Linkage Group	Position (cM)	LOD	PVE	Effect size	95% Baysean credible interval (cM)	Zebrafish chromosome (Zv9)
VAB (N = 227)			(Total: 17.3)	(0 - 7.68)		
2	23	2.38	4.1	+1.00	20.0 - 90.8	Ch5 (4.7 - 64.6) Ch20 (0.6 - 53.8) Ch24 (12.9 - 34.5)
17	49	5.69	9.6	+1.17	45.0 - 55.0	Ch8 (0.7 - 55.3)
Locomotor acitivity (N = 58)			(Total: 43.6)	(8.8 - 4371.0)		
3	42	5.73	32.5	-920.2	39.0 - 44.0	Ch4 (4.1 - 60.2)
22	41	3.42	17.6	+1604.2	37.0 – 44.0	Ch7 (27.8 - 68.4) Ch8 (23.1 - 52.6)

Additional file 4. A summary of the location and effect size of significant QTLs for foraging- and sleep-related traits.

The number of F_2 and F_3 individuals used (N), LOD is the log of odds ratio, and PVE is the percentage of phenotypic variance explained. The summed PVE of all QTL are shown at the top row of each trait (at Total:). Effect size and direction (positive and negative) of QTL refers to the magnitude of shift between homozygotes of surface fish alleles and cavefish alleles. The numbers in parentheses indicate the ranges of phenotypes. The syntenic regions of the zebrafish genome are indicated as chromosome number (syntenic region in mega base pairs, Mbp). Note, PVE at LG 22 QTL for locmotor activity can be inflated because of Beavis effect yet PVE at LG 3 is above detectable level (calculated with qtlDesign; [1, 2])

Linkage Group	Candidate gene	Expression pattern (zfin)	Gene product function
LG 2, 23 cM Syntenic to zebrafish ch 5 (4.7 - 64.6 Mb), 20 (0.6 - 53.8 Mb), 24 (12.9 - 34.5 Mb)	eya1 (eyes absent homolog 1)	Placode (nasal, otic, lateral line, trunk muscle), mature lateral line	A transcription factor,possibly maintain developmental plasticity [3]
	cdh2 (N-cadherin2, type 1)	Posterior lateral line primordium, neuromasts, brain, retina, lens, olfactory epithelium, myotome, somite,	Mediating cell adhesion through hemophilic interaction. CDH2 is involved in multiple aspects of development including the lateral line formation [4–6]
	disp1 (Dispatched 1)	Neuroectoderm, oral/pharyngeal ectoderm	Regulating the release of hedgehog protein. Involved in craniofacial formation through organizing the differentiation of neural crest cells [7]
	pcsk5a (proprotein convertase subtilsin/kexin type 5a)	Neuromasts, otic vesicle, central nervous system, liver, intestine.	A serine proteinase facilitating tissue- and substrate-specific processing of protein precursors. Involved in neuromast development and neuromast-dependent behavior [8]
	tbx1 (T-box 1)	Otic vesicle anterior lateral plate mesoderm, heart, pharyngeal arch	A transcription factor, mediating retinoic acid and hedgehog signaling so that controls otholis development [9].
	vgll2a (vestigial-like 2a)	Ventral region of forbrain, notochord, pharyngeal	A transcription co-factor, contributing pharyngeal formation by regulating neural crest cell survival and cartilage development [10].
LG 17, 49 cM Syntenic to zebrafish ch 8 (0.7 - 55.3 Mb)	gnat2 (guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 2)	Eye, retina, pineal gland	A G-protein coupled photoreceptor. null mutation makes the cone insensitive to moderate light intensity [11].
	ptch1 (patched 1)	Retina, ciliary marginal zone, forbrain, hindbrain, hypothalamus, otic vesicle, otic epithelium, gut	Hedgehog negative regulator. Null mutation causes over-proliferation of retina or no phenotype [12].

LG 3, 42 cM Syntenic to zebrafish ch 4 (4.1 - 60.2 Mb)	slc6a1l (solute carrier family 6 (neurotransmitter transporter, GABA), member 1, like)	N/A	N/A, GABAnergic system inhibit the activity of arousal system including lateral hypothalamus orexin neuron [13].
LG 22, 41 cM Syntenic to zebrafish ch 7 (27.8 - 68.4 Mb), 8 (23.1 - 52.6 Mb), 11 (43.8 - 46.5 Mb)	chrna7 (cholinergic receptor, nicotinic, alpha 7)	Hindbrain, retina	A subunit of Nicotinic acetylcholine receptor mediating sleep – arousal transition, and mutation causes epilepsy [14, 15].
	drd4b (dopamine receptor D4b)	Branchial arch, diencephalon, mid-brain, otic vesicle, spinal cord, telencephalon, tegmentum	Dopamine receptor mediates locomotor activity [16].
	gli2b (GLI family zinc finger 2b)	Cerebellum, diencephalon, dorsal thalamus, hindbrain, optic tectum	A transcription factor contributing cell differentiation expressed higher in oligodendrocyte in the wake state [17].
	tp53i11a (tumor protein p53 inducible protein 11a)	N/A	N/A, tp53 (expressed in brain pancreas, eye, optic tectum, gill, gut) is associated with narcolepsy [18].

Additional file 4 continue

Candidate genes were selected based on their expression pattern, potential contribution to the foraging and neuromast development (VAB QTL), or sleep and/or locomotor activity (Locomotor acitivity QTL). Genes whose mutations impair many tissues (for example, *mcm3*) are excluded. The number of genes after the BioMart filter was 287 for LG2, 73 for LG3, 188 for LG17, and 130 for LG22.

Additional file 4
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