Table S2. Maternal transcripts significantly enriched in the vegetal region

RefSeq ID	Name	Function	A1*	A2	V1	V2	Fold change	FDR
NM_001089043.1	*germs* (1)	components of the germ plasm	1.94	1.55	140.45	137.29	79.16	3.43E-23
NM_001088548.1	*ddx25* (2)	ATP-dependent RNA helicase	5.10	7.25	255.84	339.22	48.46	8.27E-20
NM_001087463.1	*pgat* (3)	germ plasm formation, positioning and maintenance	2.18	3.05	117.18	132.15	48.12	1.24E-19
NM_001088303.1	*dazl* (4)	RNA-binding	2.66	3.56	60.26	81.20	22.81	5.62E-13
NM_001092998.1	*pcsk6* (5)	protease; proprotein convertase	9.65	10.85	147.78	119.63	13.16	9.43E-10
NM_001095880.1	*cnppd1*	cyclin	8.81	9.59	101.51	108.35	11.42	9.73E-09
NM_001088196.1	*vegt-a* (6)	T-box transcription factor, meso-endodermal determinant	73.00	47.87	565.45	607.31	9.56	6.69E-08
NM_001091117.1	*trim36* (7)	zinc finger protein	4.82	4.64	43.40	68.48	11.70	8.55E-08
NM_001087171.1	*gk*	ribulose kinase and related carbohydrate kinases	3.09	4.54	32.95	47.78	10.64	1.54E-07
NM_001086974.1	*acsl1* (8,9)	fatty acid CoA ligase	10.93	5.97	86.42	73.91	9.34	1.69E-07
NM_001094076.1	*rtn3-b* (8)	reticulon	1.53	2.29	43.98	78.70	32.23	9.87E-07
NM_001086456.1	*snai1* (10)	zinc finger protein	7.67	2.89	50.58	42.25	8.56	1.80E-06
NM_001095591.1	*vg1* (11,12)	TGF-beta related peptide	21.63	15.83	508.78	344.14	22.72	1.80E-06
NM_001088202.1	*vegt-b* (6)	T-box transcription factor, meso-endodermal determinant	37.86	37.00	236.10	288.17	6.97	7.76E-06
NM_001093953.1	*syntabulin* (13)	nucleolar GTPase/ATPase	0.65	0.72	7.68	8.10	11.59	1.12E-05
NM_001094985.1	*lsm4*	small nuclear ribonucleoprotein	3.88	5.33	32.27	41.46	8.05	1.24E-05
NM_001091230.1	MGC81075 (8)	Trim-like protein	13.72	9.85	84.80	72.58	6.63	2.07E-05
NM_001090713.1	*tob2* (8)	transducer of ERBB2	5.22	3.85	26.83	36.48	6.87	3.57E-05
NM_001091527.1	*pgam1* (8)	phosphoglycerate mutase	13.93	20.88	96.05	126.16	6.43	4.49E-05
NM_001093074.1	*spire1* (14)	nucleolar GTPase/ATPase	25.65	14.32	133.87	103.02	5.85	7.21E-05
NM_001087479.2	*ephrin-b1* (15)	ligand for Eph receptor tyrosine kinase	3.59	3.73	29.83	29.94	8.17	1.01E-04
NM_001085868.1	*sox7* (16)	HMG-box transcription factor	10.38	5.57	82.17	58.29	8.70	1.06E-04
NM_001093628.1	*irf8*	transcription factor	4.45	5.24	23.75	35.33	6.08	1.06E-04
NM_001086196.1	MGC53832 (8)	long-chain-fatty-acid--CoA ligase 1-like	17.87	20.62	106.52	113.21	5.73	1.11E-04
NM_001087540.1	*otx1* (17)	homeodomain transcription factor	16.88	13.19	92.86	81.07	5.75	1.22E-04
NM_001095090.1	*bicc1-b* (18)	KH domain RNA-binding protein	12.79	10.51	68.36	55.25	5.30	3.54E-04
NM_001088757.1	*rnf103*	mediator of ubiquitin ligase activity	6.74	6.53	40.87	31.88	5.50	3.70E-04
NM_001095906.1	*cdk5r2*	CDK5 kinase activator	10.39	6.24	47.62	39.93	5.20	5.53E-04
NM_001097913.1	*grip2* (19,20)	PDZ domain protein	2.90	1.16	263.41	130.22	95.55	9.06E-04
NM_001095094.1	*atp2a3* (8)	Ca^{2+} transporting ATPase	5.31	6.86	28.49	30.63	4.89	1.11E-03
NM_001088491.1	*plin2* (21)	vesicular trafficking	181.10	176.38	798.04	710.26	4.23	3.85E-03
NM_001095736.1	*dsc3*	member of the cadherin gene superfamily	23.09	20.48	107.36	78.61	4.28	4.42E-03

NM_001086902.1	*elovl1*	ELOVL fatty acid elongase	16.77	18.28	61.88	89.54	4.30	4.42E-03
NM_001093340.1	MGC82549	sequence similar to PGAM1	35.96	44.72	137.77	198.77	4.17	5.78E-03
NM_001088034.1	*nanos1* (22)	RNA binding	5.09	1.49	235.07	113.47	51.88	9.18E-03
NM_001093266.1	MGC81526	sequence similar to tspan1, integral membrane protein	54.60	66.21	177.18	285.54	3.82	1.38E-02
NM_001086025.1	*acsbg2* (8)	long-chain acyl-CoA synthetases	40.03	32.67	144.06	132.11	3.78	1.43E-02
NM_001090151.1	*papola*	poly(A) polymerase and related nucleotidyltransferases	37.63	41.83	114.34	180.42	3.69	1.82E-02
NM_001097902.1	LOC100037213	uncharacterized	27.47	26.06	102.19	99.87	3.77	1.97E-02
NM_001090858.1	*wnt11b* (23)	secreted protein, developmental regulator	14.89	9.04	137.52	83.38	9.18	2.38E-02
NM_001092250.1	*rtn3-a* (8)	reticulon	55.59	44.24	174.77	174.16	3.47	3.28E-02
NM_001090817.1	*scp3* (24)	phosphatase	38.91	34.40	109.60	143.36	3.42	4.08E-02
NM_001094823.1	*aktip-b*	ubiquitin-protein ligase	45.07	45.94	132.91	179.87	3.42	4.38E-02

*A: RPKM of samples from animal blastomeres; V: RPKM of samples from vegetal blastomeres

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