Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:03:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818889.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_SRR1818889 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818889.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:03:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818889.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,045,805
Mapped reads	2,017,204 / 98.6%
Unmapped reads	28,601 / 1.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,662 / 1.5%
Read min/max/mean length	30 / 101 / 101.58
Duplicated reads (estimated)	316,013 / 15.45%
Duplication rate	12.36%
Clipped reads	2,017,516 / 98.62%

2.2. ACGT Content

Number/percentage of A's	53,350,855 / 28.56%
Number/percentage of C's	38,661,605 / 20.7%
Number/percentage of T's	52,480,943 / 28.1%
Number/percentage of G's	42,296,851 / 22.64%
Number/percentage of N's	2,509 / 0%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.7894

2.4. Mapping Quality

Mean Mapping Quality	49.23

2.5. Mismatches and indels

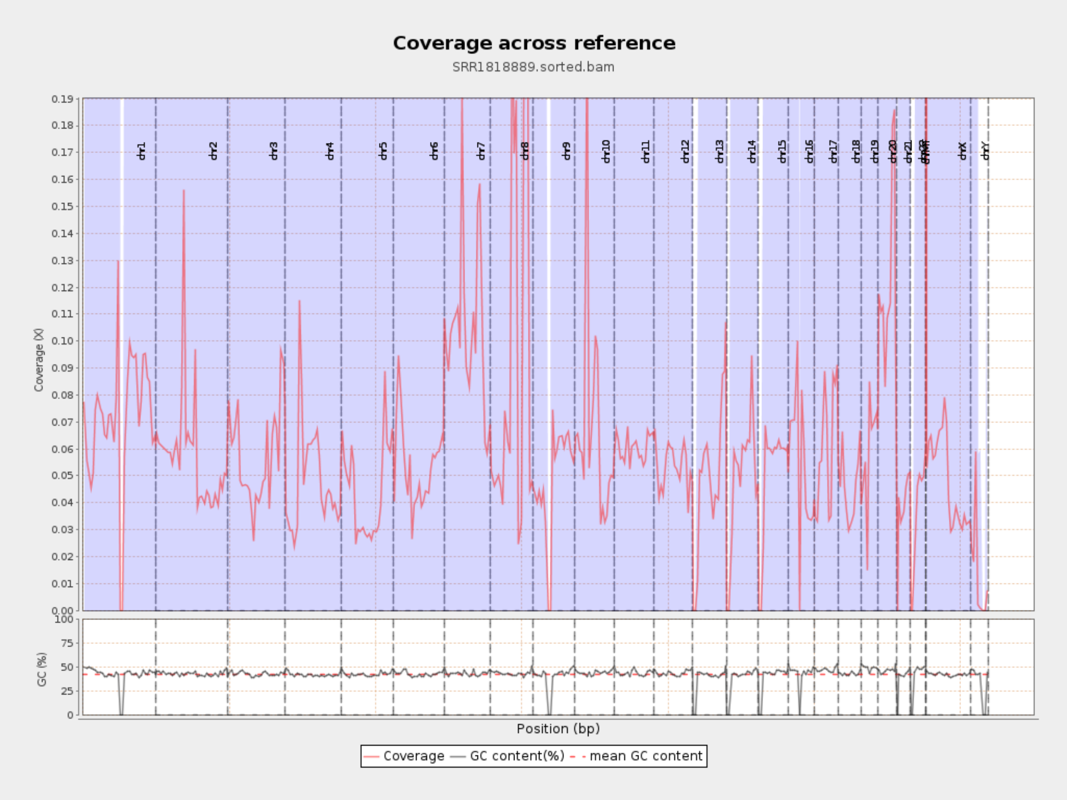
General error rate	0.65%
Mismatches	1,144,606
Insertions	28,803
Mapped reads with at least one insertion	1.39%
Deletions	55,721
Mapped reads with at least one deletion	2.7%
Homopolymer indels	39.01%

2.6. Chromosome stats

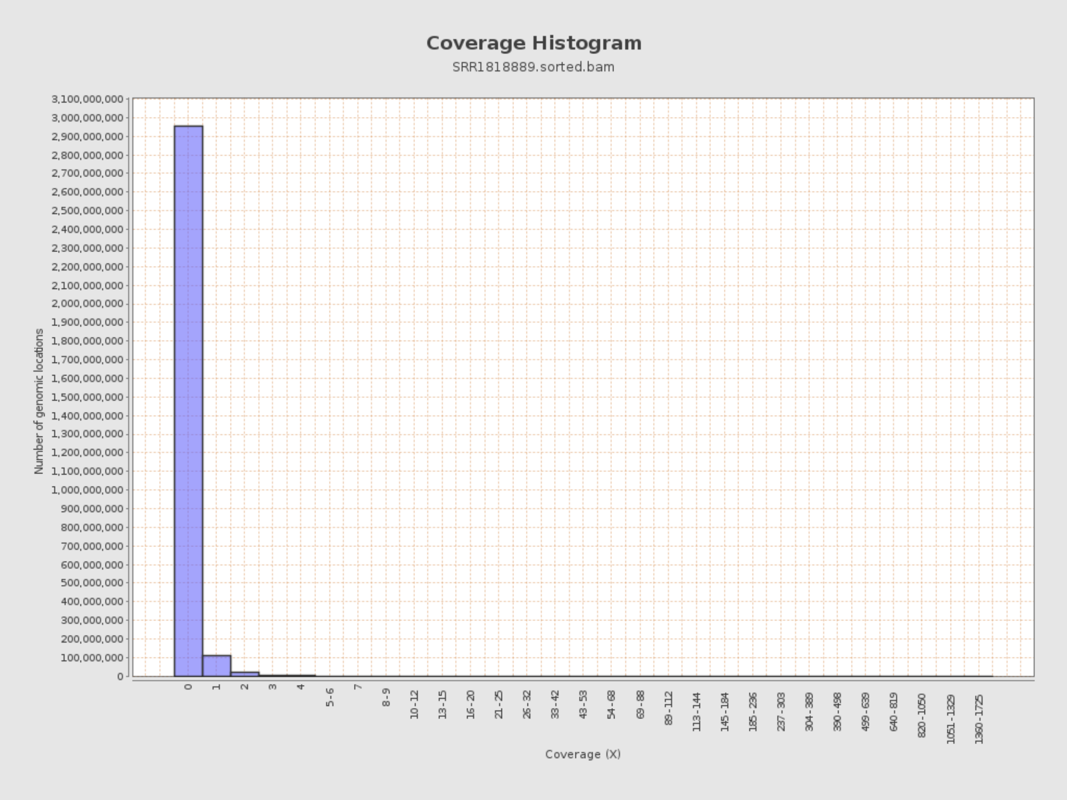
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17819355	0.0715	1.2912
chr2	243199373	14052072	0.0578	0.91
chr3	198022430	11347969	0.0573	0.3049
chr4	191154276	9324521	0.0488	0.4716
chr5	180915260	8153901	0.0451	0.2754
chr6	171115067	9179502	0.0536	0.3415
chr7	159138663	16665597	0.1047	1.7475

chr8	146364022	16040363	0.1096	0.6373
chr9	141213431	6844699	0.0485	0.6765
chr10	135534747	9074547	0.067	1.3785
chr11	135006516	8154222	0.0604	0.4336
chr12	133851895	7194563	0.0538	0.2905
chr13	115169878	5590748	0.0485	0.2719
chr14	107349540	5407185	0.0504	0.3077
chr15	102531392	5089748	0.0496	0.2755
chr16	90354753	4886578	0.0541	0.6226
chr17	81195210	4861155	0.0599	0.5163
chr18	78077248	3593778	0.046	0.803
chr19	59128983	3453363	0.0584	1.0976
chr20	63025520	7917917	0.1256	0.4992
chr21	48129895	1861655	0.0387	0.391
chr22	51304566	1765949	0.0344	0.2531
chrMT	16571	278128	16.784	10.0977
chrX	155270560	7546981	0.0486	0.3837
chrY	59373566	801129	0.0135	0.9316

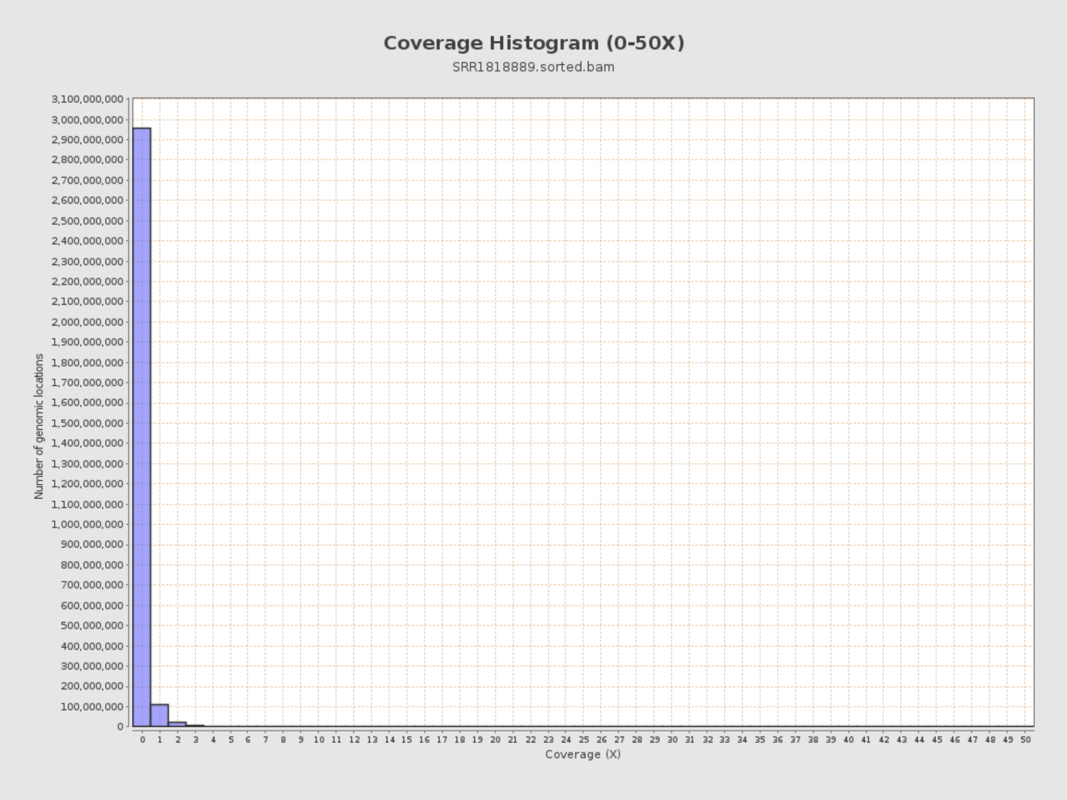
3. Results : Coverage across reference



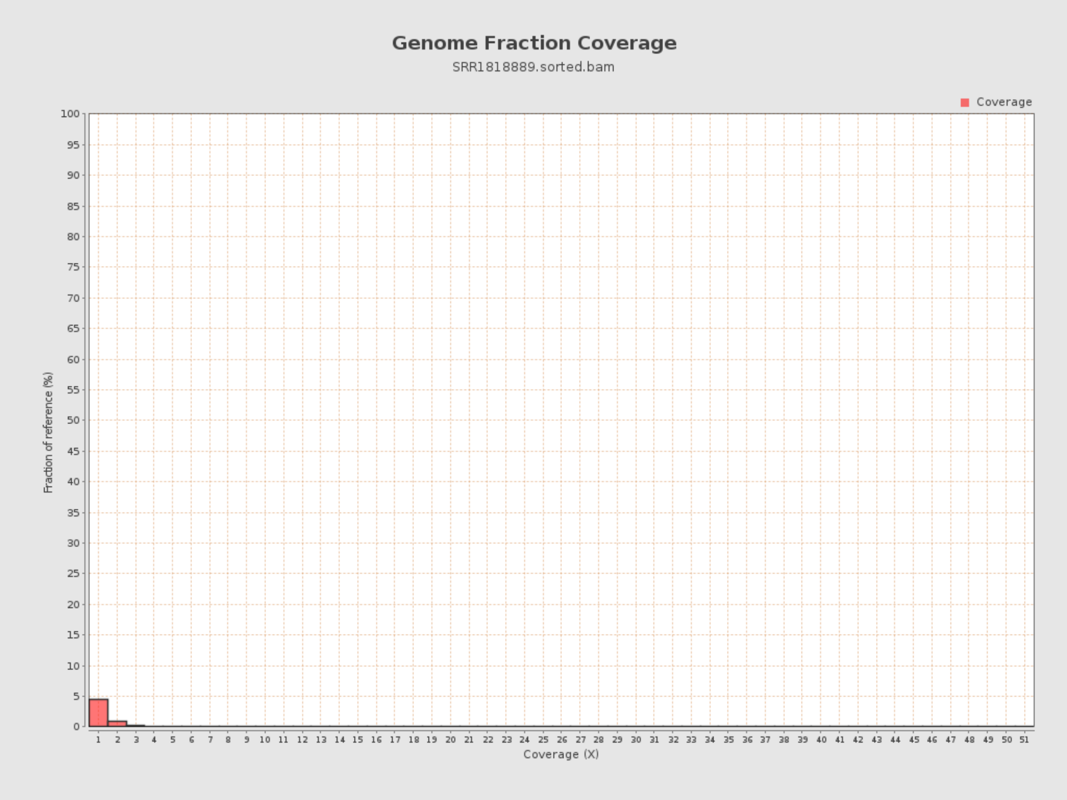
4. Results : Coverage Histogram



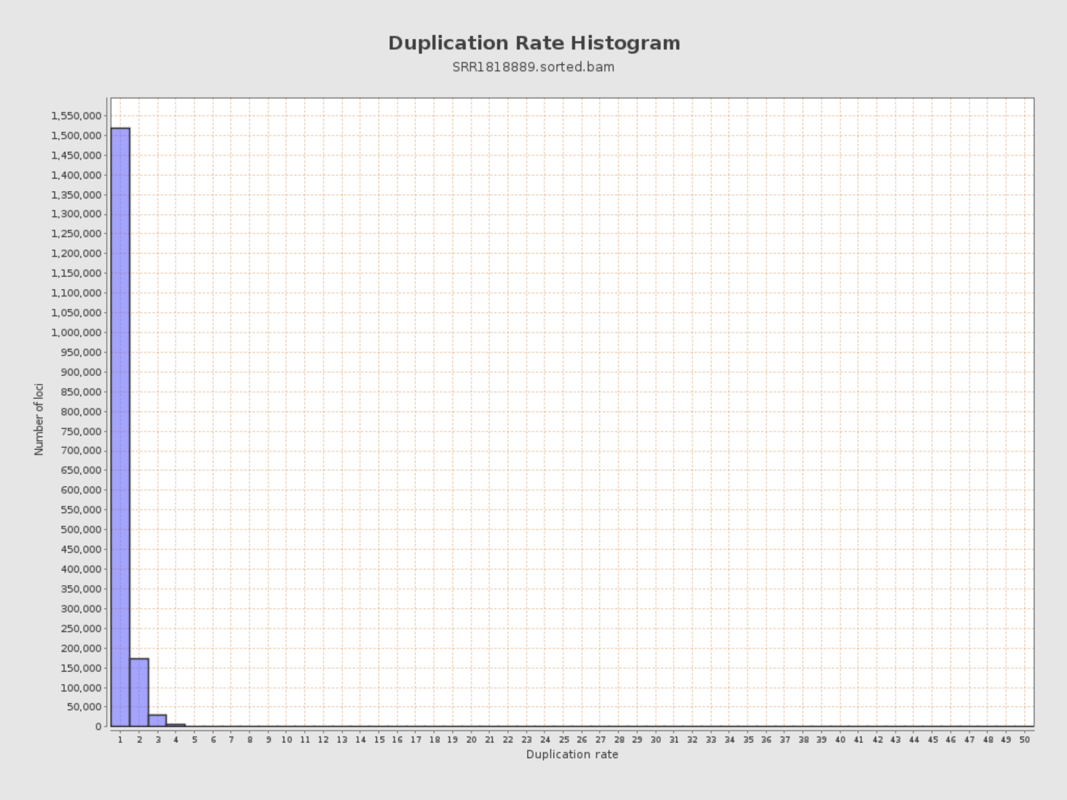
5. Results : Coverage Histogram (0-50X)



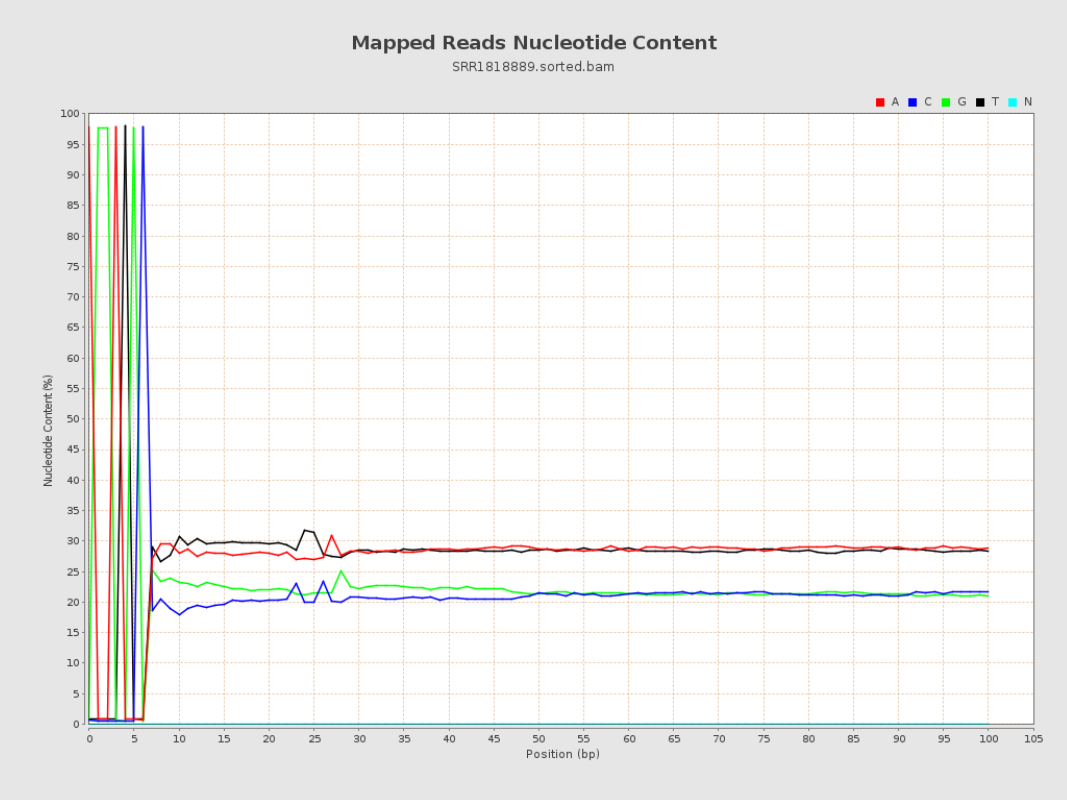
6. Results : Genome Fraction Coverage



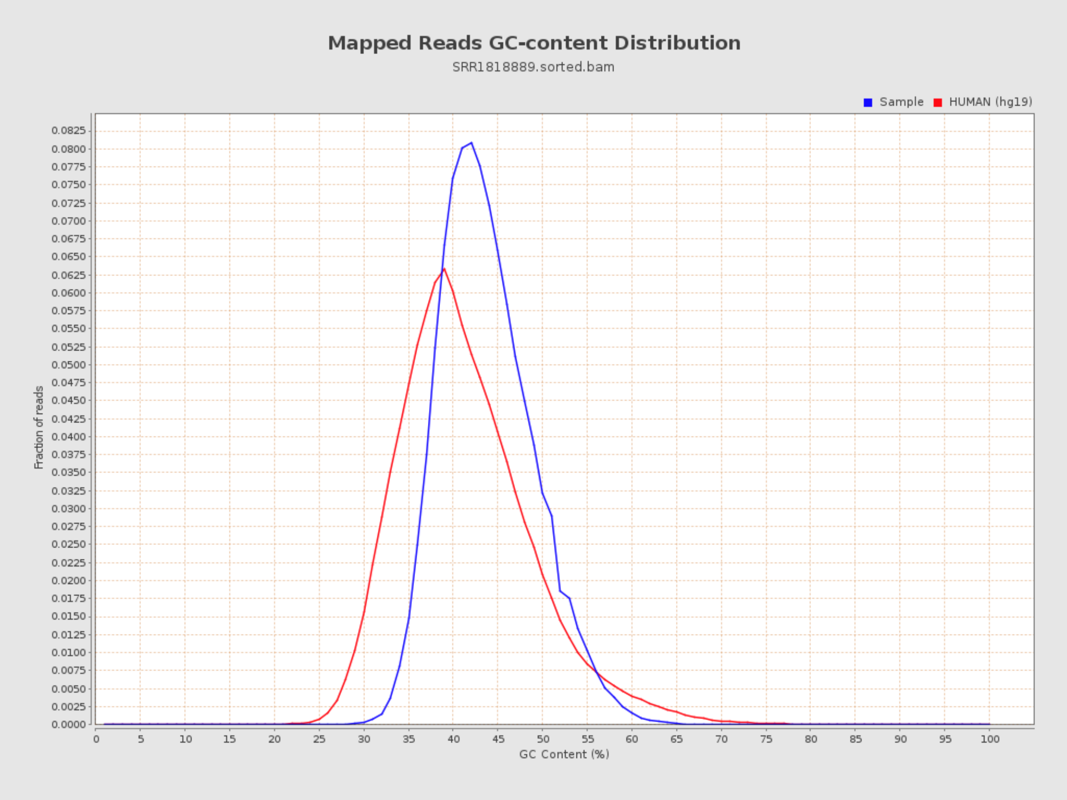
7. Results : Duplication Rate Histogram



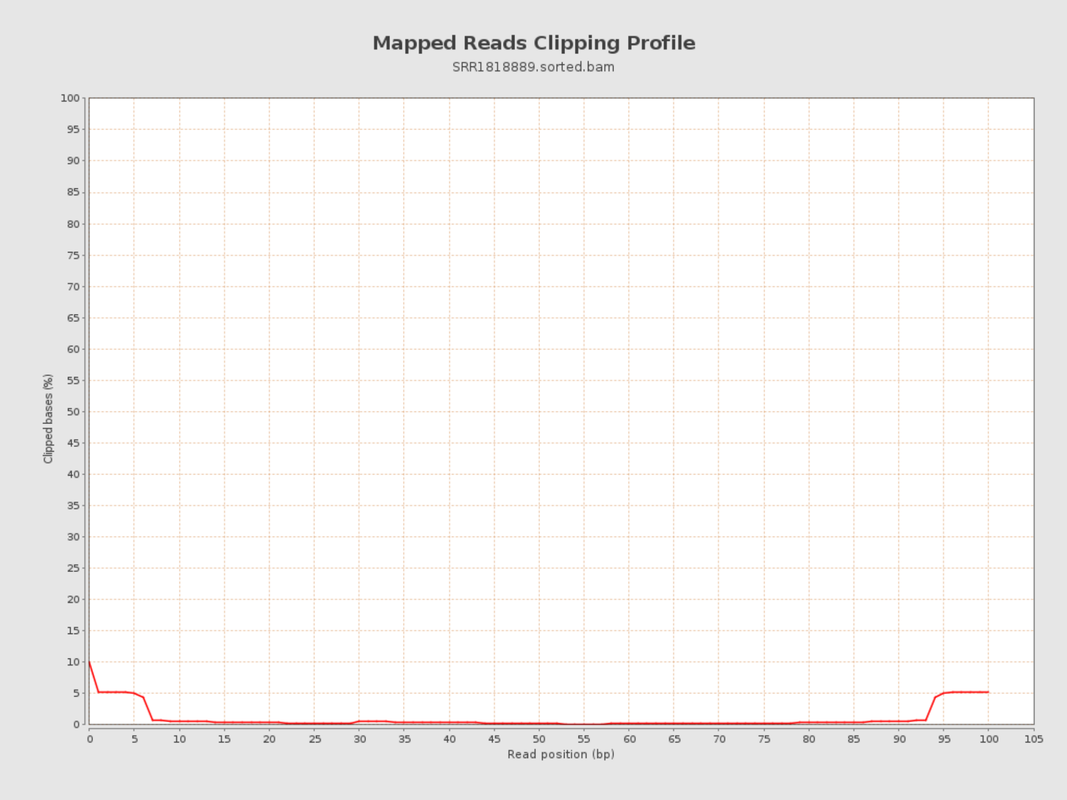
8. Results : Mapped Reads Nucleotide Content



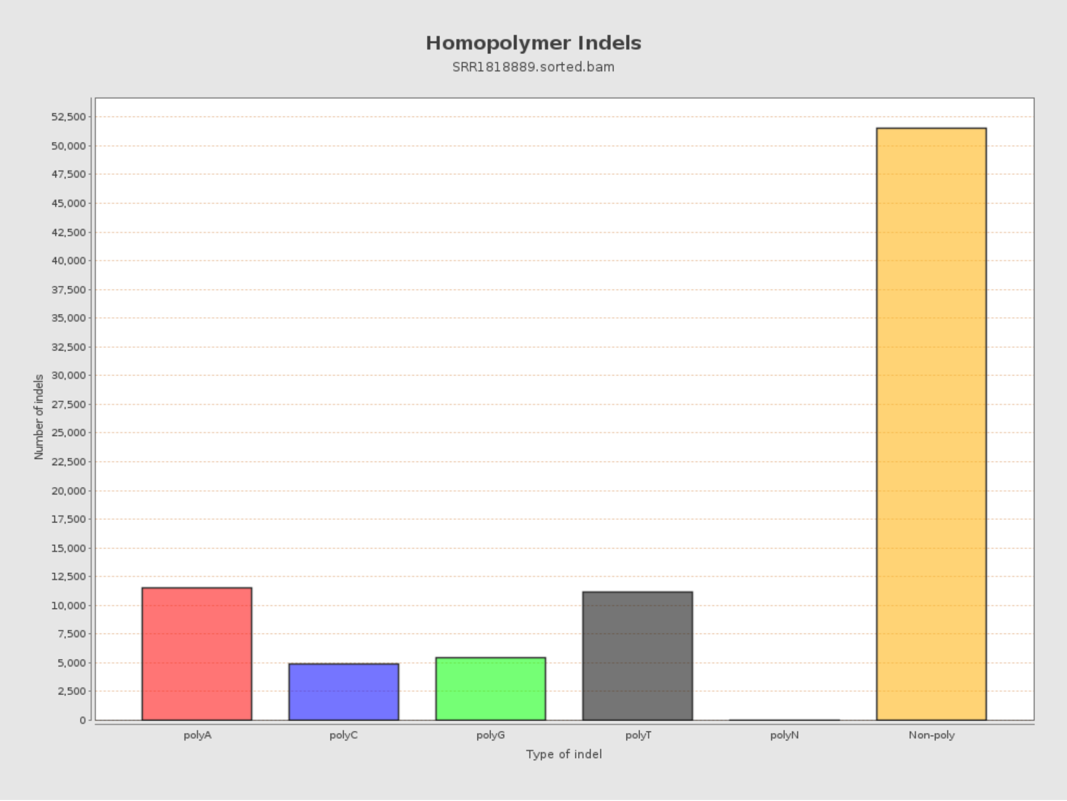
9. Results : Mapped Reads GC-content Distribution



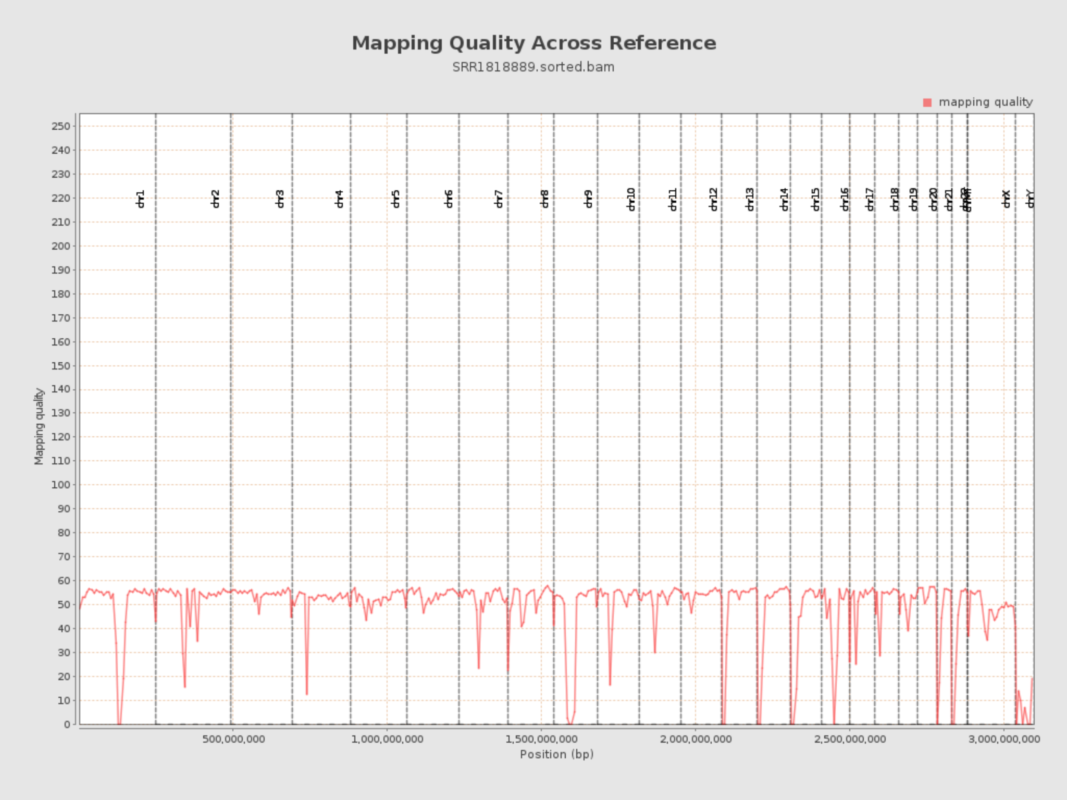
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram