Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 16:00:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514748.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_SRR5514748 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514748.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 16:00:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514748.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	53,328,309
Mapped reads	49,932,423 / 93.63%
Unmapped reads	3,395,886 / 6.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,183,418 / 13.47%
Read min/max/mean length	30 / 100 / 104.72
Duplicated reads (estimated)	38,712,070 / 72.59%
Duplication rate	42.98%
Clipped reads	25,677,384 / 48.15%

2.2. ACGT Content

Number/percentage of A's	1,453,724,581 / 31.01%
Number/percentage of C's	876,114,416 / 18.69%
Number/percentage of T's	1,440,485,890 / 30.73%
Number/percentage of G's	917,319,086 / 19.57%
Number/percentage of N's	322,117 / 0.01%
GC Percentage	38.26%

2.3. Coverage

Mean	1.5159

Standard Deviation	56.2658

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

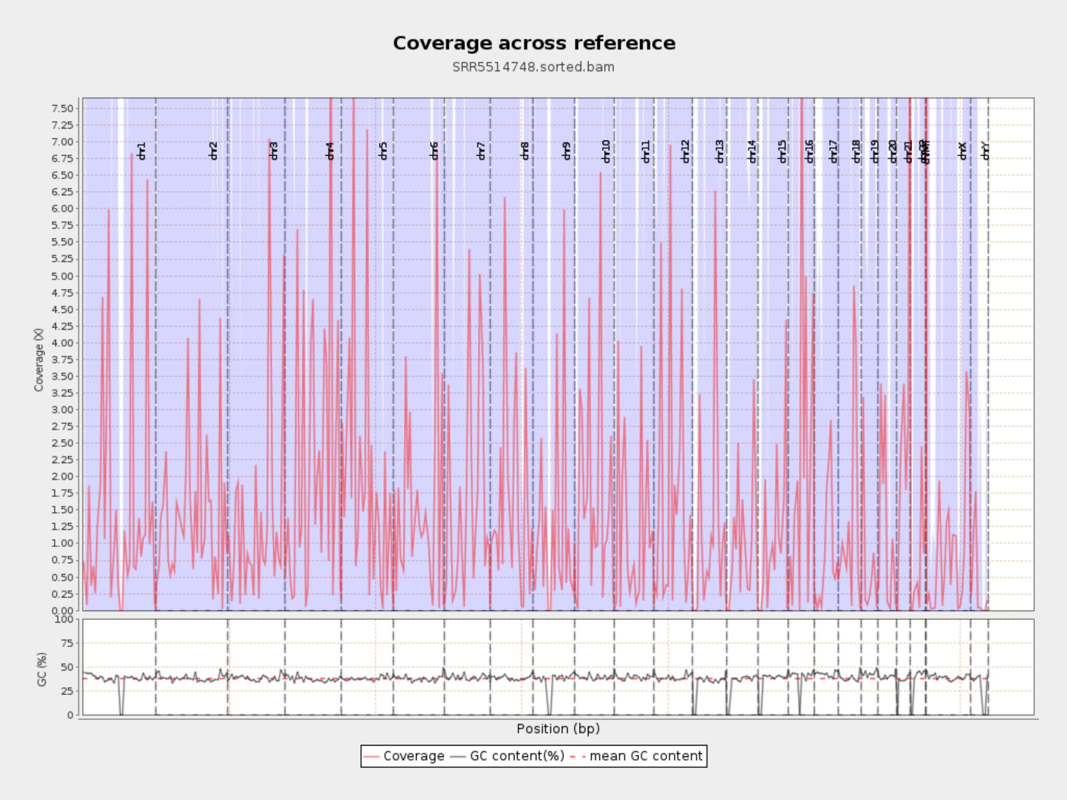
General error rate	0.74%
Mismatches	28,478,106
Insertions	3,623,455
Mapped reads with at least one insertion	6.86%
Deletions	1,637,166
Mapped reads with at least one deletion	2.99%
Homopolymer indels	46.9%

2.6. Chromosome stats

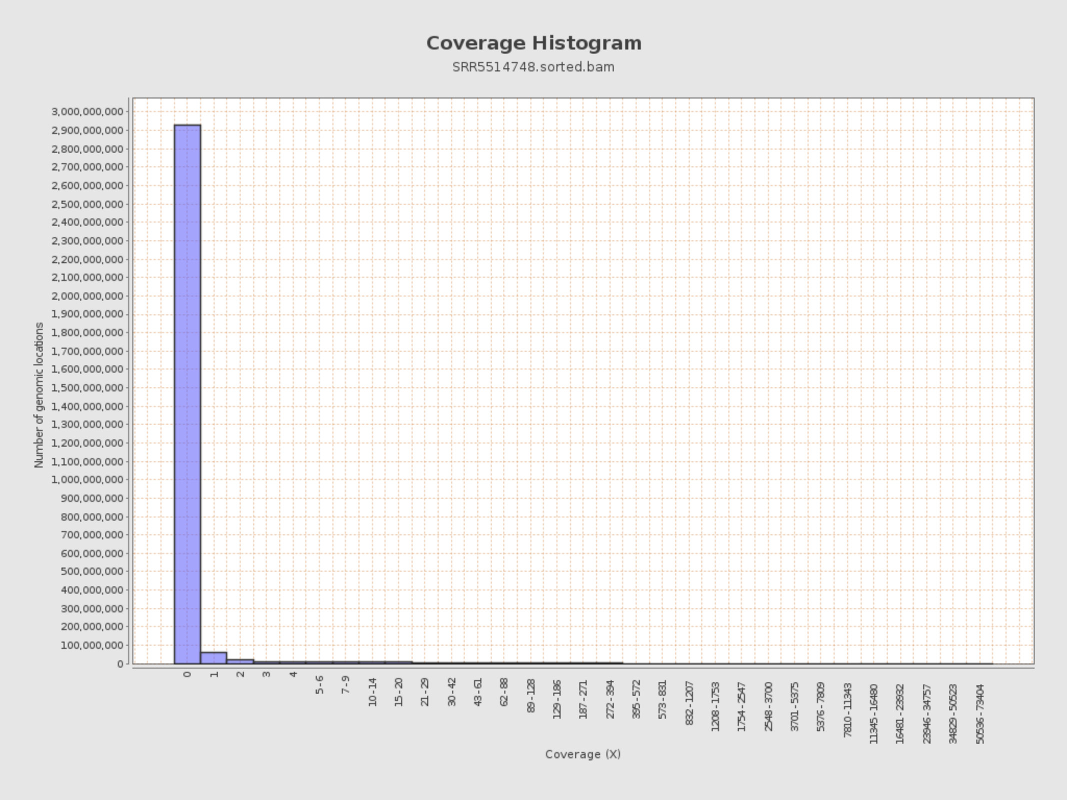
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	380648394	1.5272	45.0242
chr2	243199373	354219660	1.4565	56.3448
chr3	198022430	266180770	1.3442	32.4337
chr4	191154276	435200282	2.2767	98.9742
chr5	180915260	362862462	2.0057	31.0412
chr6	171115067	283757121	1.6583	46.0245
chr7	159138663	257167302	1.616	58.4634

chr8	146364022	245884837	1.68	88.8939
chr9	141213431	174684261	1.237	26.6883
chr10	135534747	240679457	1.7758	54.9562
chr11	135006516	168619796	1.249	21.7189
chr12	133851895	231013146	1.7259	28.1324
chr13	115169878	138165544	1.1997	44.7027
chr14	107349540	116485213	1.0851	25.0316
chr15	102531392	117244136	1.1435	32.4078
chr16	90354753	217307762	2.4051	83.7933
chr17	81195210	74836140	0.9217	28.496
chr18	78077248	110318933	1.4129	27.5947
chr19	59128983	40061313	0.6775	24.4607
chr20	63025520	81596895	1.2947	34.8613
chr21	48129895	134947107	2.8038	176.746
chr22	51304566	34127056	0.6652	38.1163
chrMT	16571	67918196	4,098.6178	3,070.488
chrX	155270560	132364865	0.8525	38.343
chrY	59373566	26388378	0.4444	11.0916

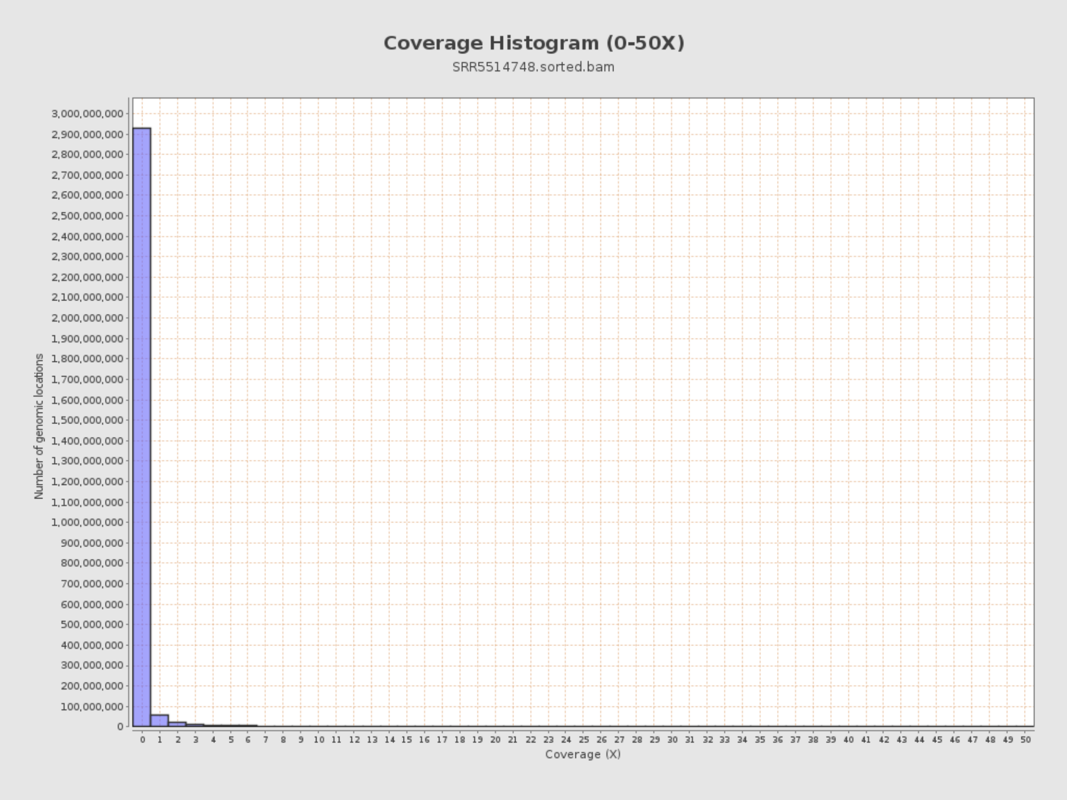
3. Results : Coverage across reference



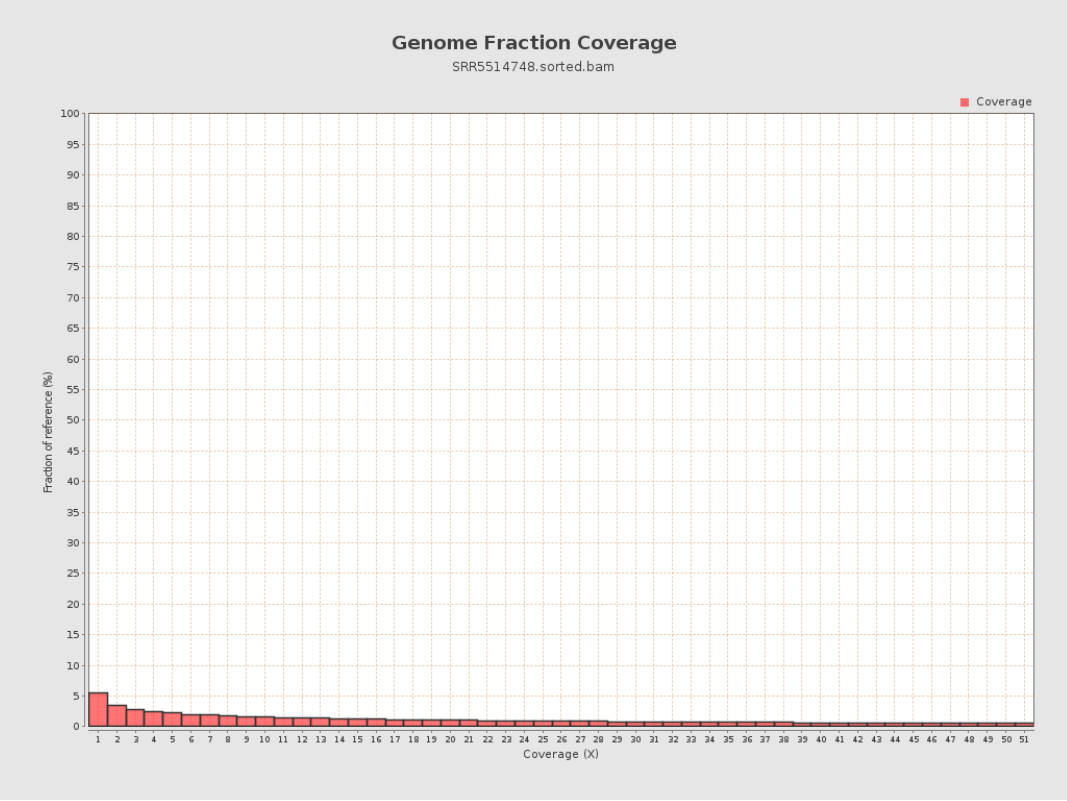
4. Results : Coverage Histogram



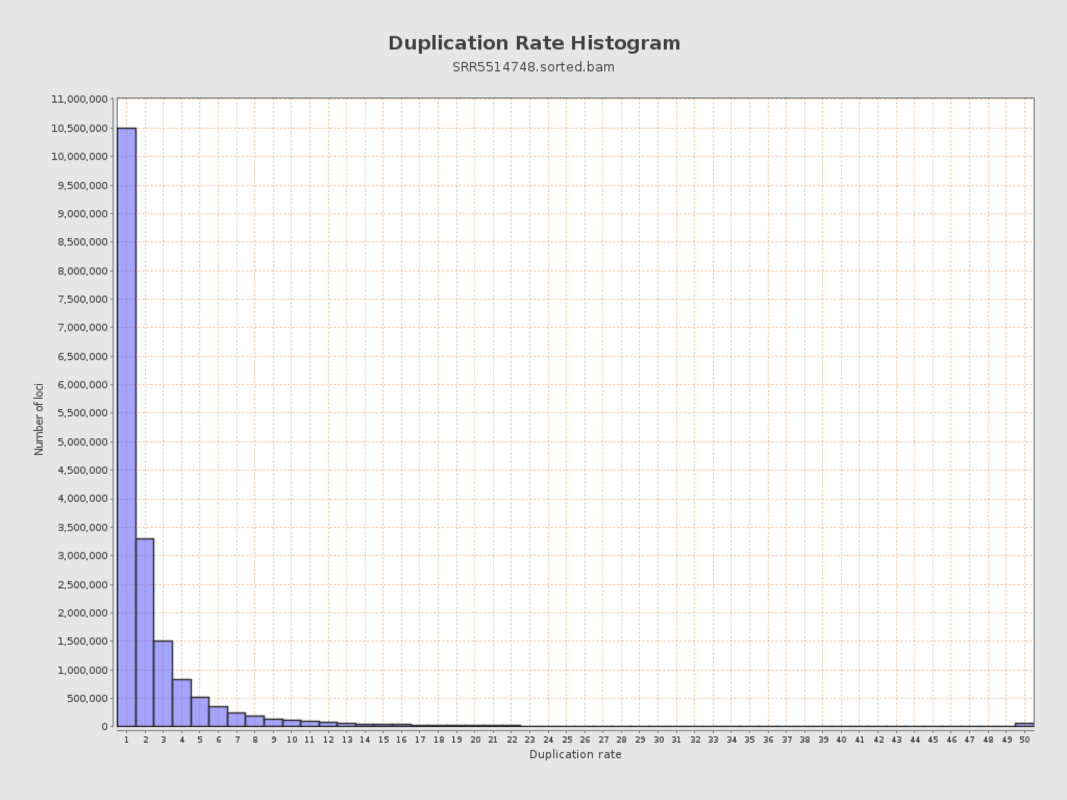
5. Results : Coverage Histogram (0-50X)



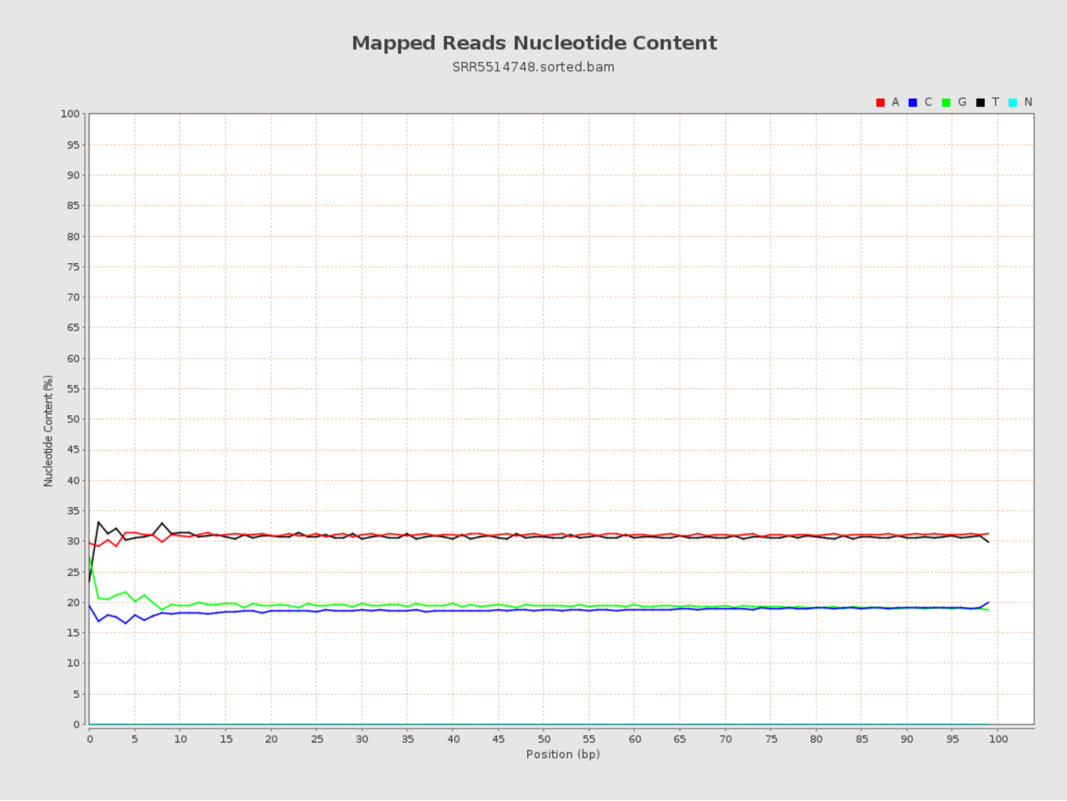
6. Results : Genome Fraction Coverage



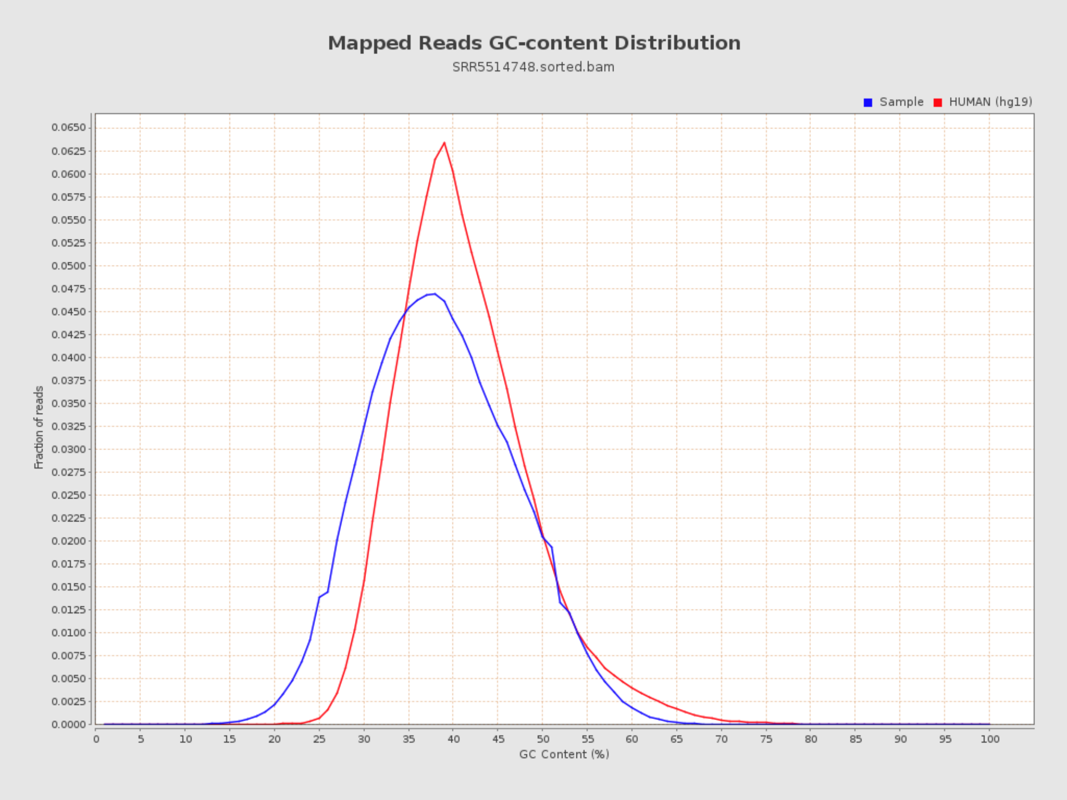
7. Results : Duplication Rate Histogram



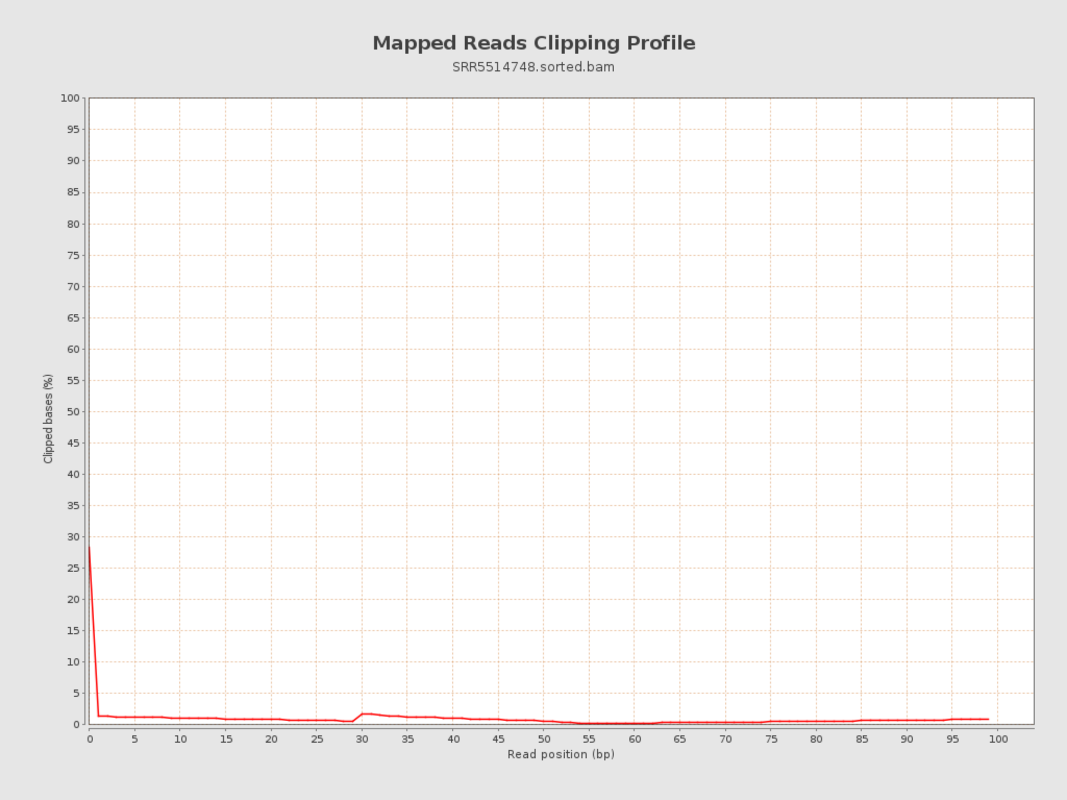
8. Results : Mapped Reads Nucleotide Content



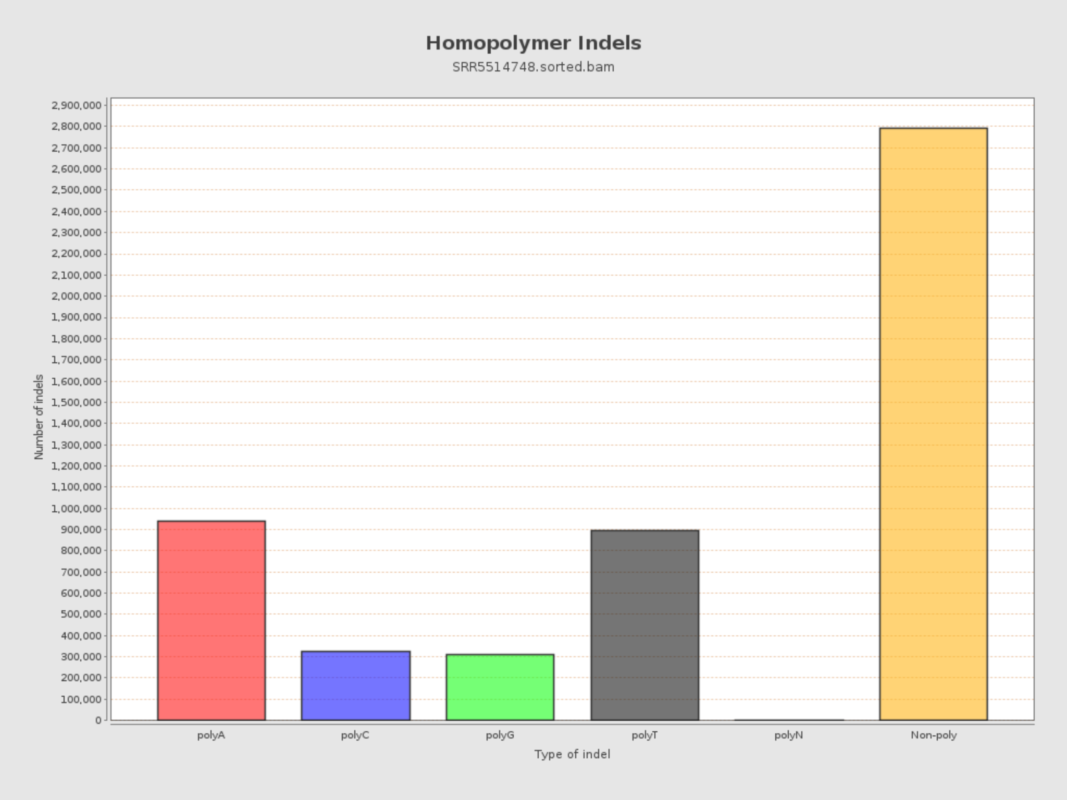
9. Results : Mapped Reads GC-content Distribution



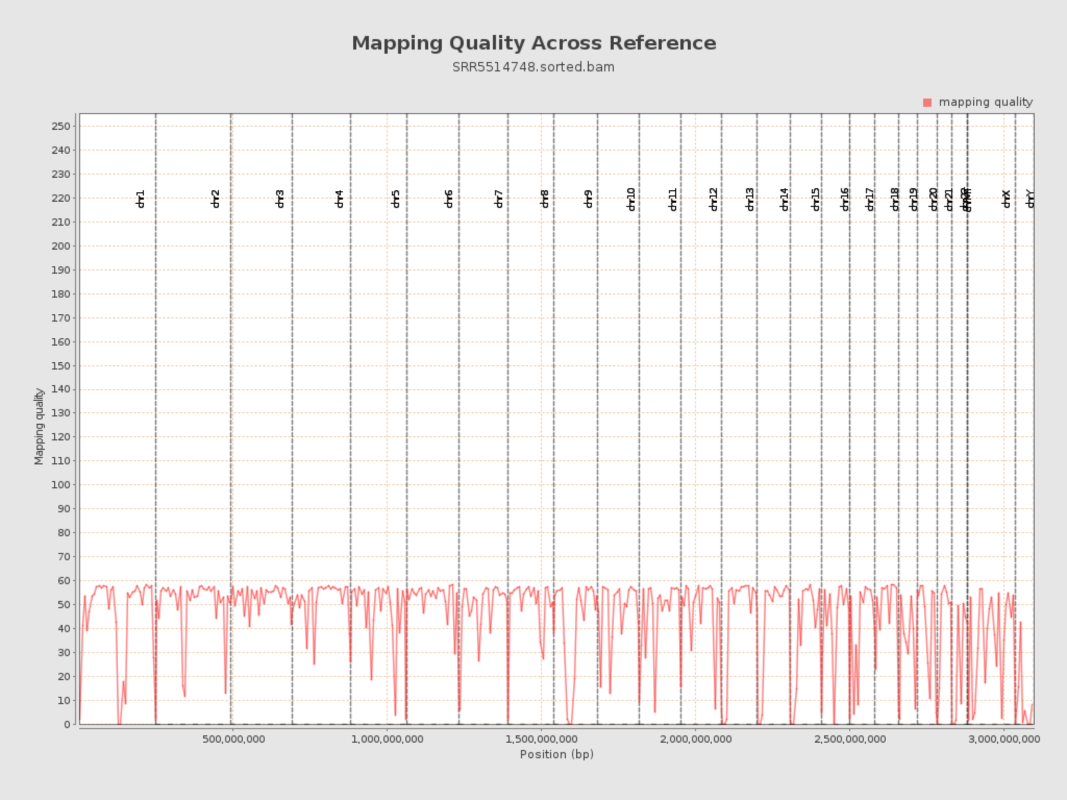
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram