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Supporting Information

Single-Cell Mass Spectrometry for Discovery Proteomics: Quantifying Translational Cell Heterogeneity in the 16-Cell Frog (*Xenopus*) Embryo

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MATERIALS AND METHODS

Materials and Reagents. Solvents and chemicals were purchased from Fisher Scientific (Pittsburg, PA) in reagent grade or higher. For MS measurements, solutions and samples were prepared using MS-grade solvents. A standard peptide mix containing angiotensin II, leucine enkephalin, and Val-Tyr-Val was from Sigma Aldrich (St. Louis, MO). Bare (uncoated) fused silica capillaries (110/40 µm outer/inner diameter) were from Polymicro Technologies (Phoenix, AZ).

Solutions. For Steinberg's solution, the following salts were dissolved at the specified concentration using Milli-Q purified water (Millipore): sodium chloride (58.2 mM), potassium chloride (0.67 mM), calcium nitrate (0.34 mM), magnesium sulfate (0.83 mM), Trisma hydrochloride (4.19 mM), and Trisma base (0.66 mM). The pH of the solution was titrated to 7.4 using 5 M sodium hydroxide. To obtain 50% Steinberg's solution, this solution was diluted two-fold.

Animals and Cell Isolation. Male and female *Xenopus laevis* adult frogs were purchased from Nasco (Fort Atkinson, WI) and maintained in a breeding colony at GW. All protocols related to the handling and manipulation of animals were approved by the GW Institutional Animal Care and Use Committee (IACUC #A311). Fertilized embryos were obtained via natural mating of adult frogs induced by gonadotropin as described previously.[2] Jelly coats surrounding the eggs were removed using cysteine solution following a standard protocol.[3] Two- to four-cell embryos with a distinct dorsal-ventral pigmentation difference were transferred into a Petri dish filled with 100% Steinberg's solution at room temperature and their development was monitored under a stereomicroscope. Embryos at the 16-cell stage (~2.75 h post fertilization) were transferred using a Pasteur pipette into 50% Steinberg's solution in a Petri dish coated with 2% agarose.

Single D11, V11, and V21 blastomeres were identified based on pigmentation and location in the embryo in reference to established fate maps.[4] Using sharpened forceps, the vitelline membrane was carefully removed from the embryos and single blastomeres were dissected following a protocol described elsewhere.[5] For each experimental condition, n = 3 biological replicates were obtained in separate 0.6 mL centrifuge tubes.

Total Protein Assay. The total protein amount was determined for the 8-, 16-, 32-, and 64-cell whole embryos using the bicinchoninic acid (BCA) assay according to the instructions of the manufacturer (Pierce Biotechnology, Inc.; Rockford, IL). For each developmental stage, n = 3 biological replicates (different embryos) were measured in 3 technical replicates (same sample quantified multiple times), allowing us to extrapolate the average cell's protein content by taking into account the total cell number in the embryo. Measurement results are shown in Figure S1. The average blastomere in the 16-cell embryo contained ~10 µg of total protein.

Sample Preparation for Bottom-Up Proteomic MS. Whole embryos and single isolated blastomeres were lysed in 50 µL and 10 µL, respectively, of a buffer containing 20 mM Tris-HCl at pH 7.5, 0.15 M NaCl, 5 mM EDTA, and 1% of sodium dodecyl sulfate (SDS) or digitonin as the detergent. To facilitate lysis, the samples were agitated on ice for 5 min in an ultrasonic bath. Afterward, proteins were reduced by dithiothreitol and alkylated using iodoacetamide. Proteins were precipitated in acetone chilled to –20°C and the precipitate was recovered by centrifugation for 10 min at 10,000 × *g* at 4°C. The supernatant was discarded, and the protein pellet was washed with cold acetone (–20°C) prior to suspension in 50 mM ammonium bicarbonate. Proteins were digested with proteomics-grade trypsin at ~1:50 ratio for protein:protease at 37°C overnight. The digested samples were dried in a vacuum concentrator (Labconco, Kansas city, MO) and reconstituted in 50% acetonitrile containing 0.05% acetic acid. Samples (blastomere digests) were centrifuged at 10,000 × *g* for 2 min prior to analysis by CE-μESI-HRMS. We note that depleting *Xenopus* samples lysates of abundant yolk platelets was recently shown to vastly improve protein identifications by MS,[6] suggesting further improvements possible in the number of proteins that are identifiable in single blastomeres.

Single-cell CE-μESI-HRMS using a Time-of-Flight Mass Spectrometer. Samples were measured using a single-cell CE-ESI system that we constructed based on our prototype instruments for small-molecules (metabolomics).[7] Briefly, 1 μL of the sample was deposited into a sample loading microvial, and ~7 nL of the peptide standard or 16 nL of the blastomere digest were hydrodynamically injected into a separation fused silica capillary (85 cm length, 40/110 μm inner/outer diameter) by elevating its inlet end 15 cm above the outlet end for 1–3 min. Afterward, the capillary inlet was transferred into a vial that contained the background electrolyte (BGE), 25% acetonitrile acidified with formic acid to pH 2.3 (~1 M) measured using a combination glass electrode. This pH was chosen to suppress ionization of capillary silanol groups to minimize peptide adsorption to the wall of the separation capillary. Peptides were electrophoretically separated by applying +19 kV on the inlet end (anode) of the separation capillary using a stable high voltage power supply (model 230-30R, Spellman; Hauppauge, NY).

Peptides migrated into a custom-built microelectrospray (μESI) interface that was constructed based on our earlier designs.[7-8] Briefly, the separation capillary was co-axially fed through a metal emitter capillary (130/260 μm inner/outer diameter) with laser-cleaved ends that supplied 50% methanol (0.1% formic acid) as electrospray sheath flow. The metal emitter was earth-grounded to complete the CE electrical circuit. To ionize separated peptides with high stability and efficiency, the microelectrospray source was maintained in the cone-jet mode, the most efficient spraying regime for ion generation in the micro-flow regime.[9] To make this possible, the emitter tip of the CE-μESI setup was precision-positioned against the sampling plate of a mass spectrometer that was held at stable –1,700 V, and the hydrodynamic behavior of the electrified liquid meniscus and the generated total ion current were continuously observed under a stereomicroscope (~5× magnification) and the mass spectrometer, respectively. Cessation of the pulsating liquid meniscus in parallel with a sudden increase in the total ion current marked the onset of the cone-jet regime.[9] Nebulizer gases, which are typically used in commercial ESI interfaces, were eliminated to help better entrain sprayed droplets into the mass spectrometer, and the CE-μESI interface was contained in an environmental chamber to minimize/eliminate air currents, which could disrupt stability of the Taylor cone. Hence, a unique aspect of this CE-μESI interface was its ability to ionize peptides in high efficiency in the cone-jet spraying regime.

Peptide ions were detected using a high-resolution Qq orthogonal acceleration time-of-flight mass spectrometer (Impact HD; Bruker Daltonics, Billerica, MA), operated at mass resolution of 40,000 full width at half maximum (FWHM). The mass spectrometer was externally mass-calibrated over the *m/z* 250–3,000 range as recommended by the vendor. Peptide ions were mass analyzed between *m/z* 250–3,000 at a data acquisition rate of 4 Hz. To facilitate the identification of peptides, ion signals (*m/z* values) were fragmented using collision-induced dissociation (CID) in nitrogen collision gas at 20–35 eV collision energy depending on the size and charge state of the ion. The data-dependent tandem HRMS (HRMS^2) was performed at 4 Hz for ion intensities lower than 3.2×10^3 counts and 15 Hz for signals above 10^5 counts per 1,000 summations.

The custom-built CE-μESI-MS instrument was characterized for analytical performance (Figure 2). Angiotensin II gave a signal-to-noise ratio of 19.9 for 167 amol peptide, indicating a lower limit of detection at ~25 amol (S/N = 3) for this peptide. The concentration calibration curve was tested linear over 3 orders of magnitude for angiotensin II and leucine encephalin, and 2 orders of magnitude for valine-tyrosine-valine (Figure 2A). Linear regression parameters: Peak area = b × concentration + a, where a/b/regression coefficient (R^2) parameters were: 1.19/–4.032/0.96 for Ang II; 1.14/–5.09/0.99 for LeuEnk; and 1.15/–4.77/0.99 for Val-Tyr-Val. Repeated measurement of 20 ng protein digest from the 16-cell embryo showed reproducible separation with a quantitative technical reproducibility of 11.5% standard error of the mean (S.E.M.) (Figure 2B). The biological reproducibility was 13.5% S.E.M. between different single cells from the same cell type in different 16-cell embryos (Figure 2B). This performance metrics agreed with those we recently determined for several metabolites (MW < 500 Da) using single-cell CE-ESI-MS,[7b] providing a robust and quantitative platform to identify and quantify protein expression in single *Xenopus* blastomeres.

CE-μESI with an Orbitrap-q-Ion Trap Mass Spectrometer. The CE-μESI platform was hyphenated to an Orbitrap Fusion (Thermo Scientific) tribrid ultrahigh-resolution tandem mass spectrometer equipped with CID, higher-energy collision dissociation (HCD), and electron transfer dissociation (ETD) cells. Minor modifications were necessary to the electrospray interface to operate the electrospray source in the cone-jet spraying regime. Briefly, the tip of the electrospray emitter was fine-positioned ~5 mm from the sampling cone of the mass spectrometer, and +2,900 V generated by a stable high voltage power supply (P350, Stanford Research System, Sunnyvale, CA) was directly applied on the electrospray emitter. CE separations were performed by applying +19 kV on the inlet end of the separation capillary, corresponding to ~16 kV effective gradient across the capillary. Generated peptide ions were mass-analyzed via data-dependent acquisition, allowing for simultaneous acquisition of MS and MS/MS spectra.

Proteins were identified and quantified in data-dependent $HRMS^2$. Survey mass spectra were measured between *m/z* 350–1,600 in the orbitrap analyzer at a resolution of ~60,000 FWHM with a maximum injection time of 100 ms. To identify proteins, precursor peptide ions were isolated in the quadrupole analyzer with an isolation window of 2 Da, routed for fragmentation via HCD using 30% relative energy in nitrogen collision gas in the multipole cell, and the fragments were detected in the ion trap with "rapid" scan rate and a maximum injection time of 50 ms. Data-dependent parameters included an exclusion time of 30 s, 10 s, and 15 s after repeated fragmentation for 7 s. Fragmentation priority was set to least intense (bottom N) with a threshold of 1,000 ion counts and a total instrument cycle of 3 s.

Quantitative measurements using tandem mass tags (TMTs; Thermo) used similar instrumental settings. Single blastomeres were prepared and digested as described previously. The resulting peptides were labeled using TMT6plex labeling reagents following the manufacturer instructions with the following changes: 10 μL of labeling reagent was added followed by 2 μL of quenching reagent to account for the smaller amount of material present. Digests of individual D11, V11, and V21 blastomeres were labeled using the TMT6-126, TMT6-127, and TMT-128 reagents, respectively. The samples were then pooled together and dried down to completeness after which 5 μL of 60% ACN in water containing 0.05% acetic acid was added. For each blastomere type, n = 3 biological replicates were measured with each analyzed in technical duplicate or quadruplet. Quantification followed the MS^2 strategy used for identification (see earlier) with minor changes to enhance quantitative coverage of the encoded proteome: maximum injection time, 50 ms; precursor isolation window, 0.8 Da; HCD collision energy, 35%; exclusion time, 10 s. Protein ratios were calculated based on the relative abundance of the reporter ions using Proteome Discoverer 2.0 (Thermo).

NanoLC-nanoESI-HRMS. Alternatively, peptides were separated using a nano-flow liquid chromatograph (Dionex Ultimate 3000 RSLCnano, Thermo) equipped with a 20-µL sampling loop. Peptides were loaded onto a trapping column (C18 PepMap 100, 300 µm ID, 5 mm length, 5 µm beads with 100 Å pore size, Thermo) and desalted for 5 min in 0.1% formic acid at 10 µL/min. The pepides were thereafter separated on a C18 PepMap RSLC analytical capillary column (75 µm ID, 500 mm length, 3 µm beads with 100 Å pore size, Thermo) using a 80 min step gradient with Solvent A (0.1% formic acid) and Solvent B (0.1% formic acid in acetonitrile) at 300 nL/min as follows: 5% B held for 5 min, B ramped from 5% to 35 % in 50 min, then ramped to 50% B in 17 min, where the solvent was held at 50% B for 5 min, before decreasing B to 5% in 5 min and equilibrating the column for 10 min. Separated peptides were ionized using a nanospray ion source that employed a fused silica capillary with 10 µm orifice (New Objective, Woburn, MA) using +2,500 V spray potential to maintain stable nanospray. The generated peptide ions were mass-analyzed using the orbitrap-quadrupole-ion trap mass spectrometer under identical instrumental setting as earlier.

Data Analysis. Data processing was comparable for data acquired on the TOF and orbitrap mass spectrometers. *(1) Processing of Qq-TOF Data (Bruker).* Time-of-flight data were converted to xml files using a script executed in data analysis 4.2 (Bruker Daltonics). The files were then submitted for proteomics search via ProteinScape 3.1 (Bruker) running Mascot 2.4 (Matrix Science, Inc., Boston, MA) as the search engine. The tandem MS were compared against *Xenopus laevis* proteome (NCBinr, updated on 10/2/2014) with the following settings: full trypsin digestion, a maximum of 2 missed cleavages allowed, methionine oxidation as variable modification, cysteine carbamidomethylation as fixed modification, and a mass accuracies of 20 ppm for MS and 0.5 Da for tandem MS. Protein identifications from the Qq-TOF experiments are reported with <5% false discovery rate (FDR) established against reversed decoy database. *(2) Processing of Orbitrap Fusion data (Thermo).* Raw (unprocessed) mass spectrometric data were processed using proteome Discoverer 1.4 (Thermo). Sequest HD and/or MSAmanda were chosen as search engines and *Xenopus laevis* proteome (canonical & isoforms) and Phrog (mRNA-derived)[6] as databases with the following search parameters: trypsin digestion with up to 2 missed cleavages; methionine oxidation as variable modification; cysteine carbamidomethylation as fixed modification; and mass errors were filtered to <15 ppm for precursor ions (MS^1) and 0.5 Da for fragments (MS^2). Peptides are reported with <1% FDR, calculated using the percolator node of Proteome Discoverer. Protein identifications are given as protein groups, where multiple isoforms of the same protein are considered as one group. Proteins from the orbitrap-quadrupole-ion trap experiments are reported with <1% FDR.

Multivariate and statistical data analysis was performed in MetaboAnalyst 3.0,[10] a data analysis and visualization pipeline. Protein abundances were estimated based on emPAI in Proteome Discoverer 2.0 and imported into MetaboAnalyst where processing used the following settings: Missing value estimation, small values ($\sim 10^{-7}$); data filtering, median value; sample normalization, median; data transformation, log transformation; data scaling, range scaling.

REFERENCES

[1] A. H. Smits, R. G. H. Lindeboom, M. Perino, S. J. van Heeringen, G. J. C. Veenstra, M. Vermeulen, *Nucleic Acids Res.* **2014**, *42*, 9880-9891.

[2] S. A. Moody, *Developmental Biology Protocols, Vol I* **2000**, *135*, 331-347.

[3] *Early development of Xenopus laevis: A laboratory manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, **2000**.

[4] a) G. Hirose, M. Jacobson, *Dev Biol* **1979**, *71*, 191-202; b) S. A. Moody, *Dev Biol* **1987**, *119*, 560-578.

[5] P. A. Grant, M. B. Herold, S. A. Moody, *Journal of Visualized Experiments* **2013**.

[6] M. Wuhr, R. M. Freeman, Jr., M. Presler, M. E. Horb, L. Peshkin, S. P. Gygi, M. W. Kirschner, *Current Biology* **2014**, *24*, 1467-1475.

[7] a) P. Nemes, S. S. Rubakhin, J. T. Aerts, J. V. Sweedler, *Nat Protoc* **2013**, *8*, 783-799; b) R. M. Onjiko, S. A. Moody, P. Nemes, *Proc. Natl. Acad. Sci. U. S. A.* **2015**, *112*, 6545-6550.

[8] P. Nemes, A. M. Knolhoff, S. S. Rubakhin, J. V. Sweedler, *Anal. Chem.* **2011**, *83*, 6810-6817.

[9] P. Nemes, I. Marginean, A. Vertes, *Anal. Chem.* **2007**, *79*, 3105-3116.

[10] J. G. Xia, I. V. Sinelnikov, B. Han, D. S. Wishart, *Nucleic Acids Res.* **2015**, *43*, W251-W257.

[11] D. Belder, A. Deege, H. Husmann, F. Kohler, M. Ludwig, *Electrophoresis* **2001**, *22*, 3813-3818.

SUPPLEMENTARY FIGURES

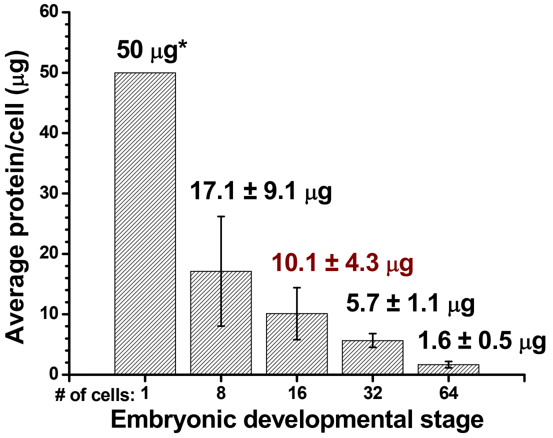

Figure S1. Average protein amounts in single blastomeres in *Xenopus* embryos at different developmental stages. Error bars show standard error of the mean. *Adopted from elsewhere.[1]

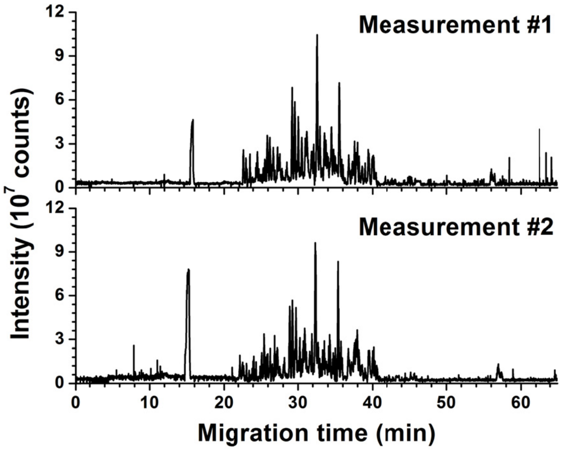

Figure S2. Base peak electropherograms showing reproducible CE separation for 20 ng protein digest from a 16-cell *Xenopus* embryo in technical duplicate.

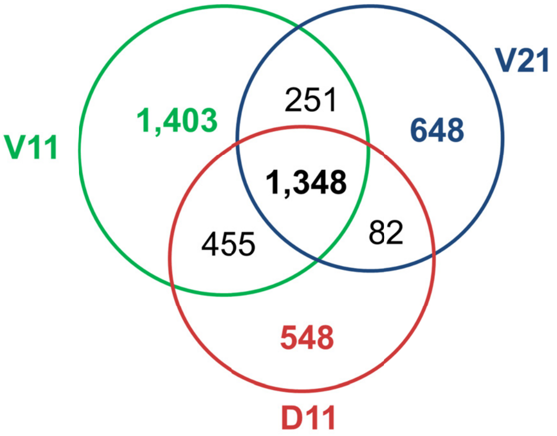

Figure S3. Peptide sequencing between single blastomeres in the 16-cell *Xenopus* embryo. The numbers indicate the total of different peptides that were identified between the D11, V11, and V21 cells with each measured in $n = 3$ biological replicates and technical duplicates.

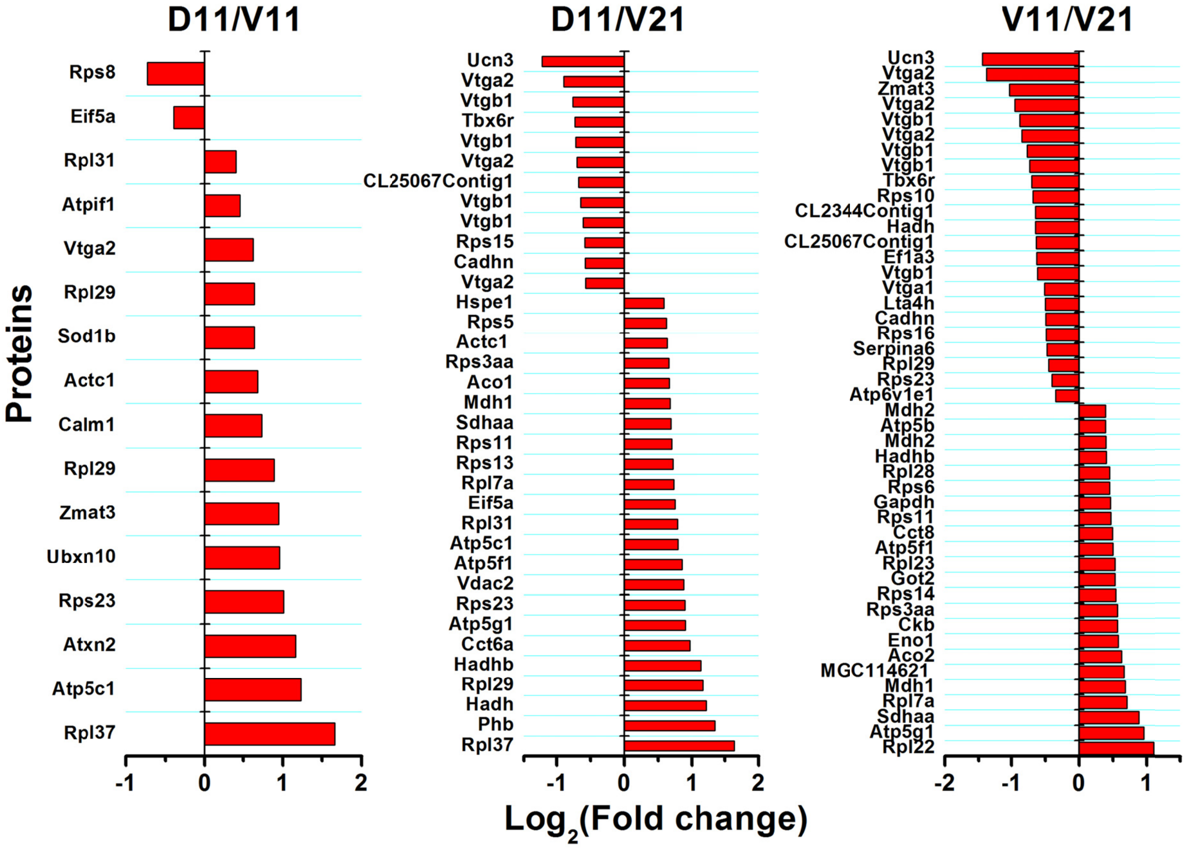

Figure S4. Translational cell heterogeneity revealing developmental asymmetry in the 16-cell embryo. Based on multiplexing quantification (see also Figure 3D), the proteins shown here were found to be significantly differentially expressed between D11/V11, V11/V21, and D11/V21 cell types ($p < 0.05$ and fold change ≥ 1.3).

SUPPLEMENTARY TABLES

Table S1. Reconfiguration of the single-cell proteomic workflow and the CE-μESI-HRMS instrument to enable progressively deeper coverage of the single-cell encoded proteome. Each new step adopted experimental conditions that were optimized in the preceding step.

Experimental Steps	Description of Experimental Conditions
1	Embryos were lysed in 1% SDS buffer and digested using trypsin (see Methods). Digests were zip-tipped (C18). Separation was performed in fused silica capillary coated with crosslinked polyvinyl alcohol using 1% formic acid as the BGE. The capillaries were coated according to the protocol described in Reference.[11]
2	Separations were performed in a bare (uncoated) fused silica capillary using 25% ACN, 1 M formic acid as the BGE. →This separation workflow was selected for the rest of the study.
3	Embryos were lysed in 0.2% digitonin, digested, and measured directly (without purification via zip-tipping).
4	Embryos were lysed in 1% SDS, digested, and measured directly (without purification via zip-tipping). →This sample preparation workflow was selected for the rest of the study.
5	Peptide sequencing was performed using: HCD with 25% collision energy, 1×fragmentation, 30-s exclusion.
6	Peptide sequencing was performed using: 35% HCD collision energy, 1×fragmentation, 30-s exclusion.
7	Peptide sequencing was performed using: 30% HCD collision energy, 1×fragmentation, 30-s exclusion. →This collision energy was selected for the rest of the study.
8	Peptide sequencing was performed using: 1×fragmentation, 10-s exclusion.
9	Peptide sequencing was performed using: 2×fragmentation, repeat for 7 s, 15-s exclusion. Protein identification was used Sequest HT with Uniprot *Xenopus* (canonical & isoform) as database. →These fragmentation conditions were selected for the rest of the study.
10	Proteins were identified using Sequest HT with a dual search engine strategy that combined Uniprot *Xenopus* (canonical & isoform) and Phrog databases.
11	Proteins were identified using a dual database strategy that accessed Uniprot *Xenopus* (canonical & isoform) and Phrog databases via Sequest HT and MSAmanda. →This dual-search engine and dual-database strategy was selected for the test of the study.
12	Proteomic data from technical duplicates were combined. →Measurement of at least two technical replicates was performed for the rest of the study.

Table S2. Identification of protein groups and peptides using the single-cell CE-μESI-HRMS(orbitrap-quadrupole-linear ion trap) platform. Each blastomere was measured in n = 3 biological replicates and technical duplicates. Error represents standard deviation. The cumulated protein groups represent all the different protein groups identified in a specific cell type.

Cell Type	Identified Protein Groups		Identified Peptides
	Groups/Cell	Cumulative	
D11	465 ± 86	829	1,399 ± 252
V11	608 ± 84	1,019	1,929 ± 482
V21	460 ± 16	815	1,401 ± 135
Total	**n/a**	**1,709**	**4,735**

Table S3. Protein identifications between D11, V11, and V21 cell types based on n = 3 biological replicates with each measured in technical duplicates.

No.	Accession Number	Description	Seq. Cover. (%)	Σ# Proteins	Σ# Unique Peptides	Σ# Peptides	Σ# PSMs
1	zeinaSSns_comp377268_c0_seq3	len=241	97.87	1	1	1	1
2	dsrrswapns_comp1430289_c0_seq1	len=213	97.62	1	1	1	1
3	Q6NTT1	LOC398508 protein (Fragment) OS=Xenopus laevis GN=L	93.00	4	23	23	1399
4	Q7ZY52	Glyceraldehyde-3-phosphate dehydrogenase OS=Xenopus	90.09	4	19	28	1976
5	BJ049851 homologue to UniRef100_Q66IR3 Cluster: MG	Rep: MGC85497 protein - Xenopus laevis (African clawed f	89.74	1	1	1	1
6	Q8AVP8;CL8Contig14	Peptidyl-prolyl cis-trans isomerase OS=Xenopus laevis GN	89.63	4	5	14	1993
7	Q6B4U5;CL4491Contig1	Malate dehydrogenase OS=Xenopus laevis GN=mdh2 PE=	88.17	9	12	28	2343
8	Q8AY70;CL7950Contig1	Glyceraldehyde-3-phosphate dehydrogenase type B OS=X	87.99	7	19	27	2882
9	Q6GR58;CL4491Contig2	Malate dehydrogenase OS=Xenopus laevis GN=mdh2 PE=	86.39	9	10	26	2392
10	CL1514Contig2	CL1514Contig2	85.25	4	3	38	2356
11	CL1514Contig1	CL1514Contig1	85.25	2	0	38	2308
12	Q7SZB1	Profilin OS=Xenopus laevis GN=MGC64293 PE=2 SV=1 - [	84.67	4	8	10	148
13	P30883;CL57Contig6	Tubulin beta-4 chain OS=Xenopus laevis GN=tubb4 PE=2	84.49	22	2	28	3016
14	Q7ZWR6	ATP synthase subunit beta OS=Xenopus laevis GN=atp5b	83.81	5	16	32	2778
15	O12975;CL1627Contig2	Fructose-bisphosphate aldolase OS=Xenopus laevis GN=a	83.79	5	3	28	2619
16	A2BDB0	Actin, cytoplasmic 2 OS=Xenopus laevis GN=actg1 PE=2	83.73	30	3	32	2492
17	CF270773 similar to UniRef100_A7SBI6 Cluster: Predict	Rep: Predicted protein - Nematostella vectensis (Starlet se	83.67	1	1	1	1
18	Q7ZY50	MGC53997 protein OS=Xenopus laevis PE=2 SV=1 - [Q7Z	82.47	15	1	27	1504
19	Q3KPP7	Fructose-bisphosphate aldolase OS=Xenopus laevis GN=M	82.14	8	2	27	1288
20	TC463468	vitellogenin (A1) [Xenopus laevis]	81.73	3	3	14	2375
21	Q8AVT0	MGC53543 protein OS=Xenopus laevis GN=eno1 PE=2 S	80.65	3	1	35	2444
22	TC462743 homologue to UniRef100_Q7SZF6 Cluster: Vi	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog)	80.54	1	14	25	5428
23	P70010	Nucleoside diphosphate kinase A1 OS=Xenopus laevis PE	79.87	3	6	10	243
24	TC435033 homologue to UniRef100_Q6NWX0 Cluster: A	Rep: ATP synthase subunit beta - Xenopus tropicalis (West	79.58	1	4	7	716
25	Q7ZWN5;CL2685Contig2	Triosephosphate isomerase OS=Xenopus laevis GN=tpi1 P	79.44	2	1	16	1325
26	Q6NUG0	MGC79030 protein OS=Xenopus laevis GN=hspe1 PE=3 S	79.41	1	4	9	249
27	O93400;CL3Contig45	Actin, cytoplasmic 1 OS=Xenopus laevis GN=actb PE=2 S	79.20	25	2	31	4744
28	CL1152Contig1	CL1152Contig1	79.13	5	19	40	1621
29	CL2685Contig3	CL2685Contig3	79.03	2	0	15	615
30	P13926	Superoxide dismutase [Cu-Zn] A OS=Xenopus laevis GN=	78.15	2	6	9	253
31	Q3B8I6	Wu:fj06d02 protein OS=Xenopus laevis GN=wu:fj06d02 PE	76.21	4	3	13	487
32	CL964Contig2	CL964Contig2	75.84	8	15	15	379
33	Q6NTT0	MGC82310 protein OS=Xenopus laevis GN=hrsp12 PE=2	74.82	3	9	9	110
34	CL1127Contig2	CL1127Contig2	74.07	3	1	12	1137
35	dsrrswapns_comp210667_c1_seq1	len=1119	73.79	2	0	15	550
36	Q7SYQ4	MGC64582 protein OS=Xenopus laevis GN=prdx6 PE=2 S	73.66	5	10	10	162
37	CL2685Contig1	CL2685Contig1	73.39	2	7	15	824
38	Q0IHG1;CL10048Contig1	MGC154377 protein OS=Xenopus laevis GN=rplp2 PE=4 S	73.04	2	5	5	102
39	CL10183Contig1	CL10183Contig1	72.85	5	1	12	360
40	Q6GPT0;CL10608Contig1	MGC82636 protein OS=Xenopus laevis GN=MGC82636 P	72.59	2	9	10	706
41	TC464539 similar to UniRef100_Q7SZF6 Cluster: Vitello	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog)	72.55	1	15	19	2012
42	Q9PSX0;CL3505Contig1	Fructose-bisphosphate aldolase OS=Xenopus laevis GN=a	72.25	3	14	17	1649
43	Q6PHL6	Rps19-prov protein OS=Xenopus laevis GN=rps19 PE=2 S	71.92	5	12	12	196
44	CL654Contig1	CL654Contig1	71.64	1	2	5	65
45	Q00387;CL13623Contig1	Serine protease inhibitor A6 OS=Xenopus laevis GN=serpi	70.18	2	27	30	4891
46	Q6NRQ9;CL5407Contig1	MGC82327 protein OS=Xenopus laevis GN=MGC82327 P	69.71	5	14	14	370
47	Q92122;CL1152Contig2	Pyruvate kinase muscle isozyme OS=Xenopus laevis GN=	69.26	5	7	31	2389
48	P18709	Vitellogenin-A2 OS=Xenopus laevis PE=1 SV=1 - [VITA2_	69.06	435	0	223	55339
49	P19011	Vitellogenin-B2 (Fragment) OS=Xenopus laevis PE=1 SV=	69.01	1	3	7	3568
50	CL6589Contig1	CL6589Contig1	68.60	204	0	213	52111
51	P45695	Cofilin-1-A OS=Xenopus laevis GN=cfl1-a PE=1 SV=3 - [C	67.86	5	5	9	110
52	CL2400Contig2	CL2400Contig2	67.37	6	6	19	829
53	Q66KY9	MGC85306 protein OS=Xenopus laevis GN=atp5d PE=2 S	67.28	3	5	5	144
54	Q6IP60;CL654Contig2	Hspd1 protein OS=Xenopus laevis GN=hspd1 PE=2 SV=1	66.84	3	7	27	1953
55	Q7ZXM8;CL3609Contig1	Ferritin OS=Xenopus laevis GN=ftmt PE=2 SV=1 - [Q7ZXM	66.67	3	7	7	167
56	EB644224 homologue to UniRef100_Q5BKG3 Cluster: M	Rep: MGC108424 protein - Xenopus tropicalis (Western cla	66.67	1	1	1	1
57	dsrrswapns_comp212871_c1_seq1	len=1347	66.47	3	7	17	521
58	P62155;CL1Contig1497	Calmodulin OS=Xenopus laevis GN=calm1 PE=1 SV=2 - [	66.44	8	5	5	1376
59	Q9PSN9	Lipovitellin 1, PCDZN=ZN(2+)- and CD(2+)-binding protein	65.91	1	1	6	788
60	P45593	Cofilin-1-B OS=Xenopus laevis GN=cfl1-b PE=1 SV=3 - [C	64.88	4	6	10	131
61	BG513260 homologue to UniRef100_Q7SZF6 Cluster: Vi	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog)	64.86	1	9	19	2549
62	zeinaSSns_comp382686_c6_seq6	len=1587	64.63	9	1	9	644
63	Q6PAB3;dsrrswapns_comp212871_c1_seq2	Malate dehydrogenase, cytoplasmic OS=Xenopus laevis G	63.77	2	6	17	620
64	Q7SZF6	Vitellogenin B1 OS=Xenopus laevis GN=vtgb1 PE=2 SV=1	63.73	3	171	202	56791
65	Q6DJI6	Putative uncharacterized protein OS=Xenopus laevis PE=4	63.06	6	3	7	172
66	dsrrswapns_comp212502_c2_seq1	len=1736	63.05	2	14	14	228
67	A4FVF5	LOC100049136 protein OS=Xenopus laevis GN=LOC1000	62.16	4	2	6	53
68	CL654Contig4	CL654Contig4	61.98	3	5	24	937
69	Q7ZXP8	Eef2-prov protein OS=Xenopus laevis GN=eef2.1 PE=2 SV	61.66	245	12	35	1178
70	TC462321 similar to UniRef100_P18709 Cluster: Vitellog	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovit	60.98	1	7	8	1689
71	P02350	40S ribosomal protein S3-A OS=Xenopus laevis GN=rps3-	59.76	3	1	14	249
72	Q7ZYT3	Rpls3-b protein OS=Xenopus laevis GN=rpls3-b PE=2 SV=	59.76	4	1	14	246
73	Q7ZWP4;CL57Contig2	MGC53205 protein OS=Xenopus laevis GN=tubb4a PE=2	59.68	7	4	21	1834
74	Q9I8J7;CL4267Contig1	MGC69114 protein OS=Xenopus laevis GN=tktl2 PE=2 SV	59.36	3	22	23	1033
75	Q7ZTL1	Acaa2-prov protein OS=Xenopus laevis GN=acaa2 PE=2 S	59.19	255	14	15	320
76	Q3ZM03;CL912Contig2	40S ribosomal protein SA OS=Xenopus laevis GN=rpsa PE	58.82	10	11	11	915
77	CL21870Contig1	CL21870Contig1	58.71	1	8	8	162

78	P15107;CL10172Contig1	Superoxide dismutase [Cu-Zn] B OS=Xenopus laevis GN=s	58.28	1	4	7	323
79	Q7ZYH7;CL3329Contig1	Pgk1-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZY	58.27	1	7	16	600
80	Q6IRQ8;CL4086Contig2	MGC81450 protein OS=Xenopus laevis GN=pgam1 PE=2	58.27	3	3	8	263
81	Q6AZP8;CL4086Contig1	MGC82549 protein OS=Xenopus laevis GN=MGC82549 P	58.27	3	3	8	106
82	G3GBS3;CL10123Contig1	Peroxiredoxin 2 OS=Xenopus laevis GN=PRDX2 PE=2 SV=	57.92	7	8	9	599
83	dsrrswapns_comp152388_c2_seq1	len=240	57.14	1	1	1	1
84	Q7SZ23;CL10303Contig1	Gstm2-prov protein OS=Xenopus laevis GN=gstm1 PE=2	57.08	2	12	12	315
85	Q5U4V6	LOC397931 protein OS=Xenopus laevis GN=LOC397931	56.89	10	2	18	762
86	Q6NRV3;CL1402Contig3	MGC81323 protein OS=Xenopus laevis GN=tuba1a PE=2	56.89	12	2	18	1249
87	Q801S3	40S ribosomal protein S3a-A OS=Xenopus laevis GN=rps3	56.44	5	14	14	265
88	Q8JHA7;CL8144Contig1	Glutathione s-transferase OS=Xenopus laevis PE=2 SV=1 -	56.19	4	6	6	418
89	Q68EY5	ATP synthase subunit alpha OS=Xenopus laevis GN=atp5a	56.06	7	3	32	1118
90	P20342	40S ribosomal protein S15 OS=Xenopus laevis GN=rps15	55.86	6	5	5	165
91	Q8AVH2;TC421129 UniRef100_Q8AVH2 Cluster: Ckb-pr	Ckb-prov protein OS=Xenopus laevis GN=ckb PE=2 SV=1 -	55.85	11	4	16	645
92	Q6GMC1;CL1Contig1214	MGC81889 protein OS=Xenopus laevis GN=rps27a PE=2	55.77	30	9	9	707
93	Q9PTK6	Fatvg OS=Xenopus laevis GN=fatvg PE=2 SV=1 - [Q9PTK	55.39	6	9	17	264
94	P70011;CL60Contig6	Nucleoside diphosphate kinase A2 OS=Xenopus laevis PE=	55.19	1	2	6	301
95	P17508;CL430Contig6	Elongation factor 1-alpha, oocyte form OS=Xenopus laevis	54.66	340	2	22	1724
96	Q6DJL4;CL12647Contig1	MGC82059 protein OS=Xenopus laevis GN=atpif1 PE=4 S	54.55	3	6	6	312
97	Q6INS0;CL10203Contig2	MGC81156 protein OS=Xenopus laevis GN=gstt1 PE=2 SV	54.55	7	9	9	176
98	Q7SY94	ATP synthase subunit alpha OS=Xenopus laevis GN=atp5a	54.25	4	2	30	1012
99	Q68FI3	D-dopachrome decarboxylase-A OS=Xenopus laevis GN=d	54.24	5	3	3	28
100	dsrrswapns_comp132298_c0_seq1	len=219	54.17	1	1	1	1
101	Q6GNF4	MGC82841 protein OS=Xenopus laevis GN=rps17 PE=2 S	54.07	3	6	6	185
102	Q52L36	MGC114755 protein OS=Xenopus laevis GN=cisd1 PE=4	53.40	5	4	4	44
103	CL45Contig21	CL45Contig21	53.21	8	2	2	10
104	TC449759 homologue to UniRef100_Q28GS7 Cluster: C	Rep: Creatine kinase, brain - Xenopus tropicalis (Western c	53.03	9	3	14	214
105	Q6DD48;CL3329Contig2	Pgk2 protein OS=Xenopus laevis GN=pgk1 PE=2 SV=1 - [	53.00	1	5	14	647
106	zeinaSSns_comp387412_c0_seq1	len=1966	52.80	4	0	29	992
107	Q7SZS3;CL137Contig1	Aspartate aminotransferase OS=Xenopus laevis GN=got2	52.69	2	10	15	409
108	CL3171Contig1	CL3171Contig1	52.63	2	1	4	166
109	Q7SZ77;CL50Contig6	Rps11 protein OS=Xenopus laevis GN=rps11 PE=2 SV=1 -	52.53	233	8	9	220
110	CL5313Contig2	CL5313Contig2	52.33	5	2	6	61
111	Q6AZS1;CL1Contig38	Histone H2A OS=Xenopus laevis GN=hist1h2ad PE=2 SV=	52.31	24	4	4	48
112	A3KMU5;CL12285Contig1	Death-associated protein-like 1-B OS=Xenopus laevis GN=	52.21	5	4	4	286
113	P41116;CL818Contig6	60S ribosomal protein L8 OS=Xenopus laevis GN=rpl8 PE=	52.14	10	12	12	262
114	TC460552 homologue to UniRef100_Q6DDD2 Cluster: H	Rep: Heat shock 10kDa protein 1 - Xenopus tropicalis (Wes	52.11	1	2	4	91
115	P49401;CL397Contig5	40S ribosomal protein S4 OS=Xenopus laevis GN=rps4 PE	52.09	12	13	13	151
116	Q6IP26	MGC79007 protein OS=Xenopus laevis GN=cox5a PE=2 S	52.03	3	5	5	120
117	CL137Contig3	CL137Contig3	52.01	1	7	12	122
118	Q8AVT1	Paics-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q8AV	52.00	3	11	11	111
119	P50886	60S ribosomal protein L22 OS=Xenopus laevis GN=rpl22 P	51.56	2	5	5	120
120	AW783929 similar to UniRef100_Q6DFA9 Cluster: Asxl1-	Rep: Asxl1-prov protein - Xenopus laevis (African clawed fr	51.47	1	1	1	2
121	P62799	Histone H4 OS=Xenopus laevis PE=1 SV=2 - [H4_XENLA]	51.46	11	5	5	41
122	CL1Contig514	CL1Contig514	51.37	10	2	10	165
123	Q4V871	MGC114621 protein OS=Xenopus laevis GN=MGC114621	51.33	5	1	2	684
124	Q6P699	MGC68562 protein OS=Xenopus laevis GN=rplp1 PE=4 SV	51.33	5	1	2	473
125	Q3B8I3;CL3171Contig2	MGC130910 protein OS=Xenopus laevis GN=rpl7 PE=2 SV	51.22	5	9	12	475
126	Q52KY1;CL6681Contig1	Vdac2 protein OS=Xenopus laevis GN=vdac2 PE=2 SV=1 -	50.88	3	8	8	388
127	Q6GNF2	MGC82844 protein OS=Xenopus laevis GN=rpl30 PE=3 SV	50.86	6	4	4	158
128	Q8AVW0;CL561Contig9	Rpl12-prov protein OS=Xenopus laevis GN=rpl12 PE=2 SV	50.30	6	6	6	403
129	CL801Contig1	CL801Contig1	49.88	16	5	27	921
130	Q6PH94;TC467404 UniRef100_Q6PH94 Cluster: 40S rib	40S ribosomal protein S12 OS=Xenopus laevis GN=rps12	49.24	8	6	6	205
131	Q3KQ54;CL6751Contig1	MGC130953 protein OS=Xenopus laevis GN=atic PE=2 SV	49.24	4	3	18	244
132	Q6NTU4	Park7 protein OS=Xenopus laevis GN=park7 PE=2 SV=1 -	49.21	8	7	7	92
133	dsrrswapns_comp215407_c5_seq3	len=354	49.09	3	1	1	1
134	Q8AVI3	Arbp-prov protein OS=Xenopus laevis GN=rplp0 PE=2 SV=	48.89	2	1	10	242
135	dsrrswapns_comp208676_c3_seq2	len=1311	48.73	2	1	10	228
136	Q76BK2;CL10087Contig1	Macrophage migration inhibitory factor OS=Xenopus laevis	48.70	1	3	3	21
137	CL5832Contig1	CL5832Contig1	48.59	1	11	17	367
138	A1L3K7	Enolase A OS=Xenopus laevis GN=LOC100037034 PE=2	48.39	2	4	21	1468
139	CL34839Contig1	CL34839Contig1	48.19	1	1	1	2
140	Q7ZYP8	LOC495278 protein (Fragment) OS=Xenopus laevis GN=L	47.77	11	14	14	164
141	Q91733	EEF1D protein OS=Xenopus laevis GN=EEF1D PE=2 SV=	47.31	20	7	8	350
142	CL348Contig2	CL348Contig2	47.14	8	3	3	42
143	P04751;CL3Contig43	Actin, alpha cardiac muscle 1 OS=Xenopus laevis GN=actc	46.95	28	2	21	2612
144	P02362	40S ribosomal protein S7 OS=Xenopus laevis GN=rps7 PE	46.91	6	6	6	48
145	Q6DJI0	40S ribosomal protein S8 OS=Xenopus laevis GN=MGC83	46.63	9	10	10	403
146	Q66KP7;CL5026Contig1	MGC85550 protein OS=Xenopus laevis GN=rps28p9 PE=4	46.38	3	3	3	12
147	Q641I6	LOC494638 protein OS=Xenopus laevis GN=LOC494638	46.04	4	6	14	285
148	P17507	Elongation factor 1-alpha, oocyte form OS=Xenopus laevis	45.99	336	1	20	938
149	Q6NTP7;CL640Contig5	LOC398139 protein OS=Xenopus laevis GN=LOC398139	45.91	4	7	21	332
150	TC428477 homologue to UniRef100_UPI00006A0177 Cl	Rep: Methylenetetrahydrofolate reductase (EC 1.5.1.20). -	45.83	1	1	1	1
151	Q6DD55;CL437Contig2	P4hb protein OS=Xenopus laevis GN=p4hb PE=2 SV=1 - [	45.45	5	10	15	299
152	Q7ZWY6	Rpl9-prov protein OS=Xenopus laevis GN=rpl9 PE=2 SV=1	44.79	294	1	7	41
153	BU910031 UniRef100_Q7ZXF2 Cluster: Hnrpa0-prov pro	Rep: Hnrpa0-prov protein - Xenopus laevis (African clawed	44.71	1	1	1	1
154	dsrrswapns_comp212852_c6_seq1	len=214	44.44	1	1	1	2
155	Q5PPT1;CL4954Contig2	LOC496089 protein OS=Xenopus laevis GN=LOC496089	44.40	3	6	7	85
156	CL1Contig1406	CL1Contig1406	44.31	9	4	14	319
157	Q6GNH1	MGC82808 protein OS=Xenopus laevis GN=rpl23 PE=2 SV	44.29	4	5	5	99
158	O42193;CL1Contig277	MGC64314 protein OS=Xenopus laevis GN=ranbp1 PE=2	44.02	4	3	5	102
159	Q3KQC9	Rps16 protein OS=Xenopus laevis GN=rps16 PE=2 SV=1 -	43.84	6	8	8	105
160	A1L2N5;CL26379Contig1	LOC100036902 protein OS=Xenopus laevis GN=LOC1000	43.50	5	2	15	1638
161	CL27242Contig1	CL27242Contig1	43.24	1	1	1	5
162	B7ZPZ8;CL315Contig4	Thymosin beta 4 peptide OS=Xenopus laevis GN=tmsb4x	43.18	4	2	2	18
163	Q5FWK8	MGC85124 protein OS=Xenopus laevis GN=alox12b PE=2	43.13	4	16	20	516

164	Q7ZTM0	Cct5-prov protein OS=Xenopus laevis GN=cct5 PE=2 SV=1	43.07	6	6	11	188
165	Q6NTR9;CL10023Contig1	MGC82428 protein OS=Xenopus laevis GN=cox6b1 PE=4	43.02	5	4	4	64
166	Q7T0N8;CL7665Contig1	Hadhsc-prov protein OS=Xenopus laevis GN=hadh PE=2 S	42.81	2	7	7	85
167	Q6GQC6;CL14883Contig1	MGC80163 protein OS=Xenopus laevis GN=MGC80163 PE	42.61	1	3	3	20
168	BJ047835 homologue to UniRef100_Q6GL21 Cluster: Re	Rep: Receptor-associated protein of the synapse, 43kD - X	42.50	1	1	1	3
169	Q7ZYF2;CL1415Contig2	Translationally-controlled tumor protein homolog OS=Xeno	42.44	2	5	5	145
170	Q6GND4	Dbia protein OS=Xenopus laevis GN=dbi PE=4 SV=1 - [Q6	42.35	3	1	3	46
171	TC427947 similar to UniRef100_UPI0000660DD4 Cluste	Rep: Homolog of Homo sapiens "Splice Isoform Long of ES	42.33	4	5	6	27
172	Q6GP33;CL5832Contig2	Glucose-6-phosphate isomerase OS=Xenopus laevis GN=	42.13	1	6	13	313
173	CF283899 homologue to UniRef100_Q642S1 Cluster: M	Rep: MGC81934 protein - Xenopus laevis (African clawed f	42.03	1	1	1	1
174	Q6AZL9	MGC86316 protein OS=Xenopus laevis GN=rps23 PE=2 S	41.96	5	6	6	65
175	dsrrswapns_comp155943_c0_seq1	len=235	41.67	1	1	1	1
176	CL1402Contig2	CL1402Contig2	41.58	6	0	9	404
177	Q7ZYF7;CL1612Contig4	MGC53103 protein OS=Xenopus laevis GN=phb PE=2 SV=	41.54	3	2	7	126
178	P51893	Adenosylhomocysteinase A OS=Xenopus laevis GN=ahcy-	41.34	5	1	13	217
179	O93477	Adenosylhomocysteinase B OS=Xenopus laevis GN=ahcy-	41.34	5	1	13	214
180	Q6INN4;CL17153Contig1	MGC82295 protein OS=Xenopus laevis GN=cox5b.2 PE=2	41.22	1	5	5	29
181	Q4QR22;CL4816Contig2	MGC114925 protein OS=Xenopus laevis GN=MGC114925	41.14	6	8	8	72
182	Q6AZJ9	40S ribosomal protein S21 OS=Xenopus laevis GN=rps21	40.96	2	3	3	8
183	CD099718 homologue to UniRef100_Q641D7 Cluster: U	Rep: Ubiquitin carboxyl-terminal hydrolase - Xenopus laevis	40.91	1	1	1	1
184	Q0IH31	MGC154809 protein OS=Xenopus laevis GN=snrpg PE=4	40.79	1	1	1	1
185	Q07254	40S ribosomal protein S10 OS=Xenopus laevis GN=rps10	40.61	233	1	6	26
186	P47904;CL48Contig2	40S ribosomal protein S27 OS=Xenopus laevis GN=rps27	40.48	5	2	4	95
187	Q6ING0	LOC443576 protein (Fragment) OS=Xenopus laevis GN=L	40.47	4	1	16	139
188	P52301;CL872Contig1	GTP-binding nuclear protein Ran OS=Xenopus laevis GN=	40.28	5	8	8	178
189	CL29572Contig1	CL29572Contig1	40.28	1	1	1	1
190	Q6GPY3	MGC82521 protein OS=Xenopus laevis GN=prdx5 PE=2 S	40.21	3	5	5	70
191	Q7ZXK4	Rpl10-prov protein OS=Xenopus laevis GN=rpl10 PE=2 SV	40.00	10	2	7	147
192	Q6DJG5	MGC84307 protein OS=Xenopus laevis GN=cox4i2 PE=2 S	39.66	4	5	5	180
193	Q6PF20;CL1Contig1255	Pcna-A protein OS=Xenopus laevis GN=pcna PE=2 SV=1 -	39.46	5	6	6	208
194	TC451860 homologue to UniRef100_Q5RJU8 Cluster: Pr	Rep: Proteasome (Prosome macropain) subunit beta type 4	39.42	2	1	2	5
195	Q6DKB9	MGC84375 protein OS=Xenopus laevis GN=aco2 PE=2 SV	39.39	3	4	18	150
196	dsrrswapns_comp141446_c0_seq1	len=239	39.34	1	1	1	1
197	CL3868Contig2	CL3868Contig2	39.19	5	1	2	285
198	Q6GR11	MGC81430 protein OS=Xenopus laevis GN=vdac3 PE=2 S	38.87	2	5	5	54
199	Q8AVE2;CL52Contig20	Hsc70 protein OS=Xenopus laevis GN=hspa1l PE=2 SV=1	38.77	23	8	18	777
200	Q66KX3	MGC85348 protein OS=Xenopus laevis GN=rpl23a PE=2 S	38.71	7	5	5	60
201	Q6AZV3;CL1Contig1336	MGC78885 protein OS=Xenopus laevis GN=rpl17 PE=2 SV	38.59	6	7	7	80
202	CL3082Contig2	CL3082Contig2	38.57	10	11	11	116
203	P26642	Elongation factor 1-gamma-A OS=Xenopus laevis GN=eef1	38.53	10	9	15	345
204	TC443713 homologue to UniRef100_Q6UTE6 Cluster: S	Rep: Superoxide dismutase - Xenopus laevis (African clawe	38.51	1	1	3	13
205	Q7SZA8;CL926Contig3	60S ribosomal protein L18 OS=Xenopus laevis GN=rpl18 P	38.30	5	2	6	93
206	CL78Contig6	CL78Contig6	38.14	26	1	12	128
207	Q7ZWU3;CL1744Contig1	Grp58-prov protein OS=Xenopus laevis GN=pdia3 PE=2 S	38.05	2	7	15	558
208	Q7SZB4	60S ribosomal protein L37a OS=Xenopus laevis GN=rpl37	38.04	4	3	3	29
209	TC447025 homologue to UniRef100_P42119 Cluster: L-l	Rep: L-lactate dehydrogenase B chain - Xenopus laevis (Af	37.90	2	3	16	520
210	CL1744Contig3	CL1744Contig3	37.89	1	3	5	90
211	dsrrswapns_comp217493_c0_seq4	len=523	37.88	1	1	1	2
212	dsrrswapns_comp203070_c1_seq1	len=343	37.76	1	1	1	1
213	Q4FZQ7	MGC116425 protein OS=Xenopus laevis GN=rpl35 PE=2 S	37.40	296	5	7	20
214	CL1Contig724	CL1Contig724	37.39	2	3	3	23
215	TC466521 homologue to UniRef100_Q28IY1 Cluster: Ba	Rep: Basic transcription factor 3 - Xenopus tropicalis (West	37.30	6	2	2	9
216	Q6NTS1;CL2114Contig3	MGC82400 protein OS=Xenopus laevis GN=MGC82400 PE	37.27	1	2	5	113
217	DC042719 homologue to UniRef100_O93400 Cluster: Ac	Rep: Actin, cytoplasmic 1 - Xenopus laevis (African clawed	37.10	1	4	16	774
218	Q4KLF5;CL749Contig1	Transcription factor BTF3 homolog 4 OS=Xenopus laevis G	36.71	1	2	2	19
219	Q8AVE3;CL2028Contig2	Hspa5 protein OS=Xenopus laevis GN=hspa5 PE=2 SV=1	36.64	7	15	15	370
220	Q9I9M9	Adenine nucleotide translocase OS=Xenopus laevis GN=sl	36.58	12	10	10	274
221	Q7SZB2;CL4738Contig1	Rpl27a protein OS=Xenopus laevis GN=rpl27a PE=2 SV=1	36.49	2	5	5	213
222	Q6PB22;CL8454Contig1	MGC68500 protein OS=Xenopus laevis GN=MGC68500 PE	36.39	3	7	7	249
223	zeinaSSns_comp30958_c0_seq1	len=202	36.36	1	1	1	1
224	Q6INB6;CL4908Contig2	ATP synthase gamma chain OS=Xenopus laevis GN=atp5c	36.05	4	3	6	37
225	Q6IRP7;CL2114Contig1	MGC82361 protein OS=Xenopus laevis GN=atp5h PE=2 S	36.02	1	2	5	56
226	dsrrswapns_comp212624_c0_seq1	len=1012	35.94	3	1	1	1
227	CL11Contig16	CL11Contig16	35.72	12	3	18	283
228	Q7ZXG3;CL107Contig4	Iff-2-prov protein OS=Xenopus laevis GN=eif5a PE=2 SV=1	35.71	6	2	4	170
229	dsrrswapns_comp187699_c1_seq1	len=281	35.59	1	1	1	1
230	CL1744Contig2	CL1744Contig2	35.55	1	2	8	91
231	Q3KQ82	Profilin OS=Xenopus laevis GN=pfn1 PE=2 SV=1 - [Q3KQ8	35.51	3	1	3	7
232	CL384Contig6	CL384Contig6	35.48	11	11	11	116
233	dsrrswapns_comp204498_c2_seq1	len=254	35.48	1	1	1	1
234	Q6AZV1	Hsp90beta OS=Xenopus laevis GN=hsp90ab1 PE=2 SV=1	35.46	14	3	20	314
235	Q7ZXH6;CL593Contig5	Ywhaq-prov protein OS=Xenopus laevis GN=ywhaq PE=2	35.37	10	2	5	110
236	Q6GP18;CL116Contig7	Superoxide dismutase OS=Xenopus laevis GN=MGC8073	35.27	3	3	5	82
237	Q5U5A6	Notch-regulated ankyrin repeat-containing protein OS=Xen	35.09	1	1	1	1
238	Q7ZYS8;CL560Contig6	60S ribosomal protein L10a OS=Xenopus laevis GN=rpl10	35.02	6	7	7	225
239	Q7SY83	MGC64447 protein OS=Xenopus laevis PE=2 SV=1 - [Q7S	34.93	4	2	7	64
240	Q6GNV0	MGC80858 protein OS=Xenopus laevis GN=pa2g4 PE=2 S	34.62	3	1	8	54
241	CL1634Contig3	CL1634Contig3	34.62	4	1	8	42
242	Q6DD58;CL18845Contig1	Mec-12 protein OS=Xenopus laevis GN=tuba4b PE=2 SV=	34.60	7	2	10	318
243	Q7SZ34;CL1198Contig2	Stathmin OS=Xenopus laevis GN=stmn1 PE=2 SV=1 - [Q7	34.48	15	5	6	29
244	dsrrswapns_comp1629_c0_seq1	len=224	34.48	1	1	1	1
245	CL1Contig796	CL1Contig796	34.42	7	1	6	135
246	Q9DED4;TC439103 UniRef100_Q9DED4 Cluster: Cold-i	Cold-inducible RNA-binding protein B OS=Xenopus laevis	34.34	11	3	6	140
247	Q6GPS9	MGC82638 protein OS=Xenopus laevis GN=hadha PE=2 S	34.34	485	1	14	108
248	dsrrswapns_comp200116_c3_seq1	len=328	34.33	1	1	1	1
249	Q6GQ64	Thioredoxin OS=Xenopus laevis GN=MGC80314 PE=3 SV	34.29	2	2	2	2

250	Q6NTT2	MGC82306 protein OS=Xenopus laevis GN=rps18 PE=2 S	34.21	7	7	7	104
251	dsrrswapns_comp482840_c0_seq1	len=431	34.15	1	1	1	1
252	Q6DJN5;dsrrswapns_comp211046_c0_seq2	60S ribosomal protein L13 OS=Xenopus laevis GN=rpl13 P	34.12	8	7	7	160
253	Q7ZSY1;CL6511Contig1	Galectin family xgalectin-VIIa OS=Xenopus laevis GN=lgals	34.10	2	7	7	74
254	Q7SZU3;TC455791 UniRef100_Q7SZU3 Cluster: Rps10-	Rps10-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q7S	33.94	5	1	5	43
255	CL569Contig8	CL569Contig8	33.93	1	1	2	25
256	Q4QR32	MGC114875 protein OS=Xenopus laevis GN=rps29 PE=4 S	33.93	1	1	2	27
257	CL24855Contig1	CL24855Contig1	33.68	1	1	3	32
258	TC427469 homologue to UniRef100_Q6GMA6 Cluster: M	Rep: MGC81949 protein - Xenopus laevis (African clawed f	33.53	2	3	3	46
259	Q7T0R9	Rps2e protein OS=Xenopus laevis GN=rps2 PE=2 SV=1 - [	33.45	15	8	8	215
260	P08429;CL92Contig5	60S ribosomal protein L4-A OS=Xenopus laevis GN=rpl4-a	33.33	501	10	12	335
261	Q6NRY1;CL6842Contig1	MGC81067 protein OS=Xenopus laevis GN=habp4 PE=2 S	33.25	1	7	7	338
262	Q8AVX2;CL1548Contig2	Rpl5-a protein OS=Xenopus laevis GN=rpl5 PE=2 SV=1 - [	33.11	3	5	7	244
263	Q6GPP8	MGC82702 protein OS=Xenopus laevis GN=hba-l5 PE=2 S	33.09	12	4	4	141
264	TC433738 homologue to UniRef100_Q6P2W6 Cluster: E	Rep: Elongation factor Tu - Xenopus tropicalis (Western cla	32.95	6	6	6	27
265	zeinaSSns_comp389457_c1_seq2	len=2398	32.95	2	1	10	93
266	BP731916 homologue to UniRef100_UPI00006A037D Cl	Rep: Pre-B-cell leukemia transcription factor 3 (Homeobox	32.79	1	1	1	1
267	P23403;CL22Contig8	40S ribosomal protein S20 OS=Xenopus laevis GN=rps20	32.77	6	3	3	141
268	Q5PQ49;CL12806Contig1	LOC495981 protein OS=Xenopus laevis GN=LOC495981	32.65	2	4	4	68
269	dsrrswapns_comp181463_c0_seq1	len=389	32.65	1	1	1	1
270	P39017;CL2323Contig1	40S ribosomal protein S6 OS=Xenopus laevis GN=rps6 PE	32.53	5	5	6	132
271	Q0IH65	LOC733268 protein OS=Xenopus laevis GN=LOC733268	32.38	3	2	2	62
272	TC469090 homologue to UniRef100_P18709 Cluster: Vit	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovit	32.37	1	7	9	1373
273	CL1144Contig4	CL1144Contig4	32.24	3	1	11	99
274	CL4254Contig2	CL4254Contig2	32.14	3	1	12	531
275	Q8AVB7;CL2995Contig1	Cct2-prov protein OS=Xenopus laevis GN=cct2 PE=2 SV=1	31.59	2	4	10	114
276	Q6GR06;CL3748Contig2	MGC81473 protein OS=Xenopus laevis GN=cbr3 PE=2 SV	31.41	1	3	5	48
277	P50143;CL5141Contig1	T-complex protein 1 subunit gamma OS=Xenopus laevis G	31.26	2	12	12	226
278	dsrrswapns_comp182460_c0_seq1	len=504	31.25	1	1	1	1
279	P24495;CL4026Contig1	Proteasome subunit alpha type-2 OS=Xenopus laevis GN=	31.20	3	4	4	18
280	dsrrswapns_comp209695_c7_seq1	len=840	31.16	1	1	1	1
281	dsrrswapns_comp145349_c0_seq1	len=620	31.11	1	1	1	1
282	A1A638;CL11731Contig1	Dbib protein OS=Xenopus laevis GN=dbi PE=4 SV=1 - [A1	31.03	2	1	3	22
283	TC456376 homologue to UniRef100_UPI000069D8DA Cl	Rep: Ubiquinol-cytochrome c reductase complex 11 kDa pr	31.03	6	1	1	28
284	CL1144Contig2	CL1144Contig2	30.85	5	9	9	89
285	Q6GN66;CL2418Contig1	T-complex protein 1 subunit delta OS=Xenopus laevis GN=	30.80	4	2	8	272
286	DR717088 homologue to UniRef100_UPI000069D998 Cl	Rep: AT-rich interactive domain-containing protein 1B (ARI	30.77	1	1	1	1
287	Q7SZ87	MGC64430 protein OS=Xenopus laevis GN=rpl28 PE=2 SV	30.66	290	1	4	25
288	Q66KV6;CL1Contig276	LOC100101273 protein OS=Xenopus laevis GN=rpl28 PE=	30.66	291	1	4	23
289	Q6DCT5;CL7695Contig1	MGC80785 protein OS=Xenopus laevis GN=aldh2 PE=2 S	30.52	1	9	9	165
290	dsrrswapns_comp195565_c1_seq1	len=284	30.51	1	1	1	1
291	A1L3K2;CL19654Contig1	Pyruvate kinase OS=Xenopus laevis GN=LOC100037030	30.32	4	1	16	1093
292	dsrrswapns_comp197002_c0_seq1	len=449	30.23	1	1	1	1
293	Q5XGW4;CL2418Contig2	T-complex protein 1 subunit delta OS=Xenopus laevis GN=	30.13	5	2	8	193
294	CL48Contig6	CL48Contig6	30.09	5	1	3	27
295	Q66KY6;CL384Contig8	MGC85310 protein OS=Xenopus laevis GN=rpl11 PE=2 SV	29.94	9	4	4	296
296	Q4FZP9	MGC116466 protein OS=Xenopus laevis GN=MGC116466	29.88	4	1	5	17
297	P09897	60S ribosomal protein L18-A OS=Xenopus laevis GN=rpl18	29.79	228	1	6	63
298	Q6NU90;CL8453Contig1	MGC81140 protein OS=Xenopus laevis GN=lap3 PE=2 SV	29.70	2	11	11	131
299	Q6DE98;CL4343Contig1	Gyg1-prov protein OS=Xenopus laevis GN=gyg1 PE=2 SV	29.70	3	2	7	77
300	TC447788 similar to UniRef100_UPI0000ECB006 Cluste	Rep: Hepatic triacylglycerol lipase precursor (EC 3.1.1.3) (H	29.67	1	1	1	3
301	CL66Contig6	CL66Contig6	29.65	4	6	6	128
302	zeinaSSns_comp385518_c1_seq2	len=534	29.49	1	1	1	1
303	P52171	Importin subunit alpha-2 OS=Xenopus laevis GN=kpna2 PE	29.45	4	3	9	161
304	Q6NTP3;CL8757Contig1	MGC83130 protein OS=Xenopus laevis GN=MGC83130 PE	29.11	3	2	2	11
305	TC453514 homologue to UniRef100_Q6DD77 Cluster: St	Rep: Stk39-prov protein - Xenopus laevis (African clawed fr	29.07	1	1	1	1
306	Q7ZYR1	Rpl3-prov protein OS=Xenopus laevis GN=rpl3 PE=2 SV=1	29.03	237	8	9	108
307	zeinaSSns_comp383101_c0_seq1	len=1454	28.92	15	2	4	12
308	Q7ZWJ2	Uqcrc1 protein OS=Xenopus laevis GN=uqcrc1 PE=2 SV=1	28.87	3	7	7	50
309	Q4FZM5;CL2718Contig3	MGC116545 protein OS=Xenopus laevis GN=cyc1 PE=2 S	28.80	2	5	5	44
310	Q5BJ43;CL26281Contig1	LOC496181 protein OS=Xenopus laevis GN=LOC496181	28.57	2	1	3	89
311	CL1011Contig3	CL1011Contig3	28.45	4	14	14	89
312	CL3941Contig2	CL3941Contig2	28.43	3	13	13	151
313	Q6GQ21;CL1684Contig2	Peptidyl-prolyl cis-trans isomerase OS=Xenopus laevis GN	28.37	4	2	2	63
314	Q7ZTL5;CL1515Contig2	Cct8-prov protein OS=Xenopus laevis GN=cct8 PE=2 SV=1	28.21	257	10	11	193
315	TC442984 similar to UniRef100_Q5HZQ5 Cluster: LOC4	Rep: LOC496332 protein - Xenopus laevis (African clawed	28.06	1	1	1	1
316	Q6GQ91;dsrrswapns_comp209386_c2_seq3	MGC80253 protein OS=Xenopus laevis GN=ndufa4 PE=4 S	28.05	2	3	3	34
317	Q6PI79;zeinaSSns_comp370372_c0_seq2	Histone H3.3 OS=Xenopus laevis PE=1 SV=3 - [H33_XEN	27.94	21	2	2	17
318	Q6NRW7;CL3725Contig3	MGC81186 protein OS=Xenopus laevis GN=clns1a PE=2 S	27.92	3	2	3	17
319	Q4KL98	MGC116533 protein OS=Xenopus laevis GN=stoml2 PE=2	27.83	5	2	2	2
320	Q91375	Elongation factor 1-gamma-B OS=Xenopus laevis GN=eef1	27.69	4	3	10	257
321	Q6GP41;CX133515 UniRef100_Q6GP41 Cluster: MGC8	MGC80700 protein OS=Xenopus laevis GN=MGC80700 P	27.50	4	3	3	39
322	Q6GPU5	MGC82602 protein OS=Xenopus laevis GN=MGC82602 P	27.46	3	1	4	114
323	Q7ZTP0;CL1Contig193	MGC53359 protein OS=Xenopus laevis GN=tuba3c PE=2 S	27.33	4	0	8	402
324	CL4288Contig3	CL4288Contig3	27.27	3	5	5	102
325	Q66J53;CL2807Contig1	MGC81873 protein OS=Xenopus laevis GN=MGC81873 P	27.25	5	6	6	710
326	Q5XHJ8;CL2211Contig2	LOC397895 protein OS=Xenopus laevis GN=gsn PE=2 SV	27.02	293	5	8	105
327	EB474857 similar to UniRef100_UPI000069F3E7 Cluster	Rep: Long palate, lung and nasal epithelium carcinoma-ass	26.85	1	1	1	1
328	Q3KPN6	Proteasome subunit alpha type OS=Xenopus laevis GN=M	26.82	4	4	4	23
329	TC443725 homologue to UniRef100_Q6DJF7 Cluster: 60	Rep: 60S ribosomal protein L6 - Xenopus laevis (African cla	26.77	3	4	6	35
330	Q6PI76;CL289Contig7	Rps14-prov protein OS=Xenopus laevis GN=rps14 PE=2 S	26.49	4	5	5	347
331	Q6PHL5;TC440338 UniRef100_Q28FP8 Cluster: 60S rib	60S ribosomal protein L27 OS=Xenopus laevis GN=rpl27 P	26.47	3	4	4	172
332	Q7ZWZ7;CL2318Contig1	Ribosomal protein L15 OS=Xenopus laevis GN=rpl15 PE=2	26.47	4	6	6	183
333	Q2VPL8	MGC131189 protein OS=Xenopus laevis GN=aldh6a1 PE=	26.39	10	6	6	98
334	CL4552Contig3	CL4552Contig3	26.37	4	2	6	105
335	Q6PAV9;CL20295Contig1	MGC68699 protein OS=Xenopus laevis GN=MGC68699 P	26.29	230	1	7	189

336	Q4QR45;CL3635Contig1	Importin subunit alpha OS=Xenopus laevis GN=kpna7 PE=	26.25	3	3	9	265
337	Q6NUC7;CL5043Contig2	Putative uncharacterized protein OS=Xenopus laevis PE=2	26.02	1	3	3	55
338	BJ093020 weakly similar to UniRef100_Q70X36 Cluster:	Rep: Transposase - Rana lessonae (Pool frog), partial (34%	25.96	5	1	1	1
339	Q7ZWS8;CL1187Contig2	Tagln2-prov protein OS=Xenopus laevis GN=tagln2 PE=2	25.89	4	4	4	26
340	EG584025 weakly similar to UniRef100_Q800A0 Cluster:	Rep: Cathepsin E precursor - Rana catesbeiana (Bull frog),	25.81	1	1	1	1
341	Q7ZYU4;TC433567 UniRef100_Q7ZYU4 Cluster: Rps9-p	Rps9-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZY	25.77	3	1	6	35
342	Q6GNX6;CL542Contig3	MGC80804 protein OS=Xenopus laevis GN=rps9 PE=2 SV	25.77	5	2	7	33
343	Q7SYU3;CL2410Contig2	MGC64490 protein OS=Xenopus laevis GN=rps5 PE=2 SV	25.62	5	4	4	105
344	Q6NU02;CL367Contig6	LOC443739 protein OS=Xenopus laevis GN=eif4a1 PE=2	25.62	27	1	7	39
345	Q6AZL6;CL367Contig5	LOC444845 protein OS=Xenopus laevis GN=LOC444845	25.62	29	1	7	26
346	Q7SZB7;CL391Contig4	60S ribosomal protein L18a OS=Xenopus laevis GN=rpl18	25.57	3	1	5	185
347	P51048	Melatonin receptor type 1A X2.0 (Fragment) OS=Xenopus	25.49	1	1	1	2
348	BG037251 similar to UniRef100_P07437 Cluster: Tubulin	Rep: Tubulin beta chain - Homo sapiens (Human), partial (	25.47	1	1	1	6
349	P02281;TC453026 UniRef100_P02281 Cluster: Histone	Histone H2B 1.1 OS=Xenopus laevis PE=1 SV=2 - [H2B11_	25.40	13	3	3	155
350	Q66KW1;CL1655Contig4	MGC85384 protein OS=Xenopus laevis GN=rpl29 PE=4 SV	25.33	3	1	2	100
351	Q7SZA5;BJ091434 UniRef100_Q7SZA5 Cluster: MGC64	MGC64312 protein OS=Xenopus laevis GN=rpl29 PE=4 SV	25.33	3	1	2	29
352	Q7ZX44;CL2985Contig2	Txndc5-prov protein OS=Xenopus laevis GN=txndc5 PE=2	25.31	1	4	7	43
353	Q7ZYQ8	60S ribosomal protein L18a (Fragment) OS=Xenopus laevis	25.28	3	1	5	75
354	Q6P7J6;CL13096Contig1	MGC68461 protein OS=Xenopus laevis GN=glrx PE=4 SV=	25.23	1	2	2	7
355	CL36962Contig1	CL36962Contig1	25.22	2	1	1	1
356	dsrrswapns_comp208692_c0_seq2	len=520	25.00	1	1	1	2
357	A5D8P9	LOC100049770 protein (Fragment) OS=Xenopus laevis G	25.00	1	1	1	1
358	Q9PSQ7	PNIXA, EP45=NI(2+)-binding serpin (Fragments) OS=Xeno	24.83	2	1	4	158
359	Q6DJJ1;zeinaSSns_comp386737_c5_seq20	MGC82151 protein OS=Xenopus laevis GN=rps25 PE=2 S	24.80	5	3	3	31
360	TC440065 homologue to UniRef100_Q6GPU5 Cluster: M	Rep: MGC82602 protein - Xenopus laevis (African clawed f	24.68	2	1	4	85
361	Q7ZY81	Nucleosome assembly protein 1-like 1-B OS=Xenopus laev	24.68	4	2	6	68
362	P05221;CL36471Contig1	Nucleoplasmin OS=Xenopus laevis PE=1 SV=1 - [NUPL_X	24.50	2	2	2	154
363	Q6DEB3;CL2313Contig1	MGC79025 protein OS=Xenopus laevis GN=phb2 PE=2 SV	24.25	4	7	7	99
364	dsrrswapns_comp11994_c0_seq1	len=224	24.24	1	1	1	1
365	Q90Z58;CL11161Contig1	Chisel OS=Xenopus laevis GN=smpx PE=4 SV=1 - [Q90Z5	24.18	1	1	1	3
366	Q5XHK2;CL84Contig4	14-3-3 protein beta/alpha-A OS=Xenopus laevis GN=ywha	24.18	12	2	4	75
367	CL2995Contig3	CL2995Contig3	24.11	2	2	8	32
368	CL593Contig1	CL593Contig1	23.98	9	1	4	51
369	zeinaSSns_comp382833_c4_seq6	len=2746	23.86	2	1	1	1
370	Q7SYT0;CL12198Contig1	Elongation factor 1-alpha OS=Xenopus laevis GN=eef1a2	23.76	329	1	12	621
371	dsrrswapns_comp207775_c3_seq1	len=557	23.75	1	1	1	1
372	TC414340 UniRef100_Q6GQ22 Cluster: Kidney mitochor	Rep: Kidney mitochondrial carrier protein 1 - Xenopus laevi	23.71	3	1	2	3
373	CL1686Contig3	CL1686Contig3	23.69	3	2	2	6
374	Q6DFL2;CL4663Contig1	Biorientation of chromosomes in cell division protein 1 OS=	23.67	1	1	1	4
375	Q8AVV6	SOSS complex subunit C OS=Xenopus laevis GN=inip PE=	23.64	1	1	1	1
376	Q7SZ26;CL2319Contig2	Peptidyl-prolyl cis-trans isomerase OS=Xenopus laevis GN	23.61	7	4	4	51
377	Q7ZX92;CL5540Contig2	MGC80929 protein OS=Xenopus laevis GN=psmd14 PE=2	23.55	1	3	3	48
378	O57468;CL1665Contig1	14-3-3 protein epsilon OS=Xenopus laevis GN=ywhae PE=	23.53	5	3	4	64
379	CL27618Contig1	CL27618Contig1	23.43	1	1	1	1
380	CL369Contig2	CL369Contig2	23.40	2	1	2	5
381	DC027108 homologue to UniRef100_Q5M7C7 Cluster: P	Rep: Protein jagunal homolog 1 - Xenopus laevis (African c	23.31	1	1	1	3
382	P49393;CL1Contig728	40S ribosomal protein S13 OS=Xenopus laevis GN=rps13	23.18	7	4	4	67
383	TC430865 similar to UniRef100_UPI0000501EBE Cluste	Rep: mitochondrial tumor suppressor 1 - Rattus norvegicus,	23.12	1	1	1	1
384	TC457286 similar to UniRef100_P18709 Cluster: Vitellog	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovit	22.78	1	5	5	370
385	Q3KPV9;CL5420Contig1	Proteasome subunit beta type OS=Xenopus laevis GN=LO	22.75	5	5	5	23
386	CL1Contig1594	CL1Contig1594	22.71	3	1	2	2
387	Q6NU46;CL5600Contig2	Acetyl-CoA acetyltransferase A, mitochondrial OS=Xenopu	22.62	3	1	5	147
388	dsrrswapns_comp194741_c2_seq1	len=959	22.60	1	1	1	1
389	dsrrswapns_comp207966_c0_seq3	len=2269	22.59	1	8	8	46
390	Q8AVD0	MGC53232 protein OS=Xenopus laevis PE=2 SV=1 - [Q8A	22.54	1	1	1	1
391	CL1Contig225	CL1Contig225	22.20	3	0	7	156
392	P79931	Pyruvate dehydrogenase E1-beta subunit (Fragment) OS=	22.01	11	7	7	59
393	CA789974 similar to UniRef100_A1A5F6 Cluster: LOC10	Rep: LOC100036684 protein - Xenopus tropicalis (Western	22.00	1	1	1	2
394	Q5EAV5;CL3725Contig2	ICLN protein OS=Xenopus laevis GN=ICLN PE=2 SV=1 - [	21.92	4	1	2	16
395	CL2691Contig4	CL2691Contig4	21.86	2	3	3	13
396	Q7SZ19	Annexin (Fragment) OS=Xenopus laevis GN=LOC398472	21.70	7	4	4	38
397	Q6PCE5;CL6542Contig1	Succinyl-CoA:3-ketoacid-coenzyme A transferase OS=Xen	21.70	3	6	6	75
398	Q7SYX2;CL10546Contig1	MGC64421 protein OS=Xenopus laevis GN=serpinb6 PE=	21.64	228	4	5	51
399	dsrrswapns_comp213847_c0_seq3	len=565	21.55	1	1	1	1
400	EG574474 similar to UniRef100_A8IIQ2 Cluster: Mitocho	Rep: Mitochondrial substrate carrier - Chlamydomonas rein	21.43	1	1	1	1
401	Q6PAB5;CL3453Contig3	MGC68609 protein OS=Xenopus laevis GN=akr1b1 PE=2	21.38	5	4	4	27
402	Q5XGW7	Cbp/p300-interacting transactivator 2 OS=Xenopus laevis	21.33	1	1	1	1
403	Q7ZYS1;CL555Contig6	60S ribosomal protein L19 OS=Xenopus laevis GN=rpl19 P	21.32	3	3	4	266
404	Q6NUB6;dsrrswapns_comp210970_c0_seq2	MGC81083 protein OS=Xenopus laevis GN=nme4 PE=2 S	21.31	1	1	1	2
405	TC432016 weakly similar to UniRef100_Q7RCA4 Cluster	Rep: Centrin - Plasmodium yoelii yoelii, partial (34%)	21.30	1	1	1	1
406	CL3748Contig3	CL3748Contig3	21.30	2	3	4	30
407	Q5XHE2;CL15613Contig1	LOC495025 protein OS=Xenopus laevis GN=uchl3 PE=2 S	21.30	2	3	3	24
408	CL3167Contig3	CL3167Contig3	21.24	1	1	1	1
409	Q7ZY48	Rpl13a-prov protein OS=Xenopus laevis GN=rpl13a PE=2	21.21	8	6	6	48
410	Q9ZZM1	Cytochrome c oxidase subunit 2 (Fragment) OS=Xenopus	21.20	3	3	3	144
411	Q6GN02	Acetyl-CoA acetyltransferase B, mitochondrial OS=Xenopu	21.19	4	1	5	138
412	Q7ZYE8;CL6531Contig1	Tyrp1-prov protein OS=Xenopus laevis GN=tyrp1 PE=2 SV	21.16	3	5	5	77
413	dsrrswapns_comp216523_c0_seq5	len=512	21.14	1	1	1	1
414	CL14169Contig1	CL14169Contig1	21.13	2	1	1	7
415	CL419Contig8	CL419Contig8	21.13	1	1	1	1
416	A0AUT4	LOC100036778 protein OS=Xenopus laevis GN=LOC1000	21.01	6	1	6	136
417	A7YYL7;CL10641Contig1	LOC100126616 protein OS=Xenopus laevis GN=mrpl32 PE	20.99	1	1	1	2
418	DC007851 similar to UniRef100_UPI00004D8D43 Cluste	Rep: C219-reactive peptide - Xenopus tropicalis, partial (12	20.89	11	1	1	1
419	dsrrswapns_comp199899_c1_seq1	len=286	20.83	1	1	1	1
420	B0LM40	Importin beta 1 OS=Xenopus laevis GN=kpnb1 PE=2 SV=1	20.78	8	8	8	90
421	Q66KR0	LOC446923 protein (Fragment) OS=Xenopus laevis GN=L	20.63	2	3	4	18

422	BI314067	BI314067	20.59	1	1	1	2
423	P79929;CL1Contig361	LOC397932 protein OS=Xenopus laevis GN=LOC397932 F	20.57	4	1	3	31
424	Q7SZA3	MGC64320 protein OS=Xenopus laevis PE=4 SV=1 - [Q7S.	20.55	2	1	1	6
425	Q66J16	MGC83352 protein OS=Xenopus laevis GN=aldh7a1 PE=2	20.55	3	5	5	23
426	Q91624;CL52Contig10	Heat shock cognate 70.I OS=Xenopus laevis GN=hsc70.I P	20.47	3	1	8	306
427	Q9IAJ7;CL4522Contig2	ATP synthase subunit B OS=Xenopus laevis GN=atp5f1 PE	20.40	3	4	4	47
428	Q3KQC0;CL5489Contig2	LOC414601 protein OS=Xenopus laevis GN=LOC414601 F	20.38	4	3	4	277
429	DC024875 homologue to UniRef100_P04751 Cluster: Ac	Rep: Actin, alpha cardiac muscle 1 - Xenopus laevis (Africa	20.34	4	3	13	485
430	Q6GPQ9;CL12997Contig1	MGC82679 protein OS=Xenopus laevis GN=ndufs6 PE=2 S	20.30	3	2	2	40
431	Q5FWM7;CL10311Contig1	MGC84940 protein OS=Xenopus laevis GN=fabp4 PE=2 SY	20.30	1	1	2	15
432	B7ZR28	N1/N2 protein OS=Xenopus laevis GN=N1/N2 PE=2 SV=1	20.27	13	5	6	135
433	CL1561Contig1	CL1561Contig1	20.22	1	1	1	2
434	Q6GPW4	Transmembrane protein 205 OS=Xenopus laevis GN=tmem	20.21	1	1	1	1
435	Q6PAY8;CL13107Contig1	Hydroxysteroid dehydrogenase-like protein 2 OS=Xenopus	20.14	1	5	5	239
436	dsrrswapns_comp209340_c0_seq1	len=500	20.13	1	1	1	1
437	dsrrswapns_comp216004_c2_seq2	len=1698	20.11	4	1	6	35
438	Q6DCJ9	Gdi2-prov protein OS=Xenopus laevis GN=gdi1 PE=2 SV=1	19.96	8	5	5	13
439	Q68A89	Proteasome subunit alpha type (Fragment) OS=Xenopus la	19.92	2	3	3	3
440	B7ZR89	Paraxis-like protein OS=Xenopus laevis GN=LOC493747 P	19.89	228	1	2	2
441	Q5PPR7;CL22579Contig1	LOC496102 protein OS=Xenopus laevis GN=LOC496102 F	19.83	1	1	1	4
442	DC047969 homologue to UniRef100_Q5PQ84 Cluster: N	Rep: Nucleoside diphosphate kinase - Xenopus laevis (Afric	19.77	4	1	1	1
443	Q6DCS9	MGC80838 protein OS=Xenopus laevis GN=ptgr1.2 PE=2 S	19.76	3	4	4	26
444	CL2090Contig1	CL2090Contig1	19.69	4	6	9	84
445	Q5M7C7;dsrrswapns_comp210647_c3_seq3	Protein jagunal homolog 1 OS=Xenopus laevis GN=jagn1 F	19.67	3	1	1	2
446	Q68F32;CL3294Contig2	MGC81977 protein OS=Xenopus laevis GN=arhgdig PE=2	19.60	4	2	2	12
447	Q566H3;CL12776Contig1	MGC114733 protein OS=Xenopus laevis GN=cebpg PE=2	19.58	1	1	1	4
448	Q640F4;CL20343Contig1	LOC494684 protein OS=Xenopus laevis GN=LOC494684 F	19.52	1	1	1	6
449	Q6IND5	MGC83495 protein OS=Xenopus laevis GN=vwa5a.2 PE=2	19.51	3	1	8	135
450	Q6NRB2	MGC84587 protein OS=Xenopus laevis GN=hibadh PE=2 S	19.51	3	3	3	24
451	P13549;CL5Contig29	Elongation factor 1-alpha, somatic form OS=Xenopus laevis	19.48	45	1	9	871
452	TC465314 UniRef100_UPI000069FFAE Cluster: Whirlin (	Rep: Whirlin (Autosomal recessive deafness type 31 protein	19.44	2	1	1	1
453	CL13435Contig1	CL13435Contig1	19.41	1	1	1	1
454	CL9216Contig2	CL9216Contig2	19.40	4	7	7	31
455	TC429806 homologue to UniRef100_Q0V9B4 Cluster: Ge	Rep: Gem protein - Xenopus tropicalis (Western clawed frog	19.40	1	1	1	1
456	A2VDA2;CL2004Contig2	LOC100037199 protein OS=Xenopus laevis GN=sri PE=2 S	19.39	4	2	3	7
457	dsrrswapns_comp116804_c0_seq1	len=382	19.33	1	1	1	1
458	Q6DE12;CL5192Contig1	M6prbp1-prov protein OS=Xenopus laevis GN=m6prbp1-pr	19.29	3	2	3	19
459	CL990Contig2	CL990Contig2	19.28	5	5	5	26
460	CL4908Contig3	CL4908Contig3	19.25	4	1	4	13
461	A1L3J7	LOC100037025 protein OS=Xenopus laevis GN=ganab PE	19.19	7	8	8	21
462	Q6AZL7	MGC86356 protein OS=Xenopus laevis GN=rps26 PE=4 SY	19.13	7	2	2	52
463	Q6PA58	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	18.95	3	3	5	70
464	CL5360Contig2	CL5360Contig2	18.93	4	1	8	108
465	Q6NTR4;CL6643Contig1	MGC83076 protein OS=Xenopus laevis GN=rpl14 PE=2 SV	18.84	3	2	2	44
466	Q8AVD7;CL3574Contig1	Ndufv1 protein OS=Xenopus laevis GN=ndufv1 PE=2 SV=1	18.68	1	4	4	19
467	A9UM19;CL14087Contig1	LOC100137677 protein OS=Xenopus laevis GN=LOC1001	18.67	1	1	2	17
468	Q66KV2	MGC85404 protein OS=Xenopus laevis GN=rpl38 PE=3 SV	18.57	2	1	1	28
469	TC453299 homologue to UniRef100_UPI000069DD4D C	Rep: Seizure 6-like protein precursor. - Xenopus tropicalis,	18.57	3	1	1	1
470	CL19436Contig1	CL19436Contig1	18.50	1	1	1	1
471	Q9DE56	Ribonucleoside-diphosphate reductase (Fragment) OS=Xer	18.46	1	2	5	70
472	dsrrswapns_comp216030_c0_seq4	len=1289	18.45	6	1	1	1
473	Q6NUH0;CL2830Contig1	60S ribosomal protein L31 OS=Xenopus laevis GN=rpl31 P	18.40	3	2	2	6
474	DR728022 homologue to UniRef100_Q5HZ68 Cluster: Gu	Rep: Guanidinoacetate N-methyltransferase B - Xenopus la	18.39	4	1	1	2
475	Q90X16;CL10849Contig1	Annexin OS=Xenopus laevis GN=anxa4 PE=2 SV=1 - [Q90	18.38	1	3	3	7
476	Q52M98	14-3-3 protein theta OS=Xenopus laevis GN=ywhaq PE=2 S	18.37	10	1	3	40
477	CB200344 homologue to UniRef100_UPI00006A0D20 Cl	Rep: Thyroglobulin precursor. - Xenopus tropicalis, partial (	18.25	1	1	1	1
478	P15126	60S ribosomal protein L5-B OS=Xenopus laevis GN=rpl5-b	18.24	3	1	3	19
479	CL42352Contig1	CL42352Contig1	18.18	2	1	1	1
480	dsrrswapns_comp216320_c1_seq1	len=333	18.18	1	1	1	3
481	CL30676Contig1	CL30676Contig1	18.07	1	1	1	1
482	dsrrswapns_comp209417_c0_seq3	len=2504	18.07	1	1	1	1
483	EB475574 weakly similar to UniRef100_Q7Q9B0 Cluster:	Rep: AGAP003346-PA - Anopheles gambiae str. PEST, pa	18.04	1	1	1	1
484	Q4FZP3	Cytochrome c oxidase subunit 6A, mitochondrial OS=Xeno	18.02	5	1	1	45
485	Q66KP4	MGC85561 protein OS=Xenopus laevis GN=uros PE=2 SV	17.94	1	1	1	1
486	A4UXD6	Toll-like receptor8 (Fragment) OS=Xenopus laevis GN=tlr8	17.92	1	1	1	1
487	zeinaSSns_comp378203_c0_seq1	len=201	17.86	5	1	1	1
488	CL2211Contig3	CL2211Contig3	17.83	4	3	6	21
489	CB562068 weakly similar to UniRef100_P08941 Cluster:	Rep: Proto-oncogene tyrosine-protein kinase ROS precurso	17.81	1	1	1	1
490	dsrrswapns_comp26597_c0_seq1	len=233	17.74	1	1	1	2
491	Q6DCM8	Hadh2-prov protein OS=Xenopus laevis GN=hsd17b10 PE=	17.69	3	2	2	9
492	TC439428 homologue to UniRef100_Q7ZTJ1 Cluster: Slc	Rep: Slc25a3-prov protein - Xenopus laevis (African clawed	17.67	6	1	3	6
493	Q6JA20;CL4546Contig2	38k protein OS=Xenopus laevis PE=2 SV=1 - [Q6JA20_XE	17.65	5	2	2	16
494	Q7ZXF3;zeinaSSns_comp386232_c2_seq1	DNA-binding protein inhibitor ID-4 OS=Xenopus laevis GN=	17.56	2	1	1	2
495	Q66IP6;CL2553Contig2	MGC86305 protein OS=Xenopus laevis GN=fam168a PE=2	17.45	1	1	1	2
496	CL3Contig34	CL3Contig34	17.43	24	3	3	5
497	CL13990Contig1	CL13990Contig1	17.36	1	1	1	2
498	CL2985Contig3	CL2985Contig3	17.33	2	3	5	18
499	Q71U00	S-phase kinase-associated protein 1 OS=Xenopus laevis G	17.18	1	1	1	1
500	CL21961Contig1	CL21961Contig1	17.17	1	1	1	2
501	zeinaSSns_comp377647_c3_seq1	len=449	17.14	1	1	1	1
502	Q63ZG6;CL22Contig15	Phosphorylase OS=Xenopus laevis GN=pygl PE=2 SV=1 -	16.96	9	10	10	251
503	Q6GNI8;CL4245Contig2	MGC82778 protein OS=Xenopus laevis GN=MGC82778 PE	16.93	1	1	1	6
504	Q4KLB0	Glyoxalase domain-containing protein 5 OS=Xenopus laevis	16.88	2	1	1	2
505	Q5U556;CL13826Contig1	LOC495364 protein OS=Xenopus laevis GN=mrpl12 PE=2	16.84	1	3	3	44
506	Q7ZX34;CL3654Contig2	MGC52616 protein OS=Xenopus laevis GN=hspa9 PE=2 S	16.72	3	7	7	32
507	NP9453667 GB	AY819241.1 AAX37552.1 c-myc	16.67	1	1	1	24

508	Q3SYN2;CL2881Contig3	MGC114703 protein OS=Xenopus laevis GN=mob3a PE=2	16.67	1	1	1	2
509	Q641G7	Actin-related protein 2/3 complex subunit 4 OS=Xenopus la	16.67	1	1	1	1
510	Q4U0Y4	Nucleosome assembly protein 1-like 1-A OS=Xenopus laev	16.58	5	1	5	63
511	Q6DJQ0	Putative uncharacterized protein OS=Xenopus laevis PE=2	16.55	4	3	3	17
512	P28024	Proteasome subunit beta type-4 (Fragment) OS=Xenopus l	16.53	4	1	2	9
513	Q5M7D5;CL6336Contig3	LOC496233 protein OS=Xenopus laevis GN=ndufs3 PE=2	16.40	4	3	3	66
514	Q6GPC4;CL12623Contig1	MGC80505 protein OS=Xenopus laevis GN=ndufb7 PE=4	16.38	1	1	1	12
515	Q6AZI4	LOC446231 protein (Fragment) OS=Xenopus laevis GN=u	16.34	3	1	1	2
516	Q6DJP1	LOC443721 protein (Fragment) OS=Xenopus laevis GN=ct	16.33	7	4	4	97
517	BG017237 similar to UniRef100_Q6DJF7 Cluster: 60S ri	Rep: 60S ribosomal protein L6 - Xenopus laevis (African cl	16.33	1	1	1	4
518	P62840	Ubiquitin-conjugating enzyme E2 D2 OS=Xenopus laevis G	16.33	2	1	1	2
519	TC428798 homologue to UniRef100_Q6GPT4 Cluster: M	Rep: MGC82630 protein - Xenopus laevis (African clawed f	16.31	3	1	1	2
520	CL5962Contig1	CL5962Contig1	16.27	2	5	5	28
521	Q6PAD3;CL1008Contig1	Psmc4 protein OS=Xenopus laevis GN=psmc4 PE=2 SV=1	16.19	2	2	2	6
522	P79951	CD3gamma/delta OS=Xenopus laevis GN=cd3g PE=2 SV=	16.17	2	2	2	3
523	CL38748Contig1	CL38748Contig1	16.15	2	1	1	1
524	dsrrswapns_comp199260_c1_seq1	len=303	16.13	1	1	1	2
525	Q6PA24	MGC68726 protein OS=Xenopus laevis GN=capza1 PE=2	16.13	1	1	1	2
526	CL9522Contig1	CL9522Contig1	16.11	1	3	3	19
527	CL11897Contig1	CL11897Contig1	16.10	1	4	4	19
528	Q7SX80	MGC64330 protein OS=Xenopus laevis GN=ctbs PE=2 SV	15.95	4	4	4	31
529	Q7ZX29;CL3649Contig1	Dia1 protein OS=Xenopus laevis GN=cyb5r3 PE=2 SV=1 -	15.95	1	3	3	15
530	CL3728Contig4	CL3728Contig4	15.79	1	1	1	1
531	Q8AVD3;CL1995Contig2	Adenylate kinase 2, mitochondrial OS=Xenopus laevis GN=	15.77	4	3	3	64
532	CL14985Contig1	CL14985Contig1	15.75	1	1	1	1
533	CL15740Contig1	CL15740Contig1	15.71	1	1	1	1
534	CL45523Contig1	CL45523Contig1	15.70	1	1	1	1
535	Q6VEU9;CL6200Contig1	H+ transporting F1 ATP synthase epsilon subunit OS=Xen	15.69	3	1	1	12
536	BJ630382 homologue to UniRef100_Q6Y211 Cluster: S6	Rep: S6 ribosomal protein - Pagrus major (Red sea bream)	15.63	1	2	2	61
537	CL1377Contig4	CL1377Contig4	15.57	4	5	6	91
538	CL38685Contig1	CL38685Contig1	15.55	2	1	1	2
539	Q4QR44	MGC114789 protein OS=Xenopus laevis GN=rps15a PE=2	15.38	2	1	1	3
540	CL16992Contig1	CL16992Contig1	15.38	1	1	1	1
541	Q641B9	Actin-related protein 2/3 complex subunit 5 OS=Xenopus la	15.33	2	1	1	2
542	Q8AVR6	Hspc177-prov protein OS=Xenopus laevis GN=chmp5 PE=	15.25	2	1	1	1
543	dsrrswapns_comp119549_c0_seq1	len=256	15.19	1	1	1	1
544	dsrrswapns_comp217115_c6_seq8	len=796	15.15	2	1	1	1
545	Q5XHE4	LOC495023 protein OS=Xenopus laevis GN=paqr4 PE=2 S	15.07	1	1	1	1
546	CL1614Contig1	CL1614Contig1	15.00	5	2	2	11
547	EB473635 homologue to UniRef100_Q09TP6 Cluster: He	Rep: Heat shock protein 70 - Sphaeroforma arctica, partial	15.00	1	1	1	3
548	dsrrswapns_comp193683_c1_seq1	len=349	14.95	1	1	1	2
549	dsrrswapns_comp212436_c4_seq1	len=421	14.91	2	1	1	1
550	Q7SY98	MGC64309 protein OS=Xenopus laevis PE=2 SV=1 - [Q7S	14.85	4	1	6	64
551	Q5U583;CL2706Contig1	Probable glutathione peroxidase 8-B OS=Xenopus laevis G	14.83	5	1	1	3
552	Q640H4	LOC494673 protein OS=Xenopus laevis GN=cth PE=2 SV=	14.82	1	1	2	2
553	A8E5Y6;CL7871Contig1	LOC100126622 protein OS=Xenopus laevis GN=ninj1 PE=	14.79	2	1	1	4
554	D2WK21	Sex-determining region Y-box 2 OS=Xenopus laevis PE=2	14.79	2	1	1	1
555	CL23927Contig1	CL23927Contig1	14.77	1	1	1	1
556	G3GBS4	Peroxiredoxin 3 OS=Xenopus laevis GN=PRDX3 PE=2 SV	14.74	4	1	7	19
557	CL44634Contig1	CL44634Contig1	14.71	1	1	1	1
558	Q7ZYL1;CL5426Contig2	Proteasome subunit beta type OS=Xenopus laevis GN=psn	14.64	2	2	2	11
559	A2VD97	LOC100037195 protein OS=Xenopus laevis GN=mccc2 PE	14.59	3	3	3	20
560	Q7T0Y7;CL7862Contig1	2o545 protein OS=Xenopus laevis GN=ccdc25 PE=2 SV=1	14.56	3	2	2	10
561	CL1501Contig1	CL1501Contig1	14.53	2	1	1	1
562	DC014590 similar to UniRef100_Q4RTC7 Cluster: Chrom	Rep: Chromosome 1 SCAF14998, whole genome shotgun	14.49	3	1	1	1
563	CB943254 homologue to UniRef100_Q52KT5 Cluster: L	Rep: LOC733227 protein - Xenopus laevis (African clawed	14.47	3	1	1	1
564	CF270399	CF270399	14.43	2	1	1	2
565	Q5XGQ8;CL9736Contig1	LOC495164 protein OS=Xenopus laevis GN=tprg1l PE=2 S	14.39	2	1	2	3
566	Q66KZ5	MGC85294 protein OS=Xenopus laevis GN=MGC85294 P	14.38	2	1	1	1
567	Q6DEA5;CL11630Contig1	Pex26-prov protein OS=Xenopus laevis GN=pex26 PE=2 S	14.37	1	1	1	45
568	Q7T0W0;CL2874Contig1	Dihydrolipoyl dehydrogenase OS=Xenopus laevis GN=dld	14.34	5	3	3	75
569	dsrrswapns_comp211056_c0_seq10	len=1398	14.29	1	1	1	1
570	Q6INT6	MGC80342 protein OS=Xenopus laevis GN=aagab PE=2 S	14.24	1	1	1	1
571	Q0IHJ5	MGC154315 protein OS=Xenopus laevis GN=MGC154315	14.16	2	1	1	1
572	Q6GQ45	MGC80353 protein OS=Xenopus laevis GN=ndufb3 PE=4	14.12	3	1	1	2
573	Q712T4	Enhancer of split related 9 OS=Xenopus laevis GN=hes9.1	14.10	1	1	1	1
574	dsrrswapns_comp120180_c0_seq1	len=262	14.04	2	1	1	1
575	P21574	Y-box-binding protein 2-A OS=Xenopus laevis GN=ybx2-a	13.99	23	3	3	61
576	CL10115Contig1	CL10115Contig1	13.94	1	1	1	2
577	dsrrswapns_comp203196_c1_seq3	len=642	13.93	1	1	1	1
578	Q6DJK5;CL3918Contig1	CNDP dipeptidase 2 (Metallopeptidase M20 family) OS=Xe	13.92	6	5	5	73
579	Q6DE30	Oat-prov protein OS=Xenopus laevis GN=oat.1 PE=2 SV=1	13.90	6	3	3	73
580	TC460857 weakly similar to UniRef100_Q90ZY4 Cluster:	Rep: Serine/threonine-protein kinase SBK1 - Danio rerio (Z	13.89	1	1	1	1
581	Q5XHC7	LOC495037 protein OS=Xenopus laevis GN=LOC495037	13.87	1	1	1	1
582	BJ627598 similar to UniRef100_Q28DA4 Cluster: Novel t	Rep: Novel trypsin family protein - Xenopus tropicalis (West	13.79	1	1	1	1
583	A9ZS93	Transmembrane, prostate androgen induced RNA OS=Xen	13.78	2	1	1	2
584	CL18181Contig1	CL18181Contig1	13.73	2	2	2	14
585	CL38387Contig1	CL38387Contig1	13.71	1	1	1	1
586	dsrrswapns_comp50253_c0_seq1	len=235	13.64	1	1	1	1
587	CL665Contig1	CL665Contig1	13.61	1	2	5	10
588	Q7LZG8	Creatine kinase (Fragment) OS=Xenopus laevis PE=3 SV=	13.58	9	1	3	31
589	Q6DDF2	Acad9-prov protein OS=Xenopus laevis GN=acad9 PE=2 S	13.50	2	4	4	31
590	Q3B8B3;CL12613Contig1	MGC132191 protein OS=Xenopus laevis GN=uchl1 PE=2	13.45	2	3	3	20
591	CL11493Contig1	CL11493Contig1	13.43	1	1	1	1
592	CL33207Contig1	CL33207Contig1	13.41	1	1	1	2
593	Q3LH63	Doublesex- and mab-3-related transcription factor 1A OS=	13.39	1	1	1	1

594	CL14060Contig1	CL14060Contig1	13.33	1	1	1	2
595	Q91926	Homeobox protein vent1 OS=Xenopus laevis GN=vent1 PE	13.26	1	1	1	1
596	zeinaSSns_comp382047_c1_seq2	len=854	13.23	2	1	1	1
597	Q8UW77;CL1026Contig6	XEB1B OS=Xenopus laevis GN=mapre1 PE=2 SV=1 - [Q8U	13.22	13	2	2	53
598	Q6GLN6	MGC84462 protein OS=Xenopus laevis GN=MGC84462 PE	13.20	1	1	1	1
599	TC450147 weakly similar to UniRef100_UPI0000ECC61A	Rep: ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic A	13.19	2	1	1	5
600	Q6PAE3	MGC68448 protein OS=Xenopus laevis GN=MGC68448 PE	13.17	4	2	8	100
601	P46472;CL5541Contig2	26S protease regulatory subunit 7 OS=Xenopus laevis GN=	13.16	292	3	4	8
602	Q7ZY16;CL9256Contig2	Adsl-prov protein OS=Xenopus laevis GN=adsl PE=2 SV=1	13.12	3	3	3	58
603	CL84Contig2	CL84Contig2	13.10	1	1	1	1
604	O42587;CL492Contig6	26S protease regulatory subunit 6A-A OS=Xenopus laevis G	13.09	6	2	2	4
605	dsrrswapns_comp200563_c0_seq1	len=269	13.04	2	1	1	14
606	Q6NTX7;CL3174Contig3	Kcnab2 protein OS=Xenopus laevis GN=kcnab2 PE=2 SV=	13.03	4	1	1	3
607	Q66KN2	MGC85584 protein OS=Xenopus laevis GN=atp5j2 PE=4 S	12.94	2	1	1	7
608	Q4V7J2	LOC733264 protein (Fragment) OS=Xenopus laevis GN=LC	12.91	2	1	1	1
609	CL46044Contig1	CL46044Contig1	12.90	1	1	1	1
610	zeinaSSns_comp381133_c0_seq2	len=1342	12.86	1	1	1	1
611	Q6DDW1	MGC81675 protein OS=Xenopus laevis GN=txnl1 PE=2 SV	12.80	1	2	2	2
612	Q6INK1	MGC82415 protein OS=Xenopus laevis GN=MGC82415 PE	12.76	2	4	4	18
613	zeinaSSns_comp388513_c0_seq2	len=2561	12.75	1	1	1	2
614	A9JS79	Proteasome subunit beta type (Fragment) OS=Xenopus lae	12.65	6	3	3	10
615	CL26319Contig1	CL26319Contig1	12.59	1	1	1	2
616	dsrrswapns_comp216613_c0_seq1	len=4193	12.57	3	7	8	66
617	TC448972 homologue to UniRef100_Q5XHJ5 Cluster: Ar	Rep: Arginine/serine-rich coiled-coil protein 2 - Xenopus tro	12.57	1	1	1	1
618	zeinaSSns_comp389334_c0_seq3	len=1094	12.54	2	1	1	1
619	Q5U4L0;CL8653Contig1	LOC100101274 protein OS=Xenopus laevis GN=LOC1001	12.50	7	2	2	34
620	dsrrswapns_comp215243_c1_seq12	len=467	12.50	10	1	1	1
621	Q66KN4;CL12856Contig1	Mitochondrial NADH dehydrogenase ubiquinone 1 alpha su	12.50	1	1	1	2
622	CL13593Contig1	CL13593Contig1	12.42	1	1	1	1
623	Q8AVB5	Sfrs1 protein (Fragment) OS=Xenopus laevis GN=Sfrs1 PE	12.37	3	1	1	3
624	Q5M781;CL1453Contig4	Dynein light chain dlc8b OS=Xenopus laevis GN=dynll2 PE	12.36	3	1	1	13
625	Q7ZTJ1;CL468Contig4	Slc25a3-prov protein OS=Xenopus laevis GN=slc25a3 PE=	12.26	6	1	3	14
626	DC034728 homologue to UniRef100_Q7ZYF0 Cluster: H	Rep: Hdac6-prov protein - Xenopus laevis (African clawed f	12.24	1	1	1	1
627	A3KNF4	LOC100049121 protein OS=Xenopus laevis GN=LOC1000	12.24	2	1	1	11
628	Q3B8E3	Phospholysine phosphohistidine inorganic pyrophosphate p	12.22	1	1	1	1
629	BP686589 homologue to UniRef100_Q801N7 Cluster: LC	Rep: LOC398570 protein - Xenopus laevis (African clawed	12.20	3	1	1	1
630	CL12084Contig1	CL12084Contig1	12.18	1	1	1	3
631	Q66L24	MGC85230 protein OS=Xenopus laevis GN=atp5l PE=4 SV	12.15	3	1	1	11
632	dsrrswapns_comp210199_c6_seq1	len=1347	12.15	3	1	1	1
633	B7ZRR7	GATA binding factor-1b OS=Xenopus laevis GN=gata1b-A	12.09	1	1	1	1
634	dsrrswapns_comp215320_c1_seq2	len=1042	12.08	2	1	1	1
635	Q05AY5	LOC414691 protein OS=Xenopus laevis GN=LOC414691 F	12.06	5	1	1	1
636	A0AUU3	Cox7a2b protein OS=Xenopus laevis GN=cox7a2 PE=4 SV	12.05	2	1	1	1
637	Q801S2;CL3774Contig1	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	12.03	1	1	3	89
638	B7ZSI6	LOC100126641 protein OS=Xenopus laevis GN=LOC1001	12.01	2	1	1	2
639	Q7ZX30	Spx-prov protein OS=Xenopus laevis GN=sf3b4 PE=2 SV=	11.94	2	1	1	1
640	Q6AXB3;CL3237Contig1	MGC79128 protein OS=Xenopus laevis GN=shmt2 PE=2 S	11.90	3	2	4	42
641	CL921Contig2	CL921Contig2	11.90	2	1	1	2
642	Q5M9A1	LOC496155 protein OS=Xenopus laevis GN=wwtr1 PE=2 S	11.81	1	1	1	1
643	CL24495Contig1	CL24495Contig1	11.81	1	1	1	3
644	CL3255Contig1	CL3255Contig1	11.74	4	1	1	1
645	CL4566Contig2	CL4566Contig2	11.70	2	1	1	1
646	CL8785Contig2	CL8785Contig2	11.64	2	1	1	1
647	Q9DFC2	Homeobox protein XHox11L2 OS=Xenopus laevis GN=tlx3	11.64	1	1	1	1
648	CL1039Contig2	CL1039Contig2	11.63	1	1	1	1
649	BJ029212 UniRef100_Q7ZX42 Cluster: Cell division prot	Rep: Cell division protein kinase 9-B - Xenopus laevis (Afric	11.56	1	1	1	1
650	Q6DJQ1;CL8372Contig1	MGC81800 protein OS=Xenopus laevis GN=mgst3 PE=2 S	11.56	1	1	1	64
651	CL71Contig1	CL71Contig1	11.54	4	1	1	2
652	dsrrswapns_comp209900_c0_seq8	len=1568	11.50	1	1	1	1
653	CL2814Contig2	CL2814Contig2	11.45	1	1	1	1
654	Q7SZ11;CL1890Contig5	Annexin OS=Xenopus laevis PE=2 SV=1 - [Q7SZ11_XENL	11.37	8	3	3	28
655	dsrrswapns_comp213683_c2_seq3	len=1326	11.36	2	1	1	1
656	Q7T0W4	Vps28-prov protein OS=Xenopus laevis GN=vps28 PE=1 S	11.31	1	1	1	1
657	Q802B7;CL5322Contig1	Ndufs1-prov protein OS=Xenopus laevis GN=ndufs1 PE=2	11.28	2	5	5	35
658	dsrrswapns_comp211238_c0_seq3	len=1138	11.25	1	1	1	1
659	Q7ZYI5;CL3906Contig2	Baf53a-pending-prov protein OS=Xenopus laevis GN=actl6	11.19	1	1	1	5
660	CD362892 homologue to UniRef100_A5A6L4 Cluster: CD	Rep: CD74 molecule, major histocompatibility complex, clas	11.19	1	1	1	1
661	B1H1N8;CL525Contig5	LOC100036826 protein OS=Xenopus laevis GN=LOC1000	11.16	10	3	3	32
662	A4PB26	Protein CDV3 homolog B OS=Xenopus laevis GN=cdv3-b F	11.16	1	1	1	1
663	Q6AZV2;CL1314Contig1	Gcdh-prov protein OS=Xenopus laevis GN=gcdh PE=2 SV=	11.14	2	2	2	6
664	Q6NTQ9;CL7675Contig2	Ndufa10b protein OS=Xenopus laevis GN=ndufa10 PE=2 S	11.11	3	2	2	8
665	dsrrswapns_comp208039_c0_seq3	len=1233	11.04	1	1	1	1
666	Q5XG13	Putative uncharacterized protein OS=Xenopus laevis PE=2	11.04	3	2	2	2
667	P54824	ATP-dependent RNA helicase ddx6 OS=Xenopus laevis GN	11.02	292	3	4	10
668	TC444012 homologue to UniRef100_UPI00004D2264 Clu	Rep: DnaJ homolog subfamily C member 14 (Dopamine rec	11.00	1	1	1	1
669	dsrrswapns_comp211746_c0_seq9	len=685	10.97	2	1	1	2
670	CD362591 weakly similar to UniRef100_Q07497 Cluster:	Rep: Ephrin type-B receptor 5 precursor - Gallus gallus (Ch	10.96	1	1	1	1
671	CL5368Contig2	CL5368Contig2	10.93	1	2	2	3
672	Q91868	Rat translocon-associated protein delta homolog OS=Xeno	10.92	1	1	1	2
673	Q4KLF3	Protein KTI12 homolog OS=Xenopus laevis GN=kti12 PE=	10.91	290	1	2	2
674	Q8AVU2	Ubiquitin-conjugating enzyme E2 S-B OS=Xenopus laevis G	10.90	1	1	1	1
675	CL11663Contig1	CL11663Contig1	10.86	2	2	2	3
676	Q6DDF9	MGC84581 protein OS=Xenopus laevis GN=MGC84581 PE	10.85	2	2	2	2
677	Q5XGQ1	LOC495170 protein OS=Xenopus laevis GN=LOC495170 F	10.84	1	1	1	1
678	Q5XGR8	Beta-lactamase-like protein 2 OS=Xenopus laevis GN=lact	10.80	227	1	2	2
679	Q0IHC9	MGC154449 protein OS=Xenopus laevis GN=nif3l1 PE=2 S	10.76	1	1	1	1

680	EB465665 weakly similar to UniRef100_Q8BGZ7 Cluster:	Rep: Keratin, type II cytoskeletal 75 - Mus musculus (Mous	10.71	1	1	1	1
681	C0J6M5	MEF2A alpha 12b isoform OS=Xenopus laevis PE=2 SV=1	10.71	1	1	1	3
682	Q7ZTB3;CL289Contig3	Heat shock protein gp96 OS=Xenopus laevis GN=hsp90b1	10.70	4	1	7	174
683	Q91840;CL994Contig4	Retinoid X receptor beta OS=Xenopus laevis GN=rxrb PE=	10.68	9	2	2	3
684	Q7ZWW3;CL7106Contig1	Ferritin OS=Xenopus laevis PE=2 SV=1 - [Q7ZWW3_XENL	10.67	3	2	2	27
685	CL4179Contig3	CL4179Contig3	10.66	5	1	2	5
686	Q6DE33;CL4688Contig1	Uqcrc2 protein OS=Xenopus laevis GN=uqcrc2 PE=2 SV=1	10.64	4	3	3	66
687	Q7ZXI5;CL2254Contig3	Snf protein OS=Xenopus laevis GN=snrpa PE=2 SV=1 - [Q	10.64	3	1	1	3
688	Q4VAE4	MGC115325 protein OS=Xenopus laevis GN=MGC115325	10.63	1	1	1	1
689	Q2T9K3	MGC131110 protein OS=Xenopus laevis GN=MGC131110	10.61	1	1	1	1
690	CL39443Contig1	CL39443Contig1	10.59	1	2	2	2
691	Q4QR21	Putative uncharacterized protein (Fragment) OS=Xenopus l	10.58	1	1	1	1
692	CL4774Contig1	CL4774Contig1	10.57	4	2	2	19
693	Q5PPY1;TC467635 similar to UniRef100_Q53DG9 Clust	Malignant T-cell-amplified sequence 1-A OS=Xenopus laev	10.50	2	1	1	5
694	Q6P7F8;CL9604Contig1	MGC68767 protein OS=Xenopus laevis GN=napsa PE=2 S	10.46	1	1	1	2
695	CL40442Contig1	CL40442Contig1	10.45	2	1	1	1
696	Q7SZ43	Mylc2a-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q7S	10.40	3	1	1	1
697	Q7ZXG1	Smarcd1 protein (Fragment) OS=Xenopus laevis GN=Smar	10.40	5	1	1	2
698	CL1Contig1051	CL1Contig1051	10.34	1	1	1	1
699	Q6DKA5	MGC84756 protein OS=Xenopus laevis GN=hsd17b11 PE=	10.33	2	1	1	1
700	Q8AXY7	Pygopus-2beta OS=Xenopus laevis PE=2 SV=1 - [Q8AXY7	10.33	1	1	1	1
701	Q52KV8	MGC115036 protein OS=Xenopus laevis GN=MGC115036	10.32	1	1	1	1
702	CL728Contig4	CL728Contig4	10.31	1	1	1	1
703	dsrrswapns_comp187784_c0_seq1	len=329	10.31	1	1	1	1
704	CX133910	CX133910	10.28	4	1	1	1
705	TC453615 similar to UniRef100_Q6GQ25 Cluster: MGC8	Rep: MGC80407 protein - Xenopus laevis (African clawed f	10.26	3	1	1	1
706	P79937	Homeobox protein Meis1 OS=Xenopus laevis GN=meis1 P	10.26	5	2	2	2
707	CL5749Contig1	CL5749Contig1	10.24	3	2	2	79
708	CL32735Contig1	CL32735Contig1	10.23	1	1	1	1
709	Q6NUB1	MGC81092 protein OS=Xenopus laevis GN=thul16 PE=2 S	10.23	1	1	1	1
710	Q90ZB7	Lymphoid enhancer factor XLEF-1B OS=Xenopus laevis G	10.22	2	1	1	1
711	CL13504Contig1	CL13504Contig1	10.21	1	1	1	1
712	CL23092Contig1	CL23092Contig1	10.19	1	1	1	1
713	TC465972 similar to UniRef100_UPI000065DF7B Cluster	Rep: Probable ATP-dependent RNA helicase DHX37 (EC 3	10.14	1	1	1	1
714	TC467277 homologue to UniRef100_Q9I8T0 Cluster: Cal	Rep: Calpain - Xenopus laevis (African clawed frog), partial	10.14	1	1	1	1
715	CL12250Contig1	CL12250Contig1	10.12	2	1	1	1
716	CL26381Contig1	CL26381Contig1	10.07	2	1	1	1
717	B7ZR65	Transcription factor Sox-9-A OS=Xenopus laevis GN=sox9-	10.06	1	1	1	1
718	Q708W2	Forkhead box protein J1-A OS=Xenopus laevis GN=foxj1-a	10.02	1	1	1	1
719	Q4QQP6;CL19376Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2	10.00	200	1	2	5
720	dsrrswapns_comp192152_c0_seq1	len=453	10.00	2	1	1	1
721	B1WBD3	LOC100158432 protein OS=Xenopus laevis GN=aars PE=	9.92	3	4	4	5
722	Q3B8D3	MGC68480 protein OS=Xenopus laevis GN=MGC68480 PE	9.91	4	1	1	20
723	Q6AZN8;CL5215Contig3	Zinc transporter 6-A OS=Xenopus laevis GN=slc30a6-a PE	9.91	1	1	1	7
724	A2VDC7	Ribonuclease kappa-A OS=Xenopus laevis GN=rnasek-a P	9.90	2	1	1	2
725	Q6IRA2;CL1Contig101	XTm4 protein OS=Xenopus laevis GN=XTm4 PE=2 SV=1 -	9.87	30	1	1	2
726	Q0IHG7	Stk4 protein OS=Xenopus laevis GN=stk4 PE=2 SV=1 - [Q	9.83	1	1	1	1
727	Q6GR45;dsrrswapns_comp203528_c0_seq3	Eukaryotic translation initiation factor 6 OS=Xenopus laevis	9.80	2	1	1	5
728	Q8QFV1	Isthmin OS=Xenopus laevis GN=ism1 PE=2 SV=1 - [ISM_X	9.80	1	1	1	1
729	TC462923 UniRef100_Q7ZXK8 Cluster: Hnrpk protein; n	Rep: Hnrpk protein - Xenopus laevis (African clawed frog),	9.78	1	1	1	1
730	CL32492Contig1	CL32492Contig1	9.75	1	1	1	3
731	Q68EX4	Proteasome subunit beta type OS=Xenopus laevis GN=psm	9.75	230	1	2	3
732	CL4179Contig1	CL4179Contig1	9.73	4	1	2	9
733	CL31289Contig1	CL31289Contig1	9.73	1	1	1	1
734	Q6DDM0	MGC83329 protein OS=Xenopus laevis GN=MGC83329 PE	9.70	544	1	3	3
735	B5MFE9	Olfactomedin-like protein 3 OS=Xenopus laevis GN=olfml3	9.69	1	1	1	1
736	CL8066Contig1	CL8066Contig1	9.68	2	1	1	1
737	dsrrswapns_comp216043_c4_seq13	len=2424	9.68	1	1	1	1
738	CL22Contig18	CL22Contig18	9.63	5	1	1	10
739	Q58E21	Proteasome subunit alpha type OS=Xenopus laevis GN=ps	9.58	6	2	2	13
740	Q3B8J8	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit,	9.57	7	3	3	12
741	Q0IHF9	Store-operated calcium entry-associated regulatory factor C	9.57	1	1	1	1
742	Q52KN0;CL14329Contig1	MGC115198 protein OS=Xenopus laevis GN=MGC115198	9.54	1	1	1	8
743	Q6GM67	MGC83388 protein OS=Xenopus laevis GN=MGC83388 PE	9.49	1	1	1	2
744	dsrrswapns_comp215263_c2_seq3	len=1750	9.47	3	1	1	2
745	Q8AVS4	Transcriptional activator protein Pur-beta-B OS=Xenopus la	9.45	1	1	1	1
746	Q6DCL1	MGC82412 protein OS=Xenopus laevis GN=bpnt1 PE=2 S	9.42	2	1	1	2
747	CL4493Contig1	CL4493Contig1	9.41	2	1	1	1
748	A2RV96	LOC496076 protein OS=Xenopus laevis GN=lrrc34 PE=2 S	9.40	1	1	1	1
749	P55863	Transcription factor Sox-3-A OS=Xenopus laevis GN=sox3-	9.39	1	1	1	1
750	Q6GNR9	Dolichyl-diphosphooligosaccharide--protein glycosyltransfer	9.36	1	1	1	1
751	CL3508Contig1	CL3508Contig1	9.35	4	1	1	2
752	CL9213Contig2	CL9213Contig2	9.31	1	1	1	2
753	Q05AW6;CL3514Contig2	MGC154502 protein OS=Xenopus laevis GN=MGC154502	9.31	2	1	1	2
754	dsrrswapns_comp198030_c0_seq1	len=1959	9.25	3	1	1	1
755	Q9W7F2;CL2204Contig2	WD repeat-containing protein 1-A OS=Xenopus laevis GN=	9.23	8	3	3	17
756	Q7ZYM3;CL5801Contig1	Gpd1 protein OS=Xenopus laevis GN=gpd1 PE=2 SV=2 - [	9.20	1	1	1	5
757	Q6IP53;CL7135Contig1	MGC78949 protein OS=Xenopus laevis GN=tekt1 PE=2 SV	9.20	3	2	2	3
758	Q6AZM8	Sh3glb2-prov protein OS=Xenopus laevis GN=sh3glb2 PE=	9.18	1	1	1	1
759	Q05AY9	LOC398450 protein OS=Xenopus laevis GN=LOC398450	9.15	7	2	2	20
760	Q2VPL7	LOC733431 protein (Fragment) OS=Xenopus laevis GN=L	9.12	2	2	2	5
761	Q6DJP2	MGC81911 protein OS=Xenopus laevis GN=ech1 PE=2 SV	9.12	2	2	2	4
762	A2VDD2	Tctex1 domain-containing protein 1-B (Fragment) OS=Xeno	9.09	2	1	1	1
763	zeinaSSns_comp338451_c0_seq1	len=210	9.09	1	1	1	1
764	CL3908Contig1	CL3908Contig1	9.09	1	1	1	1
765	Q7SZB0;CL1525Contig1	Rpl35a-prov protein OS=Xenopus laevis GN=rpl35a PE=4	9.09	4	1	1	3

