

	10	20	30	40	50	60	70	80	90	100
transcriptome	TTGCTGTTTAGAATATGGGCGGTATAGTTGGTGCCGGCCTAAGAATATTAATTCCAATTGAATGGGTGAGCCTGGGCCAATTTTCGGGGATGATCACCA									
PS96_310R	G.....C.....C.....									
Ap199.3C										
Ap200.2E										
Ap225.2C										
Ap233.1E										

	110	120	130	140	150	160	170	180	190	200
transcriptome	TATACAATGTAATTGTTACTGCTCATGGCTTTGTAATAATTTTTTTTTGGTGATGCCTATAATAATAGGGGTTTTGGTAACGATTAAATCCGTTAAT									
PS96_310R	...T.....C.....									
Ap199.3C										
Ap200.2E										
Ap225.2C										
Ap233.1E										

	210	220	230	240	250	260	270	280	290	300
transcriptome	ATTAAATAGGCCTGATATAGCTTTTCCACGGCTAAATAATATAAGATTTGGTTATTGCCTCCATCTCTGTCATTATTATTAGGGTCAAGGTTACTAGGA									
PS96_310R	G.....G.....A.....A.....A.....									
Ap199.3C	G.....G.....									
Ap200.2E										
Ap225.2C										
Ap233.1E	G.....									

	310	320	330	340	350	360	370	380	390	400
transcriptome	AGTGGGGCAGGACCGGATGAACAGTATACCCCTCCCTTGCTAAATTAACGAATCATAGAGGCGGGTCGGTCGACATAGTTATTTTTTCTTTGCATATGG									
PS96_310R	T.....									
Ap199.3C										
Ap200.2E	..C.....									
Ap225.2C										
Ap233.1E										

	410	420	430	440	450	460	470	480	490	500
transcriptome	CCGGAGCCAGAAGAATTTTAGCTTCAATTAATTTTATGGTCACATTTTATAATGGGCGGCCTAAAGCTCTAAGATATGATCGAGTAACATATTTATTTG									
PS96_310R	C.....									
Ap199.3C										
Ap200.2E										
Ap225.2C										
Ap233.1E	.T.....M.....									

	510	520	530	540	550	560	570	580	590	600
transcriptome	GTCTATTGTAGTTACGGCTATTTTATTGATTTTAGCATTGCCCGTATTAGCGGGCGCTATTACAATGTTGTTATTTGATCGAAATTTTAGAACATCTTTC									
PS96_310R										
Ap199.3C										
Ap200.2E										
Ap225.2C										
Ap233.1E										

	610	620
transcriptome	TTTGACCCCGCTGGCGGTGGCGATCC	
PS96_310R		
Ap199.3C		
Ap200.2E		
Ap225.2C		
Ap233.1E		