Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 07:13:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090133.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_SRR090133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 07:13:58 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,722,724
Mapped reads	15,788,572 / 84.33%
Unmapped reads	2,934,152 / 15.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	833 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,500,475 / 13.36%
Duplication rate	10.51%
Clipped reads	2,020,076 / 10.79%

2.2. ACGT Content

Number/percentage of A's	233,682,042 / 31.62%
Number/percentage of C's	145,153,545 / 19.64%
Number/percentage of T's	204,845,743 / 27.72%
Number/percentage of G's	155,343,824 / 21.02%
Number/percentage of N's	25,308 / 0%
GC Percentage	40.66%

2.3. Coverage

Mean	0.2388

Standard Deviation	1.528

2.4. Mapping Quality

Mean Mapping Quality	43.69

2.5. Mismatches and indels

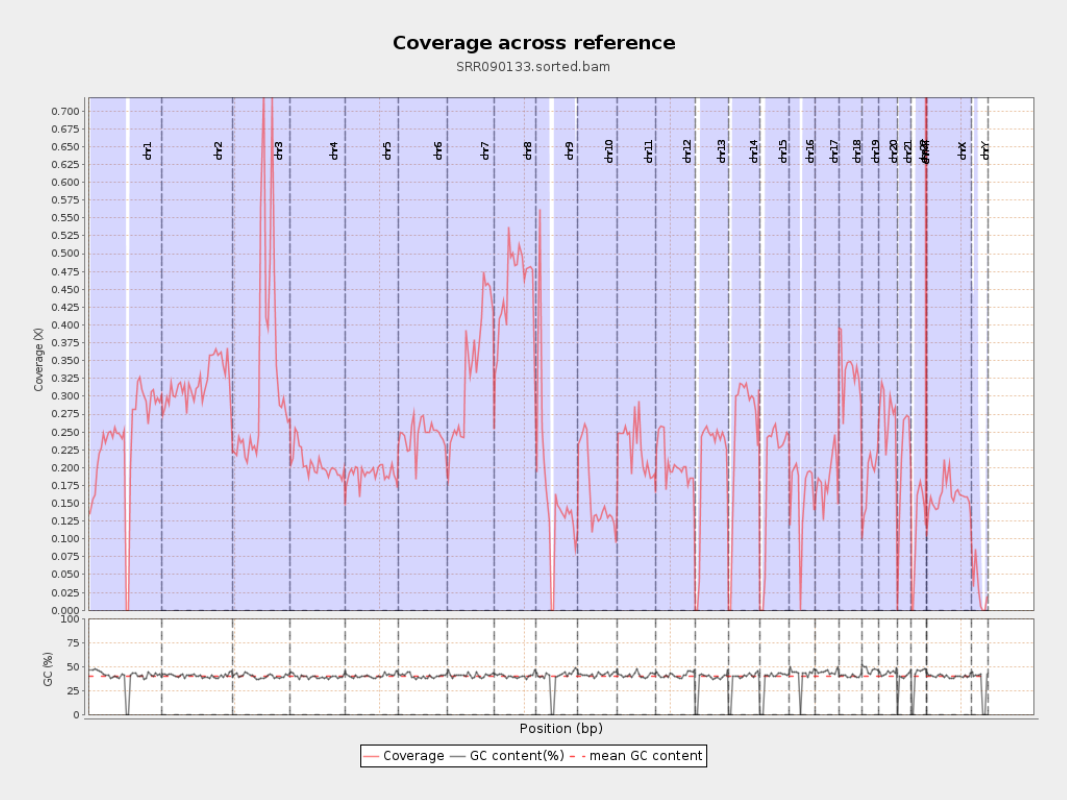
General error rate	0.41%
Mismatches	3,016,995
Insertions	32,246
Mapped reads with at least one insertion	0.2%
Deletions	100,310
Mapped reads with at least one deletion	0.63%
Homopolymer indels	45.96%

2.6. Chromosome stats

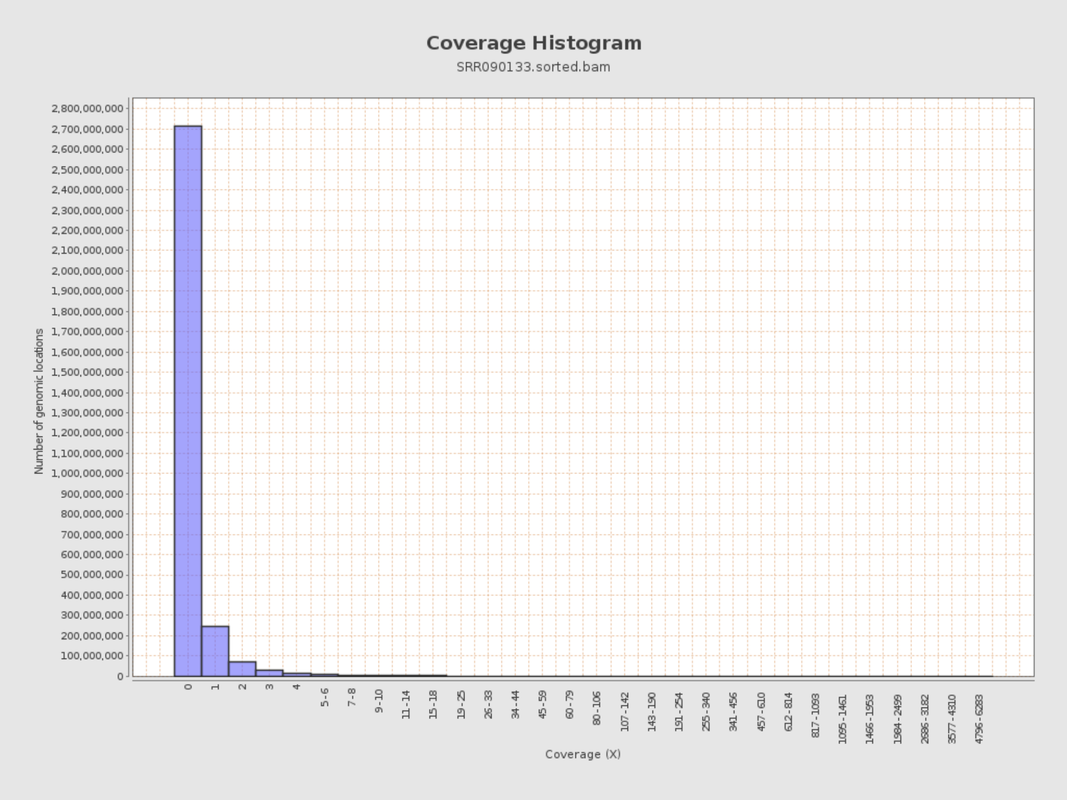
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	59610454	0.2392	1.6451
chr2	243199373	77575282	0.319	1.656
chr3	198022430	65236601	0.3294	1.4503
chr4	191154276	39150133	0.2048	0.9936
chr5	180915260	34649116	0.1915	0.9473
chr6	171115067	41972719	0.2453	1.1985
chr7	159138663	54250003	0.3409	2.3237

chr8	146364022	65983059	0.4508	3.7911
chr9	141213431	23717552	0.168	1.1348
chr10	135534747	22384994	0.1652	1.0151
chr11	135006516	30622387	0.2268	1.2154
chr12	133851895	27378315	0.2045	0.9935
chr13	115169878	23398482	0.2032	0.9984
chr14	107349540	26633567	0.2481	1.1836
chr15	102531392	19823400	0.1933	0.9902
chr16	90354753	14711637	0.1628	0.9048
chr17	81195210	14863342	0.1831	0.9535
chr18	78077248	26203028	0.3356	1.7783
chr19	59128983	11103613	0.1878	1.3788
chr20	63025520	17306867	0.2746	1.2366
chr21	48129895	9878903	0.2053	1.1062
chr22	51304566	5869467	0.1144	0.7096
chrMT	16571	401601	24.2352	25.7973
chrX	155270560	24829693	0.1599	0.9167
chrY	59373566	1646130	0.0277	0.7259

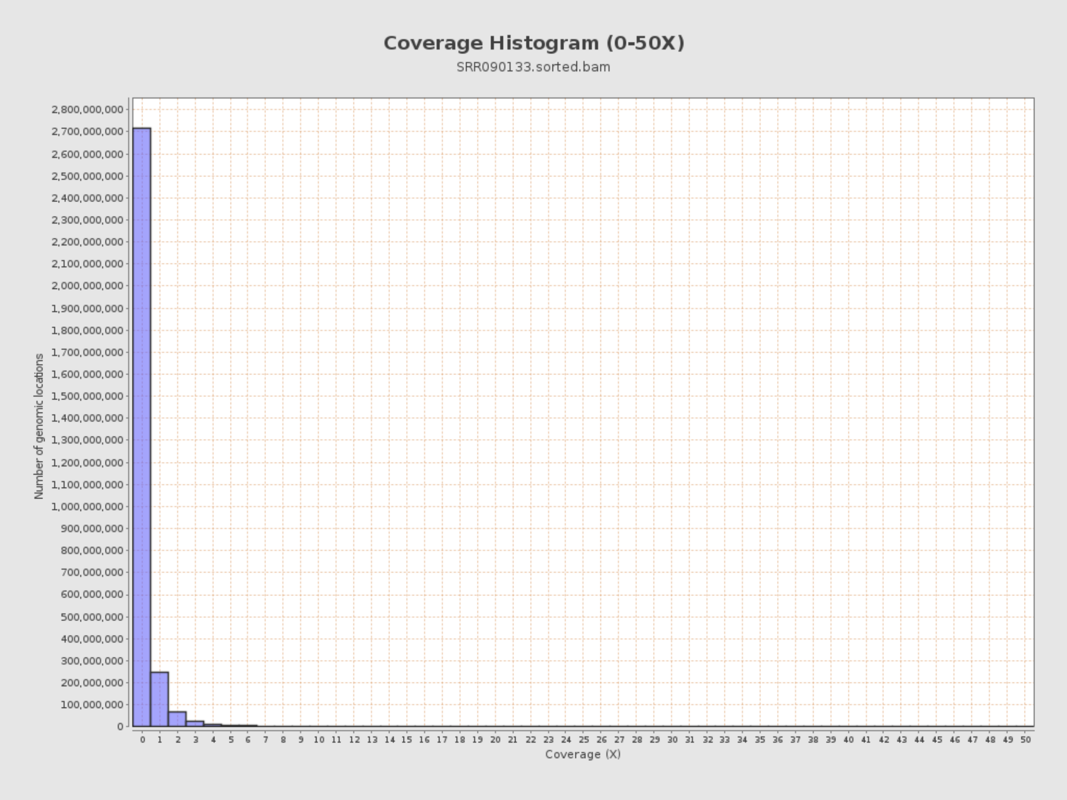
3. Results : Coverage across reference



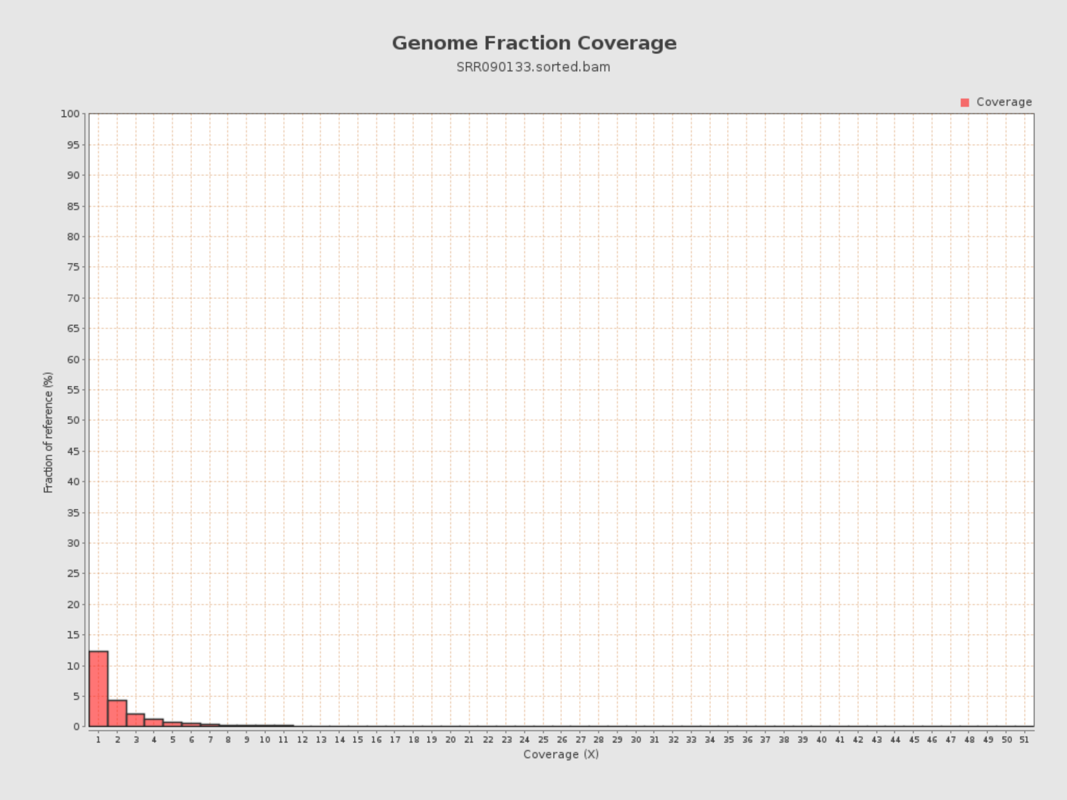
4. Results : Coverage Histogram



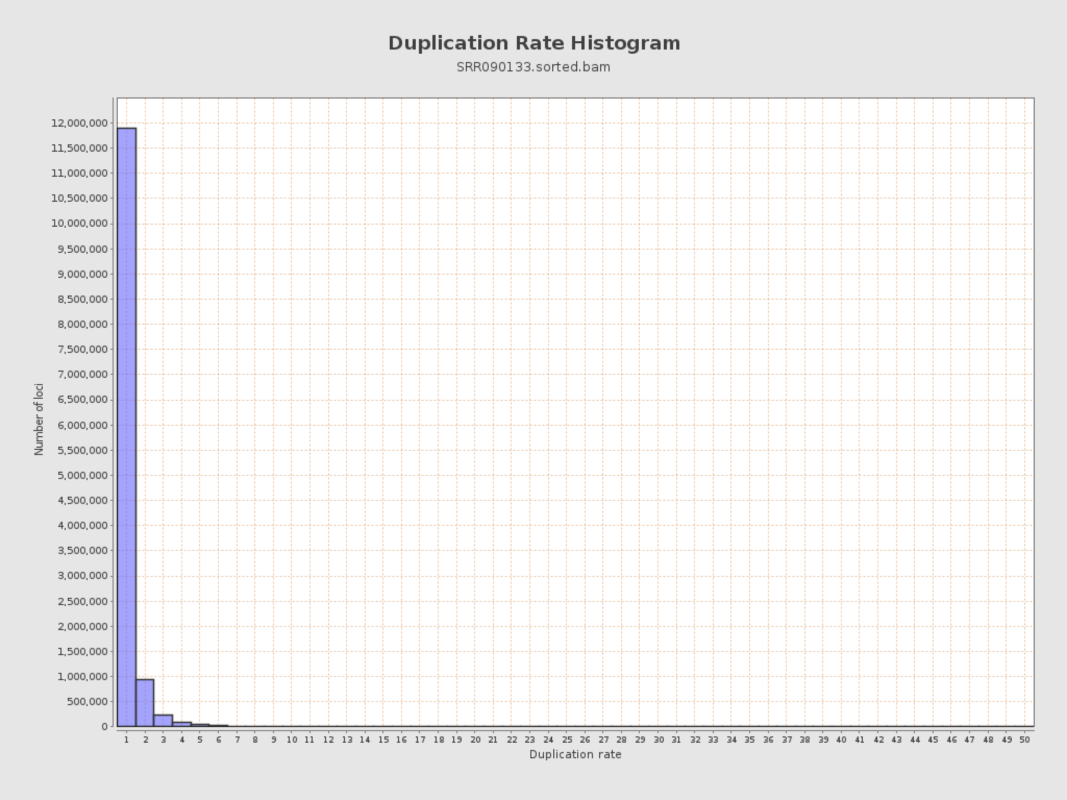
5. Results : Coverage Histogram (0-50X)



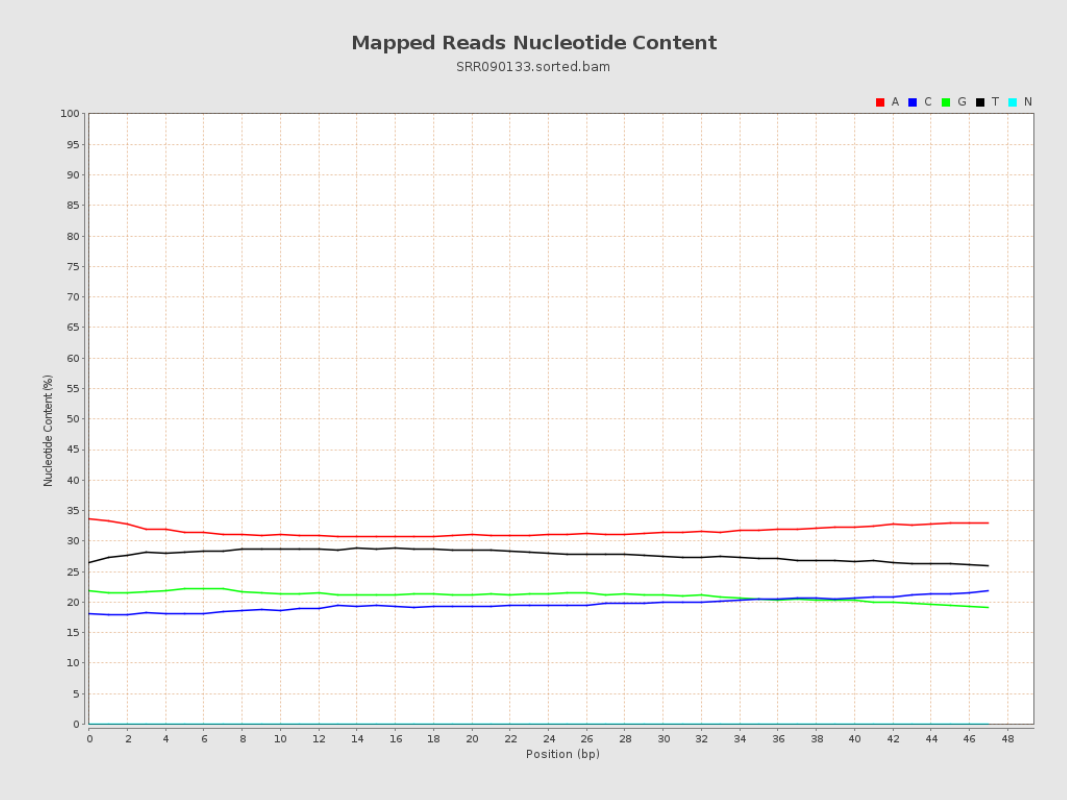
6. Results : Genome Fraction Coverage



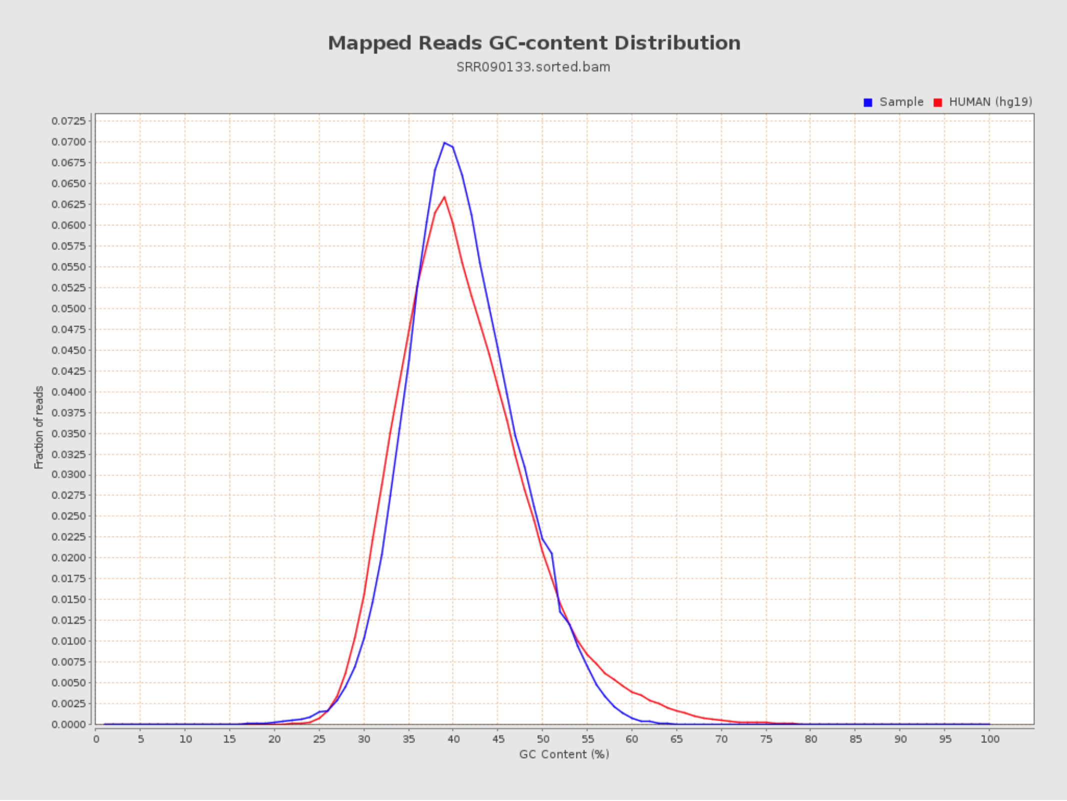
7. Results : Duplication Rate Histogram



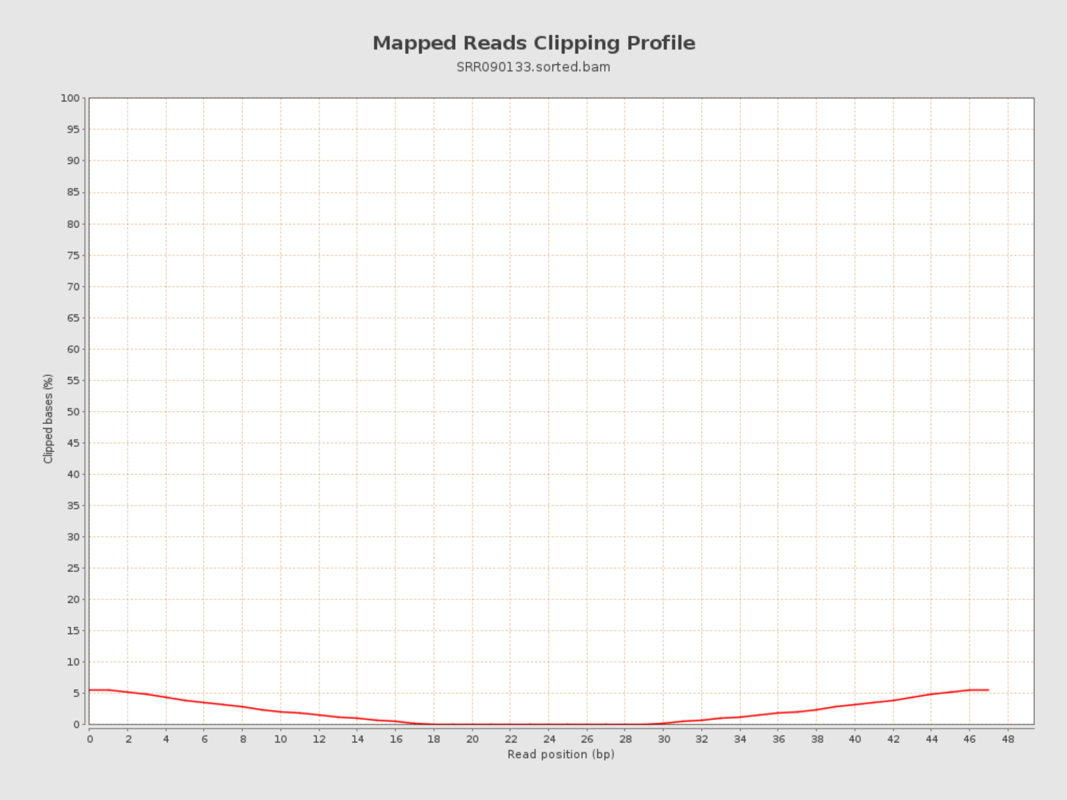
8. Results : Mapped Reads Nucleotide Content



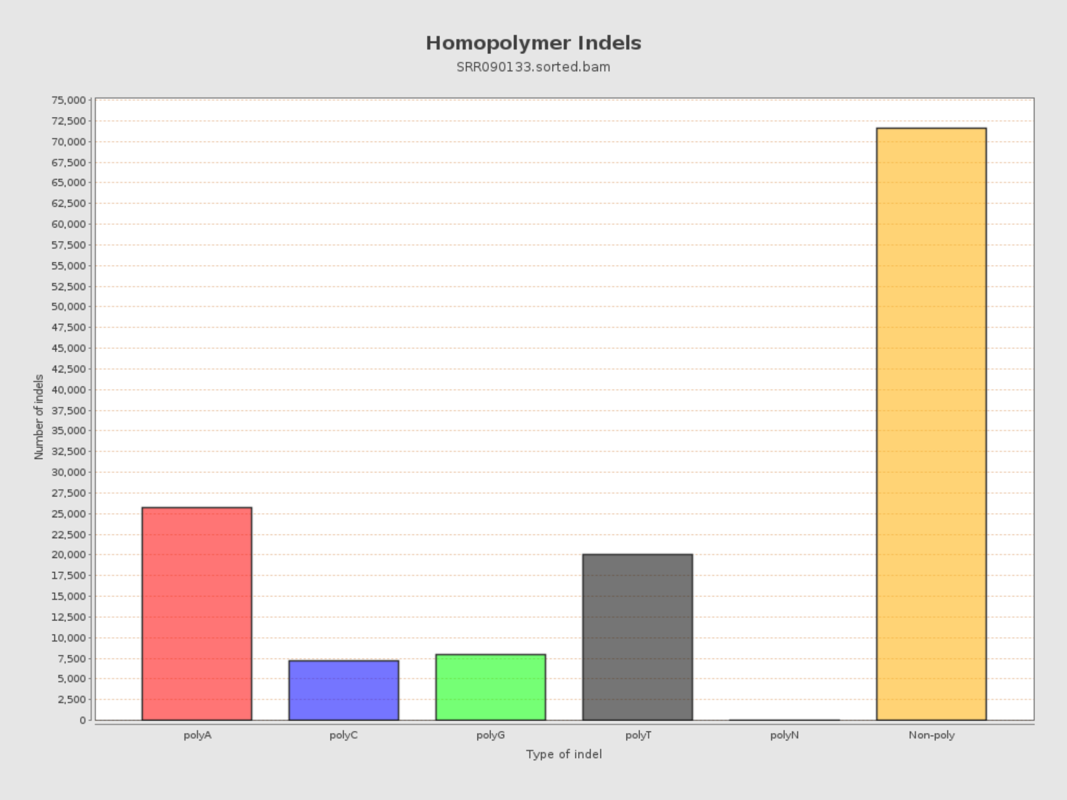
9. Results : Mapped Reads GC-content Distribution



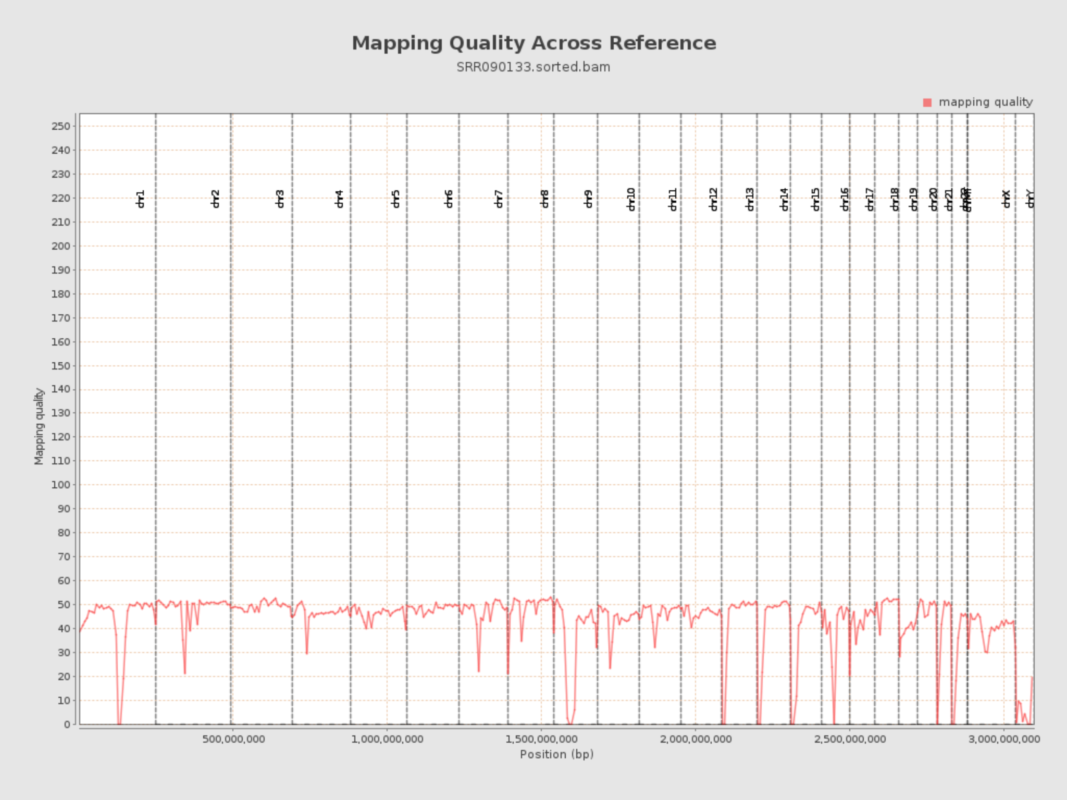
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram