Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 10:36:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514735.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_SRR5514735 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514735.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 10:36:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514735.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	131,636,473
Mapped reads	127,588,885 / 96.93%
Unmapped reads	4,047,588 / 3.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,513,769 / 2.67%
Read min/max/mean length	30 / 100 / 99.31
Duplicated reads (estimated)	97,324,113 / 73.93%
Duplication rate	43.45%
Clipped reads	21,738,177 / 16.51%

2.2. ACGT Content

Number/percentage of A's	3,084,858,832 / 25.4%
Number/percentage of C's	2,936,927,677 / 24.18%
Number/percentage of T's	3,114,615,099 / 25.64%
Number/percentage of G's	2,939,212,775 / 24.2%
Number/percentage of N's	70,581,865 / 0.58%
GC Percentage	48.38%

2.3. Coverage

Mean	3.9254

Standard Deviation	86.4427

2.4. Mapping Quality

Mean Mapping Quality	44.18

2.5. Mismatches and indels

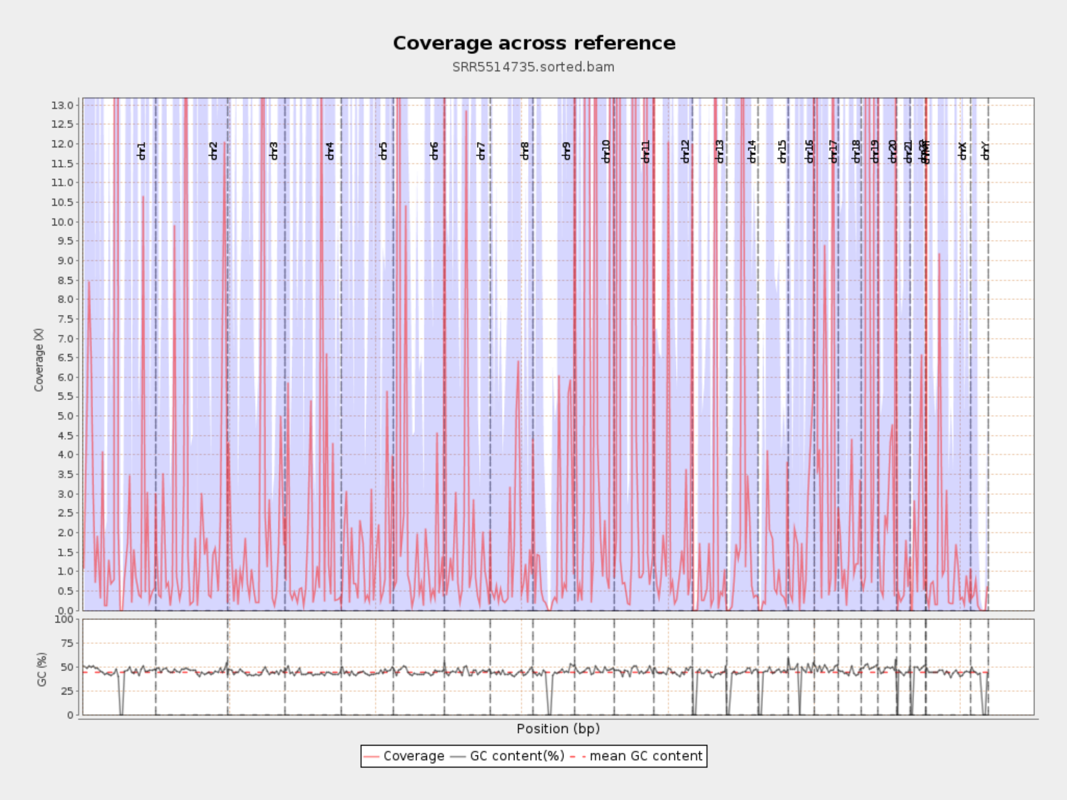
General error rate	0.99%
Mismatches	113,607,009
Insertions	4,144,711
Mapped reads with at least one insertion	3.15%
Deletions	3,066,745
Mapped reads with at least one deletion	2.34%
Homopolymer indels	46.84%

2.6. Chromosome stats

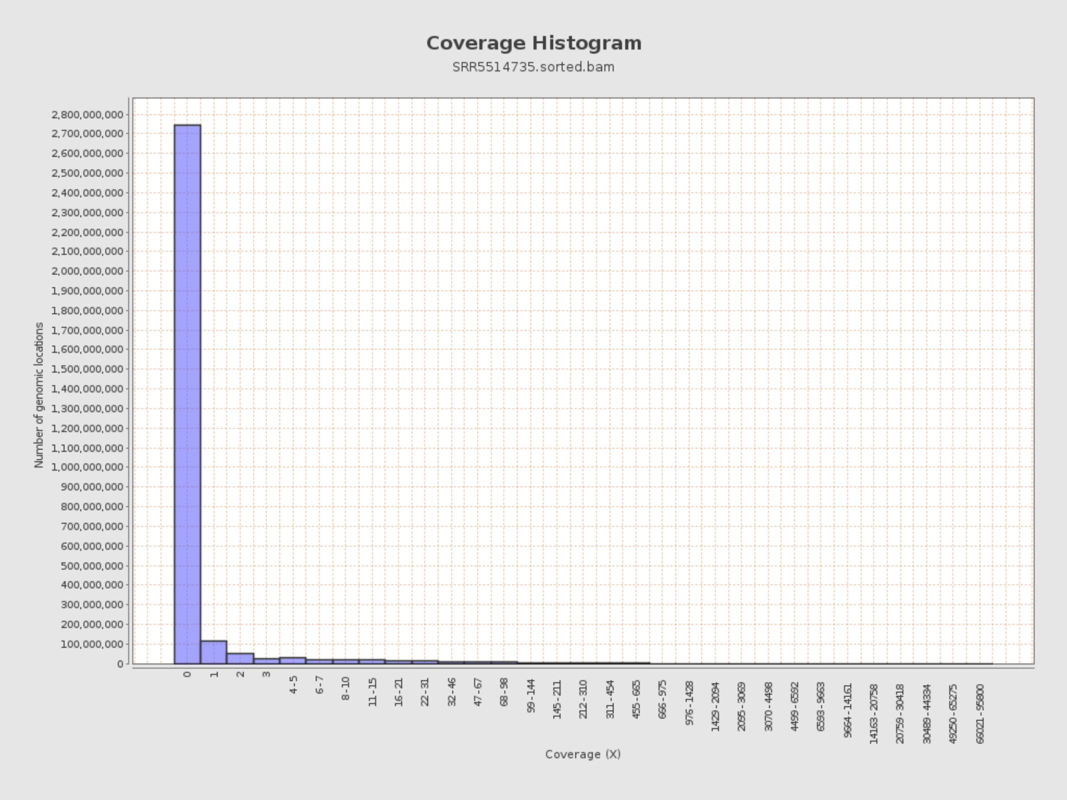
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1302426231	5.2254	129.4464
chr2	243199373	641663440	2.6384	52.2796
chr3	198022430	447677022	2.2607	24.4214
chr4	191154276	366301212	1.9163	27.5958
chr5	180915260	264085875	1.4597	33.8908
chr6	171115067	492912301	2.8806	84.5934
chr7	159138663	319974347	2.0107	21.4014

chr8	146364022	191421582	1.3078	17.1657
chr9	141213431	212071413	1.5018	18.2664
chr10	135534747	1123506156	8.2894	110.3112
chr11	135006516	1225201487	9.0751	119.6676
chr12	133851895	251412322	1.8783	22.2882
chr13	115169878	190081993	1.6504	40.8232
chr14	107349540	265264316	2.471	43.3832
chr15	102531392	99406188	0.9695	11.1115
chr16	90354753	177595636	1.9655	48.8018
chr17	81195210	887699675	10.9329	196.9022
chr18	78077248	123633399	1.5835	18.6911
chr19	59128983	3053674569	51.6443	362.6459
chr20	63025520	169953241	2.6966	110.6777
chr21	48129895	33994403	0.7063	62.6029
chr22	51304566	112276871	2.1884	25.2275
chrMT	16571	12455945	751.6713	365.3234
chrX	155270560	170610868	1.0988	15.6863
chrY	59373566	16468780	0.2774	13.0046

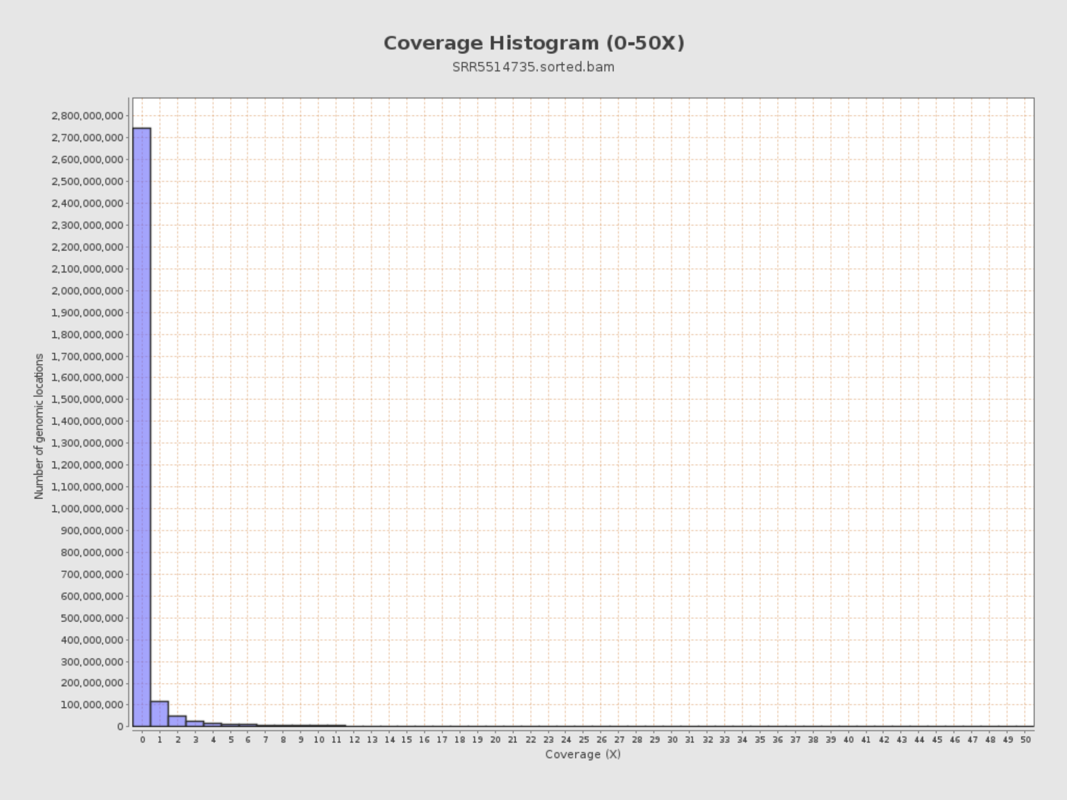
3. Results : Coverage across reference



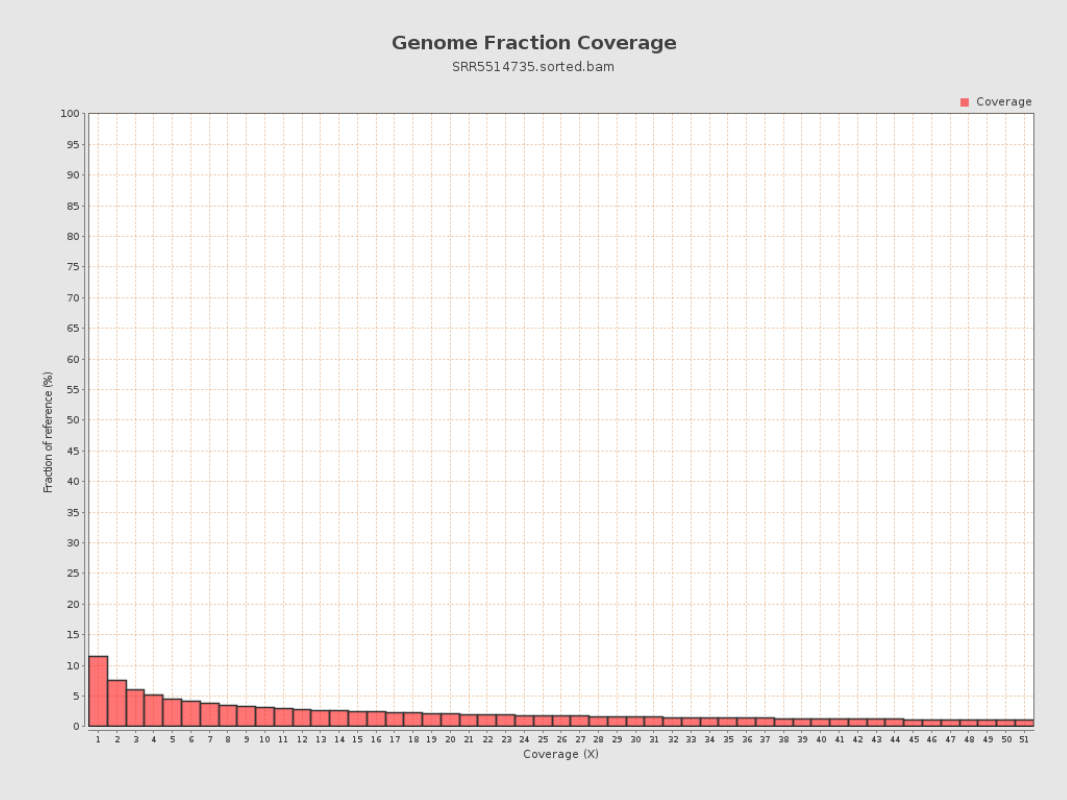
4. Results : Coverage Histogram



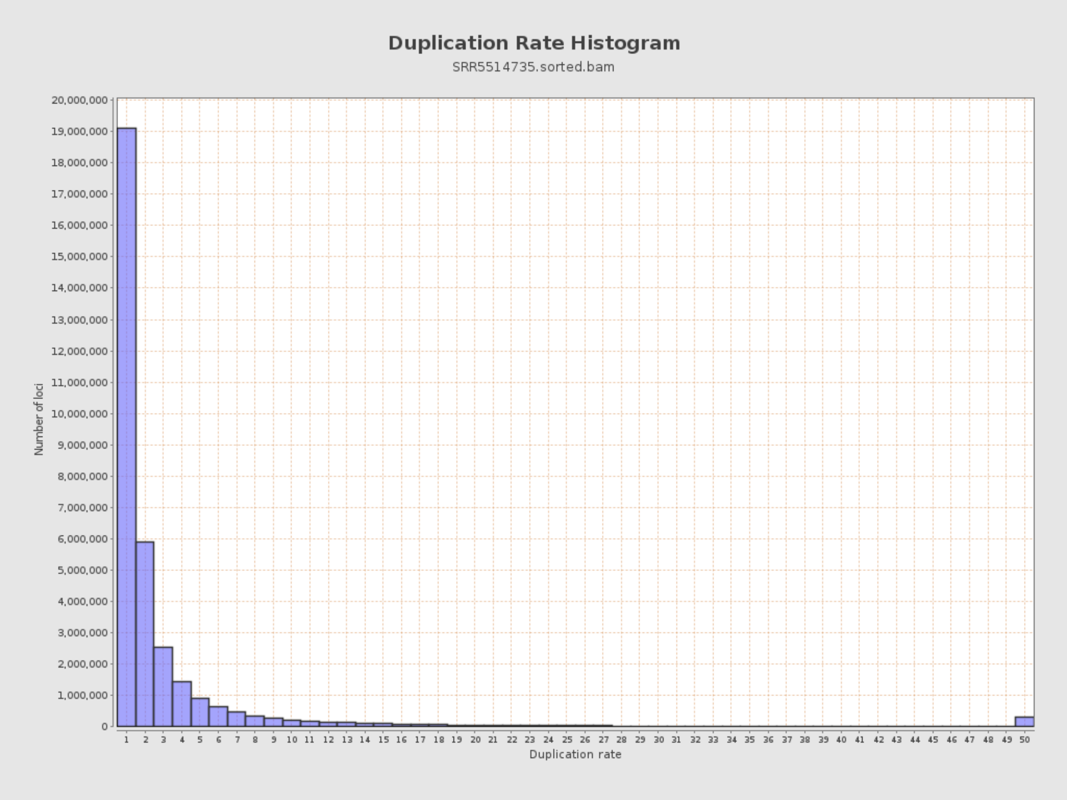
5. Results : Coverage Histogram (0-50X)



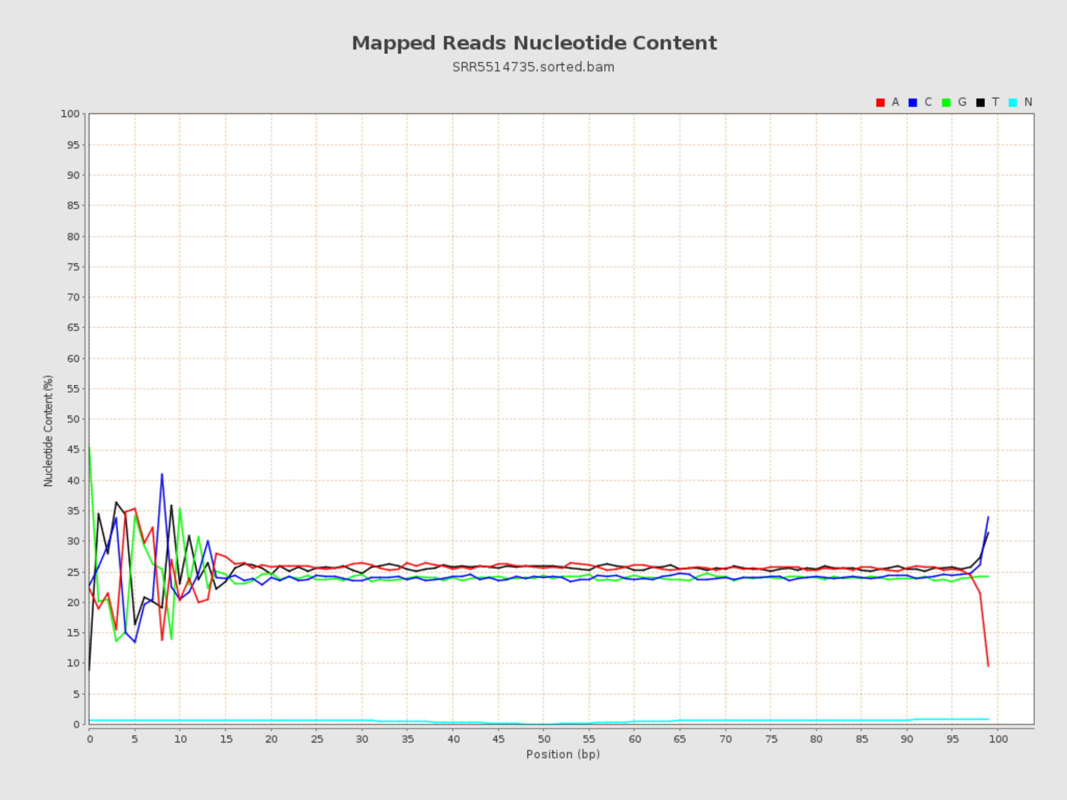
6. Results : Genome Fraction Coverage



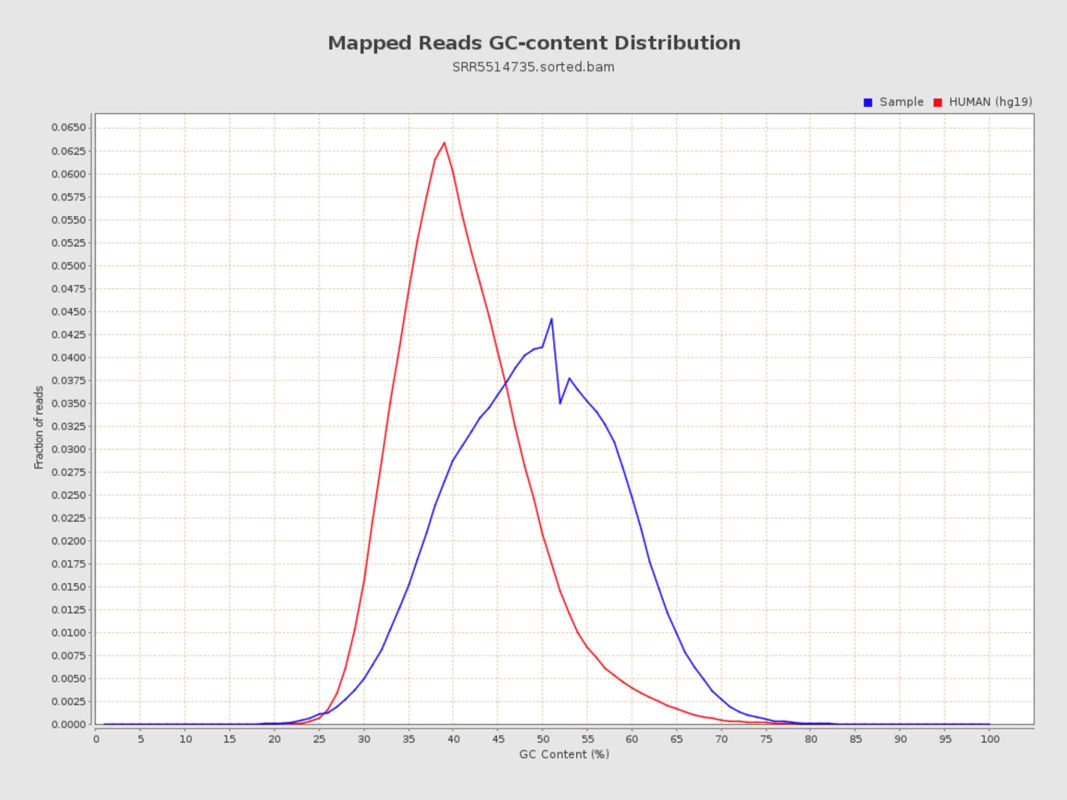
7. Results : Duplication Rate Histogram



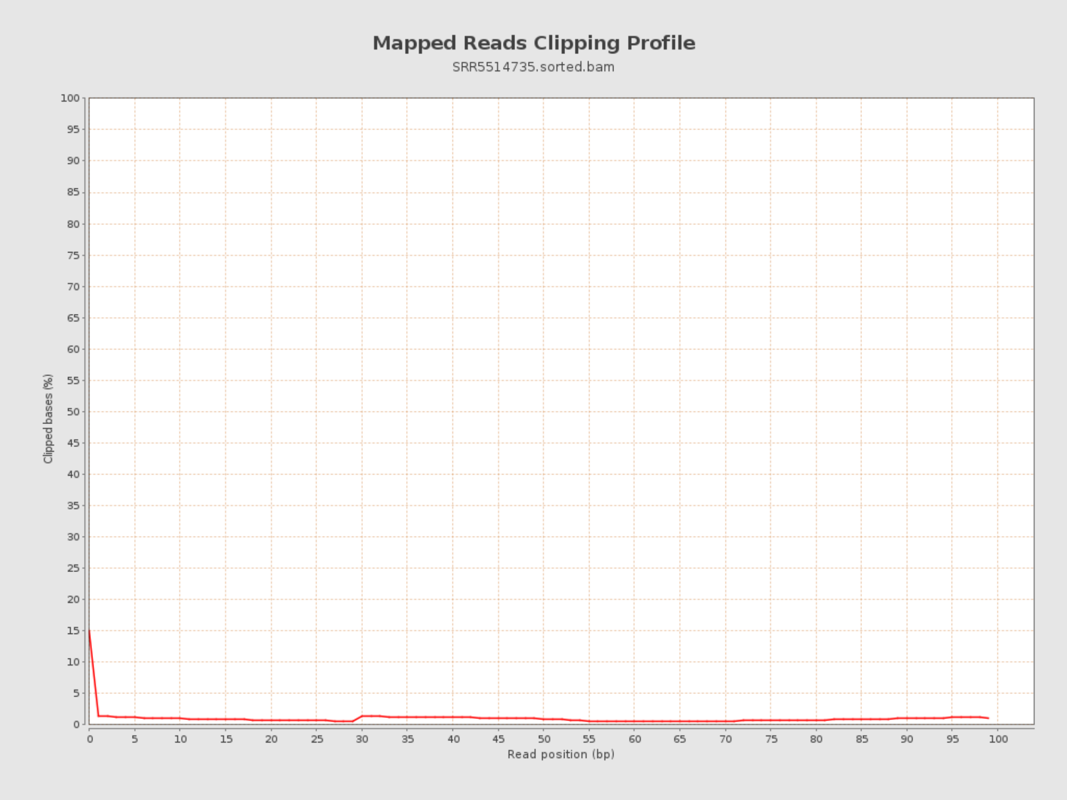
8. Results : Mapped Reads Nucleotide Content



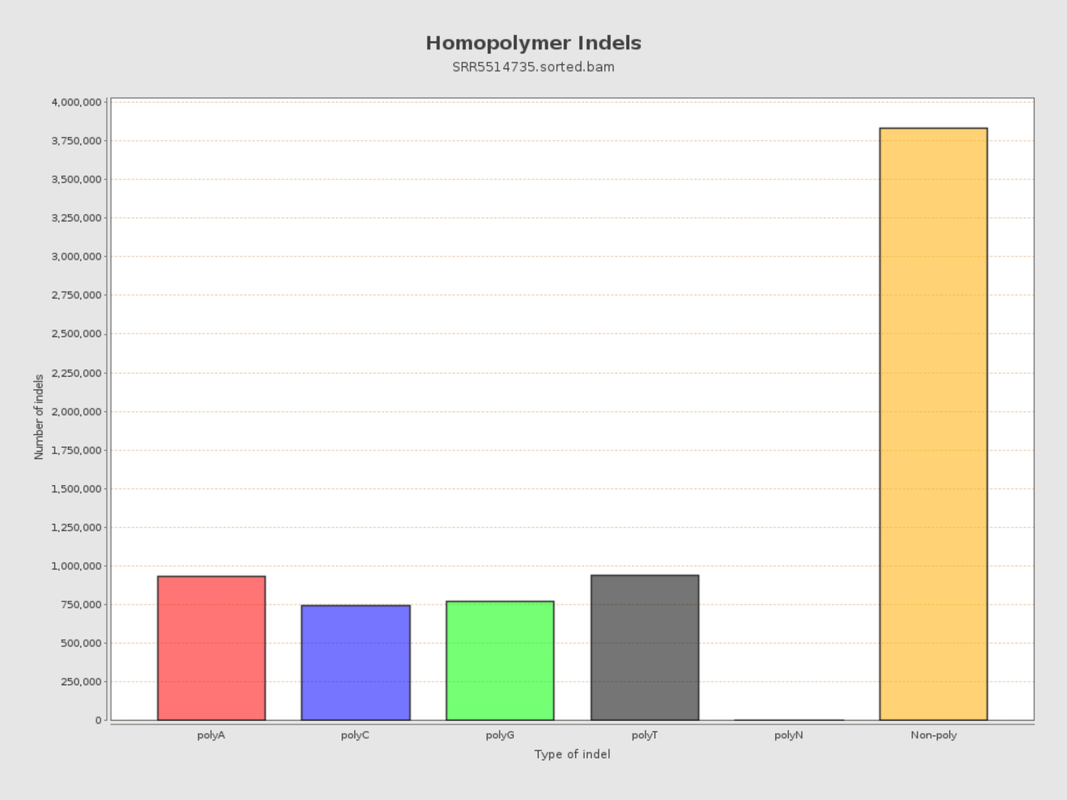
9. Results : Mapped Reads GC-content Distribution



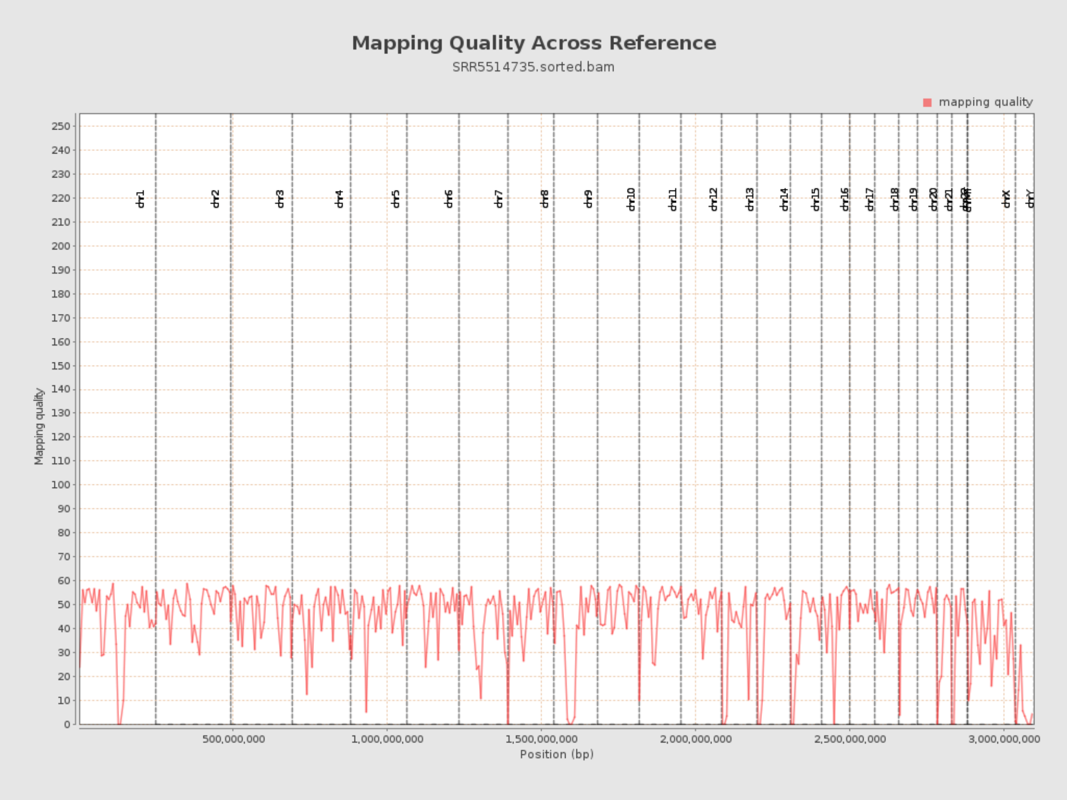
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram