

Supplemental Table S1
Individual Alligator Information

Site	JUV/ADU LT	Sex	Capture Date	Captain	Time of Capture	Total length (cm)	SVL (cm)	Tail Girth (cm)	GPS (Lat)	GPS (Long)	
AP	ADULT	M	3/31/10	Patrick	14.16	264	138	73	N 28.65189	W 81.68704	
AP	ADULT	M	3/31/10	Russ/Ditch	21.02	289.5	146	67.5	N 28.65412	W 81.69017	
AP	ADULT	M	4/9/10	Cameron	14.30	316	153	78	N 28.32701	W 80.36643	
AP	ADULT	M	3/31/10	Cameron	13.06	288	154	77.5	N 28.67602	W 81.66834	
AP	ADULT	M	4/9/10	Cameron	16.20	334	162	73	N 28.40751	W 81.39685	
AP	ADULT	M	3/31/10	Cameron	20.31	322.1	168.6	74.1	N 28.40720	W 81.39499	
AP	ADULT	M	3/31/10	Patrick/Russ	10.45	328	169	80.5			
AP	ADULT	M	4/9/10	Cameron	13.20	370	184	91	N 28.63409	W 81.69177	
AP	ADULT	M	3/31/10	Patrick/Russ	11.13	384	196	97			
AP	ADULT	M	4/9/10	Cameron	11.37	370			N 28.64828	W 81.68927	
TOTALS		10males									
							163.4				

Site	JUV/ADU LT	Sex	Capture Date	Captain	Time of Capture	Total length (cm)	SVL (cm)	Tail Girth (cm)	GPS (Lat)	GPS (Long)	
MI	ADULT	M	4/7/10	Patrick	15.00	256	124	56.5	N 28.50637	W 80.64509	
MI	ADULT	M	4/7/10	Carly/Ditch	16.40	261	127	60	N 28.30856	W 80.40598	
MI	ADULT	M	4/7/10	Patrick	13.25	260	129	60.5	N 28.50685	W 80.64771	
MI	ADULT	M	4/7/10	Cameron	15.07	257	137	62	N 28.57147	W 80.67096	
MI	ADULT	M	4/7/10	Russ/Ditch	17.45	277	137	60.5	N 28.59442	W 80.66725	
MI	ADULT	M	4/7/10	Russ/Ditch	17.10	282	140	63	N 28.59442	W 80.66725	
MI	ADULT	M	4/7/10	Patrick	11.20	301	140	74	N 28.44339	W 80.60034	
MI	ADULT	M	4/7/10	Russ/Ditch	14.35	293	147	68	N 28.64338	W 80.70582	
MI	ADULT	M	4/7/10	Russ/Ditch	13.06	298	149	67.5	N 28.59442	W 80.66725	
MI	ADULT	M	4/7/10	Russ/Ditch	10.20	301	154	63	N 28.52425	W 80.63851	
TOTALS		10 males									
							138.4				

Site	JUV/ADU LT	Sex	Capture Date	Captain	Time of Capture	Total length (cm)	SVL (cm)	Tail Girth (cm)	GPS (Lat)	GPS (Long)	
WO	ADULT	M	4/5/10	Patrick/Russ	14.30	223	118	50	N 29.09156	W 81.40450	
WO	ADULT	M	4/5/10	Cameron	14.00	252	134.5	59.3	N 29.10733	W 81.40573	
WO	ADULT	M	4/5/10	Patrick/Russ	17.17	290	140	63	N 29.09274	W 81.40385	
WO	ADULT	M	4/5/10	Patrick/Russ	17.45	288	146	65	N 29.08722	W 81.40537	
WO	ADULT	M	4/5/10	Patrick/Russ	10.40	285	149	69	N 29.09426	W 81.40544	
WO	ADULT	M	4/5/10	Arnold	11.00	325	156	78	N 29.07784	W 81.23633	
WO	ADULT	M	4/5/10	Patrick/Russ	12.35	302.6	157.3	66	N 29.08005	W 81.41041	
WO	ADULT	M	4/5/10	Patrick/Russ	15.35	286	165	63.5	N 29.13348	W 81.39153	
WO	ADULT	M	4/5/10	Patrick/Russ	11.20	336	171	69	N 29.08833	W 81.40450	
WO	ADULT	M	4/5/10	Arnold/Lou	12.15	330	176.5	72.5	N 29.07906	W 81.23619	
WO	ADULT	M	4/5/10	Patrick/Russ	13.25	325	181	78	N 29.10739	W 81.40569	
TOTALS		11 males									
							154.027				

The site (WO, AP, MI), age, sex, capture date, boat captain, time capture, total length (cm), snout-vent-length (SVL) (cm), tail girth (cm), and GPS information are listed for each alligator samples in the study.

Supplemental Table S2
Comparison: AP vs. WO DMR Gene Association

DMR Name	Chromosome	cSTART	cSTOP	Adj Oligo	Size (bp)	Description (Gene Association)	Identity	Accession
JH731055:404115-405575	JH731055	404115	405575	3	1461	Fasciola hepatica genome assembly Fhepatica_v1_scaffold scaffold1834_old	83%	LM665074.1
JH731125:503613-505040	JH731125	503613	505040	3	1428	Paralichthys olivaceus clone scaffold225_717 microsatellite sequence	90%	JN900812.1
JH731207:340484-341908	JH731207	340484	341908	3	1425	PREDICTED: Alligator mississippiensis gamma-1-syntrophin-like (LOC102569753), partial mRNA	96%	XM 006258375.1
JH731240:1092466-1093975	JH731240	1092466	1093975	3	1510	Chrysemys picta BAC clone CHY3-62H12 from chromosome unknown, complete sequence	77%	AC239227.3
JH731301:1071733-1073193	JH731301	1071733	1073193	3	1461	Alligator sinensis immunoglobulin heavy chain region genomic sequence	73%	JQ479335.1
JH731459:10190-11675	JH731459	10190	11675	3	1486	Alligator sinensis immunoglobulin heavy chain region genomic sequence	78%	JQ479335.1
JH731488:74648-76133	JH731488	74648	76133	3	1486	Chrysemys picta BAC clone CHY3-79H12 from chromosome unknown, complete sequence	87%	AC239597.1
JH731559:216471-217886	JH731559	216471	217886	3	1416	Schistocephalus solidus genome assembly S_solidus_NST_G2_scaffold SSLN_scaffold0002589	89%	LL902805.1
JH731805:276012-277476	JH731805	276012	277476	3	1465	Diphyllbothrium latum genome assembly D_latum_Geneva_scaffold DILT_contig0000309	100%	LL586140.1
JH731811:1340018-1341493	JH731811	1340018	1341493	3	1476	Mus musculus chromosome 14, clone RP23-477H13, complete sequence	84%	AC131330.25
JH731812:1496-2945	JH731812	1496	2945	3	1450	PREDICTED: Pantholops hodgsonii lectin, mannose-binding, 1 (LMAN1), mRNA	86%	XM 005972817.1
JH731855:107787-109207	JH731855	107787	109207	3	1421	PREDICTED: Alligator sinensis uncharacterized LOC102375006 (LOC102375006), misc_RNA	85%	XR 324857.1
JH731932:12968-14649	JH731932	12968	14649	3	1682	Alligator sinensis immunoglobulin heavy chain region genomic sequence	77%	JQ479335.1
JH731934:498361-500203	JH731934	498361	500203	4	1843	PREDICTED: Alligator mississippiensis syntaxin 17 (STX17), transcript variant X2, mRNA	100%	XM 006260382.1
JH732060:1153065-1154559	JH732060	1153065	1154559	3	1495	PREDICTED: Alligator mississippiensis arginyl aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1), mRNA	100%	XM 006260799.1
JH732175:382785-384210	JH732175	382785	384210	3	1426	PREDICTED: Alligator sinensis uncharacterized LOC102386692 (LOC102386692), misc_RNA	73%	XR 324702.1
JH732195:209594-211065	JH732195	209594	211065	3	1472	PREDICTED: Chaetura pelagica testis-expressed sequence 2 protein-like (LOC104386233), mRNA	83%	XM 009994809.1
JH732266:385607-387064	JH732266	385607	387064	3	1458	PREDICTED: Alligator mississippiensis septipaterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR), mRNA	100%	XM 006361301.1
JH732368:10678-12333	JH732368	10678	12333	3	1656	Chrysemys picta BAC clone CHY3-81H12 from chromosome unknown, complete sequence	84%	AC238955.2
JH732571:351468-352952	JH732571	351468	352952	3	1485	PREDICTED: Alligator mississippiensis IQ motif containing K (IQCK), transcript variant X1, mRNA	91%	XM 006259008.1
JH732676:110685-112148	JH732676	110685	112148	3	1464	PREDICTED: Alligator sinensis nucleotide-binding oligomerization domain-containing protein 2-like (LOC102387914), transcript variant X1, mRNA	86%	XM 006039339.1
JH733127:362718-364150	JH733127	362718	364150	3	1433	Acanthochelys spixii retrotransposon CR1-like LINE, complete sequence	76%	AB005891.1
JH733217:9673-11094	JH733217	9673	11094	3	1422	Alligator mississippiensis Chompy miniature inverted-repeat transposable element, partial sequence	89%	DQ063338.1
JH733220:229306-230762	JH733220	229306	230762	3	1457	PREDICTED: Alligator mississippiensis inositol-triphosphate 3-kinase A (ITPKA), partial mRNA	72%	XM 006265889.1
JH733230:73100-74516	JH733230	73100	74516	3	1417	PREDICTED: Alligator mississippiensis myosin-9-like (LOC102574832), partial mRNA	92%	XM 006266873.1
JH733567:93466-95217	JH733567	93466	95217	4	1752	Alligator sinensis immunoglobulin heavy chain region genomic sequence	67%	JQ479335.1
JH733604:95353-96821	JH733604	95353	96821	3	1469	Alligator sinensis immunoglobulin heavy chain region genomic sequence	74%	JQ479335.1
JH733615:196486-198178	JH733615	196486	198178	3	1693	PREDICTED: Alligator sinensis transmembrane protein 65 (TMEM65), mRNA	72%	XM 006028471.1
JH733615:1517983-1519448	JH733615	1517983	1519448	3	1466	PREDICTED: Alligator sinensis uncharacterized LOC102367788 (LOC102367788), transcript variant X2, misc_RNA	98%	XR 324451.1
JH733641:142951-144851	JH733641	142951	144851	3	1901	PREDICTED: Alligator sinensis uncharacterized LOC102380552 (LOC102380552), misc_RNA	70%	XR 323585.1
JH733652:523979-525397	JH733652	523979	525397	3	1419	PREDICTED: Alligator mississippiensis putative lysosomal acid lipase/cholesteryl ester hydrolase-like (LOC102562113), mRNA	81%	XM 006272247.1
JH733661:89143-90563	JH733661	89143	90563	3	1421	Mus musculus chromosome 5, clone RP23-6J21, complete sequence	93%	AC164410.5
JH733757:841901-843385	JH733757	841901	843385	3	1485	PREDICTED: Pelodiscus sinensis uncharacterized LOC102461997 (LOC102461997), ncRNA	68%	XR 333071.1
JH733767:138736-140234	JH733767	138736	140234	3	1499	Crocodylus porosus clone CpP1404 microsatellite sequence	79%	EU593421.1
JH733861:289982-291477	JH733861	289982	291477	3	1496	Alligator sinensis immunoglobulin heavy chain region genomic sequence	80%	JQ479335.1

JH733909:44053-45749	JH733909	44053	45749	3	1697	PREDICTED: Alligator mississippiensis beta-1,4-N-acetyl-galactosaminyl transferase 3 (B4GALNT3), mRNA	100%	XM 006265693.1
JH734079:74271-75705	JH734079	74271	75705	3	1435	PREDICTED: Alligator sinensis zinc finger protein 135 like (LOC102381513), mRNA	71%	XM 006036439.1
JH734173:178176-179656	JH734173	178176	179656	3	1481	PREDICTED: Chrysemys picta bellii uncharacterized LOC101942014 (LOC101942014), ncRNA	69%	XR 257523.2
JH734278:397128-398560	JH734278	397128	398560	3	1433	PREDICTED: Chrysemys picta bellii solute carrier family 16 (monocarboxylate transporter), member 7 (SLC16A7), transcript variant X2, mRNA	79%	XM 005297971.2
JH734350:68009-69455	JH734350	68009	69455	3	1447	Meriones unguiculatus clone 24 vomeronasal type 2 receptor (V2R) gene, exon 3 and partial cds	94%	KJ847402.1
JH734502:41351-43067	JH734502	41351	43067	4	1717	PREDICTED: Alligator mississippiensis uncharacterized LOC102577156 (LOC102577156), mRNA	88%	XM 006266883.1
JH734560:85523-86973	JH734560	85523	86973	3	1451	Homo sapiens chromosome X clone RP11-185O17 map p11.4, complete sequence	88%	AC092268.4
JH734878:60524-62395	JH734878	60524	62395	3	1872	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	80%	JQ479336.1
JH735001:288928-290635	JH735001	288928	290635	3	1708	Spirometra erinaceieuropaei genome assembly S_erinaceieuropaei_scaffold SPER_contig0200157	90%	LN451503.1
JH735217:599910-601383	JH735217	599910	601383	3	1474	PREDICTED: Alligator sinensis fatty acid desaturase 1-like (LOC102382251), mRNA	73%	XM 006033326.1
JH735261:93202-94650	JH735261	93202	94650	3	1449	Alligator sinensis immunoglobulin heavy chain region genomic sequence	76%	JQ479335.1
JH735392:384436-386110	JH735392	384436	386110	3	1675	PREDICTED: Alligator sinensis guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type (GNAL), partial mRNA	98%	XM 006036342.1
JH735548:319490-321215	JH735548	319490	321215	3	1726	PREDICTED: Chrysemys picta bellii ovochymase-2-like (LOC101951603), mRNA	89%	XM 008170299.1
JH735687:873877-875567	JH735687	873877	875567	4	1691	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	82%	JQ479336.1
JH736073:60550-62051	JH736073	60550	62051	3	1502	Alligator sinensis immunoglobulin heavy chain region genomic sequence	68%	JQ479335.1
JH736199:10319-11973	JH736199	10319	11973	3	1655	PREDICTED: Chrysemys picta bellii cytochrome P450 1B1 (LOC101941680), mRNA	72%	XM_008174397.1
JH736323:150041-151515	JH736323	150041	151515	3	1475	Alligator sinensis immunoglobulin heavy chain region genomic sequence	74%	JQ479335.1
JH736348:186769-188241	JH736348	186769	188241	3	1473	Gallus gallus BAC clone CH261-138H22 from chromosome ul, complete sequence	66%	AC171112.2
JH736700:4289-5719	JH736700	4289	5719	3	1431	PREDICTED: Alligator mississippiensis solute carrier family 44 (choline transporter), member 2 (SLC44A2), transcript variant X2, mRNA	74%	XM_006265591.1
JH736702:61535-62960	JH736702	61535	62960	3	1426	Acanthochelys spixii retrotransposon CR1-like LINE, complete sequence	76%	AB005891.1
JH736705:150267-151692	JH736705	150267	151692	3	1426	PREDICTED: Alligator mississippiensis epidermal growth factor (EGF), mRNA	77%	XM_006264080.1
JH736722:1115487-1116974	JH736722	1115487	1116974	3	1488	Homo sapiens 12 BAC RP11-82C23 (Roswell Park Cancer Institute Human BAC Library) complete sequence	81%	AC009773.27
JH736997:17151-18587	JH736997	17151	18587	3	1437	Alligator sinensis immunoglobulin heavy chain region genomic sequence	82%	JQ479335.1
JH737149:861047-862468	JH737149	861047	862468	3	1422	Crocodylus porosus clone CpP2514 microsatellite sequence	77%	EU593456.1
JH737202:573177-574646	JH737202	573177	574646	3	1470	Crocodylus porosus clone CpP2514 microsatellite sequence	78%	EU593456.1
JH737273:74396-76048	JH737273	74396	76048	3	1653	Mus musculus chromosome 19, clone RP24-330P23, complete sequence	90%	AC157916.2
JH737349:122248-123713	JH737349	122248	123713	3	1466	PREDICTED: Alligator sinensis magnesium transporter NIPA2-like (LOC102383552), partial mRNA	75%	XM_006026533.1
JH737379:1151972-1153421	JH737379	1151972	1153421	3	1450	PREDICTED: Alligator sinensis sorbitol dehydrogenase (SORD), mRNA	74%	XM_006020303.1
JH737791:115214-116644	JH737791	115214	116644	3	1431	PREDICTED: Alligator sinensis dynein, axonemal, heavy chain 9 (DNAH9), mRNA	80%	XM_006022043.1
JH737859:12207-13643	JH737859	12207	13643	3	1437	PREDICTED: Monodelphis domestica uncharacterized LOC103105780 (LOC103105780), ncRNA	81%	XR_467700.1
JH737933:204136-205566	JH737933	204136	205566	3	1431	PREDICTED: Alligator sinensis general transcription factor IIE subunit 2-like (LOC102385461), transcript variant X2, mRNA	84%	XM_006033990.1
JH738117:135638-137115	JH738117	135638	137115	3	1478	Crocodylus moreletii Chompy miniature inverted-repeat transposable element, partial sequence	77%	DQ063478.1
JH738181:785219-786651	JH738181	785219	786651	3	1433	PREDICTED: Alligator mississippiensis aldehyde dehydrogenase 5 family, member A1 (ALDH5A1), mRNA	76%	XM_006260546.1
JH738262:261161-262898	JH738262	261161	262898	4	1738	PREDICTED: Alligator sinensis matrix metalloproteinase 23B (MMP23B), mRNA	87%	XM_006016178.1
JH738276:975007-976972	JH738276	975007	976972	3	1966	PREDICTED: Alligator mississippiensis FERM domain containing 6 (FRMD6), mRNA	99%	XM_006276033.1

JH738335:681339-682811	JH738335	681339	682811	3	1473	PREDICTED: Alligator mississippiensis UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 18 (GALNT18), mRNA	100%	XM_006276188.1
JH738431:222669-224394	JH738431	222669	224394	4	1726	PREDICTED: Alligator sinensis class I histocompatibility antigen, F10 alpha chain-like (LOC102380209), partial mRNA	77%	XM_006034603.1
JH738473:4006858-4008341	JH738473	4006858	4008341	3	1484	Tomistoma schlegelii GG13a marker genomic sequence	82%	KP159742.1
JH738529:139176-140606	JH738529	139176	140606	3	1431	Crocodylus porosus clone CpP307 microsatellite sequence	80%	EU593353.1
JH738577:157531-159731	JH738577	157531	159731	3	2201	PREDICTED: Alligator sinensis latent transforming growth factor beta binding protein 2 (LTBP2), transcript variant X4, mRNA	87%	XM_006015345.1
JH738813:301073-302505	JH738813	301073	302505	3	1433	Latimeria menadoensis clone VMRC4-39G19, complete sequence	70%	AC150309.1
JH738843:47603-49037	JH738843	47603	49037	3	1435	Chrysemys picta BAC clone CHY3-12H12 from chromosome unknown, complete sequence	80%	AC239503.2
JH738873:51340-52825	JH738873	51340	52825	3	1486	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	77%	JQ479336.1
JH739160:115399-116863	JH739160	115399	116863	3	1465	PREDICTED: Alligator sinensis uncharacterized LOC102383386 (LOC102383386), misc_RNA	80%	XR_324864.1
JH739336:305673-307823	JH739336	305673	307823	3	2151	PREDICTED: Alligator sinensis uncharacterized LOC102379123 (LOC102379123), mRNA	99%	XM_006027934.1
JH739357:18949-20682	JH739357	18949	20682	4	1734	Crocodylus moreletii Chompy miniature inverted-repeat transposable element, partial sequence	76%	DQ063478.1
JH739357:59250-60986	JH739357	59250	60986	3	1737	Pan troglodytes BAC clone CH251-671111 from chromosome 7, complete sequence	86%	AC190158.3
JH739432:152406-153874	JH739432	152406	153874	3	1469	Mecistops cataphractus CP13 marker genomic sequence	75%	KP159689.1
JH739718:20429-21910	JH739718	20429	21910	3	1482	Alligator sinensis immunoglobulin heavy chain region genomic sequence	87%	JQ479335.1
JH739833:101919-103400	JH739833	101919	103400	3	1482	PREDICTED: Alligator sinensis methylmalonyl CoA epimerase (MCEE), transcript variant X2, mRNA	77%	XM_006020025.1

The AP vs. WO (3+ adjacent probe) DMR associated genes are presented with DMR name, chromosome (genomic contig) location, start and stop locations of the DMR, number of adjacent oligo (Adj. Oligo) in the DMR, size in base pair (bp) of the DMR, DMR associated gene description, percent (%) identity between the gene homology and DMR sequence and gene accession identification are presented for each DMR.

Supplemental Table S3
Comparison: MI vs. WO DMR Gene Association

DMR Name	Chromosome	cSTART	cSTOP	Adj Oligo	Size (bp)	Description (Gene Association)	Identity	Accession
JH731028:544624-546075	JH731028	544624	546075	3	1452	PREDICTED: Alligator mississippiensis kinesin family member 6 (KIF6), mRNA	99%	XM_006257878.1
JH731124:14052-15519	JH731124	14052	15519	3	1468	PREDICTED: Alligator sinensis C-type lectin domain family 2 member D-like (LOC102382038), mRNA	77%	XM_006038095.1
JH731181:392010-393974	JH731181	392010	393974	3	1965	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	85%	JQ479336.1
JH731275:210512-211988	JH731275	210512	211988	3	1477	Human DNA sequence from clone RP11-323P17 on chromosome 10, complete sequence	79%	AL391425.25
JH731279:152159-153815	JH731279	152159	153815	3	1657	PREDICTED: Alligator mississippiensis discs, large homolog 1 (Drosophila) (DLG1), transcript variant X2, mRNA	100%	XM_006258584.1
JH731435:44314-46031	JH731435	44314	46031	4	1718	Chrysemys picta BAC clone CHY3-63H12 from chromosome unknown, complete sequence	73%	AC239228.1
JH731438:251682-253157	JH731438	251682	253157	3	1476	Homo sapiens 3 BAC RP11-122D23 (Roswell Park Cancer Institute Human BAC Library) complete sequence	74%	AC117429.6
JH731625:506614-508048	JH731625	506614	508048	3	1435	PREDICTED: Alligator sinensis WAS/WASL interacting protein family, member 3 (WIPF3), transcript variant X1, mRNA	79%	XM_006019590.1
JH731907:91281-92776	JH731907	91281	92776	3	1496	Crocodylus novaeguineae CP13 marker genomic sequence	85%	KP159687.1
JH731976:1036096-1037529	JH731976	1036096	1037529	3	1434	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	93%	JQ479336.1
JH732028:39604-41304	JH732028	39604	41304	4	1701	Crocodylus porosus clone CpP3215 microsatellite sequence	83%	EU593482.1
JH732029:279546-281014	JH732029	279546	281014	3	1469	Crocodylus moreletii Chompy miniature inverted-repeat transposable element, partial sequence	84%	DQ063425.1
JH732498:85960-87391	JH732498	85960	87391	3	1432	PREDICTED: Alligator sinensis inhibitor of apoptosis protein-like (LOC102368067), transcript variant X1, mRNA	78%	XM_006032933.1
JH732524:169154-170833	JH732524	169154	170833	3	1680	PREDICTED: Alligator sinensis multiple epidermal growth factor-like domains protein 6-like (LOC102371633), mRNA	73%	XM_006018743.1
JH732565:273016-274471	JH732565	273016	274471	3	1456	Homo sapiens chromosome 11, clone RP13-726E6, complete sequence	95%	AC127526.11
JH732688:13797-15237	JH732688	13797	15237	3	1441	Alligator sinensis immunoglobulin heavy chain region genomic sequence	75%	JQ479335.1
JH732723:80932-82382	JH732723	80932	82382	3	1451	Haemonchus placei genome assembly H_placei_MHpl1, scaffold HPLM_scaffold0001869	70%	LM584932.1
JH732887:748219-749649	JH732887	748219	749649	3	1431	PREDICTED: Alligator sinensis uncharacterized LOC102385133 (LOC102385133), mRNA	81%	XM_006031543.1
JH732889:760906-762575	JH732889	760906	762575	3	1670	Alligator sinensis immunoglobulin heavy chain region genomic sequence	79%	JQ479335.1
JH732968:356659-358102	JH732968	356659	358102	3	1444	Homo sapiens chromosome 5 clone CTC-470C15, complete sequence	78%	AC008526.5
JH733013:1880886-1882579	JH733013	1880886	1882579	4	1694	Chrysemys picta BAC clone CHY3-94H12 from chromosome unknown, complete sequence	75%	AC239523.2
JH733097:799997-801460	JH733097	799997	801460	3	1464	PREDICTED: Pelodiscus sinensis G-protein coupled receptor 183-like (LOC102448388), transcript variant X2, mRNA	74%	XM_006115385.1
JH733396:408624-410107	JH733396	408624	410107	3	1484	Chrysemys picta BAC clone CHY3-7H12 from chromosome unknown, complete sequence	75%	AC239233.2
JH733564:87374-88805	JH733564	87374	88805	3	1432	Alligator sinensis immunoglobulin heavy chain region genomic sequence	87%	JQ479335.1
JH733614:243993-245473	JH733614	243993	245473	3	1481	PREDICTED: Chrysemys picta bellii collagen alpha-1(III) chain-like (LOC101941259), mRNA	77%	XM_005310545.1
JH733690:474234-475672	JH733690	474234	475672	3	1439	Cyprinus carpio genome assembly common carp genome, scaffold LG26	80%	LN590710.1
JH733740:46293-47759	JH733740	46293	47759	3	1467	Theobroma cacao Uncharacterized protein (TCM_004454) mRNA, complete cds	88%	XM_007050622.1
JH733745:319860-321349	JH733745	319860	321349	3	1490	Human DNA sequence from clone RP3-402H5 on chromosome 6p12.3-21.1, complete sequence	73%	AL161622.12
JH733756:246146-247559	JH733756	246146	247559	3	1414	Alligator sinensis immunoglobulin heavy chain region genomic sequence	93%	JQ479335.1
JH733781:132454-133942	JH733781	132454	133942	3	1489	Crocodylus porosus clone CpDi24 microsatellite sequence	81%	EU593293.1
JH733829:92861-94306	JH733829	92861	94306	3	1446	PREDICTED: Alligator sinensis cytochrome P450 26B1-like (LOC102388048), transcript variant X2, mRNA	76%	XM_006034634.1
JH734058:219651-221823	JH734058	219651	221823	4	2173	PREDICTED: Alligator sinensis ADP-ribosylation factor-like protein 13B-like (LOC102382571), mRNA	96%	XM_006026530.1
JH734276:203600-205051	JH734276	203600	205051	3	1452	Alligator sinensis immunoglobulin heavy chain region genomic sequence	76%	JQ479335.1
JH734340:20176-21594	JH734340	20176	21594	3	1419	Chrysemys picta BAC clone CHY3-94H12 from chromosome unknown, complete sequence	77%	AC239523.2
JH734345:27580-29040	JH734345	27580	29040	3	1461	PREDICTED: Alligator sinensis neurturin (NRTN), mRNA	95%	XM_006017519.1
JH734734:611286-612728	JH734734	611286	612728	3	1443	PREDICTED: Alligator sinensis GrpE-like 1, mitochondrial (E. coli) (GRPEL1), mRNA	94%	XM_006017017.1
JH734774:27018-28738	JH734774	27018	28738	3	1721	Chrysemys picta BAC clone CHY3-54H12 from chromosome unknown, complete sequence	81%	AC239516.2
JH734862:464575-466323	JH734862	464575	466323	3	1749	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	72%	JQ479336.1
JH734864:188264-189735	JH734864	188264	189735	3	1472	Alligator mississippiensis ornithine carbamoyltransferase (OTC), mRNA	88%	NM_001287307.1
JH734963:125128-126576	JH734963	125128	126576	3	1449	PREDICTED: Alligator mississippiensis dual specificity phosphatase 3 (DUSP3), mRNA	100%	XM_006268590.1

JH735292:425047-426526	JH735292	425047	426526	3	1480	Alligator sinensis immunoglobulin heavy chain region genomic sequence	84%	JQ479335.1
JH735370:16577-18054	JH735370	16577	18054	3	1478	Alligator sinensis immunoglobulin heavy chain region genomic sequence	96%	JQ479335.1
JH735574:92415-93871	JH735574	92415	93871	3	1457	PREDICTED: Alligator sinensis coxsackie virus and adenovirus receptor (CXADR), transcript variant X3, mRNA	74%	XM_006022916.1
JH735642:264423-265853	JH735642	264423	265853	3	1431	PREDICTED: Alligator sinensis uncharacterized LOC102372027 (LOC102372027), transcript variant X6, misc_RNA	77%	XR_325444.1
JH735680:11080-12530	JH735680	11080	12530	3	1451	Crocodylus porosus clone CpP307 microsatellite sequence	83%	EU593353.1
JH735877:123705-125428	JH735877	123705	125428	3	1724	PREDICTED: Anolis carolinensis uncharacterized LOC103279522 (LOC103279522), mRNA	95%	XM_008115102.1
JH736083:224544-225970	JH736083	224544	225970	3	1427	PREDICTED: Alligator mississippiensis OAF homolog (Drosophila) (OAF), mRNA	93%	XM_006259692.1
JH736125:2278276-2279750	JH736125	2278276	2279750	3	1475	Crocodylus porosus clone CpP3215 microsatellite sequence	79%	EU593482.1
JH736231:200698-202417	JH736231	200698	202417	3	1720	Homo sapiens chromosome 18, clone RP11-786F14, complete sequence	72%	AC091021.8
JH736511:1984-3446	JH736511	1984	3446	3	1463	Homo sapiens chromosome 10 clone RP11-423F10, complete sequence	77%	AC012047.8
JH736586:1462903-1464332	JH736586	1462903	1464332	3	1430	PREDICTED: Alligator sinensis Smith-Magenis syndrome chromosome region, candidate 8 (SMCR8), mRNA	97%	XM_006024036.1
JH736674:141958-143424	JH736674	141958	143424	3	1467	Alligator mississippiensis Sf3a2 and amAMH genes for splicing factor 3A2 and anti-mullerian hormone, partial and complete cds	75%	AB546782.1
JH736687:371416-373112	JH736687	371416	373112	4	1697	Alligator sinensis immunoglobulin heavy chain region genomic sequence	67%	JQ479335.1
JH736845:61657-63362	JH736845	61657	63362	3	1706	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	73%	JQ479336.1
JH736964:546625-548106	JH736964	546625	548106	3	1482	Alligator sinensis immunoglobulin heavy chain region genomic sequence	83%	JQ479335.1
JH736973:627286-628776	JH736973	627286	628776	3	1491	PREDICTED: Alligator sinensis wingless-type MMTV integration site family, member 11 (WNT11), transcript variant X3, mRNA	70%	XM_006021962.1
JH737063:168902-170373	JH737063	168902	170373	3	1472	Alligator mississippiensis isolate 1248all ultra conserved element locus chr3_457 genomic sequence	100%	JQ870061.1
JH737131:300064-301546	JH737131	300064	301546	3	1483	Crocodylus porosus clone CpP2708 microsatellite sequence	71%	EU593461.1
JH737153:110481-112628	JH737153	110481	112628	3	2148	Crocodylus porosus clone CpP111 microsatellite sequence	73%	EU593326.1
JH737179:197634-199113	JH737179	197634	199113	3	1480	Alligator sinensis immunoglobulin heavy chain region genomic sequence	86%	JQ479335.1
JH737248:244181-245620	JH737248	244181	245620	3	1440	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	79%	JQ479336.1
JH737283:143820-145280	JH737283	143820	145280	3	1461	PREDICTED: Alligator mississippiensis steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) (SRD5A1), mRNA	75%	XM_006271131.1
JH737421:2006056-2007706	JH737421	2006056	2007706	3	1651	PREDICTED: Alligator sinensis zinc finger protein 436-like (LOC102371443), mRNA	72%	XM_006037782.1
JH737508:64670-66609	JH737508	64670	66609	3	1940	Alligator mississippiensis Chompy miniature inverted-repeat transposable element, partial sequence	85%	DQ063331.1
JH737528:98254-1e+05	JH737528	98254	100000	3	1747	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	87%	JQ479336.1
JH737615:26189-27617	JH737615	26189	27617	3	1429	PREDICTED: Alligator sinensis biogenesis of lysosomal organelles complex-1, subunit 6, pallidin (BLOC1S6), mRNA	75%	XM_006030425.1
JH737854:72398-73874	JH737854	72398	73874	3	1477	Alligator sinensis immunoglobulin heavy chain region genomic sequence	86%	JQ479335.1
JH738122:78203-79686	JH738122	78203	79686	3	1484	Crocodylus porosus clone CpP307 microsatellite sequence	88%	EU593353.1
JH738431:43066-44963	JH738431	43066	44963	3	1898	Physcomitrella patens subsp. patens predicted protein (PHYPADRAFT_164024) mRNA, complete cds	90%	XM_001763795.1
JH738442:167010-168445	JH738442	167010	168445	3	1436	Dracunculus medinensis genome assembly		
JH738474:153750-155690	JH738474	153750	155690	3	1941	D_medinensis_Ghana, scaffold DME_scaffold0000018	89%	LK978209.1
JH738538:1532-2971	JH738538	1532	2971	3	1440	Alligator sinensis immunoglobulin heavy chain region genomic sequence	71%	JQ479335.1
JH739113:40697-42142	JH739113	40697	42142	3	1446	Chrysemys picta BAC clone CHY3-54H12 from chromosome unknown, complete sequence	83%	AC239516.2
JH739330:19933-21357	JH739330	19933	21357	3	1425	PREDICTED: Alligator mississippiensis desumoylating isopeptidase 2-like (LOC102565785), mRNA	100%	XM_006277696.1
JH739416:273343-275342	JH739416	273343	275342	3	2000	Crocodylus siamensis immunoglobulin heavy chain region genomic sequence	73%	JQ479336.1
						Mus musculus BAC clone RP24-34219 from chromosome 12, complete sequence	74%	AC159621.2

The MI vs. WO (3+ adjacent probe) DMR associated genes are presented with DMR name, chromosome (genomic contig) location, start and stop locations of the DMR, number of adjacent oligo (Adj. Oligo) in the DMR, size in base pair (bp) of the DMR, DMR associated gene description, percent (%) identity between the gene homology and DMR sequence and gene accession identification are presented for each DMR.