Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:25:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818877.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_SRR1818877 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818877.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:25:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818877.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,960,410
Mapped reads	1,909,222 / 97.39%
Unmapped reads	51,188 / 2.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,420 / 1.45%
Read min/max/mean length	30 / 101 / 101.56
Duplicated reads (estimated)	428,974 / 21.88%
Duplication rate	19.02%
Clipped reads	1,916,389 / 97.75%

2.2. ACGT Content

Number/percentage of A's	49,714,412 / 28.13%
Number/percentage of C's	37,822,398 / 21.4%
Number/percentage of T's	52,095,803 / 29.48%
Number/percentage of G's	37,082,578 / 20.98%
Number/percentage of N's	2,665 / 0%
GC Percentage	42.39%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.7204

2.4. Mapping Quality

Mean Mapping Quality	49.08

2.5. Mismatches and indels

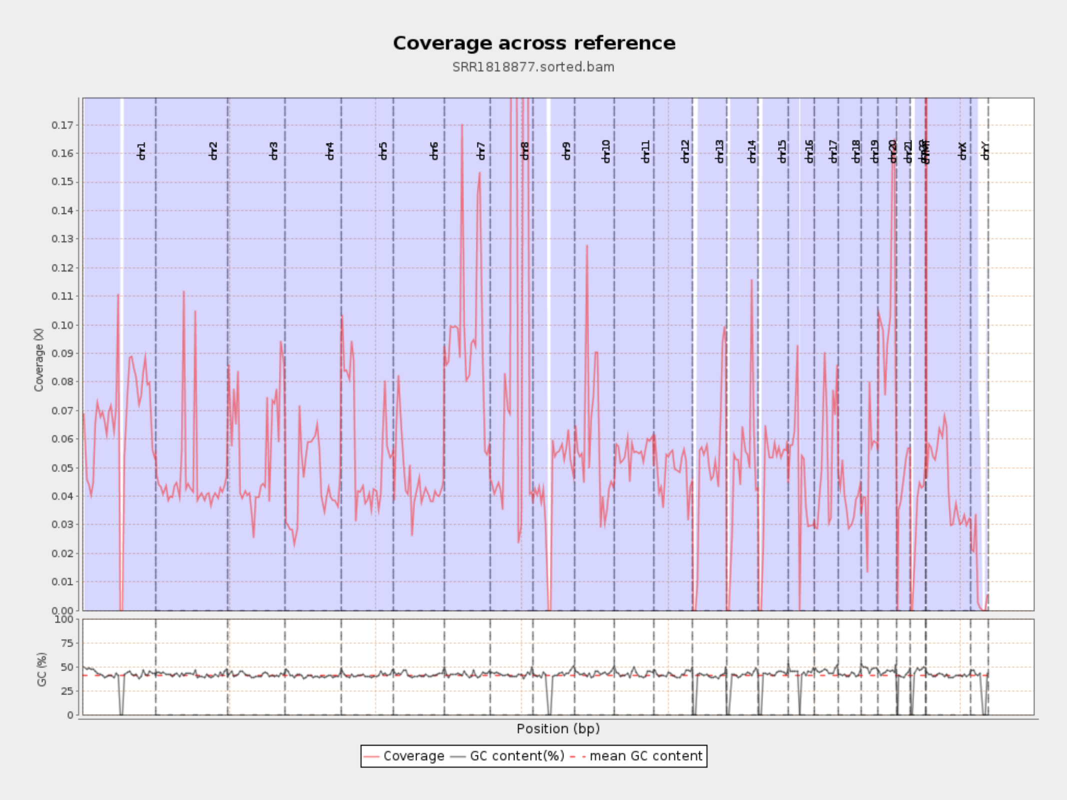
General error rate	0.65%
Mismatches	1,079,054
Insertions	26,417
Mapped reads with at least one insertion	1.33%
Deletions	57,851
Mapped reads with at least one deletion	2.96%
Homopolymer indels	42.06%

2.6. Chromosome stats

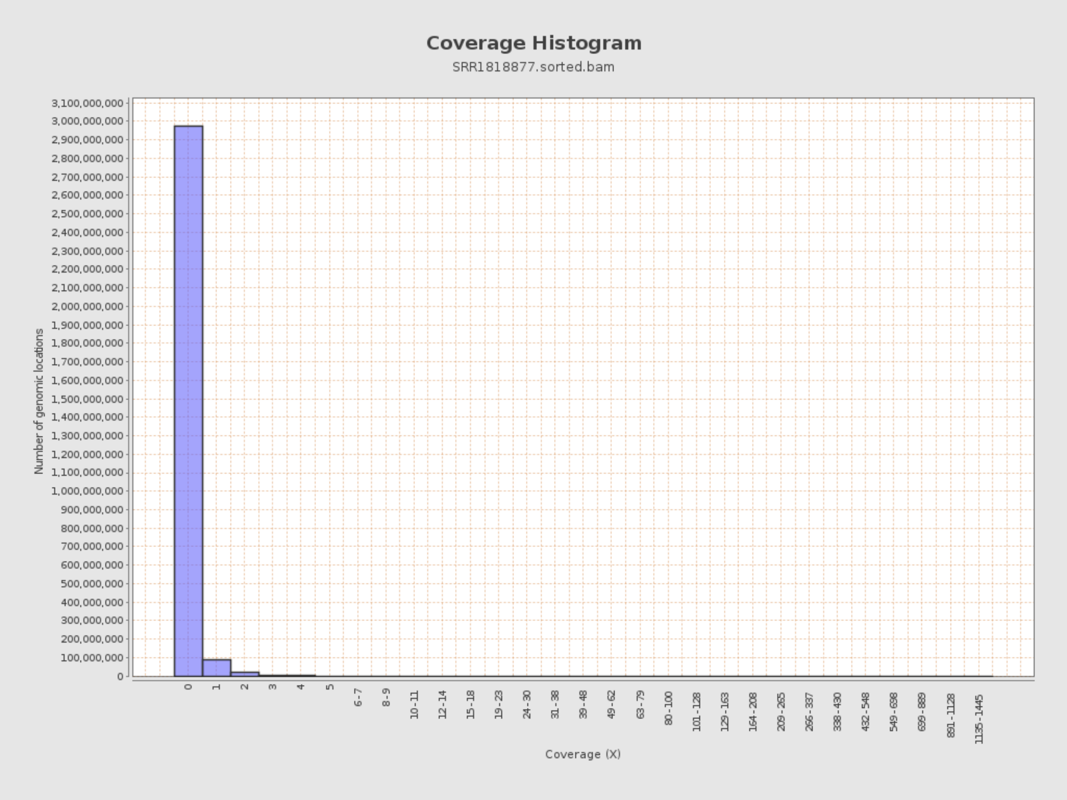
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16316187	0.0655	1.1364
chr2	243199373	11262646	0.0463	1.0496
chr3	198022430	11296982	0.057	0.3214
chr4	191154276	8549857	0.0447	0.377
chr5	180915260	10356626	0.0572	0.3428
chr6	171115067	7766658	0.0454	0.3252
chr7	159138663	15319796	0.0963	1.5791

chr8	146364022	18601579	0.1271	0.6329
chr9	141213431	6231209	0.0441	0.5272
chr10	135534747	7870574	0.0581	0.8698
chr11	135006516	7498873	0.0555	0.3906
chr12	133851895	6578071	0.0491	0.3013
chr13	115169878	5873544	0.051	0.3067
chr14	107349540	5276599	0.0492	0.3287
chr15	102531392	4730516	0.0461	0.2886
chr16	90354753	4127662	0.0457	0.7278
chr17	81195210	4340782	0.0535	0.4142
chr18	78077248	3036650	0.0389	0.5872
chr19	59128983	2905703	0.0491	1.032
chr20	63025520	6988545	0.1109	0.4871
chr21	48129895	2060716	0.0428	0.3181
chr22	51304566	1549006	0.0302	0.2768
chrMT	16571	656186	39.5985	22.8848
chrX	155270560	7035027	0.0453	0.3538
chrY	59373566	600475	0.0101	0.7967

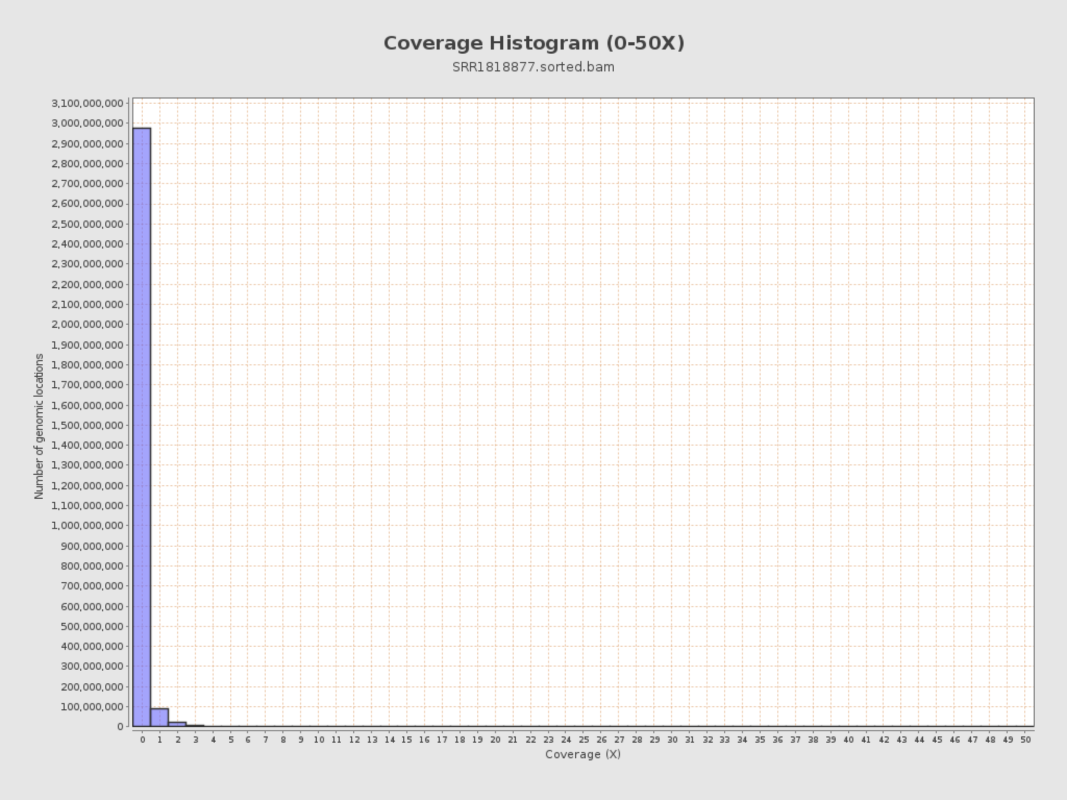
3. Results : Coverage across reference



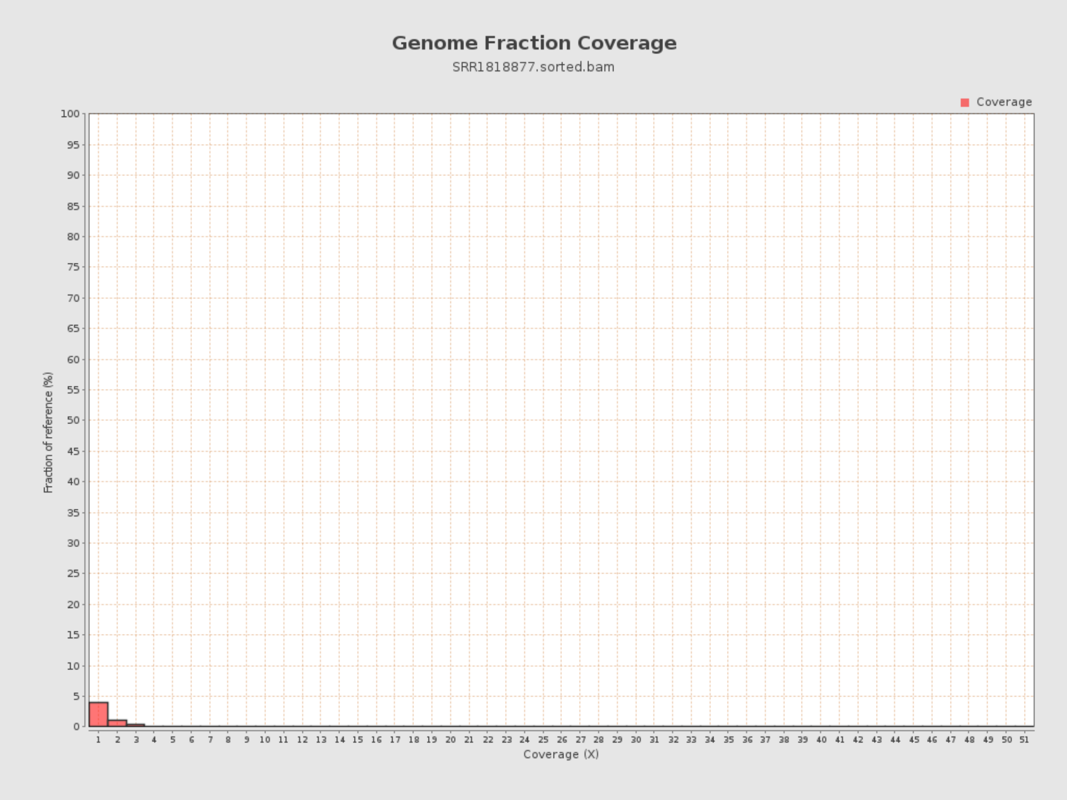
4. Results : Coverage Histogram



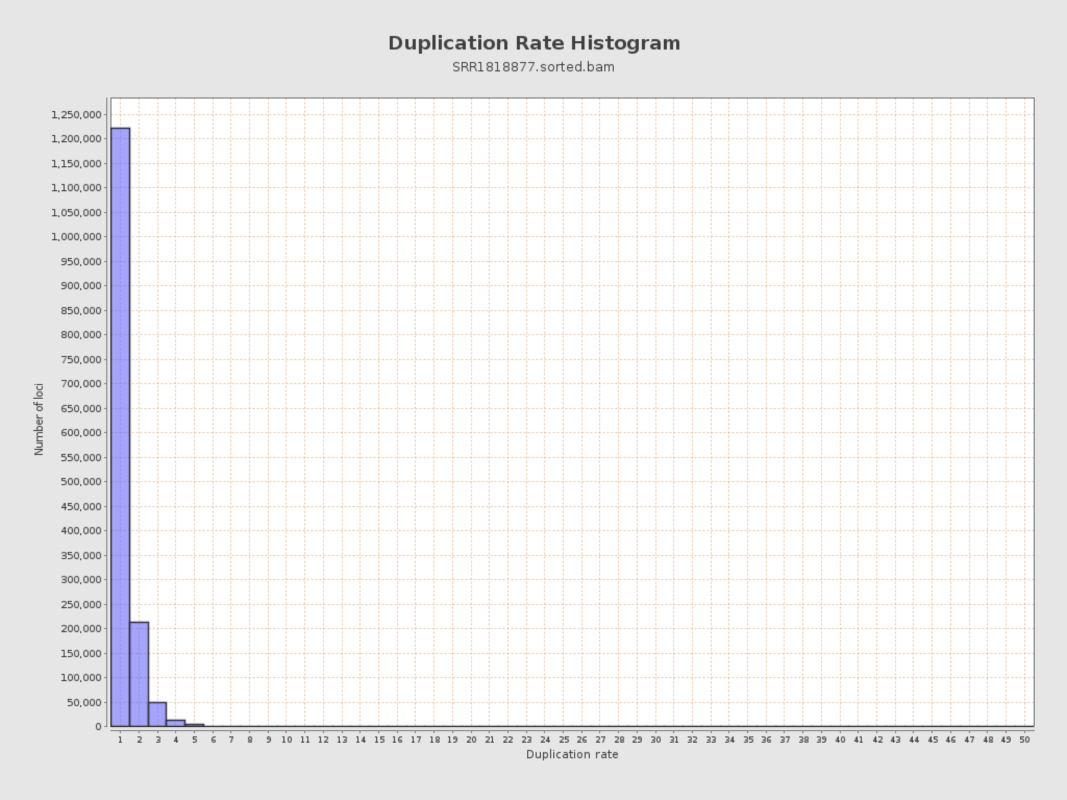
5. Results : Coverage Histogram (0-50X)



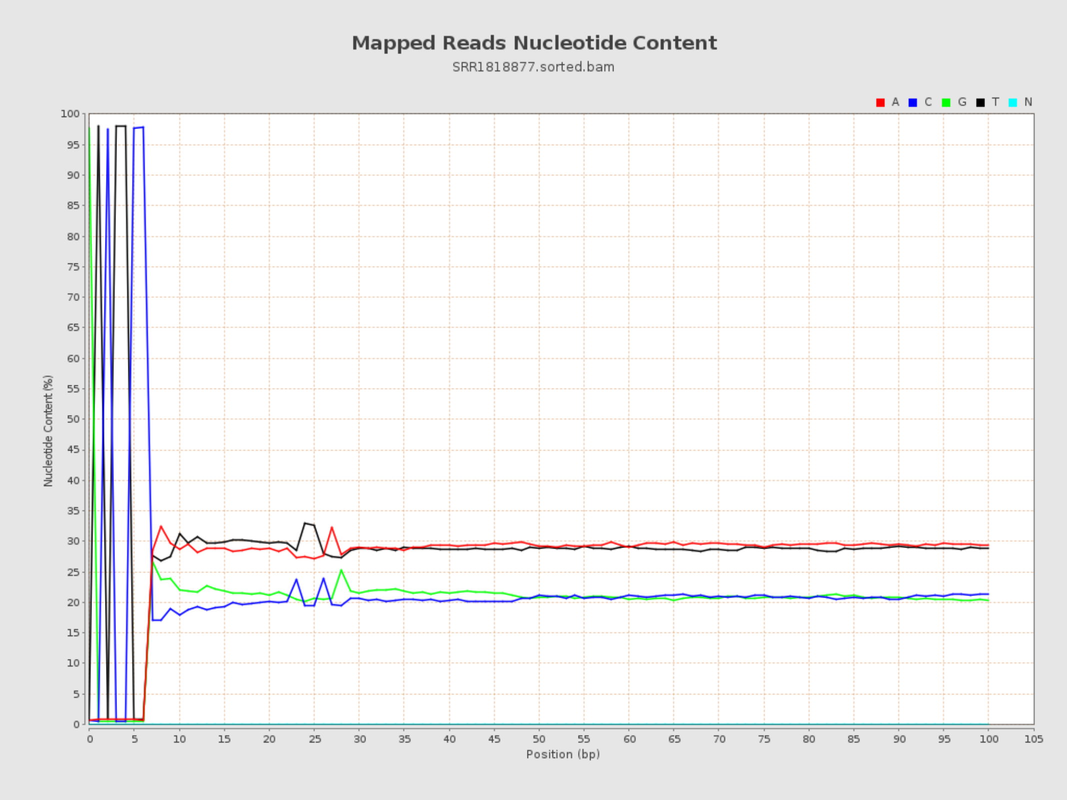
6. Results : Genome Fraction Coverage



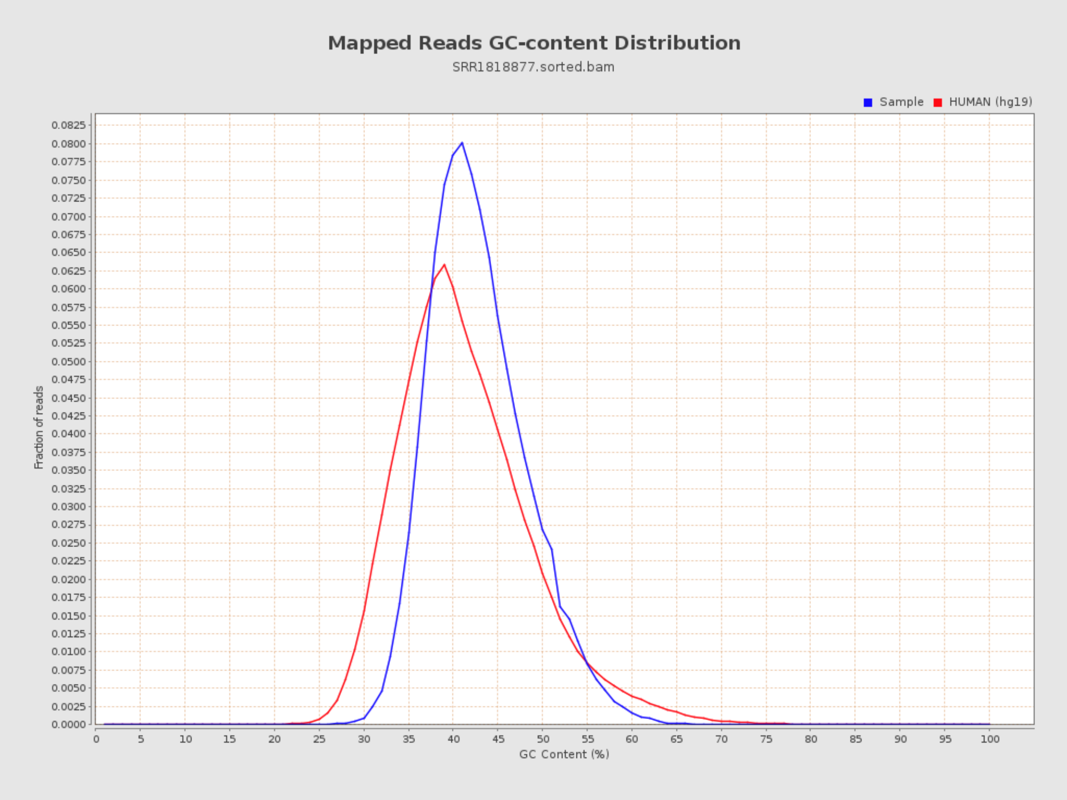
7. Results : Duplication Rate Histogram



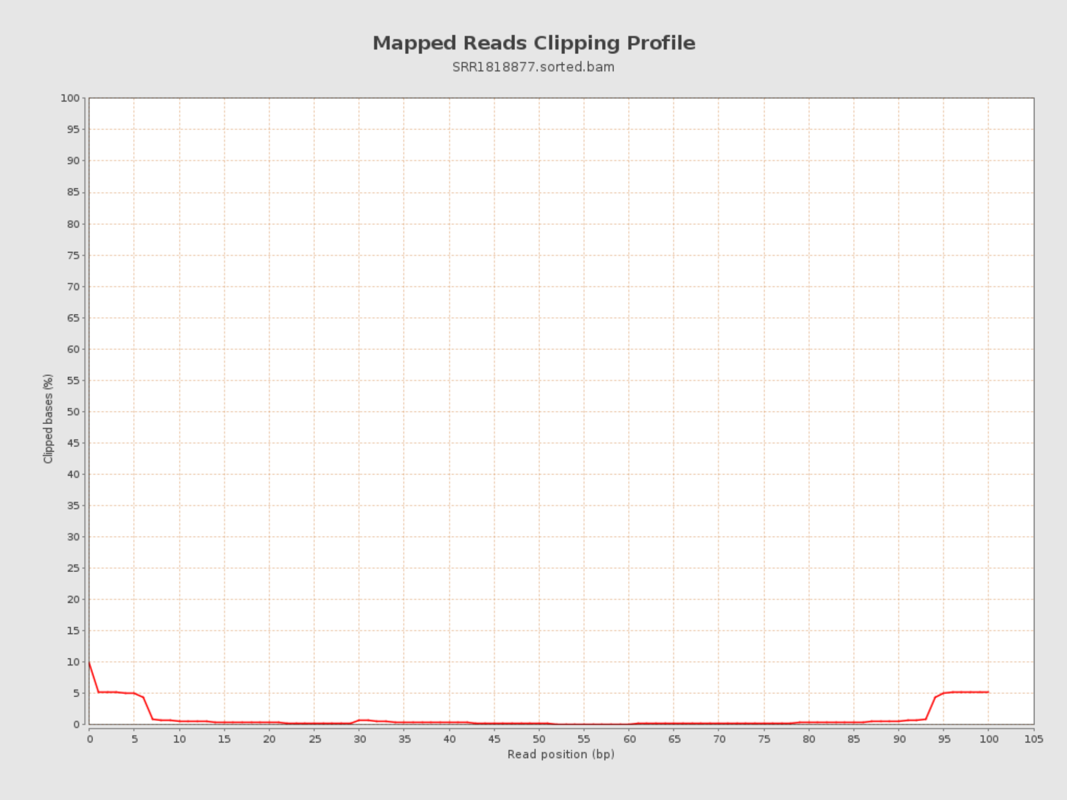
8. Results : Mapped Reads Nucleotide Content



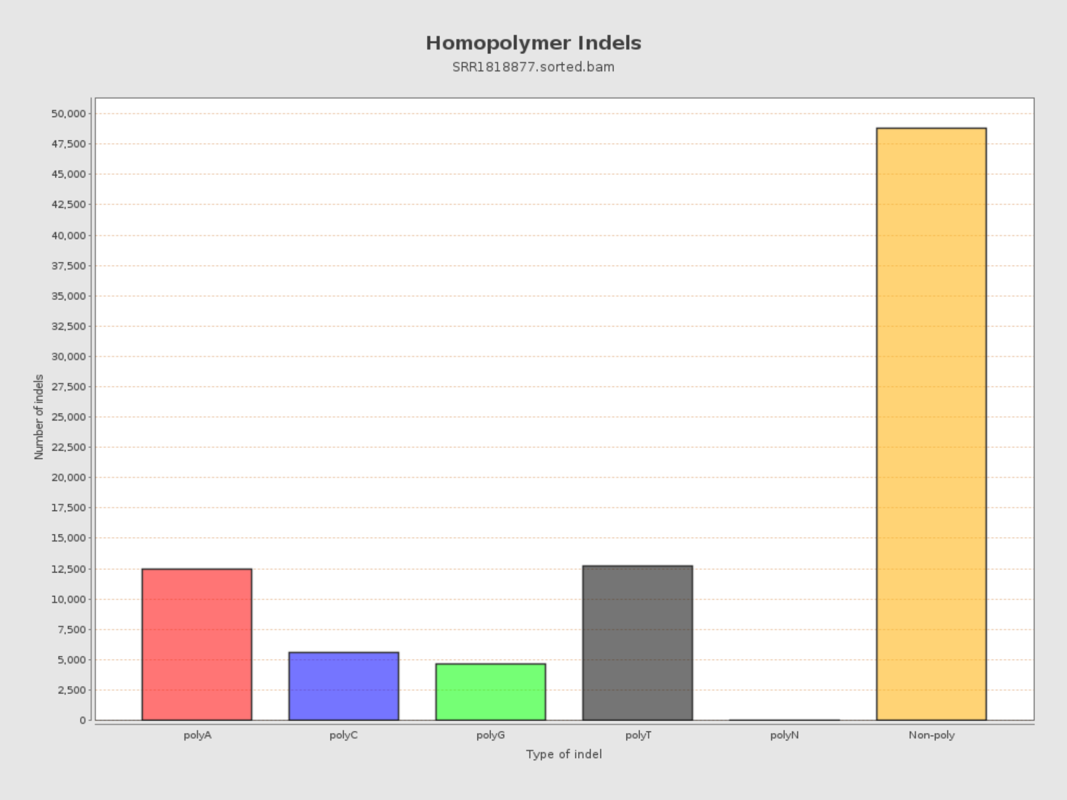
9. Results : Mapped Reads GC-content Distribution



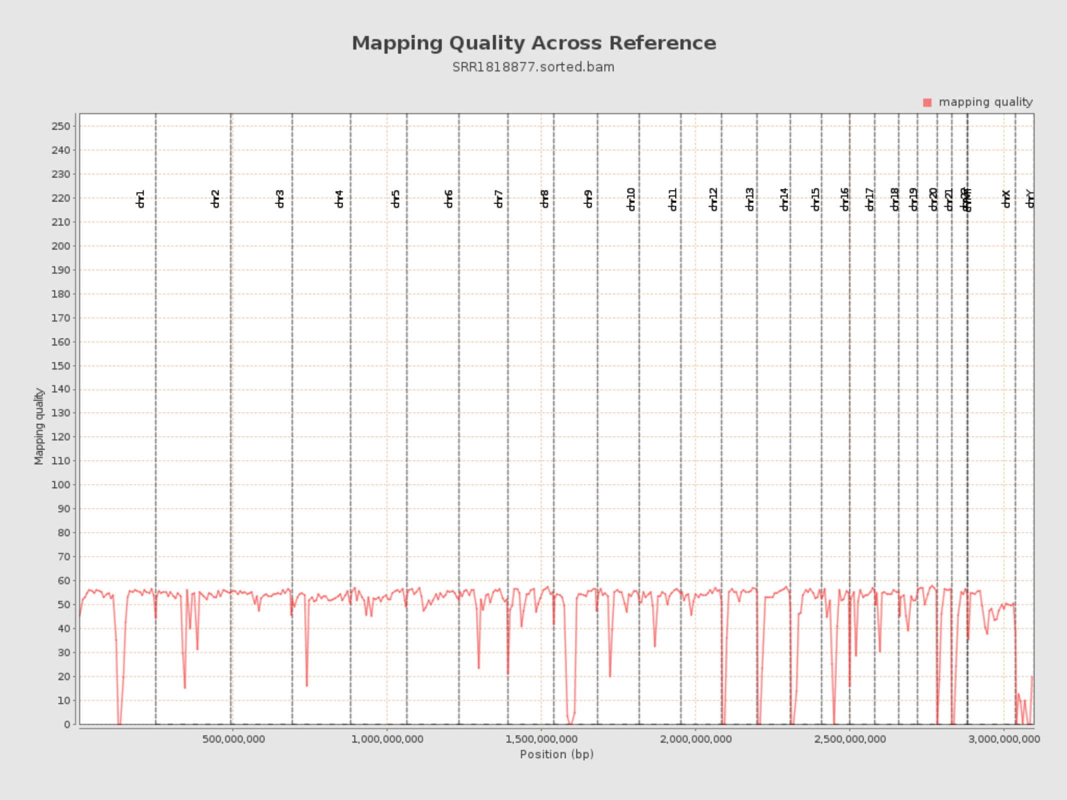
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram