Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 20:17:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082933.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_SRR3082933 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082933.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 20:17:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082933.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,005,638
Mapped reads	1,776,735 / 88.59%
Unmapped reads	228,903 / 11.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,143 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	81,413 / 4.06%
Duplication rate	3.96%
Clipped reads	795,945 / 39.69%

2.2. ACGT Content

Number/percentage of A's	31,752,658 / 26.85%
Number/percentage of C's	22,335,660 / 18.89%
Number/percentage of T's	36,963,833 / 31.26%
Number/percentage of G's	27,181,494 / 22.99%
Number/percentage of N's	5,139 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0382

Standard Deviation	0.281

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

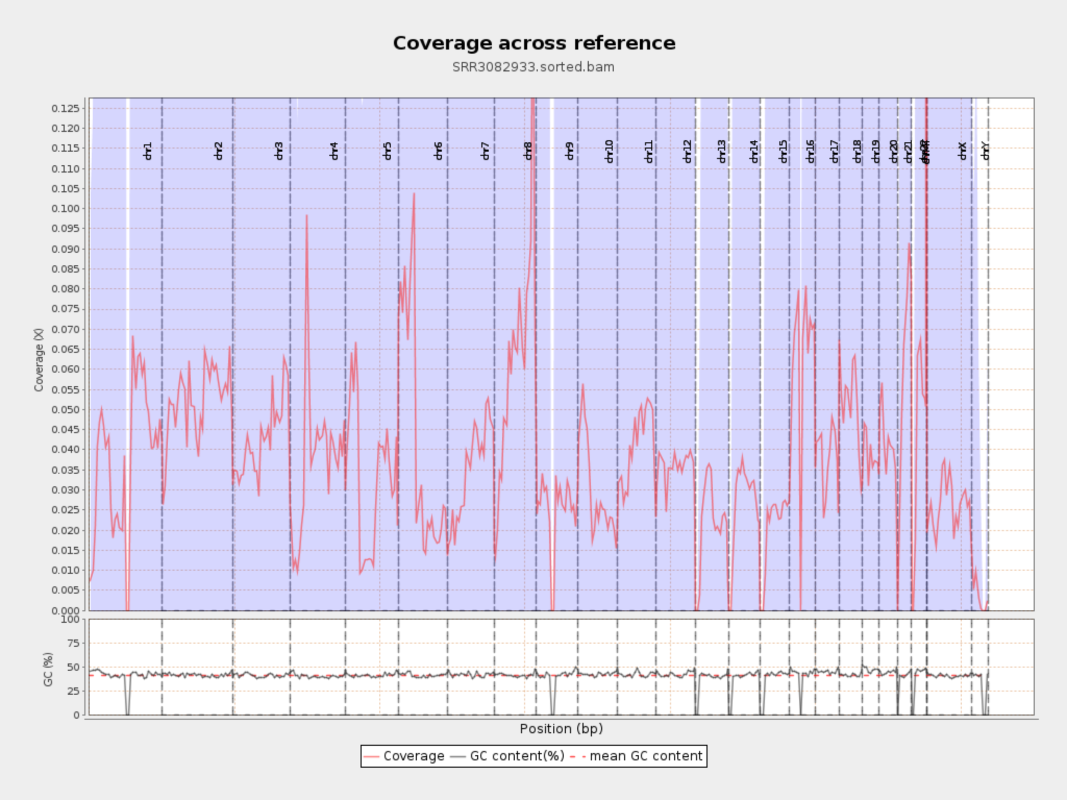
General error rate	0.76%
Mismatches	887,266
Insertions	9,382
Mapped reads with at least one insertion	0.52%
Deletions	27,323
Mapped reads with at least one deletion	1.52%
Homopolymer indels	48.53%

2.6. Chromosome stats

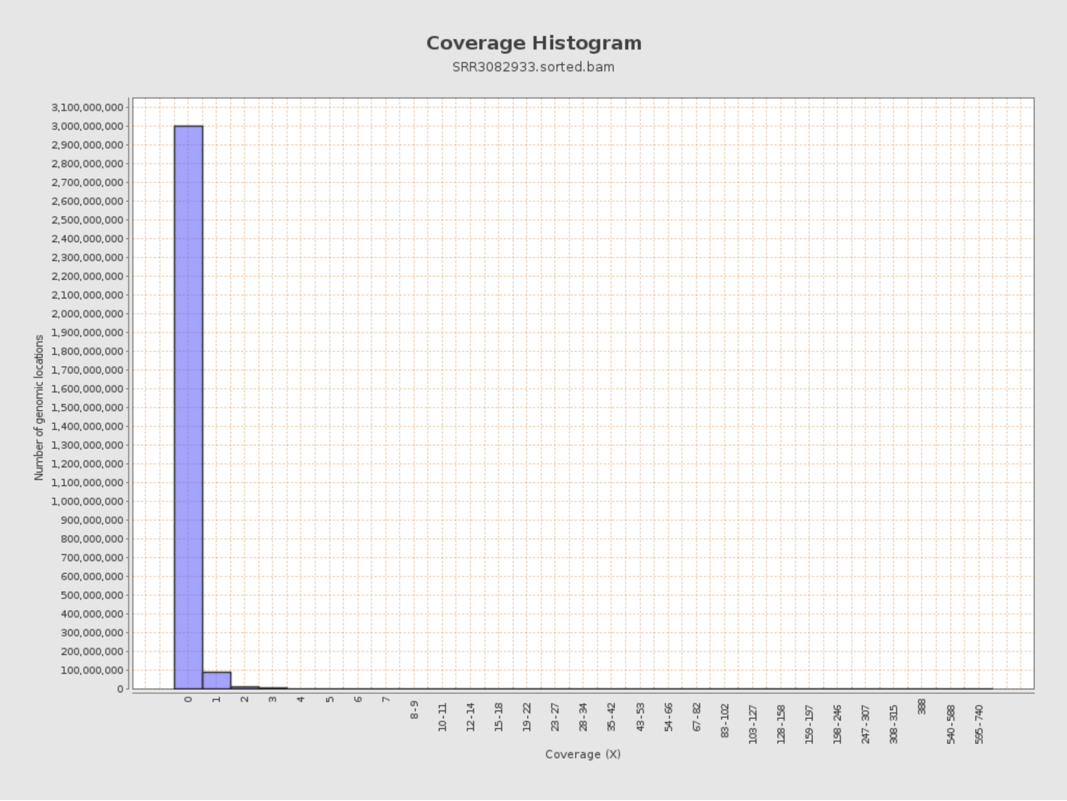
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9356775	0.0375	0.3621
chr2	243199373	12683831	0.0522	0.4253
chr3	198022430	8461743	0.0427	0.2385
chr4	191154276	7146766	0.0374	0.227
chr5	180915260	6113279	0.0338	0.2126
chr6	171115067	7292233	0.0426	0.2947
chr7	159138663	5626778	0.0354	0.2615

chr8	146364022	9337982	0.0638	0.3284
chr9	141213431	3519487	0.0249	0.2344
chr10	135534747	4132517	0.0305	0.2228
chr11	135006516	5481854	0.0406	0.276
chr12	133851895	4809638	0.0359	0.2185
chr13	115169878	2459950	0.0214	0.1689
chr14	107349540	2838039	0.0264	0.1987
chr15	102531392	2094837	0.0204	0.1676
chr16	90354753	5676456	0.0628	0.3006
chr17	81195210	3053469	0.0376	0.2398
chr18	78077248	4075941	0.0522	0.4945
chr19	59128983	2282409	0.0386	0.322
chr20	63025520	2616018	0.0415	0.2401
chr21	48129895	2812178	0.0584	0.2845
chr22	51304566	2077351	0.0405	0.2335
chrMT	16571	20664	1.247	1.3713
chrX	155270560	4099834	0.0264	0.1997
chrY	59373566	213574	0.0036	0.0762

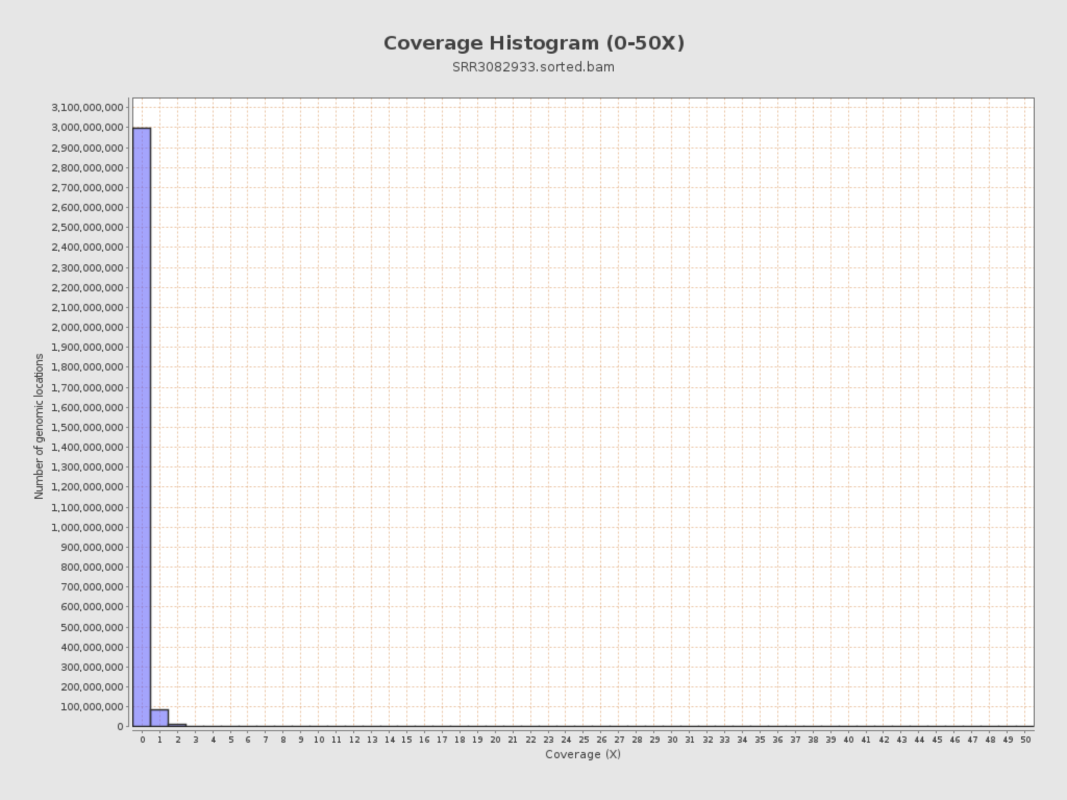
3. Results : Coverage across reference



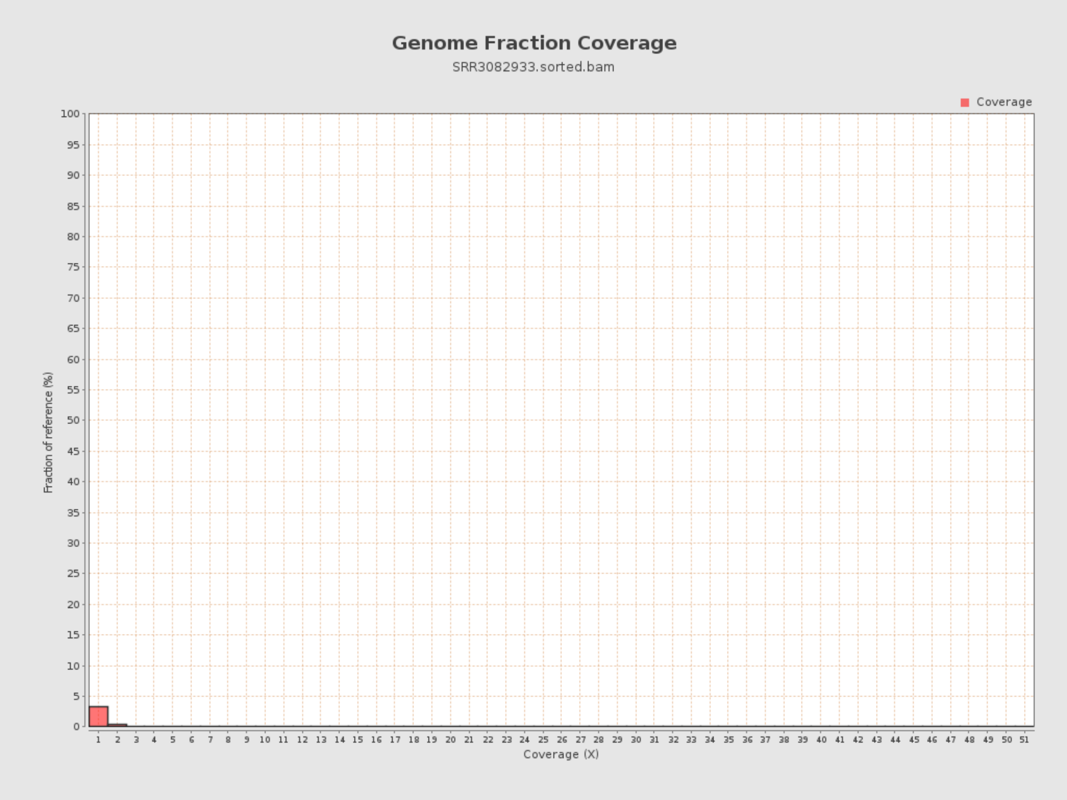
4. Results : Coverage Histogram



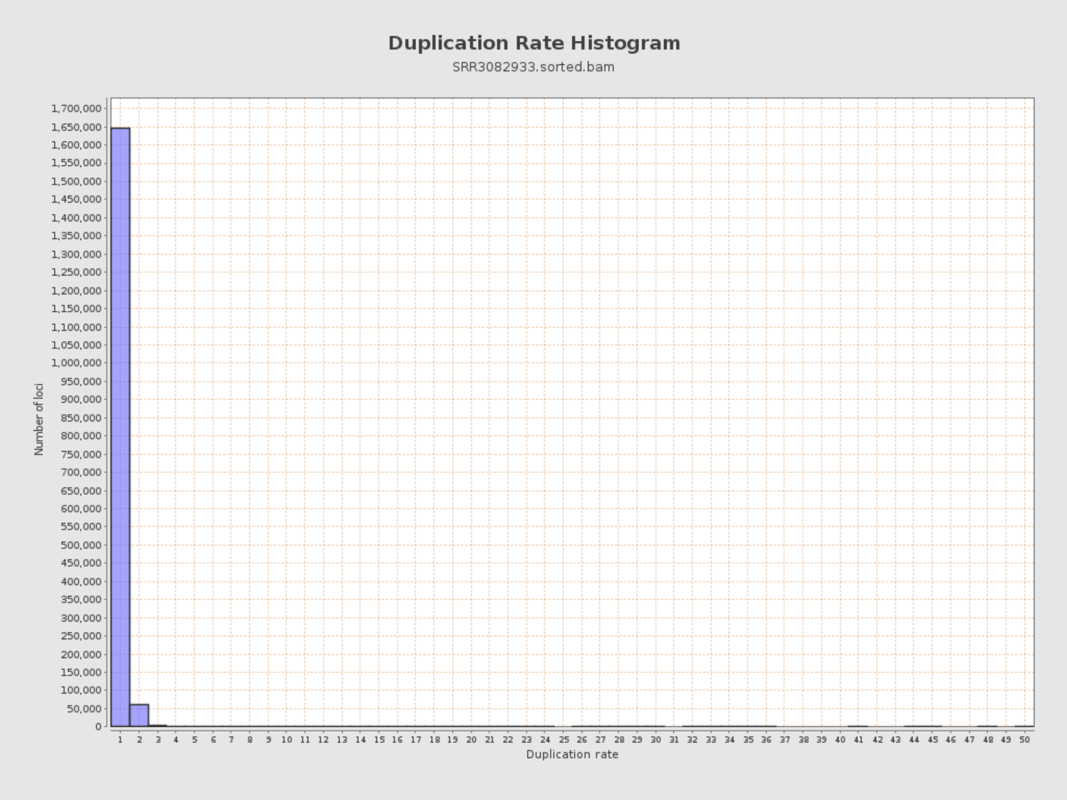
5. Results : Coverage Histogram (0-50X)



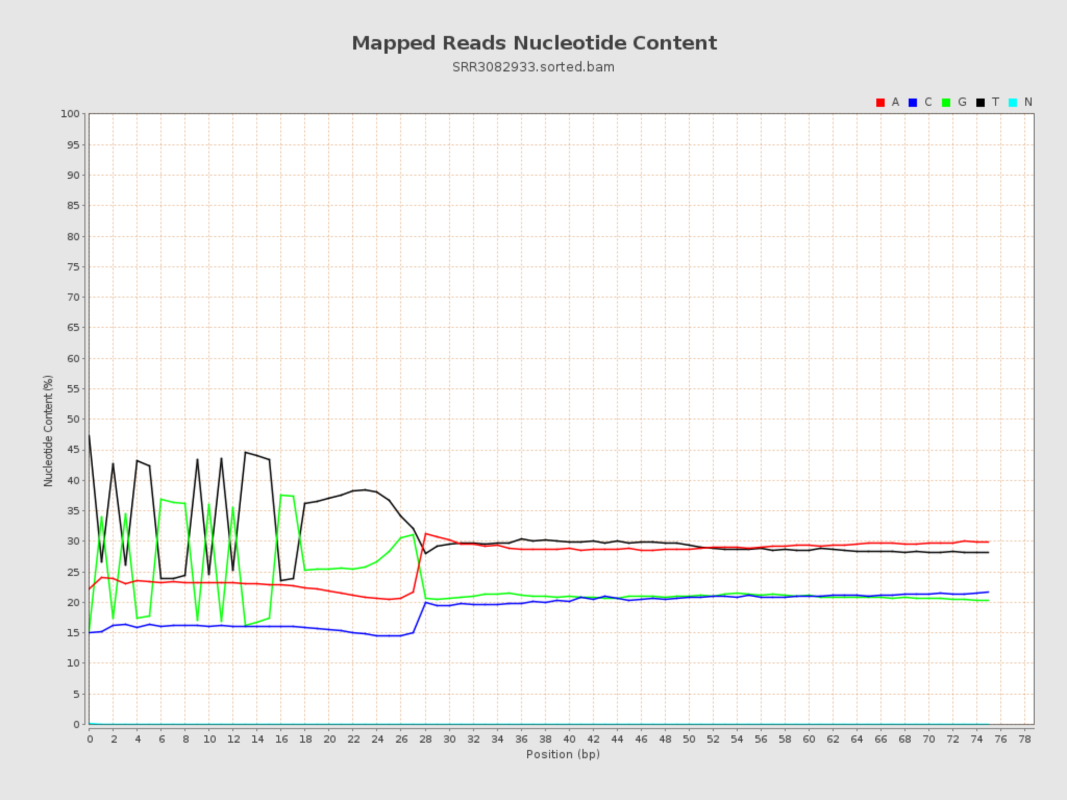
6. Results : Genome Fraction Coverage



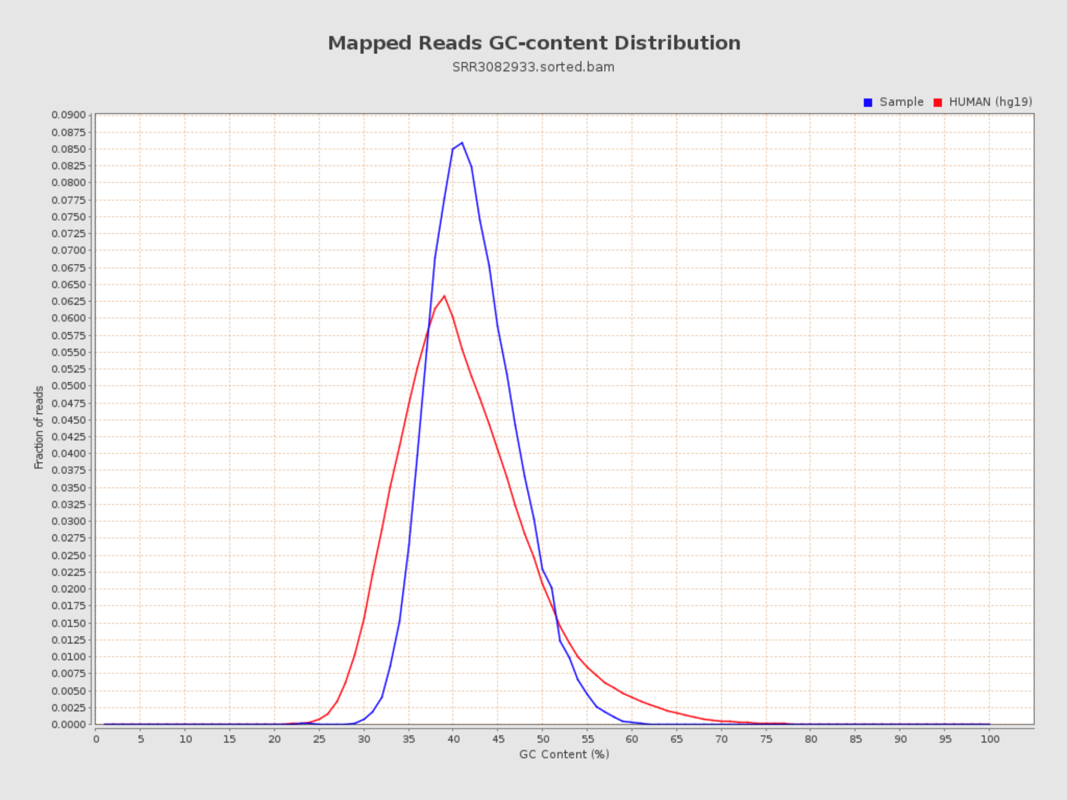
7. Results : Duplication Rate Histogram



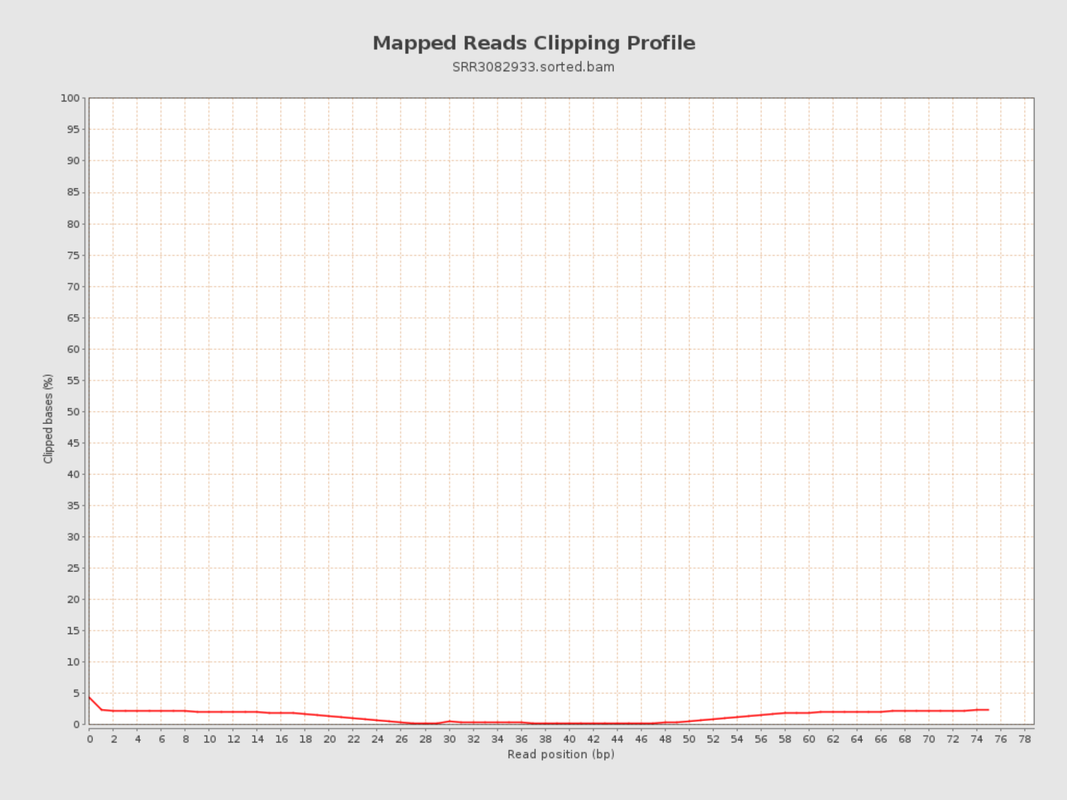
8. Results : Mapped Reads Nucleotide Content



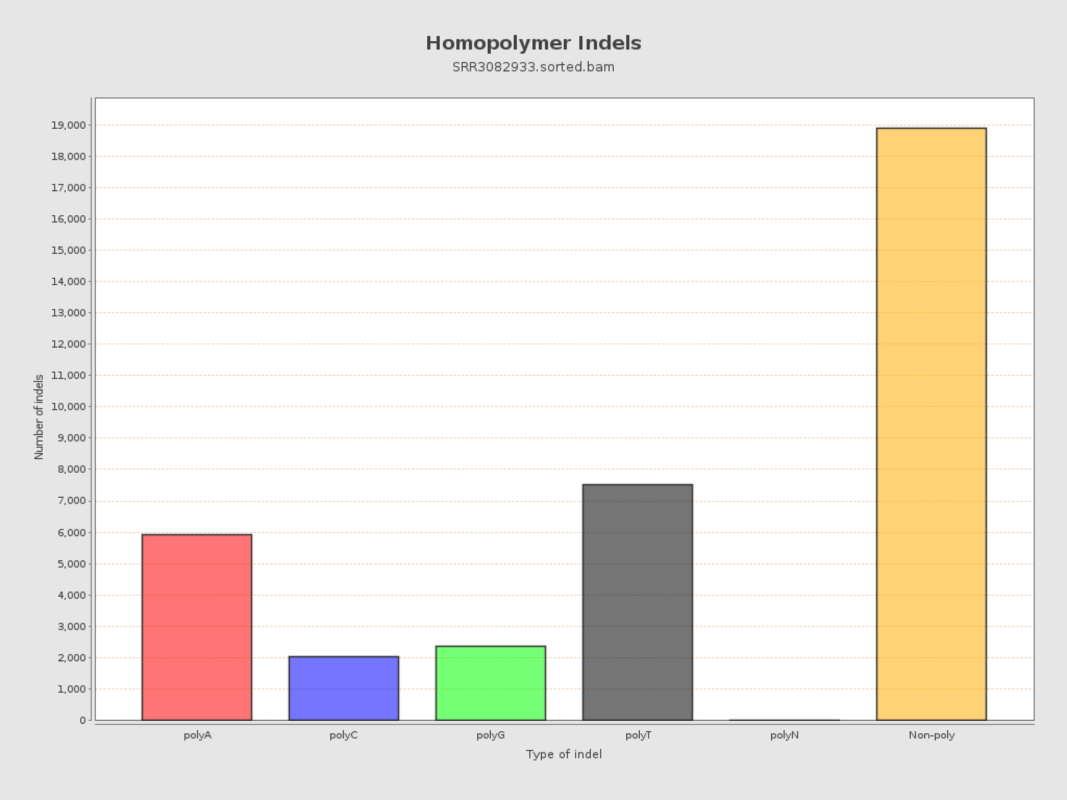
9. Results : Mapped Reads GC-content Distribution



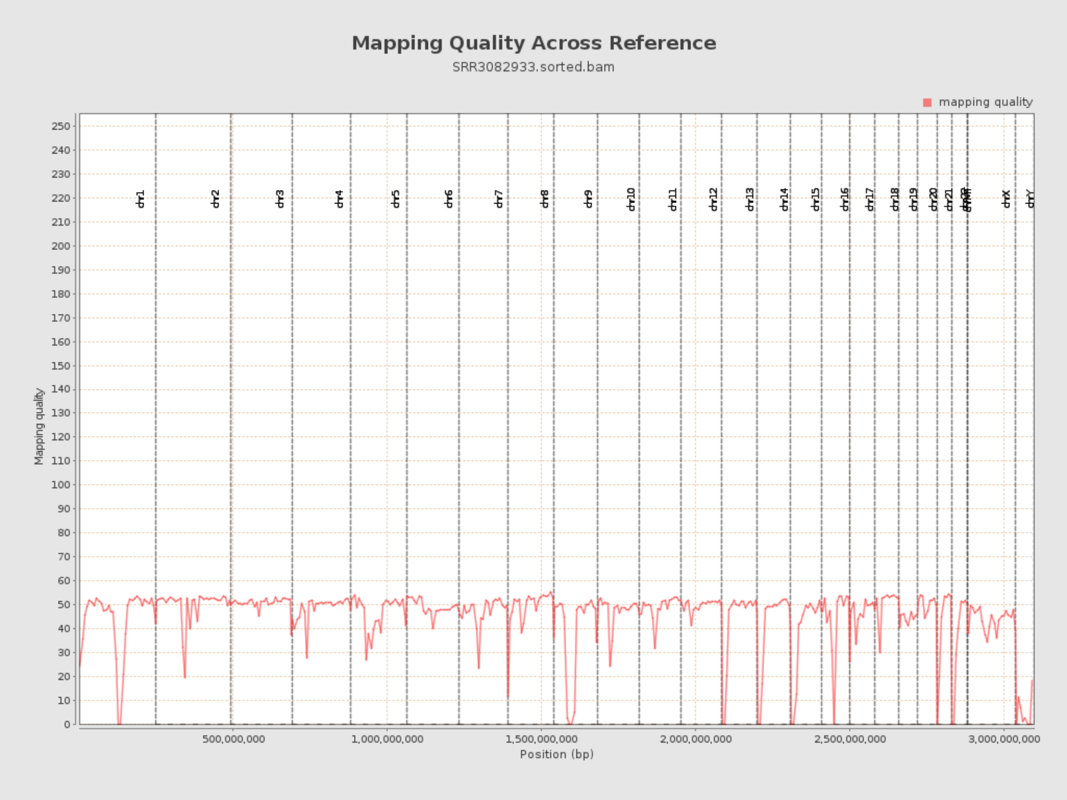
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram