

394 **Table 6.** Number of effects by variant type

	Hanwoo v1		Bovine v2		Bovine v3	
	<i>UMD3.1</i>	<i>ARS-UCD1.2</i>	<i>UMD3.1</i>	<i>ARS-UCD1.2</i>	<i>UMD3.1</i>	<i>ARS-UCD1.2</i>
3 prime UTR variant	116	198	106	176	104	166
5 prime UTR premature start codon gain variant	2	11	2	10	2	11
5 prime UTR variant downstream gene variant	17	48	18	49	17	46
intergenic region	909	1,500	822	1,377	786	1,330
intron variant	10,714	9,362	9,566	8,338	9,173	8,016
missense variant	5,592	14,545	4,899	12,918	4,736	12,392
non coding transcript exon variant	134	283	93	207	88	203
splice acceptor variant	11	26	10	24	9	24
splice donor variant	2	3	-	-	-	-
splice region variant	1	1	-	-	-	2
stop gained	28	68	25	61	24	62
synonymous variant	8	17	-	-	-	-
upstream gene variant	210	338	195	305	189	297
	828	1,369	745	1,245	723	1,185

395 In annotation results, effects were classified according to SNP type. The number of intergenic
396 region effects decreased while intron variant increased in all panels when mapping was
397 conducted using the ARS-UCD1.2 genome. Furthermore, there were minor changes and genetic
398 variations in other regions.
399

400 **Table 7.** Number of transitions and transversion variants in each SNP panel

	Hanwoo v1	Bovine v2	Bovine v3
Transition¹	18,244,942	1,592,985	466,233
Transversion²	5,905,481	498,100	145,571
Ts/Tv ratio	3.090	3.198	3.203

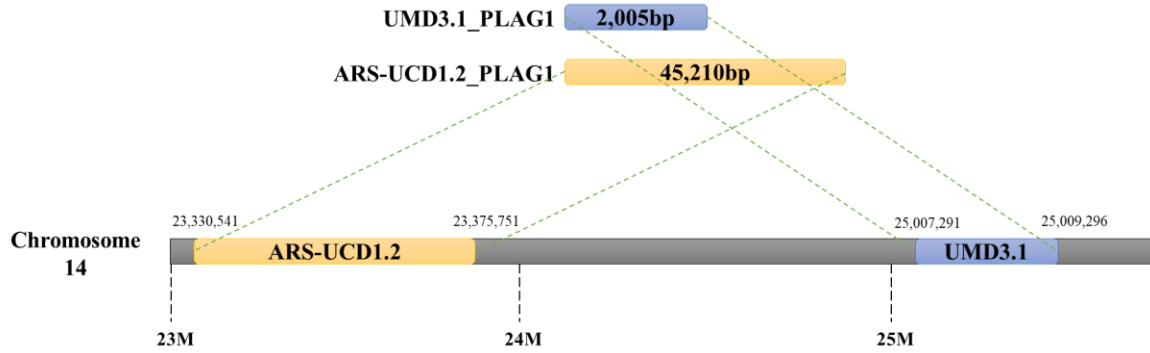
401 ¹Transition is a mutation that changes from pyrimidine to pyrimidine base or purine to purine
402 base;

403 ²Transversion is a variant of a pyrimidine-to-purine base or purine to pyrimidine base

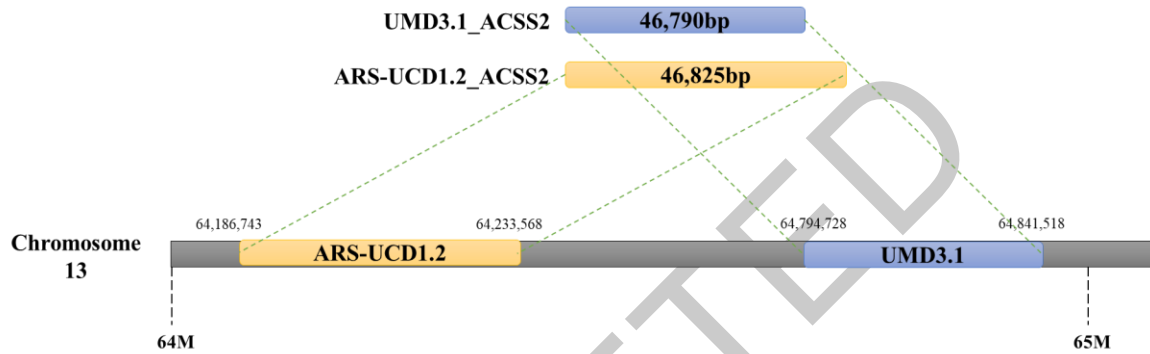
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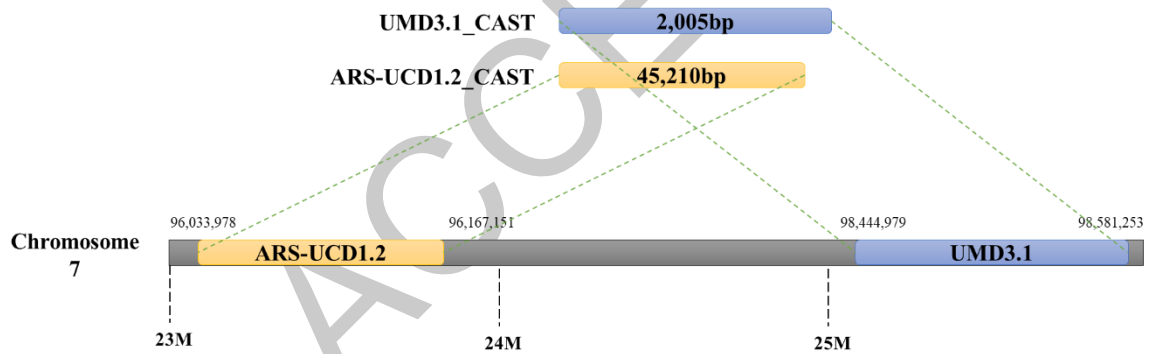
405 **Figure 2.** Gene transfer according to reference
 406 (A)



407
 408 (B)



409
 410 (C)



411
 412 In this figure, the blue box represents the gene for the *UMD3.1* genome and the yellow box for
 413 *ARS-UCD1.2* genome. And the gray box is the genome of the chromosomes. As shown in this
 414 figure, the size and the location of the gene are changed according to the reference genomes. Due
 415 to these changes, the number and the location of SNPs are changed.