Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:06:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818907.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_SRR1818907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:06:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,768,991
Mapped reads	2,643,172 / 95.46%
Unmapped reads	125,819 / 4.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,758 / 1.51%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	731,024 / 26.4%
Duplication rate	23.69%
Clipped reads	2,665,564 / 96.26%

2.2. ACGT Content

Number/percentage of A's	71,174,061 / 29.1%
Number/percentage of C's	51,151,907 / 20.92%
Number/percentage of T's	70,949,070 / 29.01%
Number/percentage of G's	51,269,043 / 20.96%
Number/percentage of N's	3,528 / 0%
GC Percentage	41.88%

2.3. Coverage

Mean	0.079

Standard Deviation	0.9447

2.4. Mapping Quality

Mean Mapping Quality	49.2

2.5. Mismatches and indels

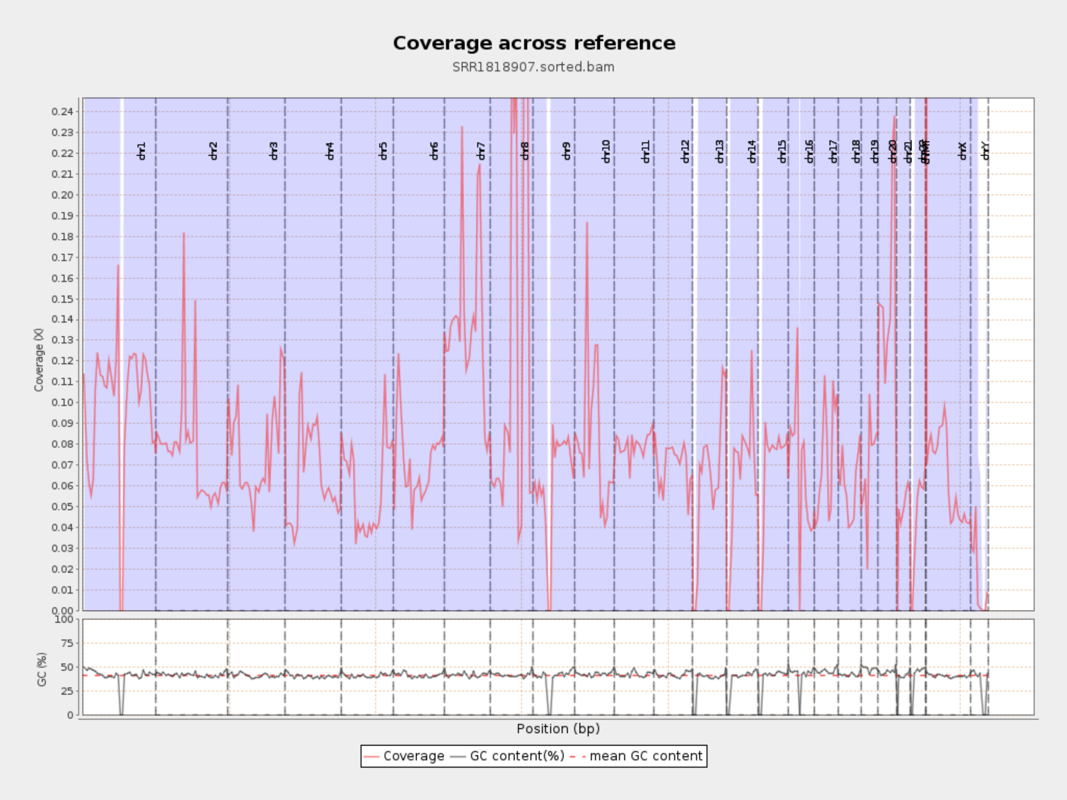
General error rate	0.65%
Mismatches	1,491,659
Insertions	35,435
Mapped reads with at least one insertion	1.3%
Deletions	81,453
Mapped reads with at least one deletion	3.01%
Homopolymer indels	40.44%

2.6. Chromosome stats

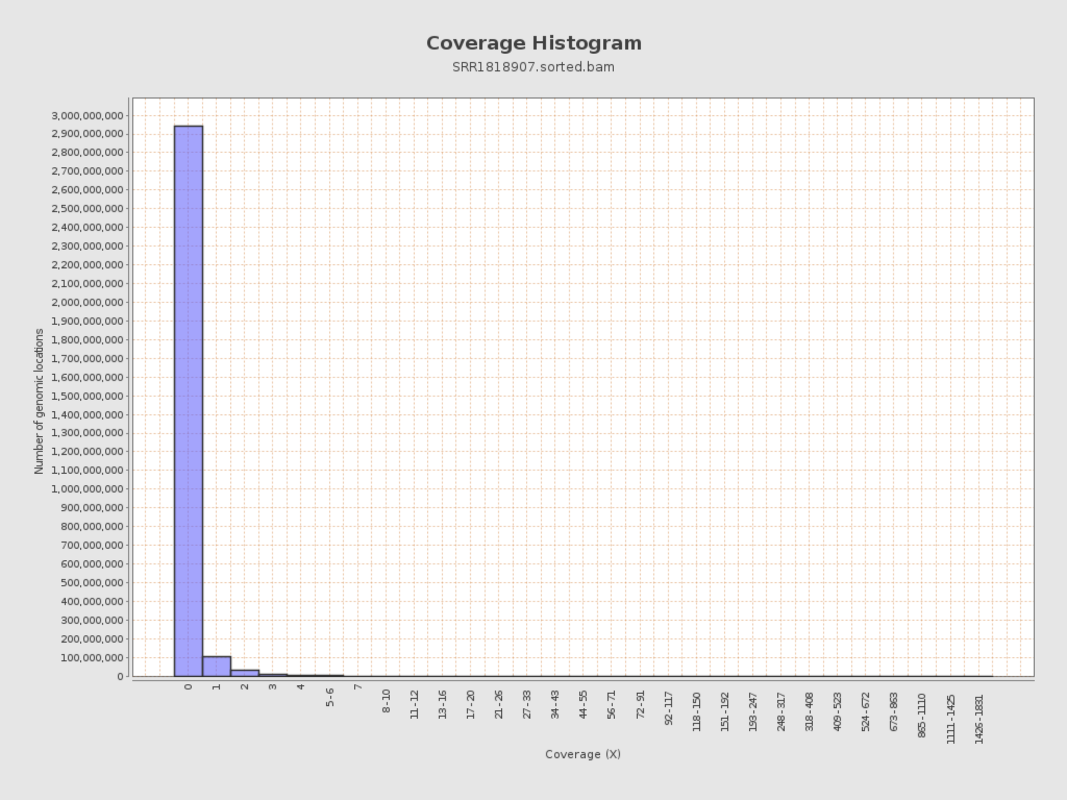
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24706828	0.0991	1.4754
chr2	243199373	18463353	0.0759	1.4127
chr3	198022430	15306297	0.0773	0.4043
chr4	191154276	12378130	0.0648	0.5121
chr5	180915260	10734401	0.0593	0.392
chr6	171115067	12187613	0.0712	0.4421
chr7	159138663	21885496	0.1375	2.0484

chr8	146364022	21243621	0.1451	0.7479
chr9	141213431	8815936	0.0624	0.7494
chr10	135534747	11061646	0.0816	1.1952
chr11	135006516	10729592	0.0795	0.5352
chr12	133851895	9445295	0.0706	0.3923
chr13	115169878	7405818	0.0643	0.3621
chr14	107349540	7071259	0.0659	0.4142
chr15	102531392	6686535	0.0652	0.3691
chr16	90354753	5954270	0.0659	0.9593
chr17	81195210	5890562	0.0725	0.5579
chr18	78077248	4710785	0.0603	0.9049
chr19	59128983	4088574	0.0691	1.2438
chr20	63025520	9941065	0.1577	0.633
chr21	48129895	2284105	0.0475	0.3934
chr22	51304566	2142820	0.0418	0.3388
chrMT	16571	767334	46.3058	27.0415
chrX	155270560	9933613	0.064	0.4639
chrY	59373566	871828	0.0147	1.1331

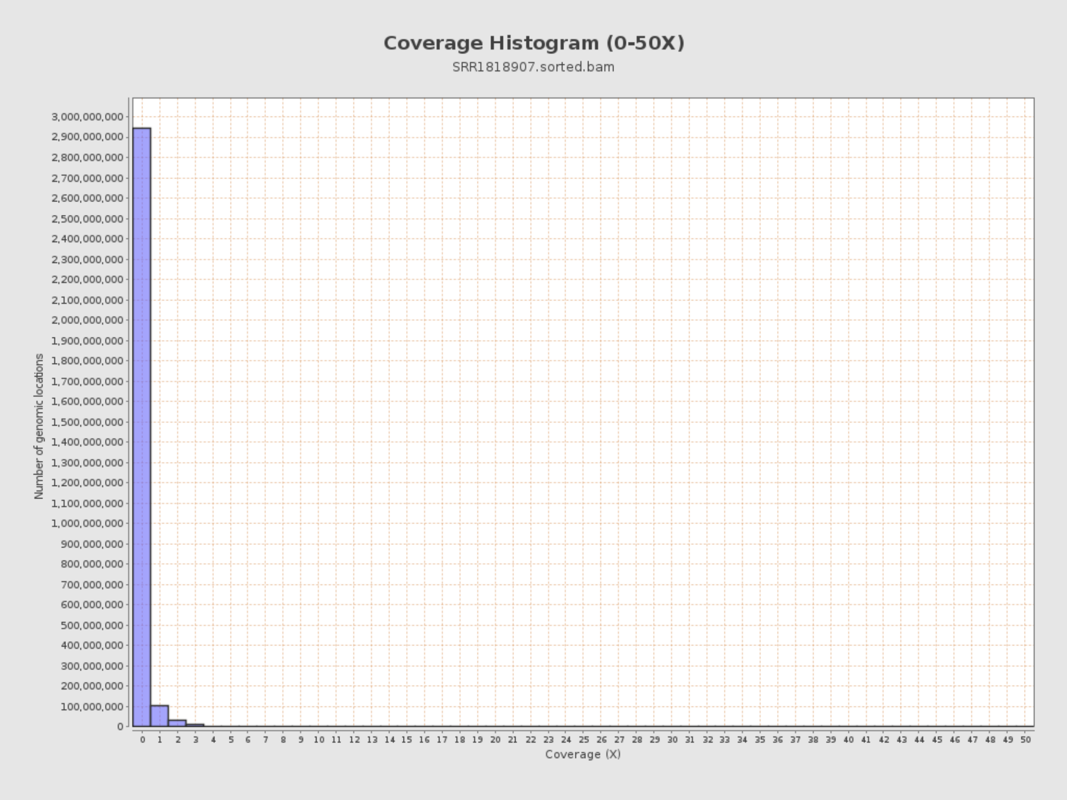
3. Results : Coverage across reference



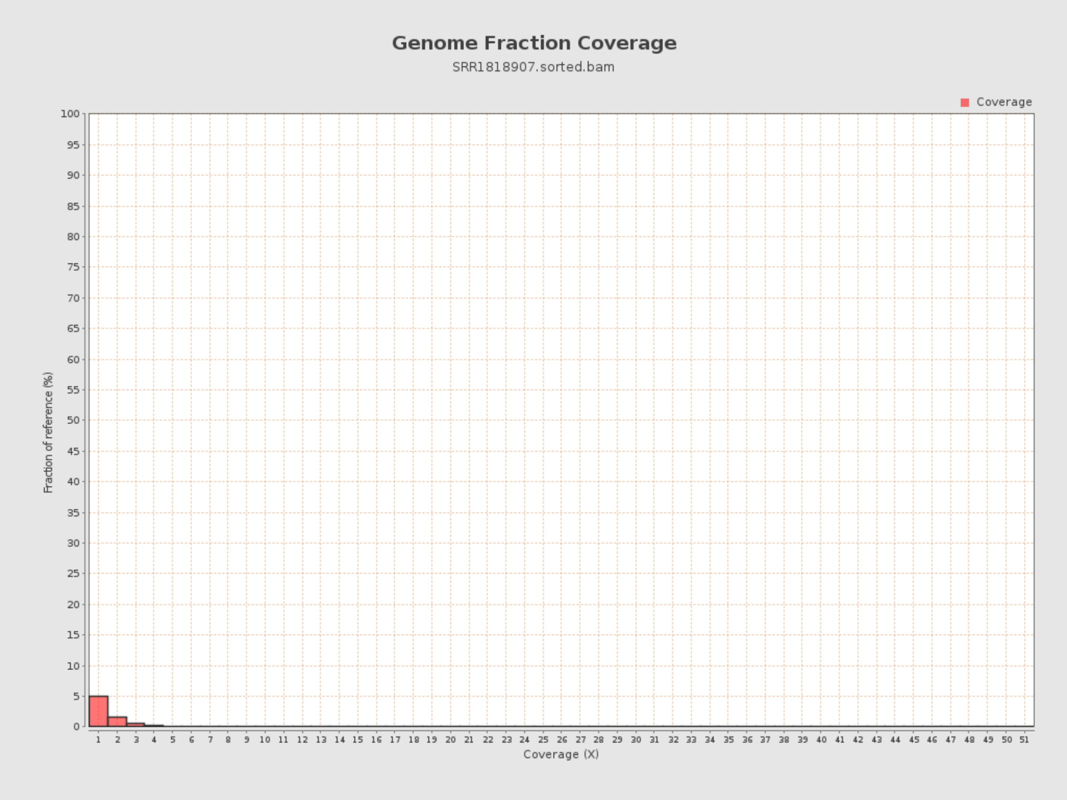
4. Results : Coverage Histogram



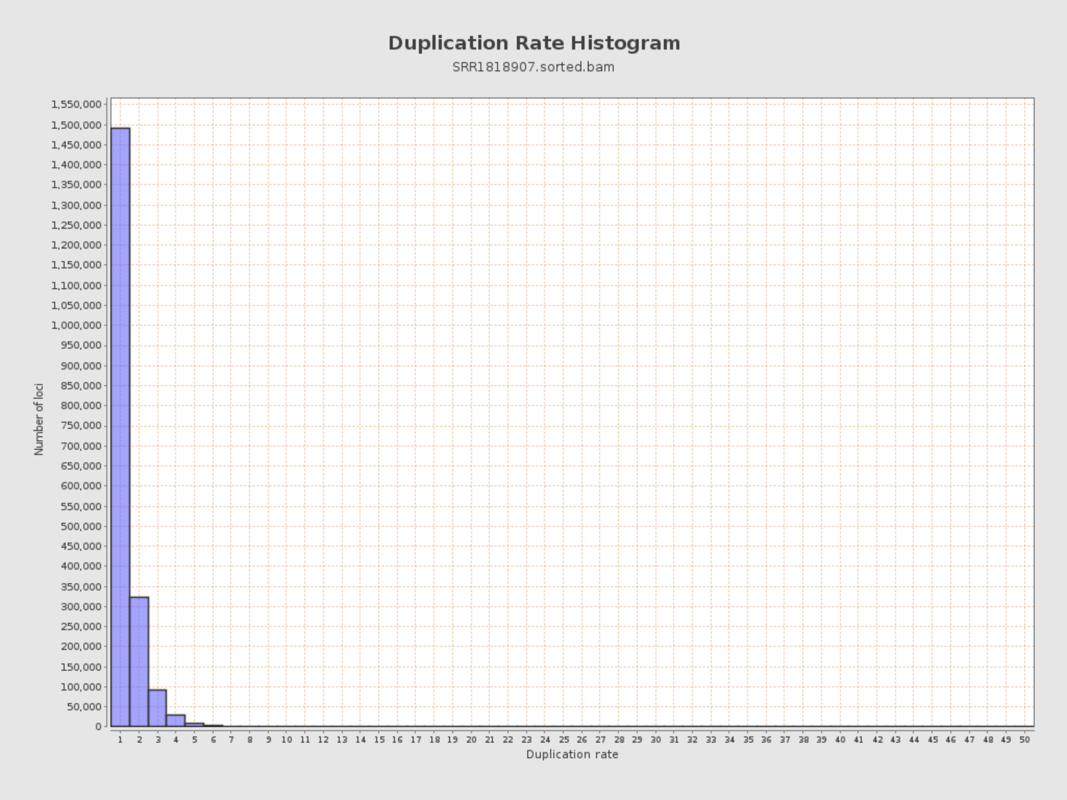
5. Results : Coverage Histogram (0-50X)



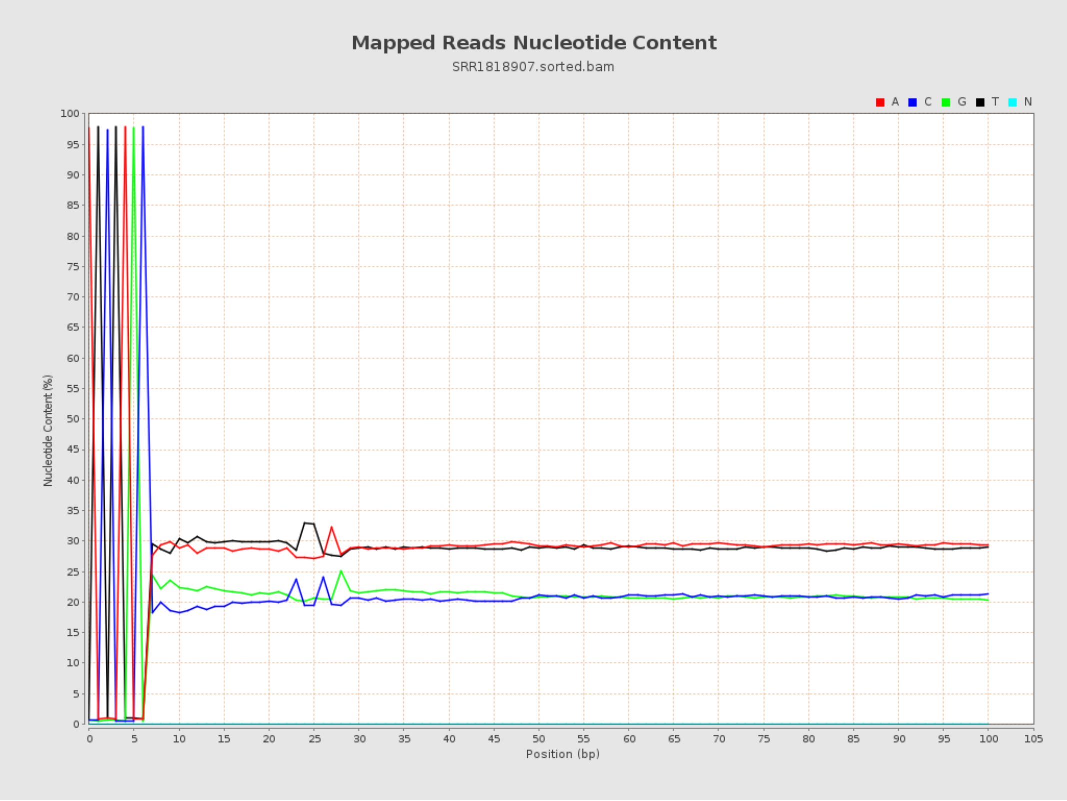
6. Results : Genome Fraction Coverage



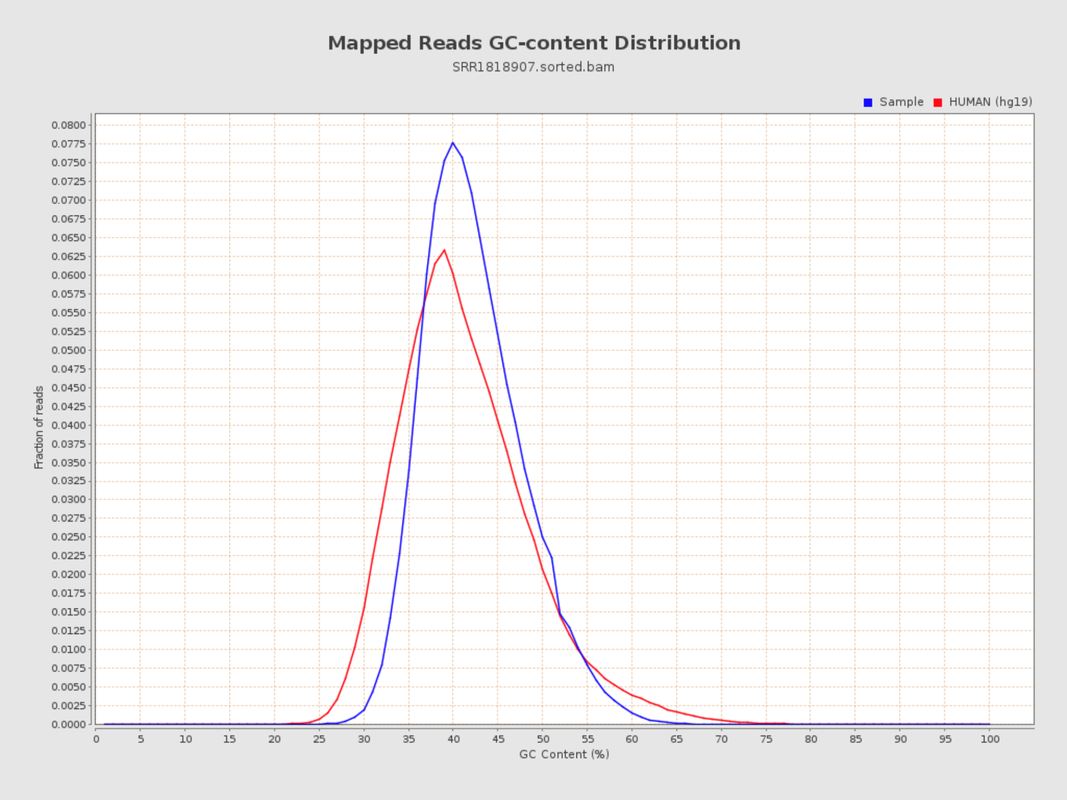
7. Results : Duplication Rate Histogram



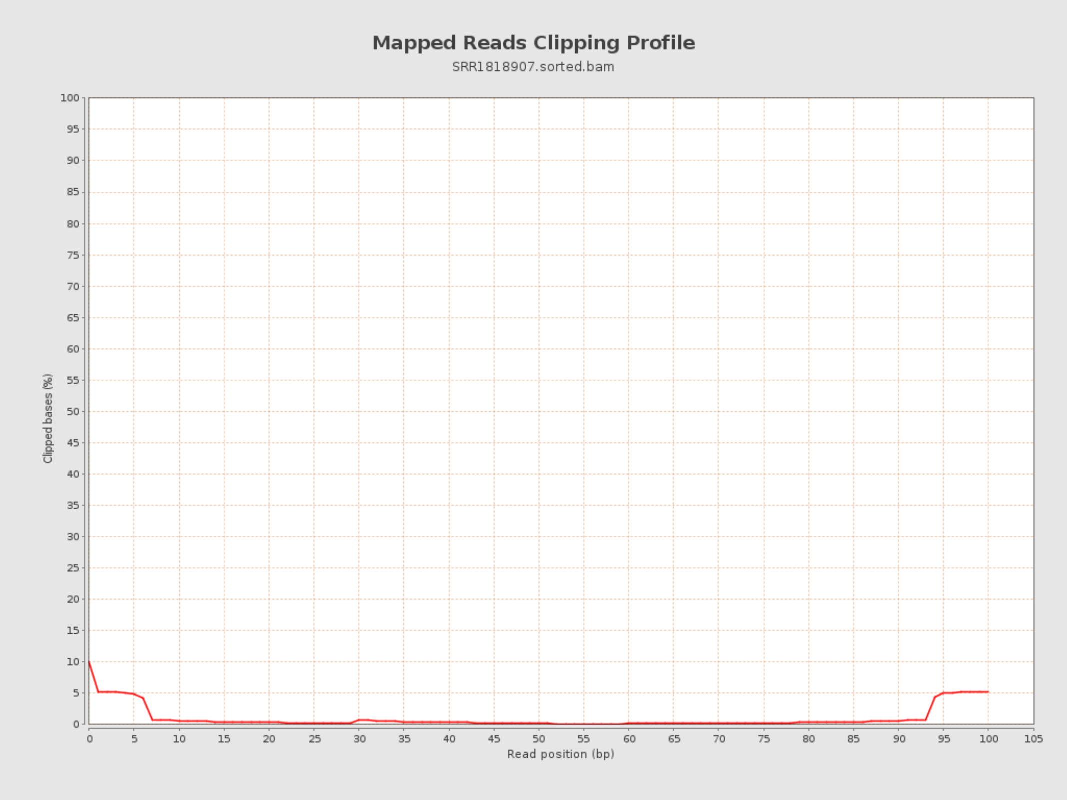
8. Results : Mapped Reads Nucleotide Content



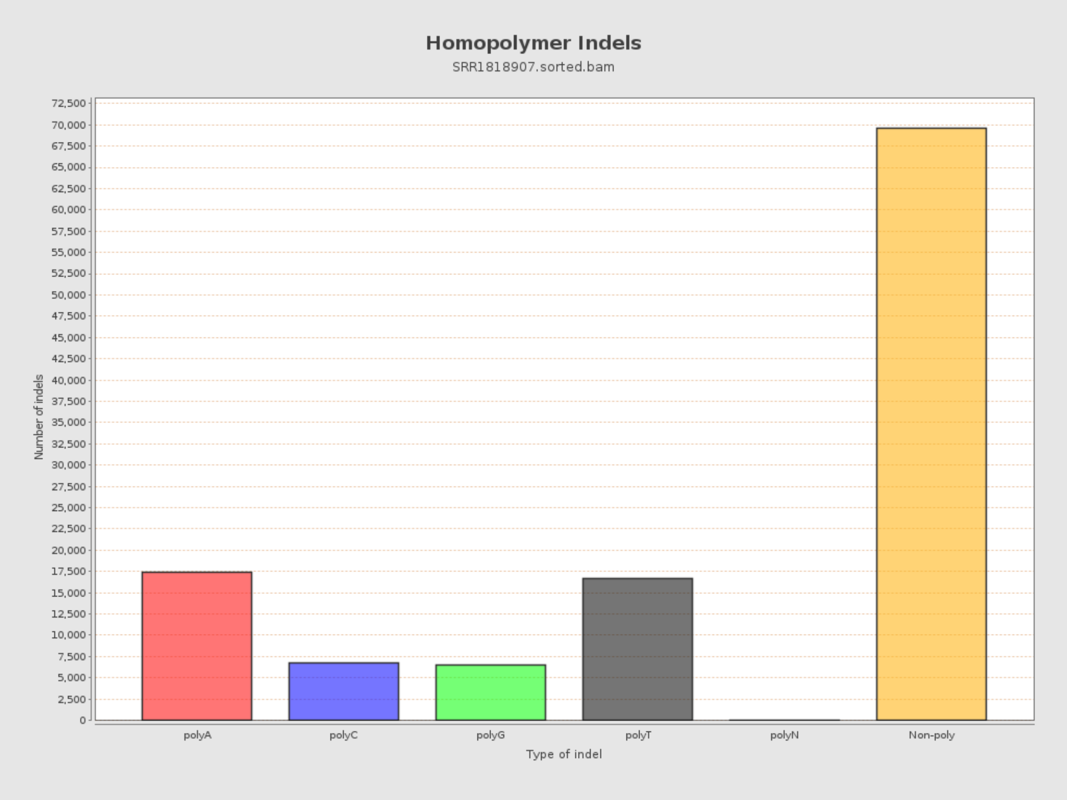
9. Results : Mapped Reads GC-content Distribution



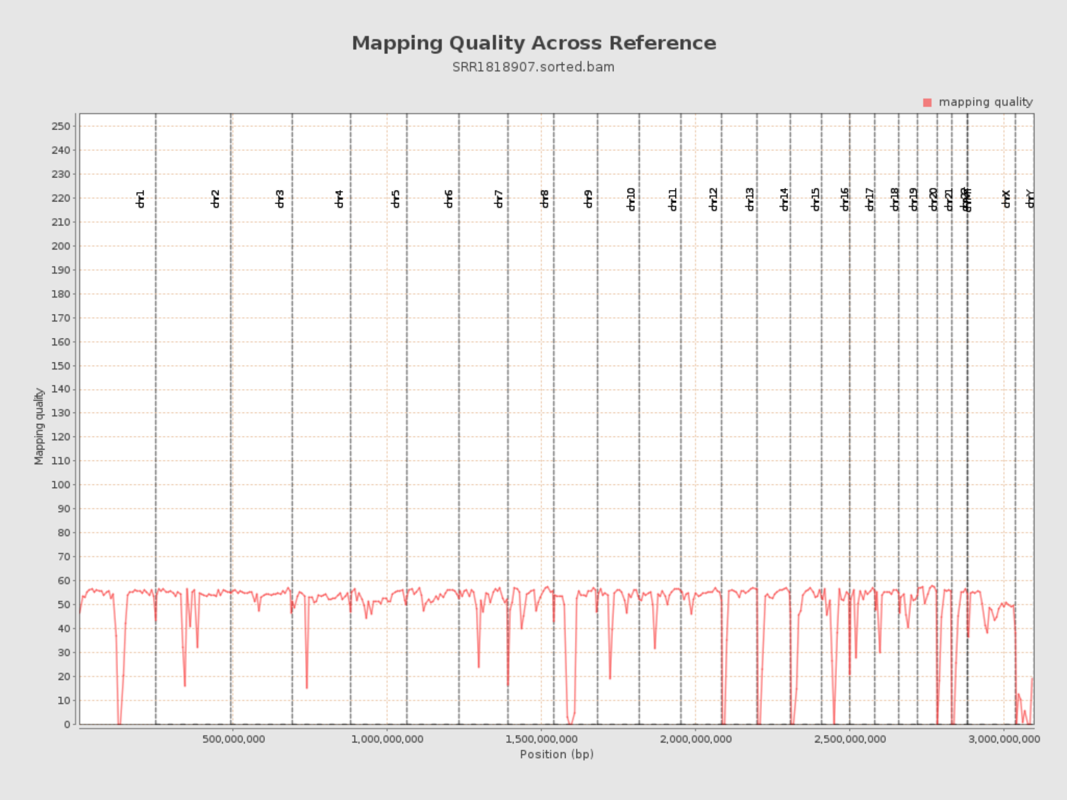
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram