Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 18:28:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548953.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_SRR1548953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548953.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 18:28:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548953.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,187,648
Mapped reads	7,959,691 / 86.63%
Unmapped reads	1,227,957 / 13.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	386,375 / 4.21%
Duplication rate	3.79%
Clipped reads	526,098 / 5.73%

2.2. ACGT Content

Number/percentage of A's	90,788,676 / 28.79%
Number/percentage of C's	66,114,350 / 20.96%
Number/percentage of T's	91,976,675 / 29.16%
Number/percentage of G's	66,502,688 / 21.09%
Number/percentage of N's	455 / 0%
GC Percentage	42.05%

2.3. Coverage

Mean	0.1019
Standard Deviation	1.1077

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

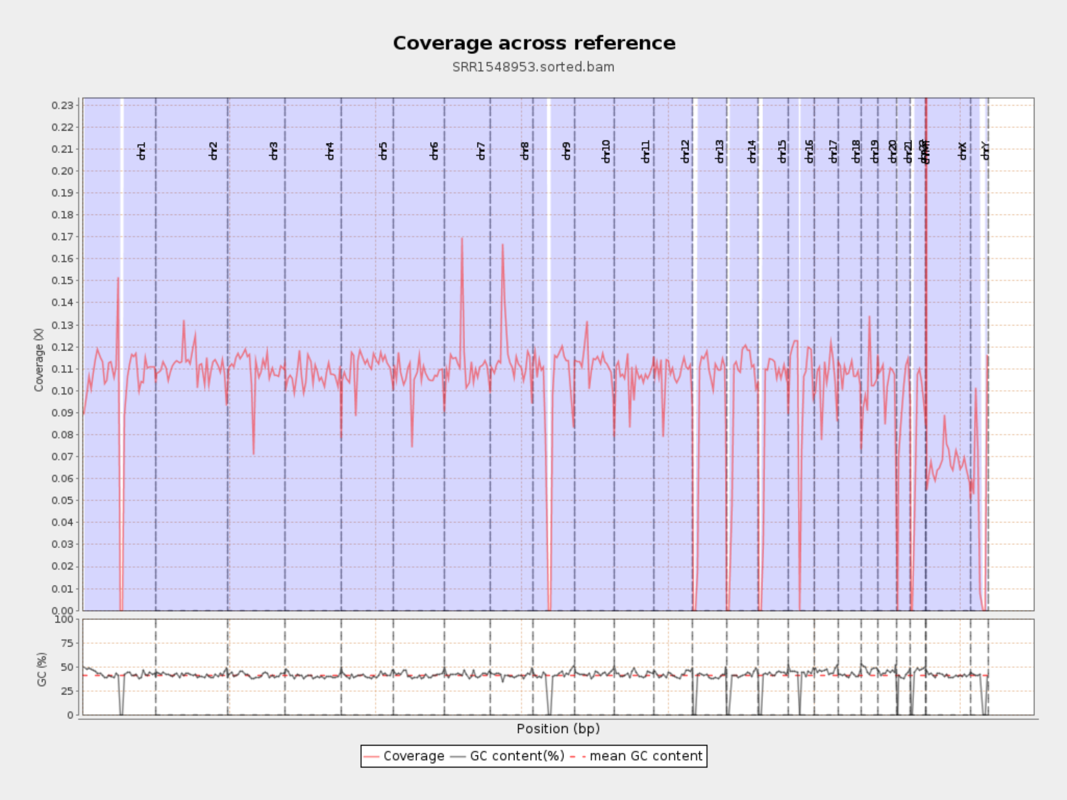
General error rate	0.24%
Mismatches	745,456
Insertions	9,007
Mapped reads with at least one insertion	0.11%
Deletions	24,538
Mapped reads with at least one deletion	0.31%
Homopolymer indels	42.43%

2.6. Chromosome stats

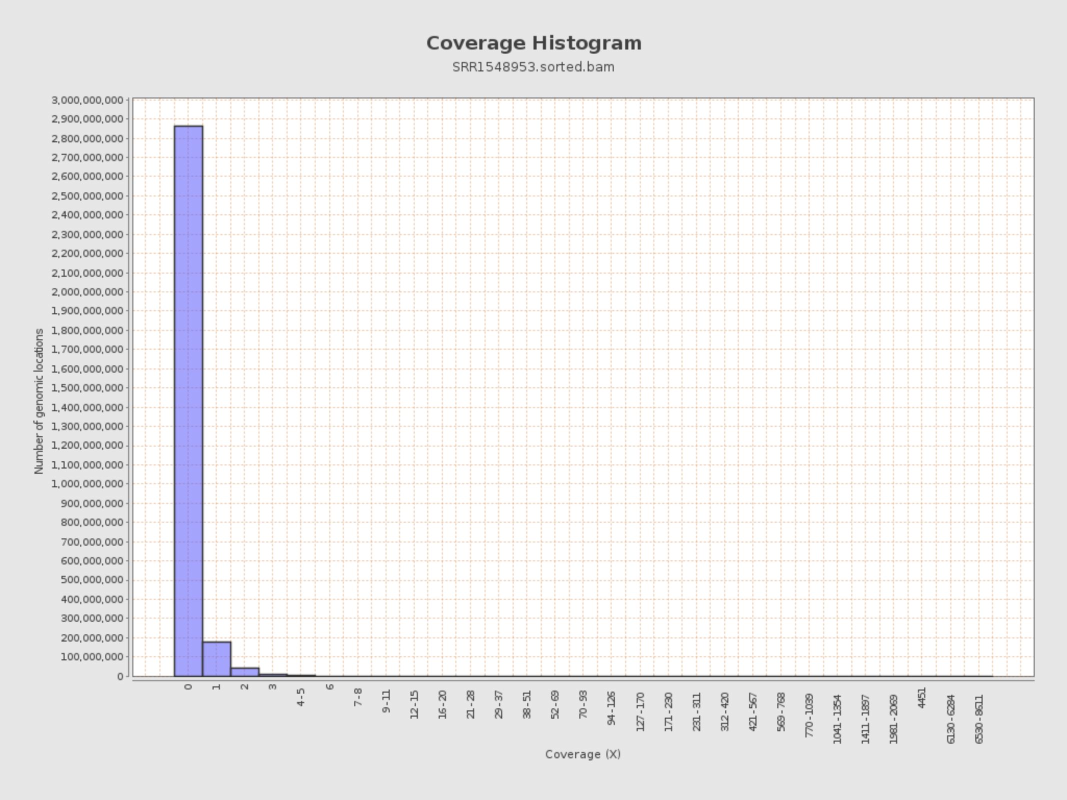
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25632103	0.1028	1.2627
chr2	243199373	27114942	0.1115	0.5733
chr3	198022430	21753525	0.1099	0.4271
chr4	191154276	20479034	0.1071	0.4409
chr5	180915260	20060367	0.1109	0.4327
chr6	171115067	18244622	0.1066	0.4381
chr7	159138663	17870067	0.1123	0.9793
chr8	146364022	16881613	0.1153	4.1937

chr9	141213431	13622882	0.0965	0.5389
chr10	135534747	15295980	0.1129	0.5561
chr11	135006516	14308229	0.106	0.5591
chr12	133851895	14439089	0.1079	0.4326
chr13	115169878	10610910	0.0921	0.388
chr14	107349540	10084272	0.0939	0.4543
chr15	102531392	9067845	0.0884	0.3791
chr16	90354753	9030899	0.0999	0.4358
chr17	81195210	8559264	0.1054	0.4356
chr18	78077248	8442876	0.1081	0.9639
chr19	59128983	6067691	0.1026	1.057
chr20	63025520	6539628	0.1038	0.4294
chr21	48129895	4214198	0.0876	0.4598
chr22	51304566	3679865	0.0717	0.4911
chrMT	16571	33683	2.0326	2.7655
chrX	155270560	10349476	0.0667	0.4033
chrY	59373566	3032681	0.0511	0.5576

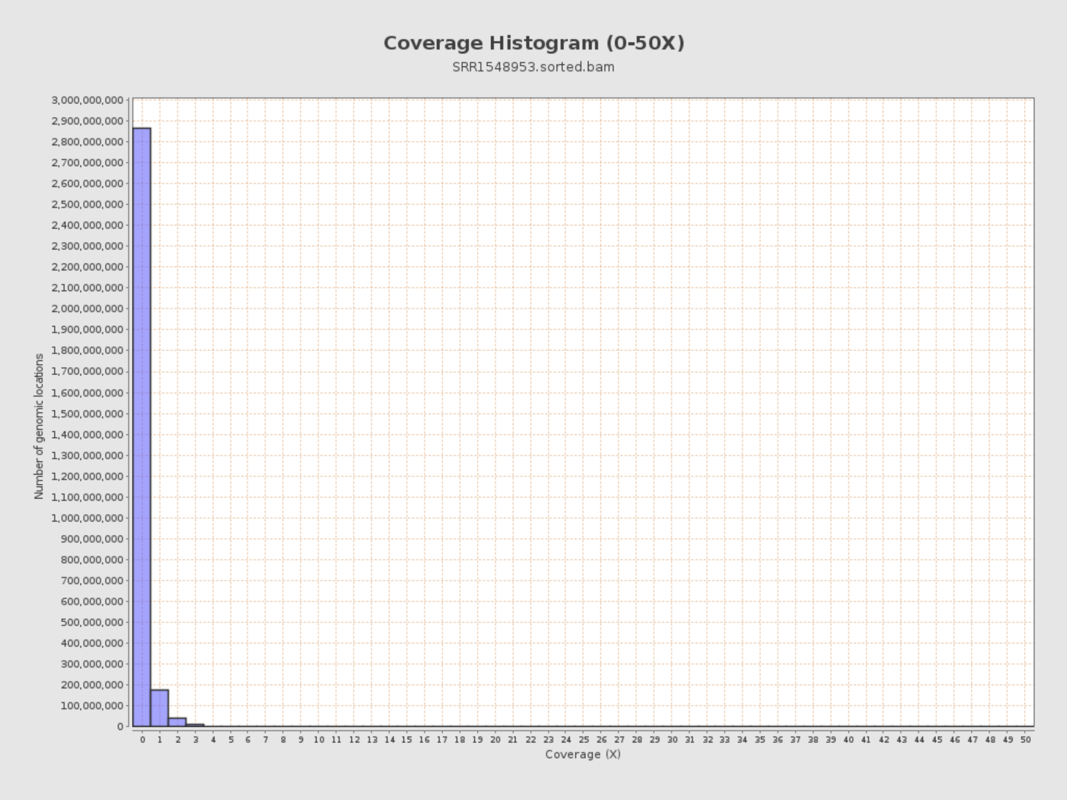
3. Results : Coverage across reference



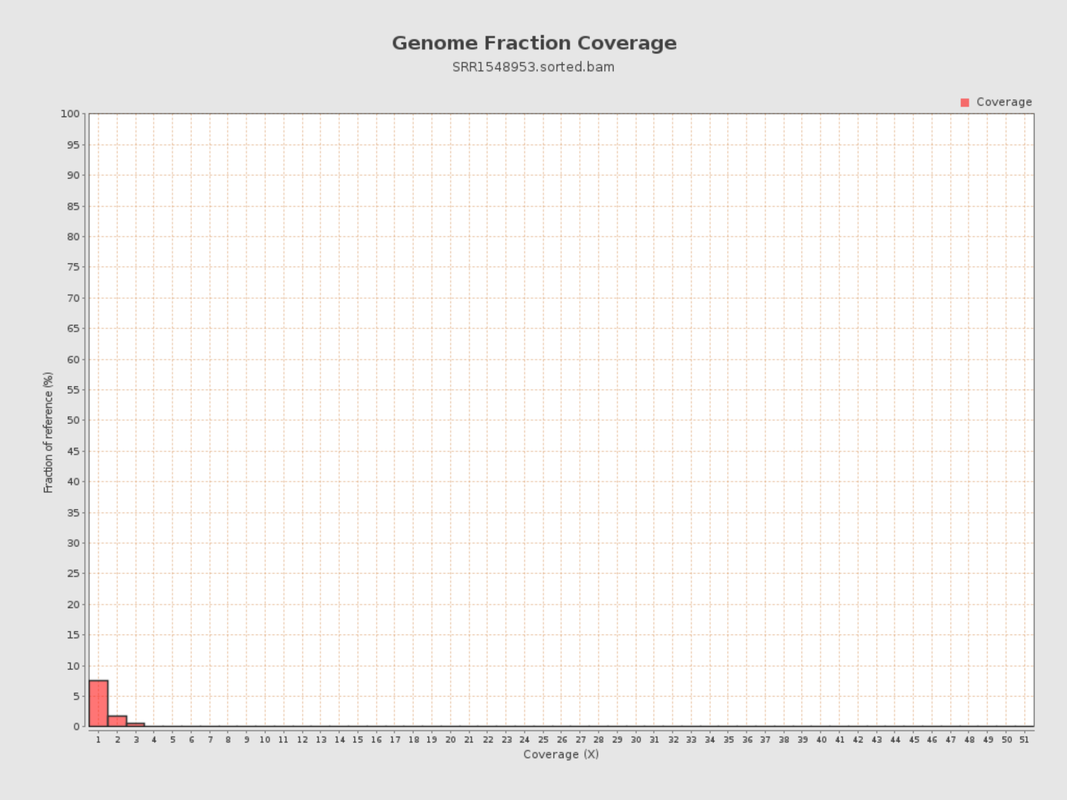
4. Results : Coverage Histogram



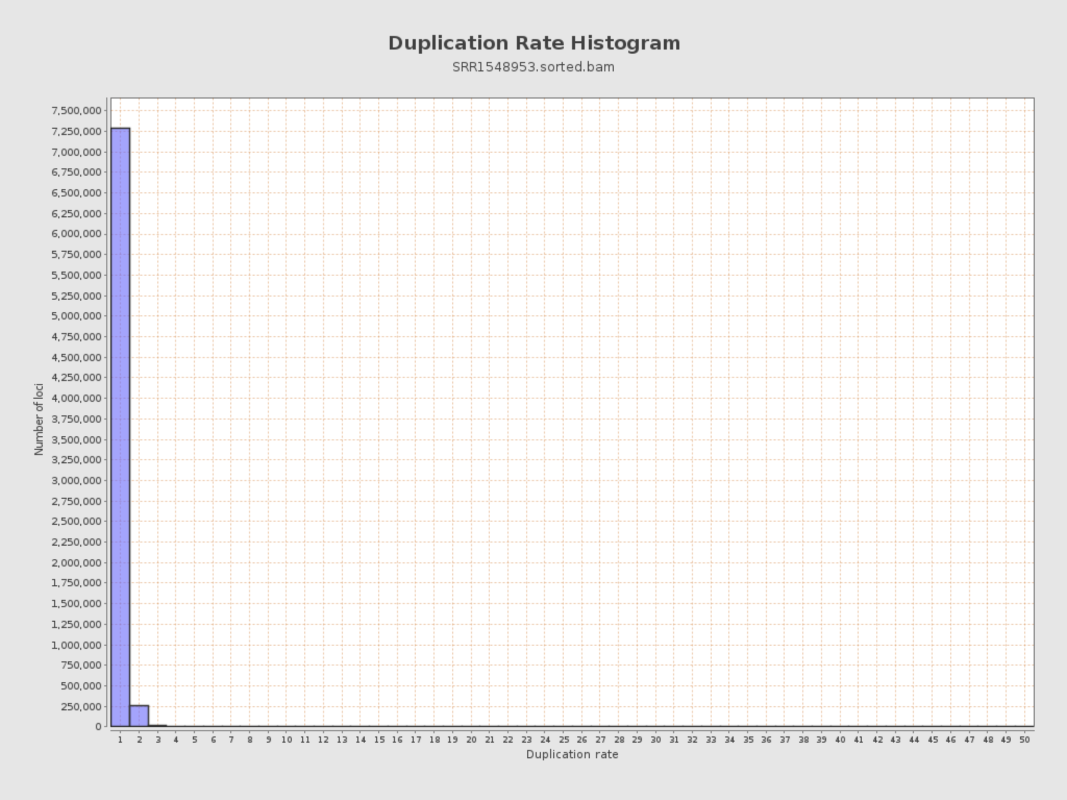
5. Results : Coverage Histogram (0-50X)



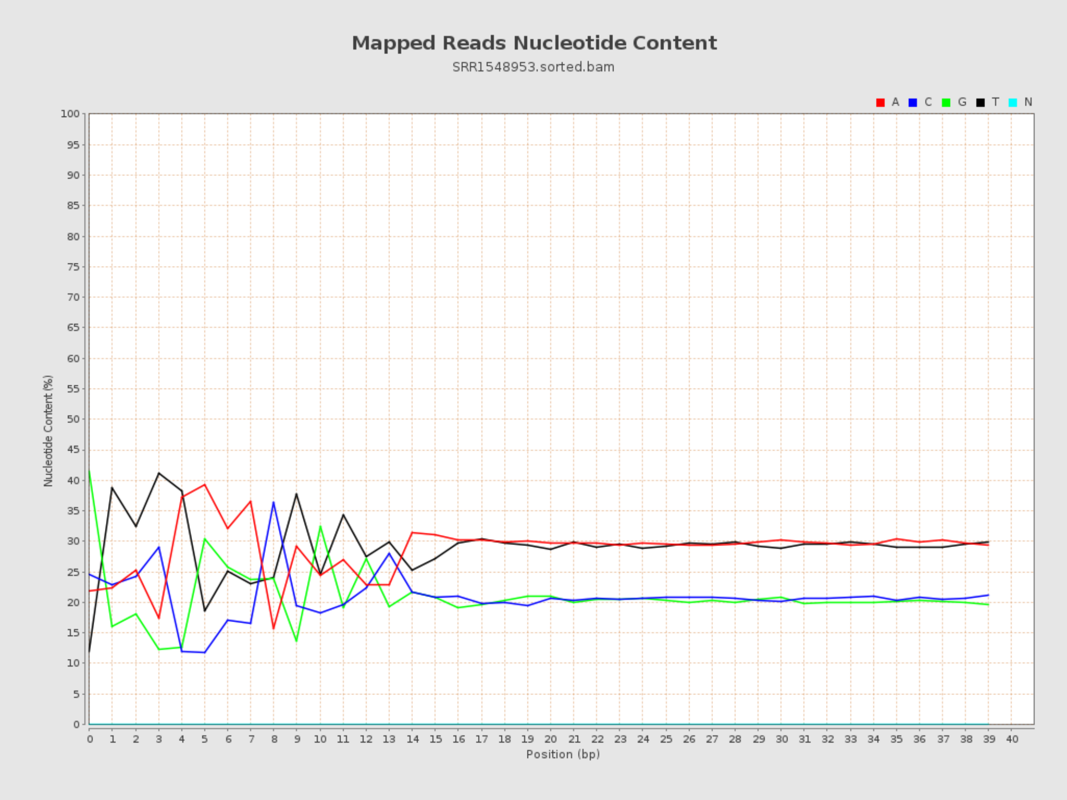
6. Results : Genome Fraction Coverage



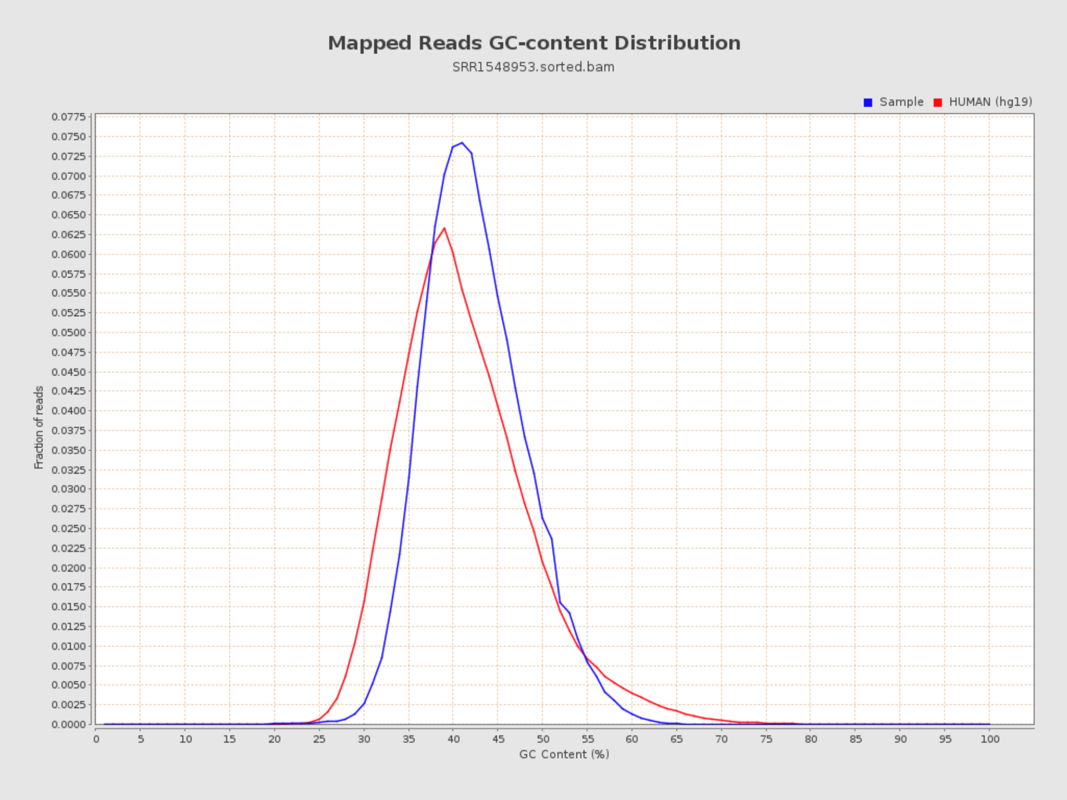
7. Results : Duplication Rate Histogram



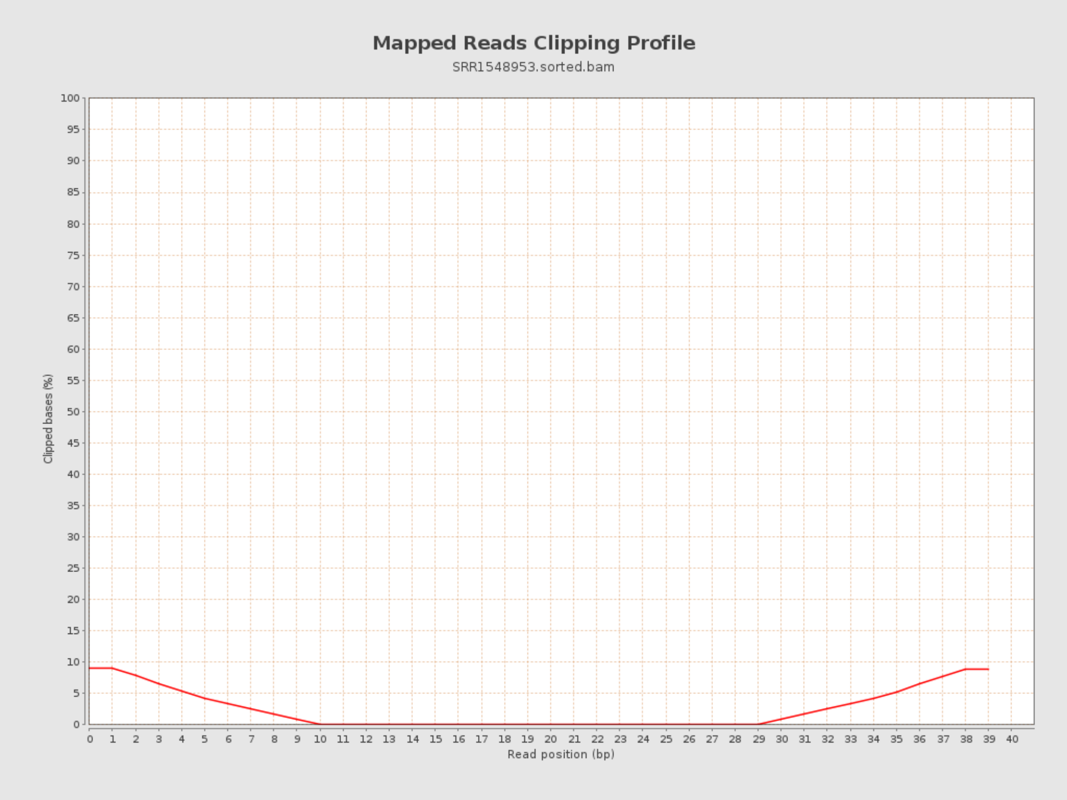
8. Results : Mapped Reads Nucleotide Content



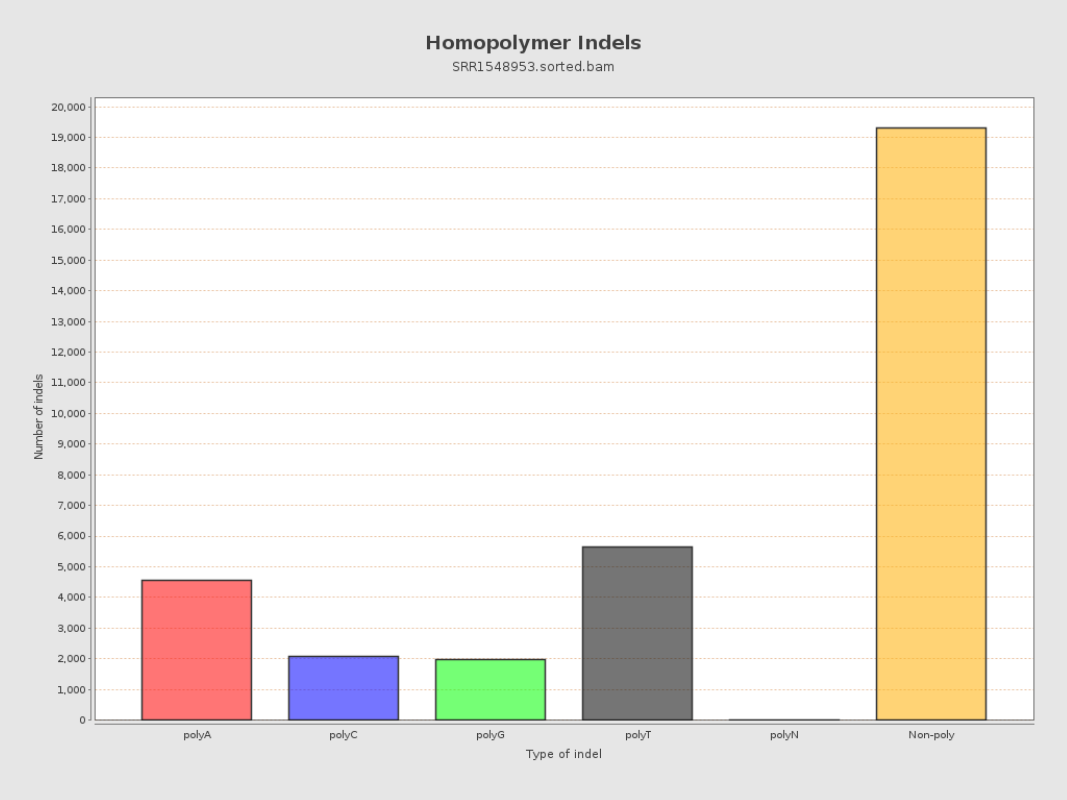
9. Results : Mapped Reads GC-content Distribution



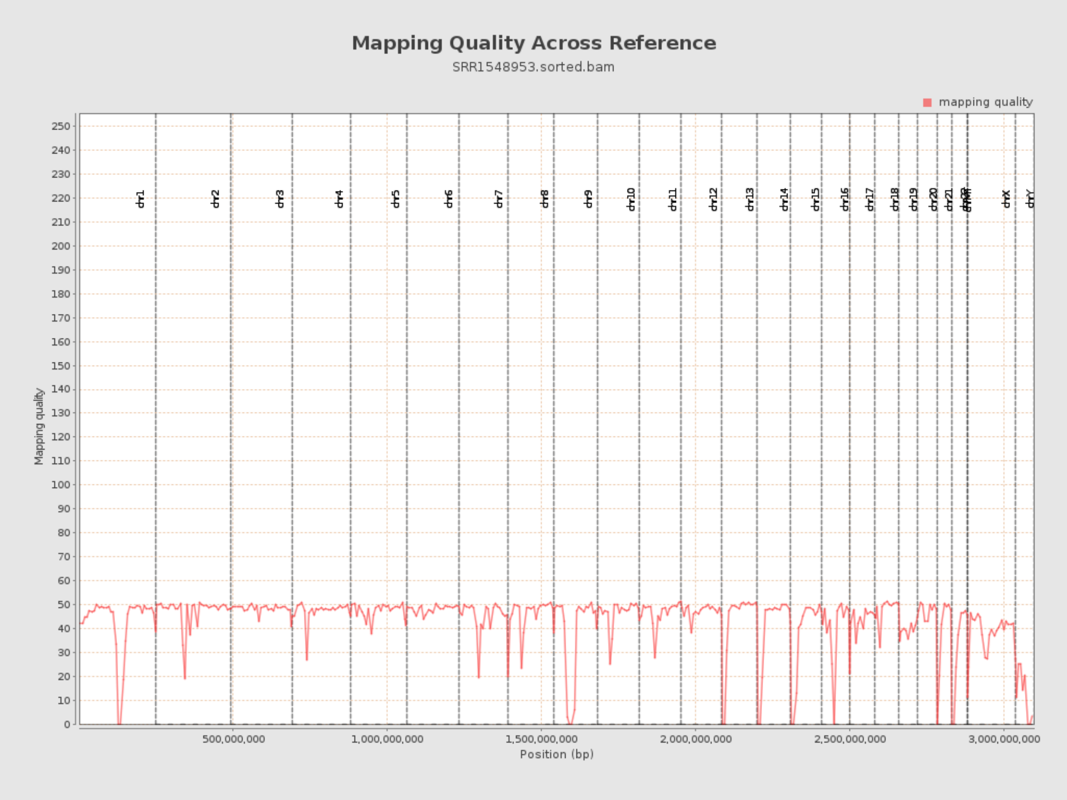
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram