Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:39:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818849.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_SRR1818849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:39:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,034,999
Mapped reads	1,022,595 / 98.8%
Unmapped reads	12,404 / 1.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,950 / 1.54%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	195,780 / 18.92%
Duplication rate	16.32%
Clipped reads	1,027,932 / 99.32%

2.2. ACGT Content

Number/percentage of A's	27,126,373 / 28.65%
Number/percentage of C's	19,558,106 / 20.66%
Number/percentage of T's	26,668,965 / 28.17%
Number/percentage of G's	21,314,949 / 22.52%
Number/percentage of N's	1,399 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0306

Standard Deviation	0.3758

2.4. Mapping Quality

Mean Mapping Quality	49.5

2.5. Mismatches and indels

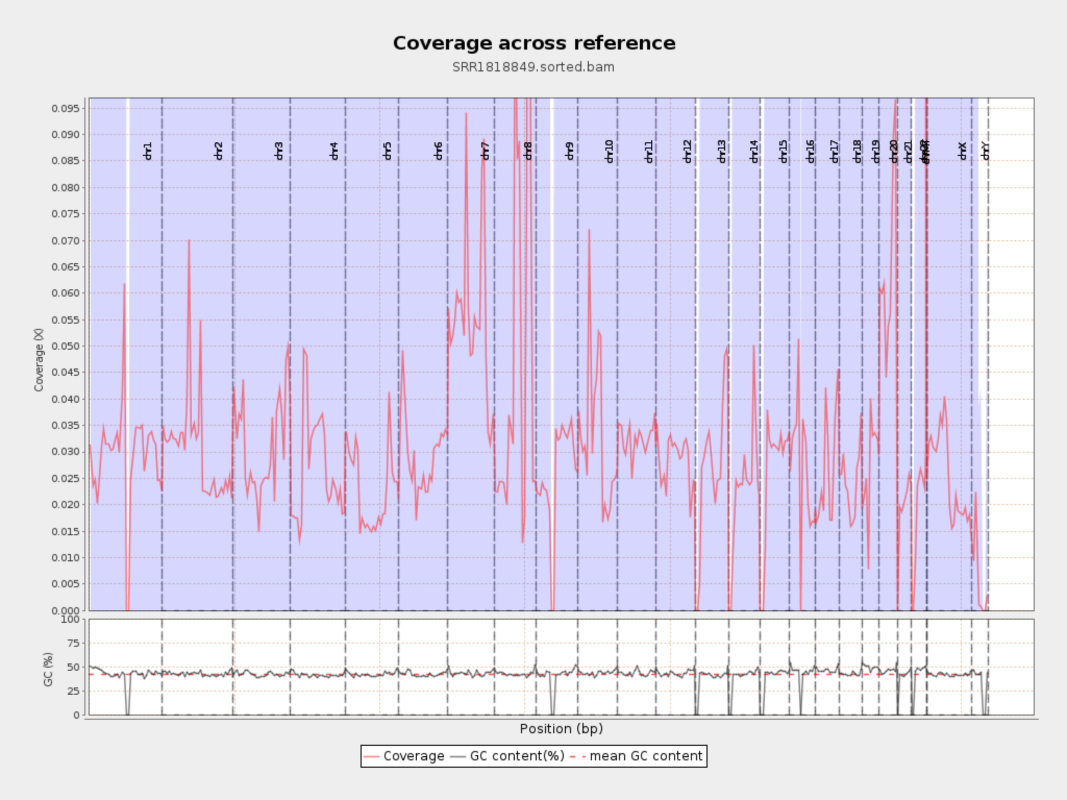
General error rate	0.64%
Mismatches	564,149
Insertions	15,278
Mapped reads with at least one insertion	1.45%
Deletions	30,879
Mapped reads with at least one deletion	2.95%
Homopolymer indels	38.93%

2.6. Chromosome stats

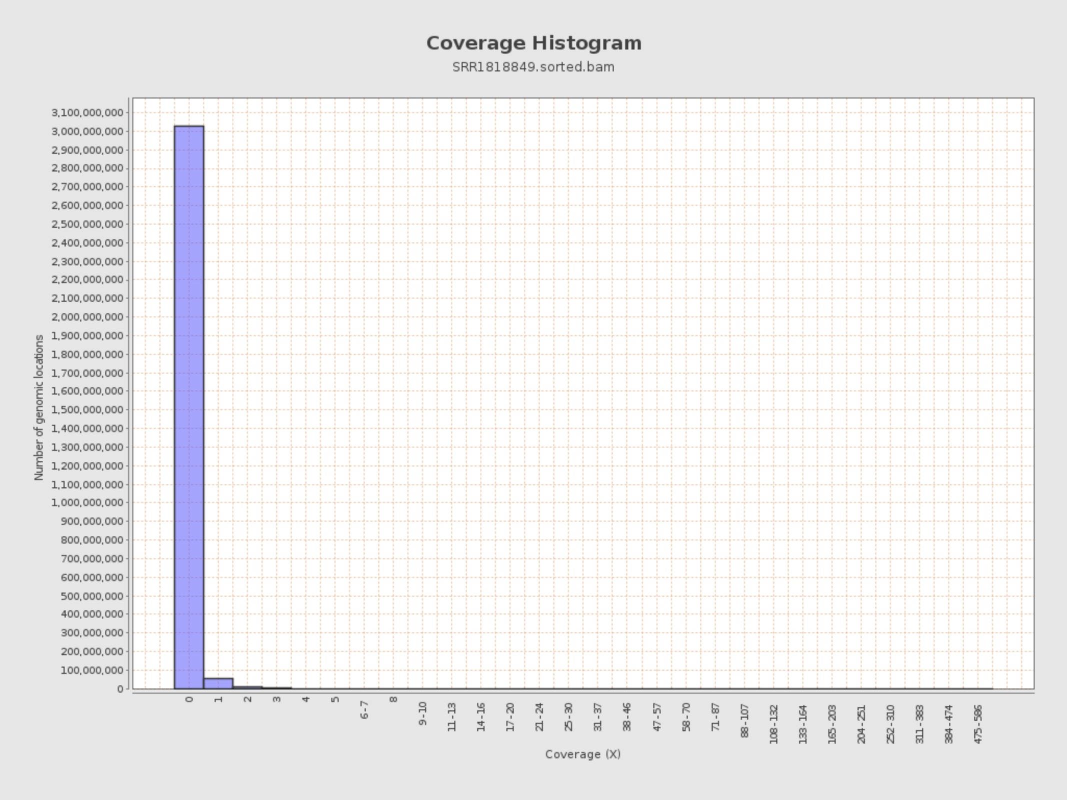
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7318252	0.0294	0.5007
chr2	243199373	7461414	0.0307	0.5077
chr3	198022430	6171223	0.0312	0.2242
chr4	191154276	5064097	0.0265	0.2694
chr5	180915260	4105376	0.0227	0.1961
chr6	171115067	4991285	0.0292	0.2288
chr7	159138663	8917397	0.056	0.865

chr8	146364022	7716580	0.0527	0.3421
chr9	141213431	3622434	0.0257	0.3144
chr10	135534747	4504820	0.0332	0.432
chr11	135006516	4379142	0.0324	0.2569
chr12	133851895	3827042	0.0286	0.2158
chr13	115169878	3092286	0.0268	0.2078
chr14	107349540	2484529	0.0231	0.2061
chr15	102531392	2678104	0.0261	0.2052
chr16	90354753	2390810	0.0265	0.377
chr17	81195210	2234979	0.0275	0.2533
chr18	78077248	1881901	0.0241	0.3428
chr19	59128983	1614753	0.0273	0.4297
chr20	63025520	4068227	0.0645	0.3423
chr21	48129895	943887	0.0196	0.2031
chr22	51304566	893473	0.0174	0.1806
chrMT	16571	57123	3.4472	2.8812
chrX	155270560	3965923	0.0255	0.2264
chrY	59373566	343486	0.0058	0.4121

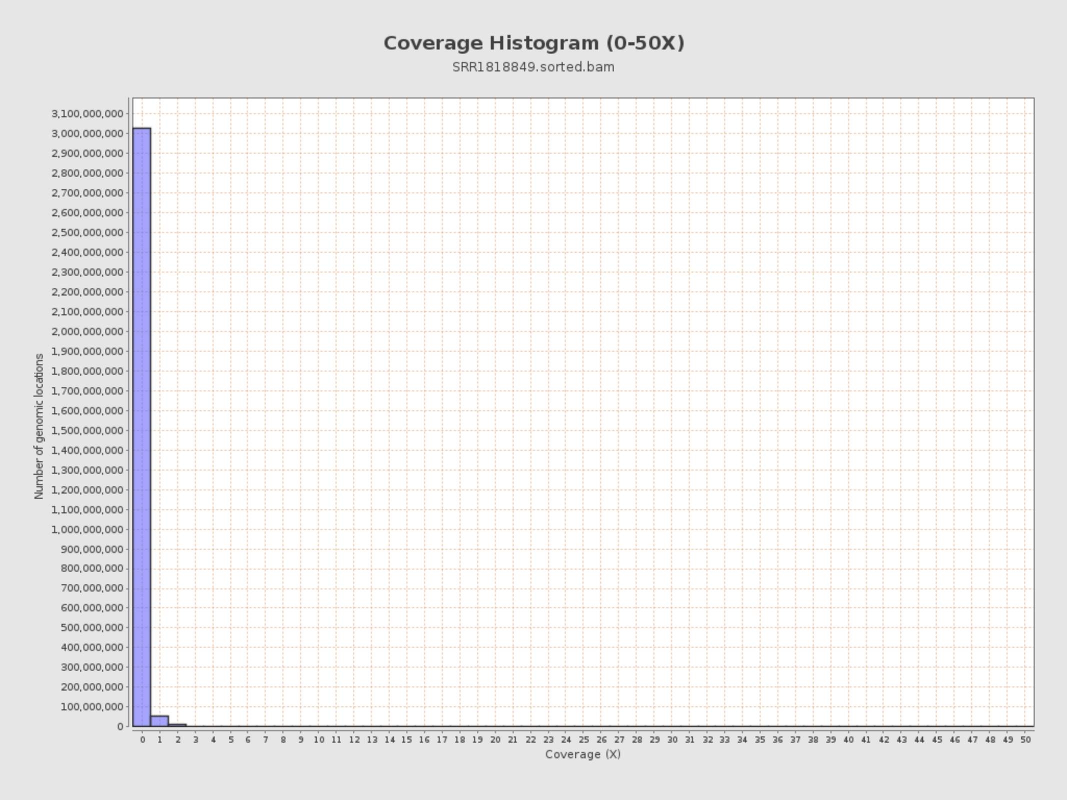
3. Results : Coverage across reference



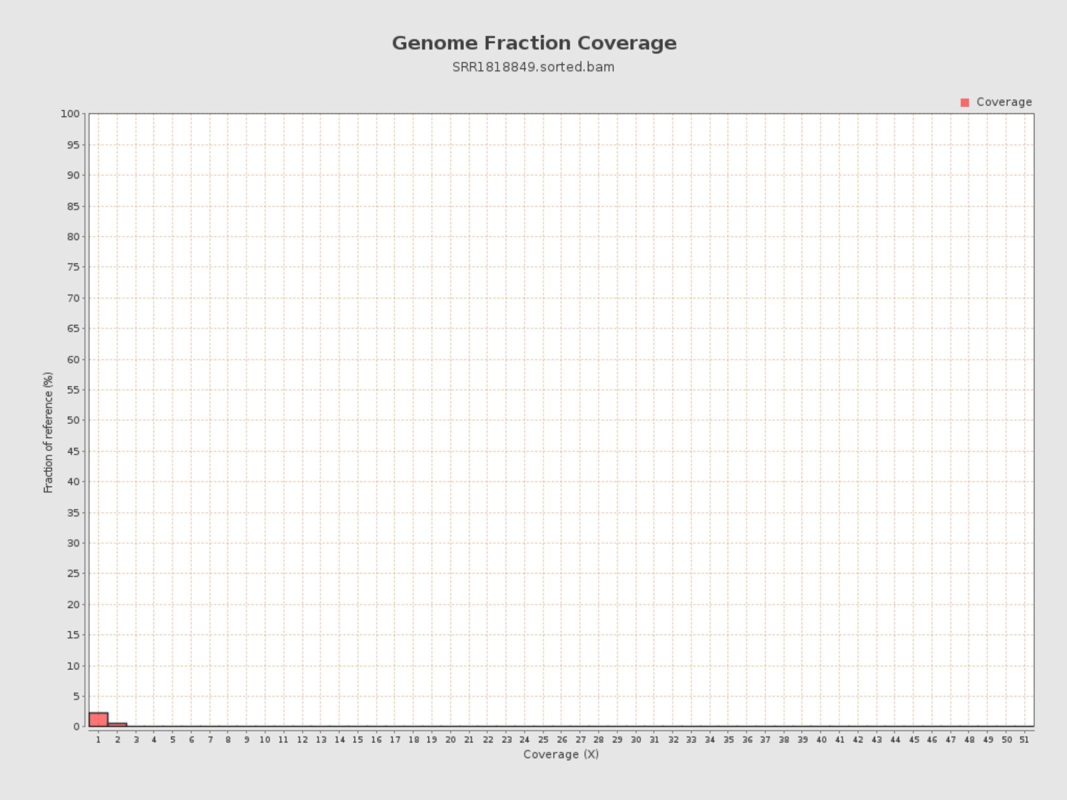
4. Results : Coverage Histogram



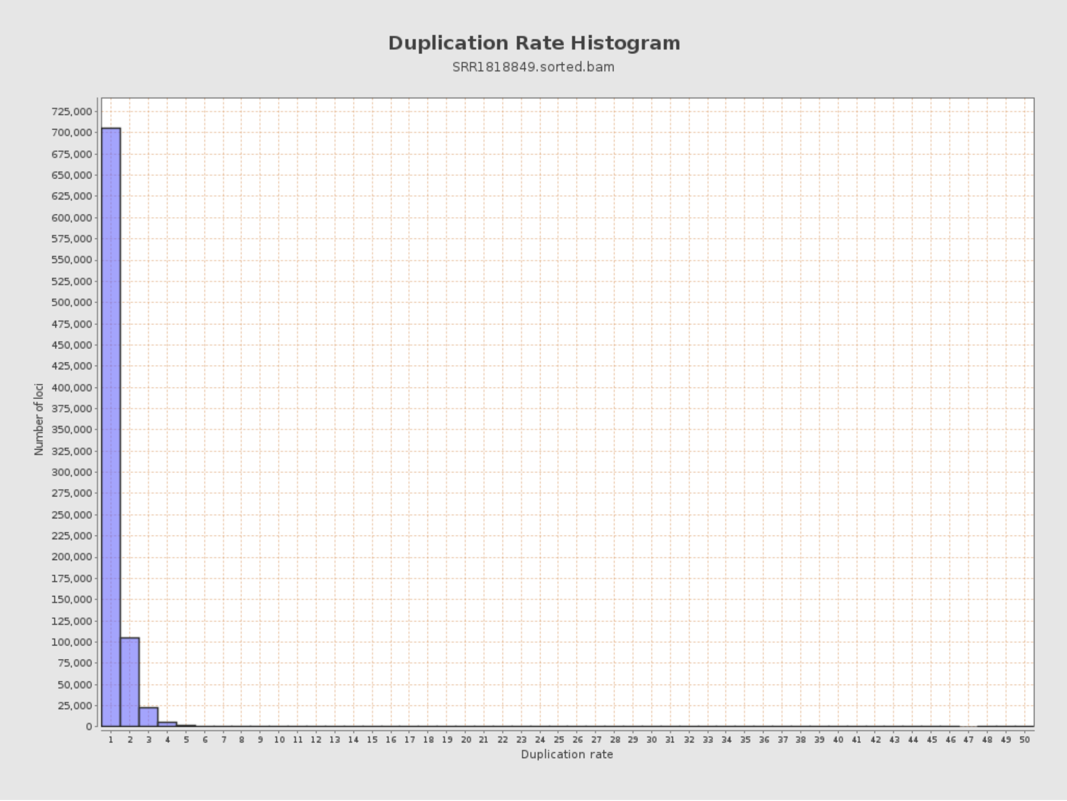
5. Results : Coverage Histogram (0-50X)



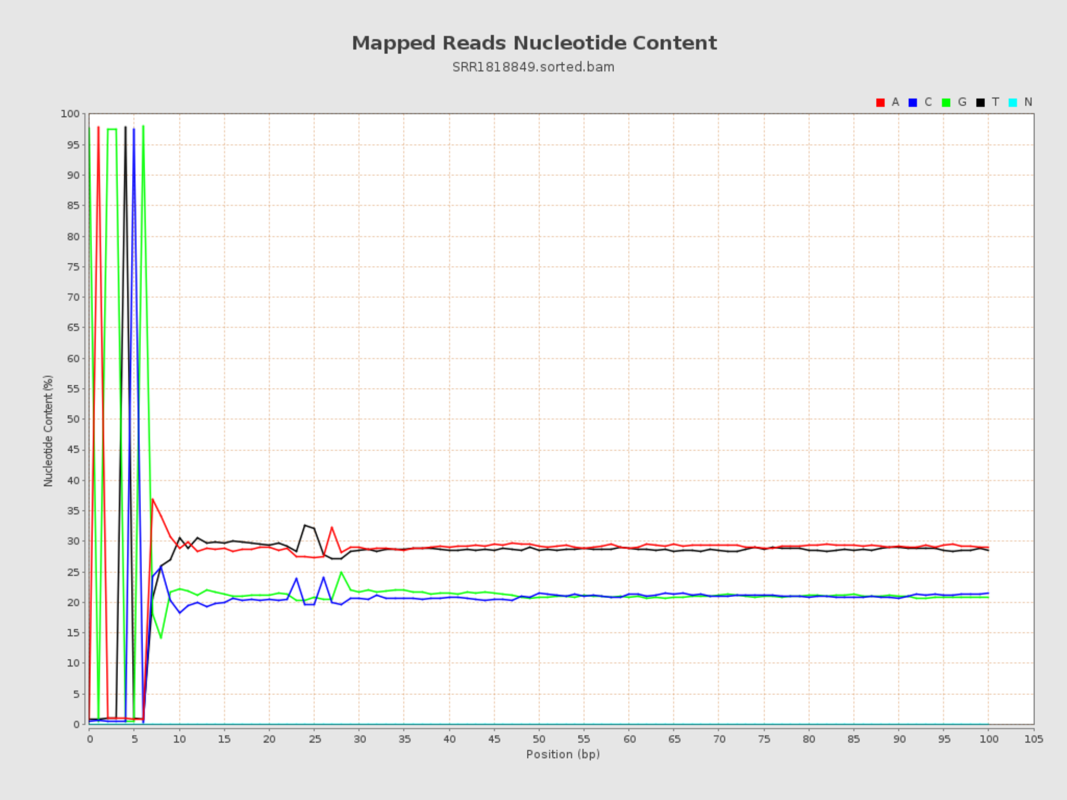
6. Results : Genome Fraction Coverage



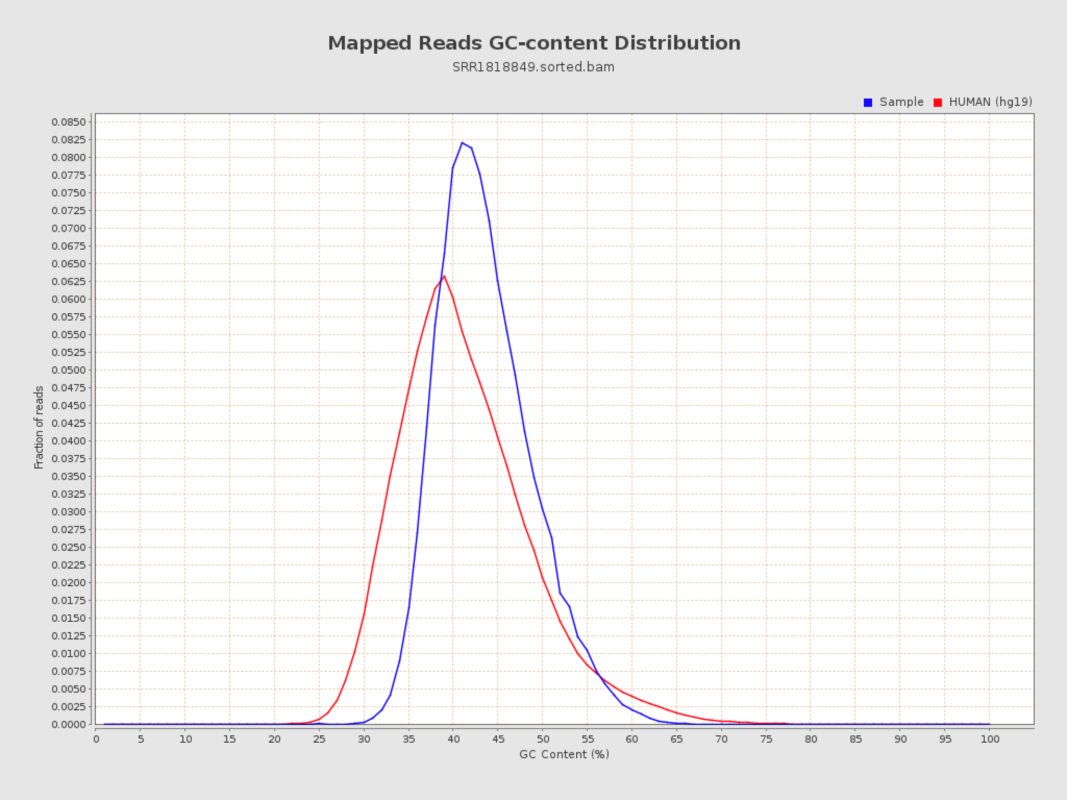
7. Results : Duplication Rate Histogram



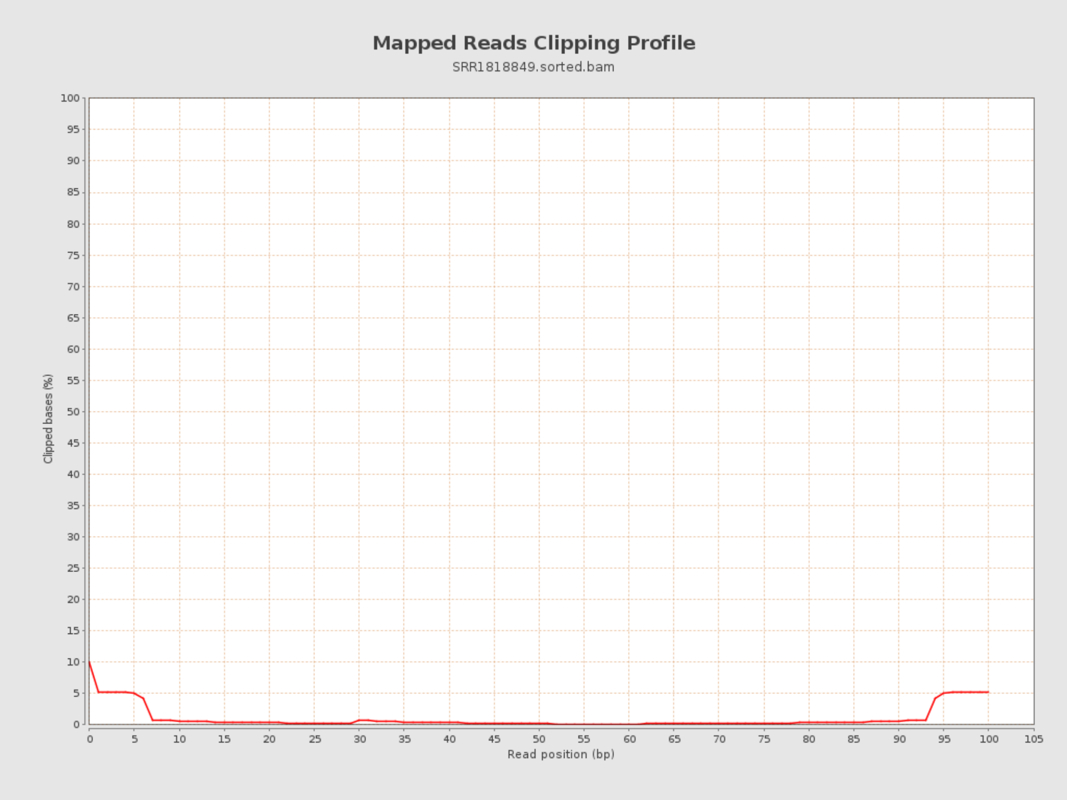
8. Results : Mapped Reads Nucleotide Content



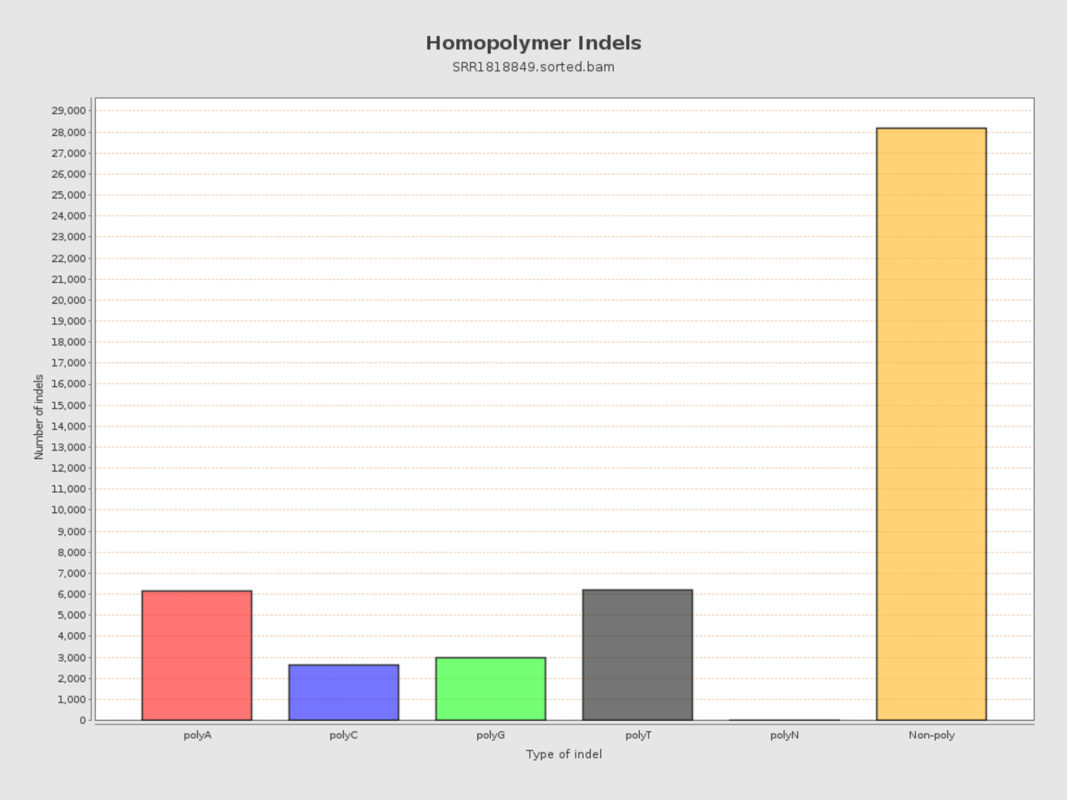
9. Results : Mapped Reads GC-content Distribution



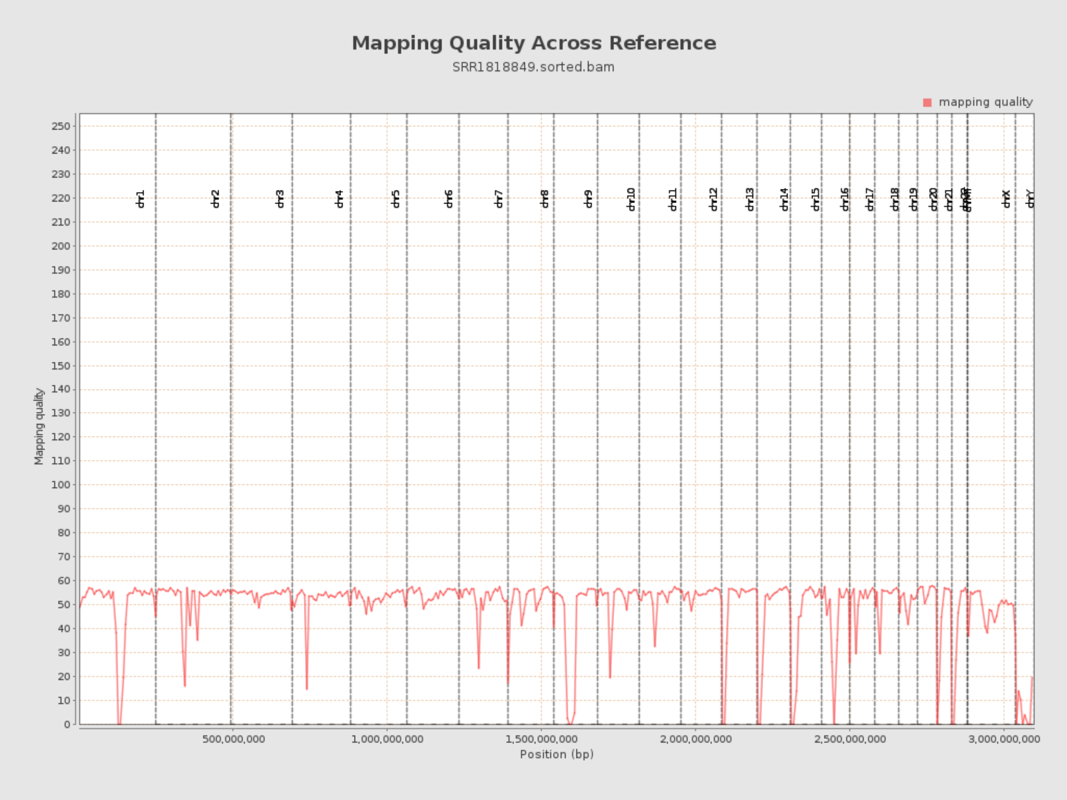
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram