Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:51:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818866.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_SRR1818866 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818866.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:51:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818866.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,854,923
Mapped reads	1,797,000 / 96.88%
Unmapped reads	57,923 / 3.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,822 / 1.61%
Read min/max/mean length	30 / 101 / 101.62
Duplicated reads (estimated)	267,717 / 14.43%
Duplication rate	11.86%
Clipped reads	1,801,516 / 97.12%

2.2. ACGT Content

Number/percentage of A's	45,494,963 / 27.36%
Number/percentage of C's	36,742,541 / 22.1%
Number/percentage of T's	48,098,208 / 28.92%
Number/percentage of G's	35,948,620 / 21.62%
Number/percentage of N's	2,635 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0537

Standard Deviation	0.6549

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

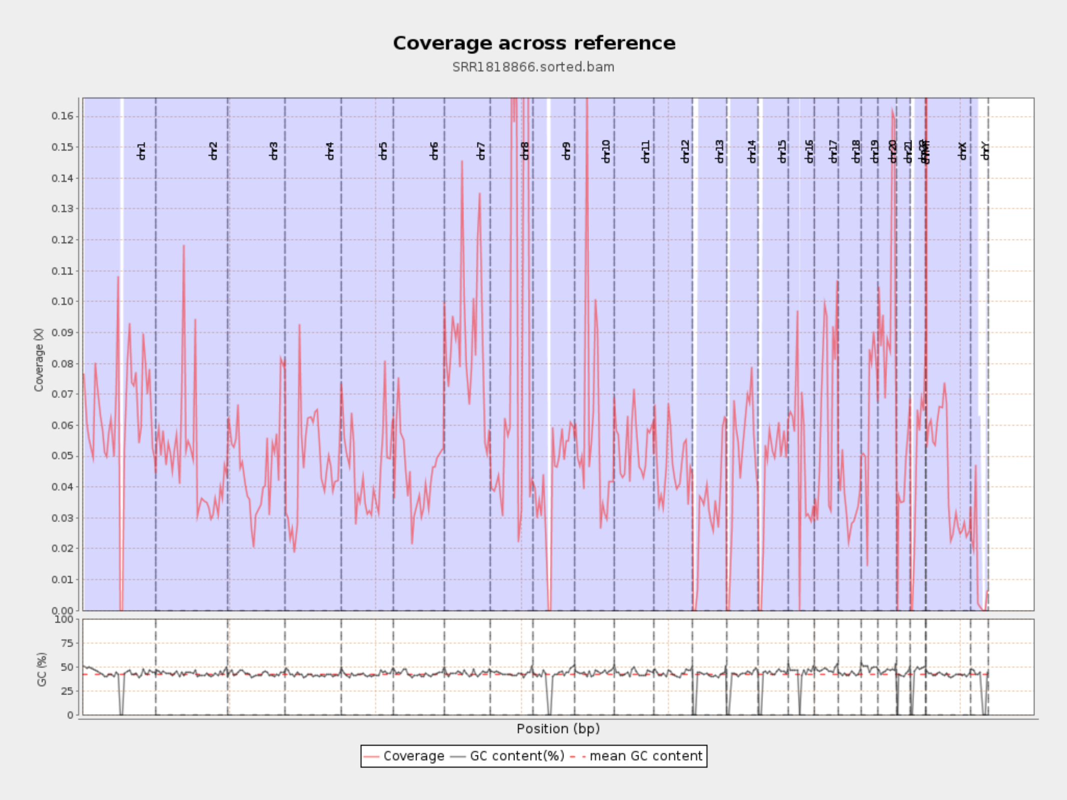
General error rate	0.66%
Mismatches	1,026,074
Insertions	25,740
Mapped reads with at least one insertion	1.38%
Deletions	51,171
Mapped reads with at least one deletion	2.78%
Homopolymer indels	39.7%

2.6. Chromosome stats

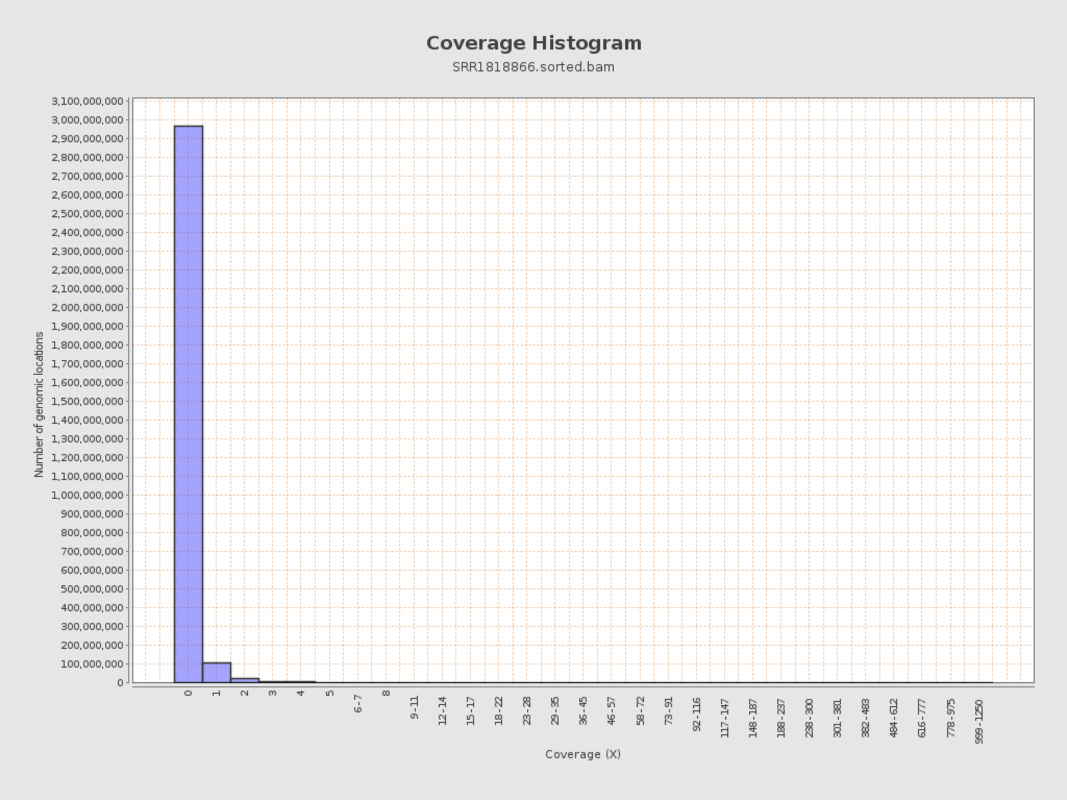
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15575357	0.0625	1.0149
chr2	243199373	11872151	0.0488	0.8902
chr3	198022430	9386657	0.0474	0.2778
chr4	191154276	9091370	0.0476	0.4081
chr5	180915260	8426237	0.0466	0.2807
chr6	171115067	7520225	0.0439	0.3005
chr7	159138663	13983486	0.0879	1.2659

chr8	146364022	14859708	0.1015	0.5244
chr9	141213431	5881894	0.0417	0.5382
chr10	135534747	7727563	0.057	1.1173
chr11	135006516	7218327	0.0535	0.3661
chr12	133851895	6292130	0.047	0.2677
chr13	115169878	3731101	0.0324	0.2174
chr14	107349540	5336940	0.0497	0.3076
chr15	102531392	4448287	0.0434	0.2528
chr16	90354753	4477681	0.0496	0.6701
chr17	81195210	5190226	0.0639	0.4306
chr18	78077248	2715695	0.0348	0.6039
chr19	59128983	3750737	0.0634	0.9816
chr20	63025520	6607736	0.1048	0.4446
chr21	48129895	2001512	0.0416	0.3299
chr22	51304566	2303946	0.0449	0.2908
chrMT	16571	457959	27.6362	17.819
chrX	155270560	6818977	0.0439	0.331
chrY	59373566	715920	0.0121	0.8918

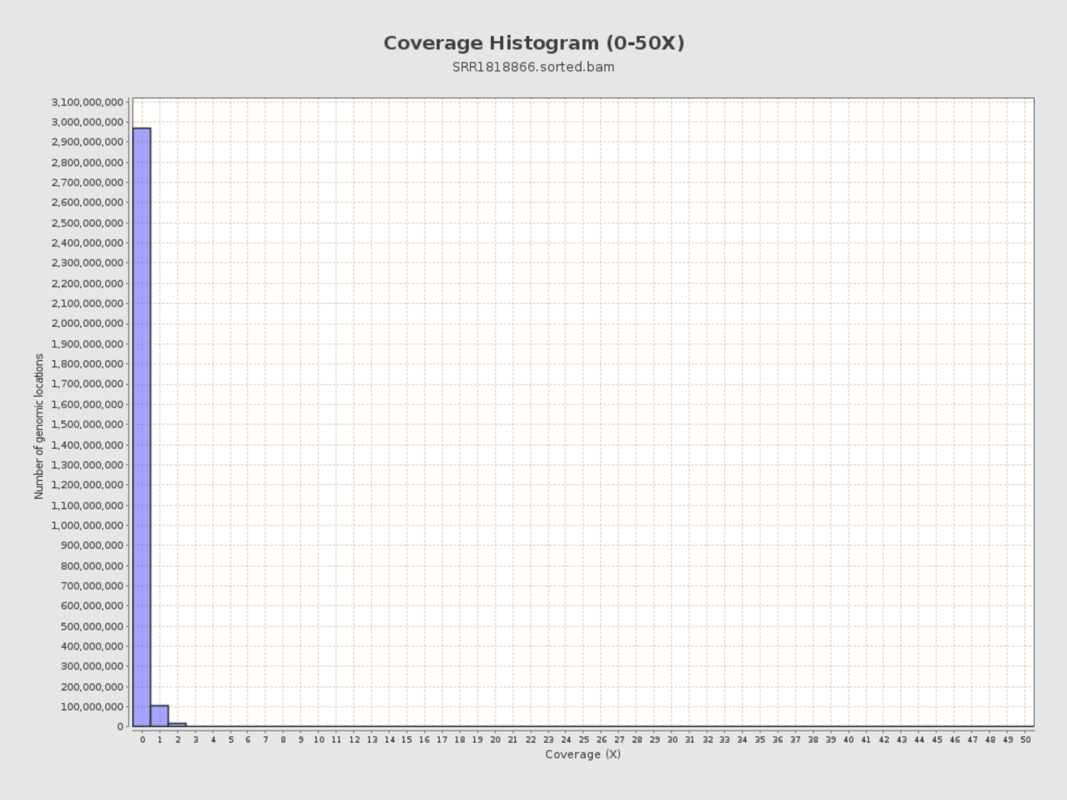
3. Results : Coverage across reference



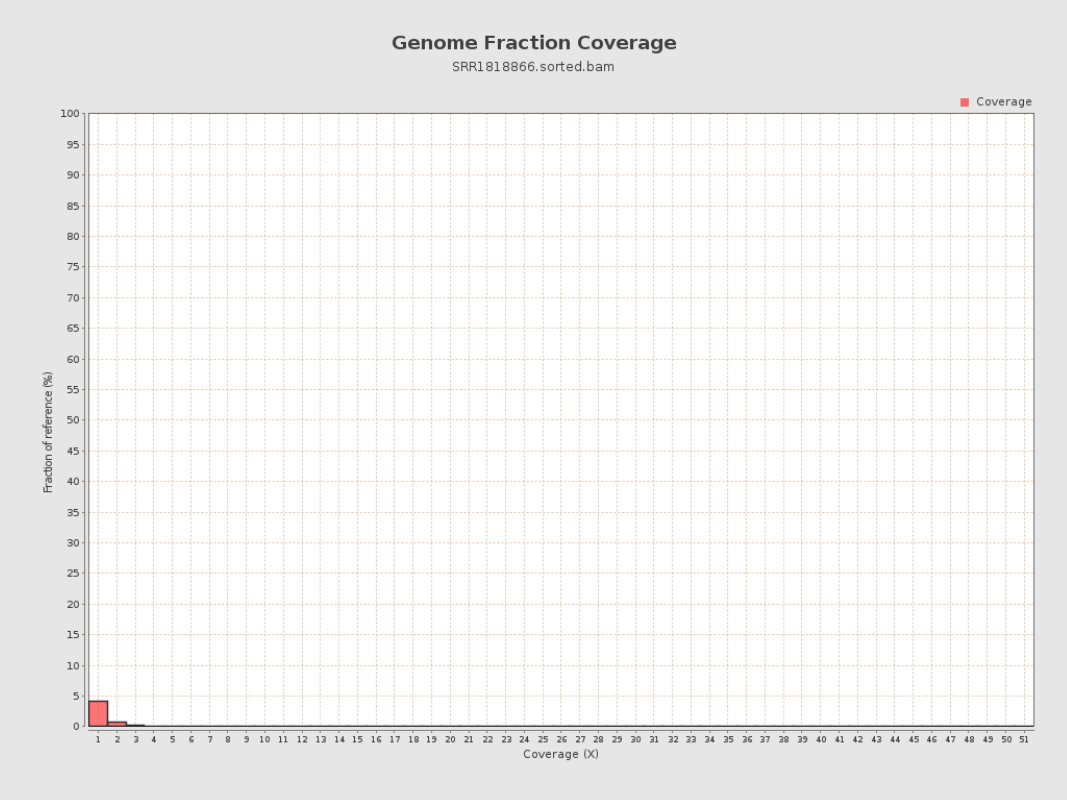
4. Results : Coverage Histogram



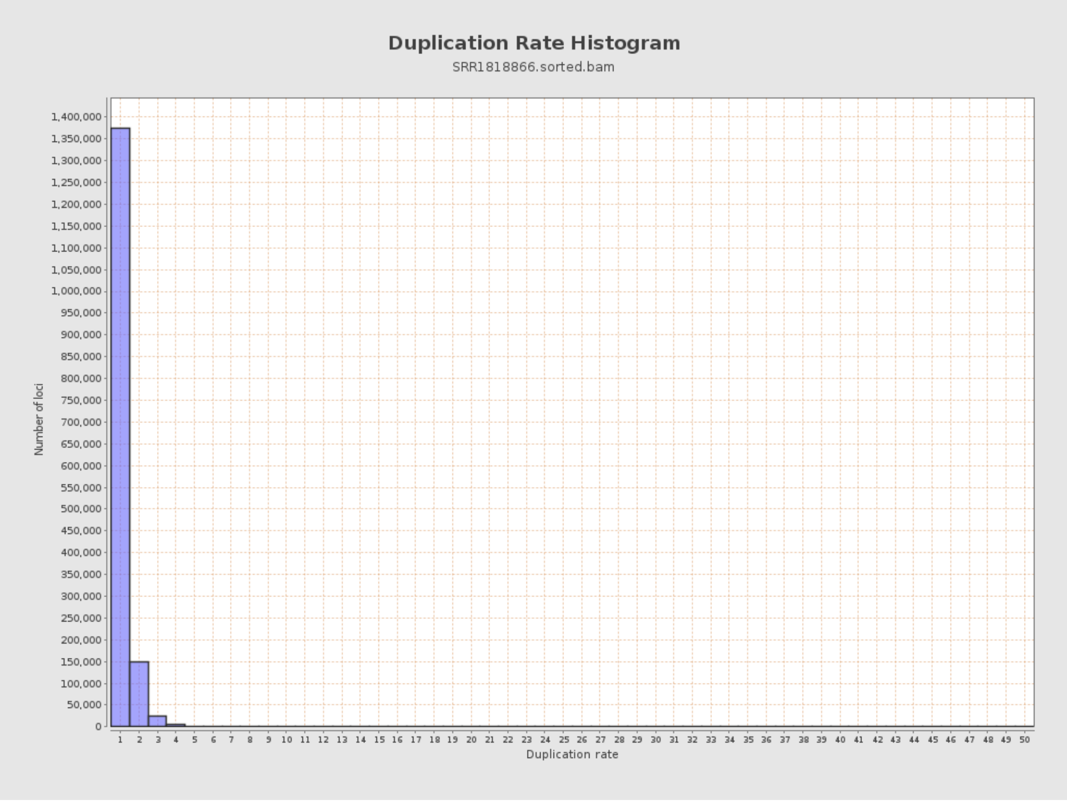
5. Results : Coverage Histogram (0-50X)



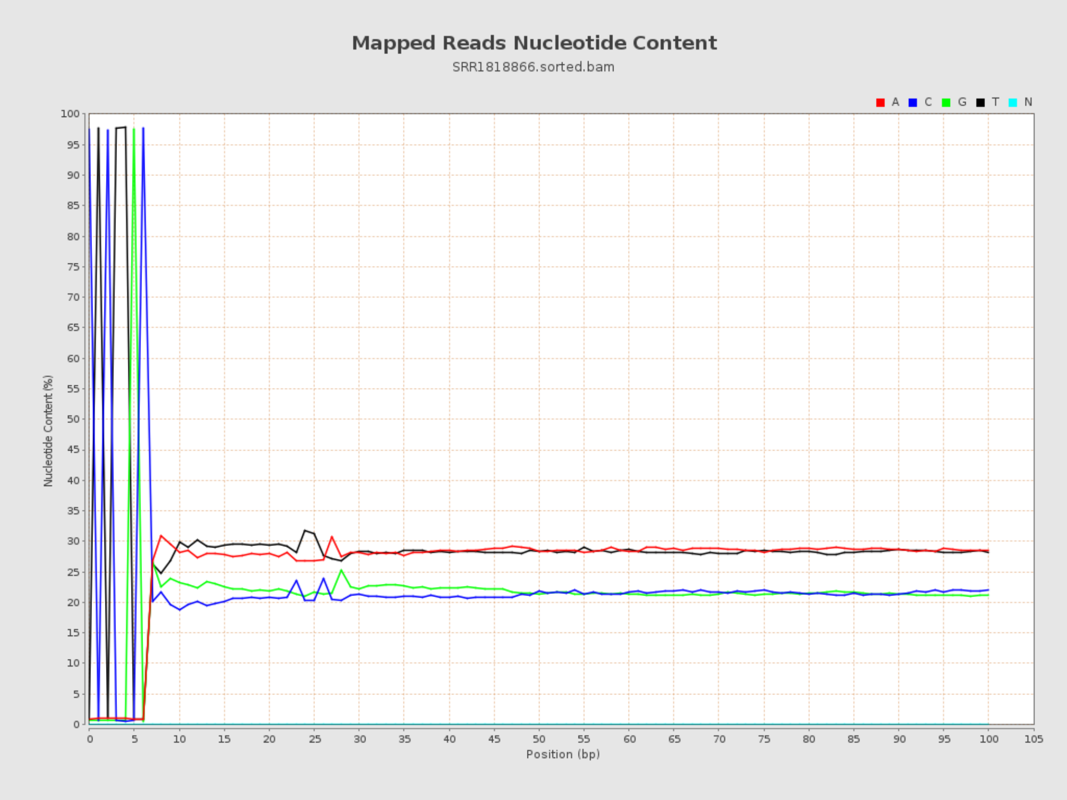
6. Results : Genome Fraction Coverage



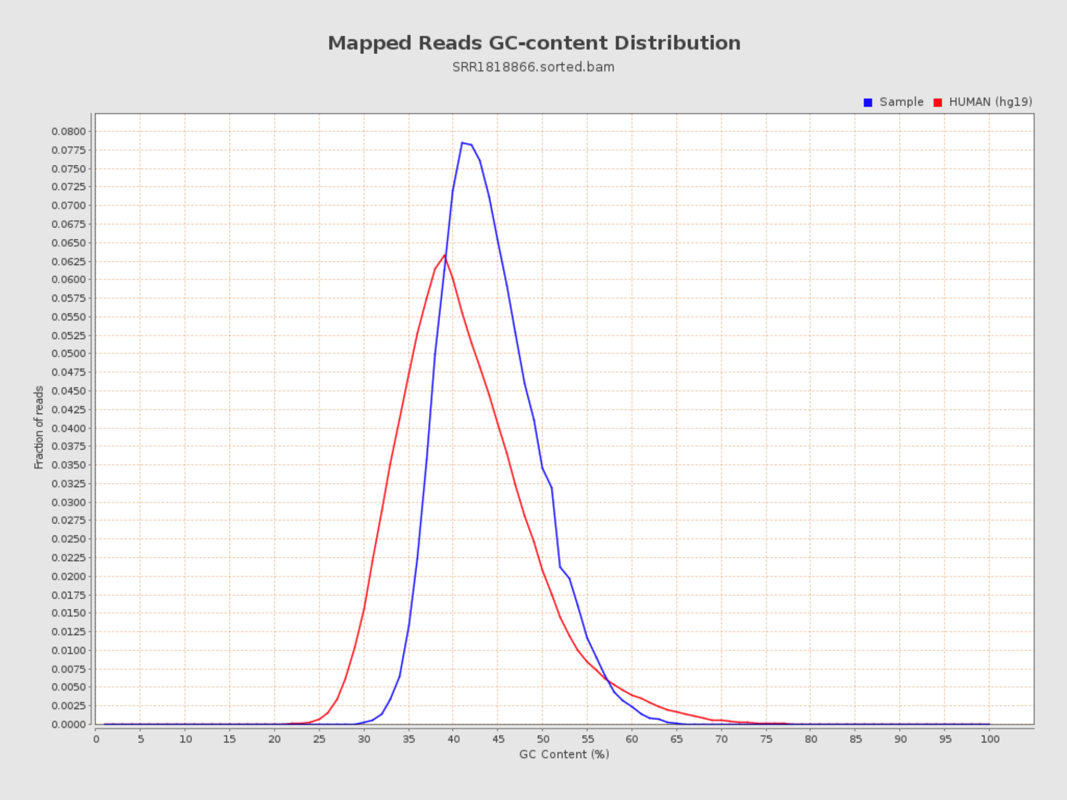
7. Results : Duplication Rate Histogram



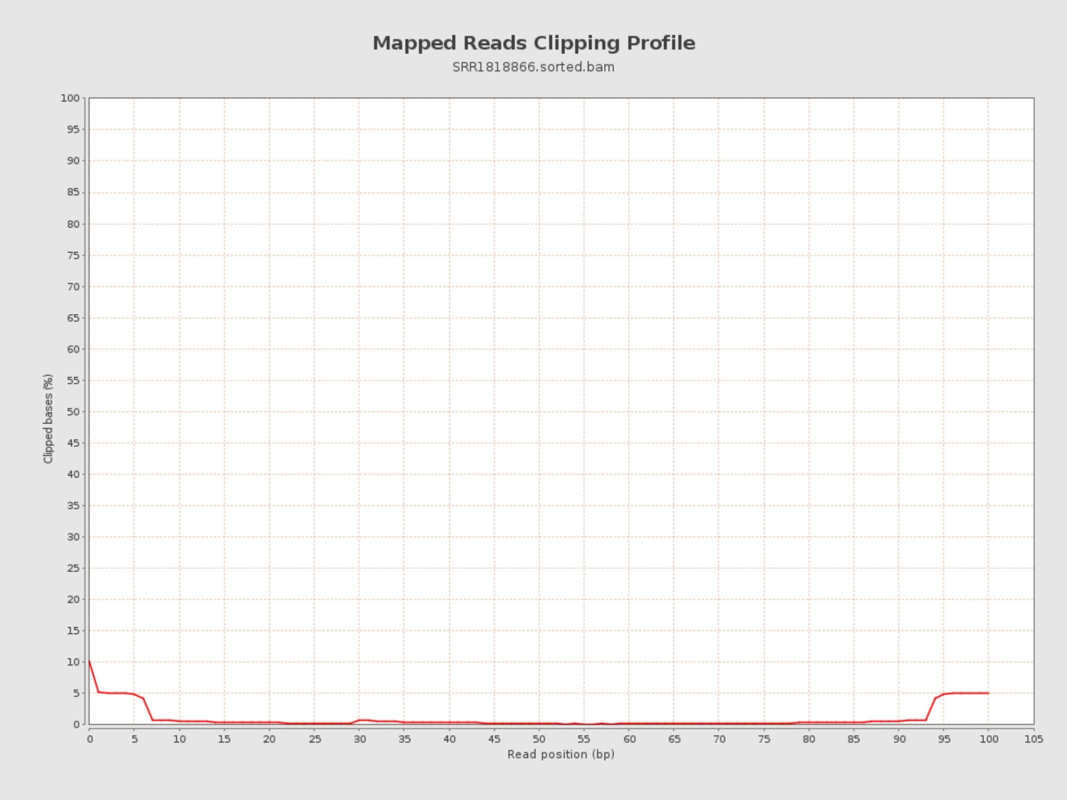
8. Results : Mapped Reads Nucleotide Content



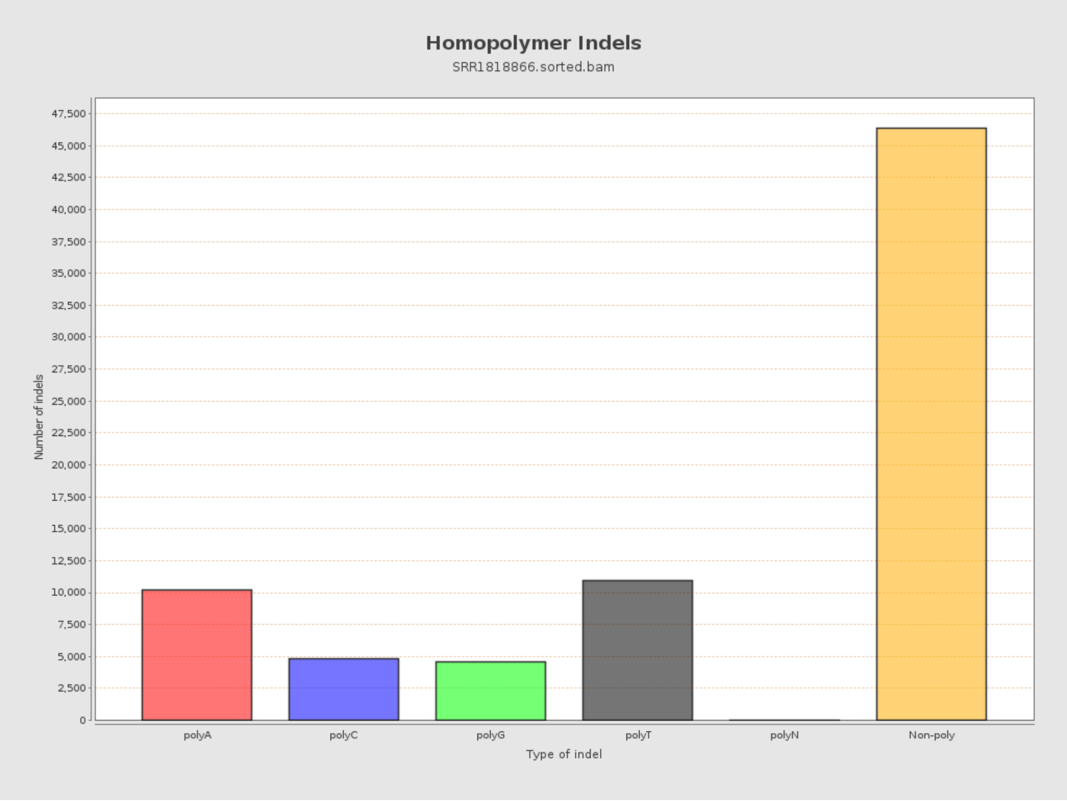
9. Results : Mapped Reads GC-content Distribution



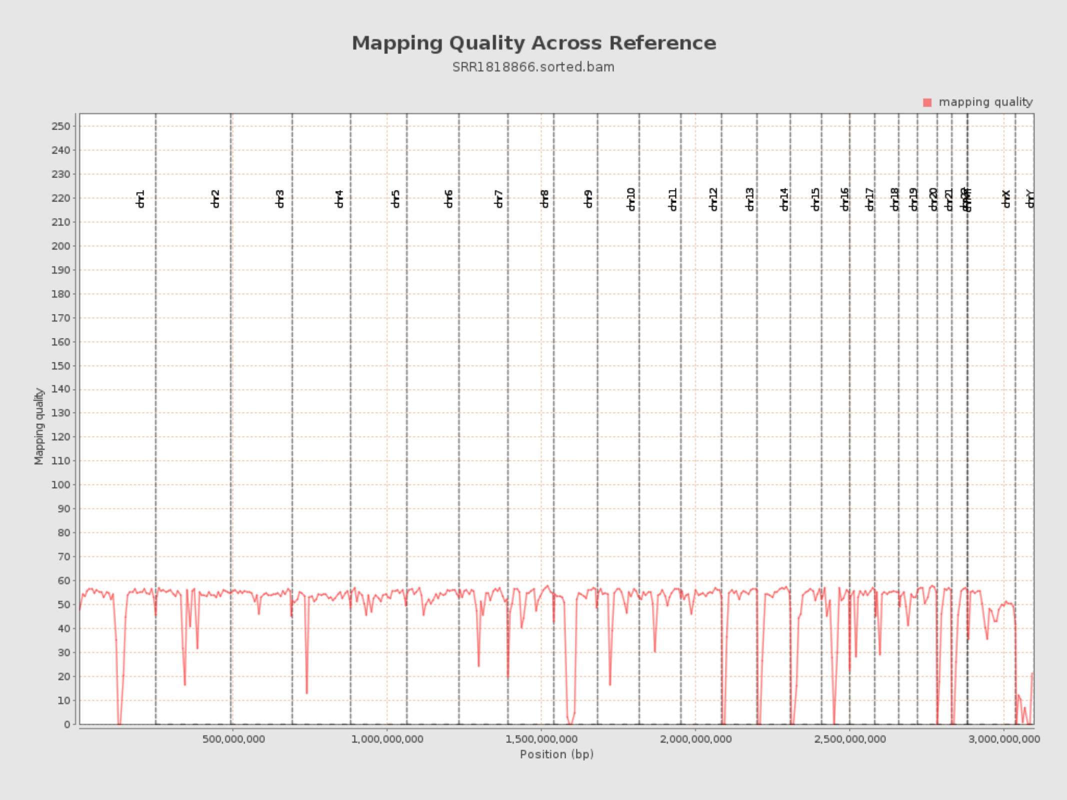
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram