Supplemental table 4. Differentially expressed genes in heifers of the PI group compared to the control heifers, day 190 of gestation.

Affymetrix Identifier	Gene Identifier	Gene Name	Ratio	Direction
Bt.552.1.S1_at	NM_175827	chemokine (C-C motif) ligand 5	2.82	Down
Bt.21883.1.S1_at	CB425639	Transcribed locus, weakly similar to NP_631937.1 placenta-specific 8 [Mus musculus]	2.69	Down
Bt.12986.1.S1_at	CK977019	MAD2 mitotic arrest deficient-like 1 (yeast)	2.42	Up
Bt.9974.1.S1_at	NM_174511	Chemokine (C-C motif) ligand 3-like 1	2.24	Down
Bt.19690.1.A1_at	CB534503	Transcribed locus, weakly similar to XP_519213.1 paraoxonase 2 [Pan troglodytes]	2.22	Down
Bt.12959.1.S1_at	CA923353	Unique Bos taurus cDNA clone 5BOV_6G5 3'	2.16	Up
Bt.9363.2.S1_at	CK945488	Transcribed locus, moderately similar to NP_001326.2 cathepsin W (lymphopain) [Homo sapiens]	2.07	Down
Bt.19462.1.A1_at	CB461397	Transcribed sequence	2.03	Down
Bt.9363.1.A1_at	BM251259	Transcribed locus, moderately similar to NP_001326.2 cathepsin W (lymphopain) [Homo sapiens]	2.01	Down
Bt.19339.3.A1_at	CB461169	Transcribed sequences	1.96	Up
Bt.26636.1.S1_at	CK775256	Transcribed locus, moderately similar to NP_077215.2 natural killer cell group 7 sequence [Mus musculus]	1.96	Down
Bt.20798.1.S1_at	CB445920	Transcribed sequences	1.94	Up
Bt.9504.1.A1_at	CB463807	Transcribed sequence with moderate similarity to protein sp:P10159 (H.sapiens) IF5A_HUMAN Initiation factor 5A	1.91	Down
Bt.5546.1.S1_at	NM_174324	adenylate cyclase-inhibiting G alpha protein	1.86	Up
Bt.16141.1.S1_at	CK778261	Transcribed locus, strongly similar to XP_519864.1 similar to cyclin E2 isoform 1; G1/S-specific cyclin E2 [Pan troglodytes]	1.85	Up
Bt.21975.1.S1_at	CK771825	Perforin 1 (pore forming protein)	1.77	Down
Bt.4266.2.A1_at	BF042221	Transcribed locus	1.75	Up
Bt.6000.2.S1_at	CF930613	Transcribed locus	1.73	Down
Bt.2173.1.S1_at	CB463330	Transcribed locus, strongly similar to XP_214478.2 similar to Succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde dehydrogenase) [Rattus norvegicus]	1.72	Up
Bt.11909.1.A1_at	CB171451	Transcribed locus, moderately similar to NP_001938.1 dual specificity phosphatase 7 [Homo sapiens]	1.71	Down
Bt.25101.1.S1_at	CF763999	Transcribed sequences	1.7	Down
Bt.18776.1.S1_at	CK979795	Transcribed locus, strongly similar to NP_055551.1 KIAA0101 [Homo sapiens]	1.7	Up
Bt.24218.1.S1_at	CK960396	Transcribed locus, strongly similar to XP_523625.1 similar to CDC6 homolog; CDC18 (cell division cycle 18, S.pombe, homolog)-like; CDC6-related protein; CDC6 (cell division cycle 6, S. cerevisiae) homolog [Pan troglodytes]	1.69	Up
Bt.17915.1.S1_at	CK957227	Transcribed locus, strongly similar to XP_526535.1 similar to chromosome condensation protein G [Pan troglodytes]	1.68	Up
Bt.27531.1.A1_at	CK846626	Transcribed sequences	1.68	Up
Bt.20277.1.S1_at	CB443446	Transcribed locus, strongly similar to XP_346407.1 topoisomerase (DNA) 2 alpha [Rattus norvegicus]	1.67	Up
Bt.19247.1.S1_at	CK837929	Transcribed locus, moderately similar to NP_006579.2 sulfotransferase family, cytosolic, 1C, member 2 [Homo sapiens]	1.66	Up
Bt.16114.1.S1_at	CB447702	Transcribed locus	1.64	Up
Bt.11587.3.A1_a_at	CK774460	Transcribed locus, strongly similar to NP_006452.2 sperm associated antigen 5 [Homo sapiens]	1.61	Up
Bt.2111.1.S1_a_at	CK847647	Transcribed locus, strongly similar to NP_004144.2 origin recognition complex, subunit 1-like (yeast) [Homo sapiens]	1.61	Up
Bt.2112.1.S1_at	BI682736	Transcribed locus	1.59	Up
Bt.27759.2.S1_at	CK962640	Transcribed locus, moderately similar to NP_002155.1 indoleamine-pyrrole 2,3 dioxygenase [Homo sapiens]	1.59	Down
Bt.29462.1.S1_at	CK972892	Transcribed locus, weakly similar to NP_689775.2 cell division cycle associated 2 [Homo sapiens]	1.59	Up
Bt.21513.1.A1_at	CK846625	Transcribed locus, moderately similar to NP_004327.1 BUB1 budding uninhibited by benzimidazoles 1 homolog (yeast) [Homo sapiens]	1.58	Up
Bt.22055.1.S1_at	CB535138	Transcribed locus	1.58	Up
Bt.24630.2.S1_at	BE723387	Transcribed locus, strongly similar to NP_653311.1 septin 10 [Homo sapiens]	1.57	Down
Bt.28366.1.A1_at	CK979039	Transcribed locus, strongly similar to NP_060568.3 epithelial cell transforming sequence 2 oncogene [Homo sapiens]	1.57	Up
Bt.15733.1.A1_at	CK971667	Transcribed locus, moderately similar to XP_524698.1 similar to TAL1 (SCL) interrupting locus; SCL interrupting locus; TAL1 (SCL) interrupting locus [Pan	1.56	Up
Bt.24844.1.S1_at	CB443429	Transcribed locus, moderately similar to NP_001804.1 centromere protein E, 312kDa [Homo sapiens]	1.56	Up
Bt.25412.1.A1_at	BE723538	Transcribed locus, moderately similar to NP_060924.4 nucleolar and spindle associated protein 1 [Homo sapiens]	1.55	Up
Bt.24288.1.A1_at	CK778639	Transcribed locus, moderately similar to NP_079133.3 hypothetical protein FLJ12735 [Homo sapiens]	1.54	Up
Bt.2353.1.S1_at	CK772080	Transcribed locus, strongly similar to NP_001159.1 baculoviral IAP repeat-containing 5 (survivin) [Homo sapiens]	1.54	Up
Bt.13954.1.S1_at	CB167572	Transcribed locus, moderately similar to XP_519489.1 similar to more than blood homolog [Pan troglodytes]	1.53	Up
Bt.13476.1.S1_at	CK950633	Transcribed locus, strongly similar to NP_612565.1 kinesin family member 23 [Homo sapiens]	1.52	Up
Bt.22461.2.A1_at	CB441743	Transcribed locus	1.51	Up
Bt.18111.1.A1_at	CB437799	Transcribed locus, weakly similar to XP_341569.1 similar to ORF4 [Rattus norvegicus]	1.51	Up
Bt.21084.1.S1_at	BI774157	Transcribed locus	1.51	Up
Bt.22699.2.A1_at	BP103971	Transcribed locus, strongly similar to NP_005586.1 nuclear factor I/A [Homo sapiens]	1.5	Up
Bt.28797.1.A1_at	CK952083	Transcribed locus, strongly similar to NP_082407.1 RIKEN cDNA 2610510J17 gene [Mus musculus]	1.5	Up
Bt.8633.1.A1_at	BI535494	Transcribed sequences	1.5	Up