Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:35:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818878.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_SRR1818878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818878.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:35:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,470,463
Mapped reads	1,447,290 / 98.42%
Unmapped reads	23,173 / 1.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,907 / 1.56%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	179,241 / 12.19%
Duplication rate	9.43%
Clipped reads	1,461,877 / 99.42%

2.2. ACGT Content

Number/percentage of A's	38,040,708 / 28.42%
Number/percentage of C's	29,367,195 / 21.94%
Number/percentage of T's	37,332,451 / 27.89%
Number/percentage of G's	29,125,928 / 21.76%
Number/percentage of N's	1,968 / 0%
GC Percentage	43.69%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.5781

2.4. Mapping Quality

Mean Mapping Quality	49.19

2.5. Mismatches and indels

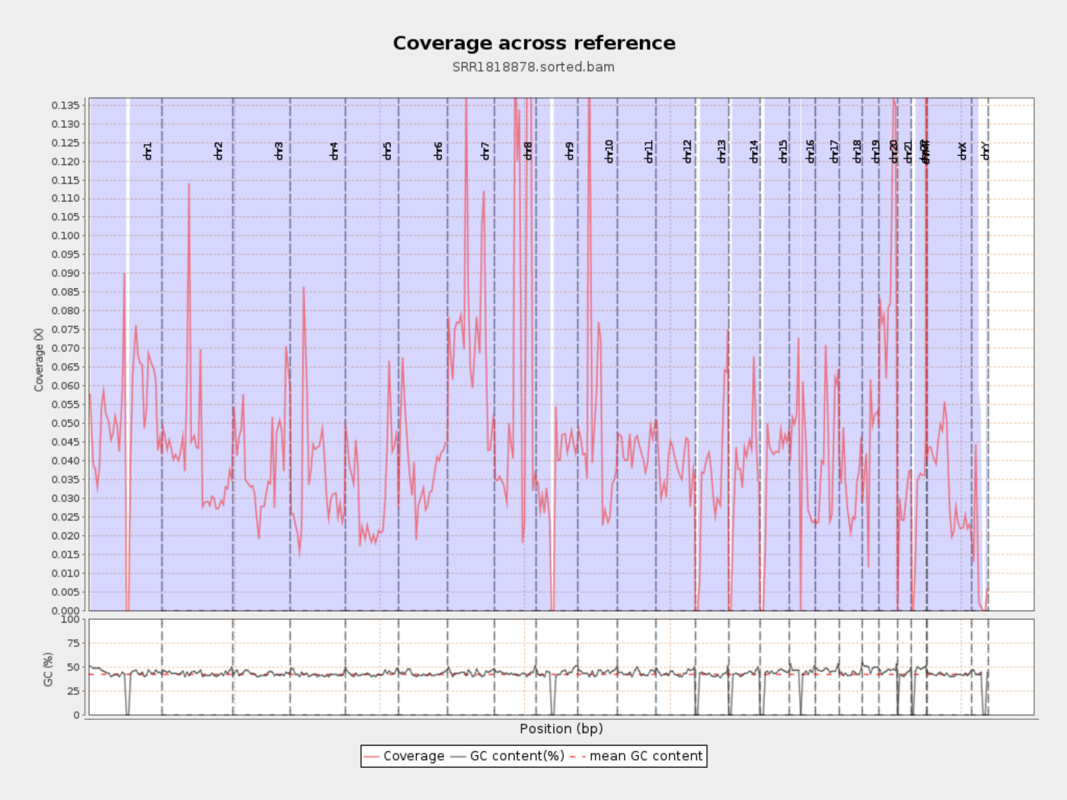
General error rate	0.64%
Mismatches	808,696
Insertions	18,511
Mapped reads with at least one insertion	1.24%
Deletions	38,738
Mapped reads with at least one deletion	2.62%
Homopolymer indels	40.64%

2.6. Chromosome stats

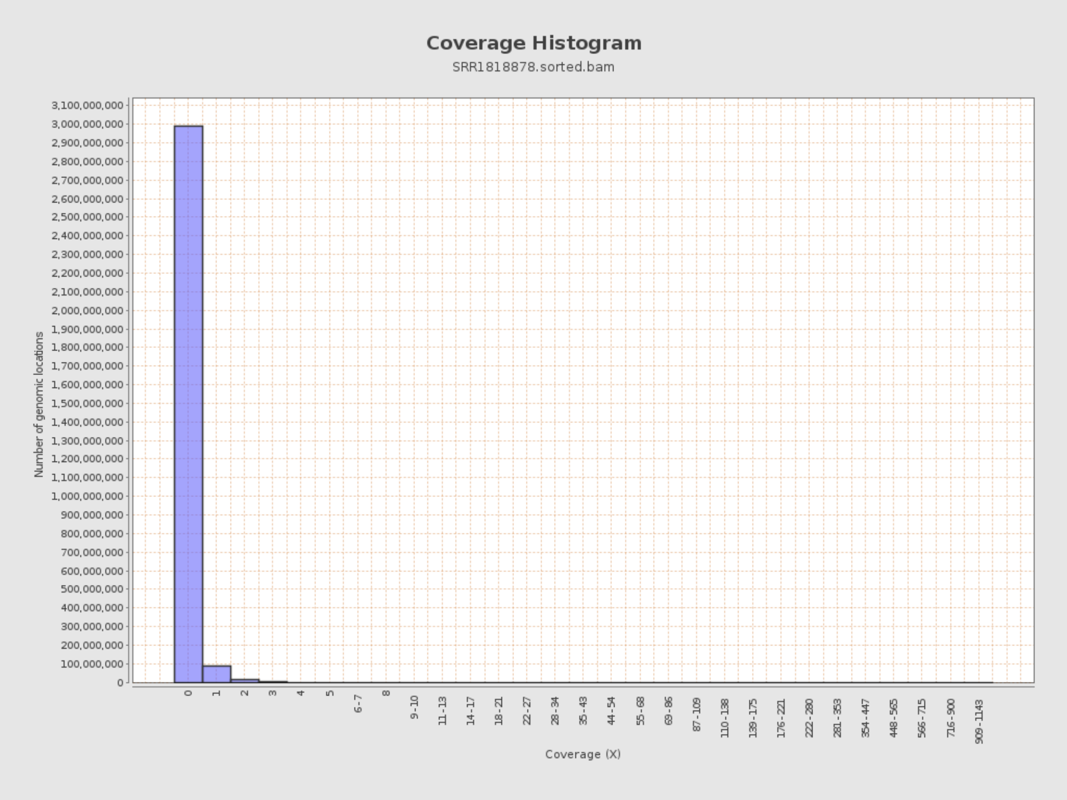
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12768228	0.0512	0.8478
chr2	243199373	10071844	0.0414	0.6823
chr3	198022430	8063220	0.0407	0.2454
chr4	191154276	6652755	0.0348	0.3708
chr5	180915260	5816793	0.0322	0.2195
chr6	171115067	6478289	0.0379	0.2624
chr7	159138663	11917727	0.0749	1.3302

chr8	146364022	11347229	0.0775	0.4634
chr9	141213431	4922424	0.0349	0.5039
chr10	135534747	6596009	0.0487	0.9906
chr11	135006516	5888329	0.0436	0.3296
chr12	133851895	5198154	0.0388	0.2335
chr13	115169878	3952290	0.0343	0.2167
chr14	107349540	3874145	0.0361	0.249
chr15	102531392	3724641	0.0363	0.2254
chr16	90354753	3547008	0.0393	0.4579
chr17	81195210	3533956	0.0435	0.4182
chr18	78077248	2575916	0.033	0.6033
chr19	59128983	2557235	0.0432	0.7918
chr20	63025520	5740853	0.0911	0.3927
chr21	48129895	1327706	0.0276	0.2722
chr22	51304566	1302118	0.0254	0.2011
chrMT	16571	161336	9.736	6.9142
chrX	155270560	5326008	0.0343	0.2996
chrY	59373566	603849	0.0102	0.7281

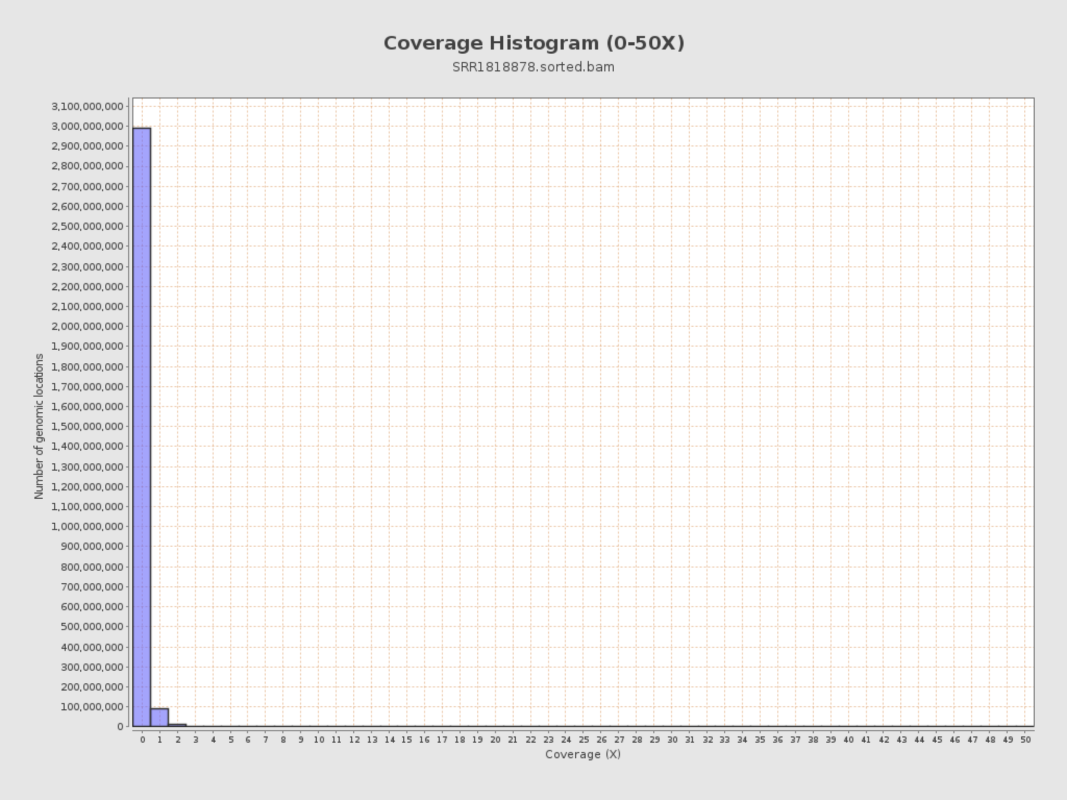
3. Results : Coverage across reference



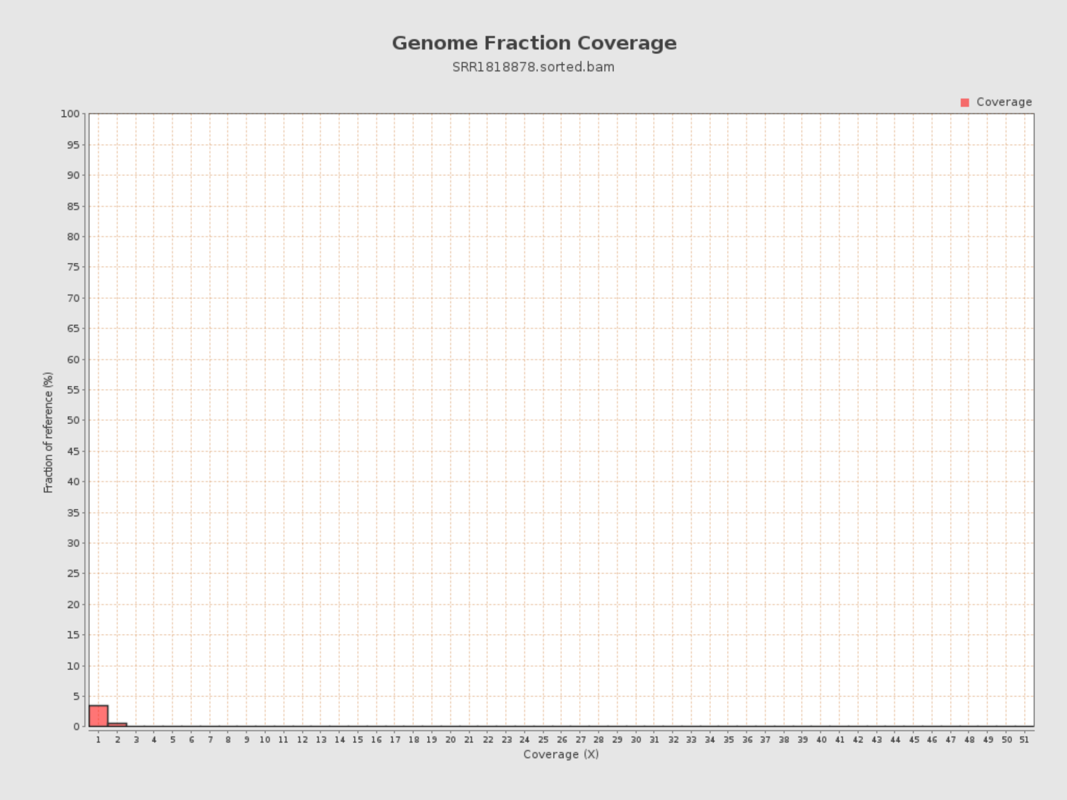
4. Results : Coverage Histogram



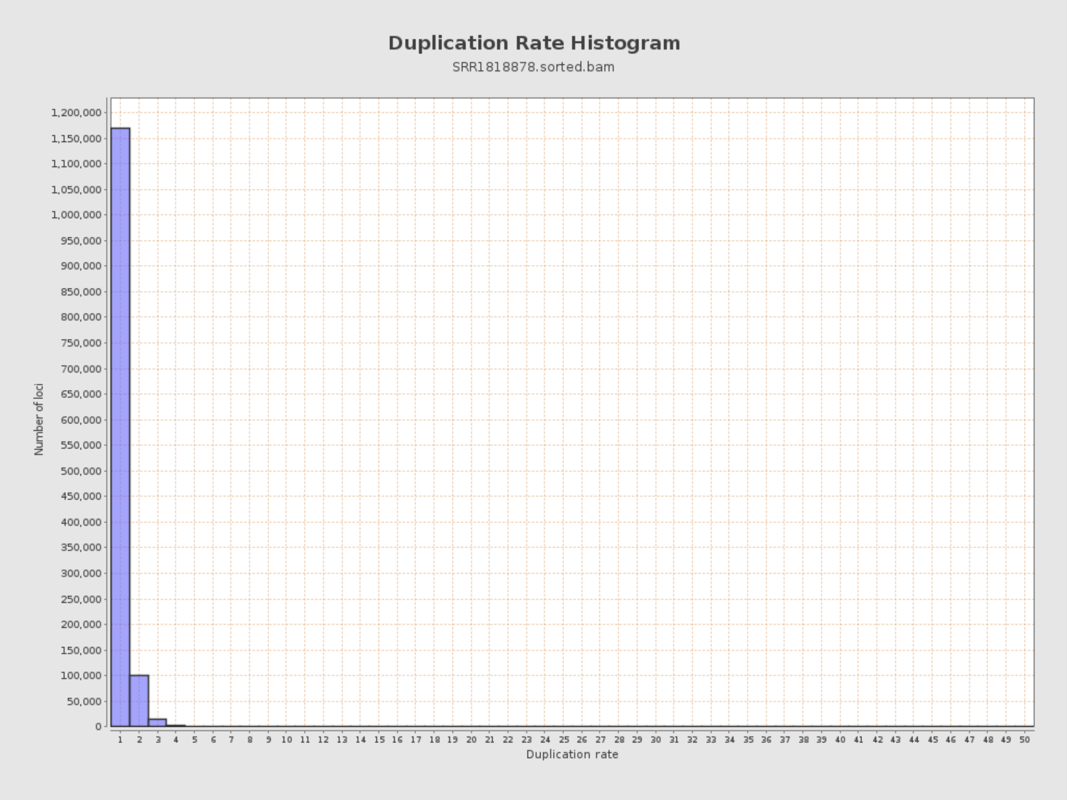
5. Results : Coverage Histogram (0-50X)



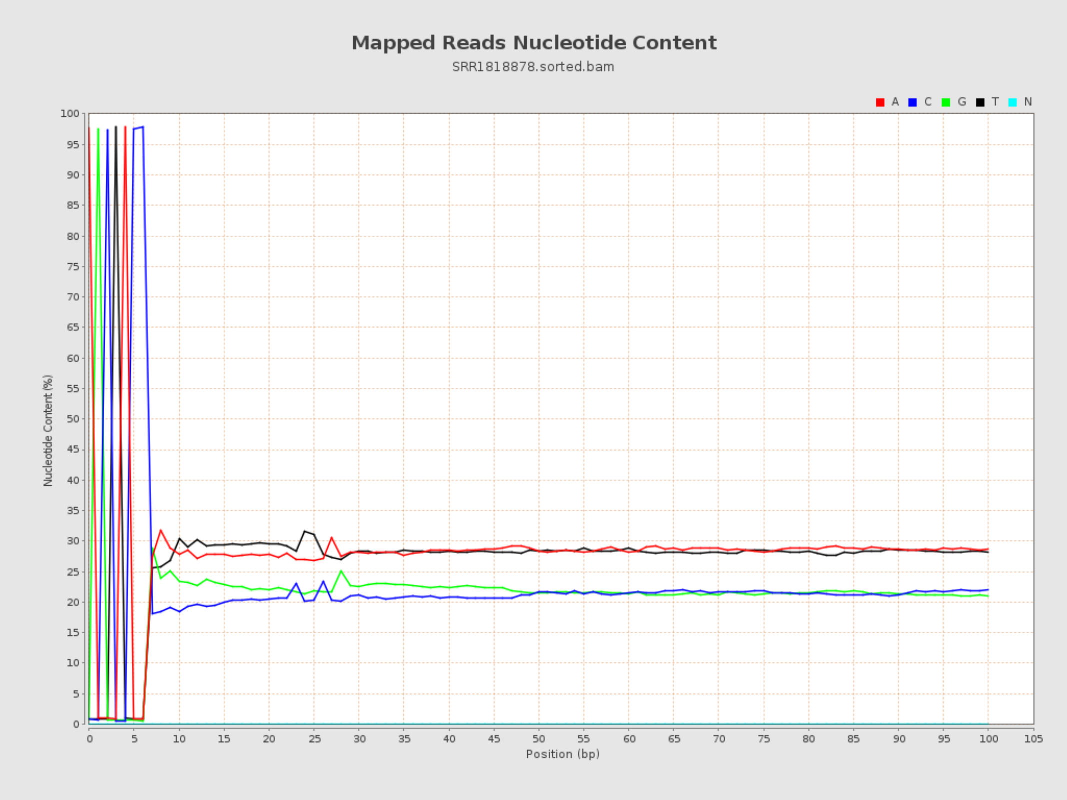
6. Results : Genome Fraction Coverage



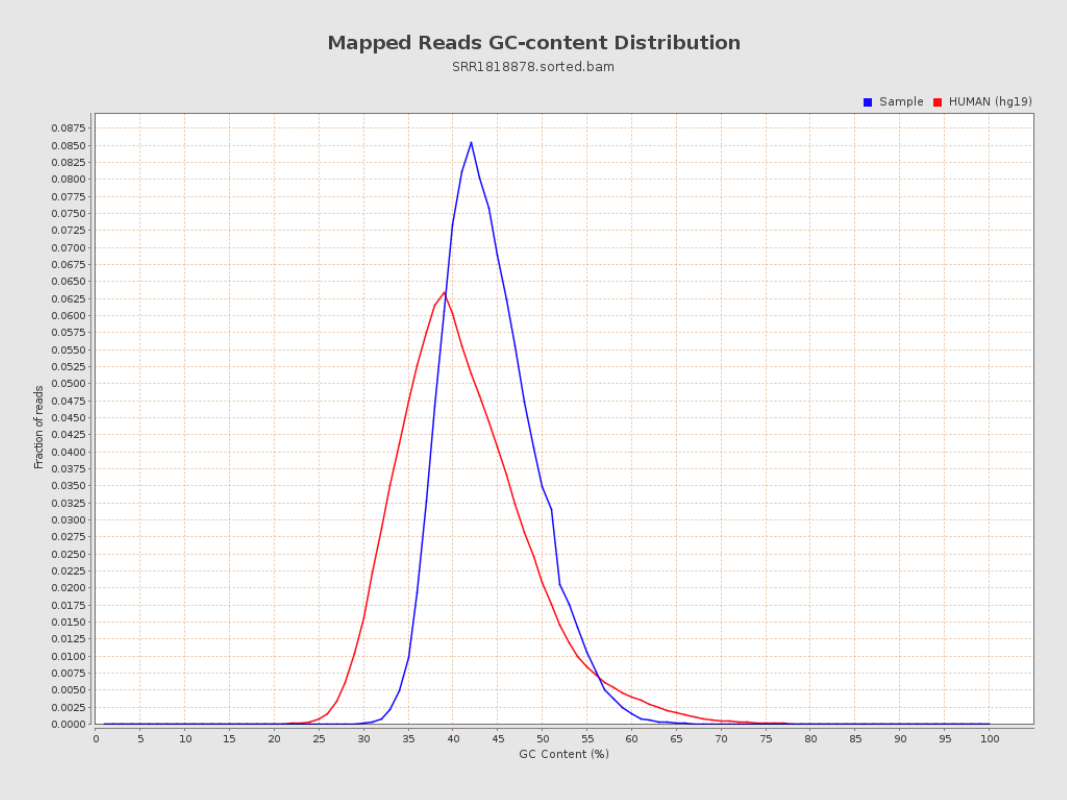
7. Results : Duplication Rate Histogram



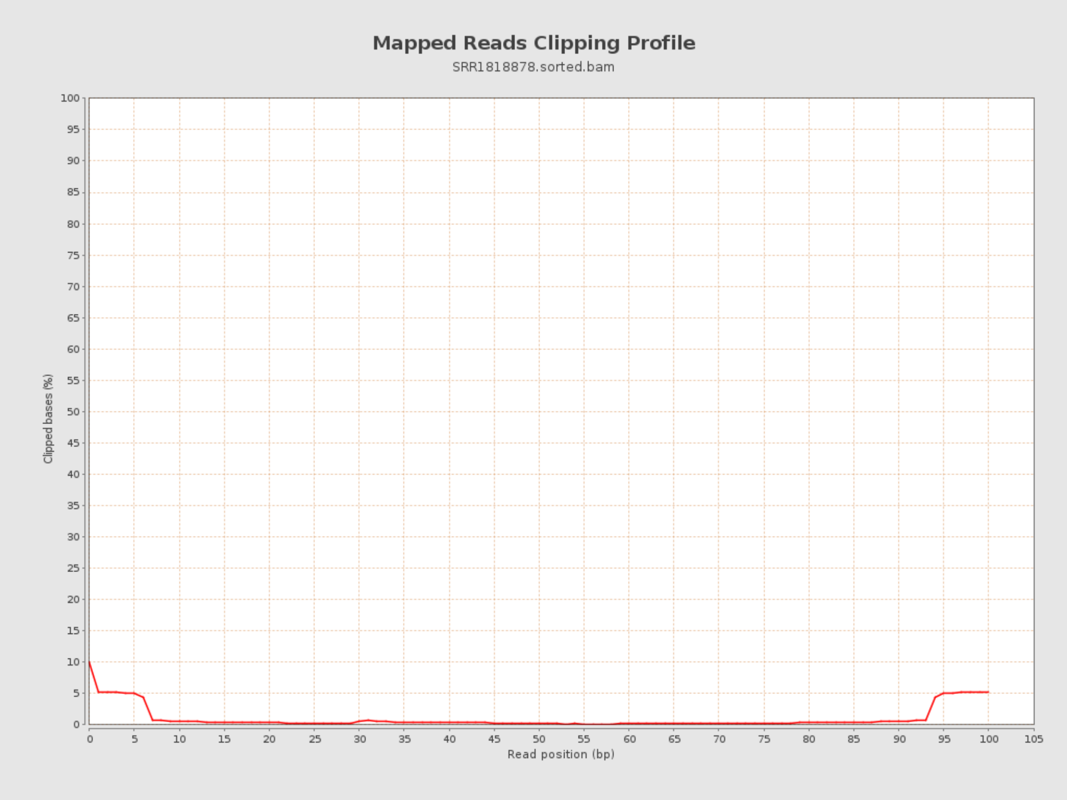
8. Results : Mapped Reads Nucleotide Content



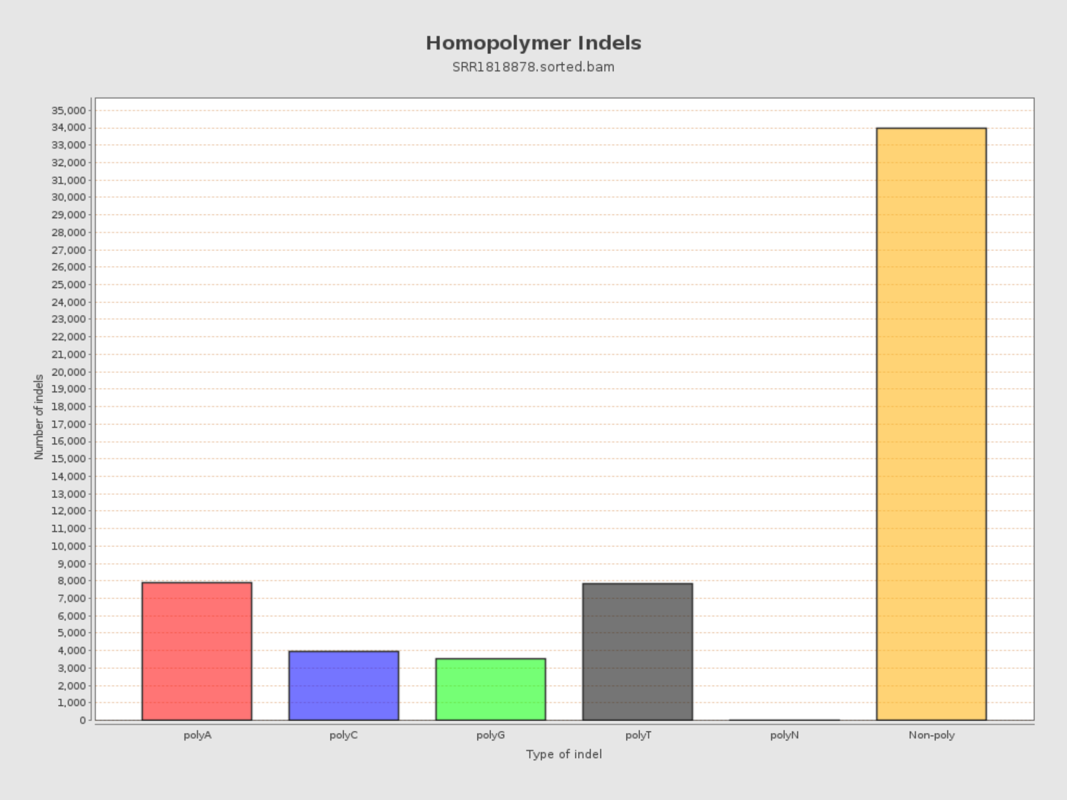
9. Results : Mapped Reads GC-content Distribution



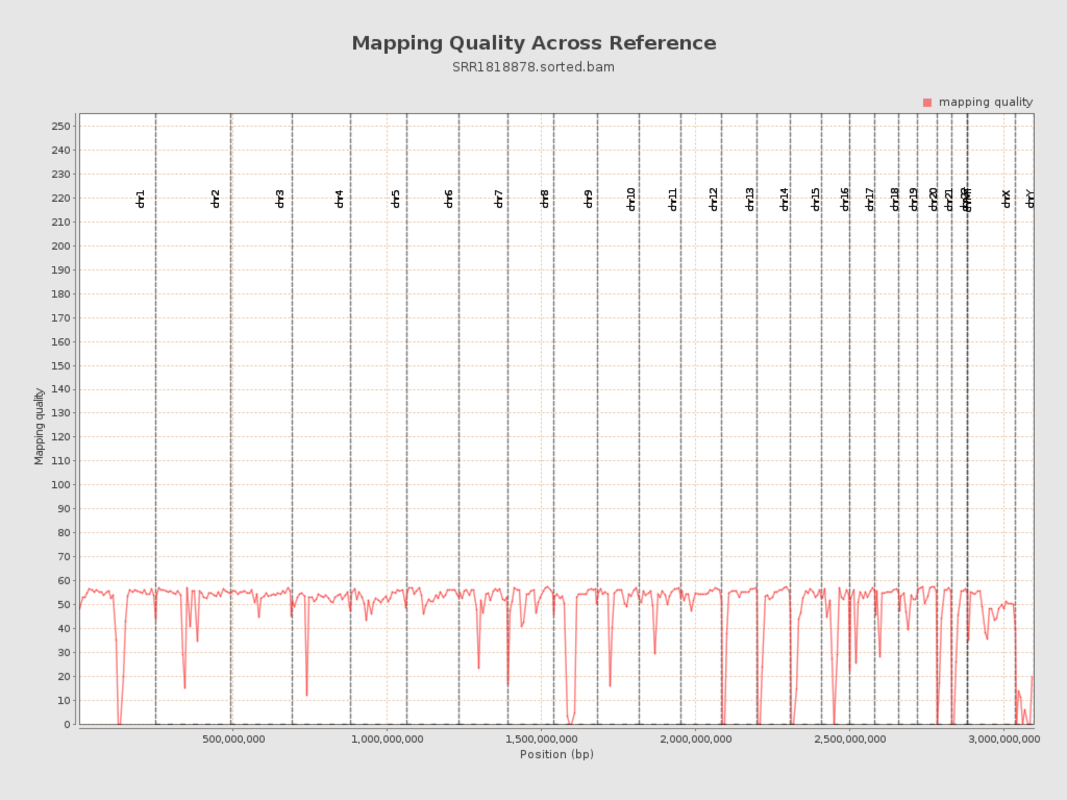
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram