Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/12 03:23:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514755.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_SRR5514755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Apr 12 03:23:12 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	88,935,803
Mapped reads	83,847,319 / 94.28%
Unmapped reads	5,088,484 / 5.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,936,482 / 13.42%
Read min/max/mean length	30 / 100 / 104.62
Duplicated reads (estimated)	69,174,779 / 77.78%
Duplication rate	48.38%
Clipped reads	39,950,647 / 44.92%

2.2. ACGT Content

Number/percentage of A's	2,496,691,909 / 31.19%
Number/percentage of C's	1,498,976,859 / 18.73%
Number/percentage of T's	2,464,920,107 / 30.8%
Number/percentage of G's	1,542,435,924 / 19.27%
Number/percentage of N's	550,068 / 0.01%
GC Percentage	38%

2.3. Coverage

Mean	2.5869

Standard Deviation	76.8255

2.4. Mapping Quality

Mean Mapping Quality	44.97

2.5. Mismatches and indels

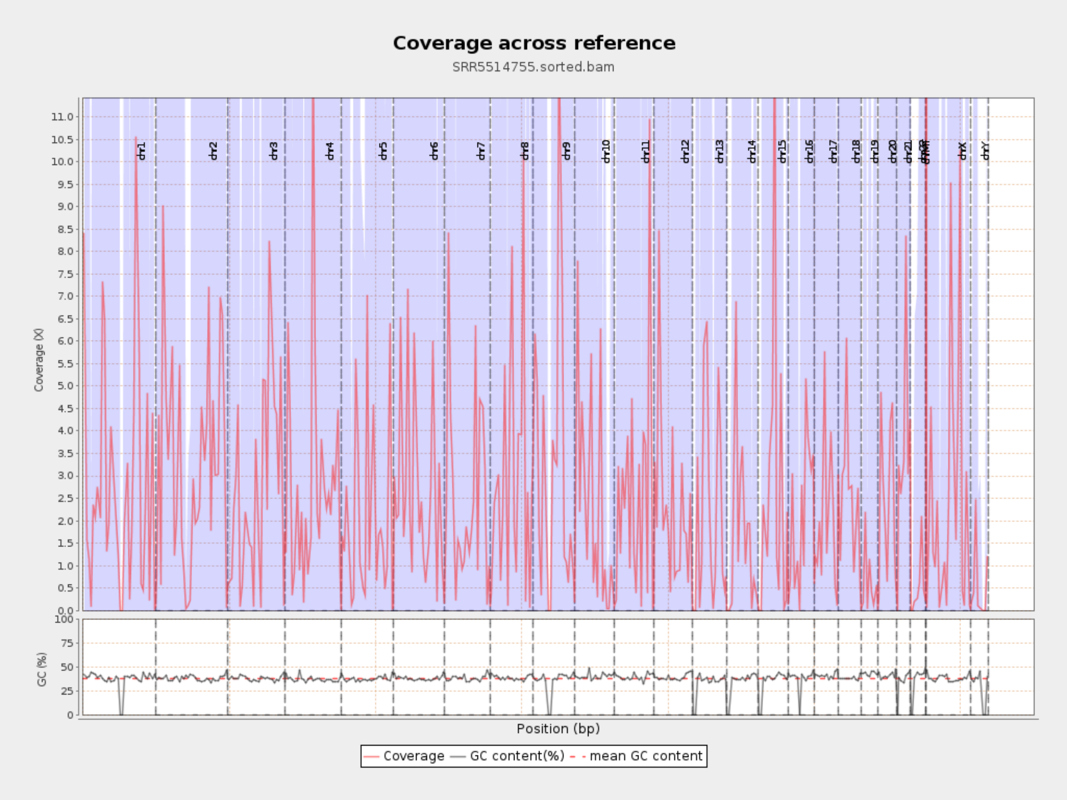
General error rate	0.59%
Mismatches	39,314,735
Insertions	5,242,864
Mapped reads with at least one insertion	6.01%
Deletions	1,790,235
Mapped reads with at least one deletion	2.01%
Homopolymer indels	56.26%

2.6. Chromosome stats

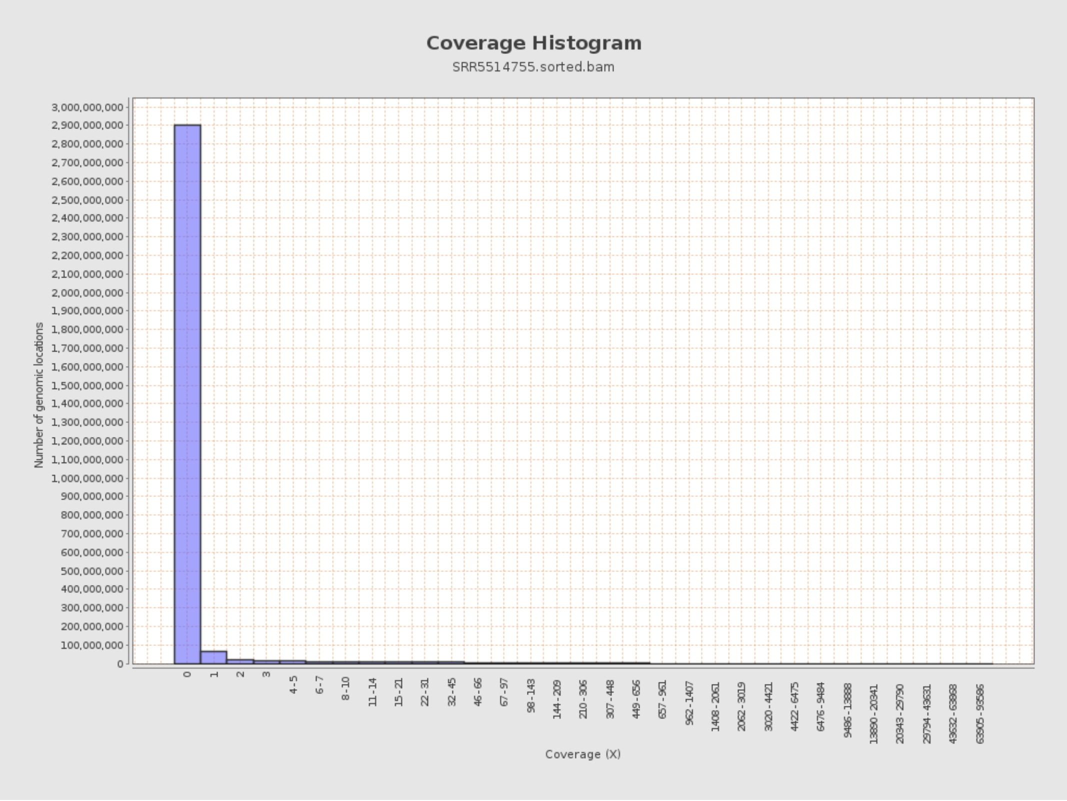
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	687765980	2.7593	66.1241
chr2	243199373	800528913	3.2917	61.2568
chr3	198022430	532709657	2.6901	42.0736
chr4	191154276	547612078	2.8648	40.0482
chr5	180915260	368757259	2.0383	35.0532
chr6	171115067	469957725	2.7464	42.3766
chr7	159138663	399036843	2.5075	42.1153

chr8	146364022	435941898	2.9785	47.4684
chr9	141213431	444892112	3.1505	160.0653
chr10	135534747	322869947	2.3822	75.8322
chr11	135006516	339870640	2.5174	42.6486
chr12	133851895	314606403	2.3504	47.7989
chr13	115169878	249481226	2.1662	46.6815
chr14	107349540	188818937	1.7589	31.5712
chr15	102531392	273834796	2.6707	57.2806
chr16	90354753	192399002	2.1294	70.2367
chr17	81195210	167102743	2.058	49.907
chr18	78077248	202076864	2.5882	33.9398
chr19	59128983	36825501	0.6228	15.024
chr20	63025520	163662961	2.5968	41.5281
chr21	48129895	179780795	3.7353	85.8681
chr22	51304566	28870912	0.5627	13.3155
chrMT	16571	242258290	14,619.4128	15,123.4573
chrX	155270560	384744039	2.4779	40.7181
chrY	59373566	33959037	0.572	16.0735

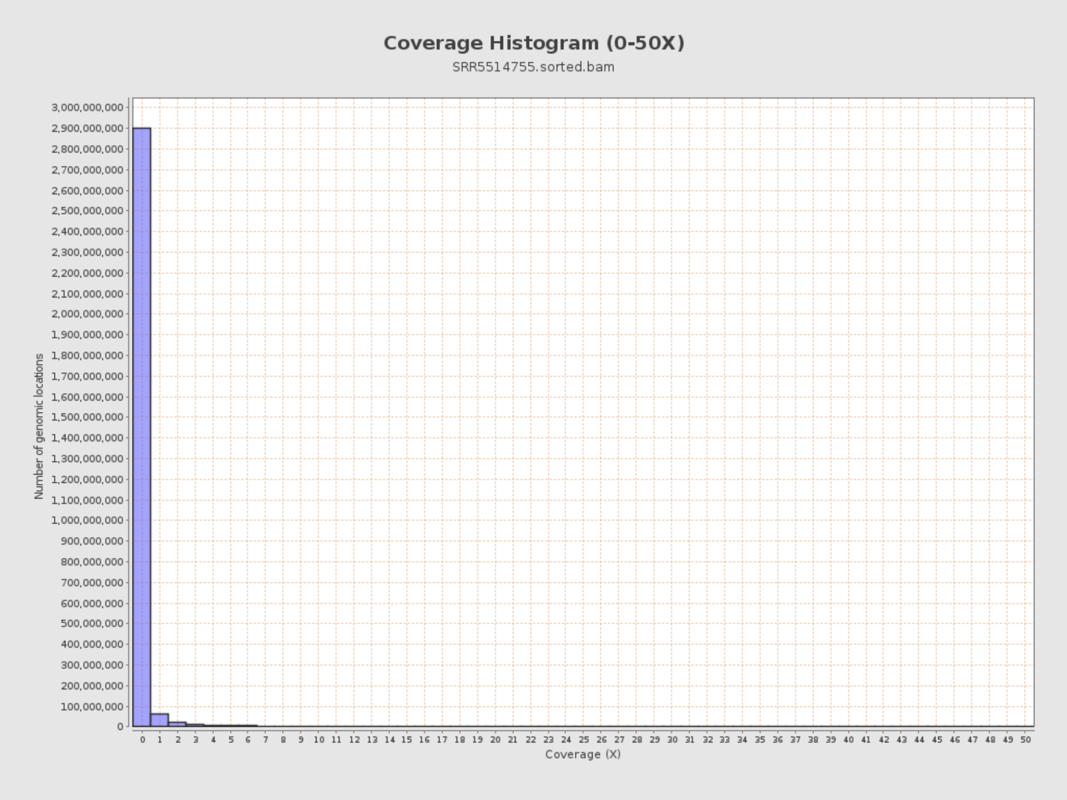
3. Results : Coverage across reference



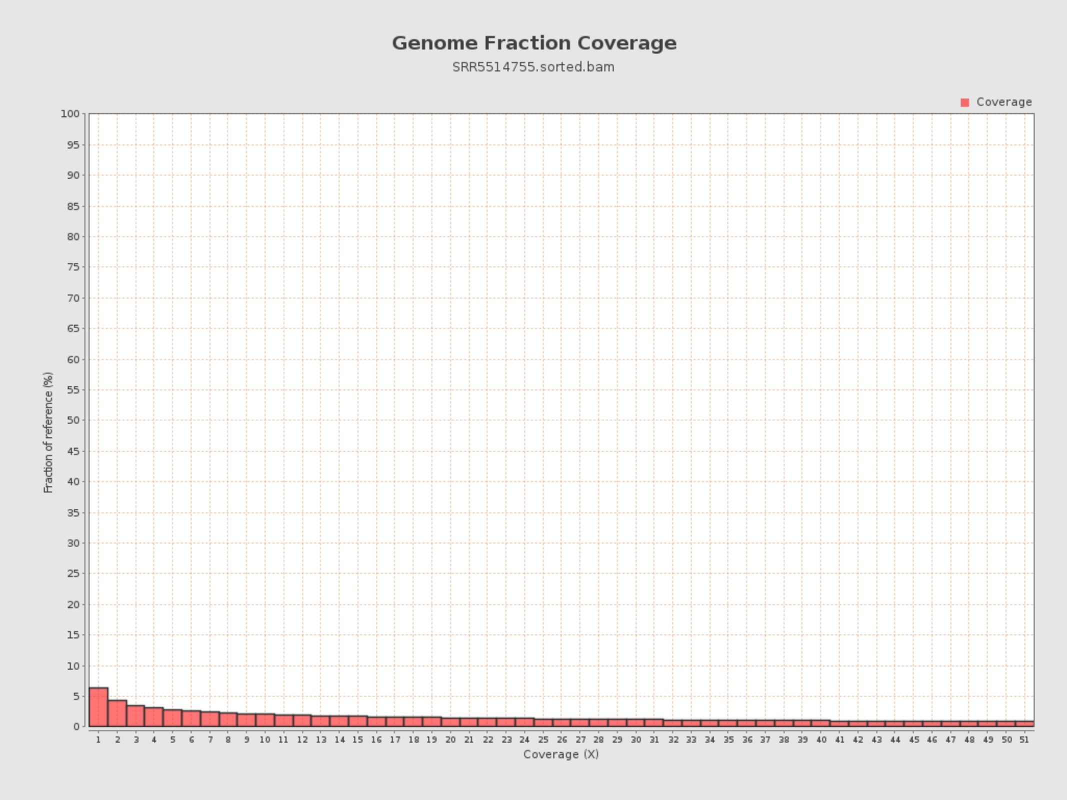
4. Results : Coverage Histogram



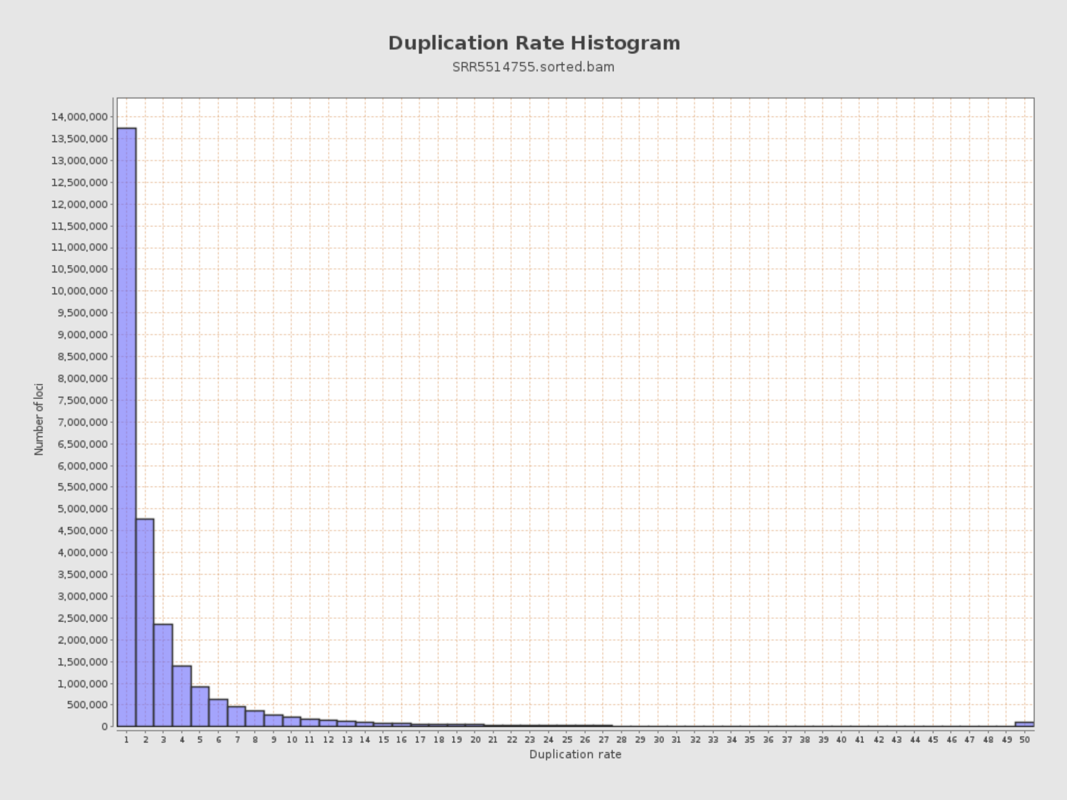
5. Results : Coverage Histogram (0-50X)



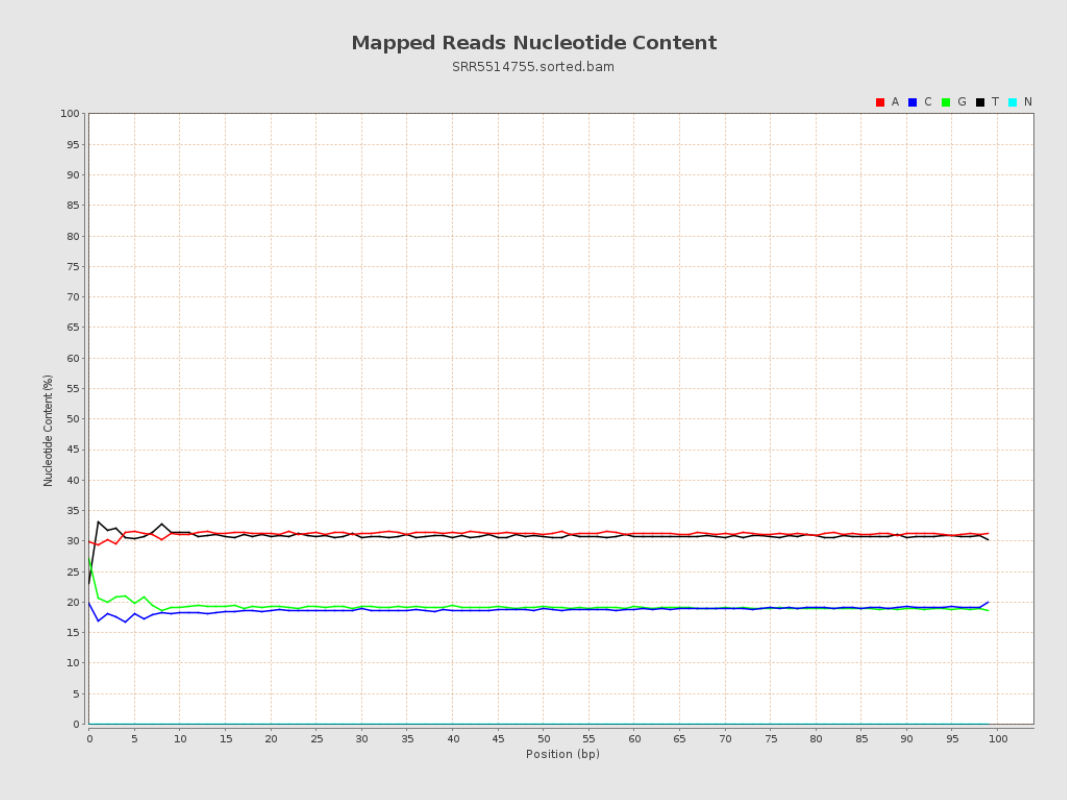
6. Results : Genome Fraction Coverage



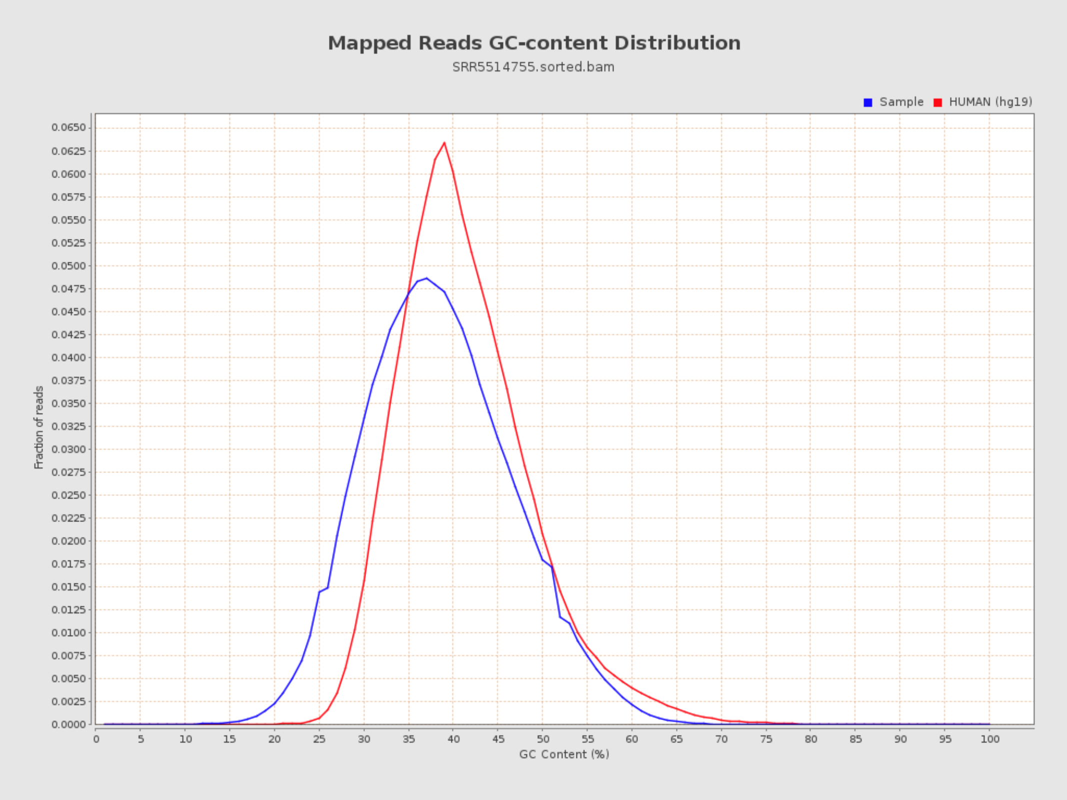
7. Results : Duplication Rate Histogram



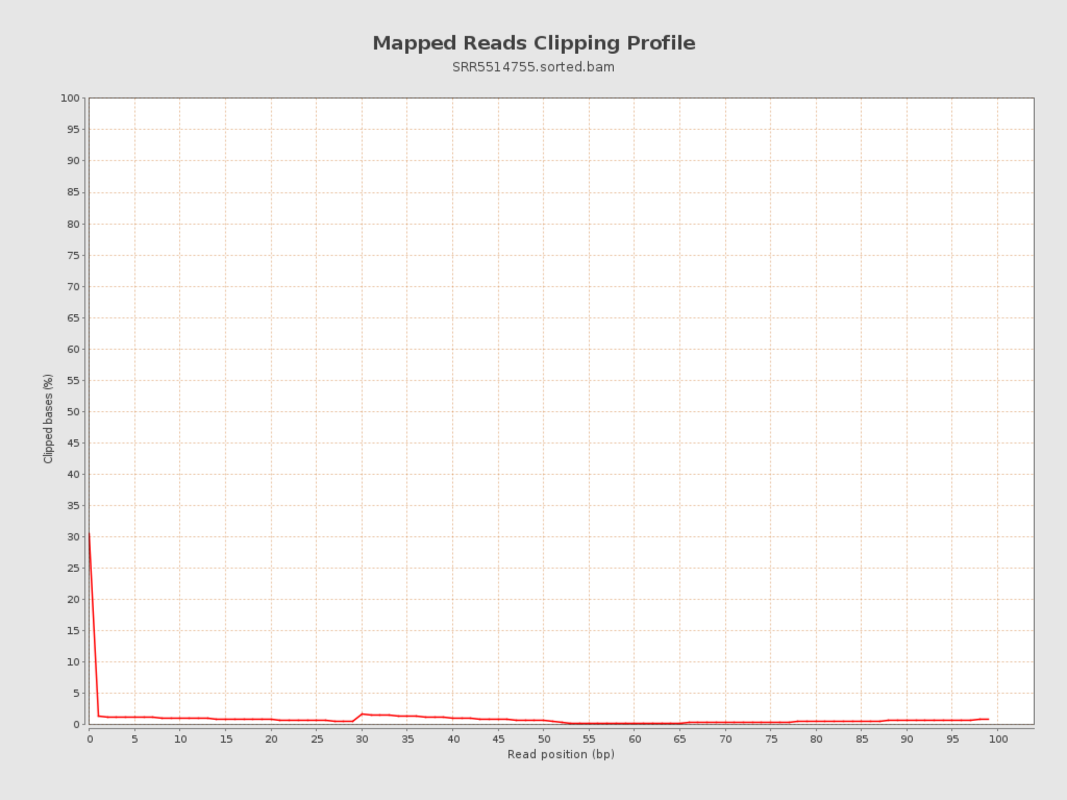
8. Results : Mapped Reads Nucleotide Content



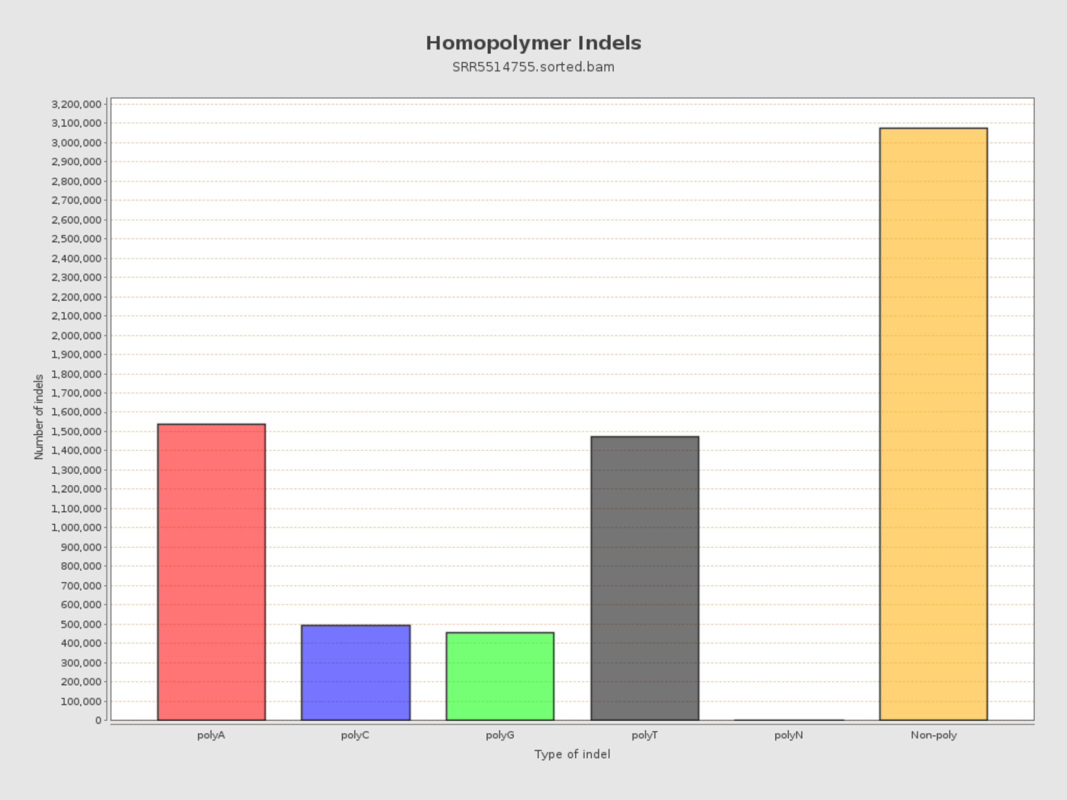
9. Results : Mapped Reads GC-content Distribution



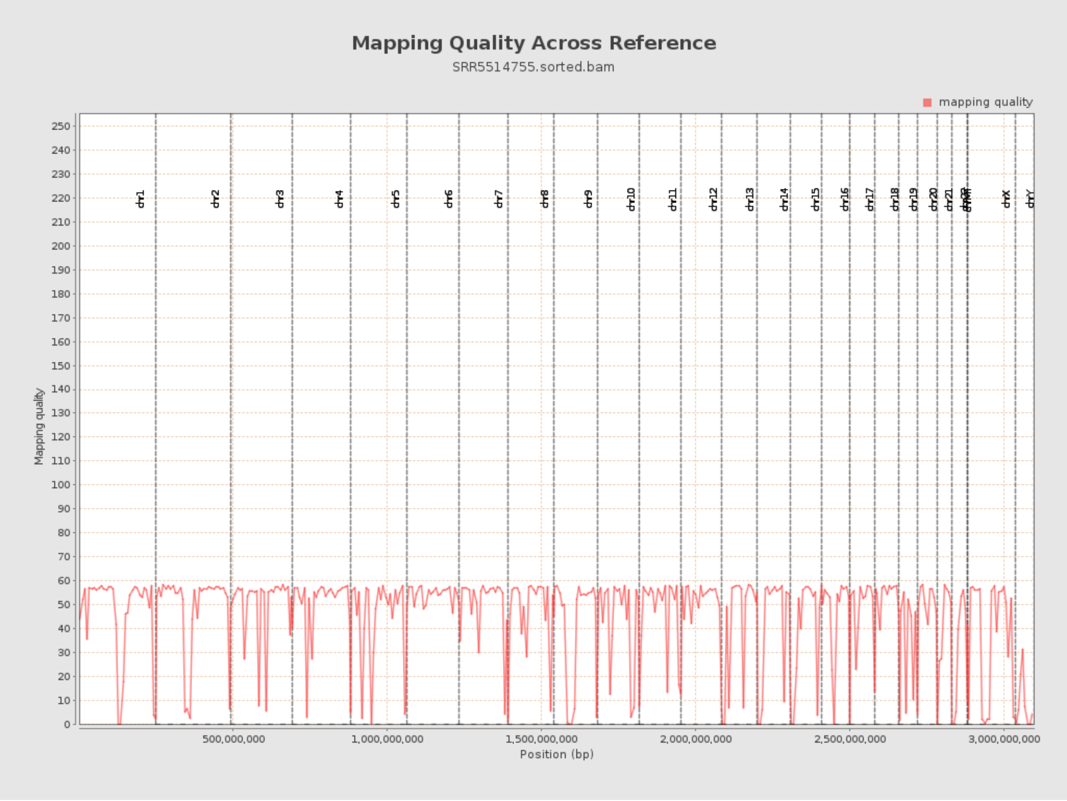
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram