Supplemental Table 1. bDNA probe sets.

Target Sequence	Function	Probe Sequence
Fan1: NM_177893		
1611-1631	CE	gggcctttacagactcgaagcTTTTTctcttggaaagaaagt
1675-1697	CE	gcttcttcgtcttccatggaatcTTTTTctcttggaaagaaagt
1741-1760	CE	aactccattcggcccagattTTTTTctcttggaaagaaagt
1782-1803	CE	gtccctgaagatctgggtcttcTTTTTctcttggaaagaaagt
1804-1826	CE	gcgtatctgatgaggtcctctctTTTTTctcttggaaagaaagt
1593-1610	LE	gaccggccagccaagtctTTTTTaggcataggacccgtgtct
1632-1649	LE	cgggcaaacacagccctaTTTTTaggcataggacccgtgtct
1698-1716	LE	accttgacccccacaagcaTTTTTaggcataggacccgtgtct
1717-1740	LE	gaccaatagcacagtagacagctgTTTTTaggcataggacccgtgtct
1761-1781	LE	cggcagatggtgtactgaggaTTTTTaggcataggacccgtgtct
1827-1844	LE	agcatgtgtgcggctgctTTTTTaggcataggacccgtgtct
1845-1866	LE	catggcagctgagatgtcactcTTTTTaggcataggacccgtgtct
1867-1885	LE	cctcccagttcccactggcTTTTTaggcataggacccgtgtct
1650-1674	BL	agtcaatgagaacagaagcaagatt
mKi67: NM_001081117		
2503-2523	CE	agactgctgctttgctgcattTTTTTctcttggaaagaaagt
2552-2570	CE	tgtttgatgctccgccgtcTTTTTctcttggaaagaaagt
2714-2738	CE	tctgttttttcattcatagtttccaTTTTTctcttggaaagaaagt
2809-2830	CE	cgttttcattgtcctgcacctgTTTTTctcttggaaagaaagt
2478-2502	LE	ccgagtactggatagcactttttctTTTTTaggcataggacccgtgtct
2571-2594	LE	ttaggagtttgcactgtgttttcaTTTTTaggcataggacccgtgtct
2595-2620	LE	caaggtcagtaatgttatggacattcTTTTTaggcataggacccgtgtct
2621-2644	LE	tctcagagaccggagtcttcttctTTTTTaggcataggacccgtgtct
2739-2760	LE	ggtgttctcagcaaggactgctTTTTTaggcataggacccgtgtct
2783-2808	LE	ttgatctactttttgttctcgaaatgTTTTTaggcataggacccgtgtct
2854-2878	LE	tttctgaaccttcacttaattcaccTTTTTaggcataggacccgtgtct
2879-2903	LE	gcacttgatctcctagctgatgtctTTTTTaggcataggacccgtgtct
2524-2551	BL	ttaaggtaggacttgcagaatatctatc
2645-2664	BL	tgcagtcttcaggggctctg
2665-2688	BL	tcttcttaacttgctcacactcga
2689-2713	BL	caagggtatgtctgagctctctaga

2761-2782	BL	tccccttaaatgtcttgctgt
2831-2853	BL	actttccttgcatctttgaggag
Top2a: NM_011623		
3587-3611	CE	agatctgatggactcttttgctttaTTTTTctcttggaaagaaagt
3659-3677	CE	tcctgcttttccttggcctTTTTTctcttggaaagaaagt
3759-3778	CE	ggatgactcttttgccccgaTTTTTctcttggaaagaaagt
3801-3824	CE	ctaattttcttctctgcctcagctTTTTTctcttggaaagaaagt
3889-3909	CE	cttctctattcgttgccggagTTTTTctcttggaaagaaagt
3541-3562	LE	cgtttctttgtttgcacagctcTTTTTaggcataggacccgtgtct
3612-3633	LE	aacagccagatcttccttccacTTTTTaggcataggacccgtgtct
3634-3658	LE	cgacaacctccagttcttcaataaaTTTTTaggcataggacccgtgtct
3698-3715	LE	ttgctttccccgcctttcTTTTTaggcataggacccgtgtct
3716-3737	LE	cacatctgtgctttcttcccctTTTTTaggcataggacccgtgtct
3871-3888	LE	gcttcctggttccgcaccTTTTTaggcataggacccgtgtct
3563-3586	BL	atgtgttgagctcttgttccttct
3678-3697	BL	caggaaggcccacttgttca
3738-3758	BL	ggagaaggcaagacgtcagca
3779-3800	BL	ttcatctccacagtcacttggg
3825-3850	BL	caacgttttcactcttaattttcttc
3851-3870	BL	atcctcagcaggggtaccct
Odc1: NM_013614		
711-735	CE	ctttgtatcttcagatccaggaaagTTTTTctcttggaaagaaagt
808-829	CE	tgcctggctcagctatgattctTTTTTctcttggaaagaaagt
967-992	CE	taaagaatgcagttaaatgatccataTTTTTctcttggaaagaaagt
1014-1033	CE	tgggtctcttctgcagcaggTTTTTctcttggaaagaaagt
689-710	LE	ccaccaccaatatcaagcagatTTTTTaggcataggacccgtgtct
762-782	LE	ttgtccagagctgggttgattTTTTTaggcataggacccgtgtct
854-874	LE	caatgatgttgactgcaagcgTTTTTaggcataggacccgtgtct
875-895	LE	ccttccacacggtttttttggTTTTTaggcataggacccgtgtct
914-939	LE	ggtttgttcatttgactcatcttcatTTTTTaggcataggacccgtgtct
940-966	LE	tactccatcattcacataatacatgaaTTTTTaggcataggacccgtgtct
993-1013	LE	gccttcacatgggcatgatcaTTTTTaggcataggacccgtgtct
1034-1058	LE	gatgagtaatacttctcgtctggctTTTTTaggcataggacccgtgtct
736-761	BL	acactggtgatctcttcaaatttaag

783-807	BL	cactccagagtctgatgggaagtac
830-853	BL	tgaaagctgatgcgacatagtatc
896-913	BL	cgtcagagccgggctgct
Sod1: NM_011434		
103-120	CE	ccatgcttccccgggagaTTTTTctcttggaaagaaagt
139-155	CE	accgtcgcccttcagcaTTTTTctcttggaaagaaagt
218-242	CE	gccttcagttaatcctgtaatttgtTTTTTctcttggaaagaaagt
71-89	LE	cctccggagggaccagagaTTTTTaggcataggacccgtgtct
121-138	LE	cgcacaccgctttcatcgTTTTTaggcataggacccgtgtct
156-173	LE	gatggttccctgcaccggTTTTTaggcataggacccgtgtct
195-217	LE	cctgacaacacaactggttcaccTTTTTaggcataggacccgtgtct
262-286	LE	ccttgtgtattgtccccatactgatTTTTTaggcataggacccgtgtct
287-309	LE	aatgaggtcctgcactggtacagTTTTTaggcataggacccgtgtct
90-102	BL	cgcgcggcggcct
174-194	BL	gcttgccttctgctcgaagtg
243-261	BL	ggacgtggaacccatgctg
Sod2: NM_013671		
169-189	CE	cgctgctctcctcagaacacgTTTTTctcttggaaagaaagt
338-356	CE	tgcagctgcatgatctgcgTTTTTctcttggaaagaaagt
417-434	CE	cccttggccagagcctcgTTTTTctcttggaaagaaagt
190-215	LE	cacaacattattgaggtttacacgacTTTTTaggcataggacccgtgtct
230-246	LE	cagcctcctgcccgtgcTTTTTaggcataggacccgtgtct
277-296	LE	tctgggaggctgtgcttgtgTTTTTaggcataggacccgtgtct
297-316	LE	cgccatagtcgtaaggcaggTTTTTaggcataggacccgtgtct
317-337	LE	cgttaatgtgtggctccagcgTTTTTaggcataggacccgtgtct
357-374	LE	gcgtggtgcttgctgtggTTTTTaggcataggacccgtgtct
375-396	LE	gttgagattgttcacgtaggccTTTTTaggcataggacccgtgtct
397-416	LE	tggtacttctcctcggtggcTTTTTaggcataggacccgtgtct
435-458	LE	agagcgacctgagttgtaacatctTTTTTaggcataggacccgtgtct
216-229	BL	tgcacgccgcccga
247-262	BL	caccggccacagggcc
263-276	BL	ccgggagcccgcgg
Cat: NM_009804		
1137-1153	CE	aaaggcggccctgaagcTTTTTctcttggaaagaaagt

1290-1310	CE	ctgttggggtaatagttggggTTTTTctcttggaaagaaagt
1330-1346	CE	tccagggctgagcgctgTTTTTctcttggaaagaaagt
1118-1136	LE	tttttgtcagggctgggctTTTTTaggcataggacccgtgtct
1189-1212	LE	cacaggtatctgcagatagttgggTTTTTaggcataggacccgtgtct
1213-1231	LE	gagcgcggtagggacagttTTTTTaggcataggacccgtgtct
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1252-1269	LE	catgcacatggggccatcTTTTTaggcataggacccgtgtct
1270-1289	LE	gcaccaccctggttgtcatgTTTTTaggcataggacccgtgtct
1347-1364	LE	gcgcactggacgctgtgcTTTTTaggcataggacccgtgtct
1154-1173	BL	gtgagtgtccgggtaggcaa
1174-1188	BL	tcccaggcggtggcg
1311-1329	BL	ctgctctggtgcgctgaag
TrxR1: NM_001042523		
770-791	CE	ggtgttcctgcttcgatctgttTTTTTctcttggaaagaaagt
833-855	CE	gttaaattcgccctctatggtctTTTTTctcttggaaagaaagt
923-945	CE	ctttccggtttttcgtttatctTTTTTctcttggaaagaaagt
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812-832	LE	cctcgctgtttgtggattgagTTTTTaggcataggacccgtgtct
856-875	LE	cctaccgccagcaacactgtTTTTTaggcataggacccgtgtct
903-922	LE	tcacgcccacggtctctaagTTTTTaggcataggacccgtgtct
968-991	LE	cgtagatgtaaggcacattggtctTTTTTaggcataggacccgtgtct
992-1011	LE	ctccaggatgtcaccgatggTTTTTaggcataggacccgtgtct
1012-1032	LE	gggagtcagctctagcttcccTTTTTaggcataggacccgtgtct
1033-1050	LE	ccccgcctggatggctacTTTTTaggcataggacccgtgtct
876-902	BL	ccaatagttctcgtacaagaatctctt
946-967	BL	gctcttcatccgtgacgggtat
c-Jun: NM_010591		
146-162	CE	gcggaggtgcggcttcaTTTTTctcttggaaagaaagt
677-696	CE	cggctcttccttcagggcttTTTTTctcttggaaagaaagt
773-792	CE	cctcatgcgcttcctctctgTTTTTctcttggaaagaaagt
828-845	CE	cgagcgatccgctccagcTTTTTctcttggaaagaaagt
870-889	CE	gctcggagttttgcgctttcTTTTTctcttggaaagaaagt

927-951	CE	gttcatgactttctgcttaagctgtTTTTTctcttggaaagaaagt
661-676	LE	gcagccgcgggtgctgTTTTTaggcataggacccgtgtct
697-714	LE	catctccggcacggtctgTTTTTaggcataggacccgtgtct
715-730	LE	gcggcgtctctcccggTTTTTaggcataggacccgtgtct
751-772	LE	ccttgatccgctcctgagactcTTTTTaggcataggacccgtgtct
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907-926	LE	gccacctgttccctgagcatTTTTTaggcataggacccgtgtct
952-971	LE	tggcacccactgttaacgtgTTTTTaggcataggacccgtgtct
972-993	LE	caactgctgcgttagcatgagtTTTTTaggcataggacccgtgtct
731-750	BL	catgtcgataggggacaggg
793-808	BL	aggcggcaatgcggtt
809-827	BL	ttccttttccggcacttgg
890-906	BL	gttggccgtggatgcca
c-Myc: NM_010849		
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1858-1880	CE	gtccttttcagaggtgagcttgtTTTTTctcttggaaagaaagt
1950-1971	CE	cagctcctcctcgagttaggtcTTTTTctcttggaaagaaagt
1695-1714	LE	tccaagacgttgtgtgtccgTTTTTaggcataggacccgtgtct
1755-1774	LE	tcagggatctggtcacgcagTTTTTaggcataggacccgtgtct
1775-1795	LE	gccttttcgttgttttccaatTTTTTaggcataggacccgtgtct
1818-1836	LE	ggatgtaggcggtggctttTTTTTaggcataggacccgtgtct
1881-1903	LE	tgttctcgtcgtttcctcaataaTTTTTaggcataggacccgtgtct
1904-1926	LE	gctgttcgagtttgtgtttcaacTTTTTaggcataggacccgtgtct
1927-1949	LE	agtttatgcaccagagtttcgaaTTTTTaggcataggacccgtgtct
1972-1996	LE	ttctccttactctcacgagagattcTTTTTaggcataggacccgtgtct
1736-1754	BL	ggcaaaaaagctgcgcttc
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Gadd45b: NM_008655		
683-707	CE	cagcgttcctctagagagatataggTTTTTctcttggaaagaaagt
800-821	CE	ggtagcctttgagggattgttcTTTTTctcttggaaagaaagt
952-970	CE	ctcttgcctgaggtgccctTTTTTctcttggaaagaaagt
1013-1030	CE	cggctgcgagcagaggctTTTTTctcttggaaagaaagt
732-752	LE	ggggacagcaactcgacagttTTTTTaggcataggacccgtgtct

753-783	LE	tgtcaaatatgtattttatttacttttttaTTTTTaggcataggacccgtgtct
897-914	LE	ggctccacagcccagaggTTTTTaggcataggacccgtgtct
915-934	LE	ccacctgtggtgctgctcctTTTTTaggcataggacccgtgtct
935-951	LE	ccttccgacctcggcgaTTTTTaggcataggacccgtgtct
995-1012	LE	ggctgcaggactgccaggTTTTTaggcataggacccgtgtct
1031-1049	LE	gcggtgtccagaccgtctgTTTTTaggcataggacccgtgtct
708-731	BL	gctttagatgtttggagtgggtct
784-799	BL	tgggggatgagggggc
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Pgc1a: NM_008904		
485-506	CE	gctgcatggttctgagtgctaaTTTTTctcttggaaagaaagt
550-571	CE	tattgctccatgaattctcggtTTTTTctcttggaaagaaagt
615-639	CE	cagatacttgagaagctctgagcagTTTTTctcttggaaagaaagt
683-704	CE	catttgtctctgctgctgttccTTTTTctcttggaaagaaagt
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507-527	LE	ctgatcctgtgggtgtggtttTTTTTaggcataggacccgtgtct
528-549	LE	cttaacaatggcagggtttgttTTTTTaggcataggacccgtgtct
594-614	LE	ggacgtctttgtggcttttgcTTTTTaggcataggacccgtgtct
640-660	LE	aggagggtcatcgtttgtggtTTTTTaggcataggacccgtgtct
661-682	LE	tgttttctgtgggtttggtgtgTTTTTaggcataggacccgtgtct
726-745	LE	gttgcgactgcggttgtgtaTTTTTaggcataggacccgtgtct
572-593	BL	tgttgacaaatgctcttcgctt
Chop: NM_007837		
231-250	CE	aatctggagagcgagggcttTTTTTctcttggaaagaaagt
251-272	CE	tgggccatagaactctgactggTTTTTctcttggaaagaaagt
273-293	CE	tgctcttcctcctcttcctccTTTTTctcttggaaagaaagt
394-415	CE	gctcgttctcttcagctagctgTTTTTctcttggaaagaaagt
416-435	CE	ctcgatttcctgcttgagccTTTTTctcttggaaagaaagt
211-230	LE	tgggatgtgcgtgtgacctcTTTTTaggcataggacccgtgtct
294-316	LE	gtttccgtttcctagttcttcctTTTTTaggcataggacccgtgtct
317-336	LE	ggctgggcactgaccactctTTTTTaggcataggacccgtgtct
354-374	LE	tcctgctccttctccttcatgTTTTTaggcataggacccgtgtct
375-393	LE	tgccactttccgctcgttcTTTTTaggcataggacccgtgtct

436-453	LE	cacctccctggtcaggcgTTTTTaggcataggacccgtgtct
454-470	LE	gcccgccgtgtggtctcTTTTTaggcataggacccgtgtct
471-490	LE	tgaccatgcggtcgatcagaTTTTTaggcataggacccgtgtct
337-353	BL	cgttgcttcccaggccg
Cpt1a: NM_013495		
372-391	CE	agagcagcaccttcagcgagTTTTTctcttggaaagaaagt
413-432	CE	gctcattttgccgtgctctgTTTTTctcttggaaagaaagt
433-451	CE	tccagattctggtgctgcgTTTTTctcttggaaagaaagt
496-516	CE	cggcagagacgtctggaagctTTTTTctcttggaaagaaagt
350-371	LE	tagcgcatagtcatgatgatcgTTTTTaggcataggacccgtgtct
392-412	LE	caaacatccagccatggtaggTTTTTaggcataggacccgtgtct
475-495	LE	gtacaacatgggctttcgaccTTTTTaggcataggacccgtgtct
534-555	LE	cctgctcacggtatctttgacaTTTTTaggcataggacccgtgtct
556-576	LE	tggcctcacagactccaggtaTTTTTaggcataggacccgtgtct
619-640	LE	caaggttgacagcaaaatcctgTTTTTaggcataggacccgtgtct
452-474	BL	cgagaagaccttgaccatagcca
517-533	BL	gctgggacaggcaggcg
577-598	BL	ggaagtctccctccttcatcag
599-617	BL	gccagtgctgtcatgcgtt
Aox1: NM_015729		
927-949	CE	gctcgcttctcttgatttcagacTTTTTctcttggaaagaaagt
971-994	CE	agagtttatactgctgcgtctgaaTTTTTctcttggaaagaaagt
1061-1081	CE	ggccaatgctctcattaatccTTTTTctcttggaaagaaagt
1141-1162	CE	cagcattggctgtccaggtagtTTTTTctcttggaaagaaagt
889-907	LE	atcgaatggcaatggtgcaTTTTTaggcataggacccgtgtct
908-926	LE	tggcgcctcacagcactgtTTTTTaggcataggacccgtgtct
950-970	LE	aatccaaaatctggggctctgTTTTTaggcataggacccgtgtct
1034-1060	LE	gcatgtaggtctcctttatgtatcttcTTTTTaggcataggacccgtgtct
1082-1101	LE	cagctcactcaggtcgccttTTTTTaggcataggacccgtgtct
1122-1140	LE	aaaagccttcagcccagctTTTTTaggcataggacccgtgtct
1163-1184	LE	gccatccgacattcttcgatacTTTTTaggcataggacccgtgtct
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1012-1033	BL	cgagaaagtggaaggcataggc
1102-1121	BL	gtgagggcatgaagctcagg

Ucp2: NM_011671		
285-305	CE	acagaggaactctgccggagtTTTTTctcttggaaagaaagt
326-346	CE	gagaaattggagaaacggggaTTTTTctcttggaaagaaagt
347-367	CE	tgctacctcccagaagatggaTTTTTctcttggaaagaaagt
511-531	CE	ctagcccttgactctccccttTTTTTctcttggaaagaaagt
246-264	LE	ctcaggctgaggcctccaaTTTTTaggcataggacccgtgtct
306-325	LE	ccttcaatcggcaagacgagTTTTTaggcataggacccgtgtct
368-390	LE	aaccaaccatgattctgatttccTTTTTaggcataggacccgtgtct
391-410	LE	gggcacatctgtggccttgaTTTTTaggcataggacccgtgtct
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492-510	LE	ggatctgcagccggaccttTTTTTaggcataggacccgtgtct
265-284	BL	tctggaggctgctttgaggt
411-432	BL	ggaacttcacagtggctgttgg
433-449	BL	agctgtcccagcccccca
471-491	BL	ggcggtatccagagggaaagt
Dgat2: NM_026384		
1663-1680	CE	cccttgcccagctagccaTTTTTctcttggaaagaaagt
1761-1777	CE	tgccctcagcctcccctTTTTTctcttggaaagaaagt
1858-1877	CE	ccagggtaggctcagattggTTTTTctcttggaaagaaagt
1998-2016	CE	ggctcaggaggatatgcgcTTTTTctcttggaaagaaagt
1681-1703	LE	atccctggagtcactaaggactgTTTTTaggcataggacccgtgtct
1724-1740	LE	gcagccacgggtgggacTTTTTaggcataggacccgtgtct
1741-1760	LE	tggtacgaggaacccgacctTTTTTaggcataggacccgtgtct
1795-1818	LE	cagtccagatgttatctaccctccTTTTTaggcataggacccgtgtct
1819-1836	LE	gcagagacccaagccgggTTTTTaggcataggacccgtgtct
1878-1898	LE	ccctagccaggagacaggaggTTTTTaggcataggacccgtgtct
1899-1917	LE	acctgtgggacagccgtgtTTTTTaggcataggacccgtgtct
1918-1937	LE	gcgagataacccaagacggcTTTTTaggcataggacccgtgtct
1959-1976	LE	ccatggtgccaacctccaTTTTTaggcataggacccgtgtct
1977-1997	LE	cagagcaacgctgagctgtgtTTTTTaggcataggacccgtgtct
1704-1723	BL	atggcctctgcctctcaaga
1778-1794	BL	ccaagtggggccagctg
1837-1857	BL	agaagagggctagggtgagga
1938-1958	BL	gagtgaaaccagccaacagca

p21: NM_0076694

42-60	CE	gcgcctgactccaattcccTTTTTctcttggaaagaaagt
124-143	CE	gctcctgtgcggaacaggtcTTTTTctcttggaaagaaagt
259-275	CE	cagcggcgtctccgtgaTTTTTctcttggaaagaaagt
312-330	CE	ggtagaccttgggcagcccTTTTTctcttggaaagaaagt
2-21	LE	gctcacacctctcggctgcTTTTTaggcataggacccgtgtct
22-41	LE	ctagactctgacaccgcggcTTTTTaggcataggacccgtgtct
166-185	LE	ctgctcactgtccacgggacTTTTTaggcataggacccgtgtct
218-235	LE	cgggcctcctggagacagTTTTTaggcataggacccgtgtct
295-311	LE	taggctccgaacgcgctTTTTTaggcataggacccgtgtct
331-347	LE	gcgggacccagggctcaTTTTTaggcataggacccgtgtct
348-365	LE	tcccaggtcgtcacggctTTTTTaggcataggacccgtgtct
61-83	BL	tgtctggatatcgctgtggatct
84-102	BL	tggtgcctgtggctctgaa
103-123	BL	ggacatcaccaggattggaca
144-165	BL	cgaagagacaacggcacacttt
186-201	BL	cgcaatcacggcgcaa
202-217	BL	cccgccatgagcgcat
236-258	BL	cgaagtcaaagttccaccgttct
276-294	BL	cccagacgaagttgccctc

Prdx: NM_0110343

412-435	CE	gcctttaagactccataatcctgaTTTTTctcttggaaagaaagt
643-668	CE	tctgcttagagaaatactctttgctcTTTTTctcttggaaagaaagt
848-873	CE	gttttctgtgactgatagaagattggTTTTTctcttggaaagaaagt
369-393	LE	tctgatattaagggaatgttcatggTTTTTaggcataggacccgtgtct
488-513	LE	agatcgtttattgttatctgtcgaagTTTTTaggcataggacccgtgtct
530-555	LE	tggactagtcgtataatctcatccacTTTTTaggcataggacccgtgtct
577-599	LE	cagctggacacacttcaccatgtTTTTTaggcataggacccgtgtct
600-619	LE	atcactgccaggtttccagcTTTTTaggcataggacccgtgtct
620-642	LE	ttattgacatcaggcttgatggtTTTTTaggcataggacccgtgtct
692-709	LE	tgctcaatgctgcctggcTTTTTaggcataggacccgtgtct
737-760	LE	acaccacatcatgtgtttaagcacTTTTTaggcataggacccgtgtct
785-802	LE	gctatccatccccagcccTTTTTaggcataggacccgtgtct
901-929	LE	tcagaattcacgtttaatagatacttaaaTTTTTaggcataggacccgtgtct

394-411	BL	gcaatggtgcgcttggga
436-459	BL	cccctgaaagagataccttcatca
460-487	BL	gatacccttatcatcaataataaaaagg
514-529	BL	agagcggccaacggga
556-576	BL	ttgtcagtgaactggaaggcc
669-691	BL	agaaaaatggtccagtgctcact
710-736	BL	gagtagagtacaagagtttcttctggc
761-784	BL	tgtaggaaaggcttatctggaatc
803-827	BL	gaccattaccaatagtggaagaaag
828-847	BL	tctgcccaaaacacagctca
874-900	BL	aaaagaagaaaaaagaattaacaggtt
α-Sma: NM_0073922		
122-140	CE	cgaagccggccttacagagTTTTTctcttggaaagaaagt
244-264	CE	cctctcttgctctgggcttcaTTTTTctcttggaaagaaagt
413-430	CE	tttctcccggttggccttTTTTTctcttggaaagaaagt
83-102	LE	accagggctgtgctgtcttcTTTTTaggcataggacccgtgtct
141-160	LE	cctgggagcatcatcaccagTTTTTaggcataggacccgtgtct
181-200	LE	cctgatgtctgggacgtcccTTTTTaggcataggacccgtgtct
201-221	LE	ggcccattccaaccattactcTTTTTaggcataggacccgtgtct
222-243	LE	tcccccacatagctgtctttttTTTTTaggcataggacccgtgtct
265-286	LE	cggatacttcagcgtcaggatcTTTTTaggcataggacccgtgtct
287-308	LE	tggtgatgatgccgtgttctatTTTTTaggcataggacccgtgtct
431-454	LE	ggtctcaaacataatctgggtcatTTTTTaggcataggacccgtgtct
103-121	BL	cccagagccattgtcgcac
161-180	BL	acgatggatgggaaaacagc
309-329	BL	tcttttccatgtcgtcccagt
330-353	BL	cgttatagaaagagtggtgccaga
354-371	BL	caggggccacacgaagct
372-392	BL	tcagcagtgtcggatgctctt
393-412	BL	agggttcagtggtgcctctg
Col1a1: NM_0077423		
4213-4232	CE	agcagggccttcttgaggttTTTTTctcttggaaagaaagt
4233-4251	CE	ctcgttggatccctggaggTTTTTctcttggaaagaaagt
4414-4434	CE	tagtccgaattcctggtctggTTTTTctcttggaaagaaagt

4130-4147	LE	cggtggacattaggcgcaTTTTTaggcataggacccgtgtct
4148-4167	LE	ggtgatgttctgggaggcctTTTTTaggcataggacccgtgtct
4191-4212	LE	gccagtctgctggtccatgtagTTTTTaggcataggacccgtgtct
4252-4271	LE	ccttcgcctctgagctcgatTTTTTaggcataggacccgtgtct
4294-4311	LE	gcagccgtccacaagggtTTTTTaggcataggacccgtgtct
4375-4393	LE	ccacatcgatgatgggcagTTTTTaggcataggacccgtgtct
4394-4413	LE	ggcaccaatgtccaagggagTTTTTaggcataggacccgtgtct
4435-4452	LE	gcaggcagggccaatgtcTTTTTaggcataggacccgtgtct
4168-4190	BL	gctacgctgttcttgcagtgata
4272-4293	BL	gctgtaggtgaagcgactgttg
4312-4332	BL	ccaagttccggtgtgactcgt
4333-4355	BL	ttgtattcgatgactgtcttgcc
4356-4374	BL	gcgggaggtcttggtggtt

Supplemental Table2

Supplemental Table 2. Real-time PCR primers.

Name	Accession No.	Forward primer	Reverse primer
Cyp7a1	NM_007824	ATCCTGGCAAACAGAAATCG	GGCCAAGTCTGGTTTCTCTG
Cyp8b1	NM_010012	AGTTGCAGCGTCTCTTCCAT	CCTTGCTCCCTCAGAAACTG
Cyp27a1	NM_024264	GAGAGTGAATCAGGGGACCA	TCAGGAATGGAGGGTTTCAG
Cyp7b1	NM_007825	GCCTTTTGGACTCGGAACAAG	AATCGGGGTGCTGAATACCTAA
Abcg5	NM_031844	AATTTTGGGGGAATTTCCAG	GTCCTGTGGTTGGCTCATCT
Abcg8	NM_026180	CCTCCGATTGCTTCTTTCAG	CTGAGAAATGCCCCCAGATA
Hnf4a1	NM_008261	GAAAATGTGCAGGTGTTGACCA	TGTGGTTCTTCCTCACGCTC
Lrh-1	NM_030676	AACGCAGAGAAAACGATGTCC	CATTGCTTGGATCACCTGAGA
Cyp1a1	NM_001136059	TTTGGTTTGGGCAAGCGAAAG	TGAAGATGCTGAGGACCAGAA
Nrf2	NM_010902	GATAGTGCCCCTGGAAGTGT	TCGTGTGAGATGAGCCTCTAA
Nqo1	NM_008706	TATCCTTCCGAGTCATCTCTAGCA	TCTGCAGCTTCCAGCTTCTTG
C/EBPβ	NM_009883	GTAATCACCTTAAAGATGTTCCTG	CTTTAATGCTCGAAACGGAAAAG
C/EBPα	NM_007678	AAGAACAGCAACGAGTACCG	GTGTCCAGTTCACGGCTCA
PPARg	NM_011146	CCCAATGGTTGCTGATTACAAA	GAGGGAGTTAGAAGGTTCTTC
PGC-1α	NM_008904	ATCACGTTCAAGGTCACCCTA	CAAAGCGGTCTCTCAATTCTG
Srebp-1c	NM_011480	TAGGTCACCGTTTCTTTGTGG	ATCCAAGGGCATCTGAGAACT
Adipsin	NM_013459	GAACCGGACAACCTGCAATCT	CACGTAACCACACCTTCGACT
Adiponectin	NM_009605	CTCTTAATCCTGCCCAGTCAT	TAGGACCAAGAAGACCTGCAT
Acly	NM_134037	CCCAGTGAACAACAGACCTAT	ACAAAGATGGTGACCTCATGC
FasN	NM_007988	GACCTTCATGGACACAATGCT	ATACCACCAGAGACCGTTATG
SCD1	NM_009127	TAGCTTTGGGTGCCTTATCTC	ACGAGGACGACAATACAATCG