Table S2: Glycosylation prediction on Tandem Repeats from Compatible and Incompatible cDNA variants

Compatible strain						
ind <sup>a</sup>	Variant id.b	splicing	TR <sup>d</sup>	glycosylation prediction in TR <sup>e</sup>		
				1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35		
C-1	C1/3.1/2r1.1	l No l	10=4			
C-1	C1/3.1/2r1.1	NO AS	2r1 2r1	++-		
Ī	C1/3.1/r1.1	IAC	-1	——		
	C1/3.1/r1.2	AS AS	r1 r1			
	C1/3.1/r1'.1	AS	r1'	— <del>□</del>		
	C1/3.1/r1'.2	AS	r1'			
ſ	C1/2/7r2.1	AS	7r2			
	C1/2/7r2.2	AS	7r2° <sup>2-4</sup>			
C - 2	C2/3.2/r1	AS	r1			
C -3	C3/2/45r2 C3/2/40r2	AbS (1)	≈ 45 <b>r2</b>			
	C3/2/25r2	AbS (1) AbS (1)	≈ 40 <b>r2</b> ≈ 25 <b>r2</b>			
ı	C3/2/11r2	NO	11 <b>r2</b> ° <sup>2</sup>			
	00/2/11/2	, NO	11112			
C - 4	C4/3.1/9r1'-r1-r1'	NO	9r1'-r1-r1'			
				<del> </del>		
	C4/2/100r2.1 C4/2/100r2.2	AS AS	≈ 100 <b>r2</b> ≈ 100 <b>r2</b> * <sup>3</sup>	<del>+++++++++++++++++++++++++++++++++++++</del>		
			100.2			
C - 5	C5/3.1/2r1'.1	NO	2r1'			
	C5/3.1/2r1'.2 C5/3.1/2r1'.3	NO NO	2r1'			
	C5/3.1/2r1'.4	NO NO	2r1' 2r1'* <sup>2</sup>			
			-			
C-6	C6/1/40r2.1	NO	≈ 40 <b>r2</b>			
	C6/1/40r2.2 C6/1/40r2.3	NO NO	≈ 40 <b>r2</b> ≈ 40 <b>r2</b>	<del></del>		
L						
	C6/2/80r2	NO	≈ 80 <b>r2</b>			
C-7	C7/2/25r2.1	NO	05- <b>0</b>			
C-7	C7/2/25r2.1	NO NO	≈ 25 <b>r2</b> ≈ 25 <b>r2</b>	<del></del>		
	C7/2/25r2.3	NO	≈ 25 <b>r2</b>			
	C7/2/25r2.4 C7/2/25r2.5	NO NO	≈ 25 <b>r2</b> ≈ 25 <b>r2</b>	<del></del>		
Ī	C7/2/30r2	NO	≈ 30 <b>r2</b>			
L	C1/2/3012	I NO	~ 3012			
C-8	C8/3.1/2r1-2r2-r1-r1'	NO	2r1-2r2*2-r1-r1'			
			12.11 2.12			
C-9	C9/3.1/2r1'.1	NO	2r1'			
	C9/3.1/2r1'.2	NO	2r1'*2			
[	C9/3.1/4r1-r1'-4r1	NO	4r1-r1'-4r1			
C - 10	C10/1/40r2.1	NO	≈ 40 <b>r2</b>			
	C10/1/40r2.2	NO	≈ 40 <b>r2</b>			
1	044/04/2	l No '	12			
C - 11	C11/3.1/4r1-r1'-4r1	NO	4r1*2-r1'-4r1	<del>                                      </del>		
[	C11/3.1/9r1'-r1-r1'	NO	9r1'-r1-r1'			
ſ	C11/1/18r2	NO	18 <b>r2</b>			
·	C11/1/15r2.1	NO	15 <b>r2</b>			
	C11/1/15r2.1	NO NO	15 <b>r2</b>			
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Incompatible strain								
ind <sup>a</sup>	Variant id. <sup>b</sup>	splicing	TR <sup>d</sup>	glycosylation prediction in TR <sup>e</sup>				
				1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35				
-								
IC - 1	IC1/3.1/9r1	NO	9r1*2					
				<del> </del>				
	IC1/3.1/2r1-2r2-r1'	NO	2r1-r2-r2*-r1'					
1	IC1/3.1/2r1.1	NO I	2 <b>r1</b>	<del></del> -				
	IC1/3.1/2r1.2	NO	2r1					
	IC1/3.1/2r1.3	NO	2r1	<del>1 1 1</del>				
	IC1/3.1/2r1.4	NO	2 <b>r1</b>					
				<del></del>				
	IC1/3.1/r1-r1'.1 IC1/3.1/r1-r1'.2	AS AS	r1-r1' r1°-r1'°	111				
	IC1/3.1/r1-r1'.2	AS	r1-r1'*	<del>4-1</del>				
	101/3.1/11-11.3	AS	11-11					
IC - 2	IC2/2/25r2.1	AbS (1)	≈ 25 <b>r2</b> *					
	IC2/2/25r2.2	NO	≈ 25 <b>r2</b>	<del>                                      </del>				
			_					
	IC2/2/15r2	AbS (1)	15 <b>r2</b>	<u>                                     </u>				
l .				<del></del>				
	IC2/2/6r2	NO	6 <b>r2</b>					
			•					
	IC2/2/4r2	AbS (3)	4r2					
•			•					
	IC2/3.1/r1-2r2-r1-r1'.1	NO	r1-2r2°2-r1-r1'					
	IC2/3.1/r1-2r2-r1-r1'.2	NO	r1-2r2-r1-r1'					
	IC2/3.1/r1-2r2-r1-r1'.3	NO	r1-2r2-r1-r1'					
				<del></del>				
	IC2/3.1/2r1-r1'	NO	2r1-r1'	<u> </u>				
IC - 3	IC3/2/40r2	NO	≈ 40 <b>r2</b>					
			•					
	IC3/2/30r2	NO	≈ 30 <b>r2</b>					
l ,	100/0/05 0	l No	1					
]	IC3/2/25r2	NO	≈ 25 <b>r2</b>					

