Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 14:24:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013177.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_SRR6013177 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013177.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 14:24:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013177.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,561,868
Mapped reads	2,293,852 / 89.54%
Unmapped reads	268,016 / 10.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,056 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	81,211 / 3.17%
Duplication rate	2.66%
Clipped reads	1,183,562 / 46.2%

2.2. ACGT Content

Number/percentage of A's	40,005,701 / 26.88%
Number/percentage of C's	28,583,281 / 19.2%
Number/percentage of T's	45,424,702 / 30.52%
Number/percentage of G's	34,801,872 / 23.38%
Number/percentage of N's	33,306 / 0.02%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0481

Standard Deviation	0.3936

2.4. Mapping Quality

Mean Mapping Quality	44.03

2.5. Mismatches and indels

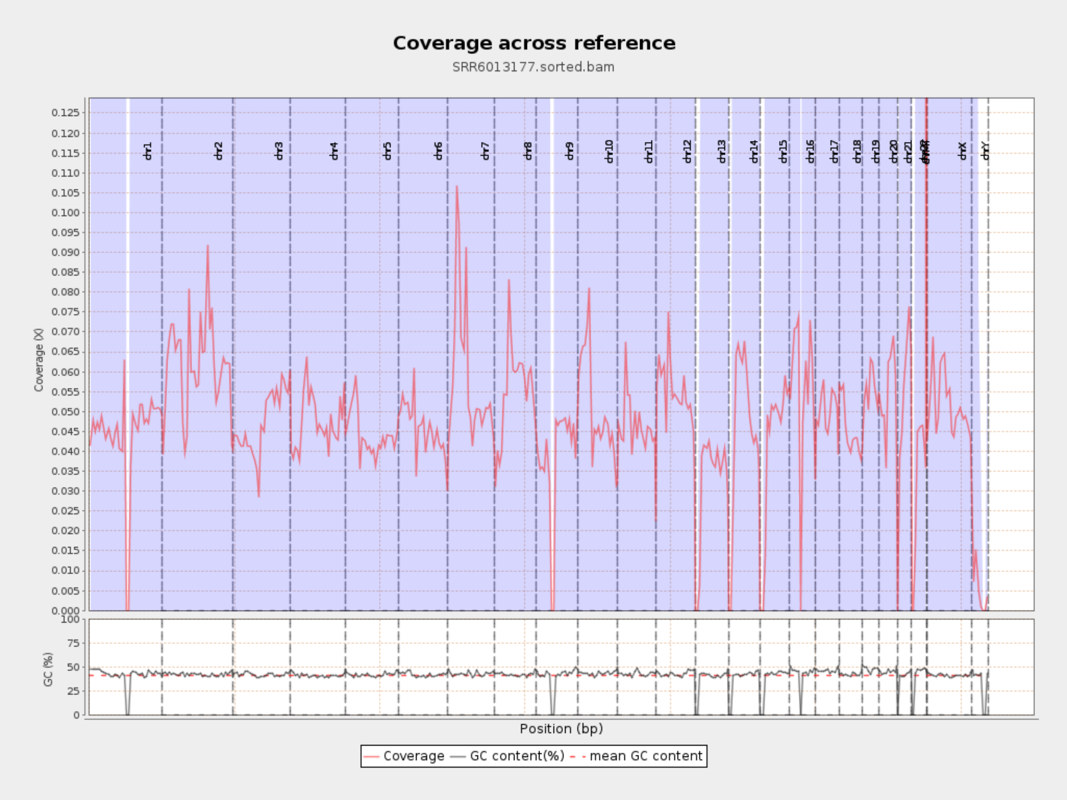
General error rate	0.8%
Mismatches	1,179,255
Insertions	10,238
Mapped reads with at least one insertion	0.44%
Deletions	35,810
Mapped reads with at least one deletion	1.54%
Homopolymer indels	44.79%

2.6. Chromosome stats

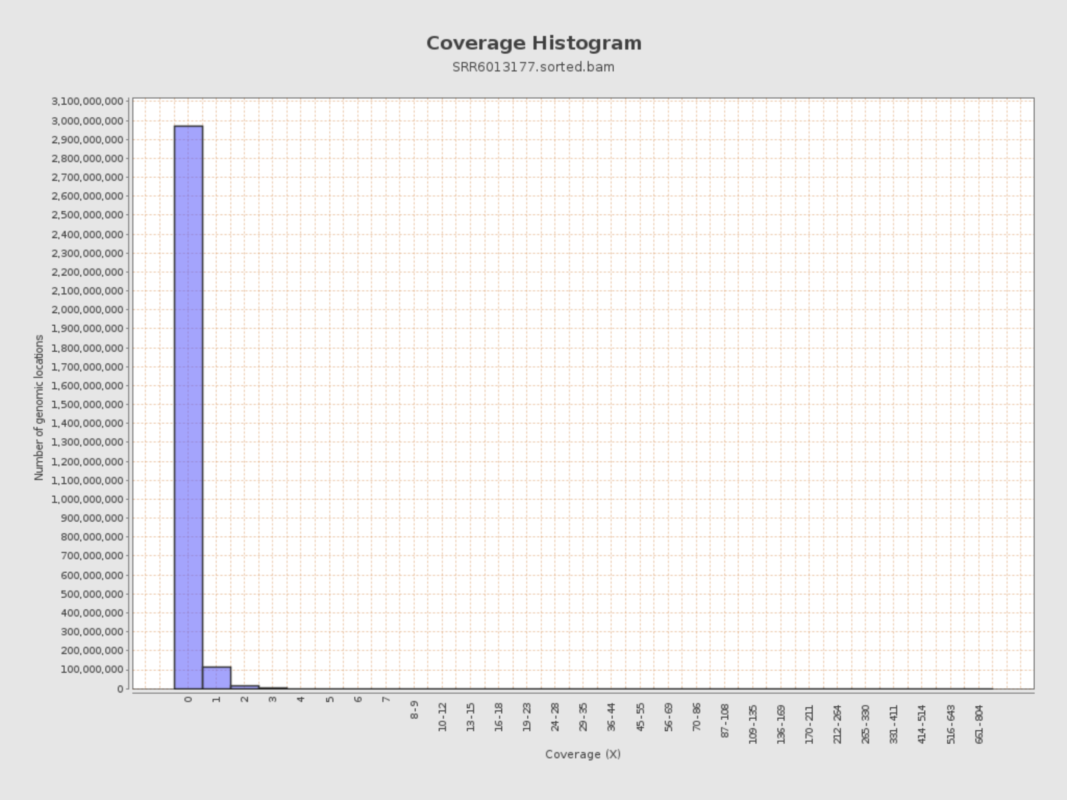
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10989412	0.0441	0.6154
chr2	243199373	15101830	0.0621	0.5107
chr3	198022430	9325769	0.0471	0.2444
chr4	191154276	9045927	0.0473	0.2541
chr5	180915260	7995543	0.0442	0.2377
chr6	171115067	7848289	0.0459	0.3
chr7	159138663	9383487	0.059	0.7181

chr8	146364022	8077944	0.0552	0.364
chr9	141213431	5343619	0.0378	0.31
chr10	135534747	6984641	0.0515	0.4149
chr11	135006516	6279508	0.0465	0.2988
chr12	133851895	7402820	0.0553	0.2702
chr13	115169878	3692268	0.0321	0.2079
chr14	107349540	4915140	0.0458	0.2573
chr15	102531392	4216113	0.0411	0.2352
chr16	90354753	5075784	0.0562	0.3026
chr17	81195210	4069976	0.0501	0.2767
chr18	78077248	3558614	0.0456	0.5641
chr19	59128983	3268292	0.0553	0.5054
chr20	63025520	3428122	0.0544	0.2687
chr21	48129895	2516682	0.0523	0.2728
chr22	51304566	1570597	0.0306	0.1963
chrMT	16571	426051	25.7106	17.9135
chrX	155270560	8048496	0.0518	0.2785
chrY	59373566	346358	0.0058	0.1222

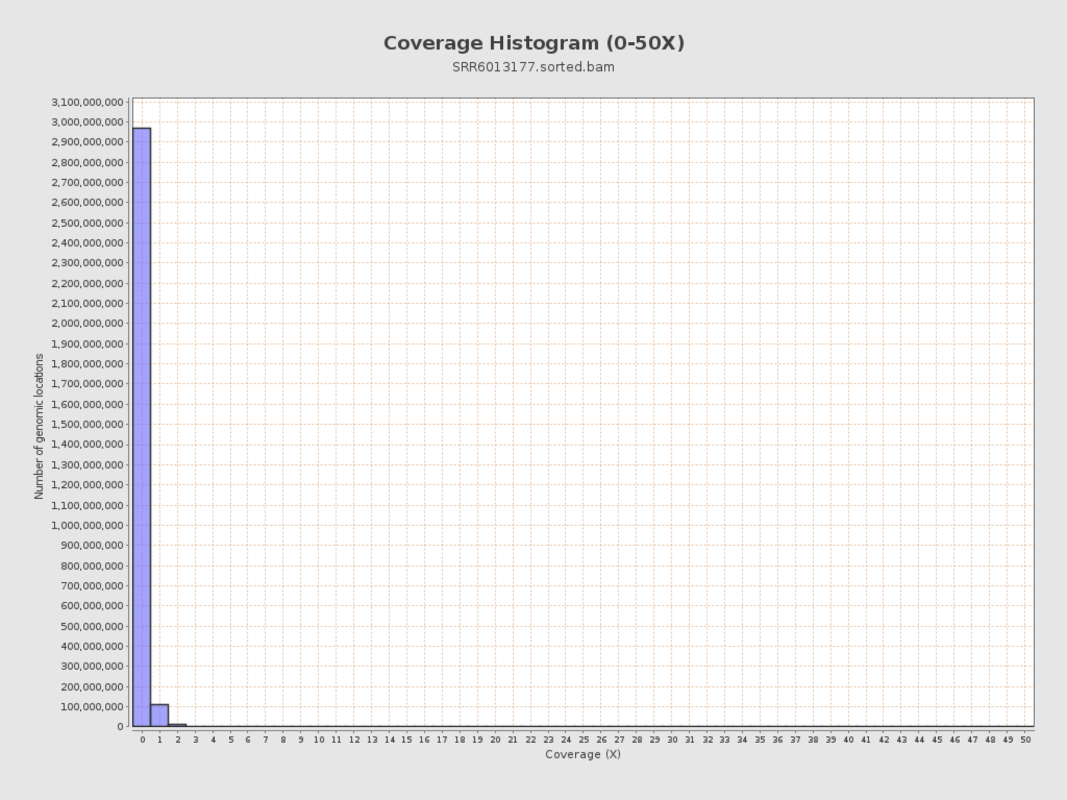
3. Results : Coverage across reference



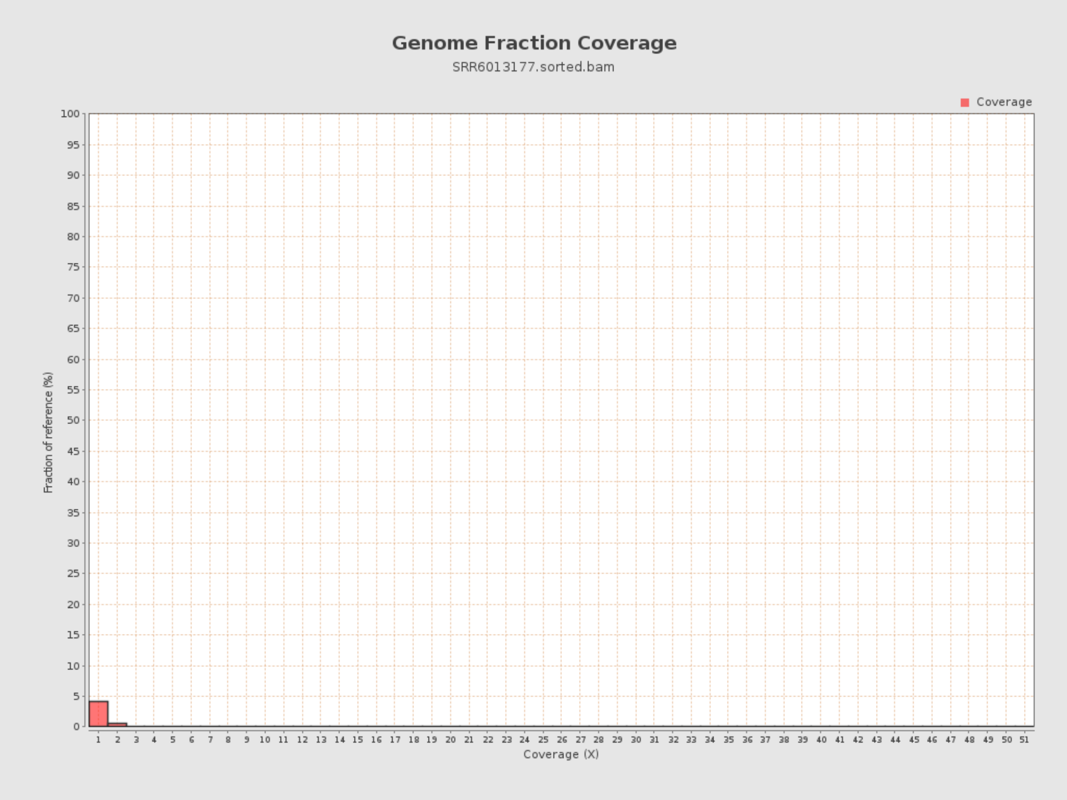
4. Results : Coverage Histogram



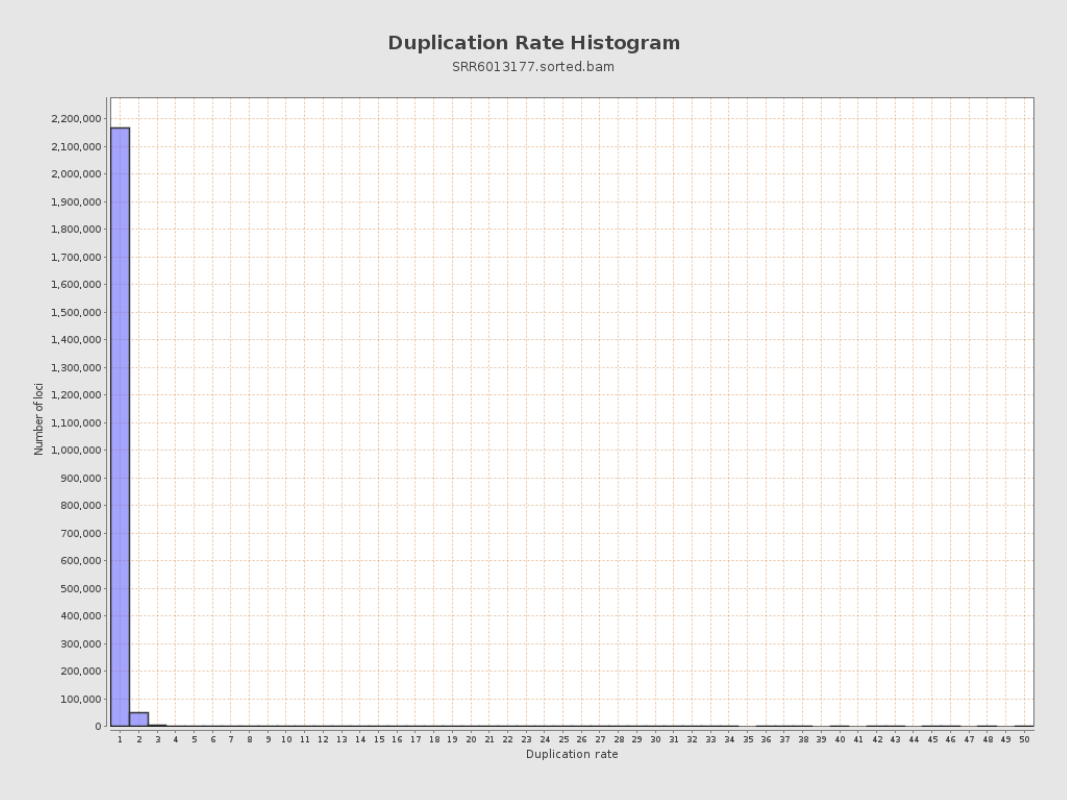
5. Results : Coverage Histogram (0-50X)



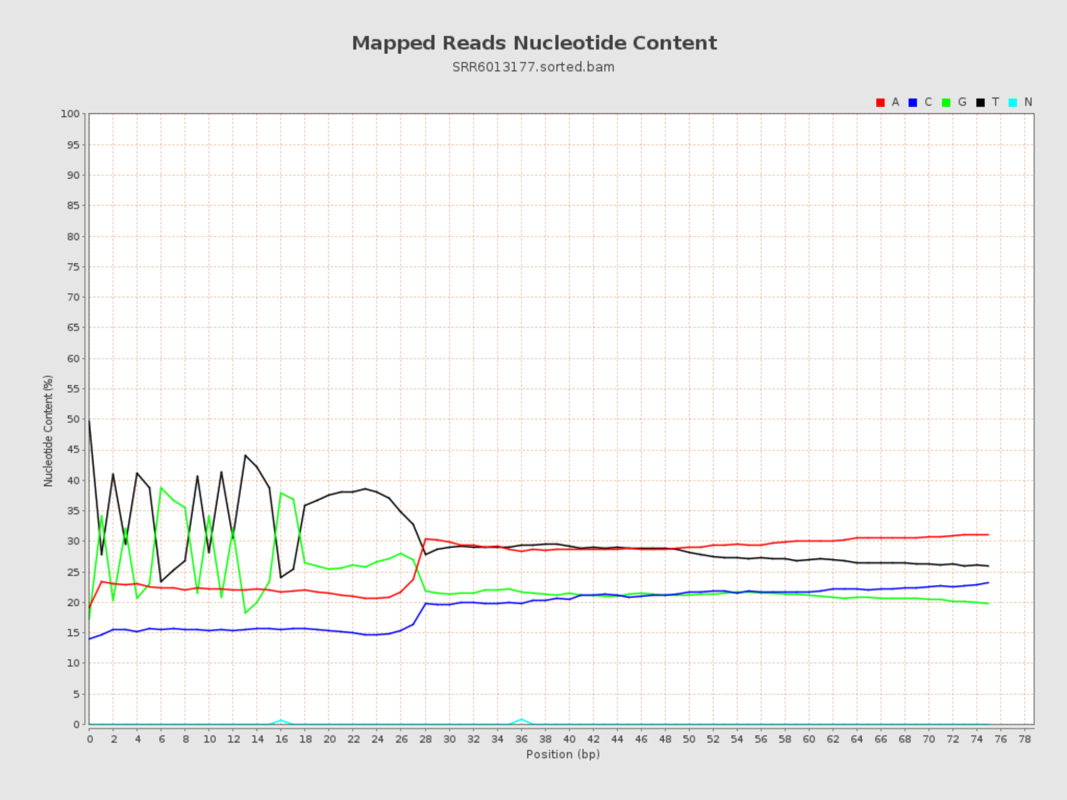
6. Results : Genome Fraction Coverage



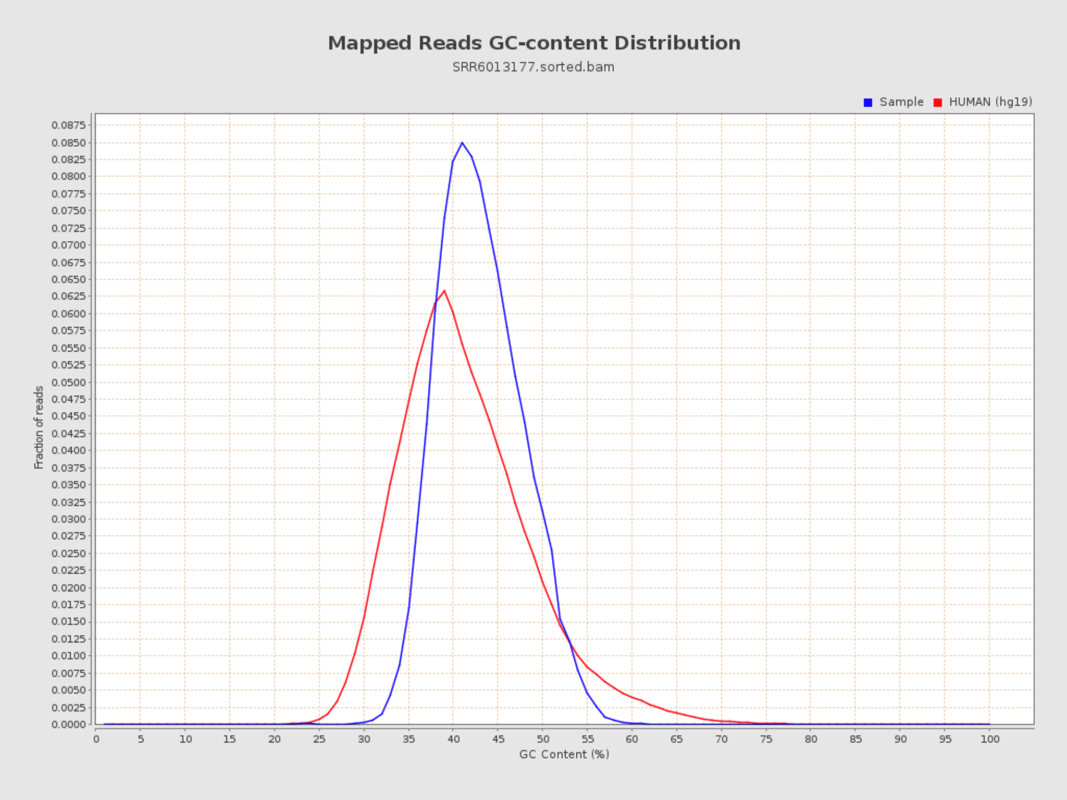
7. Results : Duplication Rate Histogram



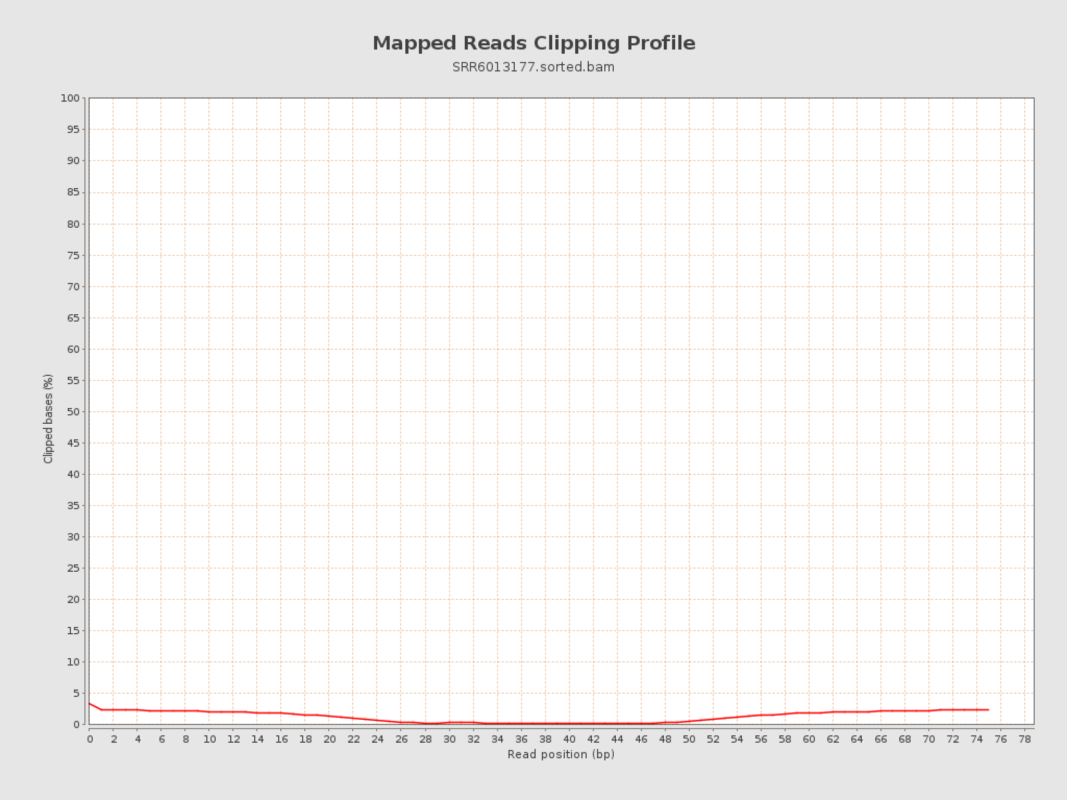
8. Results : Mapped Reads Nucleotide Content



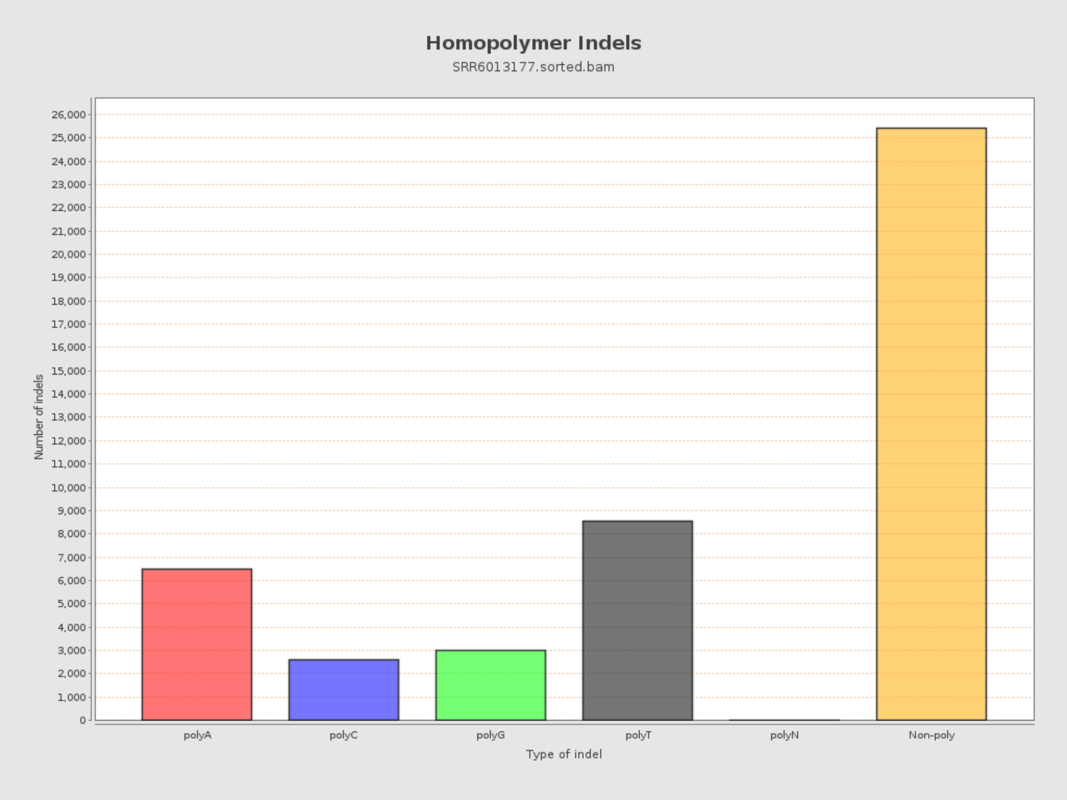
9. Results : Mapped Reads GC-content Distribution



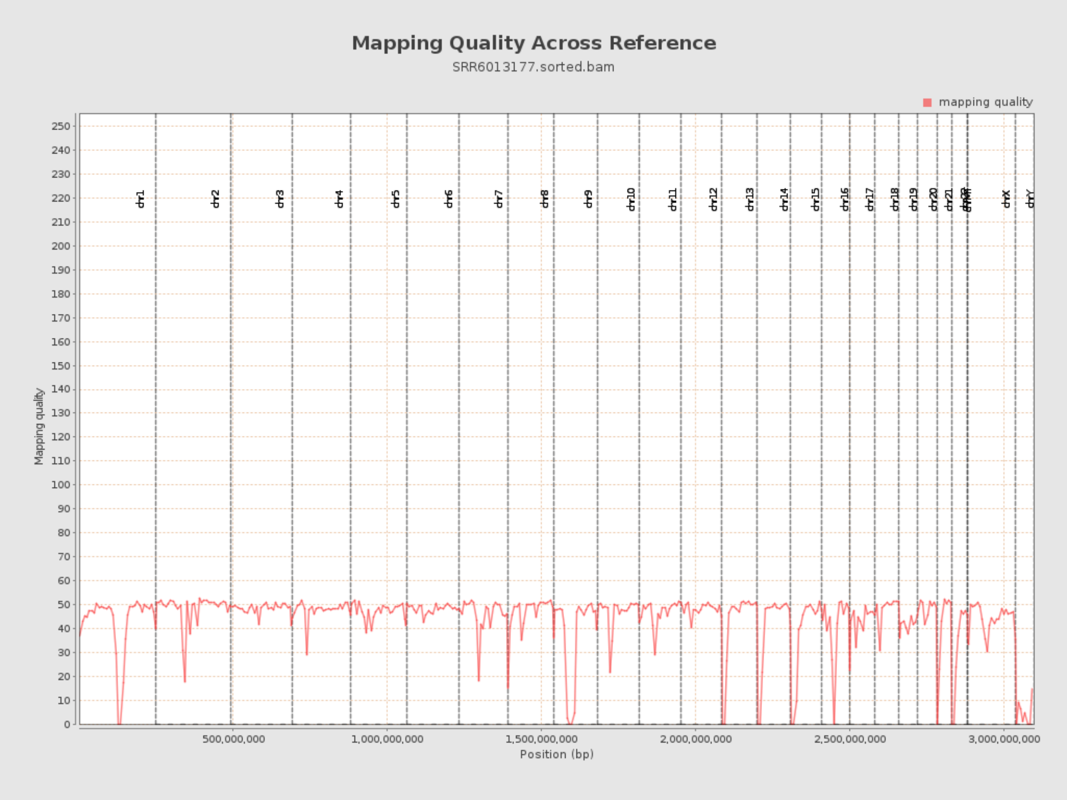
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram