Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 21:07:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514742.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_SRR5514742 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514742.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 21:07:04 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514742.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	79,555,125
Mapped reads	78,132,324 / 98.21%
Unmapped reads	1,422,801 / 1.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,040,442 / 2.56%
Read min/max/mean length	30 / 100 / 99.48
Duplicated reads (estimated)	50,915,250 / 64%
Duplication rate	42.06%
Clipped reads	12,061,723 / 15.16%

2.2. ACGT Content

Number/percentage of A's	1,917,556,444 / 25.66%
Number/percentage of C's	1,786,231,409 / 23.9%
Number/percentage of T's	1,939,498,778 / 25.95%
Number/percentage of G's	1,790,756,282 / 23.96%
Number/percentage of N's	39,873,913 / 0.53%
GC Percentage	47.86%

2.3. Coverage

Mean	2.4155

Standard Deviation	35.8595

2.4. Mapping Quality

Mean Mapping Quality	43.27

2.5. Mismatches and indels

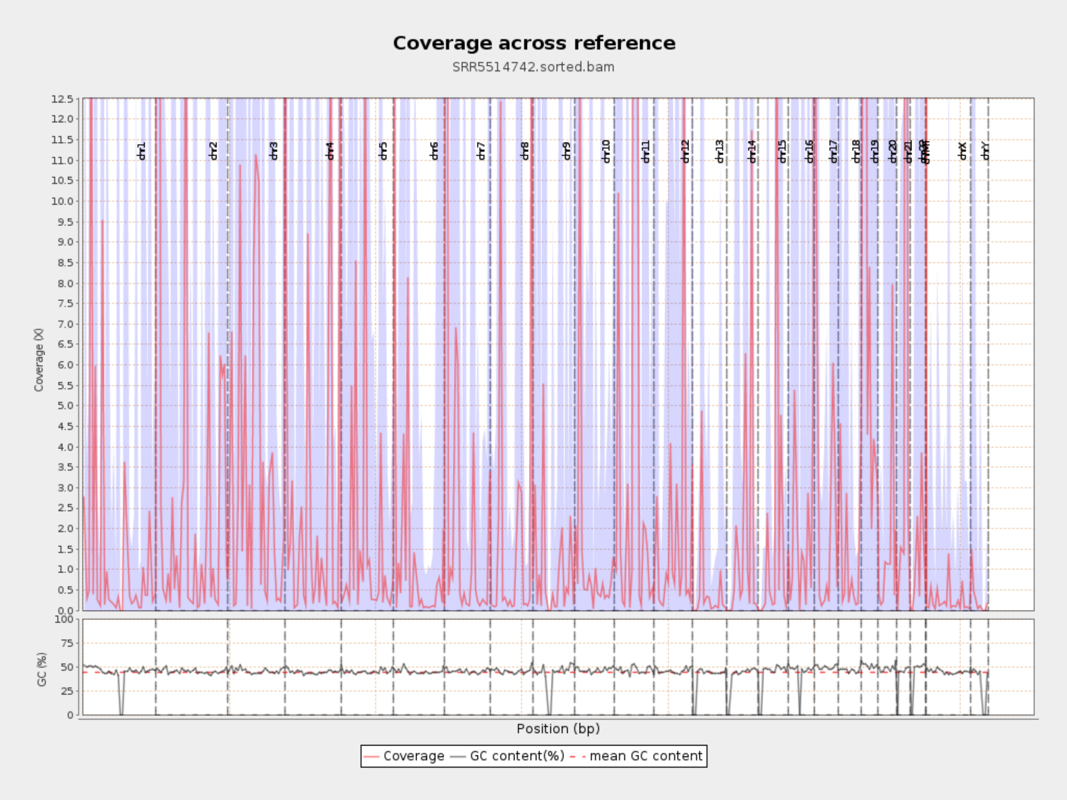
General error rate	0.84%
Mismatches	58,583,461
Insertions	2,542,408
Mapped reads with at least one insertion	3.15%
Deletions	1,952,436
Mapped reads with at least one deletion	2.43%
Homopolymer indels	46.83%

2.6. Chromosome stats

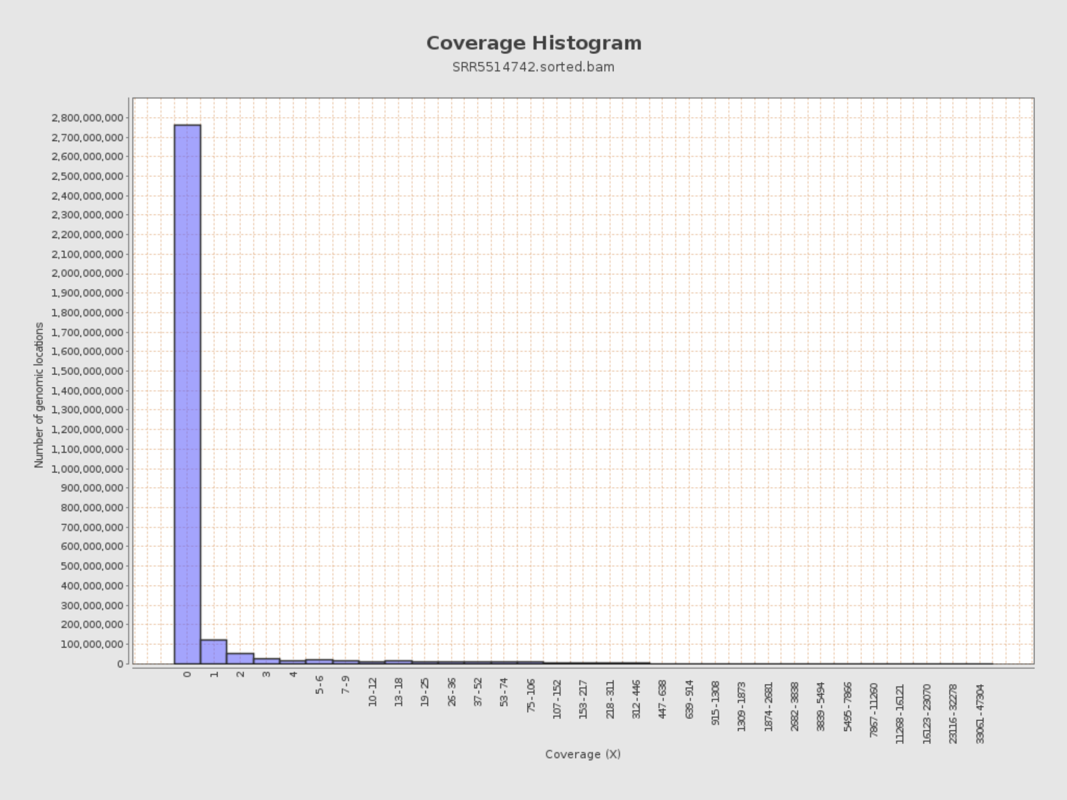
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	384990038	1.5446	22.9072
chr2	243199373	1154751770	4.7482	68.3753
chr3	198022430	649077900	3.2778	27.2696
chr4	191154276	545468414	2.8536	30.5214
chr5	180915260	335680259	1.8555	18.1299
chr6	171115067	232034349	1.356	26.3236
chr7	159138663	506536268	3.183	33.1727

chr8	146364022	310968095	2.1246	25.8581
chr9	141213431	136638852	0.9676	17.0333
chr10	135534747	193455782	1.4274	23.1235
chr11	135006516	670569921	4.9669	58.0324
chr12	133851895	257170257	1.9213	27.7426
chr13	115169878	58410479	0.5072	12.6011
chr14	107349540	188056580	1.7518	31.7722
chr15	102531392	198532156	1.9363	48.3721
chr16	90354753	174038742	1.9262	28.5282
chr17	81195210	266705595	3.2847	25.9064
chr18	78077248	96134124	1.2313	19.8614
chr19	59128983	591434964	10.0025	62.4661
chr20	63025520	102560651	1.6273	44.1274
chr21	48129895	293446392	6.097	84.2193
chr22	51304566	68038499	1.3262	17.7308
chrMT	16571	6796838	410.1646	198.5976
chrX	155270560	40109154	0.2583	4.7738
chrY	59373566	16113703	0.2714	14.7903

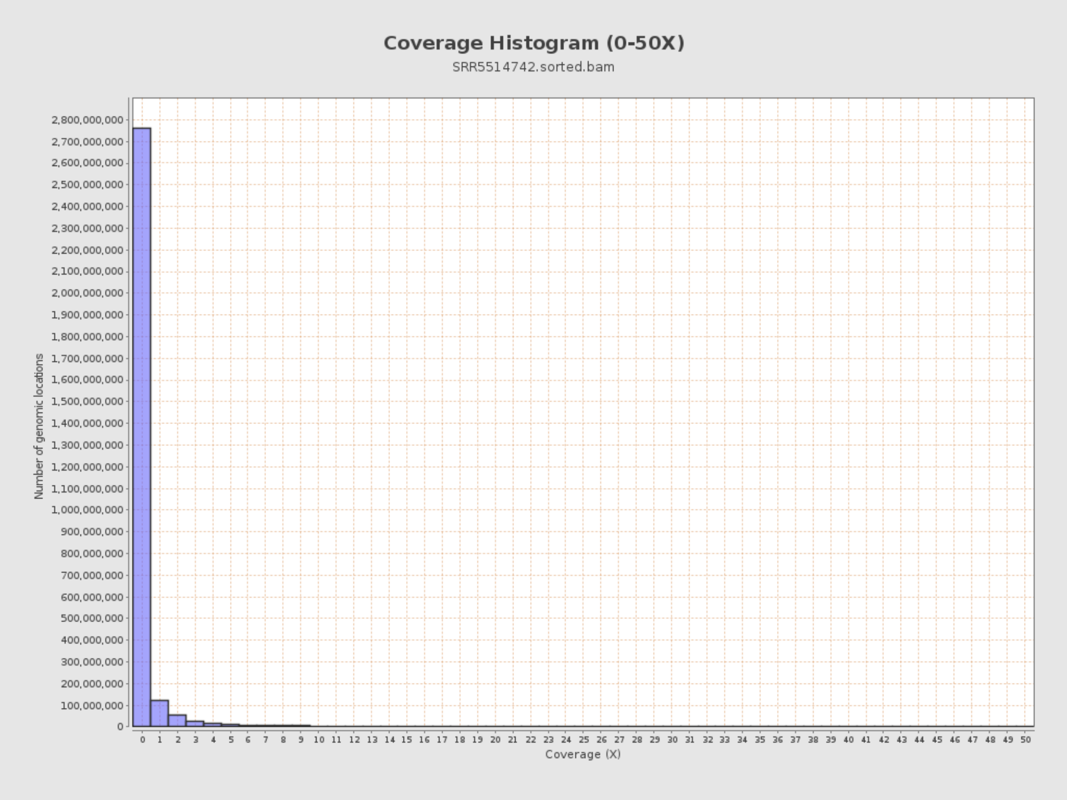
3. Results : Coverage across reference



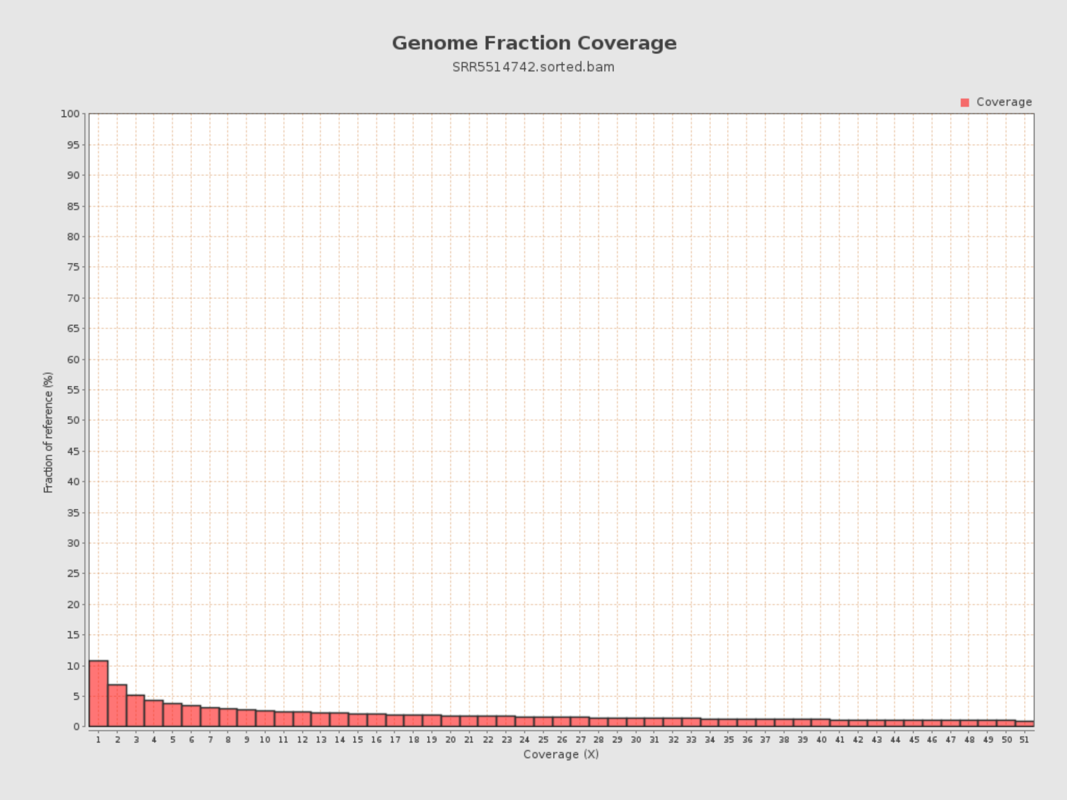
4. Results : Coverage Histogram



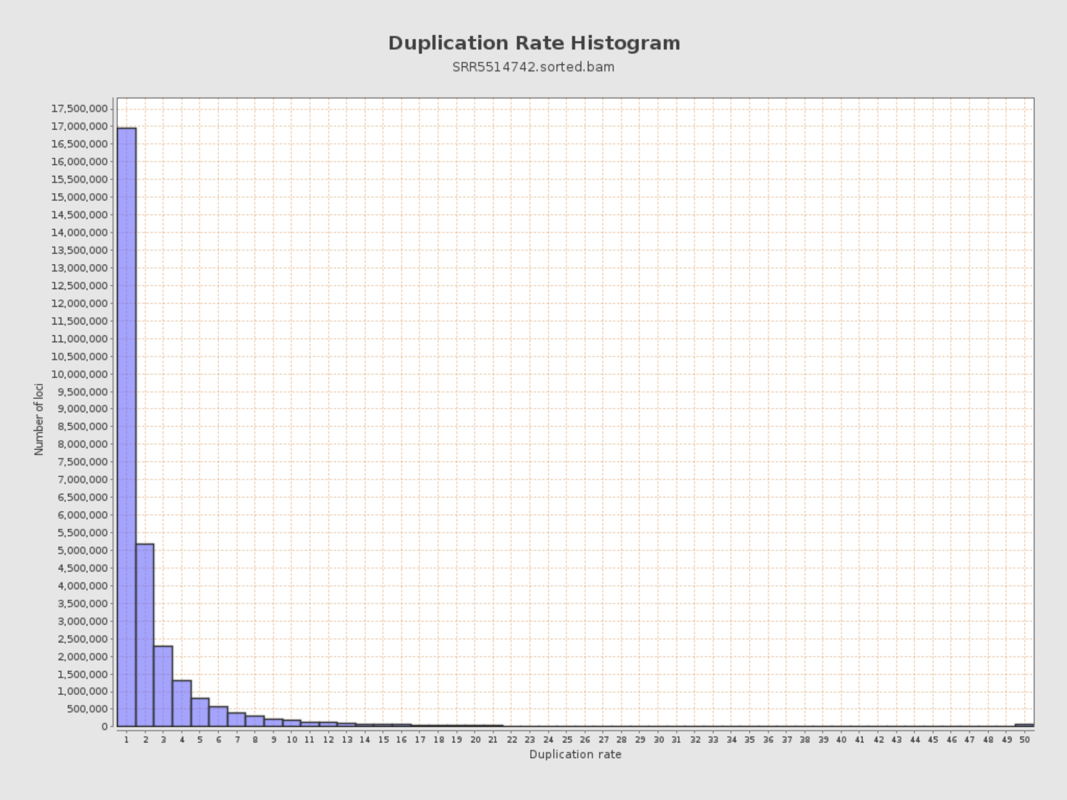
5. Results : Coverage Histogram (0-50X)



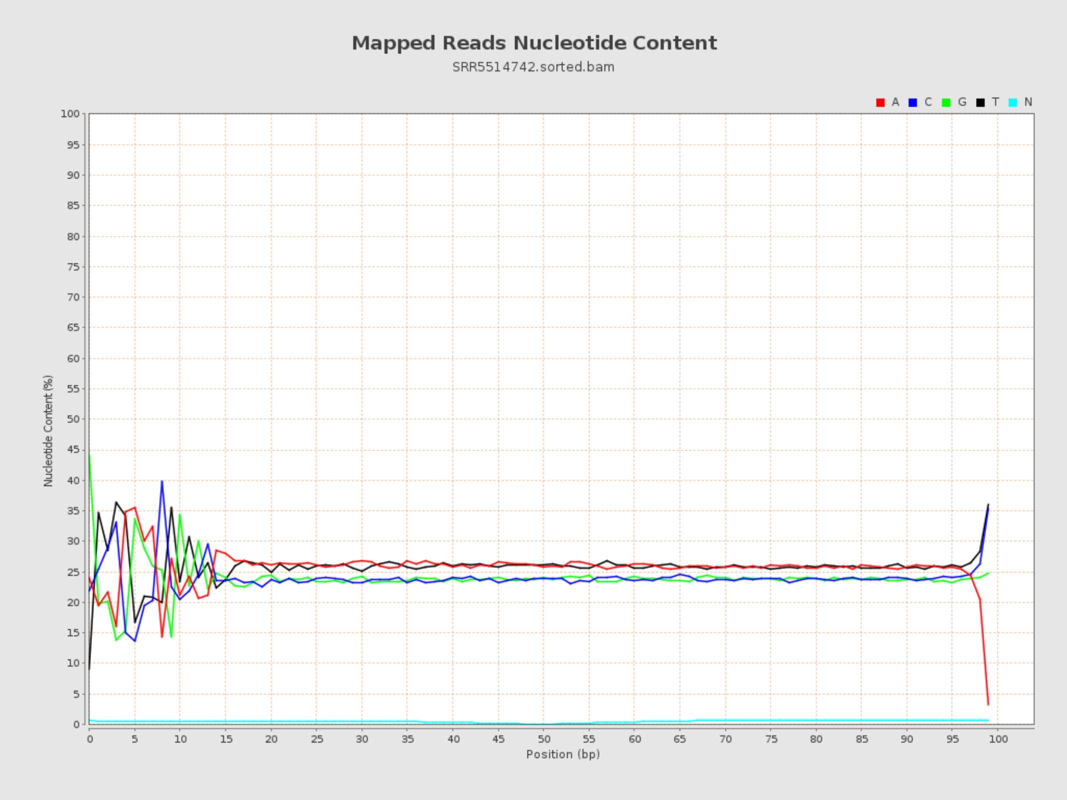
6. Results : Genome Fraction Coverage



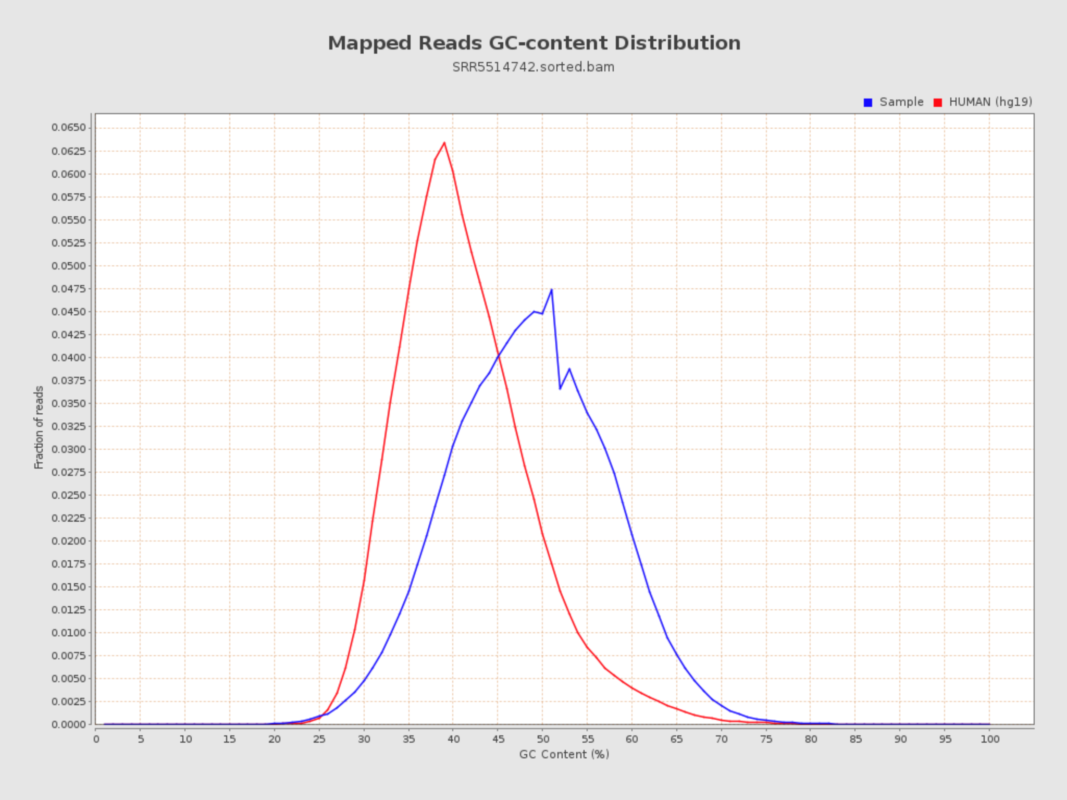
7. Results : Duplication Rate Histogram



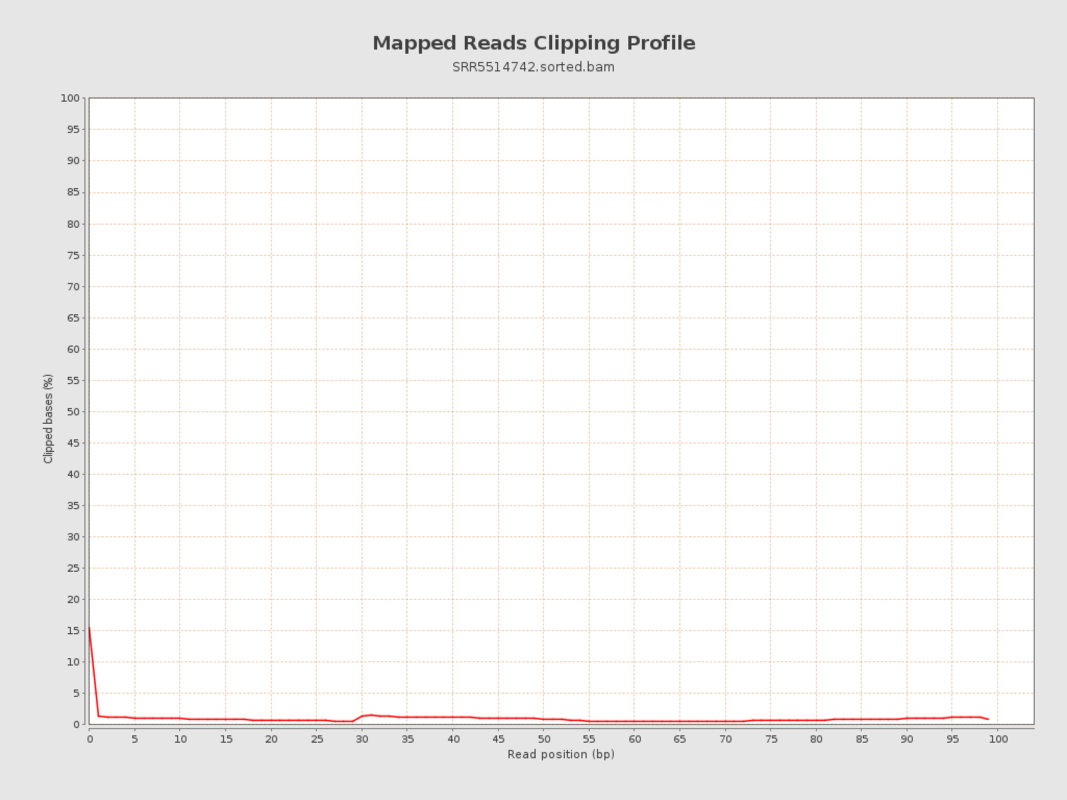
8. Results : Mapped Reads Nucleotide Content



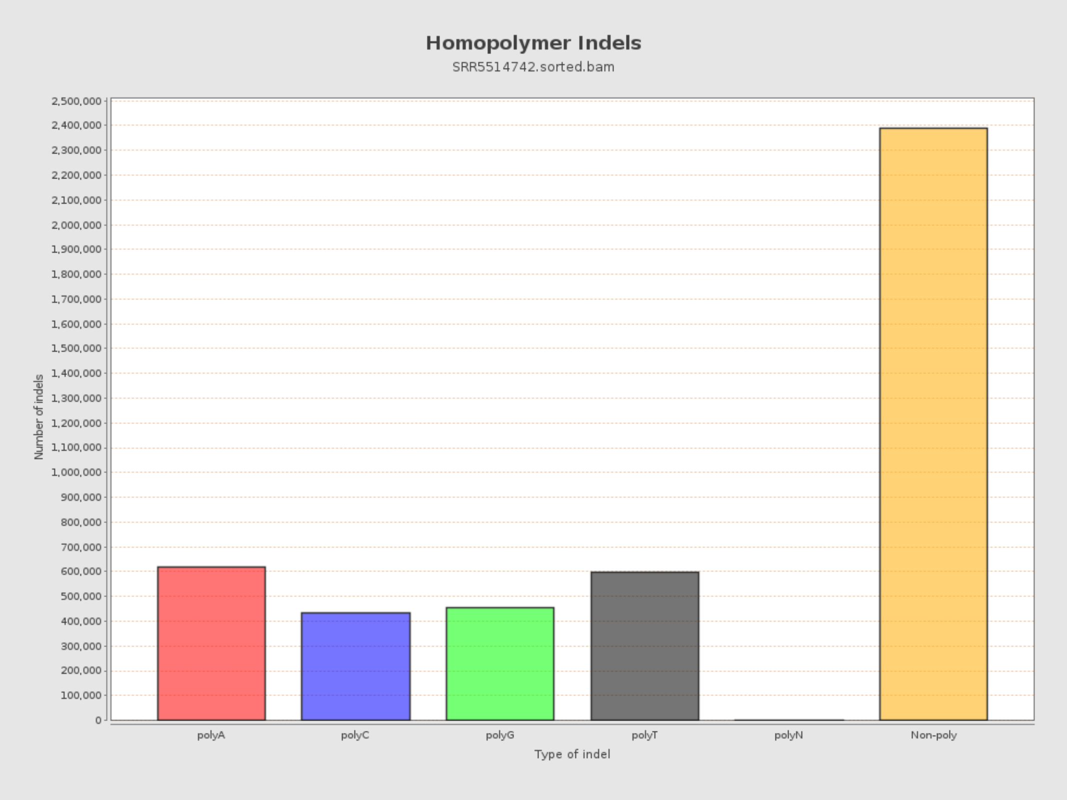
9. Results : Mapped Reads GC-content Distribution



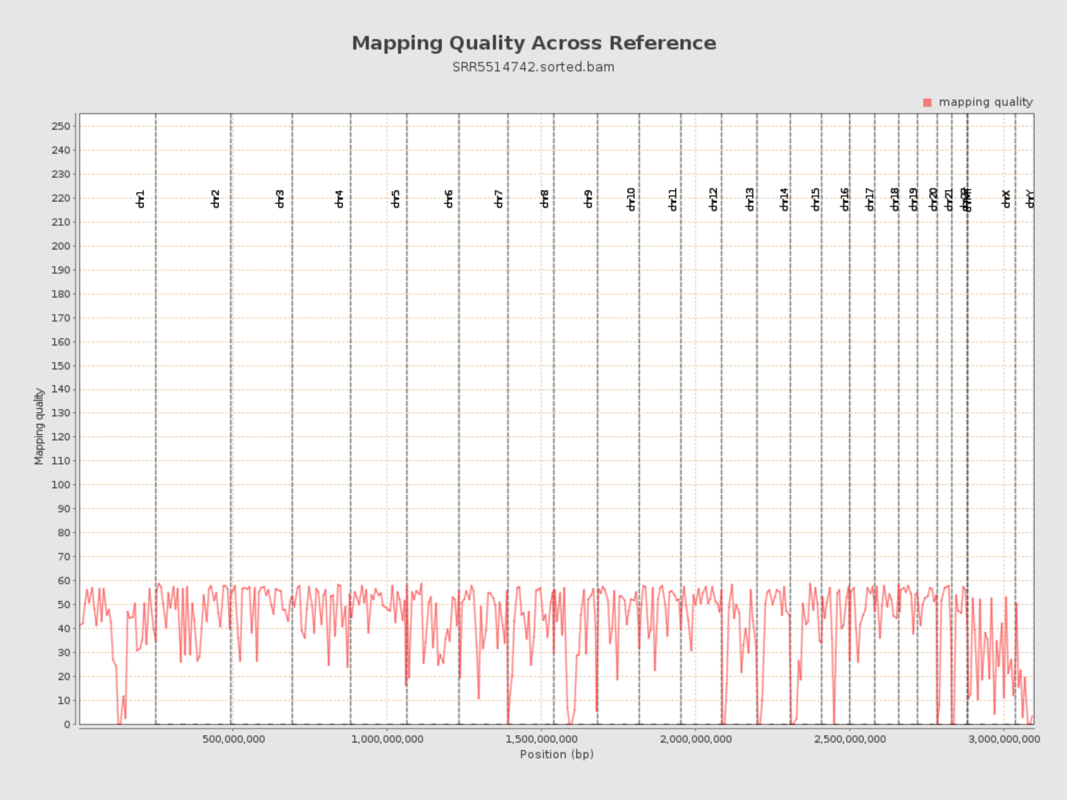
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram