Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 04:20:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514757.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_SRR5514757 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514757.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 04:20:29 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514757.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	55,550,737
Mapped reads	52,026,322 / 93.66%
Unmapped reads	3,524,415 / 6.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,084,784 / 14.55%
Read min/max/mean length	30 / 100 / 105.02
Duplicated reads (estimated)	40,938,534 / 73.7%
Duplication rate	44.45%
Clipped reads	26,974,985 / 48.56%

2.2. ACGT Content

Number/percentage of A's	1,531,066,006 / 31.11%
Number/percentage of C's	908,489,377 / 18.46%
Number/percentage of T's	1,526,708,693 / 31.03%
Number/percentage of G's	954,129,163 / 19.39%
Number/percentage of N's	336,168 / 0.01%
GC Percentage	37.85%

2.3. Coverage

Mean	1.5908

Standard Deviation	86.4841

2.4. Mapping Quality

Mean Mapping Quality	43.18

2.5. Mismatches and indels

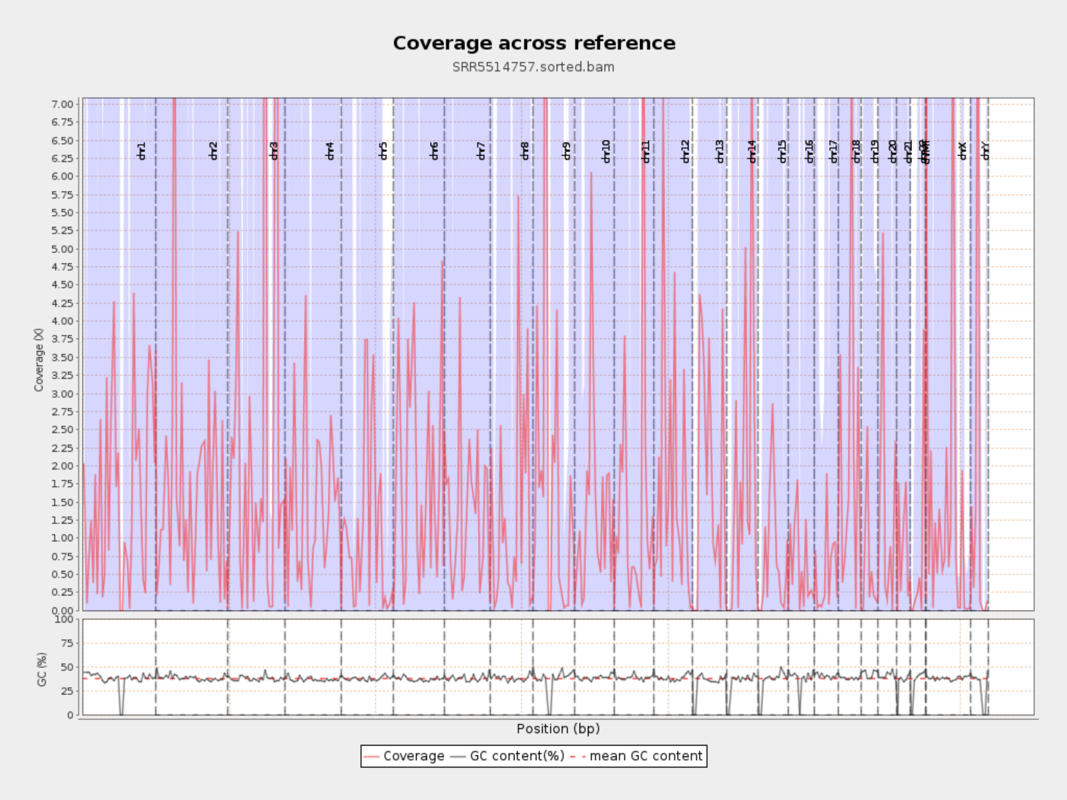
General error rate	0.64%
Mismatches	25,939,083
Insertions	3,309,633
Mapped reads with at least one insertion	6.09%
Deletions	1,339,416
Mapped reads with at least one deletion	2.42%
Homopolymer indels	49.85%

2.6. Chromosome stats

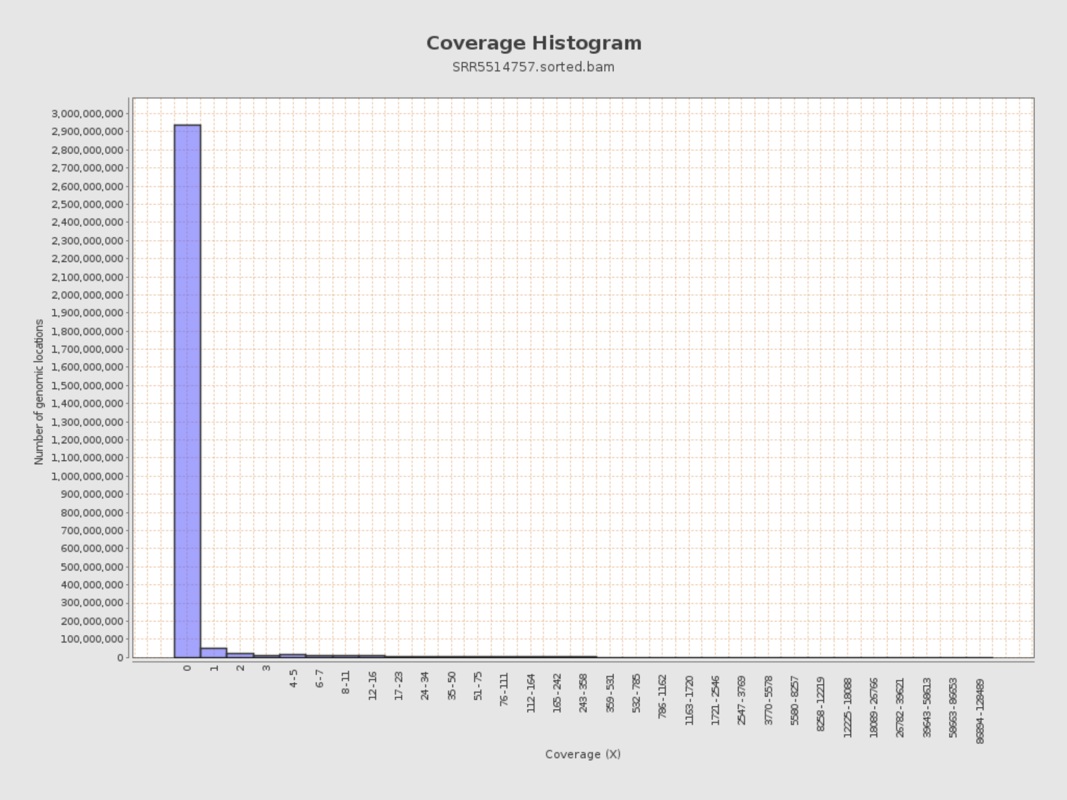
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	396233339	1.5897	29.7352
chr2	243199373	418936108	1.7226	67.0305
chr3	198022430	526834915	2.6605	224.9197
chr4	191154276	292666806	1.5311	38.3156
chr5	180915260	202873332	1.1214	19.2177
chr6	171115067	331320422	1.9362	93.3613
chr7	159138663	225333736	1.416	56.1545

chr8	146364022	192898151	1.3179	21.795
chr9	141213431	274257499	1.9421	196.3641
chr10	135534747	200241724	1.4774	24.3076
chr11	135006516	216028199	1.6001	26.9261
chr12	133851895	228109923	1.7042	23.518
chr13	115169878	217465019	1.8882	49.1039
chr14	107349540	206567411	1.9243	49.2749
chr15	102531392	76365646	0.7448	16.7456
chr16	90354753	54922613	0.6079	14.425
chr17	81195210	45044932	0.5548	14.3121
chr18	78077248	167888866	2.1503	25.0315
chr19	59128983	38011810	0.6429	12.2294
chr20	63025520	97374916	1.545	36.4759
chr21	48129895	43297980	0.8996	15.4572
chr22	51304566	36821195	0.7177	82.5368
chrMT	16571	128861136	7,776.3041	6,557.3031
chrX	155270560	203290331	1.3093	23.9707
chrY	59373566	102912427	1.7333	116.599

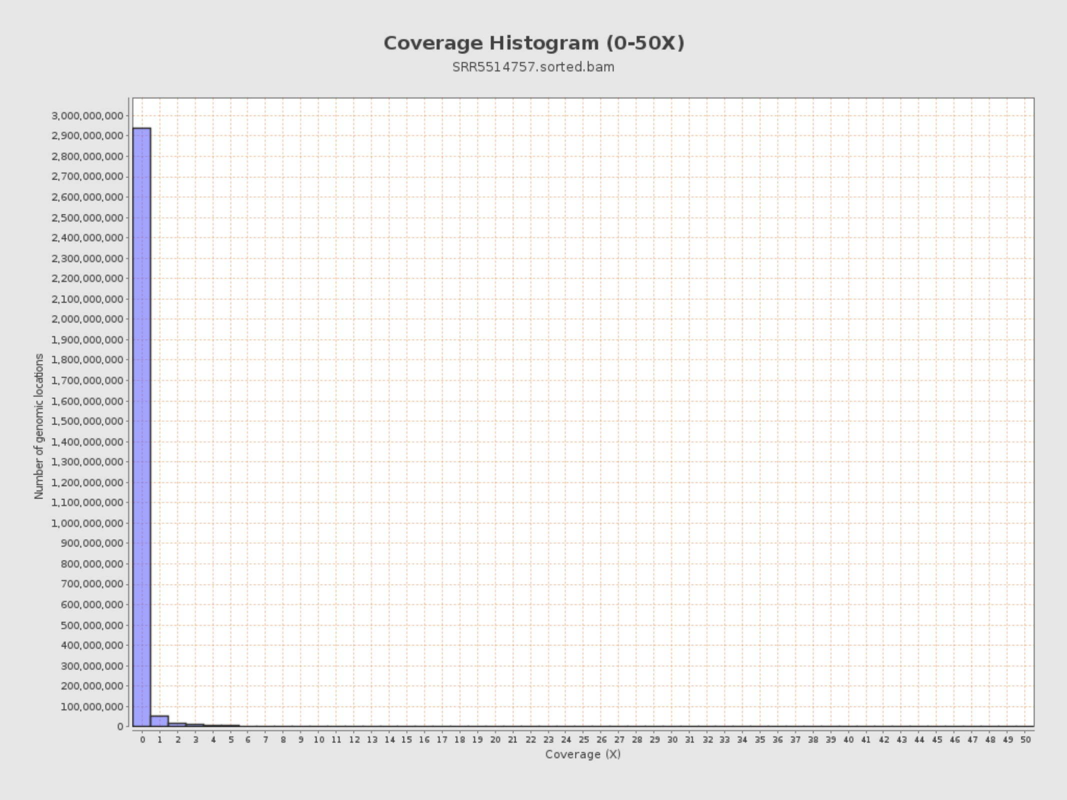
3. Results : Coverage across reference



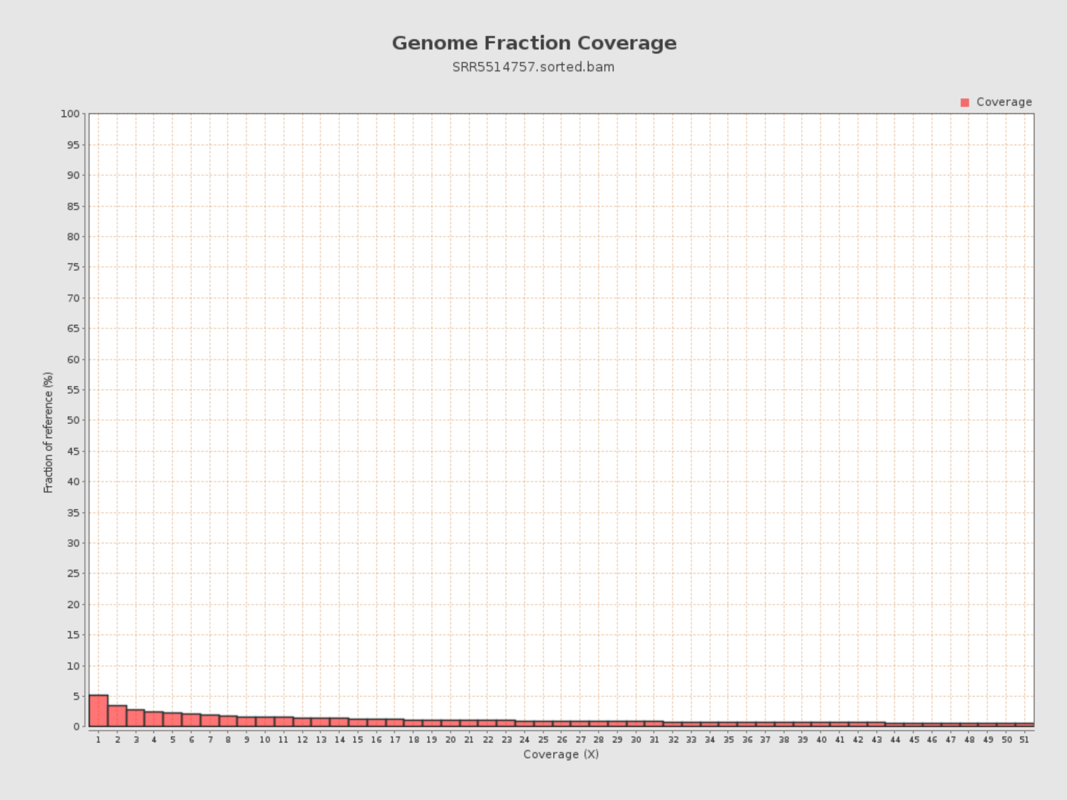
4. Results : Coverage Histogram



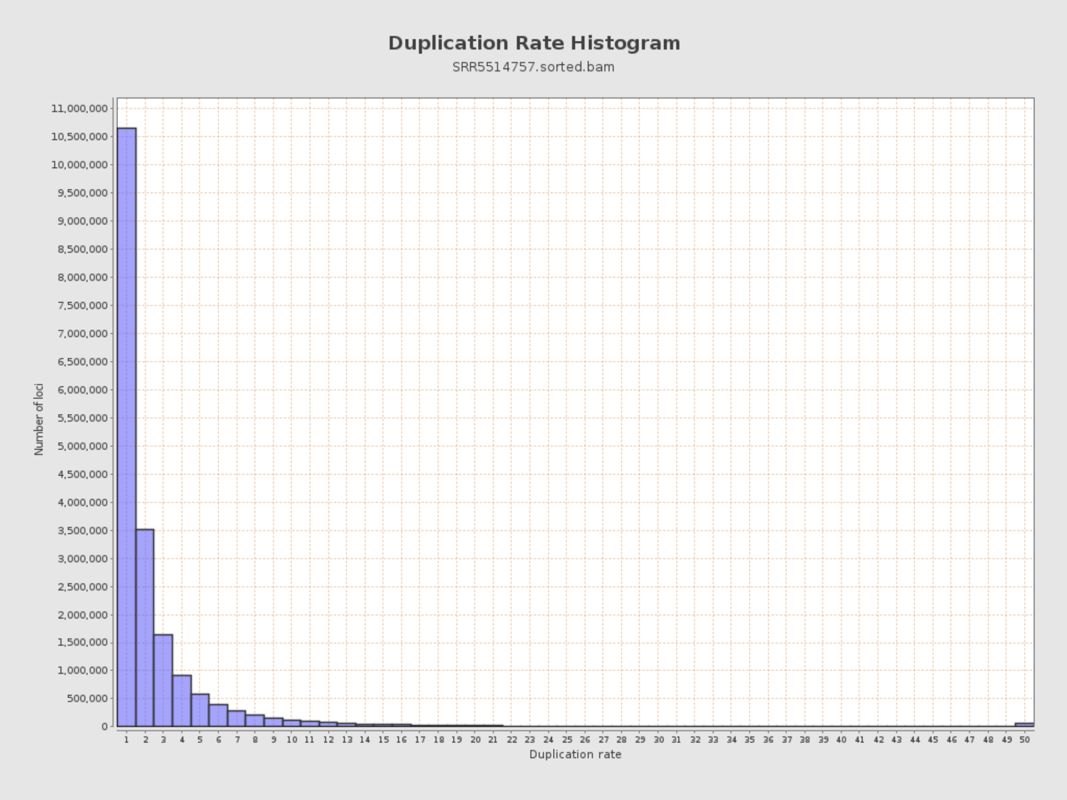
5. Results : Coverage Histogram (0-50X)



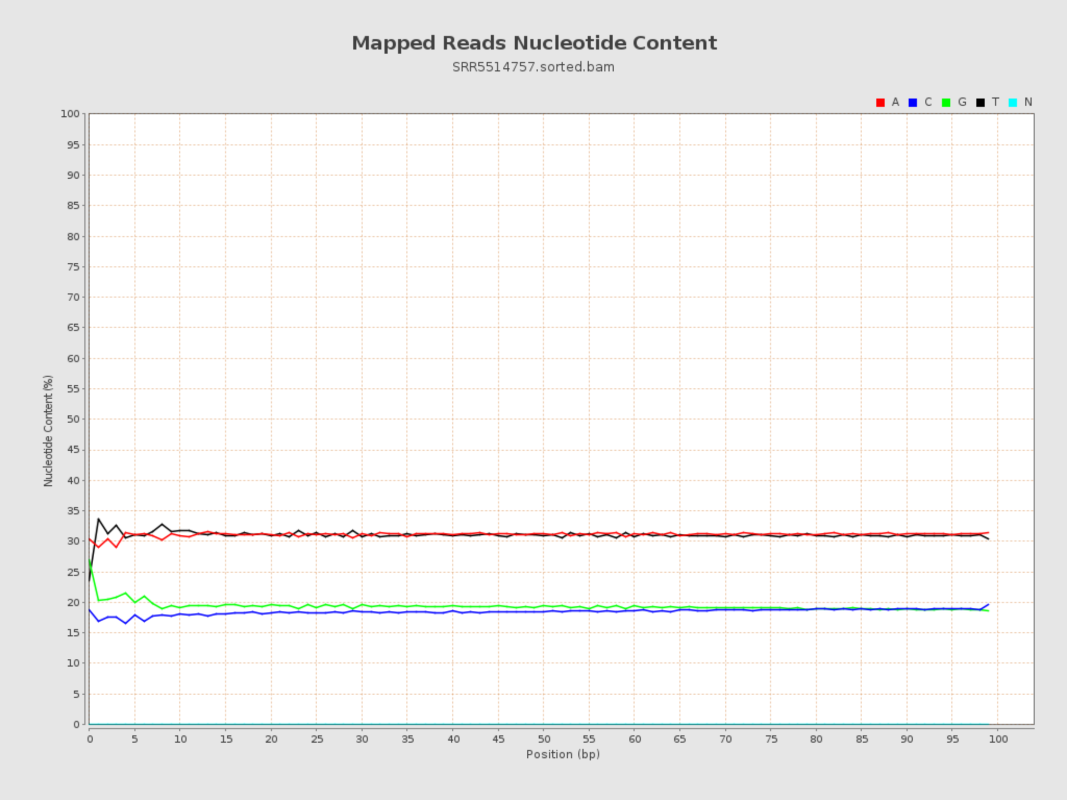
6. Results : Genome Fraction Coverage



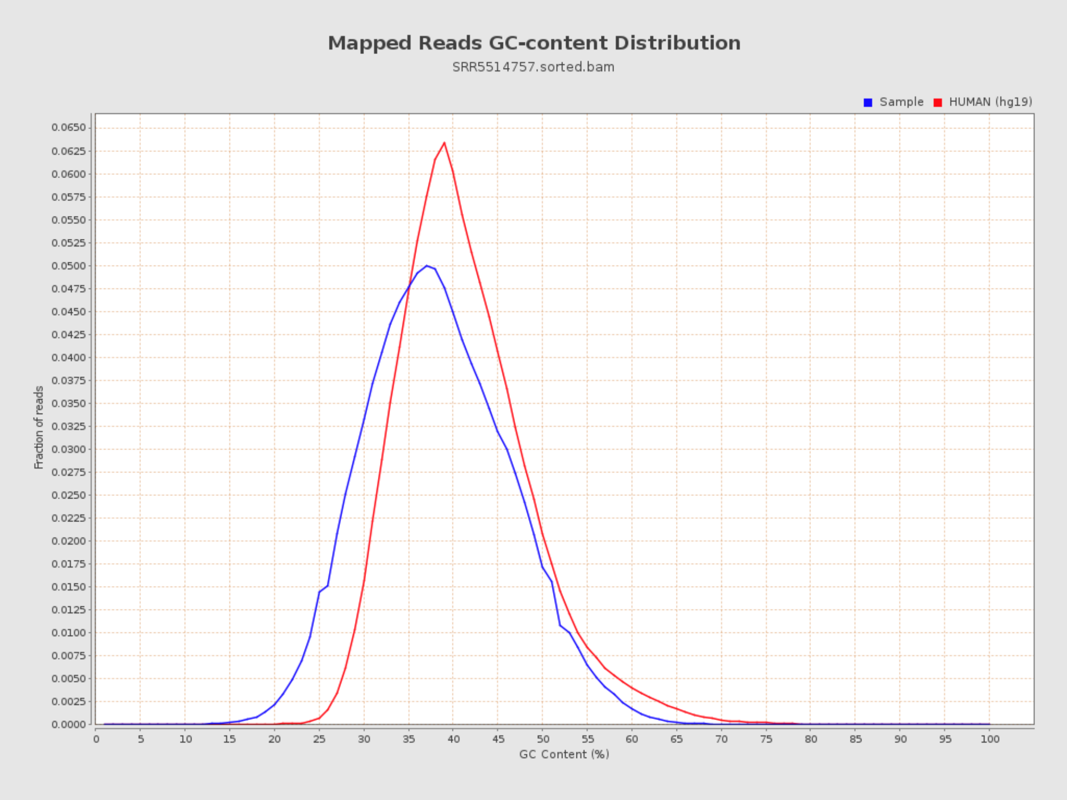
7. Results : Duplication Rate Histogram



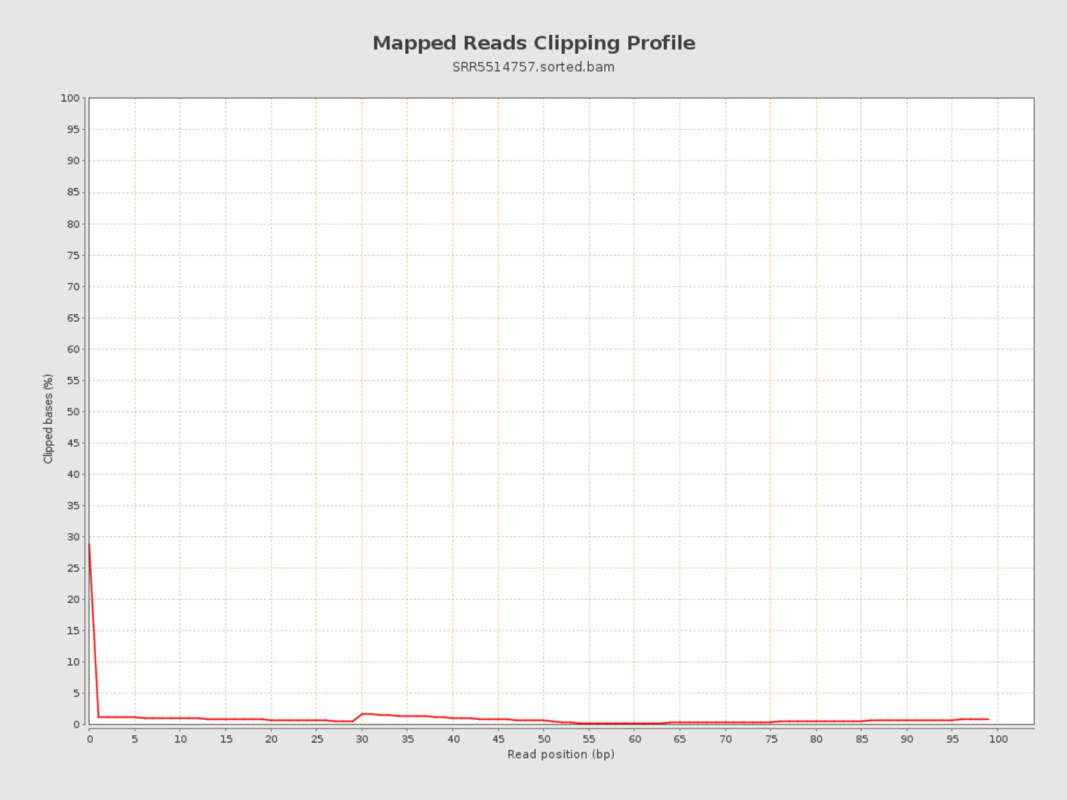
8. Results : Mapped Reads Nucleotide Content



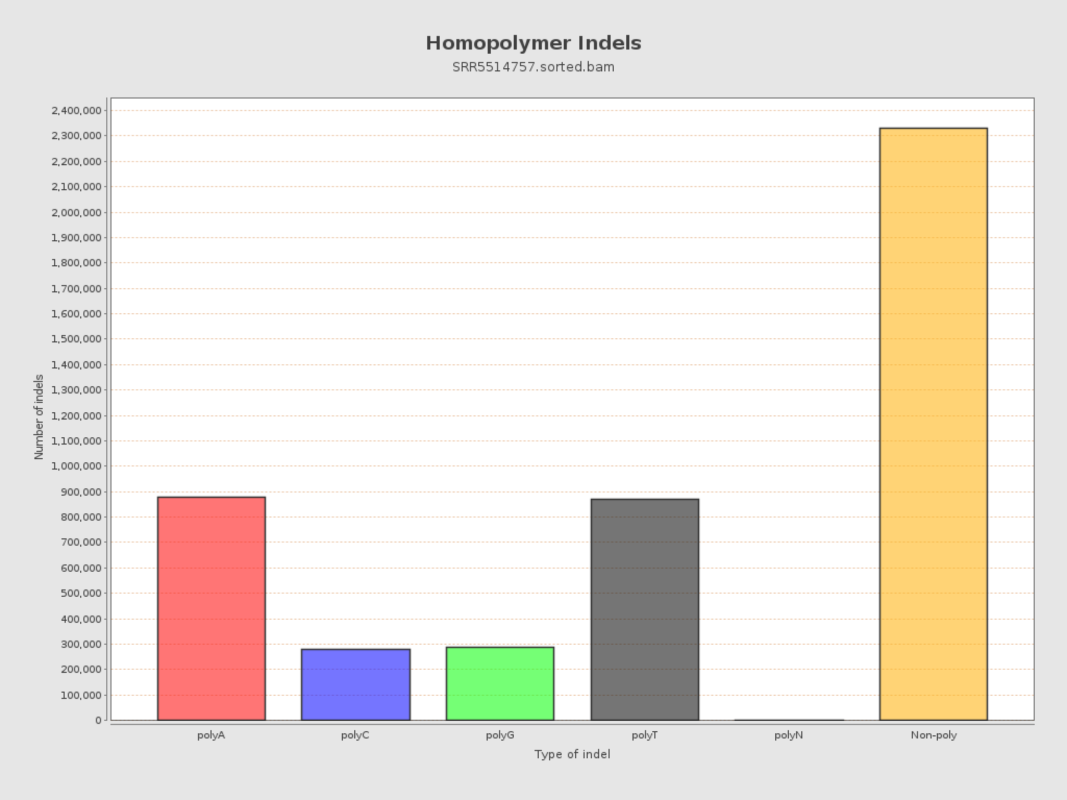
9. Results : Mapped Reads GC-content Distribution



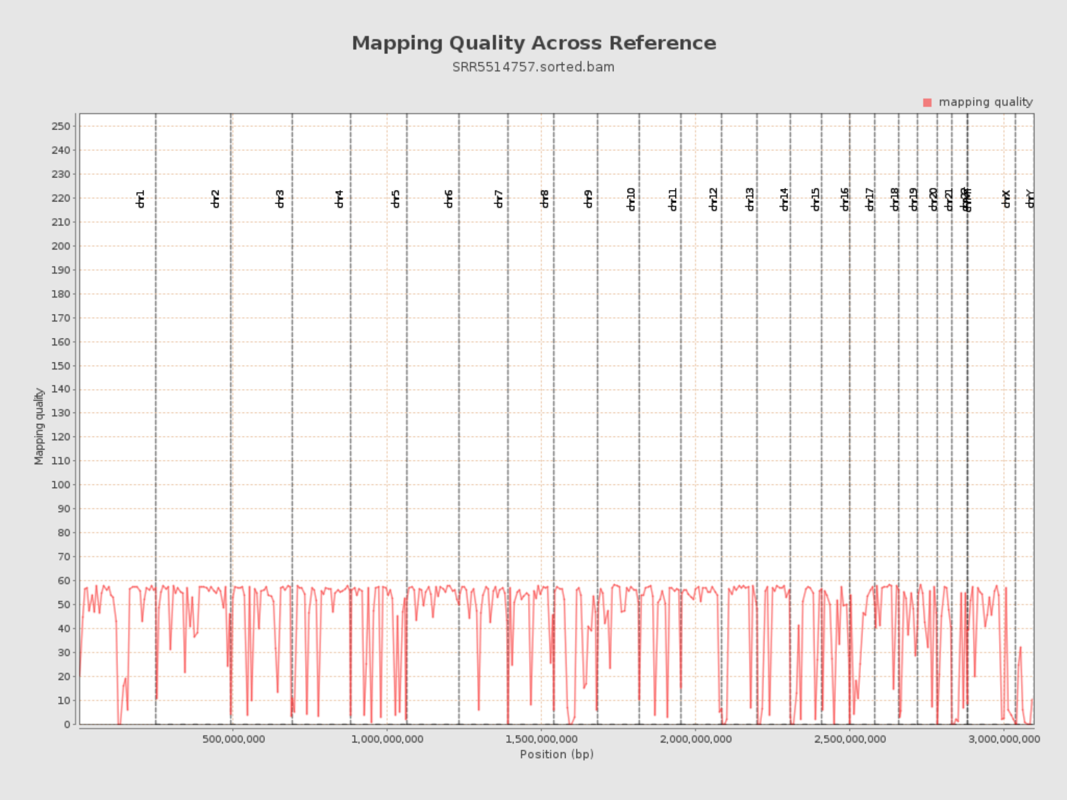
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram