Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 07:28:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514729.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_SRR5514729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514729.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 07:28:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	106,655,060
Mapped reads	100,024,744 / 93.78%
Unmapped reads	6,630,316 / 6.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,129,348 / 2.93%
Read min/max/mean length	30 / 100 / 99.06
Duplicated reads (estimated)	82,659,332 / 77.5%
Duplication rate	48.51%
Clipped reads	19,086,339 / 17.9%

2.2. ACGT Content

Number/percentage of A's	2,456,336,013 / 26.09%
Number/percentage of C's	2,206,201,751 / 23.43%
Number/percentage of T's	2,478,378,152 / 26.32%
Number/percentage of G's	2,217,644,852 / 23.56%
Number/percentage of N's	56,109,208 / 0.6%
GC Percentage	46.99%

2.3. Coverage

Mean	3.0433

Standard Deviation	110.1661

2.4. Mapping Quality

Mean Mapping Quality	40.81

2.5. Mismatches and indels

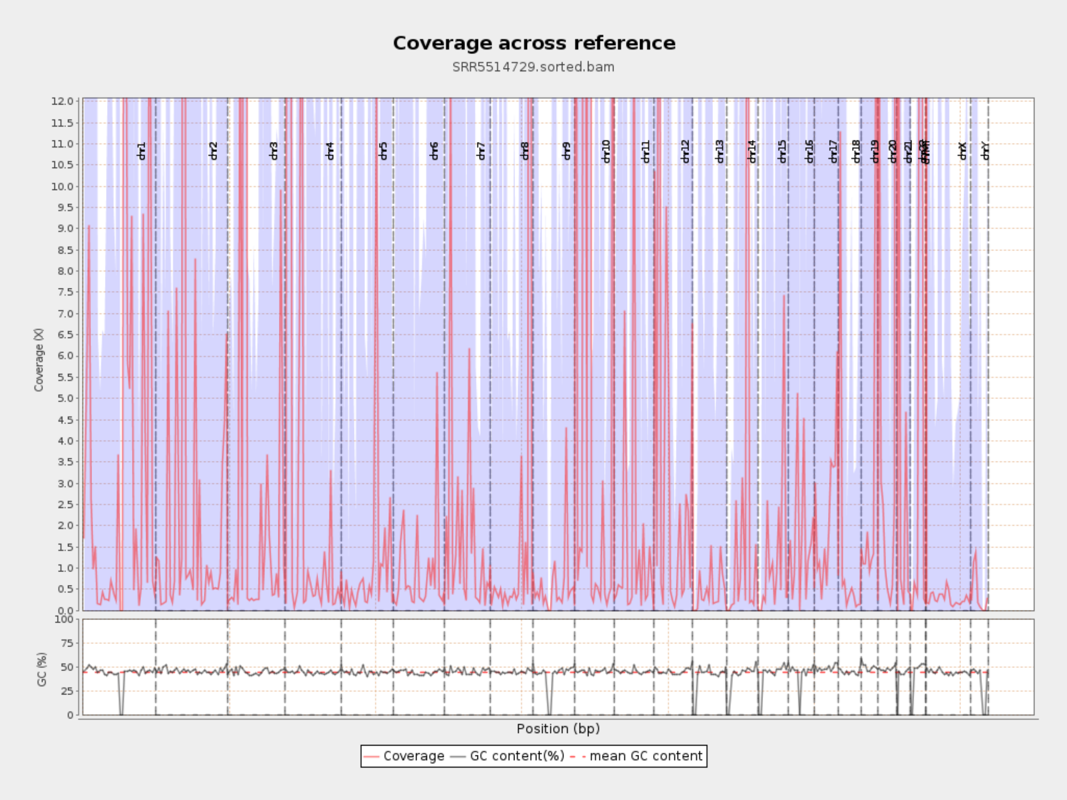
General error rate	1.02%
Mismatches	89,886,542
Insertions	3,522,152
Mapped reads with at least one insertion	3.35%
Deletions	2,752,305
Mapped reads with at least one deletion	2.65%
Homopolymer indels	41.74%

2.6. Chromosome stats

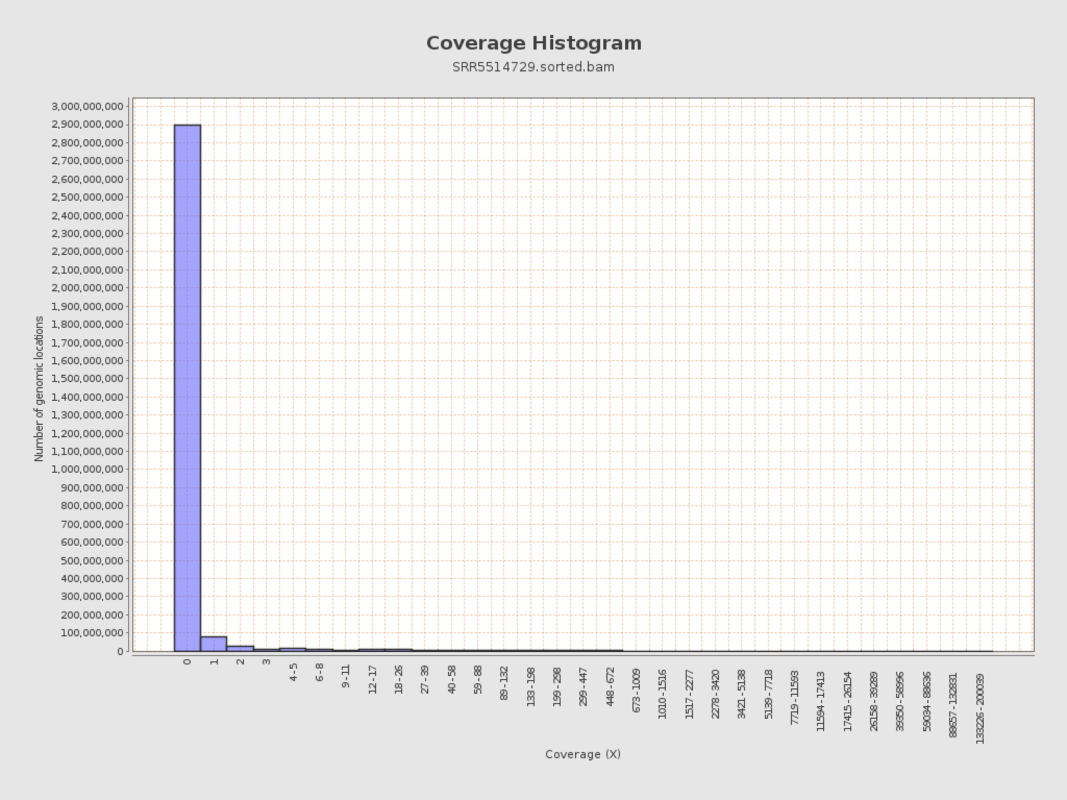
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	869127505	3.487	124.9147
chr2	243199373	758914487	3.1205	132.9173
chr3	198022430	836190496	4.2227	122.4791
chr4	191154276	964052361	5.0433	81.688
chr5	180915260	205713973	1.1371	40.2075
chr6	171115067	156157446	0.9126	35.6935
chr7	159138663	298984107	1.8788	37.7548

chr8	146364022	397482311	2.7157	150.9352
chr9	141213431	89698003	0.6352	30.2804
chr10	135534747	2156385153	15.9102	303.2084
chr11	135006516	237569625	1.7597	38.1398
chr12	133851895	499634545	3.7327	125.5247
chr13	115169878	56953369	0.4945	22.1551
chr14	107349540	282655522	2.633	59.1481
chr15	102531392	130732891	1.2751	109.327
chr16	90354753	154089314	1.7054	93.7559
chr17	81195210	176339776	2.1718	28.2479
chr18	78077248	113062103	1.4481	33.2999
chr19	59128983	209719663	3.5468	125.6498
chr20	63025520	284658647	4.5166	132.5853
chr21	48129895	164333204	3.4144	110.3928
chr22	51304566	305465378	5.954	123.1924
chrMT	16571	4299095	259.4349	160.3742
chrX	155270560	43743474	0.2817	13.0224
chrY	59373566	25123580	0.4231	41.9539

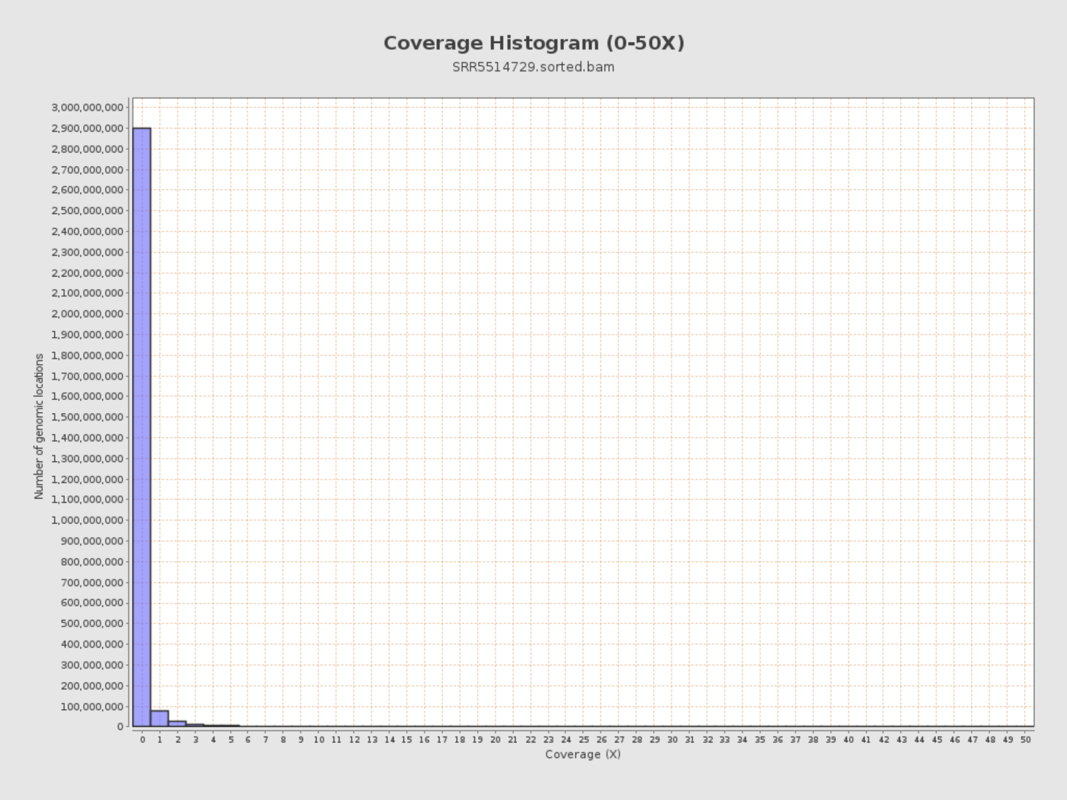
3. Results : Coverage across reference



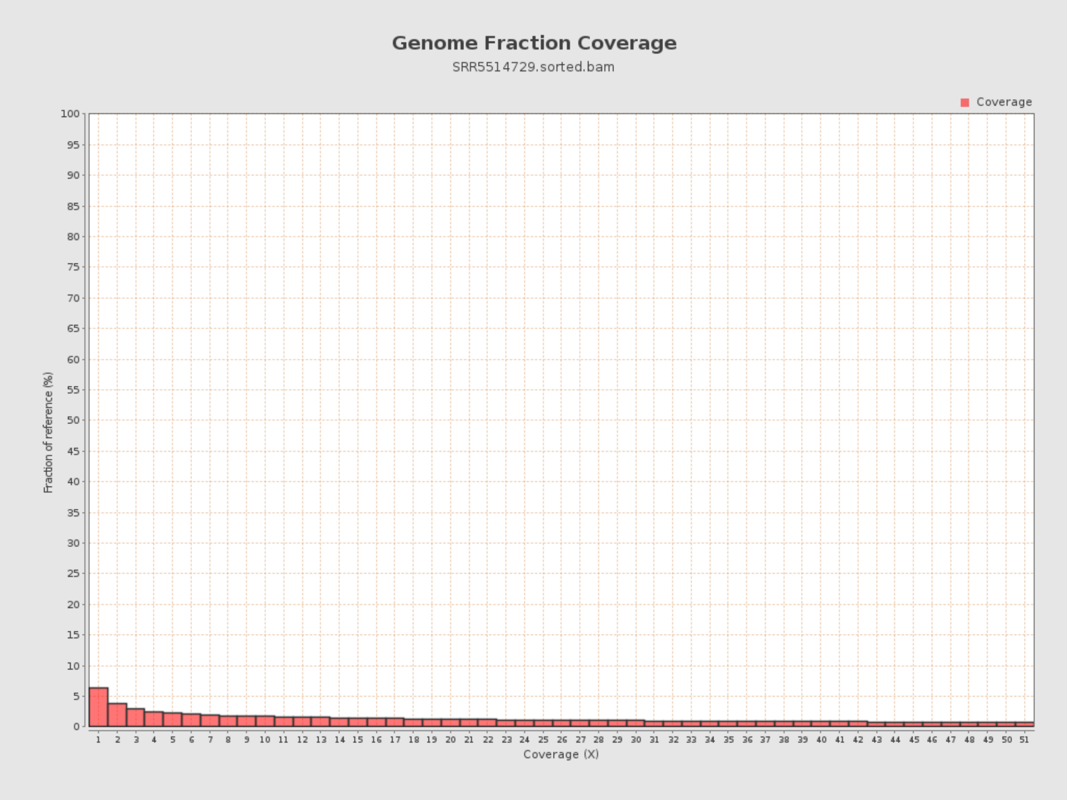
4. Results : Coverage Histogram



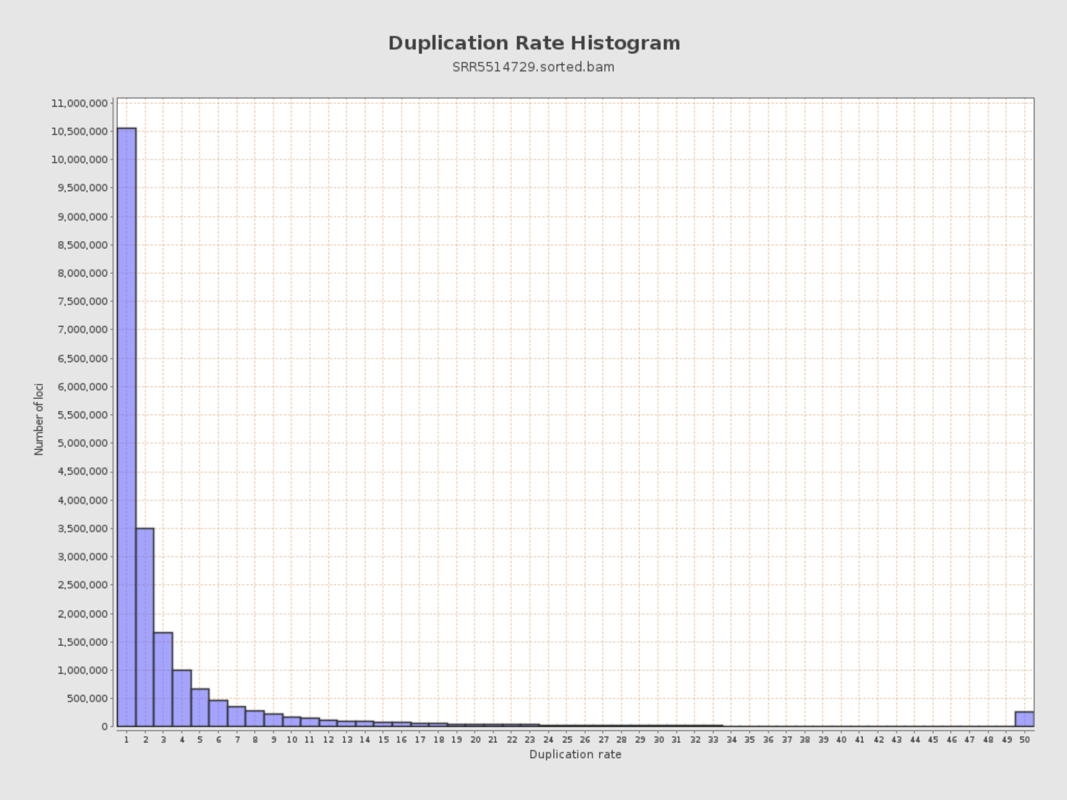
5. Results : Coverage Histogram (0-50X)



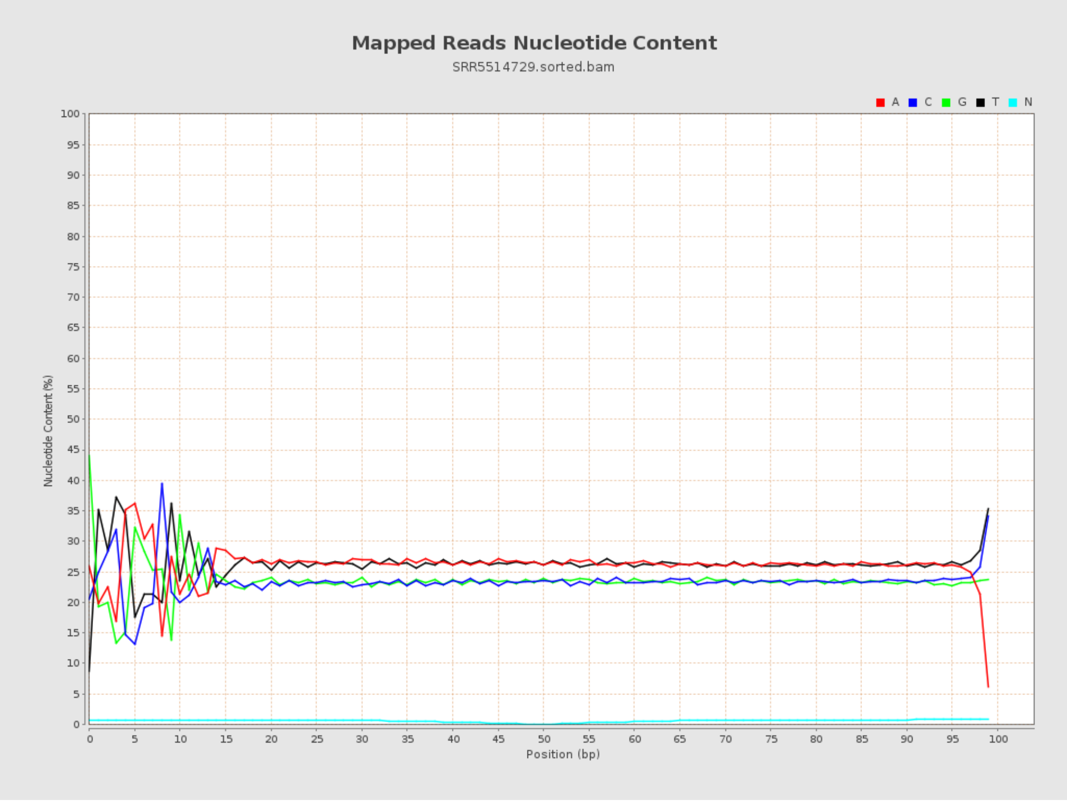
6. Results : Genome Fraction Coverage



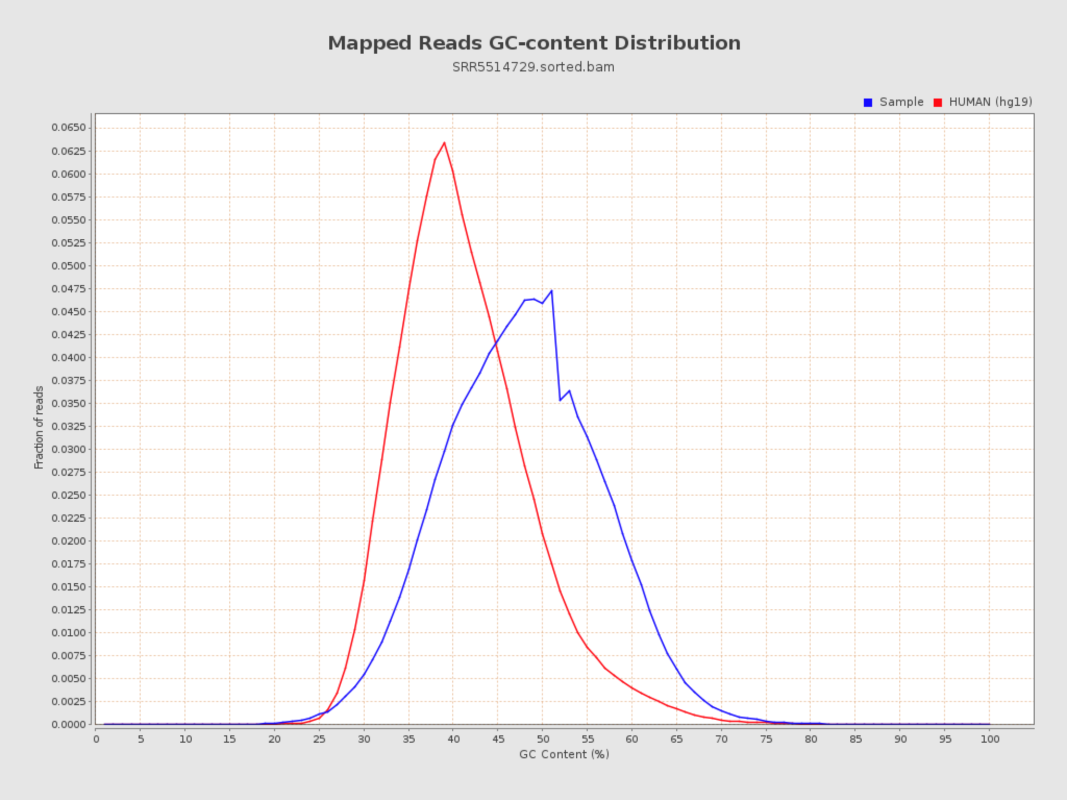
7. Results : Duplication Rate Histogram



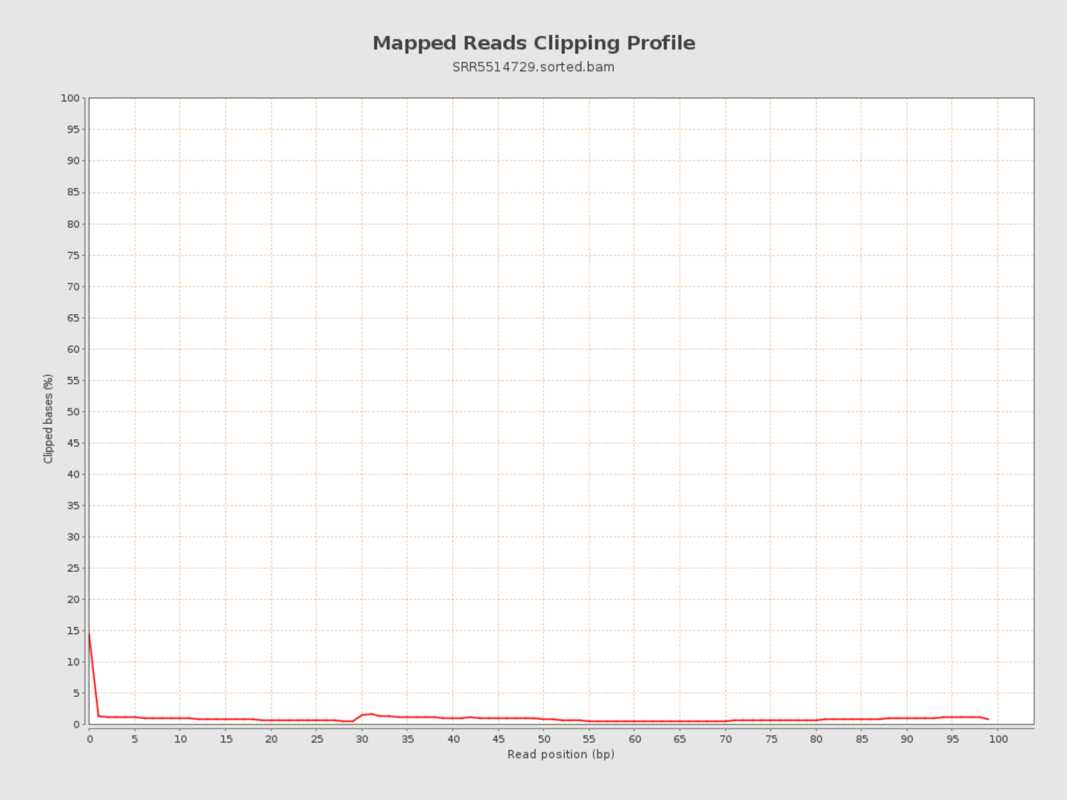
8. Results : Mapped Reads Nucleotide Content



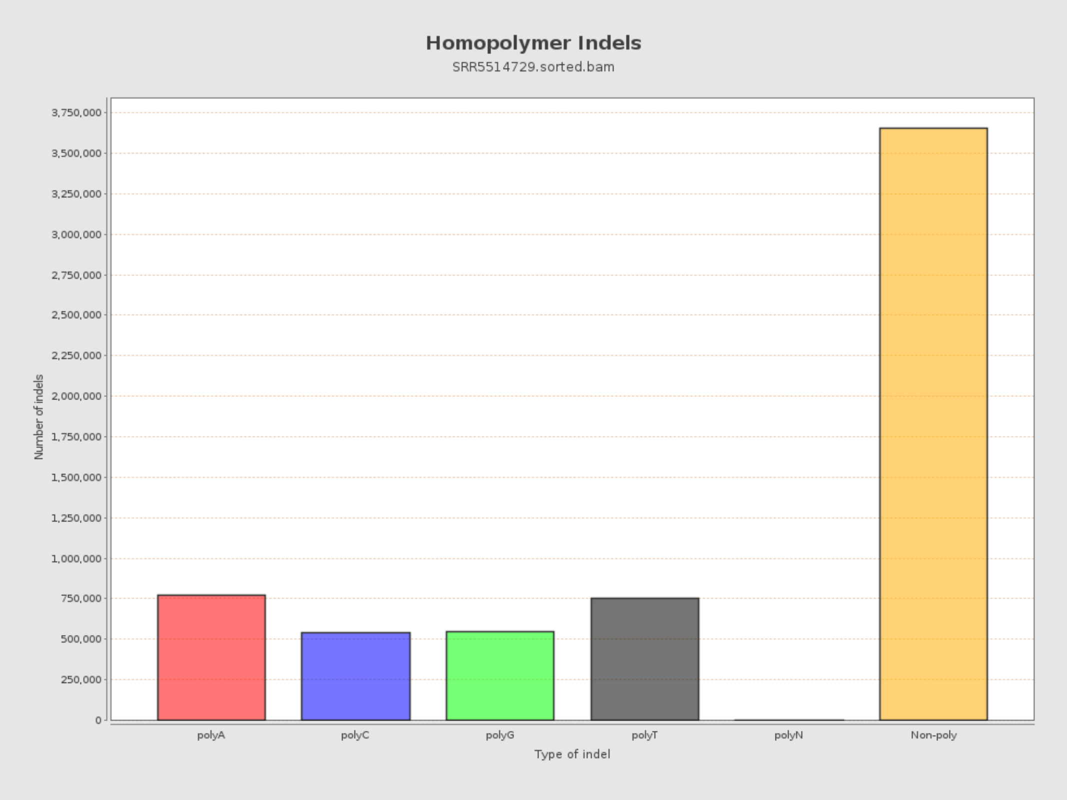
9. Results : Mapped Reads GC-content Distribution



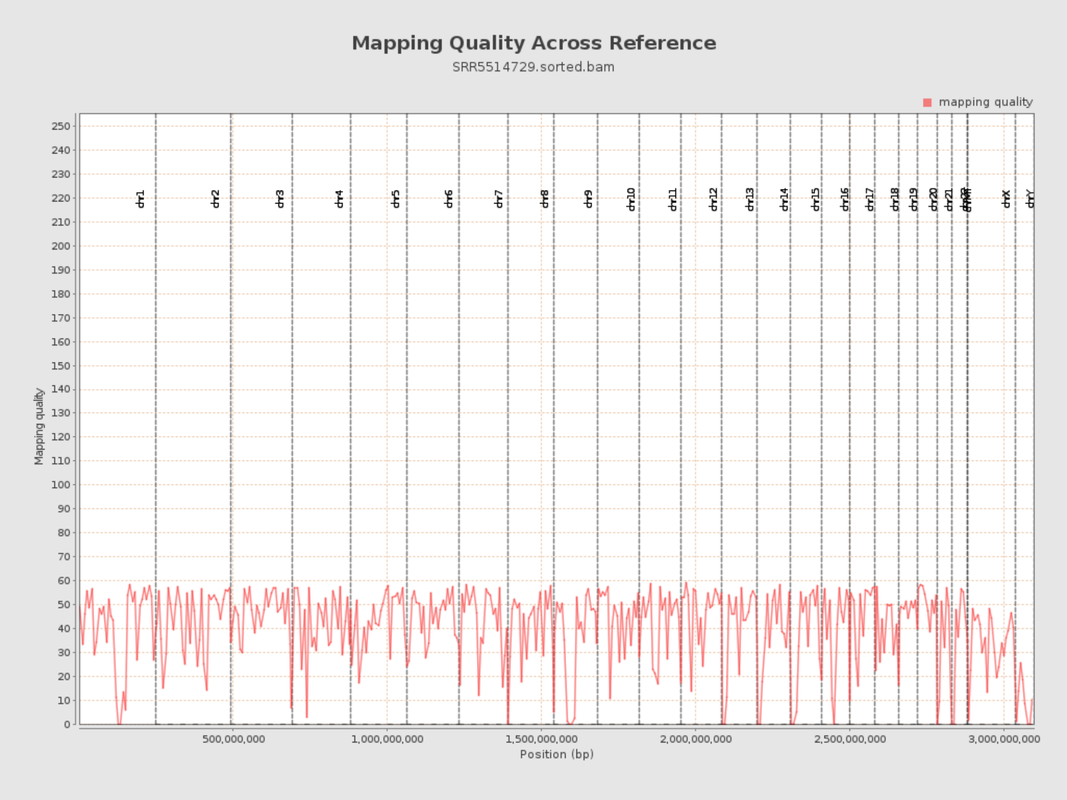
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram