

Faunes et al, Supplementary table 1

Gen	Tag (15 th base)	Transcript*	Dorsal frequency	Ventral frequency	Normalized ratio (p-val eSAGE)
<i>admp</i>	CATGTA CTGCGTTA(T)	NM_001045692.1 ENSXETT00000019176	8	0	8.2 (0.0035)
<i>cerberus</i>	CATGGATGCATCTA(C)	NM_203515.1	3	0	3.1 (0.1215)
<i>chordin*</i>	CATGATGTTACTTT(G) CATGGTTCACGATG(G)	Xt6.1-TNeu120o03.3**	3 2	0 0	3.1 (0,1215) 2.1 (0,2465)
<i>dkk-1</i>	CATGATCCTCTCTA(T)	Xt6.1-TGas131c10.3 ENSXETT00000014461	1	0	1 (0,4999)
<i>pintallavis</i>	CATGAAACCTGTTT(T)	NM_203607.1 ENSXETT00000055323	34 (32)	2	17.5 (6,65e-9)
<i>crescent (frzb2)</i>	CATGCGTGGGACCC(G)	NM_001016688.1	2	0	2.1 (0,2465)
<i>goosecoid</i>	CATGATGTGGGATC(T)	NM_001016704.2 ENSXETT00000050392	11	0	11.3 (0,0004)
<i>noggin 1</i>	CATGTTATATGCAC(T)	AY672091.1	2	0	2.1 (0,2465)
<i>otx2</i>	CATGGCTGCCTTCT(G)	NM_001016177.2 ENSXETT00000034219	5	0	5.1 (0,02955)
<i>siamois</i>	CATGAAGTTTGAAG(A)	NM_001097352.1	0	0	-
<i>sox3</i>	CATGAAAGTAAAAC(G)	NM_001007501.1	20 (18)	8	2.6 (0,0204)
<i>xnot</i>	CATGATTGTATTAT(T)	CT025280.2 ENSXETT00000025770	3	0	3.1 (0,1215)
<i>zic3</i>	CATGCAACACTGAA(A)	NM_001005691.1 ENSXETT00000052875	5 (4)	0	5.1 (0,0295)
<i>frzb</i>	CATGGACTTTAATA(C)	NM_001005438.1 ENSXETT00000002846	1	0	1 (0,4999)
<i>sfrp2</i>	CATGTTGTGCCGGT(A)	NM_203731.1 ENSXETT00000055200	1	0	1 (0,4999)
<i>follistatin</i>	CATGTAAATGTGTA(A)	NM_001008056.1	1	0	1 (0,4999)
<i>bambi</i>	CATGGTGCCAGTGA(C)	NM_001008193.1 ENSXETT00000009856	0	6	-5.8 (0,0171)
<i>bmp4</i>	CATGGAGACTCTGA(A)	AJ315161.1	0	2	-1.9 (0,2604)
<i>bmp7</i>	CATGATATTTTATC(C)	NM_001033938.2 ENSXETT00000035775	2 (1)	5	-2.5 (0,3075)
<i>crossveinless-2</i>	CATGTGAAAACCTGG(A)	NM_001044402.1	0	1	1 (0,5138)
<i>sizzled</i>	CATGCTGTATAAGA(A)	NM_001044506.1 ENSXETT00000048172	0	1	1 (0,5138)
<i>twisted</i>	CATGCTTACACTAA(T)	NM_001006747.1	0	0	-
<i>wnt8</i>	CATGTTTGGTTTGT(T)	NM_001017208.2 ENSXETT00000008323	0	1	1 (0,5138)
<i>vent1.1</i>	CATGGGAGCTATGG(C)	NM_001114235.1	0	15	-14.6 (3,8e-5)
<i>vent1.2</i>	CATGTAACCCCTGG(A)	NM_203530.1 ENSXETT00000019491	0	8	-7.8 (0,0044)
<i>vent2</i>	CATGATTTTATTCA(C)	AY187016.1 ENSXETT00000056265	8	12	-1.5 (0,4190)
<i>xbra</i>	CATGTGATGTTTTT(G)	NM_001008138.1 ENSXETT00000011786	7	3	2.4 (0,2151)
<i>odc1</i>	CATGGCATTCTCCC(T)	NM_001005441.1 ENSXETT00000007603	31	25	1.3 (0,3790)
<i>ef1alpha</i>	CATGAGGCAGACGG(T)	NM_203970.2	133 (130)	144 (137)	-1.1 (-)

Supplementary Table 1. Tags derived from control genes.

Known genes with differential expression along the dorso-ventral axis were analyzed and the most 3' tag was extracted. These tags were searched in the list of experimental tags and frequencies in each library are indicated. The 15th base of the tag is indicated between parentheses. If the frequency of occurrence of the 15-nts tag is different from the frequency of the 14-nts tag, this is indicated between parentheses.

* Sequences used to extract virtual tags are indicated. Virtual tags derived from mRNA sequences (“NM”) or Ensembl cDNAs (“ENSXETT”) are first considered. If mRNA sequence or Ensembl cDNA is not available, Unigenes and EST clusters are used.

** Virtual tag for *chordin* was obtained by comparison of sequences of *X. tropicalis* and *X. laevis* to determine the 3' end. In addition, tag derived from upstream an internal polyA tract position was considered.

Faunes et al, Supplementary table 2

DV_ID	Tag sequence	Dorsal frequency	Ventral frequency	Normalized ratio*	Matches to Genome	Tag-mapping
DV01	CATGAAACCTGTTT	34	2	17.5	23	<i>Pintallavis (forkhead box4)</i>
DV02	CATGAGTTTCTTGT	20	1	20.6	14	<i>Xt6.1-CAAM15738.5SS, Xt6.1-CAAM9567.5S, Xt6.1-CAAM4052.5</i>
DV03	CATGGGAGCTATGG	0	15	-14.6	10	<i>Vent-1.1</i>
DV04	CATGCATTAATGAA	18	2	9.3	26	Not assigned
DV05	CATGAGCTGTATGC	20	3	6.9	1482	<i>Doublecortin domain containing 2B, Str#S23608264, family with sequence similarity 119, DCN1-like protein 2, Str#S22844133, Str#S38479083</i>
DV06	CATGATGTGGGATC	11	0	11.3	2	<i>goosecoid</i>
DV07	CATGTGGCGTCCG	9	0	9.3	1	<i>Zcsl-2</i>
DV08	CATGAAAATAAAAC	9	0	9.3	82	<i>Ubadc1/ LOC496648</i>
DV09	CATGCAAGTATGTT	11	1	11.3	20	<i>Sox11</i>
DV10	CATGTACTGCGTTA	8	0	8.2	7	<i>admp</i>
DV11	CATGATGGCGGAGC	8	0	8.2	3	<i>LOC100124861</i>
DV12	CATGCTCTACCCT	13	2	6.7	9	<i>LOC549498</i>
DV13	CATGCTAGACTTTT	1	11	-10.7	12	<i>Id-2</i>
DV14	CATGTGGGAACAGA	0	8	-7.8	10	Not assigned
DV15	CATGTAACCCCTGG	0	8	-7.8	11	<i>Vent-1.2</i>
DV16	CATGCGCTGTACA	10	1	10.3	3	<i>MGC147163</i>
DV17	CATGATTGGTGCC	12	2	6.2	11	<i>Str.45862/Str.40022</i>
DV18	CATGAAAATTAAAT	12	2	6.2	68	<i>LOC548724</i>
DV19	CATGTTCACTGTTT	7	0	7.2	26	Not assigned
DV20	CATGTCTACTGCAG	7	0	7.2	20	<i>LOC394509</i>
DV21	CATGTCCTTATTAA	7	0	7.2	26	Not assigned
DV22	CATGGTTGGCTGGA	1	10	-9.7	9	<i>smagp</i>
DV23	CATGTTCCAGGTG	2	12	-5.8	19	<i>Xt6.1-CAAL21480.5S, Xt6.1-XZG37850.5S</i>
DV24	CATGGCAGCTCCAT	2	12	-5.8	44	<i>e2f5</i>
DV25	CATGATGTACAGTT	2	12	-5.8	27	<i>cyclin A2</i>
DV26	CATGTTTTAGTTTG	0	7	-6.8	45	<i>LOC549800</i>
DV27	CATGTGATACTAAG	0	7	-6.8	7	<i>MGC76280</i>
DV28	CATGTAGCTTATAC	0	7	-6.8	12	<i>hsbp1</i>
DV29	CATGTA AAACTGAA	0	7	-6.8	47	<i>LOC100038289</i>
DV30	CATGGTTAGGAGGT	0	7	-6.8	7	Not assigned
DV31	CATGGGGTGGGAGG	0	7	-6.8	42	<i>MGC75957</i>
DV32	CATGCCAATTCGC	0	7	-6.8	2	Not assigned
DV33	CATGGAGATTAGCG	9	1	9.3	4	<i>tumor protein p53</i>
DV34	CATGCCGCTCAGAC	9	1	9.3	3	<i>sympleskin</i>
DV35	CATGATGGGATTCT	11	2	5.7	12	<i>LOC100145022</i>
DV36	CATGACGAGTAGCG	11	2	5.7	0	No match to genome

DV37	CATGTGTGAGAGCA	1	9	-8.8	17	LOC550036, LOC549521
DV38	CATGTAGATATTAG	1	9	-8.8	25	<i>nap111</i>
DV39	CATGGGCAATGGGA	1	9	-8.8	16	<i>mix1</i>
DV40	CATGGAATTGAATA	1	9	-8.8	60	<i>xtr-mir-427-3</i>
DV41	CATGATTACCTTTT	1	9	-8.8	29	LOC100158535
DV42	CATGTGTTTTTATA	6	0	6.2	93	SMAD 9, splicing factor, arginine/serine-rich 10
DV43	CATGTGGCCAGCGT	6	0	6.2	6	splicing factor, arginine/serine-rich 6
DV44	CATGTGGAGATAGA	6	0	6.2	5	RNA binding motif protein 13
DV45	CATGGCCGGTACCGG	6	0	6.2	2	Str#S23705173
DV46	CATGGCACCCGATA	6	0	6.2	2	Not assigned
DV47	CATGGAATACTATA	6	0	6.2	18	<i>cone-rod homeobox (crx)</i>
DV48	CATGTCCTTCGTTA	2	11	-5.4	2	calcium activated nucleotidase 1
DV49	CATGTACCTCCAAT	2	11	-5.4	2	<i>Xt6.1-XZG44017.5</i>
DV50	CATGAAAAGGACTG	2	11	-5.4	9	transmembrane protein 32
DV51	CATGTTCTAAATGT	0	6	-5.8	44	<i>Dnajc2-prov protein</i>
DV52	CATGTTCGTGGAGG	0	6	-5.8	1	LOC496724
DV53	CATGTTACAACCTTG	0	6	-5.8	10	Integral membrane protein GPR137B (Transmembrane 7 superfamily member 1 protein)
DV54	CATGTGAGTTTGTG	0	6	-5.8	13	phosphatidylinositol transfer protein, alpha (pitpna), <i>Xt6.1-CABH10159.5SS</i>
DV55	CATGTATGTACACC	0	6	-5.8	16	<i>Xt6.1-Ttba059c13.3</i>
DV56	CATGTACTAAAAAT	0	6	-5.8	46	MGC69221
DV57	CATGGTGCCAGTGA	0	6	-5.8	16	<i>Bambi</i>
DV58	CATGGGTTAAGGTT	0	6	-5.8	19	<i>nucleobindin 1</i>
DV59	CATGGCACTTGTTT	0	6	-5.8	21	<i>fatty acid binding protein 3, muscle and heart</i>
DV60	CATGGAAGAGGCAA	0	6	-5.8	27	Str#S23215713, Str#S34494240, Uncharacterized protein KIAA0574 (Fragment)
DV61	CATGCTCAACCTGG	0	6	-5.8	5	Not assigned
DV62	CATGCTAAGTTATT	0	6	-5.8	7	Str#S22514784,
DV63	CATGATGTACAATT	0	6	-5.8	15	ENSXETT00000054938, ADP-ribosylation factor 3
DV64	CATGAAAATGCAGT	8	1	8.2	35	<i>Xt6.1-Ttba02n08.3SS</i>
DV65	CATGACAAACACAA	8	1	8.2	58	Glutathione peroxidase 7 precursor (EC 1.11.1.9) (CL683), <i>Brd7-prov protein</i>
DV66	CATGTGAAATAAAT	10	2	5.1	93	MGC75584, calcitonin gene-related peptide-receptor component protein (rcp9), <i>Xt6.1-CAAN7840.3</i> , <i>Xt6.1-CABA4576.5</i>
DV67	CATGGCGGAAGTGA	10	2	5.1	7	Ribonuclease P protein subunit p38
DV68	CATGACAAGCTAAG	10	2	5.1	5	Not assigned
DV69	CATGTACATAAGTT	1	8	-7.8	17	<i>Death-associated protein- like 1</i>

DV70	CATGTAAAGTTGAC	1	8	-7.8	12	<i>60S ribosomal protein L10a (CSA-19), Str#S20516889, Xt6.1-CAAP3220.3</i>
DV71	CATGGGGAAGTTTG	1	8	-7.8	13	Not assigned
DV72	CATGATGTAAATGC	1	8	-7.8	22	<i>zona pellucida glycoprotein 4</i>
DV73	CATGAGTACAAAAT	1	8	-7.8	24	<i>Xt6.1-CABD13995.3, Xt6.1-TNeu063n12.3SS, Xt6.1-XZG53362.5</i>
DV74	CATGTTTTTGT	2	10	-4.9	260	<i>MOBI, Mps One Binder kinase activator-like 1B, ENSXETT00000045544, Str#S16960692</i>
DV75	CATGACATTTTAGG	2	10	-4.9	17	<i>lamin B1</i>
DV76	CATGTGTGCAGAGA	5	0	5.1	29	<i>flap structure specific endonuclease 1</i>
DV77	CATGTGCCACAGTG	5	0	5.1	27	<i>Str#S42160483</i>
DV78	CATGTCTCTATTAA	5	0	5.1	21	Not assigned
DV79	CATGTCCCGTACAT	5	0	5.1	0	No match to genome
DV80	CATGTCAGAGCATC	5	0	5.1	9	<i>Xt6.1-TNeu051c17.5</i>
DV81	CATGGTTTTGGCAC	5	0	5.1	10	<i>Str#S43286247</i>
DV82	CATGGTTCACCTGT	5	0	5.1	8	<i>LOC548815</i>
DV83	CATGGTGTCTGTGT	5	0	5.1	62	<i>ADP-ribosylation factor related protein 1</i>
DV84	CATGGGAAGGCAAA	5	0	5.1	40	<i>Lysophosphatidic acid receptor 2, Xt6.1-XZF1171.3S</i>
DV85	CATGGCTGCCTTCT	5	0	5.1	18	<i>orthodenticle homeobox 2</i>
DV86	CATGGCAATGATCA	5	0	5.1	21	Not assigned
DV87	CATGGATAAGCTAC	5	0	5.1	7	Not assigned
DV88	CATGCTTTTATTTT	5	0	5.1	103	<i>Str#S17733131, Xt6.1-XZT67122.5, Xt6.1-TTbA020f14.5SS</i>
DV89	CATGCTGGTTGCAA	5	0	5.1	13	<i>Str#S26249311</i>
DV90	CATGCTGAAATTAG	5	0	5.1	23	<i>Regulator of G-protein signaling 7-binding protein (R7 family-binding protein)</i>
DV91	CATGCCTATCGGCA	5	0	5.1	1	<i>Xt6.1-TEgg042i09.3</i>
DV92	CATGCAGAGCAGAA	5	0	5.1	29	<i>UTP15, U3 small nucleolar ribonucleoprotein, homolog (utp15)</i>
DV93	CATGCAACACTGAA	5	0	5.1	19	<i>Zic family member 3 heterotaxy 1</i>
DV94	CATGATATCGTTTA	5	0	5.1	2	Not assigned
DV95	CATGACTGAATAAA	5	0	5.1	39	<i>Str#S16958610</i>
DV96	CATGAAAATGTTAA	5	0	5.1	59	<i>Xt6.1-TGas120k14.3</i>
DV97	CATGAAAATGCTAA	5	0	5.1	55	<i>Interferon-related developmental regulator 2 (SKMC15 protein)</i>
DV98	CATGTTTTACAATA	0	5	-4.9	43	<i>Xt6.1-CABJ1926.3</i>
DV99	CATGTTTATACAGTT	0	5	-4.9	37	<i>ENSXETT00000023000 (without description)</i>
DV100	CATGTTAACCAACA	0	5	-4.9	8	Not assigned
DV101	CATGTTAACATTTG	0	5	-4.9	34	Not assigned
DV102	CATGTTAACCTGA	0	5	-4.9	12	Not assigned
DV103	CATGTGCCAAAAAT	0	5	-4.9	49	<i>Str#S21734651</i>

DV104	CATGCTTACTTAC	0	5	-4.9	7	<i>Str#S37580355</i>
DV105	CATGTCATTTTGC	0	5	-4.9	57	<i>Xt6.1-XZT41995.3</i>
DV106	CATGTAAC TACCCC	0	5	-4.9	13	<i>Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2)</i>
DV107	CATGGGTGCGATGA	0	5	-4.9	2	<i>PRP31 pre-mRNA processing factor 31 homolog (prpf31)</i>
DV108	CATGGATTTGCTCA	0	5	-4.9	26	<i>CDC20 cell division cycle 20 homolog</i>
DV109	CATGCCCCCTAAGT	0	5	-4.9	4	Not assigned
DV110	CATGCCCATATATA	0	5	-4.9	41	<i>MGC145307</i>
DV111	CATGCAGAAGGAAT	0	5	-4.9	26	<i>Xt6.1-XZT56795.5</i>
DV112	CATGACTCTGTAGC	0	5	-4.9	6	<i>MAP3K12 binding inhibitory protein 1 (mbip)</i>
DV113	CATGAAGGAAATGC	0	5	-4.9	14	<i>LOC549814</i>
DV114	CATGAAAAATGTTGGG	0	5	-4.9	22	<i>protein phosphatase 1, regulatory subunit 15A, Phospholipid hydroperoxide glutathione peroxidase, mitochondrial precursor</i>
DV115	CATGTTTGATTGGT	7	1	7.2	21	<i>voltage-dependent anion channel 1 (vdac1)</i>
DV116	CATGTGTAAAAAGA	7	1	7.2	39	<i>MGC69468 protein, Xt6.1-CAA09219.3SSS</i>
DV117	CATGGTACTGGAAA	7	1	7.2	14	<i>MGC89748</i>
DV118	CATGCTTCCCACCA	7	1	7.2	10	<i>transmembrane and coiled-coil domain family 2 (tmcc2), Str#S17793010</i>
DV119	CATGTTTCTTCCAG	1	7	-6.8	17	<i>Str#S22770715</i>
DV120	CATGTGTTTATATT	1	7	-6.8	238	<i>Str#S22514775, Xt6.1-CABI14076.3SS, Xt6.1-CABD514.3SS</i>
DV121	CATGTGTATTATC	1	7	-6.8	26	<i>Str#S30067137</i>
DV122	CATGCAGGAGTTTT	1	7	-6.8	21	<i>Hairy and enhancer of split 1, (Hairy2)</i>
DV123	CATGATAAAAAAAAA	1	7	-6.8	272	<i>26 transcripts</i>
DV124	CATGACTGAGATAA	1	7	-6.8	9	<i>Str#S35898101</i>
DV125	CATGAAGGAGGGTG	1	7	-6.8	11	<i>MGC69188</i>

Supplementary Table 2. Tag-mapping of tags with significant differential expression between dorsal and ventral libraries.

Tags with statistical significant difference of frequency of occurrence between SAGE libraries (3 tests, $p < 0.05$) and a fold-ratio of 5 or higher are indicated (listed by p-value, not shown). Reliable tag-mappings (position 1, 2 or polyA-next) in the transcript databases are indicated with the description of each gene when it is present (Ensembl or NCBI). For tags without matches in Ensembl cDNAs or NCBI mRNA sequences, Unigenes and/or Gurdon EST clusters are indicated. When several matches are found, all of them are indicated, but if position 1 and position 2 are present, only transcripts with match in position 1 are indicated.

Faunes et al, Supplementary Table 3

DV_tag	rSAGE sequence	Genome position/transcript
DV01.1	CATGAAACCTGTTTTTCCTTATGTCTGTGCTATTC TTGATATTAATATATAAACTTGTTCAATTA AAAAAAAAAAAAAAAAAAAAAAAA	scaffold_474:87,681-87,744 <i>pintallavis</i>
DV01.2	CATGAAACCTGTTTTTCCTTATGTCTGTGCTATTC TTGATATTAATATATAAACTTGTTCAATTA AAAAAAAAAAAAAAAAAAAAAAAA	scaffold_474:87,681-87,744 <i>pintallavis</i>
DV01.3	CATGAAACCTGTTTTTCCTTATGTCTGTGCTATTC TTGATATTAATATATAAACTTGTTCAATTA AAAAAAAAAAAAAAAAAAAAAAAA	scaffold_474:87,681-87,744 <i>pintallavis</i>
DV04.1	CATGCATTAATGAATGTAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAA	scaffold_19023: 2428-2444
DV04.4	CATGCATTAATGAATGAAAAAAAAAAGAAAA AAAAAAAAAAAAAAAA	scaffold_19023: 2428-2444
DV04.11	CATGCATTAATGAATGAAAAAAAAAAGAAAA AGAAAAAAAA	scaffold_19023: 2428-2444
DV05.1	CATGAGCTGTATGCCACAATCATCAATATTA CAAGAAAAAAAA	178 genomic matches Cluster Str.39849
DV05.2	CATGAGCTGTATGCCACAATCATCAATATTA CAAGAAAAGGCTTGAACACTAAAAAAAA AAAAAAAAAAAAAAAA	190 genomic matches Cluster Str.39849
DV05.3	ATGAGCTGTATGCCACAATCATCAATATTA AAGAAAAGGCTTGAACACTTCAAAAA AAAAAAAAAAAAAAAA	199 genomic matches Cluster Str.39849
DV05.4	CATGAGCTGTATGCCACAATCATCAATATTA CAAGAAAAAAAAAAAAAAAAAAAAAAAA	179 genomic matches Cluster Str.39849
DV06.3	CATGATGTGGGATCTGTACATAAAGTGAAAT TATCATTTTCATTGCCTGTAAATAAAAA GCAGGCATTTGCACAGATACACTGTACTG TACTATTTATACCTTAAGTTAAAGGAATT AATAAACAGATGGCAAAAAAAAAAAAA AAAAGAAAAAAAA	scaffold_185:1,843,070-1,843,218 <i>gooseoid</i>
DV07.3	CATGTGGCGTTCCGTAAAAAAAAAAAAAAAAA	scaffold_321:185,446-185,460 (SNP G→A, BASE 14) <i>zsl-2</i>
DV08.3	CATGGAAATAAACAAAAAAAAAAAAAAAA	scaffold_1309:71,568-71,581 <i>ubadcl</i>
DV08.7	CATGGAAATAAACAAAAAAAAAAAAAAAA AAAA	scaffold_328: 504,732- 504,745 <i>LOC496648</i> scaffold_1309:71,568-71,581 <i>ubadcl</i>
DV08.8	CATGGAAATAAACCTCTTTATGCAAAAA AAAAAAAAAAAAAAAA	scaffold_328: 504,732- 504,745 <i>LOC496648</i> scaffold_1309:71,558-71,581 <i>ubadcl</i>
DV09.1	CATGCAAGTATGTTGGTAACGTTATGTCCTG AAAGGATTAATAATTAAGAAAAAAAA AAAAAAAAAAAAAAAA	scaffold_125:1,689,068-1,689,121 <i>sox11</i>
DV09.2	CATGCAAGTATGTTGGTAACGTTATGTCCTG AAAGGATTAATAATTAAGAAAAAAAAAG AAAAAAAAAAAAAAAA	scaffold_125:1,689,068-1,689,121 <i>sox11</i>
DV10.13	CATGTACTGCGTTACTCTTTGTAATATTTG TATAAGCAAATTGTTAATATATAATGCTT GTAATCTGTAACTTAACGTGTGAGGATA TCTTTTTATAAATGTACATATTAATATAT TTAAAAATAAATTTCTATGCAAGAACCTT AAAAAAAAAAAAAAAA	scaffold_112:387,252-387,420 <i>admp</i>
DV12.5	CATGCTCTTACCCTAAGGAAGGGCTGACTC AGCCCTTCCCTTCAGAGGTTTAATATGCT GATGCAGTTATAAATAAGAGGTATTTGT CTGCCAAAAAAAAACTTTCTGTAATAAAAG ATTTGAAATGTAAAAAAAAAAAAAAAA AAAAAAA	scaffold_411:704,144-704,291 <i>LOC549498</i>

DV12.6	CATGCTCTTACCCTAAGGAAGGGGCTGACTTCTC AGTCCTTCCCTTCAGAGGTTTTAACATGTCTTTCA GATGCAATTATAAATAAAGAGGTATTTTGTGTAA CTGCCAAAAAAAAAACTTTCTGTAATAAAAGCTTA ATTTGAAAGTGCAAAAAAAAAAAAAAAAAAAAAAA AAAAA	scaffold_411:704,144-704,291 <i>LOC549498</i>
DV12.8	CATGCTCTTACCCTAAGGAAGGGGCTGACTTCTC AGTCCTTCCCTTCAGAGGTTTTAATATGTCTTTCA GATGCAGTTATAAATAAAGAGGTATTTTGTGTAA CTGCCAAAAAAAAAACTTTCTGTAATAAAAGCTTA ATTTGAAATGTAAAAAAAAAAAAAAAAAAAAAA AAAAA	scaffold_411:704,144-704,291 <i>LOC549498</i>
DV12.9	CATGCTCTTACCCTAAGGAAGGGGCTGACTTCTC AGTCCTTCCCTTCAGAGGTTTTAATATGTCTTTCA GATGCAGTTATAAATAAAGAGGTATTTTGTGTAA CTGCCAAAAAAAAAACTTTCTGTAATAAAAGCTTA ATTTGAAAGGTAAAAAAAAAAAAAAAAAAAAAA AAAAA	scaffold_411:704,144-704,291 <i>LOC549498</i>
DV13.2	CATGCTAGACTTTTTATAAAAAGTTTGGTTGTAAA GCCTTTTTTTATACAGAATAAATCGATCGTGTTTA TGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	scaffold_125:418,146-418,217 <i>id-2</i>
DV13.3	CATGCTAGACTTTTTATAAAAAGTTTGGTTGTAAA GCCTTTTTTTATACAGAATAAATCGATCGTGTTTA TGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	scaffold_125:418,146-418,217 <i>id-2</i>
DV13.4	CATGCTAGACTTTTTATAAAAAGTTTGGTTGTAAA GCNCTTTTTTTATACAGAATAAATCGATCGTGTT ATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	scaffold_125:418,146-418,217 <i>id-2</i>
DV14.3	CATGTGGGAACAGATGTATATGATGATTCATTAT CTTGACATTCTTGAAATCAGATATTTTGTCAATC TCCTTCAGTAAGCGATGCCAATGAAAAAGGGAA GCATTATGTTTACAGATGTGATTATTGGAATGTTT GCCAAAATATTTGGTATCTCTAATAAACTTTGCC TCCAGCGTTGAAAAAAAAAAAAAAAAAAAAAA AAAAA	scaffold_58:1,610,508-1,610,688 Cluster Str.65896
DV16.2	CATGCGCTGTTACAAAAACCCTACTTGTACAGG AGCTGTTTGTTC AACAGAAACAGATCAATAAAT GACATCAATATTTAAAAATAAAAGAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	scaffold_353:66,955-67,035 <i>MGC147163</i>
DV16.5	CATGCGCTGTTACAAAAACCCTACTTGTACAGG AGCTGTTTGTTC AACAGAAACAGATCAATAAAT GACATCAATATTTAAAAAGAAAAAAAAAAAAAA AAAAA	scaffold_353:66,955-67,035 <i>MGC147163</i>
DV17.1	CATGATTGGTGCCCTTTAAGGAGCAAAAAAAAAA ACAAAA	scaffold_27:677,348-677,371 Cluster Str.40022
DV17.5	CATGATTGGTGCCCTTTAAGGAGCAAAAAAAAAA ACAAAATAAAAAAAAAAAAA	scaffold_27:677,348-677,371 Cluster Str.40022
DV18.1	CATGAAAATTAATGCCCGTTTCCGAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAA	scaffold_69:2,316,073-2,316,097 <i>LOC548724</i>
DV18.3	CATGAAAATTAATGCCCGTTTCCGAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAA	scaffold_69:2,316,073-2,316,097 <i>LOC548724</i>

Supplementary Table 3. Reverse SAGE sequences and transcript assignment.

For each tag, the specific rSAGE sequences of different clones and their genome and transcript matches are indicated.

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Transcript	Forward	Reverse	Annealing temperature
<i>Xenopus tropicalis</i>			
<i>ef1α</i>	ACTCAATCACCCAGGACAGATTAGTG	GTGGGTAGTCTGAGAAGGTTTCTACA	55
<i>odc1</i>	GCACATGTCAAGCCAGTTCT	TGCGCTCAGTTCTGGTACTT	60
<i>chordin</i>	ACCCAGAGAGCCAGAGACAA	ATCCACAGGGTCCACAGAAG	55
<i>sizzled</i>	CAGAAGGCCAGTTGAGTTC	TGATGGATGTCACCAGCAAT	55
<i>DV01</i>	CTGGGAGCAGATTTTGCTGT	TCAAGAATAGCACAGACATAAGGAA	59
<i>DV04</i>	CCCGGGTGGAAAATAGGTAA	GCCTCAATCGAATTGGGTAA	55
<i>DV04 probe</i>	TTGTGCTTTCGGAGCTTTTT	GCCTCAATCGAATTGGGTAA	55
<i>DV05</i>	TGGTGTGGTCCACTGTGTT	TATGGGGTTCAGGTCAGGAG	55
<i>DV05 probe</i>	TTGTGGAGAAGGACCGATTTC	ACTTGGTCGGGAATCCTTTT	55
<i>DV07</i>	TGCTTCTGATTTGCTTGCAG	CTTTGAAGAAGTCCCTTG	59
<i>DV07 probe</i>	ACTTGCCCTGACGTATGTT	CATCCCTTGCCTAGAAAACAA	55
<i>DV08</i>	AGTGGCTATTGGGTGACAGG	GTGCGGTTTAAGGTTTGAA	60
<i>DV08 probe</i>	GACGAGGATCGGGTAGATGA	GGGATTTGGTATCCGACCT	55
<i>DV09</i>	GGAAACATTCCTGCTGTCGTT	CCACAAGGCCTTTTAGATGC	55
<i>DV09 probe</i>	ACCATCAAGTCCGAGTACGG	CCCTCATCCATTTCTCTGGA	55
<i>DV11</i>	GGAGAGTGAAGGAGCACAAGG	TTTGACATTTCTGCAACA	55
<i>DV12</i>	GTGTCTCCGGTGGCATAACT	GAGAAGTCAGCCCCTCCTT	57
<i>DV12 probe</i>	ACCTGCCCTGTGTGTAGGAC	ACTGAGGGGTTCCATGTTTG	57
<i>DV13</i>	TTAAACCCGAAACGTGCAAC	AAAAAGGCTTTACAACCAACTT	56
<i>DV13 probe</i>	CTCCAGCACGTCATCGACTA	GTGCAATGCGGATGGTAAGT	56
<i>DV14</i>	CATGTGGGAACAGATGTATA	CAATGCTGGAGGCAAAGTTT	55
<i>DV14 probe</i>	TTAACGCTGGAGGCAAAGTT	AGGCCTAATGCTCAGGTCA	55
<i>DV16</i>	CACAGGCTGCATGTTTCATCT	TCTGTTGAAACAAACAGTCCT	59
<i>DV16 probe</i>	TTGTAATCGGAGGAGGATCG	GTCTCCTTCTGTGCCTTTG	55
<i>DV17</i>	CTTCTCTCGTCACCCCTCTG	ATTTTCTCTGGGCTGTGGTG	55
<i>DV18</i>	TTTGAGTGGCGGCCGAGTGC	CGGGCATTTAATTTTCATGTG	56
<i>DV18 probe</i>	ATGGACGGGTTGTAGCAAAG	GGATTCATTGTGTGGCACTG	55
<i>DV22</i>	GGAGGACTCTTTGCTGTGG	TCTTTCACCCATCTCCTTGC	60
<i>DV22 probe</i>	CCAGAGGAGGCAATAACCAA	ATAAAAGTGCTGGGCAAGGA	55
<i>DV25 probe</i>	ACAGACCCTAAAAGCGAGCA	ACTCTGCCACTTCAGGAGGA	55
<i>DV38</i>	GCATGTTCTTCACTTGCTTCAT	GCACAGCTATTGCAAGCAGA	59
<i>DV38 probe</i>	AATTGGGCACTTCTACGTG	TTCAATGGGTGTGGTCTGAA	55
<i>Xenopus laevis</i>			
<i>ef1α</i>	CCTGAACCACCCAGGCCAGATTGGTG	GAGGGTAGTCAGAGAAGCTCTCCAG	55
<i>chordin</i>	CCTCCAATCCAAGACTCCAGCAG	GGAGGAGGAGGAGCTTTGGGACAAG	55
<i>DV07</i>	TGTCATGCGACAGGTAGAGC	GGCTCTGCAACAACCTCTCC	55
<i>DV07 probe</i>	NIBB clon XI304d08ex		
<i>DV08</i>	TGCTATGCTGGATGAAGACG	TTCATCTTTGGGGTCTCTG	55
<i>DV08 probe</i>	NIBB clon XI073g09		
<i>DV09</i>	GCGCCAGTATGTACGAGGAT	TAATCGGGGAAGTCAAGTG	55
<i>DV09 probe</i>	CGAGAAAATCCCCTTCATCA	TAATCGGGGAAGTCAAGTG	55
<i>DV12</i>	CTGGTATTCACTGCCCTGT	ATAGTGGCAGCCAAAAATGG	55
<i>DV12 probe</i>	NIBB clon XI519d09ex		
<i>DV13</i>	AAACCGCATTGACTTTTTG	TAGCACCATCTCTGCCACTG	55
<i>DV13 probe</i>	TACAGGCGGCTGAATTCTCT	TAGCACCATCTCTGCCACTG	56
<i>DV14</i>	CTTGCATGCCAGAGTTGAAA	CCGAGCTTTAGTGCCAAGAC	55
<i>DV14 probe</i>	NIBB clon XI170k05		
<i>DV16</i>	TTGGGTGATTGGTAACAGCA	CTCTGAGATGTTCCGGCACAA	56
<i>DV16 probe</i>	NIBB clon XI516o04ex		
<i>DV18</i>	ACGGCAGGAAGAGAACTCA	GAGCAAGTCCCAGCAACTTC	56
<i>DV18 probe</i>	NIBB clon XI261d18ex		
<i>DV22</i>	AAGACCTTGCAATGGAGGA	CAGAGAGACCACCAGCATGA	55
<i>DV22 probe</i>	TTGCTGCCGATTCCCTAACC	AAAGCAAAGCCCTCTTGACA	55
<i>DV25 probe</i>	GCCAACAACAGCCAACTTT	AAGGATCGGCATCAATCAAG	55
<i>DV38</i>	AGCCATCCTCACTGCAGACT	ATCCTCAAGGCCACGTACAC	55
<i>DV38 probe</i>	AAAGGAGGATCCCAAAGGAA	ATCCTCAAGGCCACGTACAC	55

Supplementary Table 4. Primers and NIBB clones used in this study.

Primers used are written from 5' end to 3' end (left to right). For *X. laevis*, clones from NIBB used for generating probes are indicated.