Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 11:22:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818959.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_SRR1818959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 11:22:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,929,154
Mapped reads	2,888,976 / 98.63%
Unmapped reads	40,178 / 1.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,927 / 1.29%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	1,468,353 / 50.13%
Duplication rate	39.8%
Clipped reads	2,894,194 / 98.81%

2.2. ACGT Content

Number/percentage of A's	74,840,570 / 27.97%
Number/percentage of C's	55,188,821 / 20.63%
Number/percentage of T's	77,820,034 / 29.08%
Number/percentage of G's	59,707,960 / 22.32%
Number/percentage of N's	10,740 / 0%
GC Percentage	42.94%

2.3. Coverage

Mean	0.0865

Standard Deviation	0.9926

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

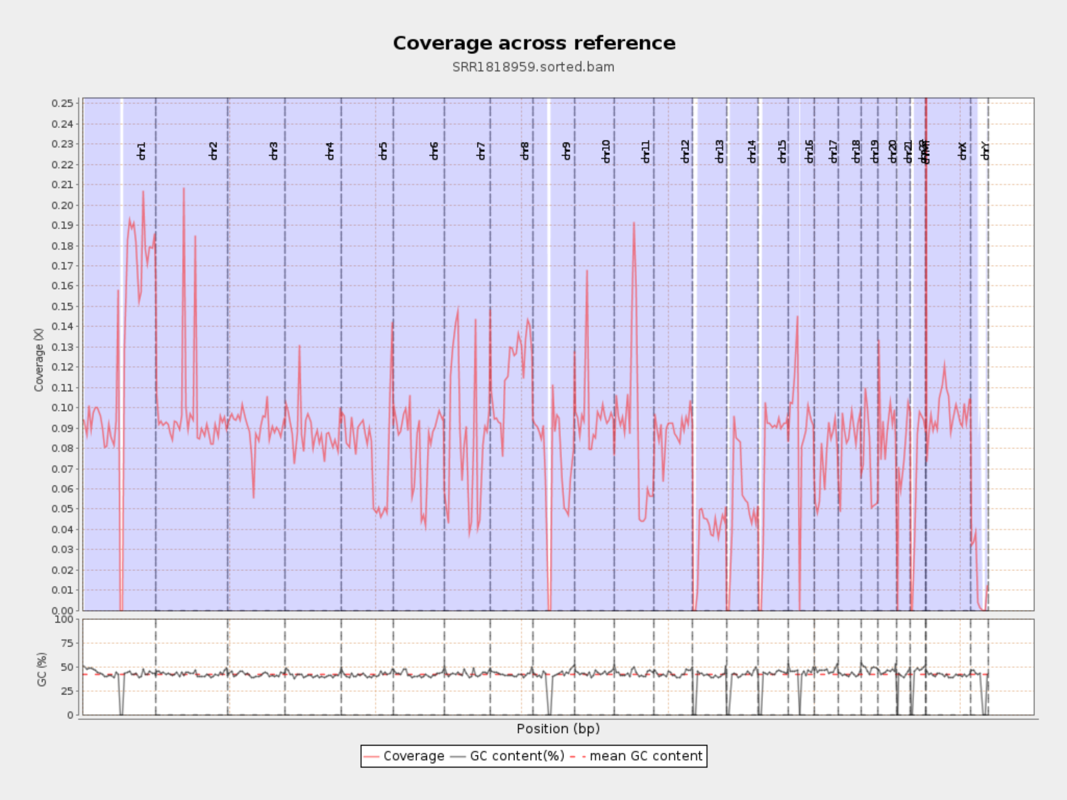
General error rate	0.66%
Mismatches	1,691,434
Insertions	36,953
Mapped reads with at least one insertion	1.24%
Deletions	83,308
Mapped reads with at least one deletion	2.82%
Homopolymer indels	41.14%

2.6. Chromosome stats

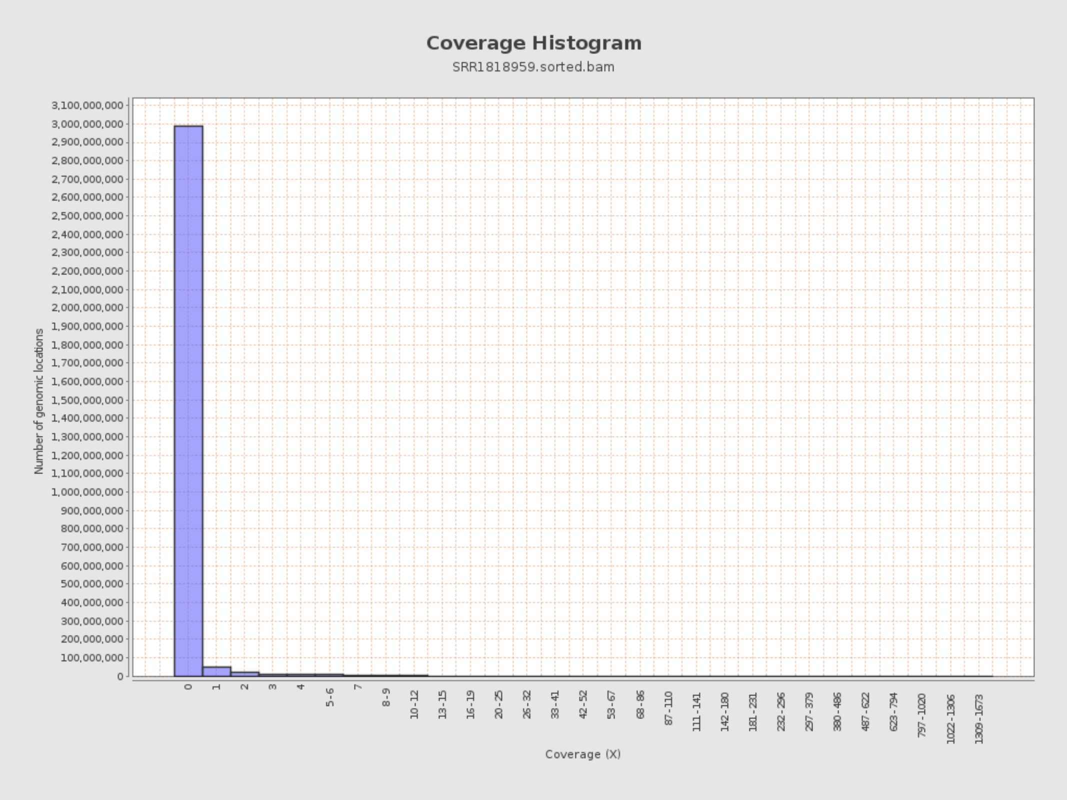
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31259259	0.1254	1.6242
chr2	243199373	23744221	0.0976	1.5867
chr3	198022430	17898410	0.0904	0.6399
chr4	191154276	16947387	0.0887	0.6973
chr5	180915260	14414379	0.0797	0.6296
chr6	171115067	14215275	0.0831	0.6791
chr7	159138663	13438699	0.0844	0.7518

chr8	146364022	17151903	0.1172	0.8426
chr9	141213431	9951267	0.0705	1.0571
chr10	135534747	13084096	0.0965	1.2141
chr11	135006516	12026620	0.0891	0.7584
chr12	133851895	11991112	0.0896	0.6586
chr13	115169878	4214287	0.0366	0.401
chr14	107349540	5723621	0.0533	0.5627
chr15	102531392	7713161	0.0752	0.5976
chr16	90354753	8212334	0.0909	1.2017
chr17	81195210	6026556	0.0742	0.6589
chr18	78077248	6632159	0.0849	1.3333
chr19	59128983	4351649	0.0736	1.471
chr20	63025520	5856374	0.0929	0.7102
chr21	48129895	3521638	0.0732	0.6542
chr22	51304566	3314814	0.0646	0.6046
chrMT	16571	14475	0.8735	2.0082
chrX	155270560	15161572	0.0976	0.7778
chrY	59373566	856762	0.0144	1.1609

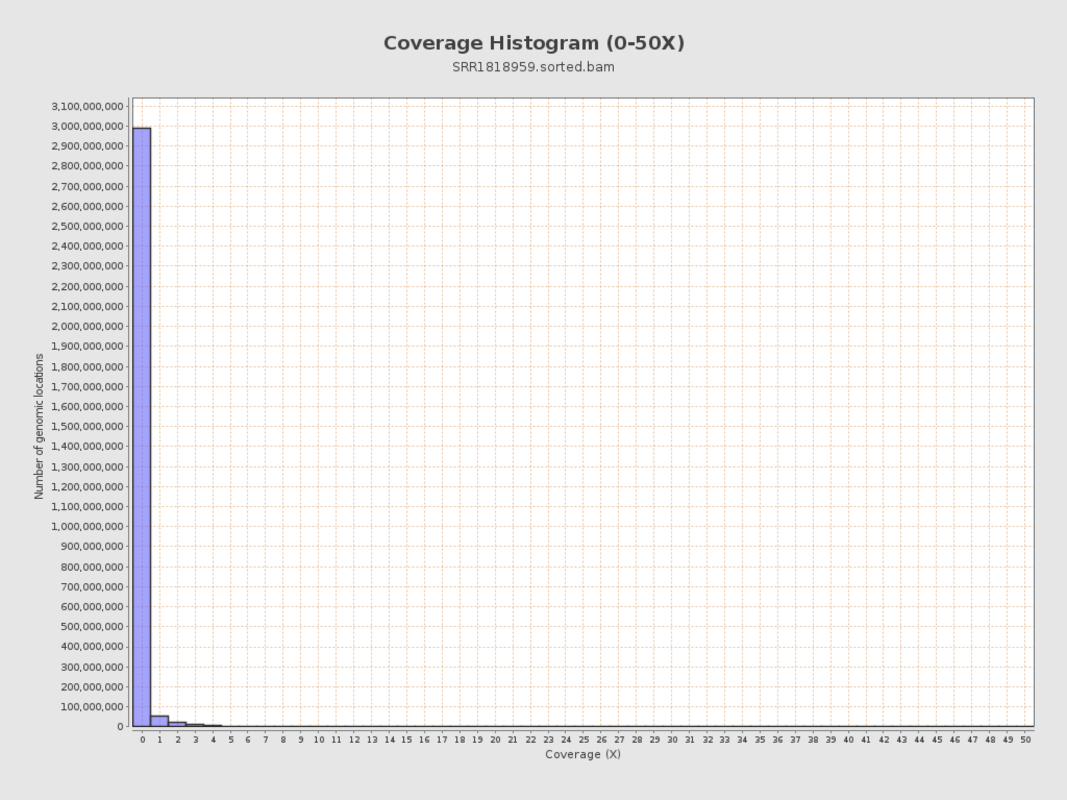
3. Results : Coverage across reference



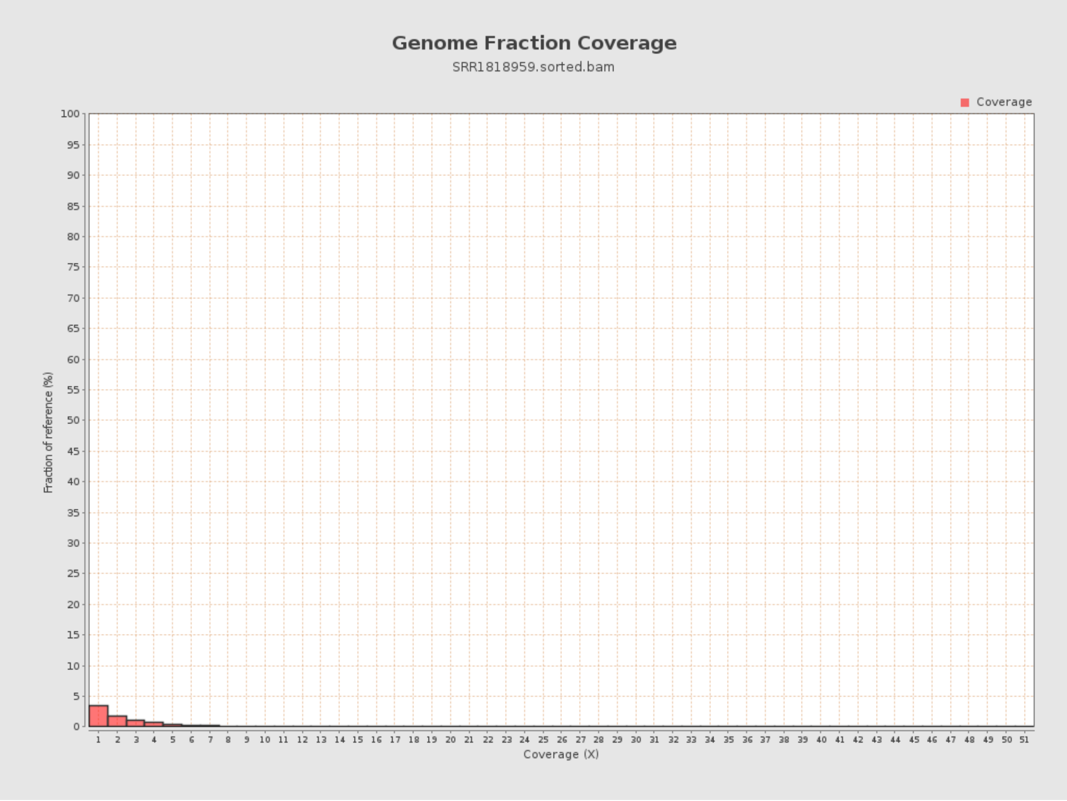
4. Results : Coverage Histogram



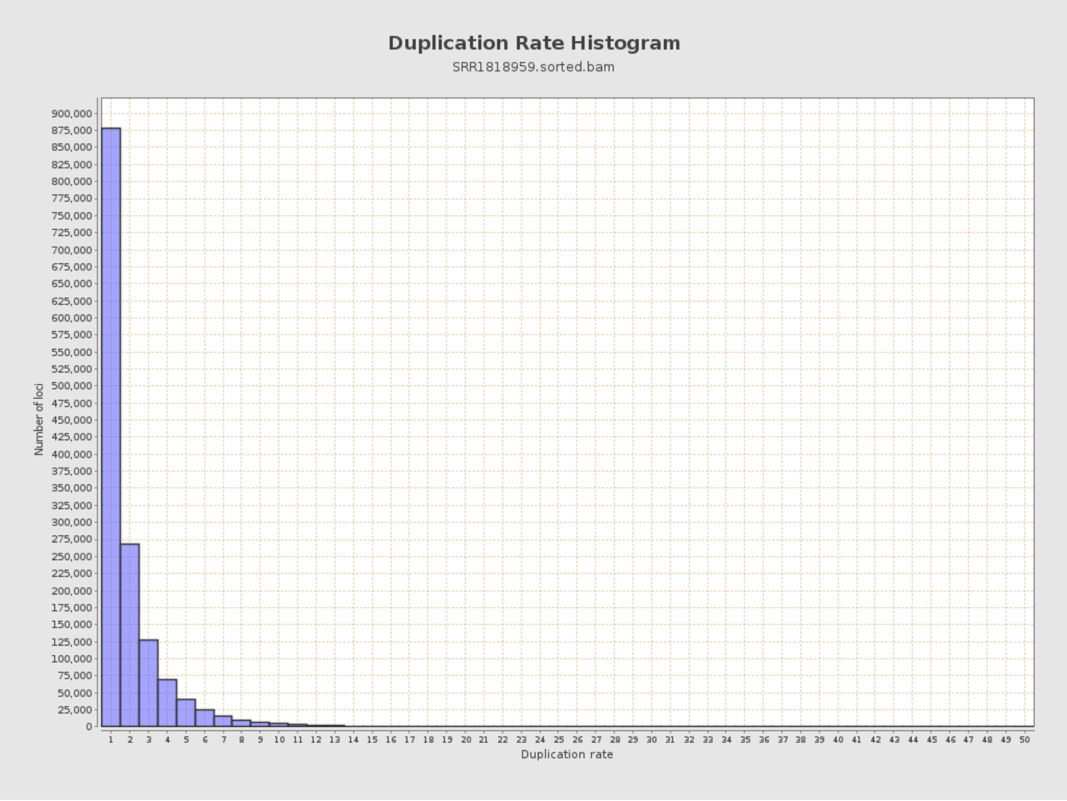
5. Results : Coverage Histogram (0-50X)



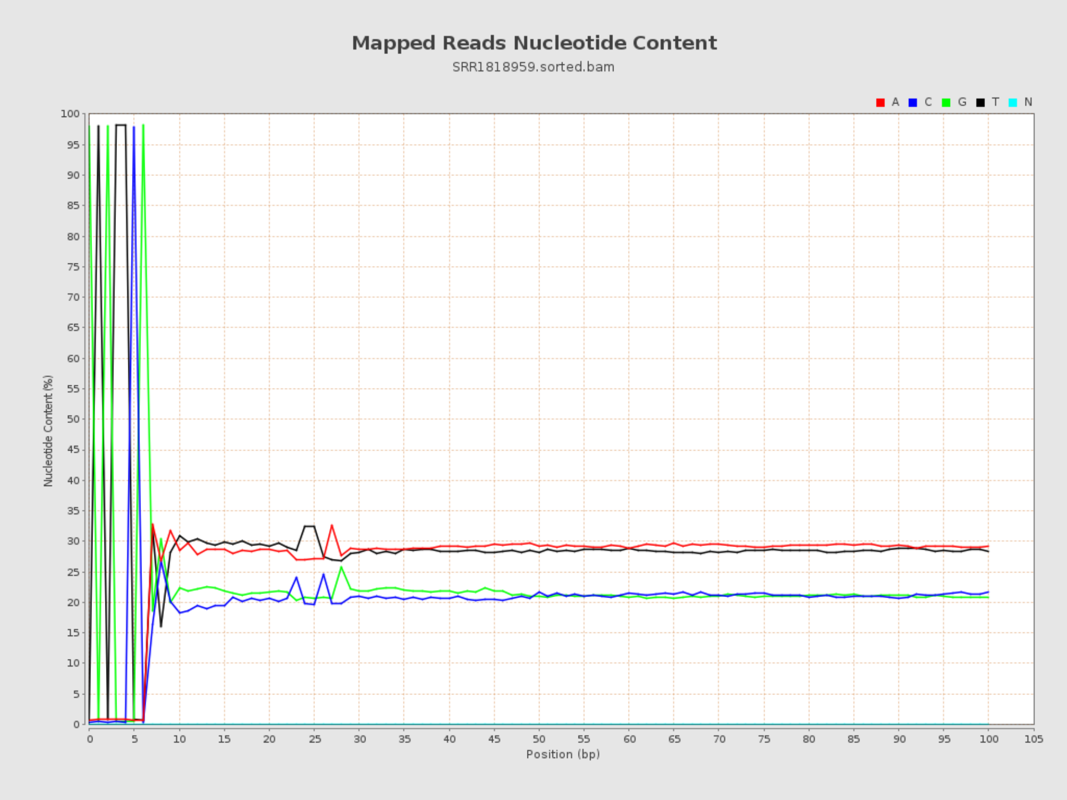
6. Results : Genome Fraction Coverage



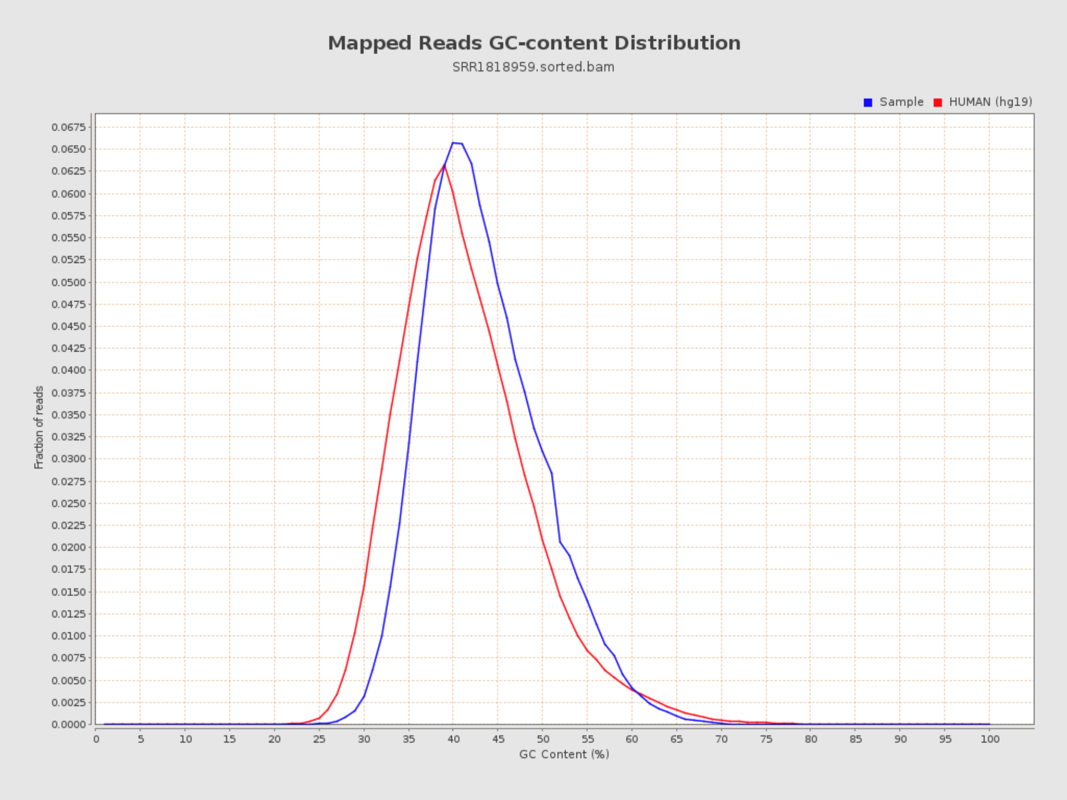
7. Results : Duplication Rate Histogram



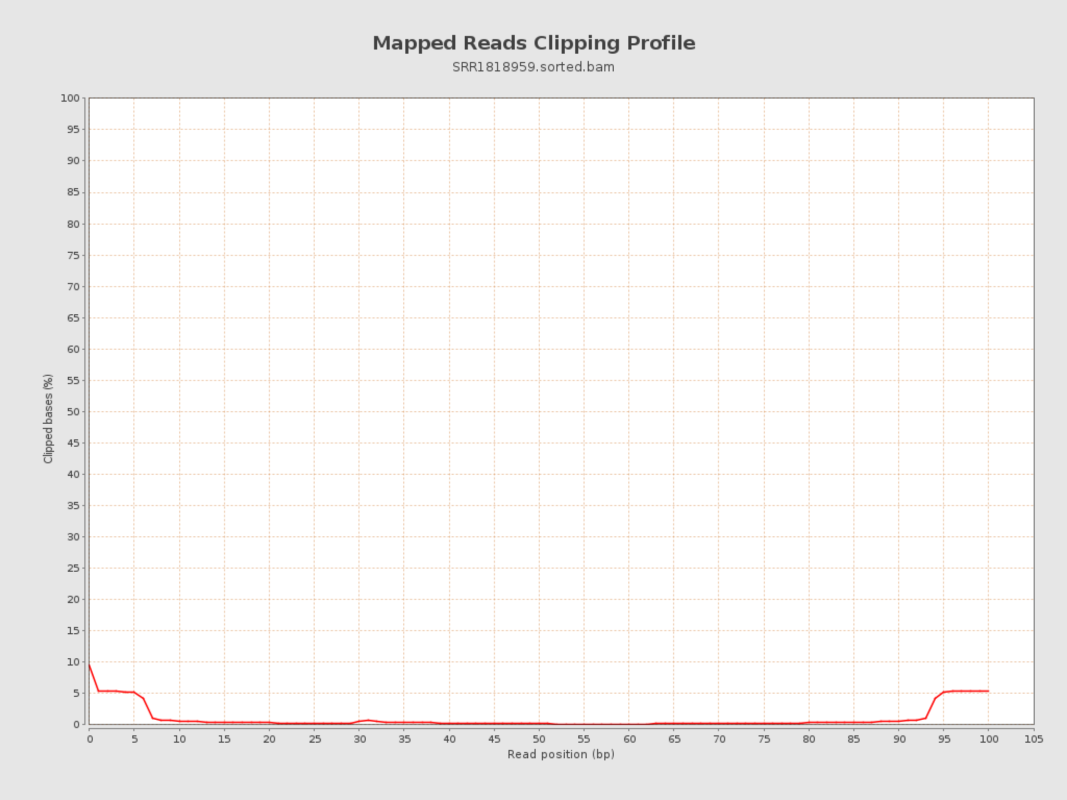
8. Results : Mapped Reads Nucleotide Content



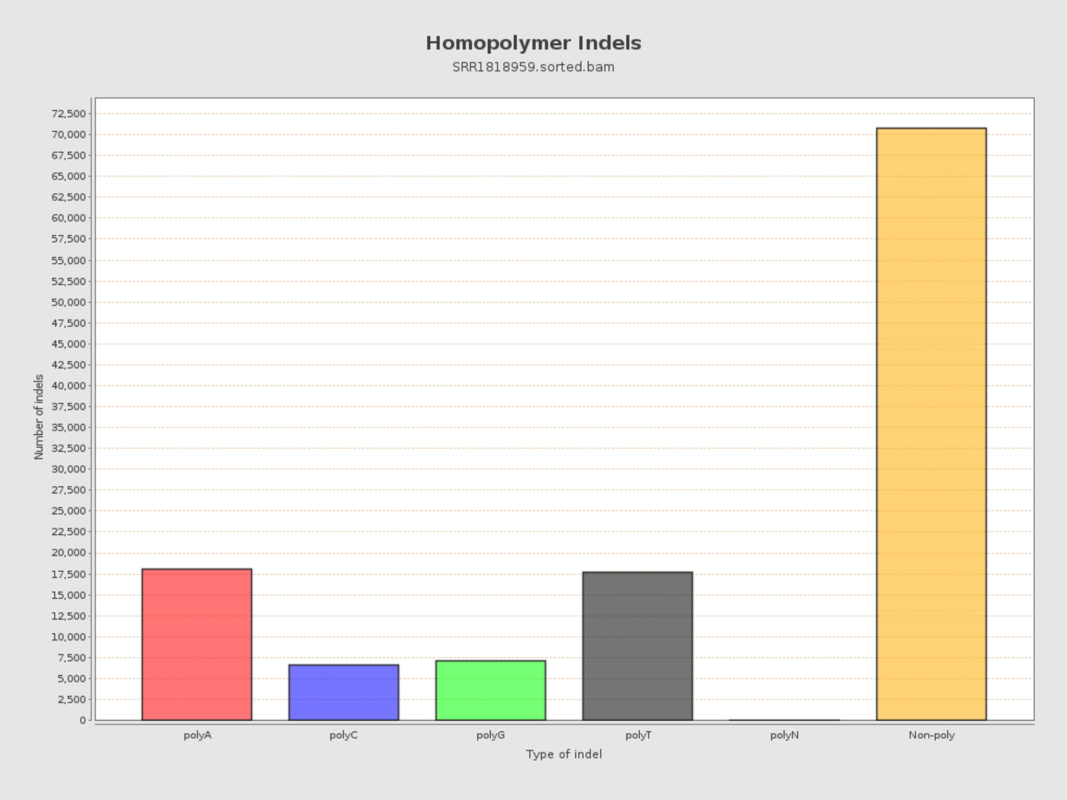
9. Results : Mapped Reads GC-content Distribution



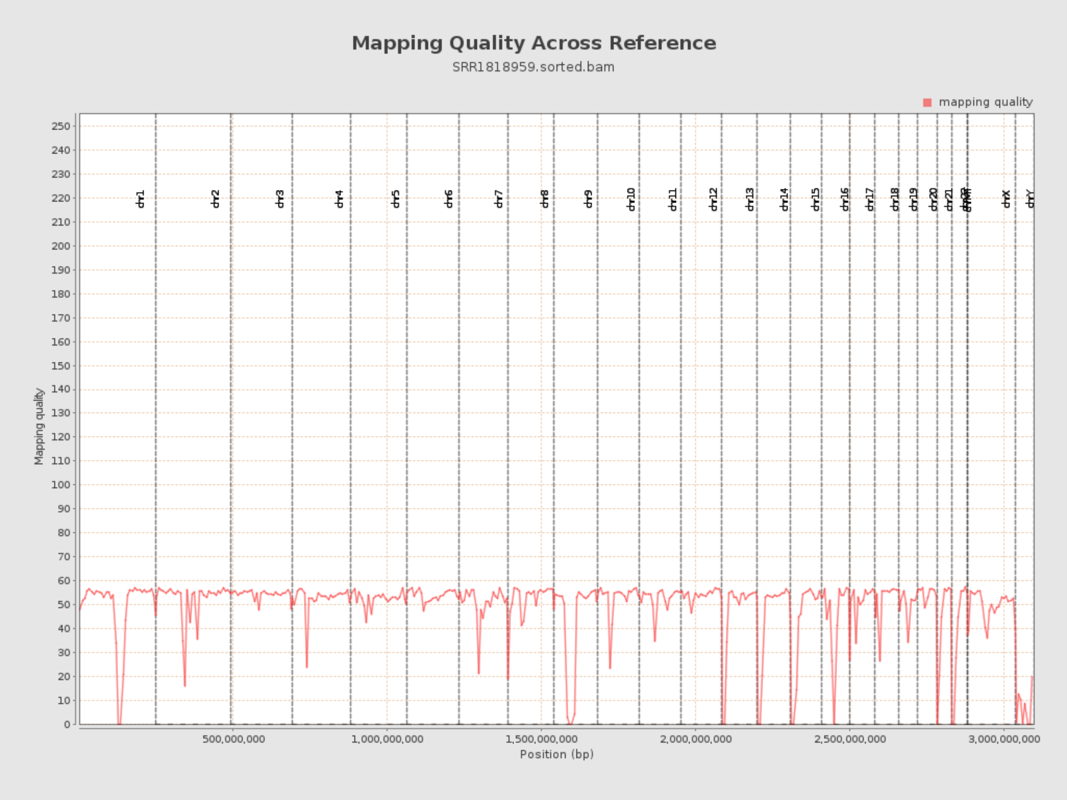
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram