Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 21:23:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818843.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_SRR1818843 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818843.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 21:23:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818843.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	774,496
Mapped reads	764,497 / 98.71%
Unmapped reads	9,999 / 1.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,569 / 1.36%
Read min/max/mean length	30 / 101 / 101.52
Duplicated reads (estimated)	95,432 / 12.32%
Duplication rate	10.39%
Clipped reads	774,289 / 99.97%

2.2. ACGT Content

Number/percentage of A's	19,628,144 / 27.73%
Number/percentage of C's	15,293,496 / 21.61%
Number/percentage of T's	19,875,404 / 28.08%
Number/percentage of G's	15,985,705 / 22.58%
Number/percentage of N's	1,030 / 0%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0229

Standard Deviation	0.2964

2.4. Mapping Quality

Mean Mapping Quality	49.28

2.5. Mismatches and indels

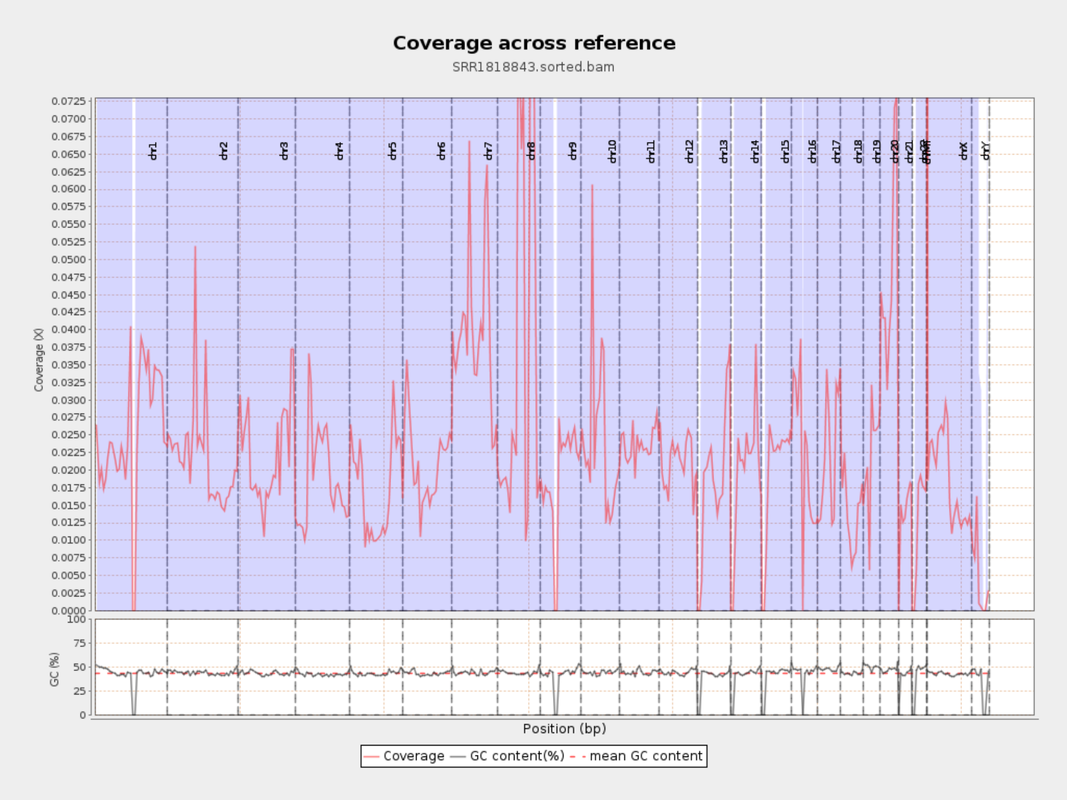
General error rate	0.63%
Mismatches	420,929
Insertions	8,344
Mapped reads with at least one insertion	1.05%
Deletions	22,102
Mapped reads with at least one deletion	2.82%
Homopolymer indels	41.7%

2.6. Chromosome stats

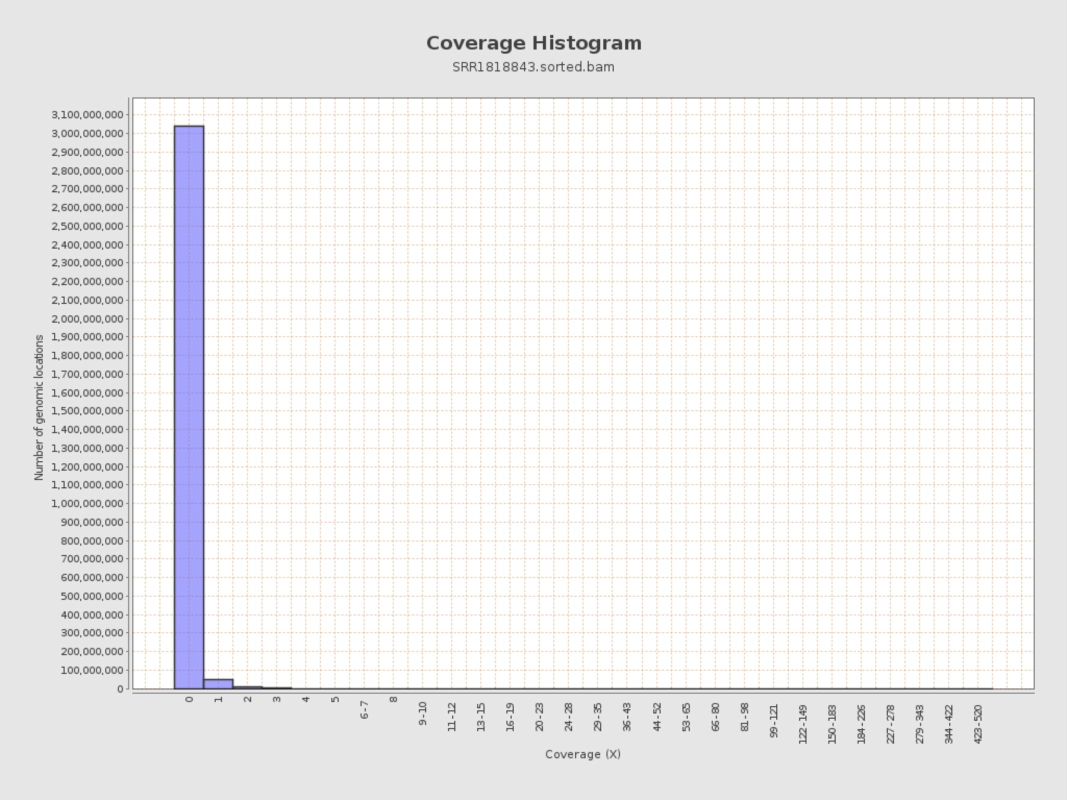
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6277045	0.0252	0.4245
chr2	243199373	5308951	0.0218	0.3682
chr3	198022430	4450869	0.0225	0.174
chr4	191154276	3621115	0.0189	0.2012
chr5	180915260	3111158	0.0172	0.1579
chr6	171115067	3558825	0.0208	0.1791
chr7	159138663	6322008	0.0397	0.622

chr8	146364022	6127262	0.0419	0.2816
chr9	141213431	2669030	0.0189	0.2632
chr10	135534747	3280805	0.0242	0.4043
chr11	135006516	3207645	0.0238	0.2045
chr12	133851895	2813887	0.021	0.1702
chr13	115169878	2143205	0.0186	0.1575
chr14	107349540	2109743	0.0197	0.171
chr15	102531392	1996014	0.0195	0.1645
chr16	90354753	1952274	0.0216	0.276
chr17	81195210	1802659	0.0222	0.2062
chr18	78077248	1056063	0.0135	0.281
chr19	59128983	1296699	0.0219	0.3991
chr20	63025520	3049770	0.0484	0.2708
chr21	48129895	667292	0.0139	0.1627
chr22	51304566	650422	0.0127	0.1374
chrMT	16571	197325	11.9079	8.2364
chrX	155270560	2894107	0.0186	0.1797
chrY	59373566	262650	0.0044	0.3044

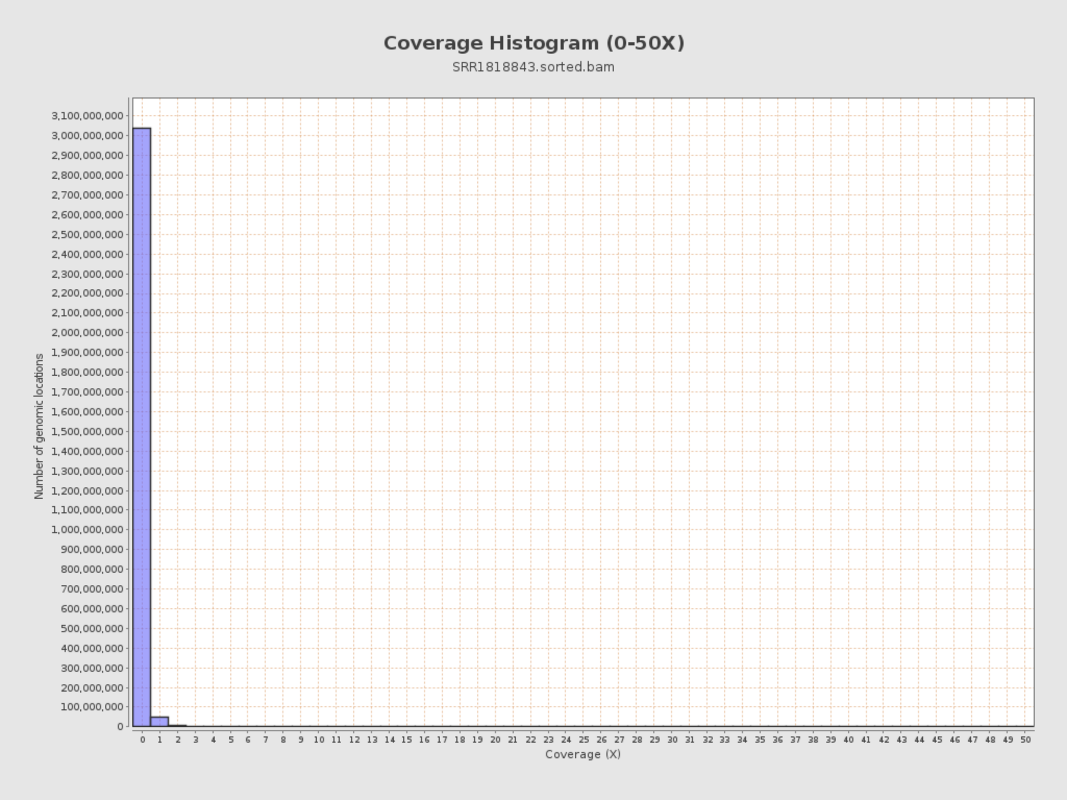
3. Results : Coverage across reference



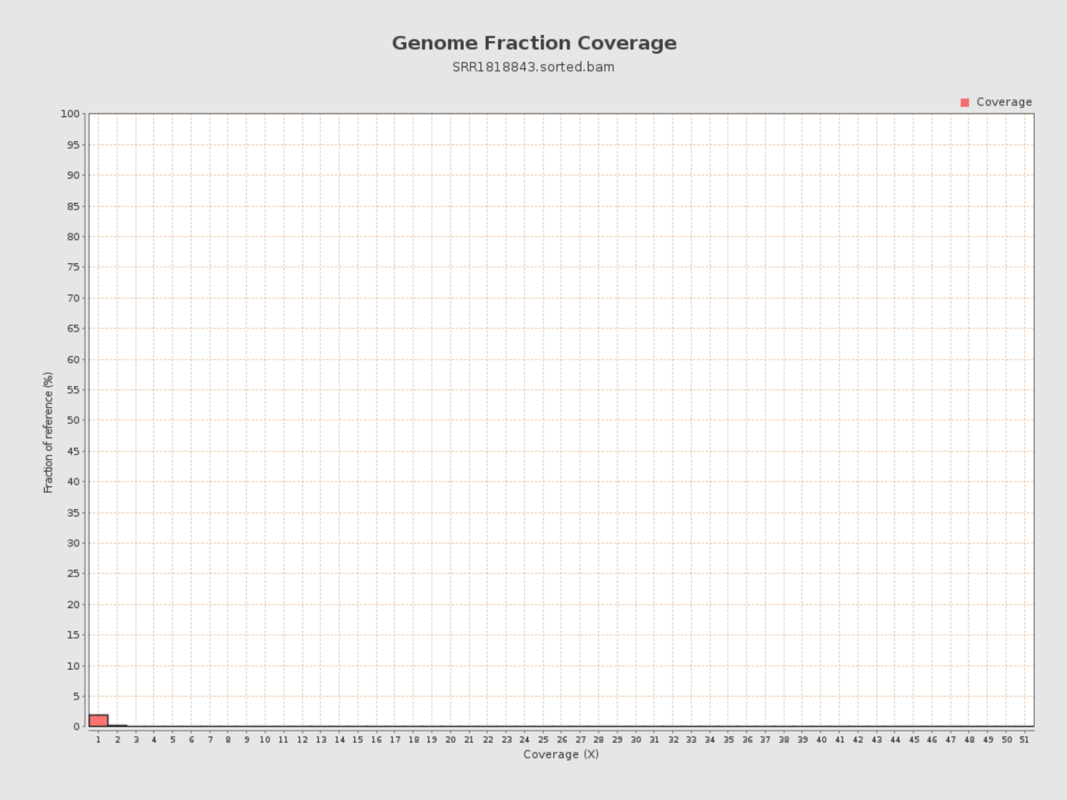
4. Results : Coverage Histogram



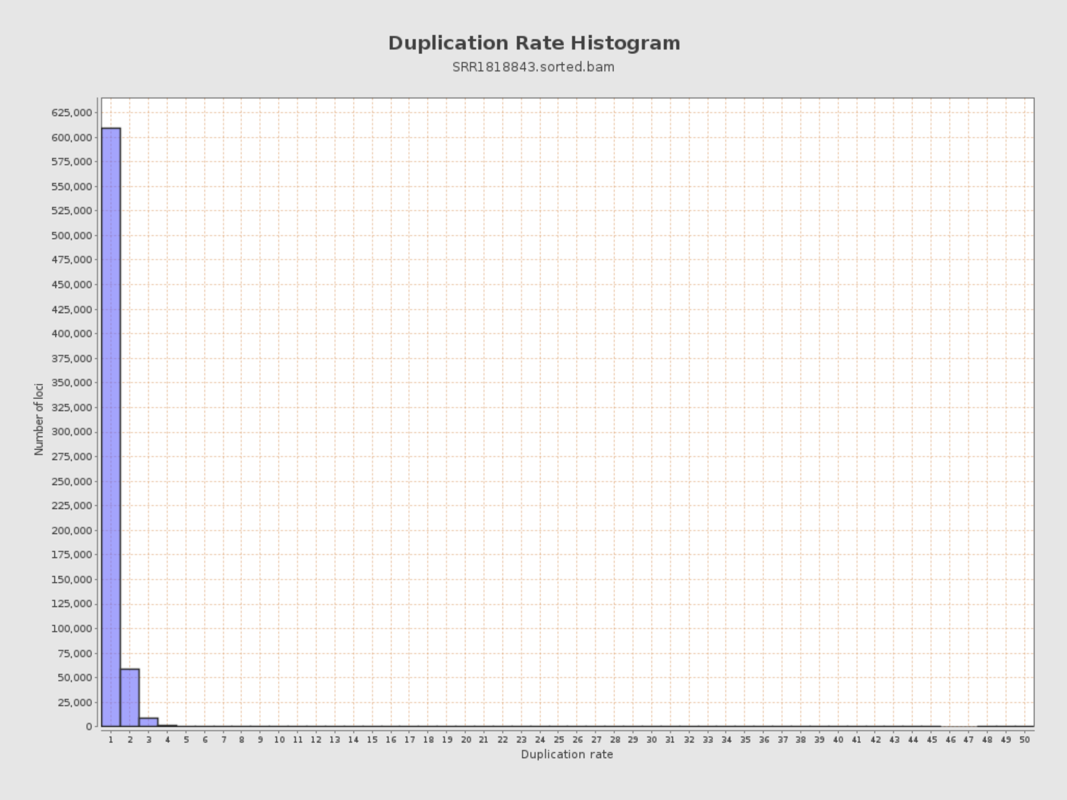
5. Results : Coverage Histogram (0-50X)



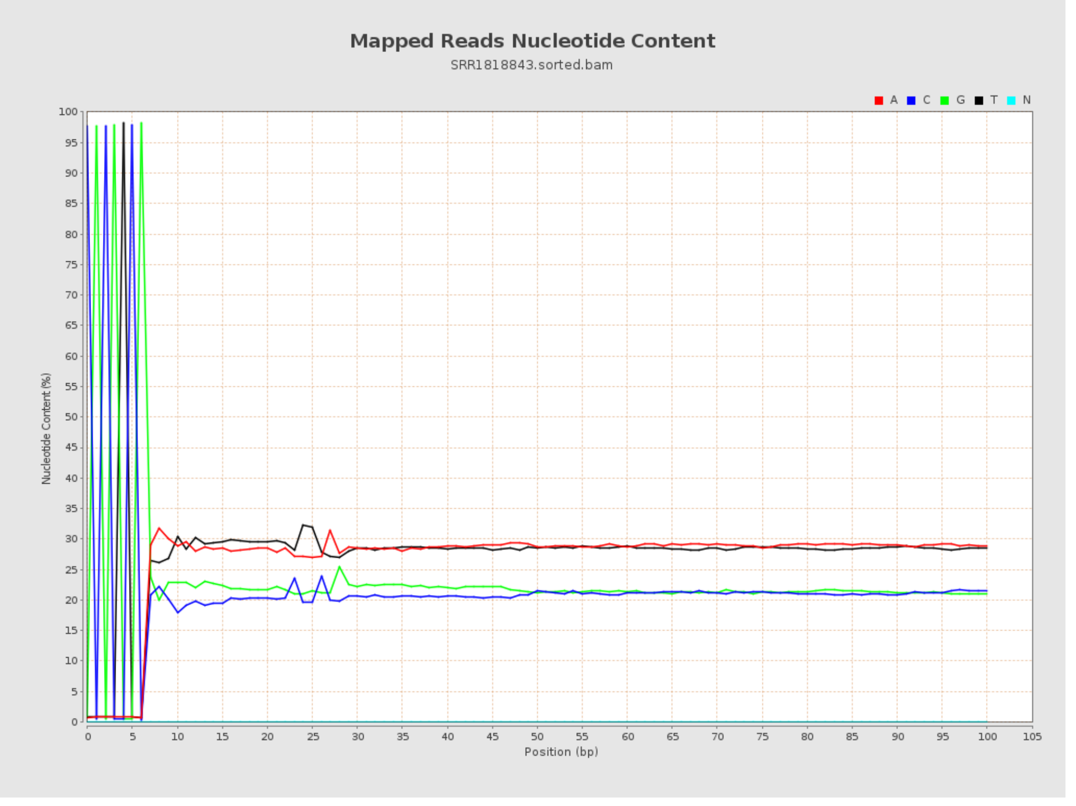
6. Results : Genome Fraction Coverage



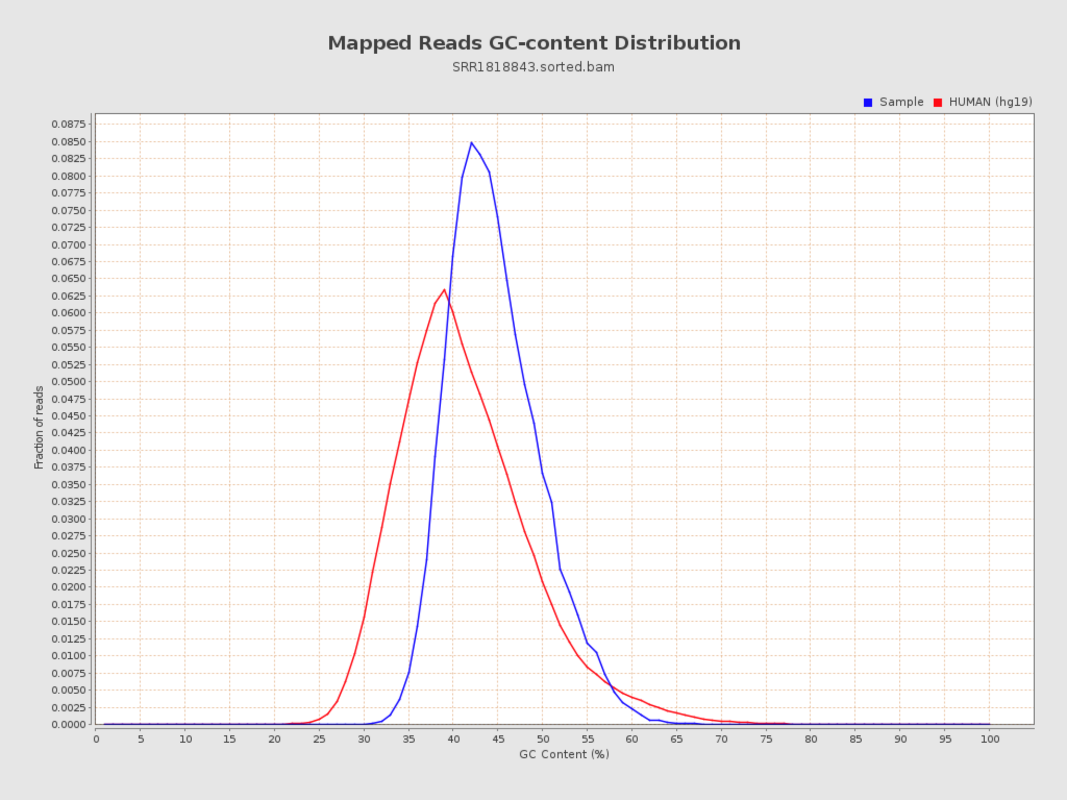
7. Results : Duplication Rate Histogram



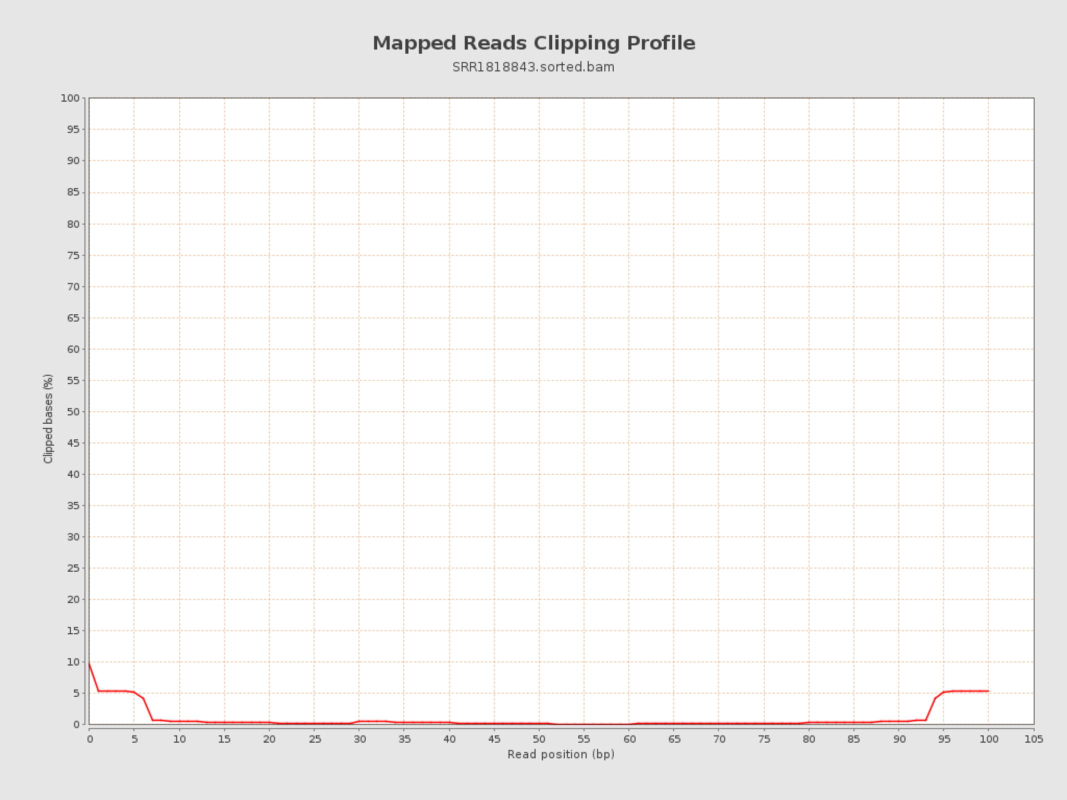
8. Results : Mapped Reads Nucleotide Content



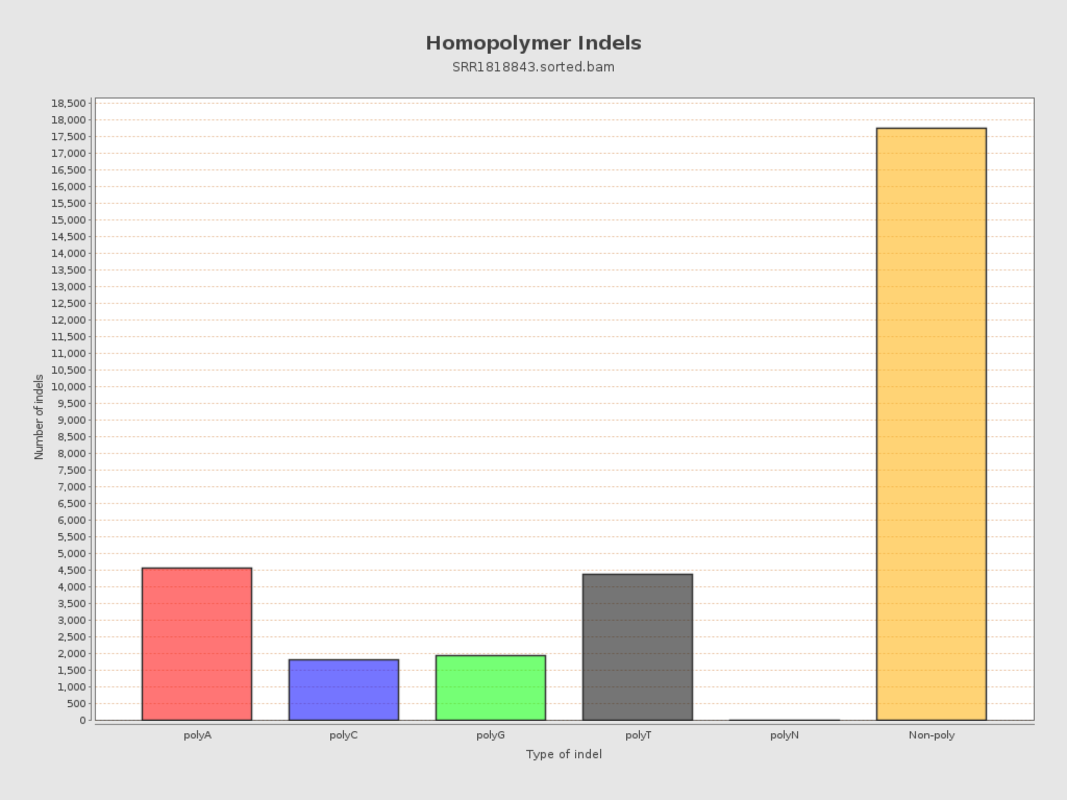
9. Results : Mapped Reads GC-content Distribution



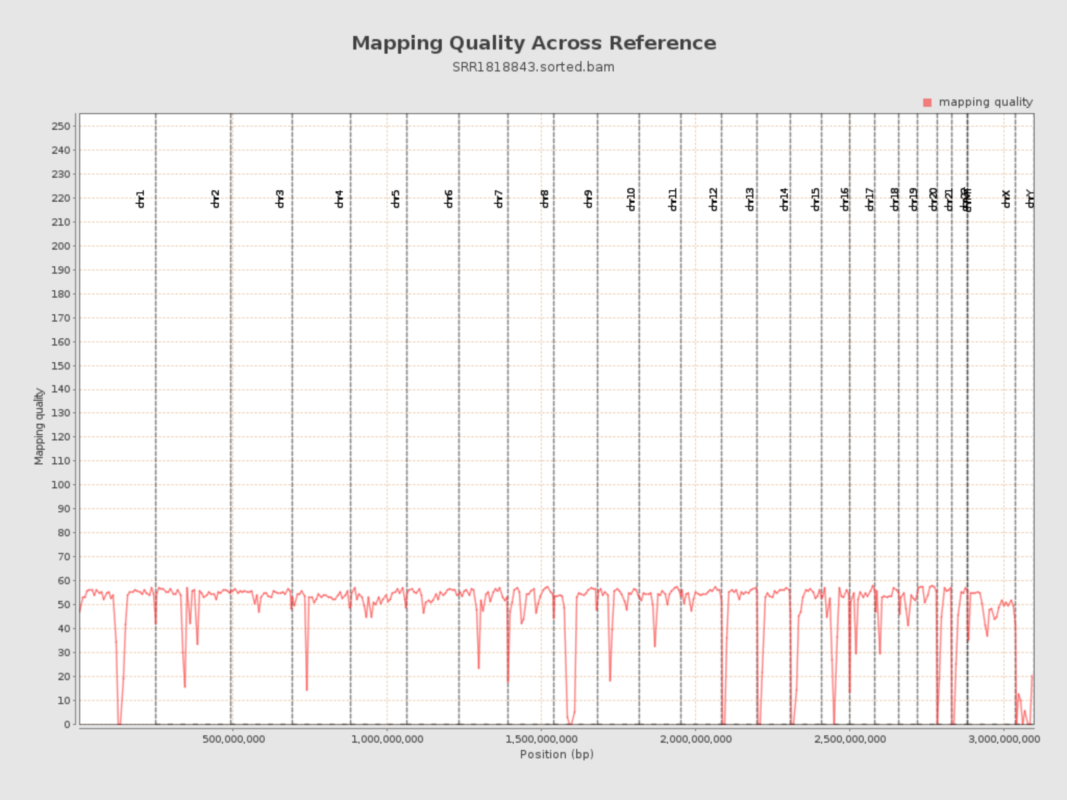
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram