Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 15:57:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082664.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_SRR3082664 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082664.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 15:57:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082664.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,197,676
Mapped reads	2,818,288 / 88.14%
Unmapped reads	379,388 / 11.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,627 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	110,364 / 3.45%
Duplication rate	3.13%
Clipped reads	1,256,508 / 39.29%

2.2. ACGT Content

Number/percentage of A's	52,143,530 / 27.74%
Number/percentage of C's	32,772,178 / 17.44%
Number/percentage of T's	62,055,482 / 33.02%
Number/percentage of G's	40,920,269 / 21.77%
Number/percentage of N's	51,971 / 0.03%
GC Percentage	39.21%

2.3. Coverage

Mean	0.0607

Standard Deviation	0.4141

2.4. Mapping Quality

Mean Mapping Quality	47.28

2.5. Mismatches and indels

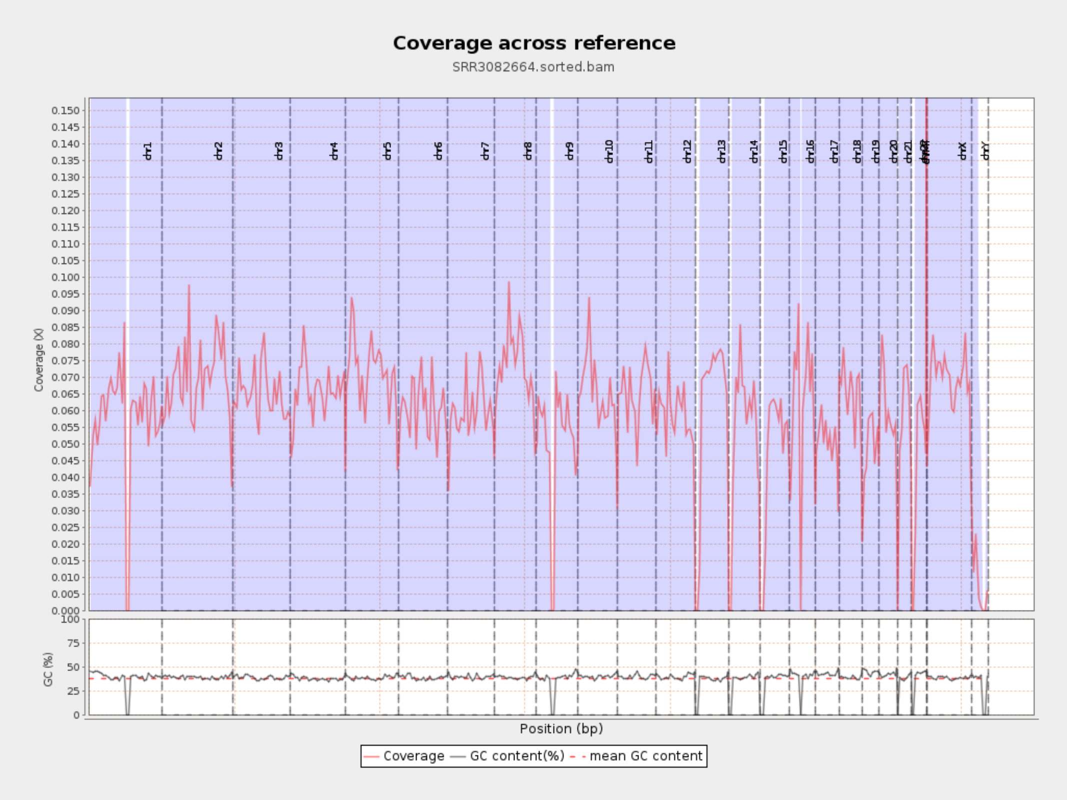
General error rate	0.96%
Mismatches	1,778,671
Insertions	17,001
Mapped reads with at least one insertion	0.6%
Deletions	44,943
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.65%

2.6. Chromosome stats

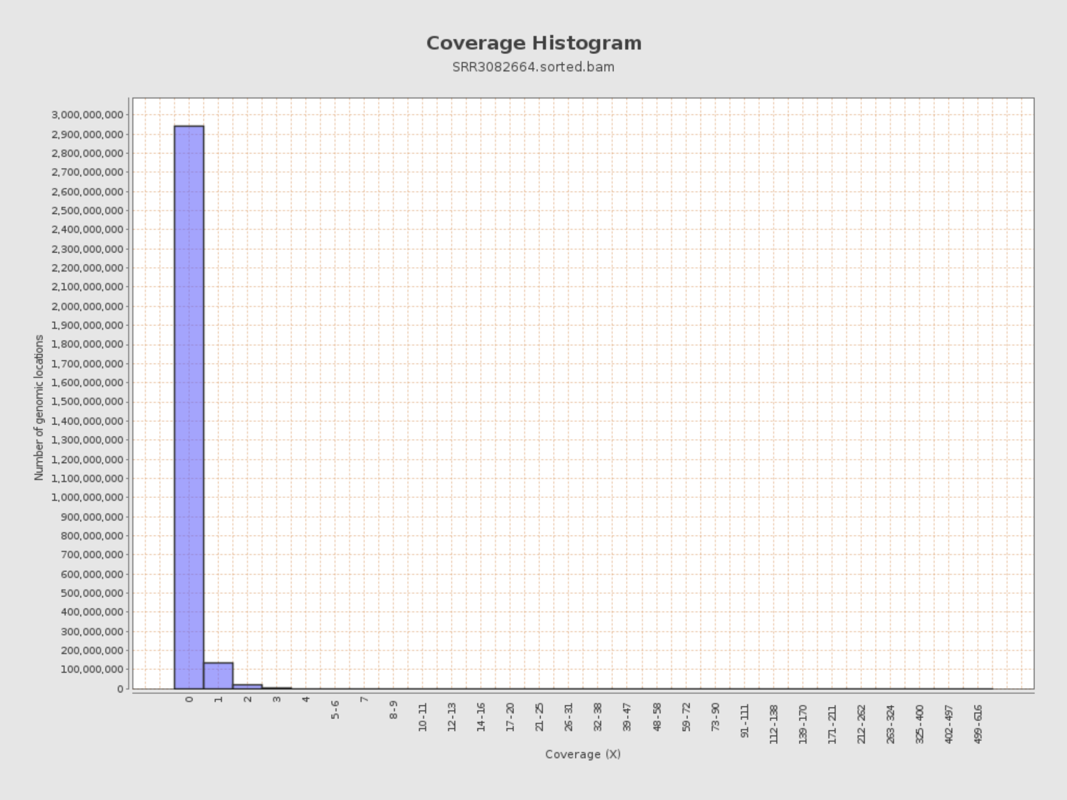
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14338384	0.0575	0.6044
chr2	243199373	16932924	0.0696	0.5228
chr3	198022430	12898753	0.0651	0.3009
chr4	191154276	12588110	0.0659	0.3216
chr5	180915260	13043025	0.0721	0.314
chr6	171115067	10332401	0.0604	0.345
chr7	159138663	9541010	0.06	0.5439

chr8	146364022	10711155	0.0732	0.4849
chr9	141213431	7155898	0.0507	0.4217
chr10	135534747	8965357	0.0661	0.4213
chr11	135006516	8731040	0.0647	0.3773
chr12	133851895	7829527	0.0585	0.2869
chr13	115169878	6954404	0.0604	0.2851
chr14	107349540	5766173	0.0537	0.3004
chr15	102531392	4727634	0.0461	0.2488
chr16	90354753	5624822	0.0623	0.3356
chr17	81195210	4094415	0.0504	0.2901
chr18	78077248	5133335	0.0657	0.7776
chr19	59128983	2910782	0.0492	0.4992
chr20	63025520	3842937	0.061	0.3041
chr21	48129895	2624747	0.0545	0.2878
chr22	51304566	2113652	0.0412	0.2335
chrMT	16571	5427	0.3275	0.5692
chrX	155270560	10697415	0.0689	0.334
chrY	59373566	452923	0.0076	0.1745

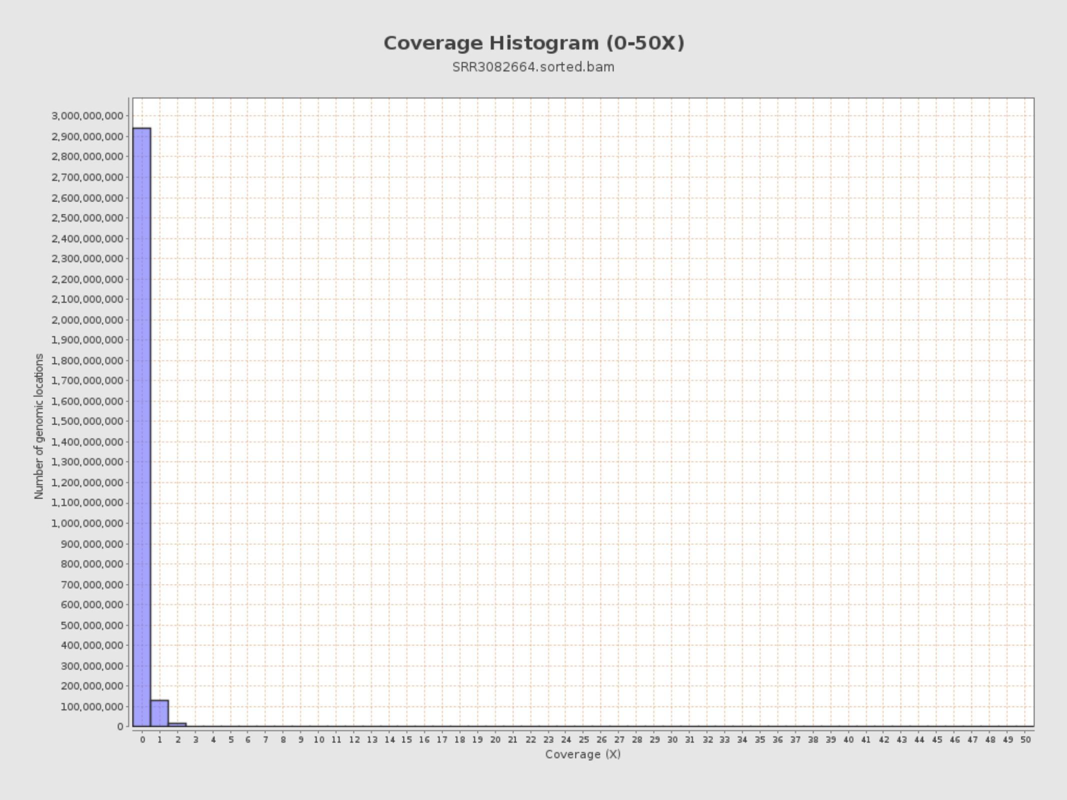
3. Results : Coverage across reference



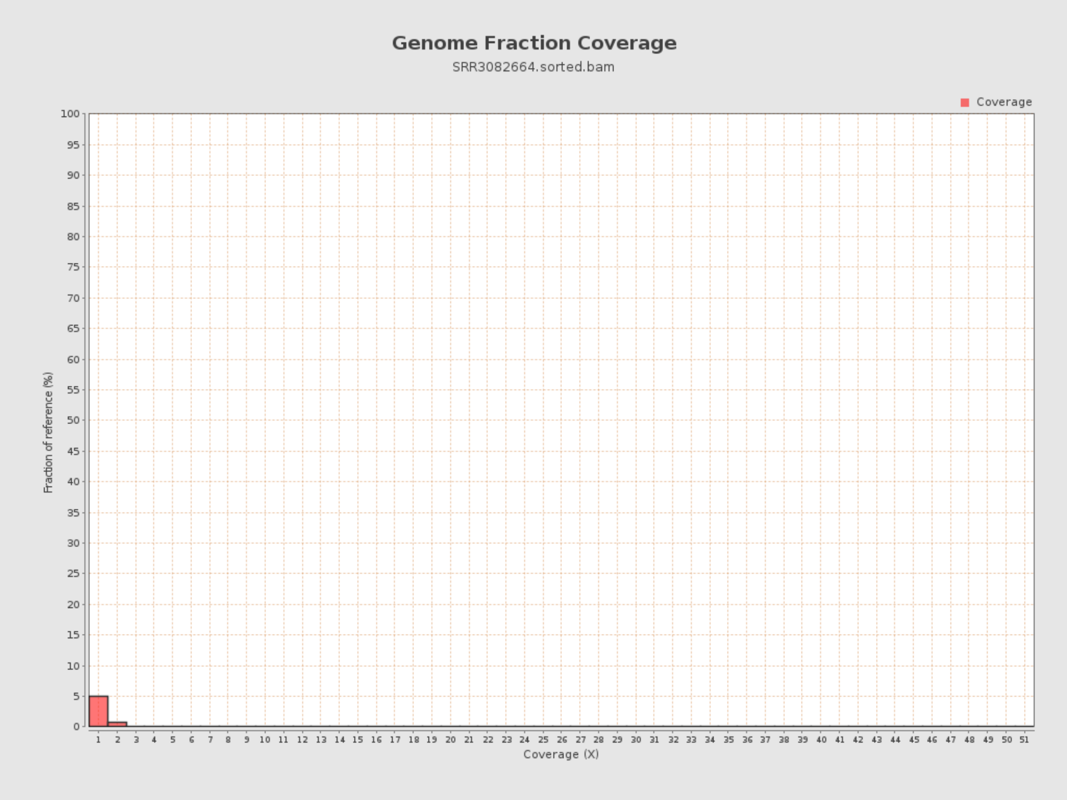
4. Results : Coverage Histogram



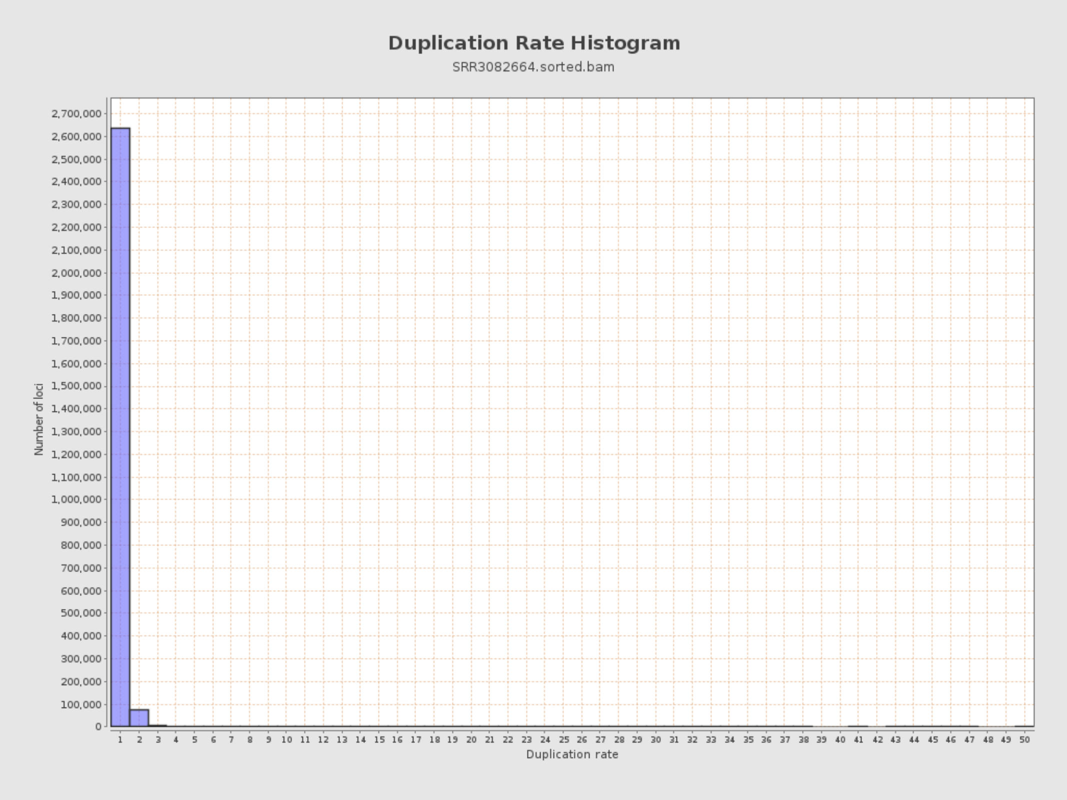
5. Results : Coverage Histogram (0-50X)



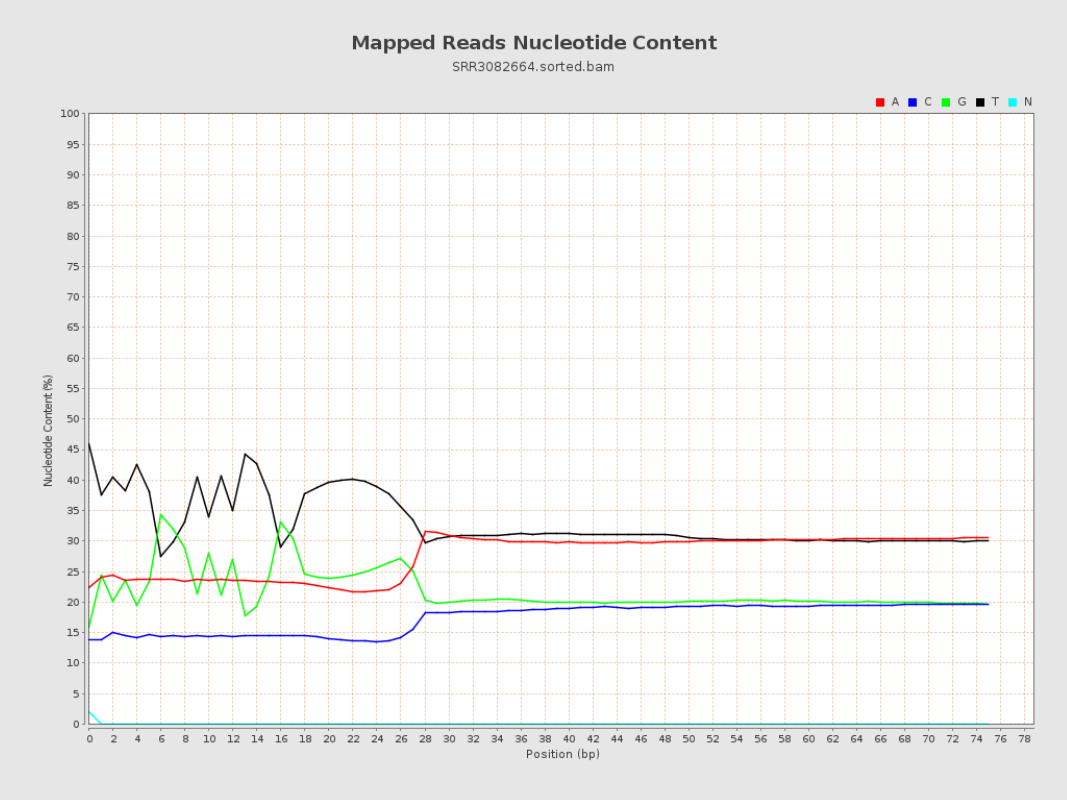
6. Results : Genome Fraction Coverage



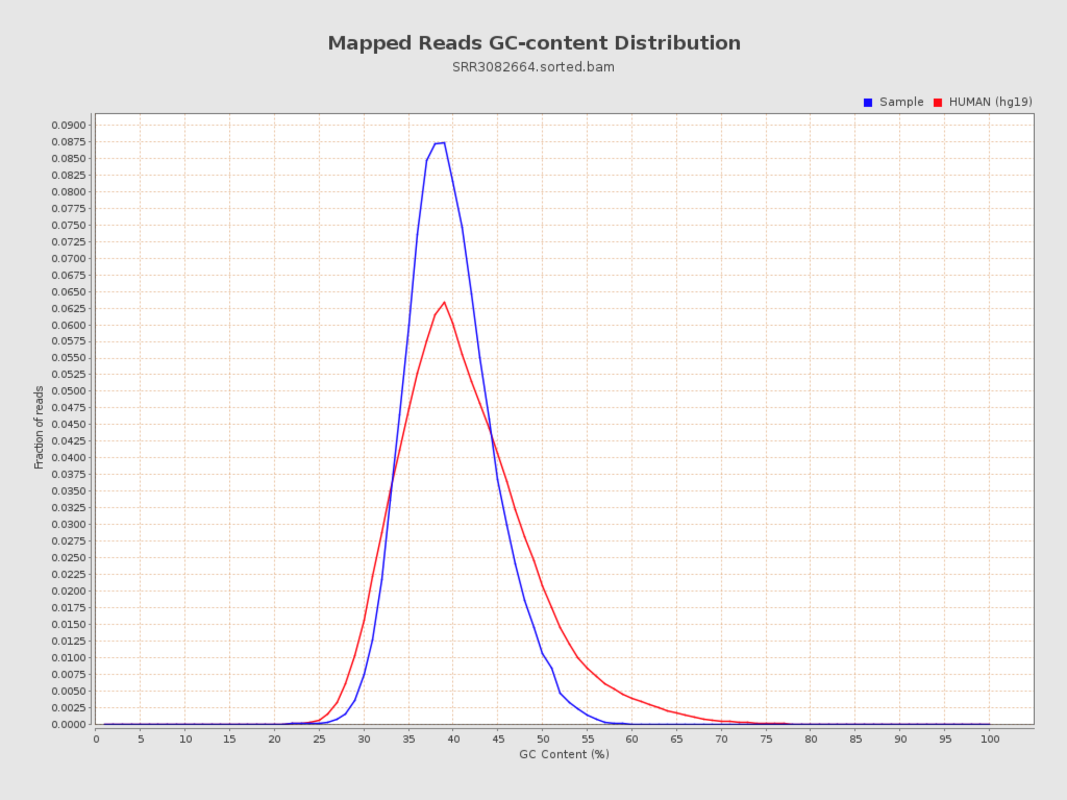
7. Results : Duplication Rate Histogram



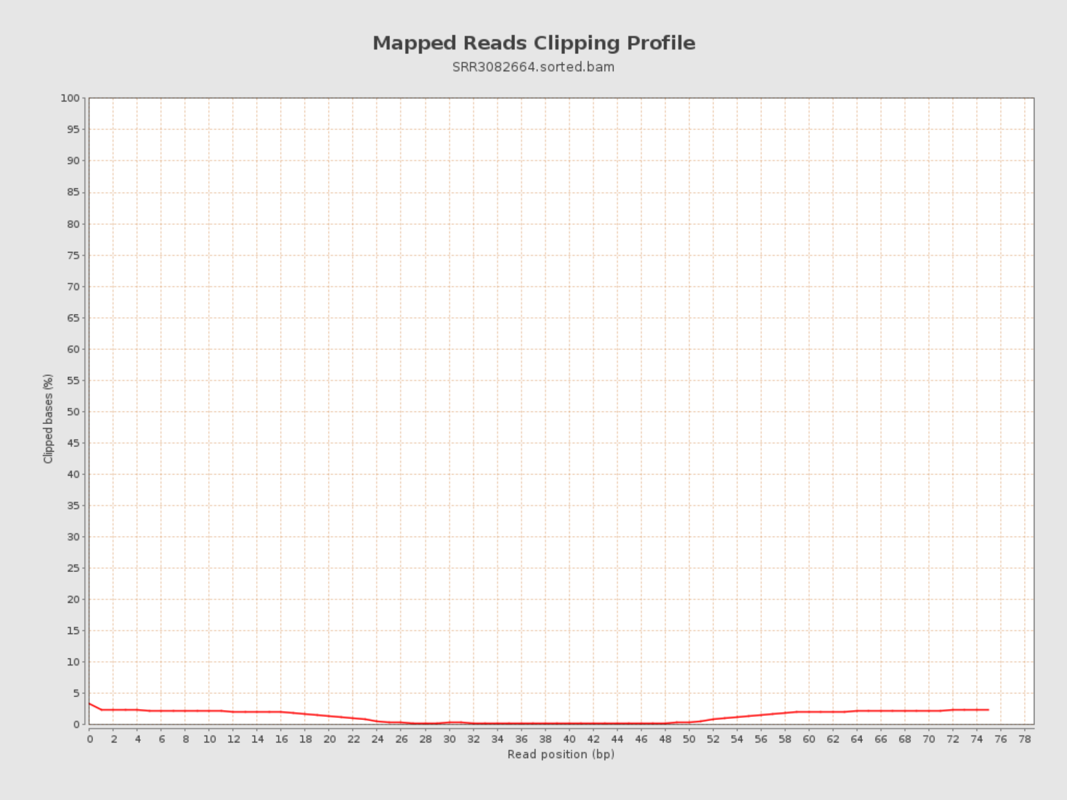
8. Results : Mapped Reads Nucleotide Content



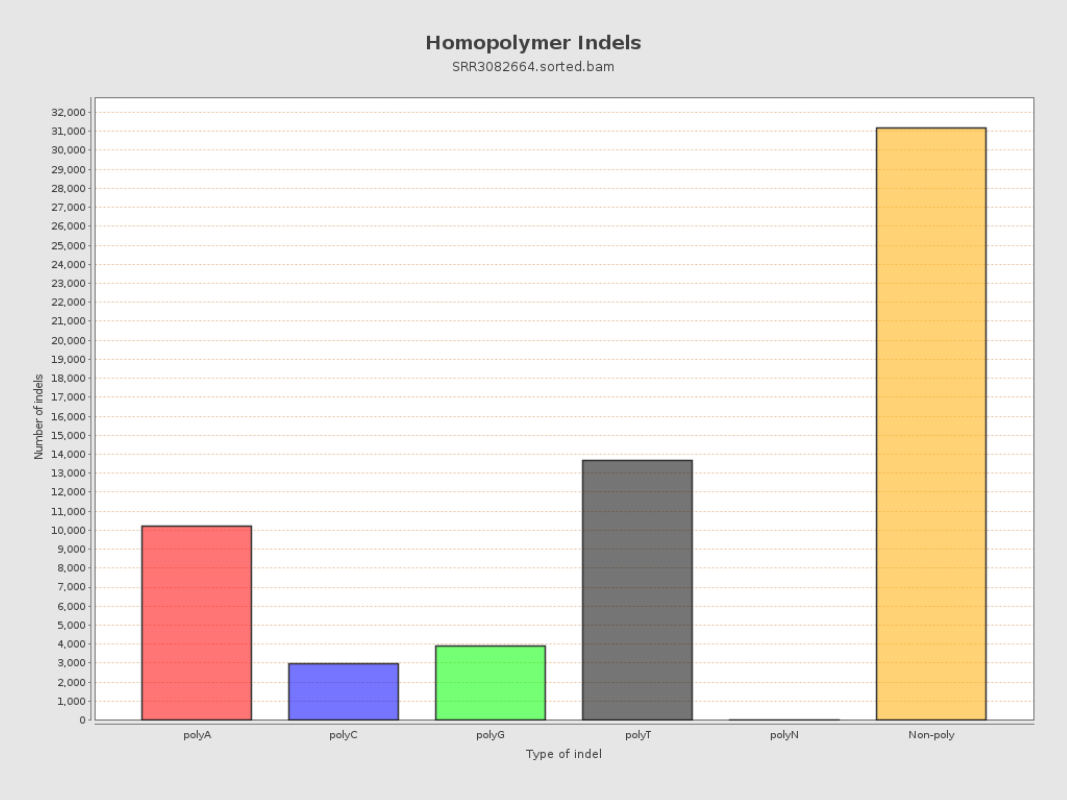
9. Results : Mapped Reads GC-content Distribution



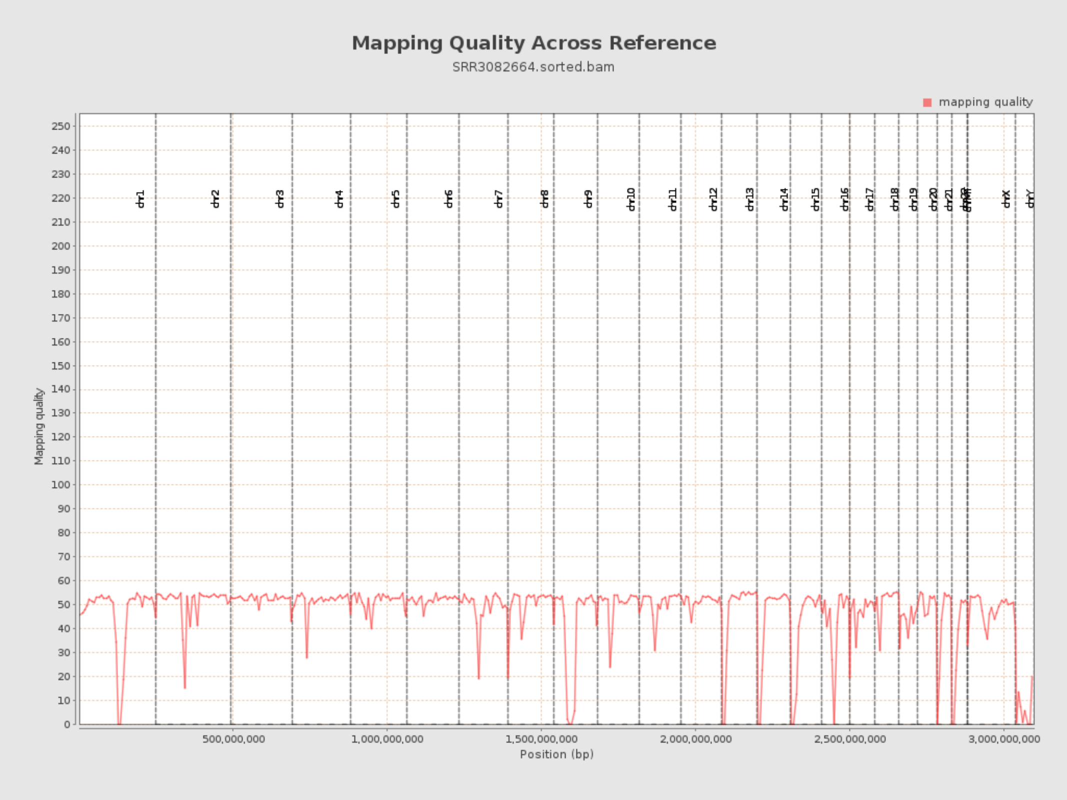
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram