Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 04:29:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818885.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_SRR1818885 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818885.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 04:29:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818885.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,916,636
Mapped reads	1,882,124 / 98.2%
Unmapped reads	34,512 / 1.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,595 / 1.54%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	372,546 / 19.44%
Duplication rate	16.57%
Clipped reads	1,903,603 / 99.32%

2.2. ACGT Content

Number/percentage of A's	50,626,831 / 29.1%
Number/percentage of C's	37,503,506 / 21.56%
Number/percentage of T's	49,453,648 / 28.42%
Number/percentage of G's	36,395,433 / 20.92%
Number/percentage of N's	2,622 / 0%
GC Percentage	42.48%

2.3. Coverage

Mean	0.0562

Standard Deviation	0.6961

2.4. Mapping Quality

Mean Mapping Quality	49.2

2.5. Mismatches and indels

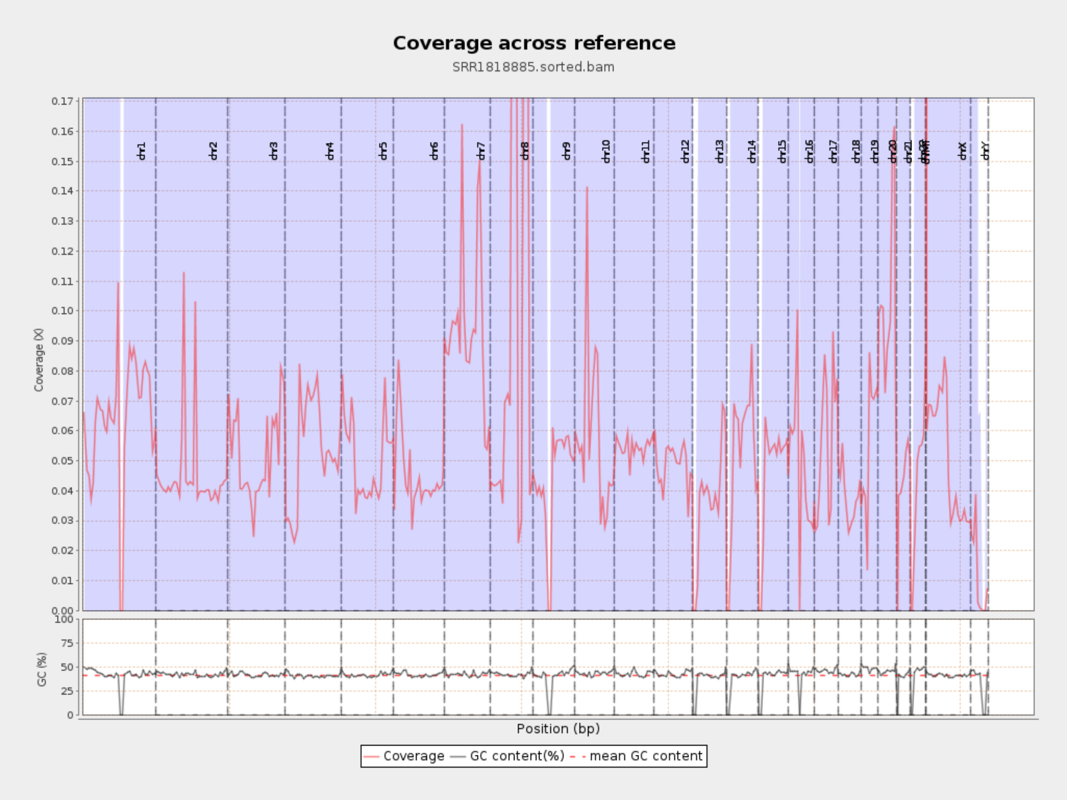
General error rate	0.65%
Mismatches	1,066,756
Insertions	24,335
Mapped reads with at least one insertion	1.25%
Deletions	57,693
Mapped reads with at least one deletion	2.99%
Homopolymer indels	41.05%

2.6. Chromosome stats

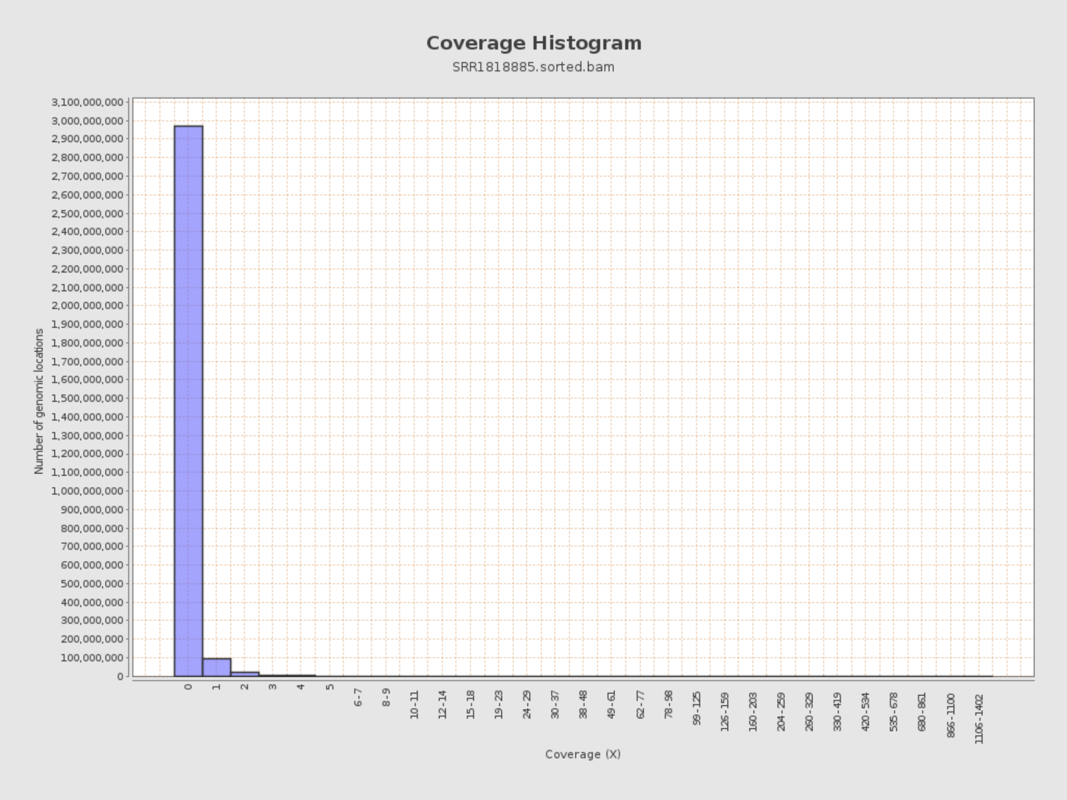
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15983756	0.0641	1.0899
chr2	243199373	11105766	0.0457	1.0012
chr3	198022430	10325554	0.0521	0.2961
chr4	191154276	10307581	0.0539	0.4077
chr5	180915260	9218971	0.051	0.3181
chr6	171115067	7710549	0.0451	0.3189
chr7	159138663	15065621	0.0947	1.4812

chr8	146364022	17068449	0.1166	0.5878
chr9	141213431	6219462	0.044	0.5404
chr10	135534747	7752141	0.0572	0.9351
chr11	135006516	7341208	0.0544	0.3947
chr12	133851895	6578710	0.0491	0.2907
chr13	115169878	4242231	0.0368	0.2463
chr14	107349540	5690771	0.053	0.336
chr15	102531392	4645029	0.0453	0.2739
chr16	90354753	4245617	0.047	0.7765
chr17	81195210	4499831	0.0554	0.4202
chr18	78077248	2992050	0.0383	0.6211
chr19	59128983	3303044	0.0559	0.9981
chr20	63025520	6812945	0.1081	0.4686
chr21	48129895	2048479	0.0426	0.318
chr22	51304566	2025414	0.0395	0.2998
chrMT	16571	269866	16.2854	10.5845
chrX	155270560	7948773	0.0512	0.3727
chrY	59373566	693716	0.0117	0.8848

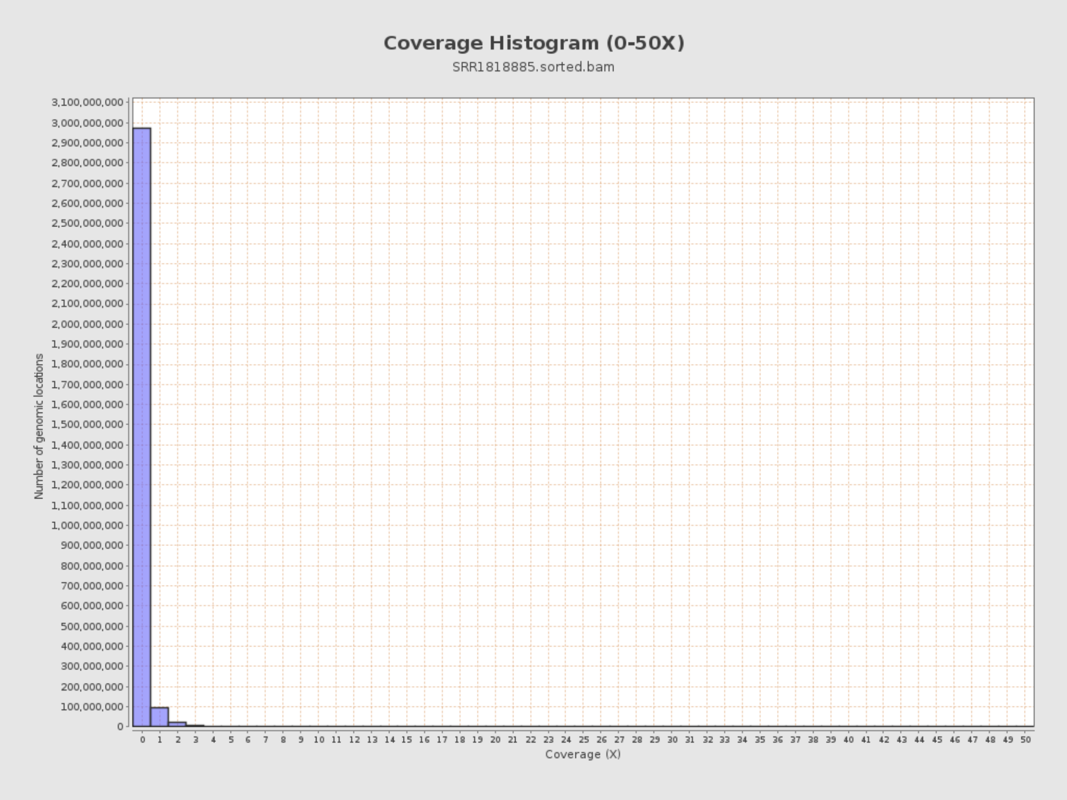
3. Results : Coverage across reference



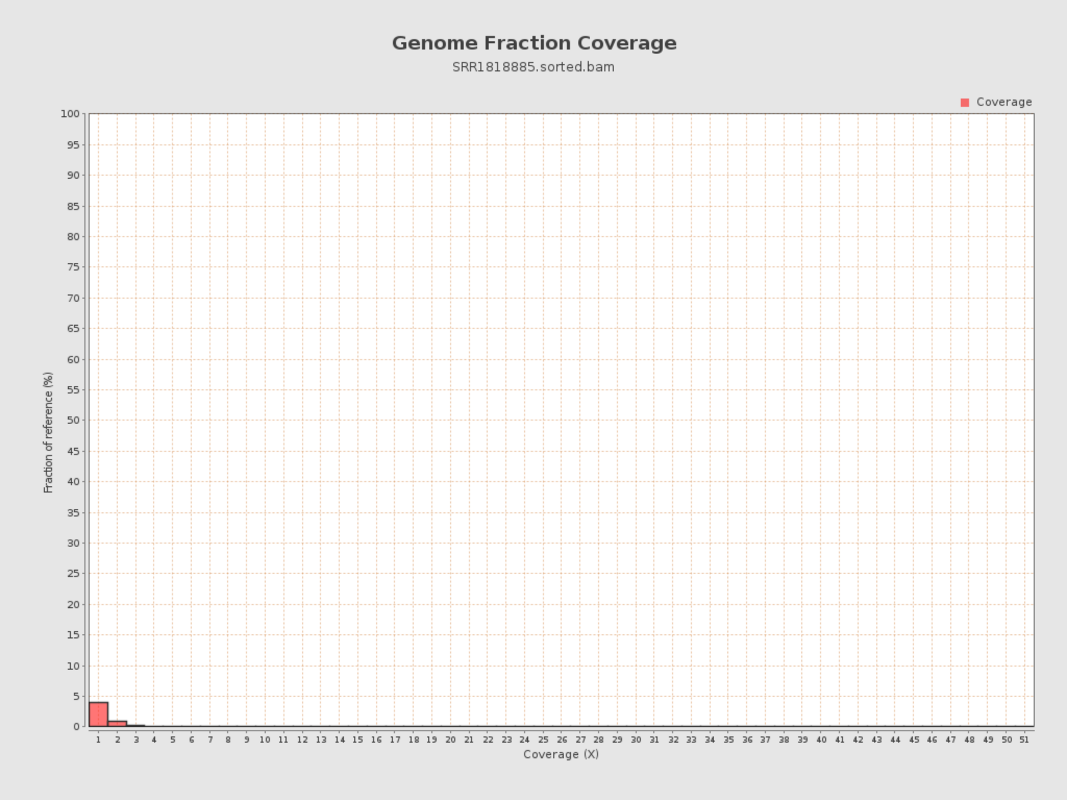
4. Results : Coverage Histogram



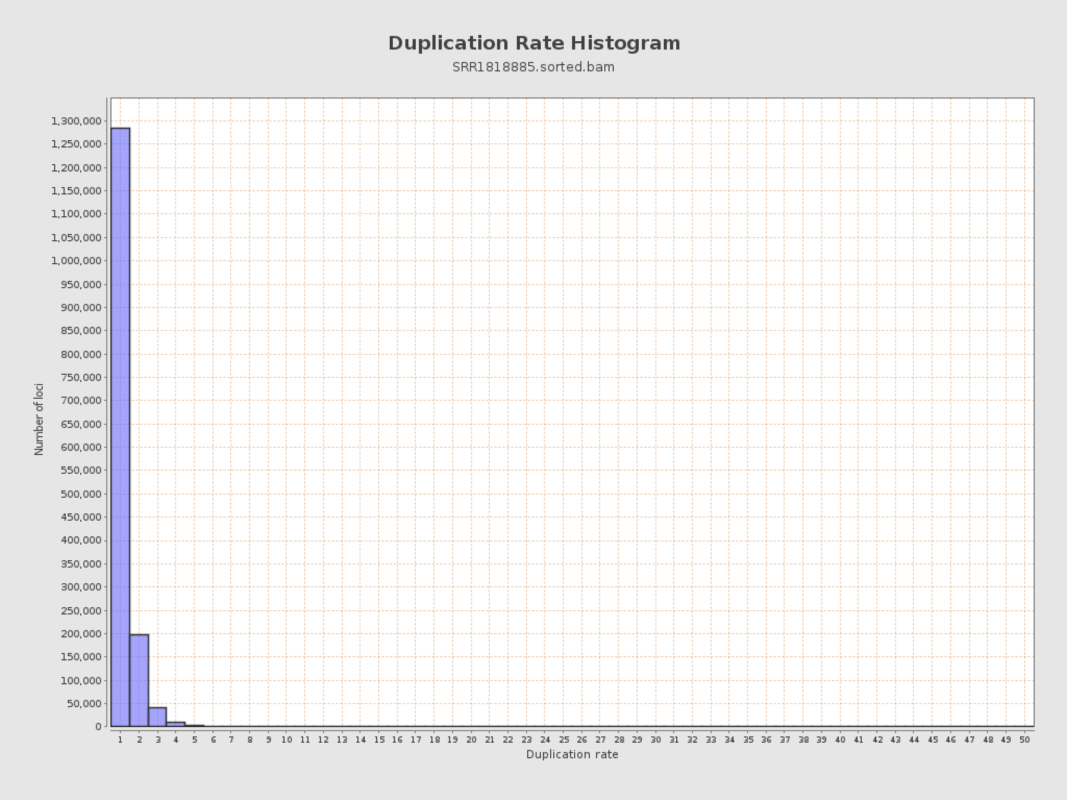
5. Results : Coverage Histogram (0-50X)



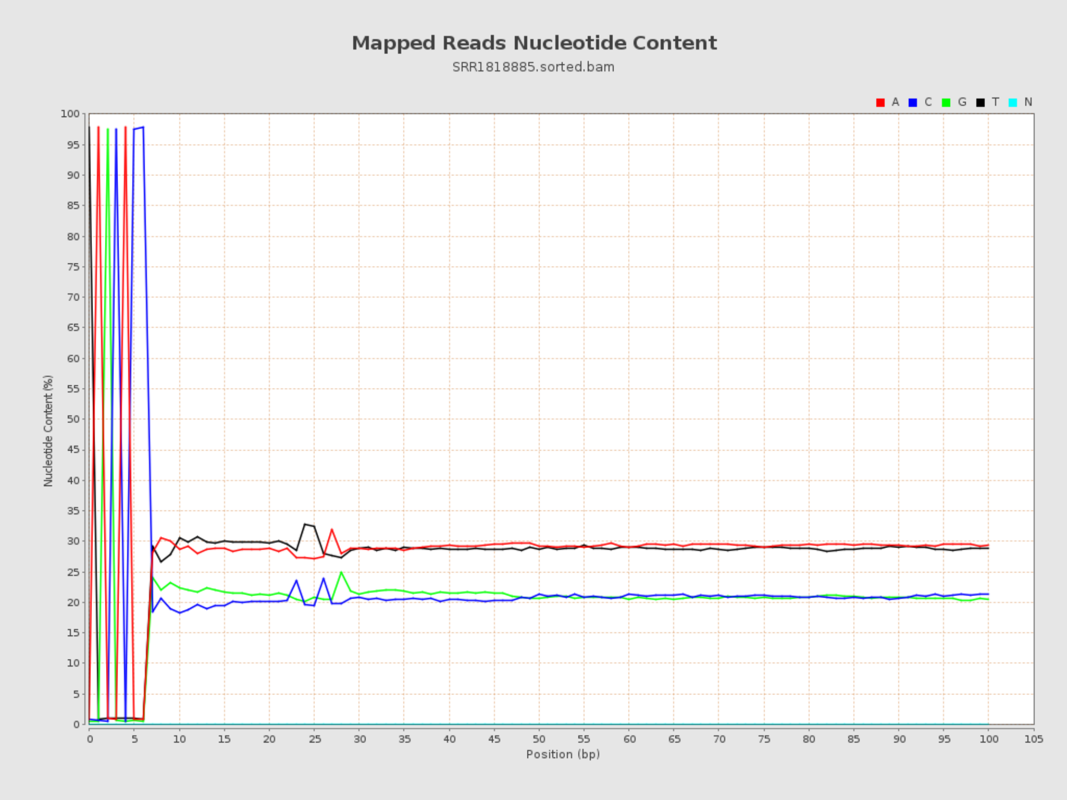
6. Results : Genome Fraction Coverage



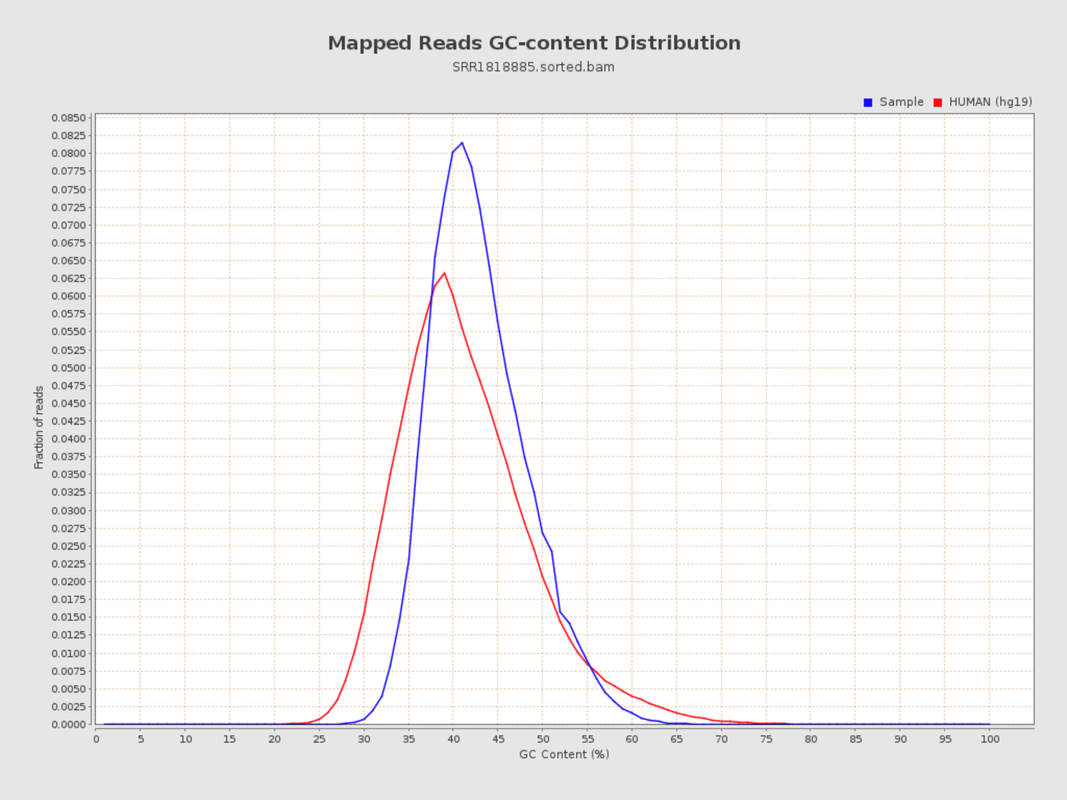
7. Results : Duplication Rate Histogram



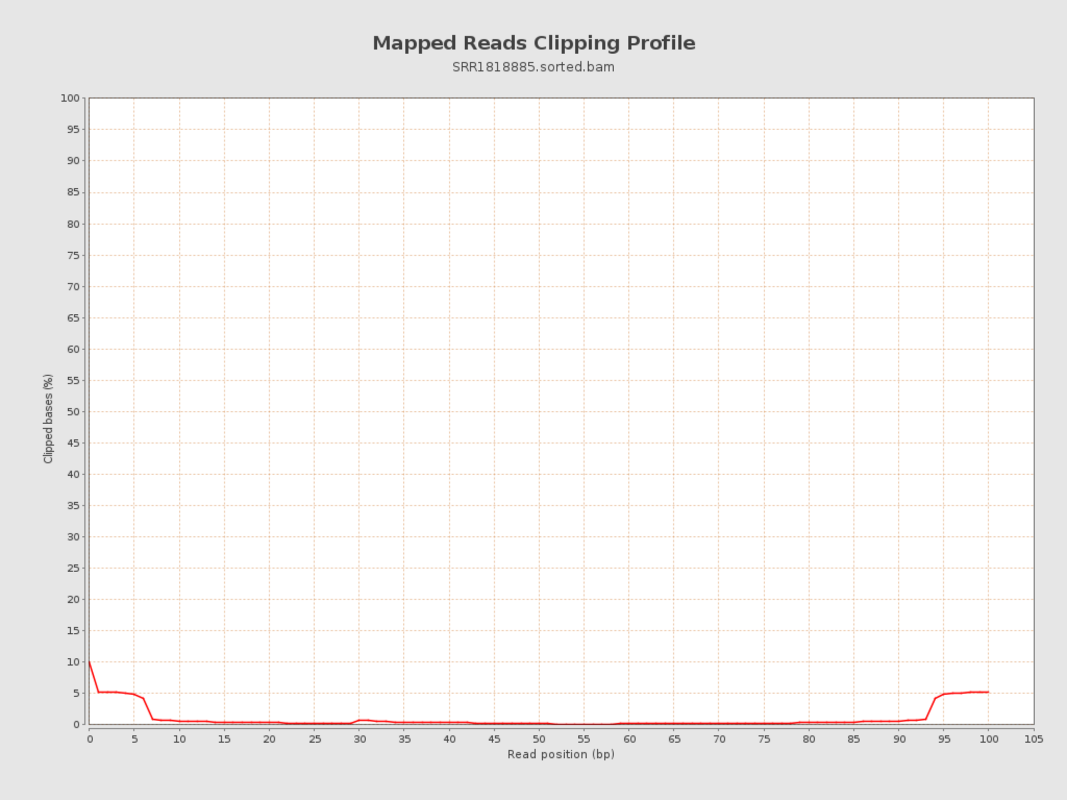
8. Results : Mapped Reads Nucleotide Content



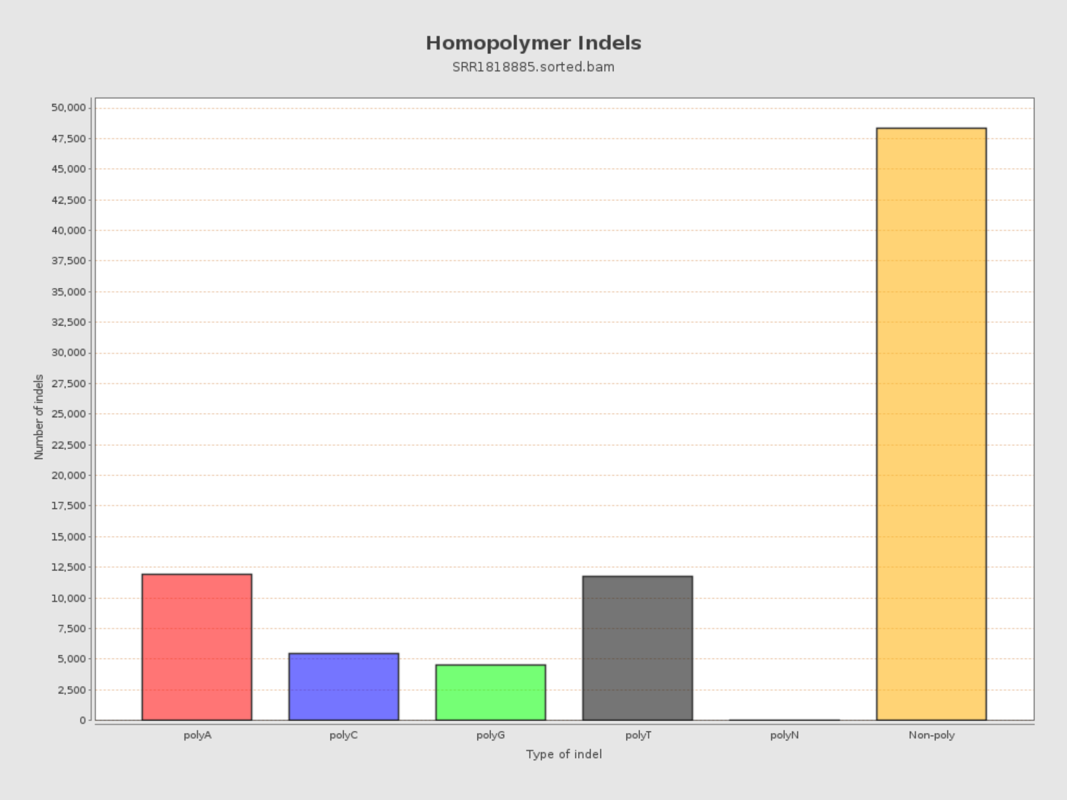
9. Results : Mapped Reads GC-content Distribution



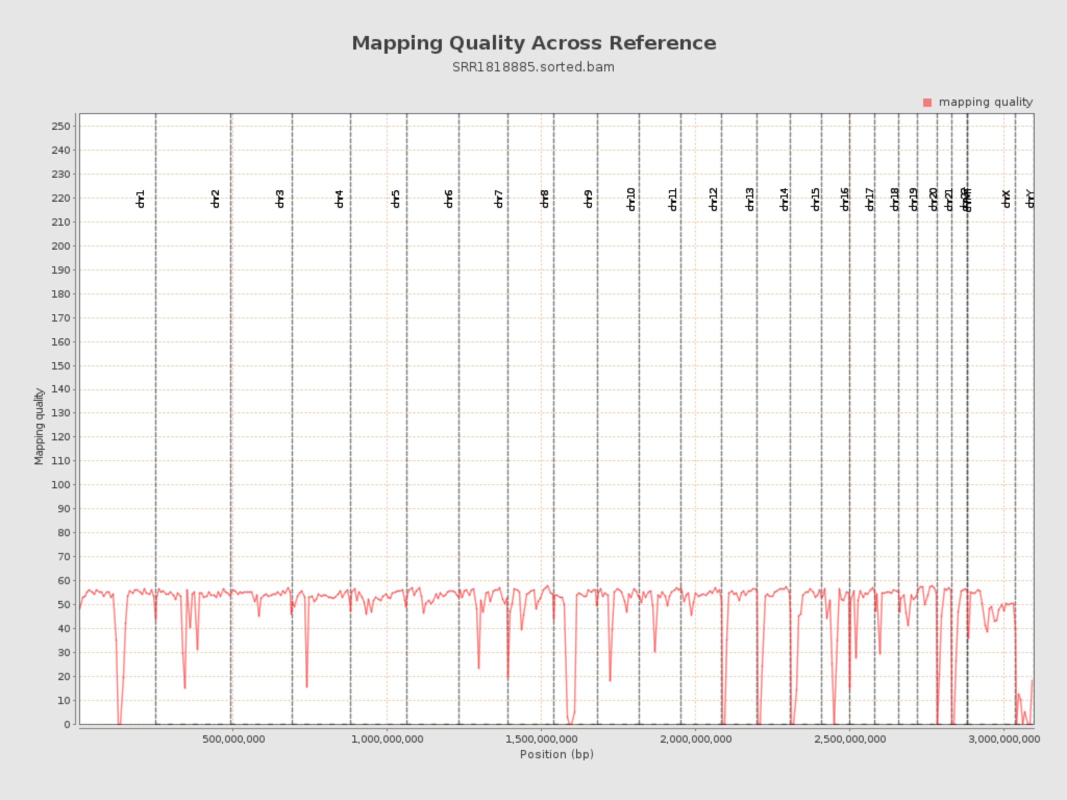
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram