	ATCAAGGGCAGTATCCTTCCCAGTGC·······AAGCAGCCAGCCCTCCTTGATGAGCCCCAGATATCGACAA	Hsap NM_001287 i05	11 1 1 OK
	ATCAAGGACAGTATCCTCCAAAGACA·······CTGCAGTACCTGTCCTTGACCATCCCTGAGACATTGACAA	Mmus NM_011930 i05	11 1 0 OK
	ATCAAGGACAGTATCCTCCAAAGACA·······CATCGGTGTCTGTCCTTGACCATCCCTGAGACATCGACAA	Rnor NM_031568 i05	11 1 0 OK
1111.003	GTGAAGGACAGTATCCTTGCATGCAG·······TAGCAGCCTTTCCTTGATCCTCCTCCACAGACATCGACAA	Ggal chr14_6468177_6468705	11 3 1 OK
	GAGAAGCTGTGTATCCTTTGCGTGGT·······TTTACACTTCCTTAACTGCACGATATTCAGATTTCGGCCT	Hsap NM_002613 i04	11 1 0 OK
	GAAAAGCTGTGTATCCTTTGCATGGT·······TCCATTCTTCCTTAACCACAAAACATTCAGATTTTGGCCT	Mmus NM_011062 i04	11 1 0 OK
	GAAAAGCTGTGTATCCTTTGCATGGT·······TCCACTCTTCCTTAACCACAAAATATTCAGATTTTGGCCT	Rnor NM_031081 i04	11 1 0 OK
1111.006	GAAAAGCTGTGTATCCTTCGAATTCT·······AATACTAGACCTTAACTTCTTAACATTCAGATTTTGGGCT	Ggal chr14_9378542_9379313	11 3 1 OK
	AAATCCAACAGTATCCTTTGGTTGTT·······TTGAAACCAGAGTCCTTAACAAGCATTGAGATATATTTCT	Hsap NM_002880 i13	11 1 0 OK
	AAATCCAACAGTATCCTTTGGTATTG·······AAACTGTCAGTCTCCTTAACAAGCATCGAGATATATTTCT	Mmus NM_029780 i13	11 1 0 OK
	AAATCCAACAGTATCCTTTGGTATTG·······GAACTGTCAGTCTCCTTAACAAGCATTGAGATATATTTCT	Rnor NM_012639 i12	11 1 0 OK
1111.010	AAATCCAATAGTATCCTTTCCTAACT·······TTCTATAGAATTTCTTTAACAGCTGTTTAGATATATTTCT	Ggal chr12_14813831_14814715	11 1 1 OK
	CTTCAGCCTAATATCCTTGGCTTCAT·······TTGCTCAGCTGGATTCCTTAACGCACGCACACCTGAACCT	Hsap NM_012305 i17	11 1 0 OK
	TCAAACTAATATCCTTGCTTAGAGGC·······GTCTGCCTGGACTCCTTAATGCACTCACATCTGAACCTGC	Mmus NM_007459 i16	01 3 1 OK?
	CTTCAAACTAATATCCTTGCTTAGAG·······TTGTCTGCCTGGACTCCTTAATGCACTCACATCTGAACCT	Mmus NM_007459 i16_fixed	11 3 1 OK
	CTTCAGACTAATATCCTTGCTTACCT·······CTGTCTGCCTGTATTCCTTAATGCACTCACATCTGAACCT	Rnor NM_031008 i17	11 2 1 OK
1111.021	CTTCAACCAAATATCCTTAAAGGCAG·······CGTTGATCGGTTTCCTTAGCTACTTTTCATGCCTGAATCT	Ggal chr5_43721038_43722042	11 3 1 OK
	TATGAGCGATATATCCTTTGGACGAG·······TTGCCTGGGATTTCCTTAATTCCCTTGCACTTGTCCTCGT	Hsap NM_016652 i06	11 1 1 OK
	TATGAACGCTATATCCTTTGAATAAG·······CCTGCTCTTTCCTTCACTCCCTGCCCGTACTTGTGCTCGT	Mmus NM_025820 i05	11 2 1 OK
	TATGAACGCTATATCCTTTGAATGAG·······GGTGCCTGCTCTTTCCTTCACTCCCCGCACTTGTGCTCGT	Rnor NM_053797 i05	11 1 1 OK
1111.024	TATGAAAGATATATCCTTTTTTAGTG·······ACTGCTACTGTTTCTTTAACATAGCTCTACTCGTTATTGT	Ggal chr3_3794338_3795173	11 1 1 OK
	GGAAGAGACTGTATCCTTCACAGGGG·······CAGTTGTATTTTCCTCAAGAAACTCCTTAGATATTGATCA	Hsap NM_139069 i06	11 1 2 OK
	GGCACTGACCGTATCCTTCCCCGCGA·······CAGTTGTATTTTCCTCAAGAAACTCCTTAGATATTGATCA	Hsap NM_002752 i06	11 1 2 OK
	GGAAGAGACTGTATCCTTCACAGGGA·······TAGTTGTATTTTCCTCAAGAGAATCCTTAGATATTGATCA	Mmus NM_016961 i07	11 2 2 OK
	GGTACTGACCGTATCCTTCCCCAGAA·······TAGCTGTGTTTTCCTCAAGAGAATCCTTAGATATTGATCA	Rnor NM_017322 i06	11 1 2 OK
1111.030	GGCACCGATCGTATCCTTCCTCACGG·······GTTGGATTTTCCTTAACTCCCAATGTCCAGATATTGACCA	Ggal chr4_44097240_44104143	11 1 0 OK