Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 12:03:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818969.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_SRR1818969 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818969.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 12:03:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818969.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	937,792
Mapped reads	902,763 / 96.26%
Unmapped reads	35,029 / 3.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,522 / 1.44%
Read min/max/mean length	30 / 101 / 101.55
Duplicated reads (estimated)	293,427 / 31.29%
Duplication rate	27.91%
Clipped reads	912,720 / 97.33%

2.2. ACGT Content

Number/percentage of A's	24,516,353 / 29.34%
Number/percentage of C's	18,016,990 / 21.56%
Number/percentage of T's	24,098,296 / 28.84%
Number/percentage of G's	16,933,702 / 20.26%
Number/percentage of N's	3,885 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.027

Standard Deviation	0.3442

2.4. Mapping Quality

Mean Mapping Quality	49.14

2.5. Mismatches and indels

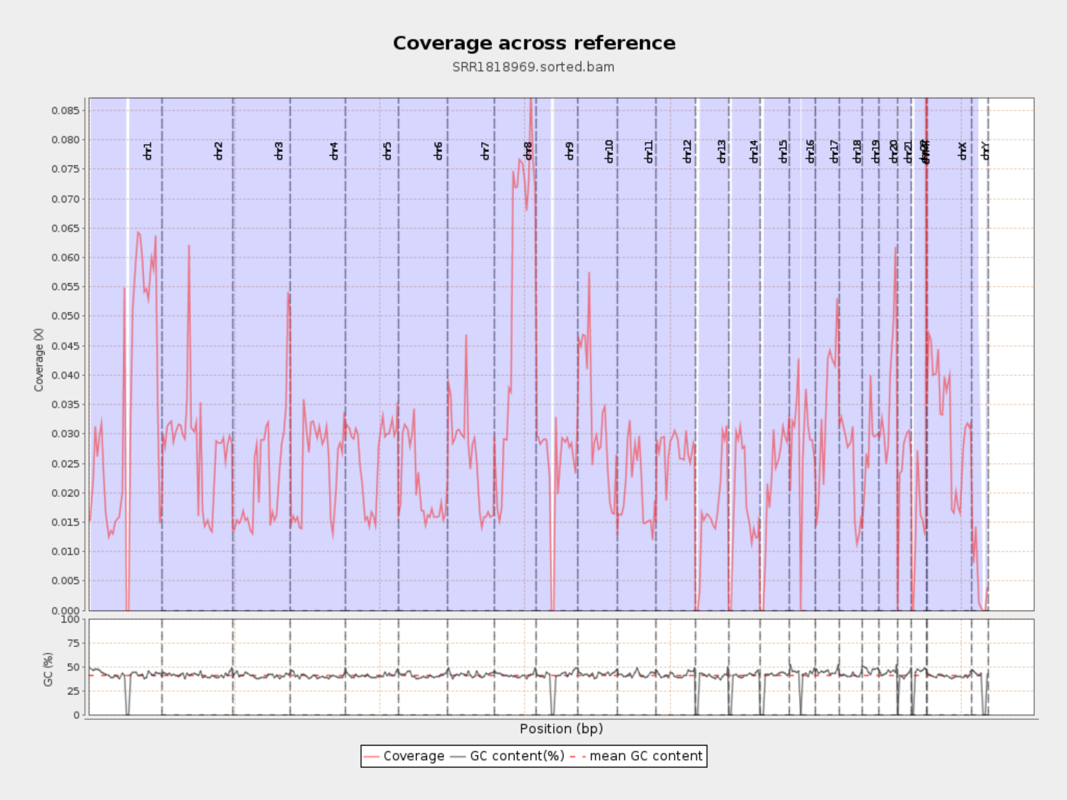
General error rate	0.63%
Mismatches	504,342
Insertions	12,052
Mapped reads with at least one insertion	1.31%
Deletions	25,792
Mapped reads with at least one deletion	2.8%
Homopolymer indels	41.68%

