Supplementary Table 2

scaffold	start-pos	end-pos	Marker Name	Development Status	Repeat Sequence	Motif	Num Rep
310	268087	268126	VVY1	Failed PCR Testing	gaagaagaagaagaagaagaagaagaagaagaagaagaa	gaa	13
310	268127	268184	VVY2	Failed PCR Testing	gaagaagaagaagaagaagaagaagaagaagaagaag

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310	363213	363237		atatatatatATATATATATATAT	at	12
310	464879	464913		agagagagagagagagagagagagagagag	ag	17
292	147230	147250		ctctctctctctctctctct	ct	10
310	152050	152070		tctctctctctctctctcTC	tc	10
292	85597	85617		agagagagagagagagag	ag	10
292	219697	219721		tgtgtgtgtgtgtgtgtgtgtg	tg	12
292	14928	14976	Design Failed	tttatttatttatttatttatttatttatttatttatttattta	ttta	12
292	143885	143907		ctctctctctctctctctct	ct	11
292	431094	431116		agagagagagagagagagag	ag	11
292	548345	548365		gagagagagagagagagaga	ga	10
310	263849	263869		gagagagagagagagagaga	ga	10
292	289216	289240		ctctctctctctctctctctct	ct	12
292	164632	164664		tctctctctctctctctctctctctctctc	tc	16
292	56767	56791		agagagagagagagagagagag	ag	12
292	535905	535927		gagagagagagagagagaga	ga	11
292	159305	159329		tctctctctctctctctctctc	tc	12
292	270741	270769		ctctctctctctctctctctctct	ct	14
292	13812	13848		acacacacacacacacacacacacacacac	ac	18
292	192288	192328		ttatttatttatttatttatttatttatttatttat	ttat	10
292	8782	8806		gagagagagagagagagagaga	ga	12
310	125214	125242		agagagagagagagagagagagagag	ag	14
292	454540	454588		tttatttatttatttatttatttatttatttatttatttattta	ttta	12
292	6913	6935		ctctctctctctctctctct	ct	11
292	623698	623720		ctctctctctctctctctct	ct	11
292	282314	282346		acacacacacacacacacacacacacac	ac	16
292	17092	17122		ctctctctctctctctctctctctct	ct	15
292	178941	178983		tctctctctctctctctctctctctctctctctctc	tc	21
292	172944	172996		atagatagatagatagatagatagatagatagatagatagatagatag	atag	13
310	191010	191030		ctctctctctctctctct	ct	10
292	112354	112390		gagagagagagagagagagagagagagagaga	ga	18
292	85795	85817		agagagagagagagagagag	ag	11
310	119600	119622		agagagagagagagagagag	ag	11
292	642113	642141		ctctctctctctctctctctctct	ct	14
292	191429	191463		agagagagagagagagagagagagagagag	ag	17
310	208327	208351		ctctctctctctctctctctct	ct	12
292	615270	615290		agagagagagagagagag	ag	10
292	21974	22026	Design Failed	atctatctatctatctatctatctatctatctatctatctatctatct	atct	13
292	392360	392392		agagagagagagagagagagagagagag	ag	16
310	175765	175789		tctctctctctctctctctctc	tc	12
292	515327	515355		tctctctctctctctctctctctctc	tc	14
310	142740	142760		tgtgtgtgtgtgtgtgtgtg	tg	10
292	15464	15494		tgtgtgtgtgtgtgtgtgtgtgtgtg	tg	15
292	642325	642345		ctctctctctctctctct	ct	10
310	174454	174506		atttatttatttatttatttatttatttatttatttatttatttattt	attt	13
310	164480	164524		atttatttatttatttatttatttatttatttatttattt	attt	11
310	228262	228302		attcattcattcattcattcattcattcattcattc	attc	10
310	233643	233691		atttatttatttatttatttatttatttatttatttatttattt	attt	12
310	118502	118524		agagagagagagagagagag	ag	11
310	144775	144797		agagagagagagagagagag	ag	11
292	110491	110531		taaataaataaataaataaataaataaataaataaataaa	taaa	10
310	170987	171009		agagagagagagagagagag	ag	11
310	124645	124679		gtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	gt	17
292	493038	493060		agagagagagagagagagag	ag	11
292	131170	131200		acacacacacacacacacacacacac	ac	15
310	497698	497738		gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	gt	20
310	369068	369090		agagagagagagagagagag	ag	11
292	380838	380862		ctctctctctctctctctct	ct	12
292	247374	247406		agagagagagagagagagagagagagagag	ag	16
310	101856	101884		ctctctctctctctctctctctct	ct	14

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292	393129	393151	agagagagagagagagagag	ag	11
310	156223	156249	tgtgtgtgtgtgtgtgtgtgtgtg	tg	13
310	63144	63192	ttatttatttatttatttatttatttatttatttatttatttat	ttat	12
310	189484	189508	gtgtgtgtgtgtgtgtgtgtgtgt	gt	12
310	176134	176170	agagagagagagagagagagagagagagagagagag	ag	18
310	187688	187716	agagagagagagagagagagagagag	ag	14
292	569176	569216	atttatttatttatttatttatttatttatttatttattt	attt	10
292	133300	133320	ctctctctctctctctctct	ct	10
292	460420	460444	agagagagagagagagagagag	ag	12
292	336036	336084	acacacacacacacacacacacacacacacacacacacacacac	ac	24
310	238383	238409	cacacacacacacacacacacaca	ca	13
310	226392	226444	ttccttccttccttccttccttccttccttccttccttccttcc	ttcc	13
292	7778	7808	agagagagagagagagagagagagag	ag	15
292	286020	286054	agagagagagagagagagagagagagagagag	ag	17
310	273945	273993	atatatatatatatatatatatatatatatatatatatatatat	at	24
292	335864	335884	agagagagagagagagagag	ag	10
292	586386	586414	acacacacacacacacacacacac	ac	14
310	392260	392280	agagagagagagagagagag	ag	10
292	353769	353793	agagagagagagagagagagag	ag	12
292	416636	416676	tgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtg	tg	20
310	181235	181261	ctctctctctctctctctctctct	ct	13
310	143431	143453	tgtgtgtgtgtgtgtgtgtg	tg	11
310	197298	197338	atagatagatagatagatagatagatagatagatagatag	atag	10
310	243807	243829	tctctctctctctctctctc	tc	11
310	297962	298002	attcattcattcattcattcattcattcattcattc	attc	10
310	361495	361535	ataaataaataaataaataaataaataaataaataaataa	ataa	10
310	123133	123161	agagagagagagagagagagagagag	ag	14
292	301275	301315	atccatccatccatccatccatccatccatccatccatccatcc	atcc	10
292	121345	121385	tccttccttccttccttccttccttccttccttccttcct	tcct	10
292	401537	401557	tatatatatatatatatata	ta	10
310	100384	100404	ctctctctctctctctctct	ct	10
310	297709	297761	tttatttatttatttatttatttatttatttatttatttatttatta	ttta	13
310	125653	125713	tatctatctatctatctatctatctatctatctatctatctatctatctatc	tatc	15
292	442968	443012	ttatttatttatttatttatttatttatttatttatttat	ttat	11
310	287578	287602	ctctctctctctctctctctct	ct	12
292	301475	301515	atccatccatccatccatccatccatccatccatccatcc	atcc	10
310	361059	361124	ttcttttcttttcttttcttttcttttcttttcttttcttttcttttcttttcttttcttt	ttctt	13
292	287875	287899	acacacacacacacacacacac	ac	12
292	287899	287919	agagagagagagagagagag	ag	10
292	440719	440784	ttattttattttattttattttattttattttattttattttattttattttattttatt	ttatt	13
310	203764	203820	tttatttatttatttatttatttatttatttatttatttatttatttatta	ttta	14
292	645095	645151	atttatttatttatttatttatttatttatttatttatttatttatttatt	attt	14
292	387484	387524	aggcaggcaggcaggcaggcaggcaggcaggcaggcaggc	aggc	10
292	387524	387616	aagaaagaaagaa

310	14578	14602	agagagagagagagagagagag	ag	12
310	34204	34248	aataaataaataaataaataaataaataaataaataaataaata	aata	11
310	80302	80332	gaagaagaagaagaagaagaagaagaagaa	gaa	10
310	103032	103058	ctctctctctctctctctctctct	ct	13
310	130227	130255	agagagagagagagagagagagagag	ag	14
310	158172	158192	tctctctctctctctctc	tc	10
310	161926	161950	tctctctctctctctctctctc	tc	12
310	162147	162175	gagagagagagagagagagagagaga	ga	14
310	194232	194262	agagagagagagagagagagagagagag	ag	15
310	248623	248653	agagagagagagagagagagagagagag	ag	15
310	276315	276387	tttatttatttat