766	dsrrswapns_comp209500_c1_seq3	len=1654	9.03	2	1	1	1
767	A1L2I8	LOC100036860 protein OS=Xenopus laevis GN=LOC1000	9.03	2	1	1	1
768	B7ZS71	Putative uncharacterized protein OS=Xenopus laevis PE=2	9.00	6	2	2	2
769	dsrrswapns_comp211447_c1_seq1	len=2210	9.00	3	1	3	3
770	Q2T9K2	Transcription factor AP-2-epsilon OS=Xenopus laevis GN=t	8.99	1	1	1	1
771	DT076135 homologue to UniRef100_Q0VFQ9 Cluster: S	Rep: Selenophosphate synthetase 2 - Xenopus tropicalis (	8.86	2	1	1	1
772	Q6DCF9;CL15Contig5	Annexin OS=Xenopus laevis GN=anxa7 PE=2 SV=1 - [Q6	8.85	293	2	3	26
773	CL2457Contig1	CL2457Contig1	8.84	2	1	1	2
774	CL14648Contig1	CL14648Contig1	8.84	2	2	2	6
775	A9UM22	LOC100137679 protein (Fragment) OS=Xenopus laevis G	8.81	2	1	1	2
776	dsrrswapns_comp215430_c0_seq1	len=990	8.81	1	1	1	1
777	Q7ZTJ4	Vha55 protein OS=Xenopus laevis GN=atp6v1b2 PE=2 SV	8.81	1	2	2	2
778	Q63ZU5	LOC494732 protein OS=Xenopus laevis GN=tsc22d1 PE=	8.76	1	1	1	1
779	CL282Contig6	CL282Contig6	8.72	5	1	1	2
780	A2BD73	LOC100037109 protein (Fragment) OS=Xenopus laevis G	8.72	1	1	1	1
781	Q5U484	LOC495520 protein (Fragment) OS=Xenopus laevis GN=L	8.71	3	1	1	3
782	Q1JQ83	MGC130971 protein OS=Xenopus laevis GN=scml2 PE=2	8.71	227	2	3	3
783	Q66KT2	MGC85457 protein OS=Xenopus laevis GN=ndufs8 PE=2	8.70	3	1	1	46
784	Q6GPD6;CL2008Contig2	MGC80474 protein OS=Xenopus laevis GN=cnpy2 PE=2 S	8.70	1	1	1	7
785	Q6IRP1	Grx5-prov protein (Fragment) OS=Xenopus laevis GN=grx5	8.67	3	1	1	2
786	CL19751Contig1	CL19751Contig1	8.66	2	1	1	2
787	Q7ZWX9	Midnolin-B OS=Xenopus laevis GN=midn-b PE=2 SV=1 - [	8.65	1	1	1	1
788	CL17316Contig1	CL17316Contig1	8.65	1	1	1	1
789	A5D8M8	LOC100049751 protein OS=Xenopus laevis GN=nqo1 PE=	8.63	2	1	1	2
790	Q7ZYS4;CL2863Contig4	MGC53685 protein OS=Xenopus laevis GN=MGC53685 P	8.62	2	1	1	2
791	dsrrswapns_comp204377_c0_seq2	len=847	8.62	2	1	1	1
792	Q2TAT7;CL10539Contig1	MGC130882 protein OS=Xenopus laevis GN=uqcrq PE=4	8.54	3	1	1	3
793	CL25612Contig1	CL25612Contig1	8.52	1	1	1	1
794	O13097;CL3156Contig1	Ephrin-B1 OS=Xenopus laevis GN=efnb1 PE=2 SV=2 - [EF	8.51	1	1	1	3
795	Q5U498	LOC495510 protein OS=Xenopus laevis GN=nxpe2 PE=2	8.49	3	1	1	3
796	Q66KU5;TC432828 UniRef100_Q66KU5 Cluster: MGC8	MGC85428 protein OS=Xenopus laevis GN=rpl36a PE=3 S	8.49	5	1	1	9
797	Q9PVY8	Forkhead box protein C2-B OS=Xenopus laevis GN=foxc2-	8.46	1	1	1	2
798	CL120Contig6	CL120Contig6	8.45	3	1	3	3
799	Q6E2P0	Urocortin 3 OS=Xenopus laevis GN=ucn3 PE=2 SV=1 - [Q	8.44	253	1	2	121
800	Q3B8H6	Pofut1 protein OS=Xenopus laevis GN=pofut1 PE=2 SV=1	8.42	2	1	1	1
801	CL791Contig1	CL791Contig1	8.41	1	1	1	1
802	A1L2I5;CL5868Contig1	Histone H2A OS=Xenopus laevis GN=h2afy PE=2 SV=1 - [	8.40	1	1	1	2
803	Q5M7C6	Glutathione peroxidase OS=Xenopus laevis GN=gpx1 PE=	8.39	1	1	1	2
804	TC448187 homologue to UniRef100_UPI00006A003E Cl	Rep: Tripartite motif-containing protein 44 (Protein DIPB). -	8.38	3	1	1	1
805	Q5M7A9	MGC81803 protein OS=Xenopus laevis GN=MGC81803 P	8.37	228	1	2	2
806	dsrrswapns_comp215388_c4_seq3	len=2200	8.33	2	1	1	3
807	Q98SU0	K-Cl cotransporter (Fragment) OS=Xenopus laevis GN=KC	8.31	1	1	1	3
808	Q6DE67	Putative uncharacterized protein OS=Xenopus laevis PE=2	8.29	1	1	1	1
809	CL6737Contig1	CL6737Contig1	8.28	1	1	1	1
810	Q3KQ55	MGC130949 protein OS=Xenopus laevis GN=uevld PE=2	8.22	1	1	1	1
811	Q63ZJ1	LOC494796 protein OS=Xenopus laevis GN=suclg1 PE=2	8.21	3	1	1	51
812	Q6GPL6	MGC83560 protein OS=Xenopus laevis GN=gca PE=2 SV=	8.21	2	1	2	2
813	Q6DFT8;CL48Contig18	Bcap31 protein OS=Xenopus laevis GN=bcap31 PE=2 SV=	8.20	3	1	1	12
814	A3KNC9	LOC100049107 protein OS=Xenopus laevis GN=zfp161 P	8.19	1	1	1	1
815	CL5478Contig2	CL5478Contig2	8.18	1	1	1	2
816	Q6GN63;CL5122Contig1	MGC82998 protein OS=Xenopus laevis GN=idh3a PE=2 S	8.15	2	3	3	21
817	Q6GM08;CL9083Contig1	MGC84065 protein OS=Xenopus laevis GN=ntm PE=2 SV=	8.12	1	1	1	3
818	Q05116;dsrrswapns_comp213483_c2_seq6	Dual specificity mitogen-activated protein kinase kinase 1 O	8.10	1	1	1	4
819	TC444688 UniRef100_Q7T0N7 Cluster: Ctsc protein; n=1	Rep: Ctsc protein - Xenopus laevis (African clawed frog), c	8.08	4	1	2	5
820	Q5M9A9	LOC496147 protein OS=Xenopus laevis GN=LOC496147	8.07	1	1	1	1
821	BQ400069 similar to UniRef100_UPI000069DA2D Cluste	Rep: Tyrosine-protein kinase receptor Tie-1 precursor (EC	8.05	2	1	1	2
822	Q640C3	LOC494728 protein OS=Xenopus laevis GN=umps PE=2 S	8.03	1	1	1	1
823	Q566F3;CL9914Contig1	MGC114950 protein OS=Xenopus laevis GN=slc45a2 PE=	8.03	1	1	1	2
824	Q5IJ69;CL32Contig6	MTGR1 OS=Xenopus laevis PE=2 SV=1 - [Q5IJ69_XENLA	8.02	3	1	1	3
825	TC454792 UniRef100_Q0IH35 Cluster: MGC154791 prot	Rep: MGC154791 protein - Xenopus laevis (African clawed	8.00	6	1	1	3
826	Q90YE5;CL4860Contig2	MAD, mothers against decapentaplegic homolog 3 OS=Xe	8.00	2	1	1	4
827	CL11416Contig1	CL11416Contig1	7.99	1	1	1	1
828	BJ042996 weakly similar to UniRef100_A4QN64 Cluster:	Rep: Zgc:162320 protein - Danio rerio (Zebrafish) (Brachyd	7.98	5	1	1	2
829	Q5FWN6	MGC85173 protein OS=Xenopus laevis GN=tbc1d19 PE=2	7.97	1	1	1	1
830	dsrrswapns_comp208635_c0_seq2	len=771	7.95	1	1	1	1
831	CL13058Contig1	CL13058Contig1	7.92	3	1	1	2
832	P05377	Acetylcholine receptor subunit alpha-1-B OS=Xenopus laev	7.88	2	1	1	1
833	Q2NLB0	UPF0469 protein KIAA0907 homolog OS=Xenopus laevis	7.86	1	1	1	1
834	Q6EE56	Aminolevulinic acid synthase 1 (Fragment) OS=Xenopus la	7.85	1	1	1	1
835	Q4KL91;CL4667Contig1	Proton-coupled amino acid transporter 4 OS=Xenopus laev	7.85	1	1	1	7
836	dsrrswapns_comp209464_c0_seq2	len=2027	7.84	2	1	1	1
837	Q0IH27	Hmg20b protein OS=Xenopus laevis GN=hmg20b PE=2 S	7.84	1	1	1	1
838	Q6DCS5	MGC80849 protein OS=Xenopus laevis GN=MGC80849 P	7.83	1	1	1	1
839	A5D8M0	Tyrosyl-DNA phosphodiesterase 2 OS=Xenopus laevis GN	7.82	1	1	1	1
840	Q7ZTK9;CL7196Contig1	Aspartate aminotransferase OS=Xenopus laevis GN=got1	7.79	291	2	3	8
841	Q6GQ37;CL8951Contig1	Protein midA homolog, mitochondrial OS=Xenopus laevis P	7.78	1	1	1	2
842	dsrrswapns_comp195977_c0_seq1	len=790	7.76	1	1	1	7
843	Q8AVW5;CL253Contig3	Ywhaz-prov protein OS=Xenopus laevis GN=ywhaz PE=2	7.76	5	1	2	42
844	CL7064Contig1	CL7064Contig1	7.71	1	1	1	1
845	P08478;CL660Contig2	Peptidyl-glycine alpha-amidating monooxygenase A OS=X	7.70	3	2	2	4
846	Q8QFW7;CL1631Contig2	Ribosomal protein L34 OS=Xenopus laevis GN=rpl34 PE=4	7.69	2	1	1	18
847	Q6P412;CL2784Contig1	MGC68722 protein OS=Xenopus laevis GN=rab15 PE=2 S	7.69	67	1	1	6
848	CL14445Contig1	CL14445Contig1	7.66	3	1	1	1
849	CL9501Contig1	CL9501Contig1	7.66	1	1	1	1
850	Q6IP78	LOC432230 protein (Fragment) OS=Xenopus laevis GN=L	7.62	5	3	3	6
851	Q6GQD7;CL206Contig9	AT-rich interactive domain-containing protein 3A OS=Xeno	7.61	2	1	1	2

852	Q5U491	LOC495515 protein (Fragment) OS=Xenopus laevis GN=LC	7.61	4	2	2	8
853	A2BD52	LOC100158263 protein (Fragment) OS=Xenopus laevis GN	7.61	3	1	1	1
854	Q32NU1;CL3333Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2	7.61	4	1	1	2
855	CL2859Contig3	CL2859Contig3	7.60	4	1	1	1
856	Q6DF71	MGC84640 protein OS=Xenopus laevis GN=znf484 PE=2 S	7.60	1	1	1	1
857	Q4V7J4	MGC115652 protein OS=Xenopus laevis GN=MGC115652	7.59	1	1	1	1
858	dsrrswapns_comp212910_c2_seq5	len=1878	7.58	2	1	1	3
859	A5PKN2	LOC100101285 protein (Fragment) OS=Xenopus laevis GN	7.56	1	1	1	1
860	Q8AVR4	Programmed cell death protein 10 OS=Xenopus laevis GN=	7.55	1	1	1	1
861	Q6GQ40;CL5428Contig3	Proteasome subunit beta type OS=Xenopus laevis GN=psm	7.54	3	1	1	3
862	Q66IY6;CL4803Contig1	MGC84052 protein OS=Xenopus laevis GN=psmd7 PE=2 S	7.50	5	1	1	8
863	Q6NTP6	Psmd2 protein OS=Xenopus laevis GN=psmd2 PE=2 SV=1	7.47	6	3	3	32
864	dsrrswapns_comp214578_c4_seq1	len=1260	7.44	2	1	1	2
865	Q66J64	MGC81783 protein OS=Xenopus laevis GN=fam222b PE=2	7.44	1	1	1	1
866	Q67FQ3	Low density lipoprotein receptor adapter protein 1-B OS=Xe	7.44	1	1	1	1
867	Q9IAB1	Putative uncharacterized protein (Fragment) OS=Xenopus l	7.44	3	1	1	1
868	Q7SZ14	MGC64316 protein OS=Xenopus laevis GN=ndufa9 PE=2 S	7.43	3	2	2	4
869	B1NA55	FcR-like protein (Fragment) OS=Xenopus laevis GN=XFL1.	7.42	256	1	2	2
870	CL16239Contig1	CL16239Contig1	7.41	1	1	1	1
871	Q6PB20;CL2763Contig1	MGC68482 protein OS=Xenopus laevis GN=bace2 PE=2 S	7.41	1	1	1	4
872	dsrrswapns_comp193427_c0_seq1	len=532	7.41	1	1	1	1
873	Q7ZXM6	Sfrp2-prov protein OS=Xenopus laevis GN=sfrp2 PE=2 SV=	7.38	1	1	1	1
874	Q6DJP0;CL2037Contig1	LOC100137615 protein OS=Xenopus laevis GN=gclc PE=2	7.38	252	1	2	3
875	Q6NTJ0	LOC414678 protein (Fragment) OS=Xenopus laevis GN=LC	7.38	8	1	1	5
876	Q6DDQ5	Protein phosphatase 1 regulatory subunit 3C OS=Xenopus	7.36	2	1	1	1
877	A5PKR6	LOC100101313 protein OS=Xenopus laevis GN=crym PE=	7.35	2	1	1	1
878	TC441790 homologue to UniRef100_Q0D2D3 Cluster: Fr	Rep: Fry protein - Xenopus tropicalis (Western clawed frog)	7.35	1	1	1	1
879	B7ZRN2	Putative uncharacterized protein OS=Xenopus laevis PE=2	7.33	2	1	1	1
880	dsrrswapns_comp217423_c2_seq11	len=1879	7.32	2	1	1	2
881	TC445670 homologue to UniRef100_Q6NX33 Cluster: My	Rep: Myosin heavy chain - Xenopus tropicalis (Western clav	7.31	3	1	1	1
882	A1L2S7	LOC100036938 protein OS=Xenopus laevis GN=LOC1000	7.30	2	1	1	1
883	Q52KW6;TC418765 UniRef100_Q52KW6 Cluster: MGC1	MGC115285 protein OS=Xenopus laevis GN=MGC115285	7.27	1	1	1	2
884	Q6DKC0;CL24Contig3	Erlin-2-B OS=Xenopus laevis GN=erlin2-b PE=2 SV=1 - [EF	7.27	3	2	2	6
885	CL5779Contig1	CL5779Contig1	7.26	1	1	1	1
886	Q6DEC9;CL9001Contig1	D-tyrosyl-tRNA(Tyr) deacylase OS=Xenopus laevis GN=dtd	7.25	1	1	1	2
887	B7ZR33	GATA binding factor-1 OS=Xenopus laevis GN=gata1a-A P	7.24	2	1	1	1
888	Q640X7	MGC84330 protein OS=Xenopus laevis GN=capns1 PE=2	7.23	1	1	1	1
889	Q6GM94;CL4854Contig2	MGC68458 protein OS=Xenopus laevis GN=abat PE=2 SV	7.20	3	1	2	17
890	TC435750 homologue to UniRef100_O93522 Cluster: No	Rep: Nonmuscle myosin II heavy chain A - Xenopus laevis	7.20	1	1	1	3
891	Q6GPB1;CL1907Contig3	MGC80559 protein OS=Xenopus laevis GN=ammecr1l PE=	7.19	227	1	2	4
892	Q6AZJ6	Fascin (Fragment) OS=Xenopus laevis GN=FSCN1 PE=2 S	7.17	7	2	2	7
893	Q7ZXX4;CL6920Contig1	MGC52697 protein OS=Xenopus laevis GN=aldh9a1 PE=2	7.14	1	2	2	9
894	Q5U4W0;CL2471Contig1	Entpd4 protein OS=Xenopus laevis GN=entpd4 PE=2 SV=1	7.14	4	2	2	6
895	Q7ZX74	MGC53501 protein OS=Xenopus laevis GN=ccdc6 PE=2 SV	7.13	292	1	2	2
896	Q2TAS0	MGC130982 protein OS=Xenopus laevis GN=tjap1 PE=2 S	7.12	1	1	1	4
897	A9ULW5;CL11158Contig1	LOC100137631 protein OS=Xenopus laevis GN=acot13 PE	7.09	1	1	1	5
898	Q7T0V9	MGC68941 protein OS=Xenopus laevis GN=asb12.2 PE=2	7.07	1	1	1	1
899	zeinaSSns_comp388666_c2_seq5	len=2890	7.06	3	1	1	8
900	CL1907Contig1	CL1907Contig1	7.06	1	1	1	3
901	Q6GP54	LOC443639 protein (Fragment) OS=Xenopus laevis GN=LC	7.02	2	1	1	1
902	Q68FK6	MGC82138 protein OS=Xenopus laevis GN=arfgap2 PE=2	7.02	1	1	1	1
903	Q7ZWU1;CL4166Contig1	Stip1-prov protein OS=Xenopus laevis GN=stip1 PE=2 SV=	7.00	2	2	2	8
904	CL1396Contig2	CL1396Contig2	7.00	1	1	1	1
905	Q66KZ8	Glutathione S-transferase (Fragment) OS=Xenopus laevis	6.98	3	1	1	2
906	Q6DDM7;CL6675Contig1	Acadl-prov protein OS=Xenopus laevis GN=acadl PE=2 SV	6.98	1	2	2	12
907	A0JPH8;CL13915Contig1	LOC100036800 protein OS=Xenopus laevis GN=LOC1000	6.97	1	2	2	50
908	zeinaSSns_comp381925_c1_seq1	len=669	6.97	2	1	1	1
909	Q6GND5	MGC82876 protein OS=Xenopus laevis GN=dnajb12 PE=2	6.97	1	1	1	1
910	Q6IRP2;CL11620Contig1	MGC83164 protein OS=Xenopus laevis GN=MGC83164 PE	6.96	2	2	2	12
911	Q6GM59;CL3818Contig1	Monocarboxylate transporter 12 OS=Xenopus laevis GN=sl	6.96	2	1	1	2
912	Q3KPT7	3-hydroxybutyrate dehydrogenase type 2 OS=Xenopus laev	6.94	2	1	1	1
913	B7ZS08	Ago61 protein OS=Xenopus laevis GN=ago61 PE=2 SV=1	6.92	2	1	1	1
914	Q5XGQ2	LOC495169 protein OS=Xenopus laevis GN=pdia4 PE=2 S	6.91	3	3	3	12
915	Q6GPB7	4-hydroxyphenylpyruvate dioxygenase OS=Xenopus laevis	6.91	1	1	1	1
916	CL5205Contig2	CL5205Contig2	6.90	3	2	2	3
917	CL7679Contig1	CL7679Contig1	6.89	1	1	1	1
918	Q2TAD9	Cysteine and histidine-rich protein 1-B OS=Xenopus laevis	6.85	1	1	1	1
919	Q3KPV4;CL10181Contig1	Transmembrane and ubiquitin-like domain-containing protei	6.82	1	1	1	4
920	CL12947Contig1	CL12947Contig1	6.81	2	1	1	2
921	Q6DD25	UBXD2 protein (Fragment) OS=Xenopus laevis GN=UBXD	6.78	1	1	1	1
922	Q91685	Homeobox protein Mix.2 OS=Xenopus laevis GN=mix-b PE	6.78	227	1	2	2
923	Q6DDP5	Ola1 protein OS=Xenopus laevis GN=ola1 PE=2 SV=1 - [Q	6.76	2	1	1	1
924	Q5U576;CL11909Contig1	LOC495345 protein OS=Xenopus laevis GN=gpr85 PE=2 S	6.76	227	1	2	3
925	B7ZRR5	Xebf-3 protein OS=Xenopus laevis GN=Xebf-3 PE=2 SV=1	6.70	2	1	1	1
926	CL303Contig2	CL303Contig2	6.70	2	1	3	12
927	dsrrswapns_comp205246_c0_seq2	len=1846	6.69	1	1	1	1
928	Q6DFI3	Tst-prov protein OS=Xenopus laevis GN=mpst PE=2 SV=1	6.69	1	1	1	1
929	dsrrswapns_comp188169_c1_seq1	len=2289	6.67	1	1	1	4
930	dsrrswapns_comp203662_c1_seq1	len=998	6.67	1	1	1	1
931	zeinaSSns_comp375133_c1_seq1	len=290	6.67	2	1	1	1
932	A2VD74	LOC100037179 protein OS=Xenopus laevis GN=mep1a PE	6.67	1	1	1	1
933	Q6GQH7	Putative uncharacterized protein (Fragment) OS=Xenopus l	6.67	2	1	1	1
934	Q5XH63;CL3193Contig1	LOC495055 protein OS=Xenopus laevis GN=LOC495055 F	6.60	4	1	1	19
935	CX133552 homologue to UniRef100_UPI00004D5784 Clu	Rep: Uncharacterized protein C21orf59. - Xenopus tropicali	6.60	1	1	1	1
936	Q5PQ95;CL11117Contig1	LOC495941 protein OS=Xenopus laevis GN=LOC495941 F	6.58	1	2	2	3
937	Q4KLA5	MGC84800 protein OS=Xenopus laevis GN=MGC84800 PE	6.58	3	1	1	1

938	Q9I9L2	Cbl proto-oncogene protein (Fragment) OS=Xenopus laevis	6.55	1	1	1	1
939	CL7498Contig1	CL7498Contig1	6.54	2	2	2	9
940	Q801S7	Uba1a protein OS=Xenopus laevis GN=uba1a PE=2 SV=1	6.52	7	2	3	6
941	Q6PAW6	MGC68638 protein OS=Xenopus laevis GN=MGC68638 PE	6.52	252	1	2	2
942	Q7ZY92	Lect1-prov protein OS=Xenopus laevis GN=lect1 PE=2 SV=	6.51	3	1	1	1
943	Q6INQ1;CL8291Contig1	MGC81422 protein OS=Xenopus laevis GN=bysl PE=2 SV=	6.50	1	1	1	4
944	Q6INM6;CL1435Contig4	MGC82347 protein OS=Xenopus laevis GN=MGC82347 PE	6.48	1	1	1	4
945	CL25284Contig1	CL25284Contig1	6.43	1	1	1	1
946	Q6GPL5	MGC83562 protein OS=Xenopus laevis GN=atpbd4 PE=2	6.42	1	1	1	2
947	Q6GLL5;CL9439Contig2	MGC84748 protein OS=Xenopus laevis GN=fgl1 PE=2 SV=	6.39	1	1	1	3
948	CL37975Contig1	CL37975Contig1	6.38	1	1	1	1
949	Q52KZ3	LOC733223 protein (Fragment) OS=Xenopus laevis GN=L	6.38	1	1	1	1
950	CL43176Contig1	CL43176Contig1	6.36	1	1	1	1
951	Q8AVH1;CL1313Contig1	Histone-binding protein RBBP7 OS=Xenopus laevis GN=rb	6.35	5	1	1	4
952	Q2VPH6	LOC432342 protein OS=Xenopus laevis GN=cops2 PE=2	6.32	252	1	2	2
953	CL9635Contig1	CL9635Contig1	6.31	1	1	1	1
954	dsrrswapns_comp21360_c1_seq1	len=389	6.31	1	1	1	1
955	Q2TAH7;CL1661Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2	6.30	2	1	1	2
956	Q6DE60;CL1365Contig1	Adenylyl cyclase-associated protein OS=Xenopus laevis G	6.30	4	2	2	13
957	dsrrswapns_comp216720_c1_seq1	len=1088	6.28	1	1	1	1
958	TC443718 homologue to UniRef100_Q5BJ90 Cluster: W	Rep: Wdr12 protein - Xenopus tropicalis (Western clawed f	6.28	1	1	1	1
959	Q5RJW9	LOC495833 protein OS=Xenopus laevis GN=ptcd1 PE=2 S	6.26	1	1	1	1
960	I3PB85;CL26Contig14	IFN-gamma-inducible-lysosomal thiol reductase OS=Xenop	6.25	2	1	1	92
961	dsrrswapns_comp216167_c0_seq12	len=818	6.25	5	1	1	27
962	Q5XGZ4	LOC779025 protein (Fragment) OS=Xenopus laevis GN=L	6.25	232	1	3	8
963	Q6DFI0	MGC83110 protein OS=Xenopus laevis GN=MGC83110 PE	6.23	3	2	2	3
964	B7ZRS3	Forkhead box transcription factor OS=Xenopus laevis GN=	6.23	2	1	1	1
965	Q7ZWN1	Inosine-5'-monophosphate dehydrogenase A OS=Xenopus	6.23	1	1	1	1
966	dsrrswapns_comp191560_c0_seq2	len=1371	6.23	1	1	1	1
967	Q63ZK5	LOC494824 protein (Fragment) OS=Xenopus laevis GN=L	6.23	2	1	1	1
968	F6KDD5	NADH dehydrogenase subunit 1 OS=Xenopus laevis GN=n	6.21	2	1	1	2
969	Q8AVM7	Basic leucine zipper and W2 domain-containing protein 1 O	6.21	1	1	1	1
970	Q498L1;CL2523Contig1	MGC114631 protein OS=Xenopus laevis GN=MGC114631	6.20	7	3	3	18
971	Q32NL8	MGC131051 protein OS=Xenopus laevis GN=slc3a1 PE=2	6.20	1	1	1	2
972	CL8769Contig1	CL8769Contig1	6.18	1	1	1	1
973	Q66J07;CL542Contig7	MGC83563 protein OS=Xenopus laevis GN=nnt PE=2 SV=	6.17	2	3	3	18
974	Q5PPT3	ATP-dependent Clp protease proteolytic subunit (Fragment)	6.17	4	1	1	2
975	CL9347Contig1	CL9347Contig1	6.16	1	2	2	4
976	Q32NS7;CL1Contig287	MGC52825 protein OS=Xenopus laevis GN=hmgb2 PE=2	6.16	16	1	1	14
977	Q6GLS2	MGC84319 protein OS=Xenopus laevis GN=tcp11l1 PE=2	6.15	1	1	1	1
978	P43695	GATA-binding factor 5-A OS=Xenopus laevis GN=gata5-a	6.15	1	1	1	1
979	Q66IS8;CL11862Contig1	Transmembrane protein 177 OS=Xenopus laevis GN=tmem	6.13	2	1	1	3
980	Q6NUD2	MGC81047 protein OS=Xenopus laevis GN=dtymk PE=2 S	6.13	2	1	1	2
981	Q802B6;CL539Contig1	Add1-a protein OS=Xenopus laevis GN=add1 PE=2 SV=1 -	6.13	2	1	1	3
982	CL10114Contig2	CL10114Contig2	6.13	1	1	1	1
983	Q3KPK3;CL25783Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2	6.12	4	2	2	6
984	Q4V7W5	Polyhomeotic-like protein 2 OS=Xenopus laevis GN=phc2	6.10	1	1	1	1
985	Q6IRQ1	70 kDa peroxisomal membrane protein OS=Xenopus laevis	6.09	1	1	1	1
986	A1L3F5	C-Maf-inducing protein OS=Xenopus laevis GN=cmip PE=2	6.09	1	2	2	4
987	Q91717;CL120Contig7	Collagen alpha-1(II) chain OS=Xenopus laevis GN=col2a1	6.06	3	2	3	7
988	Q0IHC8	MGC115147 protein OS=Xenopus laevis GN=vps37a PE=2	6.05	1	1	1	1
989	Q3KPW6	LOC733370 protein (Fragment) OS=Xenopus laevis GN=L	6.03	1	1	1	1
990	CL10840Contig1	CL10840Contig1	6.02	2	1	1	2
991	CL2715Contig5	CL2715Contig5	6.02	1	1	1	1
992	A2VDD0	LOC100037222 protein (Fragment) OS=Xenopus laevis GN	6.00	3	1	3	37
993	Q5XH25	Malic enzyme OS=Xenopus laevis GN=me2 PE=2 SV=1 - [	6.00	6	1	2	7
994	Q2TAE3	Dual specificity tyrosine-phosphorylation-regulated kinase 1	6.00	1	1	1	1
995	CL246Contig8	CL246Contig8	5.95	3	1	1	1
996	Q91560	RNA exonuclease 4 OS=Xenopus laevis GN=rexo4 PE=2	5.94	1	1	1	1
997	dsrrswapns_comp200264_c1_seq2	len=934	5.91	1	1	1	2
998	CL16756Contig1	CL16756Contig1	5.90	1	1	1	1
999	Q06271	Integrin alpha 2 subunit (Fragment) OS=Xenopus laevis PE	5.90	1	1	1	1
1000	Q91573	Mineralocorticoid receptor (Fragment) OS=Xenopus laevis	5.88	2	1	1	1
1001	Q6NRR6	MGC82267 protein OS=Xenopus laevis GN=MGC82267 PE	5.87	2	1	1	1
1002	CL6870Contig2	CL6870Contig2	5.86	1	1	1	1
1003	Q6NTL5;CL6428Contig2	MGC83205 protein OS=Xenopus laevis GN=cog6 PE=2 SV	5.86	254	1	2	3
1004	Q4V813;CL6656Contig1	Adh3 protein OS=Xenopus laevis GN=adh5 PE=2 SV=1 - [	5.85	2	1	1	4
1005	Q4KL87	MGC116558 protein OS=Xenopus laevis GN=pde9a PE=2	5.85	1	1	1	2
1006	Q7SYV2	MGC64465 protein OS=Xenopus laevis GN=pdlim1 PE=2	5.85	1	1	1	1
1007	Q6PCI1	MGC68997 protein OS=Xenopus laevis GN=nadk PE=2 SV	5.84	2	1	1	1
1008	Q6GNP1;CL9567Contig1	MGC80975 protein OS=Xenopus laevis GN=dnai1 PE=2 S	5.84	1	1	1	2
1009	Q7ZTM4;CL120Contig1	Col2a1b protein OS=Xenopus laevis GN=col2a1b PE=2 SV	5.84	4	1	3	6
1010	TC457582 similar to UniRef100_UPI00006A00F2 Cluster	Rep: Serum amyloid P-component precursor (SAP) (9.5S a	5.83	1	1	1	1
1011	Q7SYS0	Gst13-13-prov protein OS=Xenopus laevis GN=gstk1 PE=2	5.82	1	1	1	1
1012	A4FVE9	LOC100049132 protein (Fragment) OS=Xenopus laevis GN	5.82	3	1	1	2
1013	Q7ZTM9;CL5086Contig1	Eukaryotic translation initiation factor 3 subunit D OS=Xeno	5.82	253	1	2	5
1014	CL620Contig2	CL620Contig2	5.80	1	1	1	1
1015	CL9481Contig1	CL9481Contig1	5.79	2	1	1	2
1016	A5D8L8	LOC100049741 protein (Fragment) OS=Xenopus laevis GN	5.78	1	1	1	1
1017	Q4V837	Denticleless protein homolog A OS=Xenopus laevis GN=dtl	5.77	1	1	1	1
1018	Q5U511	LOC495400 protein OS=Xenopus laevis GN=vapb PE=2 S	5.76	2	1	1	1
1019	CL5041Contig1	CL5041Contig1	5.75	2	1	1	1
1020	Q7T3S2;CL2215Contig4	PP2A B'' subunit PR74 OS=Xenopus laevis GN=ppp2r3a P	5.75	229	1	2	3
1021	CL6998Contig1	CL6998Contig1	5.73	3	1	1	1
1022	Q7SYV4	Vbp1-prov protein OS=Xenopus laevis GN=vbp1 PE=2 SV=	5.73	1	1	1	1
1023	Q9I905;CL4858Contig1	MGC64562 protein OS=Xenopus laevis GN=mtch2 PE=2 S	5.72	2	1	1	4

1024	Q7ZXP5	Mct3-prov protein OS=Xenopus laevis GN=slc16a3 PE=2 S	5.72	1	1	1	1
1025	Q6NRP6	Tudor domain-containing protein 3 OS=Xenopus laevis GN=	5.69	2	2	2	2
1026	Q7ZTP9;CL8426Contig1	Slc25a20-prov protein OS=Xenopus laevis GN=slc25a20 P	5.65	1	1	1	4
1027	Q6GLT3	MGC84278 protein OS=Xenopus laevis GN=igsf21 PE=2 S	5.63	1	1	1	1
1028	Q5PQ40	LOC495989 protein OS=Xenopus laevis GN=tex26 PE=2 S	5.63	1	1	1	1
1029	Q7ZX99	Tia1 protein (Fragment) OS=Xenopus laevis GN=Tia1 PE=	5.62	1	1	1	1
1030	O93522;CL47Contig4	Nonmuscle myosin II heavy chain A OS=Xenopus laevis G	5.60	12	4	6	21
1031	dsrrswapns_comp216492_c2_seq6	len=2704	5.59	2	1	1	1
1032	CL2670Contig1	CL2670Contig1	5.57	3	1	1	1
1033	Q8AVC0	Shmt1 protein OS=Xenopus laevis GN=shmt1 PE=2 SV=1	5.57	1	1	1	1
1034	Q08B79	LOC733250 protein (Fragment) OS=Xenopus laevis GN=L	5.55	3	3	3	13
1035	Q9IBC8	T-box transcription factor TBX2-A OS=Xenopus laevis GN=	5.52	4	1	1	5
1036	CL6788Contig2	CL6788Contig2	5.49	1	1	1	1
1037	CL12Contig33	CL12Contig33	5.49	4	1	1	1
1038	dsrrswapns_comp209374_c3_seq2	len=1195	5.48	1	1	1	2
1039	dsrrswapns_comp213553_c0_seq7	len=1469	5.45	4	1	1	1
1040	Q5XHE6	LOC495021 protein OS=Xenopus laevis GN=LOC495021	5.42	2	1	1	1
1041	Q640W9	MGC84396 protein OS=Xenopus laevis GN=MGC84396 P	5.42	1	1	1	1
1042	Q66J72	MGC81721 protein OS=Xenopus laevis GN=pvrl2 PE=2 SV	5.40	3	1	1	1
1043	Q5XGW1;CL14714Contig1	LOC495263 protein OS=Xenopus laevis GN=atp5g1 PE=2	5.38	8	1	1	5
1044	Q6DFK1	Pex12-prov protein OS=Xenopus laevis GN=pex12 PE=2 S	5.38	1	1	1	1
1045	CL6622Contig2	CL6622Contig2	5.37	1	1	1	2
1046	Q6NRC5;zeinaSSns_comp387749_c1_seq4	MGC83936 protein OS=Xenopus laevis GN=dync1i2 PE=2	5.34	11	1	1	4
1047	Q6PA32	MGC68657 protein OS=Xenopus laevis GN=slco2a1 PE=2	5.34	1	2	2	2
1048	CL10567Contig1	CL10567Contig1	5.32	2	1	1	2
1049	CL2732Contig1	CL2732Contig1	5.31	2	1	1	1
1050	Q6GLY5	Protein asunder homolog OS=Xenopus laevis GN=asun PE	5.31	1	1	1	1
1051	Q4QR55	VgRBP60 protein OS=Xenopus laevis GN=VgRBP60 PE=2	5.30	2	1	1	2
1052	Q5BL86	MGC85088 protein OS=Xenopus laevis GN=blmh PE=2 SV	5.30	1	1	1	1
1053	Q501Q2	Putative uncharacterized protein OS=Xenopus laevis PE=2	5.30	3	1	1	1
1054	Q01611	Zinc finger Y-chromosomal protein 1 OS=Xenopus laevis G	5.29	228	1	2	3
1055	Q6DJJ8	Polr3c-prov protein OS=Xenopus laevis GN=polr3c PE=2 S	5.29	1	1	1	1
1056	Q6DE73;CL13437Contig1	2-oxoglutarate and iron-dependent oxygenase domain-cont	5.28	1	1	1	2
1057	CL17062Contig1	CL17062Contig1	5.26	1	1	1	1
1058	P48676	Peripherin OS=Xenopus laevis GN=prph PE=2 SV=1 - [PE	5.26	291	1	2	2
1059	A9UM24	Bix1 protein OS=Xenopus laevis GN=Bix1 PE=2 SV=1 - [A	5.24	4	1	1	1
1060	Q08B84	E3 ubiquitin-protein ligase RNF19B OS=Xenopus laevis GN	5.24	1	1	1	1
1061	CL11742Contig1	CL11742Contig1	5.23	1	1	1	1
1062	D6C652	Yes-associated protein 65 OS=Xenopus laevis GN=YAP P	5.23	1	1	1	1
1063	CL13645Contig1	CL13645Contig1	5.22	1	1	1	1
1064	P29540;CL66Contig1	General transcription factor IIE subunit 2 OS=Xenopus laev	5.21	1	1	1	32
1065	B7ZRZ7	T-box transcription factor Tbx5 OS=Xenopus laevis GN=tbx	5.20	2	1	1	1
1066	Q9IAI8	Receptor protein tyrosine phosphatase CRYP-alpha (Fragm	5.20	3	1	1	1
1067	Q66IV8;CL2891Contig1	MGC84302 protein OS=Xenopus laevis GN=syn1 PE=2 SV	5.19	1	1	1	2
1068	Q7ZYA5;CL6725Contig1	Interferon-inducible double stranded RNA-dependent protei	5.18	4	1	1	2
1069	Q6INF1	LOC432253 protein (Fragment) OS=Xenopus laevis GN=L	5.18	3	1	1	1
1070	Q6NRH1	DDB1- and CUL4-associated factor 8 OS=Xenopus laevis	5.16	1	1	1	1
1071	Q7ZX22;CL5682Contig1	WD repeat-containing protein 24 OS=Xenopus laevis GN=w	5.13	2	1	1	2
1072	Q6GP14	LOC397993 protein OS=Xenopus laevis GN=LOC397993	5.12	252	1	2	2
1073	Q569T0	MGC115178 protein OS=Xenopus laevis GN=hdac10 PE=	5.12	1	1	1	1
1074	CL1016Contig5	CL1016Contig5	5.11	2	1	1	1
1075	Q6DDR6	LOC445863 protein (Fragment) OS=Xenopus laevis GN=L	5.11	2	2	2	2
1076	Q5I016	LOC496298 protein (Fragment) OS=Xenopus laevis GN=cc	5.09	1	1	1	1
1077	CL4060Contig1	CL4060Contig1	5.06	1	1	1	1
1078	B3IXB3	RAS guanyl releasing protein 2 OS=Xenopus laevis GN=ra	5.05	3	1	1	1
1079	CL9187Contig1	CL9187Contig1	5.04	1	1	1	12
1080	Q7ZX81	MGC54008 protein OS=Xenopus laevis GN=cyp2c8.1 PE=	5.04	1	1	1	1
1081	Q6PAZ0	MGC68780 protein OS=Xenopus laevis GN=tomm70a PE=	5.03	1	1	1	1
1082	Q6NRT7	MGC81452 protein OS=Xenopus laevis GN=akt1s1 PE=2	5.02	1	1	1	2
1083	A9JS15	LOC100127283 protein OS=Xenopus laevis GN=fam110d	5.00	1	1	1	1
1084	Q66KT0	MGC85462 protein OS=Xenopus laevis GN=rnls PE=2 SV=	4.98	1	1	1	2
1085	CL6862Contig2	CL6862Contig2	4.96	2	1	1	1
1086	CL6316Contig1	CL6316Contig1	4.93	3	1	1	1
1087	CL1590Contig4	CL1590Contig4	4.92	1	1	1	1
1088	Q7ZTR0	Wu:fc55e05-prov protein OS=Xenopus laevis GN=copb2 P	4.92	4	1	1	2
1089	P30311	M-phase inducer phosphatase 3 OS=Xenopus laevis GN=c	4.90	1	1	1	1
1090	Q2VPG9;CL1Contig756	MGC132166 protein OS=Xenopus laevis GN=suclg2 PE=2	4.87	2	1	1	6
1091	Q7SYR8	Apacd-prov protein OS=Xenopus laevis GN=txndc9 PE=2	4.87	3	1	1	4
1092	Q9PWH0	Guanylate cyclase OS=Xenopus laevis GN=XGC-1 PE=2 S	4.87	483	1	3	3
1093	Q7SZJ1	Putative OFD1 protein (Fragment) OS=Xenopus laevis PE=	4.86	1	1	1	1
1094	B1NA54	Ig-like receptor 2.1 OS=Xenopus laevis GN=xilr2 PE=2 SV=	4.84	2	1	1	3
1095	CL12884Contig1	CL12884Contig1	4.84	2	1	1	1
1096	TC445443 similar to UniRef100_O74947 Cluster: Conser	Rep: Conserved fungal protein - Schizosaccharomyces pon	4.82	1	1	1	2
1097	B7ZQV9	Frizzled-8 OS=Xenopus laevis GN=xfz8 PE=2 SV=1 - [B7Z	4.80	1	1	1	2
1098	zeinaSSns_comp387346_c2_seq2	len=1947	4.79	1	1	1	1
1099	CL7840Contig1	CL7840Contig1	4.78	1	1	1	1
1100	Q6P417	MGC68516 protein OS=Xenopus laevis GN=MGC68516 P	4.76	2	1	1	3
1101	B1H1N7	Ancient ubiquitous protein 1 OS=Xenopus laevis GN=aup1	4.76	227	1	2	2
1102	Q6INJ7	LOC432278 protein (Fragment) OS=Xenopus laevis GN=L	4.73	2	1	1	1
1103	dsrrswapns_comp213982_c2_seq3	len=3721	4.72	2	1	1	1
1104	Q6NU42	MGC81264 protein OS=Xenopus laevis GN=MGC81264 P	4.71	1	1	1	1
1105	Q6S9C2	Type 7 adenylyl cyclase (Fragment) OS=Xenopus laevis P	4.71	1	1	1	1
1106	A3KNB7	LOC495502 protein OS=Xenopus laevis GN=LOC495502	4.69	4	1	1	9
1107	CL15462Contig1	CL15462Contig1	4.68	1	1	1	1
1108	CL3413Contig3	CL3413Contig3	4.67	1	1	1	1
1109	Q7ZTK1;CL1176Contig2	Slc30a1-prov protein OS=Xenopus laevis GN=slc30a1 PE=	4.66	1	1	1	3

1110	zeinaSSns_comp389585_c0_seq2	len=3397	4.66	1	1	1	1
1111	Q2TAF7	MGC132159 protein OS=Xenopus laevis GN=cep85 PE=2	4.66	292	1	2	3
1112	Q6PF58	MGC68882 protein OS=Xenopus laevis PE=2 SV=1 - [Q6P	4.62	3	1	1	1
1113	CL3394Contig2	CL3394Contig2	4.62	1	1	1	3
1114	Q5M7B8	LOC496249 protein OS=Xenopus laevis GN=aga PE=2 SV	4.61	1	1	1	1
1115	Q6NU56	Methyltransferase-like protein 14 OS=Xenopus laevis GN=r	4.61	1	1	1	2
1116	CL6944Contig2	CL6944Contig2	4.57	2	1	1	1
1117	B7ZQE3	Tbx6 protein OS=Xenopus laevis GN=tbx6 PE=2 SV=1 - [B	4.55	2	1	1	1
1118	Q6GQD0	Nuclear cap-binding protein subunit 1-B OS=Xenopus laevis	4.55	1	1	1	1
1119	Q4KLX0;CL907Contig1	MGC114675 protein OS=Xenopus laevis GN=atp6v1a PE=	4.54	3	2	2	12
1120	Q6GMY9	Exportin-2 OS=Xenopus laevis GN=cse1l PE=2 SV=1 - [XP	4.53	6	3	4	20
1121	A0JMU8	Protein CASC3 OS=Xenopus laevis GN=casc3 PE=2 SV=1	4.52	4	2	2	4
1122	B7ZQH2	XMam1 protein OS=Xenopus laevis GN=XMam1 PE=2 SV=	4.52	1	1	1	2
1123	Q7T0R2	LOC398682 protein (Fragment) OS=Xenopus laevis GN=L	4.51	2	1	1	1
1124	CB941391 homologue to UniRef100_UPI000069DDBC C	Rep: Plakophilin-1 (Band-6 protein) (B6P). - Xenopus tropic	4.49	4	1	1	3
1125	Q4V7Z2	MGC114910 protein OS=Xenopus laevis GN=msn PE=2 S	4.48	2	1	1	1
1126	CL1Contig313	CL1Contig313	4.46	2	1	2	9
1127	Q6NRI2	MGC83797 protein OS=Xenopus laevis GN=klhl7 PE=2 SV	4.46	2	1	1	1
1128	P23790	Serum response factor OS=Xenopus laevis GN=srf PE=2 S	4.46	1	1	1	1
1129	CL17976Contig1	CL17976Contig1	4.45	1	1	1	1
1130	Q9PVQ1	Proteasome subunit alpha type-7-B OS=Xenopus laevis G	4.45	2	1	1	1
1131	Q7SZ98	Annexin OS=Xenopus laevis PE=2 SV=1 - [Q7SZ98_XENL	4.44	293	1	2	12
1132	Q5I047;CL15637Contig1	Protein FAM173B OS=Xenopus laevis GN=fam173b PE=2	4.42	1	1	1	9
1133	CL22667Contig1	CL22667Contig1	4.41	1	1	1	1
1134	Q7SZT4;CL25746Contig1	Rdhl-prov protein OS=Xenopus laevis GN=dhrs9 PE=2 SV=	4.40	1	1	1	3
1135	Q9PTG8	Transforming acidic coiled-coil-containing protein 3 OS=Xe	4.40	1	1	1	1
1136	Q6DCL6;CL7918Contig1	Protein FAM69A OS=Xenopus laevis GN=fam69a PE=2 SV	4.39	3	1	1	2
1137	Q6GNA9;CL4677Contig2	MGC82910 protein OS=Xenopus laevis GN=zeb1 PE=2 SV	4.39	1	2	2	2
1138	A1L2U5	LOC100036956 protein (Fragment) OS=Xenopus laevis G	4.39	1	1	1	1
1139	H2DQ55	Interferon-gamma (Fragment) OS=Xenopus laevis PE=2 S	4.35	1	1	1	1
1140	Q7ZYP5	MGC52698 protein OS=Xenopus laevis GN=cirh1a PE=2 S	4.35	1	1	1	1
1141	Q4V847	Integrator complex subunit 8 OS=Xenopus laevis GN=ints8	4.34	1	1	1	1
1142	dsrrswapns_comp205971_c0_seq1	len=2542	4.34	1	1	1	2
1143	Q7ZXP0;CL3911Contig1	Twinfilin-2-A OS=Xenopus laevis GN=twf2-a PE=2 SV=1 - [	4.30	2	1	1	2
1144	CL14192Contig1	CL14192Contig1	4.29	1	1	1	2
1145	Q6GQI7;CL3975Contig1	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosami	4.29	2	1	1	2
1146	CL4967Contig1	CL4967Contig1	4.29	1	1	1	1
1147	Q4V7Q6	Serine/threonine-protein kinase ULK3 OS=Xenopus laevis	4.27	1	1	1	1
1148	Q6XXZ0	Transporter associated with antigen processing 1 OS=Xeno	4.27	1	1	1	2
1149	Q9DDA3	RalB-binding protein (Fragment) OS=Xenopus laevis GN=rl	4.26	2	1	1	1
1150	A9ULW6	ZPD protein OS=Xenopus laevis GN=ZPD PE=2 SV=1 - [A	4.26	1	1	1	1
1151	Q4FZM4	LOC100036775 protein (Fragment) OS=Xenopus laevis G	4.24	2	1	1	3
1152	P19102	Protein c-ets-2-A OS=Xenopus laevis GN=ets2-a PE=2 SV=	4.24	1	1	1	1
1153	Q0IH66	Ddx10 protein OS=Xenopus laevis GN=ddx10 PE=2 SV=1	4.22	6	1	1	1
1154	Q6DCT7	MGC80781 protein OS=Xenopus laevis GN=arhgap30 PE=	4.21	1	2	2	2
1155	Q4KLV8	LOC733291 protein (Fragment) OS=Xenopus laevis GN=L	4.19	6	2	2	9
1156	Q569U3	Fcp1 protein OS=Xenopus laevis GN=fcp1 PE=2 SV=1 - [Q	4.19	2	1	1	1
1157	CL12609Contig1	CL12609Contig1	4.17	1	1	1	2
1158	Q4V866	MGC114642 protein OS=Xenopus laevis GN=clpx PE=2 S	4.17	1	1	1	1
1159	CL966Contig1	CL966Contig1	4.15	1	1	1	1
1160	Q5XH38;CL4330Contig2	LOC495073 protein OS=Xenopus laevis GN=tmem184a P	4.15	1	1	1	2
1161	Q6NU97;CL5953Contig1	MGC81120 protein OS=Xenopus laevis GN=MGC81120 P	4.14	4	1	1	3
1162	Q32NR8	MGC130896 protein OS=Xenopus laevis GN=ndufs2 PE=2	4.14	1	1	1	1
1163	Q7ZYB2;CL6160Contig1	PR domain zinc finger protein 4 OS=Xenopus laevis PE=2	4.13	3	1	1	2
1164	zeinaSSns_comp388890_c0_seq6	len=1570	4.12	4	1	1	1
1165	Q6GMC8	MGC81877 protein OS=Xenopus laevis GN=ncf2 PE=2 SV	4.12	1	1	1	1
1166	Q6NRD3	E3 ubiquitin-protein ligase SH3RF1 OS=Xenopus laevis G	4.12	1	1	1	1
1167	Q7ZX27	Palmdelphin OS=Xenopus laevis GN=palmd PE=2 SV=1 - [	4.11	1	1	1	1
1168	Q6NRP9	MGC83117 protein OS=Xenopus laevis GN=ptpn4 PE=2 S	4.09	6	2	2	2
1169	Q7ZWR3	Padi2-prov protein OS=Xenopus laevis GN=padi2 PE=2 SV	4.09	1	1	1	1
1170	Q6GM62	MGC83400 protein OS=Xenopus laevis GN=idh3g PE=2 S	4.09	1	1	1	2
1171	Q5HZ81	MGC85202 protein OS=Xenopus laevis GN=cep70 PE=2 S	4.08	227	1	2	2
1172	D2CGM1	Fanconi anemia complementation group C OS=Xenopus la	4.07	1	1	1	1
1173	dsrrswapns_comp207165_c0_seq1	len=1567	4.06	2	1	1	1
1174	A0JMW2	MGC154857 protein OS=Xenopus laevis GN=heatr2 PE=2	4.05	2	1	1	1
1175	Q6NRB7	Protein FAM73A OS=Xenopus laevis GN=fam73a PE=2 SV	4.04	1	1	1	1
1176	Q6GQB6	MGC80186 protein OS=Xenopus laevis GN=MGC80186 P	4.04	2	1	1	1
1177	CL2188Contig3	CL2188Contig3	4.00	2	1	1	1
1178	CL9794Contig1	CL9794Contig1	4.00	1	1	1	1
1179	Q6P9I7;CL6420Contig1	Structural maintenance of chromosomes protein 6 OS=Xen	3.99	291	2	3	10
1180	Q4V7I2	LOC733267 protein (Fragment) OS=Xenopus laevis GN=L	3.98	2	1	1	1
1181	D3JCC3	Recombination activating protein 2 (Fragment) OS=Xenopu	3.98	21	2	3	3
1182	A2RV99	LOC445855 protein (Fragment) OS=Xenopus laevis GN=L	3.97	228	1	2	2
1183	Q5HZM8	Putative uncharacterized protein OS=Xenopus laevis GN=d	3.96	1	1	1	1
1184	CL3223Contig1	CL3223Contig1	3.95	5	1	1	1
1185	B9V8R9	Ionotropic glutamate receptor subunit GluR3(Q)flop OS=Xe	3.95	1	1	1	1
1186	CL1Contig1160	CL1Contig1160	3.94	12	2	2	4
1187	A0JMT7	LOC431931 protein OS=Xenopus laevis GN=LOC431931 P	3.94	2	1	1	1
1188	Q68F13	MGC82958 protein OS=Xenopus laevis GN=sucla2 PE=2 S	3.93	4	1	1	2
1189	CL25436Contig1	CL25436Contig1	3.93	1	1	1	1
1190	CL9991Contig1	CL9991Contig1	3.92	1	1	1	1
1191	Q32N62	LOC733423 protein (Fragment) OS=Xenopus laevis GN=L	3.91	1	1	1	1
1192	Q6GNE6	LOC443667 protein (Fragment) OS=Xenopus laevis GN=L	3.90	227	1	2	2
1193	CL9153Contig1	CL9153Contig1	3.89	2	1	1	10
1194	Q6GNR4;CL847Contig2	MGC80936 protein OS=Xenopus laevis GN=cltc PE=2 SV=	3.88	4	3	3	8
1195	CL342Contig4	CL342Contig4	3.87	2	1	1	1

1196	Q6DD71	ERO1-like protein alpha OS=Xenopus laevis GN=ero1l PE=	3.87	201	1	2	3
1197	dsrrswapns_comp211061_c2_seq3	len=3565	3.86	2	1	1	1
1198	dsrrswapns_comp208608_c7_seq4	len=1653	3.83	3	1	1	2
1199	B7ZS26	V-rel reticuloendotheliosis viral oncogene homolog B, nucle	3.82	2	1	1	1
1200	CL13527Contig1	CL13527Contig1	3.81	2	1	1	1
1201	Q5FWX4	LOC733151 protein (Fragment) OS=Xenopus laevis GN=L	3.81	2	1	1	1
1202	Q7ZTP2	Actin-related protein 2-A OS=Xenopus laevis GN=actr2-a P	3.81	2	1	1	1
1203	Q5XHM7;CL5748Contig2	Carbohydrate sulfotransferase 12 OS=Xenopus laevis GN=	3.81	2	1	1	2
1204	zeinaSSns_comp382744_c3_seq1	len=1626	3.81	3	1	1	1
1205	Q7ZXF1	Myotubularin-related protein 4 OS=Xenopus laevis GN=mtn	3.80	1	1	1	1
1206	CL13399Contig1	CL13399Contig1	3.80	1	1	1	1
1207	CL6843Contig1	CL6843Contig1	3.78	1	1	1	3
1208	Q6P286;CL8201Contig1	Probable 2-oxoglutarate dehydrogenase E1 component DH	3.78	2	1	1	7
1209	Q2VPK9	Acyl-coenzyme A oxidase OS=Xenopus laevis GN=acox1 P	3.78	227	1	2	2
1210	Q91593	Potassium channel alpha subunit Kv2.1 OS=Xenopus laevis	3.77	227	1	2	2
1211	dsrrswapns_comp211626_c8_seq3	len=725	3.74	1	1	1	4
1212	Q6GQB1	MGC80200 protein OS=Xenopus laevis GN=nrcam PE=2 S	3.74	1	2	2	3
1213	Q32N55	Pentatricopeptide repeat-containing protein 3, mitochondria	3.74	1	1	1	1
1214	CL2335Contig1	CL2335Contig1	3.71	5	2	2	6
1215	CL4517Contig2	CL4517Contig2	3.71	2	1	1	1
1216	Q6IR57	MGC82326 protein OS=Xenopus laevis GN=sec31b PE=2	3.71	1	1	1	1
1217	Q6GR23	MGC81304 protein OS=Xenopus laevis GN=irf6 PE=2 SV=	3.70	1	1	1	1
1218	CL14603Contig1	CL14603Contig1	3.69	1	1	1	1
1219	Q91819	Aurora kinase A-B OS=Xenopus laevis GN=aurka-b PE=2	3.68	1	1	1	1
1220	Q5U562	LOC495358 protein OS=Xenopus laevis GN=cib1 PE=2 SV	3.68	3	1	1	2
1221	CL19605Contig1	CL19605Contig1	3.66	1	1	1	1
1222	Q90X20	Aryl hydrocarbon receptor nuclear translocator Arnt OS=Xe	3.65	1	1	1	1
1223	Q3KQB6	CTD small phosphatase-like protein 2-B OS=Xenopus laevi	3.65	5	1	1	2
1224	Q7ZXB9;CL335Contig7	Faf1-prov protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZX	3.65	256	1	2	3
1225	Q2TAS1;CL8143Contig1	MGC130979 protein OS=Xenopus laevis GN=sptlc3 PE=2	3.64	1	1	1	3
1226	Q53I77	Exportin-6-A OS=Xenopus laevis GN=xpo6-a PE=1 SV=1 -	3.61	1	1	1	1
1227	CL1526Contig4	CL1526Contig4	3.61	1	1	1	1
1228	Q498L4	LOC734164 protein (Fragment) OS=Xenopus laevis GN=L	3.61	5	1	1	2
1229	Q6PAD5	MGC68755 protein OS=Xenopus laevis GN=pnliprp2 PE=2	3.61	1	1	1	1
1230	CL15037Contig1	CL15037Contig1	3.60	1	2	2	5
1231	Q566H1	MGC115310 protein OS=Xenopus laevis GN=crmp1 PE=2	3.59	1	1	1	2
1232	Q6GQA7;CL5376Contig2	MGC80207 protein OS=Xenopus laevis GN=dars PE=2 SV	3.58	2	1	1	2
1233	Q32NH8	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase	3.56	1	1	1	1
1234	Q8AVF3	LOC398536 protein (Fragment) OS=Xenopus laevis GN=L	3.56	1	1	1	1
1235	Q6PCK3	MGC68869 protein OS=Xenopus laevis PE=2 SV=1 - [Q6P	3.55	3	1	1	1
1236	CL7317Contig1	CL7317Contig1	3.54	3	1	1	1
1237	Q6NU47;CL6335Contig1	Serine/threonine-protein kinase pdik1l-A OS=Xenopus laevi	3.54	6	1	1	2
1238	Q91785	Kinesin-like protein KIF15-A OS=Xenopus laevis GN=kif15-	3.53	252	1	2	3
1239	CL8749Contig2	CL8749Contig2	3.53	2	1	1	1
1240	Q8QG78	Nuclear receptor corepressor 1 OS=Xenopus laevis GN=nc	3.52	2	2	2	2
1241	Q8UVR5	Bromodomain adjacent to zinc finger domain protein 1A (Fr	3.51	1	1	1	1
1242	Q561N7	LOC733199 protein (Fragment) OS=Xenopus laevis GN=L	3.51	1	1	1	1
1243	B2GTY1	LOC100158450 protein (Fragment) OS=Xenopus laevis GN	3.51	1	1	1	1
1244	dsrrswapns_comp197215_c0_seq2	len=1652	3.50	1	1	1	1
1245	dsrrswapns_comp216642_c2_seq2	len=3947	3.50	3	1	1	1
1246	Q6AX29	MGC86330 protein OS=Xenopus laevis GN=kcnj1 PE=2 S	3.49	1	1	1	1
1247	Q6NRT0;TC416396 UniRef100_Q6NRT0 Cluster: MGC8	Casein kinase I isoform gamma-1 OS=Xenopus laevis GN=	3.48	3	1	1	5
1248	B7ZSA6;CL4246Contig2	Inversin OS=Xenopus laevis GN=invs-a PE=2 SV=1 - [B7Z	3.48	291	1	2	3
1249	Q5XHD4	LOC495031 protein OS=Xenopus laevis GN=c1galt1c1 PE	3.47	1	1	1	1
1250	CL11454Contig2	CL11454Contig2	3.47	1	1	1	1
1251	Q6AZU4	MGC79131 protein OS=Xenopus laevis GN=MGC79131 P	3.46	2	1	1	1
1252	CL8237Contig1	CL8237Contig1	3.45	1	1	1	1
1253	Q641F3	Collagen alpha-1(XXI) chain OS=Xenopus laevis GN=col21	3.45	1	1	1	1
1254	zeinaSSns_comp388960_c0_seq4	len=2747	3.44	4	1	1	1
1255	B7ZQB3	LOC398954 protein OS=Xenopus laevis GN=LOC398954 P	3.41	2	1	1	1
1256	Q804I2	Germes OS=Xenopus laevis GN=LOC398520 PE=2 SV=1	3.41	1	1	1	1
1257	Q6DEA4;CL3873Contig1	MGC79068 protein OS=Xenopus laevis GN=pdia6 PE=2 S	3.39	3	1	1	2
1258	CL13100Contig1	CL13100Contig1	3.38	1	3	3	10
1259	Q641J8;CL811Contig3	E3 ubiquitin-protein ligase RNF12-A OS=Xenopus laevis G	3.38	2	1	1	2
1260	Q5FWP2	Protein Smaug homolog 1 OS=Xenopus laevis GN=samd4	3.38	1	1	1	1
1261	CL4772Contig2	CL4772Contig2	3.37	2	1	1	1
1262	CL3520Contig1	CL3520Contig1	3.36	1	1	1	1
1263	CL4145Contig1	CL4145Contig1	3.36	4	1	1	1
1264	CL2808Contig3	CL2808Contig3	3.35	1	1	1	1
1265	Q6DDQ3	Anoctamin OS=Xenopus laevis GN=ano5 PE=2 SV=1 - [Q6	3.35	1	1	1	1
1266	Q4QY31;CL2078Contig2	Aryl hydrocarbon receptor 1 alpha OS=Xenopus laevis GN=	3.35	2	1	1	2
1267	P18748	Oocyte zinc finger protein XlCOF29 OS=Xenopus laevis PE	3.35	1	1	1	1
1268	Q6GQ61	MGC80319 protein OS=Xenopus laevis GN=dnpep PE=2 S	3.34	1	1	1	1
1269	Q6IVY4;CL5230Contig1	Protein phosphatase Slingshot homolog OS=Xenopus laevi	3.33	1	1	1	4
1270	Q6DKC6	MGC84147 protein OS=Xenopus laevis GN=MGC84147 P	3.33	1	1	1	1
1271	Q2TAQ1	Putative elongator complex protein 1 OS=Xenopus laevis G	3.33	227	1	2	3
1272	CL7666Contig1	CL7666Contig1	3.32	1	1	1	1
1273	Q5XGV1	LOC398569 protein OS=Xenopus laevis GN=anln PE=2 SV	3.32	2	1	1	1
1274	Q5XHG7;CL1310Contig3	LOC398345 protein OS=Xenopus laevis GN=furin PE=2 SV	3.31	4	1	1	2
1275	A9QW72	N-methyl-D-aspartate receptor subunit NR2A OS=Xenopus	3.31	546	1	3	3
1276	B1H1X4	Serrate RNA effector molecule homolog A OS=Xenopus la	3.30	1	1	1	2
1277	CL4263Contig3	CL4263Contig3	3.30	1	1	1	2
1278	CL7240Contig1	CL7240Contig1	3.29	1	1	1	1
1279	Q98T92	Mps1/TTK OS=Xenopus laevis GN=ttk PE=2 SV=1 - [Q98T	3.29	1	1	1	1
1280	Q91687	Integrin alpha-4 OS=Xenopus laevis GN=itga4 PE=2 SV=1	3.29	1	1	1	1
1281	Q6NRS1	Inhibitor of Bruton tyrosine kinase OS=Xenopus laevis GN=	3.29	1	1	1	1

1282	Q68F30	MGC82115 protein OS=Xenopus laevis GN=alas2 PE=2 S	3.28	1	1	1	1
1283	CL8625Contig1	CL8625Contig1	3.26	2	1	1	1
1284	Q5U5A3	Immunoglobulin superfamily member 3 OS=Xenopus laevis	3.26	2	2	2	2
1285	dsrrswapns_comp217164_c6_seq9	len=2926	3.24	2	1	1	2
1286	dsrrswapns_comp216092_c0_seq2	len=2393	3.23	1	1	1	4
1287	CL7447Contig1	CL7447Contig1	3.23	1	1	1	1
1288	Q498G7	PKC-delta2 protein OS=Xenopus laevis GN=prkcd PE=2 S	3.22	4	1	1	1
1289	Q6GPK9;CL1Contig1019	Serine/threonine-protein kinase TAO2 OS=Xenopus laevis	3.22	290	1	2	3
1290	Q9W650	C-met/hepatocyte growth factor receptor OS=Xenopus laev	3.20	1	1	1	1
1291	D2DGW1	Cell division cycle associated 2 OS=Xenopus laevis PE=2	3.19	8	2	2	4
1292	CL31693Contig1	CL31693Contig1	3.19	2	1	1	1
1293	CL7008Contig1	CL7008Contig1	3.19	2	1	1	3
1294	Q6INE5	Rho GTPase-activating protein 19 OS=Xenopus laevis GN=	3.16	253	1	2	2
1295	dsrrswapns_comp196386_c1_seq2	len=2839	3.14	2	1	1	1
1296	Q5XHE3	LOC495024 protein OS=Xenopus laevis GN=cdh13 PE=1	3.10	1	1	1	1
1297	Q6IP76	RAC-beta serine/threonine-protein kinase B OS=Xenopus l	3.09	2	1	1	1
1298	A1L106;CL10855Contig1	Lgtn protein OS=Xenopus laevis GN=eif2d PE=2 SV=1 - [A	3.09	228	1	2	5
1299	CL3295Contig3	CL3295Contig3	3.07	1	1	1	2
1300	dsrrswapns_comp216121_c4_seq1	len=842	3.07	2	1	1	1
1301	dsrrswapns_comp214133_c0_seq2	len=1048	3.06	3	1	1	1
1302	Q6ZXA0	Alpha-N-acetylneuraminide alpha-2,8-sialyltransferase OS=	3.06	1	1	1	1
1303	Q498H6	MGC114937 protein OS=Xenopus laevis GN=papss1 PE=2	3.04	1	1	1	1
1304	Q63ZN4	LOC494770 protein OS=Xenopus laevis GN=cbx6 PE=2 S	3.04	290	1	2	2
1305	A7E223	LOC100125672 protein OS=Xenopus laevis GN=LOC1001	3.03	3	1	1	3
1306	A0JPG5	LOC100036792 protein (Fragment) OS=Xenopus laevis G	3.03	3	1	1	1
1307	Q5U4I3	Cyclin-D1-binding protein 1 homolog OS=Xenopus laevis G	3.02	1	1	1	1
1308	Q66J92;CL2050Contig1	Gtse1 protein OS=Xenopus laevis GN=gtse1 PE=2 SV=1 -	3.01	4	1	1	2
1309	CL2776Contig2	CL2776Contig2	3.00	2	1	1	2
1310	Q642S3	MGC81229 protein OS=Xenopus laevis GN=tubgcp4 PE=2	3.00	1	1	1	1
1311	Q66JA7;CL1690Contig2	Pdha1-b protein OS=Xenopus laevis GN=pdha1 PE=2 SV=	3.00	8	1	1	7
1312	Q6DE96	Protein IWS1 homolog A OS=Xenopus laevis GN=iws1-a P	2.99	7	2	2	2
1313	Q8AX85	RNA-binding protein VgRBP71 OS=Xenopus laevis GN=Kh	2.98	9	2	2	5
1314	Q4V7K0	Putative uncharacterized protein OS=Xenopus laevis PE=2	2.96	2	1	1	1
1315	CL303Contig6	CL303Contig6	2.96	7	2	4	11
1316	CL6506Contig2	CL6506Contig2	2.96	1	1	1	1
1317	Q5PPU1	LOC496080 protein (Fragment) OS=Xenopus laevis GN=L	2.95	2	1	1	1
1318	Q7ZXI2	Slit1 protein OS=Xenopus laevis GN=slit1 PE=2 SV=1 - [Q	2.94	1	1	2	2
1319	CL18313Contig1	CL18313Contig1	2.94	1	1	1	2
1320	Q6DFK4;CL10561Contig1	MGC81344 protein OS=Xenopus laevis GN=etaa1 PE=2 S	2.93	1	1	1	3
1321	Q6NRV4	Retinol dehydrogenase 10-B OS=Xenopus laevis GN=rdh1	2.93	1	1	1	1
1322	Q05AW7	Cytoplasmic tRNA 2-thiolation protein 1 OS=Xenopus laevi	2.93	1	1	1	1
1323	C5H606	Vitronectin OS=Xenopus laevis GN=vtn PE=2 SV=1 - [C5H	2.93	1	1	1	1
1324	Q7ZWP8;CL6523Contig2	DNA topoisomerase OS=Xenopus laevis GN=top3b PE=2	2.91	3	1	1	2
1325	CL998Contig3	CL998Contig3	2.91	1	1	1	1
1326	Q9PUU6	Frizzled-2 OS=Xenopus laevis GN=fzd2 PE=2 SV=1 - [FZD	2.90	1	1	1	1
1327	Q98SG0	Beta-amyloid protein A OS=Xenopus laevis GN=app PE=2	2.89	4	1	1	1
1328	G1ESZ8	Putative beta-N-acetylhexosaminidase (Fragment) OS=Xen	2.88	5	1	1	5
1329	CL2920Contig1	CL2920Contig1	2.88	2	1	1	1
1330	dsrrswapns_comp215363_c2_seq10	len=1552	2.85	3	1	1	1
1331	Q9I8P8;CL2106Contig1	FK506-binding protein OS=Xenopus laevis GN=fkbp10 PE=	2.84	4	1	1	15
1332	CL151Contig7	CL151Contig7	2.84	1	1	1	1
1333	Q6INE6	LOC432244 protein (Fragment) OS=Xenopus laevis GN=L	2.84	252	1	2	2
1334	dsrrswapns_comp215943_c3_seq1	len=2923	2.83	1	1	1	3
1335	Q6INT1	MGC80376 protein OS=Xenopus laevis GN=ikbkb PE=1 S	2.83	2	1	1	2
1336	Q6GPE1;CL1282Contig2	Wu:fc30a11 protein OS=Xenopus laevis GN=ap1g1 PE=2	2.83	258	1	2	5
1337	Q6GP17;CL314Contig3	Histone-lysine N-methyltransferase SUV420H1-A OS=Xen	2.81	1	1	1	4
1338	Q0IH25	Kntc2 protein OS=Xenopus laevis GN=kntc2 PE=2 SV=1 -	2.81	2	1	1	1
1339	Q641D9;CL1834Contig5	MGC81931 protein OS=Xenopus laevis GN=sec14l5 PE=2	2.80	1	1	1	2
1340	Q6EAN5	Transcription factor OS=Xenopus laevis GN=sall2 PE=2 SV	2.80	1	1	1	2
1341	Q66IT5	MGC84699 protein OS=Xenopus laevis GN=sntg2 PE=2 S	2.78	1	1	1	2
1342	Q66KR8;CL712Contig1	MGC85505 protein OS=Xenopus laevis GN=utp11l PE=2 S	2.77	1	1	1	16
1343	Q6DDK5	Acetolactate synthase-like protein OS=Xenopus laevis GN=	2.77	1	1	1	1
1344	Q7ZYL5	Kinesin-like protein KIF22-B OS=Xenopus laevis GN=kif22-	2.77	1	1	1	1
1345	Q68F42	MGC81821 protein OS=Xenopus laevis GN=dpyd PE=2 SV	2.77	1	1	1	1
1346	Q6DDZ4	LOC398498 protein OS=Xenopus laevis GN=LOC398498	2.76	3	1	1	2
1347	Q6PB11;dsrrswapns_comp214341_c2_seq3	MGC68624 protein OS=Xenopus laevis GN=nprl3 PE=2 SV	2.76	2	1	1	2
1348	CL9235Contig3	CL9235Contig3	2.76	1	1	1	1
1349	Q8QFX3	Myeloperoxidase, peroxidase 2' OS=Xenopus laevis GN=m	2.76	3	1	1	1
1350	Q640G5	LOC494678 protein (Fragment) OS=Xenopus laevis GN=L	2.75	1	1	1	1
1351	Q6GQA8	LOC443584 protein (Fragment) OS=Xenopus laevis GN=L	2.73	2	1	1	1
1352	dsrrswapns_comp189792_c1_seq1	len=1253	2.73	2	1	1	1
1353	dsrrswapns_comp209806_c1_seq5	len=893	2.72	1	1	1	1
1354	H9B3Z0	Bromodomain adjacent to zinc finger domain-like protein 2	2.72	2	1	1	1
1355	dsrrswapns_comp214613_c0_seq5	len=3333	2.72	5	1	1	1
1356	CL3320Contig1	CL3320Contig1	2.70	2	1	1	1
1357	O57526	Insulin-like growth factor 2 mRNA-binding protein 3-B OS=	2.70	2	1	1	1
1358	CL4229Contig1	CL4229Contig1	2.70	1	1	1	1
1359	O42507	Thrombospondin-3 (Fragment) OS=Xenopus laevis PE=2 S	2.70	1	1	1	1
1360	CL521Contig1	CL521Contig1	2.69	6	1	1	1
1361	Q6PA48	Protein TBRG4 OS=Xenopus laevis GN=tbrg4 PE=2 SV=1	2.69	1	1	1	1
1362	CL1401Contig6	CL1401Contig6	2.68	3	1	1	1
1363	Q7ZYF6	Bag3-A protein OS=Xenopus laevis GN=bag3 PE=2 SV=1	2.68	1	1	1	1
1364	CL13132Contig1	CL13132Contig1	2.68	1	1	1	1
1365	CL2885Contig1;Q91929	CL2885Contig1	2.67	1	1	1	4
1366	Q4V7L1	MGC115598 protein OS=Xenopus laevis GN=MGC115598	2.66	1	1	1	1
1367	Q7T106;33416619	MGC68423 protein OS=Xenopus laevis GN=10a1.1 PE=2	2.66	9	1	1	3

1368	Q6GNT1;CL1947Contig1	MGC80898 protein OS=Xenopus laevis GN=brd1 PE=2 SV	2.65	253	1	2	3
1369	Q6INT7	MGC80341 protein OS=Xenopus laevis GN=mark1 PE=2 S	2.65	227	1	2	2
1370	Q66IX2	MGC84231 protein OS=Xenopus laevis GN=psmd13 PE=2	2.65	1	1	1	1
1371	CL3876Contig1	CL3876Contig1	2.64	1	1	1	1
1372	A0JMZ1;CL1Contig964	Nucleolar and spindle-associated protein 1-B OS=Xenopus	2.62	230	1	2	3
1373	Q2TAF4;CL5014Contig2	Integrator complex subunit 6-A OS=Xenopus laevis GN=int	2.60	2	1	1	9
1374	dsrrswapns_comp217589_c0_seq4	len=5068	2.60	2	1	1	1
1375	CL6354Contig1	CL6354Contig1	2.59	1	1	1	1
1376	CL21287Contig1	CL21287Contig1	2.58	1	1	1	1
1377	A4IFX5	LOC100049142 protein (Fragment) OS=Xenopus laevis GN	2.57	1	1	1	1
1378	Q4V7V7	MGC115244 protein OS=Xenopus laevis GN=hmgxb3 PE=	2.57	1	1	1	1
1379	A1L2J4	Putative uncharacterized protein (Fragment) OS=Xenopus l	2.56	3	1	1	1
1380	Q5EAY8	Transmembrane anterior posterior transformation protein 1	2.56	227	1	2	3
1381	Q501Q8	MGC99195 protein OS=Xenopus laevis GN=sel1l PE=2 SV	2.55	1	1	1	1
1382	Q641D4	MGC82000 protein OS=Xenopus laevis GN=golm1 PE=2 S	2.54	3	1	1	15
1383	dsrrswapns_comp215656_c4_seq1	len=2897	2.53	3	1	1	1
1384	Q4KLT2	MGC115451 protein OS=Xenopus laevis GN=MGC115451	2.53	6	1	1	6
1385	A0JMY5;CL6629Contig1	NF-X1-type zinc finger protein NFXL1 OS=Xenopus laevis	2.52	1	1	1	2
1386	Q56A68	LOC733185 protein (Fragment) OS=Xenopus laevis GN=L	2.50	290	1	2	2
1387	CL19415Contig1	CL19415Contig1	2.50	1	1	1	1
1388	Q7ZXT0	Egfl7 protein OS=Xenopus laevis GN=egfl7 PE=2 SV=1 - [	2.50	2	1	1	1
1389	28386279	Xenopus laevis, Similar to propionyl Coenzyme A carboxyla	2.48	1	1	1	1
1390	Q7ZTA4	Hus1 protein OS=Xenopus laevis GN=hus1 PE=2 SV=1 - [	2.48	2	1	1	1
1391	CL11346Contig1	CL11346Contig1	2.48	2	1	1	2
1392	A1L2U3	LOC100036954 protein OS=Xenopus laevis GN=LOC1000	2.47	2	1	1	2
1393	CL24722Contig1	CL24722Contig1	2.47	2	1	1	1
1394	CL1151Contig6	CL1151Contig6	2.46	1	1	1	5
1395	Q6GQ97	MGC80235 protein OS=Xenopus laevis GN=rassf3 PE=2 S	2.46	1	1	1	1
1396	Q32NR3	DNA-binding protein RFX2 OS=Xenopus laevis GN=rfx2 P	2.45	1	1	1	4
1397	CL3570Contig2	CL3570Contig2	2.45	3	1	1	1
1398	Q4FZX3	LOC432087 protein (Fragment) OS=Xenopus laevis GN=L	2.44	13	1	1	10
1399	Q4V7N2	tRNA (cytosine(34)-C(5))-methyltransferase OS=Xenopus l	2.44	2	1	1	1
1400	CL1Contig104	CL1Contig104	2.43	4	1	1	1
1401	Q6GNZ4	MGC80774 protein OS=Xenopus laevis GN=mlh3 PE=2 SV	2.43	1	1	1	1
1402	CL5194Contig2	CL5194Contig2	2.43	2	1	1	1
1403	CL7044Contig1	CL7044Contig1	2.43	1	1	1	1
1404	CL3902Contig1	CL3902Contig1	2.42	1	1	1	1
1405	A1L3F7	LOC100036993 protein (Fragment) OS=Xenopus laevis GN	2.40	2	1	1	1
1406	Q6DJH9;dsrrswapns_comp216790_c1_seq4	MGC83433 protein OS=Xenopus laevis GN=smg7 PE=2 S	2.39	201	1	2	7
1407	A5XAW2	Kinesin heavy chain (Fragment) OS=Xenopus laevis GN=K	2.39	1	1	1	3
1408	Q7ZWS4	MGC53764 protein OS=Xenopus laevis GN=rpn2 PE=2 SV	2.38	5	1	1	17
1409	CL8729Contig1	CL8729Contig1	2.37	4	1	1	1
1410	CL9389Contig1	CL9389Contig1	2.36	1	1	1	1
1411	CL38290Contig1	CL38290Contig1	2.36	1	1	1	1
1412	CL9699Contig1	CL9699Contig1	2.36	1	1	1	1
1413	Q7ZYF4	Gfpt1-prov protein OS=Xenopus laevis GN=gfpt2 PE=2 SV	2.35	1	1	1	2
1414	Q6PCJ3	MGC68945 protein OS=Xenopus laevis GN=yeats2 PE=2	2.34	1	1	1	1
1415	CL574Contig9	CL574Contig9	2.33	1	1	1	1
1416	CL3688Contig1	CL3688Contig1	2.33	1	1	1	1
1417	Q4V7W0	MGC80416 protein OS=Xenopus laevis GN=MGC80416 P	2.33	2	1	1	1
1418	Q5HZ99;CL2118Contig4	MGC85083 protein OS=Xenopus laevis GN=dsc3 PE=2 SV	2.33	2	1	1	2
1419	A3KMH8	LOC398050 protein OS=Xenopus laevis GN=LOC398050	2.31	229	1	2	2
1420	CL5248Contig1	CL5248Contig1	2.30	1	1	1	1
1421	Q9DGF4	Prox 1 protein OS=Xenopus laevis GN=prox1 PE=2 SV=1 -	2.30	1	1	1	1
1422	Q9IBF6	Prolactin receptor OS=Xenopus laevis GN=prlr PE=2 SV=1	2.29	2	1	1	1
1423	CL6953Contig2	CL6953Contig2	2.26	1	1	1	2
1424	dsrrswapns_comp217466_c0_seq5	len=4926	2.26	3	1	1	4
1425	Q6IRN1;CL8563Contig2	MGC83880 protein OS=Xenopus laevis GN=eftud1 PE=2 S	2.26	2	1	1	10
1426	Q9DEF3	Patched-2 OS=Xenopus laevis GN=ptch2 PE=2 SV=1 - [Q	2.26	1	1	1	1
1427	CL4162Contig1	CL4162Contig1	2.25	2	1	1	1
1428	Q4KLP9;CL7902Contig1	MGC115697 protein OS=Xenopus laevis GN=parg PE=2 S	2.24	1	1	1	4
1429	CL16886Contig1	CL16886Contig1	2.24	1	1	1	9
1430	CL7485Contig1	CL7485Contig1	2.24	2	1	1	1
1431	A0AUS4;CL3713Contig3	LOC398314 protein OS=Xenopus laevis GN=dlat PE=2 SV	2.23	5	1	1	4
1432	Q6PAC8	MGC68803 protein OS=Xenopus laevis GN=MGC68803 P	2.23	1	1	1	2
1433	CL1416Contig2	CL1416Contig2	2.23	3	1	1	1
1434	CL979Contig6	CL979Contig6	2.22	2	1	1	1
1435	CL2664Contig2	CL2664Contig2	2.22	1	1	1	1
1436	A0AUT1	Trichoplein keratin filament-binding protein OS=Xenopus la	2.20	1	1	1	1
1437	CL4601Contig1	CL4601Contig1	2.18	2	1	1	1
1438	Q66KI6;CL1079Contig4	Pum1-A protein OS=Xenopus laevis GN=pum1 PE=2 SV=1	2.18	5	1	1	2
1439	Q5PPV5	Zinc finger C2HC domain-containing protein 1A OS=Xenop	2.17	3	1	1	4
1440	CL10383Contig2	CL10383Contig2	2.17	2	1	1	7
1441	Q8QFR2	Protein HIRA OS=Xenopus laevis GN=hira PE=1 SV=2 - [H	2.17	6	2	2	2
1442	CL5361Contig2	CL5361Contig2	2.17	1	1	1	1
1443	B9V5F5	Centrosomal protein of 63 kDa-A OS=Xenopus laevis GN=	2.16	290	1	2	2
1444	Q767H5	Serine/threonine protein kinase BRAF OS=Xenopus laevis	2.15	2	1	1	1
1445	CL416Contig6	CL416Contig6	2.15	2	1	1	1
1446	A4IFX0	LOC100049139 protein OS=Xenopus laevis GN=LOC1000	2.14	1	1	1	1
1447	Q6GLN2	MGC84671 protein OS=Xenopus laevis GN=wasf1 PE=2 S	2.14	1	1	1	1
1448	P70047;CL2Contig68	Myelin transcription factor 1 OS=Xenopus laevis GN=myt1	2.14	6	1	1	3
1449	Q4V801	LOC398774 protein OS=Xenopus laevis GN=LOC398774	2.14	1	1	1	1
1450	Q91757	Glycogen synthase kinase-3 beta OS=Xenopus laevis GN=	2.14	1	1	1	1
1451	CL4762Contig1	CL4762Contig1	2.14	1	1	1	1
1452	Q6IP81	MGC78867 protein OS=Xenopus laevis GN=lta4h PE=2 SV	2.13	1	1	1	2
1453	CL3733Contig2	CL3733Contig2	2.13	1	1	1	1

1454	dsrrswapns_comp216836_c3_seq1	len=3961	2.13	2	1	1	1
1455	CL952Contig1	CL952Contig1	2.12	2	1	1	4
1456	Q1W3Z6	Silencing mediator for retinoid and thyroid hormone recepto	2.12	9	4	4	4
1457	Q8AVE7;CL3384Contig1	1i973-prov protein OS=Xenopus laevis GN=gnl2 PE=2 SV=	2.12	1	1	1	2
1458	zeinaSSns_comp386979_c1_seq2	len=2448	2.11	3	1	1	2
1459	D8WX02;CL4813Contig1	Midline 1 OS=Xenopus laevis GN=mid1 PE=2 SV=1 - [D8W	2.10	1	1	1	3
1460	Q6DDF7	MGC84593 protein OS=Xenopus laevis GN=atp13a4 PE=2	2.10	9	2	2	12
1461	Q8AVF2;CL8795Contig2	MGC52738 protein OS=Xenopus laevis GN=tom1l1 PE=2	2.10	1	1	1	2
1462	Q4V7X5	LOC733254 protein (Fragment) OS=Xenopus laevis GN=L	2.09	8	1	1	1
1463	Q7ZYI2;CL621Contig2	MGC52980 protein OS=Xenopus laevis PE=2 SV=1 - [Q7Z	2.09	2	1	1	37
1464	Q1W9P0	Secretory pathway Ca,Mn-ATPase OS=Xenopus laevis GN	2.07	1	1	1	1
1465	Q5U4W7	LOC495416 protein (Fragment) OS=Xenopus laevis GN=L	2.06	253	1	2	2
1466	Q6P9I2;CL2377Contig1	MGC69046 protein OS=Xenopus laevis GN=col3a1 PE=2	2.05	3	1	2	3
1467	Q640H2	LOC494715 protein OS=Xenopus laevis GN=scp2 PE=2 S	2.05	6	1	1	5
1468	CL114Contig15	CL114Contig15	2.05	3	1	1	1
1469	Q4A520;CL7515Contig1	Putative transient receptor potential channel OS=Xenopus	2.04	1	1	1	2
1470	Q66J73	MGC81714 protein OS=Xenopus laevis GN=abcf1 PE=2 S	2.03	3	1	1	2
1471	A1L1H7	LOC733281 protein OS=Xenopus laevis GN=supt5h PE=2	2.03	1	1	1	1
1472	Q6GMC9;dsrrswapns_comp211495_c1_seq2	GMP reductase OS=Xenopus laevis GN=gmpr2 PE=2 SV=	2.02	4	1	1	2
1473	Q7ZX69;CL1735Contig1	MGC52894 protein OS=Xenopus laevis GN=MGC52894 P	2.02	3	1	1	2
1474	Q6DCM5	Ppp4r1-prov protein OS=Xenopus laevis GN=ppp4r1 PE=2	2.01	1	1	1	1
1475	Q7ZX18	MGC53357 protein OS=Xenopus laevis GN=arhgap11a.1	2.00	1	1	1	1
1476	Q2EI21	RE1-silencing transcription factor A OS=Xenopus laevis G	2.00	1	1	1	1
1477	Q7ZWV0;CL4305Contig3	Kin-1-prov protein OS=Xenopus laevis GN=prkacb PE=2 S	1.99	3	1	1	2
1478	Q66J54	Solute carrier family 22 member 6-A OS=Xenopus laevis G	1.97	1	1	1	2
1479	Q9W6C5	Programmed cell death 6-interacting protein OS=Xenopus	1.96	2	1	1	1
1480	dsrrswapns_comp212594_c0_seq1	len=1253	1.96	1	1	1	3
1481	CL2520Contig2	CL2520Contig2	1.96	1	1	1	1
1482	CL8606Contig1	CL8606Contig1	1.96	1	1	1	2
1483	Q6DDN9	Cbs-prov protein OS=Xenopus laevis GN=cbs PE=2 SV=1	1.96	2	1	1	2
1484	Q6GN12	MGC83651 protein OS=Xenopus laevis GN=tbc1d4 PE=2	1.96	1	1	1	1
1485	CL9204Contig1	CL9204Contig1	1.94	1	1	1	1
1486	CL4783Contig2	CL4783Contig2	1.94	1	1	1	1
1487	Q08AX1	LOC100158396 protein OS=Xenopus laevis GN=klhl32 PE	1.94	1	1	1	1
1488	Q6GPX8	MGC82533 protein OS=Xenopus laevis GN=pafah2 PE=2	1.93	1	1	1	1
1489	CL4122Contig1	CL4122Contig1	1.91	2	1	1	2
1490	dsrrswapns_comp196398_c0_seq1	len=1229	1.90	1	1	1	1
1491	O13124;CL7992Contig1	Vitamin D3 receptor OS=Xenopus laevis GN=vdr PE=2 SV	1.90	2	1	1	4
1492	B7ZRI3	Ret proto-oncogene OS=Xenopus laevis GN=ret-A PE=2 S	1.89	3	1	1	1
1493	dsrrswapns_comp217428_c1_seq4	len=5152	1.89	2	1	1	1
1494	Q6DCT2	UPF0668 protein C10orf76 homolog OS=Xenopus laevis P	1.89	1	1	1	1
1495	Q8AVN8;CL1362Contig1	Cdc37-prov protein OS=Xenopus laevis GN=cdc37 PE=2 S	1.89	1	1	1	5
1496	CL3689Contig1	CL3689Contig1	1.88	2	1	1	2
1497	Q9PTE5	Phosphoinositide 3 kinase catalytic subunit (Fragment) OS	1.88	4	1	1	10
1498	dsrrswapns_comp217313_c0_seq59	len=2833	1.88	6	1	1	1
1499	CL3458Contig1	CL3458Contig1	1.86	1	1	1	2
1500	Q2TAV8;CL6367Contig1	Wdhd1 protein OS=Xenopus laevis GN=wdhd1 PE=2 SV=1	1.86	3	1	1	2
1501	zeinaSSns_comp387425_c1_seq4	len=3248	1.85	2	1	1	1
1502	CL4098Contig1	CL4098Contig1	1.83	3	1	1	1
1503	B7ZRM8	MDS1 and EVI1 complex locus protein EVI1-B OS=Xenopu	1.81	1	1	1	1
1504	CL3472Contig1	CL3472Contig1	1.81	2	2	2	2
1505	D3IUT5	Treslin OS=Xenopus laevis GN=ticrr PE=1 SV=1 - [TICRR_	1.81	1	1	1	1
1506	zeinaSSns_comp388845_c0_seq6	len=3172	1.80	6	1	1	1
1507	Q5FWX5	MGC98794 protein OS=Xenopus laevis GN=MGC98794 P	1.79	1	1	1	1
1508	CL119Contig4	CL119Contig4	1.77	1	1	1	1
1509	CL212Contig6	CL212Contig6	1.74	3	2	2	7
1510	Q569Z1	Eukaryotic translation initiation factor 3 subunit B OS=Xeno	1.74	1	1	1	1
1511	Q6PCI5	Mtmr3 protein OS=Xenopus laevis GN=Mtmr3 PE=2 SV=1	1.72	1	1	1	1
1512	CL4408Contig3	CL4408Contig3	1.71	1	1	1	1
1513	Q6NUC6;CL25Contig6	Roquin OS=Xenopus laevis GN=rc3h1 PE=2 SV=1 - [RC3	1.71	4	1	1	4
1514	B7ZQN6;CL688Contig4	Cttn protein OS=Xenopus laevis GN=Cttn PE=2 SV=1 - [B7	1.70	9	1	1	2
1515	A9UMM8	LOC100137686 protein OS=Xenopus laevis GN=khnyn PE	1.69	1	1	1	1
1516	CL10344Contig2	CL10344Contig2	1.69	201	1	2	4
1517	Q5U4V0	LOC495494 protein OS=Xenopus laevis GN=tnpo1 PE=2 S	1.69	253	1	2	2
1518	CL8672Contig1	CL8672Contig1	1.68	1	1	1	2
1519	CL11069Contig2	CL11069Contig2	1.67	1	1	1	1
1520	Q642N7	LOC446968 protein (Fragment) OS=Xenopus laevis GN=L	1.65	2	1	1	1
1521	Q66JA4	MGC81147 protein OS=Xenopus laevis GN=MGC81147 P	1.65	1	1	1	2
1522	dsrrswapns_comp214315_c4_seq3	len=2467	1.64	3	1	1	1
1523	CL1459Contig2	CL1459Contig2	1.64	2	1	1	4
1524	CL1649Contig3	CL1649Contig3	1.63	2	1	1	4
1525	Q8QHA5;CL6103Contig1	DNA replication ATP-dependent helicase/nuclease DNA2 C	1.61	1	1	1	2
1526	CL3741Contig1	CL3741Contig1	1.60	2	1	1	2
1527	CL971Contig9	CL971Contig9	1.59	4	1	1	1
1528	CL170Contig6	CL170Contig6	1.59	1	1	1	2
1529	dsrrswapns_comp217415_c3_seq4	len=3082	1.57	3	1	1	1
1530	CL7944Contig1	CL7944Contig1	1.57	2	1	1	1
1531	CL7517Contig1	CL7517Contig1	1.55	1	1	1	1
1532	Q6IR70	Protein phosphatase 1 regulatory subunit 21 OS=Xenopus	1.55	1	1	1	2
1533	CL2535Contig5	CL2535Contig5	1.53	2	1	1	1
1534	CL1930Contig6	CL1930Contig6	1.52	201	1	2	3
1535	Q6NU36	MGC81278 protein OS=Xenopus laevis GN=anapc4 PE=2	1.52	1	1	1	1
1536	B7ZRE7	Breast and ovarian cancer susceptibility protein OS=Xenop	1.52	2	1	1	1
1537	Q641H7	MGC81565 protein OS=Xenopus laevis GN=lats1 PE=2 SV	1.52	1	1	1	1
1538	Q7ZWJ1	SYNE1 protein (Fragment) OS=Xenopus laevis GN=SYNE	1.52	1	1	1	1
1539	Q2TAQ2	LOC733439 protein (Fragment) OS=Xenopus laevis GN=L	1.51	1	1	1	1

1540	P42291	D(1C) dopamine receptor OS=Xenopus laevis GN=drd1c P	1.51	1	1	1	1
1541	Q6P7F7	MGC68765 protein OS=Xenopus laevis GN=smtn PE=2 SV	1.50	291	1	2	4
1542	CL1096Contig1	CL1096Contig1	1.50	2	1	1	1
1543	Q0IHJ9	MGC154309 protein OS=Xenopus laevis GN=nsun6 PE=2	1.50	1	1	1	1
1544	dsrrswapns_comp210557_c0_seq1	len=1322	1.50	1	1	1	1
1545	P08759;CL504Contig3	Serum albumin A OS=Xenopus laevis GN=alb-a PE=2 SV=	1.49	9	1	1	7
1546	Q7ZXZ0	Zygotic DNA replication licensing factor mcm3 OS=Xenopus	1.49	2	1	1	4
1547	Q801Q1	MGC53743 protein OS=Xenopus laevis GN=rrp1b PE=2 SV	1.47	4	1	1	2
1548	zeinaSSns_comp386267_c0_seq1	len=6035	1.47	2	1	1	1
1549	A1L2R9	Putative uncharacterized protein OS=Xenopus laevis PE=2	1.46	2	1	1	1
1550	Q6NS25;CL8312Contig1	MGC78791 protein OS=Xenopus laevis GN=ints2 PE=2 SV	1.45	1	1	1	3
1551	P20310	Neural cadherin-1 OS=Xenopus laevis PE=2 SV=1 - [CADH	1.44	5	1	1	31
1552	CL2010Contig3	CL2010Contig3	1.44	3	1	1	4
1553	Q641G4	Condensin-2 complex subunit H2 OS=Xenopus laevis GN=	1.44	1	1	1	2
1554	Q641B0;CL3581Contig2	Dmd protein OS=Xenopus laevis GN=dmd.1 PE=2 SV=1 - [	1.42	8	1	1	3
1555	CL4320Contig3	CL4320Contig3	1.41	1	1	1	1
1556	CL4793Contig1	CL4793Contig1	1.37	1	1	1	1
1557	P70049	Origin recognition complex protein 1 OS=Xenopus laevis G	1.35	2	1	1	1
1558	CL19729Contig1	CL19729Contig1	1.35	1	1	1	1
1559	dsrrswapns_comp217626_c0_seq5	len=5041	1.35	1	1	1	2
1560	D5JEJ8	Afadin OS=Xenopus laevis GN=mllt4 PE=2 SV=1 - [D5JEJ	1.35	1	1	1	1
1561	CL821Contig1	CL821Contig1	1.34	2	1	1	1
1562	Q6INP8	Mediator of RNA polymerase II transcription subunit 1 OS=	1.34	1	1	1	1
1563	Q6DFC7	LOC445830 protein (Fragment) OS=Xenopus laevis GN=L	1.34	296	1	2	3
1564	CL2547Contig3	CL2547Contig3	1.33	1	1	1	1
1565	Q6GN44	LOC443684 protein (Fragment) OS=Xenopus laevis GN=L	1.33	1	1	1	3
1566	Q641C5	MGC82112 protein OS=Xenopus laevis GN=MGC82112 PE	1.33	4	1	1	1
1567	Q5U4N0	LOC495463 protein (Fragment) OS=Xenopus laevis GN=L	1.32	2	1	1	3
1568	CL800Contig5	CL800Contig5	1.31	2	1	1	1
1569	CL20539Contig1	CL20539Contig1	1.31	1	1	1	1
1570	CL5444Contig1	CL5444Contig1	1.30	4	1	1	1
1571	CL11289Contig1	CL11289Contig1	1.30	2	1	1	1
1572	A8E0R9	Glutamate receptor-interacting protein 2 OS=Xenopus laevi	1.29	1	1	1	1
1573	CL465Contig2	CL465Contig2	1.29	1	1	1	1
1574	E5LG93	Centrosomal protein OS=Xenopus laevis GN=cep192 PE=	1.29	1	1	1	1
1575	zeinaSSns_comp386803_c0_seq3	len=4262	1.28	5	1	1	2
1576	P26363	Cystic fibrosis transmembrane conductance regulator OS=	1.28	1	1	1	2
1577	CL3824Contig1	CL3824Contig1	1.28	1	1	1	1
1578	Q6NU33	MGC81285 protein OS=Xenopus laevis GN=eps8 PE=2 SV	1.27	1	1	1	1
1579	Q6NU54;CL2259Contig1	MGC81241 protein OS=Xenopus laevis GN=tsc22d2 PE=2	1.27	3	1	1	9
1580	CL2871Contig3	CL2871Contig3	1.26	1	1	1	8
1581	B7ZSB1	Putative uncharacterized protein OS=Xenopus laevis PE=2	1.26	2	1	1	1
1582	A5PKN6;CL3181Contig1	LOC100101289 protein OS=Xenopus laevis GN=fam13a P	1.26	3	1	1	10
1583	Q6DDG3	Pik4ca-prov protein OS=Xenopus laevis GN=pi4ka PE=2 S	1.26	1	1	1	1
1584	Q6NRC4	LOC431827 protein (Fragment) OS=Xenopus laevis GN=L	1.26	228	1	2	2
1585	B2DCQ5;CL597Contig2	Cdc25B phosphatase OS=Xenopus laevis GN=cdc25b PE=	1.25	2	1	1	3
1586	CL6498Contig1	CL6498Contig1	1.25	2	1	1	2
1587	Q6DCU8	LOC397741 protein OS=Xenopus laevis GN=LOC397741 F	1.25	291	1	2	3
1588	Q66KF0;CL6164Contig1	MGC86497 protein OS=Xenopus laevis GN=ppp1r13l PE=	1.24	2	1	1	3
1589	CL9436Contig1	CL9436Contig1	1.23	1	1	1	1
1590	Q6DFG3;TC413472	MGC83673 protein OS=Xenopus laevis GN=MGC83673 PE	1.22	3	1	1	3
1591	CL11908Contig1	CL11908Contig1	1.22	1	1	1	1
1592	O93308	Structural maintenance of chromosomes protein 1A OS=Xe	1.22	253	1	2	2
1593	Q4V7Y7	Katanin p80 WD40-containing subunit B1 OS=Xenopus lae	1.22	1	1	1	1
1594	A8CWK9	Low density lipoprotein-related protein 2 (Fragment) OS=Xe	1.22	3	1	1	1
1595	Q7ZT76	IQ motif containing GTPase activating protein 2 OS=Xenop	1.20	544	1	3	3
1596	CL7560Contig1	CL7560Contig1	1.20	2	1	1	1
1597	Q6GPA3	LOC443632 protein (Fragment) OS=Xenopus laevis GN=L	1.20	3	1	1	1
1598	Q6GQD1	Cytoplasmic FMR1-interacting protein 2 OS=Xenopus laevi	1.20	227	1	2	2
1599	Q5XGZ5	LOC495108 protein OS=Xenopus laevis GN=snx18 PE=2 S	1.19	1	1	1	1
1600	Q6PF33	Mmp9 protein OS=Xenopus laevis GN=mmp9 PE=2 SV=1 -	1.19	3	1	1	1
1601	Q6JDF3	Schnurri 2 (Fragment) OS=Xenopus laevis PE=2 SV=1 - [Q	1.18	2	1	1	3
1602	Q6DCY9;CL8574Contig1	HAUS augmin-like complex subunit 3 OS=Xenopus laevis	1.17	1	1	1	4
1603	A6QL57	LOC100125670 protein (Fragment) OS=Xenopus laevis GN	1.16	4	1	1	2
1604	CL1161Contig2	CL1161Contig2	1.15	3	1	1	1
1605	Q642P2	Protein dopey-2 OS=Xenopus laevis GN=dopey2 PE=2 SV	1.15	1	1	1	1
1606	CL508Contig4	CL508Contig4	1.14	1	1	1	1
1607	Q6GM70	LOC443696 protein (Fragment) OS=Xenopus laevis GN=L	1.13	3	1	1	3
1608	CL2693Contig2	CL2693Contig2	1.12	2	1	1	2
1609	Q6GNU6	MGC80868 protein OS=Xenopus laevis GN=apaf1 PE=2 S	1.12	291	1	2	2
1610	Q8AVN3	Kiaa0010-prov protein OS=Xenopus laevis GN=ube3c PE=	1.11	1	1	1	1
1611	Q5HZP4;CL1727Contig2	LOC496341 protein OS=Xenopus laevis GN=ppp1r13b PE	1.11	1	1	1	7
1612	Q5XG51	LOC495282 protein (Fragment) OS=Xenopus laevis GN=L	1.10	1	1	1	1
1613	CL657Contig3	CL657Contig3	1.10	2	1	1	1
1614	Q6AX83	MGC82093 protein OS=Xenopus laevis GN=lars PE=2 SV=	1.10	1	1	1	1
1615	A1L1G6;CL1072Contig1	LOC100036836 protein OS=Xenopus laevis GN=kiaa0182	1.07	4	1	1	2
1616	CL7022Contig2	CL7022Contig2	1.04	2	1	1	1
1617	CL5186Contig1	CL5186Contig1	1.03	2	1	1	1
1618	Q6DKD7	Coatomer subunit gamma-2 OS=Xenopus laevis GN=copg	1.03	1	1	1	2
1619	Q66J90	Histone-lysine N-methyltransferase SETD1B OS=Xenopus	1.03	1	1	1	1
1620	O73732	Rho-associated kinase alpha OS=Xenopus laevis GN=rock	1.02	2	1	2	3
1621	Q6GPX6;CL1066Contig1	MGC82535 protein OS=Xenopus laevis GN=fam129b PE=	1.01	4	1	1	6
1622	B7ZSK0	Structural maintenance of chromosomes protein OS=Xeno	1.01	2	1	1	1
1623	CL15423Contig1	CL15423Contig1	1.01	2	1	1	1
1624	Q6NTR6	Ubiquitin carboxyl-terminal hydrolase 44-A OS=Xenopus la	1.01	1	1	1	1
1625	Q6DE48;CL1839Contig1	Rbbp5-prov protein OS=Xenopus laevis GN=rbbp5 PE=2 S	1.00	26	1	1	4

1626	dsrrswapns_comp216663_c2_seq9	len=3510	1.00	4	1	1	1
1627	Q6GPD0	Rho GTPase-activating protein 32 OS=Xenopus laevis GN=	0.98	1	1	1	1
1628	CL2453Contig4	CL2453Contig4	0.97	2	2	2	2
1629	CL3547Contig2	CL3547Contig2	0.97	2	1	1	1
1630	Q6GM46;CL3306Contig3	MGC83972 protein OS=Xenopus laevis GN=pde4b PE=2 S	0.97	2	1	1	4
1631	Q6AXA7	MGC80263 protein OS=Xenopus laevis GN=prpf6 PE=2 S	0.95	1	1	1	1
1632	B7ZS80;CL2280Contig1	Tyrosine-protein kinase receptor OS=Xenopus laevis GN=L	0.95	4	1	1	2
1633	Q2V0J3;CL661Contig1	Semaphorin 6D4 OS=Xenopus laevis GN=sema6d PE=2 S	0.92	6	1	1	2
1634	Q91684	DNA polymerase subunit gamma-1 OS=Xenopus laevis GN	0.92	1	1	1	1
1635	A2RV71	LOC100037140 protein OS=Xenopus laevis GN=LOC1000	0.91	2	1	1	2
1636	CL13558Contig1	CL13558Contig1	0.90	1	1	1	2
1637	CL11836Contig1	CL11836Contig1	0.89	1	1	1	1
1638	zeinaSSns_comp384061_c2_seq2	len=4918	0.89	2	1	1	3
1639	Q3KQ57	MGC130942 protein OS=Xenopus laevis GN=trappc12 PE=	0.89	1	1	1	1
1640	CL12958Contig1	CL12958Contig1	0.88	1	1	1	1
1641	CL112Contig13	CL112Contig13	0.86	3	1	1	1
1642	Q91829	V(D)J recombination-activating protein 1 OS=Xenopus laev	0.86	1	1	1	1
1643	Q566I1	INO80 complex subunit D OS=Xenopus laevis GN=ino80d	0.86	1	1	1	1
1644	Q6GQ04	MGC80529 protein OS=Xenopus laevis GN=cdc27 PE=1 S	0.84	2	1	1	6
1645	zeinaSSns_comp389497_c1_seq2	len=5283	0.83	2	1	1	1
1646	CL1424Contig5	CL1424Contig5	0.82	1	1	1	1
1647	dsrrswapns_comp217958_c1_seq1	len=15803	0.82	3	2	2	9
1648	Q6PF79;CL1865Contig1	Ctcf protein OS=Xenopus laevis GN=ctcf PE=2 SV=1 - [Q6	0.82	8	1	1	2
1649	CL9010Contig1	CL9010Contig1	0.77	1	1	1	5
1650	dsrrswapns_comp207902_c1_seq2	len=6129	0.77	1	1	1	1
1651	Q5XGY6	LOC495114 protein OS=Xenopus laevis GN=fhod1 PE=2 S	0.75	1	1	1	1
1652	Q5FWQ3	LOC733157 protein (Fragment) OS=Xenopus laevis GN=L	0.75	1	1	1	2
1653	A0JMU7	Zswim4_predicted protein OS=Xenopus laevis GN=zswim4	0.73	2	1	1	2
1654	A1L1H0	LOC100036839 protein OS=Xenopus laevis GN=rere PE=2	0.72	1	1	1	1
1655	Q640I9	Lysine-specific demethylase 2B OS=Xenopus laevis GN=k	0.71	1	1	1	1
1656	CL9129Contig1	CL9129Contig1	0.70	1	1	1	1
1657	Q860P5;CL387Contig2	Bat2-prov protein OS=Xenopus laevis GN=prrc2a PE=2 SV	0.69	8	1	1	2
1658	Q6AZS3	Uty-prov protein OS=Xenopus laevis GN=kdm6a PE=2 SV=	0.69	1	1	1	1
1659	Q7ZWK4	LOC398587 protein (Fragment) OS=Xenopus laevis GN=L	0.69	1	1	1	1
1660	Q1XG43;CL46Contig7	Scc2-2A OS=Xenopus laevis GN=SCC2-2 PE=2 SV=1 - [Q	0.67	4	1	1	2
1661	CL6529Contig1	CL6529Contig1	0.65	1	1	1	1
1662	Q5MPF8	Ataxia telangiectasia mutated OS=Xenopus laevis GN=atm	0.65	252	1	2	2
1663	Q9IBG7	Kielin/chordin-like protein OS=Xenopus laevis GN=kcp PE=	0.64	1	1	1	1
1664	Q6DFG4;CL2111Contig1	MGC83457 protein OS=Xenopus laevis GN=ephb3 PE=2 S	0.62	4	1	1	4
1665	Q6GN08	LOC398742 protein OS=Xenopus laevis GN=ncapd3 PE=2	0.60	1	1	1	1
1666	dsrrswapns_comp217697_c0_seq6	len=5729	0.59	1	1	1	11
1667	Q6GQ76;CL4342Contig3	Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase 1	0.59	8	1	1	2
1668	CL11854Contig1	CL11854Contig1	0.56	1	1	1	4
1669	D0PPG1	Costal2 OS=Xenopus laevis GN=Cos2 PE=2 SV=1 - [D0PP	0.56	4	1	1	1
1670	Q6INA9	Histone-lysine N-methyltransferase SETDB1 OS=Xenopus	0.55	1	1	1	2
1671	CL165Contig4	CL165Contig4	0.52	1	1	1	1
1672	Q6DFF2	Brd4-prov protein OS=Xenopus laevis GN=brd4 PE=2 SV=	0.51	2	1	1	3
1673	CL760Contig2	CL760Contig2	0.46	7	1	1	1
1674	CL825Contig2	CL825Contig2	0.46	1	1	1	1
1675	B7ZSC6;CL817Contig2	Slit2-a protein OS=Xenopus laevis GN=slit2-a PE=2 SV=1 -	0.46	2	1	1	2
1676	zeinaSSns_comp389539_c1_seq3	len=5153	0.43	3	1	1	2
1677	dsrrswapns_comp216350_c2_seq3	len=6139	0.43	1	1	1	1
1678	Q5U248;CL1238Contig1	LOC495689 protein OS=Xenopus laevis GN=crebbp PE=2	0.41	6	1	1	3
1679	CL742Contig3	CL742Contig3	0.40	1	1	1	61
1680	Q9DDN8	Gravin-like OS=Xenopus laevis GN=akap12 PE=2 SV=1 - [	0.28	1	1	1	1
1681	dsrrswapns_comp215471_c0_seq2	len=8484	0.27	3	1	1	1
1682	CL5147Contig1	CL5147Contig1	0.26	1	1	1	1
1683	dsrrswapns_comp213817_c0_seq2	len=15316	0.19	4	1	1	18
1684	Q4G444	Polycystic kidney disease protein 1 (Fragment) OS=Xenop	0.09	252	1	2	2
1685	CL30361Contig1	CL30361Contig1	0.00	5	1	2	2
1686	CL4370Contig2	CL4370Contig2	0.00	1	1	1	1
1687	DC044722 similar to UniRef100_A6QM14 Cluster: CCDC	Rep: CCDC95 protein - Bos taurus (Bovine), partial (27%)	0.00	1	1	1	1
1688	DC050368 homologue to UniRef100_UPI000069F0BD C	Rep: Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like pr	0.00	1	1	1	2
1689	TC468263 similar to UniRef100_Q6PAB2 Cluster: MGC6	Rep: MGC68737 protein - Xenopus laevis (African clawed f	0.00	1	1	1	1
1690	BJ035035 UniRef100_Q6DD19 Cluster: MGC80437 prot	Rep: MGC80437 protein - Xenopus laevis (African clawed f	0.00	1	1	1	1
1691	TC468342 weakly similar to UniRef100_A7SS16 Cluster:	Rep: Predicted protein - Nematostella vectensis (Starlet se	0.00	1	1	1	1
1692	BJ072460	BJ072460	0.00	1	1	1	6
1693	CL1004Contig2	CL1004Contig2	0.00	1	1	1	1
1694	CL122Contig3	CL122Contig3	0.00	1	1	1	1
1695	CL3782Contig1	CL3782Contig1	0.00	2	1	1	1
1696	CL467Contig1	CL467Contig1	0.00	1	1	1	2
1697	CL46Contig4	CL46Contig4	0.00	1	1	1	1
1698	TC428802 UniRef100_Q5MMR9 Cluster: Brg1; n=1; Xen	Rep: Brg1 - Xenopus laevis (African clawed frog), partial (2	0.00	1	1	1	1
1699	BF611644 similar to UniRef100_Q58F92 Cluster: Cytoch	Rep: Cytochrome c oxidase subunit I - Bradypus tridactylus	0.00	1	1	1	1
1700	BG235002 similar to UniRef100_P08778 Cluster: Keratin	Rep: Keratin, type I cytoskeletal 47 kDa - Xenopus laevis (	0.00	1	1	1	1
1701	DC062871 homologue to UniRef100_Q8AVT6 Cluster: M	Rep: MGC52847 protein - Xenopus laevis (African clawed f	0.00	1	2	2	2
1702	TC463837 homologue to UniRef100_Q6NRS7 Cluster: M	Rep: MGC81523 protein - Xenopus laevis (African clawed f	0.00	1	1	1	3
1703	TC440393 similar to UniRef100_Q7T0T9 Cluster: Pla2g4	Rep: Pla2g4a protein - Xenopus laevis (African clawed frog	0.00	1	1	2	2
1704	TC424140 homologue to UniRef100_Q7ZZH7 Cluster: Pr	Rep: Protein DBF4 homolog A - Xenopus laevis (African cla	0.00	1	1	1	1
1705	BI349541 homologue to UniRef100_Q6AZH2 Cluster: SI	Rep: SIPA1L1 protein - Xenopus laevis (African clawed fro	0.00	1	1	1	1
1706	TC444576 homologue to UniRef100_UPI00004D667C C	Rep: Uncharacterized protein C6orf145. - Xenopus tropicali	0.00	1	1	1	1
1707	CA974276 similar to UniRef100_Q568S8 Cluster: Zgc:11	Rep: Zgc:110113 - Danio rerio (Zebrafish) (Brachydanio rer	0.00	1	1	1	4
1708	BG023428 similar to UniRef100_A0JPF1 Cluster: Zgc:15	Rep: Zgc:153686 - Danio rerio (Zebrafish) (Brachydanio rer	0.00	1	1	2	2
1709	Q71N44	Transcription factor IIA large subunit OS=Xenopus laevis G	0.00	1	1	1	1

Table S4. Representative 45 different proteins with significant differential expression between D11, V11, and V21 cell types. Protein abundance was calculated based on emPAI and median-normalized before analysis by ANOVA-Fisher's LSD.

Accession Number	Description	p value	-Log(p)	FDR	Fisher's LSD
CL640Contig6	CL640Contig6	0.00028629	3.5432	0.24249	V21 - D11; V21 - V11
CL10183Contig1	CL10183Contig1	0.0018743	2.7272	0.36129	D11 - V11; V21 - V11
Q8AVH2	Ckb-prov protein OS=Xenopus lae	0.0022181	2.654	0.36129	D11 - V11; V21 - V11
CL6407Contig1	CL6407Contig1	0.0017882	2.7476	0.36129	D11 - V11; V21 - V11
CL2028Contig2	CL2028Contig2	0.0025593	2.5919	0.36129	D11 - V11; D11 - V21; V21 - V11
CL81Contig10	CL81Contig10	0.002426	2.6151	0.36129	D11 - V11; D11 - V21
Q6P699	MGC68562 protein OS=Xenopus l	0.0094998	2.0223	0.57188	V11 - D11; V21 - D11
Q6GMC1	MGC81889 protein OS=Xenopus l	0.018068	1.7431	0.57188	V11 - D11; V21 - D11
A3KMT2	Death-associated protein-like 1-A	0.016696	1.7774	0.57188	V21 - D11
TC447025 homologue to Un	Rep: L-lactate dehydrogenase B c	0.016565	1.7808	0.57188	V11 - D11; V11 - V21
Q66KY9	MGC85306 protein OS=Xenopus l	0.032993	1.4816	0.57188	V11 - D11; V21 - D11
Q9W7I1	Activated protein kinase C recepto	0.016443	1.784	0.57188	V11 - D11; V11 - V21
Q9PTK6	Perilipin OS=Xenopus laevis GN=f	0.014578	1.8363	0.57188	V21 - D11; V21 - V11
CL3329Contig1	CL3329Contig1	0.0055328	2.2571	0.57188	D11 - V11; V21 - V11
CL4718Contig1	CL4718Contig1	0.0060192	2.2205	0.57188	D11 - V11; V21 - V11
Q6PAB3	Malate dehydrogenase, cytoplasm	0.011283	1.9476	0.57188	D11 - V11; D11 - V21
Q6PH94	40S ribosomal protein S12 OS=Xe	0.018928	1.7229	0.57188	D11 - V11
Q6GPU5	MGC82602 protein OS=Xenopus l	0.017152	1.7657	0.57188	D11 - V11; D11 - V21
P26642	Elongation factor 1-gamma-A OS=	0.022456	1.6487	0.57188	D11 - V11; D11 - V21
CL10303Contig1	CL10303Contig1	0.016985	1.7699	0.57188	D11 - V11; D11 - V21
CL2807Contig6	CL2807Contig6	0.036802	1.4341	0.57188	D11 - V11
P13549	Elongation factor 1-alpha, somatic	0.040627	1.3912	0.57188	V21 - D11; V21 - V11
CL52Contig8	CL52Contig8	0.016186	1.7909	0.57188	D11 - V11
Q91375	Elongation factor 1-gamma-B OS=	0.034498	1.4622	0.57188	D11 - V11
CL1Contig516	CL1Contig516	0.006713	2.1731	0.57188	D11 - V11; D11 - V21
DC017479 homologue to Ur	Rep: MGC84307 protein - Xenopu	0.039108	1.4077	0.57188	V21 - V11
zeinaSSns_comp370410_c	len=541	0.038704	1.4122	0.57188	V21 - V11
CL3941Contig2	CL3941Contig2	0.01608	1.7937	0.57188	D11 - V11; D11 - V21
CL100Contig17	CL100Contig17	0.0093764	2.028	0.57188	D11 - V11; D11 - V21
CL8453Contig2	CL8453Contig2	0.041195	1.3852	0.57188	D11 - V11
CL5360Contig3	CL5360Contig3	0.042495	1.3717	0.57188	D11 - V11; V21 - V11
P06180	Histone-binding protein N1/N2 OS	0.026772	1.5723	0.57188	D11 - V11
CL1948Contig4	CL1948Contig4	0.011635	1.9342	0.57188	D11 - V11; V21 - V11
CL1948Contig1	CL1948Contig1	0.01523	1.8173	0.57188	D11 - V11; V21 - V11
Q08AW0	LOC100036826 protein (Fragment	0.045863	1.3385	0.57188	V21 - V11
P02412	60S ribosomal protein L18-B OS=	0.039454	1.4039	0.57188	D11 - V11
DC017935 homologue to Ur	Rep: MGC52825 protein - Xenopu	0.038889	1.4102	0.57188	D11 - V11
CL100Contig5	CL100Contig5	0.043003	1.3665	0.57188	D11 - V11
TC460578 homologue to Un	Rep: MGC52578 protein - Xenopu	0.038841	1.4107	0.57188	D11 - V11
TC436798 UniRef100_Q7Z	Rep: MGC52578 protein - Xenopu	0.038838	1.4107	0.57188	D11 - V11
TC440824 similar to UniRef	Rep: MGC52825 protein - Xenopu	0.038838	1.4107	0.57188	D11 - V11
Q7ZXK5	MGC52578 protein OS=Xenopus l	0.038838	1.4107	0.57188	D11 - V11
Q91764	HMG-X protein OS=Xenopus laevi	0.038838	1.4107	0.57188	D11 - V11
zeinaSSns_comp387005_c	len=2084	0.040414	1.3935	0.57188	D11 - V11
TC434817 UniRef100_Q7Z	Rep: MGC52578 protein - Xenopu	0.038854	1.4106	0.57188	D11 - V11

Table S5. Proteins with significantly different relative abundances between D11, V11, and V21 blastomeres ($p < 0.05$, ≥1.3 fold change).

D11/V11

Accession	Description	log2(ratio)	-log10(p)
Q6GN79	Ribosomal protein L37 OS=Xenopus laevis GN=rpl37 PE=3 SV=1 -	1.658337106	1.925172322
Q6INB6;CL4908Conti	ATP synthase subunit gamma OS=Xenopus laevis GN=atp5c1 PE=	1.23344343	2.364520178
CL962Contig1;Q4V7V	CL962Contig1	1.162988013	2.026819619
Q6AZL9	MGC86316 protein OS=Xenopus laevis GN=rps23 PE=2 SV=1 - [Q	1.011728168	2.085135768
A9JS40	LOC100127299 protein OS=Xenopus laevis GN=ubxn10 PE=2 SV=	0.961719714	1.572864324
Q3KPT4;dsrrswapns_	MGC131338 protein OS=Xenopus laevis GN=zmat3 PE=2 SV=1 -	0.950436286	1.909581109
Q66KW1;CL1655Con	MGC85384 protein OS=Xenopus laevis GN=rpl29 PE=4 SV=1 - [Q	0.890452367	1.870904775
P62155;CL1Contig14	Calmodulin OS=Xenopus laevis GN=calm1 PE=1 SV=2 - [CALM_X	0.734805466	1.307257941
DC024875 homologue	Rep: Actin, alpha cardiac muscle 1 - Xenopus laevis (African clawe	0.684532475	2.150460564
P15107;CL10172Con	Superoxide dismutase [Cu-Zn] B OS=Xenopus laevis GN=sod1-b	0.640270329	3.173574517
Q7SZA5;BJ091434 U	MGC64312 protein OS=Xenopus laevis GN=rpl29 PE=4 SV=1 - [Q	0.640040657	2.439410693
TC457286 similar to U	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	0.6258535	2.665281005
Q6DJL4;CL12647Con	MGC82059 protein OS=Xenopus laevis GN=atpif1 PE=4 SV=1 - [Q	0.460309036	1.415905742
Q6NUH0;CL2830Con	60S ribosomal protein L31 OS=Xenopus laevis GN=rpl31 PE=2 SV	0.393238936	1.422252163
Q8AVH2;TC421129 U	*Ckb-prov protein OS=Xenopus laevis GN=ckb PE=2 SV=1 - [Q8AV*	-0.395728246	2.880852257
Q6EE53	40S ribosomal protein S8 (Fragment) OS=Xenopus laevis PE=2 SV	-0.730405712	3.417207872

D11/V21

Accession	Description	log2(ratio)	-log10(p)
Q6GN79	Ribosomal protein L37 OS=Xenopus laevis GN=rpl37 PE=3 SV=1 -	1.640492892	1.933823271
Q7ZYF7;CL1612Cont	MGC53103 protein OS=Xenopus laevis GN=phb PE=2 SV=1 - [Q7	1.352212731	2.47394585
Q7T0N8;CL7665Cont	Hadhsc-prov protein OS=Xenopus laevis GN=hadh PE=2 SV=1 - [	1.223438266	1.984507542
Q66KW1;CL1655Con	MGC85384 protein OS=Xenopus laevis GN=rpl29 PE=4 SV=1 - [Q	1.176249409	2.186106542
CL1144Contig2	CL1144Contig2	1.142555326	2.20197089
Q6GMA6;dsrrswapns_	MGC81949 protein OS=Xenopus laevis GN=cct6a PE=2 SV=1 - [Q	0.968664633	1.662325234
Q5XGW1;CL14714Co	LOC495263 protein OS=Xenopus laevis GN=atp5g1 PE=2 SV=1 -	0.901444609	3.564714963
Q6AZL9	MGC86316 protein OS=Xenopus laevis GN=rps23 PE=2 SV=1 - [Q	0.893529102	2.193882985
Q52KY1;CL6681Cont	Vdac2 protein OS=Xenopus laevis GN=vdac2 PE=2 SV=1 - [Q52K	0.874962421	2.173484675
Q640C8;CL4522Conti	LOC494703 protein OS=Xenopus laevis GN=LOC494703 PE=2 SV	0.855134137	1.728396128
Q6INB6;CL4908Conti	ATP synthase subunit gamma OS=Xenopus laevis GN=atp5c1 PE=	0.788950505	2.871483847
Q6NUH0;CL2830Con	60S ribosomal protein L31 OS=Xenopus laevis GN=rpl31 PE=2 SV	0.784531669	1.564348832
Q7ZXG3;CL107Contig	Iff-2-prov protein OS=Xenopus laevis GN=eif5a PE=2 SV=1 - [Q7Z	0.749264488	1.608216153
Q6GQB2	MGC80199 protein OS=Xenopus laevis GN=rpl7a PE=2 SV=1 - [Q	0.72958205	2.0941971
P49393;CL1Contig72	40S ribosomal protein S13 OS=Xenopus laevis GN=rps13 PE=3 SV	0.716364168	1.428648891
Q7SZ77;CL50Contig6	Rps11 protein OS=Xenopus laevis GN=rps11 PE=2 SV=1 - [Q7SZ	0.696988492	1.711527853
Q6PA58	Succinate dehydrogenase [ubiquinone] flavoprotein subunit A, mito	0.684971693	1.439882782
dsrrswapns_comp212	*len=1347*	0.672229062	2.589035747
Q6NTP7;CL640Contig	LOC398139 protein OS=Xenopus laevis GN=LOC398139 PE=2 SV	0.66045059	1.945338719
Q801S3	40S ribosomal protein S3a-A OS=Xenopus laevis GN=rps3a-a PE=	0.657106015	2.436934689
DC024875 homologue	Rep: Actin, alpha cardiac muscle 1 - Xenopus laevis (African clawe	0.634176664	2.453248216
Q7SYU3;CL2410Cont	MGC64490 protein OS=Xenopus laevis GN=rps5 PE=2 SV=1 - [Q7	0.620531526	1.608749062
TC460552 homologue	*Rep: Heat shock 10kDa protein 1 - Xenopus tropicalis (Western cla*	0.580412599	2.905504785
Q8AVW0;CL561Conti	Rpl12-prov protein OS=Xenopus laevis GN=rpl12 PE=2 SV=1 - [Q8	0.539173679	1.336085716
Q7ZTL5;CL1515Conti	Cct8-prov protein OS=Xenopus laevis GN=cct8 PE=2 SV=1 - [Q7Z	0.513852595	2.336182452
zeinaSSns_comp3872	len=1781	0.508828857	1.665097096
P70010	Nucleoside diphosphate kinase A1 OS=Xenopus laevis PE=2 SV=1	0.501548345	1.822761083
Q7SZA5;BJ091434 U	MGC64312 protein OS=Xenopus laevis GN=rpl29 PE=4 SV=1 - [Q	0.480709857	2.447766669
Q6DJL4;CL12647Con	MGC82059 protein OS=Xenopus laevis GN=atpif1 PE=4 SV=1 - [Q	0.46816835	3.577388918
Q6GP18;CL116Contig	Superoxide dismutase OS=Xenopus laevis GN=MGC80739 PE=2	0.464674032	1.421199691
P39017;CL2323Conti	40S ribosomal protein S6 OS=Xenopus laevis GN=rps6 PE=2 SV=	0.45664967	1.379663104
CL3418Contig2	CL3418Contig2	0.435198217	1.676167357
P02350	40S ribosomal protein S3-A OS=Xenopus laevis GN=rps3-a PE=2	0.385315345	1.343267061
Q6PAY8;CL13107Cor	Hydroxysteroid dehydrogenase-like protein 2 OS=Xenopus laevis	0.384385566	2.364674981
TC463468	vitellogenin (A1) [Xenopus laevis]	-0.479986157	6.779548898
TC462321 similar to U	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-0.578666293	6.321155139
P20310	Neural cadherin-1 OS=Xenopus laevis PE=2 SV=1 - [CADHN_XEN	-0.580404744	4.606091488
P20342	40S ribosomal protein S15 OS=Xenopus laevis GN=rps15 PE=2 SV	-0.587575765	3.136999411

BG513260 homologue	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.61092132	13.57483682
TC464539 similar to U	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.645974459	8.971804995
CL25067Contig1	CL25067Contig1	-0.679233661	7.864660053
TC457286 similar to U	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-0.702073388	11.3438544
Q7SZF6	Vitellogenin B1 OS=Xenopus laevis GN=vtgb1 PE=2 SV=1 - [Q7SZ	-0.721822417	17.99764532
A0PCF2	T-box transcription factor Xtbx6r OS=Xenopus laevis GN=Xtbx6r P	-0.731187925	12.06087234
TC462743 homologue	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.763933661	14.90971422
TC469090 homologue	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-0.901169608	14.4385647
Q6E2P0	Urocortin 3 OS=Xenopus laevis GN=ucn3 PE=2 SV=1 - [Q6E2P0_	-1.231564861	10.10326666

V11/V21

Accession	Description	log2(ratio)	-log10(p)
P50886	60S ribosomal protein L22 OS=Xenopus laevis GN=rpl22 PE=2 SV	1.106282852	7.166139723
Q5XGW1;CL14714C	LOC495263 protein OS=Xenopus laevis GN=atp5g1 PE=2 SV=1 -	0.956286403	5.140405847
Q6PA58	Succinate dehydrogenase [ubiquinone] flavoprotein subunit A, mito	0.886675807	12.90792031
Q6GQB2	MGC80199 protein OS=Xenopus laevis GN=rpl7a PE=2 SV=1 - [Q	0.707105549	4.979389681
dsrrswapns_comp212	len=1347	0.681093481	4.389430469
Q4V871	MGC114621 protein OS=Xenopus laevis GN=MGC114621 PE=4 S	0.665639917	5.142113083
Q6NTP7;CL640Conti	LOC398139 protein OS=Xenopus laevis GN=LOC398139 PE=2 SV	0.626734619	4.046150439
zeinaSSns_comp3872	len=1781	0.579775042	6.284321009
Q8AVH2;TC421129 U	Ckb-prov protein OS=Xenopus laevis GN=ckb PE=2 SV=1 - [Q8AV	0.565570737	3.025112671
Q801S3	40S ribosomal protein S3a-A OS=Xenopus laevis GN=rps3a-a PE=	0.56440772	5.174805521
Q6PI76;CL289Contig7	Rps14-prov protein OS=Xenopus laevis GN=rps14 PE=2 SV=1 - [Q	0.541107791	2.567161099
Q7SZS3;CL137Conti	Aspartate aminotransferase OS=Xenopus laevis GN=got2 PE=2 SV	0.534400411	2.209633298
Q6GNH1	MGC82808 protein OS=Xenopus laevis GN=rpl23 PE=2 SV=1 - [Q	0.528354153	2.63119155
Q640C8;CL4522Conti	LOC494703 protein OS=Xenopus laevis GN=LOC494703 PE=2 SV	0.503408999	1.556967688
Q7ZTL5;CL1515Conti	Cct8-prov protein OS=Xenopus laevis GN=cct8 PE=2 SV=1 - [Q7Z	0.492556548	3.063183857
Q7SZ77;CL50Contig6	Rps11 protein OS=Xenopus laevis GN=rps11 PE=2 SV=1 - [Q7SZ7	0.469618279	2.648602252
CL3418Contig2	CL3418Contig2	0.462183946	5.557285557
P39017;CL2323Conti	40S ribosomal protein S6 OS=Xenopus laevis GN=rps6 PE=2 SV=	0.452880642	2.959055012
Q66KV6;CL1Contig27	LOC100101273 protein OS=Xenopus laevis GN=rpl28 PE=2 SV=1	0.449575732	3.222250313
CL1144Contig2	CL1144Contig2	0.400583227	1.838671666
Q6GR58;CL4491Cont	Malate dehydrogenase OS=Xenopus laevis GN=mdh2 PE=2 SV=1	0.400294977	3.804695075
CL1127Contig1	CL1127Contig1	0.389143733	5.45379494
Q6B4U5;CL4491Cont	Malate dehydrogenase OS=Xenopus laevis GN=mdh2 PE=2 SV=1	0.387545105	2.546863135
Q6AZL9	MGC86316 protein OS=Xenopus laevis GN=rps23 PE=2 SV=1 - [Q	-0.405011526	2.443926138
Q7SZA5;BJ091434 U	MGC64312 protein OS=Xenopus laevis GN=rpl29 PE=4 SV=1 - [Q	-0.448082054	1.447852842
Q00387;CL13623Con	Serine protease inhibitor A6 OS=Xenopus laevis GN=serpina6 PE=	-0.478433382	3.304595825
Q6INX6	MGC80065 protein OS=Xenopus laevis GN=rps16 PE=3 SV=1 - [Q	-0.485176981	1.926534613
P20310	Neural cadherin-1 OS=Xenopus laevis PE=2 SV=1 - [CADHN_XEN	-0.49047186	1.507131649
Q6IP81;CL11159Cont	MGC78867 protein OS=Xenopus laevis GN=lta4h PE=2 SV=1 - [Q	-0.500714351	2.975196871
TC463468	vitellogenin (A1) [Xenopus laevis]	-0.514729007	3.670437598
BG513260 homologue	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.616500961	3.189485855
P17508;CL430Contig	Elongation factor 1-alpha, oocyte form OS=Xenopus laevis PE=1 S	-0.627455233	1.459249993
CL25067Contig1	CL25067Contig1	-0.635577423	1.681761571
Q7T0N8;CL7665Cont	Hadhsc-prov protein OS=Xenopus laevis GN=hadh PE=2 SV=1 - [	-0.648205563	1.325194607
CL2344Contig1	CL2344Contig1	-0.649203361	3.56427685
Q07254	40S ribosomal protein S10 OS=Xenopus laevis GN=rps10 PE=1 S	-0.681686199	2.229020205
A0PCF2	T-box transcription factor Xtbx6r OS=Xenopus laevis GN=Xtbx6r P	-0.698812355	4.26010971
TC462743 homologue	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.729553193	4.694683576
Q7SZF6	Vitellogenin B1 OS=Xenopus laevis GN=vtgb1 PE=2 SV=1 - [Q7SZ	-0.768259066	7.397499709
TC462321 similar to U	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-0.849359798	6.33285892
TC464539 similar to U	Rep: Vitellogenin B1 - Xenopus laevis (African clawed frog), partial	-0.877021755	5.535647861
TC469090 homologue	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-0.952093563	8.892737219
Q3KPT4;dsrrswapns_	MGC131338 protein OS=Xenopus laevis GN=zmat3 PE=2 SV=1 -	-1.030106269	3.436291338
TC457286 similar to U	Rep: Vitellogenin-A2 precursor (VTG A2) [Contains: Lipovitellin I; Li	-1.380747312	3.926863535
Q6E2P0	Urocortin 3 OS=Xenopus laevis GN=ucn3 PE=2 SV=1 - [Q6E2P0_	-1.444655882	8.812761804

Table S6. Comparison of proteins identified by the single-cell mass spectrometer with transcripts that have been independently identified. A total of 998 proteins match published transcript datasets, which expands to at least 1,601 protein-transcript matches based on protein names that have been derived from mRNA-based datasets.

Accession Number for Identified Protein	Protein Description	Gene Name	Protein expected based on mRNA db? (Yes)	Quantified in This Work? (Yes)	Transcript Reported in Ref. 29?	Transcript Reported in Ref. 28b?	Transcript Reported in 28a?	Protein Matching Transcript ID? (TRUE)	Protein Likely Matching Transcript ID? (TRUE)
237402600	Xenopus laevis clone CH219-6E24, complete sequence								
27228087	Xenopus laevis clone S10-45-G5 mRNA sequence								
28386279	Xenopus laevis, Similar to propionyl	pccb			Y			TRUE	TRUE
428676593;K9YHL9	Xenopus laevis myelodysplasia syn	etv6			Y			TRUE	TRUE
7769000	Xenopus laevis clone OLT 2-1 retro	olt2							
A0A090AX62	Zygotic Mcm3 protein OS=Xenopus	mcm3			Y	Y		TRUE	TRUE
A0AUS4;CL3713Contig3	LOC398314 protein OS=Xenopus la	dlat			Y			TRUE	TRUE
A0AUT1	Trichoplein keratin filament-binding	tchp			Y			TRUE	TRUE
A0AUT2;CL2720Contig3	Ubiquitin carboxyl-terminal hydrolas	usp5							
A0AUT4	LOC100036778 protein OS=Xenopus laevis GN=LOC100036778 PE=2 SV=1 - [A0AUT4_XENLA]								
A0AUU3	Cox7a2b protein OS=Xenopus laevi	cox7a2			Y			TRUE	TRUE
A0AUU3;CL12025Contig1	Cox7a2b protein OS=Xenopus laevi	cox7a2			Y			TRUE	TRUE
A0AUU6	Wbp2 protein OS=Xenopus laevis G	wbp2							
A0JMT7	LOC431931 protein OS=Xenopus la	OC431931							
A0JMU7	Zswim4_predicted protein OS=Xeno	zswim4			Y			TRUE	TRUE
A0JMU8	Protein CASC3 OS=Xenopus laevis	casc3			Y			TRUE	TRUE
A0JMW0;CL8946Contig1	MGC154839 protein OS=Xenopus l	tmem117			Y			TRUE	TRUE
A0JMW2	MGC154857 protein OS=Xenopus l	heatr2			Y			TRUE	TRUE
A0JMY5;CL6629Contig1	NF-X1-type zinc finger protein NFXL	nfxl1			Y	Y		TRUE	TRUE
A0JMZ0	Zfp276 protein OS=Xenopus laevis	znf276			Y			TRUE	TRUE
A0JMZ1;CL1Contig964	Nucleolar and spindle-associated pr	nusap1			Y			TRUE	TRUE
A0JPG5	LOC100036792 protein (Fragment)	C100036792							
A0JPH8;CL13915Contig1	LOC100036800 protein OS=Xenopu	C100036800							
A0PCF2	T-box transcription factor Xtbx6r OS	tbx6r		Y				TRUE	TRUE
A0T1H8	Catalase OS=Xenopus laevis PE=2	cat							
A1A613	LOC733342 protein (Fragment) OS	OC733342							
A1A638;CL11731Contig1	Dbib protein OS=Xenopus laevis GN	dbi			Y			TRUE	TRUE
A1L106;CL10855Contig1	Lgtn protein OS=Xenopus laevis GN	eif2d			Y			TRUE	TRUE
A1L1G6;CL1072Contig1	LOC100036836 protein OS=Xenopu	kiaa0182			Y			TRUE	TRUE
A1L1H0	LOC100036839 protein OS=Xenopu	rere			Y			TRUE	TRUE
A1L1H6	LOC100036845 protein OS=Xenopu	C100036845							
A1L1H7	LOC733281 protein OS=Xenopus la	supt5h			Y			TRUE	TRUE
A1L2G7	Uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [A1L2G7_XENLA]								
A1L2H9	LOC100036853 protein OS=Xenopu	C100036853							
A1L2I5;CL5868Contig1	Histone H2A OS=Xenopus laevis G	h2afy			Y			TRUE	TRUE
A1L2I8	LOC100036860 protein OS=Xenopu	C100036860							
A1L2I9	Transmembrane protein 214-B OS=	mem214-b			Y			TRUE	TRUE
A1L2J4	Putative uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [A1L2J4_XENLA]								
A1L2N5;CL26379Contig1	LOC100036902 protein OS=Xenopu	a1l2n5							
A1L2Q6	Glutathione S-transferase OS=Xeno	gsta1			Y			TRUE	TRUE
A1L2R8;CL2492Contig1	LOC100036931 protein OS=Xenopu	sds			Y			TRUE	TRUE
A1L2R9	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [A1L2R9_XENLA]								
A1L2S7	LOC100036938 protein OS=Xenopu	C100036938							
A1L2U3	LOC100036954 protein OS=Xenopu	C100036954							
A1L2U5	LOC100036956 protein (Fragment)	C100036956							
A1L3F5	C-Maf-inducing protein OS=Xenopu	cmip			Y			TRUE	TRUE
A1L3F7	LOC100036993 protein (Fragment)	C100036993							
A1L3H5	LOC100037009 protein (Fragment)	C100037009							
A1L3J7	LOC100037025 protein OS=Xenopu	ganab			Y			TRUE	TRUE
A1L3K2;CL19654Contig1	Pyruvate kinase OS=Xenopus laevi	pklr			Y			TRUE	TRUE
A1L3K7	Enolase A OS=Xenopus laevis GN=	enoa							
A2BD52	LOC100158263 protein (Fragment)	C100158263							
A2BD73	LOC100037109 protein (Fragment)	C100037109							
A2BDA0;CL1Contig853	Histone H4 OS=Xenopus laevis GN	hist1h4d							
A2BDB0	Actin, cytoplasmic 2 OS=Xenopus la	actg1			Y			TRUE	TRUE
A2RV71	LOC100037140 protein OS=Xenopu	C100037140							
A2RV96	LOC496076 protein OS=Xenopus la	lrrc34				Y		TRUE	TRUE
A2RV99	LOC445855 protein (Fragment) OS	OC445855							
A2RVB7	LOC100037164 protein OS=Xenopu	cdc42ep4			Y			TRUE	TRUE
A2VCV3;CL11727Contig1	LOC100037128 protein OS=Xenopu	C100037128							
A2VD74	LOC100037179 protein OS=Xenopu	mep1a			Y			TRUE	TRUE
A2VD83	Mannose-1-phosphate guanyltransf	gmppb			Y			TRUE	TRUE
A2VD87	LOC100037189 protein OS=Xenopu	cyp3a4			Y			TRUE	TRUE
A2VD97	LOC100037195 protein OS=Xenopu	mccc2			Y			TRUE	TRUE
A2VDA1	LOC100037198 protein OS=Xenopu	tnni1							
A2VDA2;CL2004Contig2	LOC100037199 protein OS=Xenopu	sri							
A2VDA5	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [A2VDA5_XENLA]								
A2VDC7	Ribonuclease kappa-A OS=Xenopu	rnasek			Y			TRUE	TRUE
A2VDD0	LOC100037222 protein (Fragment)	C100037222							
A2VDD2	Tctex1 domain-containing protein 1-	tctex1d1			Y			TRUE	TRUE
A2VDD8	Phosphorylase (Fragment) OS=Xen	C100037229							
A3KMH8	LOC398050 protein OS=Xenopus la	OC398050							

A3KMT2	Death-associated protein-like 1-A O	dapl1			Y			TRUE	TRUE
A3KMU5;CL12285Contig1	Death-associated protein-like 1-B O	dapl1			Y			TRUE	TRUE
A3KNB7	LOC495502 protein OS=Xenopus la	OC495502							
A3KNC9	LOC100049107 protein OS=Xenopu	zfp161			Y			TRUE	TRUE
A3KNF4	LOC100049121 protein OS=Xenopus laevis GN=LOC100049121 PE=4 SV=1 - [A3KNF4_XENLA]								
A4FVE9	LOC100049132 protein (Fragment)	C100049132							
A4FVF5	LOC100049136 protein OS=Xenopus laevis GN=LOC100049136 PE=4 SV=1 - [A4FVF5_XENLA]								
A4IFX0	LOC100049139 protein OS=Xenopu	C100049139							
A4IFX5	LOC100049142 protein (Fragment)	C100049142							
A4PB26	Protein CDV3 homolog B OS=Xeno	cdv3			Y			TRUE	TRUE
A4QNS5	Uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [A4QNS5_XENLA]								
A4QNS6	LOC100049151 protein OS=Xenopu	zc3h11a							
A4UXD6	Toll-like receptor8 (Fragment) OS=X	tlr8							
A5D8L8	LOC100049741 protein (Fragment)	C100049741							
A5D8M0	Tyrosyl-DNA phosphodiesterase 2 (	tdp2			Y			TRUE	TRUE
A5D8M8	LOC100049751 protein OS=Xenopu	nqo1			Y			TRUE	TRUE
A5D8P9	LOC100049770 protein (Fragment) OS=Xenopus laevis GN=LOC100049770 PE=2 SV=1 - [A5D8P9_XENLA]								
A5PKN2	LOC100101285 protein (Fragment)	C100101285							
A5PKN6;CL3181Contig1	LOC100101289 protein OS=Xenopu	fam13a			Y			TRUE	TRUE
A5PKR6	LOC100101313 protein OS=Xenopu	crym							
A5XAW2	Kinesin heavy chain (Fragment) OS	khc							
A6QL57	LOC100125670 protein (Fragment)	C100125670							
A6YHD9	RAG1 (Fragment) OS=Xenopus lae	rag1							
A7E223	LOC100125672 protein OS=Xenopu	C100125672							
A7J1T2	Mitogen-activated protein kinase kir	map3k13			Y			TRUE	TRUE
A7UCI1	MRF4a OS=Xenopus laevis GN=MI	mrf4a							
A7YYL7;CL10641Contig1	LOC100126616 protein OS=Xenopu	mrpl32			Y			TRUE	TRUE
A8CWK9	Low density lipoprotein-related prote	lrp2			Y			TRUE	TRUE
A8E0R9	Glutamate receptor-interacting prote	grip2			Y	Y		TRUE	TRUE
A8E5Y6;CL7871Contig1	LOC100126622 protein OS=Xenopu	ninj1							
A8WH44	LOC100127250 protein OS=Xenopu	C100127250							
A9JS15	LOC100127283 protein OS=Xenopu	fam110d							
A9JS28	LOC100127294 protein OS=Xenopu	slc7a9			Y			TRUE	TRUE
A9JS40	LOC100127299 protein OS=Xenopu	ubxn10		Y	Y			TRUE	TRUE
A9JS44	LOC100127303 protein (Fragment)	C100127303							
A9JS79	Proteasome subunit beta type (Frag	psmb							
A9JS81	LOC100127334 protein OS=Xenopu	C100127334							
A9JS85	LOC100127336 protein OS=Xenopu	b3galtl							
A9JSS1	LOC100127274 protein OS=Xenopu	rnf2							
A9QW72	N-methyl-D-aspartate receptor subu	grin2a							
A9ULW5;CL11158Contig1	LOC100137631 protein OS=Xenopu	acot13			Y			TRUE	TRUE
A9ULW6	ZPD protein OS=Xenopus laevis GN	zpd			Y			TRUE	TRUE
A9ULX0	LOC100137635 protein OS=Xenopu	C100137635							
A9UM04	LOC100137663 protein (Fragment)	C100137663							
A9UM19;CL14087Contig1	LOC100137677 protein OS=Xenopus laevis GN=LOC100137677 PE=2 SV=1 - [A9UM19_XENLA]								
A9UM22	LOC100137679 protein (Fragment)	C100137679							
A9UM24	Bix1 protein OS=Xenopus laevis GN	Bix1			Y			TRUE	TRUE
A9UMM8	LOC100137686 protein OS=Xenopu	khnyn			Y			TRUE	TRUE
A9UMQ1	LOC100137703 protein (Fragment)	C100137703							
A9ZS93	Transmembrane, prostate androgen	pmepa1			Y			TRUE	TRUE
AW765098 UniRef100_Q2	Rep: LOC733431 protein - Xenopus laevis (African clawed frog), partial (34%)								
AW783929 similar to UniR	Rep: Asxl1-prov protein - Xenopus l	asxl1			Y			TRUE	TRUE
B0LM40	Importin beta 1 OS=Xenopus laevis	kpnb1			Y			TRUE	TRUE
B1B546;CL15536Contig1	Transcription factor foxp3 OS=Xenc	foxp3							
B1H1N7	Ancient ubiquitous protein 1 OS=Xe	aup1			Y			TRUE	TRUE
B1H1N8;CL525Contig5	LOC100036826 protein OS=Xenopus laevis GN=LOC100036826 PE=2 SV=1 - [B1H1N8_XENLA]								
B1H1V0	LOC495286 protein (Fragment) OS=	OC495286							
B1H1X2	LOC100158324 protein (Fragment)	C100158324							
B1H1X4	Serrate RNA effector molecule hom	srrt							
B1NA54	Ig-like receptor 2.1 OS=Xenopus lae	xilr2							
B1NA55	FcR-like protein (Fragment) OS=Xe	xfl1.7							
B1WBA3	Putative uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [B1WBA3_XENLA]								
B1WBB8;CL4228Contig1	LOC100158420 protein OS=Xenopu	C100158420							
B1WBD3	LOC100158432 protein OS=Xenopu	aars			Y	Y		TRUE	TRUE
B1WBD8	NO145 protein OS=Xenopus laevis	no145							
B1WBE0	LOC100158438 protein OS=Xenopu	eprs							
B2DCQ5;CL597Contig2	Cdc25B phosphatase OS=Xenopus	cdc25b			Y			TRUE	TRUE
B2GTY1	LOC100158450 protein (Fragment)	C100158450							
B3DLM0	LOC100174803 protein OS=Xenopu	acsl4			Y			TRUE	TRUE
B3IXB3	RAS guanyl releasing protein 2 OS=	rasgrp2							
B5DE44	Putative uncharacterized protein OS	dpp8			Y			TRUE	TRUE
B5LEQ4	RNA binding protein Bruno-like 3b (	celf2							
B5MFE9	Olfactomedin-like protein 3 OS=Xer	olfml3							
B5SVV6	Anoctamin OS=Xenopus laevis GN=	ano1			Y			TRUE	TRUE
B7ZPZ8;CL315Contig4	Thymosin beta 4 peptide OS=Xeno	tmsb4x			Y			TRUE	TRUE
B7ZQA9	POU domain, class 5, transcription	pou5f1.2							
B7ZQB3	LOC398954 protein OS=Xenopus la	OC398954							
B7ZQE3	Tbx6 protein OS=Xenopus laevis G	tbx6							
B7ZQH2	XMam1 protein OS=Xenopus laevis	mam1							
B7ZQN6;CL688Contig4	Cttn protein OS=Xenopus laevis GN	Cttn							
B7ZQQ8	CL-2 protein OS=Xenopus laevis GI	cl2							
B7ZQU5;CL4806Contig1	Protein Wnt OS=Xenopus laevis GN	wnt10a							
B7ZQU6	LOC398035 protein OS=Xenopus laevis GN=LOC398035 PE=2 SV=1 - [B7ZQU6_XENLA]								
B7ZQU9;213625150	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [B7ZQU9_XENLA]								
B7ZQV9	Frizzled-8 OS=Xenopus laevis GN=	xfz8							
B7ZR28	N1/N2 protein OS=Xenopus laevis (	n1/n2							

B7ZR30	Serine/threonine-protein kinase 10-	stk10			Y			TRUE	TRUE
B7ZR33	GATA binding factor-1 OS=Xenopu	gata1a-A							
B7ZR39	Integrin alphaV subunit OS=Xenopu	itgav			Y			TRUE	TRUE
B7ZR65	Transcription factor Sox-9-A OS=Xe	sox9			Y			TRUE	TRUE
B7ZR89	Paraxis-like protein OS=Xenopus la	tcf15							
B7ZRE7	Breast and ovarian cancer suscepti	brac1			Y			TRUE	TRUE
B7ZRI3	Ret proto-oncogene OS=Xenopus l	ret							
B7ZRI9	Nitric oxide synthase OS=Xenopus	nos1			Y			TRUE	TRUE
B7ZRL0	Fragile X mental retardation 1 OS=	fmr1-A							
B7ZRM8	MDS1 and EVI1 complex locus prot	mecom			Y			TRUE	TRUE
B7ZRN2	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [B7ZRN2_XENLA]								
B7ZRN9	Integrin alpha5 subunit OS=Xenopu	itga5			Y			TRUE	TRUE
B7ZRQ0	Uncharacterized protein OS=Xenop	C100127269							
B7ZRR5	Xebf-3 protein OS=Xenopus laevis	ebf3			Y			TRUE	TRUE
B7ZRR7	GATA binding factor-1b OS=Xenop	gata1ba							
B7ZRS3	Forkhead box transcription factor O	foxp2a							
B7ZRS8;CL9Contig15	Meis1 protein OS=Xenopus laevis	meis1			Y			TRUE	TRUE
B7ZRZ7	T-box transcription factor Tbx5 OS=	tbx5							
B7ZS08	Ago61 protein OS=Xenopus laevis	ago61							
B7ZS26	V-rel reticuloendotheliosis viral onc	relba							
B7ZS37	Bromodomain adjacent to zinc finge	baz2a			Y			TRUE	TRUE
B7ZS71	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [B7ZS71_XENLA]								
B7ZS80;CL2280Contig1	Tyrosine-protein kinase receptor O	tyr							
B7ZSA6;CL4246Contig2	Inversin OS=Xenopus laevis GN=in	invs			Y			TRUE	TRUE
B7ZSB1	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [B7ZSB1_XENLA]								
B7ZSB2	Pcm-1 protein OS=Xenopus laevis	pcm1							
B7ZSC6;CL817Contig2	Slit2-a protein OS=Xenopus laevis	slit2			Y			TRUE	TRUE
B7ZSI6	LOC100126641 protein OS=Xenopus laevis GN=LOC100126641 PE=2 SV=1 - [B7ZSI6_XENLA]								
B7ZSK0	Structural maintenance of chromoso	smc2			Y			TRUE	TRUE
B9V5F5	Centrosomal protein of 63 kDa-A O	cep63			Y	Y		TRUE	TRUE
B9V8Q8	Ionotropic glutamate receptor subur	glur5							
B9V8R7	Ionotropic glutamate receptor subur	gria1							
B9V8R9	Ionotropic glutamate receptor subur	gria3							
BF048119 similar to UniRe	Rep: Histone H3.3 - Homo sapiens	hist33							
BF427462 weakly similar t	Rep: Cytochrome c oxidase subunit	cox1							
BF611644 similar to UniRe	Rep: Cytochrome c oxidase subunit	cox1							
BF614900 similar to UniRe	Rep: Cold-inducible RNA-binding pr	cirbp			Y			TRUE	TRUE
BG017237 similar to UniRe	Rep: 60S ribosomal protein L6 - Xe	rpl6							
BG020450 homologue to U	Rep: Ubiquitin protein ligase E3C -	ube3c			Y			TRUE	TRUE
BG023428 similar to UniRe	Rep: Zgc:153686 - Danio rerio (Zebrafish) (Brachydanio rerio), partial (11%)								
BG037251 similar to UniRe	Rep: Tubulin beta chain - Homo sa	tubb			Y		Y	TRUE	TRUE
BG160380 weakly similar t	Rep: Tubulin beta-4 chain - Xenopu	tubb4			Y			TRUE	TRUE
BG234522 similar to UniRe	Rep: MGC80199 protein - Xenopus laevis (African clawed frog), partial (76%)								
BG235002 similar to UniRe	Rep: Keratin, type I cytoskeletal 47 kDa - Xenopus laevis (African clawed frog), partial (15%)								
BG513260 homologue to U	Rep: Vitellogenin B1 - Xenopus lae	vtgb1		Y				TRUE	TRUE
BI314067	BI314067								
BI349541 homologue to Ur	Rep: SIPA1L1 protein - Xenopus la	sipa1l1			Y			TRUE	TRUE
BJ029212 UniRef100_Q7Z	Rep: Cell division protein kinase 9-	cdk9			Y			TRUE	TRUE
BJ031467 similar to UniRe	Rep: LOC495262 protein - Xenopus laevis (African clawed frog), partial (4%)								
BJ035035 UniRef100_Q6D	Rep: MGC80437 protein - Xenopus laevis (African clawed frog), partial (47%)								
BJ039283	BJ039283								
BJ042270 UniRef100_Q6P	Rep: Ubiquitin carrier protein - Xenopus tropicalis (Western clawed frog) (Silurana tropicalis), partial (84%)								
BJ042996 weakly similar t	Rep: Zgc:162320 protein - Danio rerio (Zebrafish) (Brachydanio rerio), partial (7%)								
BJ047835 homologue to U	Rep: Receptor-associated protein o	rapsn							
BJ049851 homologue to U	Rep: MGC85497 protein - Xenopus laevis (African clawed frog), partial (41%)								
BJ072460	BJ072460								
BJ086436 homologue to U	Rep: 40S ribosomal protein S7 - Xe	rps7			Y			TRUE	TRUE
BJ093020 weakly similar t	Rep: Transposase - Rana lessonae (Pool frog), partial (34%)								
BJ099767 UniRef100_P33	Rep: Blastomere cadherin precursor - Xenopus laevis (African clawed frog), partial (7%)								
BJ623194 homologue to U	Rep: G3bp-prov protein - Xenopus l	g3bp			Y			TRUE	TRUE
BJ627598 similar to UniRe	Rep: Novel trypsin family protein - Xenopus tropicalis (Western clawed frog) (Silurana tropicalis), partial (16%)								
BJ630382 homologue to U	Rep: S6 ribosomal protein - Pagrus	rps6							
BJ639435	BJ639435								
BM192676 UniRef100_Q6	Rep: LOC414678 protein - Xenopus laevis (African clawed frog), partial (68%)								
BP686589 homologue to U	Rep: LOC398570 protein - Xenopus laevis (African clawed frog), partial (14%)								
BP731916 homologue to U	Rep: Pre-B-cell leukemia transcripti	pbx3							
BQ400069 similar to UniRe	Rep: Tyrosine-protein kinase recept	tie1				Y		TRUE	TRUE
BQ736408 UniRef100_UP	Rep: Multidrug resistance-associate	mrp7							
BU910031 UniRef100_Q7	Rep: Hnrpa0-prov protein - Xenopu	hnrpa0							
C0J6M5	MEF2A alpha 12b isoform OS=Xen	mef2a			Y			TRUE	TRUE
C5H606	Vitronectin OS=Xenopus laevis GN	vtn							
C5MKI3	Calcium channel voltage-dependen	cacna1a			Y			TRUE	TRUE
CA789974 similar to UniRe	Rep: LOC100036684 protein - Xenopus tropicalis (Western clawed frog) (Silurana tropicalis), partial (4%)								
CA974276 similar to UniRe	Rep: Zgc:110113 - Danio rerio (Zebrafish) (Brachydanio rerio), partial (33%)								
CA981790 weakly similar t	Rep: Gastrula zinc finger protein XlCGF49.1 - Xenopus laevis (African clawed frog), partial (39%)								
CB200344 homologue to U	Rep: Thyroglobulin precursor. - Xenopus tropicalis, partial (97%)								
CB562068 weakly similar t	Rep: Proto-oncogene tyrosine-prote	ros							
CB941391 homologue to U	Rep: Plakophilin-1 (Band-6 protein)	pkp1			Y			TRUE	TRUE
CB943254 homologue to U	Rep: LOC733227 protein - Xenopus laevis (African clawed frog), partial (52%)								
CD099718 homologue to U	Rep: Ubiquitin carboxyl-terminal hy	uchl1			Y			TRUE	TRUE
CD362591 weakly similar t	Rep: Ephrin type-B receptor 5 precu	ephb2							
CD362892 homologue to U	Rep: CD74 molecule, major histoco	hg2a							
CF270399	CF270399								
CF270562 homologue to U	Rep: MGC138012 protein - Bos tau	GC138012							
CF270676 UniRef100_Q6D	Rep: Cndp2-prov protein - Xenopus	cndp2			Y			TRUE	TRUE
CF270773 similar to UniRe	Rep: Predicted protein - Nematostella vectensis (Starlet sea anemone), partial (7%)								

CF283899 homologue to U	Rep: MGC81934 protein - Xenopus laevis (African clawed frog), partial (26%)								
CF285683 homologue to U	Rep: Arcn1 protein - Xenopus laevis	arcn1			Y			TRUE	TRUE
CF521141 similar to UniRe	Rep: Metalloreductase STEAP3 (EC	steap3			Y			TRUE	TRUE
CL1004Contig2	CL1004Contig2		Y						TRUE
CL1008Contig1;Q6PAD3	CL1008Contig1	psmc4	Y		Y			TRUE	TRUE
CL10114Contig2	CL10114Contig2		Y						TRUE
CL10115Contig1	CL10115Contig1		Y						TRUE
CL1011Contig3	CL1011Contig3		Y	Y				TRUE	TRUE
CL1014Contig3	CL1014Contig3		Y						TRUE
CL1016Contig5	CL1016Contig5		Y						TRUE
CL10183Contig1	CL10183Contig1		Y						TRUE
CL1028Contig5	CL1028Contig5		Y						TRUE
CL10344Contig2	CL10344Contig2		Y						TRUE
CL10383Contig2	CL10383Contig2		Y						TRUE
CL1039Contig2	CL1039Contig2		Y						TRUE
CL1050Contig4	CL1050Contig4		Y						TRUE
CL10567Contig1	CL10567Contig1		Y						TRUE
CL10588Contig1	CL10588Contig1		Y						TRUE
CL10642Contig1	CL10642Contig1		Y						TRUE
CL1072Contig4	CL1072Contig4		Y						TRUE
CL1073Contig2	CL1073Contig2		Y						TRUE
CL1078Contig2	CL1078Contig2		Y						TRUE
CL1079Contig2	CL1079Contig2		Y						TRUE
CL10840Contig1	CL10840Contig1		Y						TRUE
CL10967Contig1	CL10967Contig1		Y						TRUE
CL1096Contig1	CL1096Contig1		Y						TRUE
CL10981Contig1	CL10981Contig1		Y						TRUE
CL1100Contig1;Q6GN22	CL1100Contig1		Y						TRUE
CL11026Contig1	CL11026Contig1		Y						TRUE
CL11069Contig2	CL11069Contig2		Y						TRUE
CL1108Contig2	CL1108Contig2		Y						TRUE
CL1127Contig1	CL1127Contig1		Y	Y				TRUE	TRUE
CL1127Contig2	CL1127Contig2		Y						TRUE
CL11289Contig1	CL11289Contig1		Y						TRUE
CL112Contig13	CL112Contig13		Y						TRUE
CL11346Contig1	CL11346Contig1		Y						TRUE
CL11402Contig2	CL11402Contig2		Y						TRUE
CL11416Contig1	CL11416Contig1		Y						TRUE
CL1142Contig1	CL1142Contig1		Y						TRUE
CL1144Contig2	CL1144Contig2		Y	Y				TRUE	TRUE
CL1144Contig4	CL1144Contig4		Y						TRUE
CL11454Contig2	CL11454Contig2		Y						TRUE
CL11493Contig1	CL11493Contig1		Y						TRUE
CL114Contig15	CL114Contig15		Y						TRUE
CL11511Contig1	CL11511Contig1		Y						TRUE
CL1151Contig6	CL1151Contig6		Y						TRUE
CL1152Contig1	CL1152Contig1		Y	Y				TRUE	TRUE
CL11612Contig1	CL11612Contig1		Y						TRUE
CL1161Contig2	CL1161Contig2		Y						TRUE
CL11663Contig1	CL11663Contig1		Y						TRUE
CL11742Contig1	CL11742Contig1		Y						TRUE
CL1175Contig2	CL1175Contig2		Y						TRUE
CL1177Contig1	CL1177Contig1		Y						TRUE
CL11786Contig1	CL11786Contig1		Y						TRUE
CL11800Contig1	CL11800Contig1		Y						TRUE
CL11836Contig1	CL11836Contig1		Y						TRUE
CL11854Contig1	CL11854Contig1		Y						TRUE
CL11897Contig1	CL11897Contig1		Y						TRUE
CL11908Contig1	CL11908Contig1		Y						TRUE
CL11975Contig1	CL11975Contig1		Y						TRUE
CL119Contig4	CL119Contig4		Y						TRUE
CL11Contig15	CL11Contig15		Y						TRUE
CL11Contig16	CL11Contig16		Y						TRUE
CL1207Contig5	CL1207Contig5		Y						TRUE
CL12084Contig1	CL12084Contig1		Y						TRUE
CL120Contig6	CL120Contig6		Y						TRUE
CL12250Contig1	CL12250Contig1		Y						TRUE
CL12264Contig1	CL12264Contig1		Y						TRUE
CL122Contig3	CL122Contig3		Y						TRUE
CL12483Contig1	CL12483Contig1		Y						TRUE
CL12542Contig1	CL12542Contig1		Y						TRUE
CL12604Contig1	CL12604Contig1		Y						TRUE
CL12609Contig1	CL12609Contig1		Y						TRUE
CL1261Contig4	CL1261Contig4		Y						TRUE
CL1263Contig5	CL1263Contig5		Y						TRUE
CL12657Contig1	CL12657Contig1		Y						TRUE
CL127Contig15	CL127Contig15		Y						TRUE
CL12884Contig1	CL12884Contig1		Y						TRUE
CL128Contig8	CL128Contig8		Y						TRUE
CL12908Contig1	CL12908Contig1		Y						TRUE
CL12913Contig1	CL12913Contig1		Y						TRUE
CL1292Contig5	CL1292Contig5		Y						TRUE
CL12947Contig1	CL12947Contig1		Y						TRUE
CL12958Contig1	CL12958Contig1		Y						TRUE
CL12Contig33	CL12Contig33		Y						TRUE
CL13058Contig1	CL13058Contig1		Y						TRUE

CL13093Contig1	CL13093Contig1		Y						TRUE
CL13100Contig1	CL13100Contig1		Y						TRUE
CL13120Contig1	CL13120Contig1		Y						TRUE
CL13132Contig1	CL13132Contig1		Y						TRUE
CL1326Contig1	CL1326Contig1		Y						TRUE
CL13314Contig1	CL13314Contig1		Y						TRUE
CL1338Contig2	CL1338Contig2		Y						TRUE
CL13399Contig1	CL13399Contig1		Y						TRUE
CL1339Contig3	CL1339Contig3		Y						TRUE
CL13408Contig1	CL13408Contig1		Y						TRUE
CL13435Contig1	CL13435Contig1		Y						TRUE
CL13504Contig1	CL13504Contig1		Y						TRUE
CL13513Contig1	CL13513Contig1		Y						TRUE
CL13526Contig1	CL13526Contig1		Y						TRUE
CL13527Contig1	CL13527Contig1		Y						TRUE
CL13558Contig1	CL13558Contig1		Y						TRUE
CL13593Contig1	CL13593Contig1		Y						TRUE
CL13645Contig1	CL13645Contig1		Y						TRUE
CL1377Contig4	CL1377Contig4		Y						TRUE
CL137Contig3	CL137Contig3		Y						TRUE
CL1380Contig2	CL1380Contig2		Y						TRUE
CL13815Contig1	CL13815Contig1		Y						TRUE
CL13963Contig1	CL13963Contig1		Y						TRUE
CL1396Contig2	CL1396Contig2		Y						TRUE
CL13990Contig1	CL13990Contig1		Y						TRUE
CL1401Contig6	CL1401Contig6		Y						TRUE
CL1402Contig2	CL1402Contig2		Y						TRUE
CL14060Contig1	CL14060Contig1		Y						TRUE
CL14169Contig1	CL14169Contig1		Y						TRUE
CL1416Contig2	CL1416Contig2		Y						TRUE
CL1416Contig4	CL1416Contig4		Y						TRUE
CL14192Contig1	CL14192Contig1		Y						TRUE
CL1424Contig5	CL1424Contig5		Y						TRUE
CL14445Contig1	CL14445Contig1		Y						TRUE
CL14502Contig1	CL14502Contig1		Y						TRUE
CL14546Contig1	CL14546Contig1		Y						TRUE
CL1459Contig2	CL1459Contig2		Y						TRUE
CL14603Contig1	CL14603Contig1		Y						TRUE
CL14648Contig1	CL14648Contig1		Y						TRUE
CL1478Contig2	CL1478Contig2		Y						TRUE
CL14851Contig1	CL14851Contig1		Y						TRUE
CL148Contig11	CL148Contig11		Y	Y				TRUE	TRUE
CL1497Contig7	CL1497Contig7		Y						TRUE
CL14985Contig1	CL14985Contig1		Y						TRUE
CL1501Contig1	CL1501Contig1		Y						TRUE
CL15037Contig1	CL15037Contig1		Y						TRUE
CL1514Contig1	CL1514Contig1		Y						TRUE
CL1514Contig2	CL1514Contig2		Y						TRUE
CL1516Contig1	CL1516Contig1		Y						TRUE
CL151Contig7	CL151Contig7		Y						TRUE
CL1521Contig6	CL1521Contig6		Y						TRUE
CL1526Contig4	CL1526Contig4		Y						TRUE
CL15300Contig1	CL15300Contig1		Y						TRUE
CL1537Contig3	CL1537Contig3		Y						TRUE
CL15423Contig1	CL15423Contig1		Y						TRUE
CL15462Contig1	CL15462Contig1		Y						TRUE
CL1561Contig1	CL1561Contig1		Y						TRUE
CL15740Contig1	CL15740Contig1		Y						TRUE
CL1590Contig4	CL1590Contig4		Y						TRUE
CL15935Contig1	CL15935Contig1		Y						TRUE
CL15Contig35	CL15Contig35		Y						TRUE
CL16029Contig1	CL16029Contig1		Y						TRUE
CL16085Contig1	CL16085Contig1		Y						TRUE
CL1612Contig3	CL1612Contig3		Y						TRUE
CL1614Contig1	CL1614Contig1		Y						TRUE
CL16239Contig1	CL16239Contig1		Y						TRUE
CL1634Contig3	CL1634Contig3		Y						TRUE
CL1646Contig4	CL1646Contig4		Y						TRUE
CL1649Contig3	CL1649Contig3		Y						TRUE
CL165Contig4	CL165Contig4		Y						TRUE
CL16756Contig1	CL16756Contig1		Y						TRUE
CL1686Contig3	CL1686Contig3		Y						TRUE
CL16886Contig1	CL16886Contig1		Y						TRUE
CL168Contig4	CL168Contig4		Y						TRUE
CL16992Contig1	CL16992Contig1		Y						TRUE
CL17062Contig1	CL17062Contig1		Y						TRUE
CL170Contig6	CL170Contig6		Y						TRUE
CL172Contig4	CL172Contig4		Y						TRUE
CL17316Contig1	CL17316Contig1		Y						TRUE
CL1738Contig5	CL1738Contig5		Y						TRUE
CL1744Contig2	CL1744Contig2		Y						TRUE
CL1744Contig3	CL1744Contig3		Y	Y				TRUE	TRUE
CL177Contig14	CL177Contig14		Y						TRUE
CL17976Contig1	CL17976Contig1		Y						TRUE
CL179Contig6	CL179Contig6		Y						TRUE
CL18115Contig1	CL18115Contig1		Y						TRUE

CL18181Contig1	CL18181Contig1		Y						TRUE
CL18182Contig1	CL18182Contig1		Y						TRUE
CL18313Contig1	CL18313Contig1		Y						TRUE
CL18378Contig1	CL18378Contig1		Y						TRUE
CL18444Contig1	CL18444Contig1		Y						TRUE
CL18445Contig1	CL18445Contig1		Y						TRUE
CL18484Contig1	CL18484Contig1		Y						TRUE
CL18578Contig1	CL18578Contig1		Y						TRUE
CL1858Contig3	CL1858Contig3		Y						TRUE
CL1862Contig2	CL1862Contig2		Y						TRUE
CL1879Contig3	CL1879Contig3		Y						TRUE
CL18839Contig1	CL18839Contig1		Y						TRUE
CL1907Contig1	CL1907Contig1		Y						TRUE
CL1917Contig1	CL1917Contig1		Y						TRUE
CL1918Contig5	CL1918Contig5		Y						TRUE
CL19221Contig1	CL19221Contig1		Y						TRUE
CL1930Contig6	CL1930Contig6		Y						TRUE
CL19415Contig1	CL19415Contig1		Y						TRUE
CL19436Contig1	CL19436Contig1		Y						TRUE
CL19605Contig1	CL19605Contig1		Y						TRUE
CL19729Contig1	CL19729Contig1		Y						TRUE
CL19751Contig1	CL19751Contig1		Y						TRUE
CL19761Contig1	CL19761Contig1		Y						TRUE
CL1984Contig5	CL1984Contig5		Y						TRUE
CL19Contig14	CL19Contig14		Y						TRUE
CL1Contig104	CL1Contig104		Y						TRUE
CL1Contig1051	CL1Contig1051		Y						TRUE
CL1Contig1089	CL1Contig1089		Y						TRUE
CL1Contig1160	CL1Contig1160		Y						TRUE
CL1Contig1293	CL1Contig1293		Y						TRUE
CL1Contig1406	CL1Contig1406		Y						TRUE
CL1Contig1594	CL1Contig1594		Y						TRUE
CL1Contig188	CL1Contig188		Y						TRUE
CL1Contig225	CL1Contig225		Y						TRUE
CL1Contig233	CL1Contig233		Y						TRUE
CL1Contig313	CL1Contig313		Y						TRUE
CL1Contig38;Q6AZS1	CL1Contig38	hist1h2ad	Y						TRUE
CL1Contig401	CL1Contig401		Y						TRUE
CL1Contig514	CL1Contig514		Y						TRUE
CL1Contig724	CL1Contig724		Y	Y		Y		TRUE	TRUE
CL1Contig796	CL1Contig796		Y						TRUE
CL1Contig80	CL1Contig80		Y	Y				TRUE	TRUE
CL1Contig883	CL1Contig883		Y						TRUE
CL2010Contig3	CL2010Contig3		Y						TRUE
CL20231Contig1	CL20231Contig1		Y						TRUE
CL2030Contig1	CL2030Contig1		Y						TRUE
CL20326Contig1	CL20326Contig1		Y						TRUE
CL20538Contig1	CL20538Contig1		Y						TRUE
CL20539Contig1	CL20539Contig1		Y						TRUE
CL20609Contig1	CL20609Contig1		Y						TRUE
CL2090Contig1	CL2090Contig1		Y						TRUE
CL2091Contig2	CL2091Contig2		Y						TRUE
CL2097Contig2	CL2097Contig2		Y	Y				TRUE	TRUE
CL210Contig6	CL210Contig6		Y						TRUE
CL21287Contig1	CL21287Contig1		Y						TRUE
CL212Contig6	CL212Contig6		Y						TRUE
CL214Contig10	CL214Contig10		Y						TRUE
CL2159Contig1	CL2159Contig1		Y						TRUE
CL21870Contig1	CL21870Contig1		Y	Y				TRUE	TRUE
CL2188Contig3	CL2188Contig3		Y						TRUE
CL2190Contig2	CL2190Contig2		Y						TRUE
CL21961Contig1	CL21961Contig1		Y						TRUE
CL2211Contig3	CL2211Contig3		Y						TRUE
CL22213Contig1	CL22213Contig1		Y						TRUE
CL22667Contig1	CL22667Contig1		Y						TRUE
CL22Contig18	CL22Contig18		Y						TRUE
CL23092Contig1	CL23092Contig1		Y						TRUE
CL231Contig1	CL231Contig1		Y						TRUE
CL2321Contig3	CL2321Contig3		Y						TRUE
CL2335Contig1	CL2335Contig1		Y						TRUE
CL2344Contig1	CL2344Contig1		Y	Y				TRUE	TRUE
CL23662Contig1	CL23662Contig1		Y						TRUE
CL2373Contig1	CL2373Contig1		Y						TRUE
CL23927Contig1	CL23927Contig1		Y						TRUE
CL2400Contig2	CL2400Contig2		Y	Y				TRUE	TRUE
CL2402Contig2	CL2402Contig2		Y						TRUE
CL2428Contig5	CL2428Contig5		Y						TRUE
CL2431Contig4	CL2431Contig4		Y						TRUE
CL24495Contig1	CL24495Contig1		Y						TRUE
CL2453Contig4	CL2453Contig4		Y						TRUE
CL2457Contig1	CL2457Contig1		Y						TRUE
CL246Contig8	CL246Contig8		Y						TRUE
CL24722Contig1	CL24722Contig1		Y						TRUE
CL24837Contig1	CL24837Contig1		Y						TRUE
CL24838Contig1	CL24838Contig1		Y						TRUE
CL24855Contig1	CL24855Contig1		Y						TRUE

CL2502Contig4	CL2502Contig4		Y						TRUE
CL25067Contig1	CL25067Contig1		Y	Y				TRUE	TRUE
CL2520Contig2	CL2520Contig2		Y						TRUE
CL25284Contig1	CL25284Contig1		Y						TRUE
CL2535Contig5	CL2535Contig5		Y						TRUE
CL25436Contig1	CL25436Contig1		Y						TRUE
CL2547Contig3	CL2547Contig3		Y						TRUE
CL2554Contig1	CL2554Contig1		Y						TRUE
CL25612Contig1	CL25612Contig1		Y						TRUE
CL2595Contig2	CL2595Contig2		Y						TRUE
CL2615Contig3	CL2615Contig3		Y	Y				TRUE	TRUE
CL26177Contig1	CL26177Contig1		Y						TRUE
CL26319Contig1	CL26319Contig1		Y						TRUE
CL26334Contig1	CL26334Contig1		Y						TRUE
CL26381Contig1	CL26381Contig1		Y						TRUE
CL26535Contig1	CL26535Contig1		Y						TRUE
CL2663Contig2	CL2663Contig2		Y						TRUE
CL2664Contig2	CL2664Contig2		Y						TRUE
CL2667Contig4	CL2667Contig4		Y						TRUE
CL2670Contig1	CL2670Contig1		Y						TRUE
CL2685Contig1	CL2685Contig1		Y	Y				TRUE	TRUE
CL2685Contig3	CL2685Contig3		Y						TRUE
CL2691Contig4	CL2691Contig4		Y						TRUE
CL2693Contig2	CL2693Contig2		Y						TRUE
CL27024Contig1	CL27024Contig1		Y						TRUE
CL2715Contig5	CL2715Contig5		Y						TRUE
CL27242Contig1	CL27242Contig1		Y						TRUE
CL2732Contig1	CL2732Contig1		Y						TRUE
CL27337Contig1	CL27337Contig1		Y						TRUE
CL27618Contig1	CL27618Contig1		Y						TRUE
CL2776Contig2	CL2776Contig2		Y						TRUE
CL2808Contig3	CL2808Contig3		Y						TRUE
CL2814Contig2	CL2814Contig2		Y						TRUE
CL282Contig6	CL282Contig6		Y						TRUE
CL2859Contig3	CL2859Contig3		Y						TRUE
CL2865Contig2	CL2865Contig2		Y						TRUE
CL2871Contig3	CL2871Contig3		Y						TRUE
CL2885Contig1;Q91929	CL2885Contig1	sall3	Y		Y			TRUE	TRUE
CL2920Contig1	CL2920Contig1		Y						TRUE
CL2940Contig3	CL2940Contig3		Y						TRUE
CL29560Contig1	CL29560Contig1		Y						TRUE
CL29572Contig1	CL29572Contig1		Y						TRUE
CL2976Contig2	CL2976Contig2		Y						TRUE
CL2985Contig3	CL2985Contig3		Y						TRUE
CL2995Contig3	CL2995Contig3		Y						TRUE
CL29Contig2;Q52L23	CL29Contig2		Y						TRUE
CL30078Contig1	CL30078Contig1		Y						TRUE
CL30361Contig1	CL30361Contig1		Y						TRUE
CL303Contig2	CL303Contig2		Y						TRUE
CL303Contig6	CL303Contig6		Y						TRUE
CL30676Contig1	CL30676Contig1		Y						TRUE
CL3074Contig3	CL3074Contig3		Y						TRUE
CL3078Contig2	CL3078Contig2		Y						TRUE
CL3082Contig2	CL3082Contig2		Y						TRUE
CL31289Contig1	CL31289Contig1		Y						TRUE
CL313Contig1	CL313Contig1		Y						TRUE
CL3143Contig2	CL3143Contig2		Y						TRUE
CL314Contig2	CL314Contig2		Y						TRUE
CL3167Contig3	CL3167Contig3		Y						TRUE
CL31693Contig1	CL31693Contig1		Y						TRUE
CL3171Contig1	CL3171Contig1		Y						TRUE
CL3223Contig1	CL3223Contig1		Y						TRUE
CL32492Contig1	CL32492Contig1		Y						TRUE
CL3255Contig1	CL3255Contig1		Y						TRUE
CL32735Contig1	CL32735Contig1		Y						TRUE
CL3273Contig1	CL3273Contig1		Y						TRUE
CL3295Contig3	CL3295Contig3		Y						TRUE
CL33207Contig1	CL33207Contig1		Y						TRUE
CL3320Contig1	CL3320Contig1		Y						TRUE
CL3394Contig2	CL3394Contig2		Y						TRUE
CL3413Contig3	CL3413Contig3		Y						TRUE
CL3418Contig2	CL3418Contig2		Y	Y				TRUE	TRUE
CL342Contig4	CL342Contig4		Y						TRUE
CL3453Contig2	CL3453Contig2		Y						TRUE
CL3458Contig1	CL3458Contig1		Y						TRUE
CL3472Contig1	CL3472Contig1		Y						TRUE
CL34836Contig1	CL34836Contig1		Y						TRUE
CL34839Contig1	CL34839Contig1		Y						TRUE
CL348Contig2	CL348Contig2		Y						TRUE
CL3508Contig1	CL3508Contig1		Y						TRUE
CL3510Contig2	CL3510Contig2		Y						TRUE
CL3520Contig1	CL3520Contig1		Y						TRUE
CL3547Contig2	CL3547Contig2		Y						TRUE
CL3551Contig4	CL3551Contig4		Y						TRUE
CL3570Contig2	CL3570Contig2		Y						TRUE
CL35835Contig1	CL35835Contig1		Y						TRUE

CL3597Contig1	CL3597Contig1		Y						TRUE
CL359Contig3	CL359Contig3		Y						TRUE
CL363Contig1	CL363Contig1		Y						TRUE
CL3649Contig1	CL3649Contig1		Y						TRUE
CL36693Contig1	CL36693Contig1		Y						TRUE
CL3688Contig1	CL3688Contig1		Y						TRUE
CL3689Contig1	CL3689Contig1		Y						TRUE
CL36962Contig1	CL36962Contig1		Y						TRUE
CL369Contig2	CL369Contig2		Y						TRUE
CL3705Contig2	CL3705Contig2		Y						TRUE
CL3713Contig2	CL3713Contig2		Y						TRUE
CL3728Contig4	CL3728Contig4		Y						TRUE
CL3733Contig2	CL3733Contig2		Y						TRUE
CL37387Contig1	CL37387Contig1		Y						TRUE
CL3741Contig1	CL3741Contig1		Y						TRUE
CL3748Contig3	CL3748Contig3		Y						TRUE
CL3782Contig1	CL3782Contig1		Y						TRUE
CL37975Contig1	CL37975Contig1		Y						TRUE
CL3802Contig1	CL3802Contig1		Y						TRUE
CL3824Contig1	CL3824Contig1		Y						TRUE
CL38290Contig1	CL38290Contig1		Y						TRUE
CL38387Contig1	CL38387Contig1		Y						TRUE
CL384Contig6	CL384Contig6		Y						TRUE
CL38637Contig1	CL38637Contig1		Y						TRUE
CL38685Contig1	CL38685Contig1		Y						TRUE
CL3868Contig2	CL3868Contig2		Y						TRUE
CL38748Contig1	CL38748Contig1		Y						TRUE
CL3876Contig1	CL3876Contig1		Y						TRUE
CL3902Contig1	CL3902Contig1		Y						TRUE
CL3908Contig1	CL3908Contig1		Y						TRUE
CL3915Contig2	CL3915Contig2		Y						TRUE
CL3941Contig2	CL3941Contig2		Y	Y				TRUE	TRUE
CL39443Contig1	CL39443Contig1		Y						TRUE
CL39486Contig1	CL39486Contig1		Y						TRUE
CL39507Contig1	CL39507Contig1		Y						TRUE
CL39615Contig1	CL39615Contig1		Y						TRUE
CL3Contig34	CL3Contig34		Y						TRUE
CL3Contig50	CL3Contig50		Y						TRUE
CL40164Contig1	CL40164Contig1		Y						TRUE
CL40442Contig1	CL40442Contig1		Y						TRUE
CL40454Contig1	CL40454Contig1		Y						TRUE
CL4060Contig1	CL4060Contig1		Y						TRUE
CL4061Contig2	CL4061Contig2		Y						TRUE
CL4098Contig1	CL4098Contig1		Y						TRUE
CL4119Contig1	CL4119Contig1		Y						TRUE
CL4120Contig1	CL4120Contig1		Y						TRUE
CL4122Contig1	CL4122Contig1		Y						TRUE
CL4145Contig1	CL4145Contig1		Y						TRUE
CL4151Contig1	CL4151Contig1		Y						TRUE
CL4162Contig1	CL4162Contig1		Y						TRUE
CL416Contig6	CL416Contig6		Y						TRUE
CL4179Contig1	CL4179Contig1		Y						TRUE
CL4179Contig3	CL4179Contig3		Y						TRUE
CL419Contig8	CL419Contig8		Y						TRUE
CL41Contig15	CL41Contig15		Y						TRUE
CL4205Contig2	CL4205Contig2		Y						TRUE
CL42239Contig1	CL42239Contig1		Y						TRUE
CL4229Contig1	CL4229Contig1		Y						TRUE
CL42352Contig1	CL42352Contig1		Y						TRUE
CL42522Contig1	CL42522Contig1		Y						TRUE
CL4254Contig2	CL4254Contig2		Y						TRUE
CL4263Contig3	CL4263Contig3		Y						TRUE
CL4288Contig3	CL4288Contig3		Y						TRUE
CL43176Contig1	CL43176Contig1		Y						TRUE
CL4320Contig3	CL4320Contig3		Y						TRUE
CL43675Contig1	CL43675Contig1		Y						TRUE
CL4370Contig2	CL4370Contig2		Y						TRUE
CL4405Contig1	CL4405Contig1		Y						TRUE
CL4408Contig3	CL4408Contig3		Y						TRUE
CL4417Contig1	CL4417Contig1		Y						TRUE
CL44219Contig1	CL44219Contig1		Y						TRUE
CL444Contig2	CL444Contig2		Y						TRUE
CL44634Contig1	CL44634Contig1		Y						TRUE
CL4464Contig2	CL4464Contig2		Y						TRUE
CL4493Contig1	CL4493Contig1		Y						TRUE
CL4517Contig2	CL4517Contig2		Y						TRUE
CL451Contig4	CL451Contig4		Y						TRUE
CL45523Contig1	CL45523Contig1		Y						TRUE
CL4552Contig2	CL4552Contig2		Y						TRUE
CL4552Contig3	CL4552Contig3		Y						TRUE
CL45622Contig1	CL45622Contig1		Y						TRUE
CL4566Contig2	CL4566Contig2		Y						TRUE
CL4580Contig2	CL4580Contig2		Y						TRUE
CL45Contig20	CL45Contig20		Y						TRUE
CL45Contig21	CL45Contig21		Y						TRUE
CL4601Contig1	CL4601Contig1		Y						TRUE

CL4603Contig2	CL4603Contig2		Y						TRUE
CL46044Contig1	CL46044Contig1		Y						TRUE
CL463Contig1	CL463Contig1		Y						TRUE
CL4652Contig3	CL4652Contig3		Y						TRUE
CL465Contig2	CL465Contig2		Y						TRUE
CL465Contig6	CL465Contig6		Y						TRUE
CL4674Contig1	CL4674Contig1		Y						TRUE
CL467Contig1	CL467Contig1		Y						TRUE
CL4688Contig1;Q6DE33	CL4688Contig1	uqcrc2	Y		Y			TRUE	TRUE
CL46Contig4	CL46Contig4		Y						TRUE
CL471Contig2	CL471Contig2		Y						TRUE
CL4725Contig2	CL4725Contig2		Y						TRUE
CL4732Contig1	CL4732Contig1		Y						TRUE
CL4762Contig1	CL4762Contig1		Y						TRUE
CL4772Contig2	CL4772Contig2		Y						TRUE
CL4774Contig1	CL4774Contig1		Y						TRUE
CL4783Contig2	CL4783Contig2		Y						TRUE
CL4793Contig1	CL4793Contig1		Y						TRUE
CL4874Contig2	CL4874Contig2		Y						TRUE
CL489Contig1	CL489Contig1		Y						TRUE
CL48Contig6	CL48Contig6		Y						TRUE
CL4908Contig3	CL4908Contig3		Y						TRUE
CL4920Contig1	CL4920Contig1		Y						TRUE
CL4927Contig4	CL4927Contig4		Y						TRUE
CL4966Contig2	CL4966Contig2		Y	Y				TRUE	TRUE
CL4967Contig1	CL4967Contig1		Y						TRUE
CL4999Contig1	CL4999Contig1		Y						TRUE
CL5041Contig1	CL5041Contig1		Y						TRUE
CL5080Contig4	CL5080Contig4		Y						TRUE
CL508Contig4	CL508Contig4		Y						TRUE
CL5147Contig1	CL5147Contig1		Y						TRUE
CL5186Contig1	CL5186Contig1		Y						TRUE
CL5194Contig2	CL5194Contig2		Y						TRUE
CL51Contig4	CL51Contig4		Y						TRUE
CL5205Contig2	CL5205Contig2		Y						TRUE
CL521Contig1	CL521Contig1		Y						TRUE
CL5248Contig1	CL5248Contig1		Y						TRUE
CL5272Contig3	CL5272Contig3		Y						TRUE
CL5303Contig1	CL5303Contig1		Y						TRUE
CL5308Contig2	CL5308Contig2		Y						TRUE
CL5313Contig2	CL5313Contig2		Y						TRUE
CL5360Contig1	CL5360Contig1		Y						TRUE
CL5360Contig2	CL5360Contig2		Y						TRUE
CL5361Contig2	CL5361Contig2		Y						TRUE
CL5368Contig2	CL5368Contig2		Y						TRUE
CL540Contig10	CL540Contig10		Y						TRUE
CL5432Contig1	CL5432Contig1		Y						TRUE
CL5444Contig1	CL5444Contig1		Y						TRUE
CL5478Contig2	CL5478Contig2		Y						TRUE
CL5525Contig1	CL5525Contig1		Y						TRUE
CL5527Contig2	CL5527Contig2		Y						TRUE
CL5540Contig2;Q7ZX92	CL5540Contig2	psmd14	Y		Y			TRUE	TRUE
CL5553Contig1	CL5553Contig1		Y						TRUE
CL557Contig6	CL557Contig6		Y						TRUE
CL569Contig8	CL569Contig8		Y						TRUE
CL5725Contig1	CL5725Contig1		Y						TRUE
CL5749Contig1	CL5749Contig1		Y						TRUE
CL574Contig9	CL574Contig9		Y						TRUE
CL5772Contig2	CL5772Contig2		Y						TRUE
CL5779Contig1	CL5779Contig1		Y						TRUE
CL5832Contig1	CL5832Contig1		Y	Y				TRUE	TRUE
CL589Contig1	CL589Contig1		Y						TRUE
CL593Contig1	CL593Contig1		Y						TRUE
CL5962Contig1	CL5962Contig1		Y						TRUE
CL596Contig6	CL596Contig6		Y						TRUE
CL5978Contig1	CL5978Contig1		Y						TRUE
CL6016Contig1	CL6016Contig1		Y						TRUE
CL6084Contig1	CL6084Contig1		Y						TRUE
CL6135Contig2	CL6135Contig2		Y						TRUE
CL6182Contig1	CL6182Contig1		Y						TRUE
CL620Contig2	CL620Contig2		Y						TRUE
CL6214Contig1	CL6214Contig1		Y						TRUE
CL6298Contig1	CL6298Contig1		Y						TRUE
CL6316Contig1	CL6316Contig1		Y						TRUE
CL6334Contig1	CL6334Contig1		Y						TRUE
CL6354Contig1	CL6354Contig1		Y						TRUE
CL640Contig7	CL640Contig7		Y						TRUE
CL6476Contig1	CL6476Contig1		Y						TRUE
CL6498Contig1	CL6498Contig1		Y						TRUE
CL64Contig5	CL64Contig5		Y						TRUE
CL6506Contig2	CL6506Contig2		Y						TRUE
CL6521Contig1	CL6521Contig1		Y						TRUE
CL6529Contig1	CL6529Contig1		Y						TRUE
CL654Contig1	CL654Contig1		Y						TRUE
CL654Contig4	CL654Contig4		Y	Y				TRUE	TRUE
CL657Contig3	CL657Contig3		Y						TRUE

CL6589Contig1	CL6589Contig1		Y						TRUE
CL6622Contig2	CL6622Contig2		Y						TRUE
CL6653Contig3	CL6653Contig3		Y						TRUE
CL6658Contig2	CL6658Contig2		Y						TRUE
CL665Contig1	CL665Contig1		Y						TRUE
CL665Contig7	CL665Contig7		Y	Y				TRUE	TRUE
CL6693Contig1	CL6693Contig1		Y						TRUE
CL66Contig6	CL66Contig6		Y						TRUE
CL671Contig6	CL671Contig6		Y						TRUE
CL6737Contig1	CL6737Contig1		Y						TRUE
CL673Contig2	CL673Contig2		Y						TRUE
CL674Contig4	CL674Contig4		Y						TRUE
CL6751Contig3	CL6751Contig3		Y						TRUE
CL6788Contig2	CL6788Contig2		Y						TRUE
CL6843Contig1	CL6843Contig1		Y						TRUE
CL6849Contig3	CL6849Contig3		Y						TRUE
CL6862Contig2	CL6862Contig2		Y						TRUE
CL6870Contig2	CL6870Contig2		Y						TRUE
CL6944Contig2	CL6944Contig2		Y						TRUE
CL6953Contig2	CL6953Contig2		Y						TRUE
CL6998Contig1	CL6998Contig1		Y						TRUE
CL7008Contig1	CL7008Contig1		Y						TRUE
CL7022Contig2	CL7022Contig2		Y						TRUE
CL7044Contig1	CL7044Contig1		Y						TRUE
CL7064Contig1	CL7064Contig1		Y						TRUE
CL7083Contig3	CL7083Contig3		Y						TRUE
CL7087Contig1	CL7087Contig1		Y						TRUE
CL709Contig6	CL709Contig6		Y						TRUE
CL7101Contig2	CL7101Contig2		Y						TRUE
CL71Contig1	CL71Contig1		Y						TRUE
CL7240Contig1	CL7240Contig1		Y						TRUE
CL724Contig1	CL724Contig1		Y						TRUE
CL724Contig2	CL724Contig2		Y						TRUE
CL728Contig4	CL728Contig4		Y						TRUE
CL7317Contig1	CL7317Contig1		Y						TRUE
CL7394Contig1	CL7394Contig1		Y						TRUE
CL742Contig3	CL742Contig3		Y						TRUE
CL7447Contig1	CL7447Contig1		Y						TRUE
CL7485Contig1	CL7485Contig1		Y						TRUE
CL7498Contig1	CL7498Contig1		Y						TRUE
CL7517Contig1	CL7517Contig1		Y						TRUE
CL7560Contig1	CL7560Contig1		Y						TRUE
CL758Contig4	CL758Contig4		Y						TRUE
CL7602Contig2	CL7602Contig2		Y						TRUE
CL7605Contig2	CL7605Contig2		Y						TRUE
CL760Contig2	CL760Contig2		Y						TRUE
CL7666Contig1	CL7666Contig1		Y						TRUE
CL7679Contig1	CL7679Contig1		Y						TRUE
CL7768Contig1	CL7768Contig1		Y						TRUE
CL7800Contig2	CL7800Contig2		Y						TRUE
CL7840Contig1	CL7840Contig1		Y						TRUE
CL7875Contig1	CL7875Contig1		Y						TRUE
CL78Contig6	CL78Contig6		Y						TRUE
CL791Contig1	CL791Contig1		Y						TRUE
CL7944Contig1	CL7944Contig1		Y						TRUE
CL794Contig1	CL794Contig1		Y						TRUE
CL7956Contig1	CL7956Contig1		Y						TRUE
CL7985Contig2	CL7985Contig2		Y						TRUE
CL800Contig5	CL800Contig5		Y						TRUE
CL8013Contig1	CL8013Contig1		Y						TRUE
CL801Contig1	CL801Contig1		Y	Y				TRUE	TRUE
CL8066Contig1	CL8066Contig1		Y						TRUE
CL8107Contig2	CL8107Contig2		Y						TRUE
CL821Contig1	CL821Contig1		Y						TRUE
CL8237Contig1	CL8237Contig1		Y						TRUE
CL825Contig2	CL825Contig2		Y						TRUE
CL826Contig4	CL826Contig4		Y						TRUE
CL8282Contig1	CL8282Contig1		Y						TRUE
CL8325Contig2	CL8325Contig2		Y						TRUE
CL84Contig2	CL84Contig2		Y						TRUE
CL8565Contig1	CL8565Contig1		Y						TRUE
CL8587Contig2	CL8587Contig2		Y						TRUE
CL8606Contig1	CL8606Contig1		Y						TRUE
CL8625Contig1	CL8625Contig1		Y						TRUE
CL8672Contig1	CL8672Contig1		Y						TRUE
CL8729Contig1	CL8729Contig1		Y						TRUE
CL8749Contig2	CL8749Contig2		Y						TRUE
CL8769Contig1	CL8769Contig1		Y						TRUE
CL8785Contig2	CL8785Contig2		Y						TRUE
CL887Contig3	CL887Contig3		Y						TRUE
CL89Contig1	CL89Contig1		Y						TRUE
CL9010Contig1	CL9010Contig1		Y						TRUE
CL9091Contig2	CL9091Contig2		Y						TRUE
CL90Contig6	CL90Contig6		Y						TRUE
CL9129Contig1	CL9129Contig1		Y						TRUE
CL9153Contig1	CL9153Contig1		Y						TRUE

CL9187Contig1	CL9187Contig1		Y						TRUE
CL9204Contig1	CL9204Contig1		Y						TRUE
CL9213Contig2	CL9213Contig2		Y						TRUE
CL9216Contig2	CL9216Contig2		Y						TRUE
CL921Contig2	CL921Contig2		Y						TRUE
CL9235Contig3	CL9235Contig3		Y						TRUE
CL9347Contig1	CL9347Contig1		Y						TRUE
CL9389Contig1	CL9389Contig1		Y						TRUE
CL9403Contig1	CL9403Contig1		Y						TRUE
CL9406Contig2	CL9406Contig2		Y						TRUE
CL9423Contig1	CL9423Contig1		Y						TRUE
CL9436Contig1	CL9436Contig1		Y						TRUE
CL9481Contig1	CL9481Contig1		Y						TRUE
CL9501Contig1	CL9501Contig1		Y						TRUE
CL9522Contig1	CL9522Contig1		Y						TRUE
CL952Contig1	CL952Contig1		Y						TRUE
CL956Contig3	CL956Contig3		Y						TRUE
CL9618Contig1	CL9618Contig1		Y						TRUE
CL962Contig1;Q4V7W4	CL962Contig1		Y	Y				TRUE	TRUE
CL9635Contig1	CL9635Contig1		Y						TRUE
CL964Contig2	CL964Contig2		Y						TRUE
CL966Contig1	CL966Contig1		Y						TRUE
CL9699Contig1	CL9699Contig1		Y						TRUE
CL971Contig9	CL971Contig9		Y						TRUE
CL975Contig6	CL975Contig6		Y						TRUE
CL9794Contig1	CL9794Contig1		Y						TRUE
CL979Contig6	CL979Contig6		Y						TRUE
CL9851Contig1	CL9851Contig1		Y						TRUE
CL990Contig2	CL990Contig2		Y						TRUE
CL998Contig3	CL998Contig3		Y						TRUE
CL9991Contig1	CL9991Contig1		Y						TRUE
CV075495 UniRef100_Q2V	Rep: MGC131189 protein - Xenopus laevis (African clawed frog), partial (45%)								
CV523361 similar to UniRe	Rep: ATPase type 13A4 - Xenopus	atp13a4			Y			TRUE	TRUE
CX133552 homologue to U	Rep: Uncharacterized protein C21or	c21orf59			Y			TRUE	TRUE
CX133910	CX133910								
D0E8G8;CL3761Contig1	Zinc finger protein 423 OS=Xenopus	znf423			Y			TRUE	TRUE
D0EUZ9	B-cell lymphoma 9 OS=Xenopus lae	Bcl9			Y			TRUE	TRUE
D0PPG1	Costal2 OS=Xenopus laevis GN=Co	Cos2							
D2CGM1	Fanconi anemia complementation g	fancc			Y			TRUE	TRUE
D2DGW1	Cell division cycle associated 2 OS=	cdca2							
D2WK21	Sex-determining region Y-box 2 OS	sox2			Y			TRUE	TRUE
D3IUT5	Treslin OS=Xenopus laevis GN=ticr	ticrr							
D3JCC3	Recombination activating protein 2 (	rag2							
D5JEJ8	Afadin OS=Xenopus laevis GN=mllt	mllt4				Y		TRUE	TRUE
D6C652	Yes-associated protein 65 OS=Xen	yap							
D8WX02;CL4813Contig1	Midline 1 OS=Xenopus laevis GN=m	mid1			Y			TRUE	TRUE
DC007851 similar to UniRe	Rep: C219-reactive peptide - Xenopus tropicalis, partial (12%)								
DC014590 similar to UniRe	Rep: Chromosome 1 SCAF14998, whole genome shotgun sequence - Tetraodon nigroviridis (Green puffer), partial (94%)								
DC024875 homologue to U	Rep: Actin, alpha cardiac muscle 1 -	actc1		Y	Y			TRUE	TRUE
DC027108 homologue to U	Rep: Protein jagunal homolog 1 - Xe	jagn1			Y			TRUE	TRUE
DC034728 homologue to U	Rep: Hdac6-prov protein - Xenopus	hdac6			Y			TRUE	TRUE
DC035338 homologue to U	Rep: Interleukin enhancer binding fa	ilf3			Y			TRUE	TRUE
DC042719 homologue to U	Rep: Actin, cytoplasmic 1 - Xenopus	actb			Y			TRUE	TRUE
DC044722 similar to UniRe	Rep: CCDC95 protein - Bos taurus (	ccdc95							
DC047969 homologue to U	Rep: Nucleoside diphosphate kinas	nme							
DC049447 UniRef100_Q4	Rep: MGC115486 protein - Xenopus laevis (African clawed frog), partial (28%)								
DC050368 homologue to U	Rep: Filamin-B (FLN-B) (Beta-filami	flnb			Y			TRUE	TRUE
DC052197 homologue to U	Rep: Mediator of RNA polymerase I	med30							
DC053581 UniRef100_P45	Rep: Y-box-binding protein 2-B - Xe	ybx2			Y			TRUE	TRUE
DC053855 homologue to U	Rep: MGC81281 protein - Xenopus laevis (African clawed frog), partial (34%)								
DC062871 homologue to U	Rep: MGC52847 protein - Xenopus laevis (African clawed frog), partial (84%)								
DC064308 homologue to U	Rep: LOC495134 protein - Xenopus laevis (African clawed frog), partial (77%)								
DR717088 homologue to U	Rep: AT-rich interactive domain-cor	brg1							
DR720131 homologue to U	Rep: MGC64332 protein - Xenopus laevis (African clawed frog), p			Y				TRUE	TRUE
DR728022 homologue to U	Rep: Guanidinoacetate N-methyltra	gamtb							
dsrrswapns_comp116804_	len=382								
dsrrswapns_comp119549_	len=256								
dsrrswapns_comp11994_c	len=224								
dsrrswapns_comp120180_	len=262								
dsrrswapns_comp132298_	len=219								
dsrrswapns_comp141446_	len=239								
dsrrswapns_comp142531_	len=331								
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dsrrswapns_comp185310_	len=909								

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dsrrswapns_comp196070_	len=725								
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dsrrswapns_comp206214_	len=731								
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dsrrswapns_comp211061_	len=3565								
dsrrswapns_comp211238_	len=1138								
dsrrswapns_comp211245_	len=2036								
dsrrswapns_comp211248_	len=978								
dsrrswapns_comp211320_	len=1766								
dsrrswapns_comp211447_	len=2210								
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dsrrswapns_comp212594_	len=1253								
dsrrswapns_comp212612_	len=1311								
dsrrswapns_comp212624_	len=1012								
dsrrswapns_comp212669_	len=2527								
dsrrswapns_comp212852_	len=214								
dsrrswapns_comp212871_	len=1347			Y				TRUE	TRUE
dsrrswapns_comp212910_	len=1878								
dsrrswapns_comp213002_	len=1628								
dsrrswapns_comp213192_	len=1658								
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dsrrswapns_comp213316_	len=2272								
dsrrswapns_comp213553_	len=1469								
dsrrswapns_comp213599_	len=5103								
dsrrswapns_comp21360_c	len=389								
dsrrswapns_comp213683_	len=1326								
dsrrswapns_comp213703_	len=760								
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dsrrswapns_comp214667_	len=535								
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dsrrswapns_comp215727_	len=972								
dsrrswapns_comp215735_	len=2025								
dsrrswapns_comp215943_	len=2923								
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dsrrswapns_comp216043_	len=2424								
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dsrrswapns_comp216121_	len=842								
dsrrswapns_comp216131_	len=593								
dsrrswapns_comp216167_	len=818								
dsrrswapns_comp216246_	len=3435								
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dsrrswapns_comp216967_	len=3486								
dsrrswapns_comp216997_	len=3475								
dsrrswapns_comp217036_	len=682								
dsrrswapns_comp217115_	len=796								
dsrrswapns_comp217164_	len=2926								
dsrrswapns_comp217313_	len=2833								
dsrrswapns_comp217415_	len=3082								
dsrrswapns_comp217423_	len=1879								
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dsrrswapns_comp26597_c	len=233								
dsrrswapns_comp41315_c	len=209			Y				TRUE	TRUE
dsrrswapns_comp482840_	len=431								
dsrrswapns_comp50253_c	len=235								
dsrrswapns_comp678307_	len=458								
dsrrswapns_comp93611_c	len=445								
dsrrswapns_comp995798_	len=340								
DT058091	DT058091								
DT076135 homologue to U	Rep: Selenophosphate synthetase 2	sephs2			Y			TRUE	TRUE
DT080194 similar to UniRe	Rep: 6-phosphofructo-2-kinase/fruct	pfkfb1			Y			TRUE	TRUE
DY572351	DY572351								
E3URQ0;CL3362Contig2	Haspin OS=Xenopus laevis PE=2 S	gsg2							
E5LG93	Centrosomal protein OS=Xenopus l	cep192			Y			TRUE	TRUE
E7DCM0	Mogs (Fragment) OS=Xenopus laev	mogs			Y			TRUE	TRUE
E7FLL0	CST complex subunit CTC1 OS=Xe	ctc1			Y			TRUE	TRUE
EB462740 similar to UniRe	Rep: Uncharacterized protein C2orf	c2orf55							
EB465665 weakly similar to	Rep: Keratin, type II cytoskeletal 75	krt75							
EB470951 UniRef100_A8E	Rep: Alpha-tubulin - Giardia lamblia	tuba							
EB473635 homologue to U	Rep: Heat shock protein 70 - Sphae	hsp70							
EB474857 similar to UniRe	Rep: Long palate, lung and nasal ep	C20orf186							
EB475574 weakly similar to	Rep: AGAP003346-PA - Anopheles gambiae str. PEST, partial (10%)								
EB477604 homologue to U	Rep: thymidylate kinase family LPS-	cmpk2			Y			TRUE	TRUE
EB478098 similar to UniRe	Rep: uromodulin-like 1 isoform 1 - X	umodl1							
EB644224 homologue to U	Rep: MGC108424 protein - Xenopu	MGC108424							
EG574474 similar to UniRe	Rep: Mitochondrial substrate carrier - Chlamydomonas reinhardtii, partial (21%)								
EG584025 weakly similar to	Rep: Cathepsin E precursor - Rana	ctse							
F6KDD5	NADH dehydrogenase subunit 1 OS	nad1							
F7IYU6	Calcium activated chloride channel	clca6							
G1ESZ8	Putative beta-N-acetylhexosaminida	bglx							
G3CQZ6	M18BP1 isoform 1 OS=Xenopus lae	m18bp1							
G3GBS3;CL10123Contig1	Peroxiredoxin 2 OS=Xenopus laevis	prdx2		Y	Y			TRUE	TRUE
G3GBS4	Peroxiredoxin 3 OS=Xenopus laevis	prdx3			Y			TRUE	TRUE
G8HXD7	Wnt-activated inhibitory factor 1a.2	wif1			Y			TRUE	TRUE
H2DQ55	Interferon-gamma (Fragment) OS=X	ifng							
H9B3Z0	Bromodomain adjacent to zinc finge	Baz2b			Y			TRUE	TRUE
H9DRN9	Oculocerebrorenal syndrome of Low	ocrl			Y			TRUE	TRUE
I3PB85;CL26Contig14	IFN-gamma-inducible-lysosomal thi	gilt							
NP9453667 GB	AY819241.1 AAX37552.1 c-myc								
O12975;CL1627Contig2	Fructose-bisphosphate aldolase OS	aldoa		Y	Y	Y		TRUE	TRUE
O13027	Mitotic phosphoprotein 90 OS=Xeno	epn2							
O13097;CL3156Contig1	Ephrin-B1 OS=Xenopus laevis GN=	efnb1			Y	Y		TRUE	TRUE
O13124;CL7992Contig1	Vitamin D3 receptor OS=Xenopus la	vdr			Y			TRUE	TRUE
O42193;CL1Contig277	MGC64314 protein OS=Xenopus la	ranbp1			Y			TRUE	TRUE
O42469	Transducin-like enhancer protein 1	esg1							
O42507	Thrombospondin-3 (Fragment) OS=	thbs3							
O42587;CL492Contig6	26S protease regulatory subunit 6A-	psmc3			Y			TRUE	TRUE
O57345	Synaptobrevin OS=Xenopus laevis	vamp2							
O57468;CL1665Contig1	14-3-3 protein epsilon OS=Xenopus	ywhae			Y			TRUE	TRUE
O57526	Insulin-like growth factor 2 mRNA-b	igf2bp3			Y			TRUE	TRUE
O73614	TAB1 OS=Xenopus laevis GN=tab1	tab1			Y			TRUE	TRUE
O73633	Neural cell adhesion molecule OS=X	ncam1			Y			TRUE	TRUE
O73676	Lens specific OS=Xenopus laevis PE=2 SV=1 - [O73676_XENLA]								
O73732	Rho-associated kinase alpha OS=X	rock2			Y			TRUE	TRUE
O93235	Cold-inducible RNA-binding protein	cirbp			Y			TRUE	TRUE
O93308	Structural maintenance of chromoso	smc1a			Y			TRUE	TRUE
O93400;CL3Contig45	Actin, cytoplasmic 1 OS=Xenopus la	actb			Y			TRUE	TRUE
O93477	Adenosylhomocysteinase B OS=Xe	ahcy2			Y			TRUE	TRUE
O93522;CL47Contig4	Nonmuscle myosin II heavy chain A	myh9			Y			TRUE	TRUE
P02281;TC453026 UniRef1	Histone H2B 1.1 OS=Xenopus laevi	h2b11							
P02350	40S ribosomal protein S3-A OS=Xe	rps3		Y	Y			TRUE	TRUE
P02362	40S ribosomal protein S7 OS=Xeno	rps7		Y	Y			TRUE	TRUE
P04751;CL3Contig43	Actin, alpha cardiac muscle 1 OS=X	actc1		Y	Y			TRUE	TRUE
P05221;CL36471Contig1	Nucleoplasmin OS=Xenopus laevis	nupl							
P05377	Acetylcholine receptor subunit alpha	chrna1b							
P08429;CL92Contig5	60S ribosomal protein L4-A OS=Xen	rpl4		Y				TRUE	TRUE
P08478;CL660Contig2	Peptidyl-glycine alpha-amidating mo	pama							
P08537	Tubulin alpha chain OS=Xenopus la	tuba							
P08759;CL504Contig3	Serum albumin A OS=Xenopus laev	alb-a							
P09897	60S ribosomal protein L18-A OS=Xe	rpl18a			Y			TRUE	TRUE
P13549;CL5Contig29	Elongation factor 1-alpha, somatic fo	eef1as							
P13926	Superoxide dismutase [Cu-Zn] A OS	sod1			Y			TRUE	TRUE
P15107;CL10172Contig1	Superoxide dismutase [Cu-Zn] B OS	sod1		Y	Y			TRUE	TRUE
P15126	60S ribosomal protein L5-B OS=Xen	rpl5b							
P17507	Elongation factor 1-alpha, oocyte fo	eef1ao							
P17508;CL430Contig6	Elongation factor 1-alpha, oocyte fo	ef1a3		Y				TRUE	TRUE
P18709	Vitellogenin-A2 OS=Xenopus laevis	vtga2			Y			TRUE	TRUE
P18716	Gastrula zinc finger protein XlCGF2	OC101883812							
P18748	Oocyte zinc finger protein XlCOF29	xicof29							
P19011	Vitellogenin-B2 (Fragment) OS=Xen	vtgb2							
P19102	Protein c-ets-2-A OS=Xenopus laev	ets2			Y			TRUE	TRUE
P20310	Neural cadherin-1 OS=Xenopus lae	cdh1		Y	Y	Y		TRUE	TRUE
P20342	40S ribosomal protein S15 OS=Xen	rps15		Y	Y			TRUE	TRUE
P21574	Y-box-binding protein 2-A OS=Xeno	ybx2			Y			TRUE	TRUE
P23403;CL22Contig8	40S ribosomal protein S20 OS=Xen	rps20			Y			TRUE	TRUE

P23790	Serum response factor OS=Xenopu	srf			Y			TRUE	TRUE
P24033	Cyclin-dependent kinase 1-B OS=X	cdk1			Y			TRUE	TRUE
P24495;CL4026Contig1	Proteasome subunit alpha type-2 O	psma2							
P26363	Cystic fibrosis transmembrane cond	cftr			Y			TRUE	TRUE
P26642	Elongation factor 1-gamma-A OS=X	eef1ga		Y				TRUE	TRUE
P28024	Proteasome subunit beta type-4 (Fr	psmb4			Y			TRUE	TRUE
P28048	Lupus La protein homolog A OS=Xe	ssb							
P29540;CL66Contig1	General transcription factor IIE subu	gtf2e2							
P30311	M-phase inducer phosphatase 3 OS	cdc25c			Y			TRUE	TRUE
P30883;CL57Contig6	Tubulin beta-4 chain OS=Xenopus l	tubb4			Y			TRUE	TRUE
P30944	Cadherin-1 OS=Xenopus laevis GN	cdh1			Y			TRUE	TRUE
P30998;CL24Contig14	Junction plakoglobin OS=Xenopus l	jup			Y			TRUE	TRUE
P39017;CL2323Contig1	40S ribosomal protein S6 OS=Xeno	rps6		Y				TRUE	TRUE
P40650	Transcription factor Sox-11-B OS=X	sox11			Y			TRUE	TRUE
P41116;CL818Contig6	60S ribosomal protein L8 OS=Xeno	rpl8		Y	Y			TRUE	TRUE
P42291	D(1C) dopamine receptor OS=Xenc	drd1c							
P43695	GATA-binding factor 5-A OS=Xenop	gata5			Y			TRUE	TRUE
P45441	Y-box-binding protein 2-B OS=Xenc	ybx2			Y			TRUE	TRUE
P45593	Cofilin-1-B OS=Xenopus laevis GN=	cfl1			Y			TRUE	TRUE
P45695	Cofilin-1-A OS=Xenopus laevis GN=	cfl1			Y			TRUE	TRUE
P46472;CL5541Contig2	26S protease regulatory subunit 7 C	psmc2			Y			TRUE	TRUE
P47835	40S ribosomal protein S3-B OS=Xe	rps3			Y			TRUE	TRUE
P47904;CL48Contig2	40S ribosomal protein S27 OS=Xen	rps27			Y			TRUE	TRUE
P48676	Peripherin OS=Xenopus laevis GN=	prph			Y			TRUE	TRUE
P49393;CL1Contig728	40S ribosomal protein S13 OS=Xen	rps13		Y	Y			TRUE	TRUE
P49401;CL397Contig5	40S ribosomal protein S4 OS=Xeno	rps4							
P50143;CL5141Contig1	T-complex protein 1 subunit gamma	cct3		Y	Y			TRUE	TRUE
P50886	60S ribosomal protein L22 OS=Xen	rpl22		Y	Y			TRUE	TRUE
P51048	Melatonin receptor type 1A X2.0 (Fr	mtra1							
P51644;CL1057Contig4	ADP-ribosylation factor 4 OS=Xeno	arf4			Y			TRUE	TRUE
P51893	Adenosylhomocysteinase A OS=Xe	ahcy1			Y			TRUE	TRUE
P52170	Importin subunit alpha-5 OS=Xenop	kpna1			Y			TRUE	TRUE
P52171	Importin subunit alpha-2 OS=Xenop	kpna2			Y			TRUE	TRUE
P52301;CL872Contig1	GTP-binding nuclear protein Ran O	ran							
P54824	ATP-dependent RNA helicase ddx6	ddx6			Y			TRUE	TRUE
P55861	DNA replication licensing factor mcr	mcm2			Y			TRUE	TRUE
P55863	Transcription factor Sox-3-A OS=Xe	sox3			Y			TRUE	TRUE
P62155;CL1Contig1497	Calmodulin OS=Xenopus laevis GN	calm1		Y	Y			TRUE	TRUE
P62799	Histone H4 OS=Xenopus laevis PE=	hist4							
P62840	Ubiquitin-conjugating enzyme E2 D2	ube2d2							
P70010	Nucleoside diphosphate kinase A1 (	ndka1		Y				TRUE	TRUE
P70011;CL60Contig6	Nucleoside diphosphate kinase A2 (	ndka2							
P70032	Serine/threonine-protein kinase PLK	plk1			Y			TRUE	TRUE
P70039;CL1426Contig1	Adenomatous polyposis coli homolo	apc			Y		Y	TRUE	TRUE
P70047;CL2Contig68	Myelin transcription factor 1 OS=Xe	myt1			Y			TRUE	TRUE
P70049	Origin recognition complex protein 1	orc1			Y			TRUE	TRUE
P70064	Transcription factor 7-like 1-D OS=X	tcf7l1			Y			TRUE	TRUE
P79929;CL1Contig361	LOC397932 protein OS=Xenopus laevis GN=LOC397932 PE=2 SV=2 - [P79929_XENLA]								
P79931	Pyruvate dehydrogenase E1-beta su	pdhe1b1							
P79932	Pyruvate dehydrogenase E1-beta su	Pdhe1b2							
P79937	Homeobox protein Meis1 OS=Xeno	meis1			Y			TRUE	TRUE
P79951	CD3gamma/delta OS=Xenopus laev	cd3g							
Q00387;CL13623Contig1	Serine protease inhibitor A6 OS=Xe	serpina6		Y				TRUE	TRUE
Q01550	Tanabin OS=Xenopus laevis PE=2	aoc2							
Q01611	Zinc finger Y-chromosomal protein 1	zfy1							
Q05116;dsrrswapns_comp	Dual specificity mitogen-activated pr	map2k1			Y			TRUE	TRUE
Q05AW6;CL3514Contig2	MGC154502 protein OS=Xenopus l	MGC154502							
Q05AW7	Cytoplasmic tRNA 2-thiolation prote	ctu1			Y			TRUE	TRUE
Q05AX8	Lap-1 protein OS=Xenopus laevis G	lap1							
Q05AY5	LOC414691 protein OS=Xenopus laevis GN=LOC414691 PE=2 SV=1 - [Q05AY5_XENLA]								
Q05AY9	LOC398450 protein OS=Xenopus la	LOC398450							
Q06271	Integrin alpha 2 subunit (Fragment)	itga2							
Q07254	40S ribosomal protein S10 OS=Xen	rps10		Y	Y			TRUE	TRUE
Q08AW9	LOC100158398 protein OS=Xenopu	slc2a9							
Q08AX1	LOC100158396 protein OS=Xenopu	klhl32			Y			TRUE	TRUE
Q08AX4	LOC100158394 protein OS=Xenopu	OC100158394							
Q08AY2	LOC100158387 protein OS=Xenopu	OC100158387							
Q08B23	LOC733299 protein OS=Xenopus la	ngly1			Y			TRUE	TRUE
Q08B28	LOC100158365 protein OS=Xenopu	usp7							
Q08B62	LOC100158340 protein OS=Xenopu	OC100158340							
Q08B79	LOC733250 protein (Fragment) OS=	LOC733250							
Q08B84	E3 ubiquitin-protein ligase RNF19B	rnf19b			Y			TRUE	TRUE
Q09006;CL1198Contig1	Stathmin-1-A OS=Xenopus laevis G	stmn1			Y			TRUE	TRUE
Q0IH17	LOC100125665 protein OS=Xenopu	capn3			Y			TRUE	TRUE
Q0IH19	MGC154878 protein OS=Xenopus l	map1lc3c			Y			TRUE	TRUE
Q0IH25	Kntc2 protein OS=Xenopus laevis G	kntc2							
Q0IH27	Hmg20b protein OS=Xenopus laevis	hmg20b			Y			TRUE	TRUE
Q0IH31	MGC154809 protein OS=Xenopus laevis GN=snrpg PE=4 SV=1 - [Q0IH31_XENLA]								
Q0IH31;CL15343Contig1	MGC154809 protein OS=Xenopus l	snrpg			Y			TRUE	TRUE
Q0IH65	LOC733268 protein OS=Xenopus laevis GN=LOC733268 PE=2 SV=1 - [Q0IH65_XENLA]								
Q0IH66	Ddx10 protein OS=Xenopus laevis (	ddx10			Y			TRUE	TRUE
Q0IH80	MGC154542 protein OS=Xenopus l	c1ql4							
Q0IH85	LOC398205 protein OS=Xenopus la	ruvbl2			Y			TRUE	TRUE
Q0IHC8	MGC115147 protein OS=Xenopus l	vps37a			Y			TRUE	TRUE
Q0IHC9	MGC154449 protein OS=Xenopus l	nif3l1			Y			TRUE	TRUE
Q0IHE9	MGC154408 protein OS=Xenopus l	agpat6							

Q0IHF9	Store-operated calcium entry-assoc	tmem66			Y			TRUE	TRUE
Q0IHG1;CL10048Contig1	MGC154377 protein OS=Xenopus l	rplp2			Y			TRUE	TRUE
Q0IHG7	Stk4 protein OS=Xenopus laevis GN	stk4			Y			TRUE	TRUE
Q0IHH7;dsrrswapns_comp	MGC154345 protein OS=Xenopus l	MGC154345							
Q0IHI7	THAP domain-containing protein 5 (	thap5			Y			TRUE	TRUE
Q0IHJ5	MGC154315 protein OS=Xenopus laevis GN=MGC154315 PE=2 SV=1 - [Q0IHJ5_XENLA]								
Q0IHJ7;CL8685Contig1	MGC154312 protein OS=Xenopus l	MGC154312							
Q0IHJ9	MGC154309 protein OS=Xenopus l	nsun6							
Q153D9	Receptor tyrosine kinase ErbB4 OS	erbb4			Y			TRUE	TRUE
Q1JQ83	MGC130971 protein OS=Xenopus l	scml2			Y			TRUE	TRUE
Q1JV76	ADP ribosylation factor GAP protein	agd							
Q1W3Z6	Silencing mediator for retinoid and t	ncor2			Y			TRUE	TRUE
Q1W9P0	Secretory pathway Ca,Mn-ATPase (	atp2c2							
Q1XG43;CL46Contig7	Scc2-2A OS=Xenopus laevis GN=S	scc22							
Q2EI21	RE1-silencing transcription factor A	rest			Y			TRUE	TRUE
Q2KHQ3	LOC446279 protein OS=Xenopus la	daxx			Y			TRUE	TRUE
Q2NLB0	UPF0469 protein KIAA0907 homolog OS=Xenopus laevis PE=2 SV=1 - [K0907_XENLA]								
Q2NLB1	MGC130901 protein OS=Xenopus l	MGC130901							
Q2QDE3	eef2-prov protein OS=Xenopus laev	entpd3			Y			TRUE	TRUE
Q2T9K2	Transcription factor AP-2-epsilon OS	tfap2e			Y			TRUE	TRUE
Q2T9K3	MGC131110 protein OS=Xenopus l	MGC131110							
Q2TAD6	LOC431838 protein OS=Xenopus la	kifc3			Y	Y		TRUE	TRUE
Q2TAD9	Cysteine and histidine-rich protein 1	cyhr1			Y			TRUE	TRUE
Q2TAE3	Dual specificity tyrosine-phosphoryla	dyrk1a			Y			TRUE	TRUE
Q2TAF4;CL5014Contig2	Integrator complex subunit 6-A OS=	ints6			Y			TRUE	TRUE
Q2TAF7	MGC132159 protein OS=Xenopus l	cep85			Y			TRUE	TRUE
Q2TAH5;CL50Contig10	LOC495416 protein OS=Xenopus la	sec63			Y	Y		TRUE	TRUE
Q2TAH7;CL1661Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q2TAH7_XENLA]								
Q2TAQ0	MGC131229 protein OS=Xenopus l	fbxo38			Y			TRUE	TRUE
Q2TAQ1	Putative elongator complex protein	ikbkap			Y			TRUE	TRUE
Q2TAQ2	LOC733439 protein (Fragment) OS=	LOC733439							
Q2TAS0	MGC130982 protein OS=Xenopus l	tjap1							
Q2TAS1;CL8143Contig1	MGC130979 protein OS=Xenopus l	sptlc3			Y			TRUE	TRUE
Q2TAT7;CL10539Contig1	MGC130882 protein OS=Xenopus l	uqcrq			Y			TRUE	TRUE
Q2TAV8;CL6367Contig1	Wdhd1 protein OS=Xenopus laevis	wdhd1			Y			TRUE	TRUE
Q2TAV9	Putative uncharacterized protein OS	galnt6.2							
Q2V0J3;CL661Contig1	Semaphorin 6D4 OS=Xenopus laev	sema6d			Y			TRUE	TRUE
Q2VPG2	LOC733435 protein (Fragment) OS=	LOC733435							
Q2VPG9;CL1Contig756	MGC132166 protein OS=Xenopus l	suclg2			Y			TRUE	TRUE
Q2VPH0;CL1377Contig2	MGC132155 protein OS=Xenopus l	MGC132155							
Q2VPH6	LOC432342 protein OS=Xenopus la	cops2			Y			TRUE	TRUE
Q2VPK9	Acyl-coenzyme A oxidase OS=Xeno	acox1			Y			TRUE	TRUE
Q2VPL5	MGC131247 protein OS=Xenopus l	MGC131247							
Q2VPL7	LOC733431 protein (Fragment) OS=	LOC733431							
Q2VPL8	MGC131189 protein OS=Xenopus l	aldh6a1							
Q2VPN0	Zbtb7b protein OS=Xenopus laevis	zbtb7b			Y			TRUE	TRUE
Q2VPN4;CL5571Contig1	MGC52890 protein OS=Xenopus la	pnlip							
Q32N55	Pentatricopeptide repeat-containing	ptcd3			Y			TRUE	TRUE
Q32N62	LOC733423 protein (Fragment) OS=	LOC733423							
Q32NG0	Adenosine deaminase domain-conta	adad1			Y			TRUE	TRUE
Q32NH1	LOC733414 protein (Fragment) OS=	LOC733414							
Q32NH8	1-phosphatidylinositol 4,5-bisphosph	plcd4			Y			TRUE	TRUE
Q32NJ6;CL220Contig1	Uncharacterized protein OS=Xenop	yap1							
Q32NK0	MGC131089 protein OS=Xenopus l	myef2			Y			TRUE	TRUE
Q32NL8	MGC131051 protein OS=Xenopus l	slc3a1			Y	Y		TRUE	TRUE
Q32NN1	MGC131022 protein OS=Xenopus l	recql			Y	Y		TRUE	TRUE
Q32NR3	DNA-binding protein RFX2 OS=Xen	rfx2							
Q32NR8	MGC130896 protein OS=Xenopus l	ndufs2							
Q32NS5	MGC130857 protein OS=Xenopus l	abhd1							
Q32NS7;CL1Contig287	MGC52825 protein OS=Xenopus la	hmgb2			Y			TRUE	TRUE
Q32NS8	Adenylyl cyclase-associated protein	MGC52725							
Q32NU1;CL3333Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q32NU1_XENLA]								
Q32NV2	MGC78960 protein OS=Xenopus la	wdr16			Y			TRUE	TRUE
Q32NW0	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q32NW0_XENLA]								
Q3B8B3;CL12613Contig1	MGC132191 protein OS=Xenopus l	uchl1			Y			TRUE	TRUE
Q3B8C5;CL5938Contig2	MGC131368 protein OS=Xenopus l	ndufab1			Y			TRUE	TRUE
Q3B8D3	MGC68480 protein OS=Xenopus la	MGC68480							
Q3B8E3	Phospholysine phosphohistidine ino	lhpp			Y			TRUE	TRUE
Q3B8H6	Pofut1 protein OS=Xenopus laevis (	pofut1			Y			TRUE	TRUE
Q3B8I3;CL3171Contig2	MGC130910 protein OS=Xenopus l	rpl7		Y	Y			TRUE	TRUE
Q3B8I6	Wu:fj06d02 protein OS=Xenopus laevis GN=wu:fj06d02 PE=2 SV=1 - [Q3B8I6_XENLA]								
Q3B8J4	MGC130819 protein OS=Xenopus l	tekt2			Y			TRUE	TRUE
Q3B8J8	Succinate dehydrogenase [ubiquino	sdhb			Y			TRUE	TRUE
Q3KPK3	Uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q3KPK3_XENLA]								
Q3KPK3;CL25783Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q3KPK3_XENLA]								
Q3KPN6	Proteasome subunit alpha type OS=	psma							
Q3KPP7	Fructose-bisphosphate aldolase OS	aldob			Y			TRUE	TRUE
Q3KPT4;dsrrswapns_comp	MGC131338 protein OS=Xenopus l	zmat3		Y	Y			TRUE	TRUE
Q3KPT7	3-hydroxybutyrate dehydrogenase t	bdh2			Y			TRUE	TRUE
Q3KPV2	LOC398657 protein OS=Xenopus la	LOC398657							
Q3KPV4;CL10181Contig1	Transmembrane and ubiquitin-like d	tmub1			Y			TRUE	TRUE
Q3KPV9;CL5420Contig1	Proteasome subunit beta type OS=X	psmb							
Q3KPW6	LOC733370 protein (Fragment) OS=	LOC733370							
Q3KPX1	LOC733368 protein (Fragment) OS=	LOC733368							
Q3KQ21	MGC131091 protein OS=Xenopus l	slc35a3.1							
Q3KQ31	LOC733344 protein (Fragment) OS=	LOC733344							

Q3KQ47;CL20072Contig1	MGC130974 protein OS=Xenopus l	tiam1			Y			TRUE	TRUE
Q3KQ54;CL6751Contig1	MGC130953 protein OS=Xenopus l	atic			Y			TRUE	TRUE
Q3KQ55	MGC130949 protein OS=Xenopus l	uevld			Y			TRUE	TRUE
Q3KQ57	MGC130942 protein OS=Xenopus l	trappc12							
Q3KQ82	Profilin OS=Xenopus laevis GN=pfn	pfn1						TRUE	TRUE
Q3KQA5	Rab3d protein OS=Xenopus laevis G	rab3d			Y			TRUE	TRUE
Q3KQB6	CTD small phosphatase-like protein	ctdspl2b				Y		TRUE	TRUE
Q3KQC0;CL5489Contig2	LOC414601 protein OS=Xenopus laevis GN=LOC414601 PE=2 SV=1 - [Q3KQC0_XENLA]								
Q3KQC9	Rps16 protein OS=Xenopus laevis G	rps16			Y			TRUE	TRUE
Q3LH63	Doublesex- and mab-3-related trans	dmrt1a			Y			TRUE	TRUE
Q3MV19	TNF receptor-associated factor 6-A	traf6			Y			TRUE	TRUE
Q3S2E9	Carbamoyl-phosphate synthetase I	cps1							
Q3SYN2;CL2881Contig3	MGC114703 protein OS=Xenopus l	mob3a							
Q3ZM03;CL912Contig2	40S ribosomal protein SA OS=Xeno	rpsa		Y	Y			TRUE	TRUE
Q3ZPL6	Lethal giant larvae OS=Xenopus lae	llgl							
Q498E9	MGC115581 protein OS=Xenopus l	pus7			Y			TRUE	TRUE
Q498G7	PKC-delta2 protein OS=Xenopus la	prkcd			Y			TRUE	TRUE
Q498H6	MGC114937 protein OS=Xenopus l	papss1							
Q498I1	LOC398508 protein OS=Xenopus la	grhpr.2		Y	Y			TRUE	TRUE
Q498L1	MGC114631 protein OS=Xenopus l	MGC114631							
Q498L1;CL2523Contig1	MGC114631 protein OS=Xenopus l	MGC114631							
Q498L4	LOC734164 protein (Fragment) OS	LOC734164							
Q4A520;CL7515Contig1	Putative transient receptor potential	nompc							
Q4FZM4	LOC100036775 protein (Fragment)	OC100036775							
Q4FZM5;CL2718Contig3	MGC116545 protein OS=Xenopus l	cyc1			Y		Y	TRUE	TRUE
Q4FZP3	Cytochrome c oxidase subunit 6A, r	cox6a1			Y			TRUE	TRUE
Q4FZP9	MGC116466 protein OS=Xenopus laevis GN=MGC116466 PE=2 SV=1 - [Q4FZP9_XENLA]								
Q4FZQ3	Rpl34 protein OS=Xenopus laevis G	rpl34							
Q4FZQ7	MGC116425 protein OS=Xenopus l	rpl35			Y			TRUE	TRUE
Q4FZW1	LOC443587 protein (Fragment) OS	LOC443587							
Q4FZX2	LOC495168 protein OS=Xenopus la	itih2			Y			TRUE	TRUE
Q4FZX3	LOC432087 protein (Fragment) OS	LOC432087							
Q4G444	Polycystic kidney disease protein 1	pkd1			Y			TRUE	TRUE
Q4JNX8	RECQL4-helicase-like protein OS=X	rts							
Q4KL87	MGC116558 protein OS=Xenopus l	pde9a							
Q4KL91;CL4667Contig1	Proton-coupled amino acid transpor	slc36a4			Y			TRUE	TRUE
Q4KL98	MGC116533 protein OS=Xenopus l	stoml2			Y			TRUE	TRUE
Q4KLA5	MGC84800 protein OS=Xenopus la	MGC84800							
Q4KLB0	Glyoxalase domain-containing prote	glod5			Y			TRUE	TRUE
Q4KLF3	Protein KTI12 homolog OS=Xenopu	kti12			Y			TRUE	TRUE
Q4KLF5;CL749Contig1	Transcription factor BTF3 homolog 4	btf3l4			Y			TRUE	TRUE
Q4KLP7	MGC115718 protein OS=Xenopus l	esco2							
Q4KLP9;CL7902Contig1	MGC115697 protein OS=Xenopus l	parg			Y			TRUE	TRUE
Q4KLS8;CL4540Contig2	Arginine and glutamate-rich protein	arglu1			Y			TRUE	TRUE
Q4KLT2	MGC115451 protein OS=Xenopus l	MGC115451							
Q4KLV8	LOC733291 protein (Fragment) OS	LOC733291							
Q4KLW5	MGC83233 protein OS=Xenopus la	psmd2			Y			TRUE	TRUE
Q4KLX0;CL907Contig1	MGC114675 protein OS=Xenopus l	atp6v1a			Y			TRUE	TRUE
Q4QQP6;CL19376Contig1	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q4QQP6_XENLA]								
Q4QR21	Putative uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [Q4QR21_XENLA]								
Q4QR22;CL4816Contig2	MGC114925 protein OS=Xenopus laevis GN=MGC114925 PE=2 SV=1 - [Q4QR22_XENLA]								
Q4QR32	MGC114875 protein OS=Xenopus l	rps29			Y			TRUE	TRUE
Q4QR44	MGC114789 protein OS=Xenopus l	rps15a			Y			TRUE	TRUE
Q4QR45;CL3635Contig1	Importin subunit alpha OS=Xenopus	kpna7			Y			TRUE	TRUE
Q4QR49	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q4QR49_XENLA]								
Q4QR53	LOC443652 protein OS=Xenopus la	f2							
Q4QR55	VgRBP60 protein OS=Xenopus laev	vgrbp60							
Q4QR58	Eukaryotic translation initiation facto	eif3c			Y			TRUE	TRUE
Q4QY31;CL2078Contig2	Aryl hydrocarbon receptor 1 alpha G	ahr1a							
Q4U0Y4	Nucleosome assembly protein 1-like	nap1l1			Y			TRUE	TRUE
Q4V7G8	MGC115727 protein OS=Xenopus l	sirt3.2			Y			TRUE	TRUE
Q4V7I2	LOC733267 protein (Fragment) OS	LOC733267							
Q4V7J2	LOC733264 protein (Fragment) OS=Xenopus laevis GN=LOC733264 PE=2 SV=1 - [Q4V7J2_XENLA]								
Q4V7J4	MGC115652 protein OS=Xenopus l	MGC115652							
Q4V7K0	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q4V7K0_XENLA]								
Q4V7K1	MGC115622 protein OS=Xenopus l	eif4e2							
Q4V7K2	MGC115621 protein OS=Xenopus l	utp18			Y			TRUE	TRUE
Q4V7L1	MGC115598 protein OS=Xenopus l	MGC115598							
Q4V7N2	tRNA (cytosine(34)-C(5))-methyltran	nsun2			Y			TRUE	TRUE
Q4V7Q6	Serine/threonine-protein kinase ULK	ulk3			Y			TRUE	TRUE
Q4V7V6	MGC115247 protein OS=Xenopus l	prodh			Y			TRUE	TRUE
Q4V7V7	MGC115244 protein OS=Xenopus l	hmgxb3			Y			TRUE	TRUE
Q4V7W0	MGC80416 protein OS=Xenopus la	MGC80416							
Q4V7W5	Polyhomeotic-like protein 2 OS=Xen	phc2							
Q4V7X5	LOC733254 protein (Fragment) OS	LOC733254							
Q4V7Y7	Katanin p80 WD40-containing subu	katnb1			Y			TRUE	TRUE
Q4V7Z2	MGC114910 protein OS=Xenopus l	msn							
Q4V801	LOC398774 protein OS=Xenopus la	LOC398774							
Q4V813;CL6656Contig1	Adh3 protein OS=Xenopus laevis G	adh5			Y			TRUE	TRUE
Q4V837	Denticleless protein homolog A OS=	dtl							
Q4V847	Integrator complex subunit 8 OS=Xe	ints8			Y			TRUE	TRUE
Q4V866	MGC114642 protein OS=Xenopus l	clpx			Y			TRUE	TRUE
Q4V871	MGC114621 protein OS=Xenopus laevis GN=MGC114621 PE=4			Y				TRUE	TRUE
Q4VAE4	MGC115325 protein OS=Xenopus l	MGC115325							
Q501Q2	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q501Q2_XENLA]								
Q501Q8	MGC99195 protein OS=Xenopus la	sel1l			Y			TRUE	TRUE

Q52KN0;CL14329Contig1	MGC115198 protein OS=Xenopus l	MGC115198							
Q52KV8	MGC115036 protein OS=Xenopus l	MGC115036							
Q52KV9	LOC733224 protein (Fragment) OS=	LOC733224							
Q52KW6;TC418765 UniRe	MGC115285 protein OS=Xenopus l	MGC115285							
Q52KY1;CL6681Contig1	Vdac2 protein OS=Xenopus laevis (	vdac2		Y	Y			TRUE	TRUE
Q52KZ3	LOC733223 protein (Fragment) OS=	LOC733223							
Q52L09	MGC115031 protein OS=Xenopus l	hmp19							
Q52L36	MGC114755 protein OS=Xenopus l	cisd1			Y			TRUE	TRUE
Q52M98	14-3-3 protein theta OS=Xenopus la	ywhaq			Y			TRUE	TRUE
Q53I77	Exportin-6-A OS=Xenopus laevis G	xpo6			Y			TRUE	TRUE
Q561N7	LOC733199 protein (Fragment) OS=	LOC733199							
Q563C3;CL549Contig3	Sororin OS=Xenopus laevis GN=cd	cdca5		Y	Y			TRUE	TRUE
Q566F3;CL9914Contig1	MGC114950 protein OS=Xenopus l	slc45a2			Y			TRUE	TRUE
Q566H1	MGC115310 protein OS=Xenopus l	crmp1							
Q566H3;CL12776Contig1	MGC114733 protein OS=Xenopus l	cebpg			Y			TRUE	TRUE
Q566I1	INO80 complex subunit D OS=Xeno	ino80d			Y			TRUE	TRUE
Q569T0	MGC115178 protein OS=Xenopus l	hdac10			Y			TRUE	TRUE
Q569T6;CL3058Contig3	MGC115028 protein OS=Xenopus l	cnppd1			Y	Y		TRUE	TRUE
Q569U3	Fcp1 protein OS=Xenopus laevis G	fcp1							
Q569Z1	Eukaryotic translation initiation facto	eif3b			Y			TRUE	TRUE
Q56A68	LOC733185 protein (Fragment) OS=	LOC733185							
Q588Y8;CL1100Contig2	26S proteasome subunit OS=Xenop	rpn10c							
Q58E21	Proteasome subunit alpha type OS=	psma1							
Q5BIY1	MGC84975 protein OS=Xenopus la	rab11fip2			Y			TRUE	TRUE
Q5BJ43;CL26281Contig1	LOC496181 protein OS=Xenopus laevis GN=LOC496181 PE=2 SV=1 - [Q5BJ43_XENLA]								
Q5BL86	MGC85088 protein OS=Xenopus la	blmh							
Q5EAU9;CL98Contig4	Regulator of microtubule dynamics	fam82a2			Y			TRUE	TRUE
Q5EAV5;CL3725Contig2	ICLN protein OS=Xenopus laevis G	icln							
Q5EAX3	MGC85022 protein OS=Xenopus la	wrap73			Y			TRUE	TRUE
Q5EAX6	MGC84950 protein OS=Xenopus la	cog6			Y			TRUE	TRUE
Q5EAY2	Mediator of RNA polymerase II trans	med19							
Q5EAY8	Transmembrane anterior posterior t	tapt1							
Q5EE04	TPR (Fragment) OS=Xenopus laevi	tpr			Y			TRUE	TRUE
Q5EFE9	BMAL1 OS=Xenopus laevis PE=2 S	bmal1							
Q5EY87	Grainyhead-like protein 1 homolog (	grhl1			Y	Y		TRUE	TRUE
Q5F1L3	Retinal ABCA4 transporter OS=Xen	abca4							
Q5FWK8	MGC85124 protein OS=Xenopus la	alox12b							
Q5FWM7;CL10311Contig1	MGC84940 protein OS=Xenopus la	fabp4		Y	Y			TRUE	TRUE
Q5FWN6	MGC85173 protein OS=Xenopus la	tbc1d19			Y			TRUE	TRUE
Q5FWP2	Protein Smaug homolog 1 OS=Xeno	samd4a			Y			TRUE	TRUE
Q5FWQ3	LOC733157 protein (Fragment) OS=	LOC733157							
Q5FWW2	MGC98917 protein OS=Xenopus la	col6a2							
Q5FWW4	LOC398552 protein OS=Xenopus la	sgk223			Y			TRUE	TRUE
Q5FWX4	LOC733151 protein (Fragment) OS=	LOC733151							
Q5FWX5	MGC98794 protein OS=Xenopus la	MGC98794							
Q5HZ81	MGC85202 protein OS=Xenopus la	cep70							
Q5HZ99;CL2118Contig4	MGC85083 protein OS=Xenopus la	dsc3			Y			TRUE	TRUE
Q5HZM8	Putative uncharacterized protein OS	dusp11			Y			TRUE	TRUE
Q5HZN3;CL9381Contig1	NADH dehydrogenase [ubiquinone]	ndufa6			Y			TRUE	TRUE
Q5HZP4;CL1727Contig2	LOC496341 protein OS=Xenopus la	ppp1r13b			Y	Y		TRUE	TRUE
Q5HZP7	Protein kinase-like protein SgK196 (	sgk196			Y			TRUE	TRUE
Q5HZQ2	LOC496334 protein OS=Xenopus la	cdk6			Y			TRUE	TRUE
Q5HZQ5	LOC496332 protein (Fragment) OS=	LOC496332							
Q5HZZ2	LOC496311 protein OS=Xenopus la	LOC496311							
Q5I016	LOC496298 protein (Fragment) OS=	cdc42bpb			Y			TRUE	TRUE
Q5I047;CL15637Contig1	Protein FAM173B OS=Xenopus lae	fam173b			Y			TRUE	TRUE
Q5IJ69;CL32Contig6	MTGR1 OS=Xenopus laevis PE=2 S	mtgr1							
Q5M781;CL1453Contig4	Dynein light chain dlc8b OS=Xenop	dynll2			Y			TRUE	TRUE
Q5M7A9	MGC81803 protein OS=Xenopus la	MGC81803							
Q5M7B8	LOC496249 protein OS=Xenopus la	aga			Y			TRUE	TRUE
Q5M7C2	Sulfotransferase OS=Xenopus laevi	sult2a1							
Q5M7C6	Glutathione peroxidase OS=Xenopu	gpx1			Y			TRUE	TRUE
Q5M7C7;dsrrswapns_com	Protein jagunal homolog 1 OS=Xeno	jagn1			Y			TRUE	TRUE
Q5M7D5;CL6336Contig3	LOC496233 protein OS=Xenopus la	ndufs3			Y			TRUE	TRUE
Q5M7E3	5-methylcytosine rRNA methyltransf	nsun4			Y			TRUE	TRUE
Q5M7F9	Lysyl oxidase-like 1 OS=Xenopus la	loxl1							
Q5M9A1	LOC496155 protein OS=Xenopus la	wwtr1			Y			TRUE	TRUE
Q5M9A4	LOC496152 protein OS=Xenopus la	LOC496152							
Q5M9A9	LOC496147 protein OS=Xenopus la	LOC496147							
Q5MPF8	Ataxia telangiectasia mutated OS=X	atm			Y			TRUE	TRUE
Q5PPR7;CL22579Contig1	LOC496102 protein OS=Xenopus laevis GN=LOC496102 PE=2 SV=1 - [Q5PPR7_XENLA]								
Q5PPT1	LOC496089 protein OS=Xenopus la	LOC496089							
Q5PPT1;CL4954Contig2	LOC496089 protein OS=Xenopus laevis GN=LOC496089 PE=2 SV=1 - [Q5PPT1_XENLA]								
Q5PPT3	ATP-dependent Clp protease proteo	LOC496087							
Q5PPU1	LOC496080 protein (Fragment) OS=	LOC496080							
Q5PPV5	Zinc finger C2HC domain-containing	zc2hc1a							
Q5PPY1;TC467635 similar	Malignant T-cell-amplified sequence	mcts1			Y			TRUE	TRUE
Q5PPY4	Cluap1 protein OS=Xenopus laevis	cluap1			Y			TRUE	TRUE
Q5PPZ0;CL18886Contig1	LOC496039 protein OS=Xenopus la	LOC496039							
Q5PQ24;CL4416Contig2	Proteasome subunit beta type OS=X	psmb3			Y			TRUE	TRUE
Q5PQ40;CL6153Contig3	LOC495989 protein OS=Xenopus la	tex26							
Q5PQ49;CL12806Contig1	LOC495981 protein OS=Xenopus laevis GN=LOC495981 PE=2 SV=1 - [Q5PQ49_XENLA]								
Q5PQ70	LOC495963 protein OS=Xenopus la	LOC495963							
Q5PQ89	Ankyrin repeat domain-containing p	ankrd34b			Y			TRUE	TRUE
Q5PQ95;CL11117Contig1	LOC495941 protein OS=Xenopus la	LOC495941							
Q5RJW7	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q5RJW7_XENLA]								

Q5RJW9	LOC495833 protein OS=Xenopus la	ptcd1			Y			TRUE	TRUE
Q5RJX2;CL4228Contig2	Protein FAM171A1 OS=Xenopus la	fam171a1			Y			TRUE	TRUE
Q5U235	LOC495699 protein OS=Xenopus la	nomo3			Y	Y		TRUE	TRUE
Q5U248;CL1238Contig1	LOC495689 protein OS=Xenopus la	crebbp			Y			TRUE	TRUE
Q5U258;CL22014Contig1	Beta-1,3-galactosyl-O-glycosyl-glyc	gcnt3							
Q5U484	LOC495520 protein (Fragment) OS	LOC495520							
Q5U491	LOC495515 protein (Fragment) OS	LOC495515							
Q5U498	LOC495510 protein OS=Xenopus la	nxpe2							
Q5U4I3	Cyclin-D1-binding protein 1 homolo	ccndbp1							
Q5U4L0;CL8653Contig1	LOC100101274 protein OS=Xenopus laevis GN=LOC100101274 PE=2 SV=1 - [Q5U4L0_XENLA]								
Q5U4L5	LOC495501 protein OS=Xenopus la	cers5			Y			TRUE	TRUE
Q5U4N0	LOC495463 protein (Fragment) OS	LOC495463							
Q5U4T2;CL2020Contig1	LOC495440 protein OS=Xenopus la	atp2a3				Y		TRUE	TRUE
Q5U4V0	LOC495494 protein OS=Xenopus la	tnpo1			Y			TRUE	TRUE
Q5U4V6	LOC397931 protein OS=Xenopus laevis GN=LOC397931 PE=2 SV=1 - [Q5U4V6_XENLA]								
Q5U4W0;CL2471Contig1	Entpd4 protein OS=Xenopus laevis	entpd4							
Q5U4W7	LOC495416 protein (Fragment) OS	LOC495416							
Q5U511	LOC495400 protein OS=Xenopus la	vapb			Y			TRUE	TRUE
Q5U556;CL13826Contig1	LOC495364 protein OS=Xenopus la	mrpl12							
Q5U562	LOC495358 protein OS=Xenopus la	cib1			Y			TRUE	TRUE
Q5U568	LOC495352 protein OS=Xenopus la	phax			Y			TRUE	TRUE
Q5U576;CL11909Contig1	LOC495345 protein OS=Xenopus la	gpr85							
Q5U583;CL2706Contig1	Probable glutathione peroxidase 8-E	gpx8b							
Q5U592	LOC495330 protein OS=Xenopus la	olfm2							
Q5U5A2	LOC495321 protein OS=Xenopus la	LOC495321							
Q5U5A3	Immunoglobulin superfamily membe	igsf3			Y			TRUE	TRUE
Q5U5A4	LOC495319 protein OS=Xenopus la	tubb3			Y			TRUE	TRUE
Q5U5A6	Notch-regulated ankyrin repeat-cont	nrarp							
Q5U5C4;CL1634Contig2	Pa2g4 protein OS=Xenopus laevis (	pa2g4		Y	Y			TRUE	TRUE
Q5XFZ8	LOC495249 protein (Fragment) OS	LOC495249							
Q5XG13	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q5XG13_XENLA]								
Q5XG51	LOC495282 protein (Fragment) OS	LOC495282							
Q5XGK8	LOC495278 protein OS=Xenopus la	LOC495278		Y				TRUE	TRUE
Q5XGQ1	LOC495170 protein OS=Xenopus laevis GN=LOC495170 PE=2 SV=1 - [Q5XGQ1_XENLA]								
Q5XGQ2	LOC495169 protein OS=Xenopus la	pdia4			Y			TRUE	TRUE
Q5XGQ8;CL9736Contig1	LOC495164 protein OS=Xenopus la	tprg1l			Y			TRUE	TRUE
Q5XGR3;dsrrswapns_com	Peptidyl-prolyl cis-trans isomerase (	LOC495270							
Q5XGR8	Beta-lactamase-like protein 2 OS=X	lactb2			Y			TRUE	TRUE
Q5XGS8	GTP-binding protein 1 OS=Xenopus	gtpbp1			Y			TRUE	TRUE
Q5XGV1	LOC398569 protein OS=Xenopus la	anln				Y		TRUE	TRUE
Q5XGW1;CL14714Contig1	LOC495263 protein OS=Xenopus la	atp5g1		Y	Y			TRUE	TRUE
Q5XGW4;CL2418Contig2	T-complex protein 1 subunit delta O	cct4			Y			TRUE	TRUE
Q5XGW7	Cbp/p300-interacting transactivator	cited2			Y			TRUE	TRUE
Q5XGY6	LOC495114 protein OS=Xenopus la	fhod1			Y			TRUE	TRUE
Q5XGZ4	LOC779025 protein (Fragment) OS	LOC779025							
Q5XGZ5	LOC495108 protein OS=Xenopus la	snx18			Y			TRUE	TRUE
Q5XH03;dsrrswapns_comp	Erlin-2-A OS=Xenopus laevis GN=e	erlin2							
Q5XH25	Malic enzyme OS=Xenopus laevis (	me2			Y			TRUE	TRUE
Q5XH38;CL4330Contig2	LOC495073 protein OS=Xenopus la	tmem184a			Y			TRUE	TRUE
Q5XH63;CL3193Contig1	LOC495055 protein OS=Xenopus la	LOC495055							
Q5XH69	LOC495053 protein (Fragment) OS	LOC495053							
Q5XHC7	LOC495037 protein OS=Xenopus laevis GN=LOC495037 PE=2 SV=1 - [Q5XHC7_XENLA]								
Q5XHD4	LOC495031 protein OS=Xenopus la	c1galt1c1			Y			TRUE	TRUE
Q5XHE2;CL15613Contig1	LOC495025 protein OS=Xenopus la	uchl3							
Q5XHE3	LOC495024 protein OS=Xenopus la	cdh13							
Q5XHE4	LOC495023 protein OS=Xenopus la	paqr4			Y			TRUE	TRUE
Q5XHE6	LOC495021 protein OS=Xenopus la	LOC495021							
Q5XHG7;CL1310Contig3	LOC398345 protein OS=Xenopus la	furin							
Q5XHH4	LOC494998 protein OS=Xenopus la	shkbp1				Y		TRUE	TRUE
Q5XHJ3	Cellular tumor antigen p53 OS=Xen	tp53			Y			TRUE	TRUE
Q5XHJ8;CL2211Contig2	LOC397895 protein OS=Xenopus la	gsn			Y			TRUE	TRUE
Q5XHK2;CL84Contig4	14-3-3 protein beta/alpha-A OS=Xe	ywhab			Y	Y		TRUE	TRUE
Q5XHM7;CL5748Contig2	Carbohydrate sulfotransferase 12 O	chst12			Y			TRUE	TRUE
Q5XK85	Uncharacterized protein KIAA0556	kiaa0556			Y			TRUE	TRUE
Q5XK98;dsrrswapns_comp	LOC494864 protein OS=Xenopus la	msl3			Y			TRUE	TRUE
Q63ZG6;CL22Contig15	Phosphorylase OS=Xenopus laevis	pygl		Y	Y			TRUE	TRUE
Q63ZJ1	LOC494796 protein OS=Xenopus la	suclg1			Y			TRUE	TRUE
Q63ZK5	LOC494824 protein (Fragment) OS	LOC494824							
Q63ZN2	LOC445856 protein OS=Xenopus la	vps13a			Y			TRUE	TRUE
Q63ZN4	LOC494770 protein OS=Xenopus la	cbx6			Y			TRUE	TRUE
Q63ZS6	LOC494740 protein OS=Xenopus la	rpp30			Y	Y		TRUE	TRUE
Q63ZU5	LOC494732 protein OS=Xenopus la	tsc22d1			Y			TRUE	TRUE
Q63ZU7	LOC494730 protein OS=Xenopus la	gcc1			Y			TRUE	TRUE
Q640C3	LOC494728 protein OS=Xenopus la	umps			Y			TRUE	TRUE
Q640C5	D-dopachrome decarboxylase-B OS	ddt			Y			TRUE	TRUE
Q640C8;CL4522Contig1	LOC494703 protein OS=Xenopus la	LOC494703		Y				TRUE	TRUE
Q640D9	Elongation factor 1-alpha OS=Xeno	LOC494720							
Q640F4;CL20343Contig1	LOC494684 protein OS=Xenopus laevis GN=LOC494684 PE=2 SV=1 - [Q640F4_XENLA]								
Q640G5	LOC494678 protein (Fragment) OS	LOC494678							
Q640H2	LOC494715 protein OS=Xenopus la	scp2			Y			TRUE	TRUE
Q640H4	LOC494673 protein OS=Xenopus la	cth			Y			TRUE	TRUE
Q640I9	Lysine-specific demethylase 2B OS	kdm2b							
Q640J1	LOC494661 protein OS=Xenopus la	dhrs13			Y			TRUE	TRUE
Q640V5	MGC85351 protein OS=Xenopus la	mpste24							
Q640W9	MGC84396 protein OS=Xenopus la	MGC84396							
Q640X7	MGC84330 protein OS=Xenopus la	capns1			Y			TRUE	TRUE

Q640Z4	MGC83916 protein OS=Xenopus la	mta1			Y			TRUE	TRUE
Q641B0;CL3581Contig2	Dmd protein OS=Xenopus laevis Gl	dmd.1							
Q641B9	Actin-related protein 2/3 complex su	arpc5			Y			TRUE	TRUE
Q641C5	MGC82112 protein OS=Xenopus la	MGC82112							
Q641D4	MGC82000 protein OS=Xenopus la	golm1			Y			TRUE	TRUE
Q641D9;CL1834Contig5	MGC81931 protein OS=Xenopus la	sec14l5			Y			TRUE	TRUE
Q641F3	Collagen alpha-1(XXI) chain OS=Xe	col21a1							
Q641F7	MGC81732 protein OS=Xenopus la	ppid			Y			TRUE	TRUE
Q641G3;CL3592Contig3	Cell division cycle and apoptosis re	ccar1							
Q641G4	Condensin-2 complex subunit H2 O	ncaph2			Y			TRUE	TRUE
Q641G7	Actin-related protein 2/3 complex su	arpc4							
Q641H7	MGC81565 protein OS=Xenopus la	lats1			Y			TRUE	TRUE
Q641I6	LOC494638 protein OS=Xenopus laevis GN=LOC494638 PE=2 S			Y				TRUE	TRUE
Q641J8;CL811Contig3	E3 ubiquitin-protein ligase RNF12-A	rnf12							
Q642N7	LOC446968 protein (Fragment) OS	LOC446968							
Q642P2	Protein dopey-2 OS=Xenopus laevis	dopey2			Y			TRUE	TRUE
Q642S3	MGC81229 protein OS=Xenopus la	tubgcp4			Y			TRUE	TRUE
Q66IN2	Glutamine and serine-rich protein 1	qser1			Y			TRUE	TRUE
Q66IP6;CL2553Contig2	MGC86305 protein OS=Xenopus la	fam168a			Y			TRUE	TRUE
Q66IQ2	MGC86228 protein OS=Xenopus la	ablim2							
Q66IS7	MGC85220 protein OS=Xenopus la	fntb			Y			TRUE	TRUE
Q66IS8;CL11862Contig1	Transmembrane protein 177 OS=Xe	tmem177			Y			TRUE	TRUE
Q66IT5	MGC84699 protein OS=Xenopus la	sntg2							
Q66IV8;CL2891Contig1	MGC84302 protein OS=Xenopus la	syn1							
Q66IX2	MGC84231 protein OS=Xenopus la	psmd13			Y			TRUE	TRUE
Q66IY6;CL4803Contig1	MGC84052 protein OS=Xenopus la	psmd7			Y	Y		TRUE	TRUE
Q66IZ2	MGC83950 protein OS=Xenopus la	extl3			Y			TRUE	TRUE
Q66J02	MGC83799 protein OS=Xenopus la	MGC83799							
Q66J07;CL542Contig7	MGC83563 protein OS=Xenopus la	nnt			Y			TRUE	TRUE
Q66J16	MGC83352 protein OS=Xenopus la	aldh7a1			Y			TRUE	TRUE
Q66J37	MGC82041 protein OS=Xenopus la	gba3			Y			TRUE	TRUE
Q66J53;CL2807Contig1	MGC81873 protein OS=Xenopus laevis GN=MGC81873 PE=2 SV			Y				TRUE	TRUE
Q66J54	Solute carrier family 22 member 6-A	slc22a6							
Q66J64	MGC81783 protein OS=Xenopus la	fam222b							
Q66J72	MGC81721 protein OS=Xenopus la	pvrl2			Y			TRUE	TRUE
Q66J73	MGC81714 protein OS=Xenopus la	abcf1			Y	Y		TRUE	TRUE
Q66J90	Histone-lysine N-methyltransferase	setd1b			Y			TRUE	TRUE
Q66J92;CL2050Contig1	Gtse1 protein OS=Xenopus laevis G	gtse1			Y			TRUE	TRUE
Q66J94	MGC81570 protein OS=Xenopus la	asl			Y			TRUE	TRUE
Q66JA4	MGC81147 protein OS=Xenopus la	MGC81147							
Q66JA7;CL1690Contig2	Pdha1-b protein OS=Xenopus laevis	pdha1			Y			TRUE	TRUE
Q66KF0;CL6164Contig1	MGC86497 protein OS=Xenopus la	ppp1r13l			Y	Y		TRUE	TRUE
Q66KG2	LOC446299 protein (Fragment) OS	LOC446299							
Q66KI6;CL1079Contig4	Pum1-A protein OS=Xenopus laevis	pum1			Y			TRUE	TRUE
Q66KN2	MGC85584 protein OS=Xenopus la	atp5j2			Y			TRUE	TRUE
Q66KN4;CL12856Contig1	Mitochondrial NADH dehydrogenase	ndufa13							
Q66KP4	MGC85561 protein OS=Xenopus la	uros			Y			TRUE	TRUE
Q66KP7;CL5026Contig1	MGC85550 protein OS=Xenopus la	rps28p9			Y			TRUE	TRUE
Q66KQ7	MGC85526 protein OS=Xenopus la	asb5			Y			TRUE	TRUE
Q66KR0	LOC446923 protein (Fragment) OS=Xenopus laevis GN=LOC446923 PE=2 SV=1 - [Q66KR0_XENLA]								
Q66KR8;CL712Contig1	MGC85505 protein OS=Xenopus la	utp11l			Y			TRUE	TRUE
Q66KT0	MGC85462 protein OS=Xenopus la	rnls			Y			TRUE	TRUE
Q66KT2	MGC85457 protein OS=Xenopus la	ndufs8			Y			TRUE	TRUE
Q66KU5;TC432828 UniRe	MGC85428 protein OS=Xenopus la	rpl36a			Y			TRUE	TRUE
Q66KV2	MGC85404 protein OS=Xenopus la	rpl38			Y			TRUE	TRUE
Q66KV6;CL1Contig276	LOC100101273 protein OS=Xenopu	rpl28		Y	Y			TRUE	TRUE
Q66KW1;CL1655Contig4	MGC85384 protein OS=Xenopus la	rpl29		Y	Y			TRUE	TRUE
Q66KW5	MGC85374 protein OS=Xenopus la	rpl32							
Q66KX3	MGC85348 protein OS=Xenopus la	rpl23a			Y	Y		TRUE	TRUE
Q66KY6;CL384Contig8	MGC85310 protein OS=Xenopus la	rpl11		Y	Y			TRUE	TRUE
Q66KY9	MGC85306 protein OS=Xenopus la	atp5d			Y			TRUE	TRUE
Q66KZ5	MGC85294 protein OS=Xenopus laevis GN=MGC85294 PE=2 SV=1 - [Q66KZ5_XENLA]								
Q66KZ8	Glutathione S-transferase (Fragmen	LOC446920							
Q66L05	MGC85264 protein OS=Xenopus la	prss3							
Q66L23	MGC85232 protein OS=Xenopus la	rpl24			Y			TRUE	TRUE
Q66L24	MGC85230 protein OS=Xenopus la	atp5l			Y			TRUE	TRUE
Q67FQ3	Low density lipoprotein receptor ada	ldlrap1			Y	Y		TRUE	TRUE
Q68A89	Proteasome subunit alpha type (Fra	psma							
Q68A89;CL5945Contig2	Proteasome subunit alpha type (Fra	psma							
Q68EX4	Proteasome subunit beta type OS=X	psmb7			Y			TRUE	TRUE
Q68EY5	ATP synthase subunit alpha OS=Xe	atp5a1			Y			TRUE	TRUE
Q68F13	MGC82958 protein OS=Xenopus la	sucla2			Y			TRUE	TRUE
Q68F29	Vacuolar protein sorting-associated	vps26b			Y			TRUE	TRUE
Q68F30	MGC82115 protein OS=Xenopus la	alas2			Y			TRUE	TRUE
Q68F32;CL3294Contig2	MGC81977 protein OS=Xenopus la	arhgdig			Y	Y		TRUE	TRUE
Q68F42	MGC81821 protein OS=Xenopus la	dpyd			Y			TRUE	TRUE
Q68FI3	D-dopachrome decarboxylase-A OS	ddt			Y			TRUE	TRUE
Q68FJ1	ATP synthase-coupling factor 6, mit	MGC86324							
Q68FJ5	MGC86218 protein OS=Xenopus la	pdhx			Y			TRUE	TRUE
Q68FK6	MGC82138 protein OS=Xenopus la	arfgap2							
Q68FK7;CL11073Contig1	MGC81942 protein OS=Xenopus la	rufy3			Y			TRUE	TRUE
Q6AX29	MGC86330 protein OS=Xenopus la	kcnj1			Y			TRUE	TRUE
Q6AX77	XK-related protein (Fragment) OS=X	LOC446266							
Q6AX83	MGC82093 protein OS=Xenopus la	lars			Y			TRUE	TRUE
Q6AXA7	MGC80263 protein OS=Xenopus la	prpf6							
Q6AXB3;CL3237Contig1	MGC79128 protein OS=Xenopus la	shmt2		Y	Y			TRUE	TRUE

Q6AZH2	SIPA1L1 protein (Fragment) OS=Xe	sipa1l1			Y			TRUE	TRUE
Q6AZH3	CHML protein (Fragment) OS=Xeno	chml							
Q6AZI4	LOC446231 protein (Fragment) OS=	ube2l3			Y			TRUE	TRUE
Q6AZJ0	Glutamate dehydrogenase OS=Xen	glud1			Y			TRUE	TRUE
Q6AZJ6	Fascin (Fragment) OS=Xenopus lae	fscn1			Y			TRUE	TRUE
Q6AZJ9	40S ribosomal protein S21 OS=Xen	rps21			Y			TRUE	TRUE
Q6AZL6;CL367Contig5	LOC444845 protein OS=Xenopus laevis GN=LOC444845 PE=2 SV=1 - [Q6AZL6_XENLA]								
Q6AZL7	MGC86356 protein OS=Xenopus la	rps26			Y			TRUE	TRUE
Q6AZL9	MGC86316 protein OS=Xenopus la	rps23		Y	Y			TRUE	TRUE
Q6AZM8	Sh3glb2-prov protein OS=Xenopus	sh3glb2							
Q6AZN8;CL5215Contig3	Zinc transporter 6-A OS=Xenopus la	slc30a6-a			Y			TRUE	TRUE
Q6AZP8;CL4086Contig1	MGC82549 protein OS=Xenopus laevis GN=MGC82549 PE=2 SV=1 - [Q6AZP8_XENLA]								
Q6AZS1;CL1Contig38	Histone H2A OS=Xenopus laevis G	histh2ad							
Q6AZS3	Uty-prov protein OS=Xenopus laevis	kdm6a			Y			TRUE	TRUE
Q6AZU4	MGC79131 protein OS=Xenopus la	MGC79131							
Q6AZV1	Hsp90beta OS=Xenopus laevis GN	hsp90ab1			Y			TRUE	TRUE
Q6AZV2;CL1314Contig1	Gcdh-prov protein OS=Xenopus lae	gcdh							
Q6AZV3;CL1Contig1336	MGC78885 protein OS=Xenopus la	rpl17		Y	Y			TRUE	TRUE
Q6B4U5;CL4491Contig1	Malate dehydrogenase OS=Xenopu	mdh2		Y	Y			TRUE	TRUE
Q6DCC2	Pex11b-prov protein OS=Xenopus l	pex11b			Y			TRUE	TRUE
Q6DCD1	FGGY carbohydrate kinase domain-	fggy							
Q6DCF9;CL15Contig5	Annexin OS=Xenopus laevis GN=an	anxa7			Y			TRUE	TRUE
Q6DCG7	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6DCG7_XENLA]								
Q6DCG8;CL1244Contig3	Tnpo3-prov protein OS=Xenopus la	tnpo3			Y			TRUE	TRUE
Q6DCI2	XCaspase-7 protein OS=Xenopus la	casp7			Y			TRUE	TRUE
Q6DCJ9	Gdi2-prov protein OS=Xenopus laev	gdi1							
Q6DCL1	MGC82412 protein OS=Xenopus la	bpnt1			Y			TRUE	TRUE
Q6DCL5;CL4445Contig2	E3 ubiquitin-protein ligase HACE1 O	hace1			Y			TRUE	TRUE
Q6DCL6;CL7918Contig1	Protein FAM69A OS=Xenopus laevi	fam69a			Y			TRUE	TRUE
Q6DCM4	Spon2-prov protein OS=Xenopus la	spon2							
Q6DCM5	Ppp4r1-prov protein OS=Xenopus la	ppp4r1							
Q6DCM8	Hadh2-prov protein OS=Xenopus la	hsd17b10			Y	Y		TRUE	TRUE
Q6DCS5	MGC80849 protein OS=Xenopus la	MGC80849							
Q6DCS9	MGC80838 protein OS=Xenopus la	ptgr1.2			Y			TRUE	TRUE
Q6DCT2	UPF0668 protein C10orf76 homolog	c10orf76			Y			TRUE	TRUE
Q6DCT5;CL7695Contig1	MGC80785 protein OS=Xenopus la	aldh2		Y	Y			TRUE	TRUE
Q6DCT7	MGC80781 protein OS=Xenopus la	arhgap30			Y			TRUE	TRUE
Q6DCU8	LOC397741 protein OS=Xenopus la	LOC397741							
Q6DCU9	Putative uncharacterized protein OS	itga2b.1							
Q6DCY9;CL8574Contig1	HAUS augmin-like complex subunit	haus3			Y			TRUE	TRUE
Q6DD02	Nek8 protein OS=Xenopus laevis G	nek8			Y			TRUE	TRUE
Q6DD25	UBXD2 protein (Fragment) OS=Xen	ubxd2							
Q6DD48;CL3329Contig2	Pgk2 protein OS=Xenopus laevis G	pgk1			Y			TRUE	TRUE
Q6DD55;CL437Contig2	P4hb protein OS=Xenopus laevis G	p4hb		Y	Y			TRUE	TRUE
Q6DD58;CL18845Contig1	Mec-12 protein OS=Xenopus laevis	tuba4b			Y			TRUE	TRUE
Q6DD68	LOC397850 protein OS=Xenopus la	LOC397850							
Q6DD71	ERO1-like protein alpha OS=Xenop	ero1l			Y			TRUE	TRUE
Q6DDF2	Acad9-prov protein OS=Xenopus la	acad9			Y			TRUE	TRUE
Q6DDF7	MGC84593 protein OS=Xenopus la	atp13a4			Y			TRUE	TRUE
Q6DDF9	MGC84581 protein OS=Xenopus laevis GN=MGC84581 PE=2 SV=1 - [Q6DDF9_XENLA]								
Q6DDG1	LOC445874 protein (Fragment) OS=	LOC445874							
Q6DDG3	Pik4ca-prov protein OS=Xenopus la	pi4ka			Y			TRUE	TRUE
Q6DDH9	Eva1-prov protein OS=Xenopus lae	mpzl2			Y			TRUE	TRUE
Q6DDI6	WD repeat-containing protein 67 OS	wdr67			Y			TRUE	TRUE
Q6DDK5	Acetolactate synthase-like protein O	ilvbl			Y			TRUE	TRUE
Q6DDM0	MGC83329 protein OS=Xenopus la	MGC83329							
Q6DDM4	Apoptosis inhibitor 5-A OS=Xenopu	api5a			Y			TRUE	TRUE
Q6DDM7;CL6675Contig1	Acadl-prov protein OS=Xenopus lae	acadl			Y			TRUE	TRUE
Q6DDM8;CL8350Contig1	MGC83152 protein OS=Xenopus la	zfand2a			Y			TRUE	TRUE
Q6DDN7	MGC82654 protein OS=Xenopus la	hacl1			Y			TRUE	TRUE
Q6DDN9	Cbs-prov protein OS=Xenopus laev	cbs							
Q6DDP5	Ola1 protein OS=Xenopus laevis G	ola1							
Q6DDP7	Uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6DDP7_XENLA]								
Q6DDQ3	Anoctamin OS=Xenopus laevis GN=	ano5							
Q6DDQ5	Protein phosphatase 1 regulatory su	ppp1r3c			Y			TRUE	TRUE
Q6DDR6	LOC445863 protein (Fragment) OS=	LOC445863							
Q6DDV2	Znf384-prov protein OS=Xenopus la	znf384			Y			TRUE	TRUE
Q6DDW1	MGC81675 protein OS=Xenopus la	txnl1							
Q6DDX0;CL2427Contig1	Cry2 protein OS=Xenopus laevis G	cry2			Y			TRUE	TRUE
Q6DDX4	LOC445857 protein (Fragment) OS=	LOC445857							
Q6DDZ2	MGC81354 protein OS=Xenopus la	tom1			Y			TRUE	TRUE
Q6DDZ4	LOC398498 protein OS=Xenopus la	LOC398498							
Q6DE12;CL5192Contig1	M6prbp1-prov protein OS=Xenopus	m6prbp1							
Q6DE30	Oat-prov protein OS=Xenopus laevi	oat.1				Y		TRUE	TRUE
Q6DE33;CL4688Contig1	Uqcrc2 protein OS=Xenopus laevis	uqcrc2			Y			TRUE	TRUE
Q6DE48;CL1839Contig1	Rbbp5-prov protein OS=Xenopus la	rbbp5			Y			TRUE	TRUE
Q6DE60;CL1365Contig1	Adenylyl cyclase-associated protein	cap1			Y			TRUE	TRUE
Q6DE62	LOC398863 protein OS=Xenopus la	hspa4							
Q6DE67	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6DE67_XENLA]								
Q6DE73;CL13437Contig1	2-oxoglutarate and iron-dependent o	ogfod1			Y			TRUE	TRUE
Q6DE96	Protein IWS1 homolog A OS=Xenop	iws1							
Q6DE98;CL4343Contig1	Gyg1-prov protein OS=Xenopus lae	gyg1			Y			TRUE	TRUE
Q6DEA4;CL3873Contig1	MGC79068 protein OS=Xenopus la	pdia6			Y			TRUE	TRUE
Q6DEA5;CL11630Contig1	Pex26-prov protein OS=Xenopus la	pex26			Y			TRUE	TRUE
Q6DEB3;CL2313Contig1	MGC79025 protein OS=Xenopus la	phb2		Y	Y			TRUE	TRUE
Q6DEB9	LOC445848 protein (Fragment) OS=	LOC445848							

Q6DEC8;CL1892Contig1	MGC78939 protein OS=Xenopus la	st13			Y			TRUE	TRUE
Q6DEC9;CL9001Contig1	D-tyrosyl-tRNA(Tyr) deacylase OS=	dtd1			Y			TRUE	TRUE
Q6DF69	LOC445837 protein (Fragment) OS=	LOC445837							
Q6DF71	MGC84640 protein OS=Xenopus la	znf484			Y			TRUE	TRUE
Q6DF73	Fbxo11-prov protein OS=Xenopus l	fbxo11			Y			TRUE	TRUE
Q6DFA3	Rnaset2-prov protein OS=Xenopus	rnaset2			Y			TRUE	TRUE
Q6DFC7	LOC445830 protein (Fragment) OS=	LOC445830							
Q6DFF0;CL7424Contig1	MGC83705 protein OS=Xenopus la	MGC83705							
Q6DFF2	Brd4-prov protein OS=Xenopus laev	brd4			Y			TRUE	TRUE
Q6DFG3;TC413472	MGC83673 protein OS=Xenopus la	MGC83673							
Q6DFG4;CL2111Contig1	MGC83457 protein OS=Xenopus la	ephb3			Y			TRUE	TRUE
Q6DFI0	MGC83110 protein OS=Xenopus la	MGC83110							
Q6DFI3	Tst-prov protein OS=Xenopus laevis	mpst			Y			TRUE	TRUE
Q6DFJ6	Serine/threonine-protein kinase TBk	tbk1			Y			TRUE	TRUE
Q6DFK1	Pex12-prov protein OS=Xenopus la	pex12			Y			TRUE	TRUE
Q6DFK4;CL10561Contig1	MGC81344 protein OS=Xenopus la	etaa1			Y			TRUE	TRUE
Q6DFL2;CL4663Contig1	Biorientation of chromosomes in cel	bod1			Y			TRUE	TRUE
Q6DFL3	Ppp2r5e-prov protein OS=Xenopus	ppp2r5b							
Q6DFT8;CL48Contig18	Bcap31 protein OS=Xenopus laevis	bcap31			Y			TRUE	TRUE
Q6DJF7	60S ribosomal protein L6 OS=Xeno	rpl6							
Q6DJG5	MGC84307 protein OS=Xenopus la	cox4i2		Y				TRUE	TRUE
Q6DJH9;dsrrswapns_comp	MGC83433 protein OS=Xenopus la	smg7			Y			TRUE	TRUE
Q6DJI0	40S ribosomal protein S8 OS=Xeno	rps8			Y			TRUE	TRUE
Q6DJI6	Putative uncharacterized protein OS=Xenopus laevis PE=4 SV=1 - [Q6DJI6_XENLA]								
Q6DJJ1;zeinaSSns_comp3	MGC82151 protein OS=Xenopus la	rps25		Y	Y			TRUE	TRUE
Q6DJJ7;CL22Contig4	MGC82136 protein OS=Xenopus la	MGC82136							
Q6DJJ8	Polr3c-prov protein OS=Xenopus la	polr3c			Y			TRUE	TRUE
Q6DJK5;CL3918Contig1	CNDP dipeptidase 2 (Metallopeptida	cndp2			Y			TRUE	TRUE
Q6DJL3	MGC82066 protein OS=Xenopus la	rnf139			Y			TRUE	TRUE
Q6DJL4;CL12647Contig1	MGC82059 protein OS=Xenopus la	atpif1		Y	Y			TRUE	TRUE
Q6DJM2	Phosphatidate cytidylyltransferase,	tamm41							
Q6DJN5;dsrrswapns_comp	60S ribosomal protein L13 OS=Xen	rpl13							
Q6DJP0;CL2037Contig1	LOC100137615 protein OS=Xenopu	gclc			Y			TRUE	TRUE
Q6DJP1	LOC443721 protein (Fragment) OS=	ctsd			Y			TRUE	TRUE
Q6DJP2	MGC81911 protein OS=Xenopus la	ech1			Y			TRUE	TRUE
Q6DJQ0	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6DJQ0_XENLA]								
Q6DJQ1;CL8372Contig1	MGC81800 protein OS=Xenopus la	mgst3			Y			TRUE	TRUE
Q6DKA5	MGC84756 protein OS=Xenopus la	hsd17b11			Y			TRUE	TRUE
Q6DKB9	MGC84375 protein OS=Xenopus la	aco2			Y			TRUE	TRUE
Q6DKC0;CL24Contig3	Erlin-2-B OS=Xenopus laevis GN=e	erlin2							
Q6DKC6	MGC84147 protein OS=Xenopus la	MGC84147							
Q6DKD7	Coatomer subunit gamma-2 OS=Xe	copg2			Y			TRUE	TRUE
Q6DKE3;CL40282Contig1	Histone H2A OS=Xenopus laevis G	hist1h2aa			Y			TRUE	TRUE
Q6DKM0	MGC83065 protein OS=Xenopus la	cand1			Y			TRUE	TRUE
Q6DKM7	LOC443571 protein (Fragment) OS=	LOC443571							
Q6E2P0	Urocortin 3 OS=Xenopus laevis GN	ucn3		Y	Y			TRUE	TRUE
Q6EAN5	Transcription factor OS=Xenopus la	sall2			Y			TRUE	TRUE
Q6EE53	40S ribosomal protein S8 (Fragmen	rps8		Y	Y			TRUE	TRUE
Q6EE56	Aminolevulinic acid synthase 1 (Fra	alas1			Y			TRUE	TRUE
Q6GLK7	MGC84770 protein OS=Xenopus la	psmd9			Y	Y		TRUE	TRUE
Q6GLL5;CL9439Contig2	MGC84748 protein OS=Xenopus la	fgl1							
Q6GLN2	MGC84671 protein OS=Xenopus la	wasf1			Y			TRUE	TRUE
Q6GLN6	MGC84462 protein OS=Xenopus laevis GN=MGC84462 PE=2 SV=1 - [Q6GLN6_XENLA]								
Q6GLQ1	Serpin B5 OS=Xenopus laevis GN=	serpinb5							
Q6GLS2	MGC84319 protein OS=Xenopus la	tcp11l1			Y			TRUE	TRUE
Q6GLT0;CL4821Contig1	MGC84289 protein OS=Xenopus la	paics.1			Y			TRUE	TRUE
Q6GLT3	MGC84278 protein OS=Xenopus la	igsf21							
Q6GLU4	Pde6ha protein OS=Xenopus laevis	pde6h							
Q6GLX4;CL22692Contig1	Regulator of G-protein signaling 9-b	rgs9bpb							
Q6GLY0	MGC84136 protein OS=Xenopus la	sccpdh			Y			TRUE	TRUE
Q6GLY5	Protein asunder homolog OS=Xeno	asun							
Q6GM08;CL9083Contig1	MGC84065 protein OS=Xenopus la	ntm				Y		TRUE	TRUE
Q6GM32	MGC84010 protein OS=Xenopus la	fmnl1							
Q6GM46;CL3306Contig3	MGC83972 protein OS=Xenopus la	pde4b							
Q6GM50	MGC83967 protein OS=Xenopus la	rbm11			Y			TRUE	TRUE
Q6GM59;CL3818Contig1	Monocarboxylate transporter 12 OS	slc16a12			Y			TRUE	TRUE
Q6GM62	MGC83400 protein OS=Xenopus la	idh3g			Y			TRUE	TRUE
Q6GM67	MGC83388 protein OS=Xenopus la	MGC83388							
Q6GM70	LOC443696 protein (Fragment) OS=	LOC443696							
Q6GM94;CL4854Contig2	MGC68458 protein OS=Xenopus la	abat			Y			TRUE	TRUE
Q6GM98	MGC81989 protein OS=Xenopus la	slc16a3			Y			TRUE	TRUE
Q6GMA6;dsrrswapns_com	MGC81949 protein OS=Xenopus la	cct6a		Y	Y			TRUE	TRUE
Q6GMC1;CL1Contig1214	MGC81889 protein OS=Xenopus la	rps27a			Y			TRUE	TRUE
Q6GMC7	Alcohol dehydrogenase [NADP(+)] (	akr1a1			Y			TRUE	TRUE
Q6GMC8	MGC81877 protein OS=Xenopus la	ncf2							
Q6GMC9;dsrrswapns_com	GMP reductase OS=Xenopus laevis	gmpr2			Y			TRUE	TRUE
Q6GMY9	Exportin-2 OS=Xenopus laevis GN=	cse1l							
Q6GN02	Acetyl-CoA acetyltransferase B, mit	acat1b							
Q6GN08	LOC398742 protein OS=Xenopus la	ncapd3			Y			TRUE	TRUE
Q6GN10	MGC83654 protein OS=Xenopus la	rab20			Y			TRUE	TRUE
Q6GN12	MGC83651 protein OS=Xenopus la	tbc1d4			Y			TRUE	TRUE
Q6GN44	LOC443684 protein (Fragment) OS=	LOC443684							
Q6GN54	Uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [Q6GN54_XENLA]								
Q6GN59;CL5435Contig1	MGC83004 protein OS=Xenopus la	mamld1							
Q6GN63;CL5122Contig1	MGC82998 protein OS=Xenopus la	idh3a			Y			TRUE	TRUE
Q6GN66;CL2418Contig1	T-complex protein 1 subunit delta O	cct4			Y			TRUE	TRUE

Q6GN79	Ribosomal protein L37 OS=Xenopu	rpl37		Y	Y			TRUE	TRUE
Q6GNA9;CL4677Contig2	MGC82910 protein OS=Xenopus la	zeb1			Y			TRUE	TRUE
Q6GND4	Dbia protein OS=Xenopus laevis GN	dbi			Y			TRUE	TRUE
Q6GND5	MGC82876 protein OS=Xenopus la	dnajb12			Y			TRUE	TRUE
Q6GNE6	LOC443667 protein (Fragment) OS=	LOC443667							
Q6GNF2	MGC82844 protein OS=Xenopus la	rpl30			Y			TRUE	TRUE
Q6GNF4	MGC82841 protein OS=Xenopus la	rsp17		Y				TRUE	TRUE
Q6GNH1	MGC82808 protein OS=Xenopus la	rpl23		Y	Y			TRUE	TRUE
Q6GNI8;CL4245Contig2	MGC82778 protein OS=Xenopus laevis GN=MGC82778 PE=2 SV=1 - [Q6GNI8_XENLA]								
Q6GNP1;CL9567Contig1	MGC80975 protein OS=Xenopus la	dnai1			Y			TRUE	TRUE
Q6GNQ1	ATPase asna1 OS=Xenopus laevis	asna1			Y			TRUE	TRUE
Q6GNQ8	MGC80946 protein OS=Xenopus la	fes			Y			TRUE	TRUE
Q6GNR4;CL847Contig2	MGC80936 protein OS=Xenopus la	cltc							
Q6GNR9	Dolichyl-diphosphooligosaccharide-	ddost			Y			TRUE	TRUE
Q6GNS4	MGC80913 protein OS=Xenopus la	bpgm			Y			TRUE	TRUE
Q6GNS8;CL2779Contig3	MGC80906 protein OS=Xenopus la	ndufb10			Y			TRUE	TRUE
Q6GNT1;CL1947Contig1	MGC80898 protein OS=Xenopus la	brd1							
Q6GNU6	MGC80868 protein OS=Xenopus la	apaf1			Y	Y		TRUE	TRUE
Q6GNV0	MGC80858 protein OS=Xenopus la	pag2g4							
Q6GNV5	Formin-binding protein 1 homolog C	fnbp1			Y			TRUE	TRUE
Q6GNW4	Tetraspanin OS=Xenopus laevis GN	cd82			Y			TRUE	TRUE
Q6GNX6;CL542Contig3	MGC80804 protein OS=Xenopus la	rps9			Y			TRUE	TRUE
Q6GNY1;CL852Contig4	E3 ubiquitin-protein ligase mib1 OS=	mib1			Y			TRUE	TRUE
Q6GNZ4	MGC80774 protein OS=Xenopus la	mlh3			Y			TRUE	TRUE
Q6GP14	LOC397993 protein OS=Xenopus la	LOC397993							
Q6GP17;CL314Contig3	Histone-lysine N-methyltransferase	suv420h1				Y		TRUE	TRUE
Q6GP18;CL116Contig7	Superoxide dismutase OS=Xenopus	sod		Y				TRUE	TRUE
Q6GP33;CL5832Contig2	Glucose-6-phosphate isomerase OS	gpi			Y			TRUE	TRUE
Q6GP41;CX133515 UniRe	MGC80700 protein OS=Xenopus laevis GN=MGC80700 PE=2 S			Y				TRUE	TRUE
Q6GP54	LOC443639 protein (Fragment) OS=	LOC443639							
Q6GP66	MRTF-A protein OS=Xenopus laevis	mkl1			Y			TRUE	TRUE
Q6GPA3	LOC443632 protein (Fragment) OS=	LOC443632							
Q6GPA5;CL2250Contig2	Protein tweety homolog 3 OS=Xeno	ttyh3							
Q6GPB1;CL1907Contig3	MGC80559 protein OS=Xenopus la	ammecr1l			Y			TRUE	TRUE
Q6GPB7	4-hydroxyphenylpyruvate dioxygena	hpdl							
Q6GPC4;CL12623Contig1	MGC80505 protein OS=Xenopus la	ndufb7			Y			TRUE	TRUE
Q6GPD0	Rho GTPase-activating protein 32 C	arhgap32			Y			TRUE	TRUE
Q6GPD0;CL615Contig1	Rho GTPase-activating protein 32 C	arhgap32			Y			TRUE	TRUE
Q6GPD6;CL2008Contig2	MGC80474 protein OS=Xenopus la	cnpy2			Y			TRUE	TRUE
Q6GPE1;CL1282Contig2	Wu:fc30a11 protein OS=Xenopus la	ap1g1							
Q6GPK9;CL1Contig1019	Serine/threonine-protein kinase TAC	taok2				Y		TRUE	TRUE
Q6GPL5	MGC83562 protein OS=Xenopus la	atpbd4			Y			TRUE	TRUE
Q6GPL6	MGC83560 protein OS=Xenopus la	gca			Y			TRUE	TRUE
Q6GPP8	MGC82702 protein OS=Xenopus la	hbai5		Y				TRUE	TRUE
Q6GPQ9;CL12997Contig1	MGC82679 protein OS=Xenopus la	ndufs6			Y			TRUE	TRUE
Q6GPS0	MGC82653 protein OS=Xenopus la	mdn1			Y			TRUE	TRUE
Q6GPS9	MGC82638 protein OS=Xenopus la	hadha			Y			TRUE	TRUE
Q6GPT0;CL10608Contig1	MGC82636 protein OS=Xenopus la	MGC82636		Y				TRUE	TRUE
Q6GPU5	MGC82602 protein OS=Xenopus laevis GN=MGC82602 PE=2 SV=1 - [Q6GPU5_XENLA]								
Q6GPV2	LOC443605 protein (Fragment) OS=	LOC443605		Y				TRUE	TRUE
Q6GPW4	Transmembrane protein 205 OS=Xe	tmem205			Y			TRUE	TRUE
Q6GPX6;CL1066Contig1	MGC82535 protein OS=Xenopus la	fam129b			Y			TRUE	TRUE
Q6GPX8	MGC82533 protein OS=Xenopus la	pafah2			Y			TRUE	TRUE
Q6GPY3	MGC82521 protein OS=Xenopus la	prdx5			Y			TRUE	TRUE
Q6GQ04	MGC80529 protein OS=Xenopus la	cdc27			Y			TRUE	TRUE
Q6GQ13	MGC80460 protein OS=Xenopus la	lars2			Y			TRUE	TRUE
Q6GQ21;CL1684Contig2	Peptidyl-prolyl cis-trans isomerase (	ppia			Y			TRUE	TRUE
Q6GQ37;CL8951Contig1	Protein midA homolog, mitochondria	midA							
Q6GQ40;CL5428Contig3	Proteasome subunit beta type OS=X	psmb2							
Q6GQ45	MGC80353 protein OS=Xenopus la	ndufb3			Y			TRUE	TRUE
Q6GQ57	MGC80329 protein OS=Xenopus la	peli1			Y			TRUE	TRUE
Q6GQ61	MGC80319 protein OS=Xenopus la	dnpep			Y			TRUE	TRUE
Q6GQ64	Thioredoxin OS=Xenopus laevis GN	txn							
Q6GQ64;TC423515 UniRe	Thioredoxin OS=Xenopus laevis GN	MGC80314							
Q6GQ76	Cap-specific mRNA (nucleoside-2'-(	cmtr1							
Q6GQ76;CL4342Contig3	Cap-specific mRNA (nucleoside-2'-(	ftsjd2			Y			TRUE	TRUE
Q6GQ91;dsrrswapns_com	MGC80253 protein OS=Xenopus la	ndufa4							
Q6GQ97	MGC80235 protein OS=Xenopus la	rassf3			Y			TRUE	TRUE
Q6GQA7;CL5376Contig2	MGC80207 protein OS=Xenopus la	dars			Y			TRUE	TRUE
Q6GQA8	LOC443584 protein (Fragment) OS=	LOC443584							
Q6GQB1	MGC80200 protein OS=Xenopus la	nrcam							
Q6GQB2	MGC80199 protein OS=Xenopus la	rpl7a		Y	Y			TRUE	TRUE
Q6GQB6	MGC80186 protein OS=Xenopus la	MGC80186							
Q6GQC6;CL14883Contig1	MGC80163 protein OS=Xenopus laevis GN=MGC80163 PE=4 SV=1 - [Q6GQC6_XENLA]					Y		TRUE	TRUE
Q6GQD0	Nuclear cap-binding protein subunit	ncbp1-b							
Q6GQD1	Cytoplasmic FMR1-interacting prote	cyfip2			Y			TRUE	TRUE
Q6GQD7;CL206Contig9	AT-rich interactive domain-containin	arid3a			Y			TRUE	TRUE
Q6GQG6;CL5043Contig1	Npm-A protein OS=Xenopus laevis	npm2			Y			TRUE	TRUE
Q6GQH7	Putative uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [Q6GQH7_XENLA]								
Q6GQI7;CL3975Contig1	Alpha-1,3-mannosyl-glycoprotein 4-	mgat4a			Y			TRUE	TRUE
Q6GR06;CL3748Contig2	MGC81473 protein OS=Xenopus la	cbr3							
Q6GR11	MGC81430 protein OS=Xenopus la	vdac3			Y			TRUE	TRUE
Q6GR23	MGC81304 protein OS=Xenopus la	irf6			Y			TRUE	TRUE
Q6GR29	Ruvbl1 protein OS=Xenopus laevis	ruvbl1			Y			TRUE	TRUE
Q6GR45;dsrrswapns_com	Eukaryotic translation initiation facto	eif6			Y			TRUE	TRUE
Q6GR58;CL4491Contig2	Malate dehydrogenase OS=Xenopu	mdh2		Y	Y			TRUE	TRUE

Q6GR63	MGC78967 protein OS=Xenopus la	rab2b			Y			TRUE	TRUE
Q6GR67;CL1Contig211	LOC397932 protein OS=Xenopus la	LOC397932							
Q6INA9	Histone-lysine N-methyltransferase	setdb1							
Q6INB6;CL4908Contig2	ATP synthase gamma chain OS=Xe	atp5c		Y				TRUE	TRUE
Q6IND5	MGC83495 protein OS=Xenopus la	vwa5a			Y			TRUE	TRUE
Q6INE5	Rho GTPase-activating protein 19 C	arhgap19			Y	Y		TRUE	TRUE
Q6INE6	LOC432244 protein (Fragment) OS=	LOC432244							
Q6INF1	LOC432253 protein (Fragment) OS=	LOC432253							
Q6ING0	LOC443576 protein (Fragment) OS=Xenopus laevis GN=LOC443576 PE=2 SV=1 - [Q6ING0_XENLA]								
Q6INH3	MGC82600 protein OS=Xenopus la	MGC82600							
Q6INJ7	LOC432278 protein (Fragment) OS=	LOC432278							
Q6INK1	MGC82415 protein OS=Xenopus laevis GN=MGC82415 PE=2 SV=1 - [Q6INK1_XENLA]								
Q6INK3	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6INK3_XENLA]								
Q6INM6;CL1435Contig4	MGC82347 protein OS=Xenopus la	MGC82347							
Q6INN4;CL17153Contig1	MGC82295 protein OS=Xenopus la	cox5b.2		Y	Y			TRUE	TRUE
Q6INP8	Mediator of RNA polymerase II trans	med1			Y			TRUE	TRUE
Q6INQ1;CL8291Contig1	MGC81422 protein OS=Xenopus la	bysl			Y			TRUE	TRUE
Q6INR2	Pyrroline-5-carboxylate reductase C	pycr1			Y			TRUE	TRUE
Q6INS0;CL10203Contig2	MGC81156 protein OS=Xenopus la	gstt1			Y			TRUE	TRUE
Q6INT1	MGC80376 protein OS=Xenopus la	ikbkb			Y			TRUE	TRUE
Q6INT6	MGC80342 protein OS=Xenopus la	aagab			Y			TRUE	TRUE
Q6INT7	MGC80341 protein OS=Xenopus la	mark1			Y			TRUE	TRUE
Q6INU2	BSD domain-containing protein 1-A	bsdc1			Y			TRUE	TRUE
Q6INX6	MGC80065 protein OS=Xenopus la	rps16		Y	Y			TRUE	TRUE
Q6IP26	MGC79007 protein OS=Xenopus la	cox5a			Y			TRUE	TRUE
Q6IP53;CL7135Contig1	MGC78949 protein OS=Xenopus la	tekt1							
Q6IP60;CL654Contig2	Hspd1 protein OS=Xenopus laevis (	hspd1			Y			TRUE	TRUE
Q6IP76	RAC-beta serine/threonine-protein k	akt2b							
Q6IP78	LOC432230 protein (Fragment) OS=	LOC432230							
Q6IP80	MGC78878 protein OS=Xenopus la	MGC78878							
Q6IP81	MGC78867 protein OS=Xenopus la	lta4h							
Q6IP81;CL11159Contig1	MGC78867 protein OS=Xenopus la	lta4h		Y				TRUE	TRUE
Q6IR54	MGC83487 protein OS=Xenopus la	MGC83487							
Q6IR55;CL5221Contig2	E3 ubiquitin-protein ligase TM129 C	tmem129			Y			TRUE	TRUE
Q6IR57	MGC82326 protein OS=Xenopus la	sec31b			Y			TRUE	TRUE
Q6IR60	Calponin OS=Xenopus laevis GN=c	cnn2			Y			TRUE	TRUE
Q6IR70	Protein phosphatase 1 regulatory su	ppp1r21							
Q6IR71	MGC82264 protein OS=Xenopus la	MGC82264							
Q6IR73	Frs3 protein OS=Xenopus laevis GN	frs3			Y			TRUE	TRUE
Q6IRA2;CL1Contig101	XTm4 protein OS=Xenopus laevis C	tm4							
Q6IRB4	MGC78852 protein OS=Xenopus la	mapkapk2			Y			TRUE	TRUE
Q6IRM3	MGC84589 protein OS=Xenopus la	MGC84589							
Q6IRM8	MGC83924 protein OS=Xenopus la	MGC83924							
Q6IRN1;CL8563Contig2	MGC83880 protein OS=Xenopus la	eftud1			Y			TRUE	TRUE
Q6IRP1	Grx5-prov protein (Fragment) OS=X	grx5							
Q6IRP2;CL11620Contig1	MGC83164 protein OS=Xenopus la	MGC83164							
Q6IRP7;CL2114Contig1	MGC82361 protein OS=Xenopus la	atp5h			Y			TRUE	TRUE
Q6IRQ1	70 kDa peroxisomal membrane prot	abcd3			Y	Y		TRUE	TRUE
Q6IRQ8;CL4086Contig2	MGC81450 protein OS=Xenopus la	pgam1			Y			TRUE	TRUE
Q6IRR0	TOX high mobility group box family	tox4							
Q6IVY4;CL5230Contig1	Protein phosphatase Slingshot hom	ssh							
Q6JA20;CL4546Contig2	38k protein OS=Xenopus laevis PE=	x38k							
Q6JDF3	Schnurri 2 (Fragment) OS=Xenopus	shn2							
Q6JRV9	Reticulon OS=Xenopus laevis GN=I	rtn4			Y			TRUE	TRUE
Q6NRB2	MGC84587 protein OS=Xenopus la	hibadh							
Q6NRB7	Protein FAM73A OS=Xenopus laevi	fam73a			Y			TRUE	TRUE
Q6NRC4	LOC431827 protein (Fragment) OS=	LOC431827							
Q6NRC5;zeinaSSns_comp	MGC83936 protein OS=Xenopus la	dync1i2							
Q6NRD1;CL2519Contig1	MGC83915 protein OS=Xenopus la	ctns			Y			TRUE	TRUE
Q6NRD3	E3 ubiquitin-protein ligase SH3RF1	sh3rf1			Y			TRUE	TRUE
Q6NRF6;CL9526Contig1	MGC83851 protein OS=Xenopus la	tmem30b			Y			TRUE	TRUE
Q6NRH1	DDB1- and CUL4-associated factor	dcaf8			Y			TRUE	TRUE
Q6NRI2	MGC83797 protein OS=Xenopus la	klhl7			Y			TRUE	TRUE
Q6NRJ2	MGC83776 protein OS=Xenopus la	rab11fip5			Y			TRUE	TRUE
Q6NRL5	LOC431868 protein (Fragment) OS=	LOC431868							
Q6NRP3	MGC83246 protein OS=Xenopus la	slc4a7							
Q6NRP6	Tudor domain-containing protein 3 (	tdrd3			Y			TRUE	TRUE
Q6NRP7;TC434081 UniRe	MGC83147 protein OS=Xenopus la	srm			Y			TRUE	TRUE
Q6NRP9	MGC83117 protein OS=Xenopus la	ptpn4			Y			TRUE	TRUE
Q6NRQ9;CL5407Contig1	MGC82327 protein OS=Xenopus la	MGC82327		Y				TRUE	TRUE
Q6NRR6	MGC82267 protein OS=Xenopus la	MGC82267							
Q6NRS1	Inhibitor of Bruton tyrosine kinase O	ibtk			Y			TRUE	TRUE
Q6NRT0;TC416396 UniRe	Casein kinase I isoform gamma-1 C	csnk1g1			Y			TRUE	TRUE
Q6NRT2	MGC81481 protein OS=Xenopus la	scyl3			Y			TRUE	TRUE
Q6NRT7	MGC81452 protein OS=Xenopus la	akt1s1							
Q6NRV3;CL1402Contig3	MGC81323 protein OS=Xenopus la	tuba1a			Y			TRUE	TRUE
Q6NRV4	Retinol dehydrogenase 10-B OS=X	rdh10			Y			TRUE	TRUE
Q6NRW7;CL3725Contig3	MGC81186 protein OS=Xenopus la	clns1a			Y			TRUE	TRUE
Q6NRY1;CL6842Contig1	MGC81067 protein OS=Xenopus la	habp4		Y	Y			TRUE	TRUE
Q6NRY5;CL13546Contig1	MGC81049 protein OS=Xenopus la	cmc1							
Q6NRY9;CL2762Contig2	14-3-3 protein gamma-B OS=Xenop	ywhag			Y			TRUE	TRUE
Q6NS25;CL8312Contig1	MGC78791 protein OS=Xenopus la	ints2			Y			TRUE	TRUE
Q6NTJ0	LOC414678 protein (Fragment) OS=	LOC414678							
Q6NTL5;CL6428Contig2	MGC83205 protein OS=Xenopus la	cog6			Y			TRUE	TRUE
Q6NTP3;CL8757Contig1	MGC83130 protein OS=Xenopus laevis GN=MGC83130 PE=4 SV=1 - [Q6NTP3_XENLA]								
Q6NTP6	Psmd2 protein OS=Xenopus laevis	psmd2			Y			TRUE	TRUE

Q6NTP7;CL640Contig5	LOC398139 protein OS=Xenopus laevis GN=LOC398139 PE=2 S			Y				TRUE	TRUE
Q6NTQ3	LOC414455 protein (Fragment) OS	LOC414455							
Q6NTQ9;CL7675Contig2	Ndufa10b protein OS=Xenopus laev	ndufa10			Y			TRUE	TRUE
Q6NTR4;CL6643Contig1	MGC83076 protein OS=Xenopus la	rpl14			Y	Y		TRUE	TRUE
Q6NTR6;CL3218Contig1	Ubiquitin carboxyl-terminal hydrolas	usp44			Y			TRUE	TRUE
Q6NTR9;CL10023Contig1	MGC82428 protein OS=Xenopus la	cox6b1			Y			TRUE	TRUE
Q6NTS1;CL2114Contig3	MGC82400 protein OS=Xenopus laevis GN=MGC82400 PE=2 SV=1 - [Q6NTS1_XENLA]								
Q6NTS6;CL11770Contig1	SH3 domain-binding glutamic acid-r	sh3bgrl3			Y			TRUE	TRUE
Q6NTT0	MGC82310 protein OS=Xenopus la	hrsp12			Y			TRUE	TRUE
Q6NTT1	LOC398508 protein (Fragment) OS	LOC398508							
Q6NTT2	MGC82306 protein OS=Xenopus la	rps18							
Q6NTU4	Park7 protein OS=Xenopus laevis G	park7		Y	Y			TRUE	TRUE
Q6NTU8	MGC82214 protein OS=Xenopus la	grhpr.1			Y			TRUE	TRUE
Q6NTX7;CL3174Contig3	Kcnab2 protein OS=Xenopus laevis	kcnab2							
Q6NU02;CL367Contig6	LOC443739 protein OS=Xenopus la	eif4a1			Y			TRUE	TRUE
Q6NU15	LOC398496 protein OS=Xenopus la	jup			Y			TRUE	TRUE
Q6NU16;CL1235Contig4	MGC81333 protein OS=Xenopus la	eif1ax			Y			TRUE	TRUE
Q6NU33	MGC81285 protein OS=Xenopus la	eps8			Y			TRUE	TRUE
Q6NU36	MGC81278 protein OS=Xenopus la	anapc4			Y			TRUE	TRUE
Q6NU42	MGC81264 protein OS=Xenopus la	MGC81264							
Q6NU46;CL5600Contig2	Acetyl-CoA acetyltransferase A, mit	acat1							
Q6NU47;CL6335Contig1	Serine/threonine-protein kinase pdik	pdik1a							
Q6NU54;CL2259Contig1	MGC81241 protein OS=Xenopus la	tsc22d2			Y			TRUE	TRUE
Q6NU56	Methyltransferase-like protein 14 OS	mettl14			Y			TRUE	TRUE
Q6NU90;CL8453Contig1	MGC81140 protein OS=Xenopus la	lap3		Y	Y			TRUE	TRUE
Q6NU97;CL5953Contig1	MGC81120 protein OS=Xenopus la	MGC81120							
Q6NUB1	MGC81092 protein OS=Xenopus la	thul16			Y			TRUE	TRUE
Q6NUB6;dsrrswapns_com	MGC81083 protein OS=Xenopus la	nme4			Y			TRUE	TRUE
Q6NUC2	COP9 signalosome complex subuni	cops6			Y			TRUE	TRUE
Q6NUC6;CL25Contig6	Roquin OS=Xenopus laevis GN=rc3	rc3h1			Y			TRUE	TRUE
Q6NUC7;CL5043Contig2	Putative uncharacterized protein OS=Xenopus laevis PE=2 SV=1 - [Q6NUC7_XENLA]								
Q6NUD2	MGC81047 protein OS=Xenopus la	dtymk							
Q6NUD4	Putative hydroxypyruvate isomerase	hyi							
Q6NUG0	MGC79030 protein OS=Xenopus la	hspe1		Y	Y			TRUE	TRUE
Q6NUH0;CL2830Contig1	60S ribosomal protein L31 OS=Xen	rpl31		Y	Y			TRUE	TRUE
Q6P283	MGC69013 protein OS=Xenopus la	ccdc71			Y	Y		TRUE	TRUE
Q6P286;CL8201Contig1	Probable 2-oxoglutarate dehydroger	dhtkd1			Y			TRUE	TRUE
Q6P412;CL2784Contig1	MGC68722 protein OS=Xenopus la	rab15							
Q6P417	MGC68516 protein OS=Xenopus la	MGC68516							
Q6P699	MGC68562 protein OS=Xenopus la	rplp1			Y			TRUE	TRUE
Q6P7F7	MGC68765 protein OS=Xenopus la	smtn			Y			TRUE	TRUE
Q6P7F8;CL9604Contig1	MGC68767 protein OS=Xenopus la	napsa			Y			TRUE	TRUE
Q6P7J1	Hydroxysteroid 11-beta-dehydroger	hsd11b1l-a							
Q6P7J6;CL13096Contig1	MGC68461 protein OS=Xenopus la	glrx							
Q6P9I2;CL2377Contig1	MGC69046 protein OS=Xenopus la	col3a1							
Q6P9I7;CL6420Contig1	Structural maintenance of chromoso	smc6							
Q6PA07	MGC68806 protein OS=Xenopus la	ptk7			Y			TRUE	TRUE
Q6PA16;CL2923Contig2	MGC68778 protein OS=Xenopus la	brap			Y			TRUE	TRUE
Q6PA24	MGC68726 protein OS=Xenopus la	capza1							
Q6PA32	MGC68657 protein OS=Xenopus la	slco2a1							
Q6PA48	Protein TBRG4 OS=Xenopus laevis	tbrg4			Y			TRUE	TRUE
Q6PA58	Succinate dehydrogenase [ubiquino	sdha		Y				TRUE	TRUE
Q6PA74;CL7508Contig1	Dimethylaniline monooxygenase [N-	fmo2			Y			TRUE	TRUE
Q6PA94	MGC68590 protein OS=Xenopus la	MGC68590							
Q6PAB3;dsrrswapns_comp	Malate dehydrogenase, cytoplasmic	mdh1		Y	Y			TRUE	TRUE
Q6PAB5;CL3453Contig3	MGC68609 protein OS=Xenopus la	akr1b1			Y			TRUE	TRUE
Q6PAC8	MGC68803 protein OS=Xenopus la	MGC68803							
Q6PAD3;CL1008Contig1	Psmc4 protein OS=Xenopus laevis	psmc4			Y			TRUE	TRUE
Q6PAD5	MGC68755 protein OS=Xenopus la	pnliprp2							
Q6PAD8	MGC68745 protein OS=Xenopus la	MGC68745							
Q6PAE3	MGC68448 protein OS=Xenopus laevis GN=MGC68448 PE=2 SV=1 - [Q6PAE3_XENLA]								
Q6PAV9;CL20295Contig1	MGC68699 protein OS=Xenopus laevis GN=MGC68699 PE=2 SV=1 - [Q6PAV9_XENLA]								
Q6PAW6	MGC68638 protein OS=Xenopus la	MGC68638							
Q6PAX7;CL2204Contig1	WD repeat-containing protein 1-B O	wdr1			Y			TRUE	TRUE
Q6PAY8;CL13107Contig1	Hydroxysteroid dehydrogenase-like	hsdl2		Y	Y			TRUE	TRUE
Q6PAZ0	MGC68780 protein OS=Xenopus la	tomm70a			Y			TRUE	TRUE
Q6PAZ2	MGC68680 protein OS=Xenopus la	MGC68680							
Q6PAZ6;CL4518Contig2	MGC68700 protein OS=Xenopus la	MGC68700							
Q6PB01	MGC68688 protein OS=Xenopus la	siae			Y			TRUE	TRUE
Q6PB11;dsrrswapns_comp	MGC68624 protein OS=Xenopus la	nprl3			Y			TRUE	TRUE
Q6PB20;CL2763Contig1	MGC68482 protein OS=Xenopus la	bace2			Y			TRUE	TRUE
Q6PB22;CL8454Contig1	MGC68500 protein OS=Xenopus laevis GN=MGC68500 PE=2 S			Y				TRUE	TRUE
Q6PCE5;CL6542Contig1	Succinyl-CoA:3-ketoacid-coenzyme	oxct1			Y			TRUE	TRUE
Q6PCF2	MGC69167 protein OS=Xenopus la	cul2			Y			TRUE	TRUE
Q6PCF9	Putative sodium-coupled neutral am	slc38a10			Y			TRUE	TRUE
Q6PCI1	MGC68997 protein OS=Xenopus la	nadk			Y			TRUE	TRUE
Q6PCI5	Mtmr3 protein OS=Xenopus laevis (	mtmr3			Y			TRUE	TRUE
Q6PCJ3	MGC68945 protein OS=Xenopus la	yeats2			Y			TRUE	TRUE
Q6PCK3	MGC68869 protein OS=Xenopus laevis PE=2 SV=1 - [Q6PCK3_XENLA]								
Q6PCK8	MGC68835 protein OS=Xenopus la	sema5b			Y			TRUE	TRUE
Q6PF20;CL1Contig1255	Pcna-A protein OS=Xenopus laevis	pcna			Y			TRUE	TRUE
Q6PF33	Mmp9 protein OS=Xenopus laevis (	mmp9			Y			TRUE	TRUE
Q6PF36	MGC69020 protein OS=Xenopus la	zer1			Y			TRUE	TRUE
Q6PF45	Vesicular inhibitory amino acid trans	slc32a1							
Q6PF55	Actin filament-associated protein 1-l	afap1l2			Y			TRUE	TRUE
Q6PF57	MGC68883 protein OS=Xenopus la	tbc1d16			Y			TRUE	TRUE

Q6PF58	MGC68882 protein OS=Xenopus laevis PE=2 SV=1 - [Q6PF58_XENLA]								
Q6PF64	MGC68858 protein OS=Xenopus laevis PE=2 SV=1 - [Q6PF64_XENLA]								
Q6PF69;CL2844Contig1	Major vault protein OS=Xenopus lae	mvp			Y			TRUE	TRUE
Q6PF79	Ctcf protein OS=Xenopus laevis GN	ctcf			Y			TRUE	TRUE
Q6PF79;CL1865Contig1	Ctcf protein OS=Xenopus laevis GN	ctcf			Y			TRUE	TRUE
Q6PGS7	LOC398432 protein OS=Xenopus la	c1qbp							
Q6PH94;TC467404 UniRe	40S ribosomal protein S12 OS=Xen	rps12		Y	Y			TRUE	TRUE
Q6PHL5;TC440338 UniRe	60S ribosomal protein L27 OS=Xen	rpl27			Y			TRUE	TRUE
Q6PHL6	Rps19-prov protein OS=Xenopus la	rps19			Y			TRUE	TRUE
Q6PI76;CL289Contig7	Rps14-prov protein OS=Xenopus la	rps14		Y	Y			TRUE	TRUE
Q6PI79;zeinaSSns_comp3	Histone H3.3 OS=Xenopus laevis P	hist33							
Q6Q8B0	Metaxin 2 OS=Xenopus laevis GN=	mtx2			Y			TRUE	TRUE
Q6S9C2	Type 7 adenylyl cyclase (Fragment)	adcy7			Y			TRUE	TRUE
Q6UEE0	Homeodomain protein OS=Xenopus	phox2a			Y			TRUE	TRUE
Q6VEU9;CL6200Contig1	H+ transporting F1 ATP synthase e	atp5e							
Q6XXZ0	Transporter associated with antigen	tap1							
Q6ZXA0	Alpha-N-acetylneuraminide alpha-2,	st8sia1							
Q708W2	Forkhead box protein J1-A OS=Xen	foxj1			Y			TRUE	TRUE
Q70PC5	Importin subunit alpha OS=Xenopus	impa5							
Q712T4	Enhancer of split related 9 OS=Xen	hes9.1			Y			TRUE	TRUE
Q71N44	Transcription factor IIA large subuni	toa1							
Q71U00	S-phase kinase-associated protein	skp1			Y			TRUE	TRUE
Q767H5	Serine/threonine protein kinase BR	braf							
Q76BK2;CL10087Contig1	Macrophage migration inhibitory fac	mif							
Q76LD3;CL6834Contig1	DNA polymerase delta p66 subunit	pold3			Y			TRUE	TRUE
Q7LZG8	Creatine kinase (Fragment) OS=Xenopus laevis PE=3 SV=1 - [Q7LZG8_XENLA]								
Q7SX80	MGC64330 protein OS=Xenopus la	ctbs			Y			TRUE	TRUE
Q7SY83	MGC64447 protein OS=Xenopus laevis PE=2 SV=1 - [Q7SY83_XENLA]								
Q7SY94	ATP synthase subunit alpha OS=Xe	atp5a1			Y			TRUE	TRUE
Q7SY98	MGC64309 protein OS=Xenopus laevis PE=2 SV=1 - [Q7SY98_XENLA]								
Q7SYQ4	MGC64582 protein OS=Xenopus la	prdx6							
Q7SYR8	Apacd-prov protein OS=Xenopus la	txndc9			Y			TRUE	TRUE
Q7SYS0	Gst13-13-prov protein OS=Xenopus	gstk1			Y			TRUE	TRUE
Q7SYT0;CL12198Contig1	Elongation factor 1-alpha OS=Xeno	eef1a2			Y			TRUE	TRUE
Q7SYU3;CL2410Contig2	MGC64490 protein OS=Xenopus la	rps5		Y	Y			TRUE	TRUE
Q7SYV2	MGC64465 protein OS=Xenopus la	pdlim1			Y			TRUE	TRUE
Q7SYV4	Vbp1-prov protein OS=Xenopus lae	vbp1			Y			TRUE	TRUE
Q7SYV5	MGC64462 protein OS=Xenopus laevis PE=2 SV=1 - [Q7SYV5_XENLA]								
Q7SYX2;CL10546Contig1	MGC64421 protein OS=Xenopus la	serpinb6			Y			TRUE	TRUE
Q7SYY6	Cbln2-prov protein OS=Xenopus lae	cbln2							
Q7SZ11;CL1890Contig5	Annexin OS=Xenopus laevis PE=2	anx							
Q7SZ14	MGC64316 protein OS=Xenopus la	ndufa9			Y			TRUE	TRUE
Q7SZ19	Annexin (Fragment) OS=Xenopus l	anx			Y			TRUE	TRUE
Q7SZ23;CL10303Contig1	Gstm2-prov protein OS=Xenopus la	gstm1		Y	Y			TRUE	TRUE
Q7SZ25	Eno1-prov protein OS=Xenopus lae	eno1		Y	Y			TRUE	TRUE
Q7SZ26;CL2319Contig2	Peptidyl-prolyl cis-trans isomerase	ppib			Y			TRUE	TRUE
Q7SZ34;CL1198Contig2	Stathmin OS=Xenopus laevis GN=s	stmn1			Y			TRUE	TRUE
Q7SZ43	Mylc2a-prov protein OS=Xenopus l	mylc2a							
Q7SZ77;CL50Contig6	Rps11 protein OS=Xenopus laevis	rsp11		Y				TRUE	TRUE
Q7SZ87	MGC64430 protein OS=Xenopus la	rpl28			Y			TRUE	TRUE
Q7SZ98	Annexin OS=Xenopus laevis PE=2	anx							
Q7SZA3	MGC64320 protein OS=Xenopus laevis PE=4 SV=1 - [Q7SZA3_XENLA]								
Q7SZA4	60S ribosomal protein L18 OS=Xen	rpl18			Y			TRUE	TRUE
Q7SZA5;BJ091434 UniRef	MGC64312 protein OS=Xenopus la	rpl29		Y	Y			TRUE	TRUE
Q7SZA8;CL926Contig3	60S ribosomal protein L18 OS=Xen	rpl18		Y	Y			TRUE	TRUE
Q7SZB0;CL1525Contig1	Rpl35a-prov protein OS=Xenopus l	rpl35a			Y			TRUE	TRUE
Q7SZB1	Profilin OS=Xenopus laevis GN=MG	pfn							
Q7SZB2;CL4738Contig1	Rpl27a protein OS=Xenopus laevis	rpl27a		Y	Y			TRUE	TRUE
Q7SZB4	60S ribosomal protein L37a OS=Xe	rpl37a			Y			TRUE	TRUE
Q7SZB7;CL391Contig4	60S ribosomal protein L18a OS=Xe	repl18a							
Q7SZF6	Vitellogenin B1 OS=Xenopus laevis	vtgb1		Y				TRUE	TRUE
Q7SZJ1	Putative OFD1 protein (Fragment)	ofd1			Y			TRUE	TRUE
Q7SZL5	Microtubule-associated tumor suppr	mtus1			Y			TRUE	TRUE
Q7SZS3;CL137Contig1	Aspartate aminotransferase OS=Xe	got2		Y	Y			TRUE	TRUE
Q7SZT4;CL25746Contig1	Rdhl-prov protein OS=Xenopus lae	dhrs9			Y			TRUE	TRUE
Q7SZU3;TC455791 UniRe	Rps10-prov protein OS=Xenopus la	rps10			Y			TRUE	TRUE
Q7T0N8;CL7665Contig1	Hadhsc-prov protein OS=Xenopus l	hadh		Y	Y			TRUE	TRUE
Q7T0R2	LOC398682 protein (Fragment) OS	LOC398682							
Q7T0R7;CL3918Contig2	Cn2-prov protein OS=Xenopus laev	cndp2		Y	Y			TRUE	TRUE
Q7T0R9	Rps2e protein OS=Xenopus laevis	rps2							
Q7T0U6	Calcium-binding mitochondrial carri	slc25a24			Y			TRUE	TRUE
Q7T0V9	MGC68941 protein OS=Xenopus la	asb12			Y			TRUE	TRUE
Q7T0W0;CL2874Contig1	Dihydrolipoyl dehydrogenase OS=X	dld			Y			TRUE	TRUE
Q7T0W4	Vps28-prov protein OS=Xenopus la	vps28			Y			TRUE	TRUE
Q7T0Y4	Dynein regulatory complex protein 1	drc1							
Q7T0Y7;CL7862Contig1	2o545 protein OS=Xenopus laevis	ccdc25							
Q7T106;33416619	MGC68423 protein OS=Xenopus la	10a1.1			Y			TRUE	TRUE
Q7T3S2;CL2215Contig4	PP2A B" subunit PR74 OS=Xenopu	ppp2r3a			Y			TRUE	TRUE
Q7ZSY1;CL6511Contig1	Galectin family xgalectin-VIIa OS=X	lgals3			Y			TRUE	TRUE
Q7ZT76	IQ motif containing GTPase activati	iqgap2			Y			TRUE	TRUE
Q7ZTA4	Hus1 protein OS=Xenopus laevis G	hus1			Y			TRUE	TRUE
Q7ZTA9	Putative Rho family guanine-nucleo	arhgef39							
Q7ZTB3;CL289Contig3	Heat shock protein gp96 OS=Xeno	hsp90b1							
Q7ZTJ1;CL468Contig4	Slc25a3-prov protein OS=Xenopus	slc25a3			Y			TRUE	TRUE
Q7ZTJ4	Vha55 protein OS=Xenopus laevis	atp6v1b2			Y			TRUE	TRUE
Q7ZTK1;CL1176Contig2	Slc30a1-prov protein OS=Xenopus	slc30a1			Y			TRUE	TRUE

Q7ZTK6	MGC53952 protein OS=Xenopus la	hspa8			Y			TRUE	TRUE
Q7ZTK9;CL7196Contig1	Aspartate aminotransferase OS=Xe	got1							
Q7ZTL1	Acaa2-prov protein OS=Xenopus la	acaa2			Y			TRUE	TRUE
Q7ZTL5;CL1515Contig2	Cct8-prov protein OS=Xenopus laev	cct8		Y	Y			TRUE	TRUE
Q7ZTM0	Cct5-prov protein OS=Xenopus laev	cct5			Y			TRUE	TRUE
Q7ZTM4;CL120Contig1	Col2a1b protein OS=Xenopus laevis	col2a1b							
Q7ZTM9;CL5086Contig1	Eukaryotic translation initiation facto	eif3d							
Q7ZTP0;CL1Contig193	MGC53359 protein OS=Xenopus la	tuba3c			Y			TRUE	TRUE
Q7ZTP2	Actin-related protein 2-A OS=Xenop	actr2-a							
Q7ZTP9;CL8426Contig1	Slc25a20-prov protein OS=Xenopus	slc25a20			Y	Y		TRUE	TRUE
Q7ZTR0	Wu:fc55e05-prov protein OS=Xenop	copb2			Y			TRUE	TRUE
Q7ZWJ1	SYNE1 protein (Fragment) OS=Xen	syne1			Y			TRUE	TRUE
Q7ZWJ2	Uqcrc1 protein OS=Xenopus laevis	uqcrc1			Y			TRUE	TRUE
Q7ZWK0	Pck1-prov protein OS=Xenopus lae	pck1			Y			TRUE	TRUE
Q7ZWK4	LOC398587 protein (Fragment) OS	LOC398587							
Q7ZWL4	Chaperone protein DnaJ D OS=Xen	dnaja2							
Q7ZWN1	Inosine-5'-monophosphate dehydro	impdh1			Y			TRUE	TRUE
Q7ZWN5;CL2685Contig2	Triosephosphate isomerase OS=Xe	tpi1			Y			TRUE	TRUE
Q7ZWN8	LOC398560 protein (Fragment) OS	LOC398560							
Q7ZWP4;CL57Contig2	MGC53205 protein OS=Xenopus la	tubb4a							
Q7ZWP8;CL6523Contig2	DNA topoisomerase OS=Xenopus l	top3b			Y			TRUE	TRUE
Q7ZWQ0	Ribonucleoside-diphosphate reduct	rrm1			Y			TRUE	TRUE
Q7ZWR3	Padi2-prov protein OS=Xenopus lae	padi2							
Q7ZWR6	ATP synthase subunit beta OS=Xen	atp5b			Y			TRUE	TRUE
Q7ZWS4	MGC53764 protein OS=Xenopus la	rpn2			Y			TRUE	TRUE
Q7ZWS8;CL1187Contig2	Tagln2-prov protein OS=Xenopus la	tagln2			Y			TRUE	TRUE
Q7ZWU1;CL4166Contig1	Stip1-prov protein OS=Xenopus lae	stip1			Y			TRUE	TRUE
Q7ZWU3;CL1744Contig1	Grp58-prov protein OS=Xenopus la	pdia3		Y				TRUE	TRUE
Q7ZWV0;CL4305Contig3	Kin-1-prov protein OS=Xenopus lae	prkacb			Y	Y		TRUE	TRUE
Q7ZWV1	Ddx19-prov protein OS=Xenopus la	ddx19b			Y			TRUE	TRUE
Q7ZWW3;CL7106Contig1	Ferritin OS=Xenopus laevis PE=2 S	fth							
Q7ZWW5	Abcf2-prov protein OS=Xenopus lae	abcf2			Y			TRUE	TRUE
Q7ZWX9	Midnolin-B OS=Xenopus laevis GN=	midn			Y			TRUE	TRUE
Q7ZWY6	Rpl9-prov protein OS=Xenopus laev	rpl9			Y			TRUE	TRUE
Q7ZWZ7;CL2318Contig1	Ribosomal protein L15 OS=Xenopu	rpl15			Y			TRUE	TRUE
Q7ZWZ9;CL4310Contig2	Dnm1l-prov protein OS=Xenopus la	dnm1l							
Q7ZX03	Forkhead box protein K2 OS=Xenop	foxk2			Y			TRUE	TRUE
Q7ZX18	MGC53357 protein OS=Xenopus la	rhgap11a.1							
Q7ZX22;CL5682Contig1	WD repeat-containing protein 24 OS	wdr24			Y			TRUE	TRUE
Q7ZX27	Palmdelphin OS=Xenopus laevis GN	palmd							
Q7ZX29;CL3649Contig1	Dia1 protein OS=Xenopus laevis GN	cytb5r3							
Q7ZX30	Spx-prov protein OS=Xenopus laevi	sf3b4			Y	Y		TRUE	TRUE
Q7ZX34;CL3654Contig2	MGC52616 protein OS=Xenopus la	hhspa9		Y				TRUE	TRUE
Q7ZX44;CL2985Contig2	Txndc5-prov protein OS=Xenopus la	txndc5			Y			TRUE	TRUE
Q7ZX69;CL1735Contig1	MGC52894 protein OS=Xenopus la	MGC52894							
Q7ZX74	MGC53501 protein OS=Xenopus la	ccdc6							
Q7ZX81	MGC54008 protein OS=Xenopus la	cyp2c8.1							
Q7ZX92;CL5540Contig2	MGC80929 protein OS=Xenopus la	psmd14			Y			TRUE	TRUE
Q7ZX99	Tia1 protein (Fragment) OS=Xenopu	Tia1			Y			TRUE	TRUE
Q7ZXB9;CL335Contig7	Faf1-prov protein OS=Xenopus laev	faf1			Y			TRUE	TRUE
Q7ZXF1	Myotubularin-related protein 4 OS=X	mtmr4			Y			TRUE	TRUE
Q7ZXF3;zeinaSSns_comp	DNA-binding protein inhibitor ID-4 O	id4			Y			TRUE	TRUE
Q7ZXG1	Smarcd1 protein (Fragment) OS=Xe	smarcd1			Y			TRUE	TRUE
Q7ZXG3;CL107Contig4	Iff-2-prov protein OS=Xenopus laevi	eif5a		Y	Y			TRUE	TRUE
Q7ZXG7;CL54Contig1	Guanidinoacetate N-methyltransfera	gamt			Y			TRUE	TRUE
Q7ZXH6;CL593Contig5	Ywhaq-prov protein OS=Xenopus la	ywhaq			Y			TRUE	TRUE
Q7ZXI2	Slit1 protein OS=Xenopus laevis GN	slit1			Y			TRUE	TRUE
Q7ZXI5;CL2254Contig3	Snf protein OS=Xenopus laevis GN=	snrpa			Y			TRUE	TRUE
Q7ZXK4	Rpl10-prov protein OS=Xenopus lae	rpl10			Y			TRUE	TRUE
Q7ZXM6	Sfrp2-prov protein OS=Xenopus lae	sfrp2			Y			TRUE	TRUE
Q7ZXM8;CL3609Contig1	Ferritin OS=Xenopus laevis GN=ftm	ftmt			Y			TRUE	TRUE
Q7ZXP0;CL3911Contig1	Twinfilin-2-A OS=Xenopus laevis GN	twf2			Y			TRUE	TRUE
Q7ZXP5	Mct3-prov protein OS=Xenopus laev	slc16a3			Y			TRUE	TRUE
Q7ZXP8	Eef2-prov protein OS=Xenopus laev	eef2.1		Y	Y			TRUE	TRUE
Q7ZXT0	Egfl7 protein OS=Xenopus laevis G	egfl7							
Q7ZXU1	Chc1l-prov protein OS=Xenopus lae	rcbtb2			Y			TRUE	TRUE
Q7ZXV2;CL1735Contig3	MGC52808 protein OS=Xenopus la	rpn1			Y			TRUE	TRUE
Q7ZXX4;CL6920Contig1	MGC52697 protein OS=Xenopus la	aldh9a1							
Q7ZXZ0	Zygotic DNA replication licensing fa	mcm3			Y			TRUE	TRUE
Q7ZY16;CL9256Contig2	Adsl-prov protein OS=Xenopus laev	adsl			Y			TRUE	TRUE
Q7ZY19	MGC53409 protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZY19_XENLA]								
Q7ZY24;CL67Contig8	Hmgb3-prov protein OS=Xenopus la	hmgb3			Y			TRUE	TRUE
Q7ZY48	Rpl13a-prov protein OS=Xenopus la	rpl13a		Y	Y			TRUE	TRUE
Q7ZY50	MGC53997 protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZY50_X			Y				TRUE	TRUE
Q7ZY51	Profilin (Fragment) OS=Xenopus lae	MGC64293							
Q7ZY52	Glyceraldehyde-3-phosphate dehyd	gapdh			Y		Y	TRUE	TRUE
Q7ZY57	Eif2s3-prov protein OS=Xenopus la	eif2s3			Y			TRUE	TRUE
Q7ZY58	MGC53995 protein OS=Xenopus la	cdc73			Y			TRUE	TRUE
Q7ZY63	CBTF122 protein (Fragment) OS=X	cbtf122							
Q7ZY81	Nucleosome assembly protein 1-like	nap1l1			Y			TRUE	TRUE
Q7ZY84	LOC398446 protein (Fragment) OS	LOC398446							
Q7ZY92	Lect1-prov protein OS=Xenopus lae	lect1							
Q7ZY93	Methionine aminopeptidase OS=Xe	map							
Q7ZYA3	Pgm2-prov protein OS=Xenopus lae	pgm1			Y			TRUE	TRUE
Q7ZYA5;CL6725Contig1	Interferon-inducible double strandec	prkra							
Q7ZYA6	Protein CDV3 homolog A OS=Xeno	cdv3			Y			TRUE	TRUE

Q7ZYB2;CL6160Contig1	PR domain zinc finger protein 4 OS	prdm4			Y			TRUE	TRUE
Q7ZYE5;CL5229Contig2	Rheb-prov protein OS=Xenopus lae	rheb			Y			TRUE	TRUE
Q7ZYE8;CL6531Contig1	Tyrp1-prov protein OS=Xenopus lae	tyrp1			Y			TRUE	TRUE
Q7ZYF2;CL1415Contig2	Translationally-controlled tumor prot	tpt1			Y			TRUE	TRUE
Q7ZYF4	Gfpt1-prov protein OS=Xenopus lae	gfpt2			Y			TRUE	TRUE
Q7ZYF5	Calponin OS=Xenopus laevis GN=c	cnn3							
Q7ZYF6	Bag3-A protein OS=Xenopus laevis	bag3							
Q7ZYF7;CL1612Contig4	MGC53103 protein OS=Xenopus la	phb		Y				TRUE	TRUE
Q7ZYG7;CL1321Contig1	Ap2b1-prov protein OS=Xenopus la	ap2b1			Y			TRUE	TRUE
Q7ZYH3;CL653Contig1	Phf12-prov protein OS=Xenopus lae	phf12			Y			TRUE	TRUE
Q7ZYH4	Brd2-A-prov protein (Fragment) OS	brd2a			Y			TRUE	TRUE
Q7ZYH7;CL3329Contig1	Pgk1-prov protein OS=Xenopus lae	pgk1			Y			TRUE	TRUE
Q7ZYI2;CL621Contig2	MGC52980 protein OS=Xenopus laevis PE=2 SV=1 - [Q7ZYI2_XENLA]								
Q7ZYI5;CL3906Contig2	Baf53a-pending-prov protein OS=X	actl6a							
Q7ZYJ1	Pctk2-prov protein OS=Xenopus lae	cdk17			Y			TRUE	TRUE
Q7ZYL1;CL5426Contig2	Proteasome subunit beta type OS=	psmb1							
Q7ZYL5	Kinesin-like protein KIF22-B OS=Xe	kif22			Y			TRUE	TRUE
Q7ZYM3;CL5801Contig1	Gpd1 protein OS=Xenopus laevis G	gpd1			Y			TRUE	TRUE
Q7ZYM5	Sdcbp protein OS=Xenopus laevis	sdcbp							
Q7ZYP4	Ldb3-prov protein OS=Xenopus lae	ldb3							
Q7ZYP5	MGC52698 protein OS=Xenopus la	cirh1a			Y			TRUE	TRUE
Q7ZYP8	LOC495278 protein (Fragment) OS=Xenopus laevis GN=LOC495278 PE=2 SV=1 - [Q7ZYP8_XENLA]								
Q7ZYQ8	60S ribosomal protein L18a (Fragm	repl18a							
Q7ZYQ9;CL1Contig431	Ckm-prov protein OS=Xenopus lae	ckm							
Q7ZYR1	Rpl3-prov protein OS=Xenopus lae	rpl3							
Q7ZYS1;CL555Contig6	60S ribosomal protein L19 OS=Xen	rpl19			Y			TRUE	TRUE
Q7ZYS4;CL2863Contig4	MGC53685 protein OS=Xenopus la	MGC53685							
Q7ZYS8;CL560Contig6	60S ribosomal protein L10a OS=Xe	rpl10a		Y	Y			TRUE	TRUE
Q7ZYT3	Rpls3-b protein OS=Xenopus laevis	rpls3							
Q7ZYU4;TC433567 UniRe	Rps9-prov protein OS=Xenopus lae	rps9		Y	Y			TRUE	TRUE
Q801Q1	MGC53743 protein OS=Xenopus la	rrp1b			Y			TRUE	TRUE
Q801Q2;CL2424Contig1	Dtx2 protein OS=Xenopus laevis GI	dtx2			Y			TRUE	TRUE
Q801Q9;CL7416Contig1	Nkx3-1 protein OS=Xenopus laevis	nkx31							
Q801S2;CL3774Contig1	Succinate dehydrogenase [ubiquino	sdha							
Q801S3	40S ribosomal protein S3a-A OS=X	rps3a		Y	Y			TRUE	TRUE
Q801S7	Uba1a protein OS=Xenopus laevis	uba1a							
Q801T6	Alpha-1,4 glucan phosphorylase OS	pygm			Y			TRUE	TRUE
Q802B6;CL539Contig1	Add1-a protein OS=Xenopus laevis	add1							
Q802B7;CL5322Contig1	Ndufs1-prov protein OS=Xenopus la	ndufs1				Y		TRUE	TRUE
Q802C1	Grn-prov protein OS=Xenopus laevi	grn			Y			TRUE	TRUE
Q804I2	Germes OS=Xenopus laevis GN=L	LOC398520							
Q860P5;CL387Contig2	Bat2-prov protein OS=Xenopus lae	prrc2a			Y			TRUE	TRUE
Q8AVB5	Sfrs1 protein (Fragment) OS=Xenop	sfrs1							
Q8AVB7;CL2995Contig1	Cct2-prov protein OS=Xenopus lae	cct2		Y		Y		TRUE	TRUE
Q8AVC0	Shmt1 protein OS=Xenopus laevis	shmt1				Y		TRUE	TRUE
Q8AVC0;CL7997Contig2	Shmt1 protein OS=Xenopus laevis	shmt1							
Q8AVD0	MGC53232 protein OS=Xenopus laevis PE=2 SV=1 - [Q8AVD0_XENLA]								
Q8AVD3;CL1995Contig2	Adenylate kinase 2, mitochondrial C	ak2			Y	Y		TRUE	TRUE
Q8AVD7;CL3574Contig1	Ndufv1 protein OS=Xenopus laevis	ndufv1							
Q8AVE2;CL52Contig20	Hsc70 protein OS=Xenopus laevis	hspa1l							
Q8AVE3;CL2028Contig2	Hspa5 protein OS=Xenopus laevis	hspa5			Y			TRUE	TRUE
Q8AVE7;CL3384Contig1	1i973-prov protein OS=Xenopus lae	gnl2			Y			TRUE	TRUE
Q8AVF2;CL8795Contig2	MGC52738 protein OS=Xenopus la	tom1l1			Y	Y		TRUE	TRUE
Q8AVF3	LOC398536 protein (Fragment) OS=	LOC398536							
Q8AVG7	Cdc20 protein OS=Xenopus laevis	cdc20			Y			TRUE	TRUE
Q8AVH1;CL1313Contig1	Histone-binding protein RBBP7 OS=	rbbp7			Y			TRUE	TRUE
Q8AVH2;TC421129 UniRe	Ckb-prov protein OS=Xenopus laev	ckb		Y	Y			TRUE	TRUE
Q8AVI3	Arbp-prov protein OS=Xenopus lae	rplp0			Y			TRUE	TRUE
Q8AVI7;CL1548Contig4	Rpl5-b protein OS=Xenopus laevis	rpl5							
Q8AVL1	MGC53953 protein OS=Xenopus laevis PE=2 SV=1 - [Q8AVL1_XENLA]								
Q8AVM7	Basic leucine zipper and W2 domai	bzw1							
Q8AVM7;CL215Contig8	Basic leucine zipper and W2 domai	bzw1							
Q8AVN3	Kiaa0010-prov protein OS=Xenopus	ube3c			Y			TRUE	TRUE
Q8AVN8;CL1362Contig1	Cdc37-prov protein OS=Xenopus la	cdc37			Y			TRUE	TRUE
Q8AVP8;CL8Contig14	Peptidyl-prolyl cis-trans isomerase	ppia		Y	Y			TRUE	TRUE
Q8AVR4	Programmed cell death protein 10 C	pdcd10			Y			TRUE	TRUE
Q8AVR6	Hspc177-prov protein OS=Xenopus	chmp5			Y			TRUE	TRUE
Q8AVS4	Transcriptional activator protein Pur	purbb							
Q8AVT0	MGC53543 protein OS=Xenopus la	eno1			Y			TRUE	TRUE
Q8AVT1	Paics-prov protein OS=Xenopus lae	paics							
Q8AVU2	Ubiquitin-conjugating enzyme E2 S-	ube2sb				Y		TRUE	TRUE
Q8AVV6	SOSS complex subunit C OS=Xeno	inip							
Q8AVW0;CL561Contig9	Rpl12-prov protein OS=Xenopus lae	rpl12		Y	Y			TRUE	TRUE
Q8AVW5;CL253Contig3	Ywhaz-prov protein OS=Xenopus la	ywhaz			Y			TRUE	TRUE
Q8AVX2;CL1548Contig2	Rpl5-a protein OS=Xenopus laevis	rpl5							
Q8AX84	FUSE binding protein-like protein O	fubp1			Y			TRUE	TRUE
Q8AX85	RNA-binding protein VgRBP71 OS=	Khsrp			Y			TRUE	TRUE
Q8AXY7	Pygopus-2beta OS=Xenopus laevis	pygo2b							
Q8AY70;CL7950Contig1	Glyceraldehyde-3-phosphate dehyd	gapdhb		Y				TRUE	TRUE
Q8JH73	Integral membrane nucleoporin gp2	gp210							
Q8JHA7;CL8144Contig1	Glutathione s-transferase OS=Xeno	gst		Y				TRUE	TRUE
Q8QFR2	Protein HIRA OS=Xenopus laevis G	hira			Y			TRUE	TRUE
Q8QFV1	Isthmin OS=Xenopus laevis GN=isn	ism1			Y			TRUE	TRUE
Q8QFW7;CL1631Contig2	Ribosomal protein L34 OS=Xenopu	rpl34							
Q8QFX3	Myeloperoxidase, peroxidase 2' OS	mpo							
Q8QG78	Nuclear receptor corepressor 1 OS=	ncor1			Y			TRUE	TRUE

Q8QHA5;CL6103Contig1	DNA replication ATP-dependent hel	dna2			Y			TRUE	TRUE
Q8UUU4	Sp1-like zinc-finger protein XSPR-2	sp5l							
Q8UVD5	Semaphorin 4C (Fragment) OS=Xe	sema4c			Y			TRUE	TRUE
Q8UVR5	Bromodomain adjacent to zinc finge	baz1a			Y			TRUE	TRUE
Q8UW77;CL1026Contig6	XEB1B OS=Xenopus laevis GN=ma	mapre1			Y			TRUE	TRUE
Q8WM44	MHC class II antigen alpha chain D	dbag2							
Q90X16;CL10849Contig1	Annexin OS=Xenopus laevis GN=a	anxa4			Y			TRUE	TRUE
Q90X20	Aryl hydrocarbon receptor nuclear t	arnt			Y			TRUE	TRUE
Q90XW5	Iroquois-class homeodomain protei	irx5							
Q90YE5;CL4860Contig2	MAD, mothers against decapentapl	smad3			Y			TRUE	TRUE
Q90Z06	Prickle-like protein 1-A OS=Xenopu	prickle1							
Q90Z58;CL11161Contig1	Chisel OS=Xenopus laevis GN=sm	smpx							
Q90ZB7	Lymphoid enhancer factor XLEF-1B	lef1			Y			TRUE	TRUE
Q90ZL4	Lissencephaly-1 homolog OS=Xen	pafah1b1			Y			TRUE	TRUE
Q91375	Elongation factor 1-gamma-B OS=	eef1gb		Y				TRUE	TRUE
Q91560	RNA exonuclease 4 OS=Xenopus l	rexo4			Y			TRUE	TRUE
Q91573	Mineralocorticoid receptor (Fragme	nr3c2			Y			TRUE	TRUE
Q91579	CUGBP Elav-like family member 3-	tnrc4							
Q91593	Potassium channel alpha subunit K	kcnb1							
Q91598	Growth associated protein GAP-43	gap43							
Q91615	Insulin receptor substrate 1-A OS=	irs1			Y			TRUE	TRUE
Q91624;CL52Contig10	Heat shock cognate 70.I OS=Xeno	hsc70							
Q91660	Zinc finger protein GLI3 OS=Xenop	gli3			Y			TRUE	TRUE
Q91684	DNA polymerase subunit gamma-1	polg			Y			TRUE	TRUE
Q91685	Homeobox protein Mix.2 OS=Xeno	mix2							
Q91687	Integrin alpha-4 OS=Xenopus laevi	itga4			Y			TRUE	TRUE
Q91717;CL120Contig7	Collagen alpha-1(II) chain OS=Xen	col2a1			Y			TRUE	TRUE
Q91733	EEF1D protein OS=Xenopus laevis	eef1d			Y	Y		TRUE	TRUE
Q91749	Oviduct specific protein-1A OS=Xe	fosp1a							
Q91757	Glycogen synthase kinase-3 beta O	gsk3b			Y		Y	TRUE	TRUE
Q91785	Kinesin-like protein KIF15-A OS=Xe	kif15			Y			TRUE	TRUE
Q91804	NMDA receptor (Fragment) OS=Xe	nr1							
Q91819	Aurora kinase A-B OS=Xenopus la	aurka			Y			TRUE	TRUE
Q91829	V(D)J recombination-activating prot	rag1							
Q91840;CL994Contig4	Retinoid X receptor beta OS=Xeno	rxrb							
Q91868	Rat translocon-associated protein d	ssr4			Y			TRUE	TRUE
Q91896;CL253Contig8	14-3-3 protein zeta OS=Xenopus la	ywhaz			Y			TRUE	TRUE
Q91902;CL279Contig2	Delta-like protein OS=Xenopus laev	dll							
Q91926	Homeobox protein vent1 OS=Xeno	vent1							
Q92122;CL1152Contig2	Pyruvate kinase muscle isozyme O	vtga2			Y			TRUE	TRUE
Q98SG0	Beta-amyloid protein A OS=Xenopu	app							
Q98SP8	Embryonic polyadenylate-binding p	epabp-a							
Q98SU0	K-Cl cotransporter (Fragment) OS=	kcc							
Q98T92	Mps1/TTK OS=Xenopus laevis GN=	ttk			Y			TRUE	TRUE
Q98TW0	Protein kinase Cds1 OS=Xenopus l	Cds1			Y			TRUE	TRUE
Q98UD5	Collagen alpha1(IV) (Fragment) OS	col4a1							
Q9DDA3	RalB-binding protein (Fragment) OS	rlip1							
Q9DDN8	Gravin-like OS=Xenopus laevis GN	akap12			Y			TRUE	TRUE
Q9DE14	Serine/threonine-protein kinase atr	atr			Y			TRUE	TRUE
Q9DE56	Ribonucleoside-diphosphate reduct	rrm1			Y			TRUE	TRUE
Q9DED4;TC439103 UniRe	Cold-inducible RNA-binding protein	cirbp		Y	Y			TRUE	TRUE
Q9DEF3	Patched-2 OS=Xenopus laevis GN=	ptch2			Y			TRUE	TRUE
Q9DEF7	Serine/threonine-protein phosphata	ppp							
Q9DFC2	Homeobox protein XHox11L2 OS=	tlx3			Y			TRUE	TRUE
Q9DGF4	Prox 1 protein OS=Xenopus laevis	prox1				Y		TRUE	TRUE
Q9I8J7;CL4267Contig1	MGC69114 protein OS=Xenopus la	tktl2		Y	Y			TRUE	TRUE
Q9I8P8;CL2106Contig1	FK506-binding protein OS=Xenopus	fkbp10			Y			TRUE	TRUE
Q9I905;CL4858Contig1	MGC64562 protein OS=Xenopus la	mtch2							
Q9I9B1	Olfactory receptor (Fragment) OS=	xb3							
Q9I9K0	Zinc finger protein ZFPM1 (Fragme	zfpm1			Y			TRUE	TRUE
Q9I9L2	Cbl proto-oncogene protein (Fragm	Cbl							
Q9I9M9	Adenine nucleotide translocase OS	slc25a5		Y	Y			TRUE	TRUE
Q9IAB1	Putative uncharacterized protein (Fragment) OS=Xenopus laevis PE=2 SV=1 - [Q9IAB1_XENLA]								
Q9IAI8	Receptor protein tyrosine phosphat	crypa							
Q9IAJ7;CL4522Contig2	ATP synthase subunit B OS=Xenop	atp5f1			Y			TRUE	TRUE
Q9IBC8	T-box transcription factor TBX2-A O	tbx2			Y			TRUE	TRUE
Q9IBF6	Prolactin receptor OS=Xenopus lae	prlr							
Q9IBG7	Kielin/chordin-like protein OS=Xeno	kcp			Y			TRUE	TRUE
Q9PSN9	Lipovitellin 1, PCDZN=ZN(2+)- and	pcdzn							
Q9PSP4	RAN-interacting protein P10 (Fragm	ranbp10				Y		TRUE	TRUE
Q9PSQ7	PNIXA, EP45=NI(2+)-binding serpi	pnixa							
Q9PSX0;CL3505Contig1	Fructose-bisphosphate aldolase OS	aldoc			Y			TRUE	TRUE
Q9PTE5	Phosphoinositide 3 kinase catalytic	pik3c							
Q9PTG8	Transforming acidic coiled-coil-cont	tacc3			Y			TRUE	TRUE
Q9PTK6	Fatvg OS=Xenopus laevis GN=fatv	fatvg							
Q9PUU6	Frizzled-2 OS=Xenopus laevis GN=	fzd2			Y			TRUE	TRUE
Q9PVQ1	Proteasome subunit alpha type-7-B	psma7			Y			TRUE	TRUE
Q9PVY6;CL2696Contig1	Proteasome subunit alpha type-7-A	psma7			Y			TRUE	TRUE
Q9PVY8	Forkhead box protein C2-B OS=Xe	foxc2b							
Q9PWH0	Guanylate cyclase OS=Xenopus la	gc1							
Q9W650	C-met/hepatocyte growth factor rec	met							
Q9W6C5	Programmed cell death 6-interactin	pdcd6ip			Y			TRUE	TRUE
Q9W705	Nuclear receptor coactivator 2 OS=	ncoa2			Y			TRUE	TRUE
Q9W791	T-complex protein 1 subunit alpha	tcp1		Y	Y			TRUE	TRUE
Q9W7F2;CL2204Contig2	WD repeat-containing protein 1-A O	wdr1			Y			TRUE	TRUE
Q9YGY0	Axin-1 OS=Xenopus laevis GN=axi	axin1			Y		Y	TRUE	TRUE

Q9ZZM1	Cytochrome c oxidase subunit 2 (Fr	cox2							
TC414340 UniRef100_Q6(	Rep: Kidney mitochondrial carrier pi	Slc25a30			Y			TRUE	TRUE
TC424140 homologue to U	Rep: Protein DBF4 homolog A - Xer	dbf4							
TC425929 similar to UniRe	Rep: MGC69138 protein - Xenopus laevis (African clawed frog), partial (32%)								
TC426340 homologue to U	Rep: Rpl9-prov protein - Xenopus la	rpl9			Y			TRUE	TRUE
TC427469 homologue to U	Rep: MGC81949 protein - Xenopus laevis (African clawed frog), partial (37%)								
TC427947 similar to UniRe	Rep: Homolog of Homo sapiens "Sp	c21orf33							
TC428477 homologue to U	Rep: Methylenetetrahydrofolate redu	mthfr			Y			TRUE	TRUE
TC428798 homologue to U	Rep: MGC82630 protein - Xenopus laevis (African clawed frog), partial (31%)								
TC428802 UniRef100_Q5N	Rep: Brg1 - Xenopus laevis (African	brg1				Y		TRUE	TRUE
TC429244	TC429244								
TC429806 homologue to U	Rep: Gem protein - Xenopus tropica	gem			Y			TRUE	TRUE
TC429946 homologue to U	Rep: MGC97820 protein - Xenopus tropicalis (Western clawed frog) (Silurana tropicalis), partial (51%)								
TC430486 UniRef100_Q6D	Rep: Synaptobrevin homolog YKT6-	ykt6							
TC430865 similar to UniRe	Rep: mitochondrial tumor suppresso	mtus1			Y			TRUE	TRUE
TC432016 weakly similar to	Rep: Centrin - Plasmodium yoelii yo	cetn							
TC432167 UniRef100_Q68	Rep: Proteasome subunit beta type	psmb							
TC432608 homologue to U	Rep: Protein OS-9 precursor (Ampli	os9							
TC433738 homologue to U	Rep: Elongation factor Tu - Xenopus	eftu							
TC435033 homologue to U	Rep: ATP synthase subunit beta - X	atpb							
TC435583 weakly similar to	Rep: Tripartite motif-containing prot	trim68							
TC435750 homologue to U	Rep: Nonmuscle myosin II heavy ch	myh2							
TC436371 homologue to U	Rep: Snail homolog 1 - Xenopus tro	snai1			Y			TRUE	TRUE
TC439412 UniRef100_Q5E	Rep: LOC100036774 protein - Xenopus laevis (African clawed frog), partial (52%)								
TC439428 homologue to U	Rep: Slc25a3-prov protein - Xenopu	slc25a3			Y			TRUE	TRUE
TC440065 homologue to U	Rep: MGC82602 protein - Xenopus laevis (African clawed frog), complete								
TC440338 UniRef100_Q28	Rep: 60S ribosomal protein L27 - Xe	rpl27		Y	Y			TRUE	TRUE
TC440393 similar to UniRe	Rep: Pla2g4a protein - Xenopus lae	pla2g4a			Y			TRUE	TRUE
TC441388	TC441388								
TC441790 homologue to U	Rep: Fry protein - Xenopus tropicali	fry			Y			TRUE	TRUE
TC442984 similar to UniRe	Rep: LOC496332 protein - Xenopus laevis (African clawed frog), partial (40%)								
TC443713 homologue to U	Rep: Superoxide dismutase - Xenop	sod							
TC443718 homologue to U	Rep: Wdr12 protein - Xenopus tropi	wdr12			Y			TRUE	TRUE
TC443725 homologue to U	Rep: 60S ribosomal protein L6 - Xer	rpl6							
TC444012 homologue to U	Rep: DnaJ homolog subfamily C me	drip78							
TC444338 similar to UniRe	Rep: Iron(III) ABC transporter, ATP-	ct0412							
TC444576 homologue to U	Rep: Uncharacterized protein C6orf	c6orf45							
TC444688 UniRef100_Q7T	Rep: Ctsc protein - Xenopus laevis (	ctsc			Y			TRUE	TRUE
TC445443 similar to UniRe	Rep: Conserved fungal protein - Schizosaccharomyces pombe (Fission yeast), partial (5%)								
TC445670 homologue to U	Rep: Myosin heavy chain - Xenopus	mhc							
TC446929 homologue to U	Rep: U4/U6 small nuclear ribonucle	prp31							
TC447025 homologue to U	Rep: L-lactate dehydrogenase B cha	ldhb							
TC447390 weakly similar to	Rep: Neuroblast differentiation-asso	ahnak			Y			TRUE	TRUE
TC447788 similar to UniRe	Rep: Hepatic triacylglycerol lipase p	lipc							
TC448187 homologue to U	Rep: Tripartite motif-containing prot	trim44			Y			TRUE	TRUE
TC448972 homologue to U	Rep: Arginine/serine-rich coiled-coil	rsrc2			Y			TRUE	TRUE
TC449350 similar to UniRe	Rep: Protein FAM20A precursor. - (	fam20a							
TC449434 homologue to U	Rep: Zinc finger protein 326 - Xenop	znf326			Y			TRUE	TRUE
TC449583 homologue to U	Rep: AT20865p - Drosophila melanogaster (Fruit fly), partial (22%)								
TC449759 homologue to U	Rep: Creatine kinase, brain - Xenop	ckb			Y			TRUE	TRUE
TC450147 weakly similar to	Rep: ADP-ribosyl cyclase 2 precurs	bst1							
TC451860 homologue to U	Rep: Proteasome (Prosome macrop	psmb4			Y			TRUE	TRUE
TC453026 UniRef100_P02	Rep: Histone H2B 1.1 - Xenopus lae	histh2b1							
TC453211 homologue to U	Rep: LOC100037140 protein - Xenopus laevis (African clawed frog), partial (22%)								
TC453299 homologue to U	Rep: Seizure 6-like protein precurso	sez6l			Y			TRUE	TRUE
TC453514 homologue to U	Rep: Stk39-prov protein - Xenopus l	stk39			Y			TRUE	TRUE
TC453615 similar to UniRe	Rep: MGC80407 protein - Xenopus laevis (African clawed frog), partial (15%)								
TC454736 homologue to U	Rep: Ppp5c-prov protein. - Xenopus	Ppp5c				Y		TRUE	TRUE
TC454792 UniRef100_Q0I	Rep: MGC154791 protein - Xenopus laevis (African clawed frog), partial (90%)								
TC456286 homologue to U	Rep: Transmembrane protein 56-A -	temem56							
TC456376 homologue to U	Rep: Ubiquinol-cytochrome c reduct	uqcrh11							
TC457230 similar to UniRe	Rep: MGC89272 protein. - Xenopus tropicalis, partial (74%)								
TC457286 similar to UniRe	Rep: Vitellogenin-A2 precursor (VT(	vtga2		Y	Y			TRUE	TRUE
TC457517 UniRef100_UPI	Rep: Histone deacetylase 9 (HD9) (	hdac9			Y			TRUE	TRUE
TC457582 similar to UniRe	Rep: Serum amyloid P-component p	sap							
TC458492 UniRef100_Q7Z	Rep: Acaa2-prov protein - Xenopus	acaa2			Y			TRUE	TRUE
TC460552 homologue to U	Rep: Heat shock 10kDa protein 1 - X	hspe1		Y	Y			TRUE	TRUE
TC460601 UniRef100_Q66	Rep: MGC81975 protein - Xenopus laevis (African clawed frog), complete								
TC460762 similar to UniRe	Rep: LOC100049118 protein - Xenopus laevis (African clawed frog), partial (48%)								
TC460857 weakly similar to	Rep: Serine/threonine-protein kinas	sbk1							
TC461251 homologue to U	Rep: Transcription activator, effector binding - Burkholderia ambifaria MC40-6, partial (8%)								
TC461595 homologue to U	Rep: LOC100049136 protein - Xenopus laevis (African clawed frog), partial (98%)								
TC462321 similar to UniRe	Rep: Vitellogenin-A2 precursor (VT(	vtga2		Y	Y			TRUE	TRUE
TC462743 homologue to U	Rep: Vitellogenin B1 - Xenopus laev	vtgb1		Y				TRUE	TRUE
TC462923 UniRef100_Q7Z	Rep: Hnrpk protein - Xenopus laevis	hnrpk							
TC463468	vitellogenin (A1) [Xenopus laevis]	vtga1		Y				TRUE	TRUE
TC463837 homologue to U	Rep: MGC81523 protein - Xenopus laevis (African clawed frog), partial (98%)								
TC464539 similar to UniRe	Rep: Vitellogenin B1 - Xenopus laev	vtgb1		Y				TRUE	TRUE
TC464574 similar to UniRe	Rep: Krt8 protein - Xenopus laevis (African clawed frog), partial (30%)								
TC465314 UniRef100_UPI	Rep: Whirlin (Autosomal recessive (	dfnb31							
TC465972 similar to UniRe	Rep: Probable ATP-dependent RNA	dhx37			Y			TRUE	TRUE
TC466521 homologue to U	Rep: Basic transcription factor 3 - X	btf3							
TC466740 similar to UniRe	Rep: Zgc:136388 - Danio rerio (Zebrafish) (Brachydanio rerio), partial (18%)								
TC467277 homologue to U	Rep: Calpain - Xenopus laevis (Afric	capn							
TC467283 homologue to U	Rep: LOC431926 protein - Xenopus laevis (African clawed frog), partial (49%)								
TC468263 similar to UniRe	Rep: MGC68737 protein - Xenopus laevis (African clawed frog), partial (28%)								

TC468342 weakly similar t	Rep: Predicted protein - Nematostella vectensis (Starlet sea anemone), partial (48%)								
TC469090 homologue to U	Rep: Vitellogenin-A2 precursor (VT	vtga2		Y	Y			TRUE	TRUE
TC469714 homologue to U	Rep: LOC494839 protein - Xenopus laevis (African clawed frog), partial (25%)								
W6E858	Maternal effect lethal-28 OS=Xenop	mel28							
W8W3R8	Arid5B short isoform (Fragment) OS	arid5b			Y			TRUE	TRUE
zeinaSSns_comp169402_c	len=231								
zeinaSSns_comp30958_c0	len=202								
zeinaSSns_comp338451_c	len=210								
zeinaSSns_comp339972_c	len=245								
zeinaSSns_comp352393_c	len=531								
zeinaSSns_comp352424_c	len=472								
zeinaSSns_comp360359_c	len=3271								
zeinaSSns_comp375014_c	len=695								
zeinaSSns_comp375133_c	len=290								
zeinaSSns_comp377268_c	len=241								
zeinaSSns_comp377647_c	len=449								
zeinaSSns_comp378203_c	len=201								
zeinaSSns_comp381133_c	len=1342								
zeinaSSns_comp381925_c	len=669								
zeinaSSns_comp382047_c	len=854								
zeinaSSns_comp382686_c	len=1587								
zeinaSSns_comp382744_c	len=1626								
zeinaSSns_comp382833_c	len=2746								
zeinaSSns_comp383021_c	len=1221								
zeinaSSns_comp383101_c	len=1454								
zeinaSSns_comp383886_c	len=1598			Y				TRUE	TRUE
zeinaSSns_comp384061_c	len=4918								
zeinaSSns_comp385518_c	len=534								
zeinaSSns_comp385894_c	len=4516								
zeinaSSns_comp386267_c	len=6035								
zeinaSSns_comp386428_c	len=2428								
zeinaSSns_comp386578_c	len=1273								
zeinaSSns_comp386803_c	len=4262								
zeinaSSns_comp386979_c	len=2448								
zeinaSSns_comp387272_c	len=1781			Y				TRUE	TRUE
zeinaSSns_comp387330_c	len=1937								
zeinaSSns_comp387346_c	len=1947								
zeinaSSns_comp387412_c	len=1966								
zeinaSSns_comp387425_c	len=3248								
zeinaSSns_comp387445_c	len=401								
zeinaSSns_comp387680_c	len=567								
zeinaSSns_comp388100_c	len=1955								
zeinaSSns_comp388330_c	len=1496								
zeinaSSns_comp388513_c	len=2561								
zeinaSSns_comp388546_c	len=691								
zeinaSSns_comp388555_c	len=567								
zeinaSSns_comp388587_c	len=2100								
zeinaSSns_comp388666_c	len=2890								
zeinaSSns_comp388699_c	len=2647								
zeinaSSns_comp388845_c	len=3172								
zeinaSSns_comp388890_c	len=1570								
zeinaSSns_comp388960_c	len=2747								
zeinaSSns_comp389160_c	len=2130								
zeinaSSns_comp389334_c	len=1094								
zeinaSSns_comp389457_c	len=2398								
zeinaSSns_comp389497_c	len=5283								
zeinaSSns_comp389539_c	len=5153								
zeinaSSns_comp389585_c	len=3397								
zeinaSSns_comp389640_c	len=4092								