Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 19:50:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525143.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_SRR10525143 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525143.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 19:50:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525143.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,418,900
Mapped reads	1,275,161 / 89.87%
Unmapped reads	143,739 / 10.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,001 / 2.47%
Read min/max/mean length	30 / 101 / 101.91
Duplicated reads (estimated)	37,136 / 2.62%
Duplication rate	1.78%
Clipped reads	1,309,194 / 92.27%

2.2. ACGT Content

Number/percentage of A's	25,483,263 / 26.25%
Number/percentage of C's	19,421,007 / 20.01%
Number/percentage of T's	29,417,636 / 30.3%
Number/percentage of G's	22,752,020 / 23.44%
Number/percentage of N's	3,682 / 0%
GC Percentage	43.44%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.3356

2.4. Mapping Quality

Mean Mapping Quality	45.98

2.5. Mismatches and indels

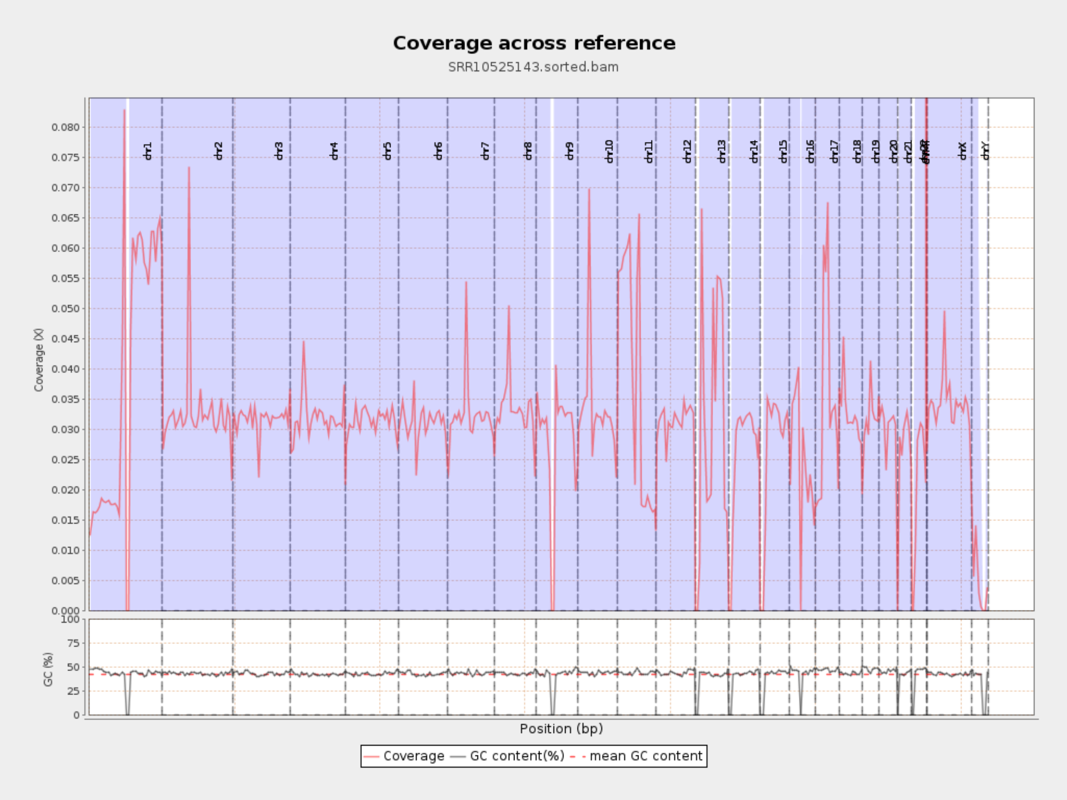
General error rate	0.75%
Mismatches	708,815
Insertions	8,190
Mapped reads with at least one insertion	0.63%
Deletions	23,827
Mapped reads with at least one deletion	1.84%
Homopolymer indels	43.42%

2.6. Chromosome stats

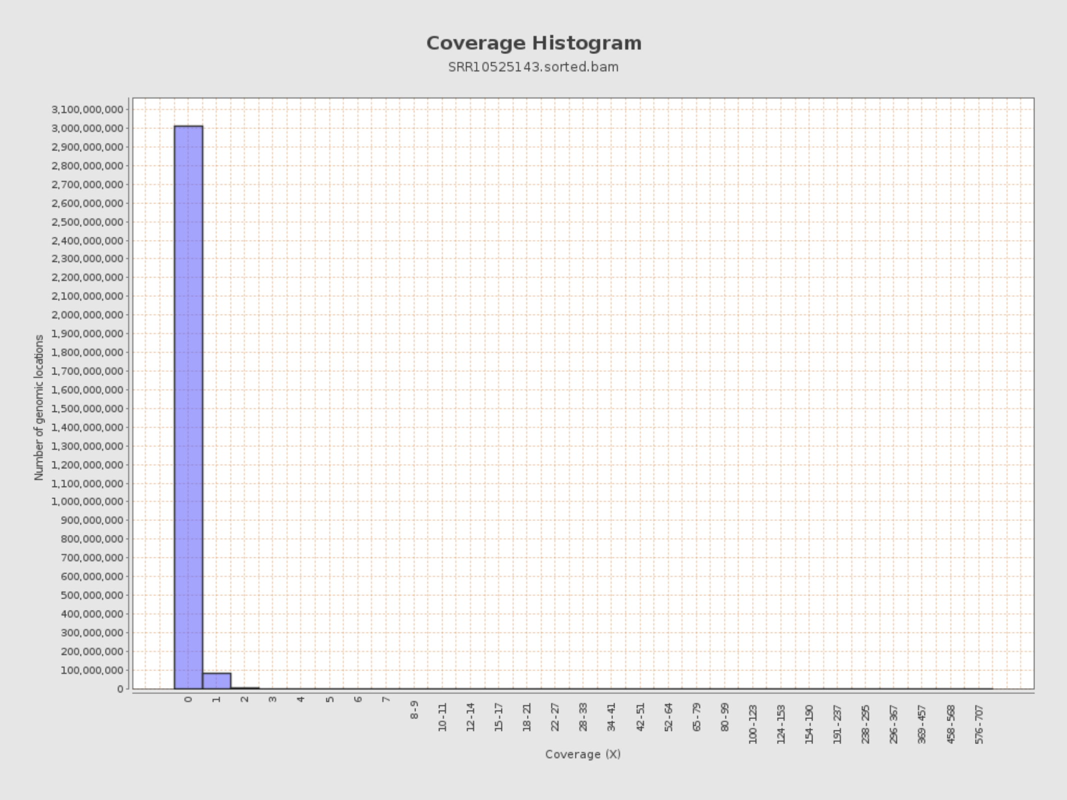
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9365315	0.0376	0.6204
chr2	243199373	8003822	0.0329	0.4206
chr3	198022430	6265668	0.0316	0.1972
chr4	191154276	6102627	0.0319	0.2054
chr5	180915260	5698971	0.0315	0.1934
chr6	171115067	5334046	0.0312	0.2156
chr7	159138663	5194569	0.0326	0.3997

chr8	146364022	4881270	0.0334	0.4226
chr9	141213431	3949460	0.028	0.2941
chr10	135534747	4543630	0.0335	0.413
chr11	135006516	5201646	0.0385	0.3616
chr12	133851895	4194226	0.0313	0.1919
chr13	115169878	3493667	0.0303	0.1893
chr14	107349540	2751621	0.0256	0.1981
chr15	102531392	2702421	0.0264	0.1743
chr16	90354753	2233758	0.0247	0.1971
chr17	81195210	2892111	0.0356	0.2415
chr18	78077248	2580869	0.0331	0.5209
chr19	59128983	1890539	0.032	0.4511
chr20	63025520	1894892	0.0301	0.1918
chr21	48129895	1262548	0.0262	0.1902
chr22	51304566	1012585	0.0197	0.1507
chrMT	16571	75922	4.5816	4.5675
chrX	155270560	5322406	0.0343	0.2542
chrY	59373566	269714	0.0045	0.1156

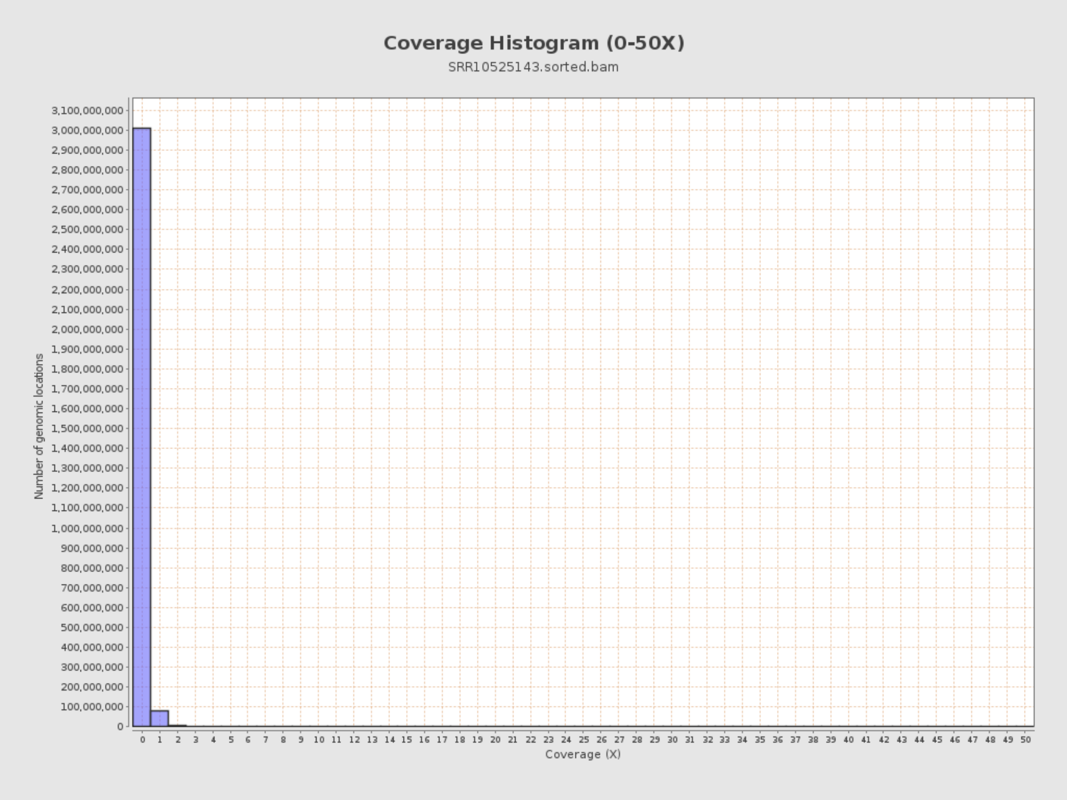
3. Results : Coverage across reference



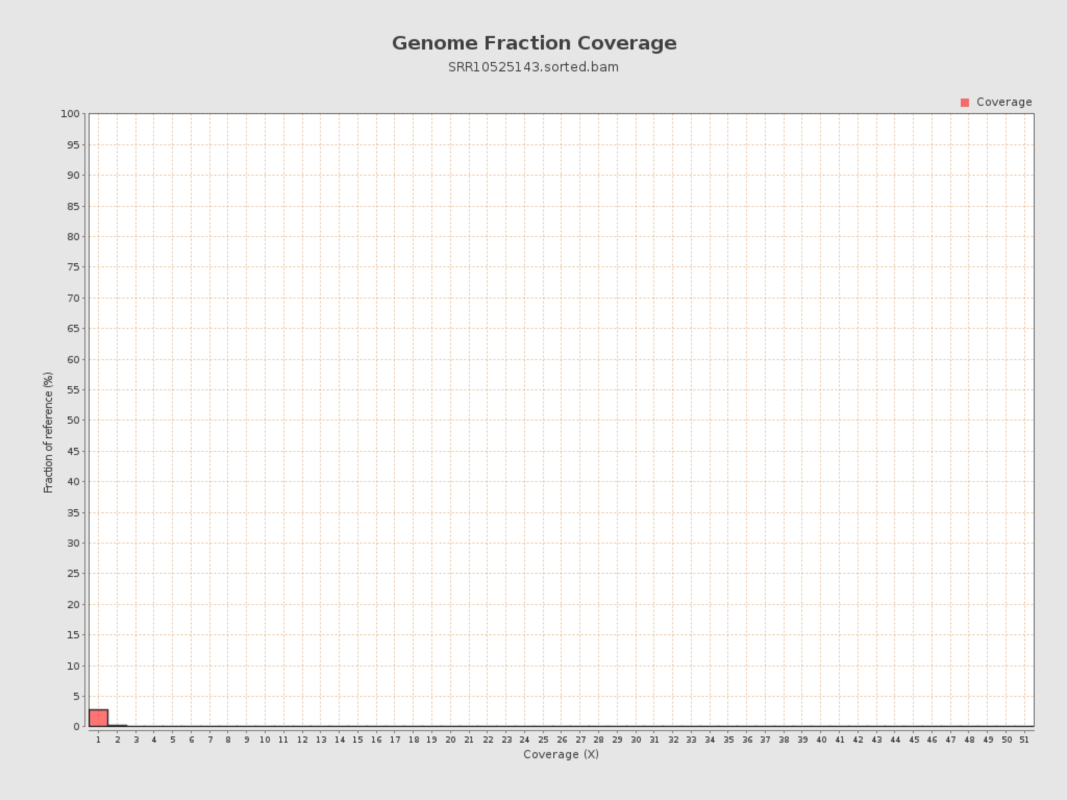
4. Results : Coverage Histogram



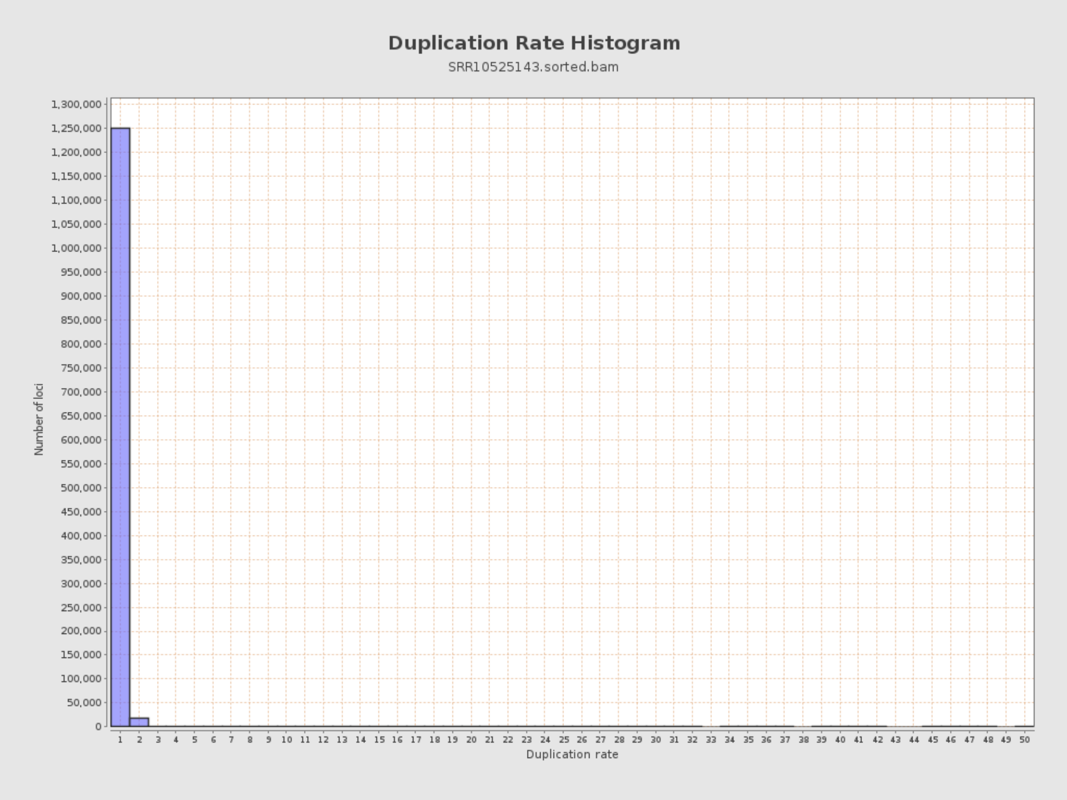
5. Results : Coverage Histogram (0-50X)



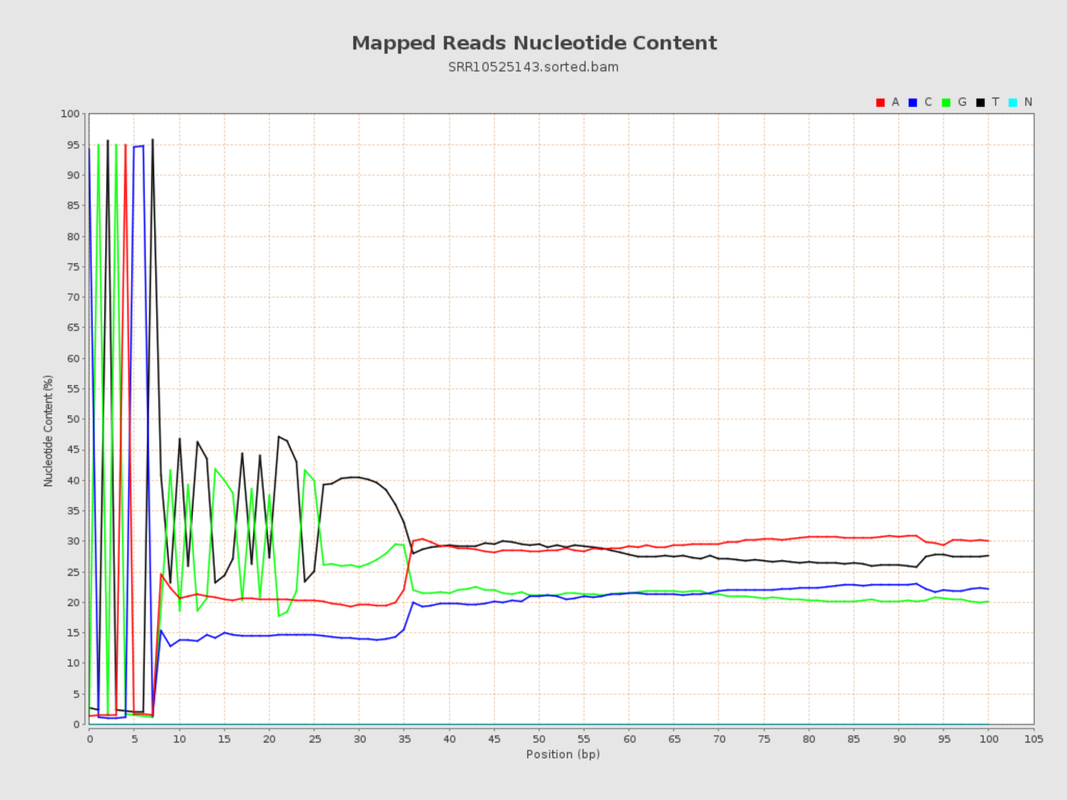
6. Results : Genome Fraction Coverage



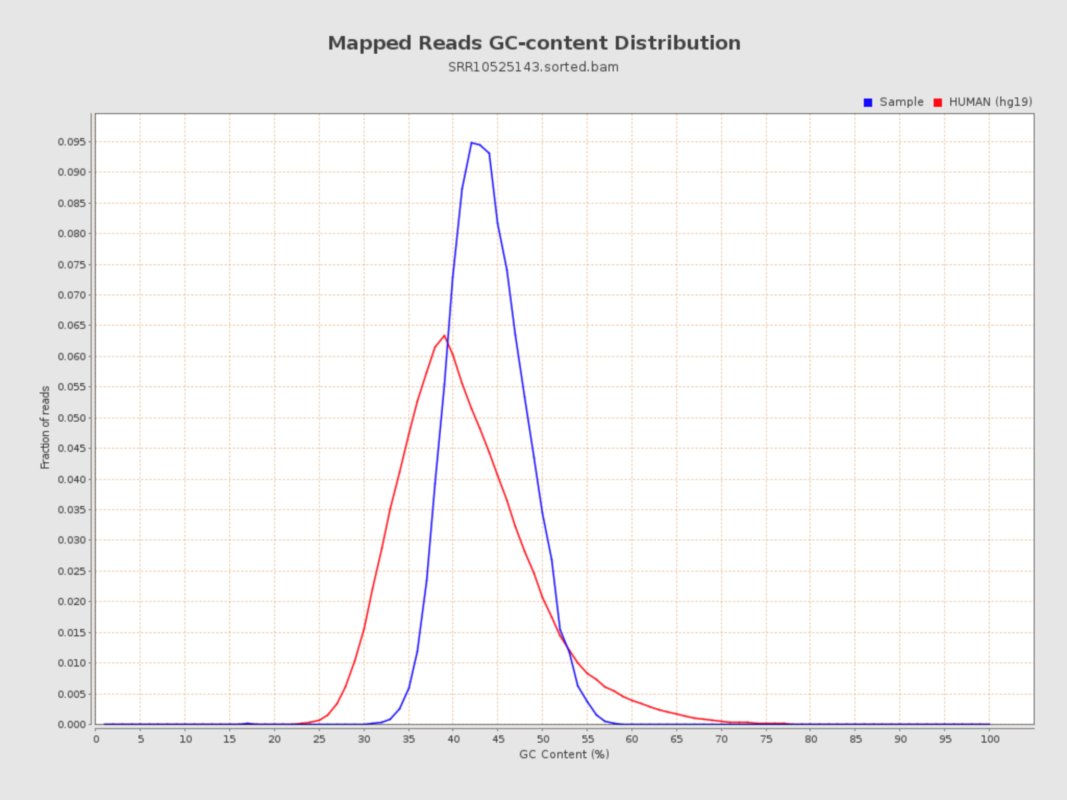
7. Results : Duplication Rate Histogram



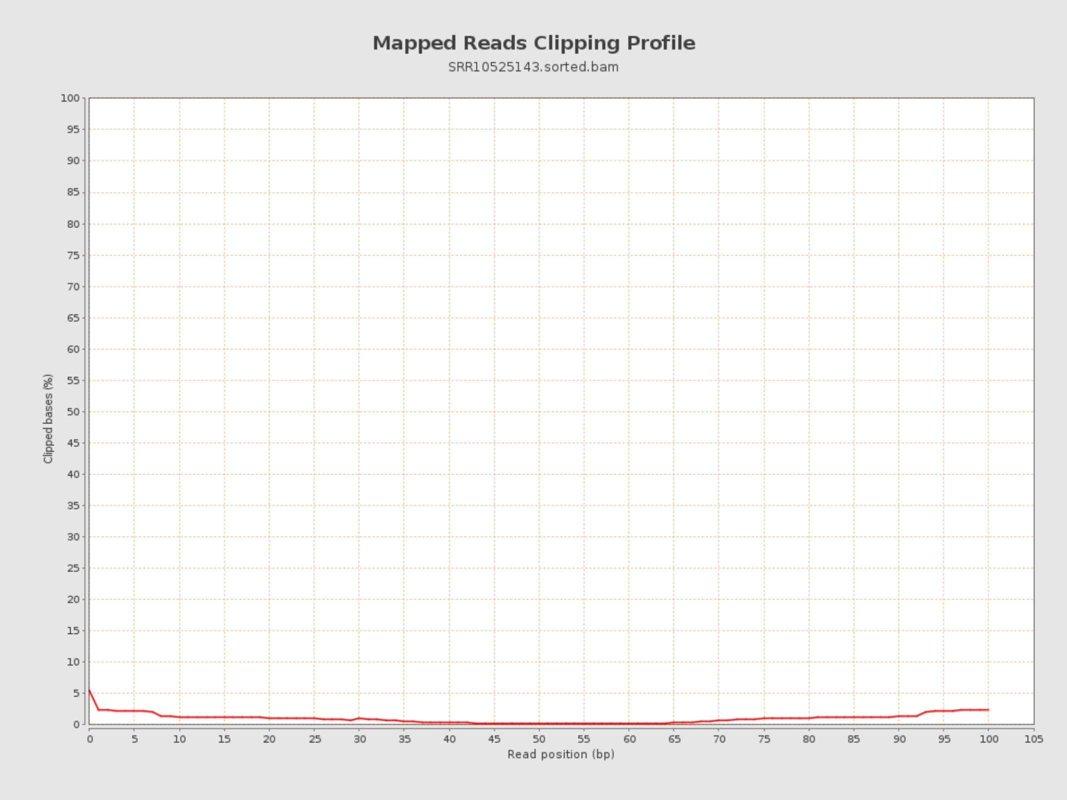
8. Results : Mapped Reads Nucleotide Content



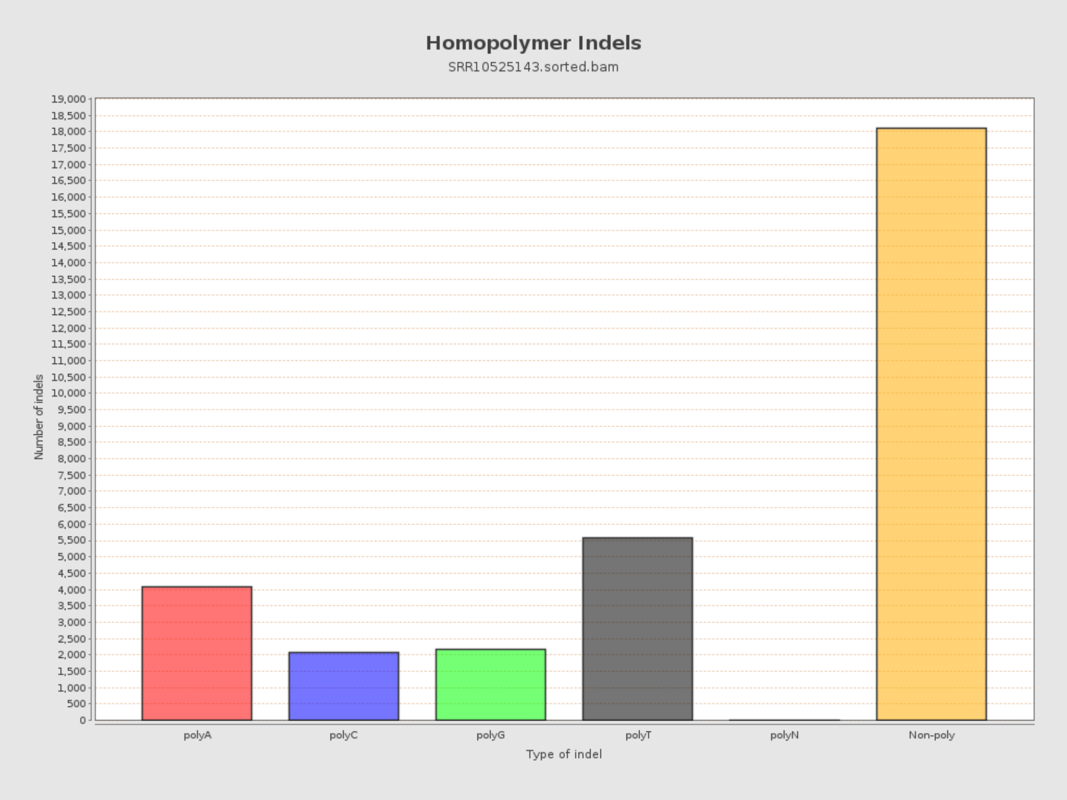
9. Results : Mapped Reads GC-content Distribution



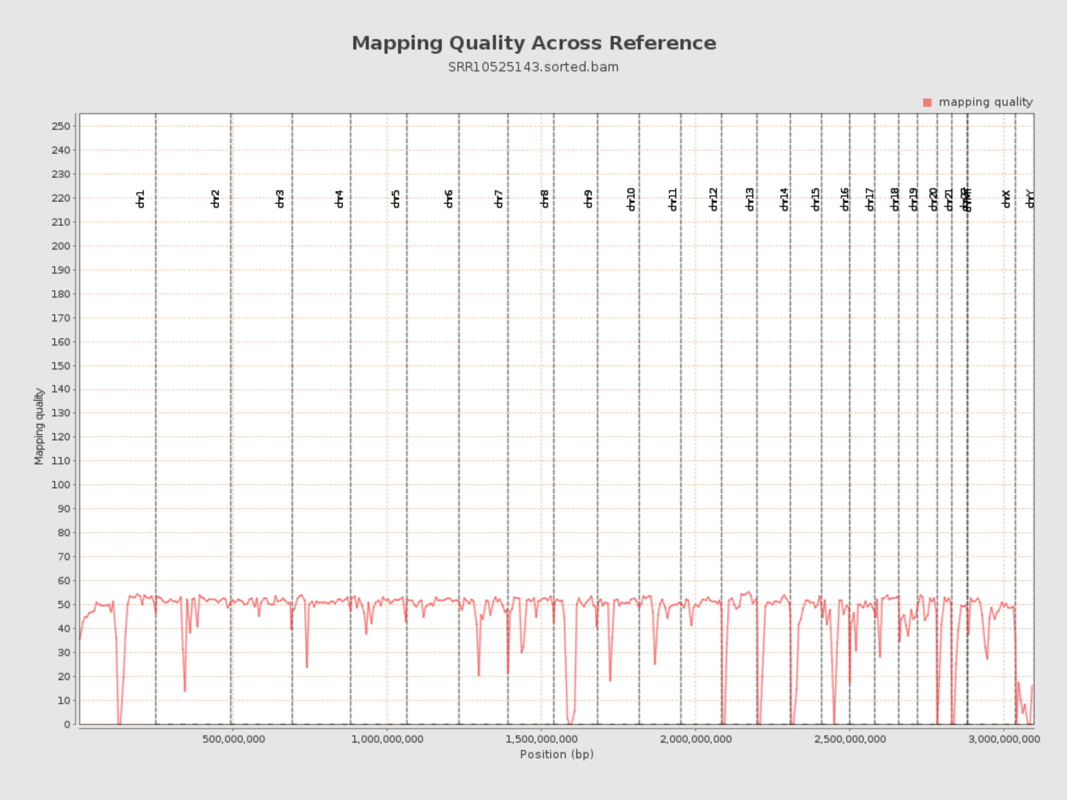
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram