Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:03:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548928.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_SRR1548928 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548928.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:03:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548928.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,398,625
Mapped reads	4,728,859 / 87.59%
Unmapped reads	669,766 / 12.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	148,840 / 2.76%
Duplication rate	2.47%
Clipped reads	255,824 / 4.74%

2.2. ACGT Content

Number/percentage of A's	54,156,851 / 28.86%
Number/percentage of C's	39,350,244 / 20.97%
Number/percentage of T's	54,641,720 / 29.12%
Number/percentage of G's	39,479,523 / 21.04%
Number/percentage of N's	1,677 / 0%
GC Percentage	42.01%

2.3. Coverage

Mean	0.0606
Standard Deviation	0.4753

2.4. Mapping Quality

Mean Mapping Quality	43.63

2.5. Mismatches and indels

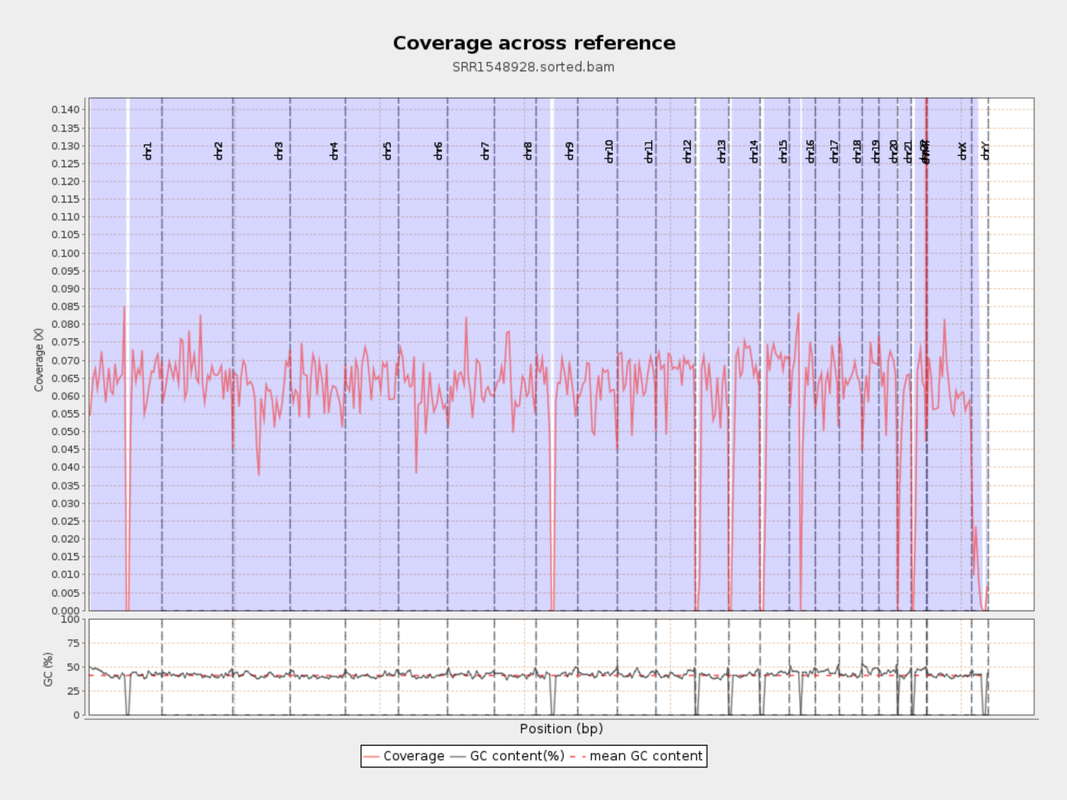
General error rate	0.24%
Mismatches	445,616
Insertions	4,583
Mapped reads with at least one insertion	0.1%
Deletions	13,516
Mapped reads with at least one deletion	0.29%
Homopolymer indels	43.88%

2.6. Chromosome stats

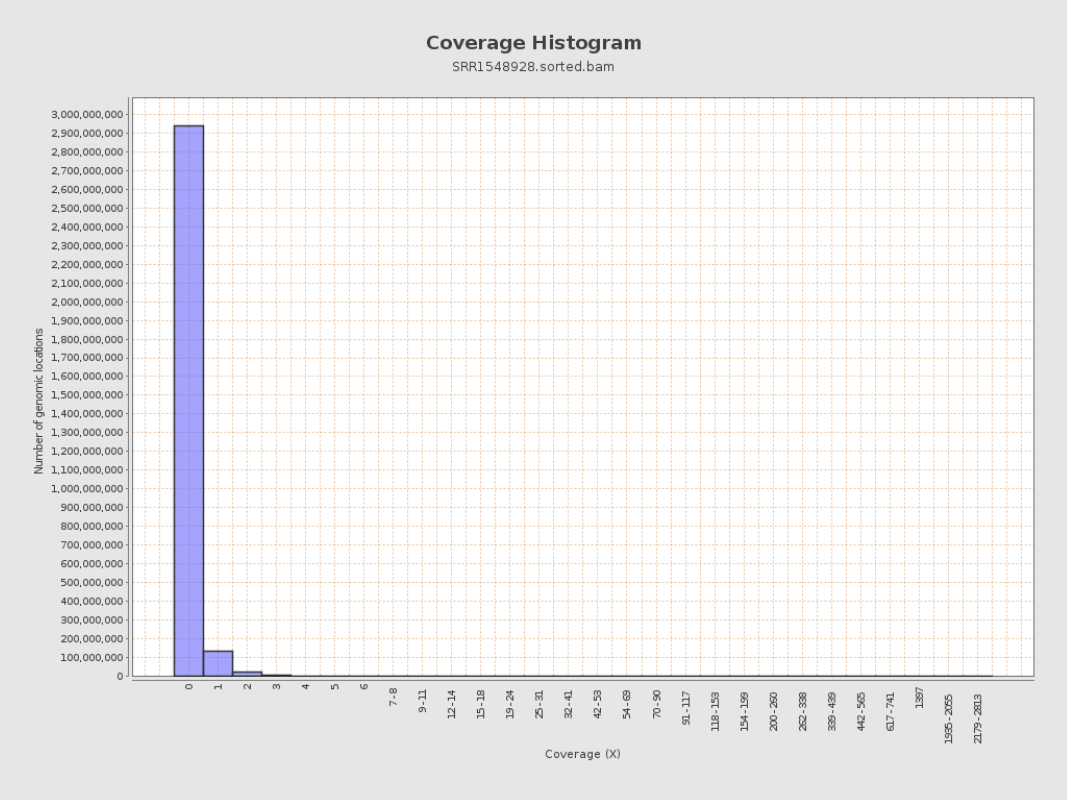
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15275731	0.0613	0.6304
chr2	243199373	16148215	0.0664	0.3584
chr3	198022430	11905420	0.0601	0.2876
chr4	191154276	11876541	0.0621	0.2969
chr5	180915260	11746070	0.0649	0.2996
chr6	171115067	10427267	0.0609	0.3128
chr7	159138663	10065550	0.0633	0.4777
chr8	146364022	9238647	0.0631	1.3918

chr9	141213431	7989320	0.0566	0.3477
chr10	135534747	8359656	0.0617	0.3391
chr11	135006516	8757959	0.0649	0.4004
chr12	133851895	9044461	0.0676	0.3078
chr13	115169878	5961522	0.0518	0.2646
chr14	107349540	6252990	0.0582	0.3009
chr15	102531392	5922364	0.0578	0.2799
chr16	90354753	5564606	0.0616	0.3058
chr17	81195210	5110074	0.0629	0.3036
chr18	78077248	5139689	0.0658	0.5661
chr19	59128983	3891533	0.0658	0.5502
chr20	63025520	4106845	0.0652	0.3035
chr21	48129895	2446957	0.0508	0.2799
chr22	51304566	2323608	0.0453	0.2571
chrMT	16571	13411	0.8093	1.4041
chrX	155270560	9563004	0.0616	0.329
chrY	59373566	516689	0.0087	0.1422

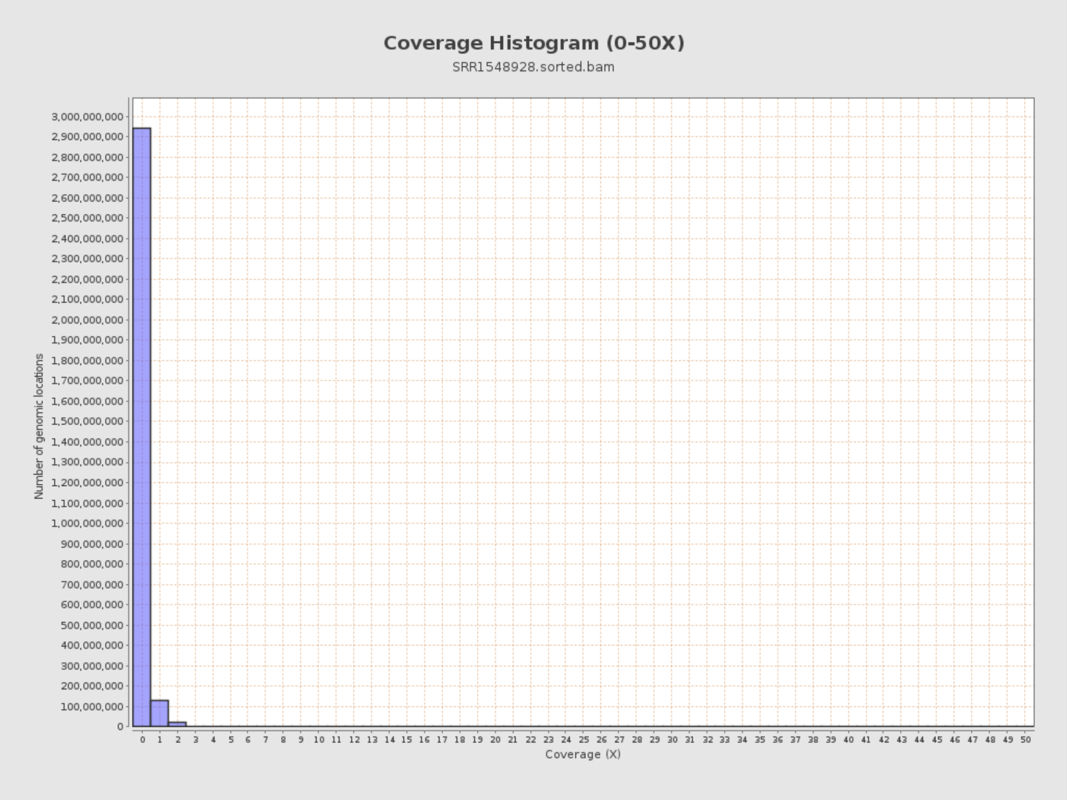
3. Results : Coverage across reference



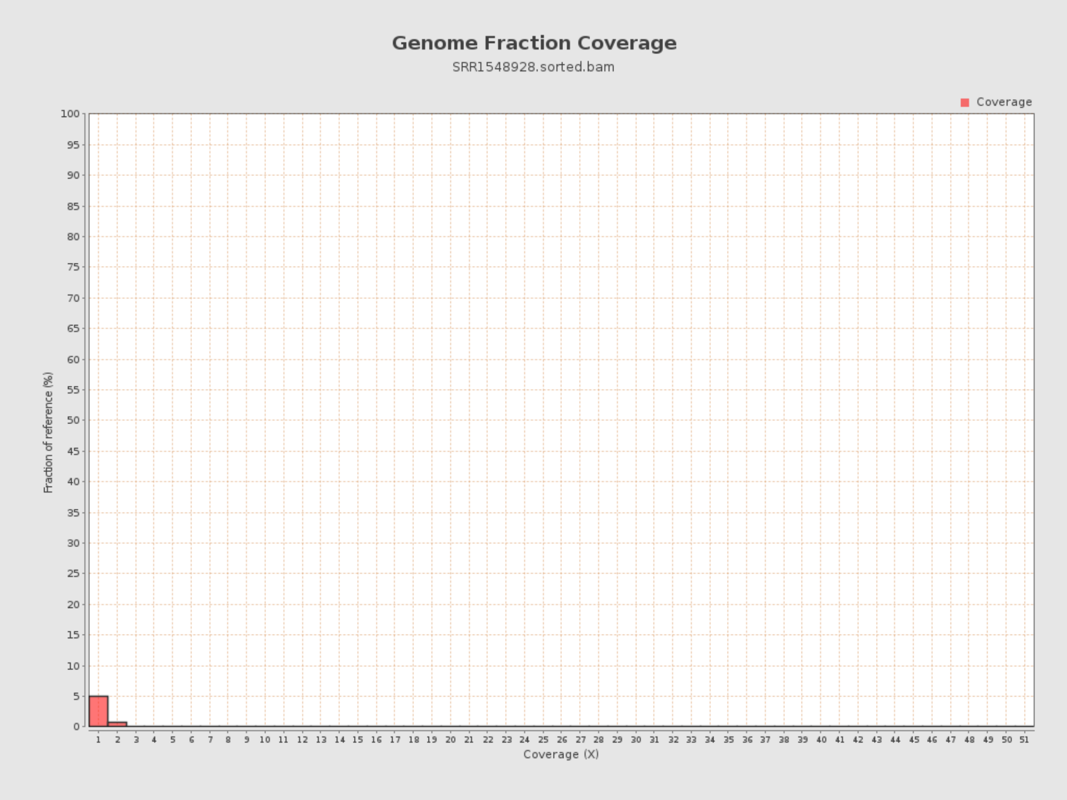
4. Results : Coverage Histogram



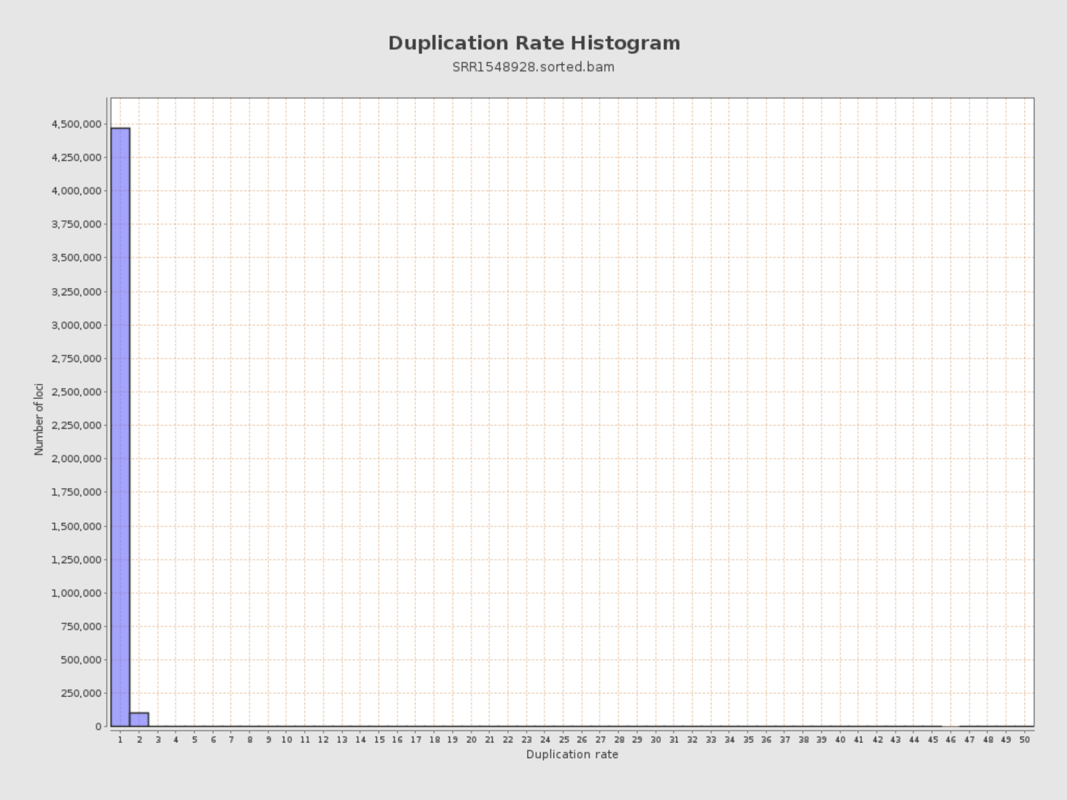
5. Results : Coverage Histogram (0-50X)



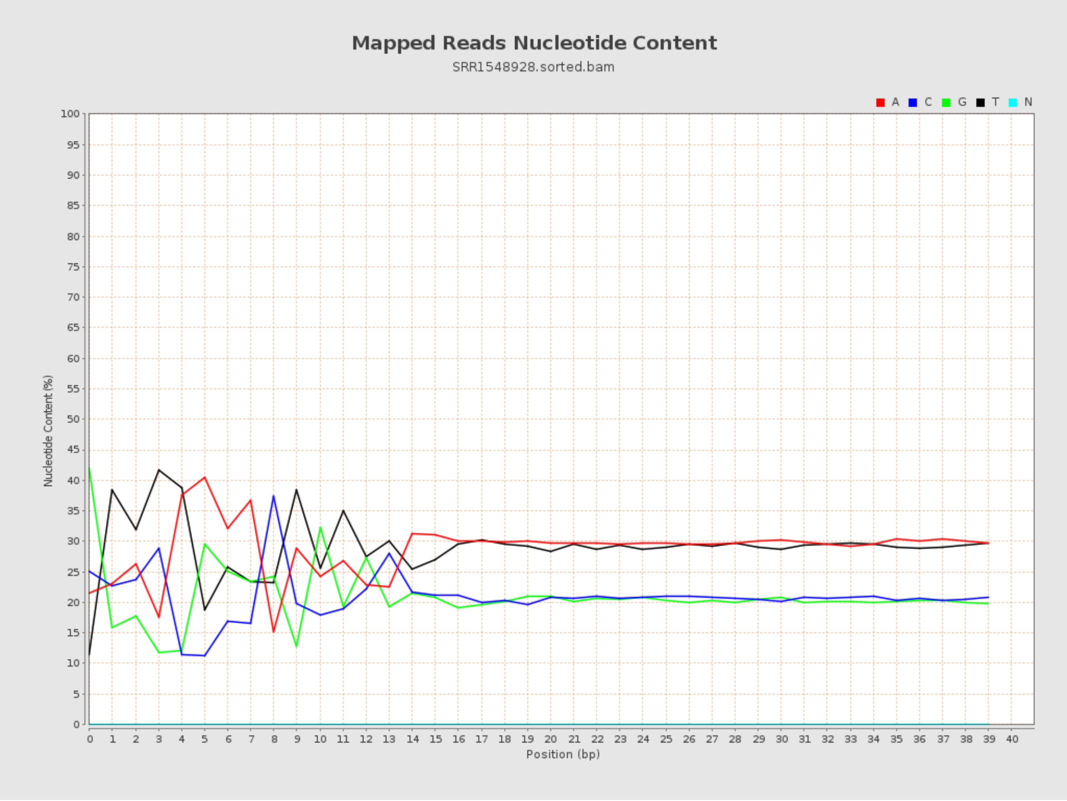
6. Results : Genome Fraction Coverage



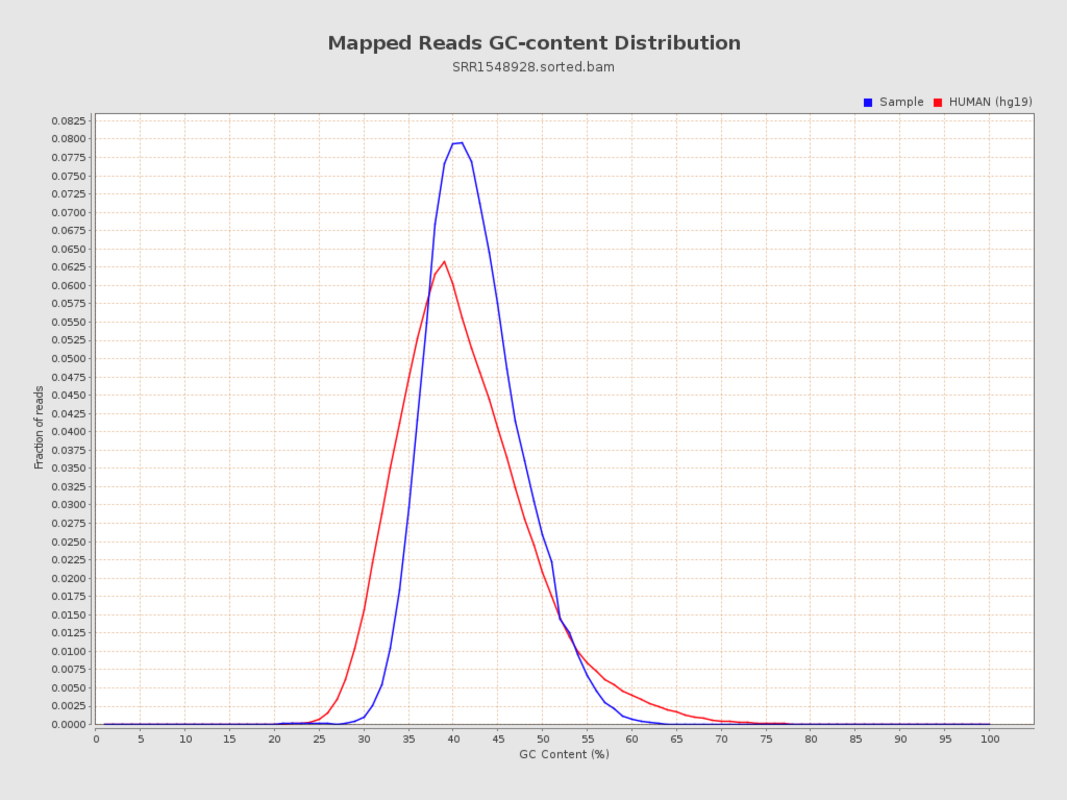
7. Results : Duplication Rate Histogram



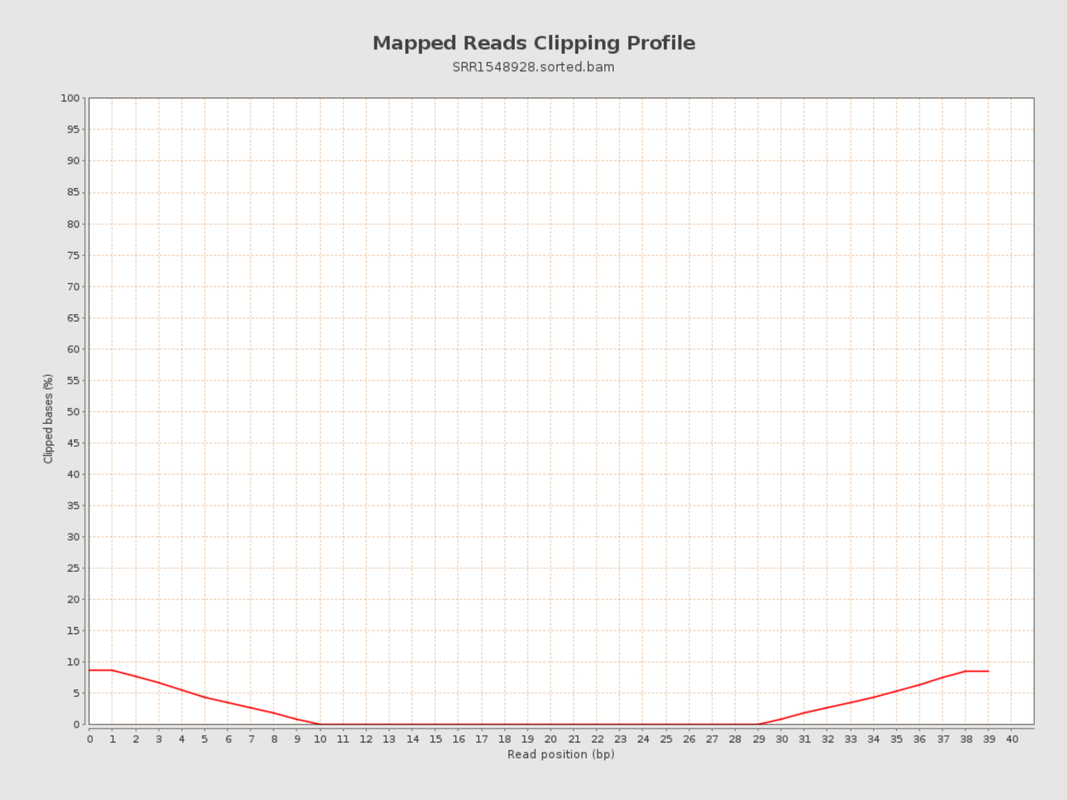
8. Results : Mapped Reads Nucleotide Content



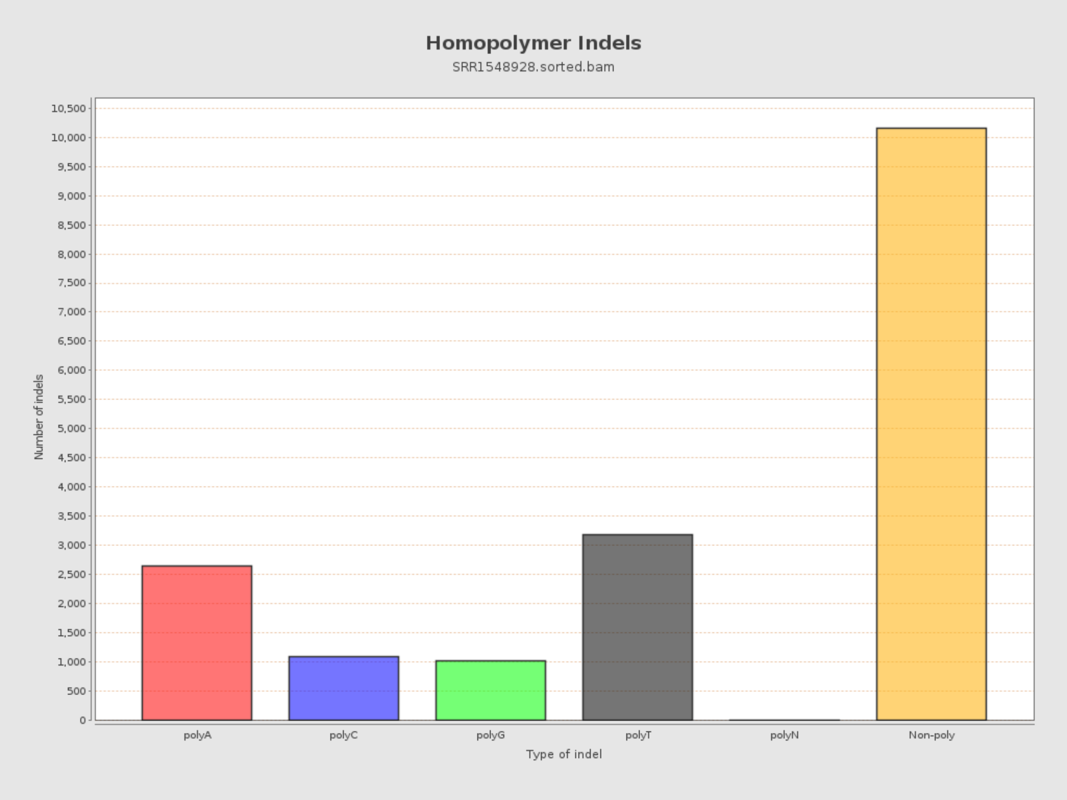
9. Results : Mapped Reads GC-content Distribution



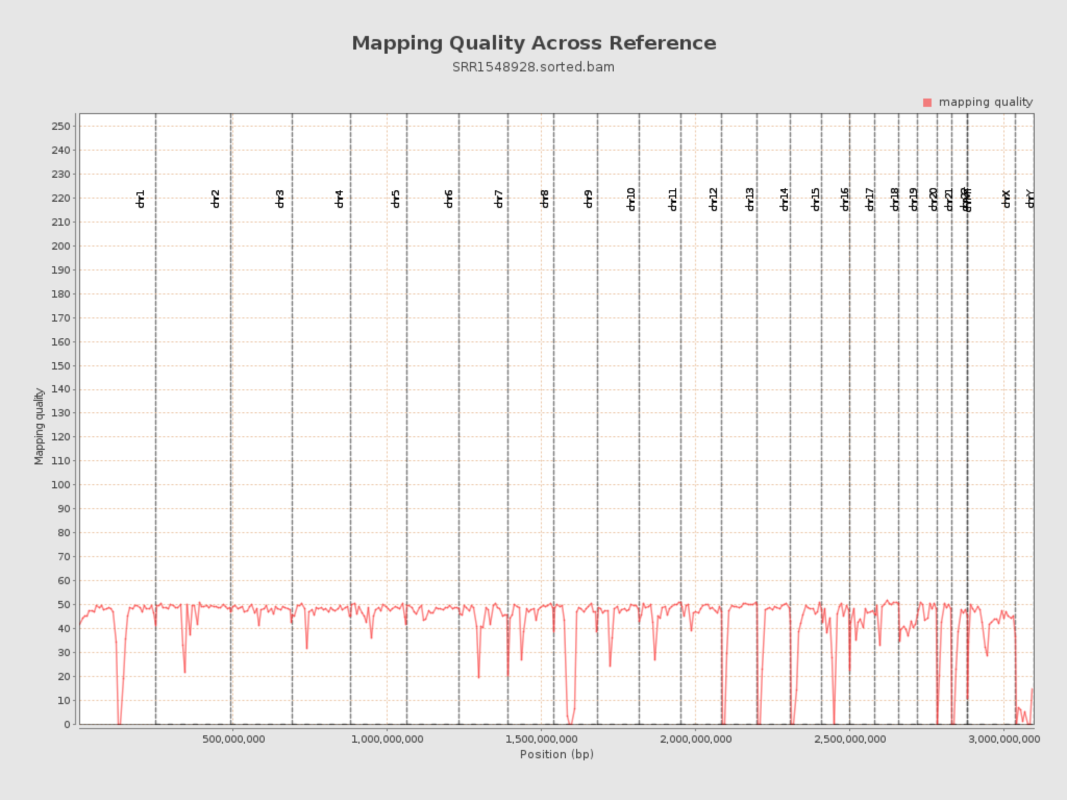
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram