Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 15:23:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525060.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_SRR10525060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 15:23:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,463,152
Mapped reads	2,263,848 / 91.91%
Unmapped reads	199,304 / 8.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,812 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	235,360 / 9.56%
Duplication rate	8.13%
Clipped reads	2,266,019 / 92%

2.2. ACGT Content

Number/percentage of A's	33,276,039 / 25.1%
Number/percentage of C's	23,496,756 / 17.72%
Number/percentage of T's	41,827,574 / 31.55%
Number/percentage of G's	33,968,425 / 25.62%
Number/percentage of N's	13,081 / 0.01%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0428

Standard Deviation	0.4095

2.4. Mapping Quality

Mean Mapping Quality	46.32

2.5. Mismatches and indels

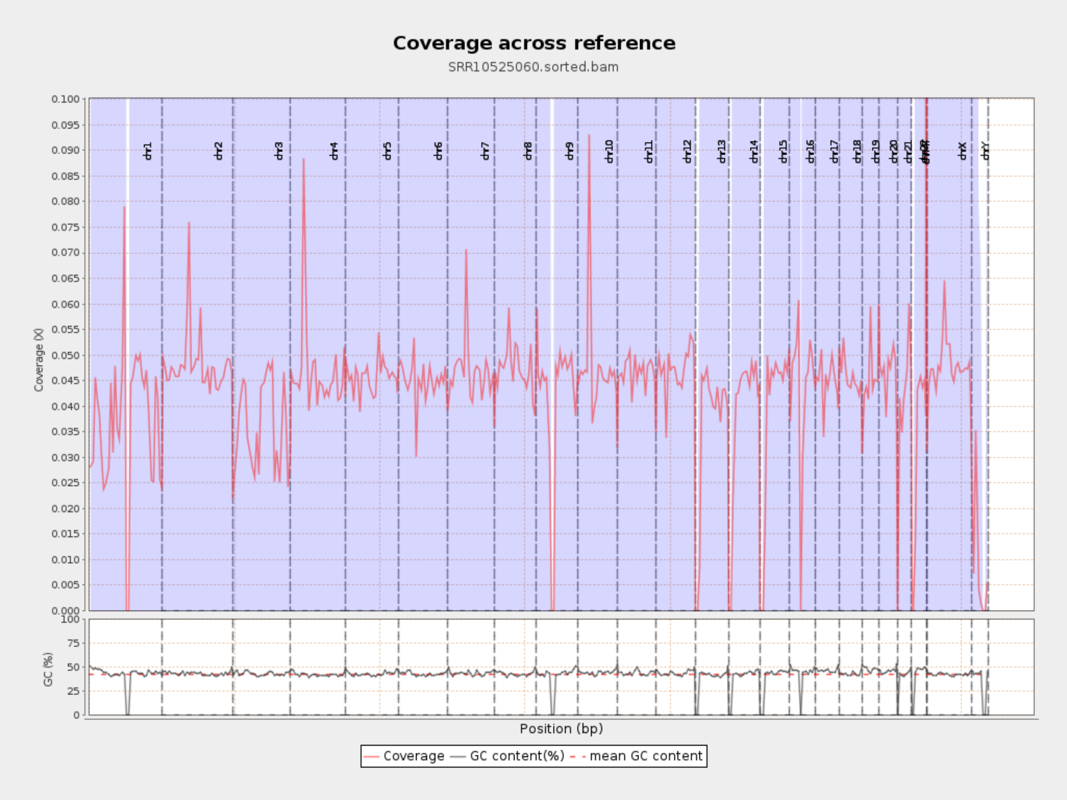
General error rate	0.49%
Mismatches	637,131
Insertions	9,270
Mapped reads with at least one insertion	0.41%
Deletions	24,947
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.66%

2.6. Chromosome stats

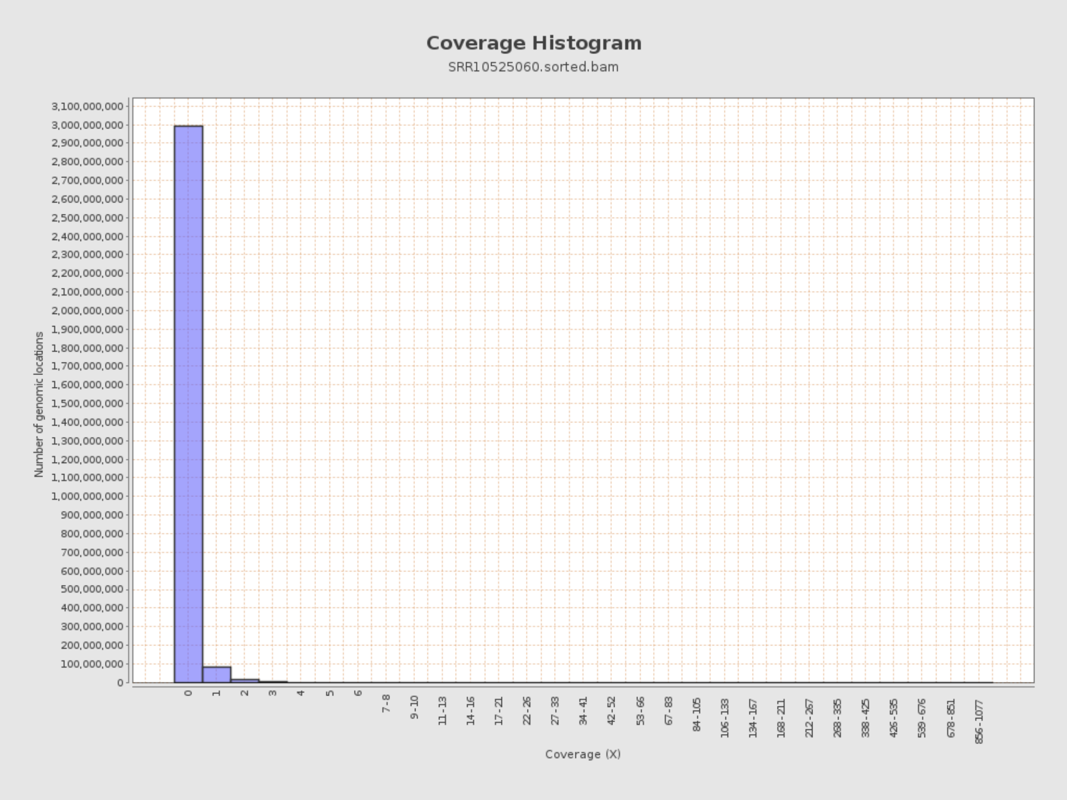
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9236397	0.0371	0.7999
chr2	243199373	11762446	0.0484	0.4952
chr3	198022430	7175662	0.0362	0.2345
chr4	191154276	8922886	0.0467	0.3251
chr5	180915260	8272658	0.0457	0.2626
chr6	171115067	7700345	0.045	0.2874
chr7	159138663	7493731	0.0471	0.4646

chr8	146364022	6935711	0.0474	0.4727
chr9	141213431	5735070	0.0406	0.3206
chr10	135534747	6471270	0.0477	0.4481
chr11	135006516	6274707	0.0465	0.3245
chr12	133851895	6314749	0.0472	0.2776
chr13	115169878	4103089	0.0356	0.2329
chr14	107349540	4070921	0.0379	0.2469
chr15	102531392	3910969	0.0381	0.2376
chr16	90354753	3926835	0.0435	0.2804
chr17	81195210	3630512	0.0447	0.2802
chr18	78077248	3593198	0.046	0.5729
chr19	59128983	2689490	0.0455	0.5589
chr20	63025520	2936162	0.0466	0.278
chr21	48129895	1971151	0.041	0.3079
chr22	51304566	1559512	0.0304	0.2137
chrMT	16571	13268	0.8007	1.0372
chrX	155270560	7421097	0.0478	0.2974
chrY	59373566	499954	0.0084	0.3492

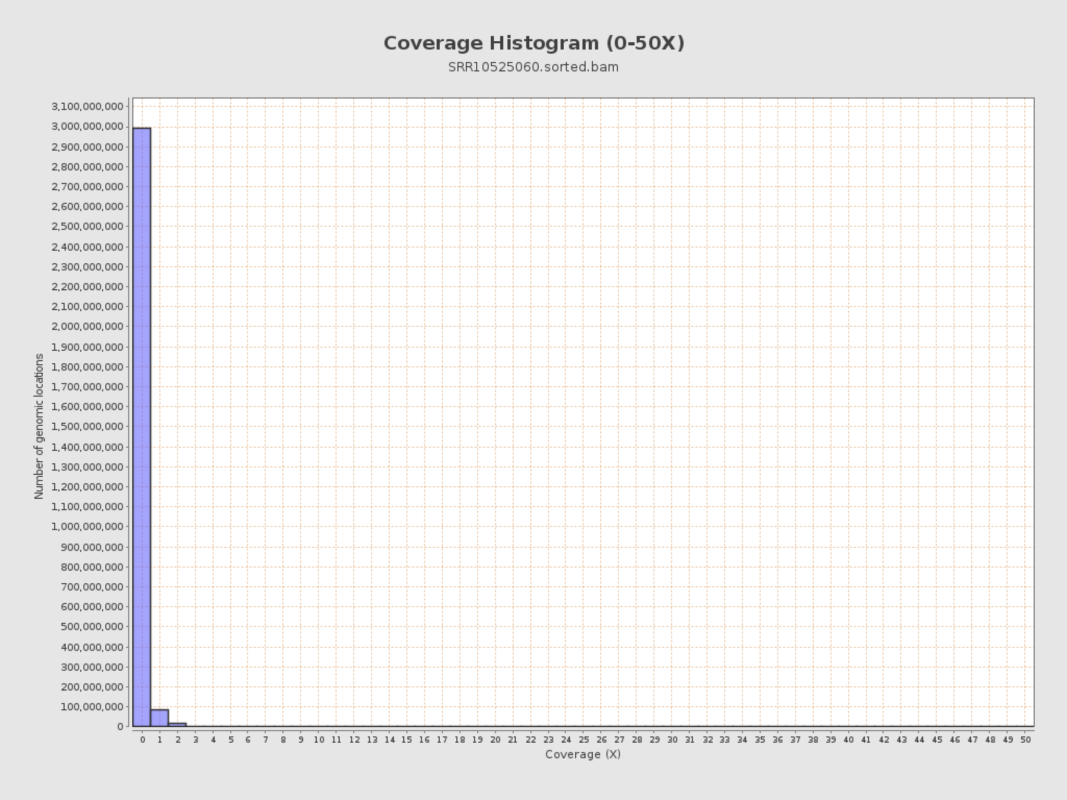
3. Results : Coverage across reference



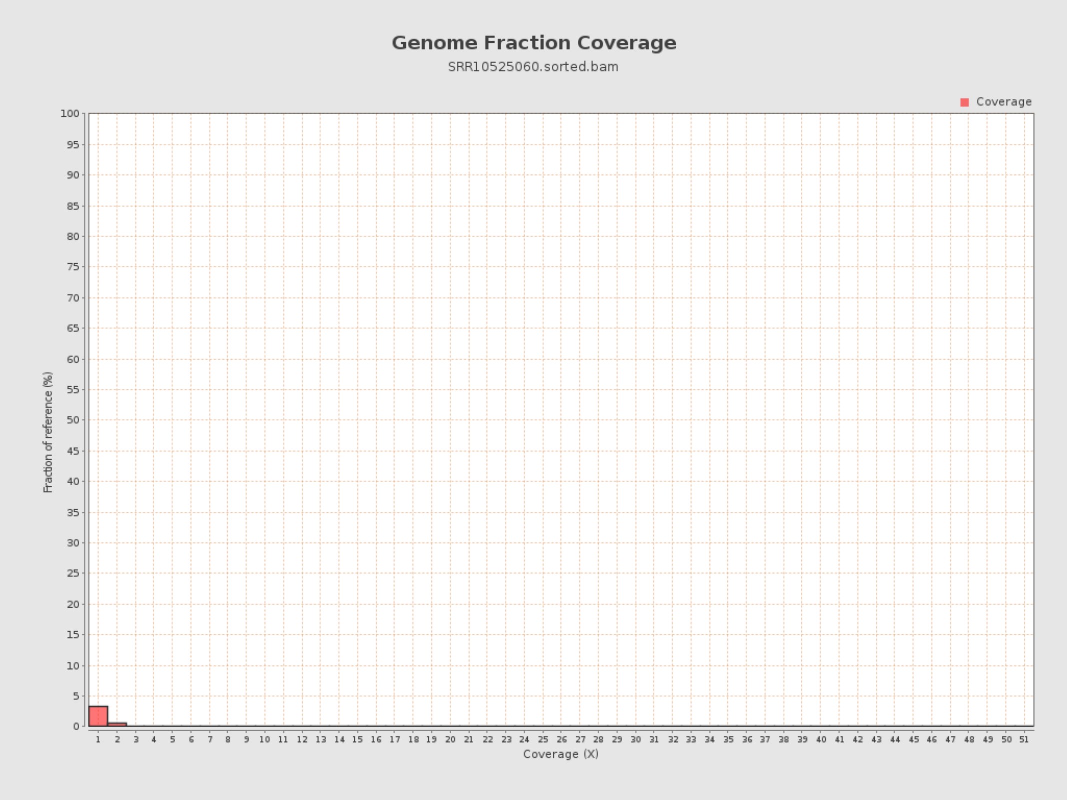
4. Results : Coverage Histogram



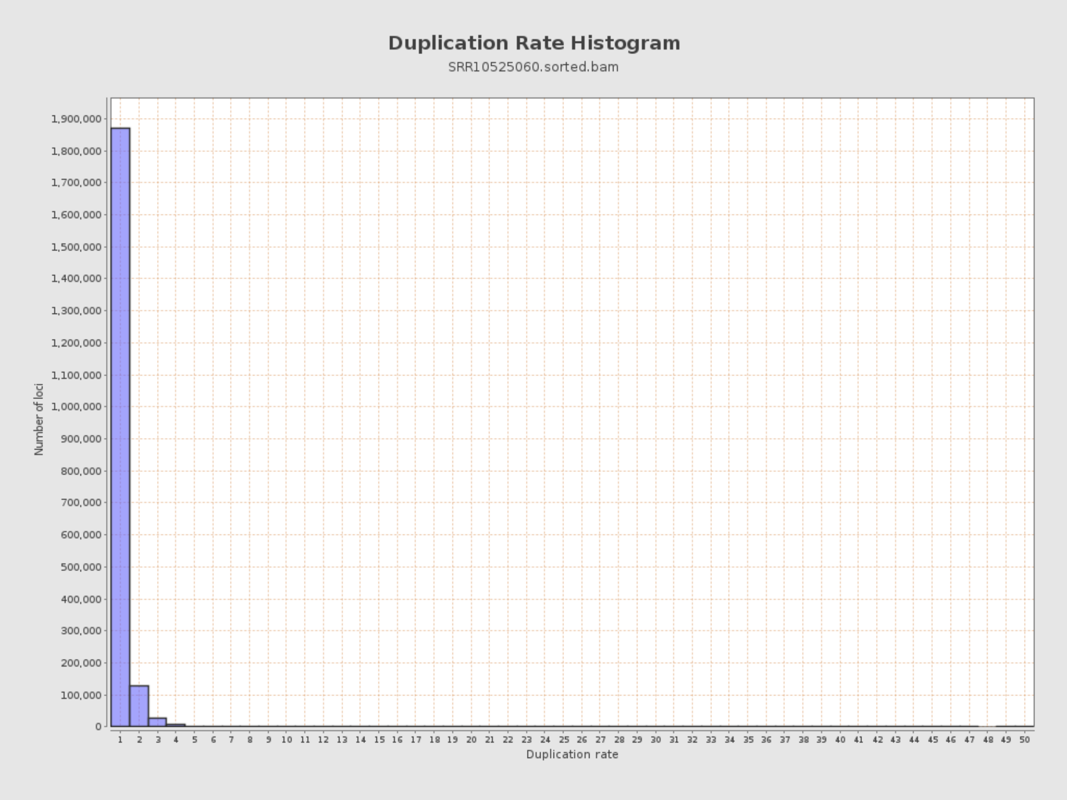
5. Results : Coverage Histogram (0-50X)



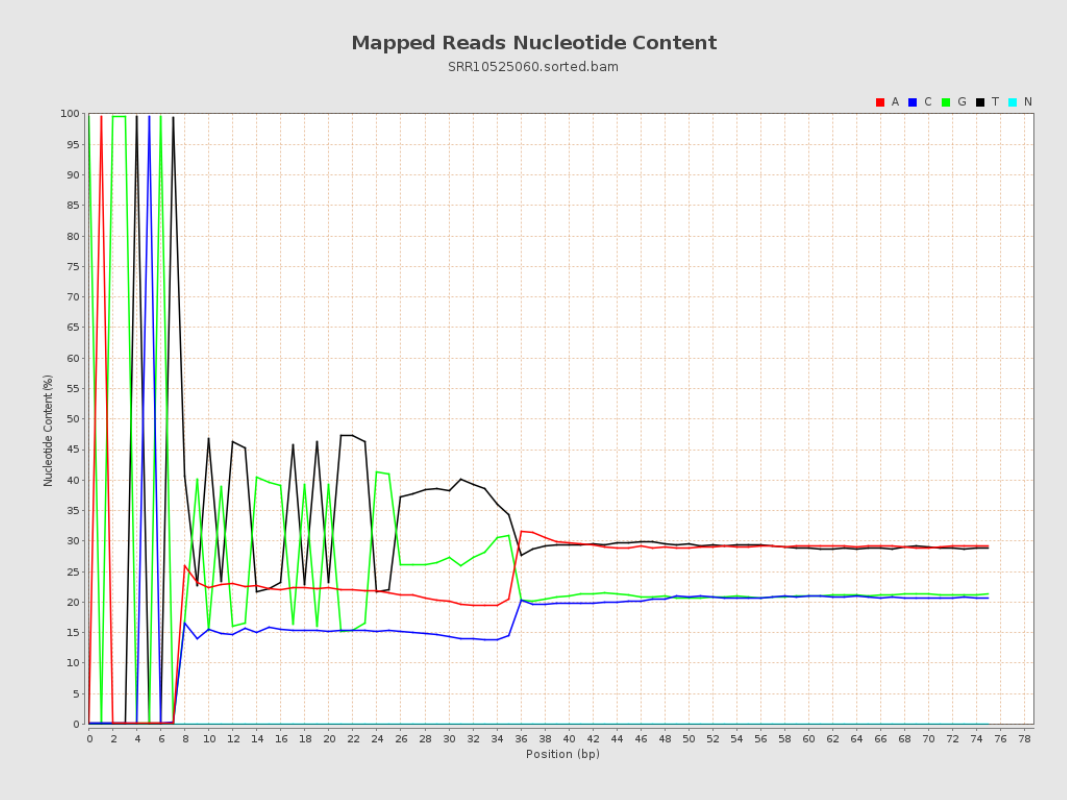
6. Results : Genome Fraction Coverage



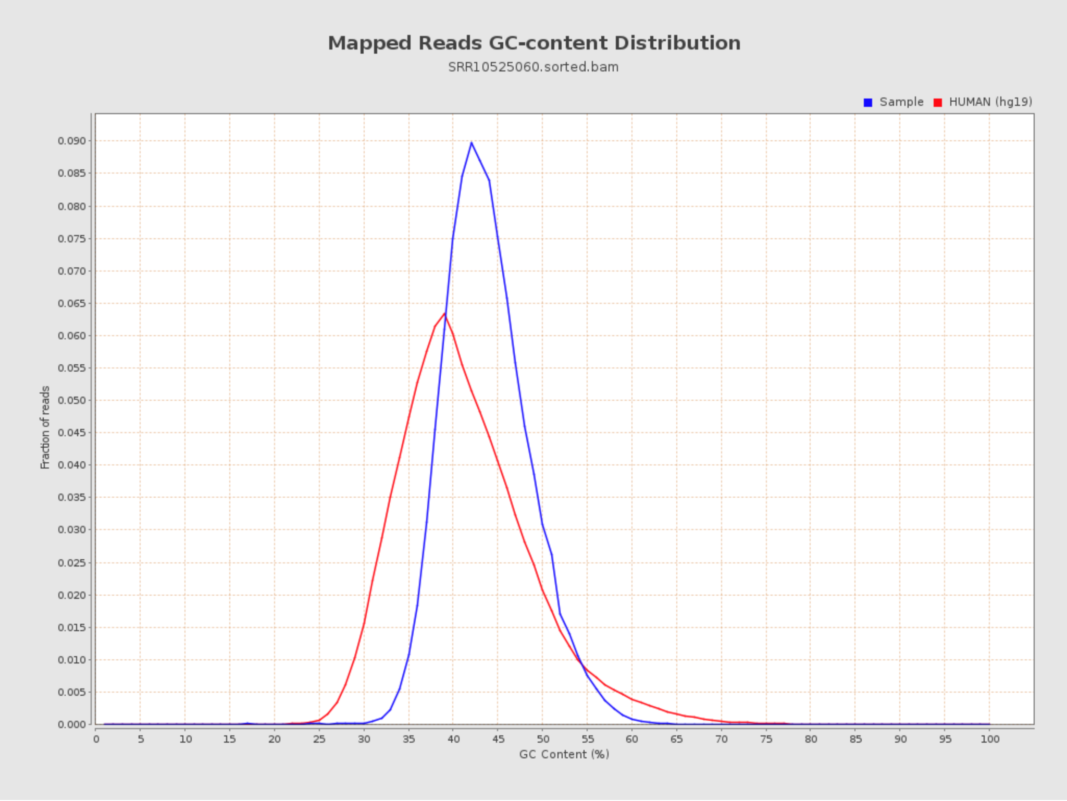
7. Results : Duplication Rate Histogram



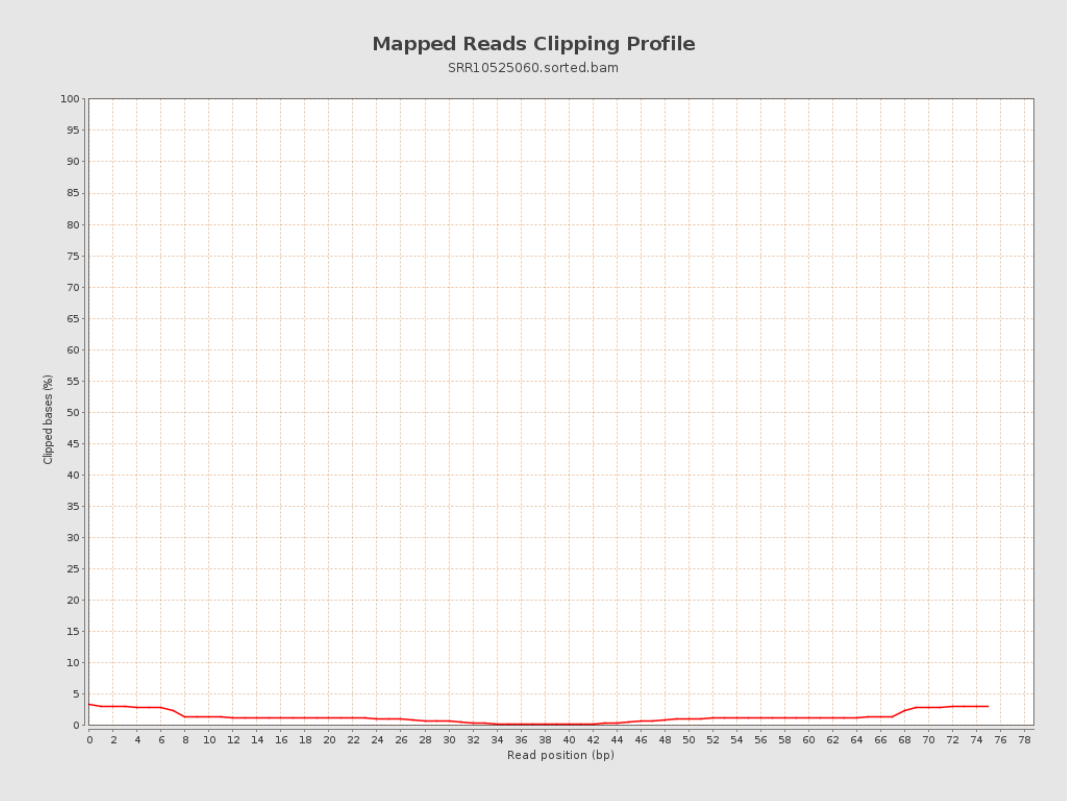
8. Results : Mapped Reads Nucleotide Content



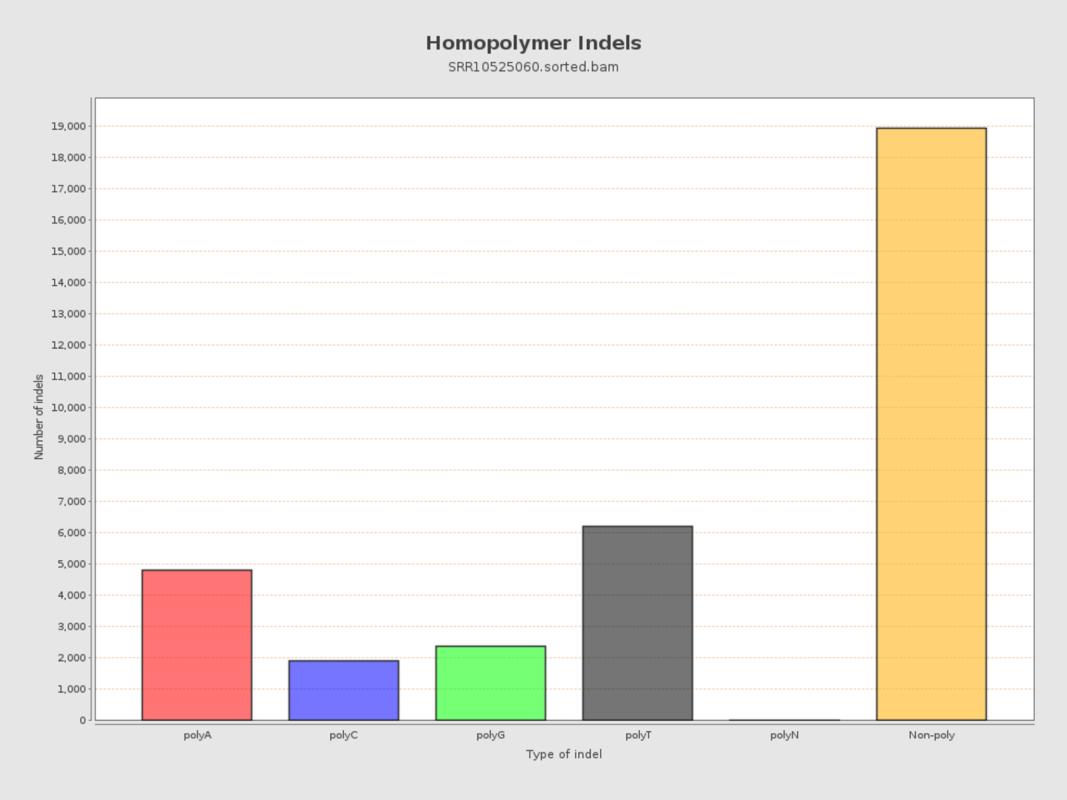
9. Results : Mapped Reads GC-content Distribution



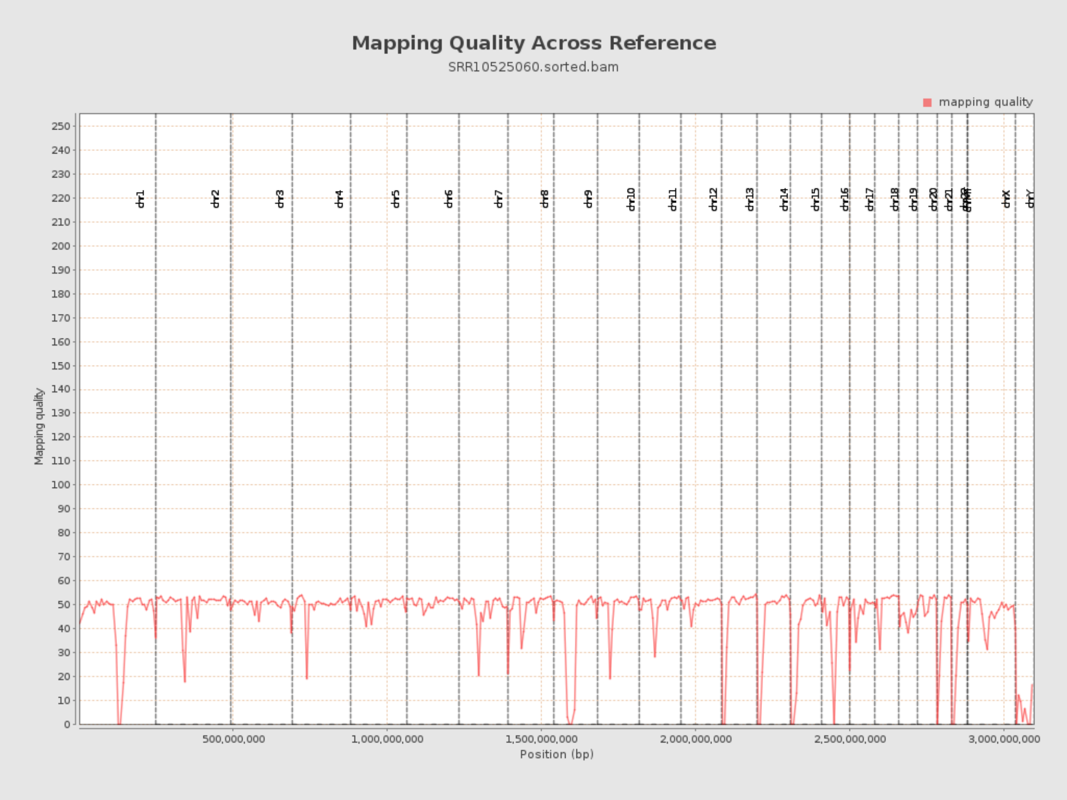
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram