Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:14:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818869.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_SRR1818869 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818869.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:14:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818869.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	768,795
Mapped reads	757,625 / 98.55%
Unmapped reads	11,170 / 1.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,228 / 1.59%
Read min/max/mean length	30 / 101 / 101.61
Duplicated reads (estimated)	133,258 / 17.33%
Duplication rate	14.91%
Clipped reads	766,137 / 99.65%

2.2. ACGT Content

Number/percentage of A's	20,084,302 / 28.67%
Number/percentage of C's	15,581,871 / 22.24%
Number/percentage of T's	19,584,832 / 27.95%
Number/percentage of G's	14,812,053 / 21.14%
Number/percentage of N's	918 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.285

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

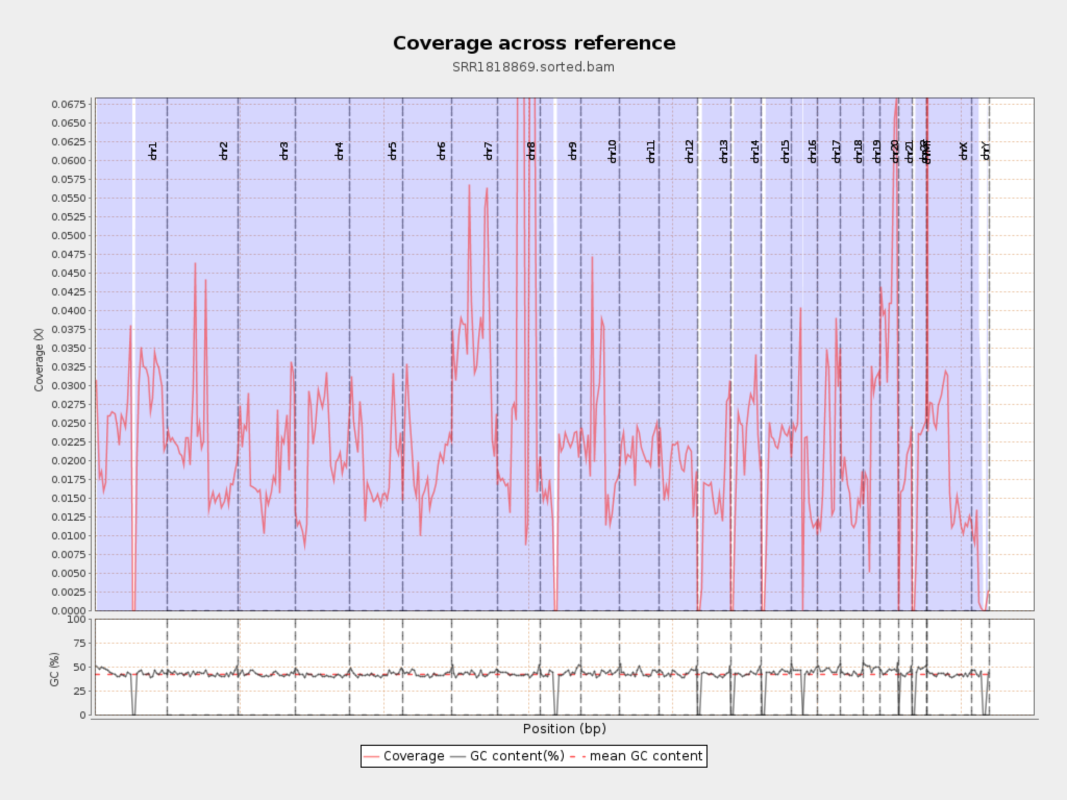
General error rate	0.64%
Mismatches	421,740
Insertions	9,871
Mapped reads with at least one insertion	1.26%
Deletions	23,577
Mapped reads with at least one deletion	3.04%
Homopolymer indels	40.62%

2.6. Chromosome stats

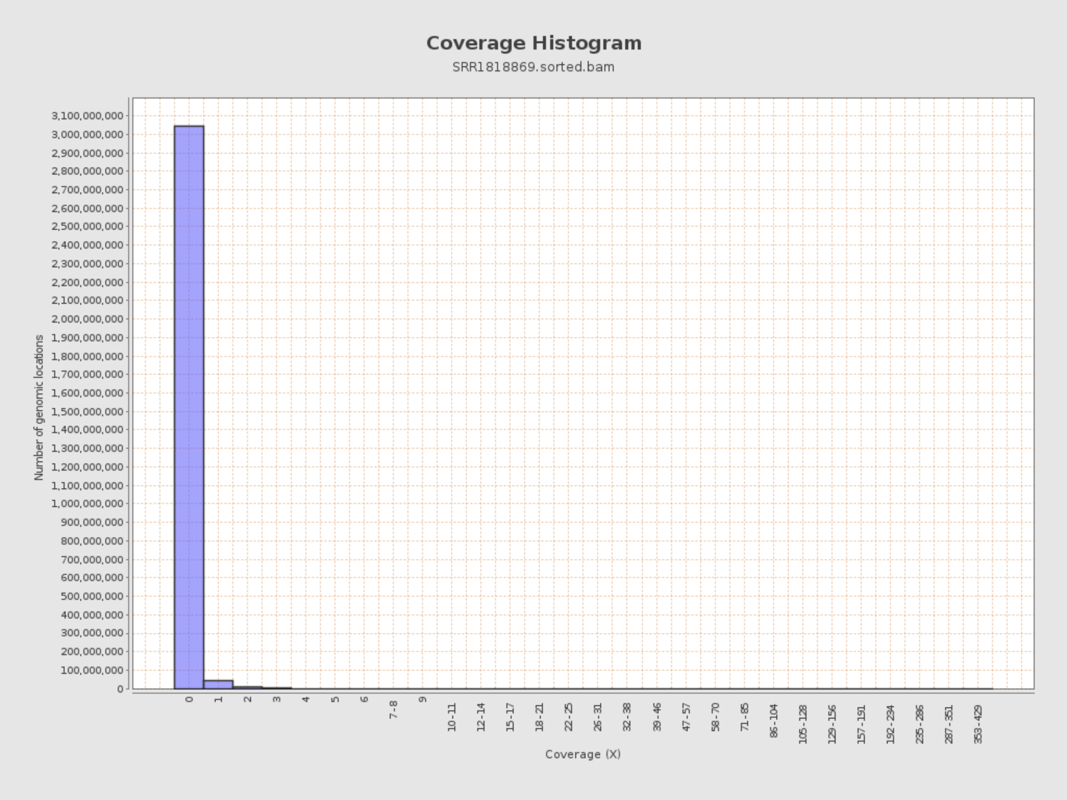
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6250675	0.0251	0.3671
chr2	243199373	5104758	0.021	0.4376
chr3	198022430	4045870	0.0204	0.1774
chr4	191154276	3989373	0.0209	0.2124
chr5	180915260	3601749	0.0199	0.181
chr6	171115067	3292426	0.0192	0.1843
chr7	159138663	5885718	0.037	0.5017

chr8	146364022	6692826	0.0457	0.2972
chr9	141213431	2496182	0.0177	0.2436
chr10	135534747	3129785	0.0231	0.3573
chr11	135006516	2923919	0.0217	0.2014
chr12	133851895	2577211	0.0193	0.1725
chr13	115169878	1710958	0.0149	0.1513
chr14	107349540	2269301	0.0211	0.1865
chr15	102531392	1940271	0.0189	0.1714
chr16	90354753	1723833	0.0191	0.3493
chr17	81195210	1885336	0.0232	0.2119
chr18	78077248	1188726	0.0152	0.2514
chr19	59128983	1380148	0.0233	0.3372
chr20	63025520	2873740	0.0456	0.2805
chr21	48129895	832942	0.0173	0.1827
chr22	51304566	872067	0.017	0.1731
chrMT	16571	92548	5.5849	4.1239
chrX	155270560	3090784	0.0199	0.1899
chrY	59373566	258966	0.0044	0.3215

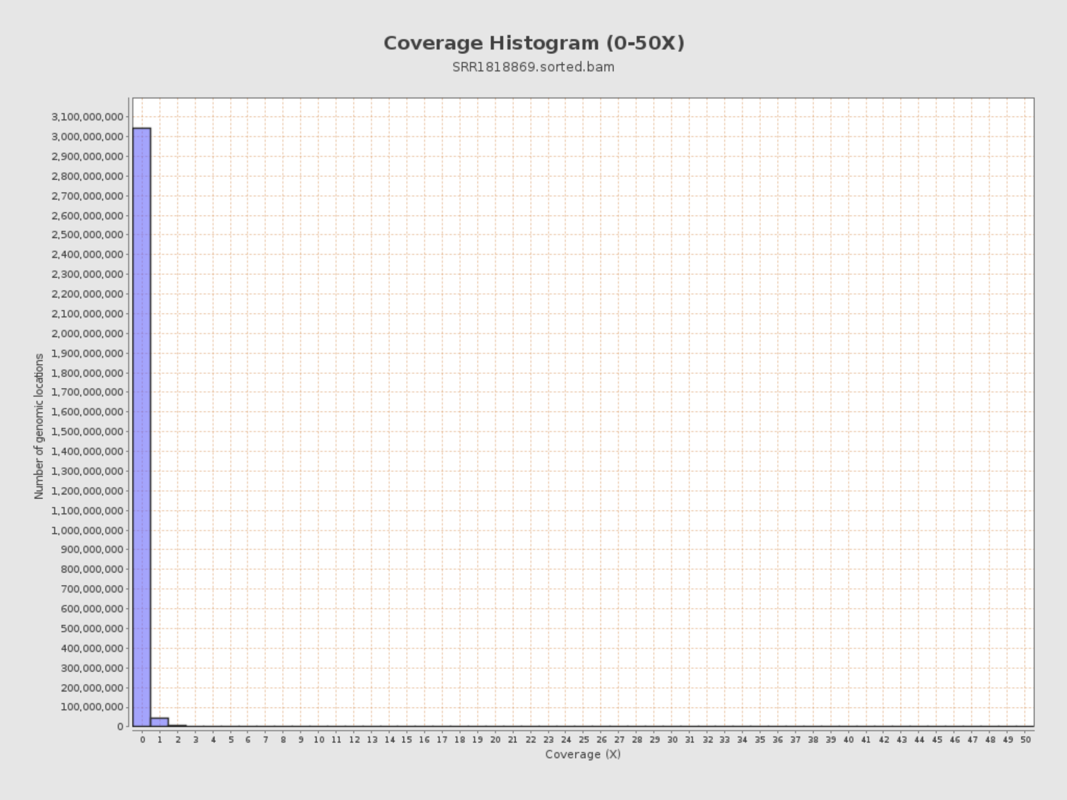
3. Results : Coverage across reference



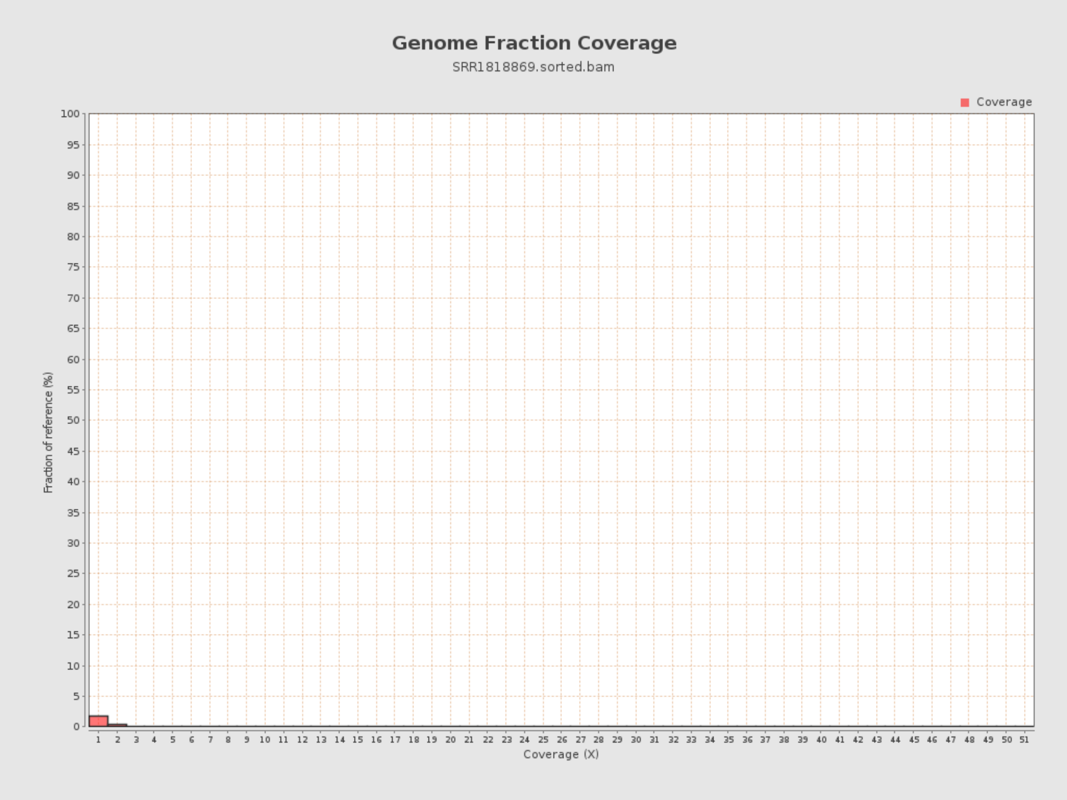
4. Results : Coverage Histogram



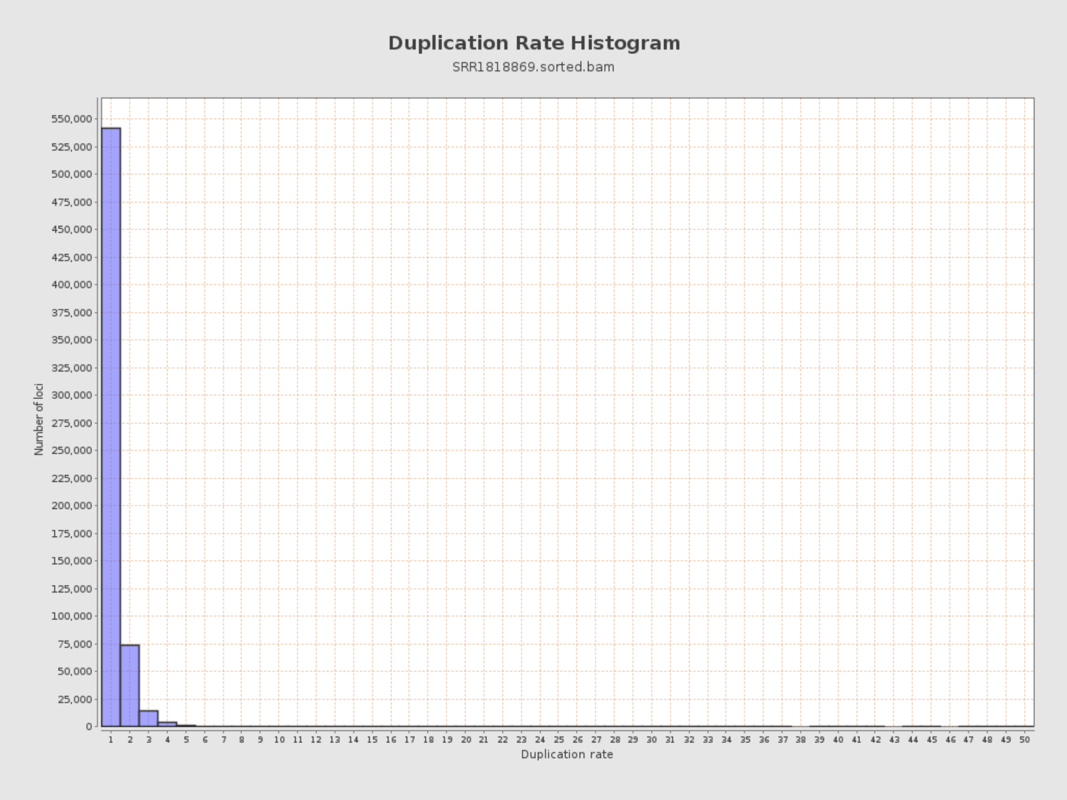
5. Results : Coverage Histogram (0-50X)



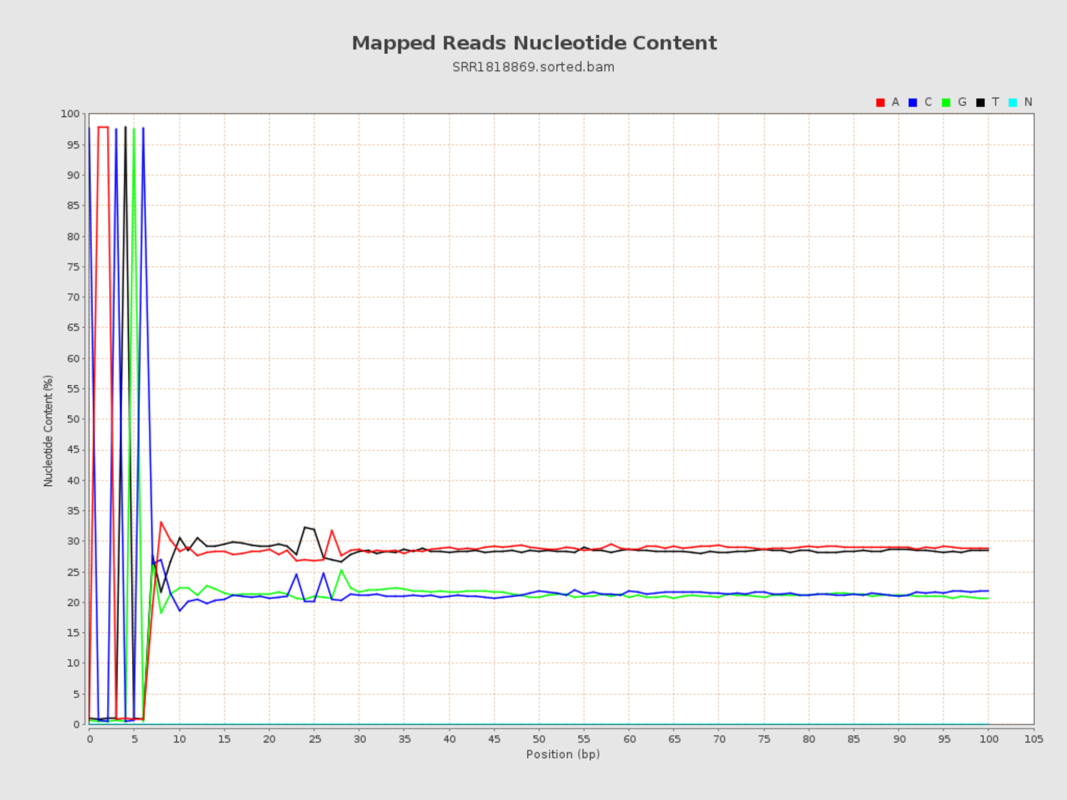
6. Results : Genome Fraction Coverage



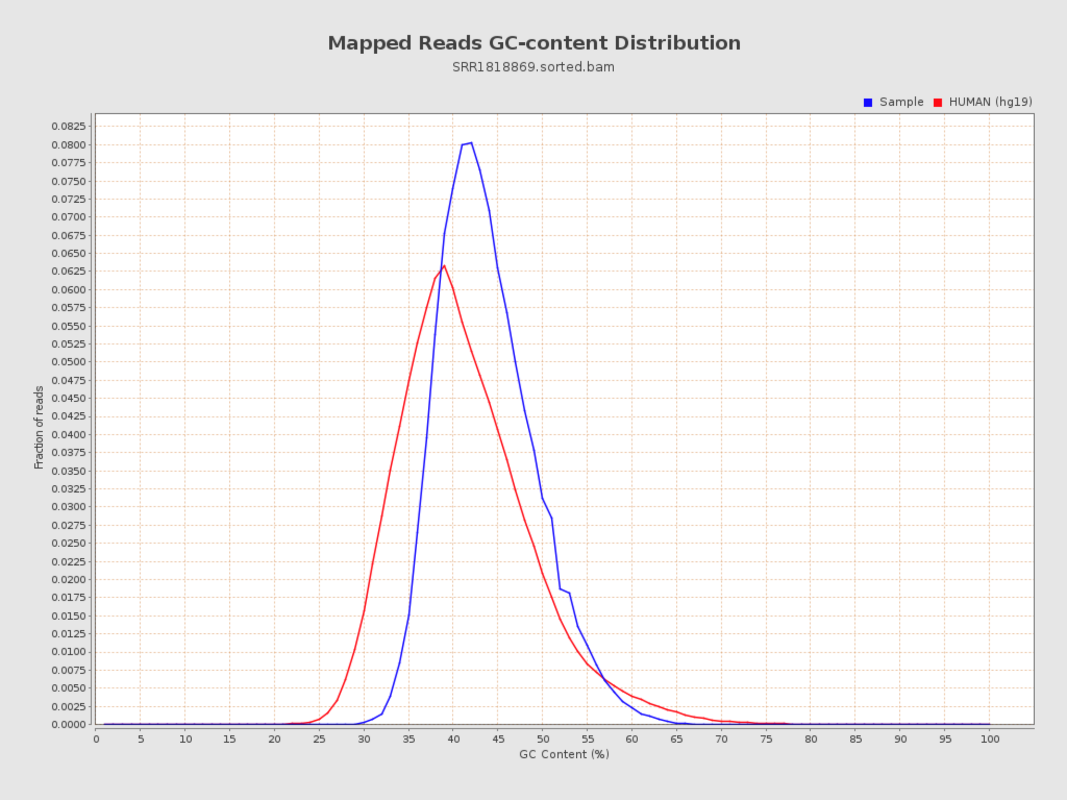
7. Results : Duplication Rate Histogram



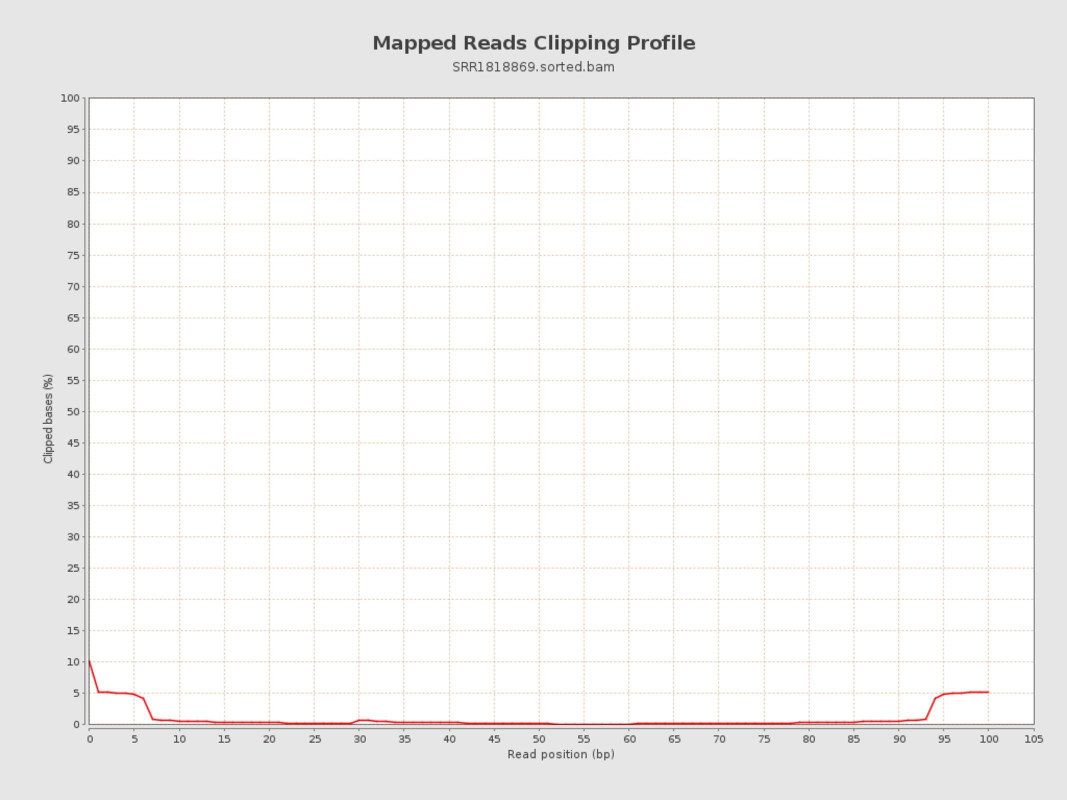
8. Results : Mapped Reads Nucleotide Content



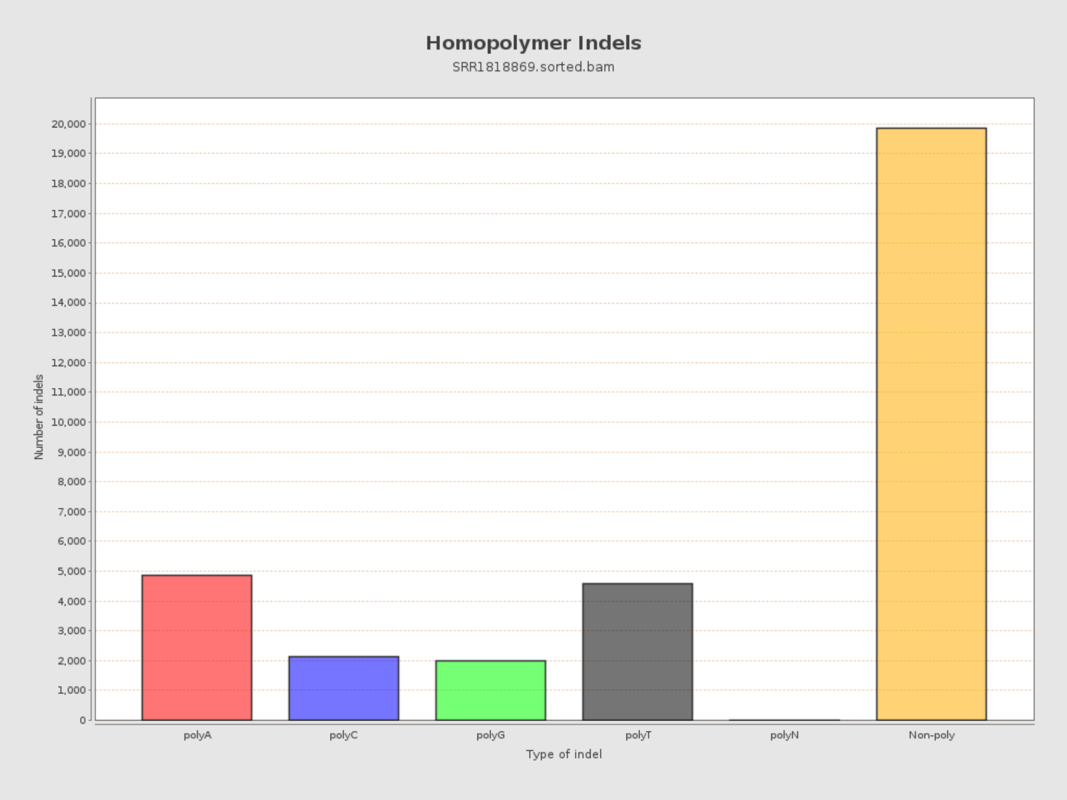
9. Results : Mapped Reads GC-content Distribution



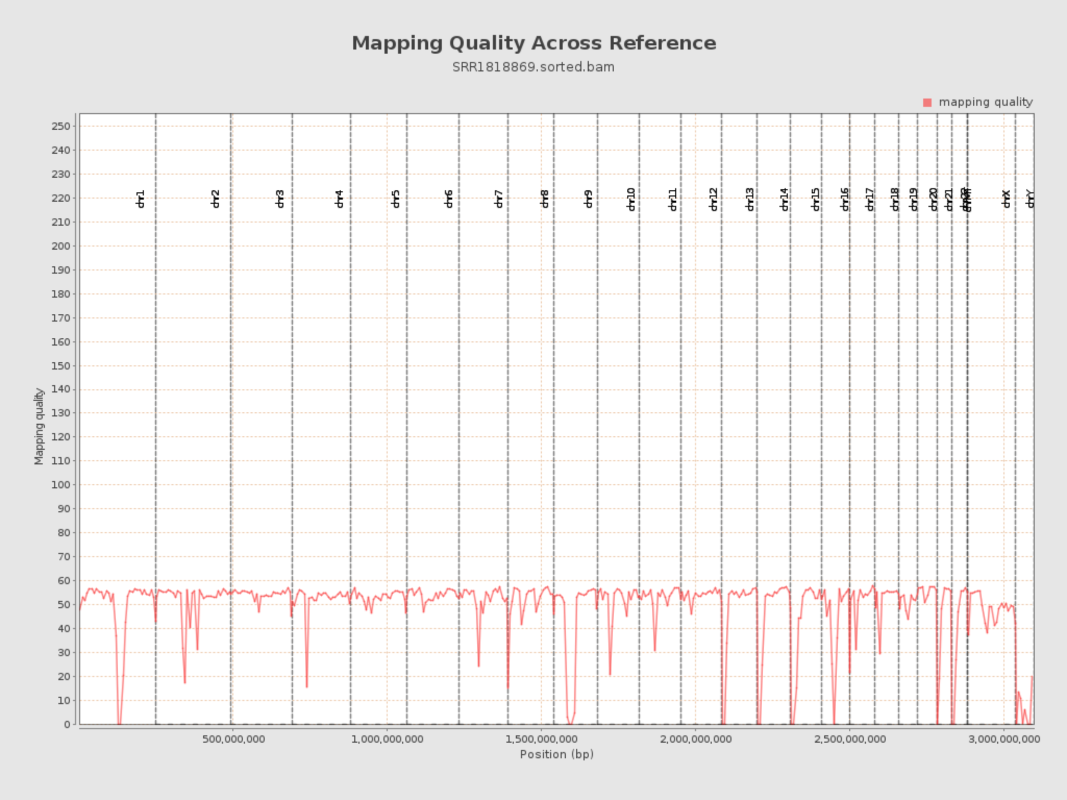
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram