Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:37:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525115.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_SRR10525115 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525115.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:37:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525115.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,239,373
Mapped reads	2,038,606 / 91.03%
Unmapped reads	200,767 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,509 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	82,559 / 3.69%
Duplication rate	3.05%
Clipped reads	2,041,261 / 91.15%

2.2. ACGT Content

Number/percentage of A's	28,339,819 / 24.27%
Number/percentage of C's	23,867,121 / 20.44%
Number/percentage of T's	37,111,875 / 31.78%
Number/percentage of G's	27,446,699 / 23.51%
Number/percentage of N's	3,616 / 0%
GC Percentage	43.94%

2.3. Coverage

Mean	0.0377

Standard Deviation	0.3289

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

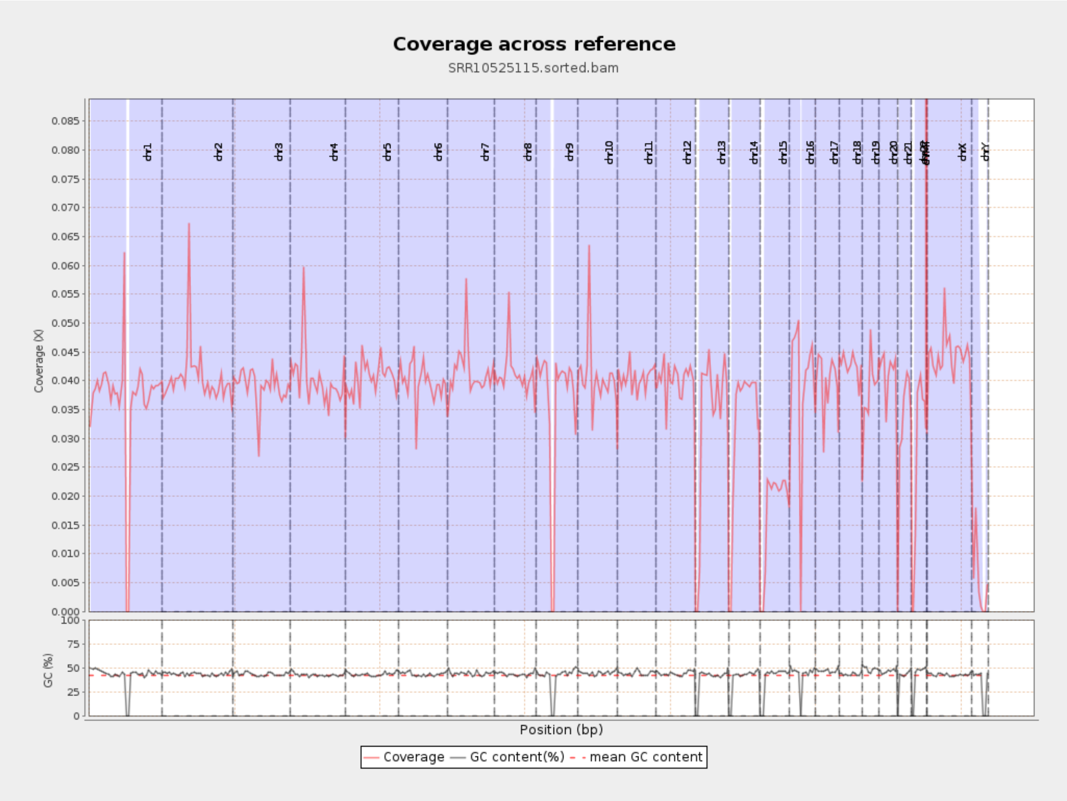
General error rate	0.5%
Mismatches	565,340
Insertions	7,675
Mapped reads with at least one insertion	0.37%
Deletions	19,479
Mapped reads with at least one deletion	0.95%
Homopolymer indels	41.78%

2.6. Chromosome stats

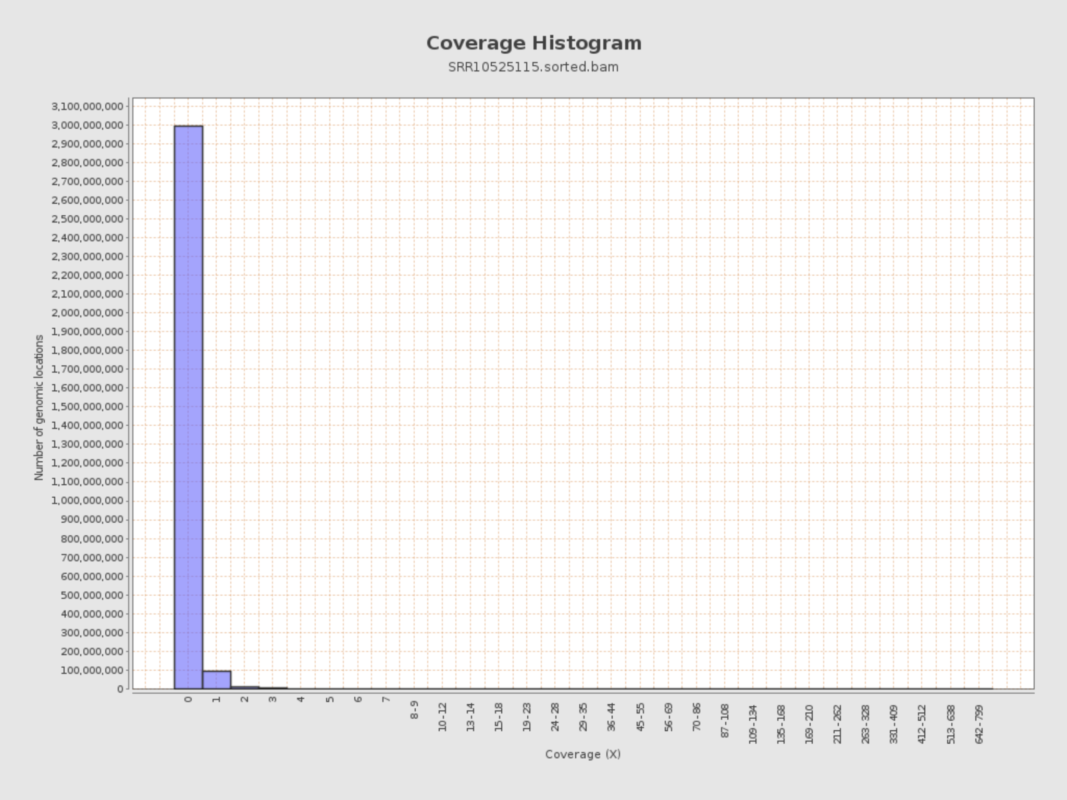
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9149060	0.0367	0.6312
chr2	243199373	9876457	0.0406	0.3501
chr3	198022430	7725363	0.039	0.2184
chr4	191154276	7687362	0.0402	0.245
chr5	180915260	7337620	0.0406	0.2254
chr6	171115067	6803884	0.0398	0.2447
chr7	159138663	6635140	0.0417	0.3636

chr8	146364022	6026354	0.0412	0.3854
chr9	141213431	5067406	0.0359	0.3165
chr10	135534747	5533288	0.0408	0.3106
chr11	135006516	5445747	0.0403	0.2989
chr12	133851895	5355174	0.04	0.2306
chr13	115169878	3802160	0.033	0.2013
chr14	107349540	3460841	0.0322	0.2236
chr15	102531392	1802678	0.0176	0.1495
chr16	90354753	3584659	0.0397	0.2401
chr17	81195210	3198476	0.0394	0.2346
chr18	78077248	3333538	0.0427	0.5221
chr19	59128983	2279919	0.0386	0.4563
chr20	63025520	2587079	0.041	0.2318
chr21	48129895	1535093	0.0319	0.2283
chr22	51304566	1343932	0.0262	0.1788
chrMT	16571	46257	2.7914	2.3645
chrX	155270560	6855534	0.0442	0.2737
chrY	59373566	328396	0.0055	0.1313

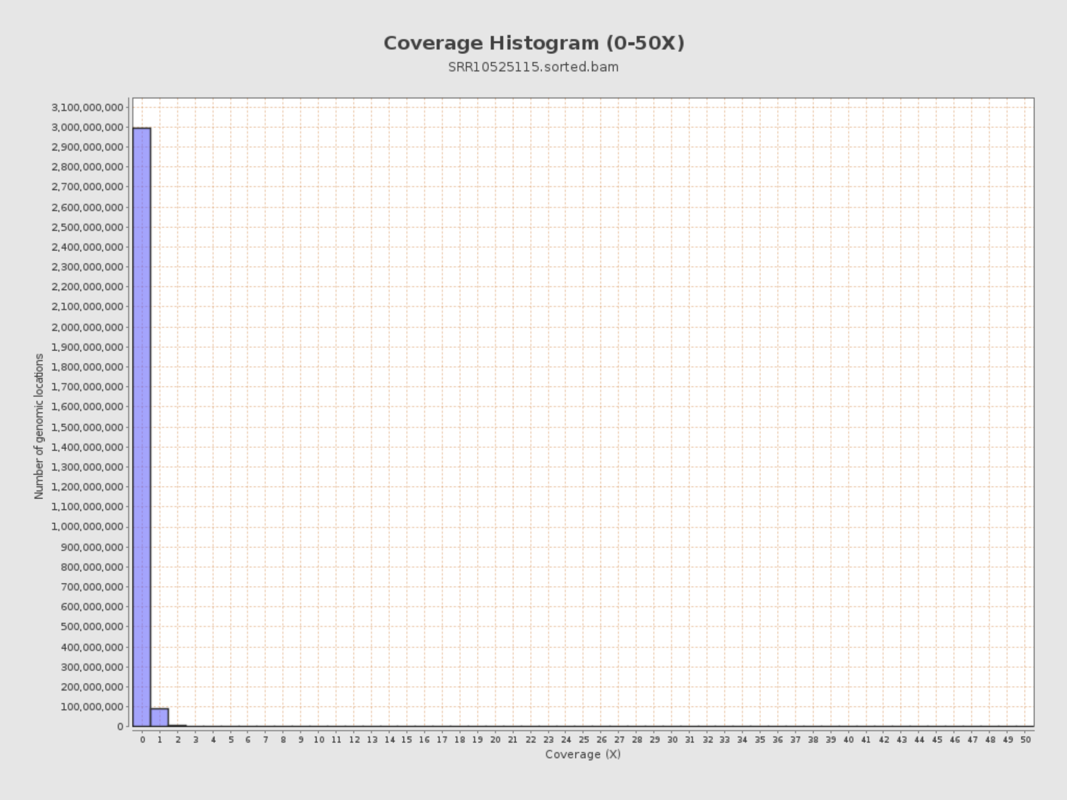
3. Results : Coverage across reference



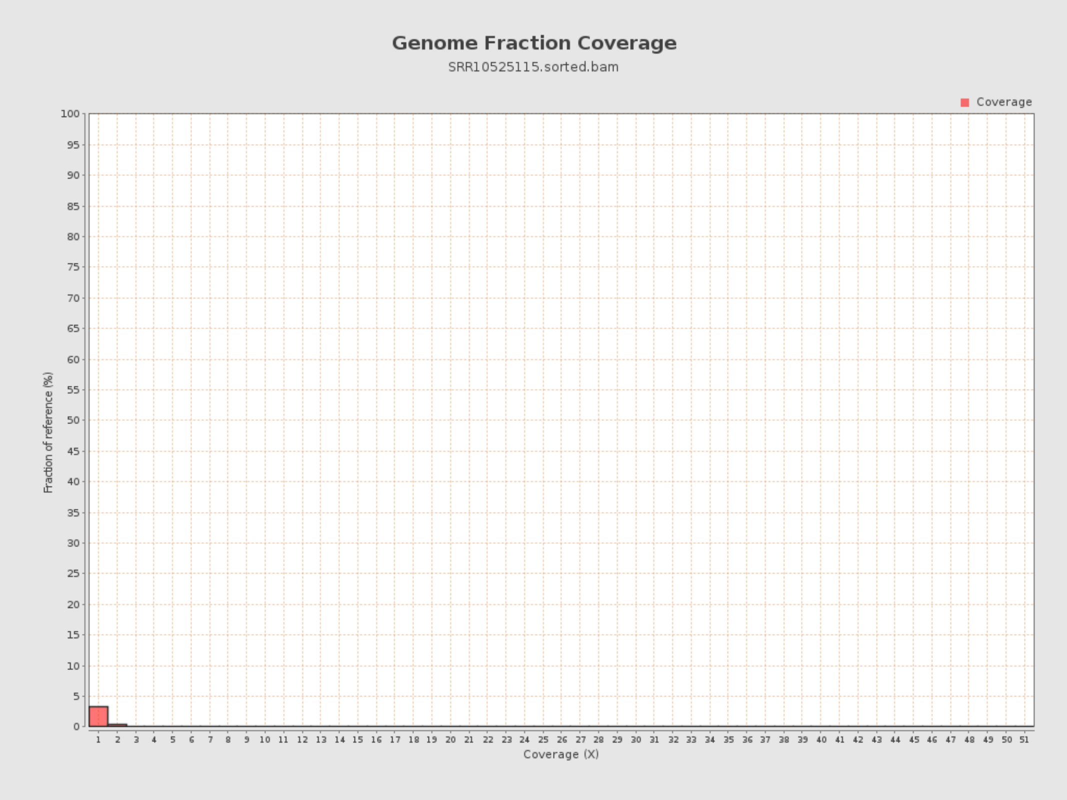
4. Results : Coverage Histogram



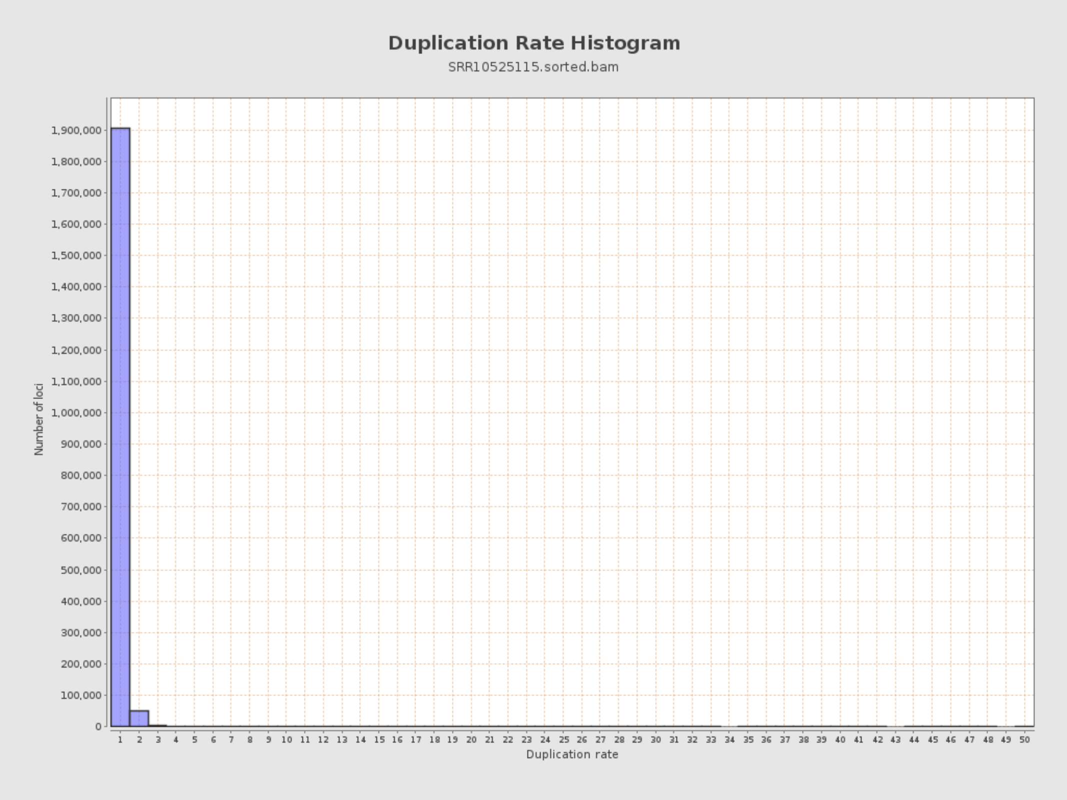
5. Results : Coverage Histogram (0-50X)



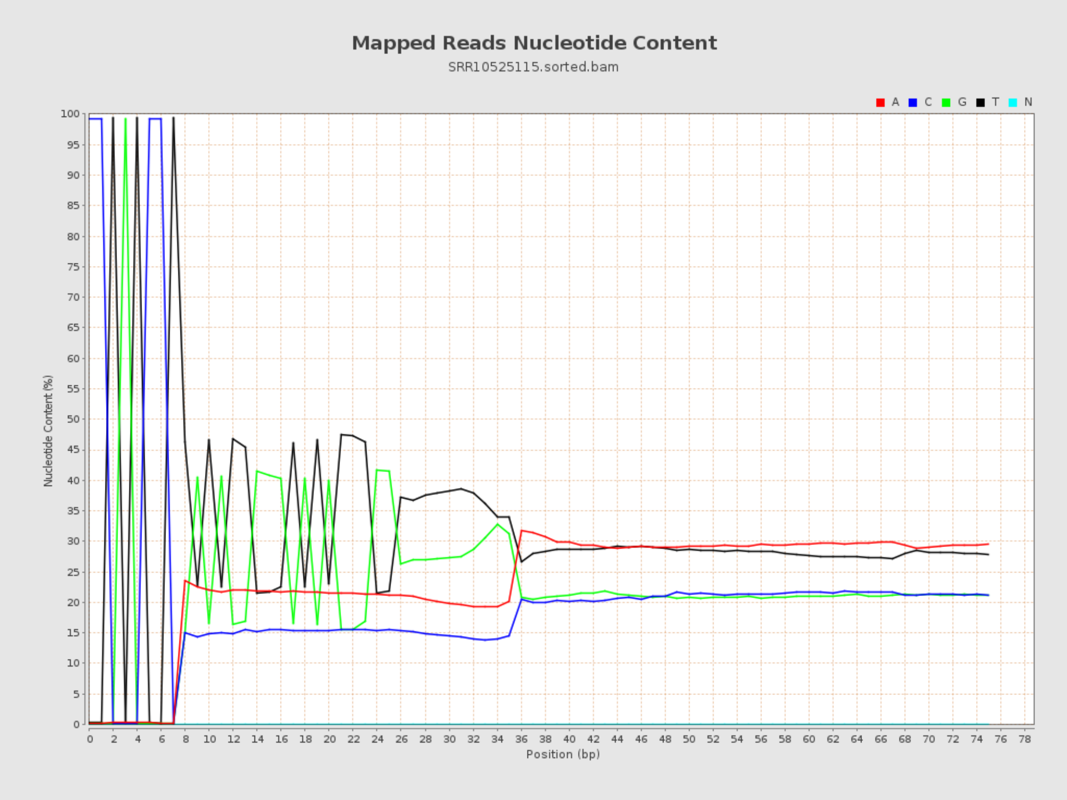
6. Results : Genome Fraction Coverage



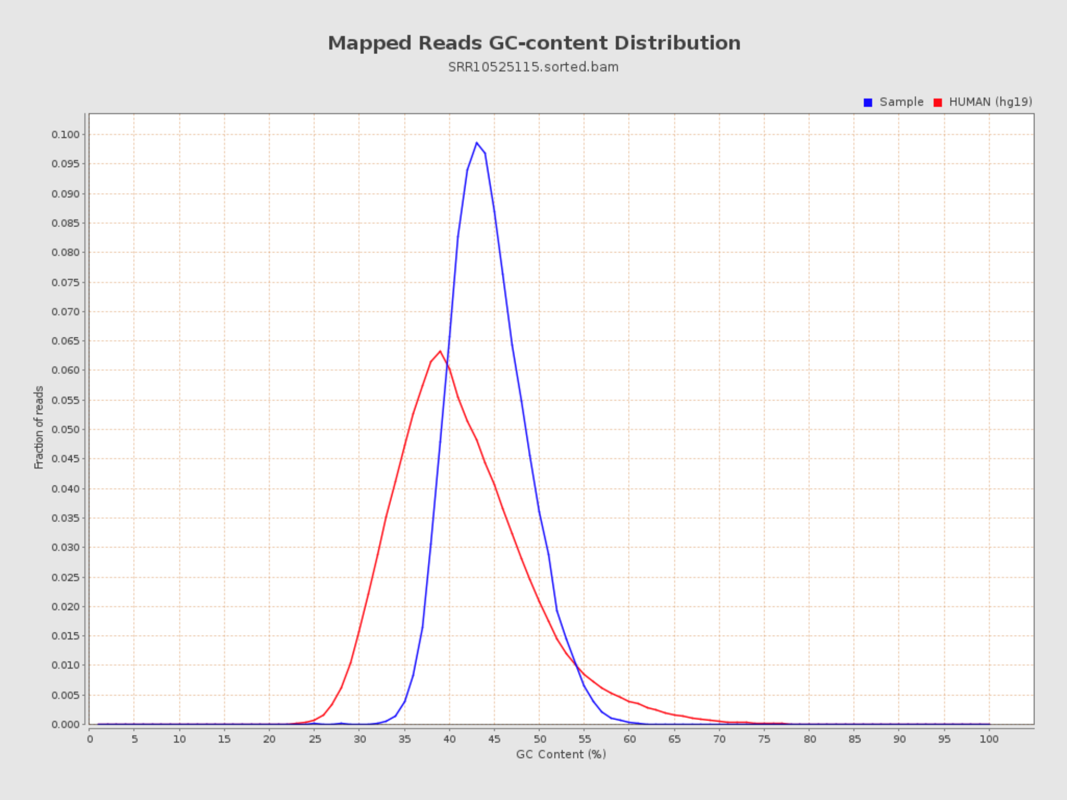
7. Results : Duplication Rate Histogram



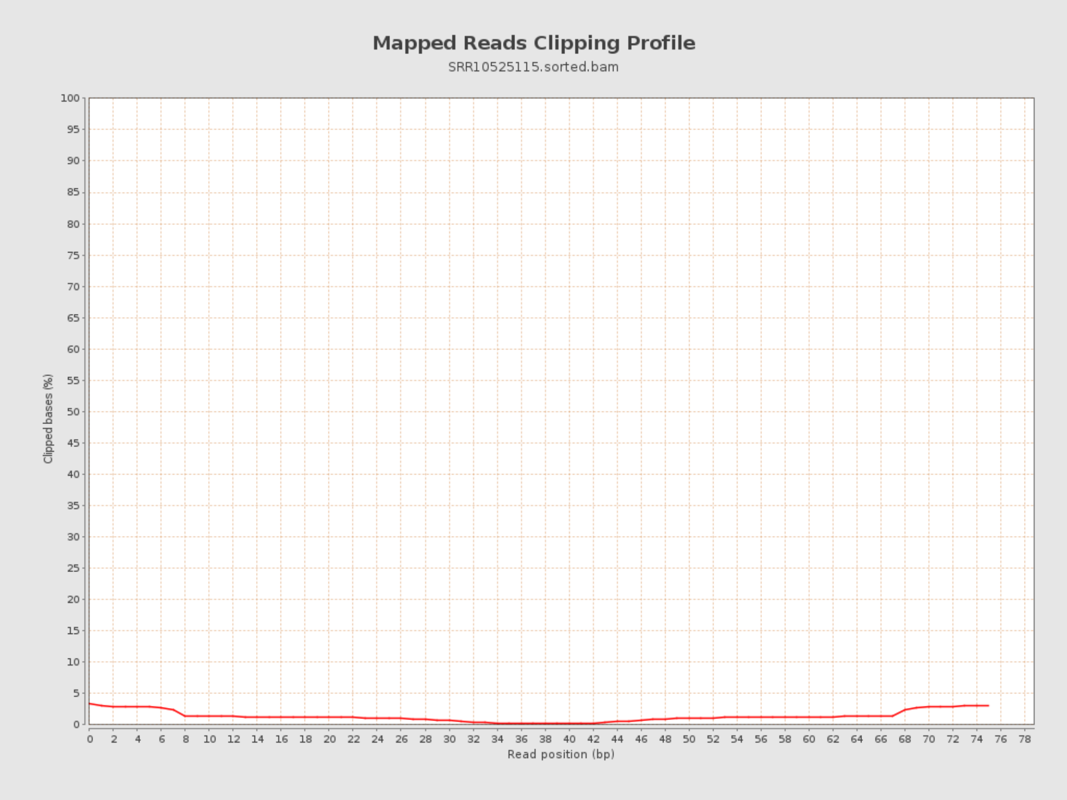
8. Results : Mapped Reads Nucleotide Content



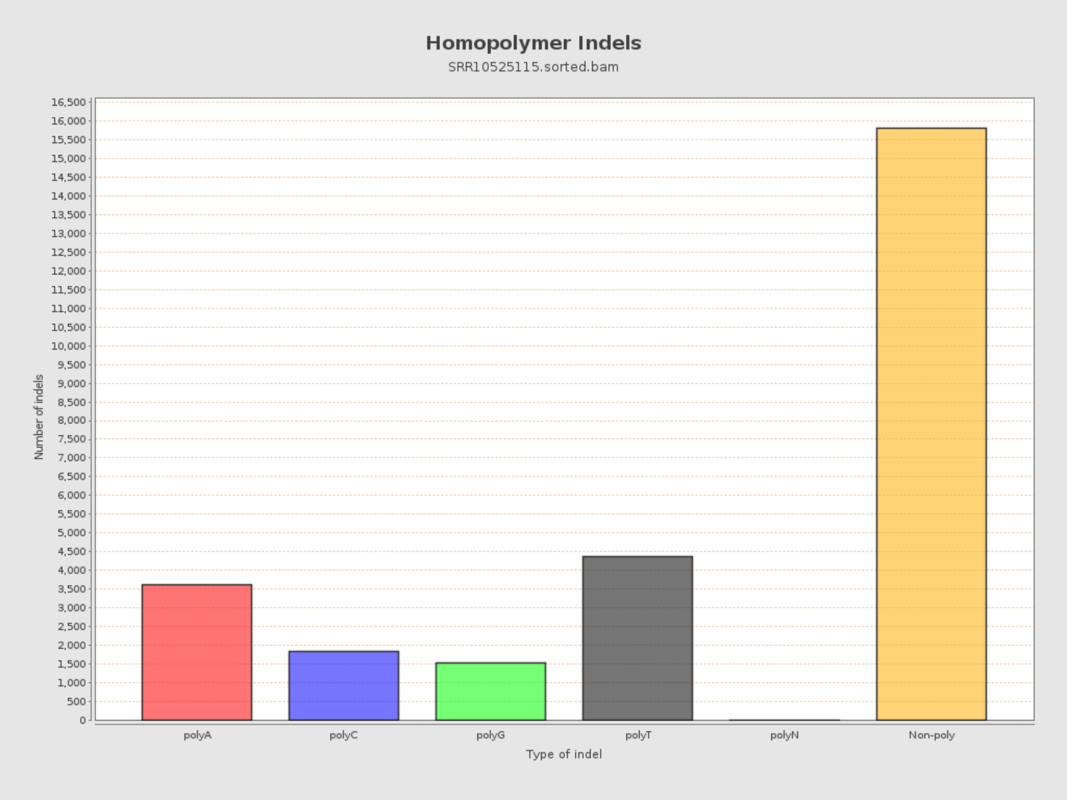
9. Results : Mapped Reads GC-content Distribution



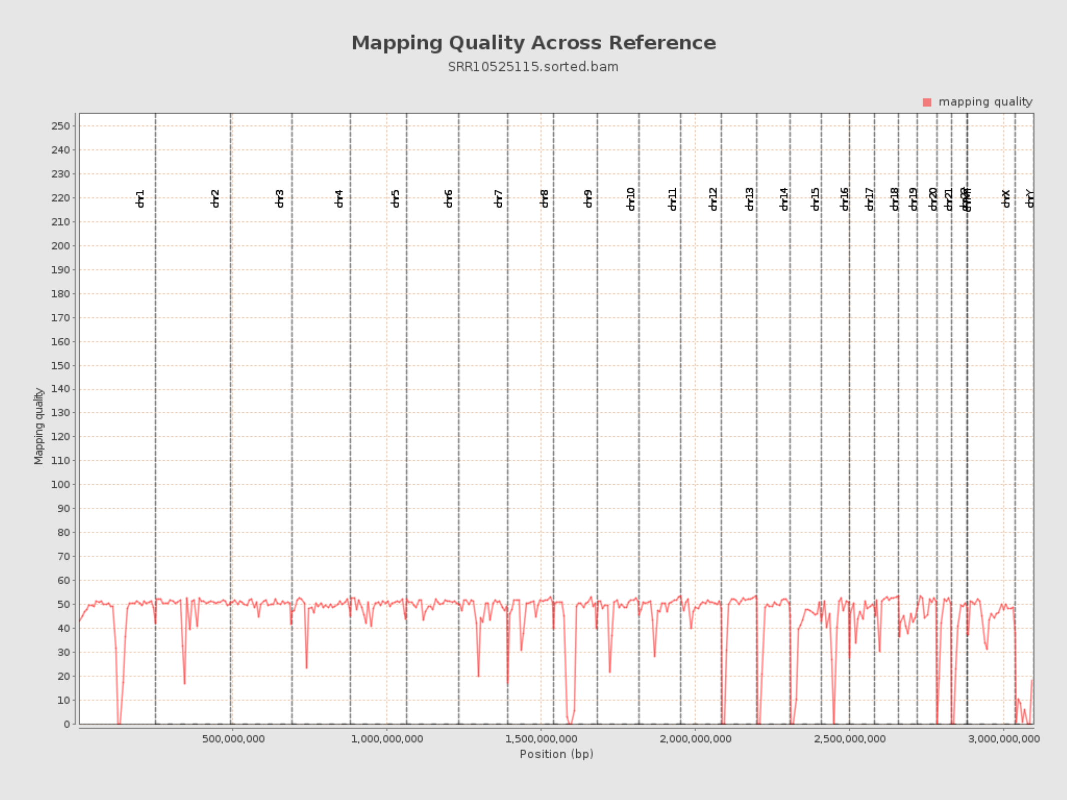
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram