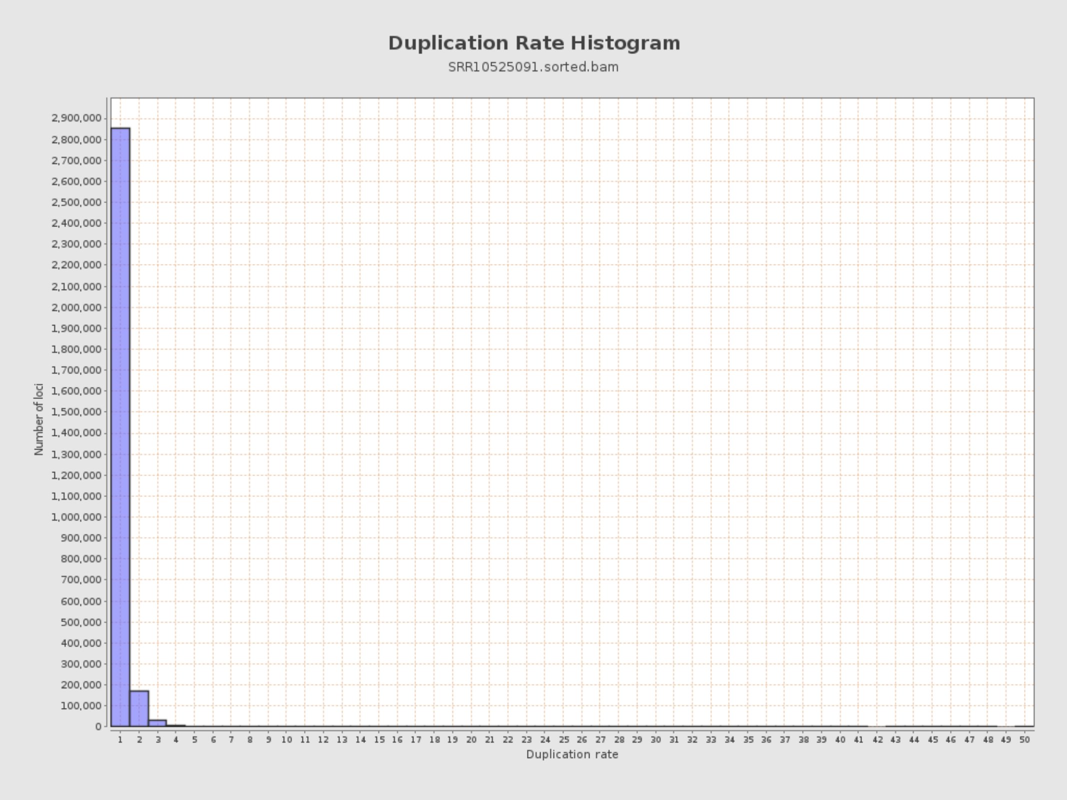
5. Results : Coverage Histogram (0-50X)



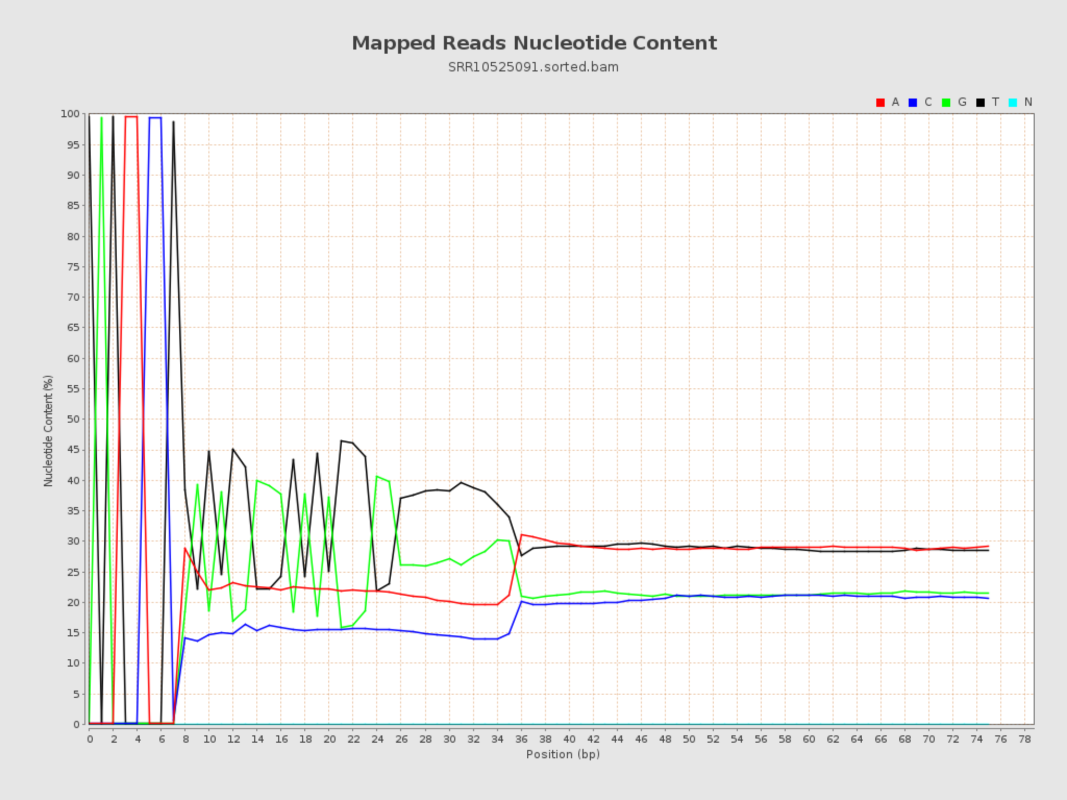
6. Results : Genome Fraction Coverage



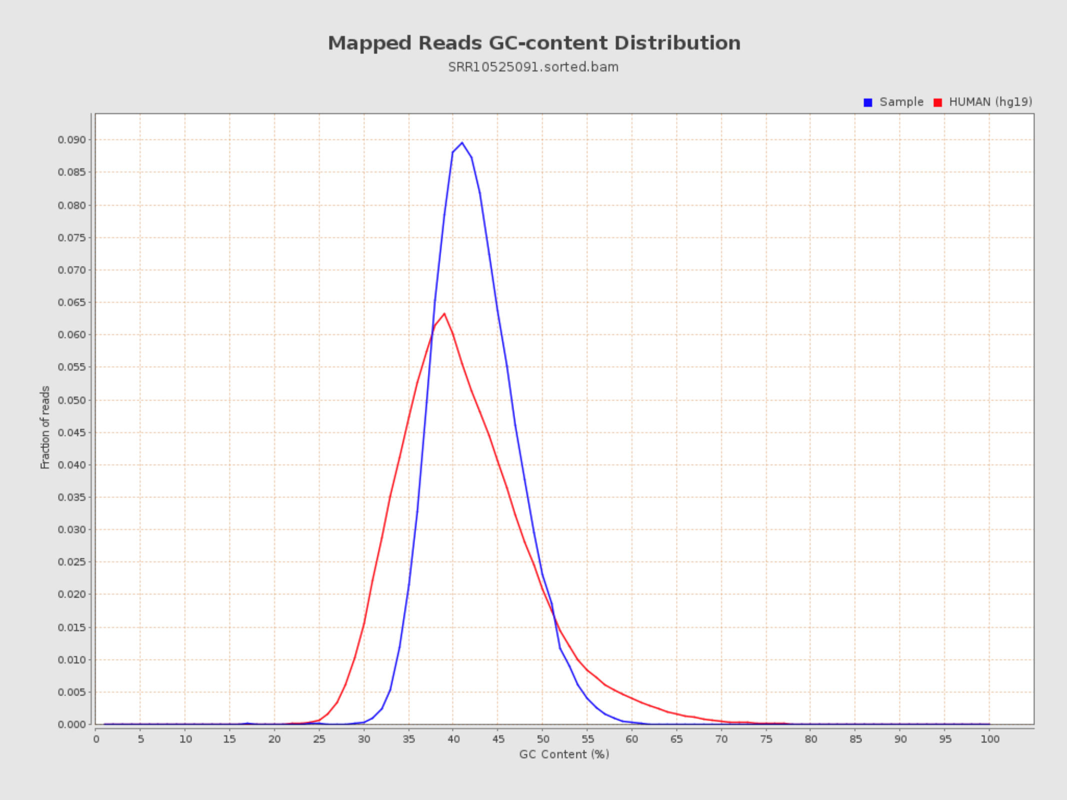
7. Results : Duplication Rate Histogram



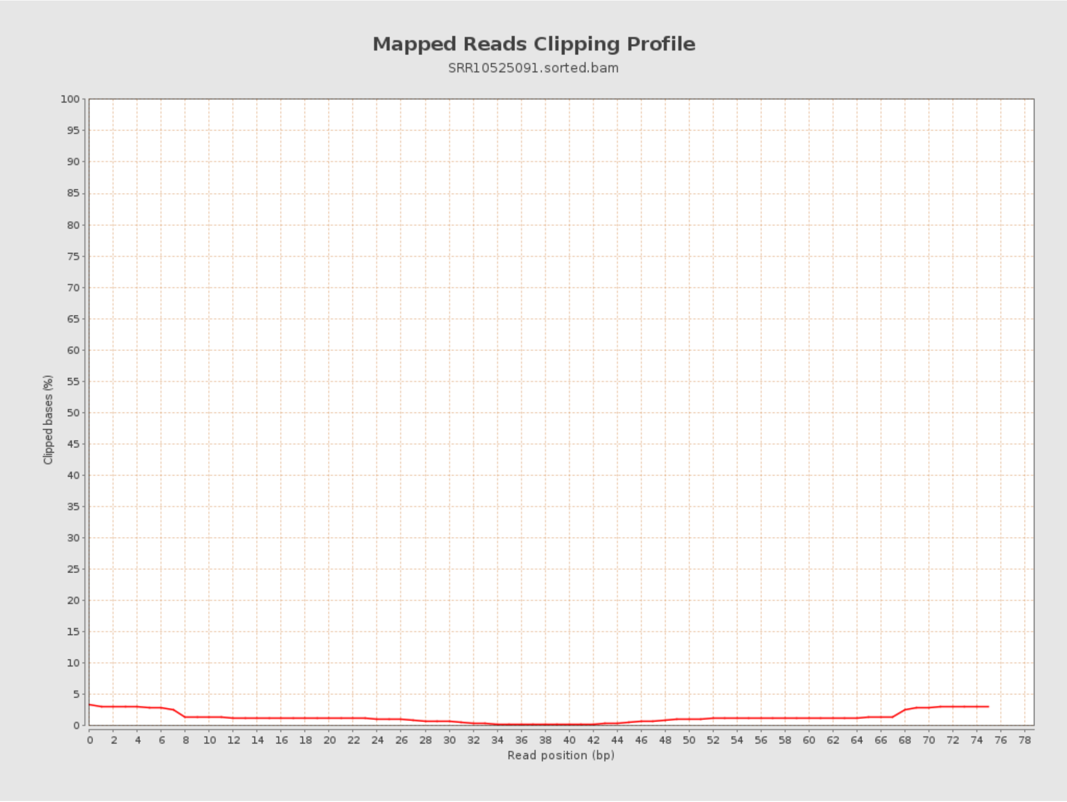
8. Results : Mapped Reads Nucleotide Content



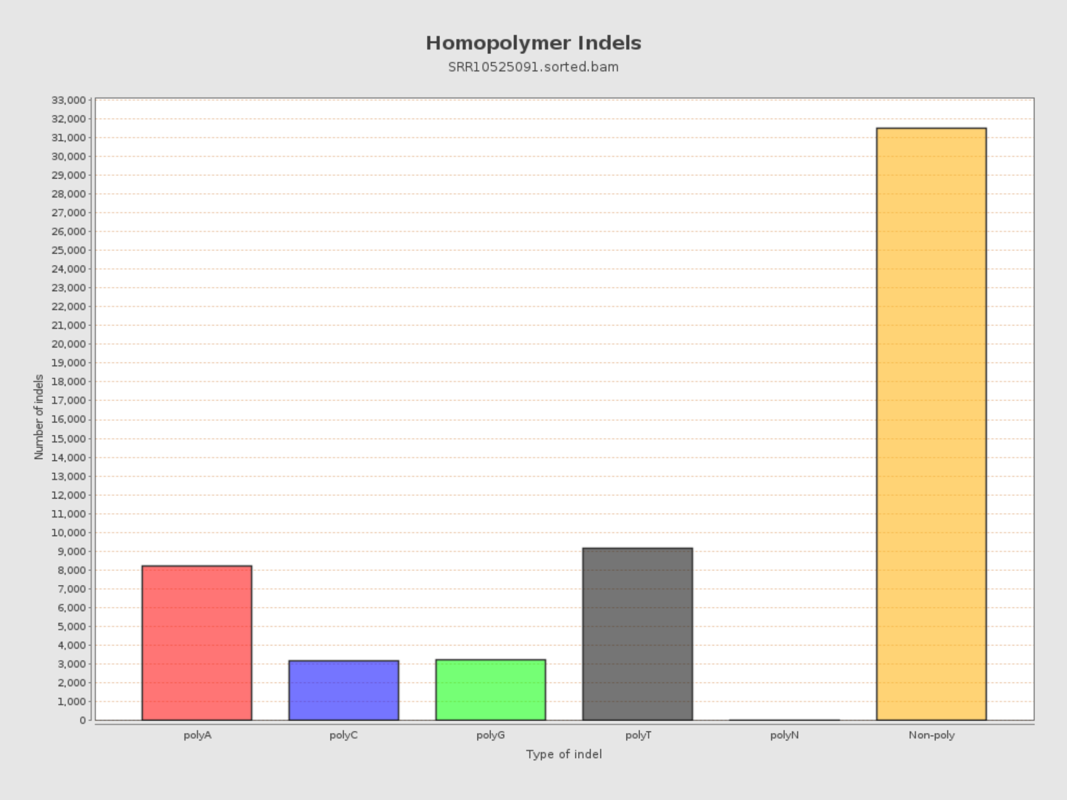
9. Results : Mapped Reads GC-content Distribution



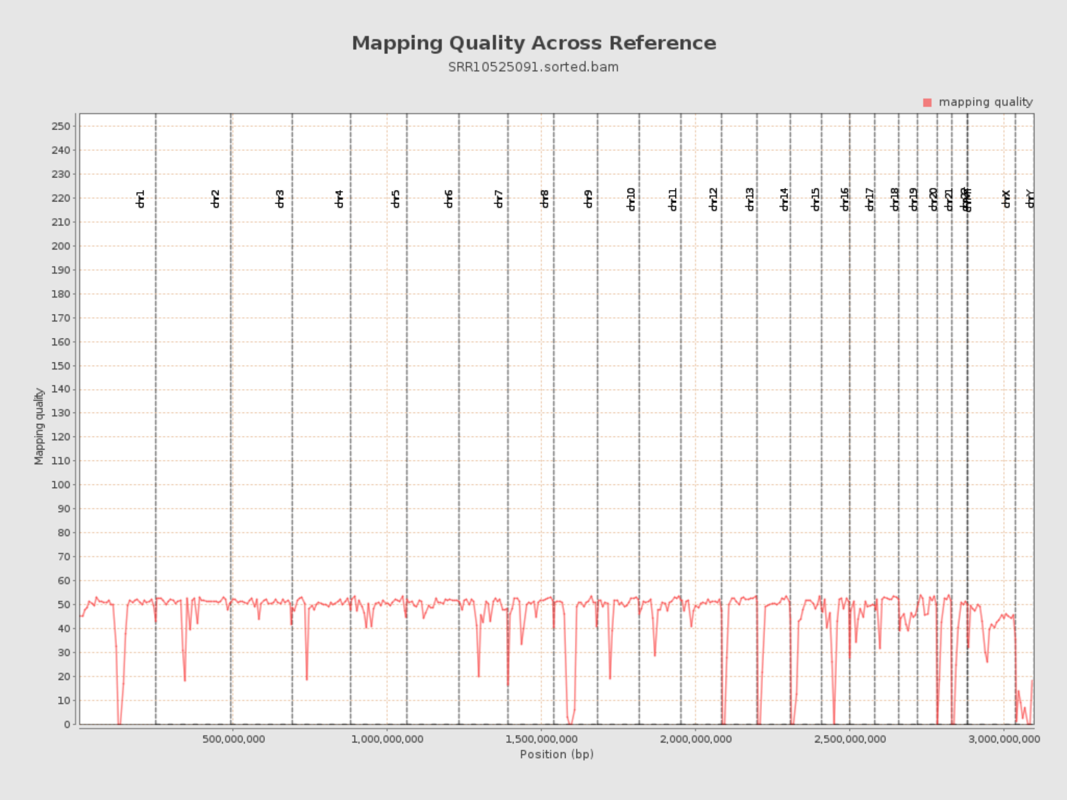
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram