Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:01:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525125.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_SRR10525125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:01:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,863,357
Mapped reads	1,601,795 / 85.96%
Unmapped reads	261,562 / 14.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,623 / 2.56%
Read min/max/mean length	30 / 101 / 101.94
Duplicated reads (estimated)	50,368 / 2.7%
Duplication rate	1.89%
Clipped reads	1,647,917 / 88.44%

2.2. ACGT Content

Number/percentage of A's	31,488,769 / 26.16%
Number/percentage of C's	23,496,145 / 19.52%
Number/percentage of T's	36,890,815 / 30.65%
Number/percentage of G's	28,469,293 / 23.66%
Number/percentage of N's	4,922 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0389

Standard Deviation	0.3821

2.4. Mapping Quality

Mean Mapping Quality	45.25

2.5. Mismatches and indels

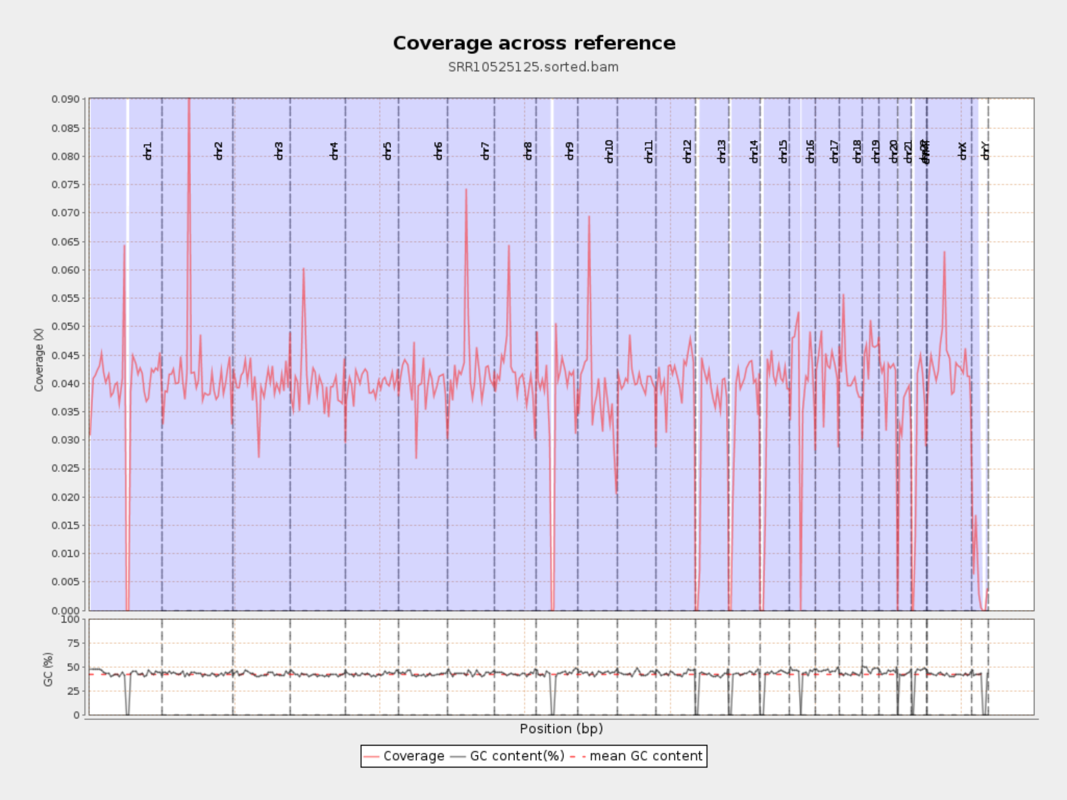
General error rate	0.78%
Mismatches	919,695
Insertions	10,648
Mapped reads with at least one insertion	0.66%
Deletions	27,788
Mapped reads with at least one deletion	1.71%
Homopolymer indels	41.67%

2.6. Chromosome stats

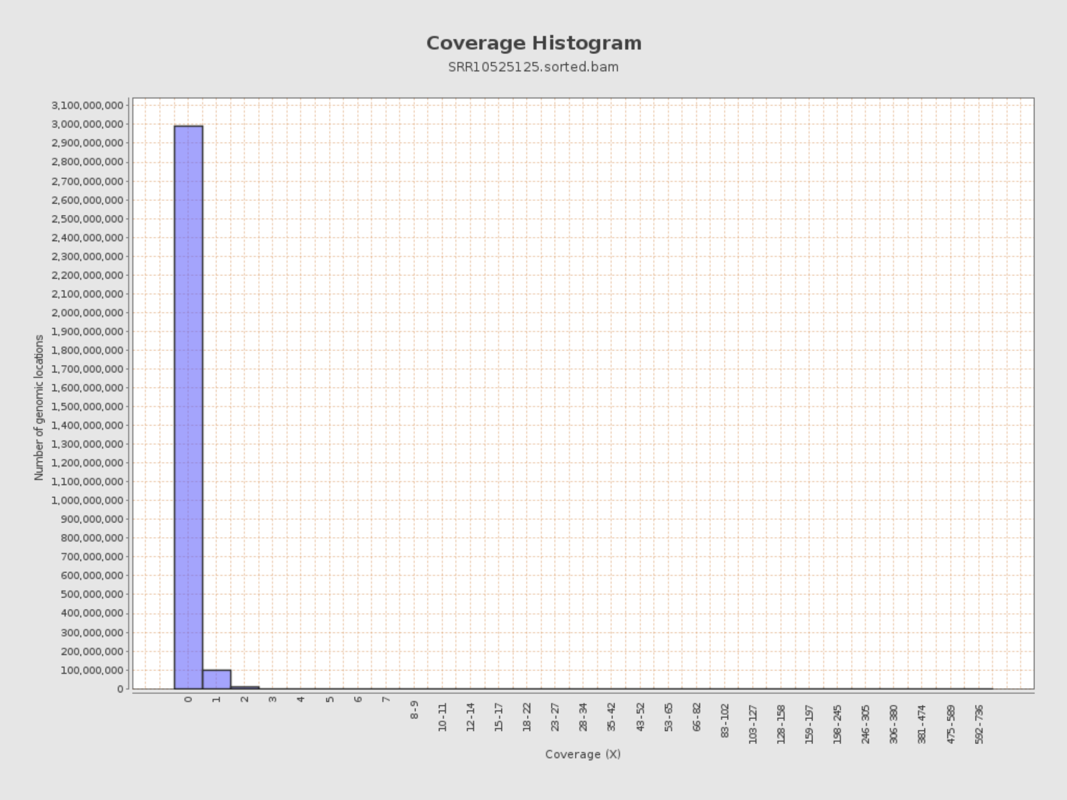
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9708522	0.039	0.5511
chr2	243199373	10211852	0.042	0.609
chr3	198022430	7918135	0.04	0.2182
chr4	191154276	7639797	0.04	0.2469
chr5	180915260	7229494	0.04	0.2239
chr6	171115067	6839434	0.04	0.2605
chr7	159138663	6826399	0.0429	0.5587

chr8	146364022	6125000	0.0418	0.5182
chr9	141213431	5110329	0.0362	0.3733
chr10	135534747	5218478	0.0385	0.3633
chr11	135006516	5455113	0.0404	0.3847
chr12	133851895	5522973	0.0413	0.2249
chr13	115169878	3785831	0.0329	0.1973
chr14	107349540	3671328	0.0342	0.2414
chr15	102531392	3488459	0.034	0.2026
chr16	90354753	3616702	0.04	0.2437
chr17	81195210	3425296	0.0422	0.2651
chr18	78077248	3277873	0.042	0.6206
chr19	59128983	2689795	0.0455	0.4368
chr20	63025520	2558947	0.0406	0.2311
chr21	48129895	1545946	0.0321	0.2206
chr22	51304566	1436209	0.028	0.1827
chrMT	16571	518	0.0313	0.174
chrX	155270560	6780360	0.0437	0.3104
chrY	59373566	315447	0.0053	0.1369

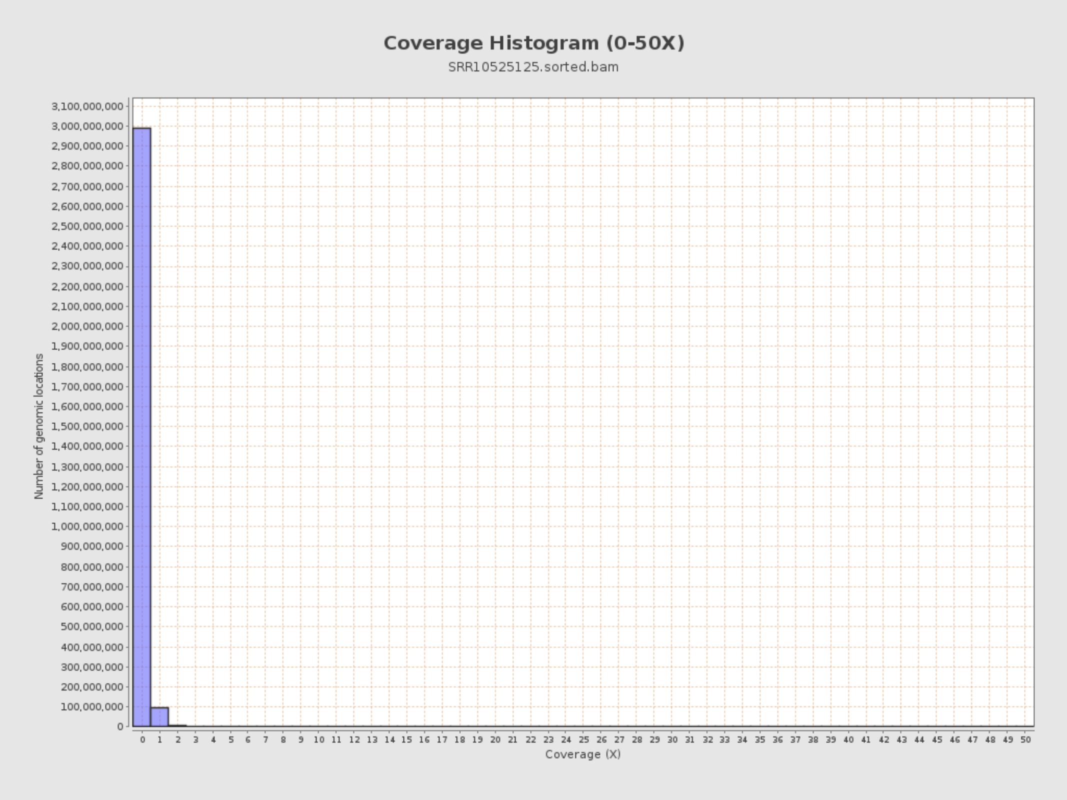
3. Results : Coverage across reference



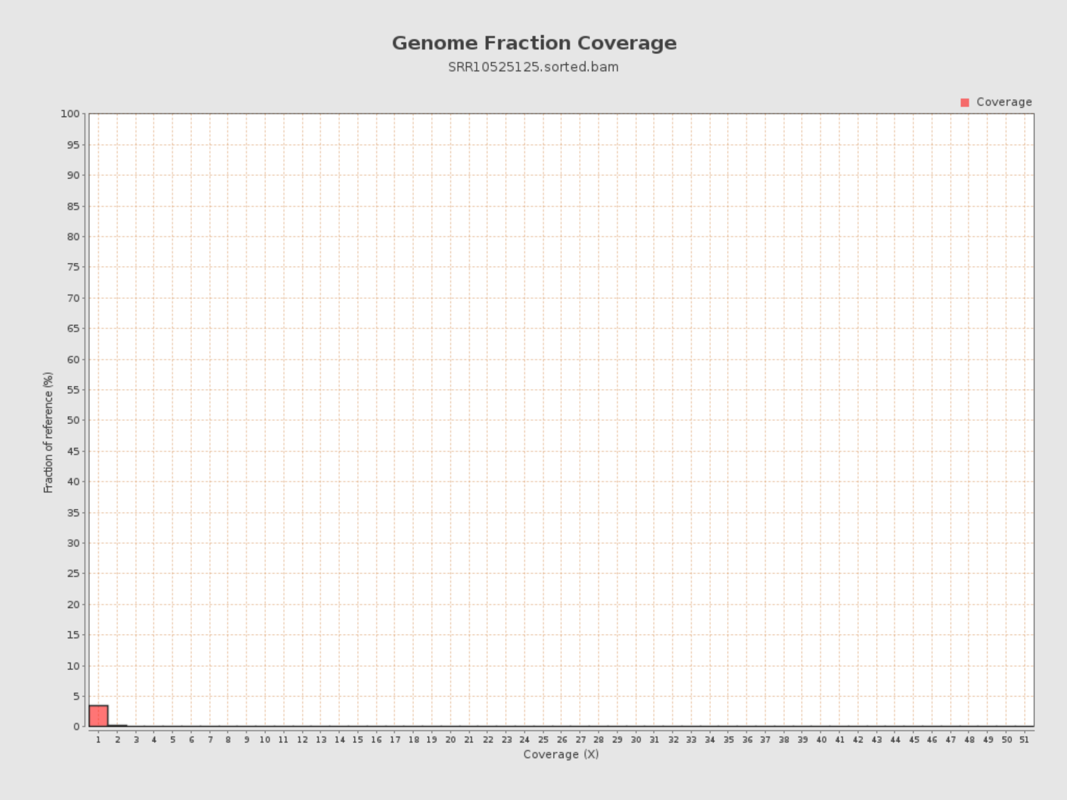
4. Results : Coverage Histogram



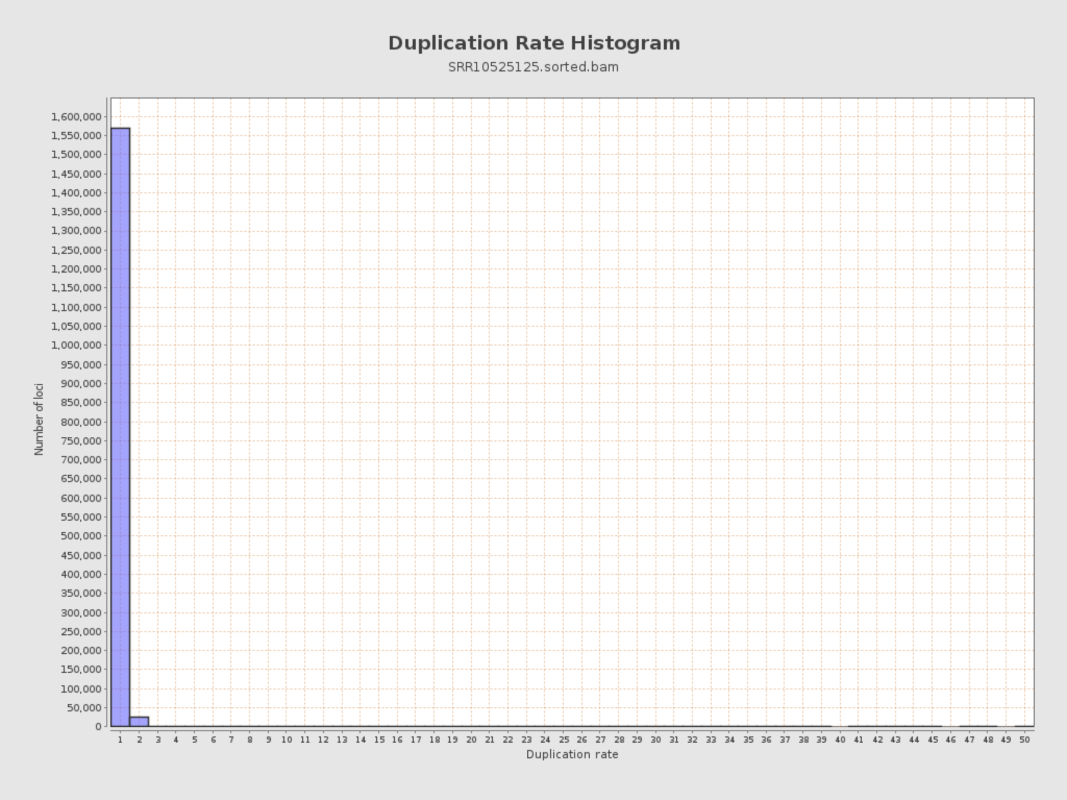
5. Results : Coverage Histogram (0-50X)



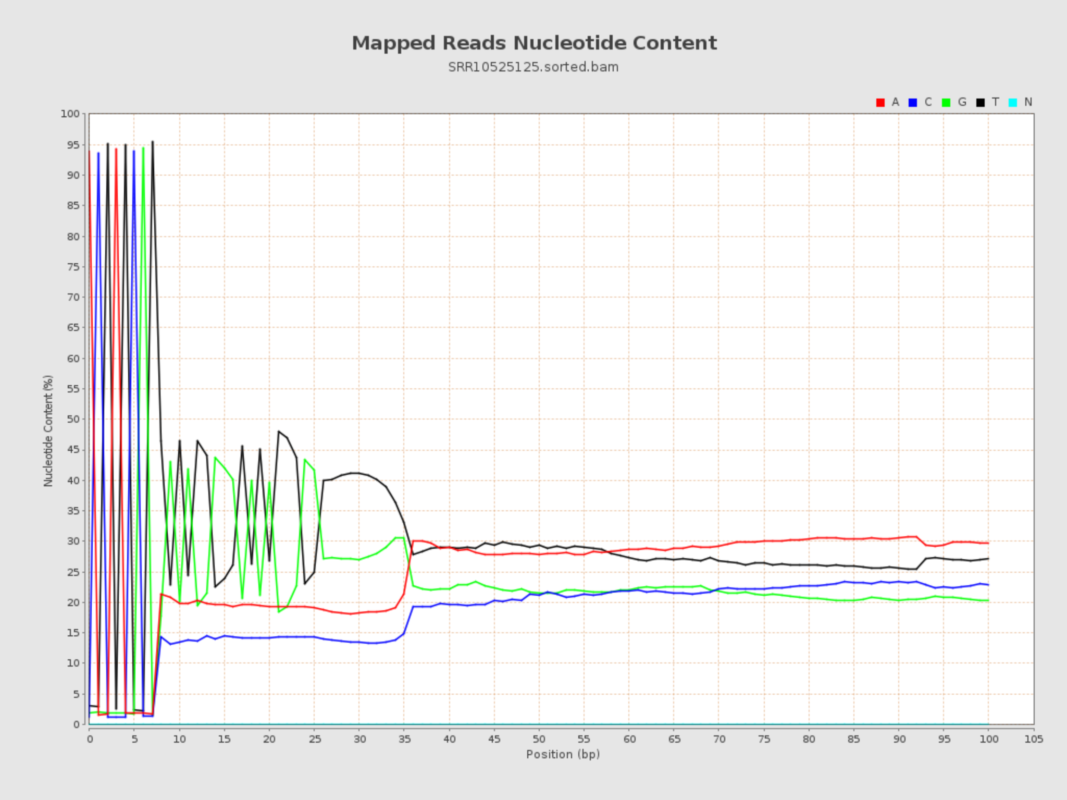
6. Results : Genome Fraction Coverage



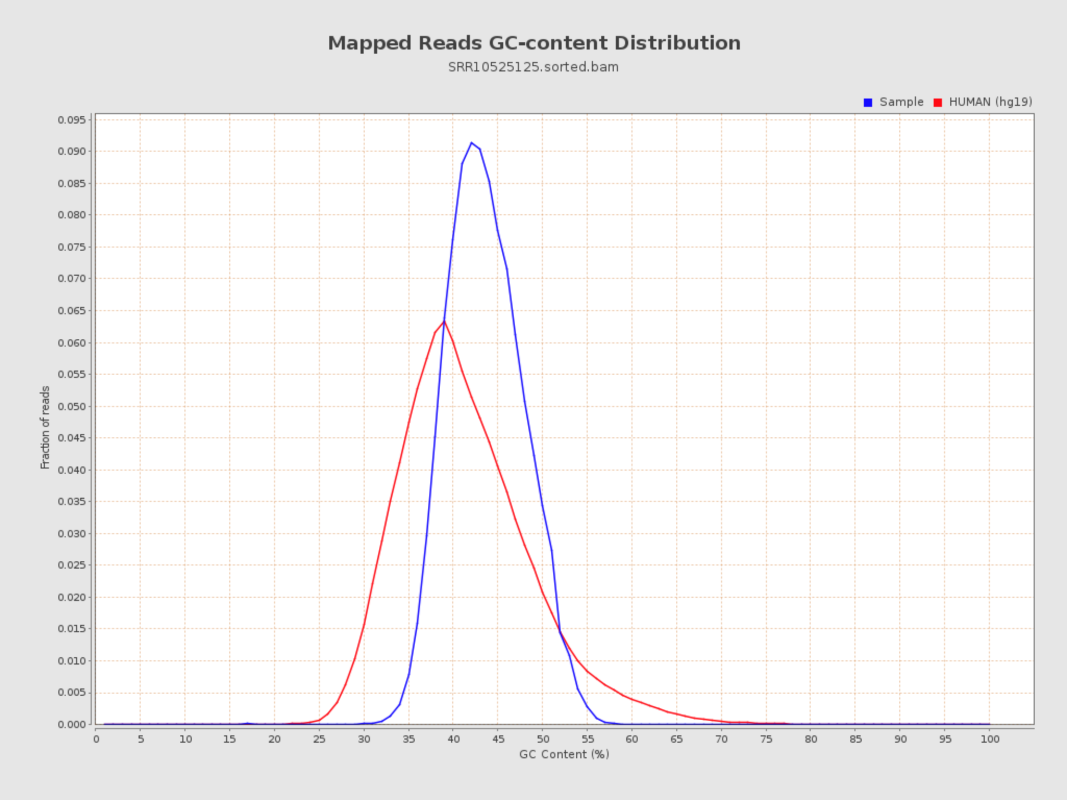
7. Results : Duplication Rate Histogram



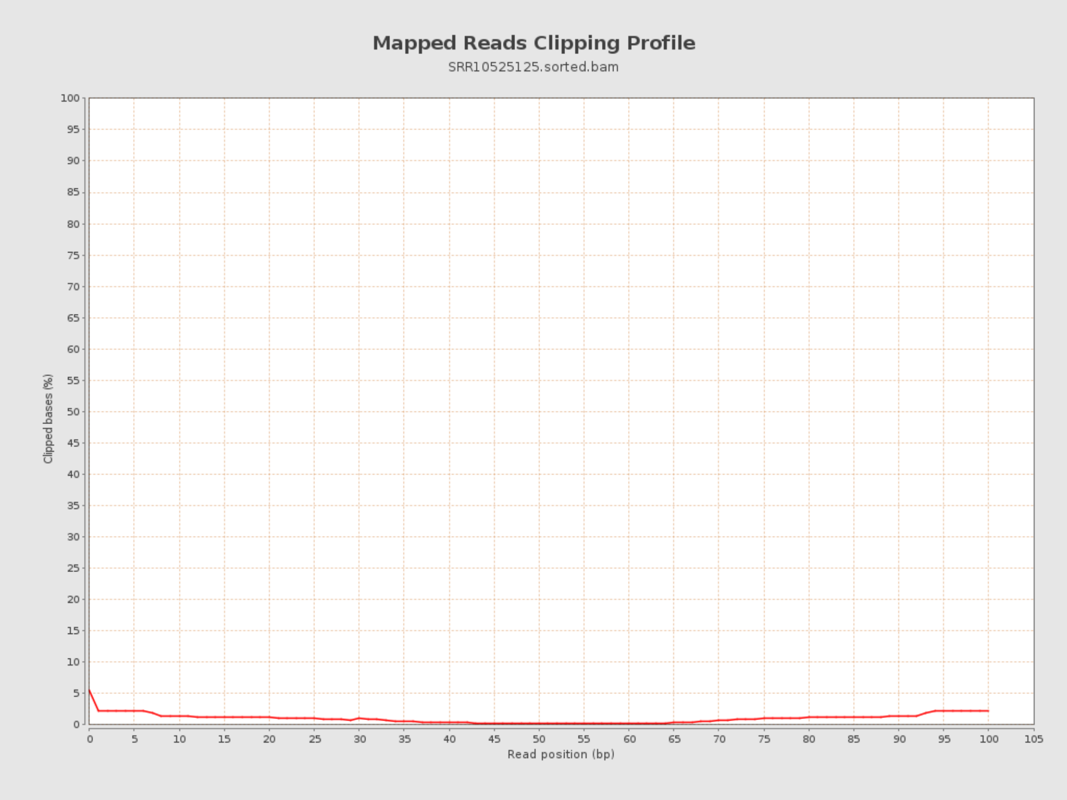
8. Results : Mapped Reads Nucleotide Content



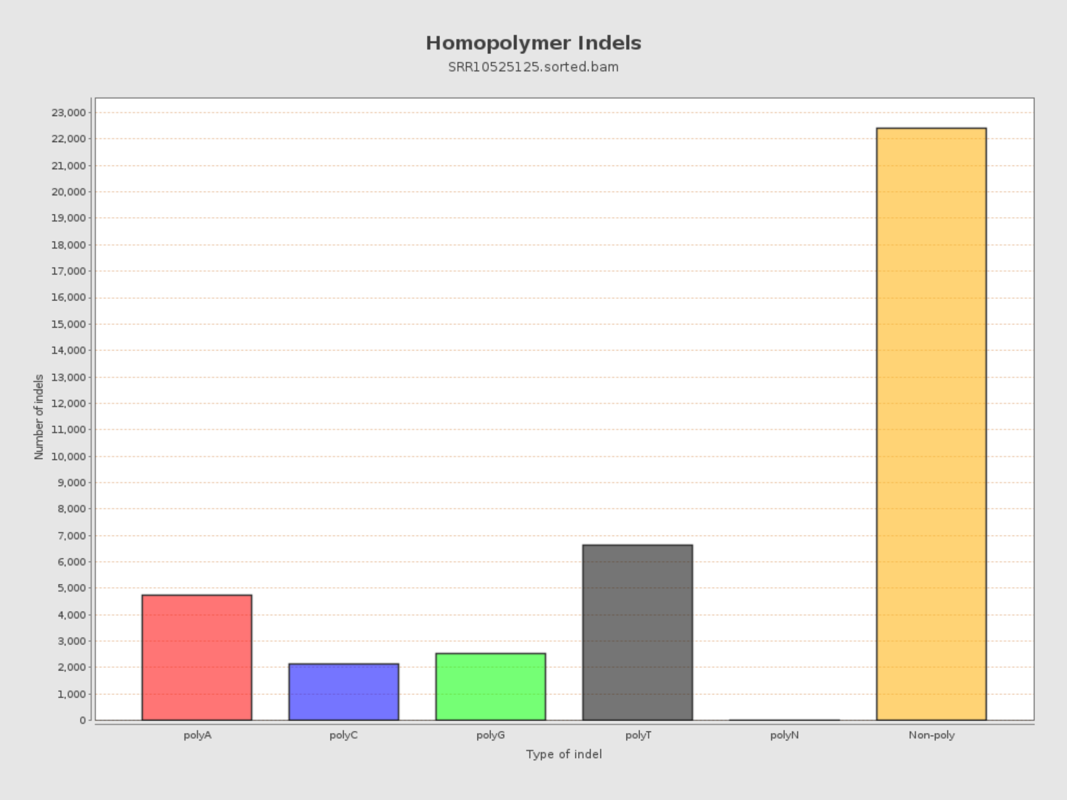
9. Results : Mapped Reads GC-content Distribution



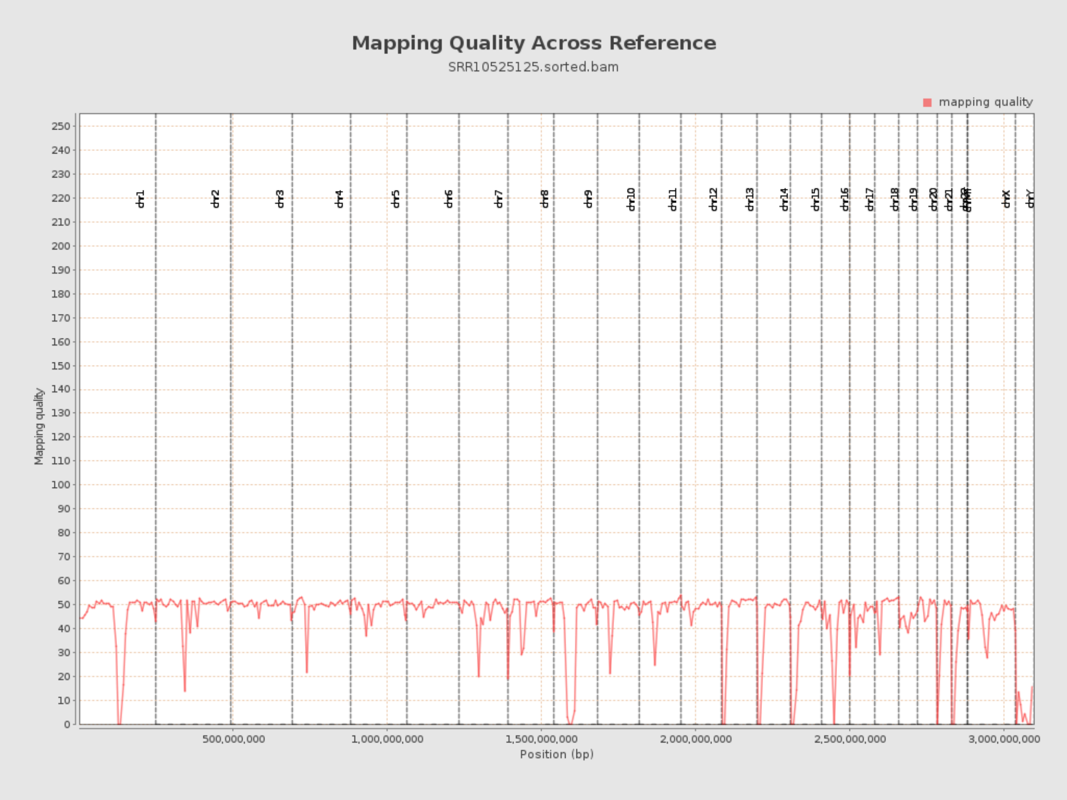
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram