Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 22:34:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013345.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_SRR6013345 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013345.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 22:34:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013345.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,324,432
Mapped reads	2,076,667 / 89.34%
Unmapped reads	247,765 / 10.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,218 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	90,356 / 3.89%
Duplication rate	3.45%
Clipped reads	947,007 / 40.74%

2.2. ACGT Content

Number/percentage of A's	37,485,409 / 27.16%
Number/percentage of C's	26,274,418 / 19.03%
Number/percentage of T's	42,918,730 / 31.09%
Number/percentage of G's	31,328,078 / 22.69%
Number/percentage of N's	34,368 / 0.02%
GC Percentage	41.73%

2.3. Coverage

Mean	0.0446

Standard Deviation	0.3745

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

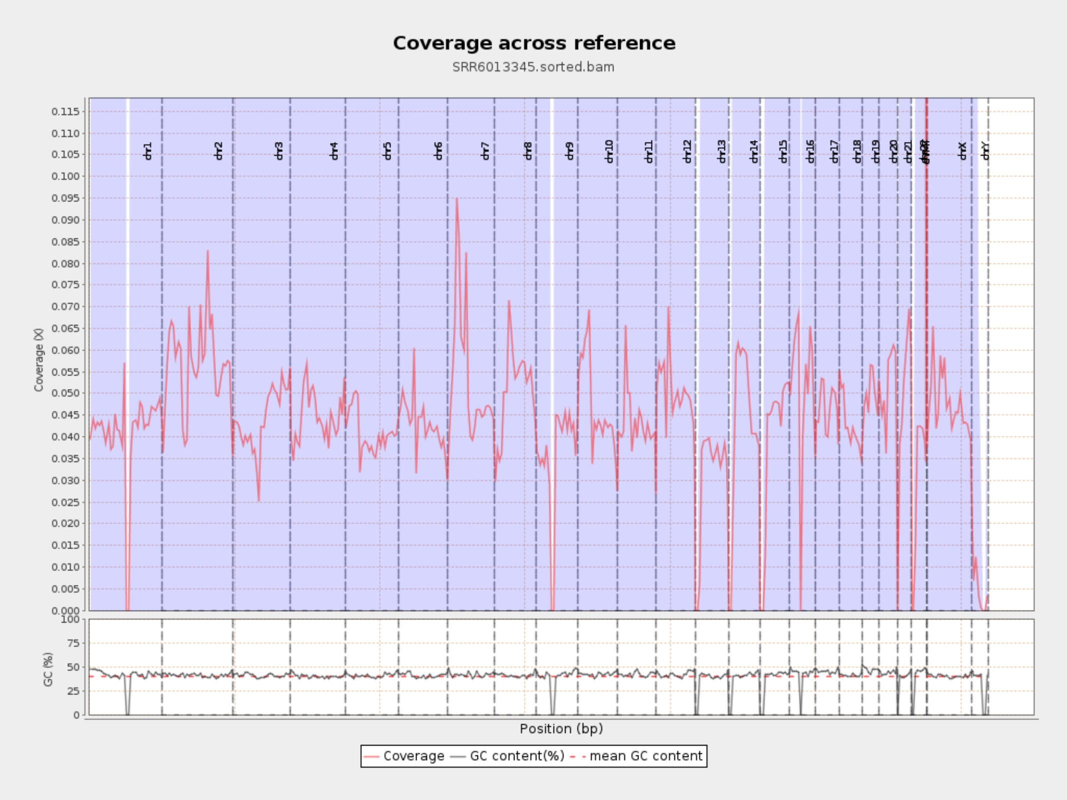
General error rate	0.81%
Mismatches	1,100,867
Insertions	9,663
Mapped reads with at least one insertion	0.46%
Deletions	33,959
Mapped reads with at least one deletion	1.62%
Homopolymer indels	45.3%

2.6. Chromosome stats

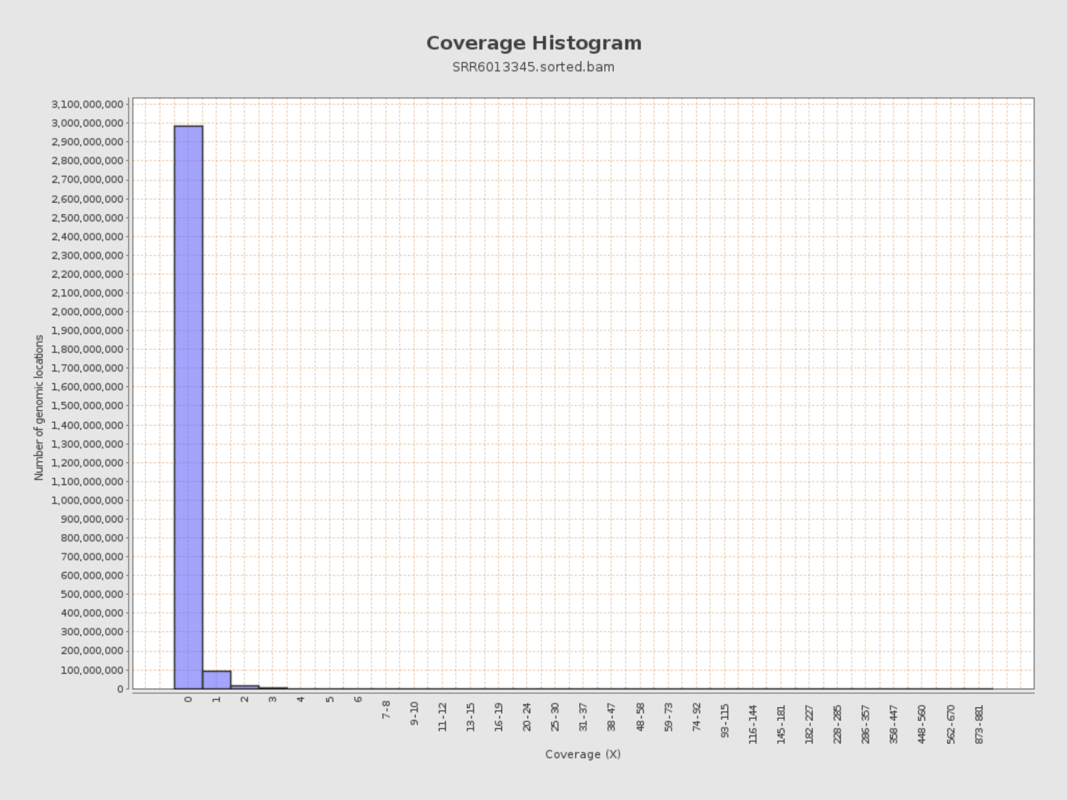
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10134292	0.0407	0.5698
chr2	243199373	13854151	0.057	0.5048
chr3	198022430	8701059	0.0439	0.2467
chr4	191154276	8526575	0.0446	0.2558
chr5	180915260	7401637	0.0409	0.2399
chr6	171115067	7379998	0.0431	0.3001
chr7	159138663	8598681	0.054	0.6268

chr8	146364022	7463867	0.051	0.3828
chr9	141213431	4966798	0.0352	0.3011
chr10	135534747	6487414	0.0479	0.3796
chr11	135006516	5853273	0.0434	0.2849
chr12	133851895	6806872	0.0509	0.2691
chr13	115169878	3516580	0.0305	0.2127
chr14	107349540	4608948	0.0429	0.2583
chr15	102531392	3945379	0.0385	0.23
chr16	90354753	4649909	0.0515	0.2972
chr17	81195210	3768052	0.0464	0.2815
chr18	78077248	3357503	0.043	0.5276
chr19	59128983	2939556	0.0497	0.4611
chr20	63025520	3244087	0.0515	0.2719
chr21	48129895	2353739	0.0489	0.2757
chr22	51304566	1460049	0.0285	0.1972
chrMT	16571	419257	25.3006	15.4047
chrX	155270560	7376403	0.0475	0.2738
chrY	59373566	285583	0.0048	0.1107

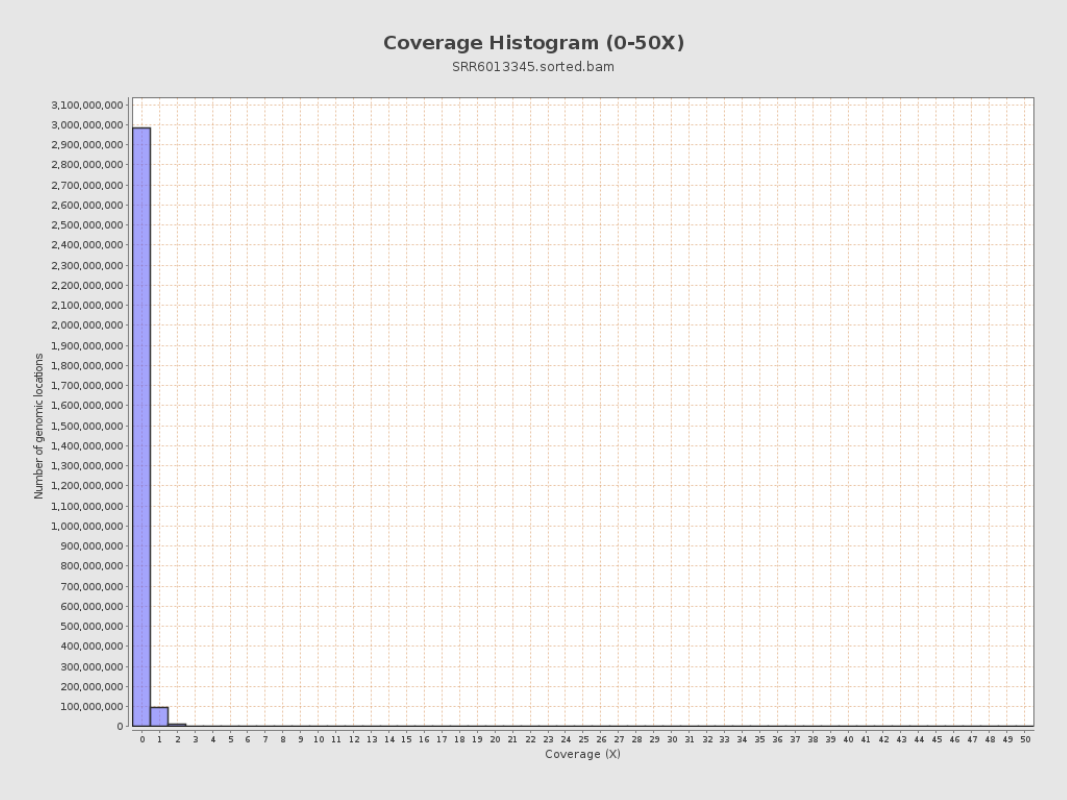
3. Results : Coverage across reference



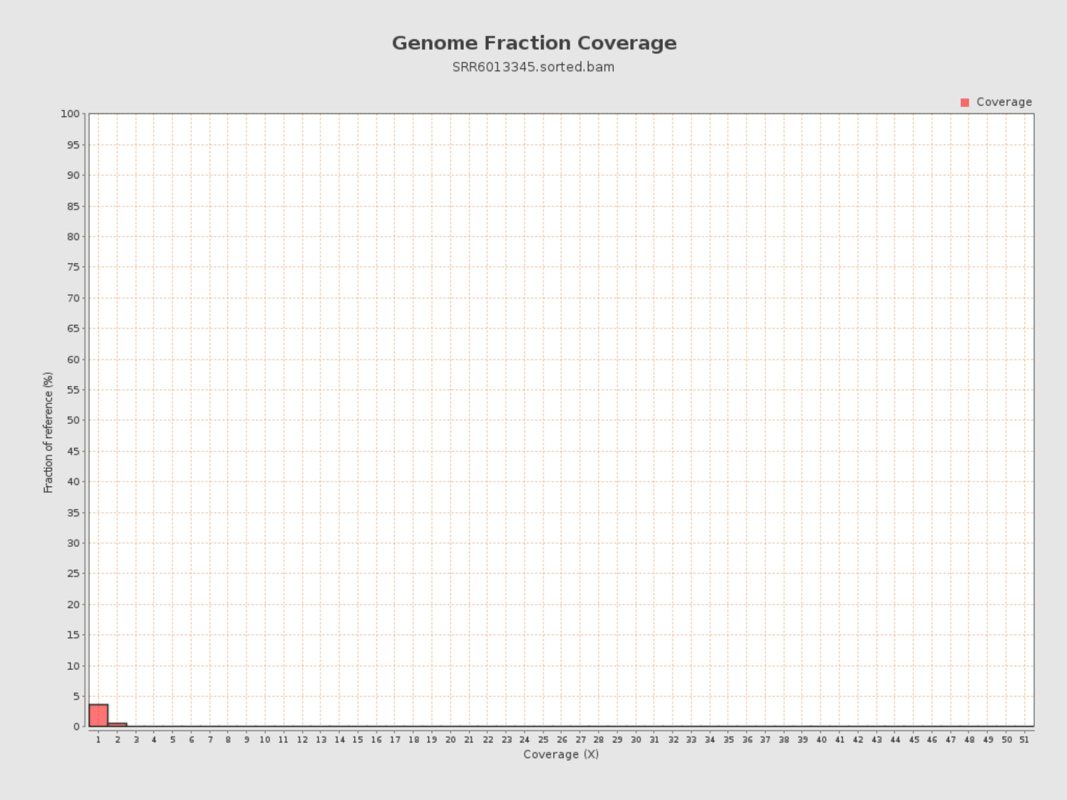
4. Results : Coverage Histogram



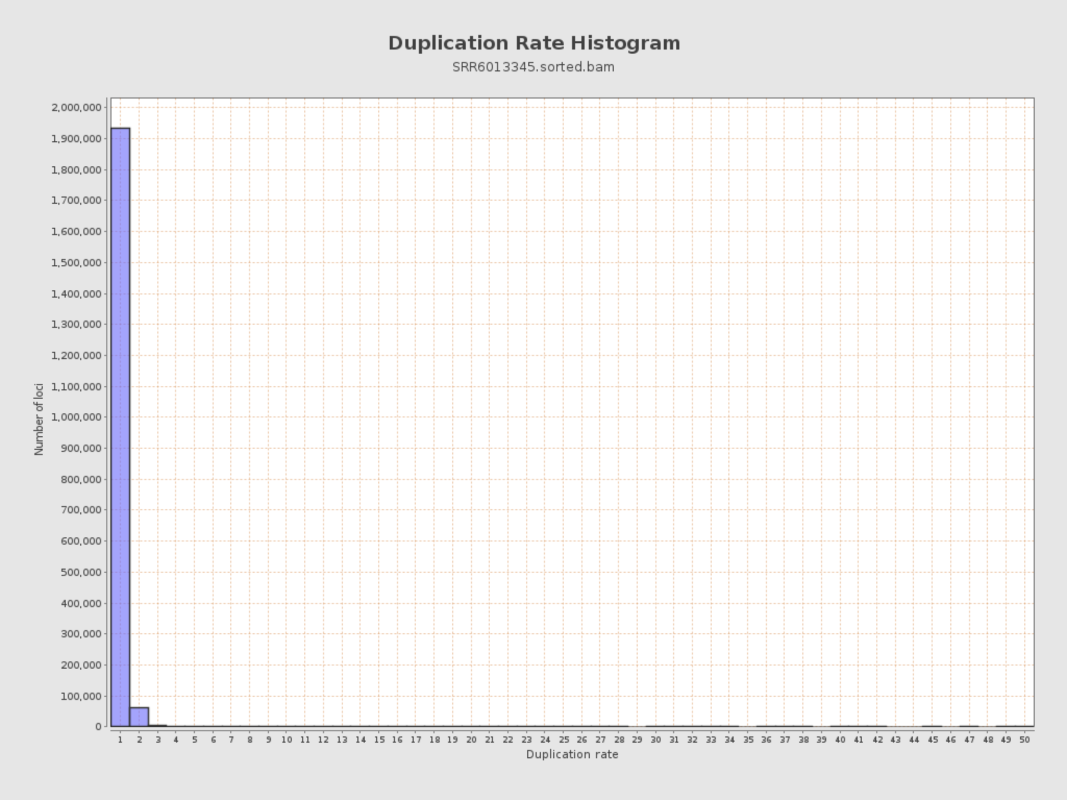
5. Results : Coverage Histogram (0-50X)



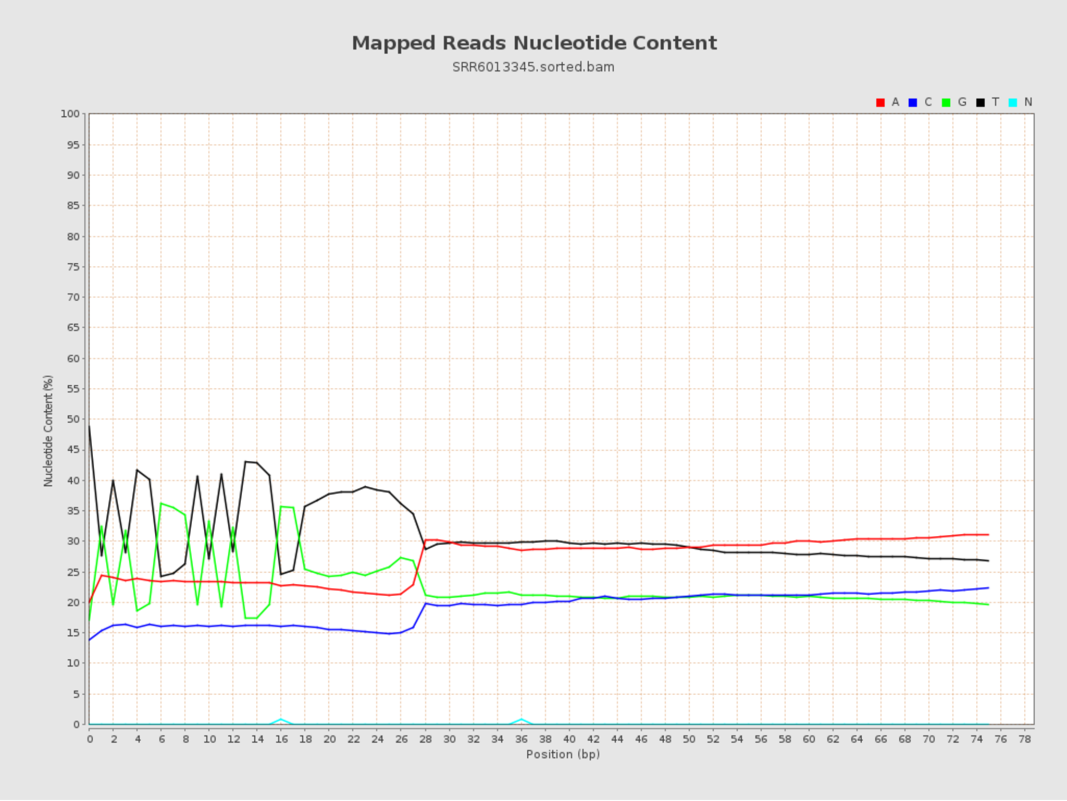
6. Results : Genome Fraction Coverage



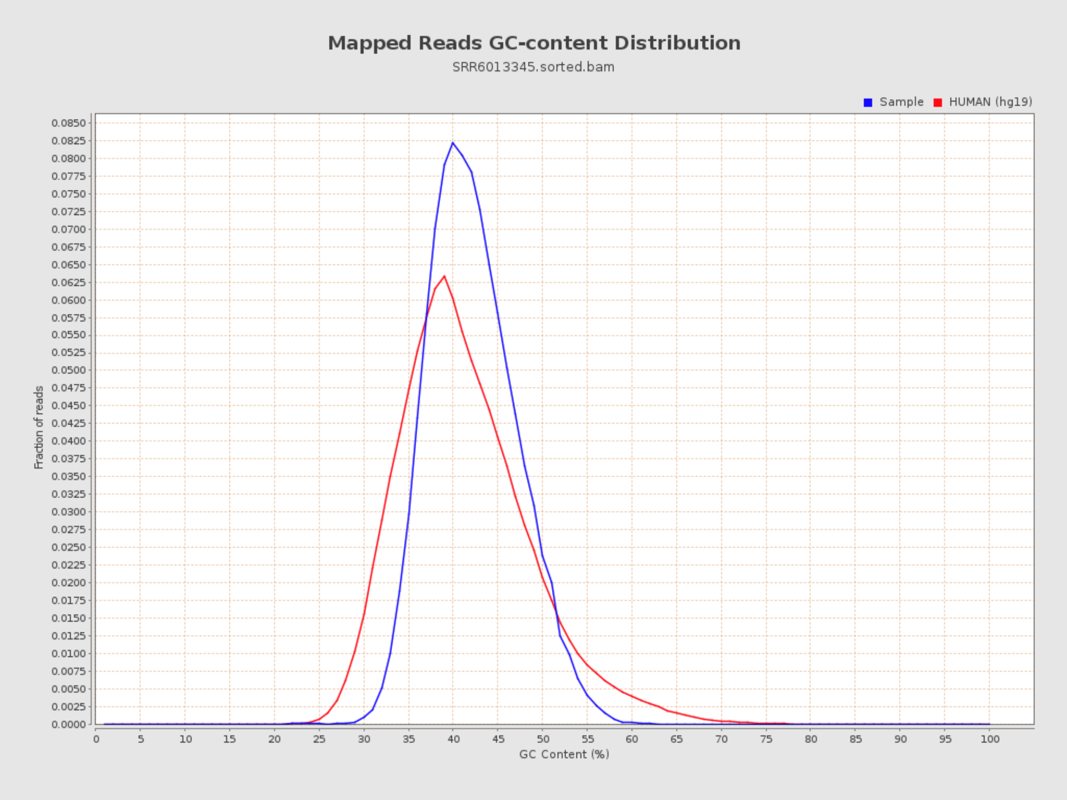
7. Results : Duplication Rate Histogram



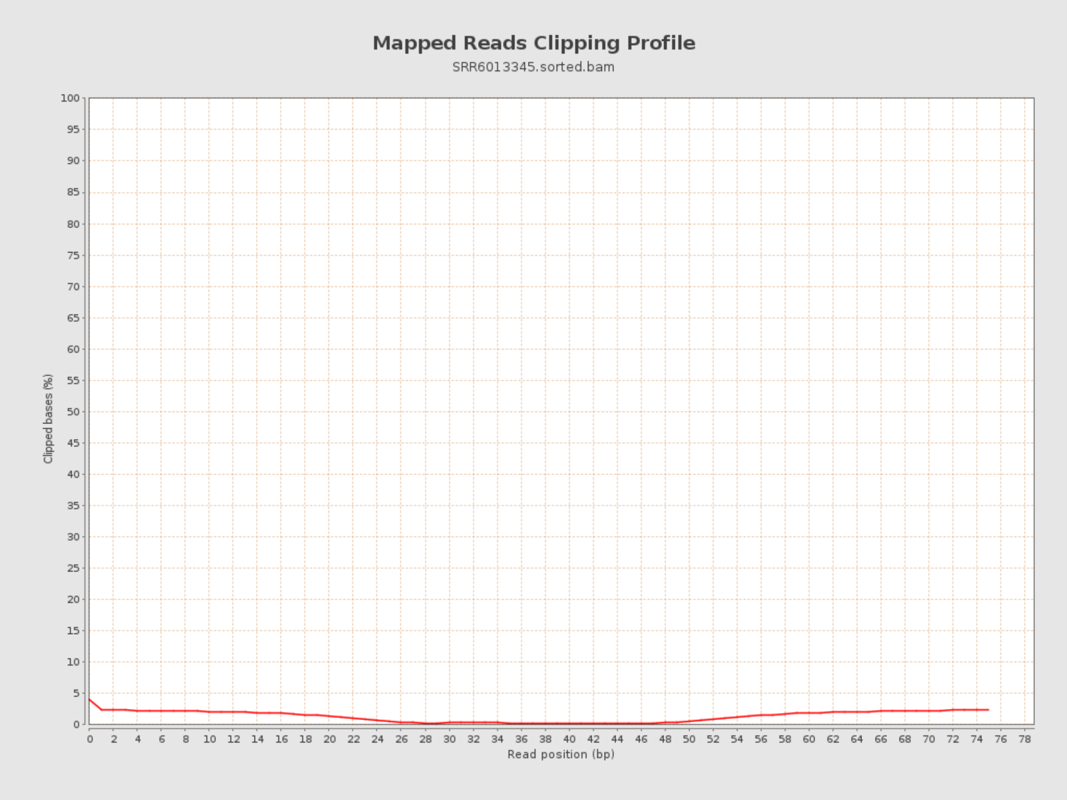
8. Results : Mapped Reads Nucleotide Content



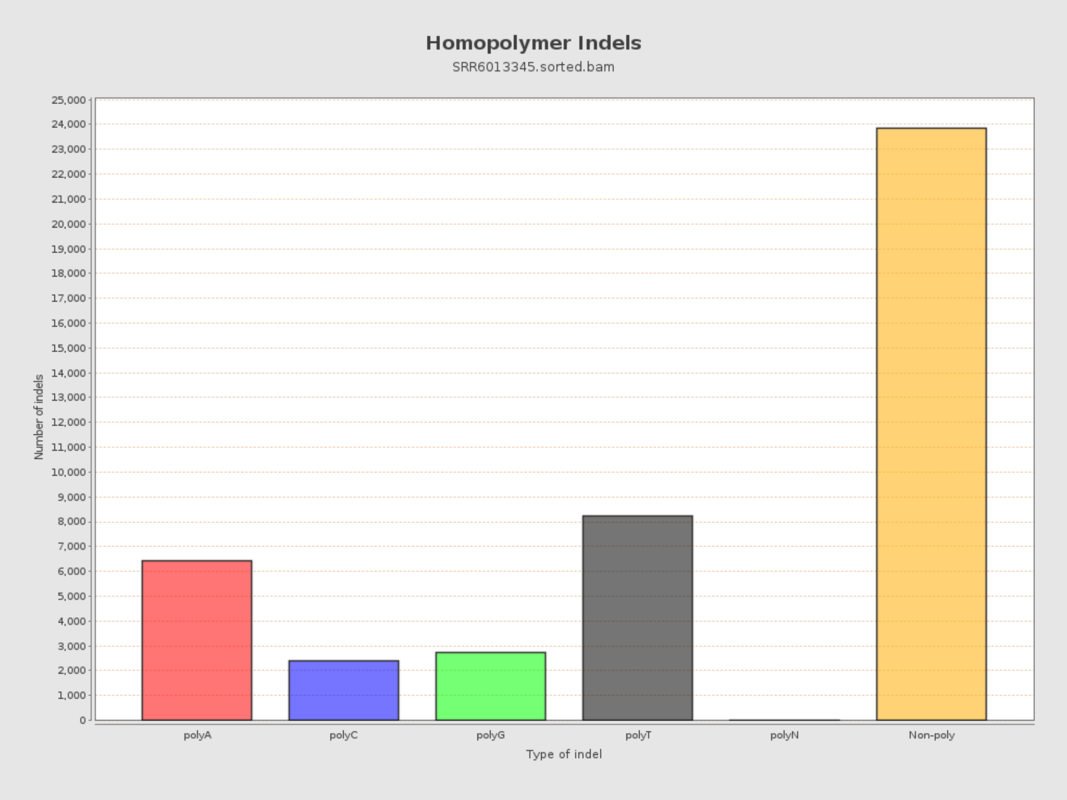
9. Results : Mapped Reads GC-content Distribution



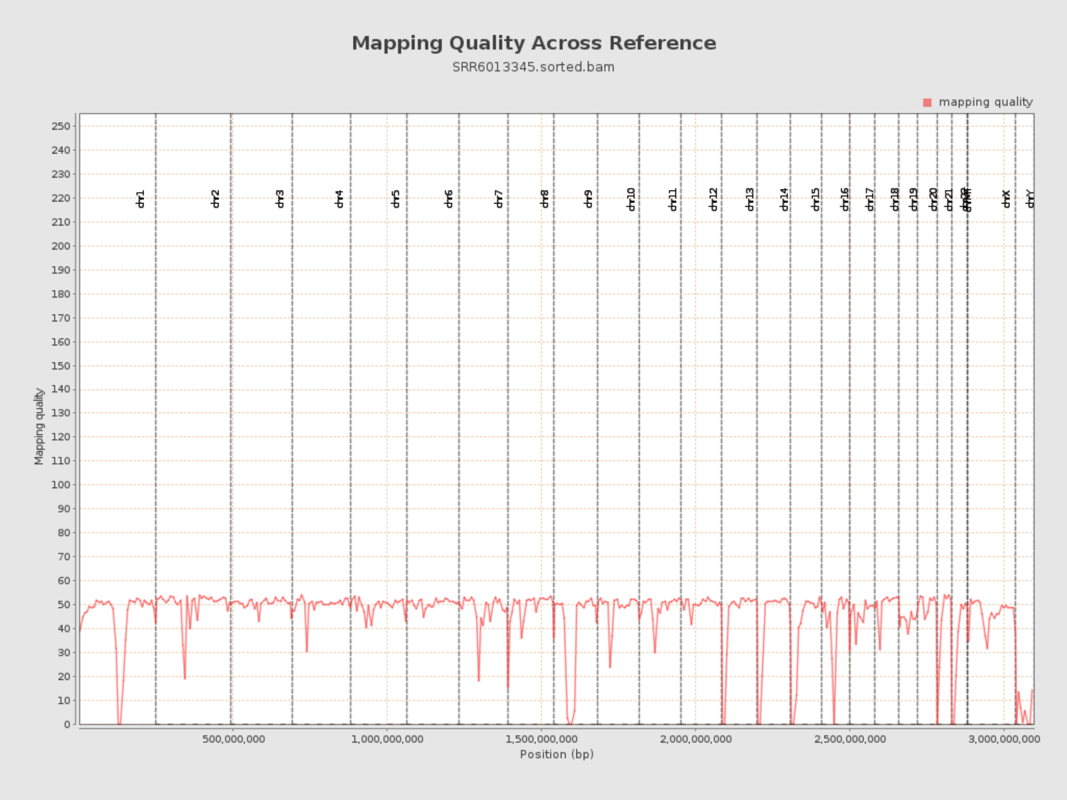
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram