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gi	2468545382	ref	XM_001172077.6	/217-2515	CAGCTACGGT	TTCCGTCTGG	GCTTCCTTGCA	TTCTGGGACA
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gi	82502903	gb	DQ286964.1	/209-2512	CAGCTACGGT	TTCCGTCTGG	GCTTCCTTGCA	TTCTGGGACA
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gi	1012955506	gb	JN214348.1	/1-2294	CAGCTACGGT	TTCCGTCTGG	GCTTCCTTGCA	TTCTGGGACA
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gi	2491632765	ref	XM_055256596.1	/219-2498	CAGCTACGGT	TTCCGTCTGG	GCTTCCTTGCA	TTCTGGAACG
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gi	724818526	ref	XM_010362387.1	/219-2500	CAGCTACGGT	TTCCGTCTGG	GCTTCCTTGCA	TTCTGGAACA
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gi	23491728	dbj	AB082923.1	/138-2432
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gi	2464112530	ref	XM_002826974.5	/217-2510
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gi	369762889	gb	JN900492.1	/1-2296
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gi	1820556254	ref	XM_032139337.2	/219-2505
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gi	1482600679	ref	XM_023193314.2	/219-2502
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gi	795219223	ref	XM_011994541.1	/216-2498
gi	795284149	ref	XM_011958559.1	/216-2508
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gi	724818526	ref	XM_010362387.1	/219-2500
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gi	1622875777	ref	XM_028835713.1	/104-2379
gi	2161852967	ref	XM_045375423.1	/104-2379
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gi	631786534	tpe	HG975427.1	/217-2512	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1889531459	ref	NM_001276761.3	/214-2509	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	11066969	gb	AF307851.1	AF307851/205-2499	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	13097806	gb	BC003596.1	/195-2489	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2468545382	ref	XM_001172077.6	/217-2515	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2490746137	ref	XM_003810066.4	/217-2504	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	82502895	gb	DQ191317.1	/216-2519	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	208342285	gb	FJ207420.1	/210-2513	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	82502903	gb	DQ286964.1	/209-2512	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	23491728	dbj	AB082923.1	/138-2432	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2246031073	ref	NM_001407262.1	/104-2399	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
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gi	2493367174	ref	XM_004058511.4	/124-2413	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2464112530	ref	XM_002826974.5	/217-2510	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2463445091	ref	XM_054457336.1	/217-2510	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2493367171	ref	XM_055367400.1	/104-2393	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	369762889	gb	JN900492.1	/1-2296	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1894803100	ref	NM_001126118.2	/1-2296	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1743179656	ref	XM_030800485.1	/219-2506	GCCATGGCCA	TCTACAAGCA	ATCAAGCAC	ATGACGGAGG
gi	1012955506	gb	JN214348.1	/1-2294	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
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gi	2491632765	ref	XM_055256596.1	/219-2498	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2468545380	ref	XM_016931470.3	/1-2299	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2516461531	ref	XM_057300362.1	/1-2288	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1482600679	ref	XM_023193314.2	/219-2502	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	795239330	ref	XM_012052423.1	/219-2503	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1777287103	ref	XM_003912272.5	/219-2502	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	795219218	ref	XM_011994540.1	/219-2501	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	795284141	ref	XM_011958558.1	/219-2511	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1411121371	ref	XM_025363516.1	/219-2502	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
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gi	795284149	ref	XM_011958559.1	/216-2508	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1411121369	ref	XM_025363515.1	/219-2505	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1825912814	ref	XM_033184717.1	/219-2500	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1411121373	ref	XM_025363517.1	/216-2499	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1938907787	ref	XM_008010194.2	/219-2504	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2161852969	ref	XM_005582787.3	/216-2491	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	724818526	ref	XM_010362387.1	/219-2500	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	1059108540	ref	XM_017850545.1	/219-2500	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
gi	2161852970	ref	XM_045375424.1	/213-2488	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
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gi	1059108538	ref	XM_017850544.1	/104-2385	GCCATGGCCA	TCTACAAGCA	GTCAAGCAC	ATGACGGAGG
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gi	1889531459	ref	NM_001276761.3	/214-2509	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
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gi	2468545382	ref	XM_001172077.6	/217-2515	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	2490746137	ref	XM_003810066.4	/217-2504	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	82502895	gb	DQ191317.1	/216-2519	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	208342285	gb	FJ207420.1	/210-2513	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	82502903	gb	DQ286964.1	/209-2512	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
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gi	2246031073	ref	NM_001407262.1	/104-2399	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
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gi	2246031054	ref	NM_001407265.1	/103-2398	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TCGTTGAGGCG	CTGTCCCCAC	CATGAGCGCT	GCTCAGATAG
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gi	2491632765	ref	XM_055256596.1	/219-2498	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
gi	2516461531	ref	XM_057300362.1	/1-2288	TTGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGATAG
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gi	795239330	ref	XM_012052423.1	/219-2503	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
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gi	795284141	ref	XM_011958558.1	/219-2511	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	1411121371	ref	XM_025363516.1	/219-2502	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
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gi	795284149	ref	XM_011958559.1	/216-2508	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
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gi	1825912814	ref	XM_033184717.1	/219-2500	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
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gi	1938907787	ref	XM_008010194.2	/219-2504	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	2161852969	ref	XM_005582787.3	/216-2491	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	724818526	ref	XM_010362387.1	/219-2500	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	1059108540	ref	XM_017850545.1	/219-2500	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	2161852970	ref	XM_045375424.1	/213-2488	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
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gi	1059108538	ref	XM_017850544.1	/104-2385	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TCGTTGAGGCG	CTGCCCCCAC	CATGAGCGCT	GCTCAGACAG

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gi	11066969	gb	AF307851.1	AF307851/205-2499	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
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gi	82502895	gb	DQ191317.1	/216-2519	CGATGGTCTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	208342285	gb	FJ207420.1	/210-2513	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	82502903	gb	DQ286964.1	/209-2512	CGATGGTCTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	23491728	dbj	AB082923.1	/138-2432	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	2246031073	ref	NM_001407262.1	/104-2399	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
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gi	2493367174	ref	XM_004058511.4	/124-2413	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
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gi	2468545380	ref	XM_016931470.3	/1-2299	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	2516461531	ref	XM_057300362.1	/1-2288	CGATGGTCTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	1482600679	ref	XM_023193314.2	/219-2502	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	795239330	ref	XM_012052423.1	/219-2503	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	1777287103	ref	XM_003912272.5	/219-2502	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	795219218	ref	XM_011994540.1	/219-2501	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	795284141	ref	XM_011958558.1	/219-2511	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	1411121371	ref	XM_025363516.1	/219-2502	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	795219223	ref	XM_011994541.1	/216-2498	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	795284149	ref	XM_011958559.1	/216-2508	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	1411121369	ref	XM_025363515.1	/219-2505	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	1825912814	ref	XM_033184717.1	/219-2500	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	1411121373	ref	XM_025363517.1	/216-2499	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	1938907787	ref	XM_008010194.2	/219-2504	CGATGGACTG	GCCCCTCCTC	AACATCTTAT	CCGAGTGGAA
gi	2161852969	ref	XM_005582787.3	/216-2491	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
gi	724818526	ref	XM_010362387.1	/219-2500	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
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gi	2161852970	ref	XM_045375424.1	/213-2488	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
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gi	1622875777	ref	XM_028835713.1	/104-2379	CGATGGACTG	GCCCCTCCTC	AGCACCTTAT	CCGAGTGGAA
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gi	1059108538	ref	XM_017850544.1	/104-2385	CGATGGACTG	GCCCCTCCTC	AGCATCTTAT	CCGAGTGGAA
gi	1938907785	ref	XM_008010192.2	/1-2286	CGATGGACTG	GCCCCTCCTC	AACATCTTAT	CCGAGTGGAA

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gi	1889531459	ref	NM_001276761.3	/214-2509	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	11066969	gb	AF307851.1	AF307851/205-2499	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	13097806	gb	BC003596.1	/195-2489	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2468545382	ref	XM_001172077.6	/217-2515	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2490746137	ref	XM_003810066.4	/217-2504	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	82502895	gb	DQ191317.1	/216-2519	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	208342285	gb	FJ207420.1	/210-2513	GTAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	82502903	gb	DQ286964.1	/209-2512	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	23491728	dbj	AB082923.1	/138-2432	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2246031073	ref	NM_001407262.1	/104-2399	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2246031052	ref	NM_001407266.1	/104-2399	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2246031054	ref	NM_001407265.1	/103-2398	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2493367174	ref	XM_004058511.4	/124-2413	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2464112530	ref	XM_002826974.5	/217-2510	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2463445091	ref	XM_054457336.1	/217-2510	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2493367171	ref	XM_055367400.1	/104-2393	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	369762889	gb	JN900492.1	/1-2296	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	1894803100	ref	NM_001126118.2	/1-2296	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	1743179656	ref	XM_030800485.1	/219-2506	GGCAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	1012955506	gb	JN214348.1	/1-2294	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	1820556254	ref	XM_032139337.2	/219-2505	GGCAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2491632765	ref	XM_055256596.1	/219-2498	GGCAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2468545380	ref	XM_016931470.3	/1-2299	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	2516461531	ref	XM_057300362.1	/1-2288	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	1482600679	ref	XM_023193314.2	/219-2502	GGAAA	TTTGC	GTGTGGAGTA	TTTGGATGAC	AGAAACACTT
gi	795239330	ref	XM_012052423.1	/219-2503	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1777287103	ref	XM_003912272.5	/219-2502	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	795219218	ref	XM_011994540.1	/219-2501	GGAAA	TTTGC	GTGTGGAGTA	TTCCAGATGAC	AGAAACACTT
gi	795284141	ref	XM_011958558.1	/219-2511	GGAAA	TTTGC	ATGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1411121371	ref	XM_025363516.1	/219-2502	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	795219223	ref	XM_011994541.1	/216-2498	GGAAA	TTTGC	GTGTGGAGTA	TTCCAGATGAC	AGAAACACTT
gi	795284149	ref	XM_011958559.1	/216-2508	GGAAA	TTTGC	ATGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1411121369	ref	XM_025363515.1	/219-2505	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1825912814	ref	XM_033184717.1	/219-2500	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1411121373	ref	XM_025363517.1	/216-2499	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1938907787	ref	XM_008010194.2	/219-2504	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	2161852969	ref	XM_005582787.3	/216-2491	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	724818526	ref	XM_010362387.1	/219-2500	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1059108540	ref	XM_017850545.1	/219-2500	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	2161852970	ref	XM_045375424.1	/213-2488	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	2309385734	ref	XM_050765347.1	/104-2390	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	2309385732	ref	XM_050765346.1	/104-2390	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1622875777	ref	XM_028835713.1	/104-2379	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	2161852967	ref	XM_045375423.1	/104-2379	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1059108538	ref	XM_017850544.1	/104-2385	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT
gi	1938907785	ref	XM_008010192.2	/1-2286	GGAAA	TTTGC	GTGTGGAGTA	TTCCGGATGAC	AGAAACACTT

gi	1808862652	ref	NM_000546.6	/217-2512	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	631786534	tpe	HG975427.1	/217-2512	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1889531459	ref	NM_001276761.3	/214-2509	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	13097806	gb	BC003596.1	/195-2489	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2468545382	ref	XM_001172077.6	/217-2515	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2490746137	ref	XM_003810066.4	/217-2504	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	82502895	gb	DQ191317.1	/216-2519	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	208342285	gb	FJ207420.1	/210-2513	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	82502903	gb	DQ286964.1	/209-2512	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	23491728	dbj	AB082923.1	/138-2432	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2246031073	ref	NM_001407262.1	/104-2399	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2246031052	ref	NM_001407266.1	/104-2399	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2246031054	ref	NM_001407265.1	/103-2398	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2493367174	ref	XM_004058511.4	/124-2413	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2464112530	ref	XM_002826974.5	/217-2510	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2463445091	ref	XM_054457336.1	/217-2510	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2493367171	ref	XM_055367400.1	/104-2393	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	369762889	gb	JN900492.1	/1-2296	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1894803100	ref	NM_001126118.2	/1-2296	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1743179656	ref	XM_030800485.1	/219-2506	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1012955506	gb	JN214348.1	/1-2294	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1820556254	ref	XM_032139337.2	/219-2505	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2491632765	ref	XM_055256596.1	/219-2498	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2468545380	ref	XM_016931470.3	/1-2299	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2516461531	ref	XM_057300362.1	/1-2288	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1482600679	ref	XM_023193314.2	/219-2502	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCAGAGGT
gi	795239330	ref	XM_012052423.1	/219-2503	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1777287103	ref	XM_003912272.5	/219-2502	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	795219218	ref	XM_011994540.1	/219-2501	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	795284141	ref	XM_011958558.1	/219-2511	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1411121371	ref	XM_025363516.1	/219-2502	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	795219223	ref	XM_011994541.1	/216-2498	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	795284149	ref	XM_011958559.1	/216-2508	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1411121369	ref	XM_025363515.1	/219-2505	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1825912814	ref	XM_033184717.1	/219-2500	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1411121373	ref	XM_025363517.1	/216-2499	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1938907787	ref	XM_008010194.2	/219-2504	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2161852969	ref	XM_005582787.3	/216-2491	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	724818526	ref	XM_010362387.1	/219-2500	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1059108540	ref	XM_017850545.1	/219-2500	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2161852970	ref	XM_045375424.1	/213-2488	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2309385734	ref	XM_050765347.1	/104-2390	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2309385732	ref	XM_050765346.1	/104-2390	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1622875777	ref	XM_028835713.1	/104-2379	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	2161852967	ref	XM_045375423.1	/104-2379	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1059108538	ref	XM_017850544.1	/104-2385	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT
gi	1938907785	ref	XM_008010192.2	/1-2286	TTCGACATAG	TGTGGTGGTG	CCCTATGAGC	CGCCTGAGGT

gi	1808862652	ref	NM_000546.6	/217-2512	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	631786534	tpe	HG975427.1	/217-2512	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1889531459	ref	NM_001276761.3	/214-2509	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	13097806	gb	BC003596.1	/195-2489	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2468545382	ref	XM_001172077.6	/217-2515	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2490746137	ref	XM_003810066.4	/217-2504	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	82502895	gb	DQ191317.1	/216-2519	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	208342285	gb	FJ207420.1	/210-2513	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	82502903	gb	DQ286964.1	/209-2512	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	23491728	dbj	AB082923.1	/138-2432	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2246031073	ref	NM_001407262.1	/104-2399	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2246031052	ref	NM_001407266.1	/104-2399	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2246031054	ref	NM_001407265.1	/103-2398	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2493367174	ref	XM_004058511.4	/124-2413	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2464112530	ref	XM_002826974.5	/217-2510	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2463445091	ref	XM_054457336.1	/217-2510	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2493367171	ref	XM_055367400.1	/104-2393	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	369762889	gb	JN900492.1	/1-2296	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1894803100	ref	NM_001126118.2	/1-2296	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1743179656	ref	XM_030800485.1	/219-2506	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1012955506	gb	JN214348.1	/1-2294	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1820556254	ref	XM_032139337.2	/219-2505	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2491632765	ref	XM_055256596.1	/219-2498	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2468545380	ref	XM_016931470.3	/1-2299	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2516461531	ref	XM_057300362.1	/1-2288	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1482600679	ref	XM_023193314.2	/219-2502	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	795239330	ref	XM_012052423.1	/219-2503	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1777287103	ref	XM_003912272.5	/219-2502	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	795219218	ref	XM_011994540.1	/219-2501	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	795284141	ref	XM_011958558.1	/219-2511	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1411121371	ref	XM_025363516.1	/219-2502	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	795219223	ref	XM_011994541.1	/216-2498	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	795284149	ref	XM_011958559.1	/216-2508	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1411121369	ref	XM_025363515.1	/219-2505	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1825912814	ref	XM_033184717.1	/219-2500	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1411121373	ref	XM_025363517.1	/216-2499	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1938907787	ref	XM_008010194.2	/219-2504	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2161852969	ref	XM_005582787.3	/216-2491	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	724818526	ref	XM_010362387.1	/219-2500	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1059108540	ref	XM_017850545.1	/219-2500	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2161852970	ref	XM_045375424.1	/213-2488	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2309385734	ref	XM_050765347.1	/104-2390	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2309385732	ref	XM_050765346.1	/104-2390	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1622875777	ref	XM_028835713.1	/104-2379	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	2161852967	ref	XM_045375423.1	/104-2379	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1059108538	ref	XM_017850544.1	/104-2385	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT
gi	1938907785	ref	XM_008010192.2	/1-2286	TGGCTCTGAC	TGTACCACCA	TCCACTACAA	CTACATGTGT

gi	1808862652	ref	NM_000546.6	/217-2512	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	631786534	tpe	HG975427.1	/217-2512	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1889531459	ref	NM_001276761.3	/214-2509	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	11066969	gb	AF307851.1	AF307851/205-2499	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	13097806	gb	BC003596.1	/195-2489	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2468545382	ref	XM_001172077.6	/217-2515	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2490746137	ref	XM_003810066.4	/217-2504	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	82502895	gb	DQ191317.1	/216-2519	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	208342285	gb	FJ207420.1	/210-2513	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	82502903	gb	DQ286964.1	/209-2512	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	23491728	dbj	AB082923.1	/138-2432	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2246031073	ref	NM_001407262.1	/104-2399	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2246031052	ref	NM_001407266.1	/104-2399	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2246031054	ref	NM_001407265.1	/103-2398	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2493367174	ref	XM_004058511.4	/124-2413	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2464112530	ref	XM_002826974.5	/217-2510	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2463445091	ref	XM_054457336.1	/217-2510	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2493367171	ref	XM_055367400.1	/104-2393	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	369762889	gb	JN900492.1	/1-2296	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1894803100	ref	NM_001126118.2	/1-2296	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1743179656	ref	XM_030800485.1	/219-2506	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1012955506	gb	JN214348.1	/1-2294	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1820556254	ref	XM_032139337.2	/219-2505	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2491632765	ref	XM_055256596.1	/219-2498	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2468545380	ref	XM_016931470.3	/1-2299	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2516461531	ref	XM_057300362.1	/1-2288	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1482600679	ref	XM_023193314.2	/219-2502	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	795239330	ref	XM_012052423.1	/219-2503	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1777287103	ref	XM_003912272.5	/219-2502	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	795219218	ref	XM_011994540.1	/219-2501	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	795284141	ref	XM_011958558.1	/219-2511	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1411121371	ref	XM_025363516.1	/219-2502	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	795219223	ref	XM_011994541.1	/216-2498	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	795284149	ref	XM_011958559.1	/216-2508	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1411121369	ref	XM_025363515.1	/219-2505	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1825912814	ref	XM_033184717.1	/219-2500	AACAGTTCCT	GCATGGGCGG	CATGAATCGT	AGGCCCATTC
gi	1411121373	ref	XM_025363517.1	/216-2499	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1938907787	ref	XM_008010194.2	/219-2504	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2161852969	ref	XM_005582787.3	/216-2491	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	724818526	ref	XM_010362387.1	/219-2500	AACAGTTCCT	GCATGGGCGG	CATGAATCGG	AGGCCCATTC
gi	1059108540	ref	XM_017850545.1	/219-2500	AACAGTTCCT	GCATGGGCGG	CATGAATCGG	AGGCCCATTC
gi	2161852970	ref	XM_045375424.1	/213-2488	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2309385734	ref	XM_050765347.1	/104-2390	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2309385732	ref	XM_050765346.1	/104-2390	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1622875777	ref	XM_028835713.1	/104-2379	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	2161852967	ref	XM_045375423.1	/104-2379	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC
gi	1059108538	ref	XM_017850544.1	/104-2385	AACAGTTCCT	GCATGGGCGG	CATGAATCGG	AGGCCCATTC
gi	1938907785	ref	XM_008010192.2	/1-2286	AACAGTTCCT	GCATGGGCGG	CATGAACCGG	AGGCCCATCC

gi	1808862652	ref	NM_000546.6	/217-2512	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	631786534	tpe	HG975427.1	/217-2512	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1889531459	ref	NM_001276761.3	/214-2509	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	11066969	gb	AF307851.1	/AF307851/205-2499	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	13097806	gb	BC003596.1	/195-2489	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2468545382	ref	XM_001172077.6	/217-2515	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2490746137	ref	XM_003810066.4	/217-2504	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	82502895	gb	DQ191317.1	/216-2519	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	208342285	gb	FJ207420.1	/210-2513	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	82502903	gb	DQ286964.1	/209-2512	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	23491728	dbj	AB082923.1	/138-2432	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2246031073	ref	NM_001407262.1	/104-2399	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2246031052	ref	NM_001407266.1	/104-2399	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2246031054	ref	NM_001407265.1	/103-2398	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2493367174	ref	XM_004058511.4	/124-2413	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2464112530	ref	XM_002826974.5	/217-2510	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2463445091	ref	XM_054457336.1	/217-2510	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2493367171	ref	XM_055367400.1	/104-2393	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	369762889	gb	JN900492.1	/1-2296	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1894803100	ref	NM_001126118.2	/1-2296	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1743179656	ref	XM_030800485.1	/219-2506	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1012955506	gb	JN214348.1	/1-2294	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1820556254	ref	XM_032139337.2	/219-2505	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2491632765	ref	XM_055256596.1	/219-2498	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2468545380	ref	XM_016931470.3	/1-2299	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2516461531	ref	XM_057300362.1	/1-2288	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1482600679	ref	XM_023193314.2	/219-2502	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	795239330	ref	XM_012052423.1	/219-2503	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1777287103	ref	XM_003912272.5	/219-2502	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	795219218	ref	XM_011994540.1	/219-2501	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	795284141	ref	XM_011958558.1	/219-2511	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1411121371	ref	XM_025363516.1	/219-2502	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	795219223	ref	XM_011994541.1	/216-2498	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	795284149	ref	XM_011958559.1	/216-2508	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1411121369	ref	XM_025363515.1	/219-2505	TCACCATCAT	CACACTGGAA	GACTCCAGTA			GTGGTAATCT
gi	1825912814	ref	XM_033184717.1	/219-2500	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1411121373	ref	XM_025363517.1	/216-2499	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1938907787	ref	XM_008010194.2	/219-2504	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2161852969	ref	XM_005582787.3	/216-2491	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	724818526	ref	XM_010362387.1	/219-2500	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1059108540	ref	XM_017850545.1	/219-2500	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2161852970	ref	XM_045375424.1	/213-2488	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2309385734	ref	XM_050765347.1	/104-2390	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2309385732	ref	XM_050765346.1	/104-2390	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1622875777	ref	XM_028835713.1	/104-2379	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	2161852967	ref	XM_045375423.1	/104-2379	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1059108538	ref	XM_017850544.1	/104-2385	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT
gi	1938907785	ref	XM_008010192.2	/1-2286	TCACCATCAT	CACACTGGAA	GACTCC	---	A	GTGGTAATCT

gi	1808862652	ref	NM_000546.6	/217-2512	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	631786534	tpe	HG975427.1	/217-2512	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	1889531459	ref	NM_001276761.3	/214-2509	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	13097806	gb	BC003596.1	/195-2489	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2468545382	ref	XM_001172077.6	/217-2515	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2490746137	ref	XM_003810066.4	/217-2504	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	82502895	gb	DQ191317.1	/216-2519	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	208342285	gb	FJ207420.1	/210-2513	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	82502903	gb	DQ286964.1	/209-2512	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	23491728	dbj	AB082923.1	/138-2432	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2246031073	ref	NM_001407262.1	/104-2399	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2246031052	ref	NM_001407266.1	/104-2399	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2246031054	ref	NM_001407265.1	/103-2398	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2493367174	ref	XM_004058511.4	/124-2413	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2464112530	ref	XM_002826974.5	/217-2510	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2463445091	ref	XM_054457336.1	/217-2510	ACTGGGACGG	AACAGCTTTG	AGGTGCGCGT	TTGTGCCTGT
gi	2493367171	ref	XM_055367400.1	/104-2393	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	369762889	gb	JN900492.1	/1-2296	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	1894803100	ref	NM_001126118.2	/1-2296	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	1743179656	ref	XM_030800485.1	/219-2506	ACTGGGACGG	AACAGCTTTG	AGGTGCGCGT	TTGTGCCTGT
gi	1012955506	gb	JN214348.1	/1-2294	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	1820556254	ref	XM_032139337.2	/219-2505	ACTGGGACGG	AACAGCTTTG	AGGTGCGCGT	TTGTGCCTGT
gi	2491632765	ref	XM_055256596.1	/219-2498	ACTGGGACGG	AACAGCTTTG	AGGTGCGCGT	TTGTGCCTGT
gi	2468545380	ref	XM_016931470.3	/1-2299	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	2516461531	ref	XM_057300362.1	/1-2288	ACTGGGACGG	AACAGCTTTG	AGGTGCGTGT	TTGTGCCTGT
gi	1482600679	ref	XM_023193314.2	/219-2502	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	795239330	ref	XM_012052423.1	/219-2503	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1777287103	ref	XM_003912272.5	/219-2502	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	795219218	ref	XM_011994540.1	/219-2501	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	795284141	ref	XM_011958558.1	/219-2511	ACTGGGACGA	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGC
gi	1411121371	ref	XM_025363516.1	/219-2502	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	795219223	ref	XM_011994541.1	/216-2498	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	795284149	ref	XM_011958559.1	/216-2508	ACTGGGACGA	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGC
gi	1411121369	ref	XM_025363515.1	/219-2505	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1825912814	ref	XM_033184717.1	/219-2500	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1411121373	ref	XM_025363517.1	/216-2499	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1938907787	ref	XM_008010194.2	/219-2504	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	2161852969	ref	XM_005582787.3	/216-2491	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	724818526	ref	XM_010362387.1	/219-2500	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1059108540	ref	XM_017850545.1	/219-2500	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	2161852970	ref	XM_045375424.1	/213-2488	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	2309385734	ref	XM_050765347.1	/104-2390	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	2309385732	ref	XM_050765346.1	/104-2390	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1622875777	ref	XM_028835713.1	/104-2379	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	2161852967	ref	XM_045375423.1	/104-2379	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1059108538	ref	XM_017850544.1	/104-2385	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT
gi	1938907785	ref	XM_008010192.2	/1-2286	ACTGGGACGG	AACAGCTTTG	AGGTGCGAGT	TTGTGCCTGT

gi	1808862652	ref	NM_000546.6	/217-2512	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	631786534	tpe	HG975427.1	/217-2512	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	1889531459	ref	NM_001276761.3	/214-2509	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	11066969	gb	AF307851.1	/AF307851/205-2499	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	13097806	gb	BC003596.1	/195-2489	GCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2468545382	ref	XM_001172077.6	/217-2515	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2490746137	ref	XM_003810066.4	/217-2504	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	82502895	gb	DQ191317.1	/216-2519	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	208342285	gb	FJ207420.1	/210-2513	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	82502903	gb	DQ286964.1	/209-2512	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	23491728	dbj	AB082923.1	/138-2432	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2246031073	ref	NM_001407262.1	/104-2399	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2246031052	ref	NM_001407266.1	/104-2399	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2246031054	ref	NM_001407265.1	/103-2398	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2493367174	ref	XM_004058511.4	/124-2413	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2464112530	ref	XM_002826974.5	/217-2510	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2463445091	ref	XM_054457336.1	/217-2510	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2493367171	ref	XM_055367400.1	/104-2393	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	369762889	gb	JN900492.1	/1-2296	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	1894803100	ref	NM_001126118.2	/1-2296	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	1743179656	ref	XM_030800485.1	/219-2506	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCACA
gi	1012955506	gb	JN214348.1	/1-2294	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	1820556254	ref	XM_032139337.2	/219-2505	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCACA
gi	2491632765	ref	XM_055256596.1	/219-2498	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCACA
gi	2468545380	ref	XM_016931470.3	/1-2299	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	2516461531	ref	XM_057300362.1	/1-2288	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATCTCCGCA
gi	1482600679	ref	XM_023193314.2	/219-2502	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	795239330	ref	XM_012052423.1	/219-2503	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	1777287103	ref	XM_003912272.5	/219-2502	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	795219218	ref	XM_011994540.1	/219-2501	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	795284141	ref	XM_011958558.1	/219-2511	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAA	AATTTCCGCA
gi	1411121371	ref	XM_025363516.1	/219-2502	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	795219223	ref	XM_011994541.1	/216-2498	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	795284149	ref	XM_011958559.1	/216-2508	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAA	AATTTCCGCA
gi	1411121369	ref	XM_025363515.1	/219-2505	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	1825912814	ref	XM_033184717.1	/219-2500	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	1411121373	ref	XM_025363517.1	/216-2499	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGTA
gi	1938907787	ref	XM_008010194.2	/219-2504	CCTGGGAGAG	ACCGGCGCAC	GGAGGAAGAG	AATTTCCGCA
gi	2161852969	ref	XM_005582787.3	/216-2491	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	724818526	ref	XM_010362387.1	/219-2500	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTACCGCA
gi	1059108540	ref	XM_017850545.1	/219-2500	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTACCGCA
gi	2161852970	ref	XM_045375424.1	/213-2488	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2309385734	ref	XM_050765347.1	/104-2390	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2309385732	ref	XM_050765346.1	/104-2390	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	1622875777	ref	XM_028835713.1	/104-2379	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	2161852967	ref	XM_045375423.1	/104-2379	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTTCCGCA
gi	1059108538	ref	XM_017850544.1	/104-2385	CCTGGGAGAG	ACCGGCGCAC	AGAGGAAGAG	AATTACCGCA
gi	1938907785	ref	XM_008010192.2	/1-2286	CCTGGGAGAG	ACCGGCGCAC	GGAGGAAGAG	AATTTCCGCA

gi	1808862652	ref	NM_000546.6	/217-2512	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	631786534	tpe	HG975427.1	/217-2512	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	1889531459	ref	NM_001276761.3	/214-2509	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	11066969	gb	AF307851.1	AF307851/205-2499	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	13097806	gb	BC003596.1	/195-2489	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2468545382	ref	XM_001172077.6	/217-2515	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2490746137	ref	XM_003810066.4	/217-2504	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	82502895	gb	DQ191317.1	/216-2519	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	208342285	gb	FJ207420.1	/210-2513	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	82502903	gb	DQ286964.1	/209-2512	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	23491728	dbj	AB082923.1	/138-2432	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2246031073	ref	NM_001407262.1	/104-2399	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2246031052	ref	NM_001407266.1	/104-2399	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2246031054	ref	NM_001407265.1	/103-2398	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2493367174	ref	XM_004058511.4	/124-2413	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2464112530	ref	XM_002826974.5	/217-2510	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2463445091	ref	XM_054457336.1	/217-2510	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2493367171	ref	XM_055367400.1	/104-2393	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	369762889	gb	JN900492.1	/1-2296	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	1894803100	ref	NM_001126118.2	/1-2296	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	1743179656	ref	XM_030800485.1	/219-2506	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1012955506	gb	JN214348.1	/1-2294	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	1820556254	ref	XM_032139337.2	/219-2505	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2491632765	ref	XM_055256596.1	/219-2498	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2468545380	ref	XM_016931470.3	/1-2299	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	2516461531	ref	XM_057300362.1	/1-2288	AGAAAGGGGA	GCCTCACCAC	GAGCTGCCCC	CAGGGAGCAC
gi	1482600679	ref	XM_023193314.2	/219-2502	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	795239330	ref	XM_012052423.1	/219-2503	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1777287103	ref	XM_003912272.5	/219-2502	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	795219218	ref	XM_011994540.1	/219-2501	AGAAAGGGGA	GCCTTGCCAT	GAGCTGCCCC	CTGGGAGCAC
gi	795284141	ref	XM_011958558.1	/219-2511	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1411121371	ref	XM_025363516.1	/219-2502	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	795219223	ref	XM_011994541.1	/216-2498	AGAAAGGGGA	GCCTTGCCAT	GAGCTGCCCC	CTGGGAGCAC
gi	795284149	ref	XM_011958559.1	/216-2508	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1411121369	ref	XM_025363515.1	/219-2505	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1825912814	ref	XM_033184717.1	/219-2500	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1411121373	ref	XM_025363517.1	/216-2499	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1938907787	ref	XM_008010194.2	/219-2504	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2161852969	ref	XM_005582787.3	/216-2491	AGAAAGGGGA	GCCTTGCCAC	CAGCTGCCCC	CTGGGAGCAC
gi	724818526	ref	XM_010362387.1	/219-2500	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1059108540	ref	XM_017850545.1	/219-2500	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	2161852970	ref	XM_045375424.1	/213-2488	AGAAAGGGGA	GCCTTGCCAC	CAGCTGCCCC	CTGGGAGCAC
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gi	2309385732	ref	XM_050765346.1	/104-2390	AGAAAGGGGA	GCCTTGCCAC	CAGCTGCCCC	CTGGGAGCAC
gi	1622875777	ref	XM_028835713.1	/104-2379	AGAAAGGGGA	GCCTTGCCAC	CAGCTGCCCC	CTGGGAGCAC
gi	2161852967	ref	XM_045375423.1	/104-2379	AGAAAGGGGA	GCCTTGCCAC	CAGCTGCCCC	CTGGGAGCAC
gi	1059108538	ref	XM_017850544.1	/104-2385	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC
gi	1938907785	ref	XM_008010192.2	/1-2286	AGAAAGGGGA	GCCTTGCCAC	GAGCTGCCCC	CTGGGAGCAC

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gi	631786534	tpe	HG975427.1	/217-2512	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	1889531459	ref	NM_001276761.3	/214-2509	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	13097806	gb	BC003596.1	/195-2489	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2468545382	ref	XM_001172077.6	/217-2515	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2490746137	ref	XM_003810066.4	/217-2504	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	82502895	gb	DQ191317.1	/216-2519	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	208342285	gb	FJ207420.1	/210-2513	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	82502903	gb	DQ286964.1	/209-2512	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	23491728	dbj	AB082923.1	/138-2432	TAAGCGAGCA	CTGTCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2246031073	ref	NM_001407262.1	/104-2399	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2246031052	ref	NM_001407266.1	/104-2399	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2246031054	ref	NM_001407265.1	/103-2398	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2463445091	ref	XM_054457336.1	/217-2510	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2493367171	ref	XM_055367400.1	/104-2393	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	369762889	gb	JN900492.1	/1-2296	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
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gi	1743179656	ref	XM_030800485.1	/219-2506	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	1012955506	gb	JN214348.1	/1-2294	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	1820556254	ref	XM_032139337.2	/219-2505	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2491632765	ref	XM_055256596.1	/219-2498	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2516461531	ref	XM_057300362.1	/1-2288	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
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gi	795219218	ref	XM_011994540.1	/219-2501	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
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gi	1411121371	ref	XM_025363516.1	/219-2502	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
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gi	724818526	ref	XM_010362387.1	/219-2500	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
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gi	2309385732	ref	XM_050765346.1	/104-2390	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	1622875777	ref	XM_028835713.1	/104-2379	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	2161852967	ref	XM_045375423.1	/104-2379	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG
gi	1059108538	ref	XM_017850544.1	/104-2385	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCGCAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TAAGCGAGCA	CTGCCCCAACA	ACACCAGCTC	CTCTCCCCAG

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gi	1889531459	ref	NM_001276761.3	/214-2509
gi	11066969	gb	AF307851.1	AF307851/205-2499
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gi	2468545382	ref	XM_001172077.6	/217-2515
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gi	82502895	gb	DQ191317.1	/216-2519
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gi	1889531459	ref	NM_001276761.3	/214-2509	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	11066969	gb	AF307851.1	AF307851/205-2499	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	13097806	gb	BC003596.1	/195-2489	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	2468545382	ref	XM_001172077.6	/217-2515	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	2490746137	ref	XM_003810066.4	/217-2504	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	82502895	gb	DQ191317.1	/216-2519	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	208342285	gb	FJ207420.1	/210-2513	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	82502903	gb	DQ286964.1	/209-2512	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	2493367174	ref	XM_004058511.4	/124-2413	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	369762889	gb	JN900492.1	/1-2296	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	1894803100	ref	NM_001126118.2	/1-2296	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	2491632765	ref	XM_055256596.1	/219-2498	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	2161852969	ref	XM_005582787.3	/216-2491	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	724818526	ref	XM_010362387.1	/219-2500	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
gi	1059108540	ref	XM_017850545.1	/219-2500	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAACT
gi	2161852970	ref	XM_045375424.1	/213-2488	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	1622875777	ref	XM_028835713.1	/104-2379	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT
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gi	1059108538	ref	XM_017850544.1	/104-2385	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAACT
gi	1938907785	ref	XM_008010192.2	/1-2286	AGATCCGTTGG	GCGTGAGCGC	TTCGAGATGT	TCCGAGAGCT

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gi	631786534	tpe	HG975427.1	/217-2512	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1889531459	ref	NM_001276761.3	/214-2509	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	13097806	gb	BC003596.1	/195-2489	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2468545382	ref	XM_001172077.6	/217-2515	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2490746137	ref	XM_003810066.4	/217-2504	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	82502895	gb	DQ191317.1	/216-2519	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	208342285	gb	FJ207420.1	/210-2513	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	82502903	gb	DQ286964.1	/209-2512	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	23491728	dbj	AB082923.1	/138-2432	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2246031073	ref	NM_001407262.1	/104-2399	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2246031052	ref	NM_001407266.1	/104-2399	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2246031054	ref	NM_001407265.1	/103-2398	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2493367174	ref	XM_004058511.4	/124-2413	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2464112530	ref	XM_002826974.5	/217-2510	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2463445091	ref	XM_054457336.1	/217-2510	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2493367171	ref	XM_055367400.1	/104-2393	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	369762889	gb	JN900492.1	/1-2296	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1894803100	ref	NM_001126118.2	/1-2296	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1743179656	ref	XM_030800485.1	/219-2506	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1012955506	gb	JN214348.1	/1-2294	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1820556254	ref	XM_032139337.2	/219-2505	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2491632765	ref	XM_055256596.1	/219-2498	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2468545380	ref	XM_016931470.3	/1-2299	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	2516461531	ref	XM_057300362.1	/1-2288	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAG
gi	1482600679	ref	XM_023193314.2	/219-2502	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	795239330	ref	XM_012052423.1	/219-2503	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1777287103	ref	XM_003912272.5	/219-2502	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	795219218	ref	XM_011994540.1	/219-2501	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	795284141	ref	XM_011958558.1	/219-2511	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1411121371	ref	XM_025363516.1	/219-2502	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	795219223	ref	XM_011994541.1	/216-2498	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	795284149	ref	XM_011958559.1	/216-2508	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1411121369	ref	XM_025363515.1	/219-2505	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1825912814	ref	XM_033184717.1	/219-2500	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1411121373	ref	XM_025363517.1	/216-2499	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1938907787	ref	XM_008010194.2	/219-2504	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	2161852969	ref	XM_005582787.3	/216-2491	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	724818526	ref	XM_010362387.1	/219-2500	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1059108540	ref	XM_017850545.1	/219-2500	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	2161852970	ref	XM_045375424.1	/213-2488	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	2309385734	ref	XM_050765347.1	/104-2390	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	2309385732	ref	XM_050765346.1	/104-2390	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1622875777	ref	XM_028835713.1	/104-2379	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	2161852967	ref	XM_045375423.1	/104-2379	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1059108538	ref	XM_017850544.1	/104-2385	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA
gi	1938907785	ref	XM_008010192.2	/1-2286	GAATGAGGCC	TTGGAAC TCA	AGGATGCCCCA	GGCTGGGAAA

gi	1808862652	ref	NM_000546.6	/217-2512	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	631786534	tpe	HG975427.1	/217-2512	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1889531459	ref	NM_001276761.3	/214-2509	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	13097806	gb	BC003596.1	/195-2489	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2468545382	ref	XM_001172077.6	/217-2515	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2490746137	ref	XM_003810066.4	/217-2504	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	82502895	gb	DQ191317.1	/216-2519	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	208342285	gb	FJ207420.1	/210-2513	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	82502903	gb	DQ286964.1	/209-2512	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	23491728	dbj	AB082923.1	/138-2432	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2246031073	ref	NM_001407262.1	/104-2399	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
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gi	2246031054	ref	NM_001407265.1	/103-2398	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2493367174	ref	XM_004058511.4	/124-2413	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2464112530	ref	XM_002826974.5	/217-2510	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2463445091	ref	XM_054457336.1	/217-2510	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2493367171	ref	XM_055367400.1	/104-2393	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	369762889	gb	JN900492.1	/1-2296	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1894803100	ref	NM_001126118.2	/1-2296	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1743179656	ref	XM_030800485.1	/219-2506	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1012955506	gb	JN214348.1	/1-2294	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1820556254	ref	XM_032139337.2	/219-2505	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2491632765	ref	XM_055256596.1	/219-2498	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2468545380	ref	XM_016931470.3	/1-2299	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2516461531	ref	XM_057300362.1	/1-2288	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1482600679	ref	XM_023193314.2	/219-2502	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	795239330	ref	XM_012052423.1	/219-2503	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1777287103	ref	XM_003912272.5	/219-2502	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	795219218	ref	XM_011994540.1	/219-2501	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	795284141	ref	XM_011958558.1	/219-2511	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1411121371	ref	XM_025363516.1	/219-2502	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
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gi	795284149	ref	XM_011958559.1	/216-2508	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1411121369	ref	XM_025363515.1	/219-2505	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1825912814	ref	XM_033184717.1	/219-2500	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1411121373	ref	XM_025363517.1	/216-2499	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1938907787	ref	XM_008010194.2	/219-2504	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2161852969	ref	XM_005582787.3	/216-2491	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	724818526	ref	XM_010362387.1	/219-2500	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1059108540	ref	XM_017850545.1	/219-2500	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2161852970	ref	XM_045375424.1	/213-2488	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2309385734	ref	XM_050765347.1	/104-2390	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2309385732	ref	XM_050765346.1	/104-2390	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1622875777	ref	XM_028835713.1	/104-2379	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	2161852967	ref	XM_045375423.1	/104-2379	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1059108538	ref	XM_017850544.1	/104-2385	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT
gi	1938907785	ref	XM_008010192.2	/1-2286	GAGCCAGGGG	GGAGCAGGGC	TCACTCCAGC	CACCTGAAGT

gi	1808862652	ref	NM_000546.6	/217-2512	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	631786534	tpe	HG975427.1	/217-2512	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1889531459	ref	NM_001276761.3	/214-2509	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	13097806	gb	BC003596.1	/195-2489	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2468545382	ref	XM_001172077.6	/217-2515	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2490746137	ref	XM_003810066.4	/217-2504	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	82502895	gb	DQ191317.1	/216-2519	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	208342285	gb	FJ207420.1	/210-2513	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	82502903	gb	DQ286964.1	/209-2512	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	23491728	dbj	AB082923.1	/138-2432	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2246031073	ref	NM_001407262.1	/104-2399	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
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gi	2246031054	ref	NM_001407265.1	/103-2398	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2493367174	ref	XM_004058511.4	/124-2413	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2464112530	ref	XM_002826974.5	/217-2510	CCAAGAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2463445091	ref	XM_054457336.1	/217-2510	CCAAGAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2493367171	ref	XM_055367400.1	/104-2393	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	369762889	gb	JN900492.1	/1-2296	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1894803100	ref	NM_001126118.2	/1-2296	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1743179656	ref	XM_030800485.1	/219-2506	CCAAGAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTTAT
gi	1012955506	gb	JN214348.1	/1-2294	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1820556254	ref	XM_032139337.2	/219-2505	CCAAGAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTTAT
gi	2491632765	ref	XM_055256596.1	/219-2498	CCAAGAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTTAT
gi	2468545380	ref	XM_016931470.3	/1-2299	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2516461531	ref	XM_057300362.1	/1-2288	CCAAAAAGGG	TCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1482600679	ref	XM_023193314.2	/219-2502	CCAAGAAGGG	GCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	795239330	ref	XM_012052423.1	/219-2503	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	1777287103	ref	XM_003912272.5	/219-2502	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	795219218	ref	XM_011994540.1	/219-2501	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	795284141	ref	XM_011958558.1	/219-2511	CCAAGAAGGG	GCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1411121371	ref	XM_025363516.1	/219-2502	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	795219223	ref	XM_011994541.1	/216-2498	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
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gi	1411121369	ref	XM_025363515.1	/219-2505	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	1825912814	ref	XM_033184717.1	/219-2500	CCAAGAAGGG	GCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1411121373	ref	XM_025363517.1	/216-2499	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	1938907787	ref	XM_008010194.2	/219-2504	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	2161852969	ref	XM_005582787.3	/216-2491	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	724818526	ref	XM_010362387.1	/219-2500	CCAAGAAGGG	GCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	1059108540	ref	XM_017850545.1	/219-2500	CCAAGAAGGG	GCAGTCTACC	TCCCGCCATA	AAAAACTCAT
gi	2161852970	ref	XM_045375424.1	/213-2488	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
gi	2309385734	ref	XM_050765347.1	/104-2390	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT
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gi	1938907785	ref	XM_008010192.2	/1-2286	CCAAGAAGGG	GCAATCTACC	TCCCGCCATA	AAAAATTCAT

gi	1808862652	ref	NM_000546.6	/217-2512	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
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gi	1889531459	ref	NM_001276761.3	/214-2509	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	11066969	gb	AF307851.1	AF307851/205-2499	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	13097806	gb	BC003596.1	/195-2489	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	2468545382	ref	XM_001172077.6	/217-2515	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	2490746137	ref	XM_003810066.4	/217-2504	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	82502895	gb	DQ191317.1	/216-2519	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	208342285	gb	FJ207420.1	/210-2513	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	82502903	gb	DQ286964.1	/209-2512	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	23491728	dbj	AB082923.1	/138-2432	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	2246031073	ref	NM_001407262.1	/104-2399	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
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gi	2493367174	ref	XM_004058511.4	/124-2413	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	2464112530	ref	XM_002826974.5	/217-2510	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCG
gi	2463445091	ref	XM_054457336.1	/217-2510	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTTTG
gi	2493367171	ref	XM_055367400.1	/104-2393	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	369762889	gb	JN900492.1	/1-2296	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
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gi	1743179656	ref	XM_030800485.1	/219-2506	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCG
gi	1012955506	gb	JN214348.1	/1-2294	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	1820556254	ref	XM_032139337.2	/219-2505	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCG
gi	2491632765	ref	XM_055256596.1	/219-2498	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCG
gi	2468545380	ref	XM_016931470.3	/1-2299	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	2516461531	ref	XM_057300362.1	/1-2288	GTTCAAGACA	GAAGGGCCTG	ACTCAGACTG	ACATTCTCCA
gi	1482600679	ref	XM_023193314.2	/219-2502	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	795239330	ref	XM_012052423.1	/219-2503	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1777287103	ref	XM_003912272.5	/219-2502	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	795219218	ref	XM_011994540.1	/219-2501	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	795284141	ref	XM_011958558.1	/219-2511	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1411121371	ref	XM_025363516.1	/219-2502	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	795219223	ref	XM_011994541.1	/216-2498	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	795284149	ref	XM_011958559.1	/216-2508	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1411121369	ref	XM_025363515.1	/219-2505	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1825912814	ref	XM_033184717.1	/219-2500	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1411121373	ref	XM_025363517.1	/216-2499	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1938907787	ref	XM_008010194.2	/219-2504	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	2161852969	ref	XM_005582787.3	/216-2491	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	724818526	ref	XM_010362387.1	/219-2500	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1059108540	ref	XM_017850545.1	/219-2500	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	2161852970	ref	XM_045375424.1	/213-2488	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	2309385734	ref	XM_050765347.1	/104-2390	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	2309385732	ref	XM_050765346.1	/104-2390	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1622875777	ref	XM_028835713.1	/104-2379	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	2161852967	ref	XM_045375423.1	/104-2379	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1059108538	ref	XM_017850544.1	/104-2385	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG
gi	1938907785	ref	XM_008010192.2	/1-2286	GTTCAAGACA	GAGGGGCCTG	ACTCAGACTG	ACATTCTCAG

gi	1808862652	ref	NM_000546.6	/217-2512	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	631786534	tpe	HG975427.1	/217-2512	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1889531459	ref	NM_001276761.3	/214-2509	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	13097806	gb	BC003596.1	/195-2489	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2468545382	ref	XM_001172077.6	/217-2515	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2490746137	ref	XM_003810066.4	/217-2504	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	82502895	gb	DQ191317.1	/216-2519	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	208342285	gb	FJ207420.1	/210-2513	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCCTC	CCCCATCTCT
gi	82502903	gb	DQ286964.1	/209-2512	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	23491728	dbj	AB082923.1	/138-2432	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2246031073	ref	NM_001407262.1	/104-2399	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2246031052	ref	NM_001407266.1	/104-2399	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2246031054	ref	NM_001407265.1	/103-2398	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2493367174	ref	XM_004058511.4	/124-2413	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2464112530	ref	XM_002826974.5	/217-2510	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2463445091	ref	XM_054457336.1	/217-2510	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2493367171	ref	XM_055367400.1	/104-2393	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	369762889	gb	JN900492.1	/1-2296	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1894803100	ref	NM_001126118.2	/1-2296	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1743179656	ref	XM_030800485.1	/219-2506	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1012955506	gb	JN214348.1	/1-2294	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1820556254	ref	XM_032139337.2	/219-2505	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2491632765	ref	XM_055256596.1	/219-2498	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2468545380	ref	XM_016931470.3	/1-2299	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2516461531	ref	XM_057300362.1	/1-2288	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1482600679	ref	XM_023193314.2	/219-2502	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	795239330	ref	XM_012052423.1	/219-2503	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	1777287103	ref	XM_003912272.5	/219-2502	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	795219218	ref	XM_011994540.1	/219-2501	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	795284141	ref	XM_011958558.1	/219-2511	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1411121371	ref	XM_025363516.1	/219-2502	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	795219223	ref	XM_011994541.1	/216-2498	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	795284149	ref	XM_011958559.1	/216-2508	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1411121369	ref	XM_025363515.1	/219-2505	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	1825912814	ref	XM_033184717.1	/219-2500	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1411121373	ref	XM_025363517.1	/216-2499	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	1938907787	ref	XM_008010194.2	/219-2504	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT
gi	2161852969	ref	XM_005582787.3	/216-2491	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	724818526	ref	XM_010362387.1	/219-2500	CTTCTTGTGTTG	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1059108540	ref	XM_017850545.1	/219-2500	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	2161852970	ref	XM_045375424.1	/213-2488	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	2309385734	ref	XM_050765347.1	/104-2390	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	2309385732	ref	XM_050765346.1	/104-2390	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	1622875777	ref	XM_028835713.1	/104-2379	CTTAATTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	2161852967	ref	XM_045375423.1	/104-2379	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCA----T
gi	1059108538	ref	XM_017850544.1	/104-2385	CTTCTTGTGTT-	CCCCACTGAC	AGCCTCCCAC	CCCCATCTCT
gi	1938907785	ref	XM_008010192.2	/1-2286	CTTCTTGTGTTG	CCCCACTG--	AGCCTCCCAC	CCCCATCTCT

gi	1808862652	ref	NM_000546.6	/217-2512	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	631786534	tpe	HG975427.1	/217-2512	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	1889531459	ref	NM_001276761.3	/214-2509	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	13097806	gb	BC003596.1	/195-2489	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2468545382	ref	XM_001172077.6	/217-2515	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2490746137	ref	XM_003810066.4	/217-2504	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	82502895	gb	DQ191317.1	/216-2519	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	208342285	gb	FJ207420.1	/210-2513	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	82502903	gb	DQ286964.1	/209-2512	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	23491728	dbj	AB082923.1	/138-2432	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2246031073	ref	NM_001407262.1	/104-2399	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2246031052	ref	NM_001407266.1	/104-2399	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2246031054	ref	NM_001407265.1	/103-2398	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2493367174	ref	XM_004058511.4	/124-2413	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2464112530	ref	XM_002826974.5	/217-2510	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2463445091	ref	XM_054457336.1	/217-2510	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2493367171	ref	XM_055367400.1	/104-2393	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	369762889	gb	JN900492.1	/1-2296	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	1894803100	ref	NM_001126118.2	/1-2296	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	1743179656	ref	XM_030800485.1	/219-2506	CCCTCCCCCTG	CCATTTTGGG	TTTTGGATCT	TTGAACCCCTT
gi	1012955506	gb	JN214348.1	/1-2294	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	1820556254	ref	XM_032139337.2	/219-2505	CCCTCCCCCTG	CCATTTTGGG	TTTTGGATCT	TTGAACCCCTT
gi	2491632765	ref	XM_055256596.1	/219-2498	CCCTCCCCCTG	CCATTTTGGG	TTTTGGATCT	TTGAACCCCTT
gi	2468545380	ref	XM_016931470.3	/1-2299	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	2516461531	ref	XM_057300362.1	/1-2288	CCCTCCCCCTG	CCATTTTGGG	TTTTGGGTCT	TTGAACCCCTT
gi	1482600679	ref	XM_023193314.2	/219-2502	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAACCCCTT
gi	795239330	ref	XM_012052423.1	/219-2503	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	1777287103	ref	XM_003912272.5	/219-2502	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	795219218	ref	XM_011994540.1	/219-2501	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	795284141	ref	XM_011958558.1	/219-2511	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAACCCCTT
gi	1411121371	ref	XM_025363516.1	/219-2502	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	795219223	ref	XM_011994541.1	/216-2498	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	795284149	ref	XM_011958559.1	/216-2508	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAACCCCTT
gi	1411121369	ref	XM_025363515.1	/219-2505	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	1825912814	ref	XM_033184717.1	/219-2500	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAACCAATT
gi	1411121373	ref	XM_025363517.1	/216-2499	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	1938907787	ref	XM_008010194.2	/219-2504	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	2161852969	ref	XM_005582787.3	/216-2491	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	724818526	ref	XM_010362387.1	/219-2500	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAACCCCTT
gi	1059108540	ref	XM_017850545.1	/219-2500	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAAACCTT
gi	2161852970	ref	XM_045375424.1	/213-2488	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	2309385734	ref	XM_050765347.1	/104-2390	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	2309385732	ref	XM_050765346.1	/104-2390	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	1622875777	ref	XM_028835713.1	/104-2379	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	2161852967	ref	XM_045375423.1	/104-2379	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT
gi	1059108538	ref	XM_017850544.1	/104-2385	CCCTCCCCCTG	CCATTTTGGAG	TTTTGGGTCT	TTAAAACCTT
gi	1938907785	ref	XM_008010192.2	/1-2286	CCCTCCCCCTG	CCATTTTGGAG	TTCTGGGTCT	TTAAACCCCTT

gi	1808862652	ref	NM_000546.6	/217-2512	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	631786534	tpe	HG975427.1	/217-2512	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1889531459	ref	NM_001276761.3	/214-2509	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	11066969	gb	AF307851.1	AF307851/205-2499	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	13097806	gb	BC003596.1	/195-2489	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2468545382	ref	XM_001172077.6	/217-2515	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2490746137	ref	XM_003810066.4	/217-2504	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	82502895	gb	DQ191317.1	/216-2519	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	208342285	gb	FJ207420.1	/210-2513	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	82502903	gb	DQ286964.1	/209-2512	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	23491728	dbj	AB082923.1	/138-2432	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2246031073	ref	NM_001407262.1	/104-2399	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2246031052	ref	NM_001407266.1	/104-2399	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2246031054	ref	NM_001407265.1	/103-2398	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2493367174	ref	XM_004058511.4	/124-2413	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2464112530	ref	XM_002826974.5	/217-2510	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2463445091	ref	XM_054457336.1	/217-2510	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCG
gi	2493367171	ref	XM_055367400.1	/104-2393	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	369762889	gb	JN900492.1	/1-2296	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1894803100	ref	NM_001126118.2	/1-2296	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1743179656	ref	XM_030800485.1	/219-2506	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCG
gi	1012955506	gb	JN214348.1	/1-2294	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCG
gi	1820556254	ref	XM_032139337.2	/219-2505	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCG
gi	2491632765	ref	XM_055256596.1	/219-2498	GCTTGCAATA	GGTGTGCATC	AGAAGCACCC	AGGACTTCCG
gi	2468545380	ref	XM_016931470.3	/1-2299	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	2516461531	ref	XM_057300362.1	/1-2288	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1482600679	ref	XM_023193314.2	/219-2502	GCTTGCAATA	GGTGTGCATC	AGAAGCACCC	AGGACTTCCA
gi	795239330	ref	XM_012052423.1	/219-2503	GCTTGCAATA	GGTGTGCATC	AGAAGCACCC	AGGAGTTCCG
gi	1777287103	ref	XM_003912272.5	/219-2502	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
gi	795219218	ref	XM_011994540.1	/219-2501	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
gi	795284141	ref	XM_011958558.1	/219-2511	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1411121371	ref	XM_025363516.1	/219-2502	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
gi	795219223	ref	XM_011994541.1	/216-2498	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
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gi	1411121369	ref	XM_025363515.1	/219-2505	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
gi	1825912814	ref	XM_033184717.1	/219-2500	GCTTGCATA	GGTGTGCGTC	AGAAGCACCC	AGGACTTCCA
gi	1411121373	ref	XM_025363517.1	/216-2499	GCTTGCAATA	GGTGTGCGTC	AGAAGCACCC	AGGAGTTCCG
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gi	2161852969	ref	XM_005582787.3	/216-2491	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	724818526	ref	XM_010362387.1	/219-2500	GCTTCCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTT-CA
gi	1059108540	ref	XM_017850545.1	/219-2500	GCTTCCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTT-CA
gi	2161852970	ref	XM_045375424.1	/213-2488	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	2309385734	ref	XM_050765347.1	/104-2390	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	2309385732	ref	XM_050765346.1	/104-2390	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	1622875777	ref	XM_028835713.1	/104-2379	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	2161852967	ref	XM_045375423.1	/104-2379	GCTTGCAATA	GGTGTGCATC	AGGAGCACCC	AGGAGTTCCG
gi	1059108538	ref	XM_017850544.1	/104-2385	GCTTCCAATA	GGTGTGCGTC	AGAAGCACCC	AGGACTT-CA
gi	1938907785	ref	XM_008010192.2	/1-2286	GCTTGCAATA	GGTGTGTGTC	AGAAGCACCC	AGGAGTTCCG

gi	1808862652	ref	NM_000546.6	/217-2512	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	631786534	tpe	HG975427.1	/217-2512	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	1889531459	ref	NM_001276761.3	/214-2509	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	13097806	gb	BC003596.1	/195-2489	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	2468545382	ref	XM_001172077.6	/217-2515	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2490746137	ref	XM_003810066.4	/217-2504	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	82502895	gb	DQ191317.1	/216-2519	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	208342285	gb	FJ207420.1	/210-2513	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	82502903	gb	DQ286964.1	/209-2512	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	23491728	dbj	AB082923.1	/138-2432	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	2246031073	ref	NM_001407262.1	/104-2399	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	2246031052	ref	NM_001407266.1	/104-2399	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	2246031054	ref	NM_001407265.1	/103-2398	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	2493367174	ref	XM_004058511.4	/124-2413	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2464112530	ref	XM_002826974.5	/217-2510	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2463445091	ref	XM_054457336.1	/217-2510	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2493367171	ref	XM_055367400.1	/104-2393	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	369762889	gb	JN900492.1	/1-2296	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	1894803100	ref	NM_001126118.2	/1-2296	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	1743179656	ref	XM_030800485.1	/219-2506	TTTGGCTTTGT	CCCAGGGGCTC	GAC	TGAACAG	GTTGGCCTGC
gi	1012955506	gb	JN214348.1	/1-2294	TTTGGCTTTGT	CCCGGGGGCTC	CAC	TGAACAA	GTTGGCCTGC
gi	1820556254	ref	XM_032139337.2	/219-2505	TTTGGCTTTGT	CCCAGGGGCTC	GAC	TGAACAG	GTTGGCCTGC
gi	2491632765	ref	XM_055256596.1	/219-2498	TTTGGCTTTGT	CCCAGGGGCTC	GAC	TGAACAG	GTTGGCCTGC
gi	2468545380	ref	XM_016931470.3	/1-2299	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2516461531	ref	XM_057300362.1	/1-2288	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1482600679	ref	XM_023193314.2	/219-2502	TTTACTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	795239330	ref	XM_012052423.1	/219-2503	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1777287103	ref	XM_003912272.5	/219-2502	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	795219218	ref	XM_011994540.1	/219-2501	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	795284141	ref	XM_011958558.1	/219-2511	TTTACTTTGT	CCCTGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1411121371	ref	XM_025363516.1	/219-2502	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	795219223	ref	XM_011994541.1	/216-2498	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	795284149	ref	XM_011958559.1	/216-2508	TTTACTTTGT	CCCTGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1411121369	ref	XM_025363515.1	/219-2505	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1825912814	ref	XM_033184717.1	/219-2500	TTTCTTTGT	CCCAGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1411121373	ref	XM_025363517.1	/216-2499	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1938907787	ref	XM_008010194.2	/219-2504	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2161852969	ref	XM_005582787.3	/216-2491	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	724818526	ref	XM_010362387.1	/219-2500	TTTACTTTGT	CCCAGGGGCTT	GAC	TGAACAA	GTTGGCCTGC
gi	1059108540	ref	XM_017850545.1	/219-2500	TTTACTTTGT	CCCAGGGGCTT	GAC	TGAACAA	GTTGGCCTGC
gi	2161852970	ref	XM_045375424.1	/213-2488	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2309385734	ref	XM_050765347.1	/104-2390	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2309385732	ref	XM_050765346.1	/104-2390	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1622875777	ref	XM_028835713.1	/104-2379	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	2161852967	ref	XM_045375423.1	/104-2379	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC
gi	1059108538	ref	XM_017850544.1	/104-2385	TTTACTTTGT	CCCAGGGGCTT	GAC	TGAACAA	GTTGGCCTGC
gi	1938907785	ref	XM_008010192.2	/1-2286	TTTGGCTTTGT	CCCGGGGGCTC	GAC	TGAACAA	GTTGGCCTGC

gi	1808862652	ref	NM_000546.6	/217-2512	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	631786534	tpe	HG975427.1	/217-2512	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1889531459	ref	NM_001276761.3	/214-2509	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	11066969	gb	AF307851.1	AF307851/205-2499	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	13097806	gb	BC003596.1	/195-2489	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2468545382	ref	XM_001172077.6	/217-2515	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2490746137	ref	XM_003810066.4	/217-2504	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	82502895	gb	DQ191317.1	/216-2519	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	208342285	gb	FJ207420.1	/210-2513	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	82502903	gb	DQ286964.1	/209-2512	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	23491728	dbj	AB082923.1	/138-2432	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2246031073	ref	NM_001407262.1	/104-2399	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2246031052	ref	NM_001407266.1	/104-2399	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2246031054	ref	NM_001407265.1	/103-2398	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2493367174	ref	XM_004058511.4	/124-2413	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2464112530	ref	XM_002826974.5	/217-2510	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2463445091	ref	XM_054457336.1	/217-2510	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2493367171	ref	XM_055367400.1	/104-2393	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	369762889	gb	JN900492.1	/1-2296	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1894803100	ref	NM_001126118.2	/1-2296	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1743179656	ref	XM_030800485.1	/219-2506	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1012955506	gb	JN214348.1	/1-2294	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1820556254	ref	XM_032139337.2	/219-2505	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2491632765	ref	XM_055256596.1	/219-2498	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2468545380	ref	XM_016931470.3	/1-2299	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	2516461531	ref	XM_057300362.1	/1-2288	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGAGTAGGAC
gi	1482600679	ref	XM_023193314.2	/219-2502	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	795239330	ref	XM_012052423.1	/219-2503	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1777287103	ref	XM_003912272.5	/219-2502	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	795219218	ref	XM_011994540.1	/219-2501	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	795284141	ref	XM_011958558.1	/219-2511	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGACAGGAC
gi	1411121371	ref	XM_025363516.1	/219-2502	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	795219223	ref	XM_011994541.1	/216-2498	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	795284149	ref	XM_011958559.1	/216-2508	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGACAGGAC
gi	1411121369	ref	XM_025363515.1	/219-2505	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1825912814	ref	XM_033184717.1	/219-2500	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1411121373	ref	XM_025363517.1	/216-2499	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1938907787	ref	XM_008010194.2	/219-2504	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	2161852969	ref	XM_005582787.3	/216-2491	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	724818526	ref	XM_010362387.1	/219-2500	ACTGGTGT	TTT	TGTTGTAGGG	AGGAGGATGG	GGGGTAGGAC
gi	1059108540	ref	XM_017850545.1	/219-2500	ACTGGTGT	TTT	TGTTGTAGGG	AGGAGGATGG	GGGGTAGGAC
gi	2161852970	ref	XM_045375424.1	/213-2488	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	2309385734	ref	XM_050765347.1	/104-2390	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	2309385732	ref	XM_050765346.1	/104-2390	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1622875777	ref	XM_028835713.1	/104-2379	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	2161852967	ref	XM_045375423.1	/104-2379	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC
gi	1059108538	ref	XM_017850544.1	/104-2385	ACTGGTGT	TTT	TGTTGTAGGG	AGGAGGATGG	GGGGTAGGAC
gi	1938907785	ref	XM_008010192.2	/1-2286	ACTGGTGT	TTT	TGTTGTGGGG	AGGAGGATGG	GGGGTAGGAC

gi	1808862652	ref	NM_000546.6	/217-2512	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	631786534	tpe	HG975427.1	/217-2512	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1889531459	ref	NM_001276761.3	/214-2509	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	11066969	gb	AF307851.1	AF307851/205-2499	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	13097806	gb	BC003596.1	/195-2489	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2468545382	ref	XM_001172077.6	/217-2515	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2490746137	ref	XM_003810066.4	/217-2504	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	82502895	gb	DQ191317.1	/216-2519	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	208342285	gb	FJ207420.1	/210-2513	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	82502903	gb	DQ286964.1	/209-2512	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	23491728	dbj	AB082923.1	/138-2432	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2246031073	ref	NM_001407262.1	/104-2399	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2246031052	ref	NM_001407266.1	/104-2399	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2246031054	ref	NM_001407265.1	/103-2398	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2493367174	ref	XM_004058511.4	/124-2413	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2464112530	ref	XM_002826974.5	/217-2510	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2463445091	ref	XM_054457336.1	/217-2510	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2493367171	ref	XM_055367400.1	/104-2393	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	369762889	gb	JN900492.1	/1-2296	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1894803100	ref	NM_001126118.2	/1-2296	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1743179656	ref	XM_030800485.1	/219-2506	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGG---
gi	1012955506	gb	JN214348.1	/1-2294	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1820556254	ref	XM_032139337.2	/219-2505	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGG---
gi	2491632765	ref	XM_055256596.1	/219-2498	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGG---
gi	2468545380	ref	XM_016931470.3	/1-2299	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2516461531	ref	XM_057300362.1	/1-2288	AT-ACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1482600679	ref	XM_023193314.2	/219-2502	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	795239330	ref	XM_012052423.1	/219-2503	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1777287103	ref	XM_003912272.5	/219-2502	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	795219218	ref	XM_011994540.1	/219-2501	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	795284141	ref	XM_011958558.1	/219-2511	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1411121371	ref	XM_025363516.1	/219-2502	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	795219223	ref	XM_011994541.1	/216-2498	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	795284149	ref	XM_011958559.1	/216-2508	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1411121369	ref	XM_025363515.1	/219-2505	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1825912814	ref	XM_033184717.1	/219-2500	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1411121373	ref	XM_025363517.1	/216-2499	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1938907787	ref	XM_008010194.2	/219-2504	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2161852969	ref	XM_005582787.3	/216-2491	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	724818526	ref	XM_010362387.1	/219-2500	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1059108540	ref	XM_017850545.1	/219-2500	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2161852970	ref	XM_045375424.1	/213-2488	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2309385734	ref	XM_050765347.1	/104-2390	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2309385732	ref	XM_050765346.1	/104-2390	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1622875777	ref	XM_028835713.1	/104-2379	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	2161852967	ref	XM_045375423.1	/104-2379	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1059108538	ref	XM_017850544.1	/104-2385	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG
gi	1938907785	ref	XM_008010192.2	/1-2286	ATAACCAGCT	TAGATTTTAA	GGTTTTTACT	GTGAGGGATG

gi	1808862652	ref	NM_000546.6	/217-2512	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	631786534	tpe	HG975427.1	/217-2512	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	1889531459	ref	NM_001276761.3	/214-2509	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	13097806	gb	BC003596.1	/195-2489	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	2468545382	ref	XM_001172077.6	/217-2515	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2490746137	ref	XM_003810066.4	/217-2504	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	82502895	gb	DQ191317.1	/216-2519	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	208342285	gb	FJ207420.1	/210-2513	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	82502903	gb	DQ286964.1	/209-2512	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	23491728	dbj	AB082923.1	/138-2432	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	2246031073	ref	NM_001407262.1	/104-2399	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	2246031052	ref	NM_001407266.1	/104-2399	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	2246031054	ref	NM_001407265.1	/103-2398	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2463445091	ref	XM_054457336.1	/217-2510	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2493367171	ref	XM_055367400.1	/104-2393	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	369762889	gb	JN900492.1	/1-2296	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	1894803100	ref	NM_001126118.2	/1-2296	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	1743179656	ref	XM_030800485.1	/219-2506	-----AT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1012955506	gb	JN214348.1	/1-2294	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGT	TAAGGGTTAG
gi	1820556254	ref	XM_032139337.2	/219-2505	-----AT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2491632765	ref	XM_055256596.1	/219-2498	-----AT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2516461531	ref	XM_057300362.1	/1-2288	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1482600679	ref	XM_023193314.2	/219-2502	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	795239330	ref	XM_012052423.1	/219-2503	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1777287103	ref	XM_003912272.5	/219-2502	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	795219218	ref	XM_011994540.1	/219-2501	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	795284141	ref	XM_011958558.1	/219-2511	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1411121371	ref	XM_025363516.1	/219-2502	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	795219223	ref	XM_011994541.1	/216-2498	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	795284149	ref	XM_011958559.1	/216-2508	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1411121369	ref	XM_025363515.1	/219-2505	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1825912814	ref	XM_033184717.1	/219-2500	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1411121373	ref	XM_025363517.1	/216-2499	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1938907787	ref	XM_008010194.2	/219-2504	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2161852969	ref	XM_005582787.3	/216-2491	TTTGGGAAAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	724818526	ref	XM_010362387.1	/219-2500	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1059108540	ref	XM_017850545.1	/219-2500	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2161852970	ref	XM_045375424.1	/213-2488	TTTGGGAAAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2309385734	ref	XM_050765347.1	/104-2390	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2309385732	ref	XM_050765346.1	/104-2390	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1622875777	ref	XM_028835713.1	/104-2379	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	2161852967	ref	XM_045375423.1	/104-2379	TTTGGGAAAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1059108538	ref	XM_017850544.1	/104-2385	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TTTGGGAGAT	GTAAGAAATG	TTCTTGCAGG	TAAGGGTTAG

gi	1808862652	ref	NM_000546.6	/217-2512	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	631786534	tpe	HG975427.1	/217-2512	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1889531459	ref	NM_001276761.3	/214-2509	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	13097806	gb	BC003596.1	/195-2489	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2468545382	ref	XM_001172077.6	/217-2515	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2490746137	ref	XM_003810066.4	/217-2504	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	82502895	gb	DQ191317.1	/216-2519	TTTACAATCA	GCCACATTC	AGG	TAGGTAG	GGGCCCACCTT
gi	208342285	gb	FJ207420.1	/210-2513	TTTACAATCA	GCCACATTC	AGG	TAGGTAG	GGGCCCACCTT
gi	82502903	gb	DQ286964.1	/209-2512	TTTACAATCA	GCCACATTC	AGG	TAGGTAG	GGGCCCACCTT
gi	23491728	dbj	AB082923.1	/138-2432	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2246031073	ref	NM_001407262.1	/104-2399	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2246031052	ref	NM_001407266.1	/104-2399	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2246031054	ref	NM_001407265.1	/103-2398	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2493367174	ref	XM_004058511.4	/124-2413	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2464112530	ref	XM_002826974.5	/217-2510	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2463445091	ref	XM_054457336.1	/217-2510	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2493367171	ref	XM_055367400.1	/104-2393	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	369762889	gb	JN900492.1	/1-2296	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1894803100	ref	NM_001126118.2	/1-2296	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1743179656	ref	XM_030800485.1	/219-2506	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1012955506	gb	JN214348.1	/1-2294	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1820556254	ref	XM_032139337.2	/219-2505	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2491632765	ref	XM_055256596.1	/219-2498	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2468545380	ref	XM_016931470.3	/1-2299	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	2516461531	ref	XM_057300362.1	/1-2288	TTTACAATCA	GCCACATTC	---	TAGGTAG	GGGCCCACCTT
gi	1482600679	ref	XM_023193314.2	/219-2502	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	795239330	ref	XM_012052423.1	/219-2503	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1777287103	ref	XM_003912272.5	/219-2502	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	795219218	ref	XM_011994540.1	/219-2501	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	795284141	ref	XM_011958558.1	/219-2511	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1411121371	ref	XM_025363516.1	/219-2502	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	795219223	ref	XM_011994541.1	/216-2498	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	795284149	ref	XM_011958559.1	/216-2508	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1411121369	ref	XM_025363515.1	/219-2505	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1825912814	ref	XM_033184717.1	/219-2500	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1411121373	ref	XM_025363517.1	/216-2499	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1938907787	ref	XM_008010194.2	/219-2504	TTTACAATCA	GCCACATTC	---	TAGGTGA	CACCCCACCTT
gi	2161852969	ref	XM_005582787.3	/216-2491	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	724818526	ref	XM_010362387.1	/219-2500	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1059108540	ref	XM_017850545.1	/219-2500	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	2161852970	ref	XM_045375424.1	/213-2488	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	2309385734	ref	XM_050765347.1	/104-2390	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	2309385732	ref	XM_050765346.1	/104-2390	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1622875777	ref	XM_028835713.1	/104-2379	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	2161852967	ref	XM_045375423.1	/104-2379	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1059108538	ref	XM_017850544.1	/104-2385	TTTACAATCA	GCCACATTC	---	TAGGTGG	CACCCCACCTT
gi	1938907785	ref	XM_008010192.2	/1-2286	TTTACAATCA	GCCACATTC	---	TAGGTGA	CACCCCACCTT

gi	1808862652	ref	NM_000546.6	/217-2512	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	631786534	tpe	HG975427.1	/217-2512	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1889531459	ref	NM_001276761.3	/214-2509	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	13097806	gb	BC003596.1	/195-2489	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2468545382	ref	XM_001172077.6	/217-2515	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2490746137	ref	XM_003810066.4	/217-2504	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	82502895	gb	DQ191317.1	/216-2519	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	-TGTTGAATT
gi	208342285	gb	FJ207420.1	/210-2513	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	-TGTTGAATT
gi	82502903	gb	DQ286964.1	/209-2512	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	-TGTTGAATT
gi	23491728	dbj	AB082923.1	/138-2432	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2246031073	ref	NM_001407262.1	/104-2399	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2246031052	ref	NM_001407266.1	/104-2399	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2246031054	ref	NM_001407265.1	/103-2398	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2493367174	ref	XM_004058511.4	/124-2413	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2464112530	ref	XM_002826974.5	/217-2510	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2463445091	ref	XM_054457336.1	/217-2510	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2493367171	ref	XM_055367400.1	/104-2393	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	369762889	gb	JN900492.1	/1-2296	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1894803100	ref	NM_001126118.2	/1-2296	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1743179656	ref	XM_030800485.1	/219-2506	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1012955506	gb	JN214348.1	/1-2294	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1820556254	ref	XM_032139337.2	/219-2505	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2491632765	ref	XM_055256596.1	/219-2498	CACCACTACTA	ACCAGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2468545380	ref	XM_016931470.3	/1-2299	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2516461531	ref	XM_057300362.1	/1-2288	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1482600679	ref	XM_023193314.2	/219-2502	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	795239330	ref	XM_012052423.1	/219-2503	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1777287103	ref	XM_003912272.5	/219-2502	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	795219218	ref	XM_011994540.1	/219-2501	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	795284141	ref	XM_011958558.1	/219-2511	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	1411121371	ref	XM_025363516.1	/219-2502	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTATTGAATT
gi	795219223	ref	XM_011994541.1	/216-2498	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	795284149	ref	XM_011958559.1	/216-2508	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	1411121369	ref	XM_025363515.1	/219-2505	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTATTGAATT
gi	1825912814	ref	XM_033184717.1	/219-2500	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	1411121373	ref	XM_025363517.1	/216-2499	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTATTGAATT
gi	1938907787	ref	XM_008010194.2	/219-2504	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTCAATT
gi	2161852969	ref	XM_005582787.3	/216-2491	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	724818526	ref	XM_010362387.1	/219-2500	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	1059108540	ref	XM_017850545.1	/219-2500	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	2161852970	ref	XM_045375424.1	/213-2488	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2309385734	ref	XM_050765347.1	/104-2390	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2309385732	ref	XM_050765346.1	/104-2390	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1622875777	ref	XM_028835713.1	/104-2379	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	2161852967	ref	XM_045375423.1	/104-2379	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTGAATT
gi	1059108538	ref	XM_017850544.1	/104-2385	CACCACTACTA	ACCAGGGAAG	CTGTCCCTCG	CTGTTGAATT
gi	1938907785	ref	XM_008010192.2	/1-2286	CACCGTACTA	ACCAGGGAAG	CTGTCCCTCA	CTGTTCAATT

gi	1808862652	ref	NM_000546.6	/217-2512	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	631786534	tpe	HG975427.1	/217-2512	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	1889531459	ref	NM_001276761.3	/214-2509	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	13097806	gb	BC003596.1	/195-2489	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2468545382	ref	XM_001172077.6	/217-2515	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2490746137	ref	XM_003810066.4	/217-2504	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	82502895	gb	DQ191317.1	/216-2519	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	208342285	gb	FJ207420.1	/210-2513	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	82502903	gb	DQ286964.1	/209-2512	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	23491728	dbj	AB082923.1	/138-2432	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2246031073	ref	NM_001407262.1	/104-2399	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2246031052	ref	NM_001407266.1	/104-2399	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2246031054	ref	NM_001407265.1	/103-2398	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2493367174	ref	XM_004058511.4	/124-2413	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2464112530	ref	XM_002826974.5	/217-2510	TTCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2463445091	ref	XM_054457336.1	/217-2510	TTCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2493367171	ref	XM_055367400.1	/104-2393	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	369762889	gb	JN900492.1	/1-2296	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	1894803100	ref	NM_001126118.2	/1-2296	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	1743179656	ref	XM_030800485.1	/219-2506	TTCTCTAACT	TCAAGGCCCT	TATCTATGAA	ATGCTGGCAT
gi	1012955506	gb	JN214348.1	/1-2294	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	1820556254	ref	XM_032139337.2	/219-2505	TTCTCTAACT	TCAAGGCCCT	TATCTATGAA	ATGCTGGCAT
gi	2491632765	ref	XM_055256596.1	/219-2498	TTCTCTAACT	TCAAGGCCCT	TATCTATGAA	ATGCTGGCAT
gi	2468545380	ref	XM_016931470.3	/1-2299	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	2516461531	ref	XM_057300362.1	/1-2288	TTCTCTAACT	TCAAGGCCCA	TATCTGTGAA	ATGCTGGCAT
gi	1482600679	ref	XM_023193314.2	/219-2502	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	795239330	ref	XM_012052423.1	/219-2503	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1777287103	ref	XM_003912272.5	/219-2502	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	795219218	ref	XM_011994540.1	/219-2501	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	795284141	ref	XM_011958558.1	/219-2511	TCCTCTAACT	TCAAGGTCCA	TATCTATGAA	ATGCTGGCAT
gi	1411121371	ref	XM_025363516.1	/219-2502	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	795219223	ref	XM_011994541.1	/216-2498	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	795284149	ref	XM_011958559.1	/216-2508	TCCTCTAACT	TCAAGGTCCA	TATCTATGAA	ATGCTGGCAT
gi	1411121369	ref	XM_025363515.1	/219-2505	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1825912814	ref	XM_033184717.1	/219-2500	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1411121373	ref	XM_025363517.1	/216-2499	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1938907787	ref	XM_008010194.2	/219-2504	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2161852969	ref	XM_005582787.3	/216-2491	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	724818526	ref	XM_010362387.1	/219-2500	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1059108540	ref	XM_017850545.1	/219-2500	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2161852970	ref	XM_045375424.1	/213-2488	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2309385734	ref	XM_050765347.1	/104-2390	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2309385732	ref	XM_050765346.1	/104-2390	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1622875777	ref	XM_028835713.1	/104-2379	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	2161852967	ref	XM_045375423.1	/104-2379	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1059108538	ref	XM_017850544.1	/104-2385	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT
gi	1938907785	ref	XM_008010192.2	/1-2286	TCCTCTAACT	TCAAGGCCCA	TATCTATGAA	ATGCTGGCAT

gi	1808862652	ref	NM_000546.6	/217-2512	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	631786534	tpe	HG975427.1	/217-2512	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	1889531459	ref	NM_001276761.3	/214-2509	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	13097806	gb	BC003596.1	/195-2489	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2468545382	ref	XM_001172077.6	/217-2515	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2490746137	ref	XM_003810066.4	/217-2504	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	82502895	gb	DQ191317.1	/216-2519	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	208342285	gb	FJ207420.1	/210-2513	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	82502903	gb	DQ286964.1	/209-2512	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	23491728	dbj	AB082923.1	/138-2432	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2246031073	ref	NM_001407262.1	/104-2399	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2246031052	ref	NM_001407266.1	/104-2399	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2246031054	ref	NM_001407265.1	/103-2398	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2493367174	ref	XM_004058511.4	/124-2413	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2464112530	ref	XM_002826974.5	/217-2510	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2463445091	ref	XM_054457336.1	/217-2510	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2493367171	ref	XM_055367400.1	/104-2393	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	369762889	gb	JN900492.1	/1-2296	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	1894803100	ref	NM_001126118.2	/1-2296	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	1743179656	ref	XM_030800485.1	/219-2506	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1012955506	gb	JN214348.1	/1-2294	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	1820556254	ref	XM_032139337.2	/219-2505	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2491632765	ref	XM_055256596.1	/219-2498	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2468545380	ref	XM_016931470.3	/1-2299	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	2516461531	ref	XM_057300362.1	/1-2288	TTGCAACCTAC	CTCACAGAGT	GCATTGTGAG	GGTTAATGAA
gi	1482600679	ref	XM_023193314.2	/219-2502	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	795239330	ref	XM_012052423.1	/219-2503	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1777287103	ref	XM_003912272.5	/219-2502	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	795219218	ref	XM_011994540.1	/219-2501	TTGCAACCTAC	CTCGCAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	795284141	ref	XM_011958558.1	/219-2511	TTGCAACCTAC	CTCACAGAGT	GCATCGTGAG	GGTTAATGAA
gi	1411121371	ref	XM_025363516.1	/219-2502	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	795219223	ref	XM_011994541.1	/216-2498	TTGCAACCTAC	CTCGCAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	795284149	ref	XM_011958559.1	/216-2508	TTGCAACCTAC	CTCACAGAGT	GCATCGTGAG	GGTTAATGAA
gi	1411121369	ref	XM_025363515.1	/219-2505	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1825912814	ref	XM_033184717.1	/219-2500	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1411121373	ref	XM_025363517.1	/216-2499	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1938907787	ref	XM_008010194.2	/219-2504	TTGCAACCTAC	CTCACAGAGT	GTGTTGTGAG	GGTTAATGAA
gi	2161852969	ref	XM_005582787.3	/216-2491	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	724818526	ref	XM_010362387.1	/219-2500	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1059108540	ref	XM_017850545.1	/219-2500	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2161852970	ref	XM_045375424.1	/213-2488	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2309385734	ref	XM_050765347.1	/104-2390	TTGCAACCTAC	CTCACAGAGT	GTGTTGTGAG	GGTTAATGAA
gi	2309385732	ref	XM_050765346.1	/104-2390	TTGCAACCTAC	CTCACAGAGT	GTGTTGTGAG	GGTTAATGAA
gi	1622875777	ref	XM_028835713.1	/104-2379	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	2161852967	ref	XM_045375423.1	/104-2379	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1059108538	ref	XM_017850544.1	/104-2385	TTGCAACCTAC	CTCACAGAGT	GCGTTGTGAG	GGTTAATGAA
gi	1938907785	ref	XM_008010192.2	/1-2286	TTGCAACCTAC	CTCACAGAGT	GTGTTGTGAG	GGTTAATGAA

gi	1808862652	ref	NM_000546.6	/217-2512	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	631786534	tpe	HG975427.1	/217-2512	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1889531459	ref	NM_001276761.3	/214-2509	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	11066969	gb	AF307851.1	AF307851/205-2499	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	13097806	gb	BC003596.1	/195-2489	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2468545382	ref	XM_001172077.6	/217-2515	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2490746137	ref	XM_003810066.4	/217-2504	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	82502895	gb	DQ191317.1	/216-2519	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	208342285	gb	FJ207420.1	/210-2513	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	82502903	gb	DQ286964.1	/209-2512	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	23491728	dbj	AB082923.1	/138-2432	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2246031073	ref	NM_001407262.1	/104-2399	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2246031052	ref	NM_001407266.1	/104-2399	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2246031054	ref	NM_001407265.1	/103-2398	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2493367174	ref	XM_004058511.4	/124-2413	ATAATGTACA	TCTGGCCTTG	AAATCAACCTT	TTATTACATG
gi	2464112530	ref	XM_002826974.5	/217-2510	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2463445091	ref	XM_054457336.1	/217-2510	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2493367171	ref	XM_055367400.1	/104-2393	ATAATGTACA	TCTGGCCTTG	AAATCAACCTT	TTATTACATG
gi	369762889	gb	JN900492.1	/1-2296	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1894803100	ref	NM_001126118.2	/1-2296	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1743179656	ref	XM_030800485.1	/219-2506	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1012955506	gb	JN214348.1	/1-2294	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1820556254	ref	XM_032139337.2	/219-2505	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2491632765	ref	XM_055256596.1	/219-2498	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2468545380	ref	XM_016931470.3	/1-2299	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2516461531	ref	XM_057300362.1	/1-2288	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1482600679	ref	XM_023193314.2	/219-2502	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	795239330	ref	XM_012052423.1	/219-2503	ATAATGTACG	TTTGGCCTTG	AAACCAACCTT	TTATTACTTG
gi	1777287103	ref	XM_003912272.5	/219-2502	ATAATGTACG	TTTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	795219218	ref	XM_011994540.1	/219-2501	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	795284141	ref	XM_011958558.1	/219-2511	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1411121371	ref	XM_025363516.1	/219-2502	ATAATGTACG	TTTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	795219223	ref	XM_011994541.1	/216-2498	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	795284149	ref	XM_011958559.1	/216-2508	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1411121369	ref	XM_025363515.1	/219-2505	ATAATGTACG	TTTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1825912814	ref	XM_033184717.1	/219-2500	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1411121373	ref	XM_025363517.1	/216-2499	ATAATGTACG	TTTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1938907787	ref	XM_008010194.2	/219-2504	ATAATGTATG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2161852969	ref	XM_005582787.3	/216-2491	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	724818526	ref	XM_010362387.1	/219-2500	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1059108540	ref	XM_017850545.1	/219-2500	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2161852970	ref	XM_045375424.1	/213-2488	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2309385734	ref	XM_050765347.1	/104-2390	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2309385732	ref	XM_050765346.1	/104-2390	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1622875777	ref	XM_028835713.1	/104-2379	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	2161852967	ref	XM_045375423.1	/104-2379	ATAATGTACA	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1059108538	ref	XM_017850544.1	/104-2385	ATAATGTACG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG
gi	1938907785	ref	XM_008010192.2	/1-2286	ATAATGTATG	TCTGGCCTTG	AAACCAACCTT	TTATTACATG

gi	1808862652	ref	NM_000546.6	/217-2512	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	631786534	tpe	HG975427.1	/217-2512	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1889531459	ref	NM_001276761.3	/214-2509	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	11066969	gb	AF307851.1	AF307851/205-2499	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	13097806	gb	BC003596.1	/195-2489	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2468545382	ref	XM_001172077.6	/217-2515	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2490746137	ref	XM_003810066.4	/217-2504	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	82502895	gb	DQ191317.1	/216-2519	GGGTCCTAAAA	CTTGACCCCC	TTGAGGGTGC	CTGTTCCCTC	
gi	208342285	gb	FJ207420.1	/210-2513	GGGTCCTAAAA	CTTGACCCCC	TTGAGGGTGC	CTGTTCCCTC	
gi	82502903	gb	DQ286964.1	/209-2512	GGGTCCTAAAA	CTTGACCCCC	TTGAGGGTGC	CTGTTCCCTC	
gi	23491728	dbj	AB082923.1	/138-2432	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2246031073	ref	NM_001407262.1	/104-2399	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2246031052	ref	NM_001407266.1	/104-2399	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2246031054	ref	NM_001407265.1	/103-2398	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2493367174	ref	XM_004058511.4	/124-2413	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2464112530	ref	XM_002826974.5	/217-2510	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2463445091	ref	XM_054457336.1	/217-2510	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2493367171	ref	XM_055367400.1	/104-2393	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	369762889	gb	JN900492.1	/1-2296	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1894803100	ref	NM_001126118.2	/1-2296	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1743179656	ref	XM_030800485.1	/219-2506	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1012955506	gb	JN214348.1	/1-2294	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1820556254	ref	XM_032139337.2	/219-2505	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2491632765	ref	XM_055256596.1	/219-2498	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2468545380	ref	XM_016931470.3	/1-2299	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2516461531	ref	XM_057300362.1	/1-2288	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1482600679	ref	XM_023193314.2	/219-2502	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	795239330	ref	XM_012052423.1	/219-2503	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	1777287103	ref	XM_003912272.5	/219-2502	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	795219218	ref	XM_011994540.1	/219-2501	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	795284141	ref	XM_011958558.1	/219-2511	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1411121371	ref	XM_025363516.1	/219-2502	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	795219223	ref	XM_011994541.1	/216-2498	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	795284149	ref	XM_011958559.1	/216-2508	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1411121369	ref	XM_025363515.1	/219-2505	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	1825912814	ref	XM_033184717.1	/219-2500	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTAT	-----
gi	1411121373	ref	XM_025363517.1	/216-2499	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	1938907787	ref	XM_008010194.2	/219-2504	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	2161852969	ref	XM_005582787.3	/216-2491	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	724818526	ref	XM_010362387.1	/219-2500	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1059108540	ref	XM_017850545.1	/219-2500	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	2161852970	ref	XM_045375424.1	/213-2488	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	2309385734	ref	XM_050765347.1	/104-2390	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	2309385732	ref	XM_050765346.1	/104-2390	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	1622875777	ref	XM_028835713.1	/104-2379	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	2161852967	ref	XM_045375423.1	/104-2379	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----
gi	1059108538	ref	XM_017850544.1	/104-2385	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TTGT	-----
gi	1938907785	ref	XM_008010192.2	/1-2286	GGGTCCTAGAA	CTTGACCCCC	TTGAGGGTGC	TCGT	-----

gi	1808862652	ref	NM_000546.6	/217-2512	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	631786534	tpe	HG975427.1	/217-2512	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1889531459	ref	NM_001276761.3	/214-2509	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	13097806	gb	BC003596.1	/195-2489	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2468545382	ref	XM_001172077.6	/217-2515	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAA
gi	2490746137	ref	XM_003810066.4	/217-2504	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAA
gi	82502895	gb	DQ191317.1	/216-2519	TCCCCTCTCCC	TGTTGGCTGG	TGGGTTGGTA	GTTTCTACAG
gi	208342285	gb	FJ207420.1	/210-2513	TCCCCTCTCCC	TGTTGGCTGG	TGGGTTGGTA	GTTTCTACAG
gi	82502903	gb	DQ286964.1	/209-2512	TCCCCTCTCCC	TGTTGGCTGG	TGGGTTGGTA	GTTTCTACAG
gi	23491728	dbj	AB082923.1	/138-2432	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2246031073	ref	NM_001407262.1	/104-2399	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
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gi	2246031054	ref	NM_001407265.1	/103-2398	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2463445091	ref	XM_054457336.1	/217-2510	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2493367171	ref	XM_055367400.1	/104-2393	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	369762889	gb	JN900492.1	/1-2296	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1894803100	ref	NM_001126118.2	/1-2296	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1743179656	ref	XM_030800485.1	/219-2506	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1012955506	gb	JN214348.1	/1-2294	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1820556254	ref	XM_032139337.2	/219-2505	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2491632765	ref	XM_055256596.1	/219-2498	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAA
gi	2516461531	ref	XM_057300362.1	/1-2288	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAA
gi	1482600679	ref	XM_023193314.2	/219-2502	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	795239330	ref	XM_012052423.1	/219-2503	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1777287103	ref	XM_003912272.5	/219-2502	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	795219218	ref	XM_011994540.1	/219-2501	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	ATTTCTACAG
gi	795284141	ref	XM_011958558.1	/219-2511	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1411121371	ref	XM_025363516.1	/219-2502	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	795219223	ref	XM_011994541.1	/216-2498	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	ATTTCTACAG
gi	795284149	ref	XM_011958559.1	/216-2508	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1411121369	ref	XM_025363515.1	/219-2505	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1825912814	ref	XM_033184717.1	/219-2500	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1411121373	ref	XM_025363517.1	/216-2499	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1938907787	ref	XM_008010194.2	/219-2504	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2161852969	ref	XM_005582787.3	/216-2491	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	724818526	ref	XM_010362387.1	/219-2500	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1059108540	ref	XM_017850545.1	/219-2500	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2161852970	ref	XM_045375424.1	/213-2488	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2309385734	ref	XM_050765347.1	/104-2390	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2309385732	ref	XM_050765346.1	/104-2390	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1622875777	ref	XM_028835713.1	/104-2379	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	2161852967	ref	XM_045375423.1	/104-2379	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1059108538	ref	XM_017850544.1	/104-2385	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TCCCCTCTCCC	TGTTGGTCGG	TGGGTTGGTA	GTTTCTACAG

gi	1808862652	ref	NM_000546.6	/217-2512	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	631786534	tpe	HG975427.1	/217-2512	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	1889531459	ref	NM_001276761.3	/214-2509	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	13097806	gb	BC003596.1	/195-2489	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2468545382	ref	XM_001172077.6	/217-2515	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2490746137	ref	XM_003810066.4	/217-2504	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	82502895	gb	DQ191317.1	/216-2519	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCT-TG
gi	208342285	gb	FJ207420.1	/210-2513	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCT-TG
gi	82502903	gb	DQ286964.1	/209-2512	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCT-TG
gi	23491728	dbj	AB082923.1	/138-2432	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2246031073	ref	NM_001407262.1	/104-2399	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2246031052	ref	NM_001407266.1	/104-2399	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2246031054	ref	NM_001407265.1	/103-2398	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2493367174	ref	XM_004058511.4	/124-2413	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2464112530	ref	XM_002826974.5	/217-2510	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2463445091	ref	XM_054457336.1	/217-2510	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	2493367171	ref	XM_055367400.1	/104-2393	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	369762889	gb	JN900492.1	/1-2296	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	1894803100	ref	NM_001126118.2	/1-2296	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	1743179656	ref	XM_030800485.1	/219-2506	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	1012955506	gb	JN214348.1	/1-2294	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	1820556254	ref	XM_032139337.2	/219-2505	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	2491632765	ref	XM_055256596.1	/219-2498	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	2468545380	ref	XM_016931470.3	/1-2299	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	2516461531	ref	XM_057300362.1	/1-2288	TTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGT	CAAGTCTCTG
gi	1482600679	ref	XM_023193314.2	/219-2502	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	795239330	ref	XM_012052423.1	/219-2503	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CGAGTCCCTG
gi	1777287103	ref	XM_003912272.5	/219-2502	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	795219218	ref	XM_011994540.1	/219-2501	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	795284141	ref	XM_011958558.1	/219-2511	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTC--TG
gi	1411121371	ref	XM_025363516.1	/219-2502	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	795219223	ref	XM_011994541.1	/216-2498	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	795284149	ref	XM_011958559.1	/216-2508	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTC--TG
gi	1411121369	ref	XM_025363515.1	/219-2505	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	1825912814	ref	XM_033184717.1	/219-2500	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	1411121373	ref	XM_025363517.1	/216-2499	CTGGGCAGCT	-GTTAGGTAG	AGGAAGTTGC	CAAGTCCCTG
gi	1938907787	ref	XM_008010194.2	/219-2504	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	2161852969	ref	XM_005582787.3	/216-2491	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	724818526	ref	XM_010362387.1	/219-2500	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	1059108540	ref	XM_017850545.1	/219-2500	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	2161852970	ref	XM_045375424.1	/213-2488	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	2309385734	ref	XM_050765347.1	/104-2390	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	2309385732	ref	XM_050765346.1	/104-2390	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	1622875777	ref	XM_028835713.1	/104-2379	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	2161852967	ref	XM_045375423.1	/104-2379	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG
gi	1059108538	ref	XM_017850544.1	/104-2385	CTGGGCAGCT	GGTTAGGTAG	AGGGAGTTGC	CAAGTCTCTG
gi	1938907785	ref	XM_008010192.2	/1-2286	CTGGGCAGCT	-GTTAGGTAG	AGGGAGTTGC	CAAGTCCCTG

gi	1808862652	ref	NM_000546.6	/217-2512	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	631786534	tpe	HG975427.1	/217-2512	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	1889531459	ref	NM_001276761.3	/214-2509	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	11066969	gb	AF307851.1	AF307851/205-2499	CTGGCCCAGC	CAAACCC-TG	TCTGACCACC	TCTTGGTGAA
gi	13097806	gb	BC003596.1	/195-2489	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2468545382	ref	XM_001172077.6	/217-2515	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2490746137	ref	XM_003810066.4	/217-2504	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	82502895	gb	DQ191317.1	/216-2519	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTCGA
gi	208342285	gb	FJ207420.1	/210-2513	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTCGA
gi	82502903	gb	DQ286964.1	/209-2512	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTCGA
gi	23491728	dbj	AB082923.1	/138-2432	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2246031073	ref	NM_001407262.1	/104-2399	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2246031052	ref	NM_001407266.1	/104-2399	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
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gi	2493367174	ref	XM_004058511.4	/124-2413	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2464112530	ref	XM_002826974.5	/217-2510	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
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gi	2493367171	ref	XM_055367400.1	/104-2393	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	369762889	gb	JN900492.1	/1-2296	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
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gi	1743179656	ref	XM_030800485.1	/219-2506	CTGGCCITGGC	CAAACCC-TG	TCTGACAACC	TCCTGGTGAA
gi	1012955506	gb	JN214348.1	/1-2294	CTGGCCCAGC	CAAACCC-TG	TCTGACCACC	TCTTGGTGAA
gi	1820556254	ref	XM_032139337.2	/219-2505	CTGGCCCTGGC	CAAACCC-TG	TCTGACAACC	TCCTGGTGAA
gi	2491632765	ref	XM_055256596.1	/219-2498	CTGGCCITGGC	CAAACCC-TG	TCTGACAACC	TCCTGGTGAA
gi	2468545380	ref	XM_016931470.3	/1-2299	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	2516461531	ref	XM_057300362.1	/1-2288	CTGGCCCAGC	CAAACCC-TG	TCTGACAACC	TCTTGGTGAA
gi	1482600679	ref	XM_023193314.2	/219-2502	CTGGCCCGGC	CAAACCC-TG	TCTGAGAACC	CGTTGGTGAA
gi	795239330	ref	XM_012052423.1	/219-2503	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	1777287103	ref	XM_003912272.5	/219-2502	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	795219218	ref	XM_011994540.1	/219-2501	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	795284141	ref	XM_011958558.1	/219-2511	CTGGCCITGGC	CAAACCC-TG	TCTGAGAACC	CGTTGGTGAA
gi	1411121371	ref	XM_025363516.1	/219-2502	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	795219223	ref	XM_011994541.1	/216-2498	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	795284149	ref	XM_011958559.1	/216-2508	CTGGCCITGGC	CAAACCC-TG	TCTGAGAACC	CGTTGGTGAA
gi	1411121369	ref	XM_025363515.1	/219-2505	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	1825912814	ref	XM_033184717.1	/219-2500	CTGGCCCGGC	CAAACCC-TG	TCTGAGAACC	CGTTGGTGAA
gi	1411121373	ref	XM_025363517.1	/216-2499	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	1938907787	ref	XM_008010194.2	/219-2504	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	2161852969	ref	XM_005582787.3	/216-2491	TTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	724818526	ref	XM_010362387.1	/219-2500	CTGGCCCGGC	CAAACCC-TG	TCTGAGAACC	CGTTGGTGAA
gi	1059108540	ref	XM_017850545.1	/219-2500	CTGGCCCGGC	CAAACCC-TG	TCTGAGAACC	CAITGGTGAA
gi	2161852970	ref	XM_045375424.1	/213-2488	TTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
gi	2309385734	ref	XM_050765347.1	/104-2390	TTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
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gi	1622875777	ref	XM_028835713.1	/104-2379	TTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA
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gi	1059108538	ref	XM_017850544.1	/104-2385	CTGGCCCGGC	CAAACCC-TG	TCTGAGAACC	CAITGGTGAA
gi	1938907785	ref	XM_008010192.2	/1-2286	CTGGCCCGGC	CAAACCCTTG	TCTGAGAACC	TGTTGGTGAA

gi	1808862652	ref	NM_000546.6	/217-2512	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	631786534	tpe	HG975427.1	/217-2512	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1889531459	ref	NM_001276761.3	/214-2509	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	11066969	gb	AF307851.1	AF307851/205-2499	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	13097806	gb	BC003596.1	/195-2489	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2468545382	ref	XM_001172077.6	/217-2515	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2490746137	ref	XM_003810066.4	/217-2504	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	82502895	gb	DQ191317.1	/216-2519	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	208342285	gb	FJ207420.1	/210-2513	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	82502903	gb	DQ286964.1	/209-2512	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	23491728	dbj	AB082923.1	/138-2432	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2246031073	ref	NM_001407262.1	/104-2399	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2246031052	ref	NM_001407266.1	/104-2399	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2246031054	ref	NM_001407265.1	/103-2398	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2493367174	ref	XM_004058511.4	/124-2413	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2464112530	ref	XM_002826974.5	/217-2510	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2463445091	ref	XM_054457336.1	/217-2510	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2493367171	ref	XM_055367400.1	/104-2393	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	369762889	gb	JN900492.1	/1-2296	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1894803100	ref	NM_001126118.2	/1-2296	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1743179656	ref	XM_030800485.1	/219-2506	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1012955506	gb	JN214348.1	/1-2294	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1820556254	ref	XM_032139337.2	/219-2505	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2491632765	ref	XM_055256596.1	/219-2498	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2468545380	ref	XM_016931470.3	/1-2299	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2516461531	ref	XM_057300362.1	/1-2288	CCTTAGTACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1482600679	ref	XM_023193314.2	/219-2502	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	795239330	ref	XM_012052423.1	/219-2503	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1777287103	ref	XM_003912272.5	/219-2502	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
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gi	795284141	ref	XM_011958558.1	/219-2511	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1411121371	ref	XM_025363516.1	/219-2502	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
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gi	1411121369	ref	XM_025363515.1	/219-2505	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1825912814	ref	XM_033184717.1	/219-2500	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1411121373	ref	XM_025363517.1	/216-2499	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1938907787	ref	XM_008010194.2	/219-2504	CCTTAGCACC	TAAAAAGGAAA	TCTCATCCCA	TCCCACACCC
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gi	724818526	ref	XM_010362387.1	/219-2500	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1059108540	ref	XM_017850545.1	/219-2500	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2161852970	ref	XM_045375424.1	/213-2488	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2309385734	ref	XM_050765347.1	/104-2390	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	2309385732	ref	XM_050765346.1	/104-2390	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1622875777	ref	XM_028835713.1	/104-2379	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
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gi	1059108538	ref	XM_017850544.1	/104-2385	CCTTAGCACC	TAAAAAGGAAA	TCTCACCCCA	TCCCACACCC
gi	1938907785	ref	XM_008010192.2	/1-2286	CCTTAGCACC	TAAAAAGGAAA	TCTCATCCCA	TCCCACACCC

gi	1808862652	ref	NM_000546.6	/217-2512	TGGAGGATTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	631786534	tpe	HG975427.1	/217-2512	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1889531459	ref	NM_001276761.3	/214-2509	TGGAGGATTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	11066969	gb	AF307851.1	AF307851/205-2499	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	13097806	gb	BC003596.1	/195-2489	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2468545382	ref	XM_001172077.6	/217-2515	TGGAGGATAT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2490746137	ref	XM_003810066.4	/217-2504	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	82502895	gb	DQ191317.1	/216-2519	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	208342285	gb	FJ207420.1	/210-2513	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	82502903	gb	DQ286964.1	/209-2512	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	23491728	dbj	AB082923.1	/138-2432	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2246031073	ref	NM_001407262.1	/104-2399	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2246031052	ref	NM_001407266.1	/104-2399	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2246031054	ref	NM_001407265.1	/103-2398	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2493367174	ref	XM_004058511.4	/124-2413	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2464112530	ref	XM_002826974.5	/217-2510	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2463445091	ref	XM_054457336.1	/217-2510	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2493367171	ref	XM_055367400.1	/104-2393	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	369762889	gb	JN900492.1	/1-2296	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1894803100	ref	NM_001126118.2	/1-2296	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1743179656	ref	XM_030800485.1	/219-2506	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1012955506	gb	JN214348.1	/1-2294	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1820556254	ref	XM_032139337.2	/219-2505	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2491632765	ref	XM_055256596.1	/219-2498	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2468545380	ref	XM_016931470.3	/1-2299	TGGAGGATAT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	2516461531	ref	XM_057300362.1	/1-2288	TGGAGGATTTT	CATCTCTTGT	ATATGATGAT	CTGGATCCAC
gi	1482600679	ref	XM_023193314.2	/219-2502	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	795239330	ref	XM_012052423.1	/219-2503	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	1777287103	ref	XM_003912272.5	/219-2502	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	795219218	ref	XM_011994540.1	/219-2501	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	795284141	ref	XM_011958558.1	/219-2511	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	1411121371	ref	XM_025363516.1	/219-2502	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	795219223	ref	XM_011994541.1	/216-2498	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	795284149	ref	XM_011958559.1	/216-2508	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	1411121369	ref	XM_025363515.1	/219-2505	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	1825912814	ref	XM_033184717.1	/219-2500	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	1411121373	ref	XM_025363517.1	/216-2499	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	1938907787	ref	XM_008010194.2	/219-2504	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	2161852969	ref	XM_005582787.3	/216-2491	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	724818526	ref	XM_010362387.1	/219-2500	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	1059108540	ref	XM_017850545.1	/219-2500	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	2161852970	ref	XM_045375424.1	/213-2488	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	2309385734	ref	XM_050765347.1	/104-2390	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	2309385732	ref	XM_050765346.1	/104-2390	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	1622875777	ref	XM_028835713.1	/104-2379	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	2161852967	ref	XM_045375423.1	/104-2379	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC
gi	1059108538	ref	XM_017850544.1	/104-2385	TGGAGGATTTT	CATCTCTTGT	CTAGGATGAT	CTGGATCCAC
gi	1938907785	ref	XM_008010192.2	/1-2286	TGGAGGATTTT	CATCTCTTGT	CTATGATGAT	CTGGATCCAC

gi	1808862652	ref	NM_000546.6	/217-2512	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	631786534	tpe	HG975427.1	/217-2512	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	1889531459	ref	NM_001276761.3	/214-2509	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	11066969	gb	AF307851.1	AF307851/205-2499	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	13097806	gb	BC003596.1	/195-2489	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2468545382	ref	XM_001172077.6	/217-2515	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	TT
gi	2490746137	ref	XM_003810066.4	/217-2504	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	82502895	gb	DQ191317.1	/216-2519	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	208342285	gb	FJ207420.1	/210-2513	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	82502903	gb	DQ286964.1	/209-2512	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	23491728	dbj	AB082923.1	/138-2432	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2246031073	ref	NM_001407262.1	/104-2399	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2246031052	ref	NM_001407266.1	/104-2399	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2246031054	ref	NM_001407265.1	/103-2398	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2493367174	ref	XM_004058511.4	/124-2413	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2464112530	ref	XM_002826974.5	/217-2510	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2463445091	ref	XM_054457336.1	/217-2510	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	2493367171	ref	XM_055367400.1	/104-2393	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	369762889	gb	JN900492.1	/1-2296	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	1894803100	ref	NM_001126118.2	/1-2296	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	1743179656	ref	XM_030800485.1	/219-2506	C-AGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTTT	TT
gi	1012955506	gb	JN214348.1	/1-2294	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	1820556254	ref	XM_032139337.2	/219-2505	C-AGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTTT	T
gi	2491632765	ref	XM_055256596.1	/219-2498	C-AGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTT	----
gi	2468545380	ref	XM_016931470.3	/1-2299	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTTT	TT
gi	2516461531	ref	XM_057300362.1	/1-2288	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTTTC	--
gi	1482600679	ref	XM_023193314.2	/219-2502	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	795239330	ref	XM_012052423.1	/219-2503	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	1777287103	ref	XM_003912272.5	/219-2502	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	795219218	ref	XM_011994540.1	/219-2501	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	795284141	ref	XM_011958558.1	/219-2511	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	1411121371	ref	XM_025363516.1	/219-2502	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	795219223	ref	XM_011994541.1	/216-2498	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	795284149	ref	XM_011958559.1	/216-2508	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	1411121369	ref	XM_025363515.1	/219-2505	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	1825912814	ref	XM_033184717.1	/219-2500	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	1411121373	ref	XM_025363517.1	/216-2499	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	1938907787	ref	XM_008010194.2	/219-2504	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	2161852969	ref	XM_005582787.3	/216-2491	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	724818526	ref	XM_010362387.1	/219-2500	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	1059108540	ref	XM_017850545.1	/219-2500	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	2161852970	ref	XM_045375424.1	/213-2488	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	2309385734	ref	XM_050765347.1	/104-2390	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	TT--
gi	2309385732	ref	XM_050765346.1	/104-2390	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	TT--
gi	1622875777	ref	XM_028835713.1	/104-2379	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	2161852967	ref	XM_045375423.1	/104-2379	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----
gi	1059108538	ref	XM_017850544.1	/104-2385	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	ATTTTC	----
gi	1938907785	ref	XM_008010192.2	/1-2286	CAAGACTTGT	TTTATGCTCA	GGGTCAATTT	CTTTTC	----

gi	1808862652	ref	NM_000546.6	/217-2512	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	631786534	tpe	HG975427.1	/217-2512	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1889531459	ref	NM_001276761.3	/214-2509	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	11066969	gb	AF307851.1	AF307851/205-2499	--	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	13097806	gb	BC003596.1	/195-2489	--	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2468545382	ref	XM_001172077.6	/217-2515	---	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2490746137	ref	XM_003810066.4	/217-2504	-----	T	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	82502895	gb	DQ191317.1	/216-2519	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	208342285	gb	FJ207420.1	/210-2513	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	82502903	gb	DQ286964.1	/209-2512	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	23491728	dbj	AB082923.1	/138-2432	--	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2246031073	ref	NM_001407262.1	/104-2399	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2246031052	ref	NM_001407266.1	/104-2399	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2246031054	ref	NM_001407265.1	/103-2398	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2493367174	ref	XM_004058511.4	/124-2413	-----	TTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2464112530	ref	XM_002826974.5	/217-2510	---	TTTTTTTC	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2463445091	ref	XM_054457336.1	/217-2510	---	TTTTTTTC	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2493367171	ref	XM_055367400.1	/104-2393	-----	TTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	369762889	gb	JN900492.1	/1-2296	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1894803100	ref	NM_001126118.2	/1-2296	-	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1743179656	ref	XM_030800485.1	/219-2506	---	TTTTTTTTTT	TTTTTT	--	CATTT	TATC	TTTTT	TTT	TGAGACTGGG
gi	1012955506	gb	JN214348.1	/1-2294	--	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1820556254	ref	XM_032139337.2	/219-2505	---	TTTTTTTTTT	TTTTTT	--	CATTT	TATC	TTTTT	TTT	TGAGACTGGG
gi	2491632765	ref	XM_055256596.1	/219-2498	----	TTTTTTTT	TTTTTT	--	CATTT	TATC	TTTTT	TTT	TGAGACTGGG
gi	2468545380	ref	XM_016931470.3	/1-2299	---	TTTTTTTTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	2516461531	ref	XM_057300362.1	/1-2288	-----	T	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1482600679	ref	XM_023193314.2	/219-2502	-----	T	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	795239330	ref	XM_012052423.1	/219-2503	-----	TTTT	TTTTTT	--	TTT	TC	TTTTTTC	TTT	TGAGACTGGG
gi	1777287103	ref	XM_003912272.5	/219-2502	-----	TTT	TTTTTC	--	TTT	TTA	TTTTTTC	TTT	TGAGACTGGG
gi	795219218	ref	XM_011994540.1	/219-2501	-----	T	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	795284141	ref	XM_011958558.1	/219-2511	---	TTTTTTTTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1411121371	ref	XM_025363516.1	/219-2502	-----	TTT	TTTTTT	--	TTT	TTTTTTTTTTTT	TTT	TGAGACTGGG	
gi	795219223	ref	XM_011994541.1	/216-2498	-----	T	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	795284149	ref	XM_011958559.1	/216-2508	---	TTTTTTTTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1411121369	ref	XM_025363515.1	/219-2505	-----	TTT	TTTTTT	--	TTT	TTTTTTTTTTTT	TTT	TGAGACTGGG	
gi	1825912814	ref	XM_033184717.1	/219-2500	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1411121373	ref	XM_025363517.1	/216-2499	-----	TTT	TTTTTT	--	TTT	TTTTTTTTTTTT	TTT	TGAGACTGGG	
gi	1938907787	ref	XM_008010194.2	/219-2504	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	2161852969	ref	XM_005582787.3	/216-2491	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	724818526	ref	XM_010362387.1	/219-2500	-----	TTTT	TTTTTC	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1059108540	ref	XM_017850545.1	/219-2500	-----	TTTT	TTTTTC	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	2161852970	ref	XM_045375424.1	/213-2488	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	2309385734	ref	XM_050765347.1	/104-2390	---	TTTTTTTTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	2309385732	ref	XM_050765346.1	/104-2390	---	TTTTTTTTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1622875777	ref	XM_028835713.1	/104-2379	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	2161852967	ref	XM_045375423.1	/104-2379	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1059108538	ref	XM_017850544.1	/104-2385	-----	TTTT	TTTTTC	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	
gi	1938907785	ref	XM_008010192.2	/1-2286	-----	TTTT	TTTTTT	--	TTT	TTTTTTTTT	TTT	TGAGACTGGG	

gi	1808862652	ref	NM_000546.6	/217-2512	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	631786534	tpe	HG975427.1	/217-2512	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1889531459	ref	NM_001276761.3	/214-2509	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	13097806	gb	BC003596.1	/195-2489	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2468545382	ref	XM_001172077.6	/217-2515	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2490746137	ref	XM_003810066.4	/217-2504	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	82502895	gb	DQ191317.1	/216-2519	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	208342285	gb	FJ207420.1	/210-2513	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	82502903	gb	DQ286964.1	/209-2512	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	23491728	dbj	AB082923.1	/138-2432	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2246031073	ref	NM_001407262.1	/104-2399	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2246031052	ref	NM_001407266.1	/104-2399	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2246031054	ref	NM_001407265.1	/103-2398	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2493367174	ref	XM_004058511.4	/124-2413	TCTCACTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCA
gi	2464112530	ref	XM_002826974.5	/217-2510	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2463445091	ref	XM_054457336.1	/217-2510	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2493367171	ref	XM_055367400.1	/104-2393	TCTCACTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCA
gi	369762889	gb	JN900492.1	/1-2296	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1894803100	ref	NM_001126118.2	/1-2296	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1743179656	ref	XM_030800485.1	/219-2506	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1012955506	gb	JN214348.1	/1-2294	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1820556254	ref	XM_032139337.2	/219-2505	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2491632765	ref	XM_055256596.1	/219-2498	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2468545380	ref	XM_016931470.3	/1-2299	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2516461531	ref	XM_057300362.1	/1-2288	TCTCGCTTTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1482600679	ref	XM_023193314.2	/219-2502	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	795239330	ref	XM_012052423.1	/219-2503	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1777287103	ref	XM_003912272.5	/219-2502	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	795219218	ref	XM_011994540.1	/219-2501	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	795284141	ref	XM_011958558.1	/219-2511	TCTCACTCTG	TTGCCCAGGC	TGGAG	TGGAG	TGGAGTGGCG
gi	1411121371	ref	XM_025363516.1	/219-2502	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	795219223	ref	XM_011994541.1	/216-2498	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	795284149	ref	XM_011958559.1	/216-2508	TCTCACTCTG	TTGCCCAGGC	TGGAG	TGGAG	TGGAGTGGCG
gi	1411121369	ref	XM_025363515.1	/219-2505	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1825912814	ref	XM_033184717.1	/219-2500	TCTCTCTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1411121373	ref	XM_025363517.1	/216-2499	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1938907787	ref	XM_008010194.2	/219-2504	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2161852969	ref	XM_005582787.3	/216-2491	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	724818526	ref	XM_010362387.1	/219-2500	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1059108540	ref	XM_017850545.1	/219-2500	TCTCACACTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	2161852970	ref	XM_045375424.1	/213-2488	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	2309385734	ref	XM_050765347.1	/104-2390	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	2309385732	ref	XM_050765346.1	/104-2390	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	1622875777	ref	XM_028835713.1	/104-2379	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	2161852967	ref	XM_045375423.1	/104-2379	TCTCACTCTG	TTGCCCAGGC	-----	TGAAG	TGGAGTGGCG
gi	1059108538	ref	XM_017850544.1	/104-2385	TCTCACACTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG
gi	1938907785	ref	XM_008010192.2	/1-2286	TCTCACTCTG	TTGCCCAGGC	-----	TGGAG	TGGAGTGGCG

gi	1808862652	ref	NM_000546.6	/217-2512	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	631786534	tpe	HG975427.1	/217-2512	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	1889531459	ref	NM_001276761.3	/214-2509	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	13097806	gb	BC003596.1	/195-2489	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	2468545382	ref	XM_001172077.6	/217-2515	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2490746137	ref	XM_003810066.4	/217-2504	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CTGGCTCAAG
gi	82502895	gb	DQ191317.1	/216-2519	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	208342285	gb	FJ207420.1	/210-2513	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	82502903	gb	DQ286964.1	/209-2512	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	23491728	dbj	AB082923.1	/138-2432	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	2246031073	ref	NM_001407262.1	/104-2399	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	2246031052	ref	NM_001407266.1	/104-2399	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	2246031054	ref	NM_001407265.1	/103-2398	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2463445091	ref	XM_054457336.1	/217-2510	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2493367171	ref	XM_055367400.1	/104-2393	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	369762889	gb	JN900492.1	/1-2296	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	1894803100	ref	NM_001126118.2	/1-2296	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	1743179656	ref	XM_030800485.1	/219-2506	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CTGGCTCGAG
gi	1012955506	gb	JN214348.1	/1-2294	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCGAG
gi	1820556254	ref	XM_032139337.2	/219-2505	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CTGGCCCCAAG
gi	2491632765	ref	XM_055256596.1	/219-2498	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CTGGCTCAAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2516461531	ref	XM_057300362.1	/1-2288	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CTGGCTCAAG
gi	1482600679	ref	XM_023193314.2	/219-2502	TGATCTTGGC	TCACTGTAGC	CTTTGCCTCC	CCGGCTCAAG
gi	795239330	ref	XM_012052423.1	/219-2503	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1777287103	ref	XM_003912272.5	/219-2502	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	795219218	ref	XM_011994540.1	/219-2501	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CTGGCTCAAG
gi	795284141	ref	XM_011958558.1	/219-2511	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1411121371	ref	XM_025363516.1	/219-2502	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	795219223	ref	XM_011994541.1	/216-2498	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CTGGCTCAAG
gi	795284149	ref	XM_011958559.1	/216-2508	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1411121369	ref	XM_025363515.1	/219-2505	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1825912814	ref	XM_033184717.1	/219-2500	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1411121373	ref	XM_025363517.1	/216-2499	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1938907787	ref	XM_008010194.2	/219-2504	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2161852969	ref	XM_005582787.3	/216-2491	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	724818526	ref	XM_010362387.1	/219-2500	TGATCTTGGC	TTACTGCAGC	CTTTGCCTCC	CCAGCTCAAG
gi	1059108540	ref	XM_017850545.1	/219-2500	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCAGCTCAAG
gi	2161852970	ref	XM_045375424.1	/213-2488	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2309385734	ref	XM_050765347.1	/104-2390	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2309385732	ref	XM_050765346.1	/104-2390	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1622875777	ref	XM_028835713.1	/104-2379	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	2161852967	ref	XM_045375423.1	/104-2379	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG
gi	1059108538	ref	XM_017850544.1	/104-2385	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCAGCTCAAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TGATCTTGGC	TCACTGCAGC	CTTTGCCTCC	CCGGCTCAAG

gi	1808862652	ref	NM_000546.6	/217-2512	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	631786534	tpe	HG975427.1	/217-2512	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1889531459	ref	NM_001276761.3	/214-2509	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	13097806	gb	BC003596.1	/195-2489	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2468545382	ref	XM_001172077.6	/217-2515	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2490746137	ref	XM_003810066.4	/217-2504	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	82502895	gb	DQ191317.1	/216-2519	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	208342285	gb	FJ207420.1	/210-2513	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	82502903	gb	DQ286964.1	/209-2512	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	23491728	dbj	AB082923.1	/138-2432	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2246031073	ref	NM_001407262.1	/104-2399	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2246031052	ref	NM_001407266.1	/104-2399	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2246031054	ref	NM_001407265.1	/103-2398	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2493367174	ref	XM_004058511.4	/124-2413	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2464112530	ref	XM_002826974.5	/217-2510	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2463445091	ref	XM_054457336.1	/217-2510	CAGTCCCTGCT	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2493367171	ref	XM_055367400.1	/104-2393	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	369762889	gb	JN900492.1	/1-2296	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1894803100	ref	NM_001126118.2	/1-2296	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
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gi	1012955506	gb	JN214348.1	/1-2294	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1820556254	ref	XM_032139337.2	/219-2505	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAAGT
gi	2491632765	ref	XM_055256596.1	/219-2498	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAAGT
gi	2468545380	ref	XM_016931470.3	/1-2299	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2516461531	ref	XM_057300362.1	/1-2288	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1482600679	ref	XM_023193314.2	/219-2502	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
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gi	1777287103	ref	XM_003912272.5	/219-2502	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	795219218	ref	XM_011994540.1	/219-2501	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	795284141	ref	XM_011958558.1	/219-2511	CAGTCCCTGCC	ACAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1411121371	ref	XM_025363516.1	/219-2502	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	795219223	ref	XM_011994541.1	/216-2498	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	795284149	ref	XM_011958559.1	/216-2508	CAGTCCCTGCC	ACAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1411121369	ref	XM_025363515.1	/219-2505	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1825912814	ref	XM_033184717.1	/219-2500	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1411121373	ref	XM_025363517.1	/216-2499	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1938907787	ref	XM_008010194.2	/219-2504	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2161852969	ref	XM_005582787.3	/216-2491	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	724818526	ref	XM_010362387.1	/219-2500	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1059108540	ref	XM_017850545.1	/219-2500	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2161852970	ref	XM_045375424.1	/213-2488	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2309385734	ref	XM_050765347.1	/104-2390	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2309385732	ref	XM_050765346.1	/104-2390	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1622875777	ref	XM_028835713.1	/104-2379	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	2161852967	ref	XM_045375423.1	/104-2379	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1059108538	ref	XM_017850544.1	/104-2385	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT
gi	1938907785	ref	XM_008010192.2	/1-2286	CAGTCCCTGCC	TCAGCCTCCG	GAGTAGCTGG	GACCACAGGT

gi	1808862652	ref	NM_000546.6	/217-2512	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	631786534	tpe	HG975427.1	/217-2512	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	1889531459	ref	NM_001276761.3	/214-2509	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	13097806	gb	BC003596.1	/195-2489	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2468545382	ref	XM_001172077.6	/217-2515	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2490746137	ref	XM_003810066.4	/217-2504	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	82502895	gb	DQ191317.1	/216-2519	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	208342285	gb	FJ207420.1	/210-2513	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	82502903	gb	DQ286964.1	/209-2512	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	23491728	dbj	AB082923.1	/138-2432	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2246031073	ref	NM_001407262.1	/104-2399	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2246031052	ref	NM_001407266.1	/104-2399	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2246031054	ref	NM_001407265.1	/103-2398	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2493367174	ref	XM_004058511.4	/124-2413	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2464112530	ref	XM_002826974.5	/217-2510	TCACGCCGCC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2463445091	ref	XM_054457336.1	/217-2510	TCACGCCGCC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2493367171	ref	XM_055367400.1	/104-2393	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	369762889	gb	JN900492.1	/1-2296	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	1894803100	ref	NM_001126118.2	/1-2296	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	1743179656	ref	XM_030800485.1	/219-2506	TCATGCCACC	ATGGCCAGCC	AGTTTTTGCA	CGTTTTGTAG
gi	1012955506	gb	JN214348.1	/1-2294	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	1820556254	ref	XM_032139337.2	/219-2505	TCATGCCACC	ATGGCCAGCC	AGTTTTTGCA	TGTTTTGTAG
gi	2491632765	ref	XM_055256596.1	/219-2498	TCATGCCACC	ATGGCCAGCC	AGTTTTTGCA	TGTTTTGTAG
gi	2468545380	ref	XM_016931470.3	/1-2299	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	2516461531	ref	XM_057300362.1	/1-2288	TCATGCCACC	ATGGCCAGCC	AACTTTTGCA	TGTTTTGTAG
gi	1482600679	ref	XM_023193314.2	/219-2502	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
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gi	795284141	ref	XM_011958558.1	/219-2511	TCATGCCACC	ACGGCCGCC	AATTTTTGCA	TGTTTGGTAG
gi	1411121371	ref	XM_025363516.1	/219-2502	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TATTTGGTAG
gi	795219223	ref	XM_011994541.1	/216-2498	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
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gi	1411121369	ref	XM_025363515.1	/219-2505	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TATTTGGTAG
gi	1825912814	ref	XM_033184717.1	/219-2500	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAA
gi	1411121373	ref	XM_025363517.1	/216-2499	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TATTTGGTAG
gi	1938907787	ref	XM_008010194.2	/219-2504	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	2161852969	ref	XM_005582787.3	/216-2491	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	724818526	ref	XM_010362387.1	/219-2500	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	1059108540	ref	XM_017850545.1	/219-2500	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	2161852970	ref	XM_045375424.1	/213-2488	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	2309385734	ref	XM_050765347.1	/104-2390	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	2309385732	ref	XM_050765346.1	/104-2390	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	1622875777	ref	XM_028835713.1	/104-2379	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	2161852967	ref	XM_045375423.1	/104-2379	TCATGCCACC	ATGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	1059108538	ref	XM_017850544.1	/104-2385	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG
gi	1938907785	ref	XM_008010192.2	/1-2286	TCATGCCACC	ACGGCCAGCC	AATTTTTGCA	TGTTTGGTAG

gi	1808862652	ref	NM_000546.6	/217-2512	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	631786534	tpe	HG975427.1	/217-2512	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1889531459	ref	NM_001276761.3	/214-2509	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	11066969	gb	AF307851.1	AF307851/205-2499	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	13097806	gb	BC003596.1	/195-2489	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2468545382	ref	XM_001172077.6	/217-2515	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2490746137	ref	XM_003810066.4	/217-2504	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	82502895	gb	DQ191317.1	/216-2519	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	208342285	gb	FJ207420.1	/210-2513	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	82502903	gb	DQ286964.1	/209-2512	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	23491728	dbj	AB082923.1	/138-2432	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2246031073	ref	NM_001407262.1	/104-2399	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2246031052	ref	NM_001407266.1	/104-2399	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2246031054	ref	NM_001407265.1	/103-2398	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2493367174	ref	XM_004058511.4	/124-2413	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2464112530	ref	XM_002826974.5	/217-2510	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2463445091	ref	XM_054457336.1	/217-2510	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2493367171	ref	XM_055367400.1	/104-2393	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	369762889	gb	JN900492.1	/1-2296	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1894803100	ref	NM_001126118.2	/1-2296	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1743179656	ref	XM_030800485.1	/219-2506	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1012955506	gb	JN214348.1	/1-2294	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1820556254	ref	XM_032139337.2	/219-2505	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2491632765	ref	XM_055256596.1	/219-2498	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2468545380	ref	XM_016931470.3	/1-2299	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2516461531	ref	XM_057300362.1	/1-2288	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1482600679	ref	XM_023193314.2	/219-2502	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	795239330	ref	XM_012052423.1	/219-2503	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1777287103	ref	XM_003912272.5	/219-2502	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	795219218	ref	XM_011994540.1	/219-2501	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	795284141	ref	XM_011958558.1	/219-2511	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1411121371	ref	XM_025363516.1	/219-2502	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	795219223	ref	XM_011994541.1	/216-2498	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	795284149	ref	XM_011958559.1	/216-2508	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1411121369	ref	XM_025363515.1	/219-2505	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1825912814	ref	XM_033184717.1	/219-2500	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1411121373	ref	XM_025363517.1	/216-2499	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1938907787	ref	XM_008010194.2	/219-2504	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2161852969	ref	XM_005582787.3	/216-2491	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
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gi	2161852970	ref	XM_045375424.1	/213-2488	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
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gi	2309385732	ref	XM_050765346.1	/104-2390	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1622875777	ref	XM_028835713.1	/104-2379	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	2161852967	ref	XM_045375423.1	/104-2379	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1059108538	ref	XM_017850544.1	/104-2385	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC
gi	1938907785	ref	XM_008010192.2	/1-2286	AGATGGGGTC	TCACAGTGTT	GCCCAGGCTG	GTCTCAAAC

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gi	1889531459	ref	NM_001276761.3	/214-2509	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	11066969	gb	AF307851.1	AF307851/205-2499	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	13097806	gb	BC003596.1	/195-2489	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2468545382	ref	XM_001172077.6	/217-2515	CCTGGGCTCA	GGTGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2490746137	ref	XM_003810066.4	/217-2504	CCTGGGCTCA	GGTGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	82502895	gb	DQ191317.1	/216-2519	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	208342285	gb	FJ207420.1	/210-2513	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	82502903	gb	DQ286964.1	/209-2512	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	23491728	dbj	AB082923.1	/138-2432	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2246031073	ref	NM_001407262.1	/104-2399	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2246031052	ref	NM_001407266.1	/104-2399	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2246031054	ref	NM_001407265.1	/103-2398	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2493367174	ref	XM_004058511.4	/124-2413	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2464112530	ref	XM_002826974.5	/217-2510	CCTGGGCTCA	GGCGATCCGC	CTGTCTCAGC	CTCCCAGAGT
gi	2463445091	ref	XM_054457336.1	/217-2510	CCTGGGCTCA	GGCGATCCGC	CTGTCTCAGC	CTCCCAGAGT
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gi	369762889	gb	JN900492.1	/1-2296	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	1894803100	ref	NM_001126118.2	/1-2296	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	1743179656	ref	XM_030800485.1	/219-2506	CCTGGGCTCA	GGCGATCCGC	CTGCCTCAGC	CTCCCAGAGT
gi	1012955506	gb	JN214348.1	/1-2294	CCTGGGCTCA	GGCGATCCAC	CTGTCTCAGC	CTCCCAGAGT
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gi	2491632765	ref	XM_055256596.1	/219-2498	CCTGGGCTCA	GGCGATCCGC	CTGCCTCAGC	CTCCCAGAGT
gi	2468545380	ref	XM_016931470.3	/1-2299	CCTGGGCTCA	GGTGATCCAC	CTGTCTCAGC	CTCCCAGAGT
gi	2516461531	ref	XM_057300362.1	/1-2288	CCTGGGCTCA	GGTGATCCAC	CTGTCTCAGC	CTCCCAGAGT
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gi	1938907785	ref	XM_008010192.2	/1-2286	CCTGGGCTCA	GGTGATCCGC	CTGCCTCAGC	CTCCCAGAGT

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gi	82502895	gb	DQ191317.1	/216-2519
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gi	795284141	ref	XM_011958558.1	/219-2511
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gi	1622875777	ref	XM_028835713.1	/104-2379
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gi	1889531459	ref	NM_001276761.3	/214-2509	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
gi	11066969	gb	AF307851.1	AF307851/205-2499	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
gi	13097806	gb	BC003596.1	/195-2489	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
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gi	208342285	gb	FJ207420.1	/210-2513	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
gi	82502903	gb	DQ286964.1	/209-2512	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
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gi	2493367174	ref	XM_004058511.4	/124-2413	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
gi	2464112530	ref	XM_002826974.5	/217-2510	GAGTCAACAT	CTTTTACATT	CTGCAAGCAC	GTCTGCATTT
gi	2463445091	ref	XM_054457336.1	/217-2510	GAGTCAACAT	CTTTTACATT	CTGCAAGCAC	GTCTGCATTT
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gi	369762889	gb	JN900492.1	/1-2296	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
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gi	1012955506	gb	JN214348.1	/1-2294	GGGTCAAACAT	CTTTTACATT	CTGCAAGCAC	ATCTGCATTT
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gi	1482600679	ref	XM_023193314.2	/219-2502	GGGTCAAACCT	CTTTTACATT	CTGCAAGCAC	GTCTGCATTT
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gi	13097806	gb	BC003596.1	/195-2489	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
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gi	2490746137	ref	XM_003810066.4	/217-2504	TCACCCCTACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	82502895	gb	DQ191317.1	/216-2519	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	208342285	gb	FJ207420.1	/210-2513	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	82502903	gb	DQ286964.1	/209-2512	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	23491728	dbj	AB082923.1	/138-2432	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	2246031073	ref	NM_001407262.1	/104-2399	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
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gi	1012955506	gb	JN214348.1	/1-2294	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	1820556254	ref	XM_032139337.2	/219-2505	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	2491632765	ref	XM_055256596.1	/219-2498	TCACCCCACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	2468545380	ref	XM_016931470.3	/1-2299	TCACCCCTACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	2516461531	ref	XM_057300362.1	/1-2288	TCACCCCTACC	CTTCCCCCTCC	TTCTCCCCTTT	TTATATCCCA
gi	1482600679	ref	XM_023193314.2	/219-2502	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	795239330	ref	XM_012052423.1	/219-2503	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1777287103	ref	XM_003912272.5	/219-2502	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	795219218	ref	XM_011994540.1	/219-2501	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	795284141	ref	XM_011958558.1	/219-2511	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1411121371	ref	XM_025363516.1	/219-2502	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	795219223	ref	XM_011994541.1	/216-2498	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	795284149	ref	XM_011958559.1	/216-2508	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1411121369	ref	XM_025363515.1	/219-2505	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1825912814	ref	XM_033184717.1	/219-2500	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1411121373	ref	XM_025363517.1	/216-2499	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1938907787	ref	XM_008010194.2	/219-2504	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	2161852969	ref	XM_005582787.3	/216-2491	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	724818526	ref	XM_010362387.1	/219-2500	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1059108540	ref	XM_017850545.1	/219-2500	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	2161852970	ref	XM_045375424.1	/213-2488	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	2309385734	ref	XM_050765347.1	/104-2390	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	2309385732	ref	XM_050765346.1	/104-2390	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	1622875777	ref	XM_028835713.1	/104-2379	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	2161852967	ref	XM_045375423.1	/104-2379	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCAA
gi	1059108538	ref	XM_017850544.1	/104-2385	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA
gi	1938907785	ref	XM_008010192.2	/1-2286	TCACCCCACC	CTTCCCCCTC	--CTCCCCTTT	TTATATCCCA

gi	1808862652	ref	NM_000546.6	/217-2512	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
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gi	1889531459	ref	NM_001276761.3	/214-2509	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	11066969	gb	AF307851.1	AF307851/205-2499	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	13097806	gb	BC003596.1	/195-2489	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	2468545382	ref	XM_001172077.6	/217-2515	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	2490746137	ref	XM_003810066.4	/217-2504	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	82502895	gb	DQ191317.1	/216-2519	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	208342285	gb	FJ207420.1	/210-2513	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	82502903	gb	DQ286964.1	/209-2512	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
gi	23491728	dbj	AB082923.1	/138-2432	TTTTTATATC	GATCTCTTAT	TTTACAATAA	AACTTTGCTG
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gi	2464112530	ref	XM_002826974.5	/217-2510	TTTTTATATC	AAATCTCTTAT	TTTACAATAA	AACTTTGCTG
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