2.6. Chromosome stats

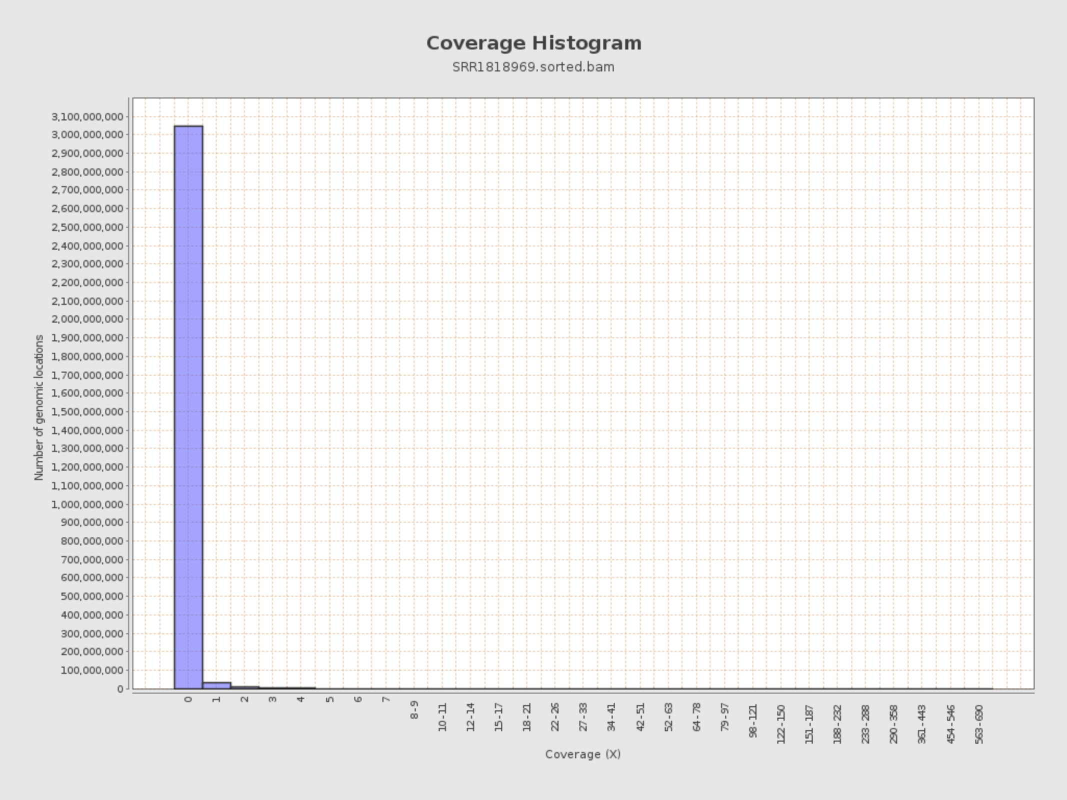
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8407925	0.0337	0.6027
chr2	243199373	6829582	0.0281	0.4242
chr3	198022430	4475614	0.0226	0.2258
chr4	191154276	4744544	0.0248	0.2531
chr5	180915260	4715573	0.0261	0.2479
chr6	171115067	3575935	0.0209	0.236
chr7	159138663	4113549	0.0258	0.421

chr8	146364022	7909693	0.054	0.3834
chr9	141213431	3445961	0.0244	0.3192
chr10	135534747	4456314	0.0329	0.3897
chr11	135006516	2786935	0.0206	0.2401
chr12	133851895	3669411	0.0274	0.2535
chr13	115169878	1905845	0.0165	0.1938
chr14	107349540	1877727	0.0175	0.2086
chr15	102531392	2167676	0.0211	0.2187
chr16	90354753	2590244	0.0287	0.3512
chr17	81195210	2858238	0.0352	0.3037
chr18	78077248	1898085	0.0243	0.3542
chr19	59128983	1651747	0.0279	0.5415
chr20	63025520	2380908	0.0378	0.3117
chr21	48129895	1182532	0.0246	0.2474
chr22	51304566	668598	0.013	0.1833
chrMT	16571	10023	0.6049	1.2167
chrX	155270560	5013893	0.0323	0.3029
chrY	59373566	280029	0.0047	0.2428

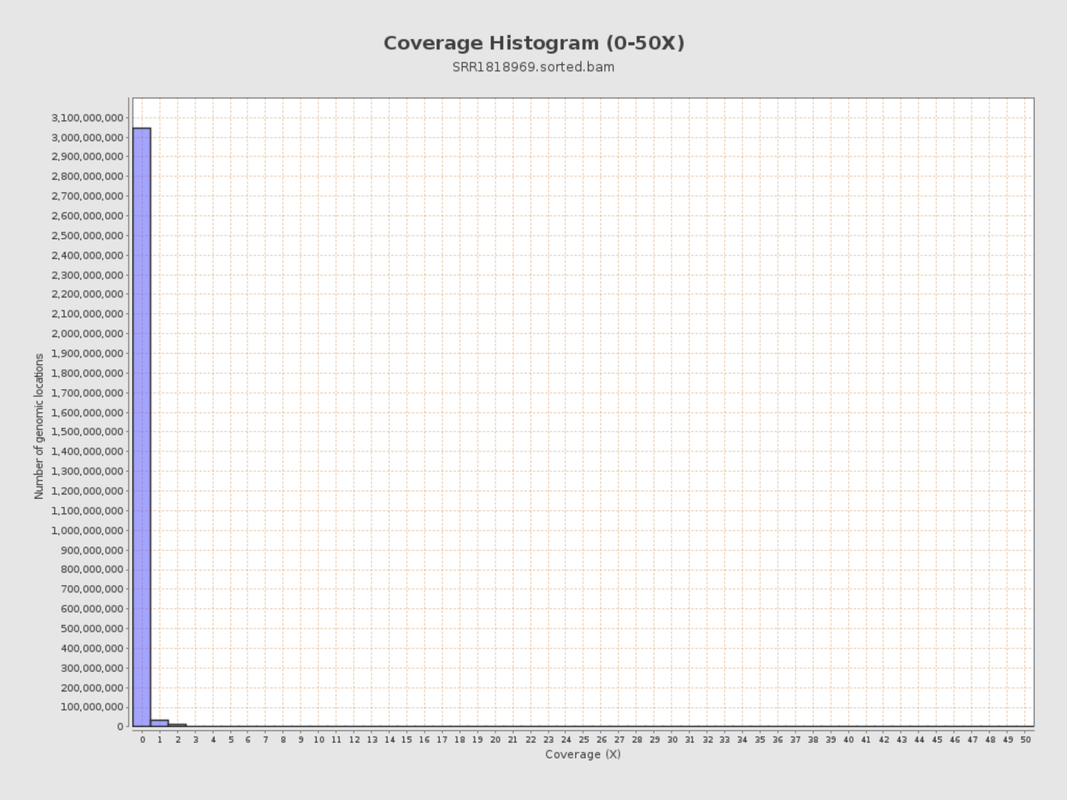
3. Results : Coverage across reference



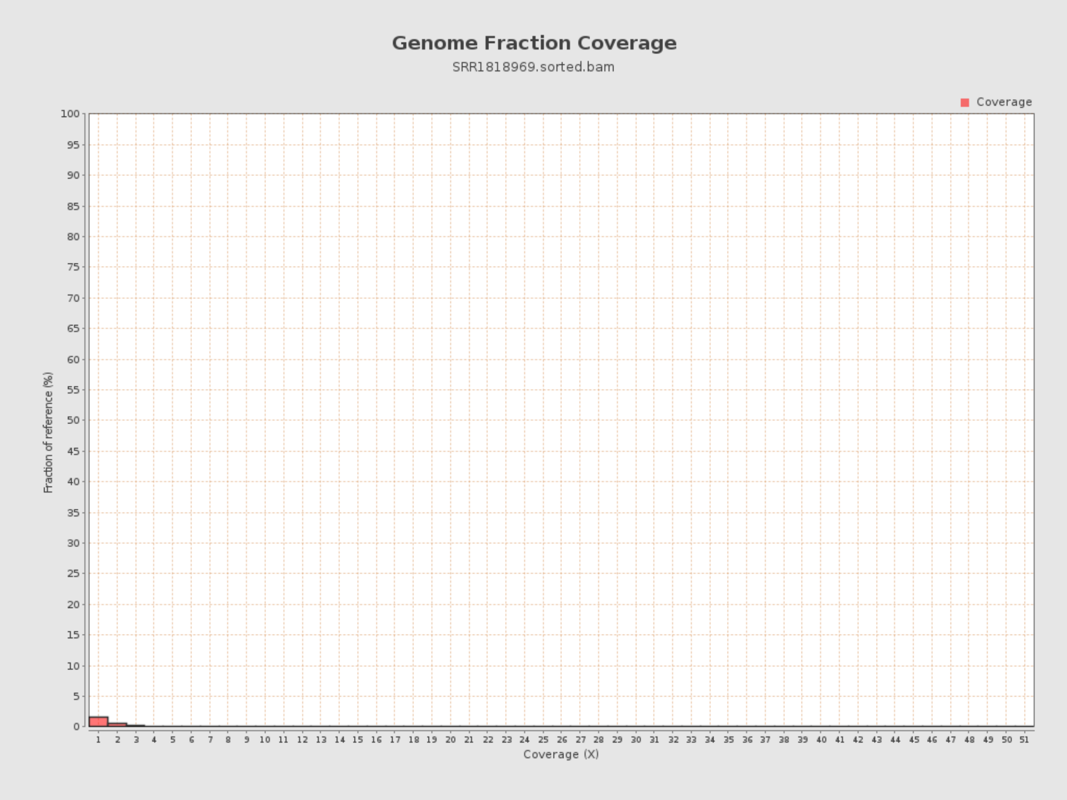
4. Results : Coverage Histogram



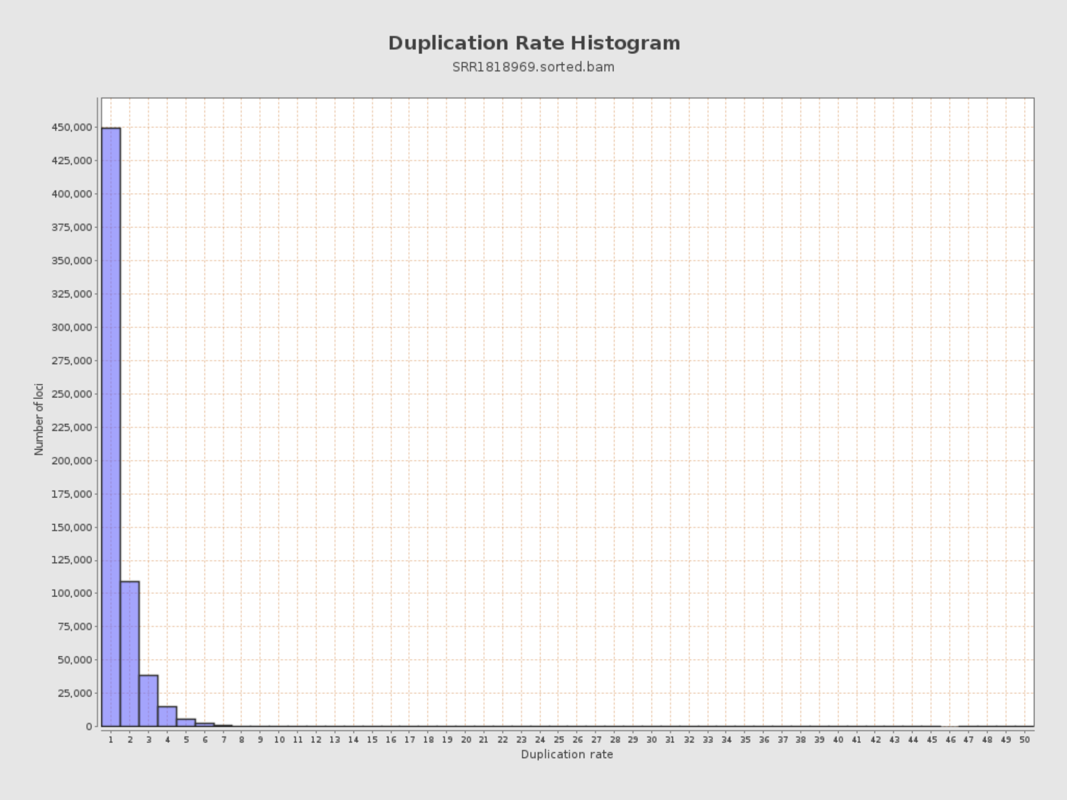
5. Results : Coverage Histogram (0-50X)



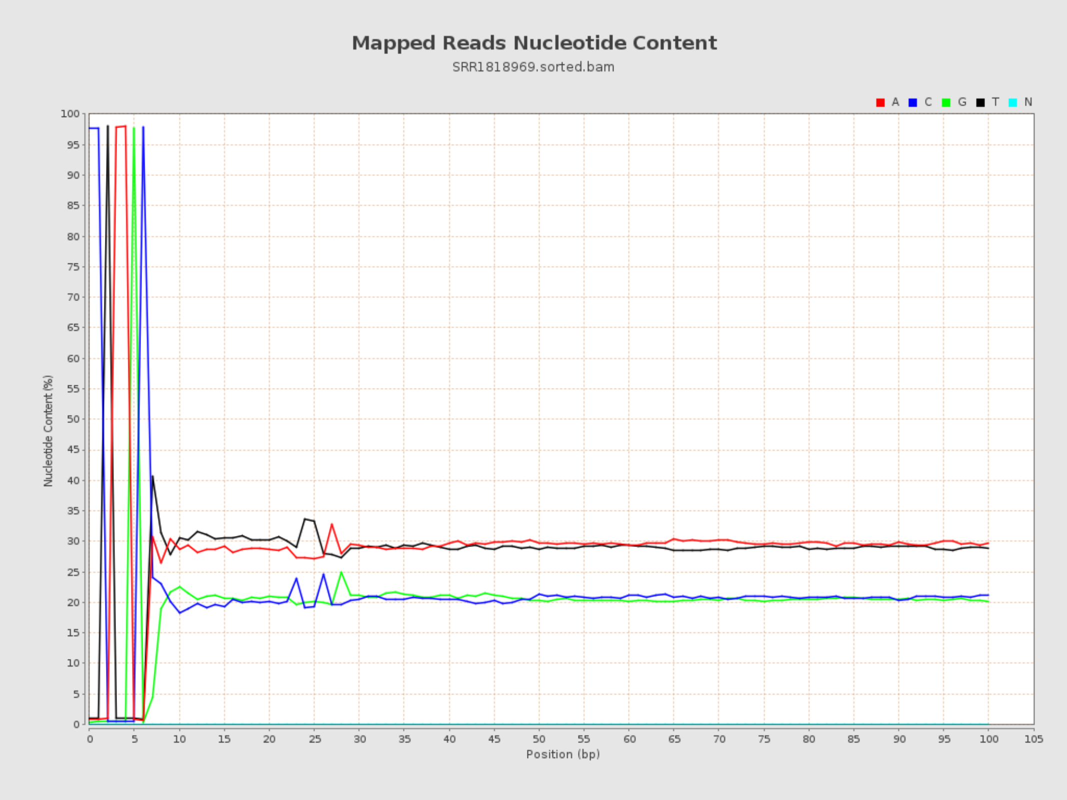
6. Results : Genome Fraction Coverage



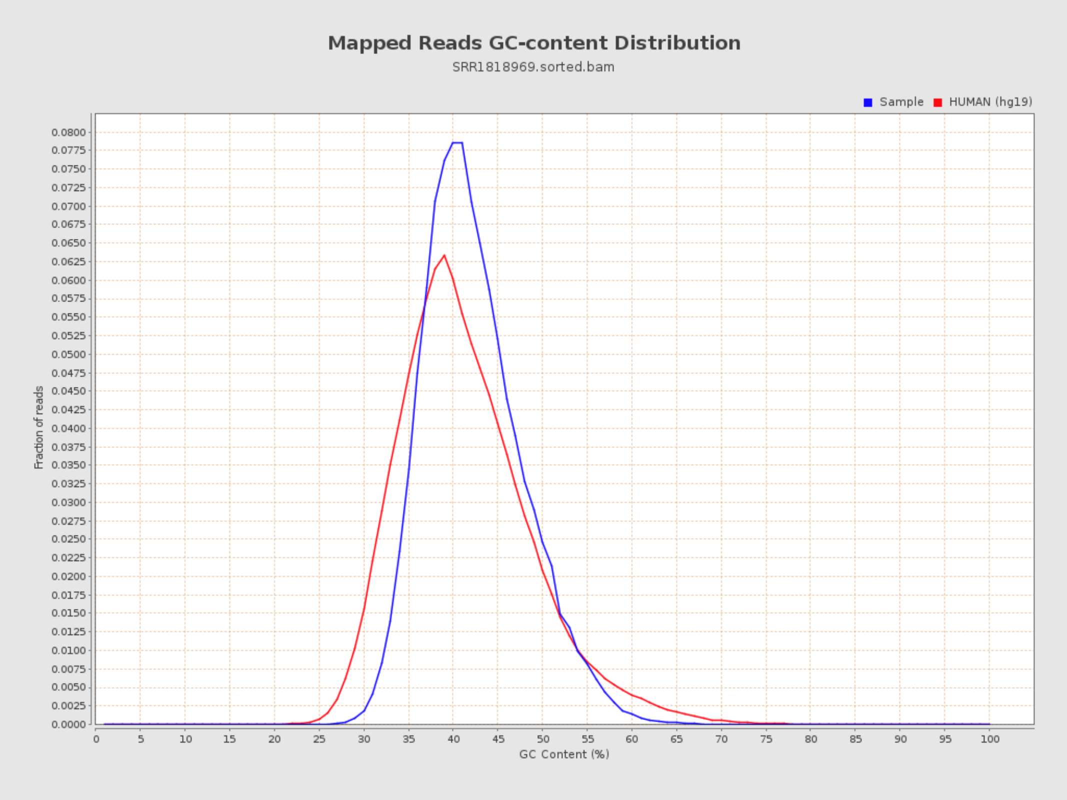
7. Results : Duplication Rate Histogram



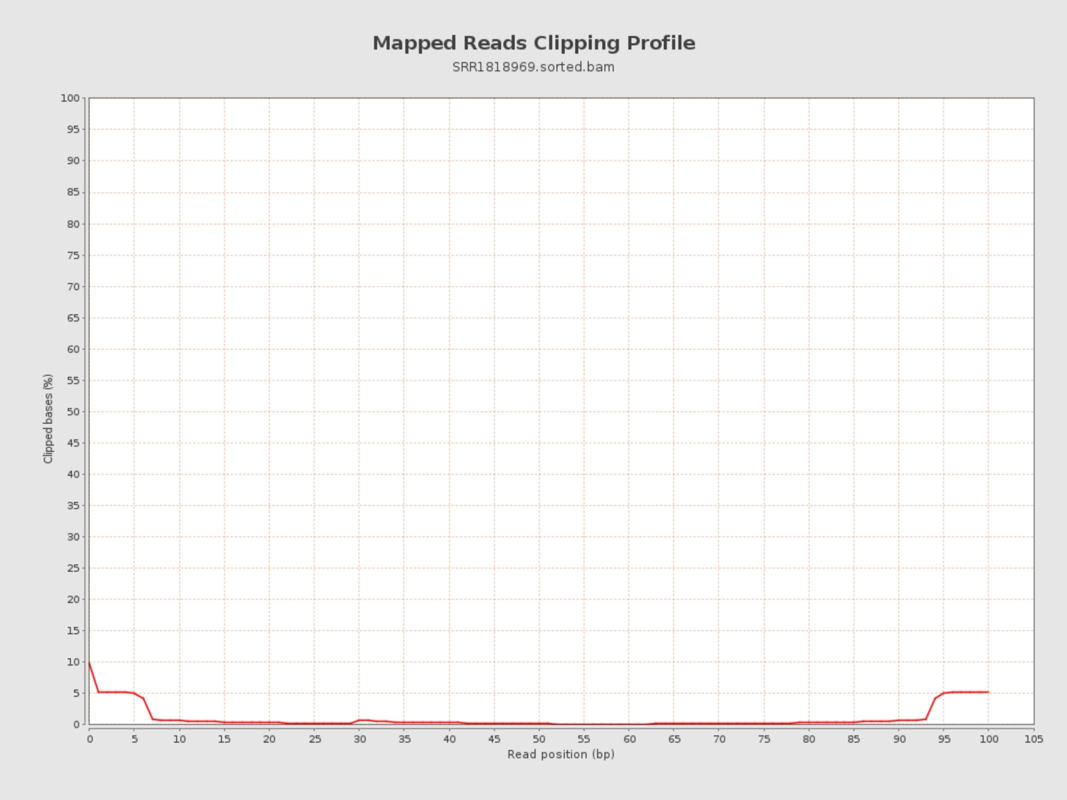
8. Results : Mapped Reads Nucleotide Content



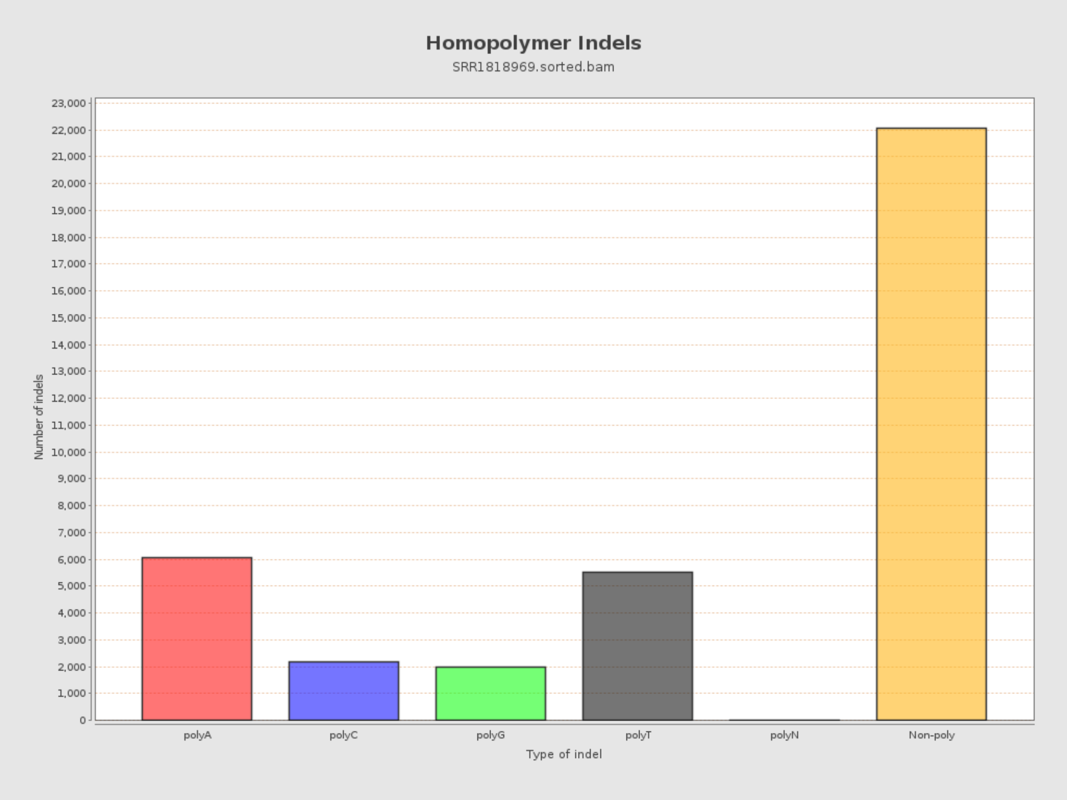
9. Results : Mapped Reads GC-content Distribution



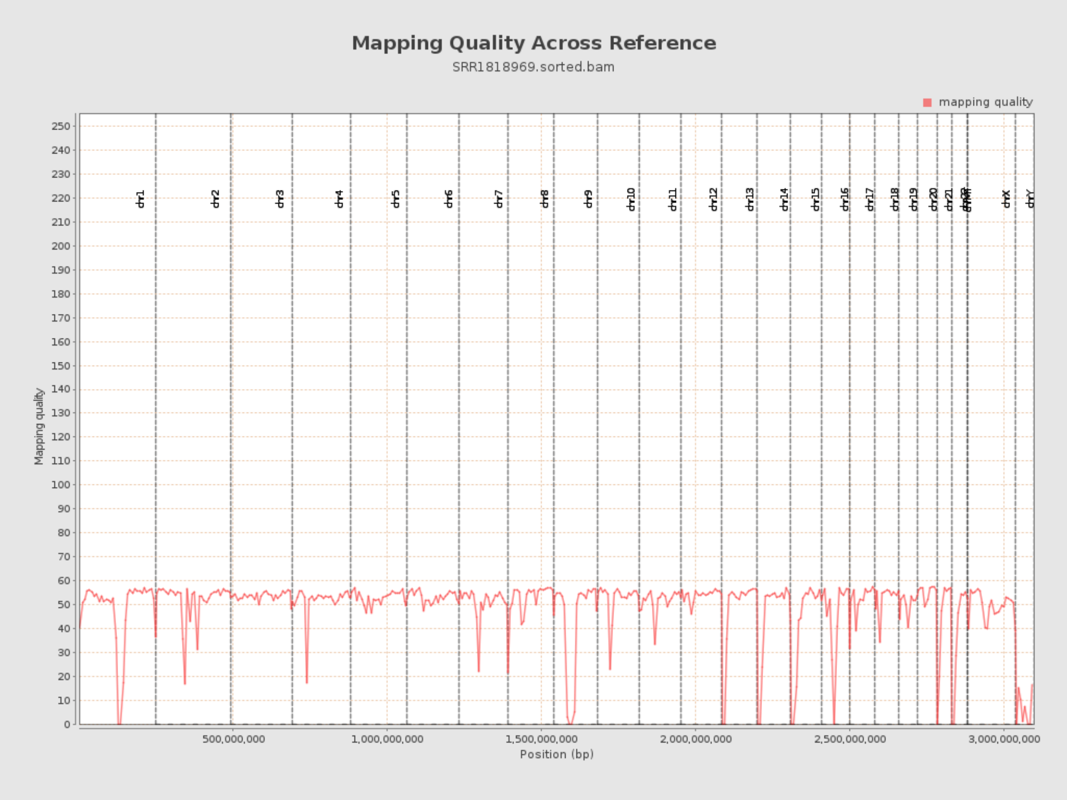
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram