Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:45:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818887.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_SRR1818887 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818887.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:45:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818887.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,586,960
Mapped reads	1,420,928 / 89.54%
Unmapped reads	166,032 / 10.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,626 / 1.3%
Read min/max/mean length	30 / 101 / 101.5
Duplicated reads (estimated)	218,655 / 13.78%
Duplication rate	12.47%
Clipped reads	1,435,673 / 90.47%

2.2. ACGT Content

Number/percentage of A's	38,228,088 / 29.06%
Number/percentage of C's	26,830,838 / 20.4%
Number/percentage of T's	37,413,028 / 28.44%
Number/percentage of G's	29,081,396 / 22.11%
Number/percentage of N's	1,875 / 0%
GC Percentage	42.5%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.5521

2.4. Mapping Quality

Mean Mapping Quality	49.15

2.5. Mismatches and indels

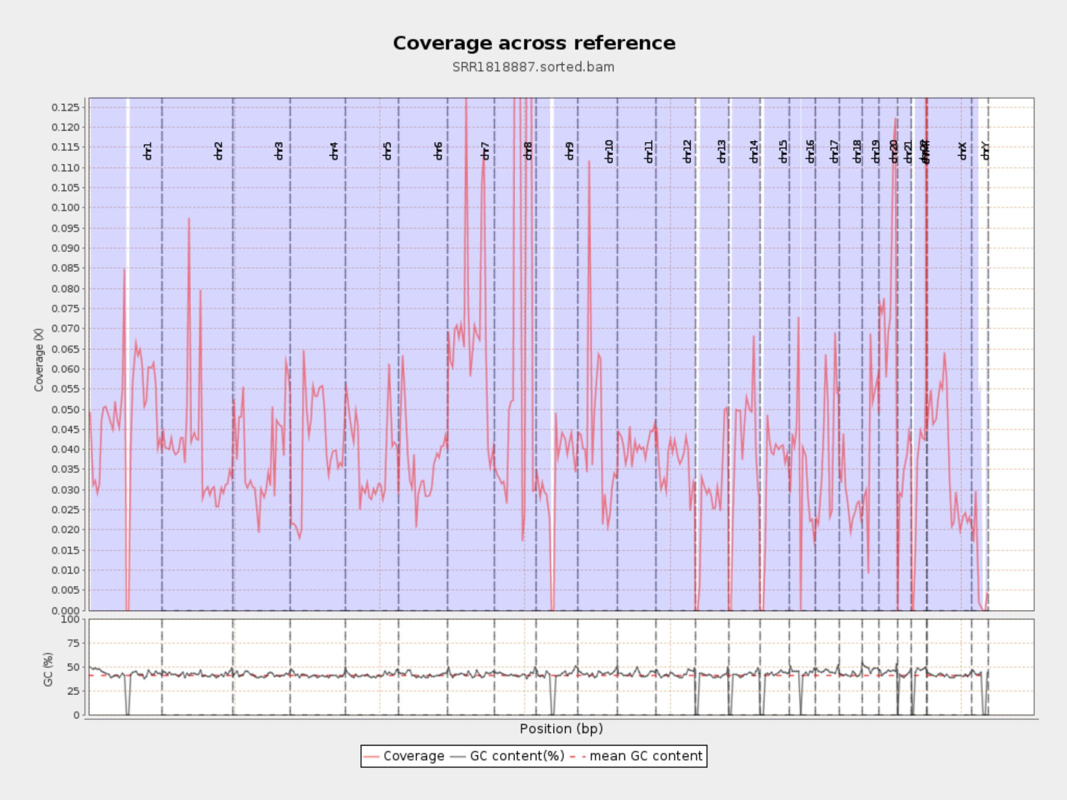
General error rate	0.63%
Mismatches	787,626
Insertions	16,784
Mapped reads with at least one insertion	1.14%
Deletions	43,094
Mapped reads with at least one deletion	2.96%
Homopolymer indels	42%

2.6. Chromosome stats

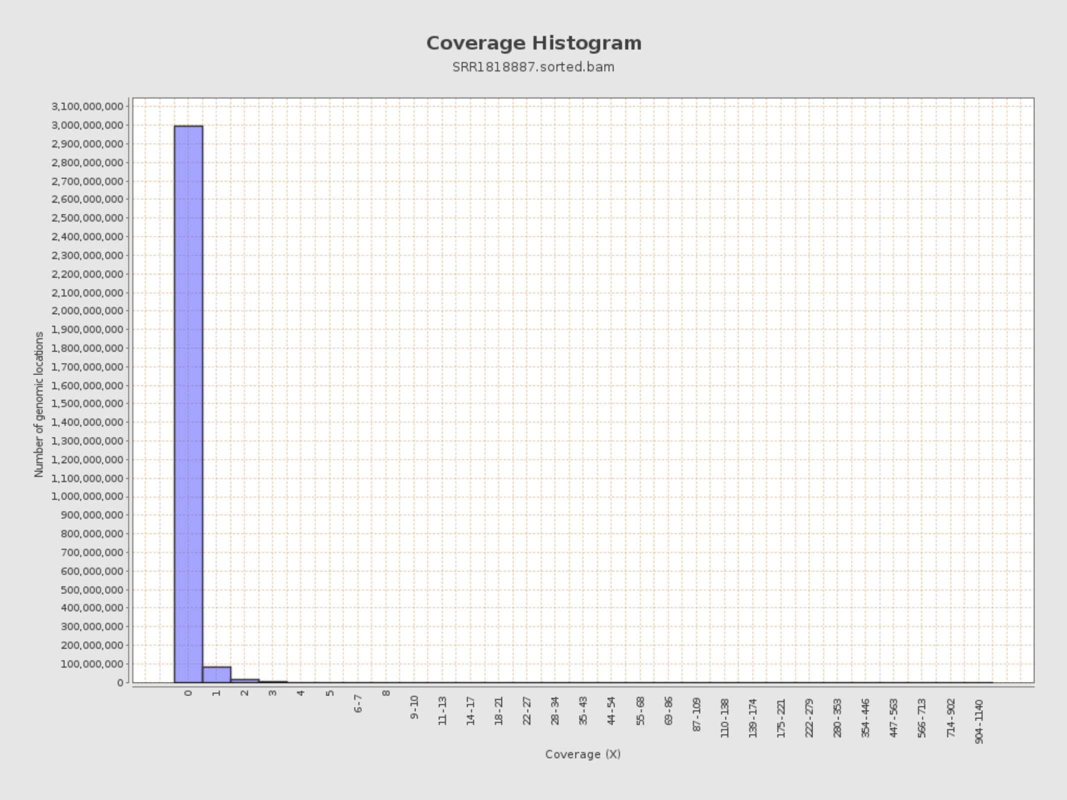
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11850537	0.0475	0.8801
chr2	243199373	9643266	0.0397	0.7927
chr3	198022430	7735240	0.0391	0.2437
chr4	191154276	7619399	0.0399	0.3285
chr5	180915260	6851592	0.0379	0.2538
chr6	171115067	6270934	0.0366	0.2621
chr7	159138663	11153918	0.0701	1.1709

chr8	146364022	12715372	0.0869	0.4622
chr9	141213431	4605556	0.0326	0.4439
chr10	135534747	5867482	0.0433	0.7264
chr11	135006516	5558075	0.0412	0.3202
chr12	133851895	4933621	0.0369	0.2401
chr13	115169878	3197794	0.0278	0.2023
chr14	107349540	4258973	0.0397	0.2747
chr15	102531392	3379127	0.033	0.2212
chr16	90354753	3027299	0.0335	0.5351
chr17	81195210	3372824	0.0415	0.3353
chr18	78077248	2199822	0.0282	0.508
chr19	59128983	2496756	0.0422	0.8428
chr20	63025520	5149037	0.0817	0.3778
chr21	48129895	1555281	0.0323	0.2667
chr22	51304566	1518425	0.0296	0.2322
chrMT	16571	221550	13.3697	8.4669
chrX	155270560	5937573	0.0382	0.286
chrY	59373566	521847	0.0088	0.632

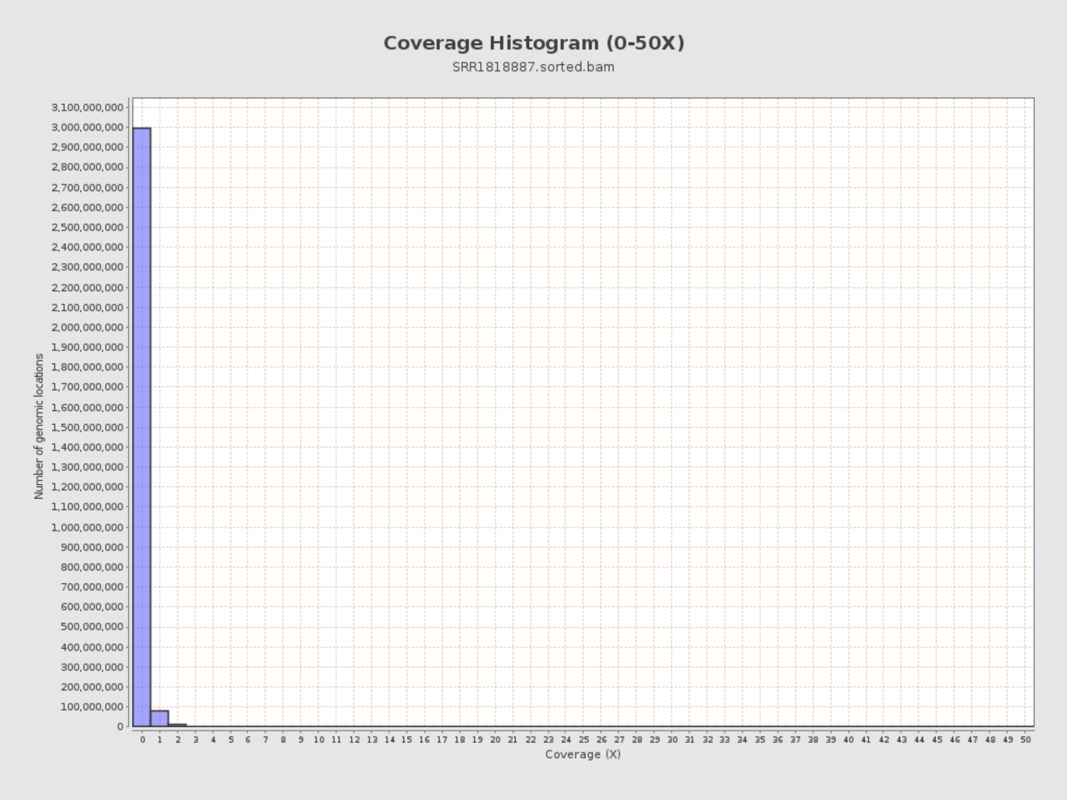
3. Results : Coverage across reference



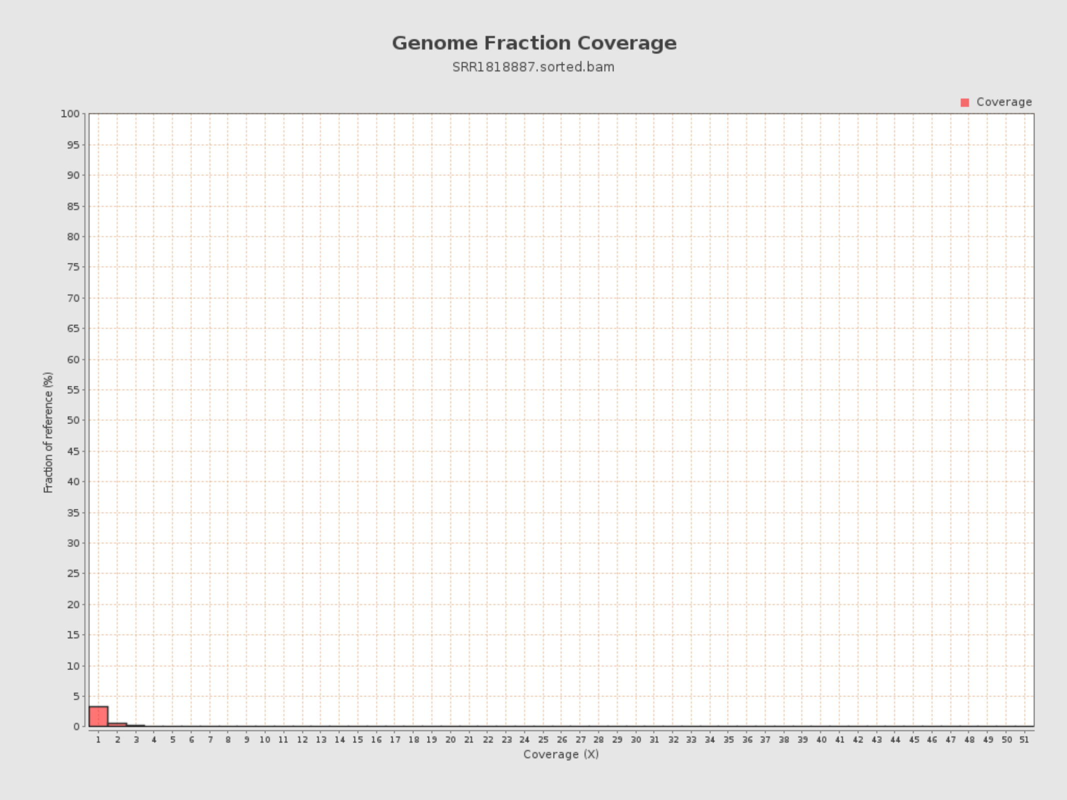
4. Results : Coverage Histogram



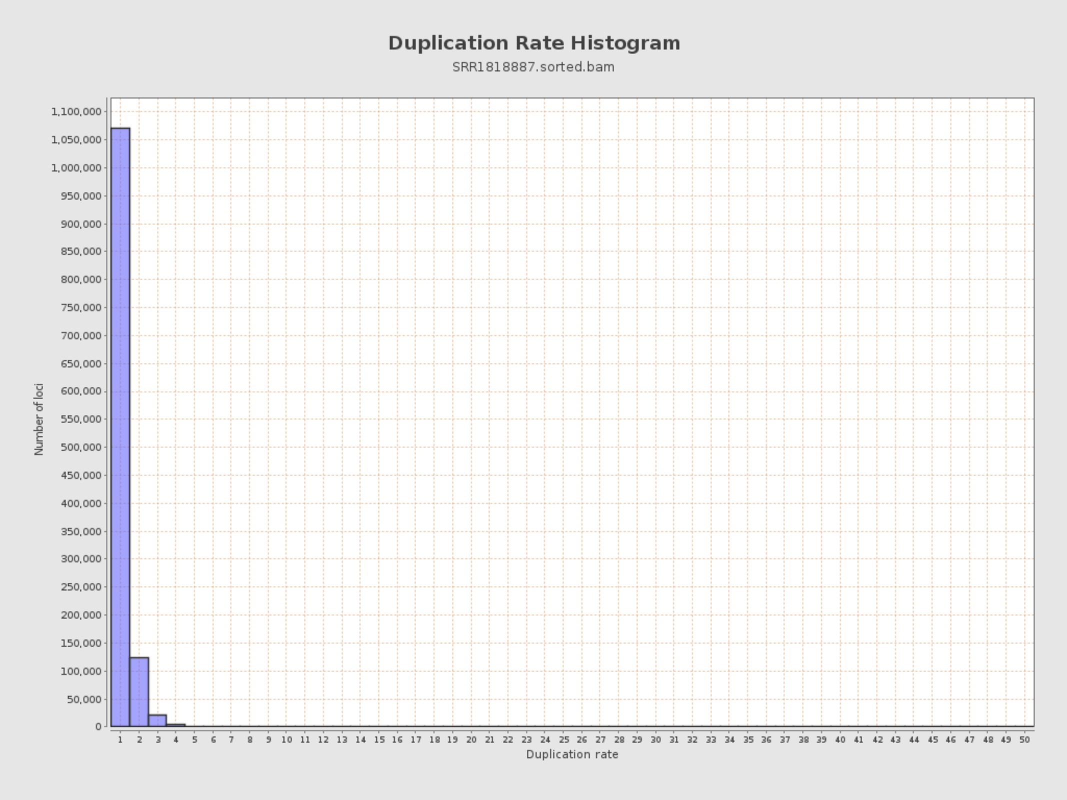
5. Results : Coverage Histogram (0-50X)



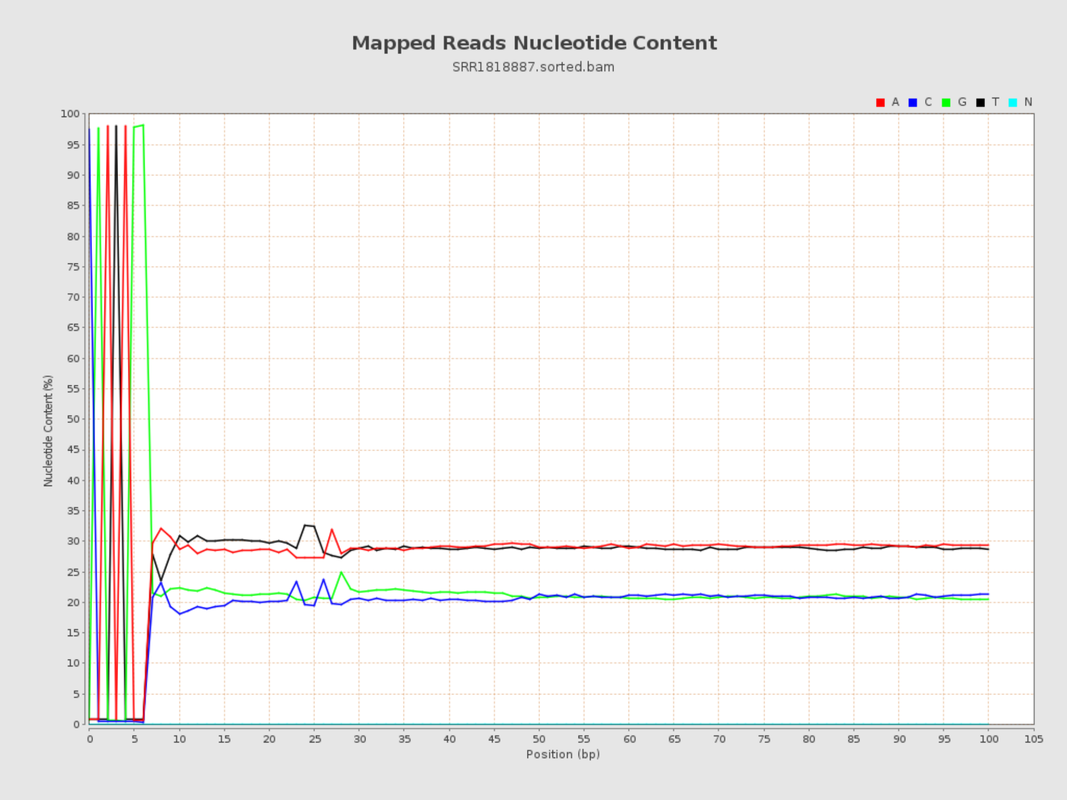
6. Results : Genome Fraction Coverage



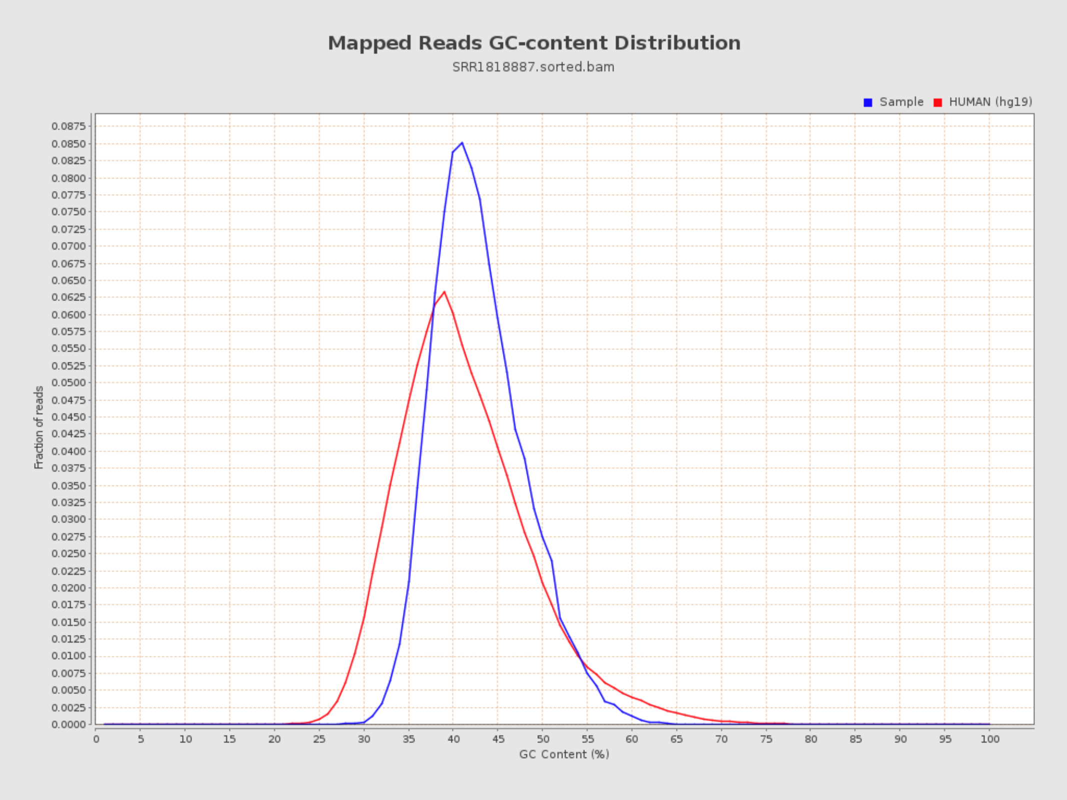
7. Results : Duplication Rate Histogram



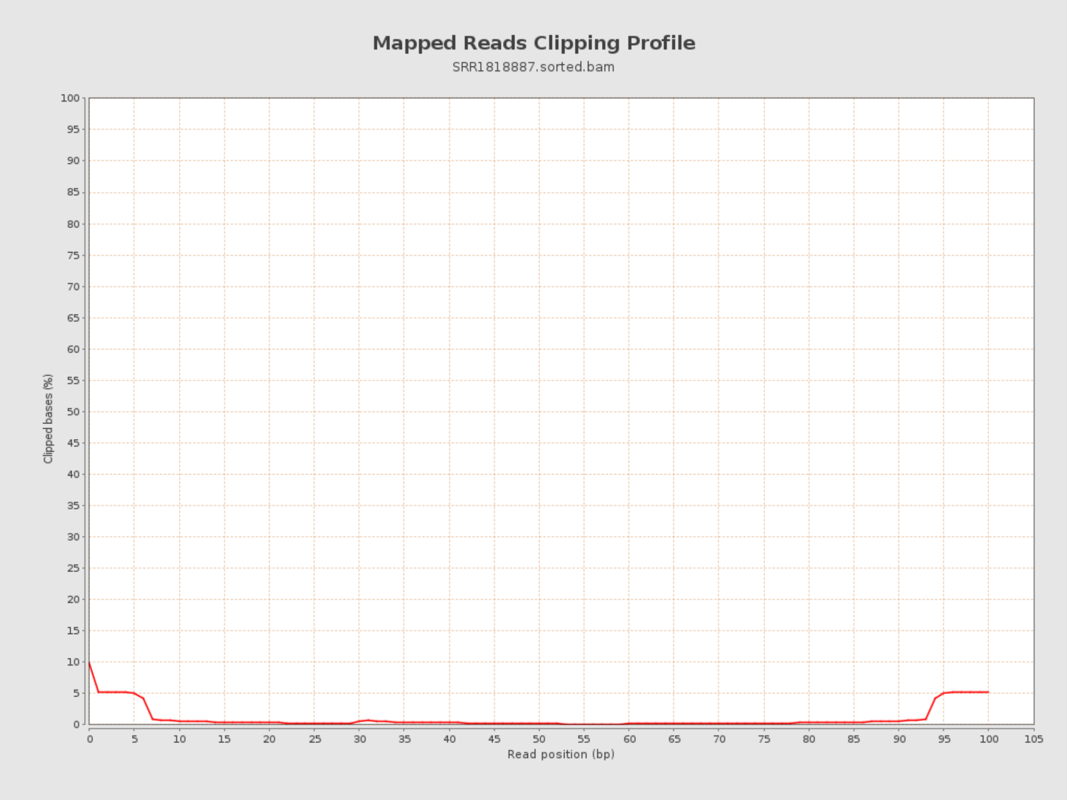
8. Results : Mapped Reads Nucleotide Content



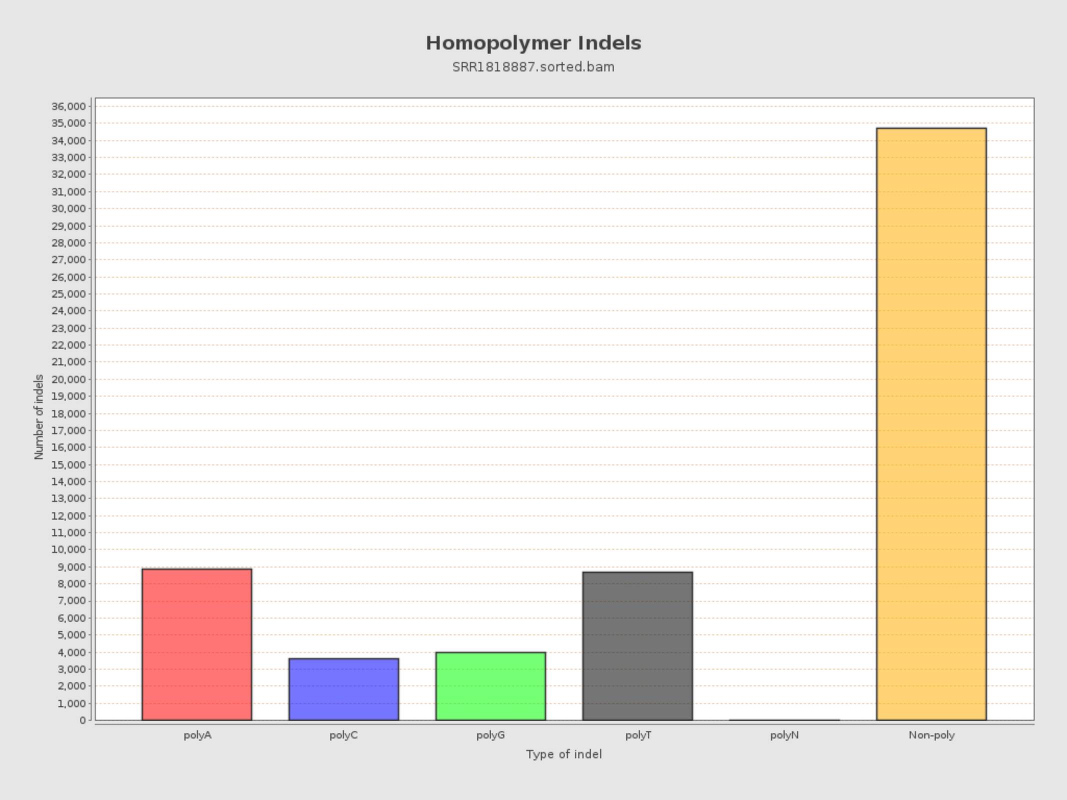
9. Results : Mapped Reads GC-content Distribution



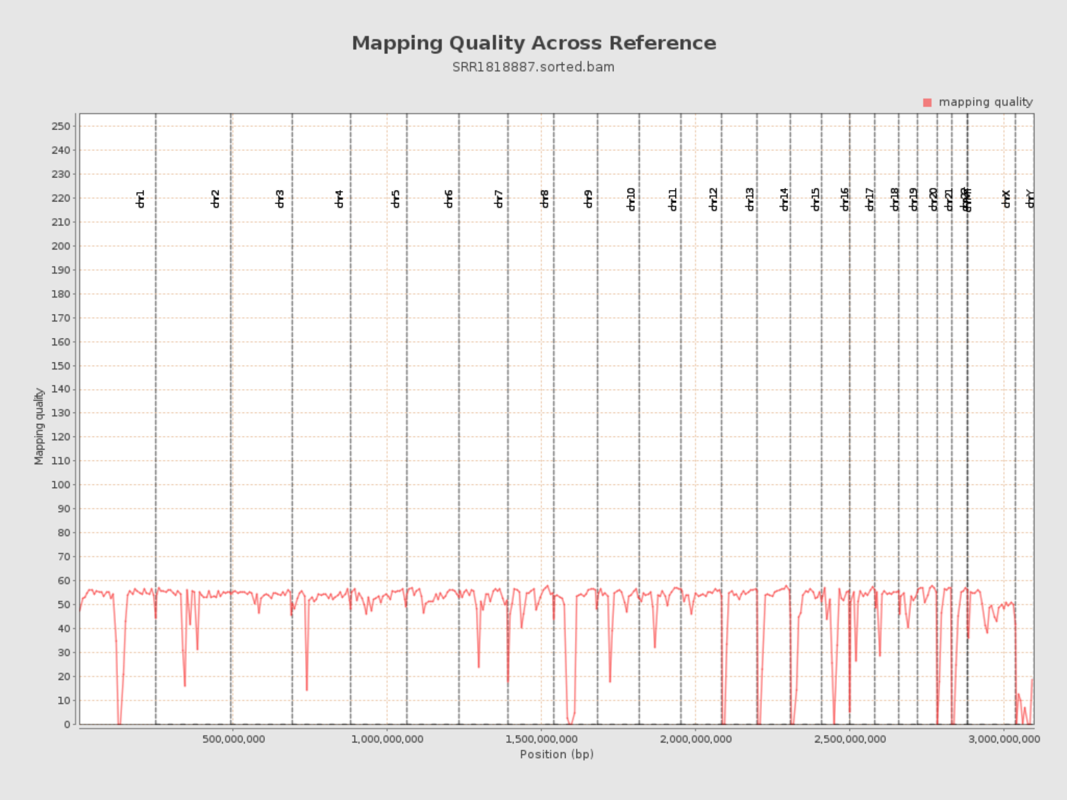
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram