Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:07:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818875.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_SRR1818875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818875.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:07:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,512,167
Mapped reads	1,471,322 / 97.3%
Unmapped reads	40,845 / 2.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,202 / 1.47%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	305,658 / 20.21%
Duplication rate	17.78%
Clipped reads	1,485,344 / 98.23%

2.2. ACGT Content

Number/percentage of A's	38,838,060 / 28.53%
Number/percentage of C's	30,063,890 / 22.09%
Number/percentage of T's	39,203,557 / 28.8%
Number/percentage of G's	28,004,227 / 20.57%
Number/percentage of N's	1,847 / 0%
GC Percentage	42.66%

2.3. Coverage

Mean	0.044

Standard Deviation	0.5286

2.4. Mapping Quality

Mean Mapping Quality	49.34

2.5. Mismatches and indels

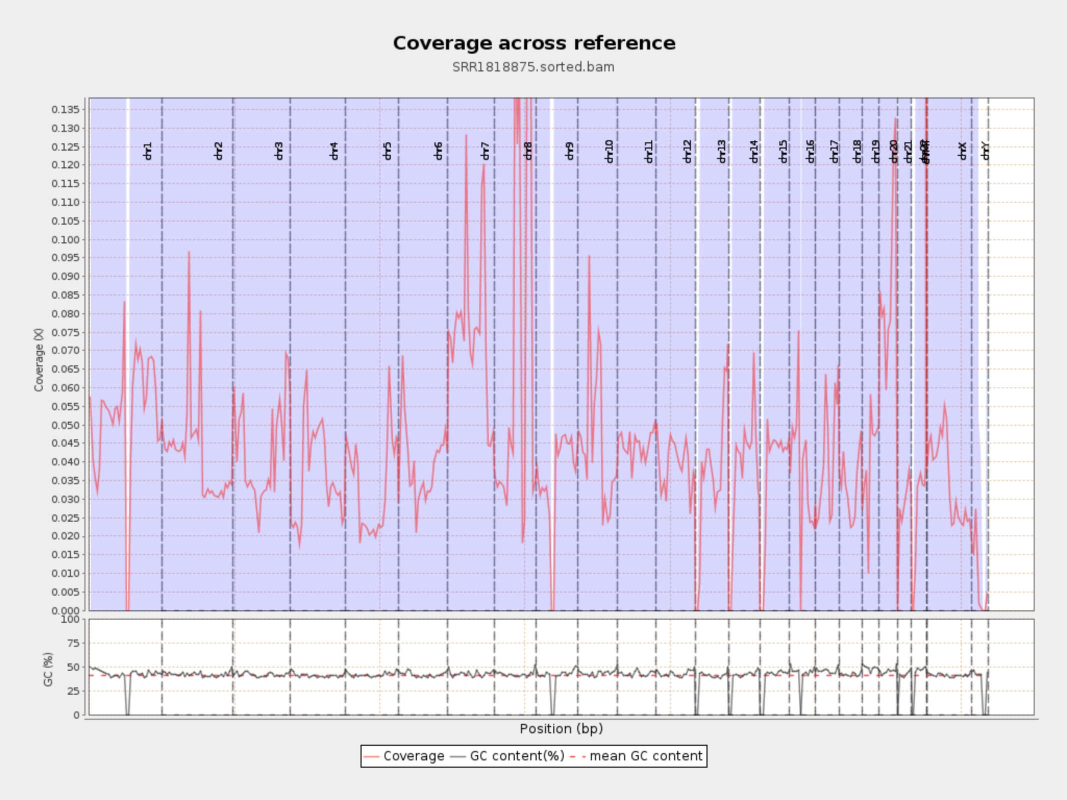
General error rate	0.64%
Mismatches	822,376
Insertions	19,941
Mapped reads with at least one insertion	1.31%
Deletions	44,786
Mapped reads with at least one deletion	2.97%
Homopolymer indels	41.54%

2.6. Chromosome stats

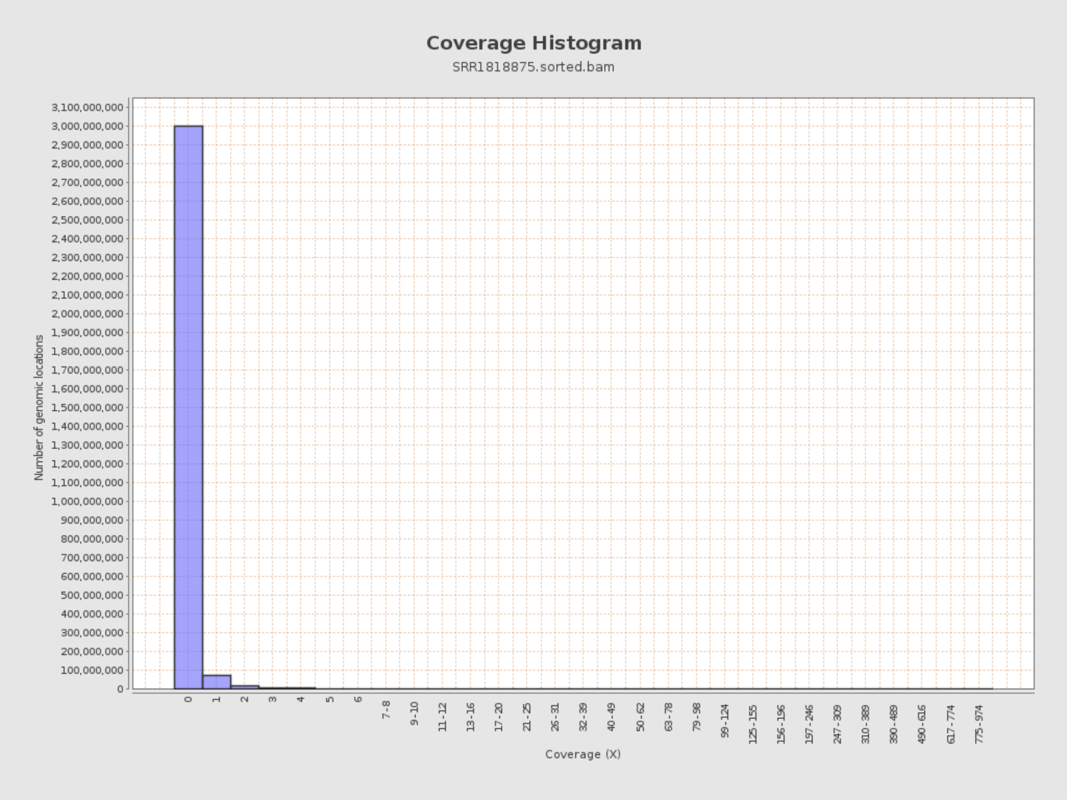
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13055103	0.0524	0.7939
chr2	243199373	10308032	0.0424	0.7571
chr3	198022430	8501767	0.0429	0.2713
chr4	191154276	6905081	0.0361	0.3149
chr5	180915260	6018426	0.0333	0.2519
chr6	171115067	6754802	0.0395	0.2904
chr7	159138663	12260110	0.077	1.134

chr8	146364022	11768548	0.0804	0.4698
chr9	141213431	4968080	0.0352	0.4419
chr10	135534747	6234354	0.046	0.6466
chr11	135006516	6015550	0.0446	0.3364
chr12	133851895	5320530	0.0397	0.2625
chr13	115169878	4146125	0.036	0.247
chr14	107349540	4031584	0.0376	0.2736
chr15	102531392	3759213	0.0367	0.2511
chr16	90354753	3339771	0.037	0.5635
chr17	81195210	3363842	0.0414	0.3443
chr18	78077248	2632011	0.0337	0.4671
chr19	59128983	2373195	0.0401	0.6422
chr20	63025520	5570297	0.0884	0.4206
chr21	48129895	1317911	0.0274	0.249
chr22	51304566	1235647	0.0241	0.2248
chrMT	16571	338353	20.4184	12.902
chrX	155270560	5508268	0.0355	0.2997
chrY	59373566	471253	0.0079	0.5946

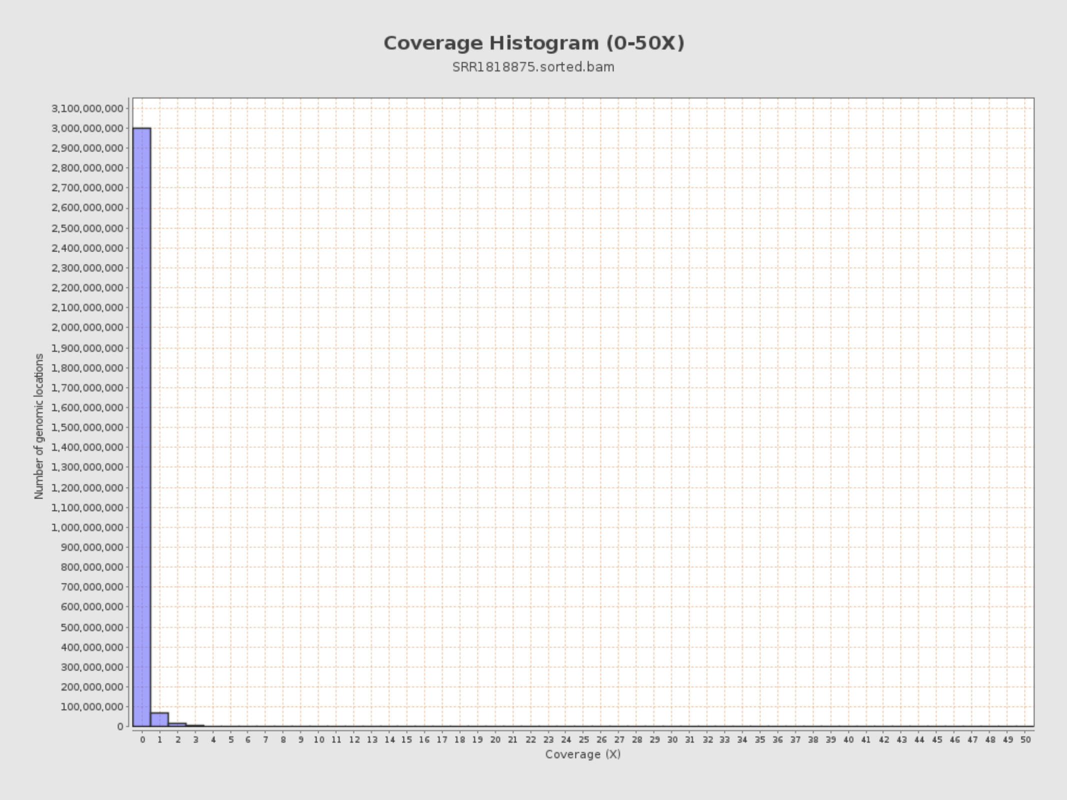
3. Results : Coverage across reference



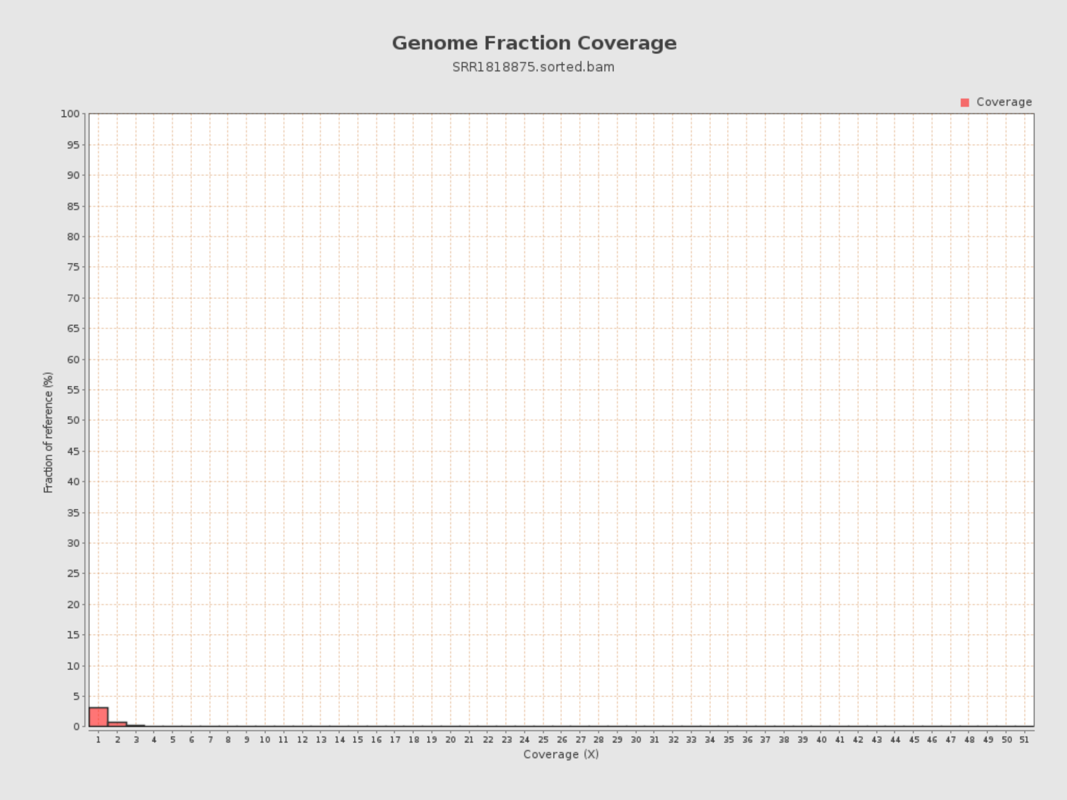
4. Results : Coverage Histogram



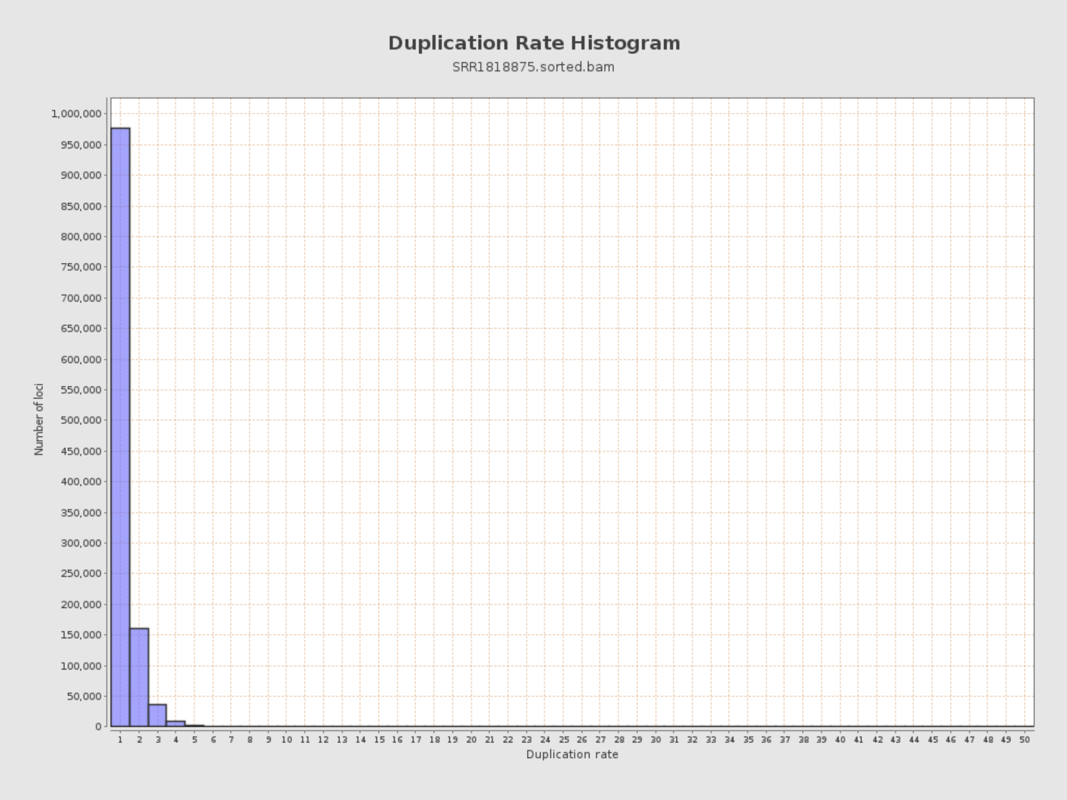
5. Results : Coverage Histogram (0-50X)



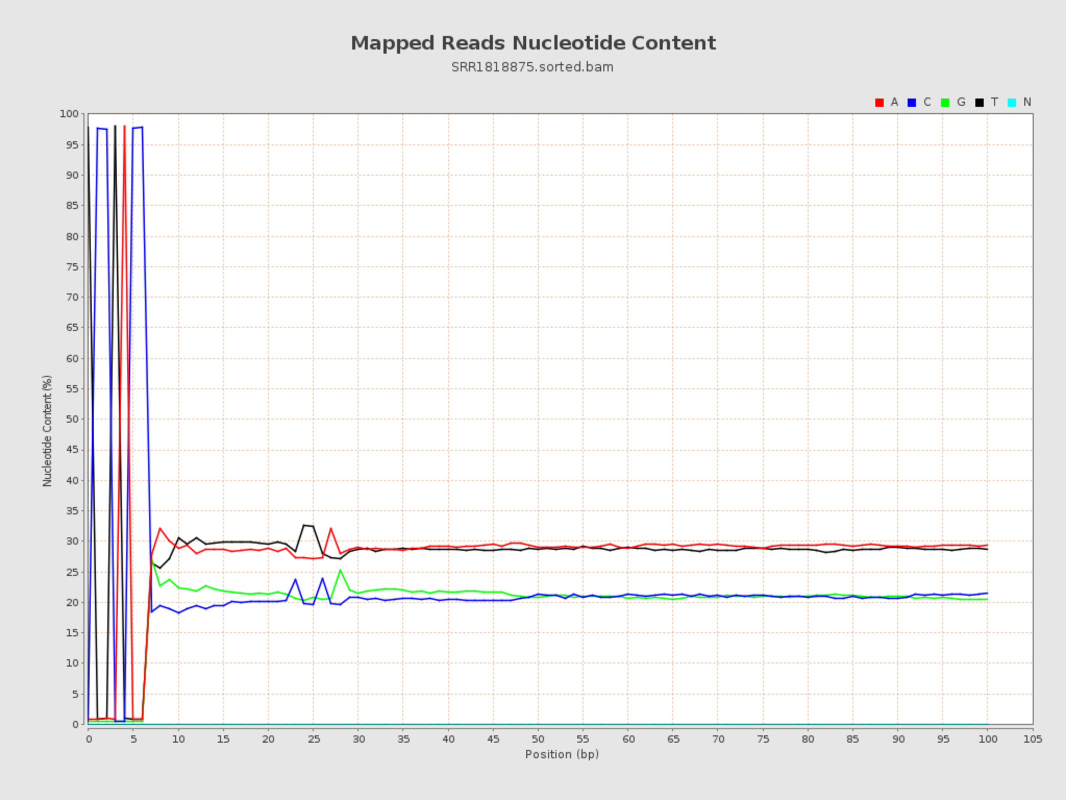
6. Results : Genome Fraction Coverage



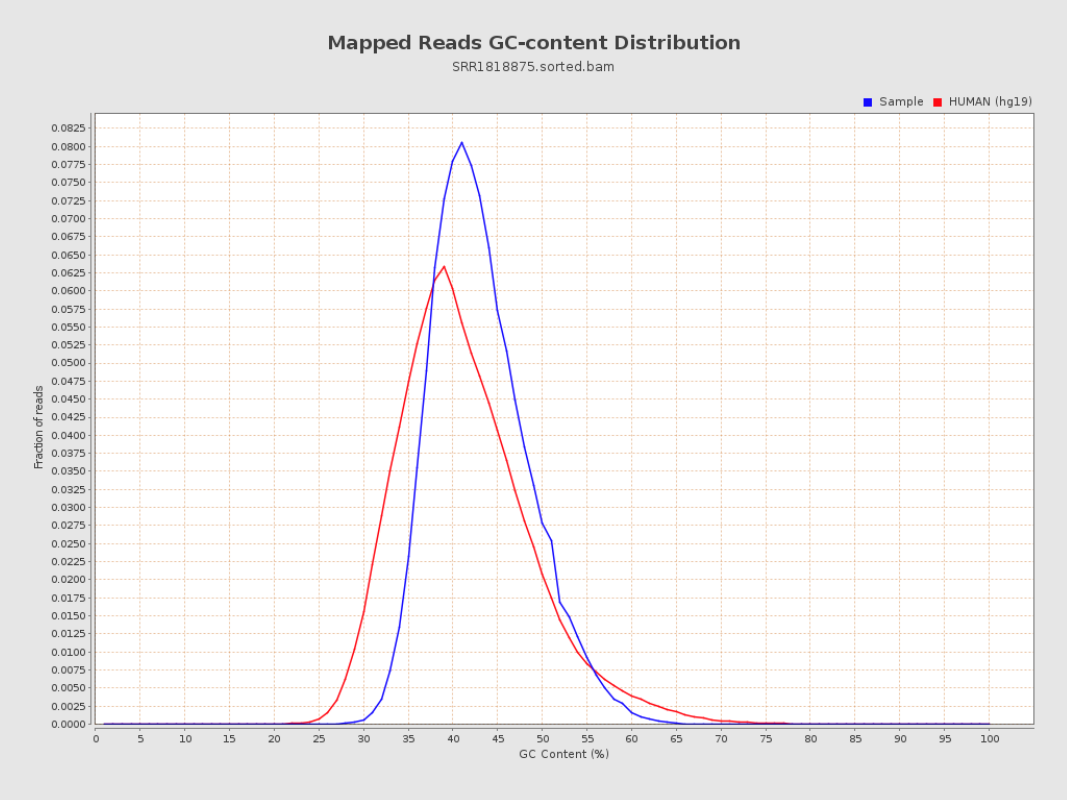
7. Results : Duplication Rate Histogram



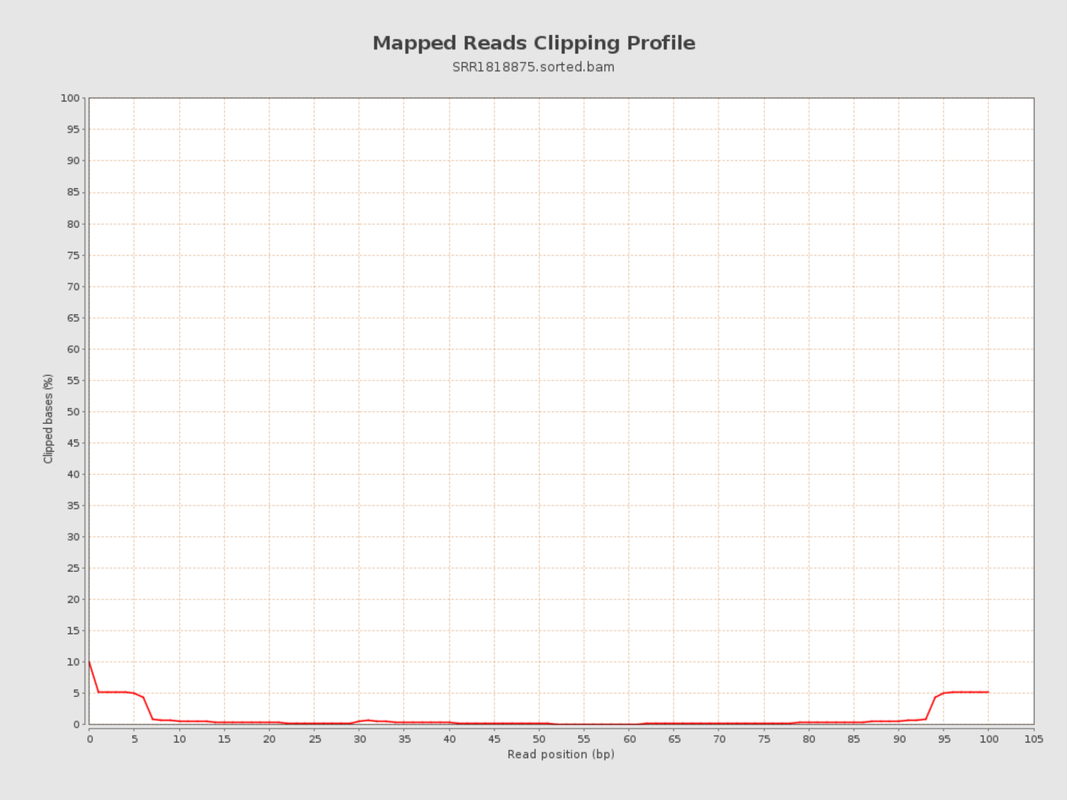
8. Results : Mapped Reads Nucleotide Content



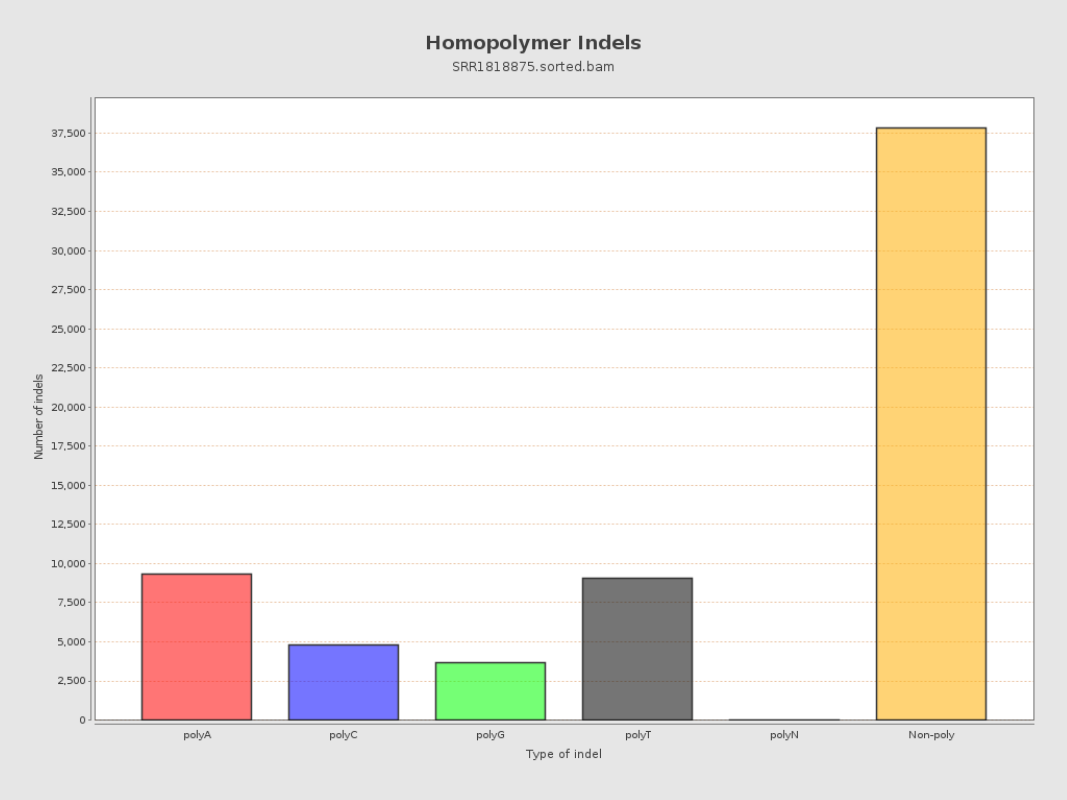
9. Results : Mapped Reads GC-content Distribution



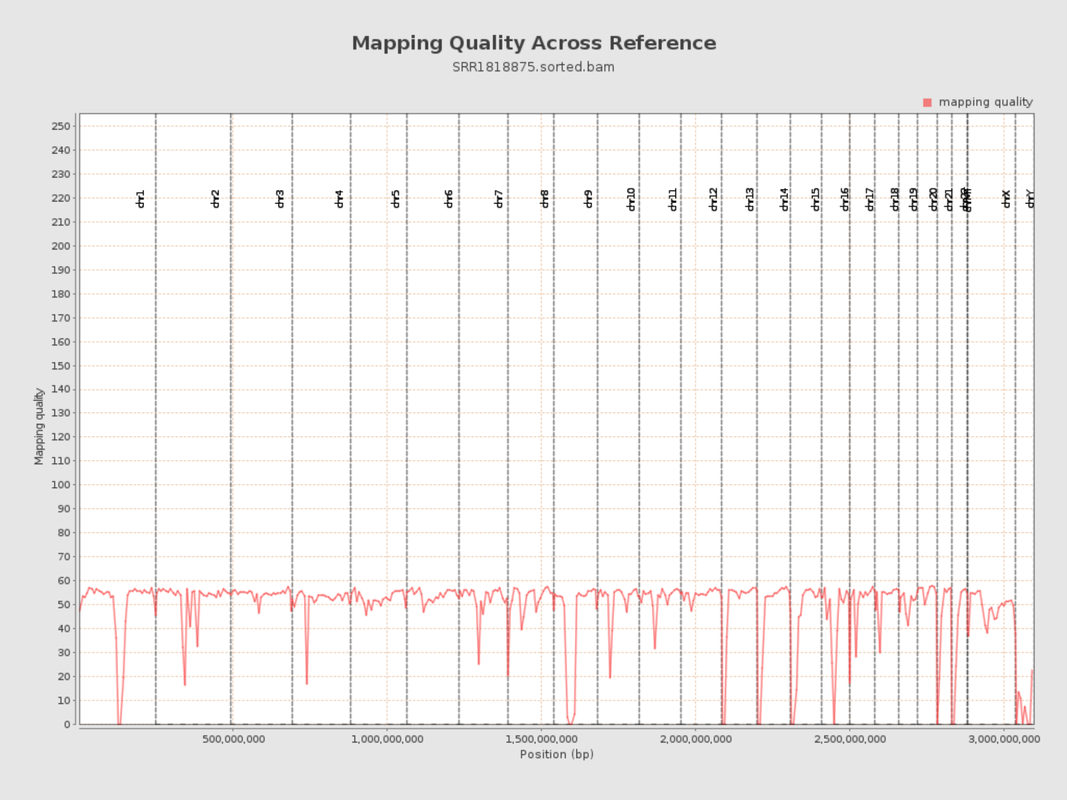
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram