Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:15:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525089.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_SRR10525089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525089.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:15:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525089.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,812,794
Mapped reads	4,332,487 / 90.02%
Unmapped reads	480,307 / 9.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,851 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	277,476 / 5.77%
Duplication rate	4.9%
Clipped reads	4,341,173 / 90.2%

2.2. ACGT Content

Number/percentage of A's	65,084,415 / 26.11%
Number/percentage of C's	47,258,735 / 18.96%
Number/percentage of T's	78,924,062 / 31.66%
Number/percentage of G's	57,990,821 / 23.26%
Number/percentage of N's	7,599 / 0%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0805

Standard Deviation	0.5684

2.4. Mapping Quality

Mean Mapping Quality	45.56

2.5. Mismatches and indels

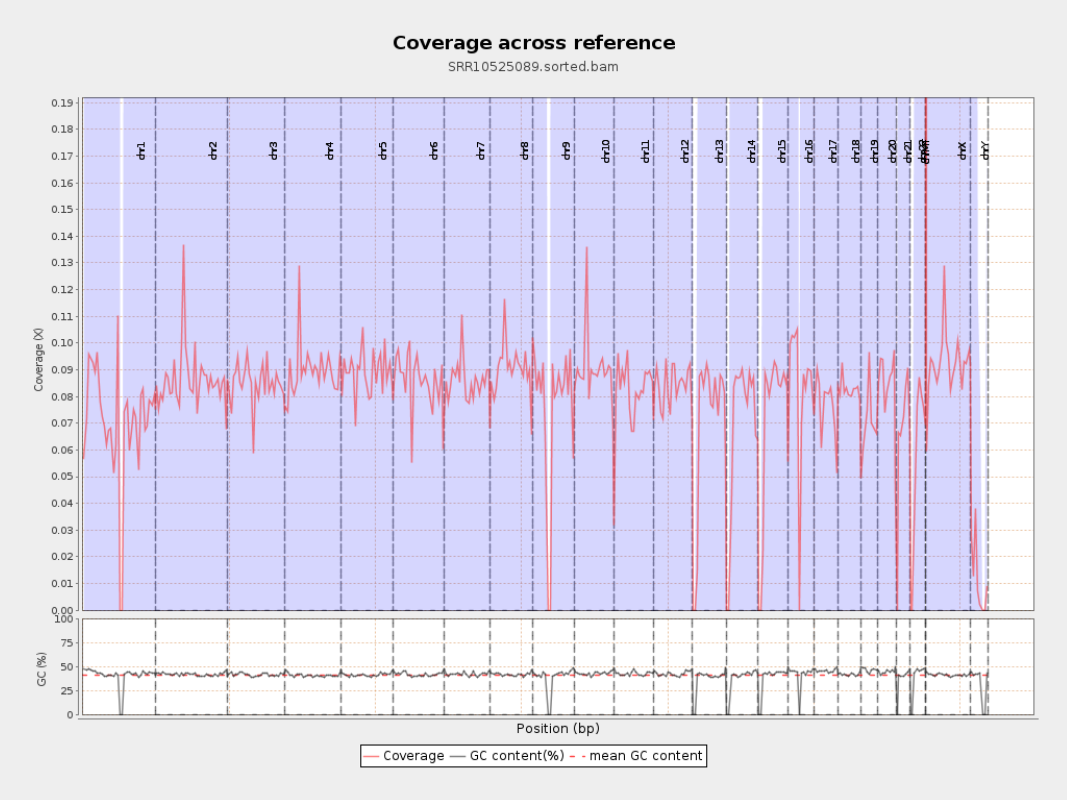
General error rate	0.48%
Mismatches	1,172,619
Insertions	17,989
Mapped reads with at least one insertion	0.41%
Deletions	38,191
Mapped reads with at least one deletion	0.88%
Homopolymer indels	41.55%

2.6. Chromosome stats

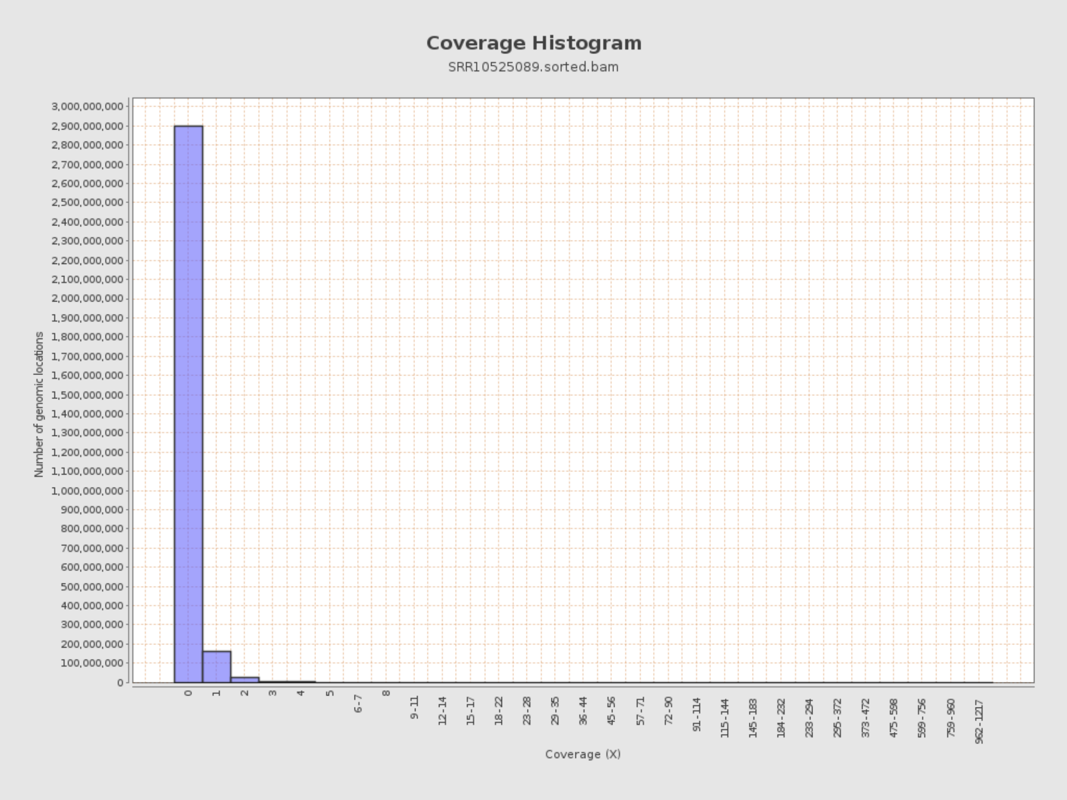
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17558004	0.0704	1.0028
chr2	243199373	21098421	0.0868	0.6419
chr3	198022430	16856648	0.0851	0.3556
chr4	191154276	17149477	0.0897	0.4294
chr5	180915260	16050284	0.0887	0.3689
chr6	171115067	14719349	0.086	0.4016
chr7	159138663	13710800	0.0862	0.7011

chr8	146364022	13225704	0.0904	0.7267
chr9	141213431	10576078	0.0749	0.5656
chr10	135534747	12265830	0.0905	0.5654
chr11	135006516	11128534	0.0824	0.5207
chr12	133851895	11284033	0.0843	0.3763
chr13	115169878	8048829	0.0699	0.3197
chr14	107349540	7517532	0.07	0.3714
chr15	102531392	7142084	0.0697	0.3248
chr16	90354753	7333894	0.0812	0.3876
chr17	81195210	6298376	0.0776	0.3749
chr18	78077248	6475305	0.0829	1.0174
chr19	59128983	4195373	0.071	0.7739
chr20	63025520	5415109	0.0859	0.3798
chr21	48129895	3256461	0.0677	0.3914
chr22	51304566	2858847	0.0557	0.2869
chrMT	16571	116848	7.0514	4.7155
chrX	155270560	14366245	0.0925	0.4599
chrY	59373566	680812	0.0115	0.2456

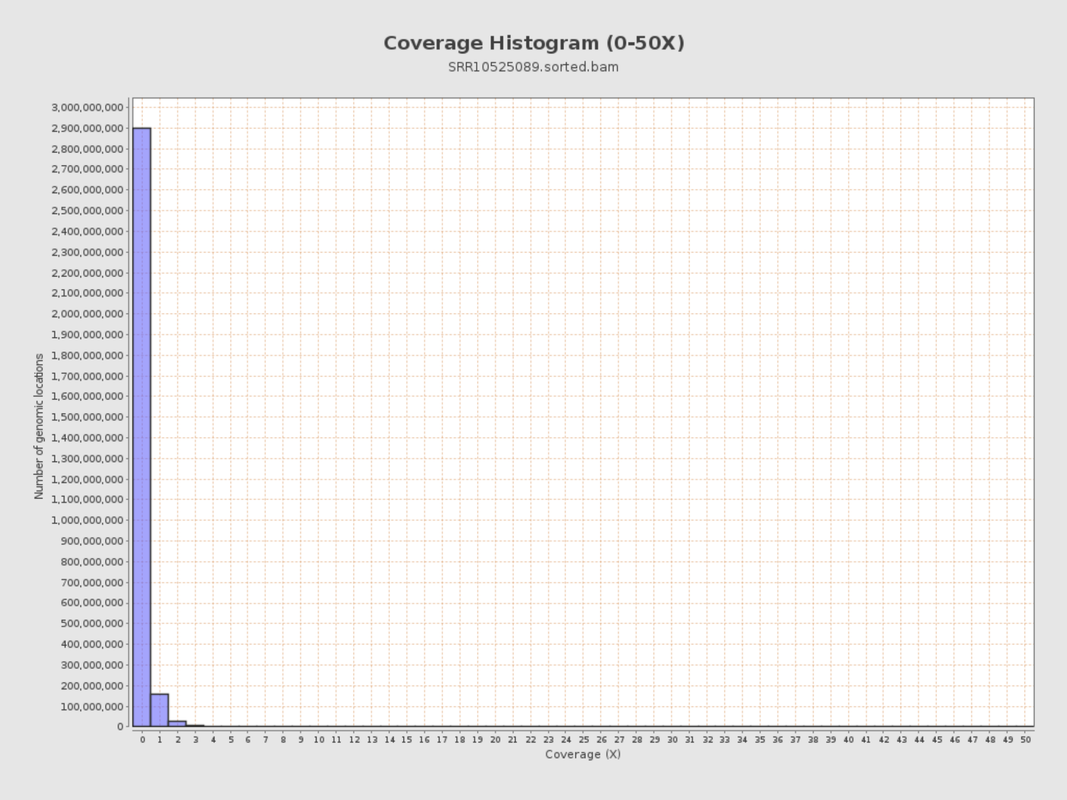
3. Results : Coverage across reference



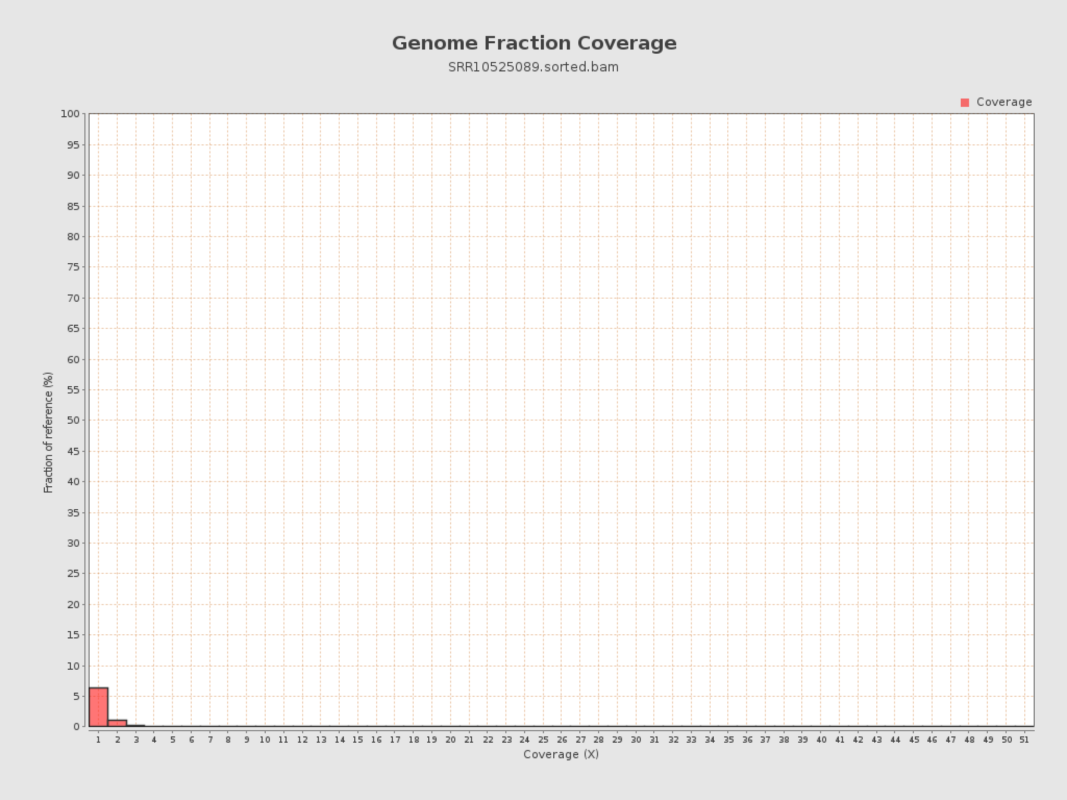
4. Results : Coverage Histogram



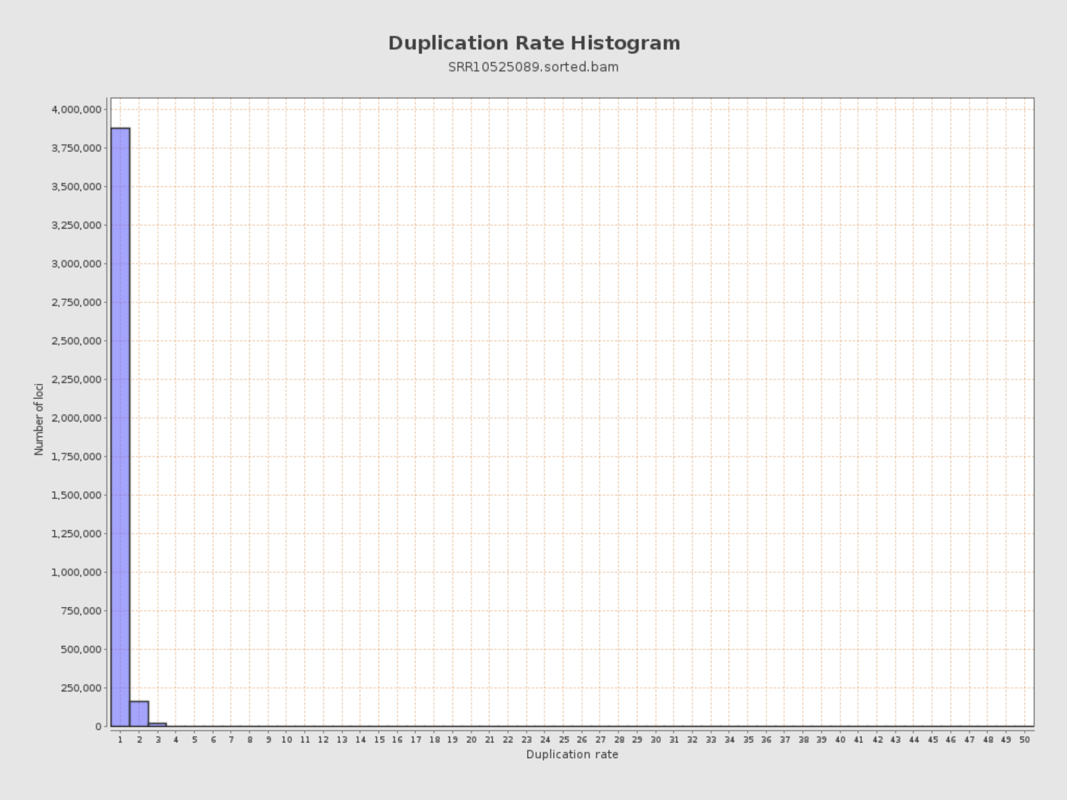
5. Results : Coverage Histogram (0-50X)



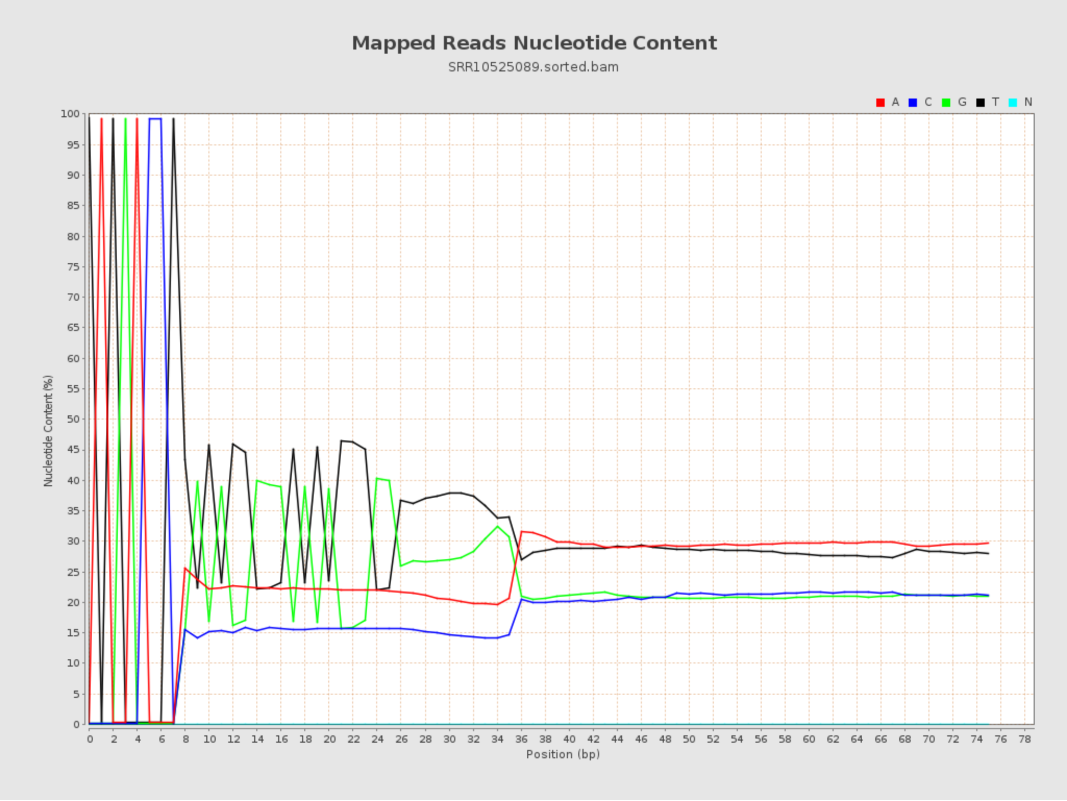
6. Results : Genome Fraction Coverage



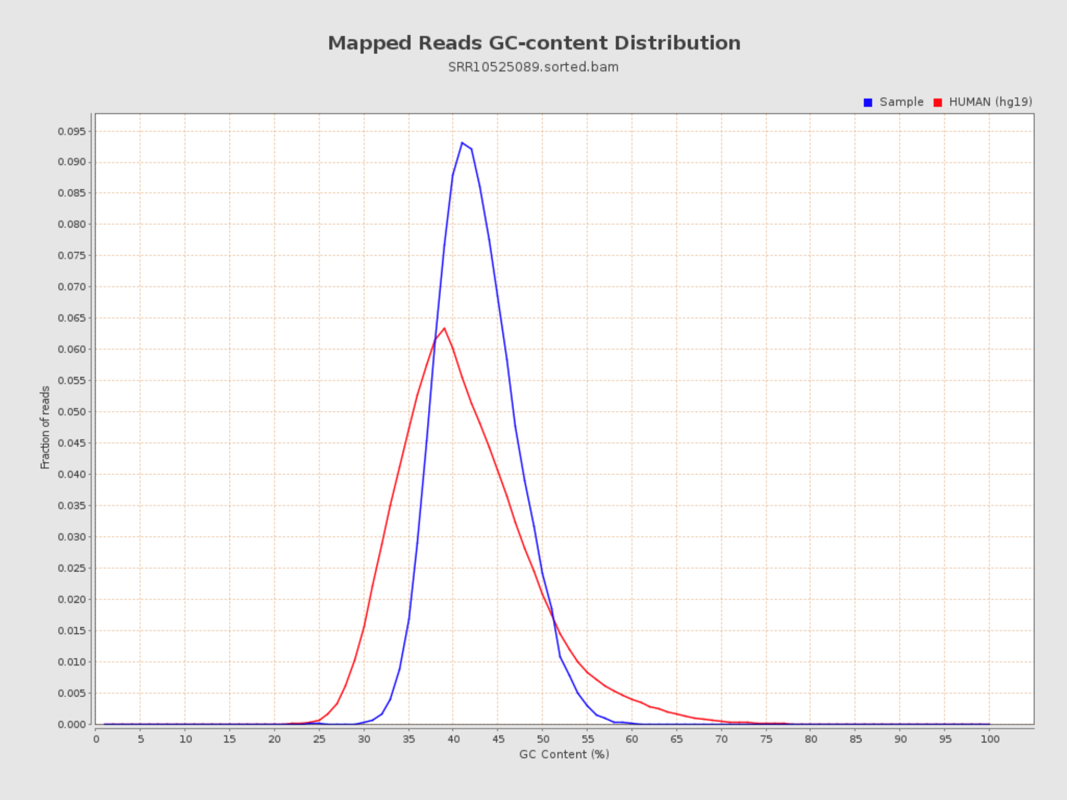
7. Results : Duplication Rate Histogram



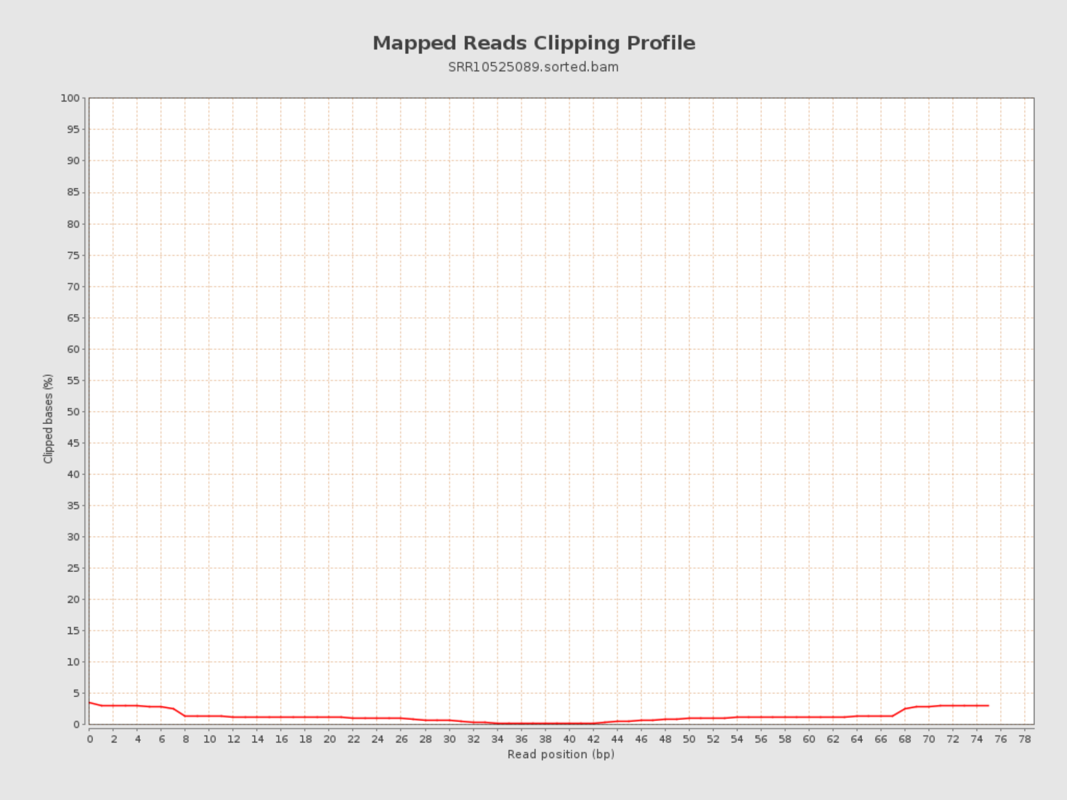
8. Results : Mapped Reads Nucleotide Content



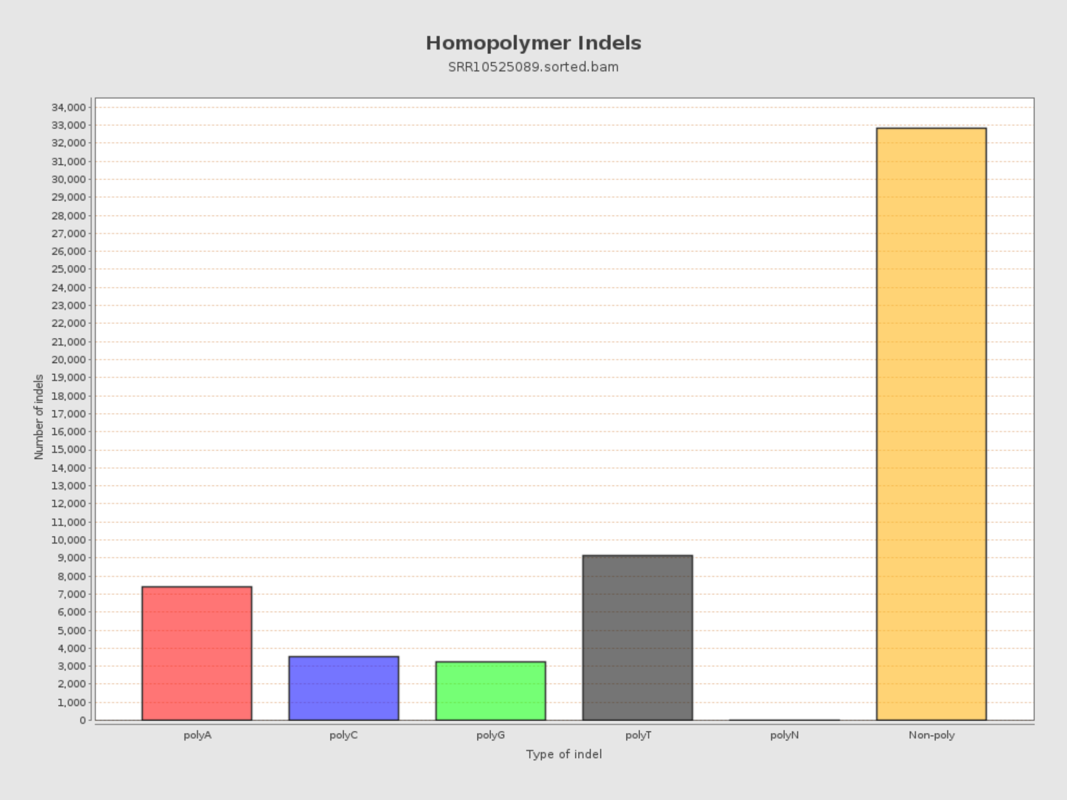
9. Results : Mapped Reads GC-content Distribution



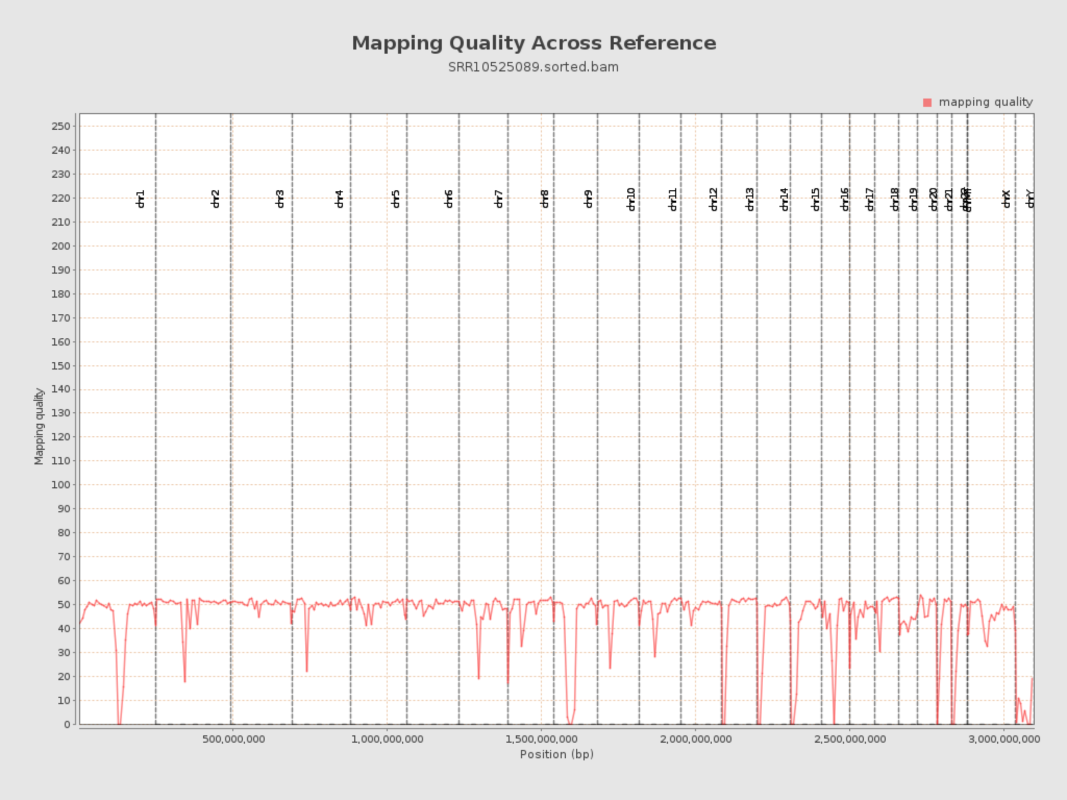
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram