Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 20:28:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525157.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_SRR10525157 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525157.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 20:28:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525157.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,969,236
Mapped reads	1,150,890 / 58.44%
Unmapped reads	818,346 / 41.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,820 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	26,541 / 1.35%
Duplication rate	1.66%
Clipped reads	1,150,468 / 58.42%

2.2. ACGT Content

Number/percentage of A's	18,972,735 / 27.38%
Number/percentage of C's	12,730,460 / 18.37%
Number/percentage of T's	20,901,578 / 30.16%
Number/percentage of G's	16,699,973 / 24.1%
Number/percentage of N's	1,656 / 0%
GC Percentage	42.46%

2.3. Coverage

Mean	0.0224

Standard Deviation	0.2164

2.4. Mapping Quality

Mean Mapping Quality	45.42

2.5. Mismatches and indels

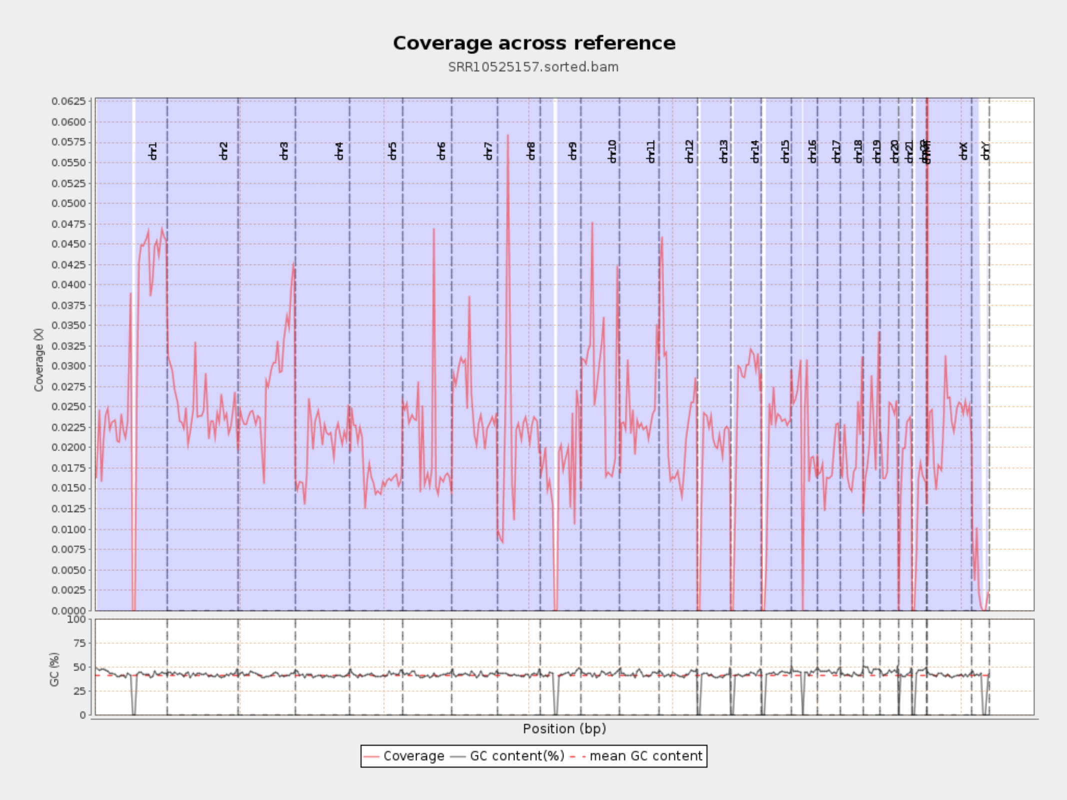
General error rate	0.5%
Mismatches	335,313
Insertions	5,563
Mapped reads with at least one insertion	0.48%
Deletions	13,655
Mapped reads with at least one deletion	1.18%
Homopolymer indels	42.98%

2.6. Chromosome stats

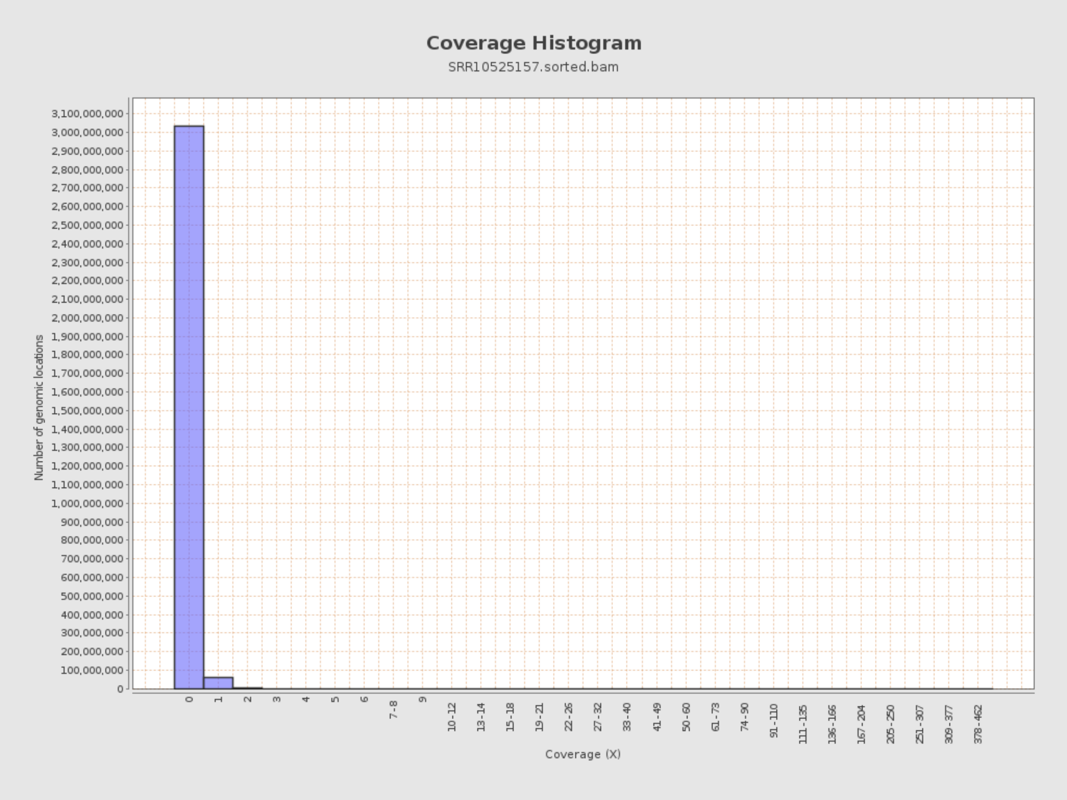
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7567432	0.0304	0.3856
chr2	243199373	6004649	0.0247	0.2628
chr3	198022430	5515940	0.0279	0.1778
chr4	191154276	3946037	0.0206	0.1579
chr5	180915260	3147693	0.0174	0.1397
chr6	171115067	3554390	0.0208	0.1676
chr7	159138663	4114137	0.0259	0.2872

chr8	146364022	3232304	0.0221	0.1863
chr9	141213431	2308300	0.0163	0.1603
chr10	135534747	3847886	0.0284	0.2498
chr11	135006516	3212339	0.0238	0.1899
chr12	133851895	3196027	0.0239	0.1646
chr13	115169878	2185460	0.019	0.1455
chr14	107349540	2663953	0.0248	0.1716
chr15	102531392	1963979	0.0192	0.1519
chr16	90354753	1967973	0.0218	0.1696
chr17	81195210	1458029	0.018	0.1468
chr18	78077248	1506519	0.0193	0.3114
chr19	59128983	1301744	0.022	0.2763
chr20	63025520	1334508	0.0212	0.1562
chr21	48129895	882041	0.0183	0.1486
chr22	51304566	592437	0.0115	0.114
chrMT	16571	50945	3.0743	2.3941
chrX	155270560	3582499	0.0231	0.1688
chrY	59373566	191207	0.0032	0.0991

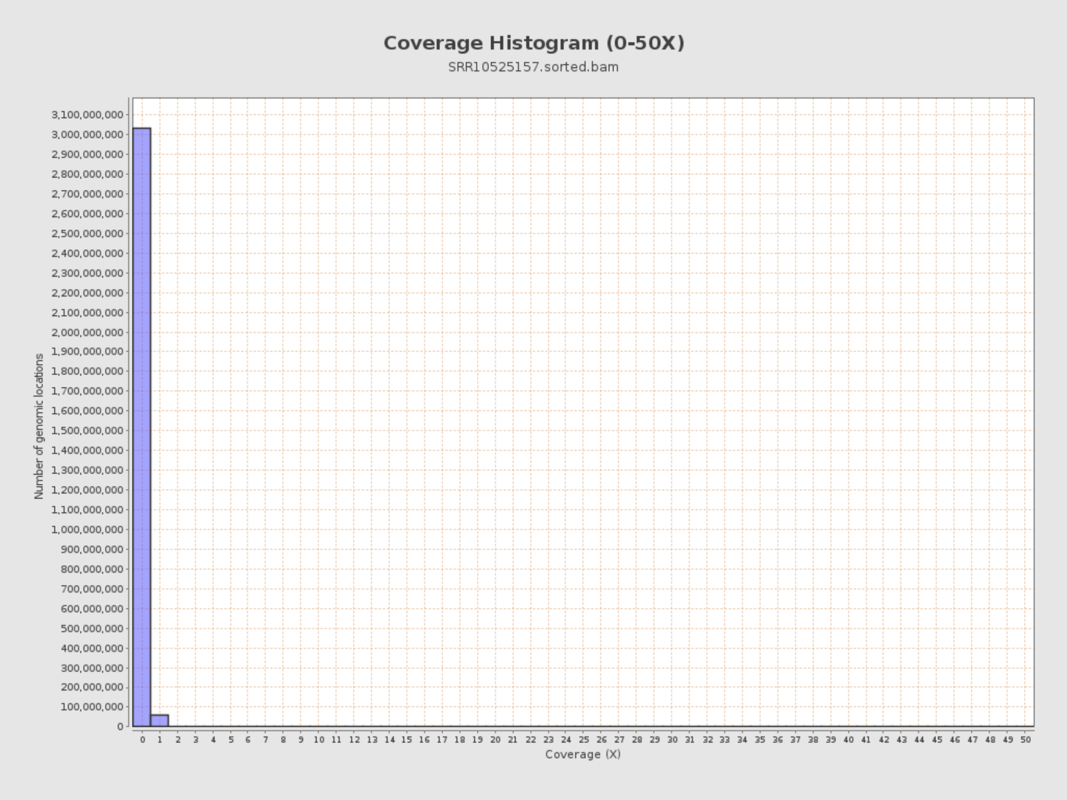
3. Results : Coverage across reference



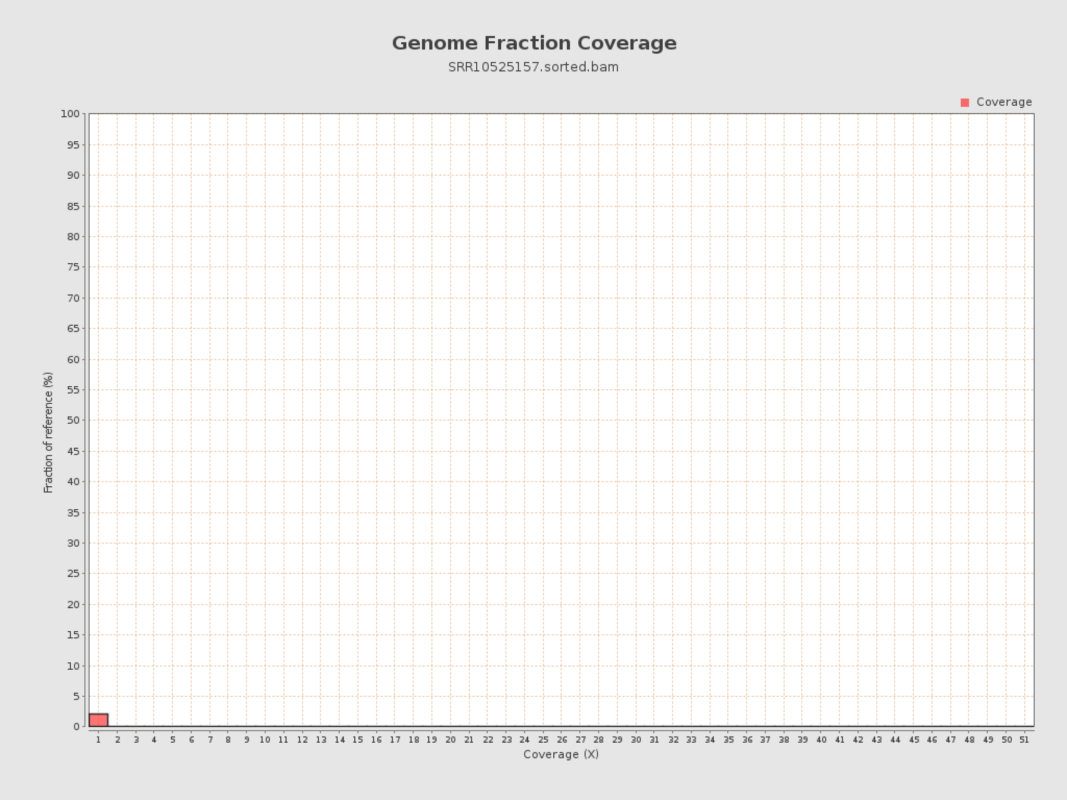
4. Results : Coverage Histogram



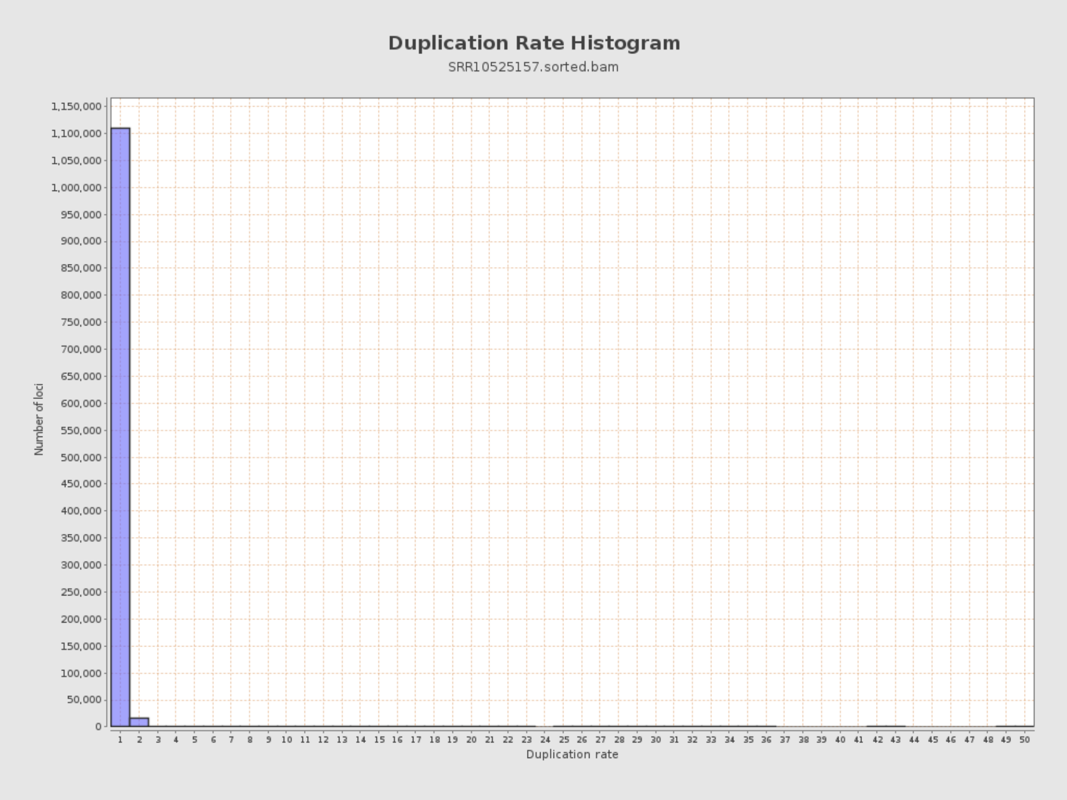
5. Results : Coverage Histogram (0-50X)



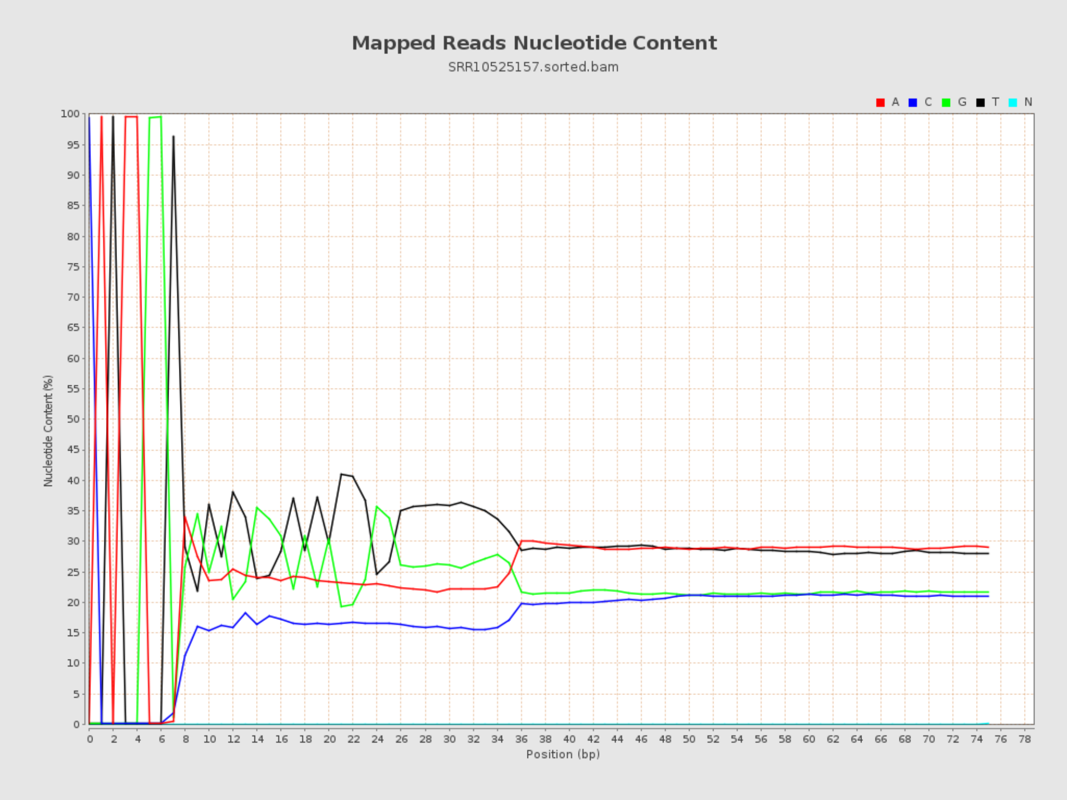
6. Results : Genome Fraction Coverage



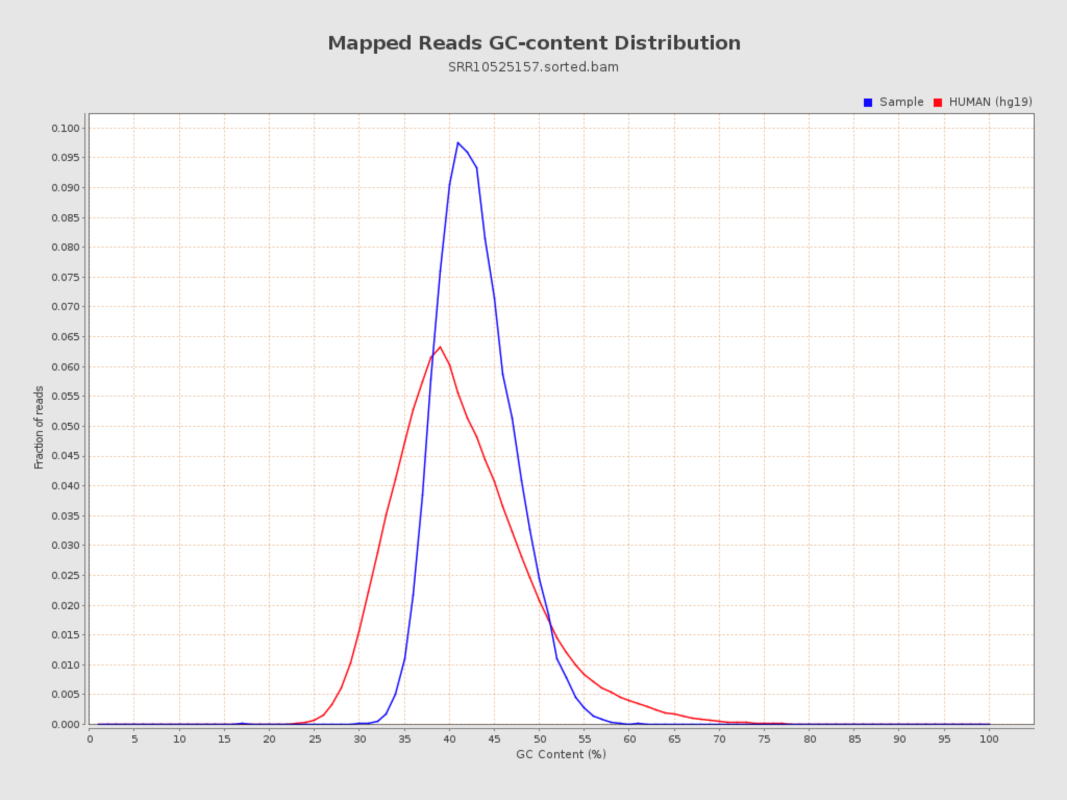
7. Results : Duplication Rate Histogram



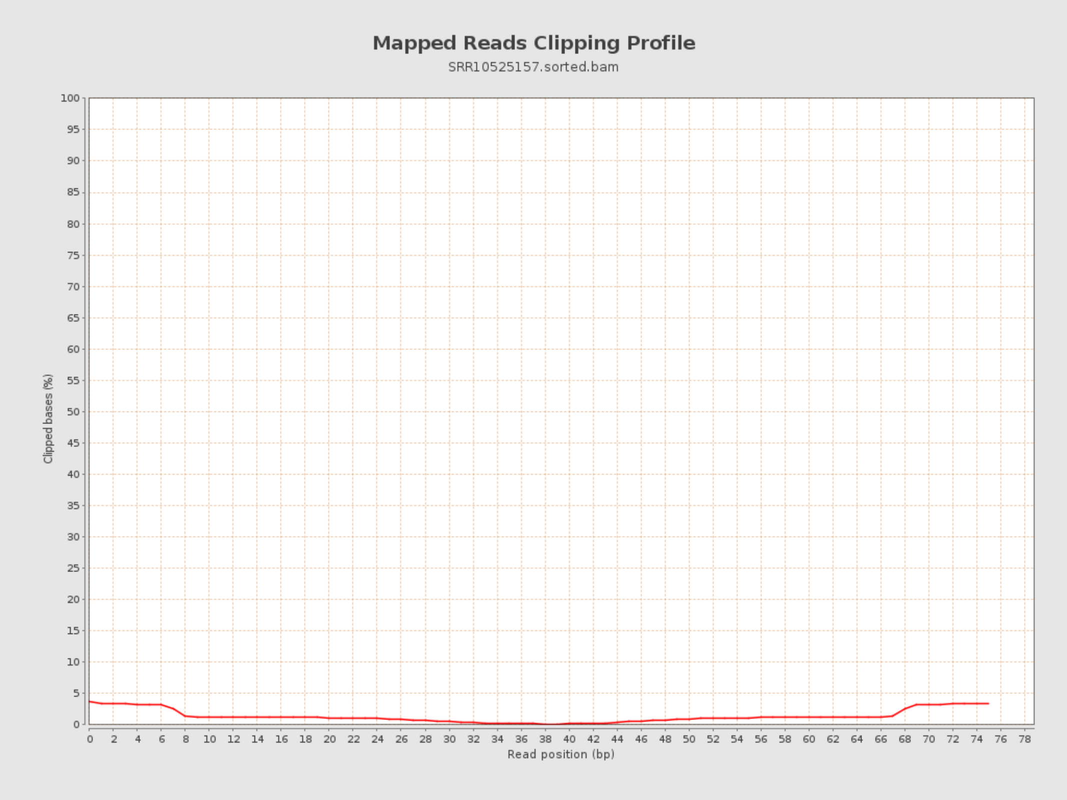
8. Results : Mapped Reads Nucleotide Content



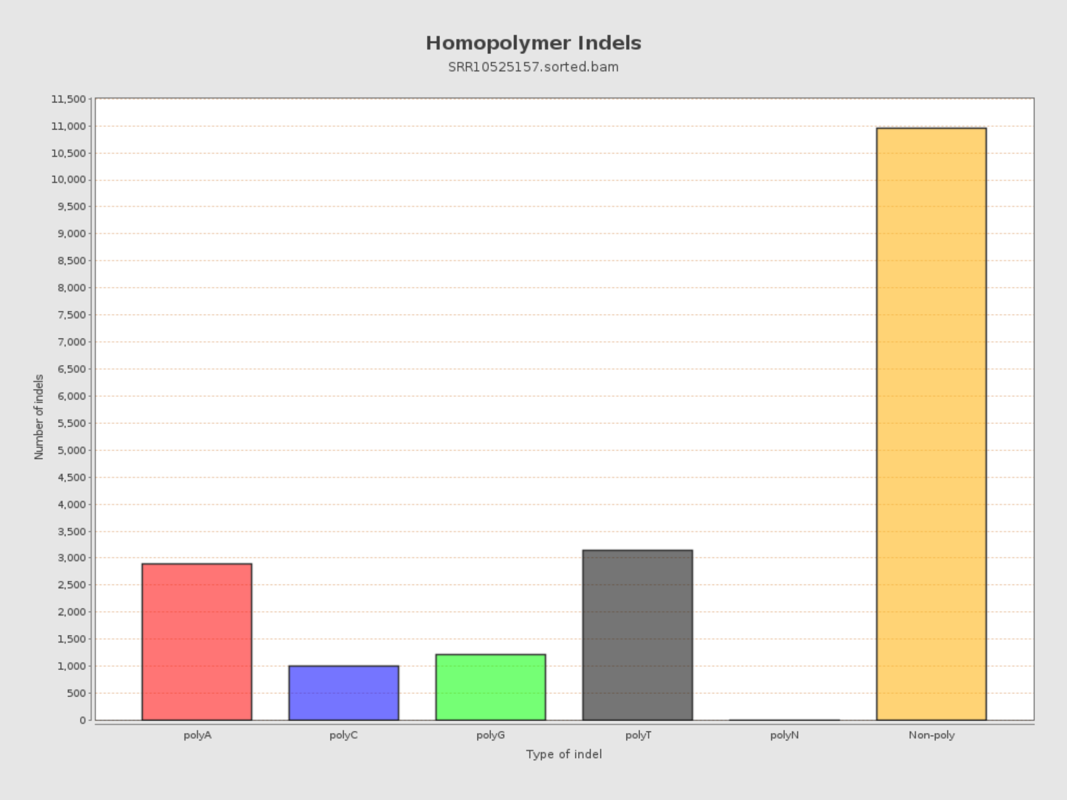
9. Results : Mapped Reads GC-content Distribution



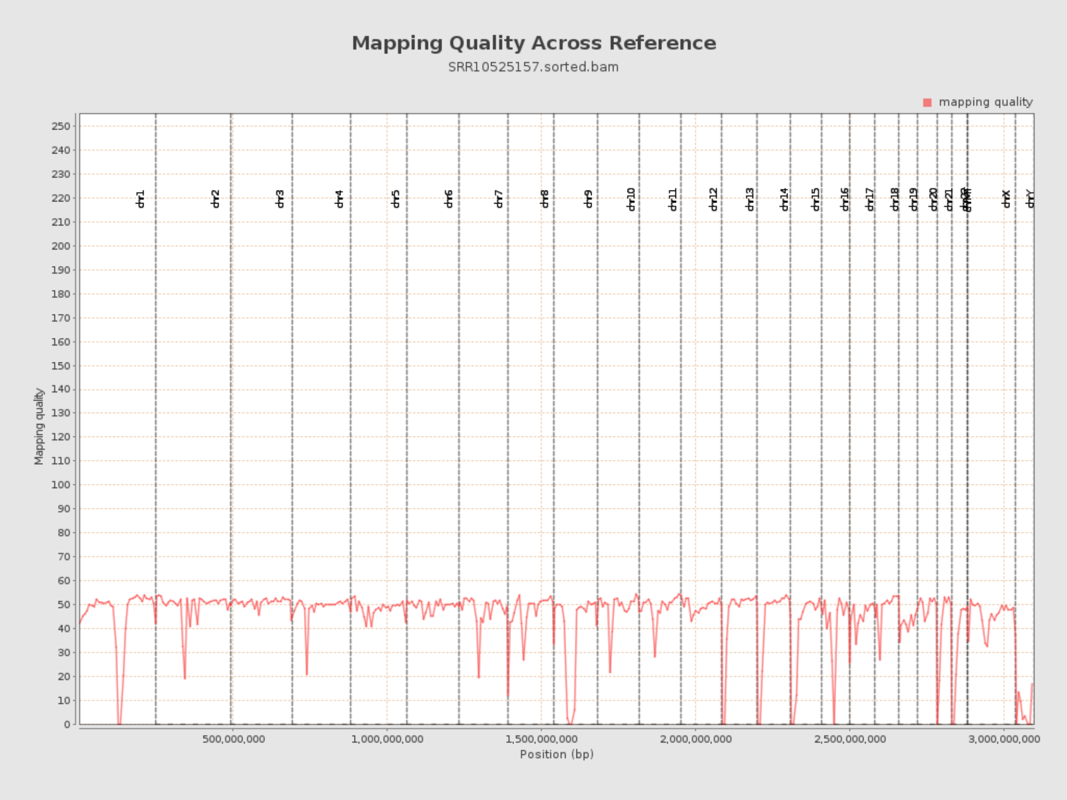
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram