

**Supplemental Table 1** Oligonucleotide probes used for analysis of mouse gene expression by bDNA signal amplification assay

Gene	Accession no.	Target region	Function	Sequence
GSTA1	NM_008181	177—200	CE	cccgagtttcagaaatcttTTTTctctggaaagaaagt
		285—308	CE	tgtagtggagaatggcttggctTTTTctctggaaagaaagt
		333—354	CE	gctctcctcatgtcctccTTTTctctggaaagaaagt
		424—443	CE	ttgctcttctcctcaggTTTTctctggaaagaaagt
		119—137	LE	gctccattctcccctgccccTTTTtaggcataggaccgtgtct
		138—156	LE	gccaagagccaccggatagTTTTtaggcataggaccgtgtct
		157—176	LE	caaaactccacaccagctgcaTTTTtaggcataggaccgtgtct
		201—221	LE	ttcgtaacctgccaggctcatTTTTtaggcataggaccgtgtct
		265—284	LE	gcaccaggttcatcccctgTTTTtaggcataggaccgtgtct
		355—379	LE	tcctctgtgacatgcaatgatTTTTtaggcataggaccgtgtct
		380—400	LE	cattatcccagatccgccacTTTTtaggcataggaccgtgtct
		486—507	LE	ttcaacacctttcaaggcagTTTTtaggcataggaccgtgtct
		531—549	LE	ctgctcagcctgtgccaTTTTtaggcataggaccgtgtct
		550—569	LE	caaccagggaataatcagccTTTTtaggcataggaccgtgtct
		222—243	BL	tggaacatcagactcccatcac
		244—264	BL	atctctaccatgggcactg
		309—332	BL	catagagggtgattggaggcaa
		401—423	BL	ggcatgtggggtaataagagaat
		444—463	BL	ttcctgatctggcaaggc
		464—485	BL	ggaagtaacggctcctggttg
508—530	BL	cgagataatctgtccatggctc		
GSTA4	NM_010357	612—634	CE	atctgtcttaaatgcctgcagTTTTctctggaaagaaagt
		807—831	CE	tctatatacctgtctctggaatcTTTTctctggaaagaaagt
		832—852	CE	tgaagagctgtactcctgggaTTTTctctggaaagaaagt
		481—504	LE	ctccgtggtctttaaactcttTTTTtaggcataggaccgtgtct
		525—545	LE	gatgtctgcccaactgagctgTTTTtaggcataggaccgtgtct
		546—567	LE	tcaaaatggctcttaggagctgTTTTtaggcataggaccgtgtct
		568—588	LE	gggcaactgagttctccaccaTTTTtaggcataggaccgtgtct
		661—679	LE	tgactccgggtgcaggaTTTTtaggcataggaccgtgtct
		680—700	LE	ccatctggaggagctctcTTTTtaggcataggaccgtgtct
		722—746	LE	gctgcactagaactcaggacaatcTTTTtaggcataggaccgtgtct
		747—766	LE	tgggtgccacctaagcacTTTTtaggcataggaccgtgtct
		789—806	LE	tctgcagctggcctgtggTTTTtaggcataggaccgtgtct
		432—459	BL	tttagctctgacagatcaaatcata
		460—480	BL	caaacactgggaagtaacggg
		505—524	BL	gttgccaacgagaaaagcct
		589—611	BL	cagagggaagtcggacagtacag
		635—660	BL	acttctaattgtaggaatgtgctg
701—721	BL	ctgaccacctcaacatagggg		
767—788	BL	tgacactgcaatggaacctg		
GSTM1	NM_010358	345—364	CE	aactggctcagcaggactgacTTTTctctggaaagaaagt
		467—488	CE	tccaggcccagctgaaactTTTTctctggaaagaaagt
		729—747	CE	tgtctgcacggatcctctcTTTTctctggaaagaaagt
		765—786	CE	tgagctgatcgggtgtTTTTctctggaaagaaagt
		324—344	LE	ggacaaaacagcgggtcccTTTTtaggcataggaccgtgtct
		411—429	LE	gctgggtgtggtcttcaTTTTtaggcataggaccgtgtct
		430—446	LE	gtatcccagatcatagggatgTTTTtaggcataggaccgtgtct
		447—466	LE	catgaggatcgggtgtgTTTTtaggcataggaccgtgtct
		489—511	LE	gcttgagtctgtattccaggagTTTTtaggcataggaccgtgtct
		512—529	LE	tctcattcagccactggctcTTTTtaggcataggaccgtgtct
		530—552	LE	cgcaggatggcattgctctgTTTTtaggcataggaccgtgtct
		598—623	LE	ggctcttcgggcaaggatTTTTtaggcataggaccgtgtct
		685—709	LE	ccatgacctggttccacaaTTTTtaggcataggaccgtgtct
		365—387	LE	gtcagggtgtaacagagcatgaTTTTtaggcataggaccgtgtct
		388—410	LE	aactctggctctgcttctcaaaTTTTtaggcataggaccgtgtct
		553—574	BL	cagactactagagaaactgtgggca
		575—597	BL	tgtgtgttgaggtgactttata
624—640	BL	agtccgaggagctcca		
641—660	BL	ccatggtgatctctctcatcata		
661—684	BL	tgtcaagtcgggagcgtca		
710—728	BL	caagtaaggcagattgggaag		
748—764	BL	ggtgatctgtgtatccatgat		

Supplemental Table 1 Continued

Gene	Accession no.	Target region	Function	Sequence		
GSTM2	NM_008183	674—695	CE	caaagattggctggagaggaaTTTTTctcttgaaagaaagt		
		763—783	CE	taagagctaggccagcagagTTTTTctcttgaaagaaagt		
		784—804	CE	ggagaagaaagctgcacgtggTTTTTctcttgaaagaaagt		
		847—865	CE	accagaggctggctgagTTTTTctcttgaaagaaagt		
		629—651	LE	gatatcttctcaggccctcaaaTTTTTAggcataggaccctgtct		
		717—740	LE	tctggccttgatcctactttgTTTTTAggcataggaccctgtct		
		741—762	LE	cactcatgagtattccccaggTTTTTAggcataggaccctgtct		
		887—911	LE	agacaagggataggaggactaatTTTTTAggcataggaccctgtct		
		950—973	LE	ggattctcgggtctagtacattccTTTTTAggcataggaccctgtct		
		990—1013	LE	ggcagcacacagacagatctaacTTTTTAggcataggaccctgtct		
		652—673	BL	gcggctgctctcatgtagtca		
		696—716	BL	ggttcaaaaaggccatcttg		
		805—826	BL	atggaggaaatagggaatggaa		
		827—846	BL	ggaagggctgggaagaggaa		
		866—886	BL	gaagaatggagagccaagg		
		912—928	BL	ggctggatgcagggcag		
		929—949	BL	tccaacctcactgagggaag		
		974—989	BL	tctcaggccaggccgg		
		GSTM3	NM_010359	335—355	CE	tcatgagctgtatcgggtgtTTTTTctcttgaaagaaagt
				356—376	CE	aatcgggactgcagcagactaTTTTTctcttgaaagaaagt
378—400	CE			agaactctggctctgctctcaTTTTTctcttgaaagaaagt		
401—420	CE			tttctcagggatggccttcaTTTTTctcttgaaagaaagt		
141—159	LE			cagccactggctcggctcaTTTTTAggcataggaccctgtct		
160—182	LE			aggccaagattgaattctcactTTTTTAggcataggaccctgtct		
229—247	LE			ggatggcattgctctgggtTTTTTAggcataggaccctgtct		
266—288	LE			tgtctctccacacagggtgtgtctTTTTTAggcataggaccctgtct		
289—309	LE			cacacggatcctctcctctcTTTTTAggcataggaccctgtct		
421—445	LE			ccaggaactcagagtagagcttcatTTTTTAggcataggaccctgtct		
512—534	LE			gggctcaaacatacgatactggTTTTTAggcataggaccctgtct		
183—202	BL			agggcagattgggaaaatcc		
203—226	BL			ccttgtgtgacctcaattaagt		
249—264	BL			ccggccaaggtagcgc		
310—334	BL			ccataactggttctccaagtac		
446—464	BL			gcaaacctggcctcttgc		
465—486	BL			cacataggtgacctgtcccct		
487—511	BL	caagaatgtcataagcaaggaaatc				