

36B4	NM_001002	(193+) AGATGCAGCAGATCCGCAT
		(322-) ATATGAGGCAGCAGTTTCTCCAG
		FAM-AGGCTGTGGTGCTGATGGGCAAGAA-TAMRA
FABP4	NM_001442	(294+) GGATGGAAAATCAACCACCA
		(375-)GGAAGTGACGCCTTTCATGA
		FAM-ATTCCACCACCAGTTTATCATCCTCTCGTT-TAMRA
CD1d	NM_001766	(957+) GAGGCCCCACTTTGGGTAA
		(1025-) CACTGTTTCCCTCGTCCACTT
		FAM-TGGCCATTCAAGTGCTCAACCAGG-TAMRA
CD1a	NM_001763	(1357+) ACCTGTCCTGTCTGGGTGAA
		(1435-) CCCACGGAAGTGTGATGCT
		FAM-CAGTCTAGAGGGCCAGGACATCGTCCT-TAMRA
PPARa	NM_005036	(459+) CATTACGGAGTCCACGCGT
		(527-) ACCAGCTTGAGTCGAATCGTT
		FAM-AGGCTGCAAGGGCTTCTTTCGGCG-TAMRA
PPARd	NM_006238	(595+) AGCATCCTCACCGGCAAAG
		(660-) CCACAATGTCTCGATGTCGTG
		FAM-CAGCCACACGGCGCCCTTTG-TAMRA
PPARg	NM_005037	(1313+) GATGACAGCGACTTGGCAA
		(1397-) CTTCAATGGGCTTACATTCA
		FAM-CAAACCTGGGCGGTCTCCACTGAG-TAMRA