

seed-m8 TCTCACCC	7
hsa-miR-1229-3p CTCTCACCACTGCCCTCCCACAG	23
hsa-mir-1229	GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCAGGGGACACCCTCTCACCACTGCCCTCCCACAG	69
panTro6	GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCGGGGACACCCTCTCAGCGCTGCCCTCCCACAG	69
gorGor6	GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCGGGGACACCCTCTCAGCGCTGCCCTCCCACAG	69
ponAbe3	GTGGGTAGGGTTTGGGGGAGAGCGTGGGCTGGGGTTCGGGGACACCCTCTCAGCGCTGCCCTCCCACAG	69
consensus	*****!!!!!!!!!	