Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:03:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525103.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_SRR10525103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:03:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	667,296
Mapped reads	557,939 / 83.61%
Unmapped reads	109,357 / 16.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,346 / 2.3%
Read min/max/mean length	30 / 101 / 101.85
Duplicated reads (estimated)	11,000 / 1.65%
Duplication rate	1.23%
Clipped reads	572,449 / 85.79%

2.2. ACGT Content

Number/percentage of A's	11,140,821 / 26.13%
Number/percentage of C's	8,111,656 / 19.02%
Number/percentage of T's	13,368,024 / 31.35%
Number/percentage of G's	10,019,801 / 23.5%
Number/percentage of N's	1,601 / 0%
GC Percentage	42.52%

2.3. Coverage

Mean	0.0138

Standard Deviation	0.167

2.4. Mapping Quality

Mean Mapping Quality	46.54

2.5. Mismatches and indels

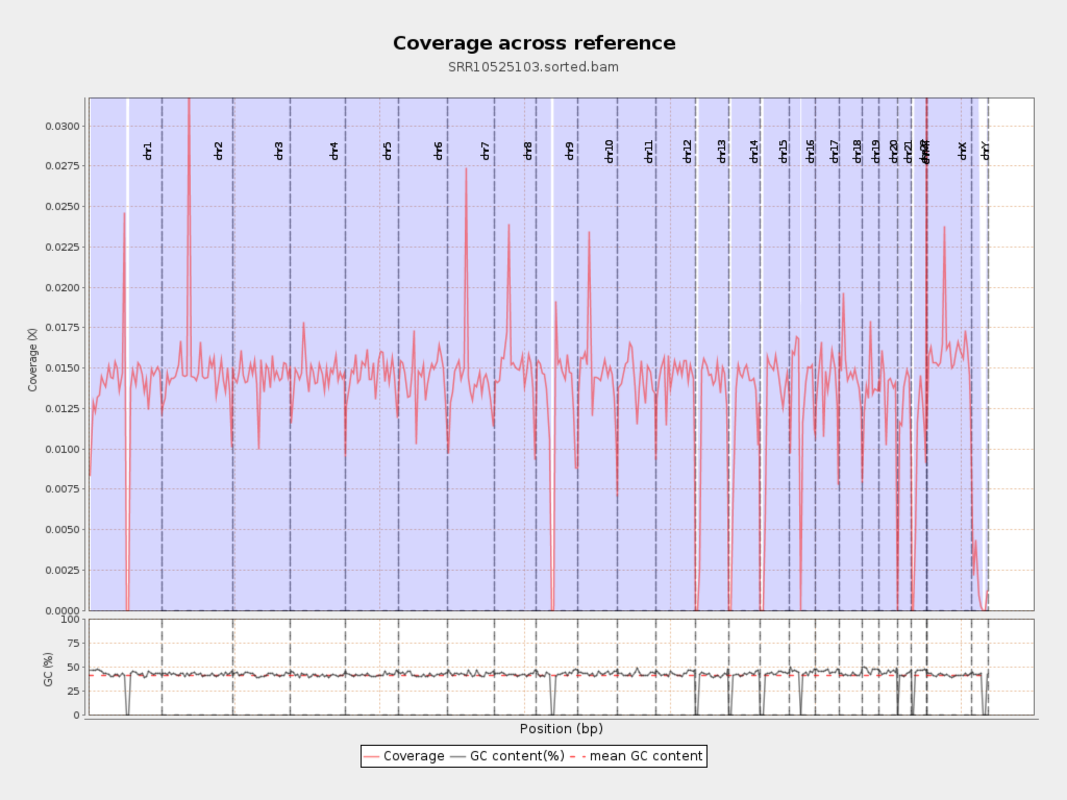
General error rate	0.76%
Mismatches	314,912
Insertions	3,845
Mapped reads with at least one insertion	0.68%
Deletions	9,903
Mapped reads with at least one deletion	1.75%
Homopolymer indels	43.37%

2.6. Chromosome stats

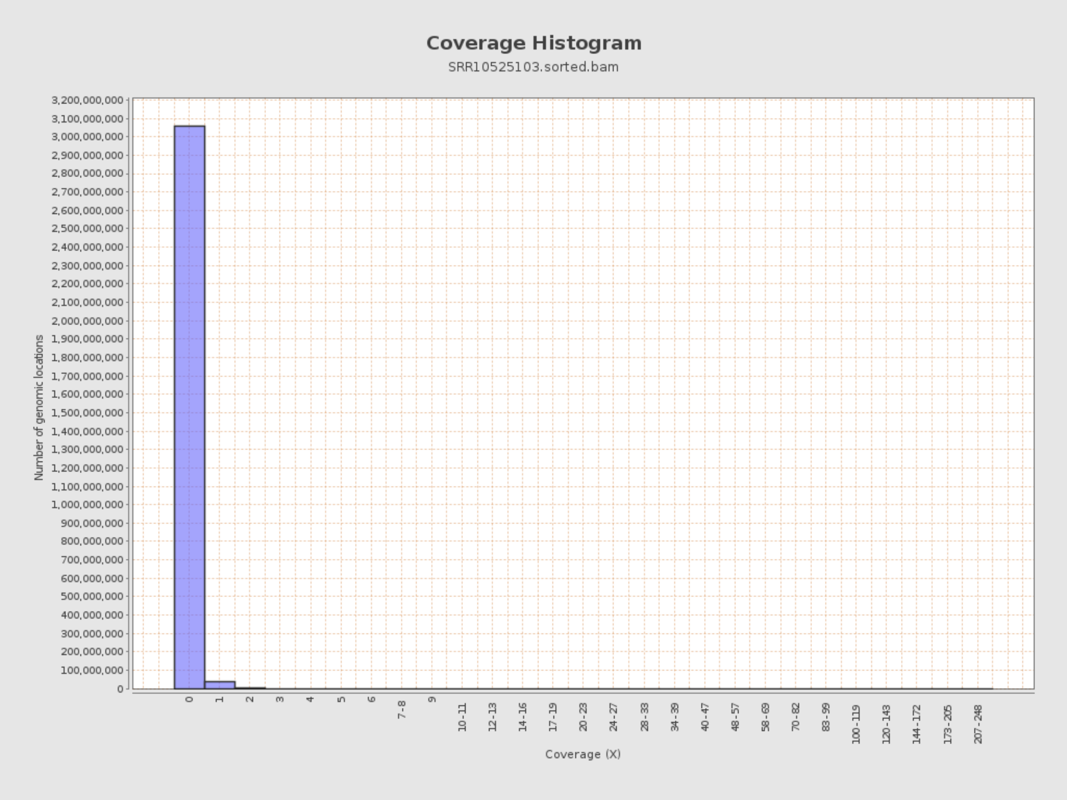
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3363833	0.0135	0.2272
chr2	243199373	3675931	0.0151	0.2277
chr3	198022430	2880137	0.0145	0.1255
chr4	191154276	2783688	0.0146	0.1273
chr5	180915260	2650056	0.0146	0.1267
chr6	171115067	2478417	0.0145	0.1359
chr7	159138663	2311335	0.0145	0.2302

chr8	146364022	2231439	0.0152	0.212
chr9	141213431	1803025	0.0128	0.1675
chr10	135534747	2024341	0.0149	0.1675
chr11	135006516	1918775	0.0142	0.1735
chr12	133851895	1943566	0.0145	0.1258
chr13	115169878	1384874	0.012	0.1135
chr14	107349540	1263734	0.0118	0.117
chr15	102531392	1212042	0.0118	0.1124
chr16	90354753	1196330	0.0132	0.1232
chr17	81195210	1122584	0.0138	0.1428
chr18	78077248	1172687	0.015	0.2413
chr19	59128983	810222	0.0137	0.1849
chr20	63025520	851839	0.0135	0.1218
chr21	48129895	559582	0.0116	0.1153
chr22	51304566	439869	0.0086	0.0957
chrMT	16571	625	0.0377	0.2183
chrX	155270560	2485509	0.016	0.1527
chrY	59373566	94328	0.0016	0.049

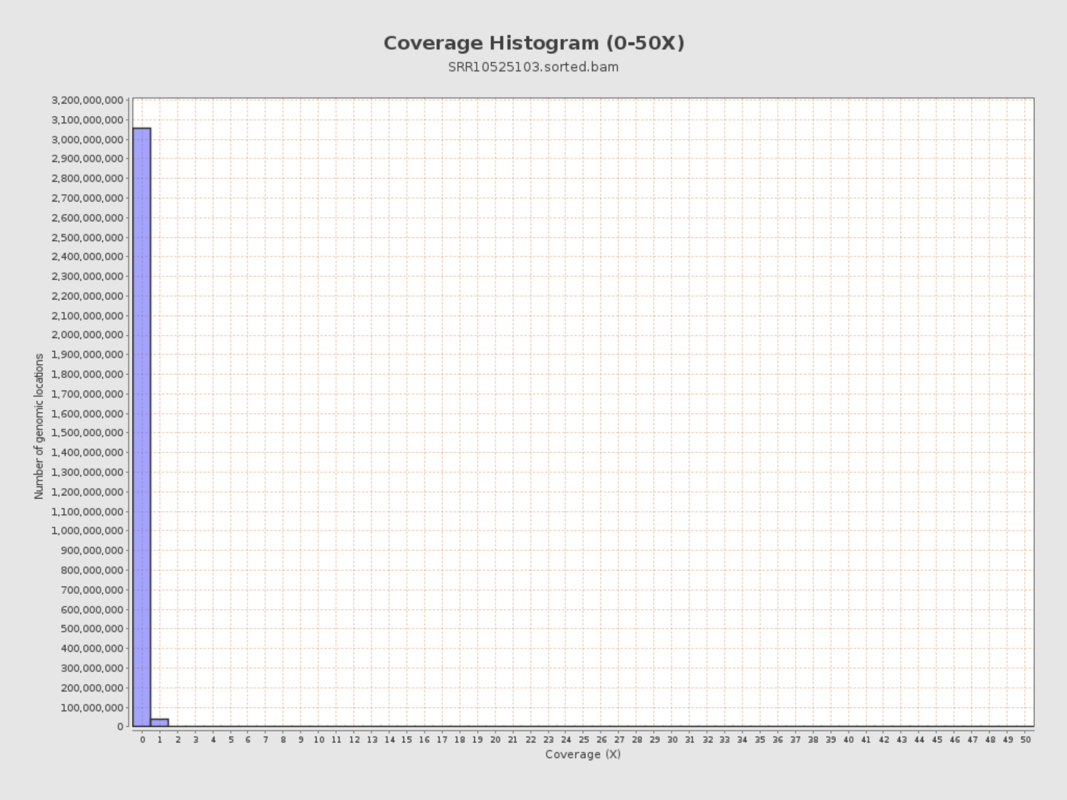
3. Results : Coverage across reference



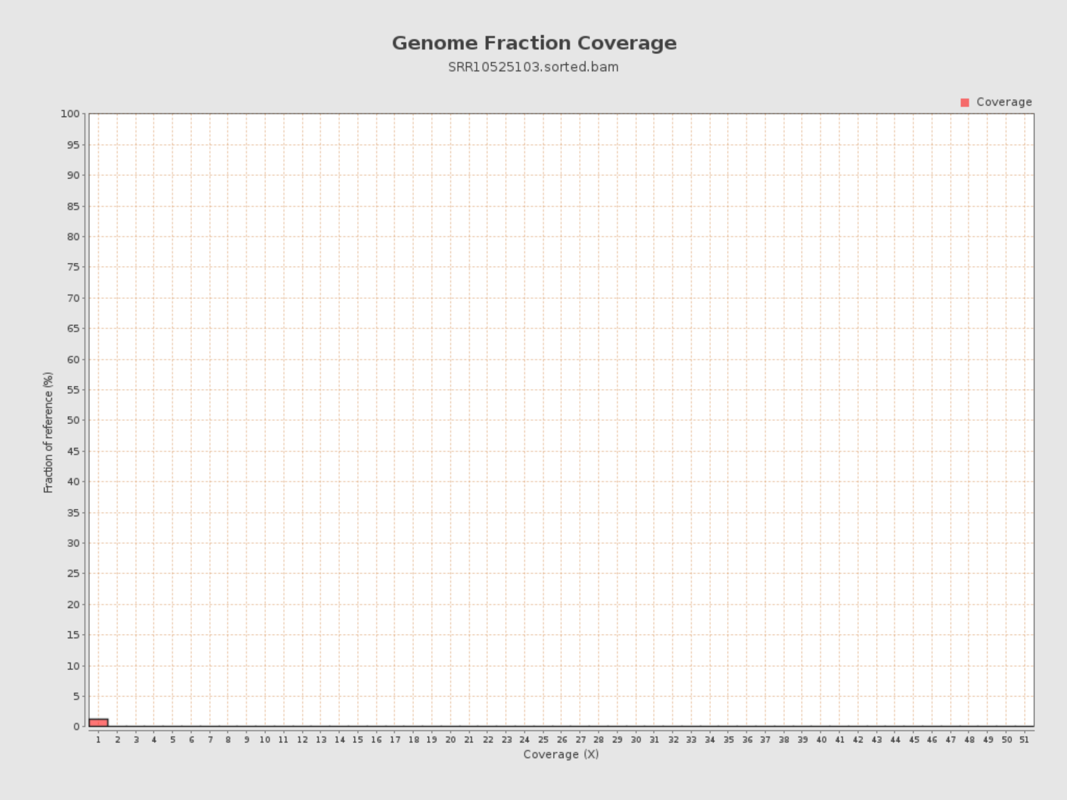
4. Results : Coverage Histogram



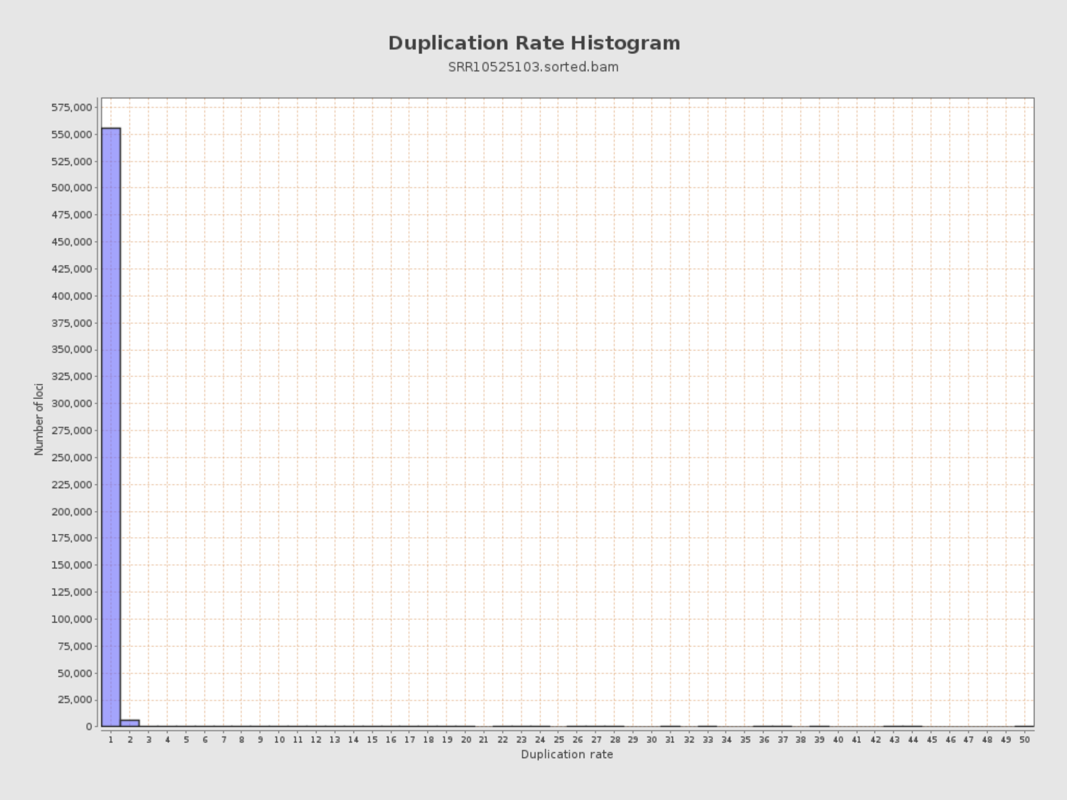
5. Results : Coverage Histogram (0-50X)



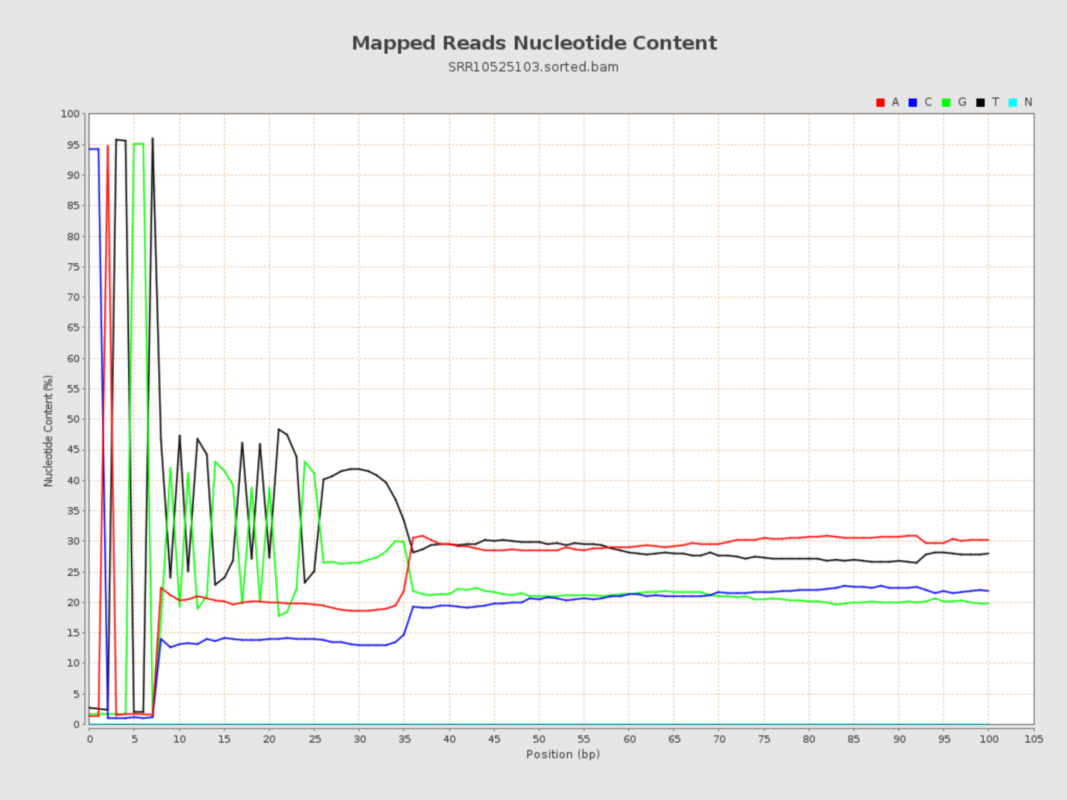
6. Results : Genome Fraction Coverage



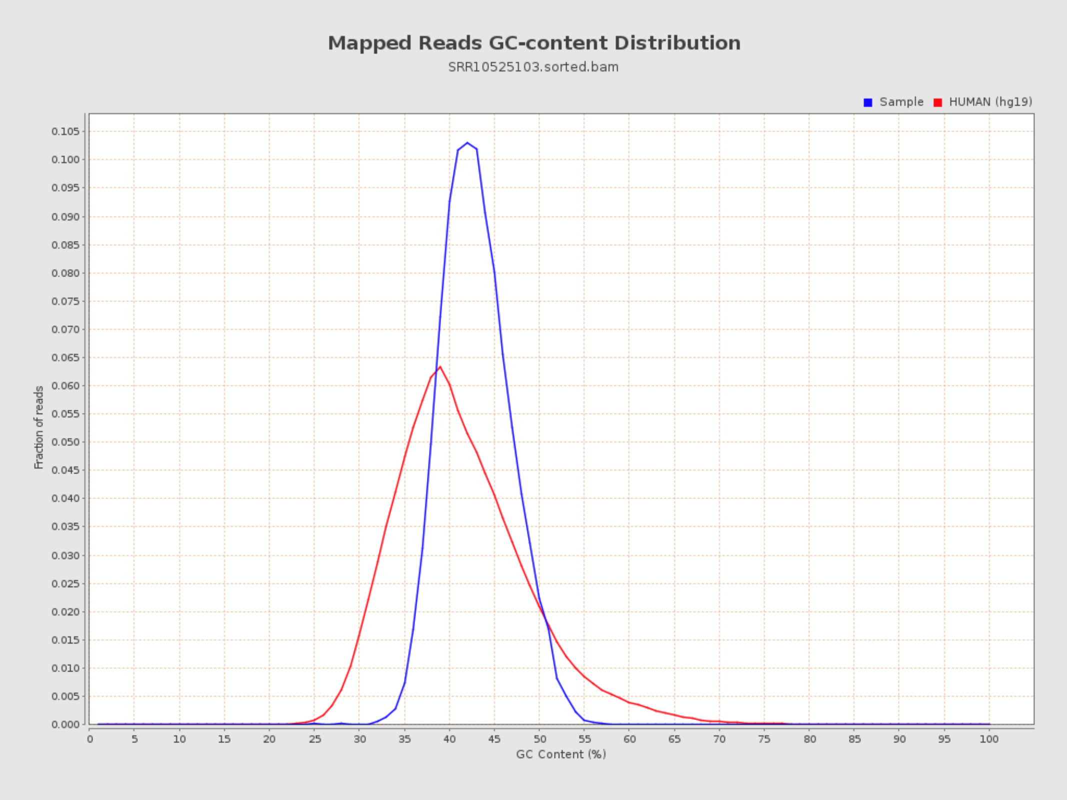
7. Results : Duplication Rate Histogram



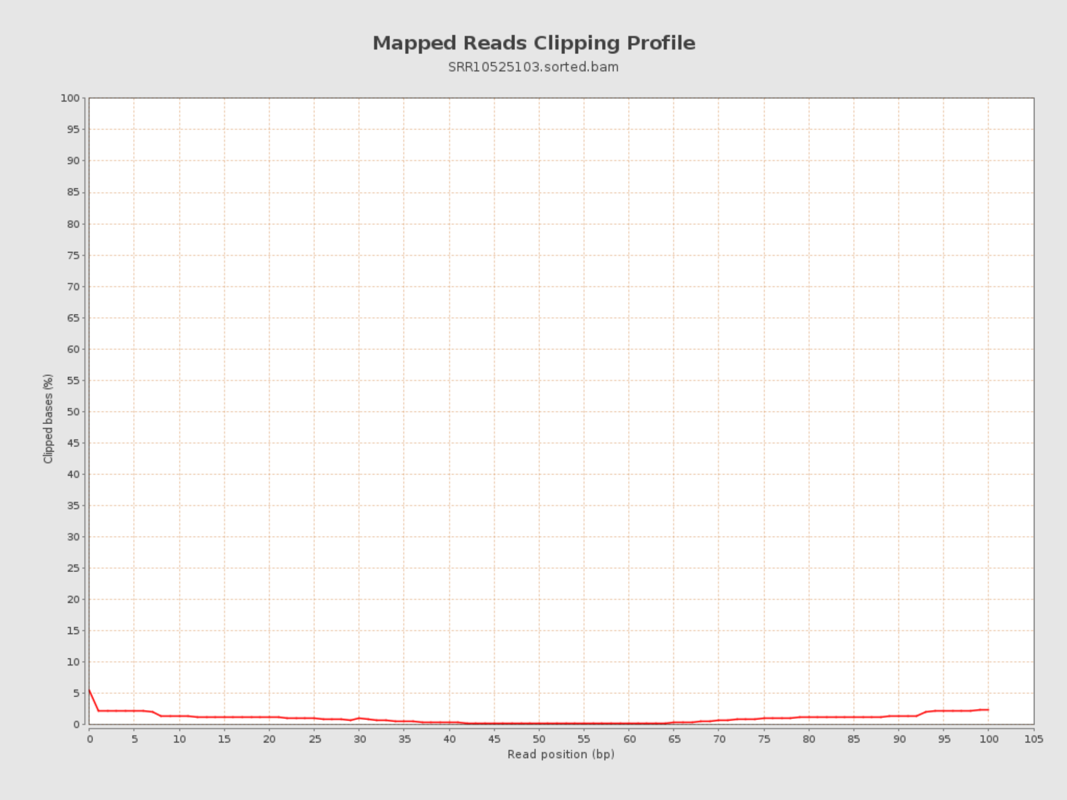
8. Results : Mapped Reads Nucleotide Content



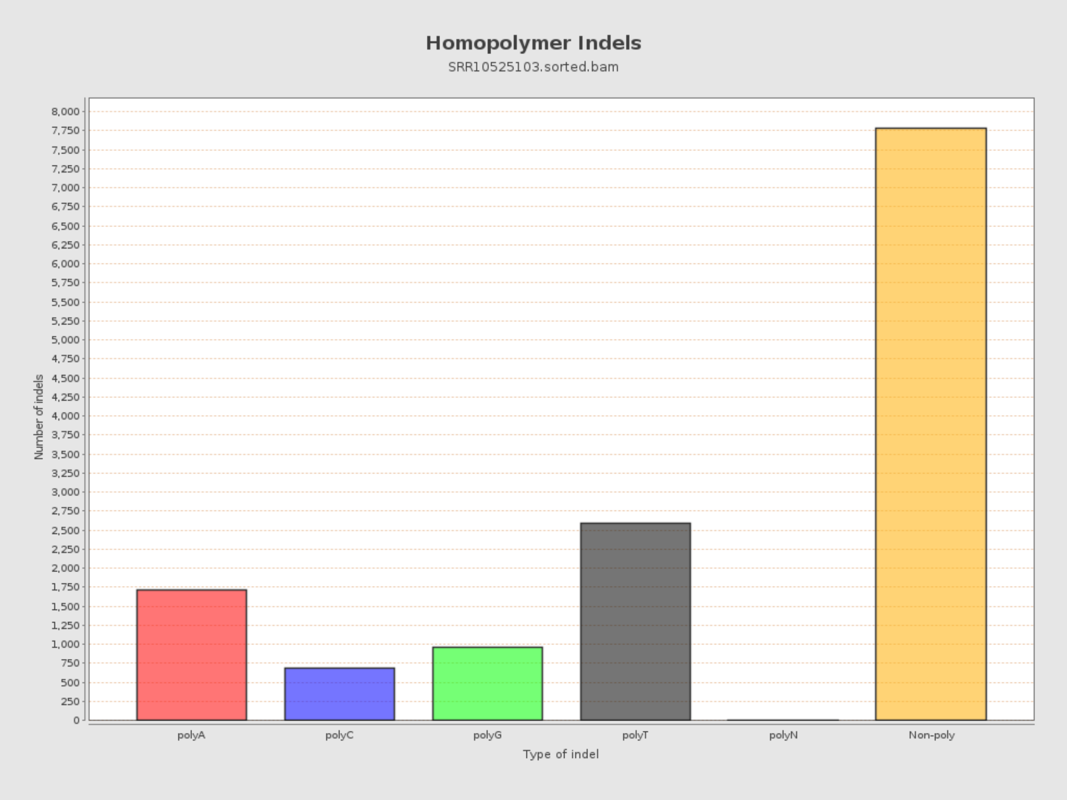
9. Results : Mapped Reads GC-content Distribution



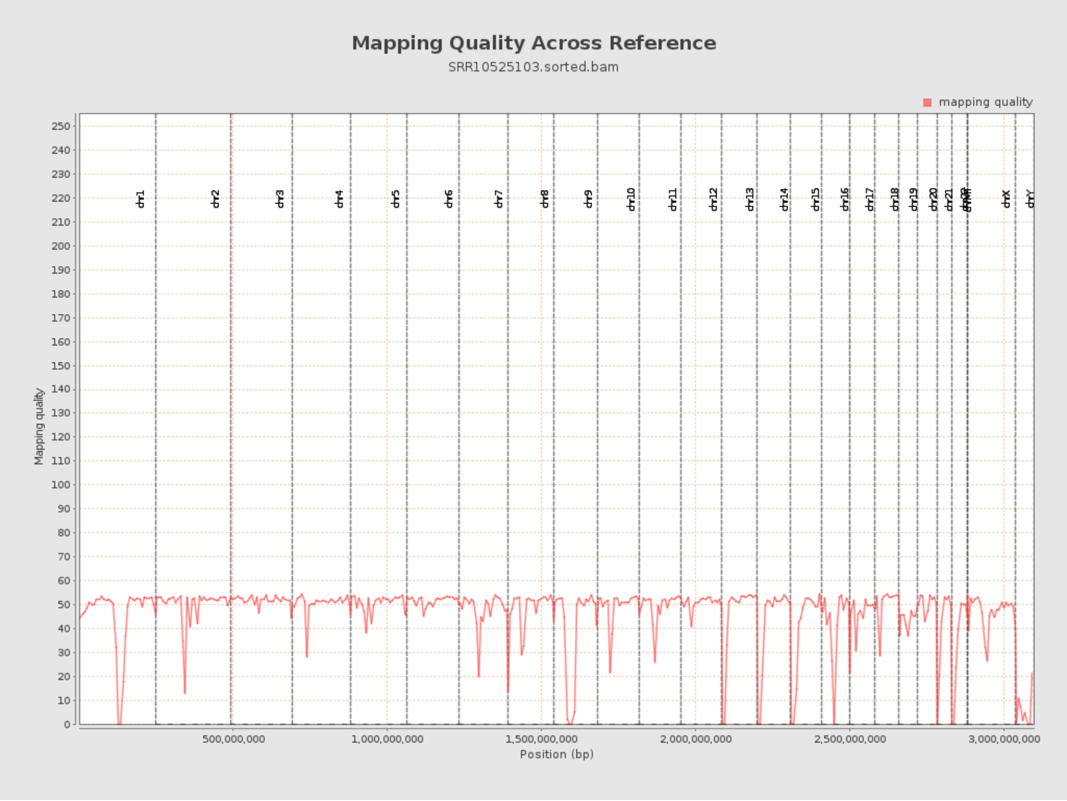
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram