Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:38:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080783.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_SRR3080783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:38:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,588,033
Mapped reads	2,260,570 / 87.35%
Unmapped reads	327,463 / 12.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,481 / 0.98%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	92,980 / 3.59%
Duplication rate	3.52%
Clipped reads	1,058,881 / 40.91%

2.2. ACGT Content

Number/percentage of A's	43,067,522 / 28.63%
Number/percentage of C's	28,870,027 / 19.19%
Number/percentage of T's	46,075,303 / 30.63%
Number/percentage of G's	32,407,634 / 21.54%
Number/percentage of N's	2,924 / 0%
GC Percentage	40.74%

2.3. Coverage

Mean	0.0486

Standard Deviation	0.325

2.4. Mapping Quality

Mean Mapping Quality	46.31

2.5. Mismatches and indels

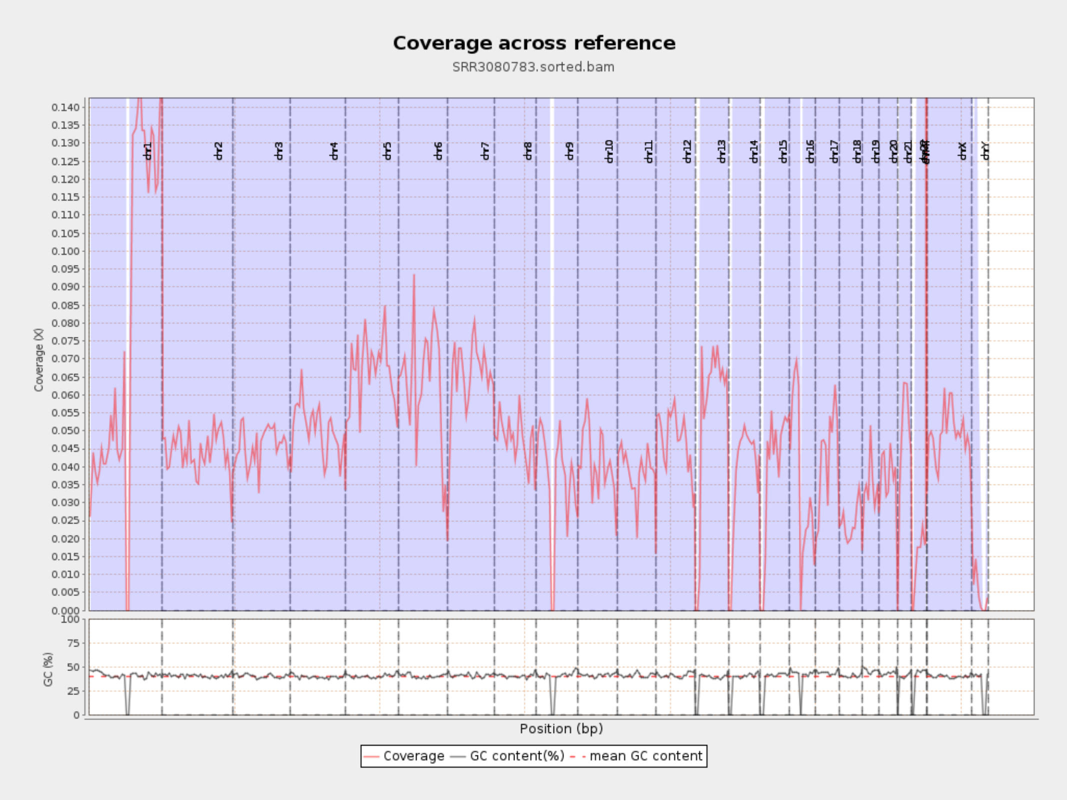
General error rate	0.76%
Mismatches	1,123,338
Insertions	11,212
Mapped reads with at least one insertion	0.49%
Deletions	32,876
Mapped reads with at least one deletion	1.44%
Homopolymer indels	48.1%

2.6. Chromosome stats

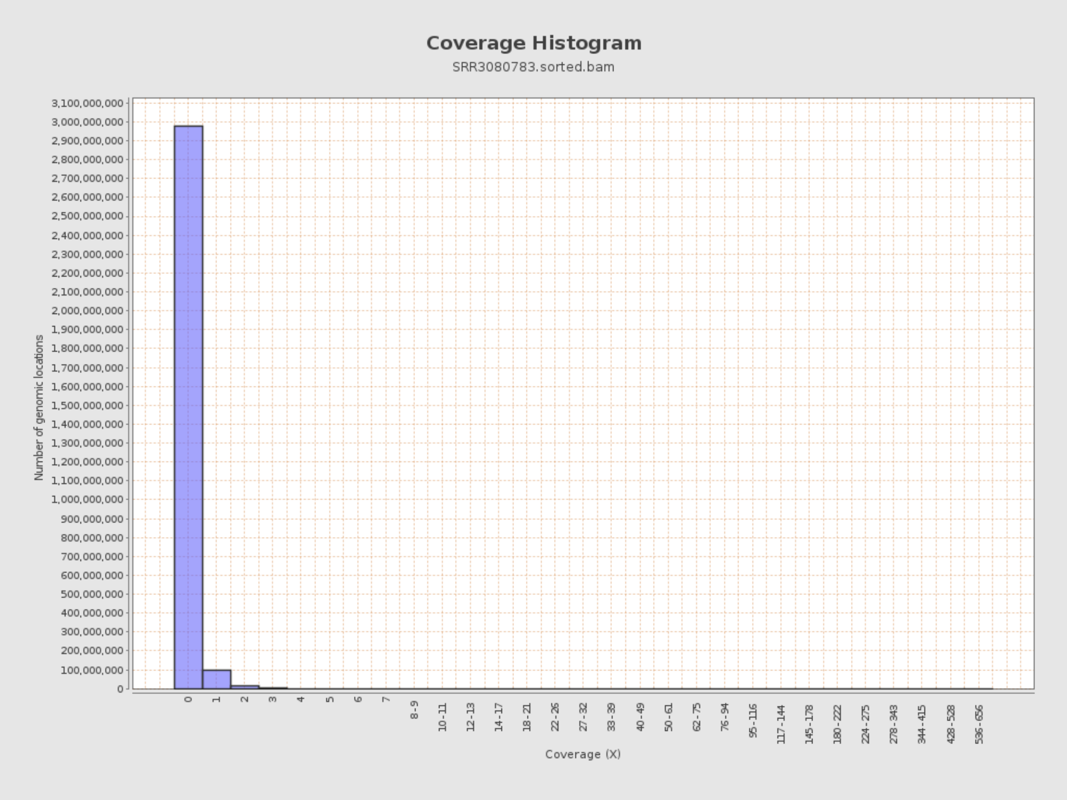
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19684707	0.079	0.524
chr2	243199373	10797860	0.0444	0.3753
chr3	198022430	9081706	0.0459	0.2583
chr4	191154276	9643536	0.0504	0.274
chr5	180915260	12108085	0.0669	0.3122
chr6	171115067	10795803	0.0631	0.3543
chr7	159138663	10477307	0.0658	0.3477

chr8	146364022	6964884	0.0476	0.4273
chr9	141213431	5176184	0.0367	0.2664
chr10	135534747	5654158	0.0417	0.2934
chr11	135006516	5213295	0.0386	0.2505
chr12	133851895	6418965	0.048	0.265
chr13	115169878	6310186	0.0548	0.2839
chr14	107349540	4016603	0.0374	0.2426
chr15	102531392	3997127	0.039	0.2468
chr16	90354753	3256959	0.036	0.24
chr17	81195210	3489462	0.043	0.2602
chr18	78077248	1937374	0.0248	0.3284
chr19	59128983	2040957	0.0345	0.3407
chr20	63025520	2376340	0.0377	0.2385
chr21	48129895	2237446	0.0465	0.2659
chr22	51304566	705902	0.0138	0.1377
chrMT	16571	202454	12.2174	6.7162
chrX	155270560	7581400	0.0488	0.2758
chrY	59373566	306962	0.0052	0.1009

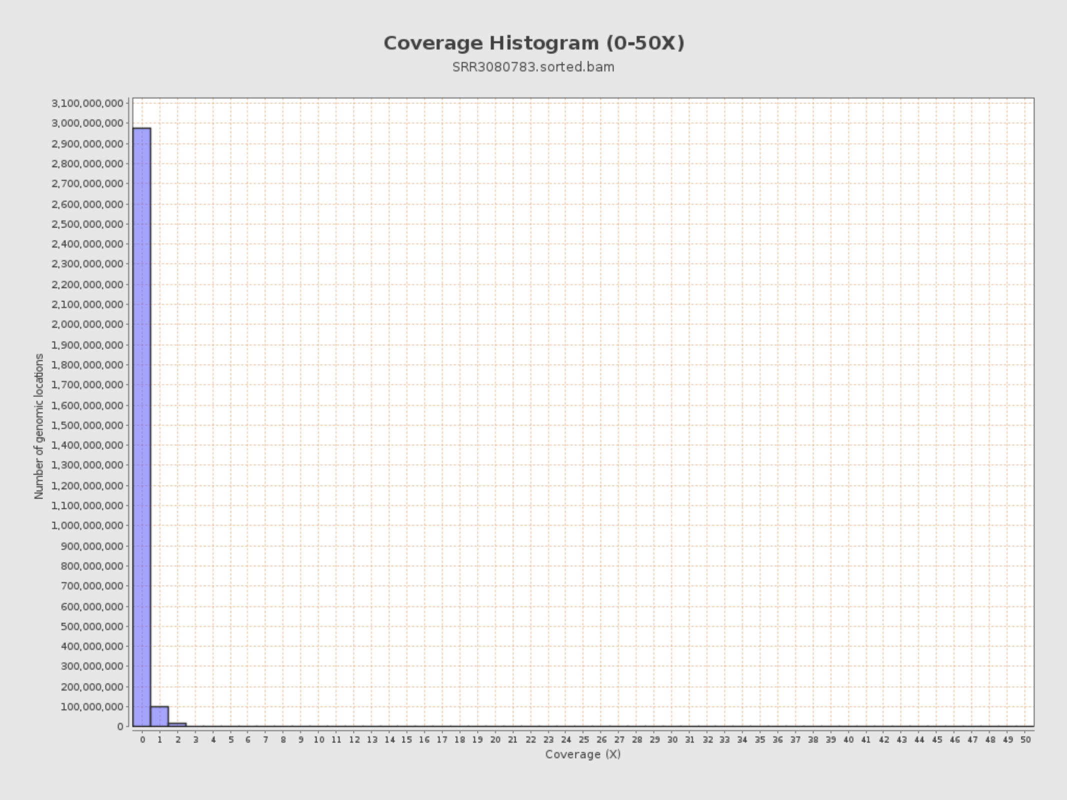
3. Results : Coverage across reference



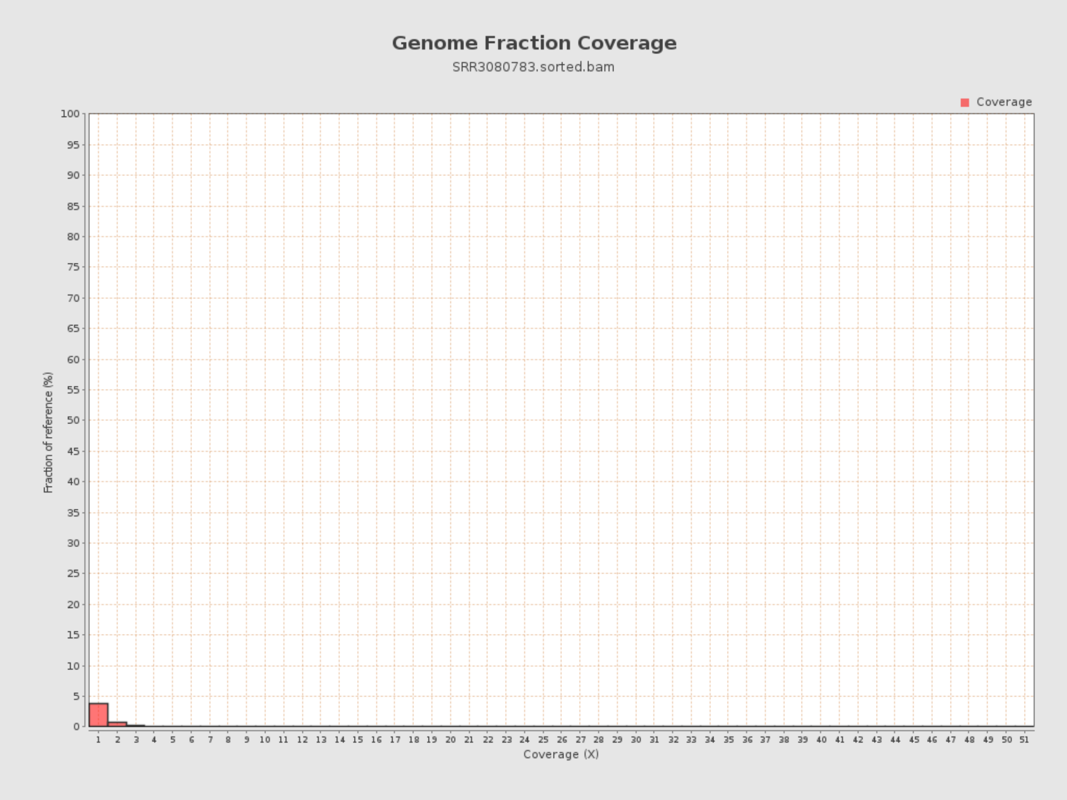
4. Results : Coverage Histogram



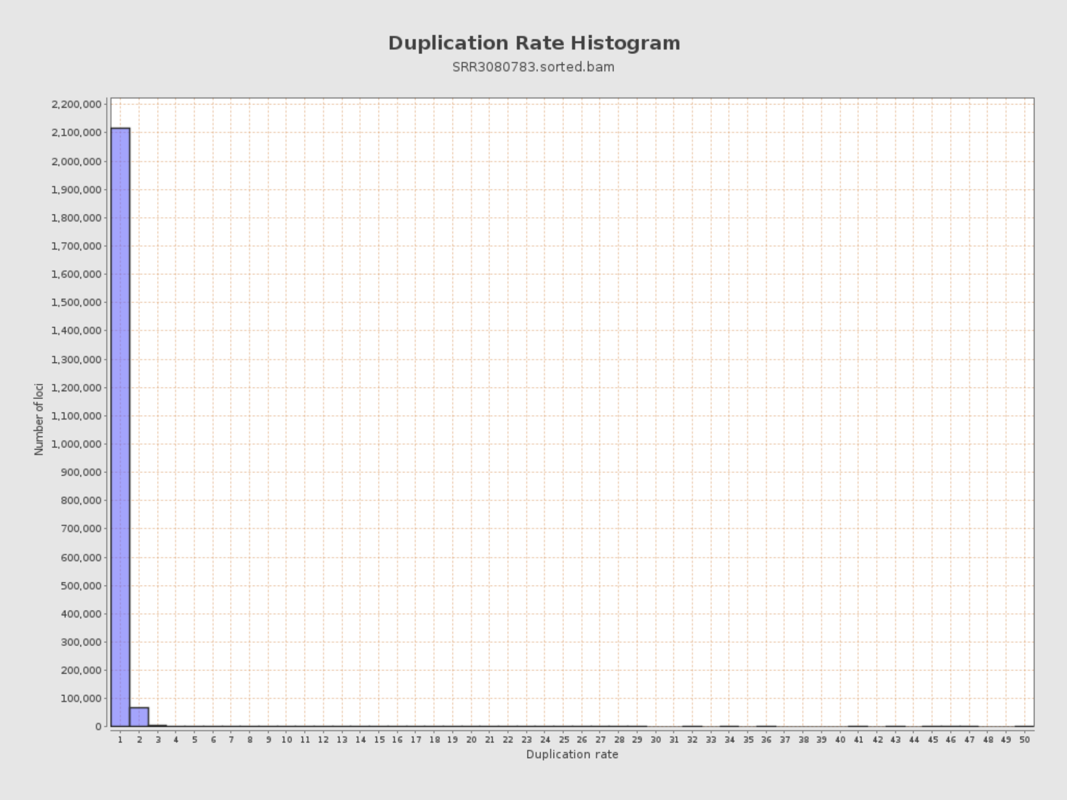
5. Results : Coverage Histogram (0-50X)



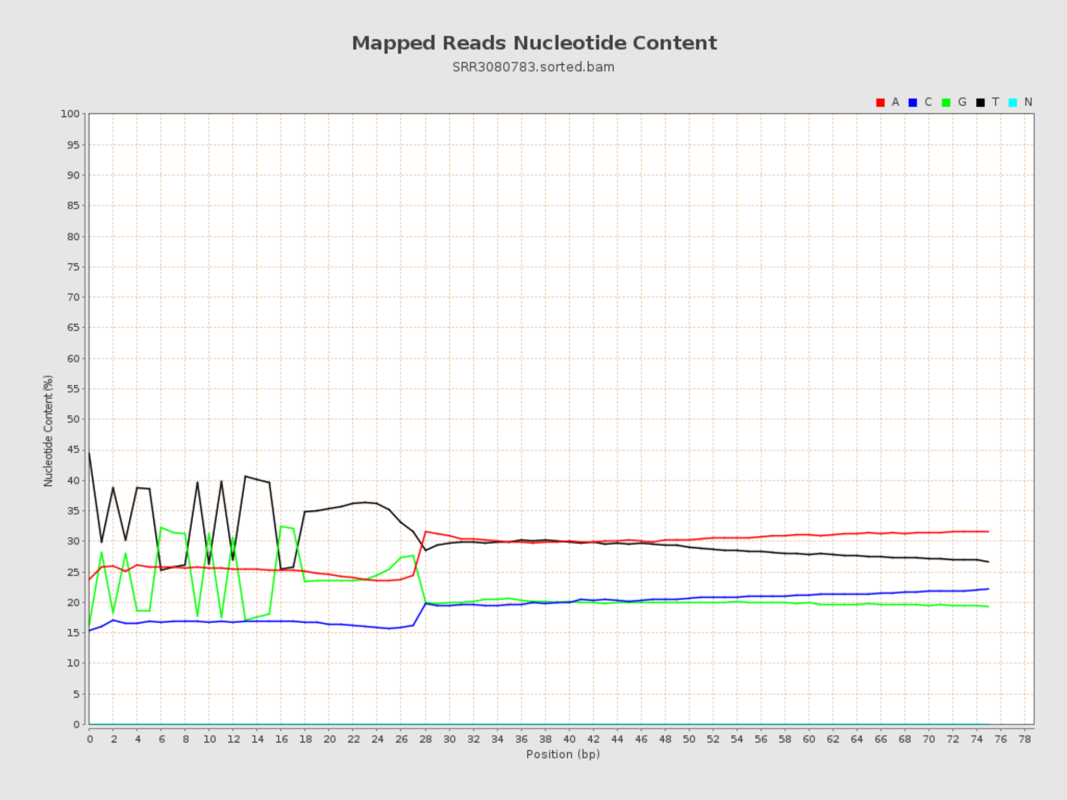
6. Results : Genome Fraction Coverage



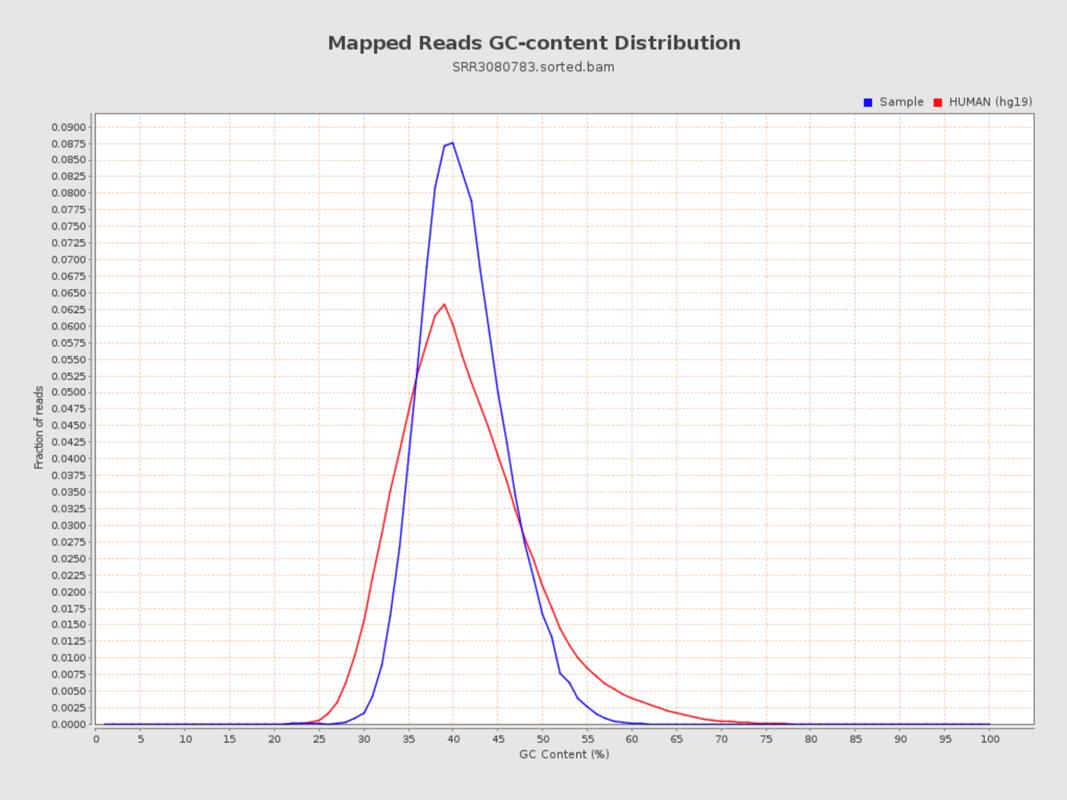
7. Results : Duplication Rate Histogram



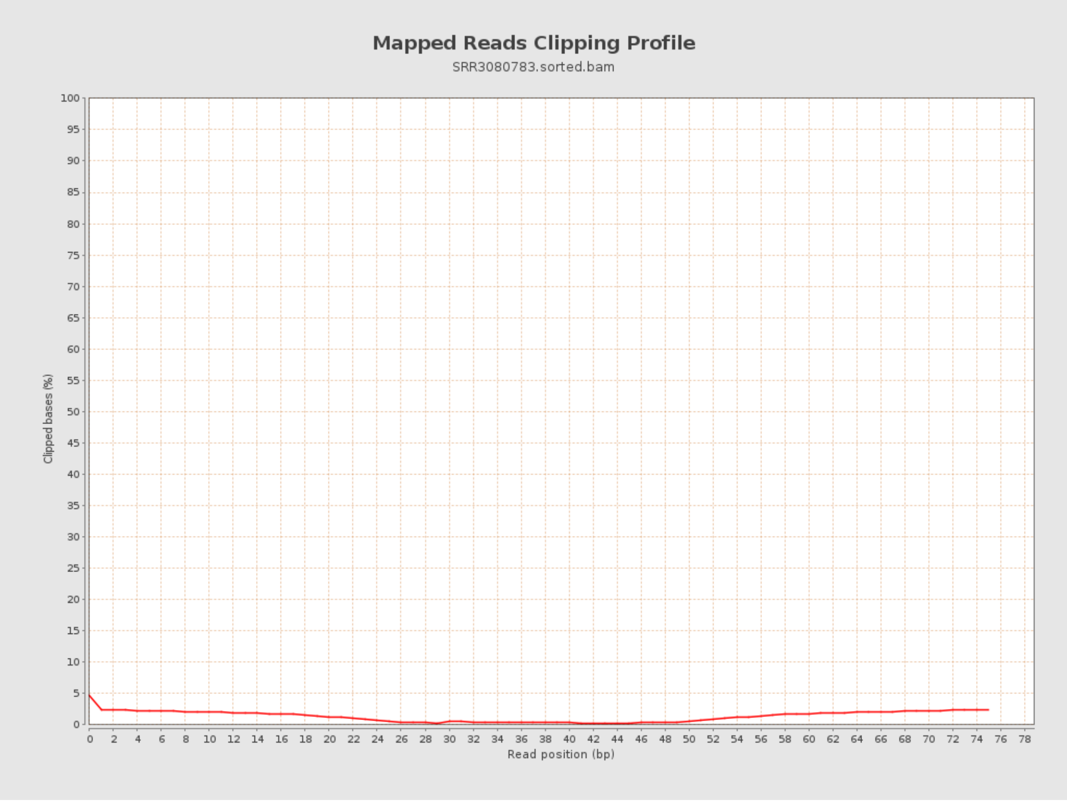
8. Results : Mapped Reads Nucleotide Content



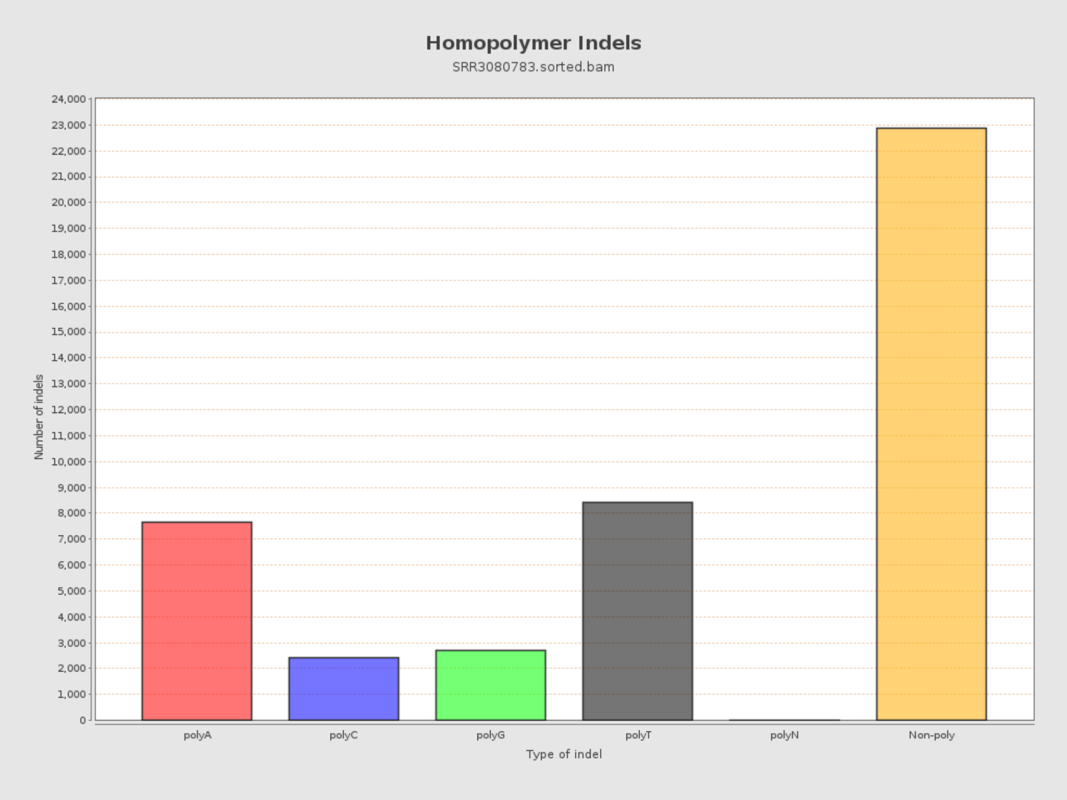
9. Results : Mapped Reads GC-content Distribution



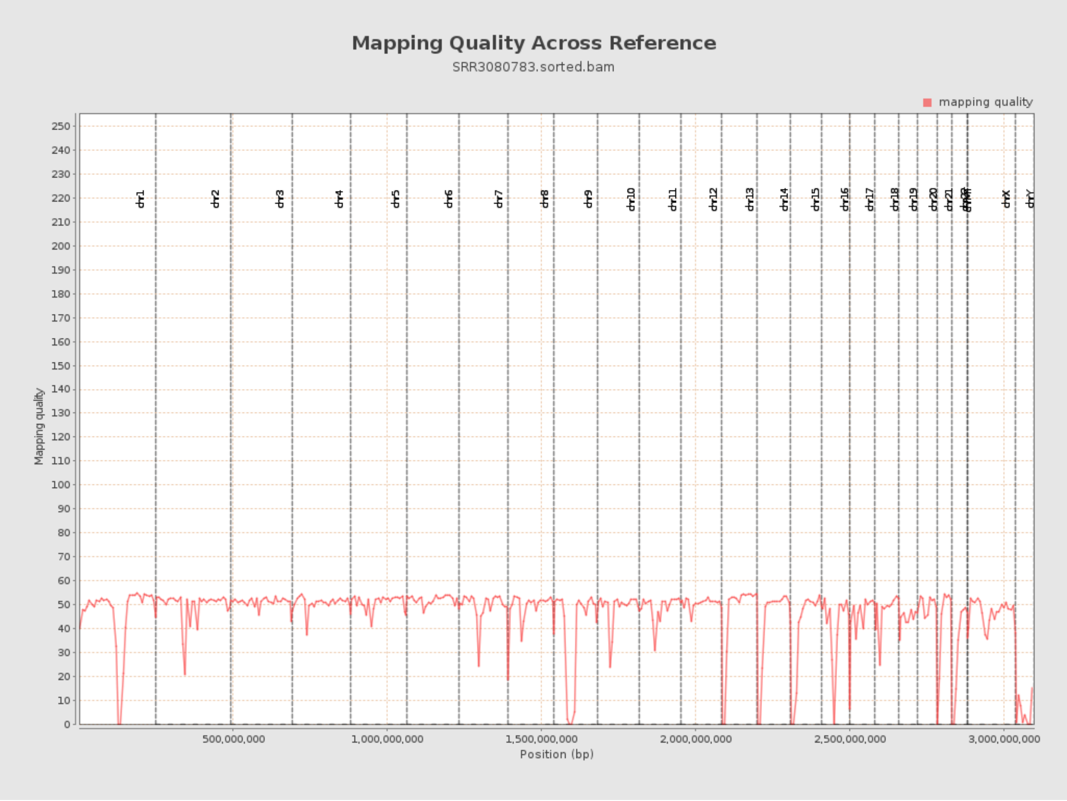
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram