

1101.056	AGCACCTCCTTATATCCCTTCCAGAG.....AGGCTGCTGTCCCTTAACTCACCACACCTGGAGATCC AGCACCTCCTTATATCCCTTCCAGAG.....GAGATAGCTGCTTAACTCACCACACCTGGAGATCC AGCACCTCCTTATATCCCTTCCAGAG.....GCTGTGATGAGGCTCCTTAACTCACCACACCTGGAGATCC	Hsap NM_001923 i25 Mmus NM_015735 i25 Ggal chr5_53229366_53229366	11 1 0 OK 11 1 1 OK 11 1 0 OK
1101.062	GGAAGGGACTGTATCCTTGTGCTGCT.....GGAGTATTTTCTTAGCTACTTGAATATAGATTATGATCA GGAAGGGACTGTATCCTTGTGCTGCT.....GGAGTATTTTCTTAGCTACTTGAATATAGATTATGATCA GGAAGGGACTGTATCCTTGTGCTGCT.....CACTGTTTCTCTTAGCTGTGTAACTTAAATATATGATCA	Hsap NM_002750 i06 Mmus NM_016700 i07 Ggal chr6_17436831_17439489	11 2 2 OK 11 2 2 OK 11 1 2 OK
1101.063	GGAAGGGACTGTATCCTTGTACCTTT.....TCTTTTCCCTTAAAGTTCATATTCAGATTATGACCA GGAAGGGACTGTATCCTTGTACCTTT.....TCTTTTCCCTTAAAGTTCATATTCAGATTATGACCA GCAACGATCCTGTATCCTTCCCTACGG.....GTGGATTTCCTTAACTCCCAATGTCAGATTATGACCA	Hsap NM_002753 i09 Mmus NM_009158 i07 Ggal chr4_44097240_44104143	11 1 1 OK 11 3 1 OK 11 1 0 OK
1101.065	AGAGAAGATCTATCCTTCTTCTTC.....CCATCTTGGCTTCTTAACTTTCGTTTCAGATTATGACCA AGAGAAGATCTATCCTTCTTCTTC.....TGTGATACCACTTAACTTTCGTTTCAGATTATGACCA TTTGAATGATGATCAGTGCAGGGGGA.....ATCCGAAATATCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_002869 i07 Mmus NM_024287 i07 Ggal chr4_522520_522984	11 1 1 OK 11 1 0 OK 01 2 2 OK?
1101.067	GGATTGCCCTGTATCCTTGGCAGT.....TCTCTTCCGTTCCTTAACTTCTGAACCAGTCTAGCAAT GGATTGCCCTGTATCCTTGGCAGT.....TCTCTTCCGTTCCTTAACTTCTGAACCAGTCTAGCAAT GATCTGCTCCTGTATCCTTCCACCTTT.....GCACTGTTTCCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_003145 i03 Mmus NM_025448 i02 Ggal chrUn_96932473_96933034	11 1 0 OK 11 1 0 OK 11 1 2 OK
1101.069	TTGAGTATGATATCCTTCTTGGCCCA.....TGTGCAATGCTTCTTAACTTTCGTTTCAGATTATGACCA TTGAGTATGATATCCTTCTTGGCCCA.....TGTGCAATGCTTCTTAACTTTCGTTTCAGATTATGACCA TTGAGTATGATATCCTTCTTGGCCCA.....TGTGCAATGCTTCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_003504 i10 Mmus NM_009862 i11 Ggal chr15_660173_660807	11 1 0 OK 01 1 0 OK 10 2 0 OK
1101.072	GACGCTGACTGTATCCTTATTTTGG.....ACTTGTCTATATCTTAACTTTCGTTTCAGATTATGACCA GATGCTGACTGTATCCTTATTTTGG.....ACTTGTCTATATCTTAACTTTCGTTTCAGATTATGACCA GATGCTGACTGTATCCTTATTTTGG.....ACTTGTCTATATCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_003757 i03 Mmus NM_018799 i03 Ggal chr23_1073072_1073801	11 1 1 OK 11 1 1 OK 11 1 1 OK
1101.074	TTTGACAGCTGTATCCTTGAAGCAG.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TTTGACAGCTGTATCCTTGAAGCAG.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TCCATGACAGCTGTATCCTTGAAGCAG.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_004301 i05 Mmus NM_019673 i05 Ggal chr9_17034817_17035724	11 3 1 OK 11 2 1 OK 11 2 2 OK
1101.075	TATGTTAGAGATATCCTTCTTGGCCCA.....TACCCTTAACTTTCGTTTCAGATTATGACCA TATGTTAGAGATATCCTTCTTGGCCCA.....TACCCTTAACTTTCGTTTCAGATTATGACCA TATGTTAGAGATATCCTTCTTGGCCCA.....TACCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_004595 i06 Mmus NM_009214 i06 Mmus NM_009214 i06_fixed Ggal chr1_75870459_75871073	11 3 0 OK 01 2 1 OK? 11 2 1 OK 11 2 1 OK
1101.077	TATCTTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TATCTTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TATCTTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_004632 i05 Mmus NM_022994 i05 Ggal chrE26C13_82869_83508	11 1 1 OK 01 1 1 OK 01 1 0 OK
1101.097	GACGAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GACGAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GATGAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_006598 i23 Mmus NM_011390 i23 Ggal chr11_3397409_3399238 Ggal chr20_10116442_10116901	11 1 1 OK 11 3 1 OK 11 2 0 OK 11 1 0 OK
1101.101	GTTGATCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GTTGATCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GTTGATCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_006773 i13 Mmus NM_025860 i12 Ggal chr7_7737371_7738259 Ggal chr7_7737371_7738259	11 3 1 OK 11 3 0 OK 11 1 1 OK 11 1 1 OK
1101.111	TACTATGTTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TACTATGTTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TACTATGTTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_014060 i04 Mmus NM_026902 i04 Ggal chr4_74501311_74502503	11 3 2 OK 11 1 2 OK 11 1 2 OK
1101.114	GGGAGTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GGGAGTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GGGAGTCTGCTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_014845 i07 Mmus NM_139939 i07 Ggal chr3_43399277_43401571	11 2 1 OK 11 1 2 OK 11 1 1 OK
1101.116	AAGAAAGCTGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AAGAAAGCTGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AAGAAAGCTGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_014970 i07 Mmus NM_010629 i07 Ggal chr8_4995386_4996027 Ggal chrUn_76644081_76644723	11 1 0 OK 11 1 0 OK 11 1 0 OK 11 1 0 OK
1101.119	TTTGGAAATGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TTTGGAAATGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TTTGGAAATGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_015336 i10 Mmus NM_172554 i10 Mmus NM_172554 i10_fixed Ggal chr1_35064335_35071988	11 1 0 OK 01 1 0 OK? 11 1 0 OK 11 1 0 OK
1101.132	CCGAAAGAAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA CCGAAAGAAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA CCGAAAGAAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_018052 i08 Mmus NM_146216 i08 Ggal chr11_1581346_1581798	11 1 2 OK 11 1 2 OK 11 1 2 OK
1101.133	TCCAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TCCAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TCCAGAAGTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_018052 i16 Mmus NM_146216 i16 Ggal chr11_1617479_1619208 Ggal chr11_1617479_1619208_fixed	11 1 0 OK 11 3 0 OK 11 1 0 OK? 11 1 0 OK
1101.136	TACTGTTACAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TACTGTTACAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA TACTGTTACAAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_018142 i15 Mmus NM_027590 i15 Ggal chr4_34616973_34618289	11 1 2 OK 11 1 2 OK 11 2 1 OK
1101.138	ATCAGATACATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA ATCAGATACATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA ATCAGATACATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_018247 i06 Mmus NM_133718 i06 Ggal chr3_79111988_79114287	11 1 2 OK 11 2 2 OK 10 2 0 OK
1101.143	AGACAGATCAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AGACAGATCAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AGACAGATCAATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_021940 i03 Mmus NM_028534 i03 Ggal chr3_27688511_27692611	11 1 1 OK 11 1 1 OK 11 2 1 OK
1101.150	AGTCAATGCTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AGTCAATGCTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA AGTCAATGCTGTATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_024561 i03 Mmus NM_025832 i03 Ggal chr1_158070247_158074115	11 1 0 OK 11 1 0 OK 11 2 0 OK
1101.163	GATAATACAGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GATAATACAGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA GATAATACAGATATCCTTCTTGGCCCA.....TACTTCTTTCCTTAACTTTCGTTTCAGATTATGACCA	Hsap NM_030877 i04 Mmus NM_028580 i04 Ggal chr20_3508778_3512132	11 1 1 OK 11 1 0 OK 11 1 0 OK

1101.169	CACCACTGCCGTATCCTTTTGGCTTC.....GATTCCTAGTCCCTTAATCAATTCCCAACCAGCCCTGGCTAAA	Hsap	NM_032327	i05	11	2	1	OK
	CATCACTGCCGTATCCTTTTGGTCTC.....TGTTCCTTCCCTTAATGATTCCTTCAGGAGCCCTGGCTAAA	Mmus	NM_023740	i06	11	2	1	OK
	CACCACTGCCGTATCCTTCAAGAGTA.....ACAGTTCAGTCCCTTAAGCCAGAGGAGCCCTGGCTCAA	Ggal	chr6_12423980_12424336		11	1	2	OK
1101.182	AGCAGCAATAGTATCCTTTAAAAAAA.....TTGTTTGATGCTCCATAACTCCATATTAGATAACTTTT	Hsap	NM_152905	i02	11	1	1	OK
	AGCAGCAATAGTATCCTTTAAAAAAA.....CTGCTTTGATGCTGCTTAAGTCTTCATTTAGATAACTTTCT	Mmus	NM_008682	i02	11	2	1	OK
	GCAGCAATAGTATCCTTTAAGGCTT.....TACAGTTATGTCCATAACTTGTCACTAAGATAGCTTCT	Ggal	chr1_42833877_42835893		11	1	1	OK
1101.183	GGATGCTGATGTATCCTTTCCTGGT.....ATTATGTTCTTAACGTGGAATTTCTTAGCTGATGAAA	Hsap	NM_152991	i04	11	2	1	OK
	AGATGCTGATGTATCCTTTCTCAAT.....ATTANGTTCTTAACGTGGATTTCCTCAGCAGATGAAA	Mmus	NM_021876	i04	11	2	1	OK
	GGATGCTGATGTATCCTTTAAATAA.....CTCTCTGTTGTTCCCTTAAGATGAGATGTAGCAGATGAAA	Ggal	chrUn_146990432_146991360		11	1	0	OK
	GGATGCTGATGTATCCTTTAAATAA.....CTCTCTGTTGTTCCCTTAAGATGAGATGTAGCAGATGAAA	Ggal	chrUn_97137162_97138090		11	1	0	OK
1101.184	CITTTGCAATGTATCCTTCAAAACAT.....GTGGTTTTTCCTGAACTTTCCTTCTGCAGCAAAGTTCTA	Hsap	NM_153354	i05	11	1	1	OK
	CITTTGCAATGTATCCTTCAAAACAT.....GTGGTTTTTCCTGAACTTTCCTTCTGCAGCAAAGTTCTA	Mmus	NM_175187	i05	11	1	1	OK
	CITTTGCAATGTATCCTTCTCTGTT.....TAAALTTTCCTTGAACTTTTCTTCTGCTAGTAAAGGTAATG	Ggal	chrUn_156584238_156588825		11	2	0	OK