Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 15:15:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514733.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_SRR5514733 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514733.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 15:15:45 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514733.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	62,164,627
Mapped reads	60,916,991 / 97.99%
Unmapped reads	1,247,636 / 2.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,398,186 / 2.25%
Read min/max/mean length	30 / 100 / 99.21
Duplicated reads (estimated)	38,256,613 / 61.54%
Duplication rate	41.94%
Clipped reads	8,668,649 / 13.94%

2.2. ACGT Content

Number/percentage of A's	1,528,589,373 / 26.19%
Number/percentage of C's	1,365,918,367 / 23.4%
Number/percentage of T's	1,545,224,931 / 26.47%
Number/percentage of G's	1,369,295,978 / 23.46%
Number/percentage of N's	28,280,021 / 0.48%
GC Percentage	46.86%

2.3. Coverage

Mean	1.8864

Standard Deviation	24.6543

2.4. Mapping Quality

Mean Mapping Quality	39.99

2.5. Mismatches and indels

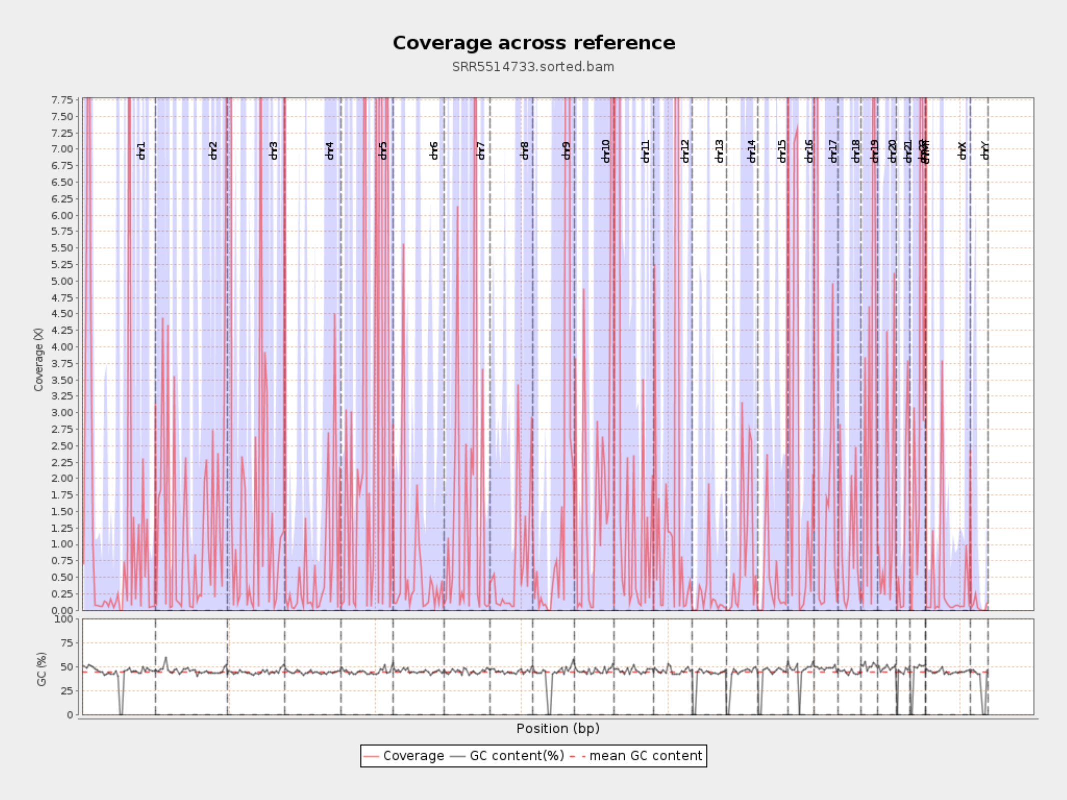
General error rate	0.88%
Mismatches	48,826,992
Insertions	1,765,307
Mapped reads with at least one insertion	2.83%
Deletions	1,380,821
Mapped reads with at least one deletion	2.22%
Homopolymer indels	48.26%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	340434426	1.3658	21.4779
chr2	243199373	331717231	1.364	17.1583
chr3	198022430	1017218572	5.1369	54.4817
chr4	191154276	125192400	0.6549	8.2834
chr5	180915260	583135029	3.2232	26.5344
chr6	171115067	101343476	0.5923	14.3856
chr7	159138663	270087951	1.6972	15.6867

chr8	146364022	104987683	0.7173	10.7095
chr9	141213431	336940886	2.386	32.7702
chr10	135534747	323519264	2.387	26.3868
chr11	135006516	441914093	3.2733	25.0962
chr12	133851895	287838467	2.1504	24.0238
chr13	115169878	28600361	0.2483	3.5095
chr14	107349540	93879835	0.8745	11.2608
chr15	102531392	55288659	0.5392	6.4989
chr16	90354753	201315123	2.2281	22.0808
chr17	81195210	524809482	6.4636	54.1511
chr18	78077248	77153795	0.9882	12.567
chr19	59128983	175054212	2.9605	27.3269
chr20	63025520	97236130	1.5428	20.7422
chr21	48129895	60032376	1.2473	13.9967
chr22	51304566	190319826	3.7096	30.642
chrMT	16571	6213969	374.9906	162.1976
chrX	155270560	61285777	0.3947	9.6347
chrY	59373566	4173337	0.0703	2.7492

3. Results : Coverage across reference



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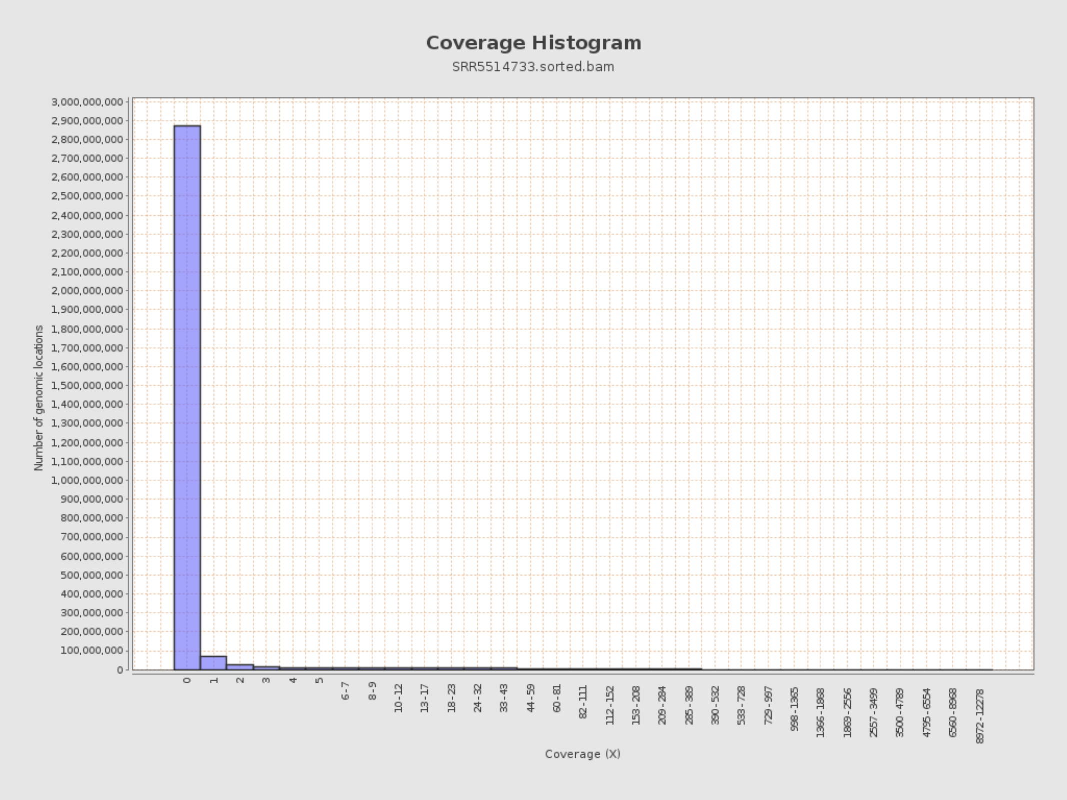
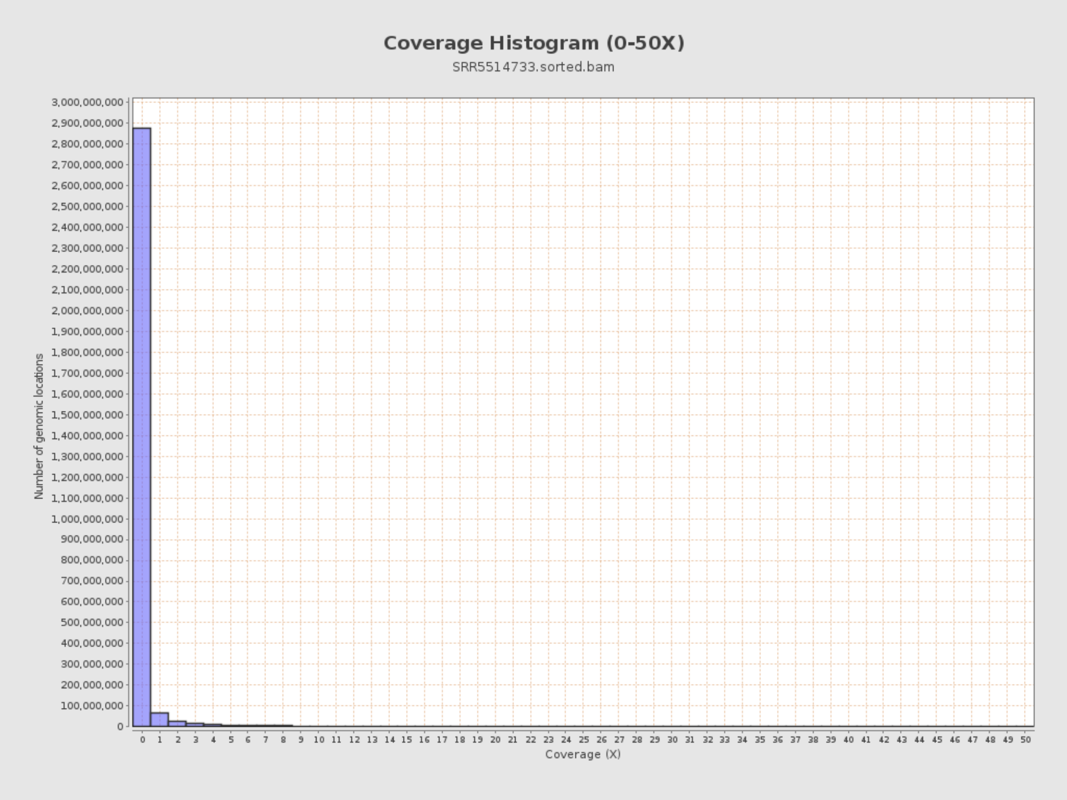
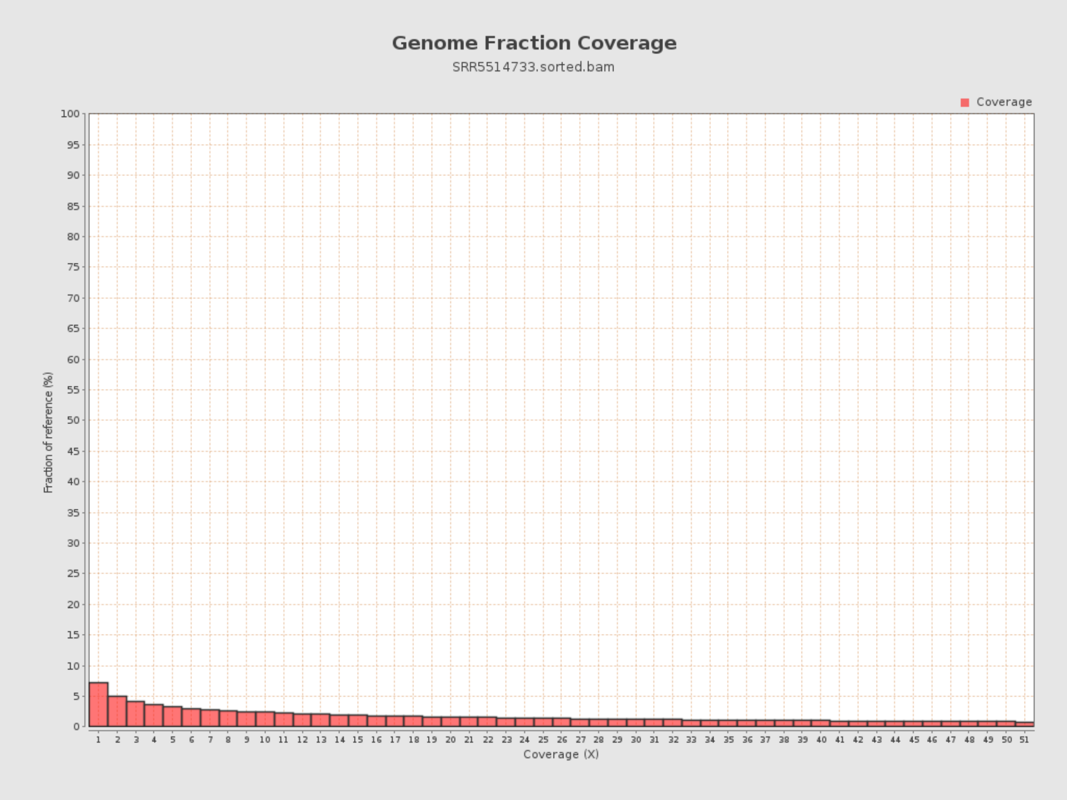
4. Results : Coverage Histogram



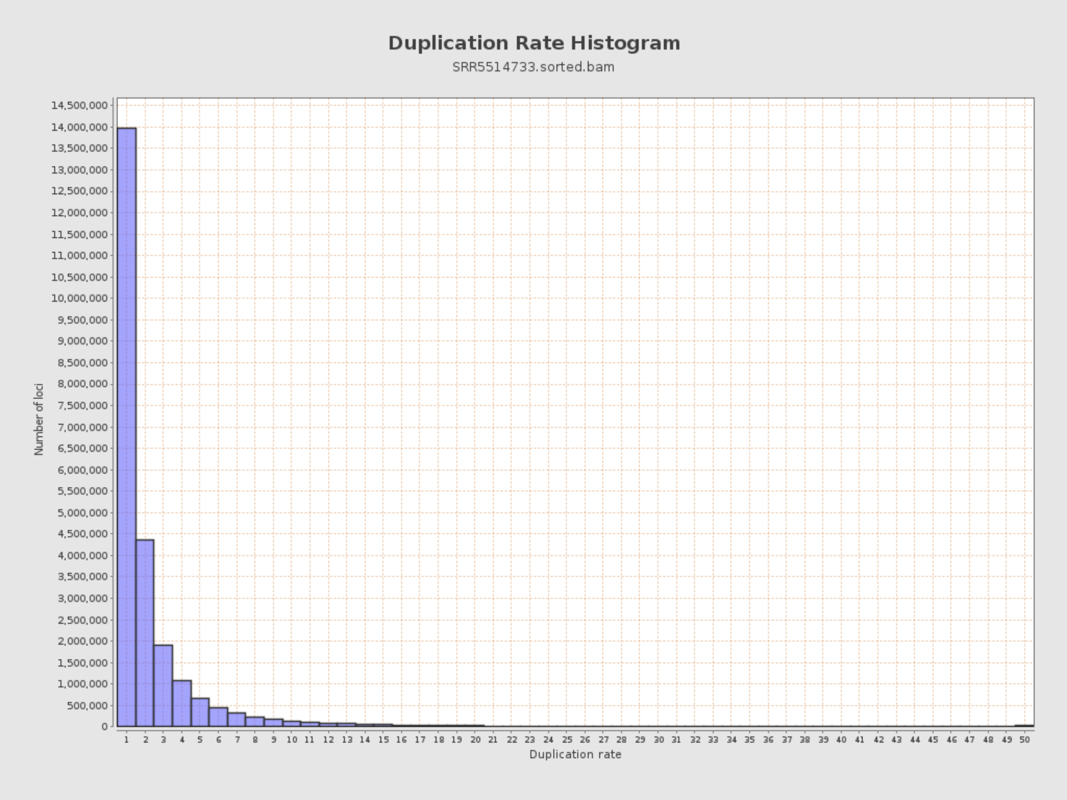
5. Results : Coverage Histogram (0-50X)



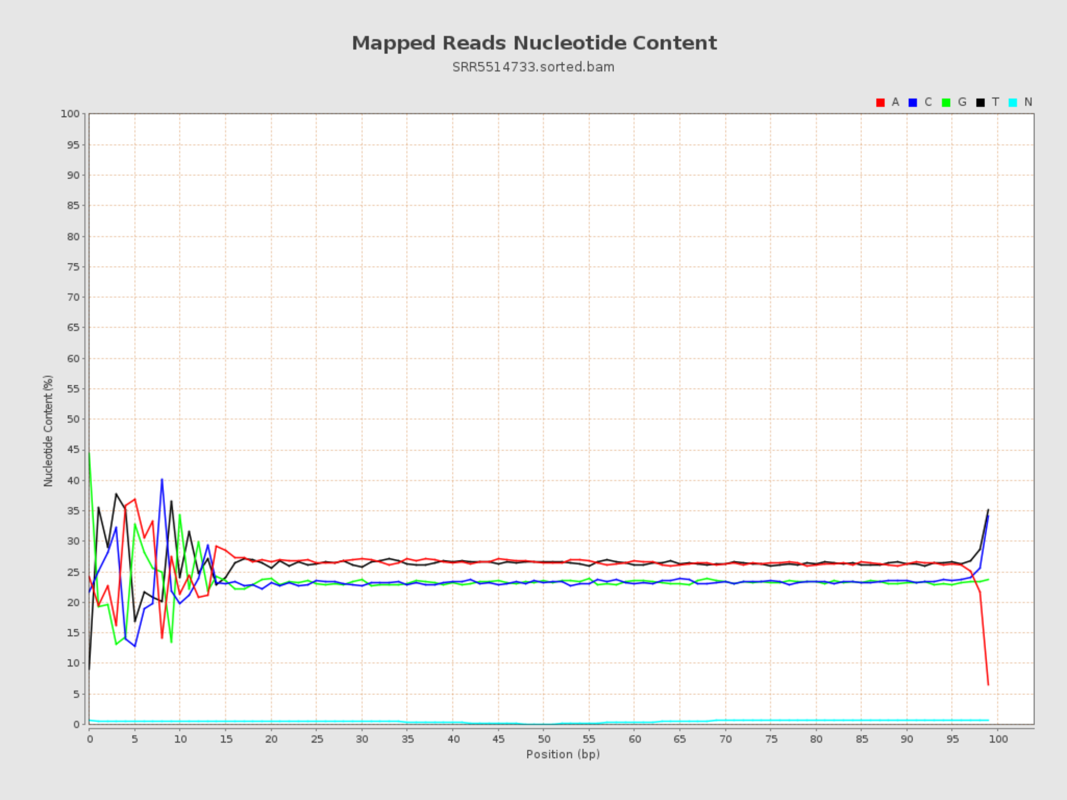
6. Results : Genome Fraction Coverage



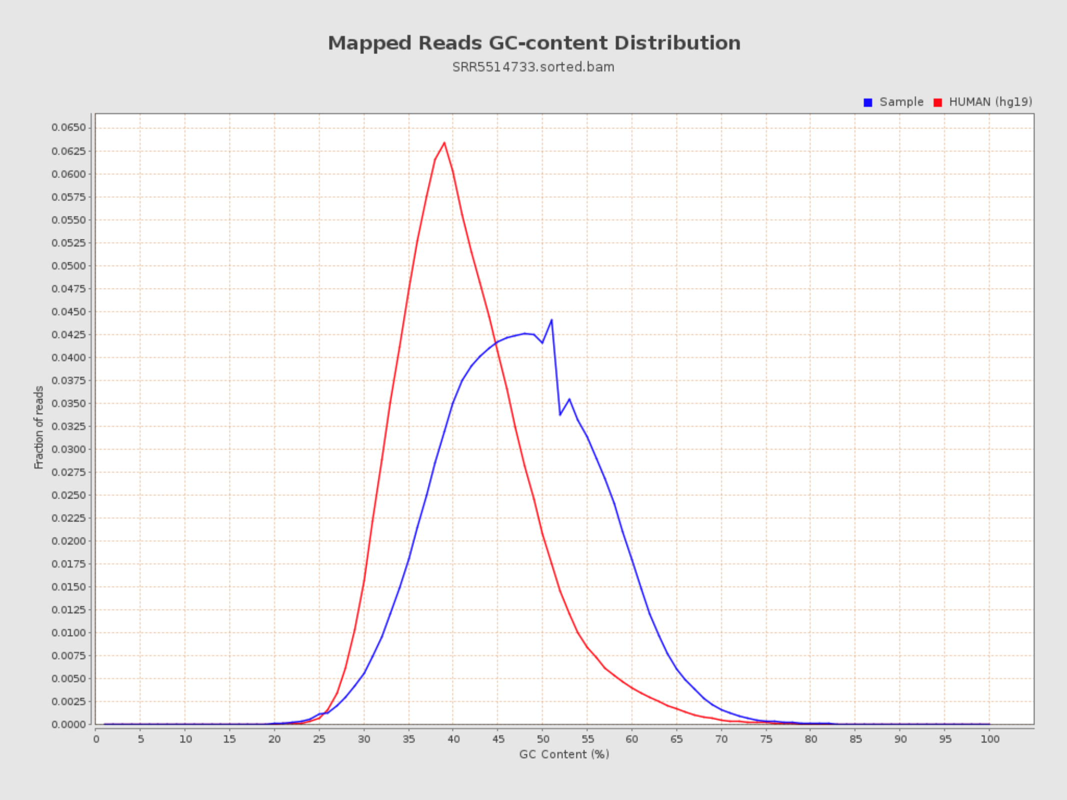
7. Results : Duplication Rate Histogram



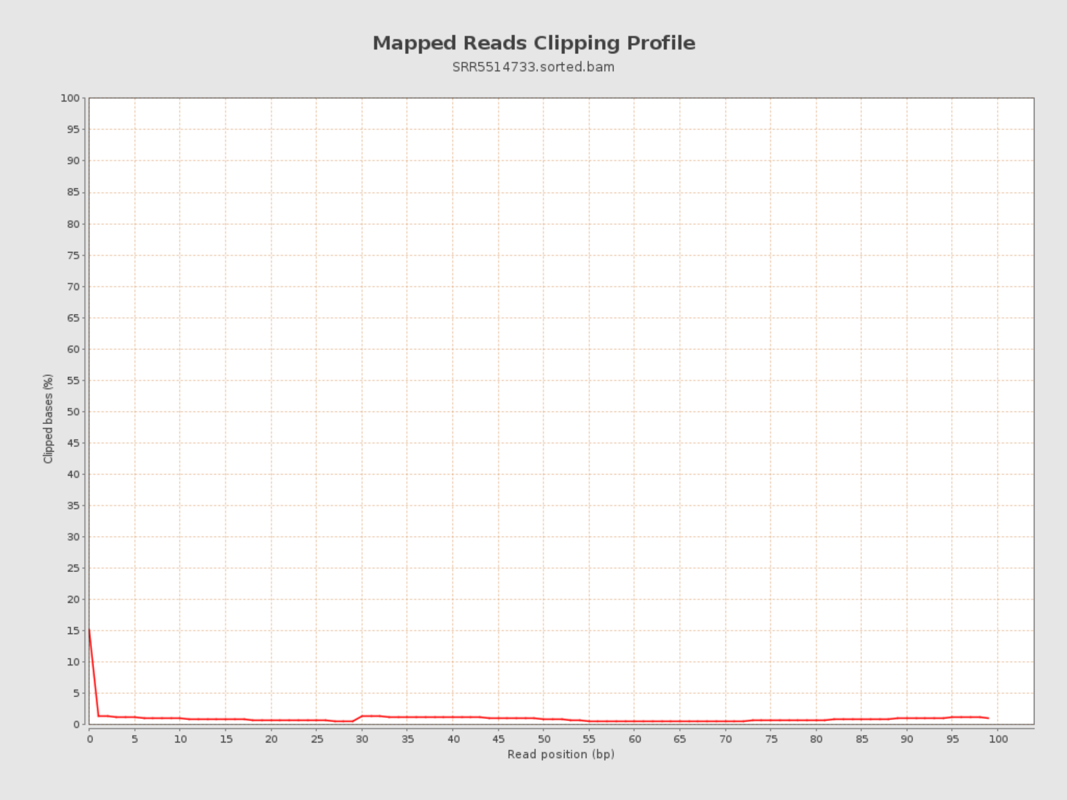
8. Results : Mapped Reads Nucleotide Content



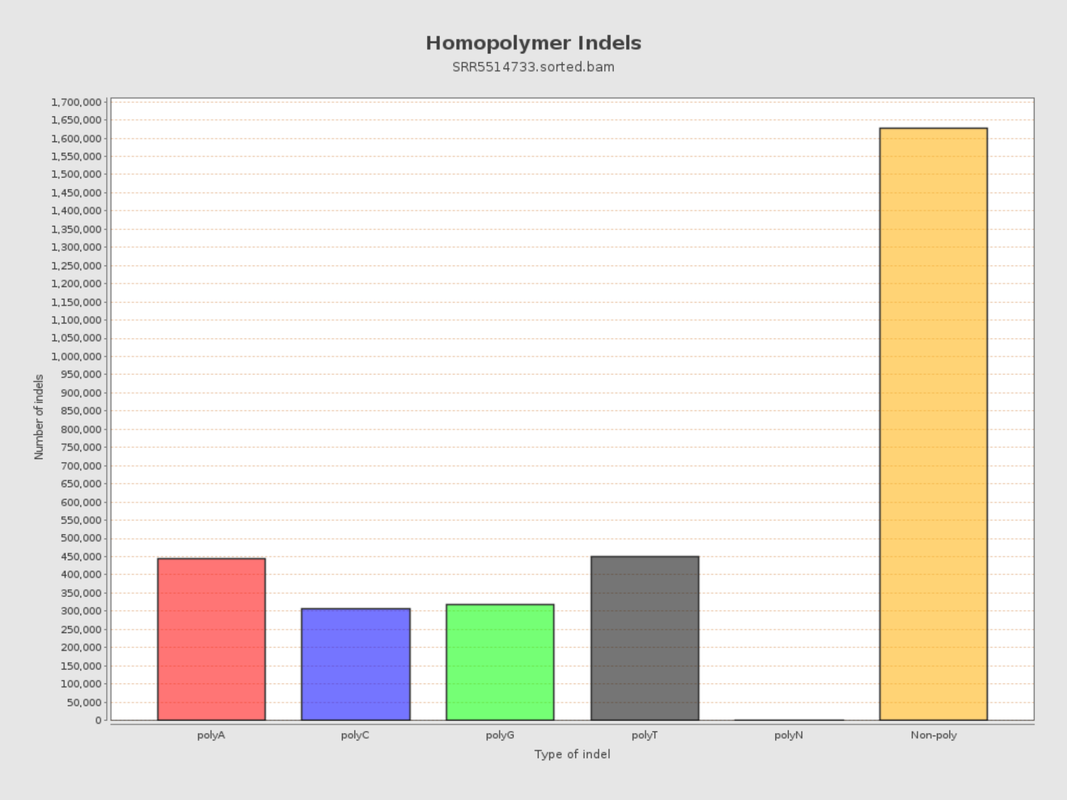
9. Results : Mapped Reads GC-content Distribution



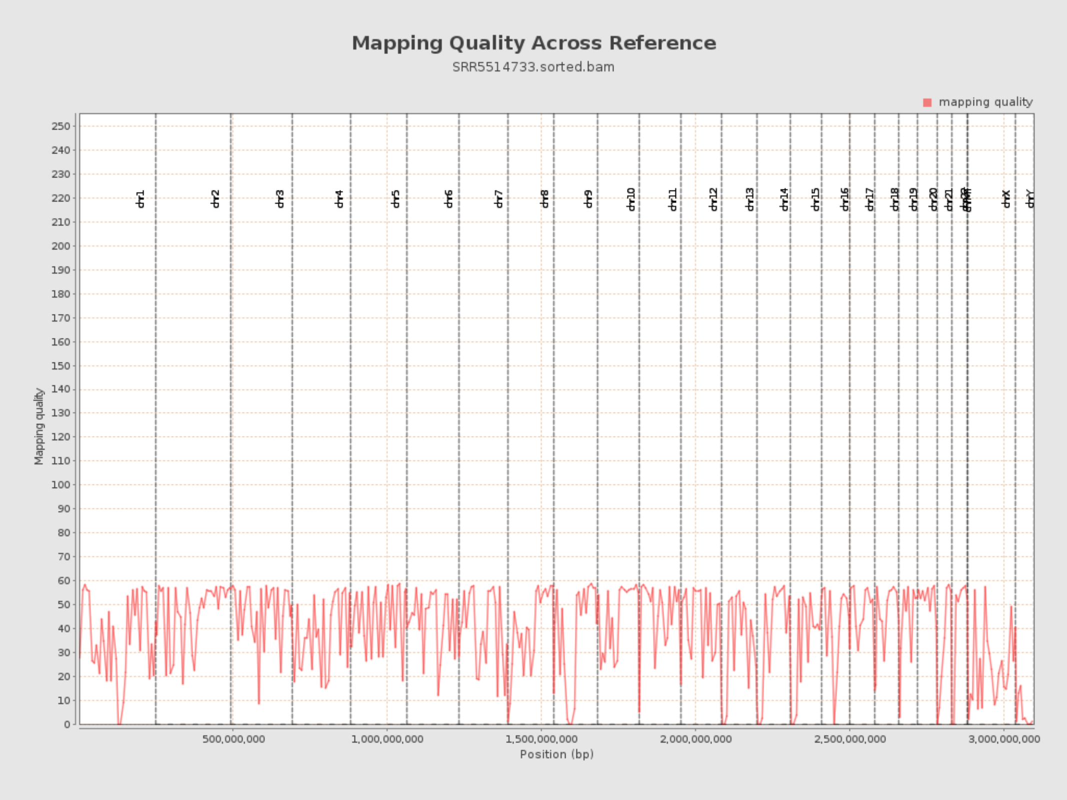
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram