Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:14:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818908.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_SRR1818908 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818908.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818908.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,970,723
Mapped reads	1,942,362 / 98.56%
Unmapped reads	28,361 / 1.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,674 / 1.4%
Read min/max/mean length	30 / 101 / 101.54
Duplicated reads (estimated)	442,473 / 22.45%
Duplication rate	19.12%
Clipped reads	1,957,172 / 99.31%

2.2. ACGT Content

Number/percentage of A's	52,271,026 / 29.07%
Number/percentage of C's	38,733,196 / 21.54%
Number/percentage of T's	50,919,143 / 28.32%
Number/percentage of G's	37,872,410 / 21.06%
Number/percentage of N's	2,609 / 0%
GC Percentage	42.61%

2.3. Coverage

Mean	0.0581

Standard Deviation	0.714

2.4. Mapping Quality

Mean Mapping Quality	49.25

2.5. Mismatches and indels

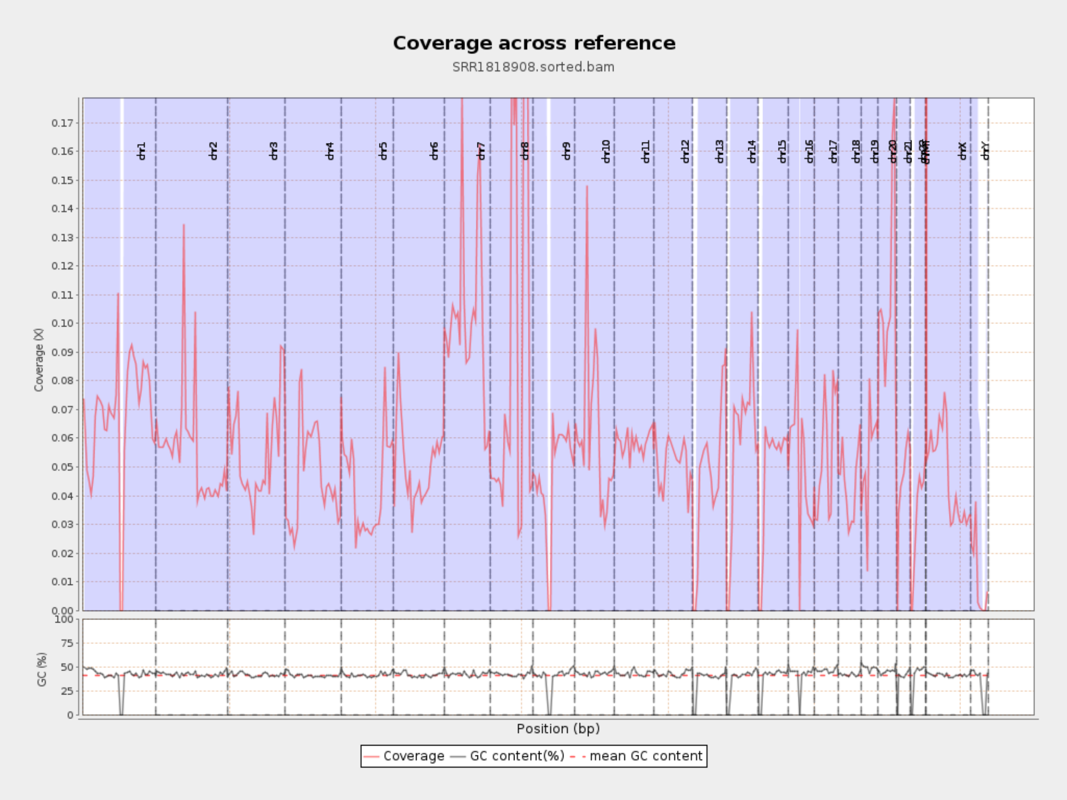
General error rate	0.64%
Mismatches	1,092,069
Insertions	25,499
Mapped reads with at least one insertion	1.27%
Deletions	58,006
Mapped reads with at least one deletion	2.92%
Homopolymer indels	41.73%

2.6. Chromosome stats

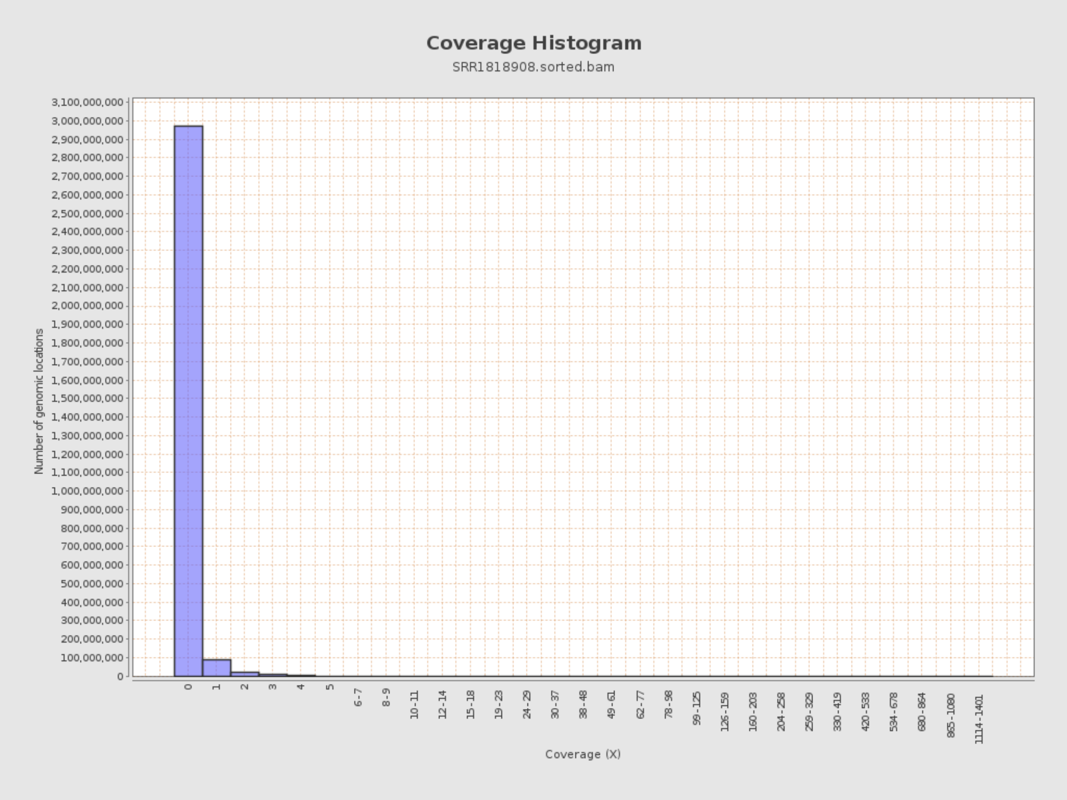
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16820123	0.0675	1.0697
chr2	243199373	13539279	0.0557	0.9724
chr3	198022430	11072844	0.0559	0.3208
chr4	191154276	8971232	0.0469	0.3986
chr5	180915260	7835746	0.0433	0.2971
chr6	171115067	8672605	0.0507	0.337
chr7	159138663	16209188	0.1019	1.6628

chr8	146364022	15491893	0.1058	0.587
chr9	141213431	6632479	0.047	0.642
chr10	135534747	8333106	0.0615	0.9362
chr11	135006516	7876214	0.0583	0.422
chr12	133851895	6964562	0.052	0.3131
chr13	115169878	5447633	0.0473	0.2929
chr14	107349540	6380418	0.0594	0.357
chr15	102531392	4877974	0.0476	0.2915
chr16	90354753	4525483	0.0501	0.6506
chr17	81195210	4410207	0.0543	0.4308
chr18	78077248	3472298	0.0445	0.7221
chr19	59128983	3133626	0.053	0.9713
chr20	63025520	7249783	0.115	0.4982
chr21	48129895	2162457	0.0449	0.3341
chr22	51304566	1595439	0.0311	0.271
chrMT	16571	259657	15.6694	10.7192
chrX	155270560	7331382	0.0472	0.3664
chrY	59373566	644242	0.0109	0.7957

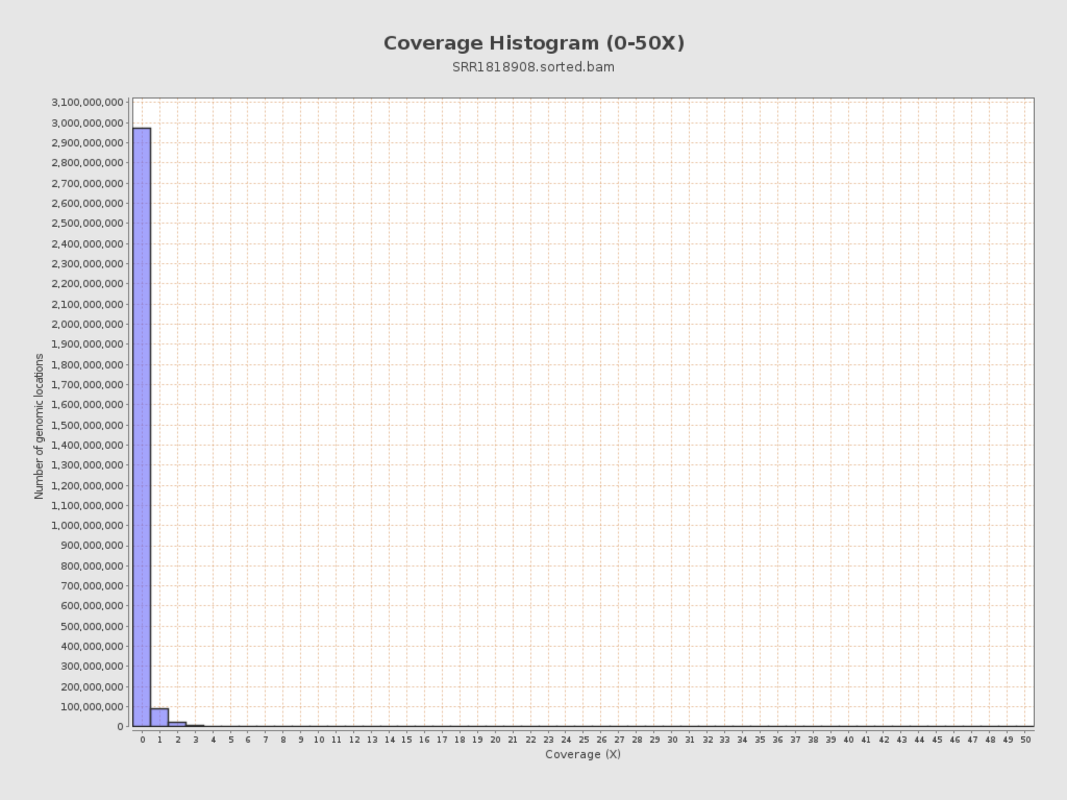
3. Results : Coverage across reference



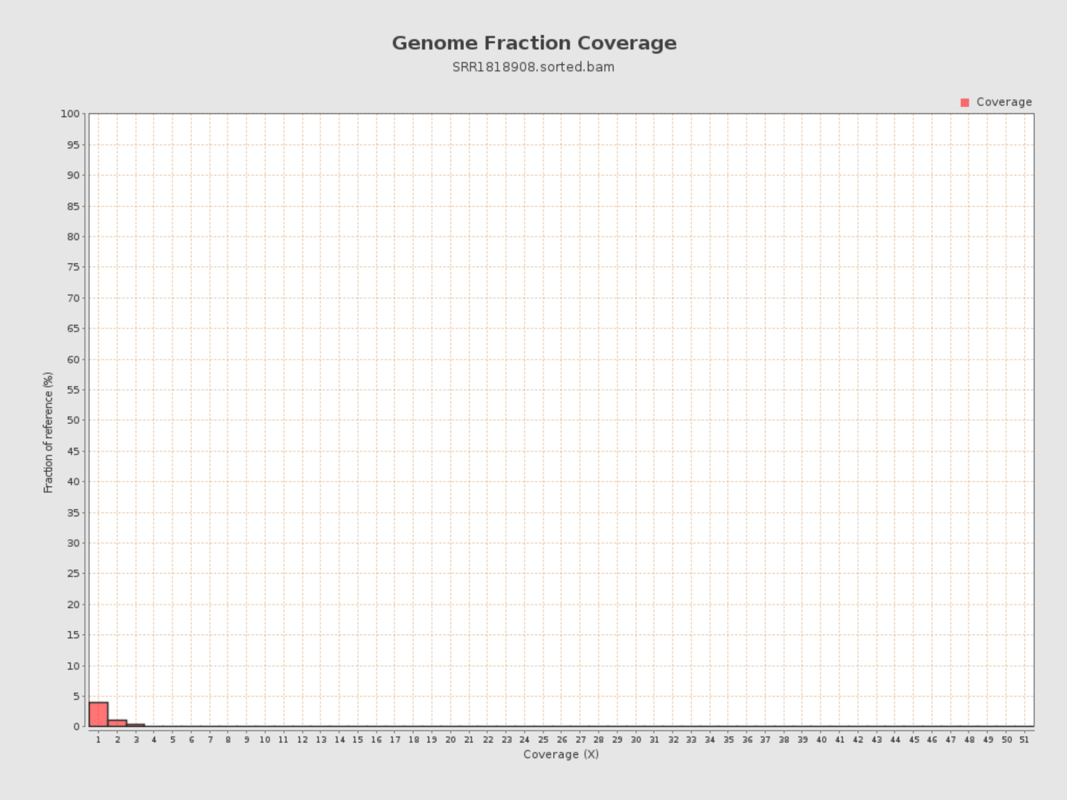
4. Results : Coverage Histogram



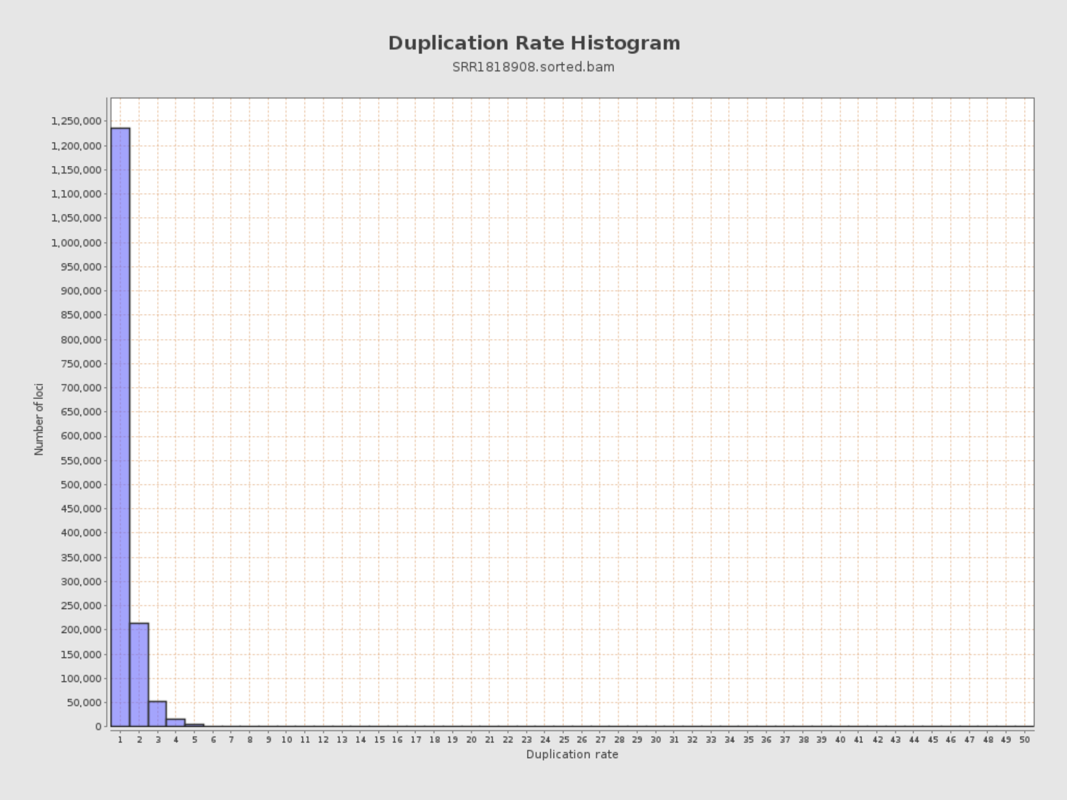
5. Results : Coverage Histogram (0-50X)



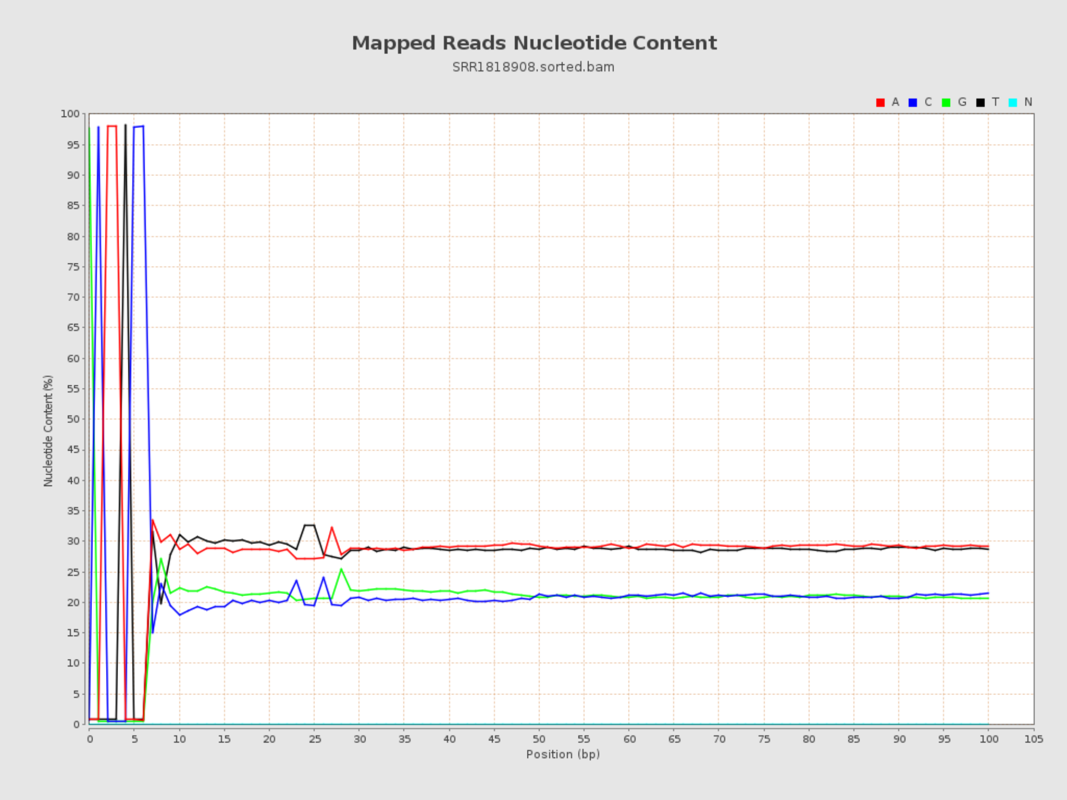
6. Results : Genome Fraction Coverage



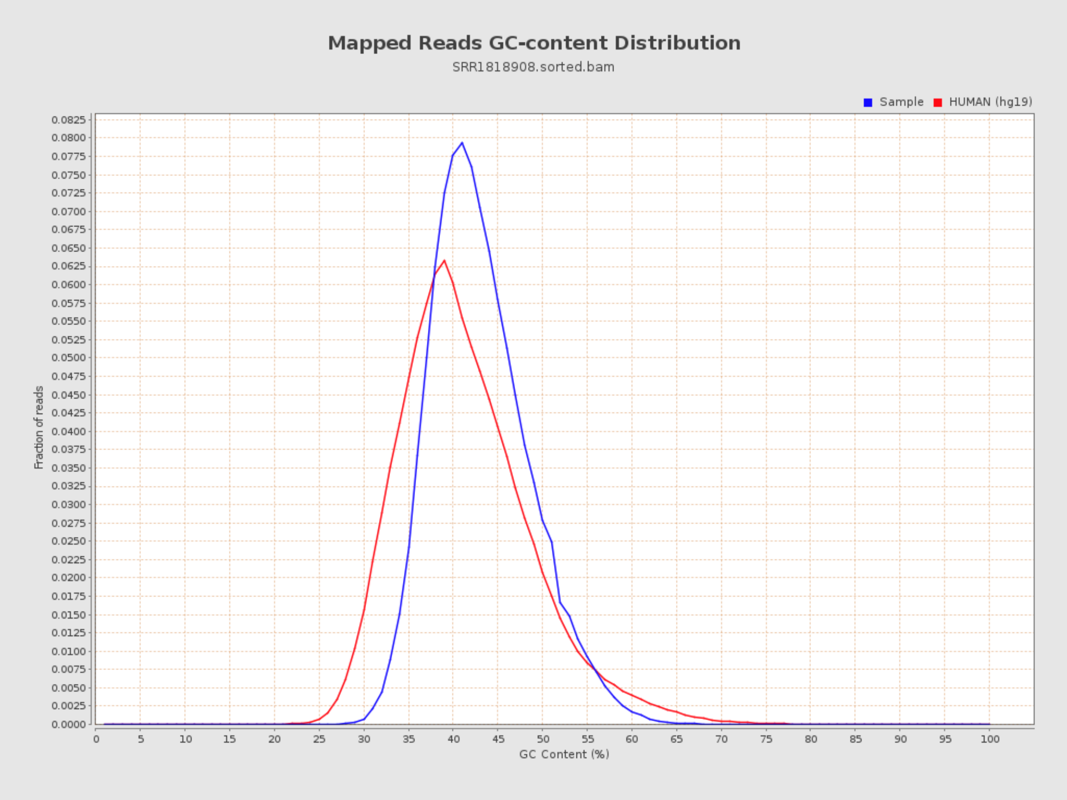
7. Results : Duplication Rate Histogram



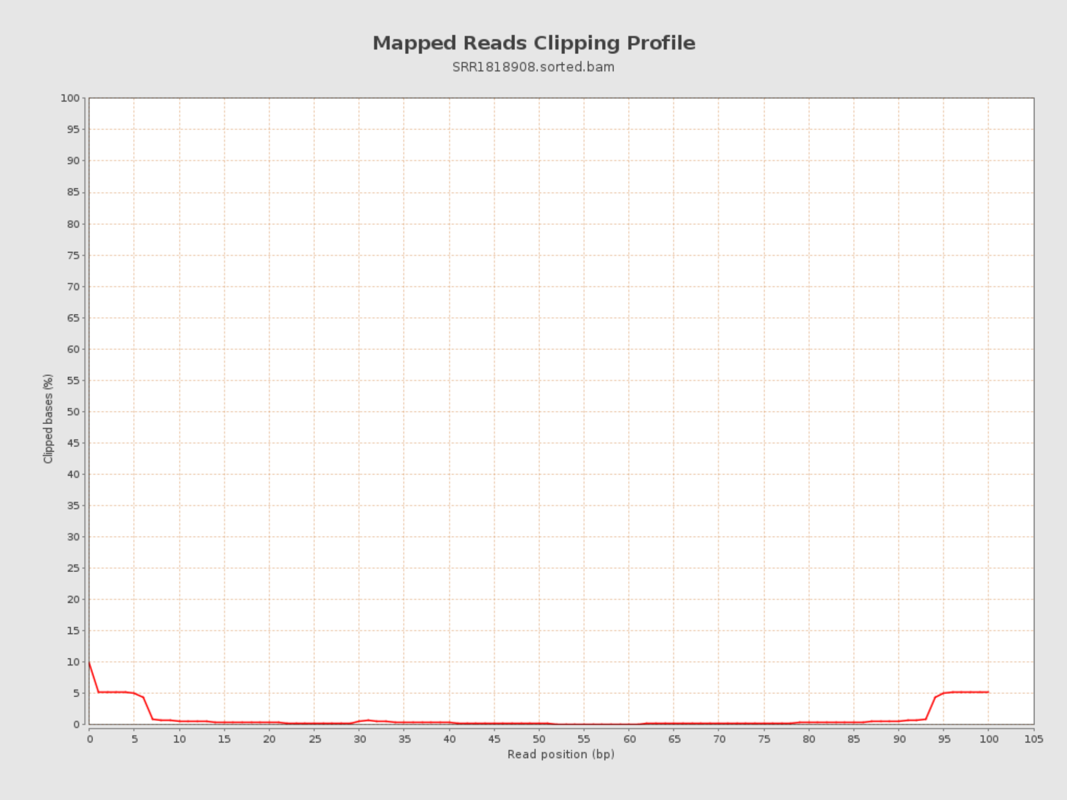
8. Results : Mapped Reads Nucleotide Content



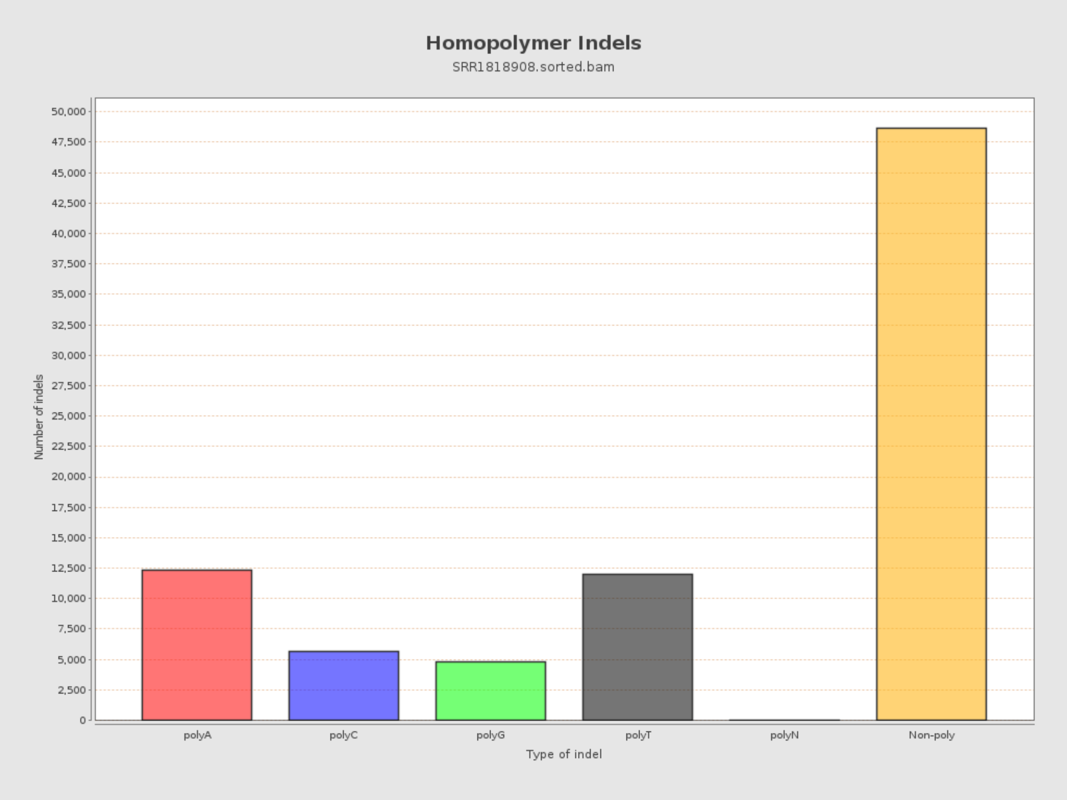
9. Results : Mapped Reads GC-content Distribution



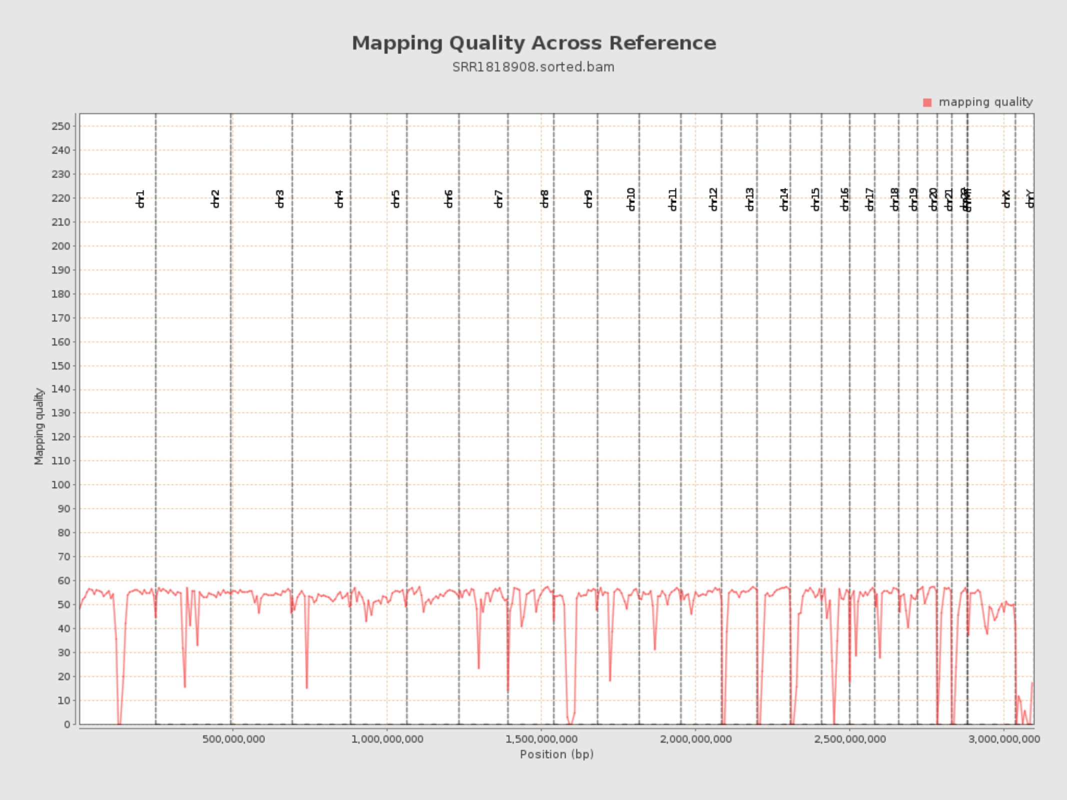
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram