Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 01:02:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818860.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_SRR1818860 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818860.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 01:01:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818860.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	747,751
Mapped reads	683,054 / 91.35%
Unmapped reads	64,697 / 8.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,606 / 1.69%
Read min/max/mean length	30 / 101 / 101.65
Duplicated reads (estimated)	116,286 / 15.55%
Duplication rate	14.47%
Clipped reads	689,913 / 92.27%

2.2. ACGT Content

Number/percentage of A's	18,110,864 / 28.7%
Number/percentage of C's	12,747,890 / 20.2%
Number/percentage of T's	18,399,333 / 29.16%
Number/percentage of G's	13,835,990 / 21.93%
Number/percentage of N's	983 / 0%
GC Percentage	42.13%

2.3. Coverage

Mean	0.0204

Standard Deviation	0.2714

2.4. Mapping Quality

Mean Mapping Quality	49.09

2.5. Mismatches and indels

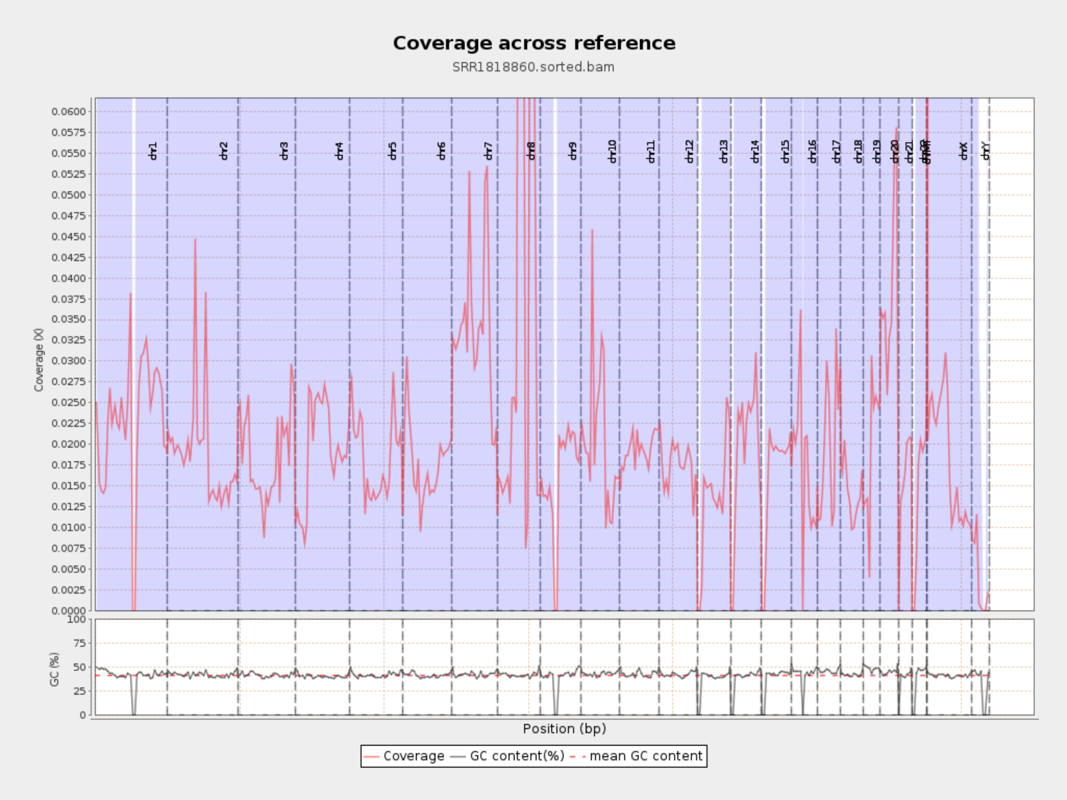
General error rate	0.65%
Mismatches	390,251
Insertions	8,944
Mapped reads with at least one insertion	1.27%
Deletions	21,534
Mapped reads with at least one deletion	3.07%
Homopolymer indels	41.38%

2.6. Chromosome stats

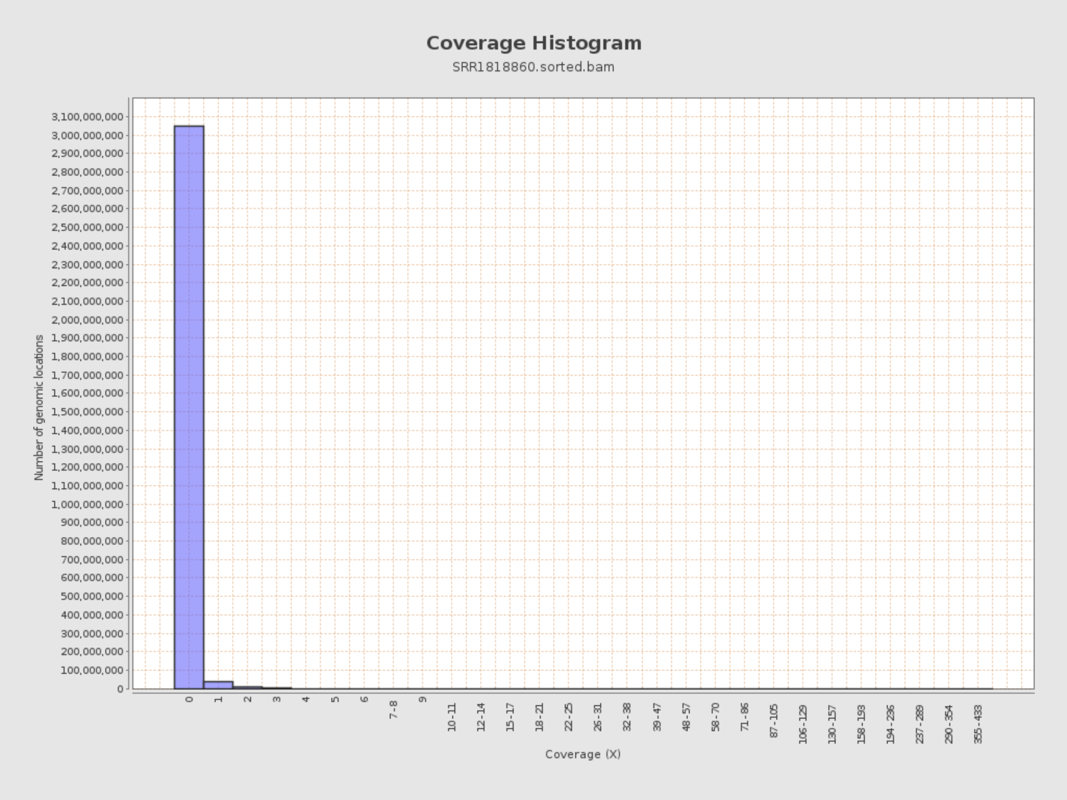
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5673608	0.0228	0.3941
chr2	243199373	4587478	0.0189	0.3876
chr3	198022430	3681976	0.0186	0.1704
chr4	191154276	3698429	0.0193	0.1903
chr5	180915260	3323721	0.0184	0.1717
chr6	171115067	2989655	0.0175	0.1727
chr7	159138663	5416567	0.034	0.4827

chr8	146364022	6074031	0.0415	0.2892
chr9	141213431	2247802	0.0159	0.2267
chr10	135534747	2783584	0.0205	0.3346
chr11	135006516	2612554	0.0194	0.1924
chr12	133851895	2334151	0.0174	0.1634
chr13	115169878	1556509	0.0135	0.143
chr14	107349540	2056154	0.0192	0.1796
chr15	102531392	1652375	0.0161	0.1536
chr16	90354753	1527971	0.0169	0.2882
chr17	81195210	1622383	0.02	0.2002
chr18	78077248	1094318	0.014	0.2593
chr19	59128983	1140281	0.0193	0.3415
chr20	63025520	2455053	0.039	0.2545
chr21	48129895	761052	0.0158	0.1686
chr22	51304566	706923	0.0138	0.1578
chrMT	16571	63937	3.8584	3.4255
chrX	155270560	2853318	0.0184	0.1883
chrY	59373566	223178	0.0038	0.3022

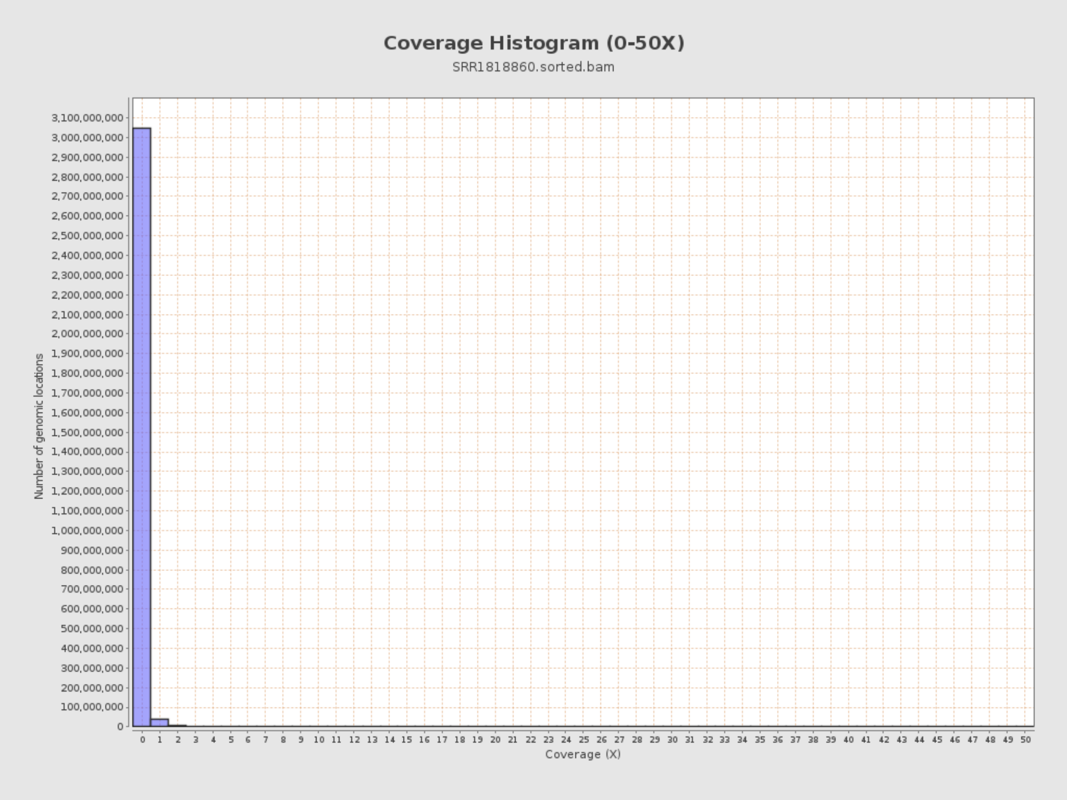
3. Results : Coverage across reference



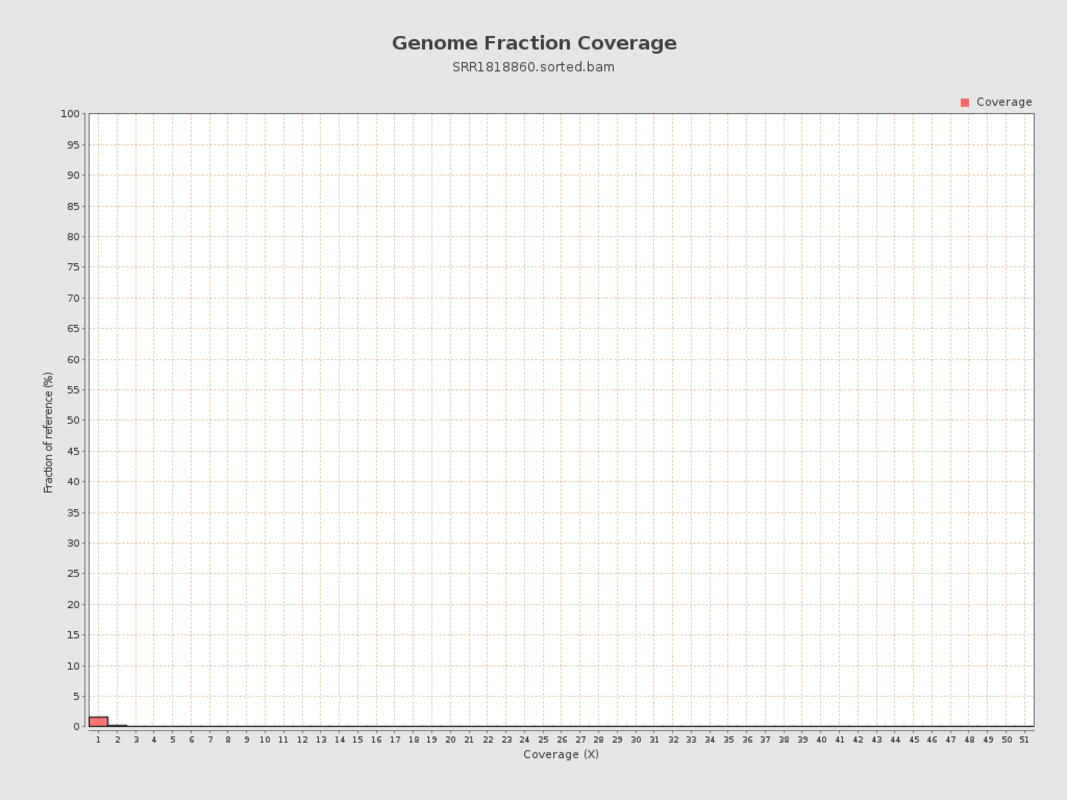
4. Results : Coverage Histogram



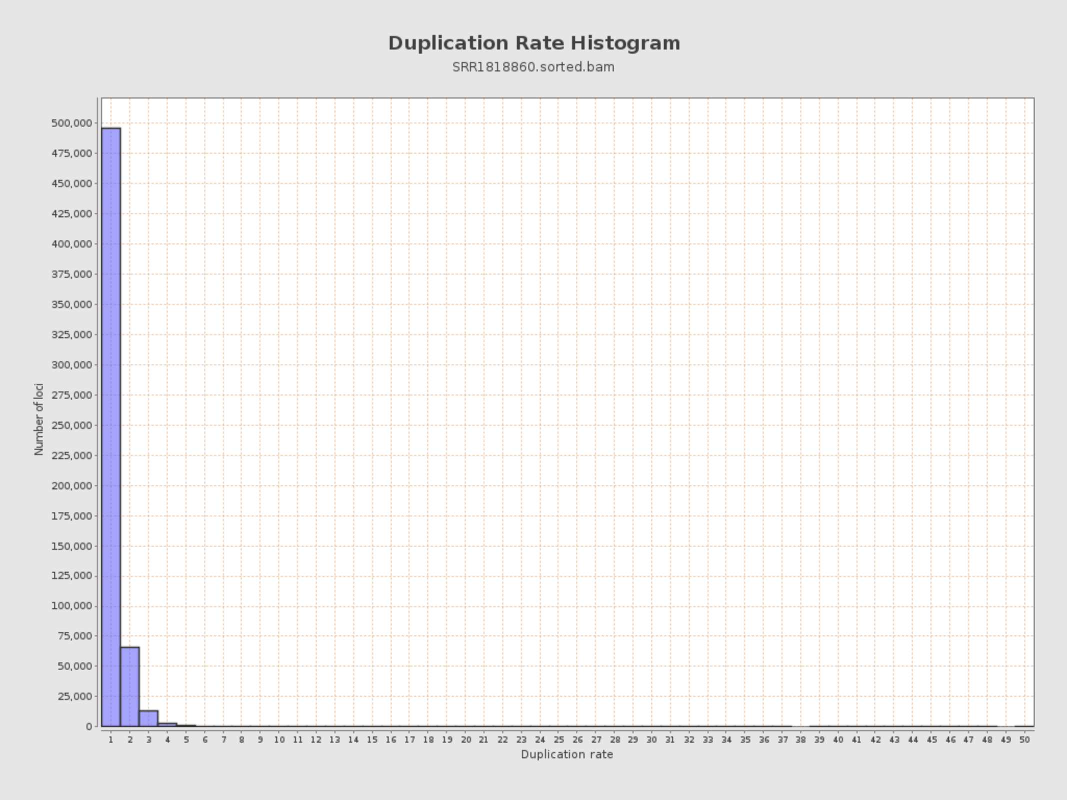
5. Results : Coverage Histogram (0-50X)



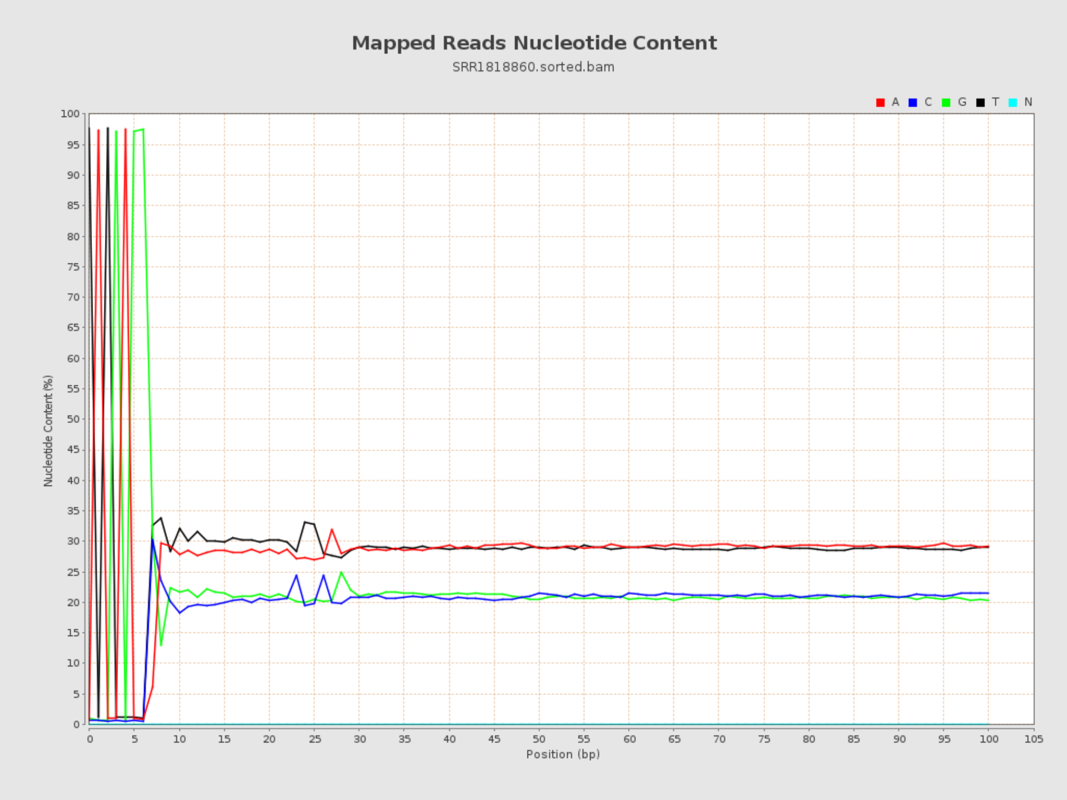
6. Results : Genome Fraction Coverage



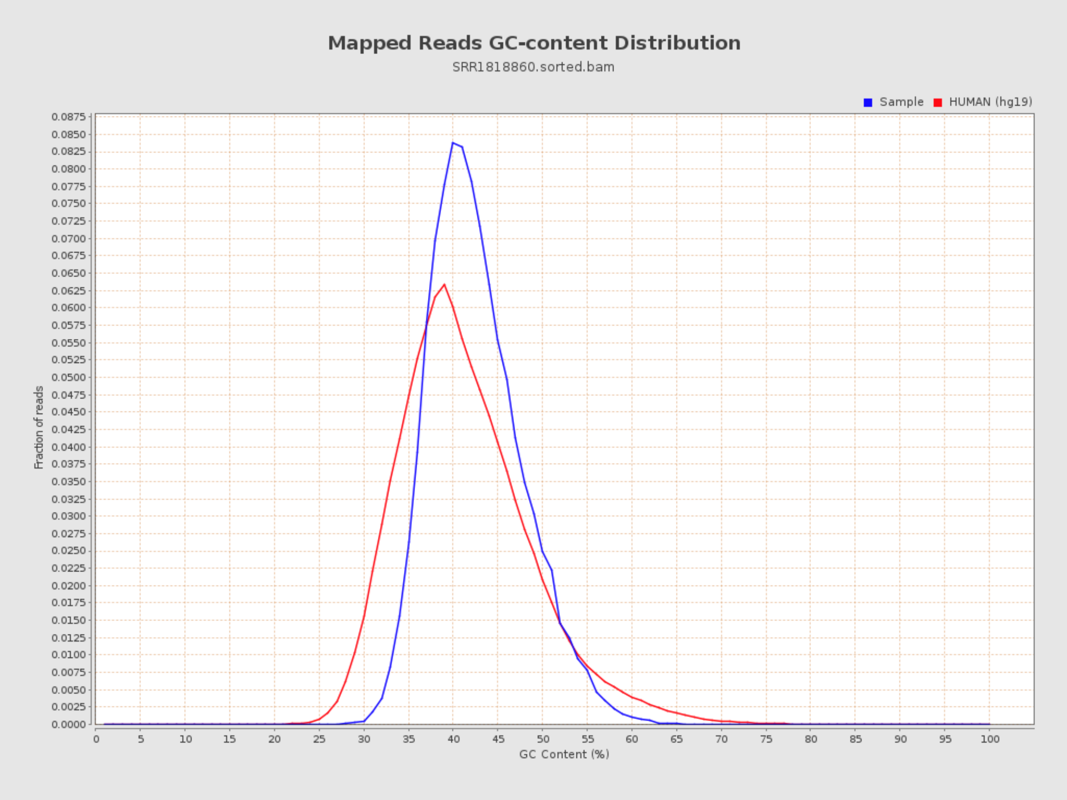
7. Results : Duplication Rate Histogram



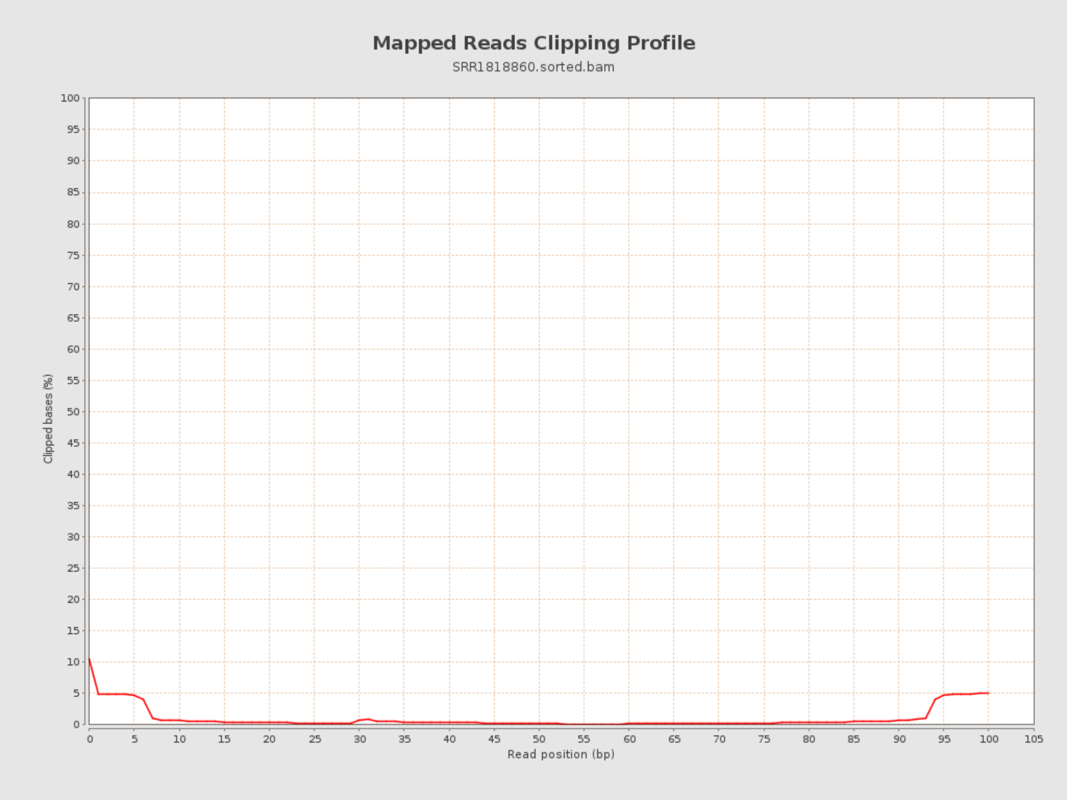
8. Results : Mapped Reads Nucleotide Content



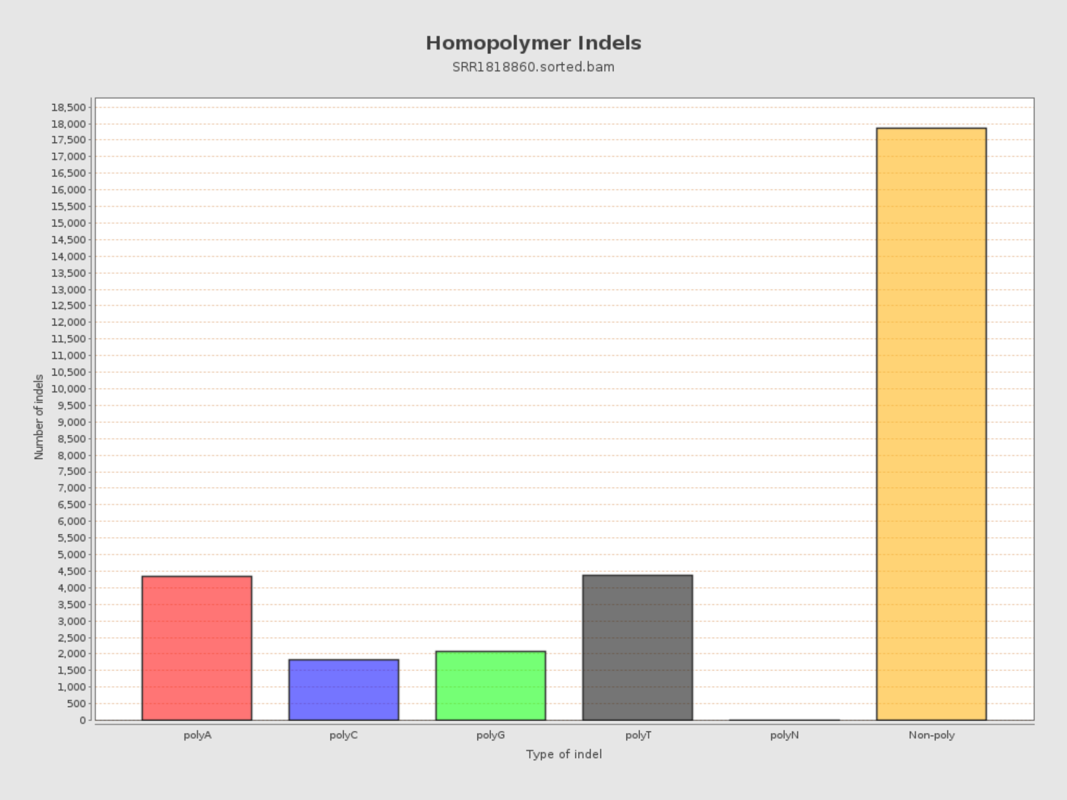
9. Results : Mapped Reads GC-content Distribution



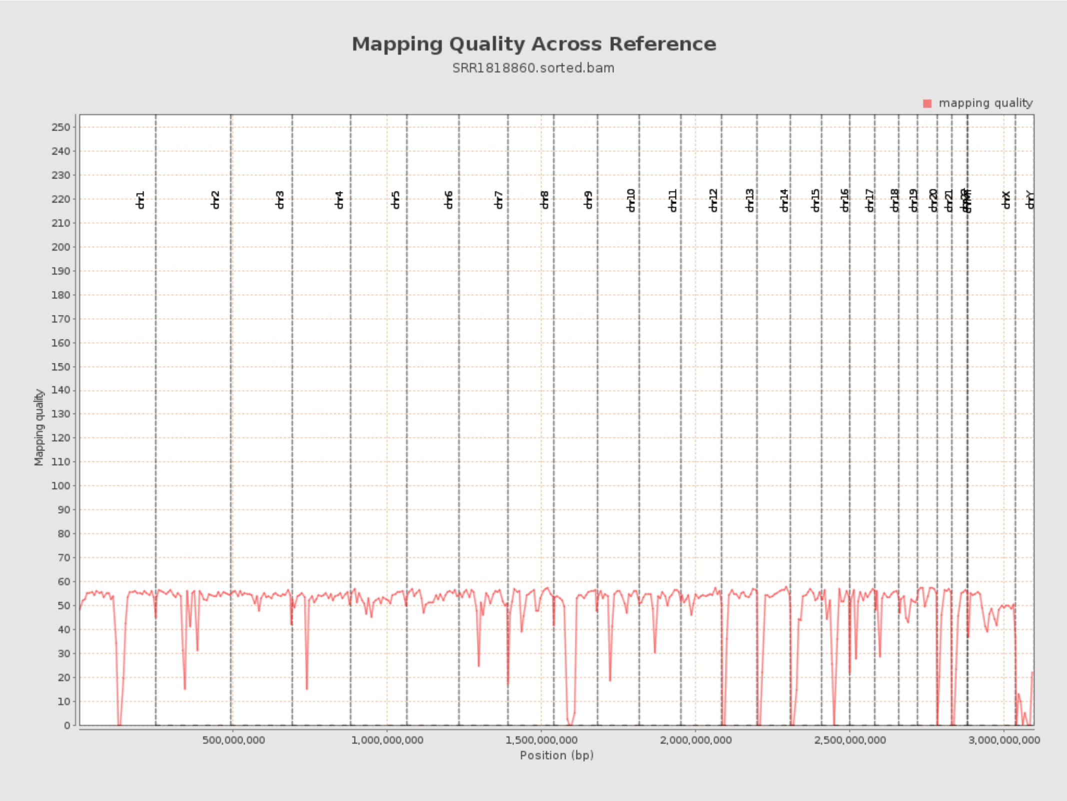
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram