Table 1. Top list of genes showing the highest expression level in the AI vs. IVF-ET profile in bovine caruncular endometrium

Top list of the 100 most regulated genes in the [AI *vs.* IVF-ET] profiles in caruncles									
Gene accession N°	**Unigene ID**	**Bovine gene name**	**Bovine gene symbol**	**Human gene symbol**	**Log ratio**	**variance**	**stat.test**	**group**	**BH**
BM361913	Hs.181244	MHC Class I JSP.1	JSP.1	HLA-A	1.5119	0.1382	-3.8177	3	0.1382
CR453977	Hs.639	calbindin 3, (vitamin D-dependent calcium binding protein)	CALB3	S100G	-0.9995	0.1370	4.4243	3	0.1370
CN433519	Hs.446574	thymosin, beta 10	TMSB10	TMSB10	-0.7867	0.0455	-5.0322	4	0.0455
AW466018	Hs.155097	carbonic anhydrase II	CA2	CA2	0.6815	0.1382	-4.1700	3	0.1382
CR456021	Hs.644618	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	SLC25A5	SLC25A5	0.6263	0.1199	-4.9293	3	0.1199
BF042057	Hs.591967	similar to interleukin-18 binding protein	LOC617470	IL18BP	-0.5509	0.0908	-5.7304	3	0.0908
AW465810	Hs.645068	zinc finger protein 36, C3H type-like 2	ZFP36L2	ZFP36L2	0.5043	0.1382	6.6847	2	0.1382
CN440850	Hs.561411	similar to Embigin homolog (mouse)	LOC785366	0	0.4918	0.0263	3.8447	4	0.0263
X55389	Hs.271135	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	ATP5C1	ATP5C1	0.4726	0.0263	6.3848	3	0.0263
AW464920	Hs.247916	natriuretic peptide precursor C	NPPC	NPPC	-0.4441	0.1382	-4.2772	3	0.1382
CN441344	Hs.82045	midkine (neurite growth-promoting factor 2)	MDK	MDK	0.4371	0.1382	-3.5405	3	0.1382
BF044858	Hs.279529	px19-like protein	PX19	PRELID1	0.4332	0.0516	5.7208	4	0.0516
CN786320	Hs.494496	fructose-1,6-bisphosphatase 2	FBP2	FBP1	0.4209	0.1382	-3.5025	3	0.1382
BF046702	Hs.139389	cystatin E/M	CST6	CST6	0.4138	0.1524	-4.9752	2	0.1524
CN433528	Hs.485262	similar to mitochondrial carrier homolog 1	LOC781257	MTCH1	-0.3888	0.0327	7.2484	3	0.0327
CN439210	Hs.524390	similar to alpha-tubulin	LOC407195	TUBA1A	-0.3663	0.0942	3.2287	4	0.0942
NG010005A10G09	Hs.474783	thiosulfate sulfurtransferase (rhodanese)	TST	TST	-0.3565	0.1382	5.3617	2	0.1382
AW267059	Hs.460558	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	SULT1A1	SULT1A4	0.3535	0.1764	5.6652	1	0.1764

CR552920	Hs.62886	similar to SPARC-like protein 1 precursor (High endothelial venule protein) (Hevin) (MAST 9)	MGC127494	SPARCL1	0.3502	0.1658	-5.9905	1	0.1658
BF041945	Hs.644065	similar to KIAA0669 protein	LOC541277	TSC22D2	0.3467	0.1382	-3.9938	3	0.1382
CN433809	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C3 (subunit 9)	ATP5G3	ATP5G3	0.3379	0.1204	4.7467	3	0.1204
CR456010	Hs.587979	prostate tumor over expressed gene 1	PTOV1	PTOV1	-0.3345	0.1656	4.3817	2	0.1656
CN441786	Hs.518662	Transcribed locus	0	FAM129A	0.3221	0.1370	-4.4749	3	0.1370
BF045543	Hs.74034	caveolin 1, caveolae protein, 22kDa	CAV1	CAV1	-0.3198	0.1403	-5.2184	2	0.1403
CR453935	Hs.521487	similar to transmembrane protein 66	MGC139371	TMEM66	-0.3157	0.1382	-5.5481	2	0.1382
CB536391	Hs.490817	similar to VIP2 receptor	LOC790124	VIPR2	-0.3053	0.1515	-5.0248	2	0.1515
BF039310	Hs.428214	0	0	MAML2	-0.3036	0.1382	-6.5624	2	0.1382
AW464441	Hs.290404	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	SLC25A3	SLC25A3	0.3002	0.1382	4.3232	3	0.1382
BF046620	Hs.25338	hypothetical LOC538575	MGC139156	PRSS23	-0.2979	0.1676	4.0261	2	0.1676
BM364565	Hs.445129	hypothetical LOC510651	LOC510651	C12orf35	0.2966	0.0770	3.6503	4	0.0770
CN435672	Hs.615223	hypothetical LOC618459	LOC618459	FAM101B	0.2933	0.1658	-4.2187	2	0.1658
CR452973	Hs.127897	similar to Rap guanine nucleotide exchange factor (GEF) 1	LOC520454	RAPGEF1	-0.2884	0.1403	5.2482	2	0.1403
AW465340	Hs.373550	similar to TG-interacting factor	LOC510050	TGIF1	0.2842	0.0353	4.6058	4	0.0353
CN441335	Hs.76884	inhibitor of DNA binding 3	ID3	ID3	-0.2829	0.1382	-3.6488	3	0.1382
NG010006B21A01	Hs.199763	Transcribed locus	0	SSH1	-0.2790	0.0263	3.9925	4	0.0263
BF042291	Mm.103246	hypothetical protein LOC782395	LOC782395	Mfhas1	0.2745	0.0722	3.5422	6	0.0722
BF042780	Hs.488835	similar to transmembrane protein induced by tumor necrosis factor alpha	LOC520173	TMPIT	-0.2731	0.1619	-4.5821	2	0.1619
NG010008A10G02	Hs.200100	hypothetical LOC615685	LOC615685	C7orf41	-0.2710	0.1619	-4.4658	2	0.1619
BF045597	Hs.172772	Transcribed locus, weakly similar to XP_578119.2 similar to transcription elongation factor B (SIII), polypeptide 2 [Rattus	0	TCEB2	-0.2705	0.1382	-3.9613	3	0.1382

		norvegicus]							
AW465707	Hs.522789	similar to mammalian retrotransposon derived 8b	MGC140692	FAM127A	-0.2688	0.1382	-4.2503	3	0.1382
CN434811	Hs.631602	similar to nucleobindin 1	MGC143428	NUCB1	-0.2679	0.1619	-4.5544	2	0.1619
BF041910	Hs.460468	similar to exportin 6	LOC510797	XPO6	0.2642	0.1134	5.1092	3	0.1134
CR553375	Hs.134296	similar to Deleted in liver cancer 1	LOC511433	DLC1	-0.2590	0.1619	4.4717	2	0.1619
BF040173	Hs.550155	similar to Ankyrin repeat domain-containing protein 13B	LOC616514	ANKRD13B	0.2576	0.0263	-4.0568	4	0.0263
NG010008A20G04	Hs.210891	similar to TBC1 domain family, member 4	LOC534649	TBC1D4	0.2521	0.1382	-3.3009	3	0.1382
AW462339	Hs.592048	Ubiquinol-cytochrome c reductase core protein II	UQCRC2	UQCRC2	0.2508	0.1764	-3.9104	2	0.1764
CR453487	Hs.417004	S100 calcium binding protein A11 (calgizzarin)	S100A11	S100A11	-0.2476	0.1515	3.1374	3	0.1515
NM_173982	Hs.652217	advanced glycosylation end product-specific receptor	AGER	AGER	-0.2399	0.1619	-6.4562	1	0.1619
BCAZ0017eo21	0	0	0	0	0.2386	0.0999	5.1617	3	0.0999
BF044376	Hs.567328	similar to Rab5B	LOC539150	RAB5B	-0.2377	0.1515	5.0578	2	0.1515
CN441812	Hs.482587	similar to Secretory carrier-associated membrane protein 1 (Secretory carrier membrane protein 1)	LOC535352	SCAMP1	0.2367	0.0737	3.7800	4	0.0737
CR452523	Hs.410596	Transcribed locus	0	WDR68	-0.2359	0.1382	5.5658	2	0.1382
CR551679	Hs.458332	pyrroline-5-carboxylate reductase 1	PYCR1	PYCR1	-0.2326	0.0263	6.9646	3	0.0263
CN438842	Hs.643279	Transcribed locus	0	EIF4EBP2	-0.2321	0.1382	3.6951	3	0.1382
CN441754	Hs.309641	RING finger protein 11	RNF11	RNF11	0.2280	0.1417	3.2677	3	0.1417
CR455706	Hs.126497	similar to AE binding protein 2	MGC142819	AEBP2	0.2231	0.1204	-4.7134	3	0.1204
AW464058	Hs.530291	annexin A11	ANXA11	ANXA11	-0.2219	0.1382	6.9761	2	0.1382
AW462229	Hs.5333	Transcribed locus	0	KBTBD11	0.2151	0.1382	-4.3906	3	0.1382
AW267074	Hs.652329	LAG1 homolog, ceramide synthase 2 (S. cerevisiae)	LASS2	LASS2	-0.2136	0.1608	4.6450	2	0.1608

CN439691	Hs.530904	cysteine and glycine-rich protein 2	CSRP2	CSRP2	-0.2119	0.1620	-4.4174	2	0.1620
CR455904	Hs.534333	similar to NADH dehydrogenase	LOC785629	NDUFA2	-0.2115	0.1382	-5.4580	2	0.1382
AW465346	Hs.105134	similar to CHCR	LOC540550	MBNL3	0.1996	0.0941	-5.3990	3	0.0941
CN442418	Bt.45855	similar to fibroblast growth factor 9	LOC613731	LOC613731	0.1975	0.1382	5.6127	2	0.1382
BM363499	Hs.514821	chemokine (C-C motif) ligand 5	CCL5	CCL5	-0.1965	0.1524	-3.1162	3	0.1524
CN432898	Hs.501140	similar to KIAA1598 protein	LOC532603	KIAA1598	-0.1948	0.1382	3.6962	3	0.1382
CN439268	Hs.533613	troponin T type 2 (cardiac)	TNNT2	TNNT2	0.1945	0.0722	-7.1856	4	0.0722
CN433434	Hs.164853	similar to ubiquitin-conjugating enzyme UbcH6	LOC615599	UBE2E1	0.1941	0.1619	4.5649	2	0.1619
BP240034B20G10	Mm.27620	similar to SMF protein	LOC509419	A630042L21Rik	-0.1936	0.1561	6.7870	1	0.1561
AV597541	Hs.432752	similar to KIAA1513 protein	LOC539790	POGK	-0.1916	0.1619	-4.6216	2	0.1619
BF044278	Hs.471768	similar to SINK-homologous serine/threonine kinase	MGC139116	STK40	0.1909	0.0942	-5.2545	3	0.0942
CR454066	Hs.445387	Transcribed locus	0	RPS6KA3	0.1901	0.1656	4.3958	2	0.1656
CK773418	Hs.441072	similar to DNA-directed RNA polymerase II 7.6 kDa polypeptide (RPB10) (RPB7.6) (RPABC5)	LOC617375	POLR2L	-0.1899	0.1382	3.7159	3	0.1382
AW465457	Hs.534591	similar to Y106G6H.8	MGC136990	C17orf61	-0.1899	0.0722	6.2246	4	0.0722
CR456060	Hs.435120	similar to Kinesin family member 1C	LOC514928	KIF1C	-0.1871	0.1204	-4.6529	3	0.1204
BF046544	Hs.55041	mitochondrial ribosomal protein L2	MRPL2	MRPL2	0.1869	0.1382	6.2141	2	0.1382
BF044717	0	0	0	0	0.1863	0.1382	-3.9859	3	0.1382
CR452280	Hs.156369	similar to tenascin N	LOC517433	TNN	0.1828	0.1658	4.2175	2	0.1658
AW463527	Hs.523855	similar to Syntaxin 12	LOC505538	STX12	-0.1817	0.1524	-4.9826	2	0.1524
BU01002X1E09	#N/A	#N/A	#N/A	#N/A	-0.1799	0.1382	3.7709	3	0.1382
CR553968	Hs.181163	similar to put. HMG-17 protein	LOC512161	HMGN2	-0.1794	0.1656	4.2984	2	0.1656
CN441254	Hs.15591	hypothetical LOC512756	LOC512756	COPS6	0.1793	0.1619	6.4916	1	0.1619
CR452002	Hs.525899	C6orf49-like protein	LOC505031	C6orf49	-0.1762	0.0722	-4.8765	5	0.0722
BF039693	Bt.87214	similar to BRG1-Associated Factor 250a	LOC783818	LOC783818	0.1712	0.1503	-3.2163	3	0.1503
CN440524	Hs.436040	cadherin 13, H-cadherin (heart)	CDH13	CDH13	0.1710	0.1134	4.9806	3	0.1134
CN438132	Hs.445665	abhydrolase domain containing 4	ABHD4	ABHD4	-0.1681	0.1370	-4.5000	3	0.1370
CR454741	Hs.632191	similar to RS21-C6 protein	MGC133613	XTP3TPA	0.1666	0.1382	-7.9103	1	0.1382
CR550709	Hs.511801	similar to CG32955-PF	MGC134279	C17orf49	-0.1663	0.1742	-5.7172	1	0.1742

CN441769	Hs.317190	FAD-dependent oxidoreductase domain containing 1	FOXRED1	FOXRED1	-0.1637	0.1382	-3.5359	3	0.1382
BF041456	Hs.162877	similar to protein kinase C and casein kinase substrate in neurons 2	MGC137898	PACSIN2	-0.1611	0.1382	-4.0245	3	0.1382
BF039699	Hs.213198	similar to paraspeckle protein 1	MGC139047	PSPC1	0.1611	0.1382	6.4570	2	0.1382
BF045636	Mm.34775	pyruvate dehydrogenase E1 component alpha subunit precursor	PDHA	Pdha1	0.1589	0.1382	-3.9479	3	0.1382
BF039711	Hs.75277	hypothetical LOC516731	LOC516731	RMND5A	0.1581	0.1656	-6.3627	1	0.1656
BP230036000G7	Hs.479898	sulfotransferase, estrogen-preferring	STE	SULT1E1	0.1458	0.1382	8.7596	1	0.1382
BP230036000G2	0	0	0	0	0.1445	0.1619	6.6143	1	0.1619
BF043536	Hs.517546	similar to Oxysterol binding protein 2	LOC510311	OSBP2	0.1395	0.1714	5.8135	1	0.1714
BF040119	Hs.78960	similar to LATS, large tumor suppressor, homolog 2 (Drosophila)	LOC508208	LATS2	-0.1314	0.1658	-4.2741	2	0.1658
CN436096	Hs.13366	similar to Chromosome 6 open reading frame 151	LOC513601	C6orf151	-0.1293	0.1619	-4.5073	2	0.1619
BM364411	Hs.8008	similar to DNMT1 associated protein-1	MGC139005	DMAP1	0.1288	0.1658	-4.2301	2	0.1658
BP230036000D6	Bt.1656	msh homeobox 1	MSX1	MSX1	0.1267	0.1524	-3.0864	3	0.1524
BI535499	Hs.389461	similar to SMAP-1b	LOC535692	UNC45A	-0.1249	0.1764	-5.5652	1	0.1764