Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 06:34:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514767.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_SRR5514767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 06:34:16 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,154,609
Mapped reads	61,660,303 / 99.2%
Unmapped reads	494,306 / 0.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,672,607 / 7.52%
Read min/max/mean length	30 / 100 / 100.77
Duplicated reads (estimated)	56,726,888 / 91.27%
Duplication rate	49.32%
Clipped reads	17,839,025 / 28.7%

2.2. ACGT Content

Number/percentage of A's	1,716,907,032 / 29.28%
Number/percentage of C's	1,208,117,215 / 20.6%
Number/percentage of T's	1,699,177,594 / 28.98%
Number/percentage of G's	1,232,103,369 / 21.01%
Number/percentage of N's	7,565,142 / 0.13%
GC Percentage	41.61%

2.3. Coverage

Mean	1.8957

Standard Deviation	128.9348

2.4. Mapping Quality

Mean Mapping Quality	49.51

2.5. Mismatches and indels

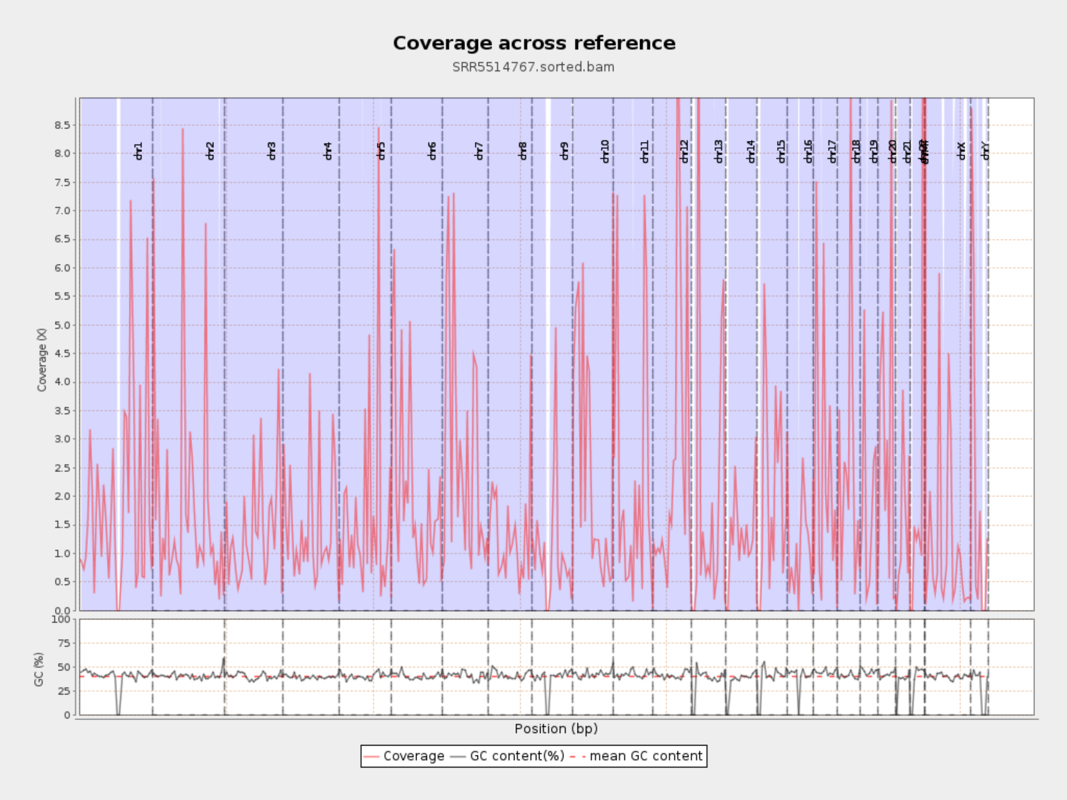
General error rate	0.74%
Mismatches	38,924,770
Insertions	2,825,308
Mapped reads with at least one insertion	4.42%
Deletions	2,028,566
Mapped reads with at least one deletion	3.1%
Homopolymer indels	42.65%

2.6. Chromosome stats

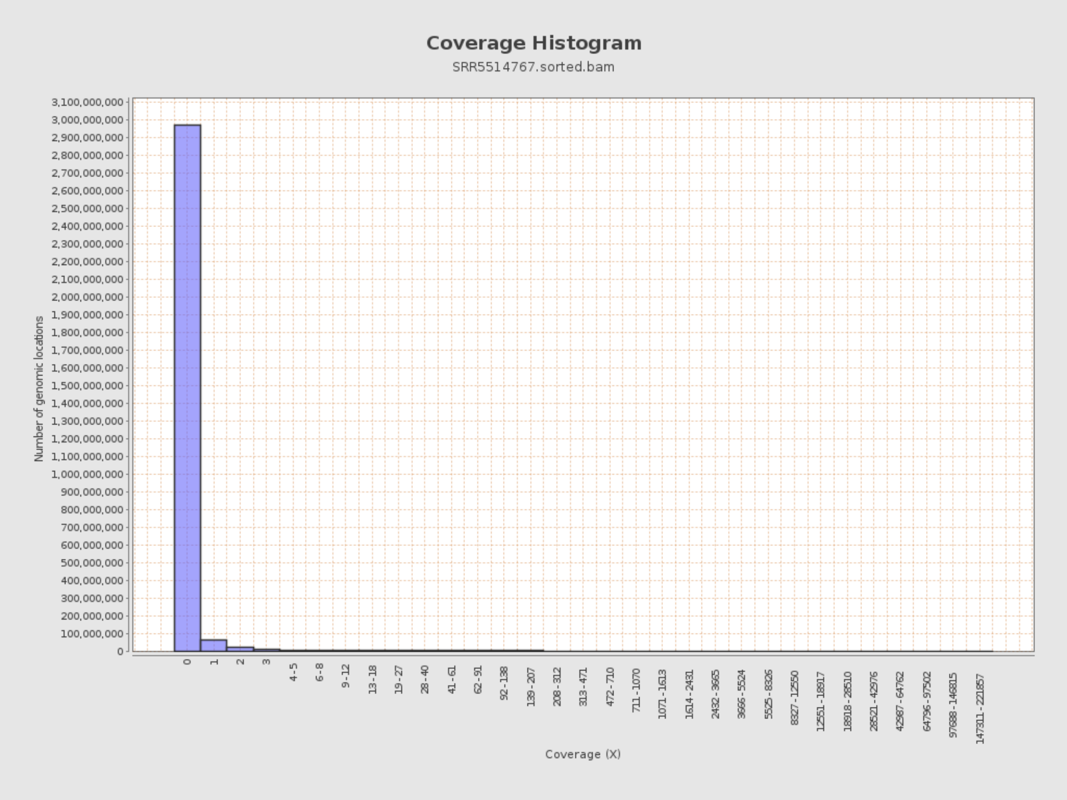
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	471810888	1.8929	89.611
chr2	243199373	446237719	1.8349	91.8475
chr3	198022430	284482495	1.4366	62.5642
chr4	191154276	285296515	1.4925	61.4416
chr5	180915260	304179515	1.6813	103.2303
chr6	171115067	350191558	2.0465	95.3472
chr7	159138663	425339253	2.6728	182.4951

chr8	146364022	197104435	1.3467	72.3092
chr9	141213431	144920454	1.0263	42.0095
chr10	135534747	319581717	2.3579	127.6362
chr11	135006516	315391682	2.3361	144.0104
chr12	133851895	346864705	2.5914	237.9583
chr13	115169878	256008732	2.2229	124.0421
chr14	107349540	140358653	1.3075	81.2512
chr15	102531392	207056233	2.0194	89.7307
chr16	90354753	99726084	1.1037	58.0583
chr17	81195210	194016524	2.3895	54.0621
chr18	78077248	210044254	2.6902	75.1898
chr19	59128983	114495529	1.9364	69.8509
chr20	63025520	191934540	3.0453	262.2728
chr21	48129895	75355095	1.5657	63.6551
chr22	51304566	184430546	3.5948	486.6481
chrMT	16571	1787831	107.8891	186.7747
chrX	155270560	179702031	1.1573	98.9224
chrY	59373566	122217700	2.0585	112.2726

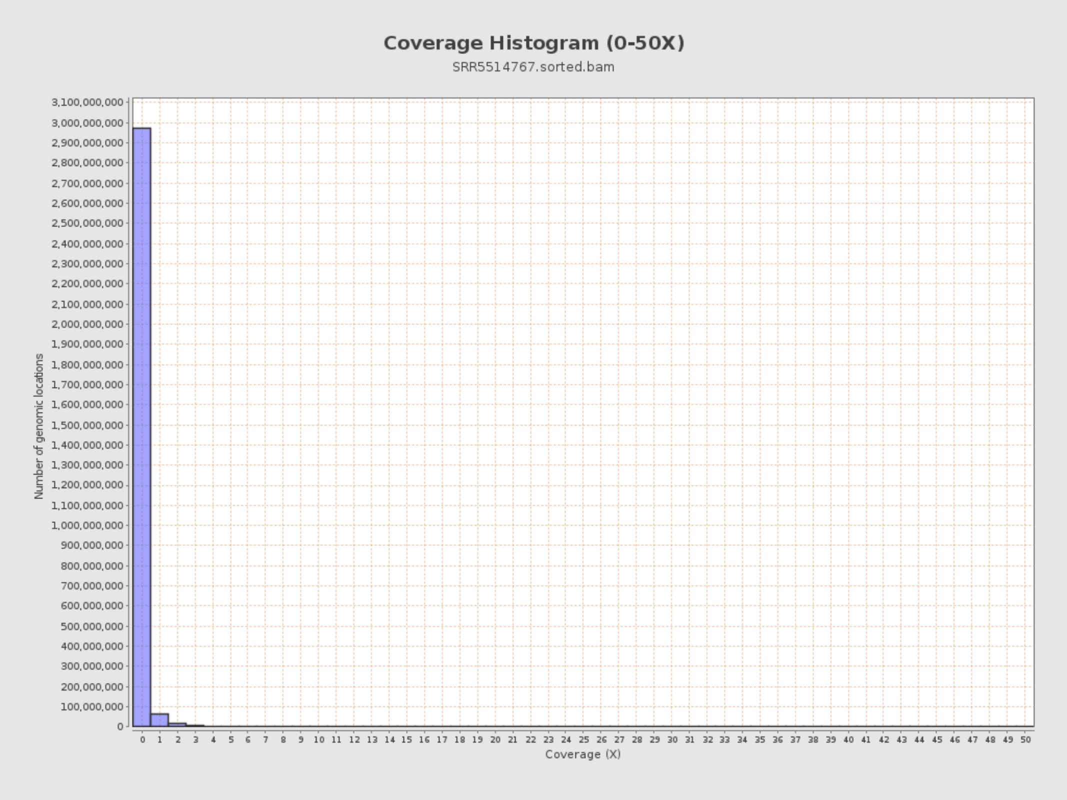
3. Results : Coverage across reference



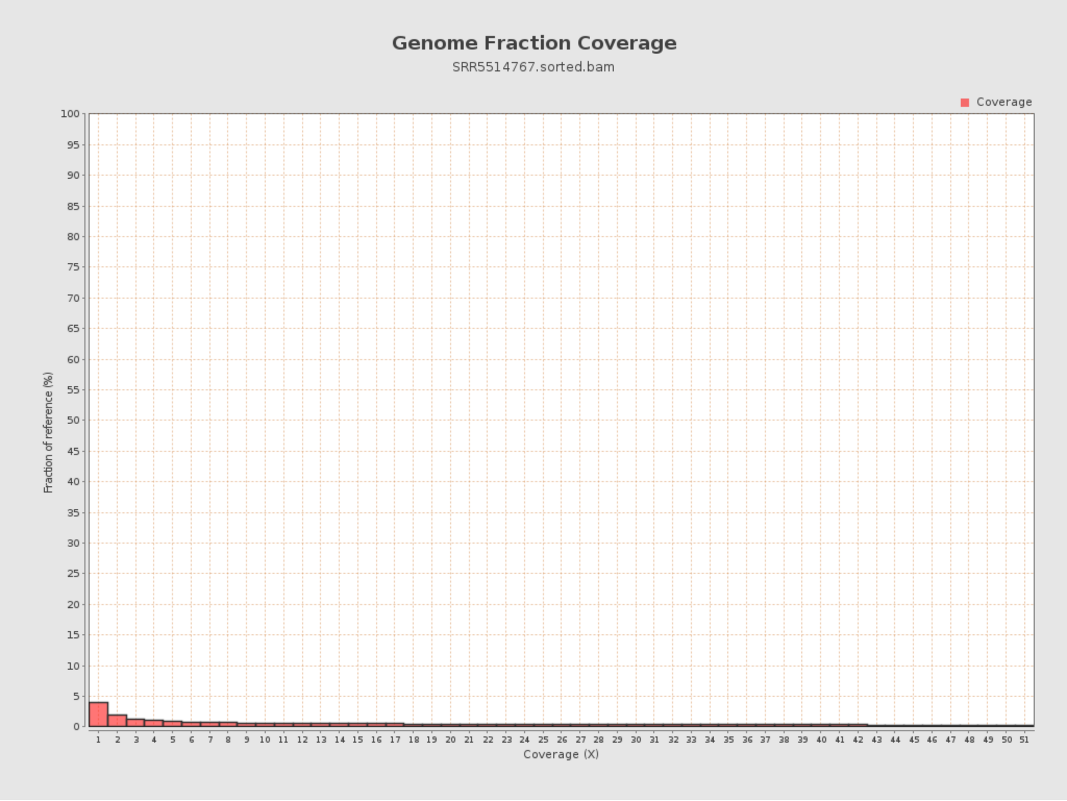
4. Results : Coverage Histogram



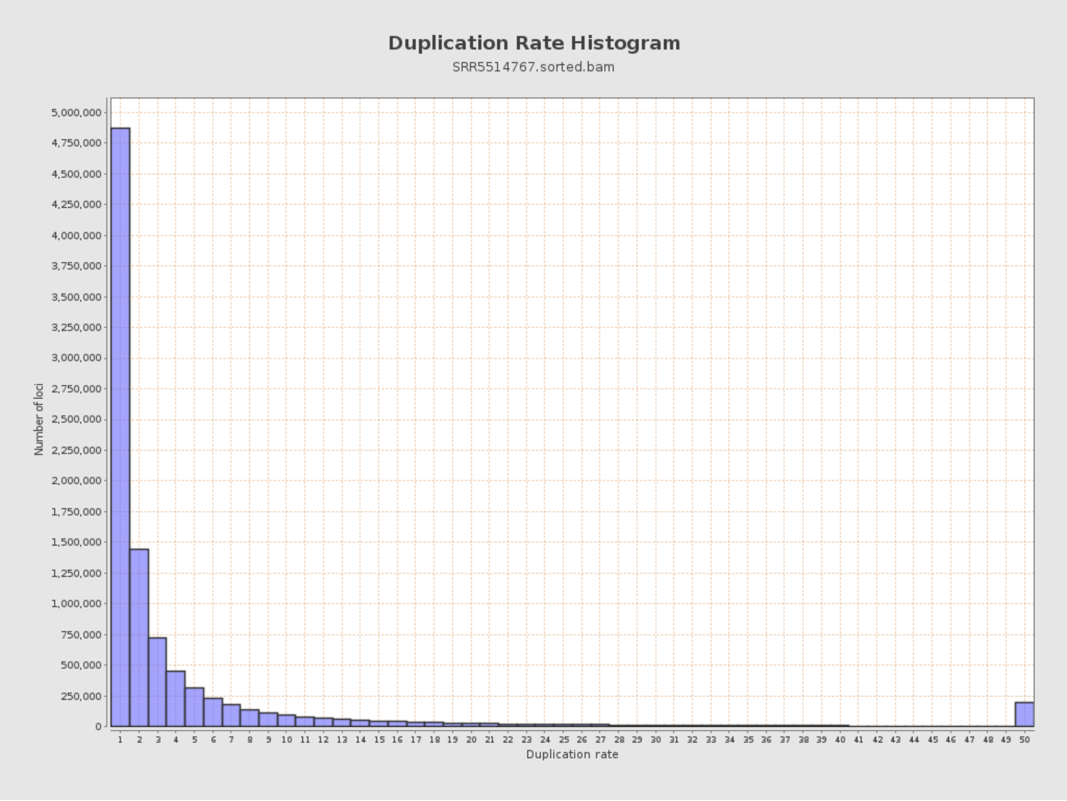
5. Results : Coverage Histogram (0-50X)



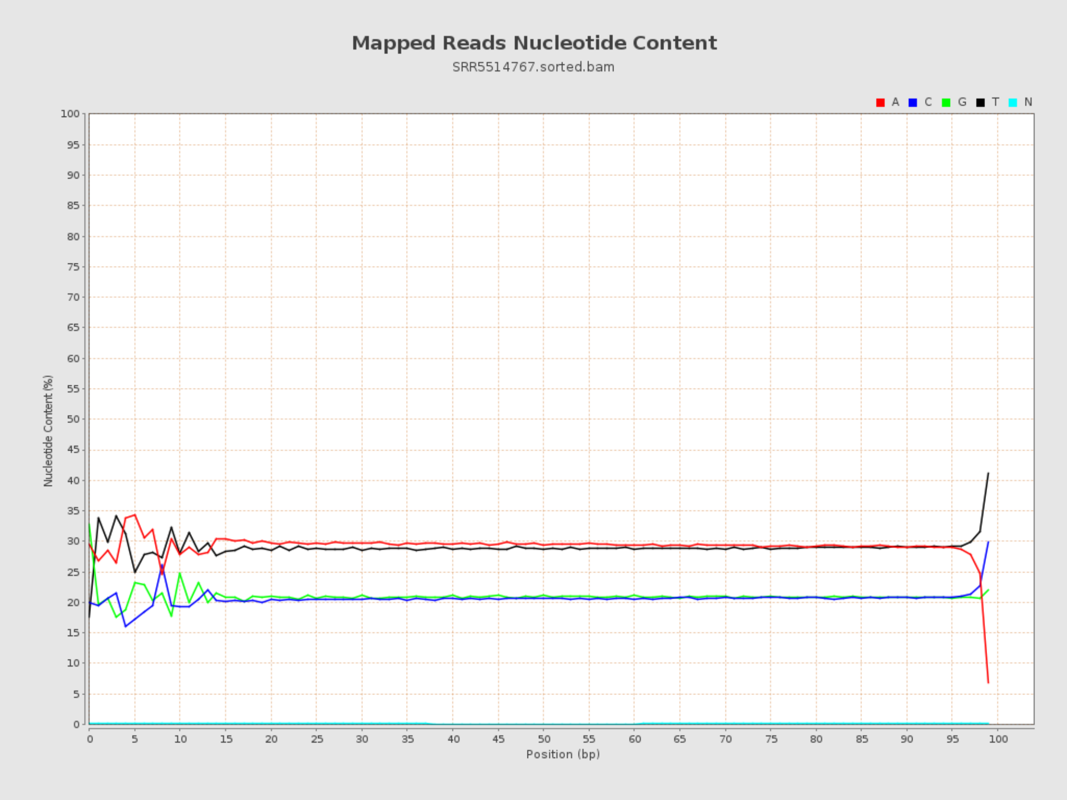
6. Results : Genome Fraction Coverage



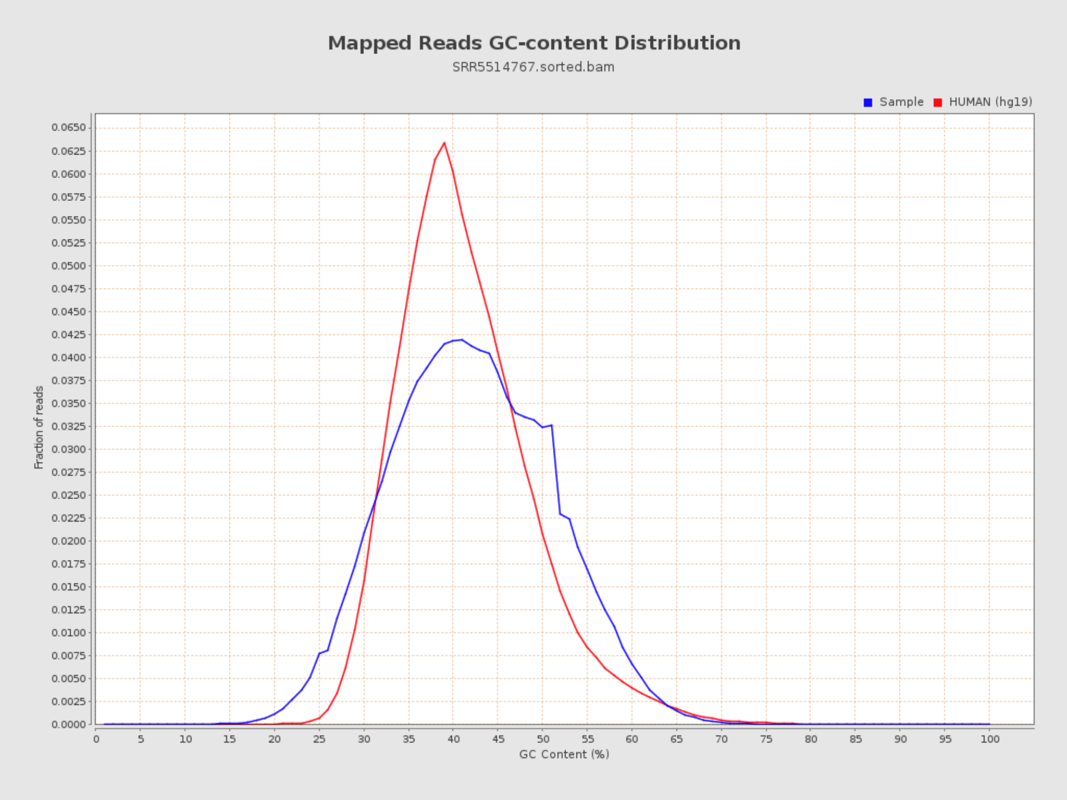
7. Results : Duplication Rate Histogram



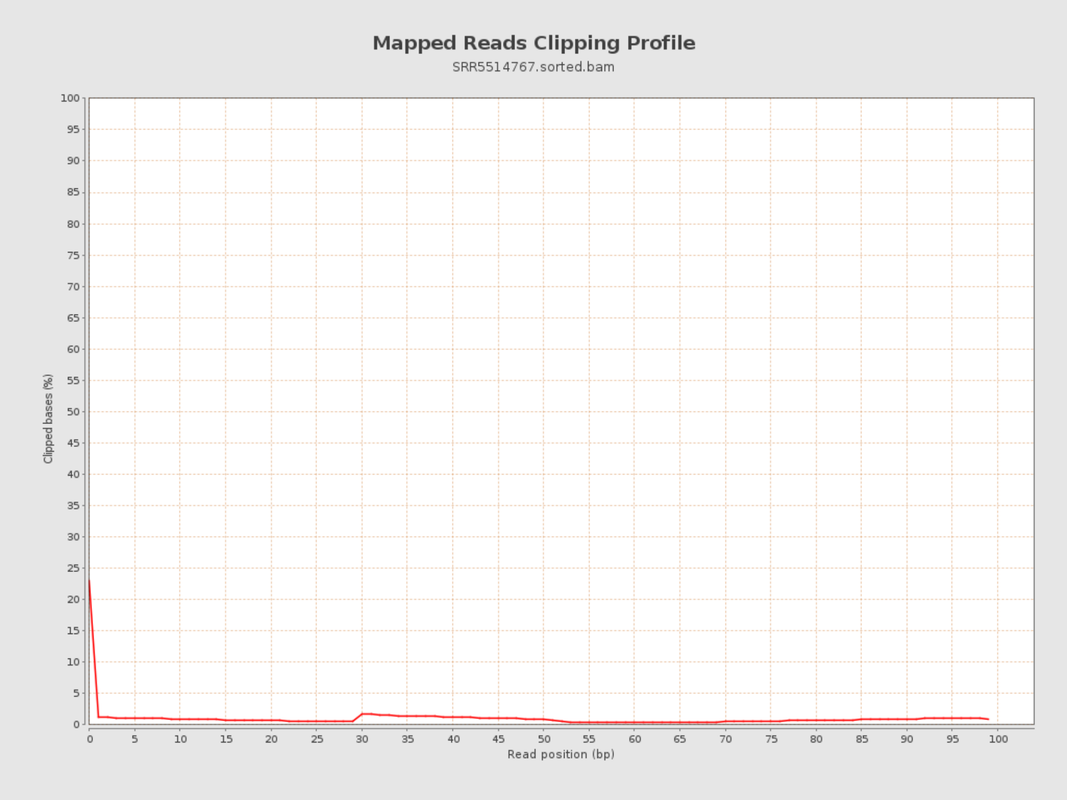
8. Results : Mapped Reads Nucleotide Content



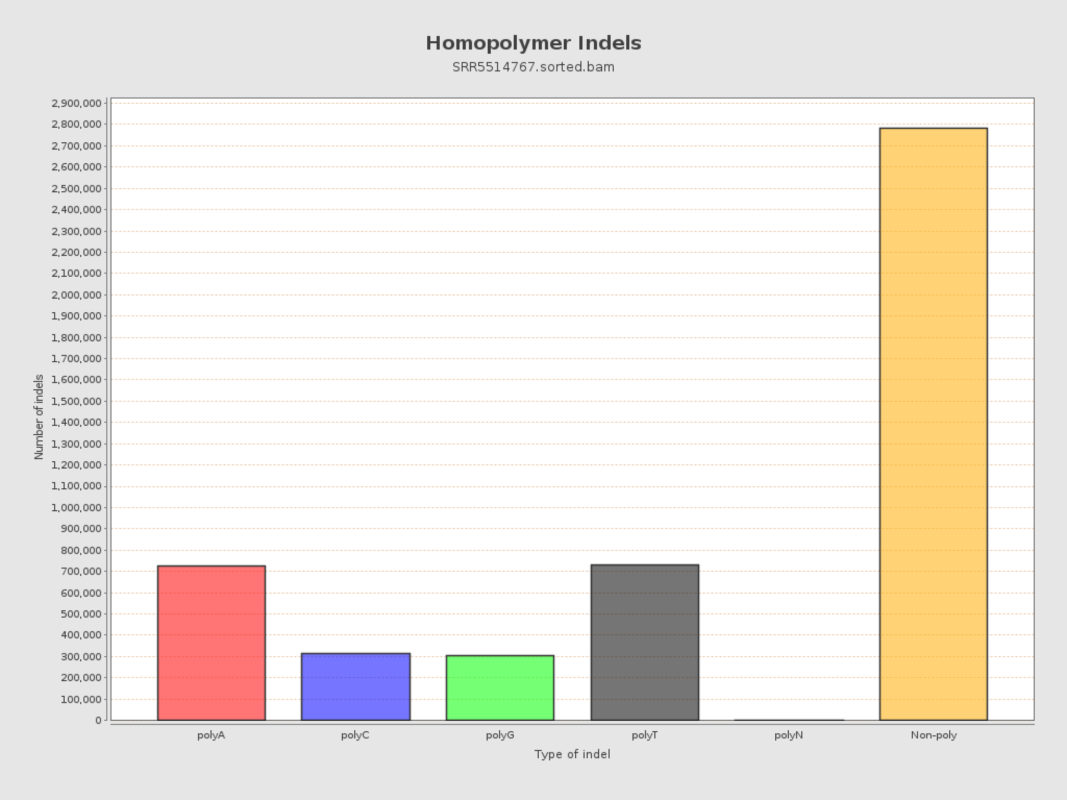
9. Results : Mapped Reads GC-content Distribution



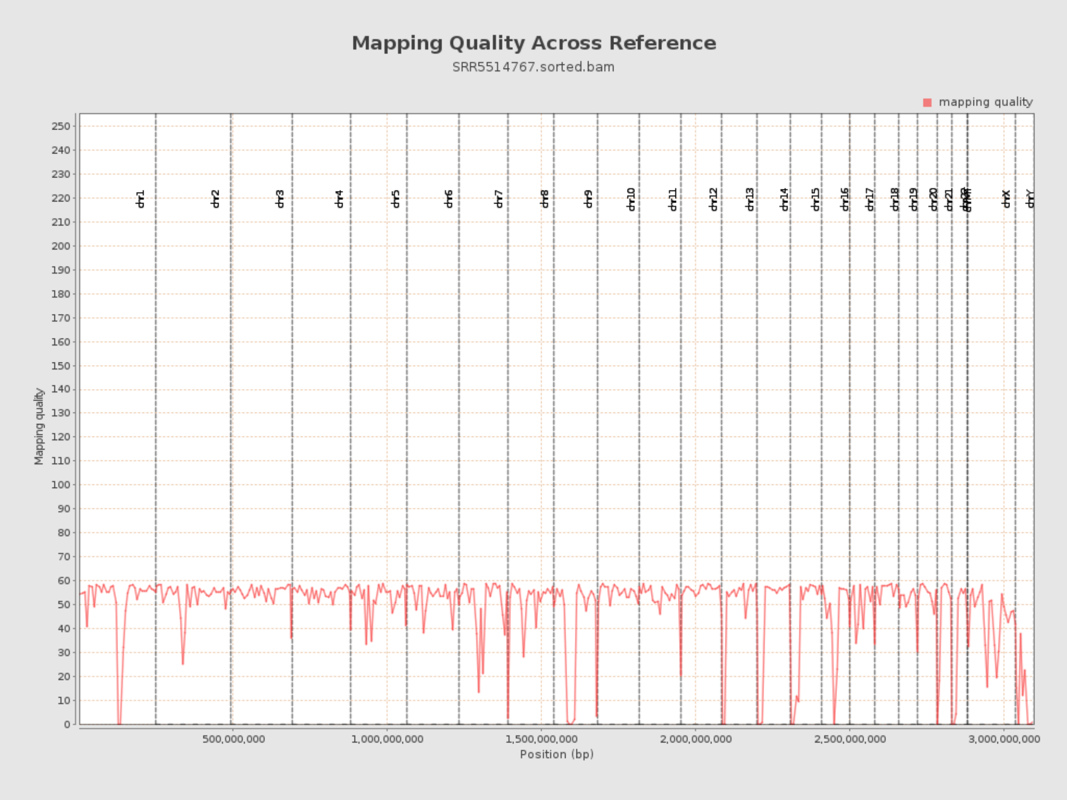
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram