Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 05:48:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514762.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_SRR5514762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 05:48:09 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,479,126
Mapped reads	18,200,717 / 88.87%
Unmapped reads	2,278,409 / 11.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,744,801 / 13.4%
Read min/max/mean length	30 / 100 / 104.47
Duplicated reads (estimated)	12,205,905 / 59.6%
Duplication rate	37.61%
Clipped reads	9,259,135 / 45.21%

2.2. ACGT Content

Number/percentage of A's	536,217,305 / 31.11%
Number/percentage of C's	325,283,867 / 18.87%
Number/percentage of T's	526,702,437 / 30.55%
Number/percentage of G's	335,532,481 / 19.46%
Number/percentage of N's	115,544 / 0.01%
GC Percentage	38.33%

2.3. Coverage

Mean	0.5572

Standard Deviation	22.0235

2.4. Mapping Quality

Mean Mapping Quality	43.12

2.5. Mismatches and indels

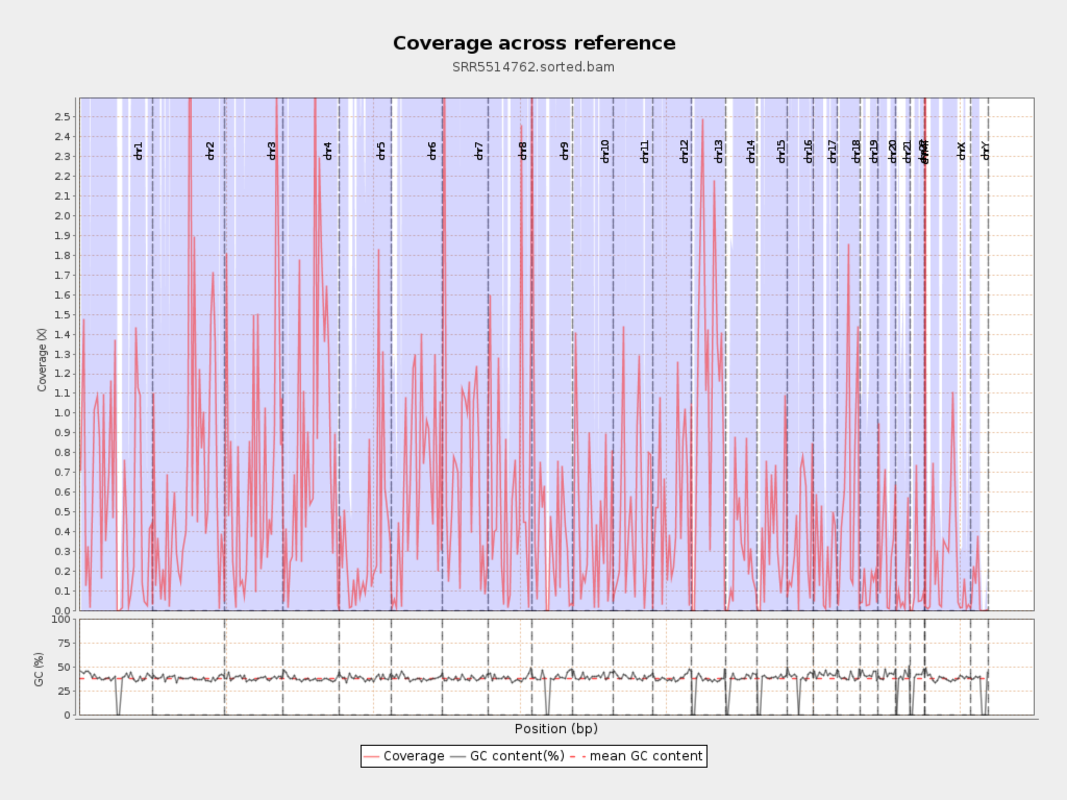
General error rate	0.61%
Mismatches	8,887,138
Insertions	982,431
Mapped reads with at least one insertion	5.18%
Deletions	371,494
Mapped reads with at least one deletion	1.94%
Homopolymer indels	53.2%

2.6. Chromosome stats

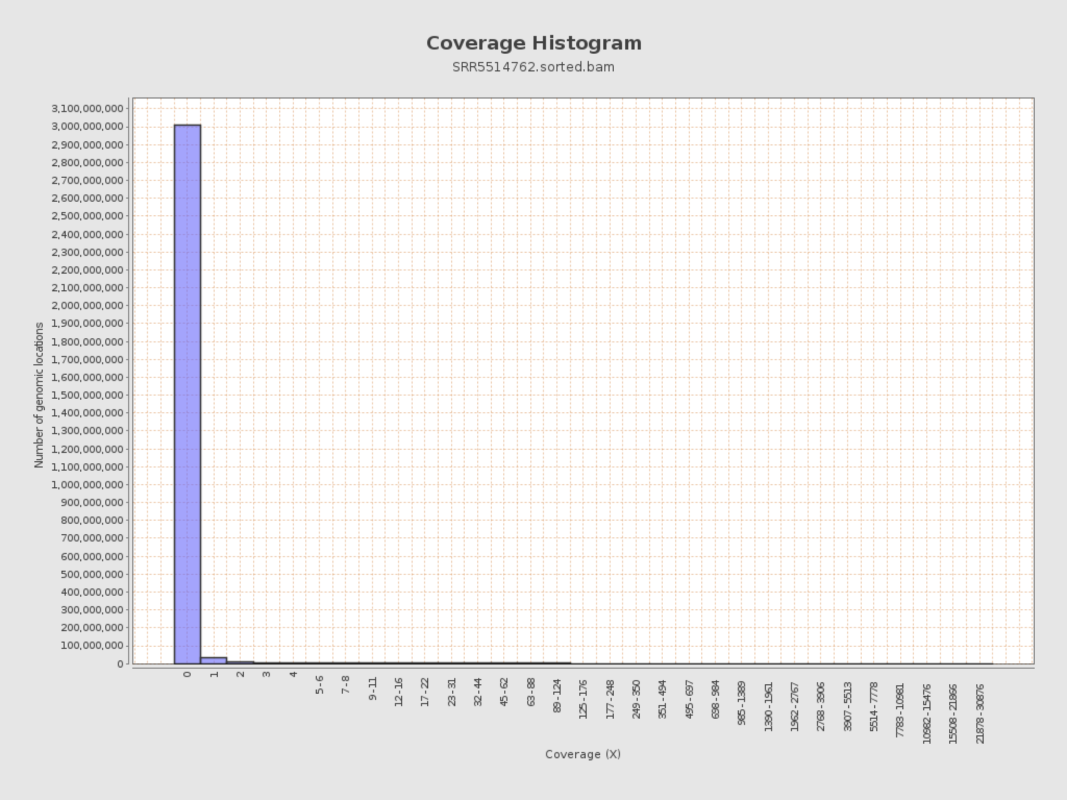
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	137001480	0.5497	13.606
chr2	243199373	170116145	0.6995	33.0045
chr3	198022430	142032379	0.7173	13.6583
chr4	191154276	168279678	0.8803	15.947
chr5	180915260	66501419	0.3676	13.2549
chr6	171115067	111148172	0.6496	11.5047
chr7	159138663	119377301	0.7501	14.9568

chr8	146364022	91762581	0.6269	38.2021
chr9	141213431	60367084	0.4275	13.9042
chr10	135534747	52588149	0.388	12.6372
chr11	135006516	66097374	0.4896	10.6974
chr12	133851895	69816143	0.5216	12.7743
chr13	115169878	136145653	1.1821	25.3848
chr14	107349540	33259345	0.3098	7.3728
chr15	102531392	41177479	0.4016	7.445
chr16	90354753	33623073	0.3721	8.1993
chr17	81195210	20640861	0.2542	9.4956
chr18	78077248	51450155	0.659	13.7243
chr19	59128983	6862867	0.1161	8.1844
chr20	63025520	22424040	0.3558	18.0945
chr21	48129895	6122232	0.1272	6.0338
chr22	51304566	7735379	0.1508	4.0936
chrMT	16571	66298488	4,000.8743	4,233.4304
chrX	155270560	38032584	0.2449	8.4444
chrY	59373566	6035187	0.1016	3.4494

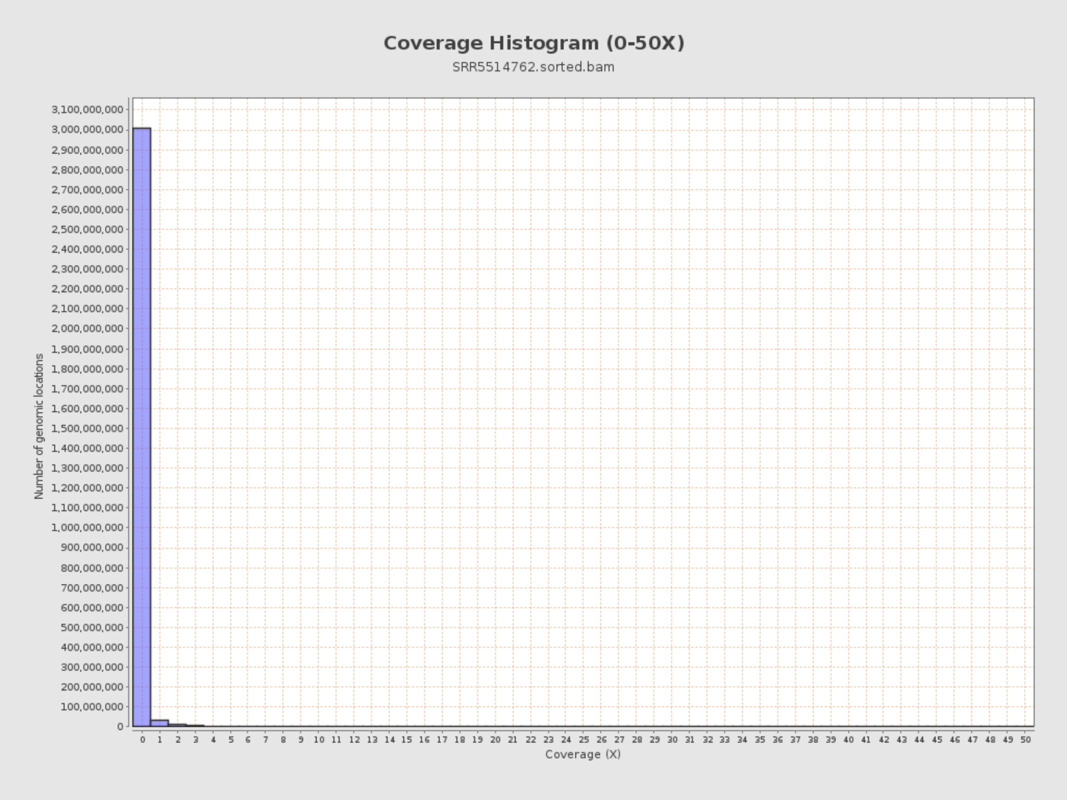
3. Results : Coverage across reference



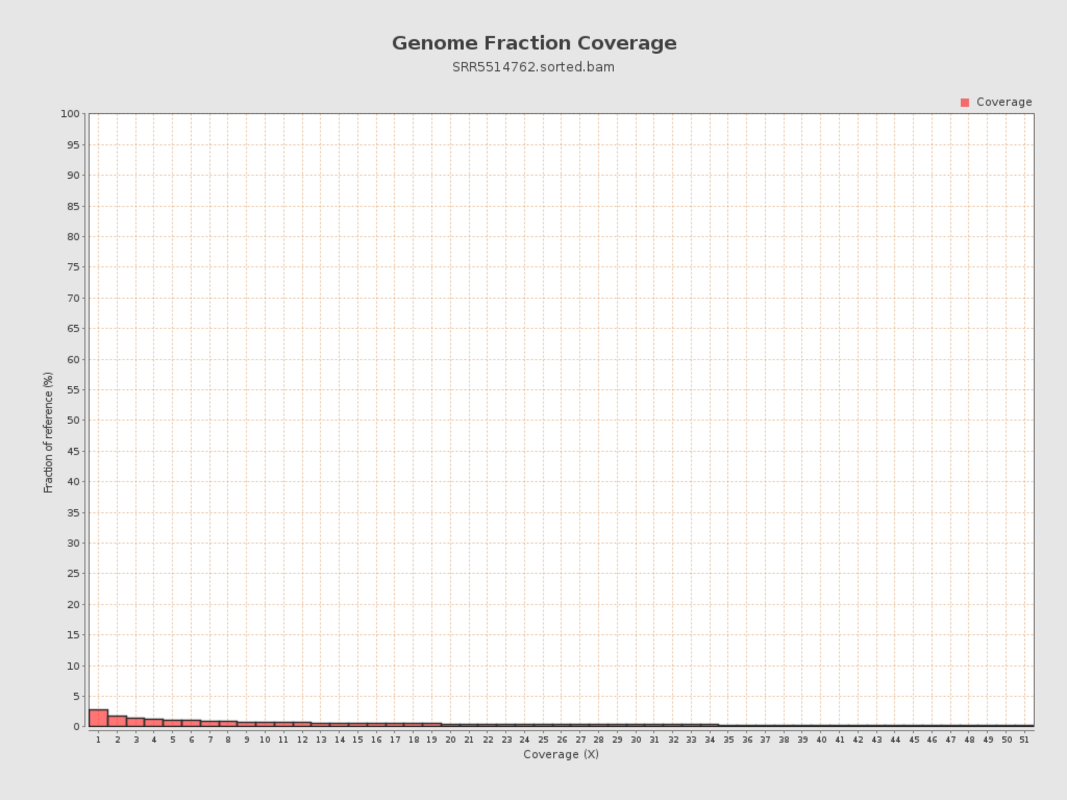
4. Results : Coverage Histogram



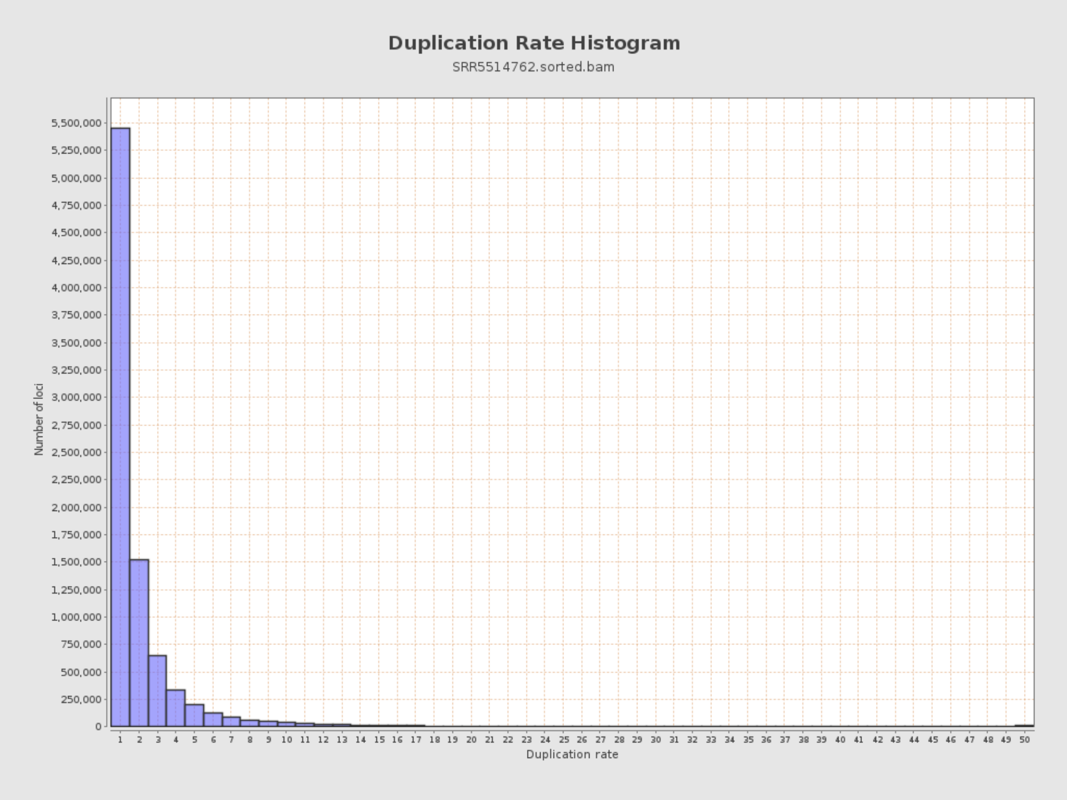
5. Results : Coverage Histogram (0-50X)



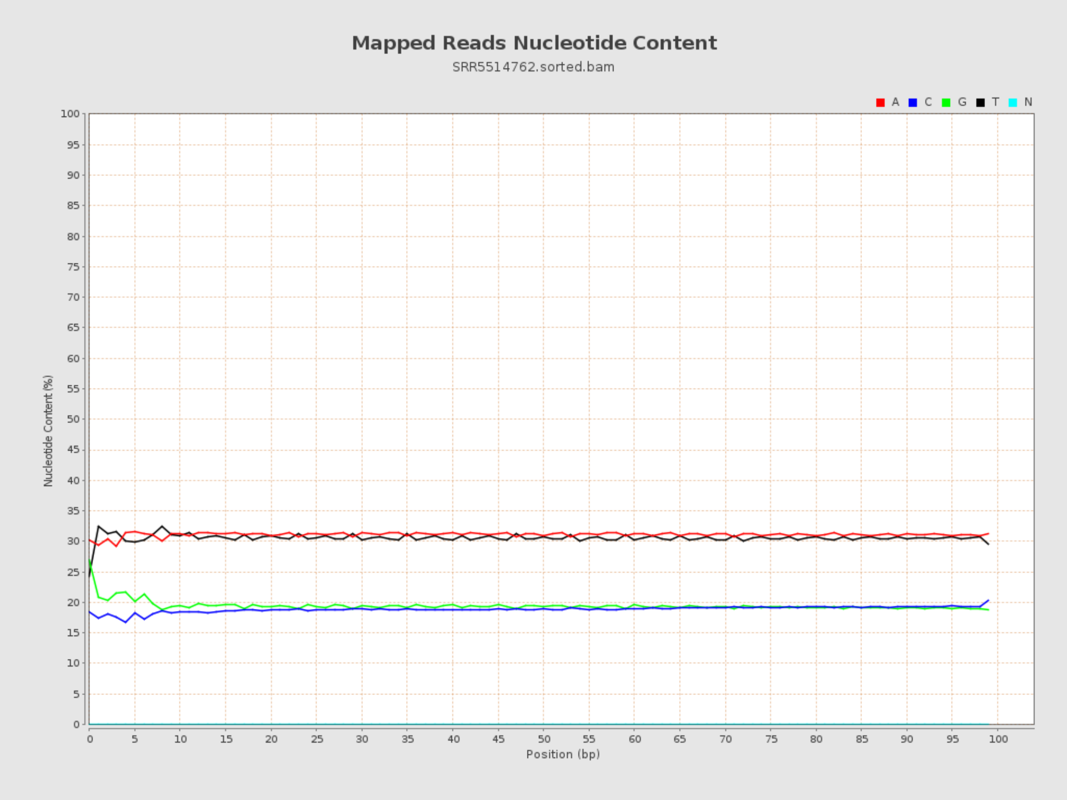
6. Results : Genome Fraction Coverage



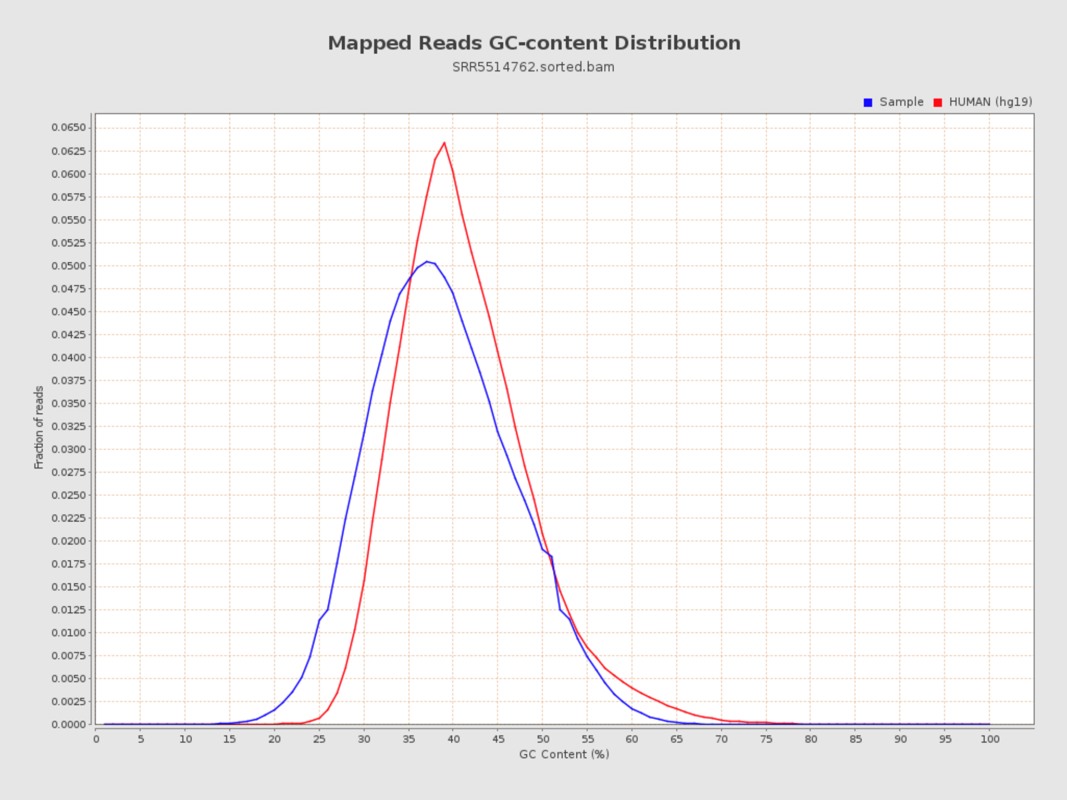
7. Results : Duplication Rate Histogram



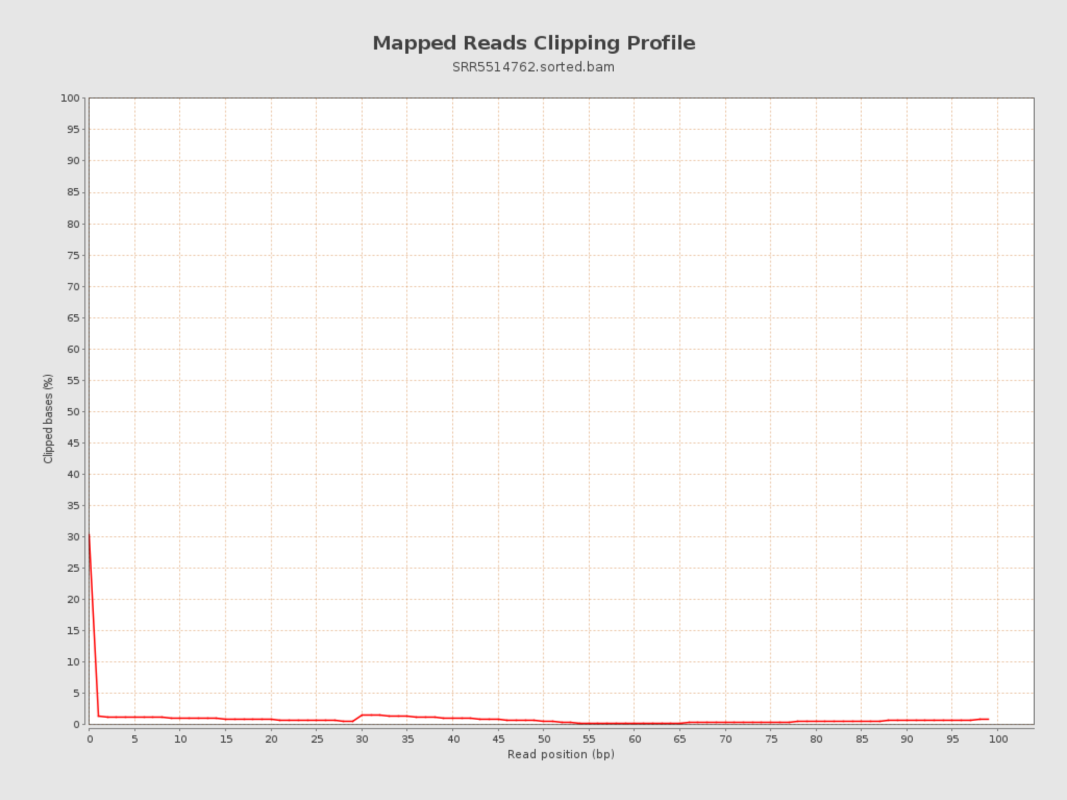
8. Results : Mapped Reads Nucleotide Content



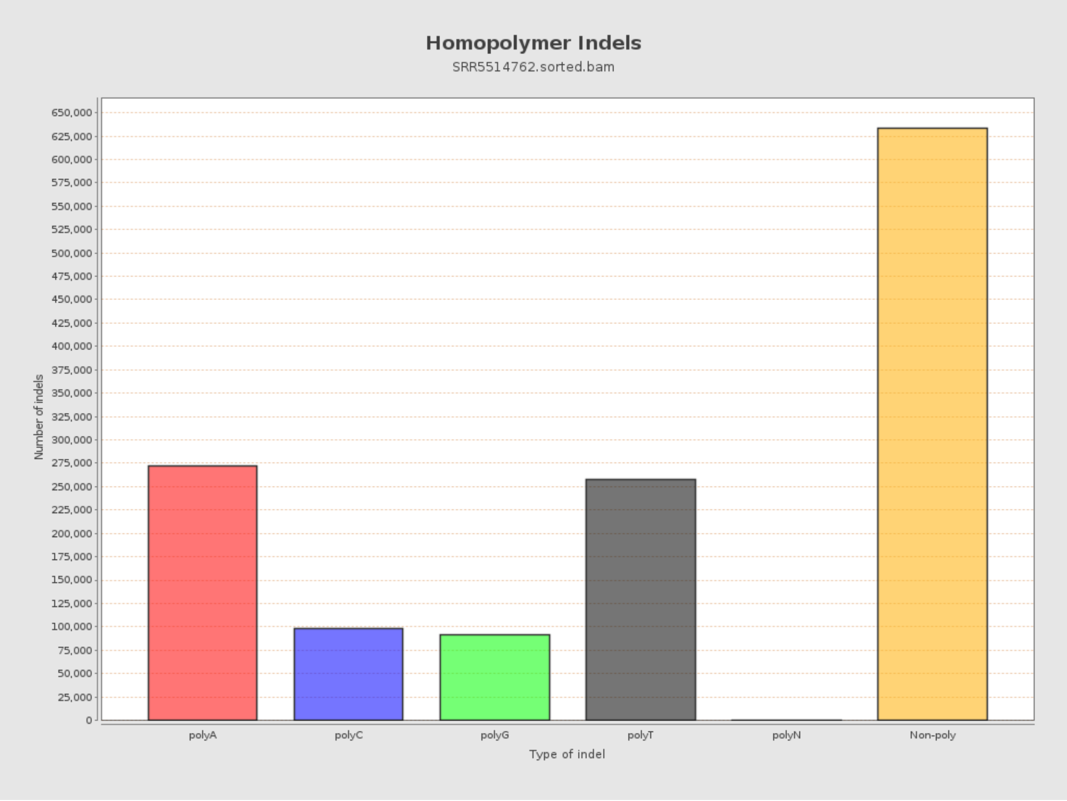
9. Results : Mapped Reads GC-content Distribution



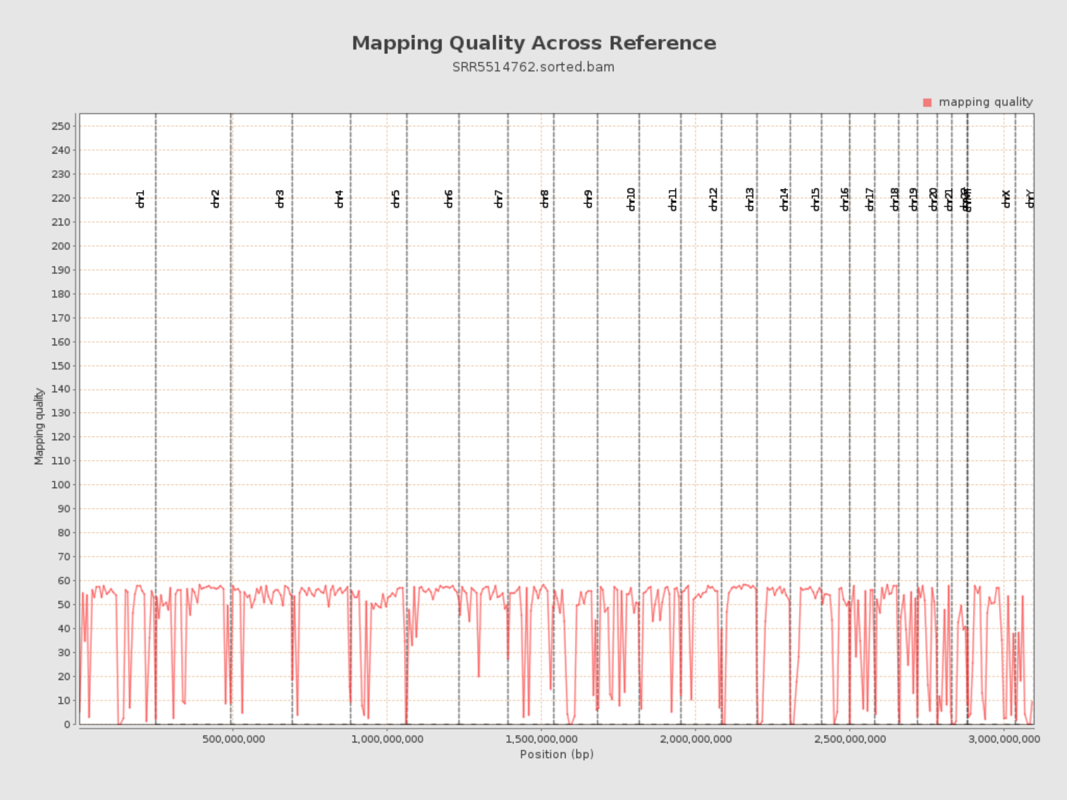
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram