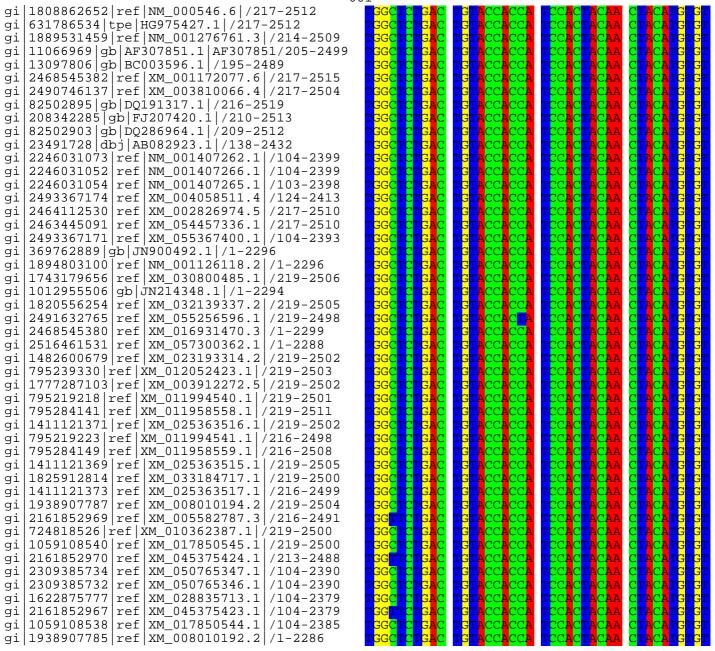
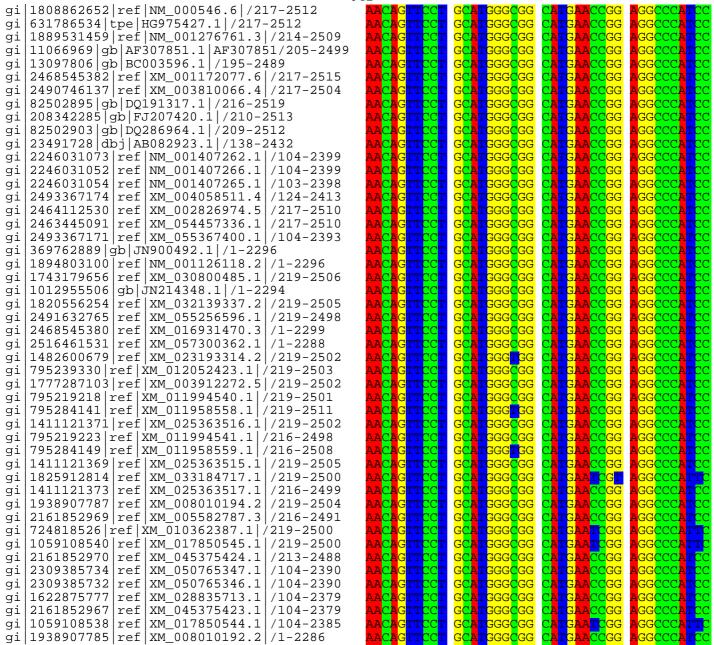
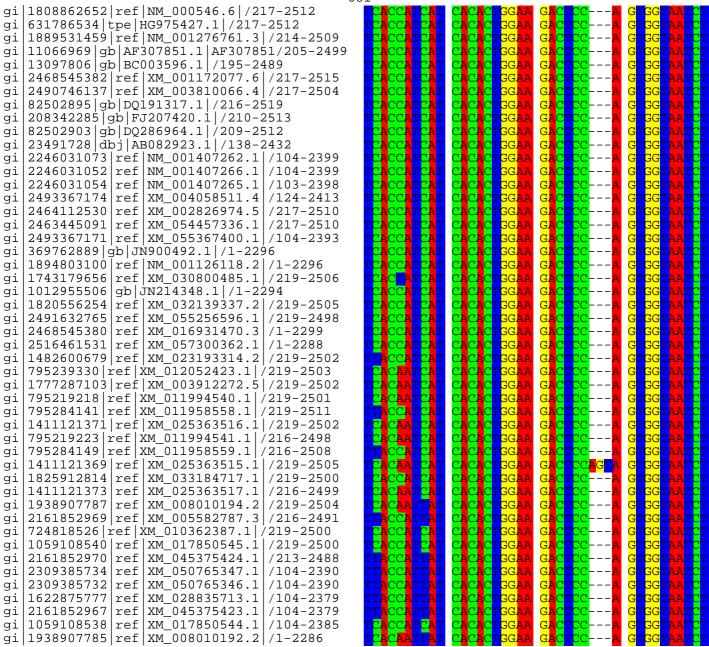


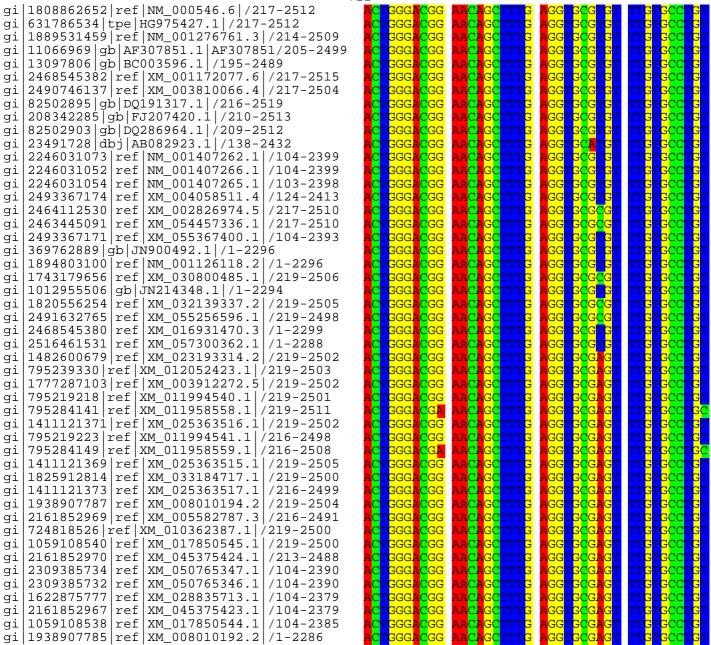
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gi	1808862652 ref NM_000546.6 /217-2512	GGAAA <mark>TTT</mark> GC	CTCTCCACTA	TTTCCATCAC	ACAAACACTT					
					2 (2 2 2 2 (2 2 2 2 2 2 2 2 2 2 2 2 2 2					
gı	631786534 tpe HG975427.1 /217-2512	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGAGTA</mark>	TTTGGATGAC	AGAAACACTTI					
gi	1889531459 ref NM_001276761.3 /214-2509	GGAAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CA CTT					
gi	11066969 gb AF307851.1 AF307851/205-2499	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT					
gi	13097806 gb BC003596.1 /195-2489	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTT <mark>GGA</mark> TGAC	A <mark>GAAA</mark> CAC <mark>TT</mark>					
qi	2468545382 ref XM 001172077.6 /217-2515	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTTGGATGAC	AGAAA CA CTT					
gi	2490746137 ref XM 003810066.4 /217-2504	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT					
	· · · · · · · · · · · · · · · · · · ·		GIGIGGAGIA		AGAAACACTI					
gı	82502895 gb DQ191317.1 /216-2519	GGAAA <mark>TTTGC</mark>	GIGIAGIA	TTT <mark>GGA</mark> TGAC	AGAAACACITT					
gi	208342285 gb FJ207420.1 /210-2513	GTAAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	82502903 gb DQ286964.1 /209-2512	GGAAA <mark>TTTGC</mark>	CTCTCCACTA	TTTGGATGAC	ACAAA <mark>CACTT</mark>					
9.			GIGIGGAGIA		AGAAACACTI					
gi	23491728 dbj AB082923.1 /138-2432	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGAGTA</mark>	TTTGGATGAC	A <mark>GAAA</mark> CACTT					
gi	2246031073 ref NM 001407262.1 /104-2399	GGAAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	2246031052 ref NM 001407266.1 /104-2399	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT					
	I I — I				AGAAA CACTT					
gi	2246031054 ref NM_001407265.1 /103-2398	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGAGTA</mark>	TTT <mark>GGA</mark> T <mark>GA</mark> C	AGAAACACTTI					
gi	2493367174 ref XM 004058511.4 /124-2413	GGAAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	2464112530 ref XM 002826974.5 /217-2510	GGAAA <mark>TTT</mark> GC	G <mark>TGTGGAGTA</mark>	TTTGGATGAC	ACAAA <mark>CACTT</mark>					
			CHCHCCAC		A CA A A CA CHIL					
gi	2463445091 ref XM_054457336.1 /217-2510	GGAAA <mark>TTTGC</mark>	GIGIGGAGIA	TTTGGATGAC	AGAAACACTT					
gi	2493367171 ref XM_055367400.1 /104-2393	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	369762889 gb JN900492.1 /1-2296	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAA <mark>CACTT</mark>					
	1									
gi	· · · · · · · · · · · · · · · · · · ·	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTTGGATGAC	AGAAA CA CTT					
gi	1743179656 ref XM_030800485.1 /219-2506	GGCAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	1012955506 gb JN214348.1 /1-2294	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT					
	1820556254 ref XM 032139337.2 / 219-2505				A CA A A CA CITIT					
gi			GTGTGGAGTA		AGAAACACII					
gi	2491632765 ref XM_055256596.1 /219-2498	GGCAATTTGC	GTGTGGAGTA	TTT <mark>GGATGA</mark> C	A <mark>GAAA</mark> CAC <mark>TT</mark>					
gi	2468545380 ref XM 016931470.3 /1-2299	GGAAATTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAA CACTT					
gi	2516461531 ref XM 057300362.1 /1-2288	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTTGGATGAC						
					AGAAACACTI					
gi	1482600679 ref XM_023193314.2 /219-2502	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTTGGATGAC	AGAAA <mark>CACTT</mark>					
gi	795239330 ref XM_012052423.1 /219-2503	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCCGATGAC	AGAAA CACTT					
gi	1777287103 ref XM_003912272.5 /219-2502	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCGGATGAC	AGAAACAC <mark>TT</mark>					
	· · · · · · · · · · · · · · · · · · ·				ACARACACTI					
gi	795219218 ref XM_011994540.1 /219-2501	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGA</mark> GTA	TTC <mark>AGATGA</mark> C	AGAAACACTT					
gi	795284141 ref XM_011958558.1 /219-2511	GGAAA <mark>TTTG</mark> C	ATGTGGAGTA	TTCGGATGAC	AGAAA CACTT					
gi	1411121371 ref XM 025363516.1 /219-2502	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTCGGATGAC	AGAAACAC <mark>TT</mark>					
	· · · · · · · · · · · · · · · · · · ·									
дi	795219223 ref XM_011994541.1 /216-2498	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TT <mark>CAGATGA</mark> C	AGAAACACTT					
gı	795284149 ref XM_011958559.1 /216-2508	GGAAA <mark>TTT</mark> GC	ATGTGGAGTA	TTCGGATGAC	AGAAA CACTT					
gi	1411121369 ref XM 025363515.1 /219-2505	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTCGGATGAC	AGAAACACTT					
	1825912814 ref XM 033184717.1 /219-2500	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA		AGAAA <mark>CACTT</mark>					
gi	, , <u> </u>			TTCGGATGAC						
gi	1411121373 ref XM_025363517.1 /216-2499	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGAGTA</mark>	TTCGGATGAC	A <mark>GAAA</mark> CACTT					
gi	1938907787 ref XM 008010194.2 /219-2504	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCGGATGAC	AGAAA CACTT					
gi	2161852969 ref XM 005582787.3 /216-2491	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCGGATGAC	ACAAA <mark>CACTT</mark>					
	,				ACARACACTI					
gı	724818526 ref XM_010362387.1 /219-2500	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTCGGATGAC	AGAAACAC <mark>TT</mark>					
gi	1059108540 ref XM_017850545.1 /219-2500	GGAAA <mark>TTT</mark> GC	G <mark>TG</mark> TGGAG <mark>TA</mark>	TTCGGATGAC	A <mark>G</mark> AAA <mark>CAC</mark> TT					
gi	2161852970 ref XM_045375424.1 /213-2488	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCGGATGAC	AGAAACACTT					
			CTCTCCACTA		A CA A A CA CEE					
gi	2309385734 ref XM_050765347.1 /104-2390	GGAAA <mark>TTTGC</mark>	GTGTGGAGTA	TTCGGATGAC	A <mark>GAAA</mark> CACTT					
gi	2309385732 ref XM_050765346.1 /104-2390	GGAAA <mark>TTT</mark> GC	G <mark>TGTGGAGTA</mark>	TTCGGATGAC	A <mark>G</mark> AAA <mark>CACTT</mark>					
gi	1622875777 ref XM 028835713.1 /104-2379	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTCGGATGAC	AGAAA <mark>CACTT</mark>					
	2161852967 ref XM_045375423.1 /104-2379	GGAAATTTGC		TTCGGATGAC						
gi			GTGTGGAGTA		AGAAACACTT					
gi	1059108538 ref XM_017850544.1 /104-2385	GGAAA <mark>TTTGC</mark>	G <mark>TGTGGAGTA</mark>	TTCGGATGAC	A <mark>GAAA</mark> CACTT					
qi	1938907785 ref XM 008010192.2 /1-2286	GGAAA <mark>TTT</mark> GC	GTGTGGAGTA	TTCGGATGAC	AGAAA <mark>CACTT</mark>					

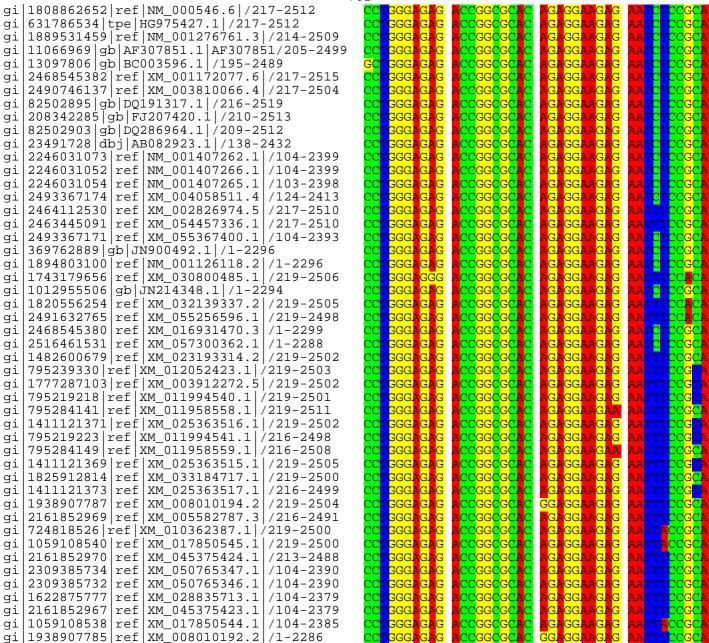


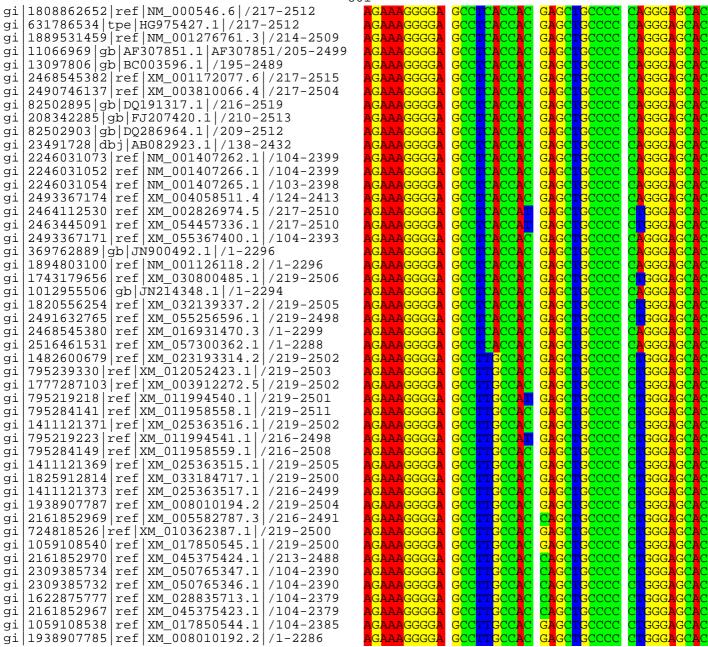


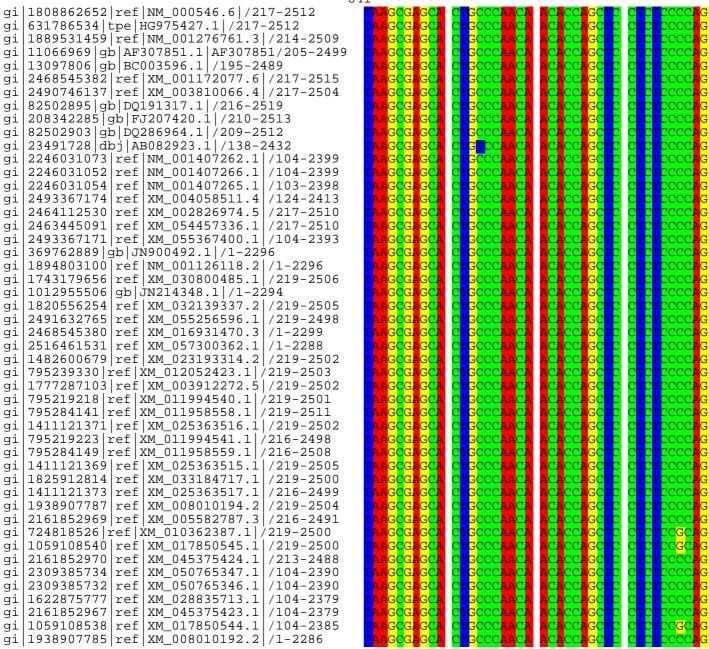


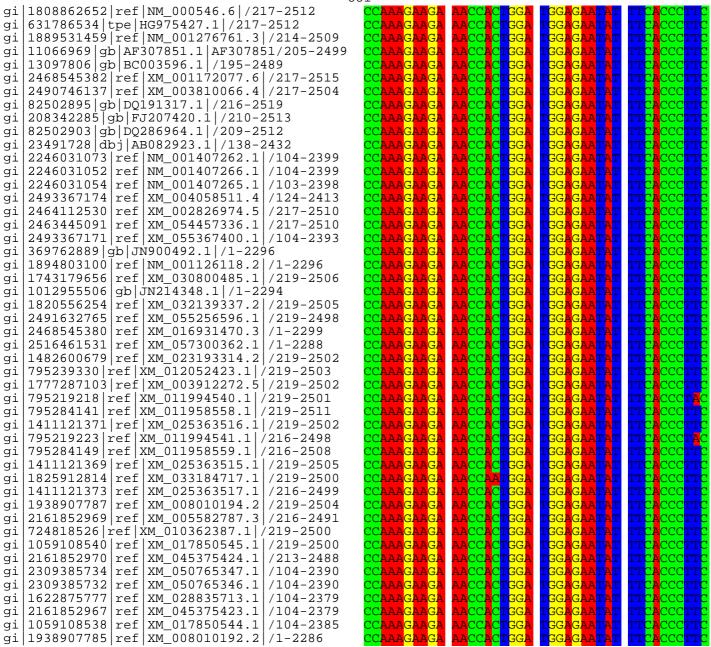




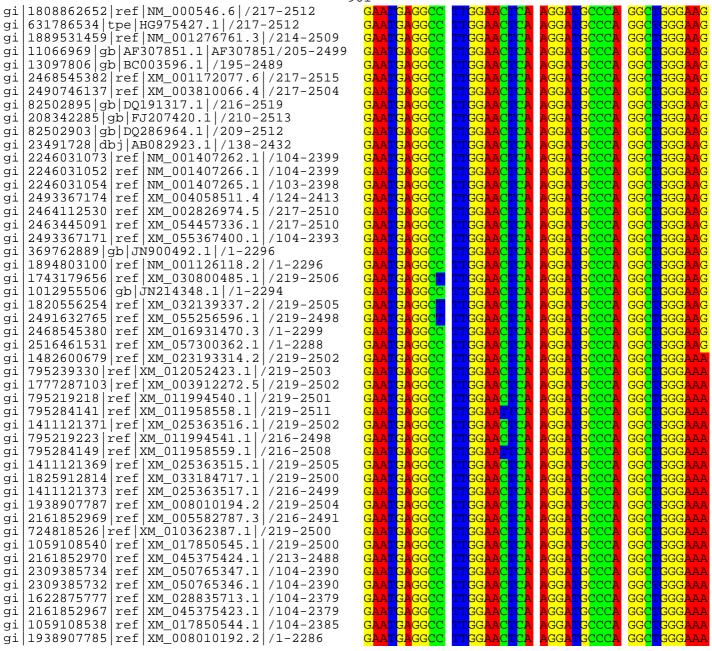


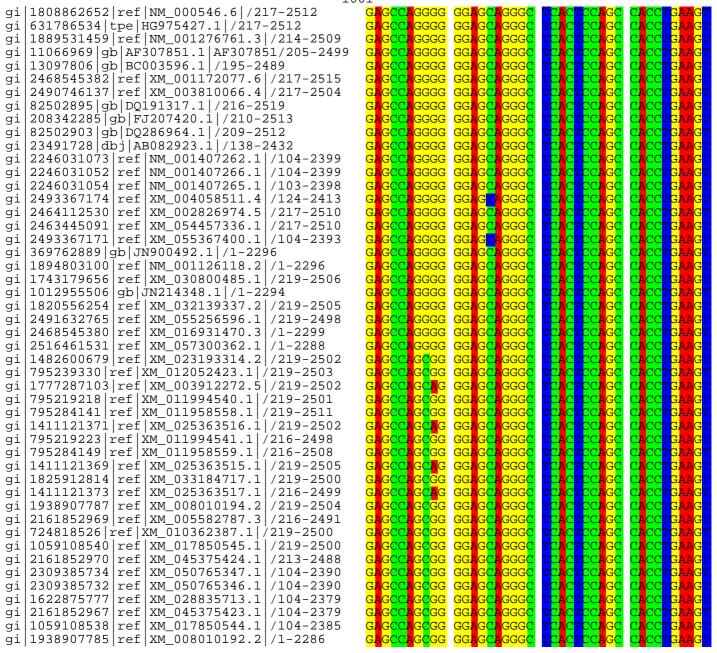


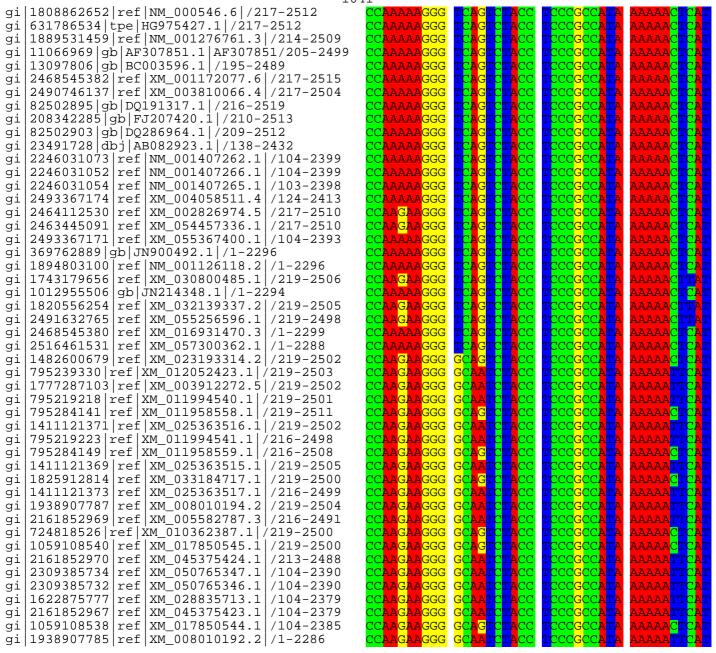


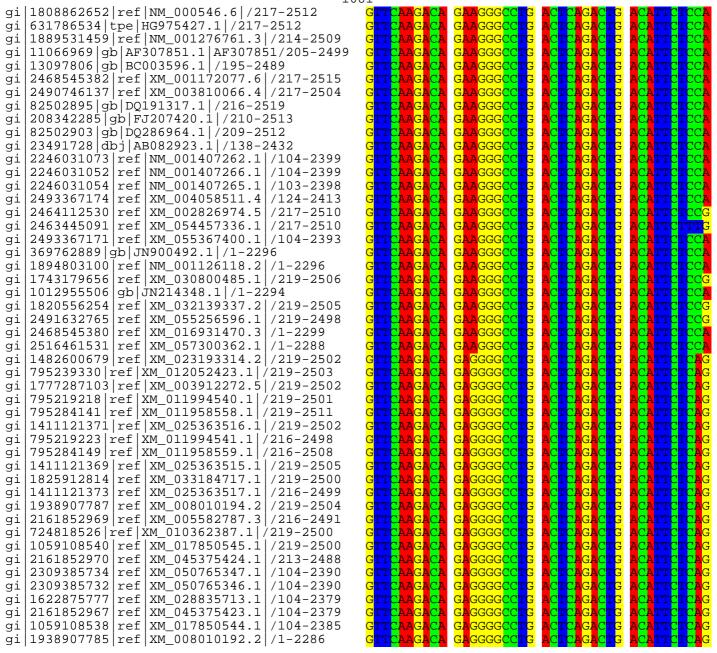


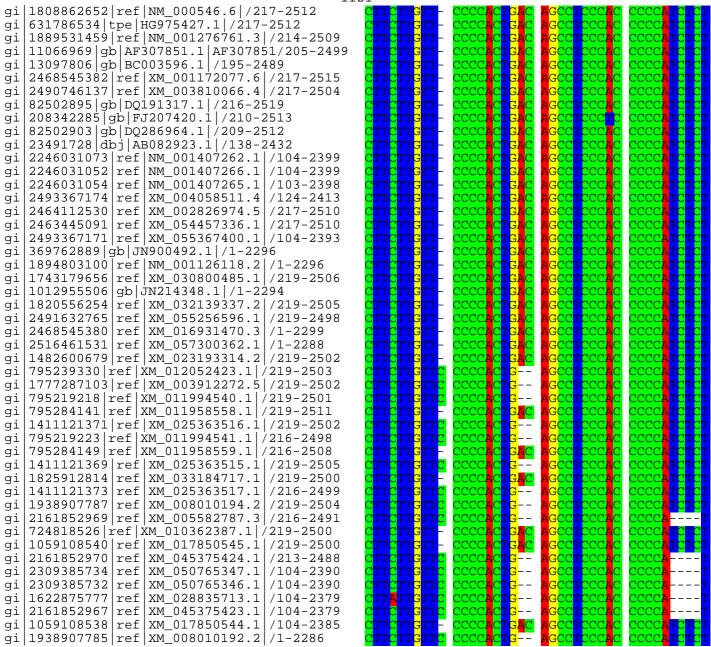


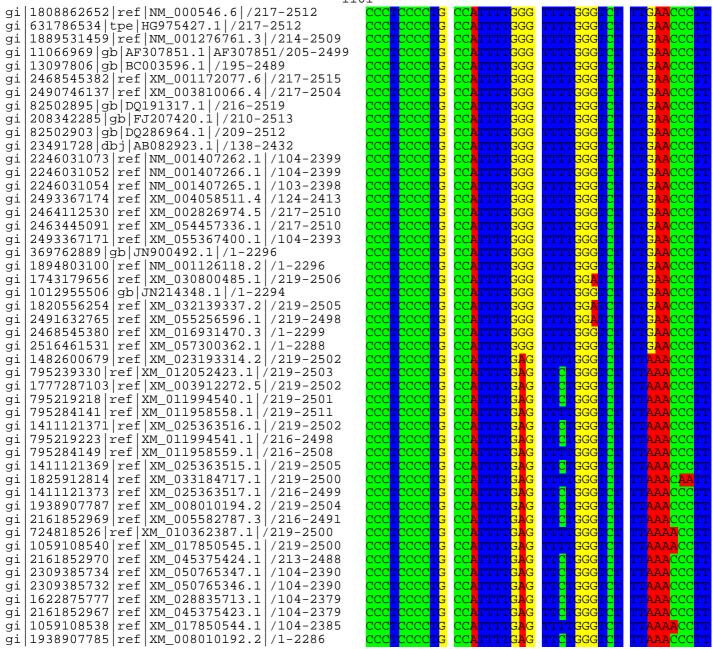


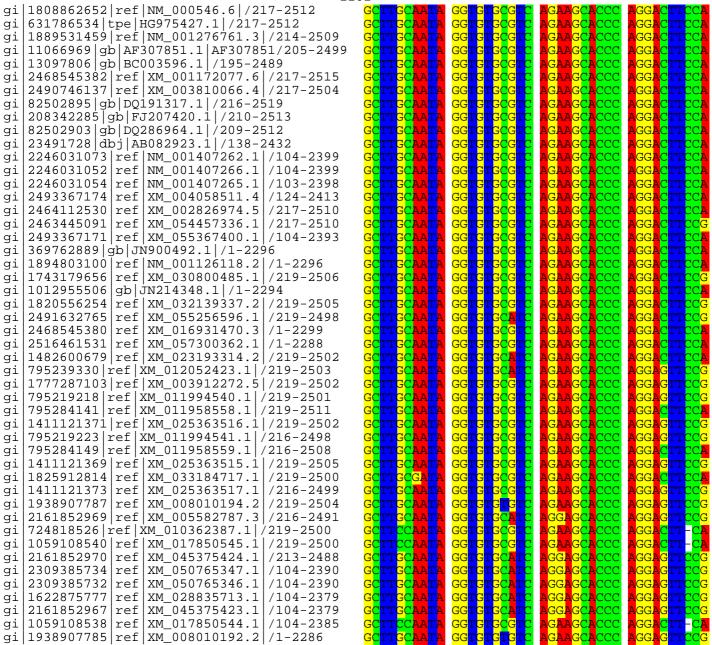


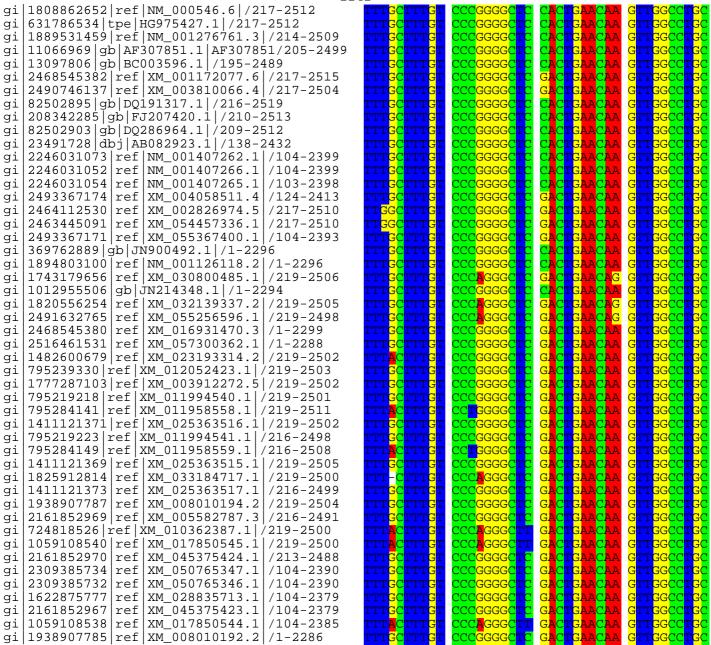




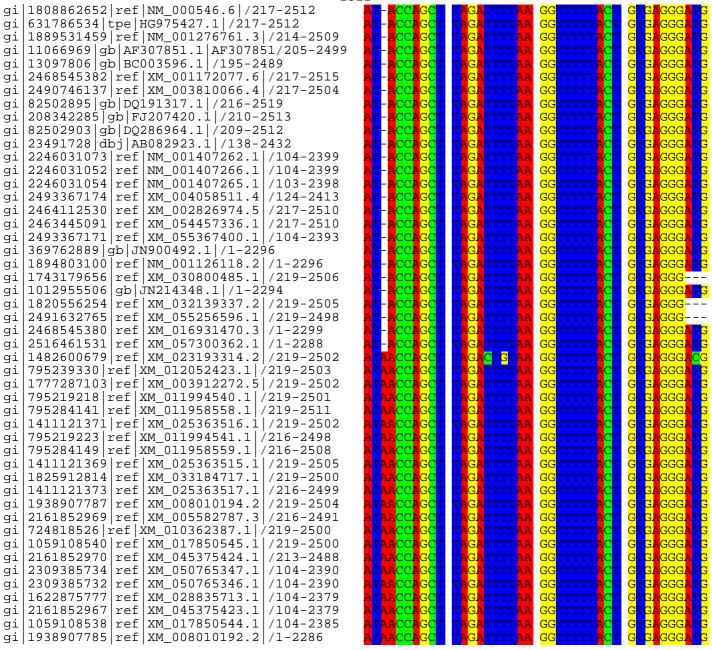


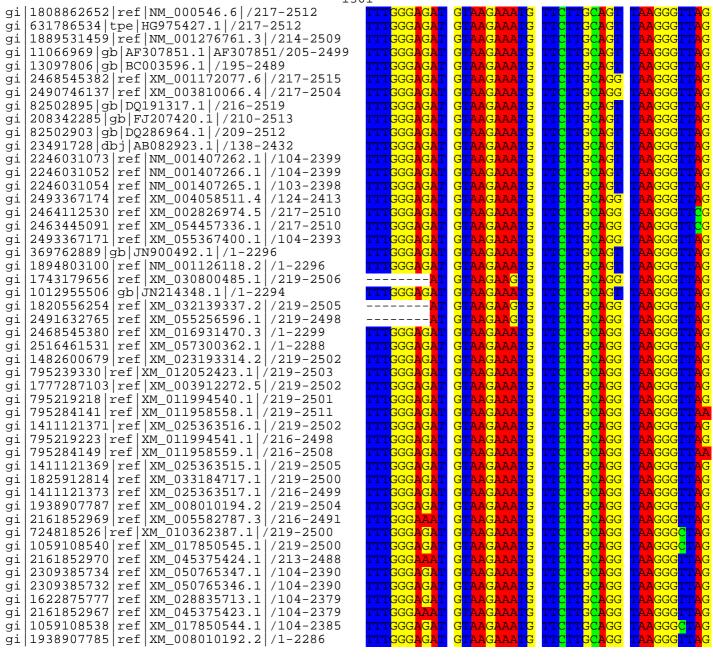


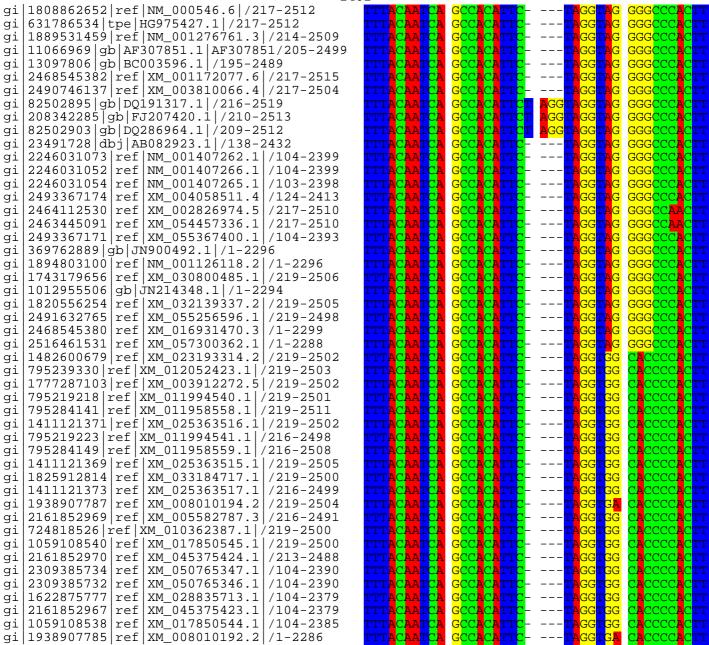


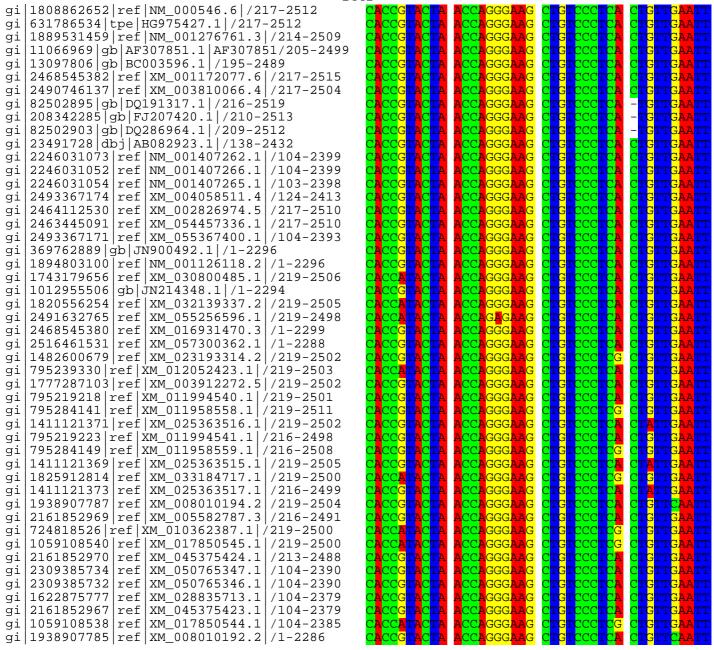


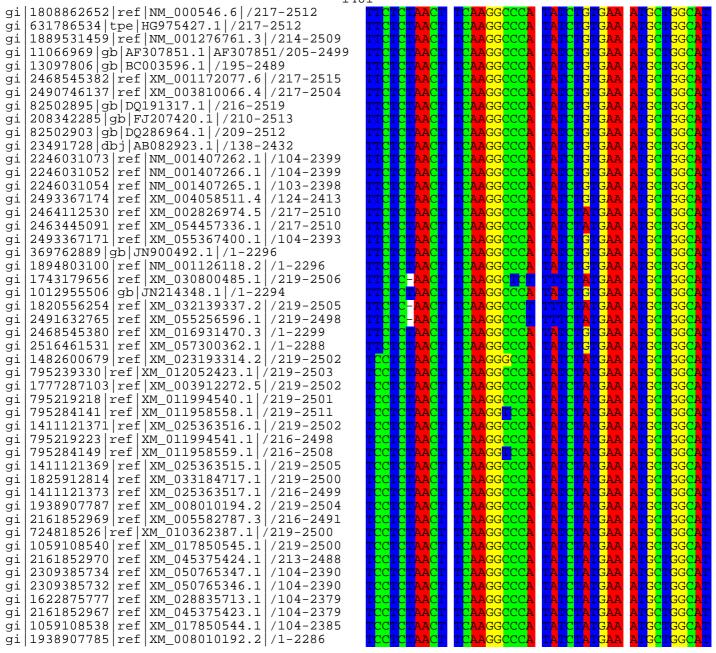
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1 189531459 ref NM_001276761.3 /214-2509			ACTGGTGTTT			
1 1889531459 ref NM_001276761.3 /214-2509 ci	gi	631786534 tpe HG975427.1 /217-2512	ACTGGTGTTT	TGTTGTGGGG .	AGGAGGA <mark>T</mark> GG GG <i>I</i>	G <mark>TA</mark> GGAC
11066969 gi Ar307851.1 Ar307851/205-2499 ci		1889531459 ref NM 001276761.3 / 214-2509	ACTGGTGTTT	TGTTGTGGGG	AGGAGGA <mark>T</mark> GG GG	GTAGGAC
13097806 g BC003596.1 195-2489			A CTCCTCTTT	TCTTCTCCCC	ACCACCATEC CCA	CTACCAC
1						
1 2490746137 ref XM_003810066.4 /217-2504 COGGCCTT COGGGGGGG GG.GGGGTG GG.GG.GGG GG.GGGTG GG.GG.GG GG.GGGTG	· .					
1	gı		ACTGGTGTTT			
1	gi	2490746137 ref XM_003810066.4 /217-2504	ACTGGTGTTT	TGTGGTGGGG .	A <mark>GGA</mark> GGA <mark>T</mark> GG GG	G <mark>TA</mark> GGAC
1	αi	82502895 ab D0191317.1 / 216-2519	ACTCCTCTTT	TGTTGTGGGG	AGGAGGA <mark>T</mark> GG GGZ	GTAGGAC
1						
13491728						
1246031052 ref NM_001407266.1 /104-2399 ref						
gi 2246031052 ref NM_001407265.1 /104-2398 cTGGTGTTT GTTGTGGGG GG_GGLTGGAC GG_GGLTGGAC	gi	23491728 dbj AB082923.1 /138-2432	ACTGGTGTTT	TGTTGTGGGG .	A <mark>GGA</mark> GGA <mark>T</mark> GG GG <i>I</i>	G <mark>TA</mark> GGAC
gi 2246031052 ref NM_001407265.1 /104-2398 cTGGTGTTT GTTGTGGGG GG_GGLTGGAC GG_GGLTGGAC	gi	2246031073 ref NM_001407262.1 /104-2399	ACTGGTGTTT	TGTTGTGGGG .	A <mark>GGA</mark> GGA <mark>T</mark> GG GG	G <mark>TA</mark> GGAC
1		2246031052 ref NM 001407266.1 /104-2399	ACTCCTCTTT	TGTTGTGGGG	AGGAGGA <mark>T</mark> GG GGZ	GTAGGAC
12493367174 ref XM_002826974.5 /217-2510 CTGCGTTT CTTT GGG AGG.GG.TG GG.CT. GGAC GG.GT. GGAC GG.CT. GGAC GG.GT. GGAC G		· · · · - · · · · · · · · · · · · · · ·				
12464112530 ref XM_002826974.5 /217-2510 2673675771 GTTGTGGGG GGGGTGG GGGTTGGGGT GGGTTGGGT GTTGTGGGG GGGTGGGGTTGGGT GGTGGGTTT GTTGTGGGG GGGGTGGGGTTGGGGT GGGTTGGGT GGGTTGGGT GGGTTGGGGT GGGTTGGGGT GGGTTGGGGT GGGTTGGGT GGGTTGGGGT GGGTTGG	91					
2463445091 ref XM_055367400.1 /104-2393						
1493367171 ref XM_055367400.1 7104-2393 369762889 3b ymb00492.1 71-2296 1894803100 ref XM_030800485.1 71-2296 3193487175556 3b ymb1214348.1 71-2294 31820556254 ref XM_0318037.2 7219-2505 3182556596 3b ymb1214348.1 71-2294 31820556254 ref XM_03133337.2 7219-2505 3182556596 31825566596 31825566596 31825566596 31825566596 31825566596 31825666666 3182566666 3182566666 3182566666 3182566666 31825666666 3182566666 31825666666 31825666666 31825666666 31825666666 31825666666 31825666666 318256666666666 31825666	gi	2464112530 ref XM_002826974.5 /217-2510	ACTGGTGTTT	TGTTGTGGGG .	A <mark>GGA</mark> GGA <mark>T</mark> GG GG <i>I</i>	G <mark>TA</mark> GGAC
2493367171 ref xm_055367400.1 /104-2393 36762889 gb JN900492.1 /1-2296 1894803100 ref Nm_001126118.2 /1-2296 1894803100 ref Nm_0030800485.1 /219-2506 gi 1743179656 ref xm_030800485.1 /219-2505 182595506 gb JN214348.1 /1-2294 2491632765 ref xm_032139337.2 /219-2505 2491632765 ref xm_055256596.1 /219-2498 2488545380 ref xm_055256596.1 /219-2498 2488545380 ref xm_057300362.1 /1-2288 ref xm_057300362.1 /1-2288 ref xm_00530362.1 /219-2502 ref xm_00331470.3 /12299 2491632765 ref xm_00331470.3 /12299 2491632765 ref xm_00530362.1 /219-2502 ref xm_00530362.1 /219-2503 ref xm_003912272.5 /219-2502 ref xm_00194540.1 /219-2501 ref xm_011994540.1 /219-2501 ref xm_011994541.1 /216-2498 ref xm_011994541.1 /216-2498 ref xm_011994541.1 /216-2498 ref xm_011994541.1 /216-2498 ref xm_0033184717.1 /219-2500 ref xm_005363515.1 /219-2500 ref xm_005863515.1 /219-2500 ref xm_00586374.1 /216-2499 ref xm_00586377.3 /216-2499 ref xm_00586377.3 /216-2499 ref xm_00586377.3 /216-2499 ref xm_00586377.3 /216-2500 ref xm_00586377.3 /216-2500 ref xm_00586377.3 /216-2500 ref xm_0058637.3 /216-2500 ref xm_0058637.3 /216-2499 ref xm_0058637.3 /216-2500 ref xm_0058637.3 /216-2499 ref xm_0058637.3 /216-2499 ref xm_0058637.3 /21	gi	2463445091 ref XM_054457336.1 /217-2510	ACTGGTGTTT	TGTTGTGGGG	A <mark>GGA</mark> GGA <mark>T</mark> GG GG	G <mark>TA</mark> GGAC
		2493367171 ref xm 055367400 1 /104-2393	ACTCCTCTTT	TCTTCTCCCC	AGGAGGA <mark>T</mark> GG GGZ	GTAGGAC
189480310		,				
1743179656						
gi 1012955506 gb \[\bar{J}\text{N2}\]14348.1 \/1-2294	· .					
1820556254 ref XM_032139337.2 /219-2505 XCTGGTGTTT TGTTGTGGGG AGGAGGATGG GGAGGATGG GGAGGATGG GGAGGATGG C468845380 ref XM_016931470.3 /1-2298 ACTGGTGTTT TGTTGTGGGG AGGAGGATGG GGAGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC GGAGGATGG GGAGGATGG GGGGTAGGAC GGAGGATGG GGAGGATGG GGGGTAGGAC GGAGGATGG	gi	l	ACTGGTGTTT	TGTTGTGGGG .	a <mark>gga</mark> gga <mark>t</mark> gg gga	G <mark>TA</mark> GGAC
1820556254 ref XM_032139337.2 /219-2505 ACTGGTG TIT TGTGGGG GGGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC GGAGGATGG GGGGTAGGAC	gi	1012955506 gb JN214348.1 /1-2294	ACTGGTGTTT	TGTTGTGGGG	A <mark>GGA</mark> GGA <mark>T</mark> GG GG	G <mark>TA</mark> GGAC
gi		1 ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' ' '	ACTCCTCTTT	TGTTGTGGGG	AGGAGGA <mark>T</mark> GG GGZ	GTAGGAC
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gi		1 1 -				
Gelocation Gel	gı					
Gelocation Gel	gi	2516461531 ref XM_057300362.1 /1-2288	ACTGGTGTTT	TGTGGTGGGG .	agg <mark>a</mark> gga <mark>t</mark> gg gga	G <mark>TA</mark> GGAC
gi 795239330 ref XM_012052423.1 /219-2503 gi 1777287103 ref XM_013912272.5 /219-2502 gi 795219218 ref XM_011994540.1 /219-2501 gi 1795284141 ref XM_011958558.1 /219-2501 gi 1795284141 ref XM_025363516.1 /219-2502 gi 795219223 ref XM_011994541.1 /216-2498 gi 795219223 ref XM_011994541.1 /216-2498 gi 1411121369 ref XM_025363515.1 /219-2505 gi 1411121373 ref XM_025363515.1 /219-2505 gi 1411121373 ref XM_025363515.1 /219-2505 gi 12398907787 ref XM_008010194.2 /219-2504 gi 12161852969 ref XM_017850545.1 /219-2500 gi 2161852970 ref XM_017850545.1 /219-2500 gi 2309385734 ref XM_045375424.1 /213-2488 gi 2309385737 ref XM_050765347.1 /04-2390 gi 1622875777 ref XM_028357313.1 /04-2379 gi 1059108548 ref XM_017850544.1 /104-2385		1482600679 ref XM 023193314.2 /219-2502	ACTGGTGTTT	TGTTGTGGGG	AGG <mark>A</mark> GG <mark>AT</mark> GG GGG	GTAGGAC
gi 1777287103 ref XM_003912272.5 /219-2502 gi 795219218 ref XM_011994540.1 /219-2501 gi 795219223 ref XM_011958558.1 /219-2502 gi 795219223 ref XM_011994541.1 /216-2498 gi 795284149 ref XM_011958559.1 /216-2508 gi 1411121369 ref XM_011958559.1 /219-2505 gi 1411121373 ref XM_025363515.1 /219-2505 gi 1411121373 ref XM_025363515.1 /219-2505 gi 1411121373 ref XM_033184717.1 /219-2505 gi 1411121373 ref XM_008010194.2 /219-2504 gi 1938907787 ref XM_008010194.2 /219-2504 gi 2161852969 ref XM_017850545.1 /219-2500 gi 1059108540 ref XM_017850545.1 /219-2500 gi 2309385734 ref XM_045375424.1 /213-2488 gi 2309385732 ref XM_050765346.1 /104-2390 gi 1622875777 ref XM_050765346.1 /104-2379 gi 2161852967 ref XM_045375423.1 /104-2379 gi 1059108538 ref XM_045375423.1 /104-2379 gi 2161852967 ref XM_045375423.1 /104-2379 gi 1059108538 ref XM_045375423.1 /104-2379 gi XM_045375423.1 /104-2379 gi XM_045375423.1 /104-2379 gi XM_045375423.1 /104-2385 XM_045375423.1			ACTCCTCTTT	TGTTGCGGGG		
Type						
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gi 2161852969 ref XM_005582787.3 /216-2491 ACTGGTGTTT TGTTGTGGGG AGGAGGATGG AGGA	gi	1411121373 ref XM_025363517.1 /216-2499	ACTGGTGTTT	TGTTGCGGGG	A <mark>GGA</mark> GGA <mark>T</mark> GG GGG	G <mark>TA</mark> GGAC
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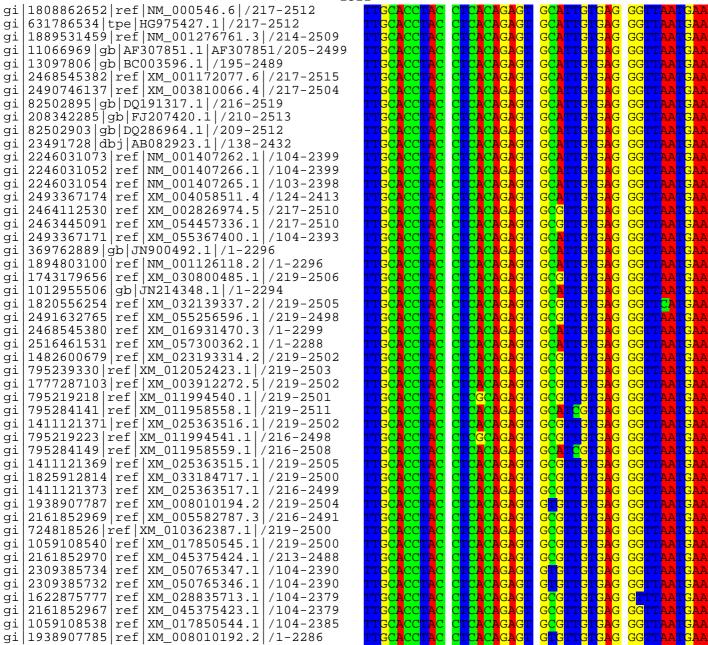


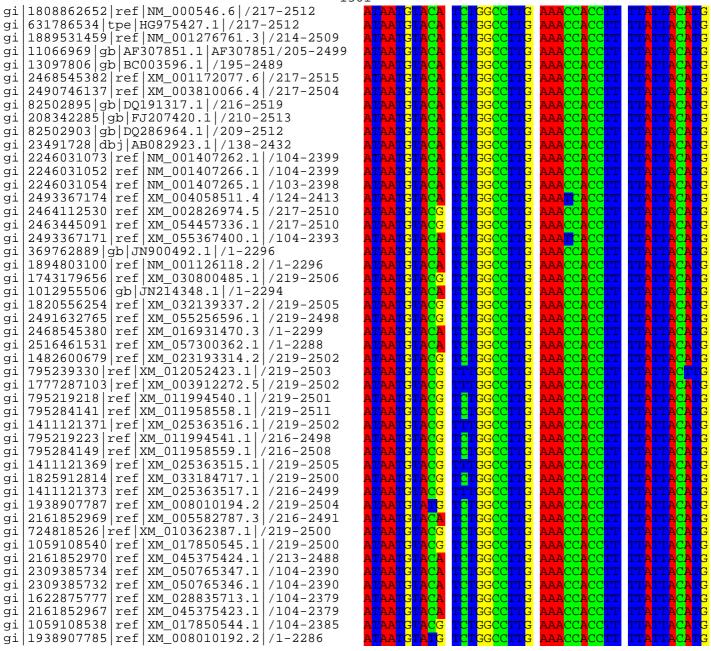


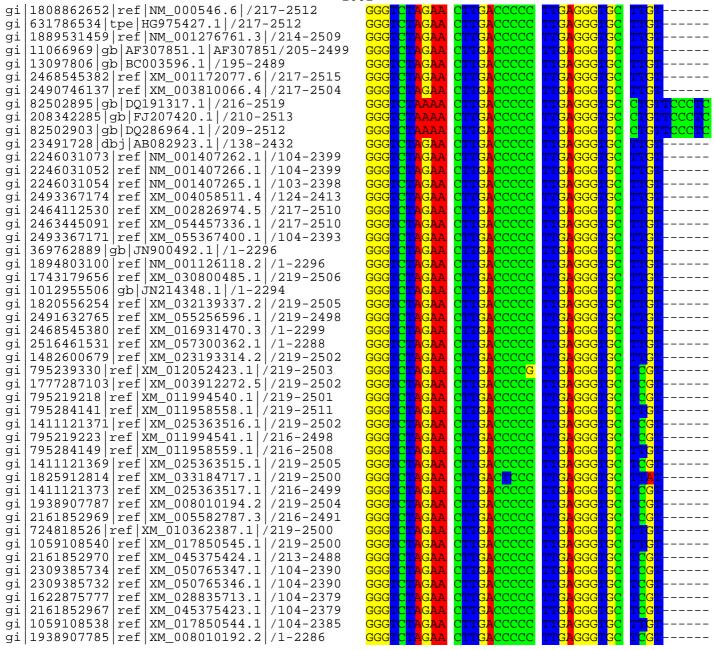


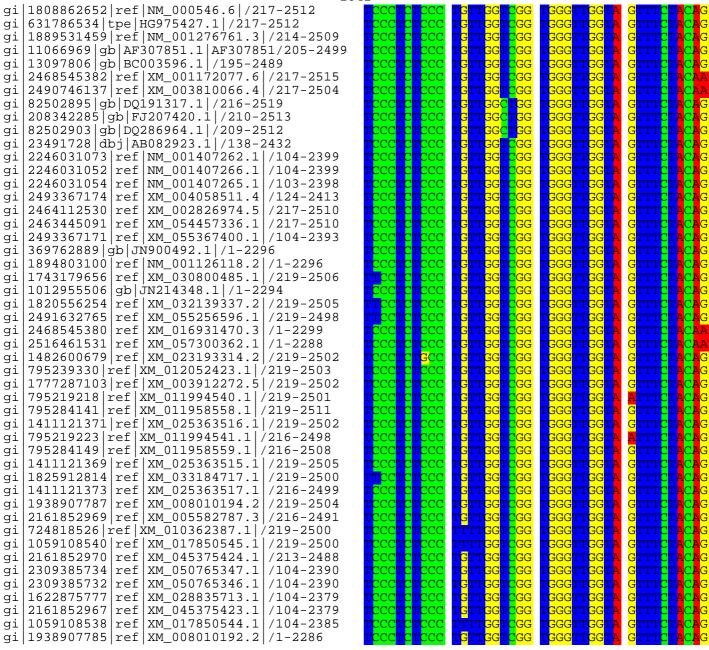


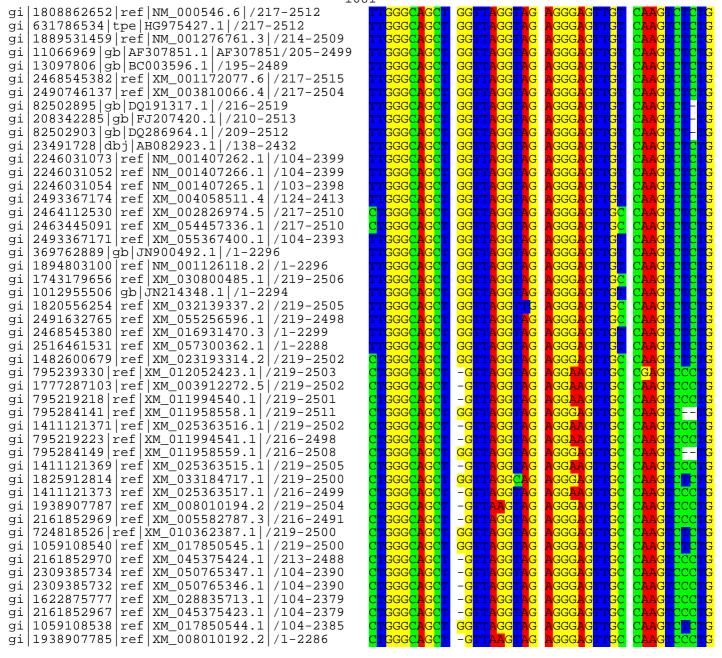


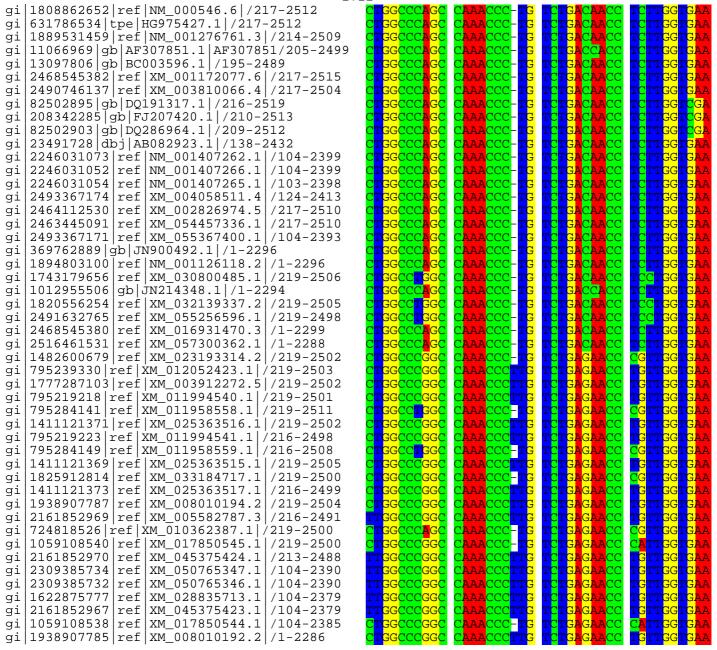


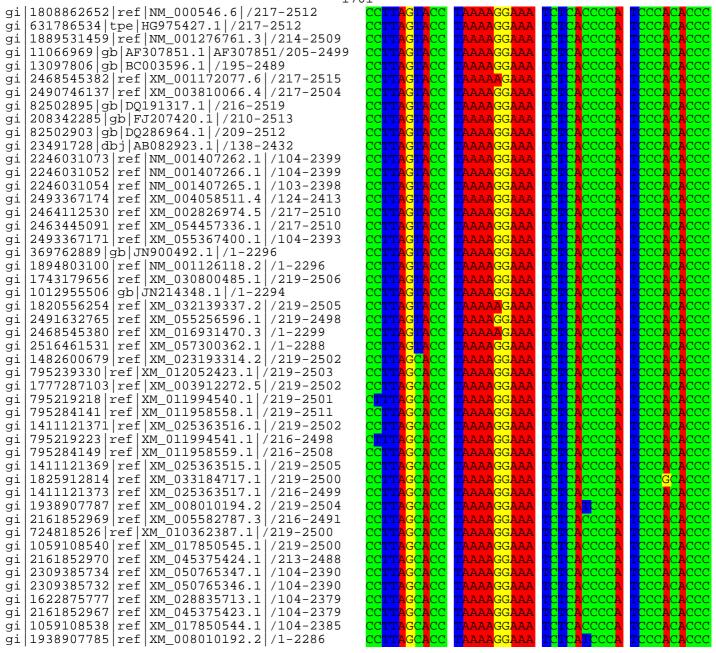


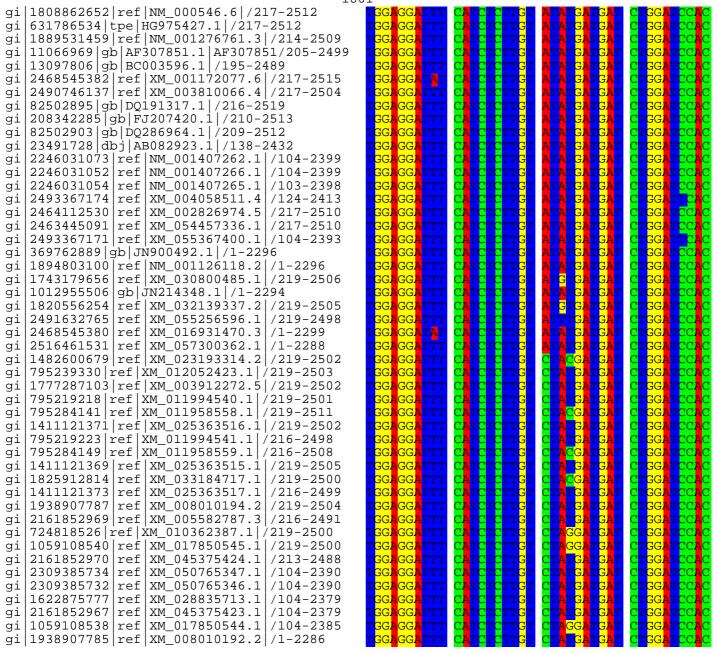


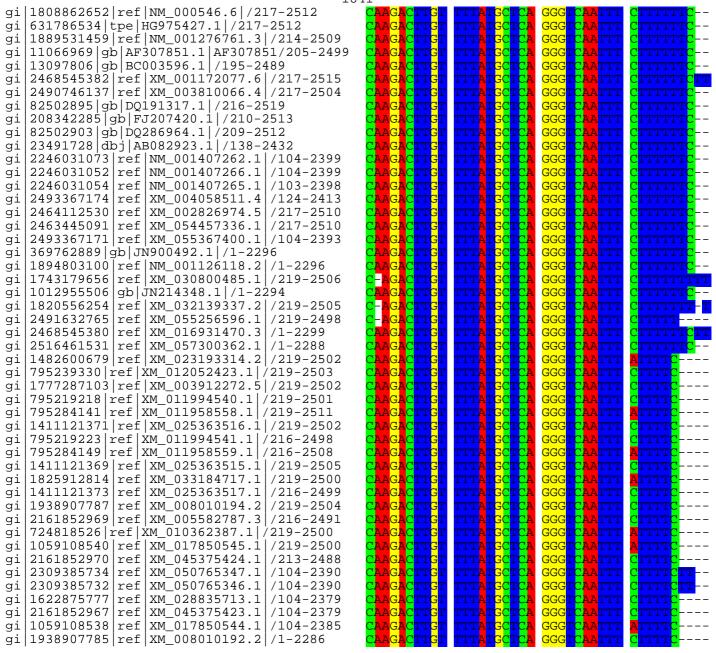


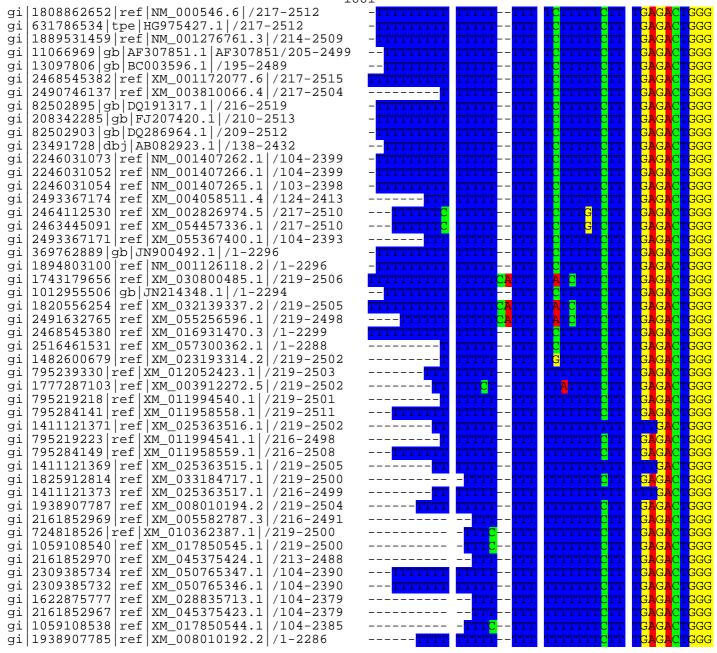


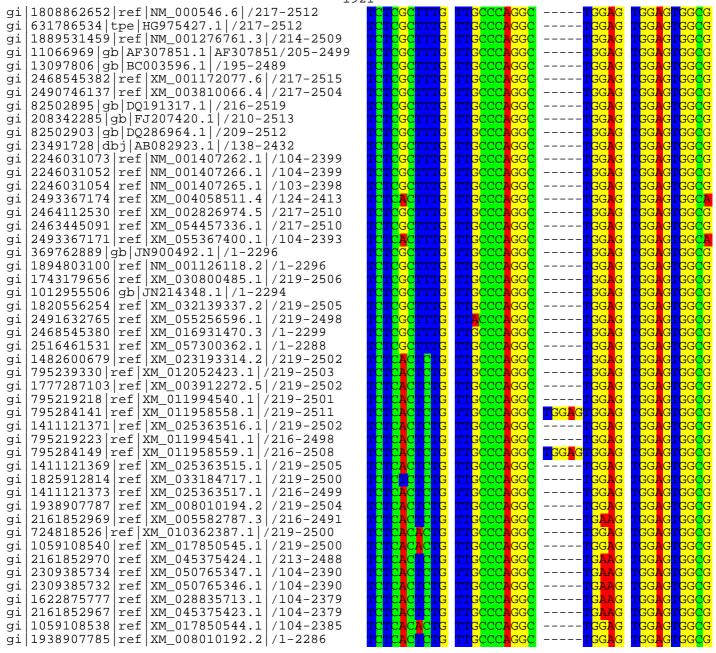


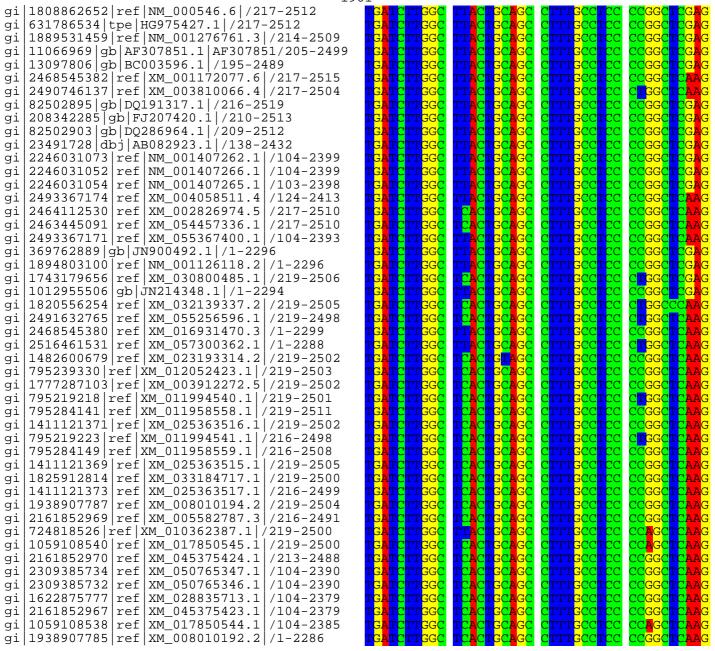




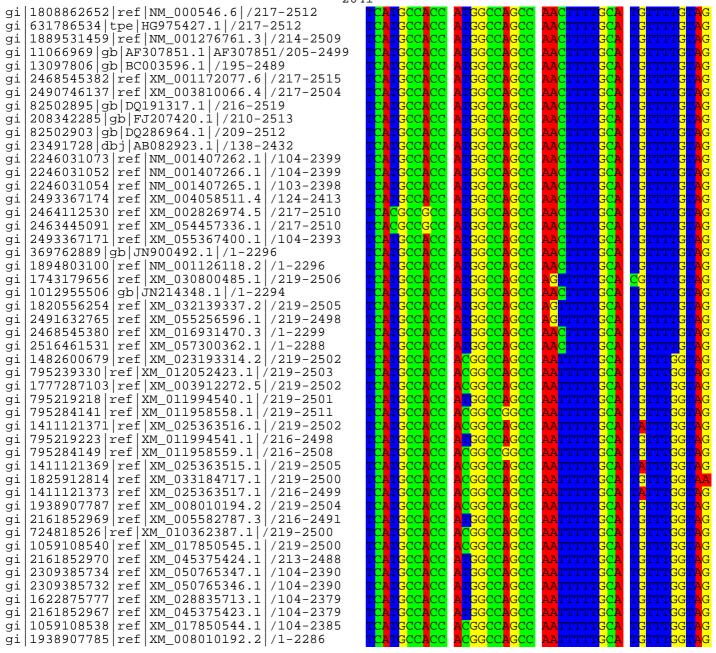


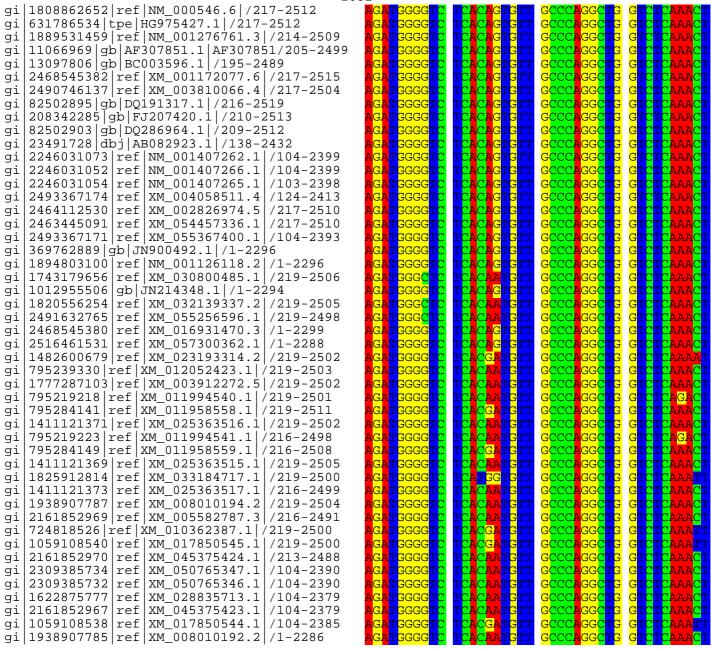


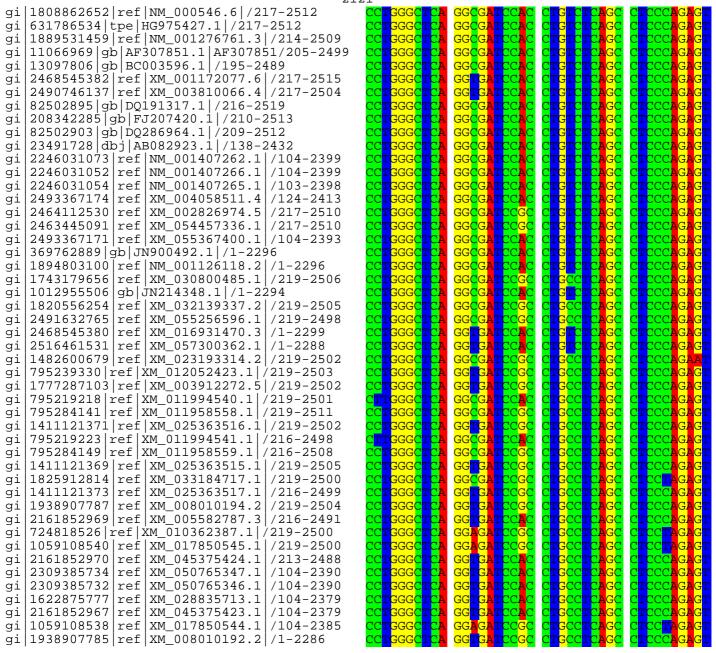


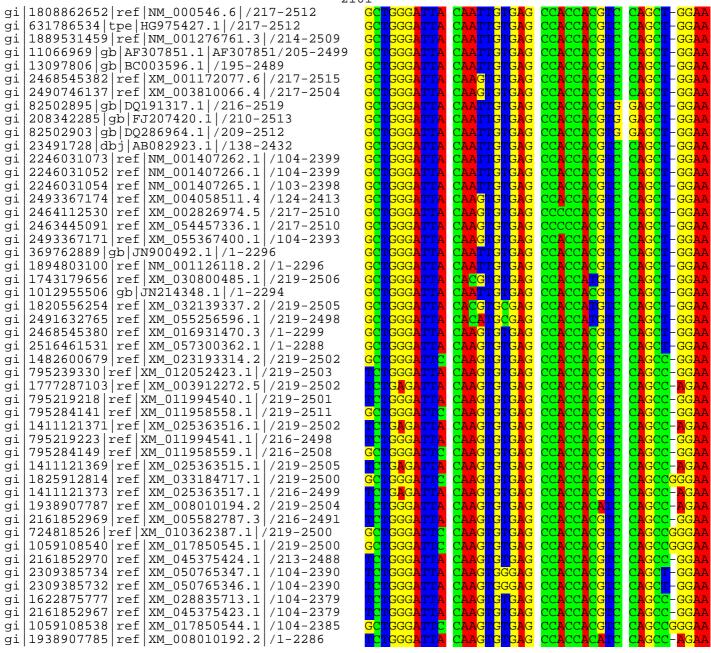


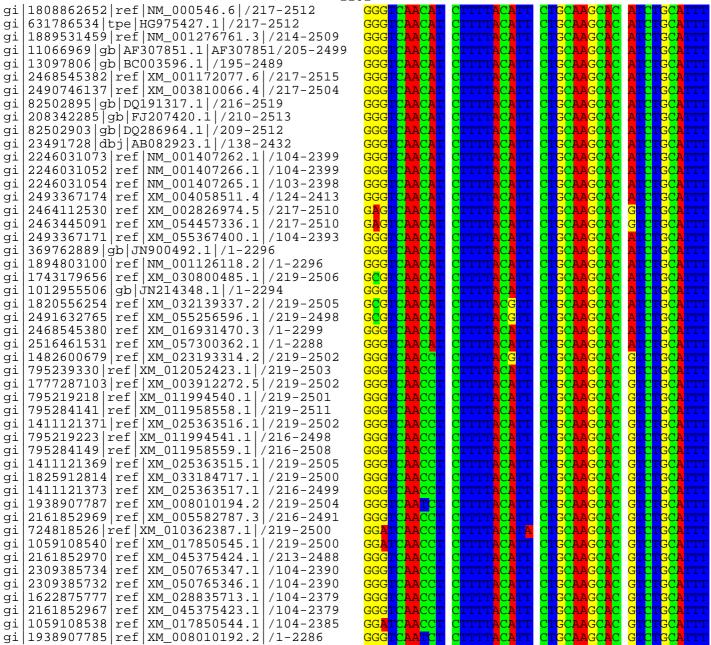


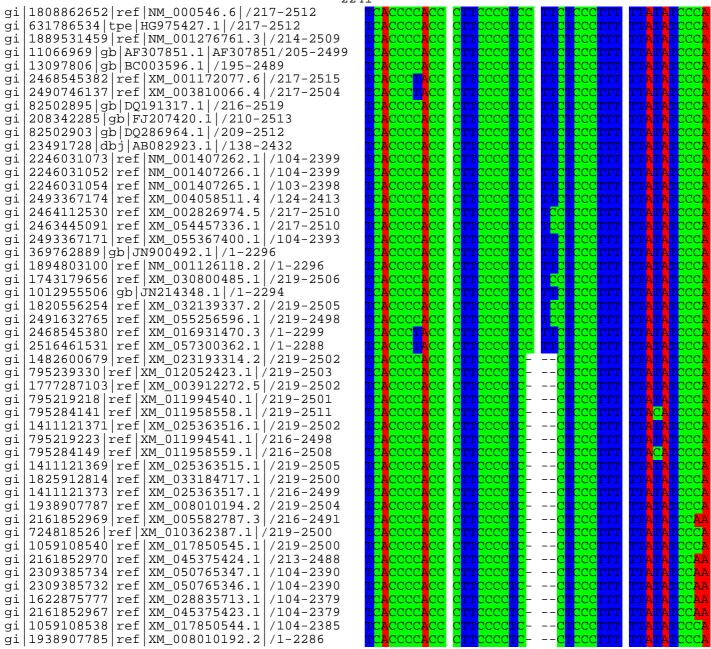


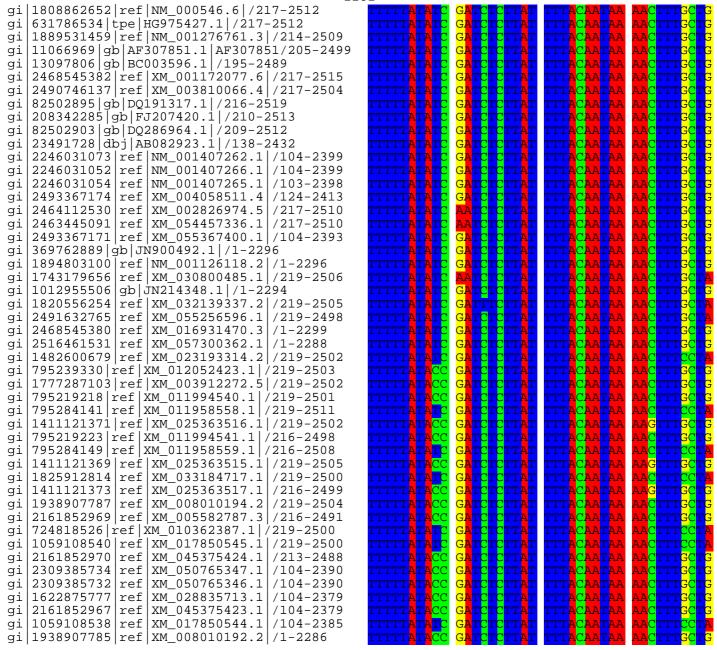












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