Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:42:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525117.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_SRR10525117 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525117.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:42:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525117.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,032,154
Mapped reads	1,829,710 / 90.04%
Unmapped reads	202,444 / 9.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,790 / 2.35%
Read min/max/mean length	30 / 101 / 101.86
Duplicated reads (estimated)	64,111 / 3.15%
Duplication rate	2.2%
Clipped reads	1,876,508 / 92.34%

2.2. ACGT Content

Number/percentage of A's	37,176,259 / 26.93%
Number/percentage of C's	27,257,233 / 19.74%
Number/percentage of T's	42,207,251 / 30.57%
Number/percentage of G's	31,411,898 / 22.75%
Number/percentage of N's	4,908 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.4393

2.4. Mapping Quality

Mean Mapping Quality	46.25

2.5. Mismatches and indels

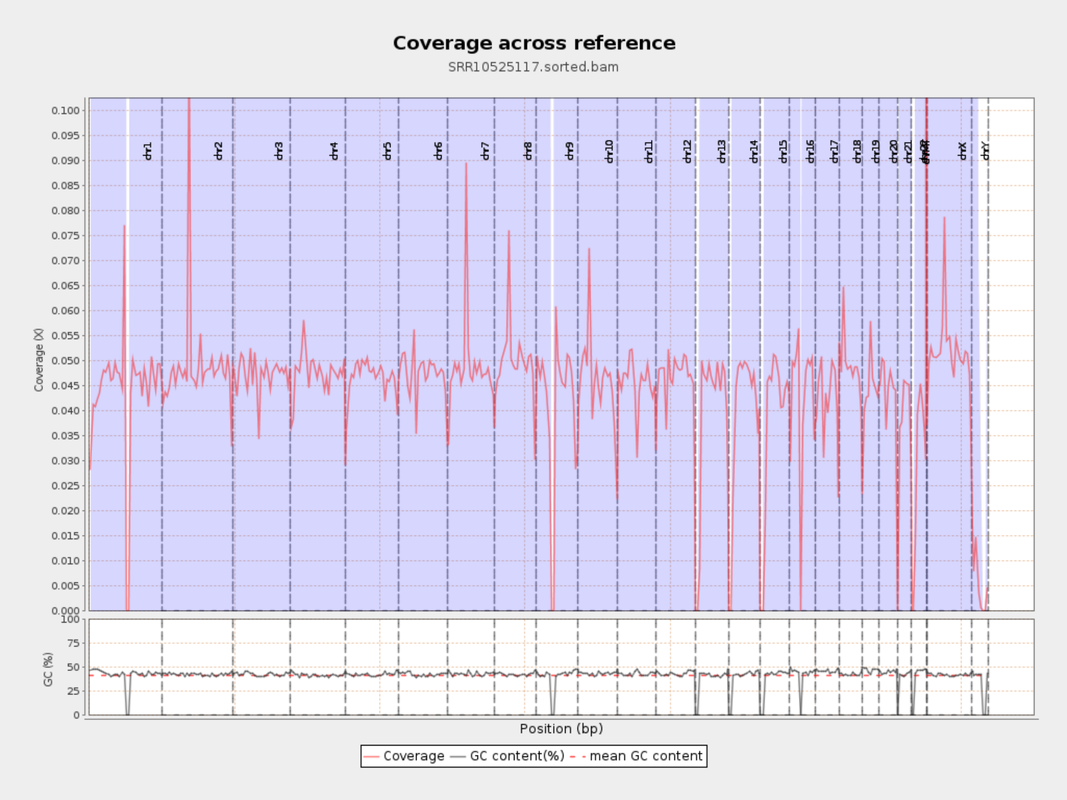
General error rate	0.74%
Mismatches	1,003,372
Insertions	10,710
Mapped reads with at least one insertion	0.58%
Deletions	30,112
Mapped reads with at least one deletion	1.62%
Homopolymer indels	42.85%

2.6. Chromosome stats

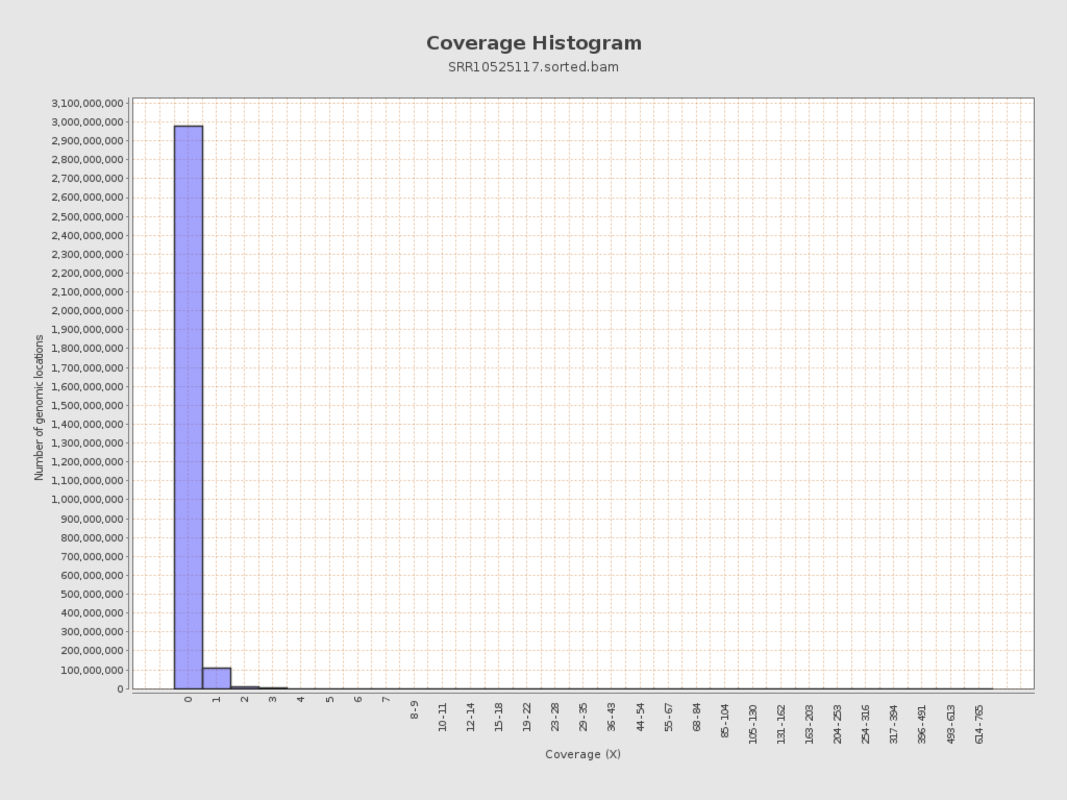
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10919316	0.0438	0.6563
chr2	243199373	11965554	0.0492	0.6591
chr3	198022430	9365996	0.0473	0.2425
chr4	191154276	9084065	0.0475	0.2559
chr5	180915260	8452845	0.0467	0.2483
chr6	171115067	8114324	0.0474	0.2867
chr7	159138663	7836901	0.0492	0.6915

chr8	146364022	7296839	0.0499	0.6266
chr9	141213431	5812683	0.0412	0.4313
chr10	135534747	6324127	0.0467	0.4124
chr11	135006516	6092175	0.0451	0.4471
chr12	133851895	6286291	0.047	0.2448
chr13	115169878	4455452	0.0387	0.218
chr14	107349540	4161213	0.0388	0.2754
chr15	102531392	3821431	0.0373	0.2157
chr16	90354753	3844787	0.0426	0.2579
chr17	81195210	3410982	0.042	0.2875
chr18	78077248	3871959	0.0496	0.7318
chr19	59128983	2622628	0.0444	0.4963
chr20	63025520	2780997	0.0441	0.2408
chr21	48129895	1774445	0.0369	0.2365
chr22	51304566	1414084	0.0276	0.1838
chrMT	16571	9114	0.55	0.957
chrX	155270560	8070909	0.052	0.3639
chrY	59373566	319915	0.0054	0.1165

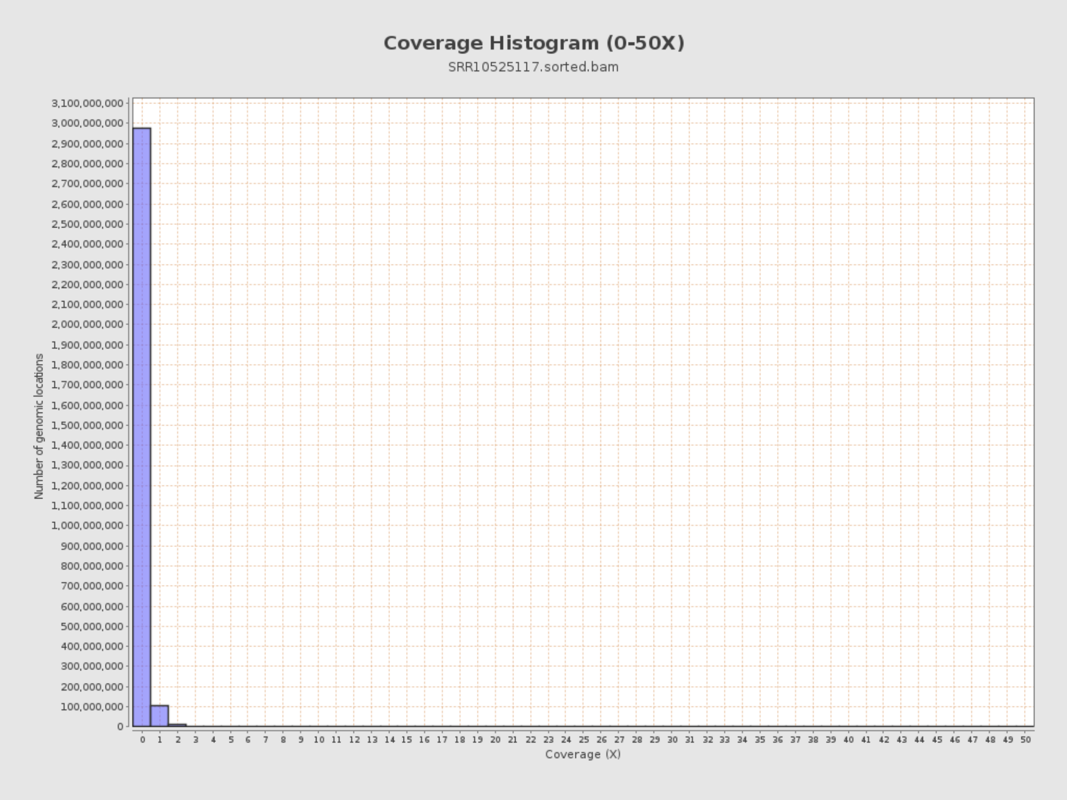
3. Results : Coverage across reference



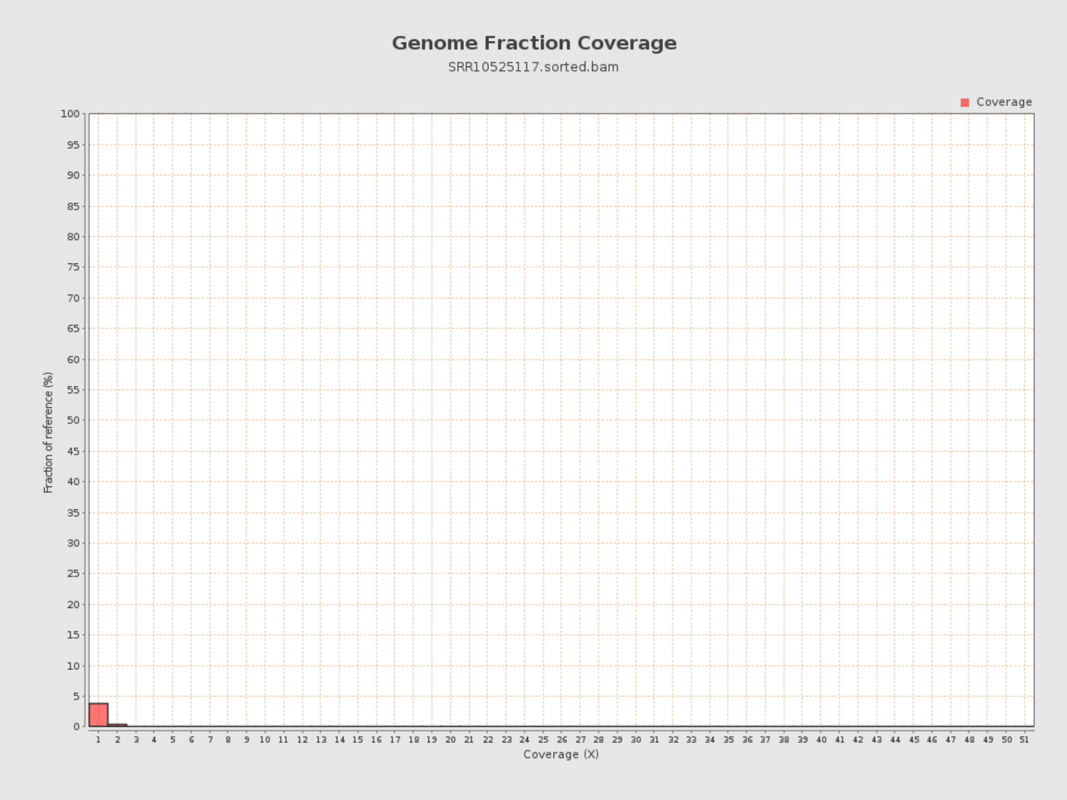
4. Results : Coverage Histogram



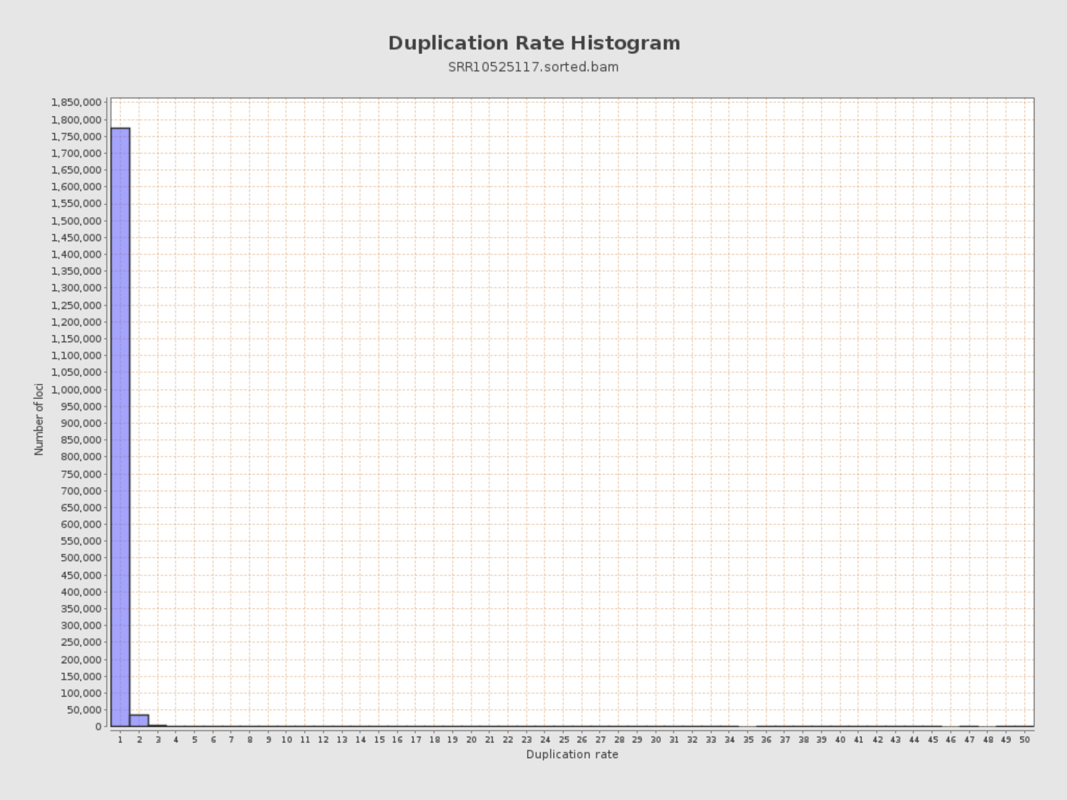
5. Results : Coverage Histogram (0-50X)



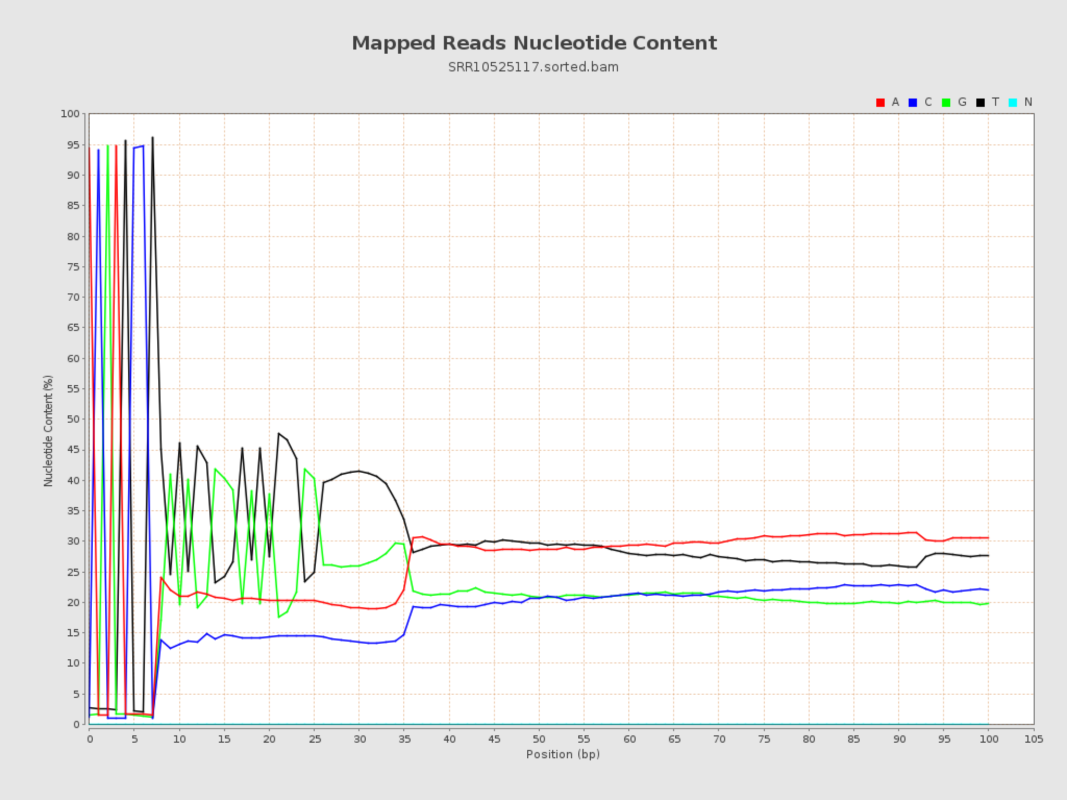
6. Results : Genome Fraction Coverage



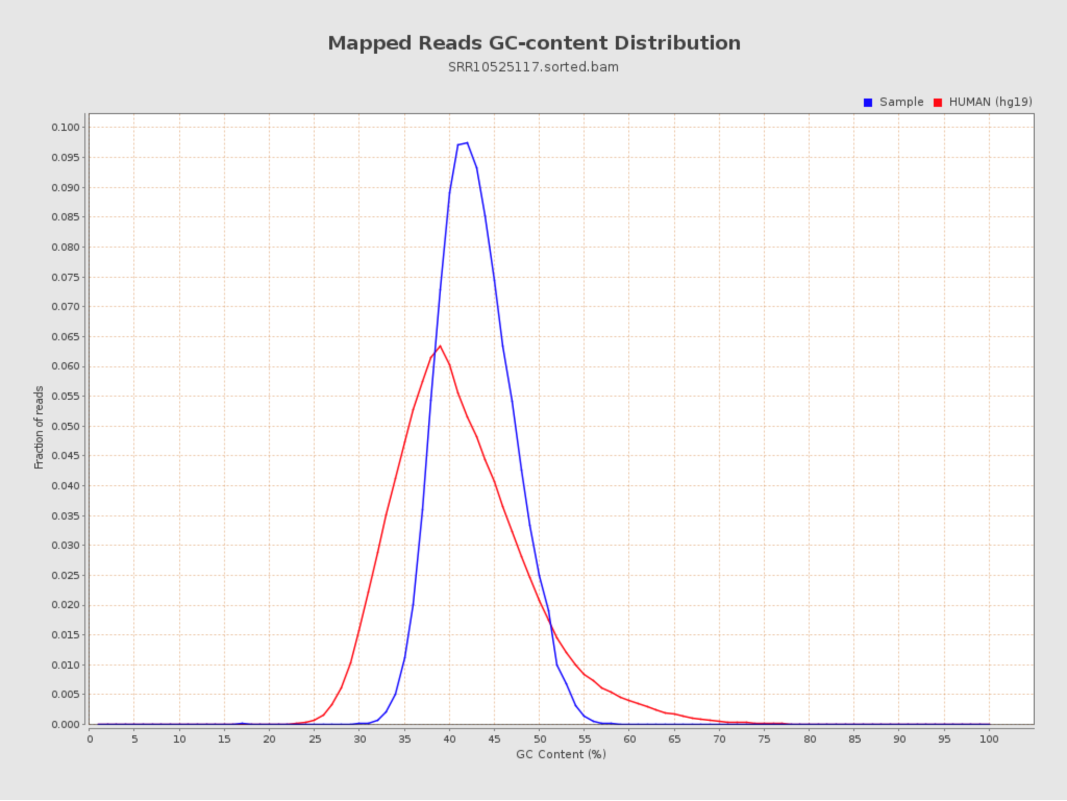
7. Results : Duplication Rate Histogram



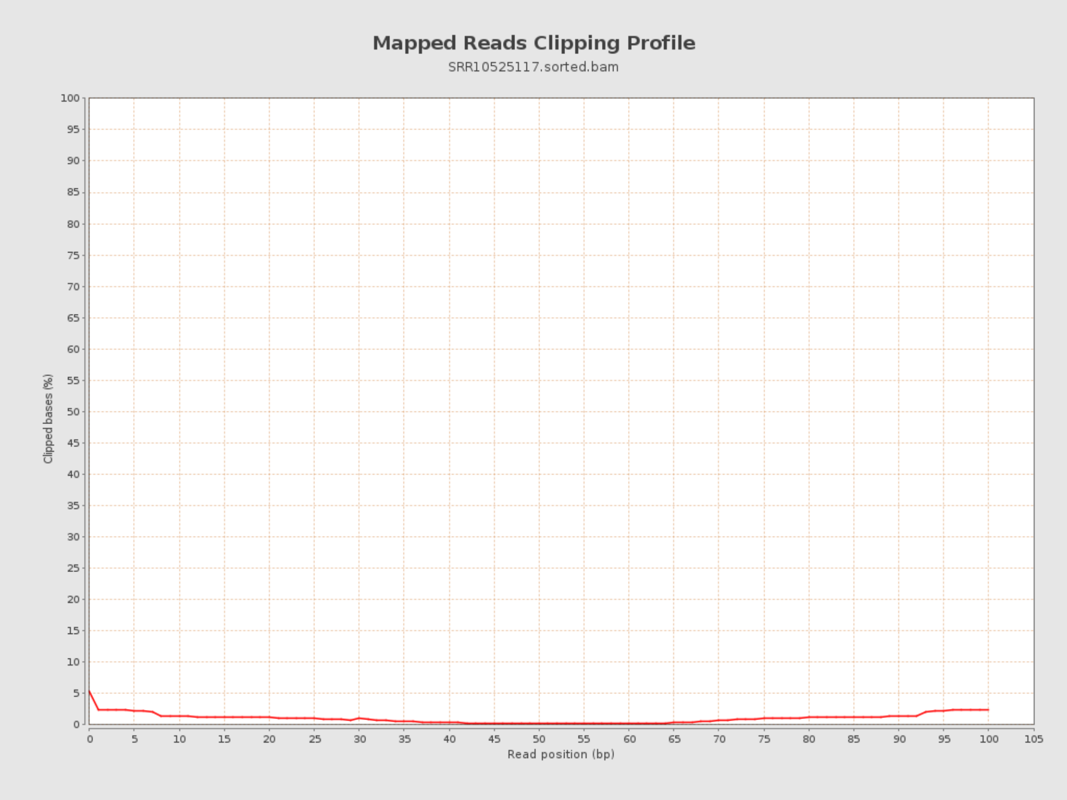
8. Results : Mapped Reads Nucleotide Content



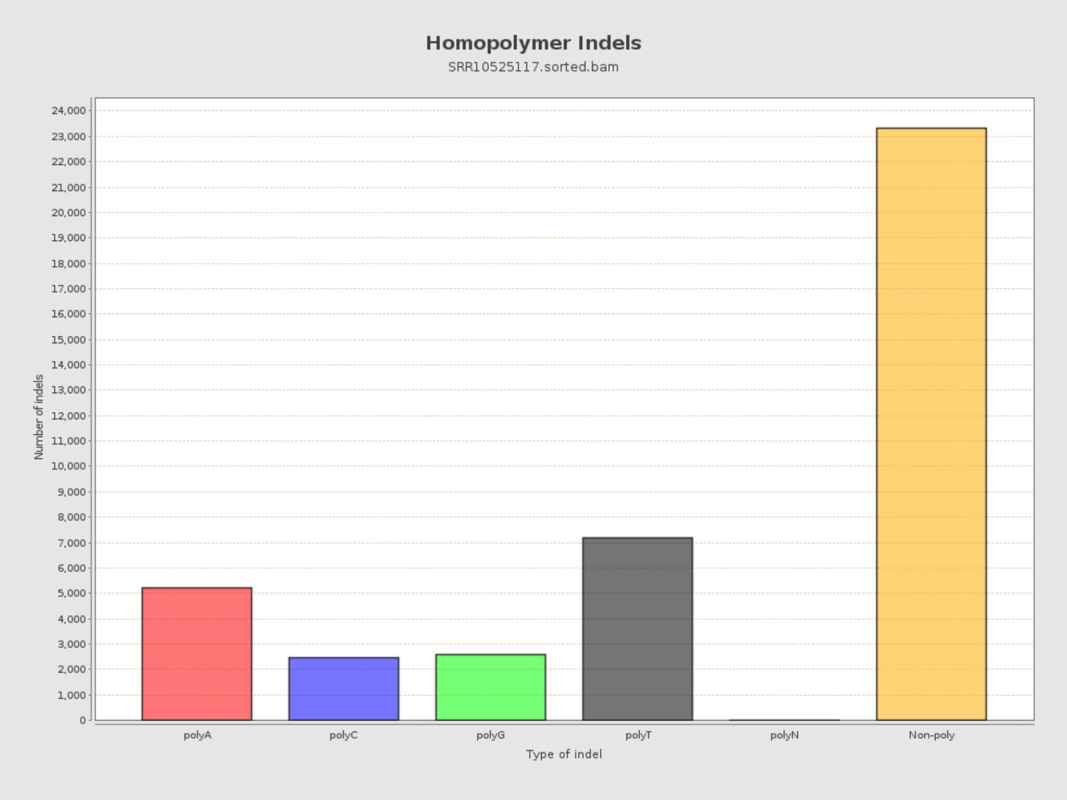
9. Results : Mapped Reads GC-content Distribution



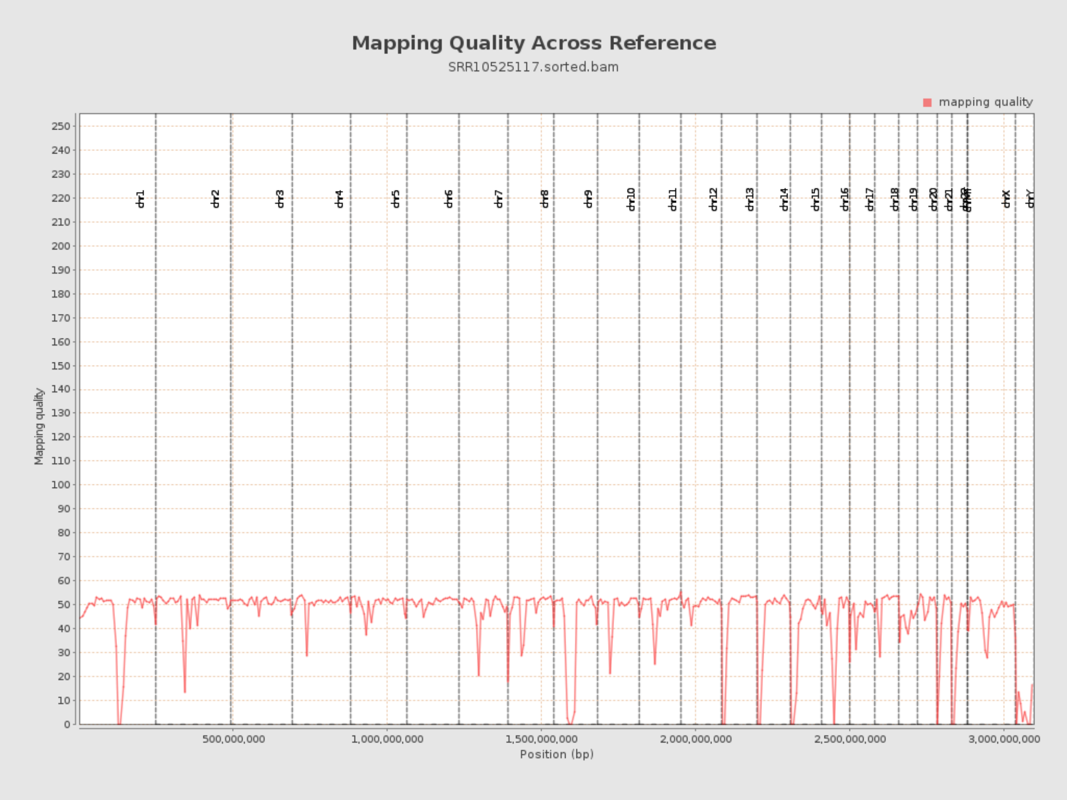
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram