Table 3. Summary of *in situ* hybridization

		Distribution of hybridization signals in MBs†						
Gene	Probe*	(-)	(±)	(+)	(++)	No. of MBs	Total point‡	Rank‡
CG4842	GH15220	96.7	3.3	0.0	0.0	30	3.3	D
CG13244	GH27987	100.0	0.0	0.0	0.0	42	0.0	D
CG13297	RE64858	66.7	33.3	0.0	0.0	24	33.3	C
CG32473	RE62048	68.3	0.0	31.7	0.0	60	63.4	B
Rab10	LD39986	3.1	15.6	43.8	37.5	32	215.7	A
CG12866	Genomic PCR	83.3	16.7	0.0	0.0	24	16.7	D
CG5476	RE59605	23.3	10.0	46.7	20.0	30	163.4	A
CG18266	GH11218	63.3	23.3	6.7	6.7	30	56.8	B
Kif3C	GH04118	63.2	10.5	7.9	18.4	38	81.5	B
CG13312	Genomic PCR	60.7	28.6	10.7	0.0	28	50.0	B
CG2070	LP06328	35.3	26.5	26.5	11.8	34	114.9	A
CG2196	Genomic PCR	29.4	17.6	26.5	26.5	34	150.1	A
CG13350	SD03057	81.3	12.5	6.3	0.0	32	25.1	C
CG11164	RE50056	100.0	0.0	0.0	0.0	32	0.0	D
CG14313	Genomic PCR	87.5	0.0	12.5	0.0	56	25.0	C
CG13566	Genomic PCR	92.6	7.4	0.0	0.0	27	7.4	D
CG32676	GH03394	69.2	3.8	15.4	11.5	26	69.1	B
Hr46	GH21112	36.0	0.0	20.0	44.0	50	172.0	A
Dhod	GH24729	81.2	0.0	18.8	0.0	80	37.6	C
CG14446	GM27257	62.9	0.0	37.1	0.0	62	74.2	B
CG2267	GH11073	28.9	10.5	13.2	47.4	38	179.1	A
CG3994	RE54080	90.0	10.0	0.0	0.0	30	10.0	D
CG15185	Genomic PCR	56.8	27.3	6.8	9.1	44	68.2	B

CG14014	RE73577	45.5	0.0	54.5	0.0	22	109.0	A
CG14628	Genomic PCR	94.7	5.3	0.0	0.0	38	5.3	D
CG3371	GH13810	85.5	0.0	14.5	0.0	62	29.0	C
CG3818	Genomic PCR	76.7	23.3	0.0	0.0	30	23.3	C
CG14911	Genomic PCR	38.5	26.9	34.6	0.0	26	96.1	B
CG4575	Genomic PCR	100.0	0.0	0.0	0.0	32	0.0	D
CG14460	Genomic PCR	100.0	0.0	0.0	0.0	30	0.0	D
CG10205	LP09070	100.0	0.0	0.0	0.0	26	0.0	D
fkh	RE03865	41.2	0.0	38.2	20.6	68	138.2	A
trio	GH01987	50.0	21.9	28.1	0.0	32	78.1	B
CG33143	Genomic PCR	80.0	6.7	3.3	10.0	30	43.3	C
CG13444	RE33441	82.1	0.0	3.6	14.3	28	50.1	B
CG7945	LD01950	37.5	0.0	62.5	0.0	32	125.0	A
jing	LD36562	45.3	0.0	54.7	0.0	86	109.4	A
CG6974	Genomic PCR	94.1	5.9	0.0	0.0	34	5.9	D
CG7846	LD24980	96.4	3.6	0.0	0.0	28	3.6	D
CG13716	Genomic PCR	84.4	12.5	3.1	0.0	32	18.7	D
CG12301	LD31322	73.8	0.0	26.2	0.0	42	52.4	B
CG4940	Genomic PCR	79.2	16.7	4.2	0.0	24	25.1	C
CG10505	Genomic PCR	96.9	0.0	0.0	3.1	32	9.3	D
CG31559	RE15313	33.3	66.7	0.0	0.0	30	66.7	B
CG6372	GH13022	80.6	0.0	19.4	0.0	36	38.8	C
CG31530	RE24196	9.4	0.0	15.6	75.0	32	256.2	A
Brf	LD32109	50.0	0.0	50.0	0.0	12	100.0	A
CG12744	GH03826	100.0	0.0	0.0	0.0	48	0.0	D

CG13604	LD48066	65.4	3.8	23.1	7.7	26	73.1	B
klg	GH05072	74.0	0.0	24.0	2.0	50	54.0	B
CG15057	Genomic PCR	93.3	6.7	0.0	0.0	30	6.7	D
RluA-1	RH09496	66.7	33.3	0.0	0.0	30	33.3	C
CG13159	RE25177	96.4	3.6	0.0	0.0	28	3.6	D
ey	pBSEyE10.1.1	33.3	0.0	31.3	35.4	48	168.8	A
CG17319	Genomic PCR	15.8	3.7	57.9	2.6	38	127.3	A
CG11178	LD19061	61.8	0.0	29.4	8.8	34	85.2	B
CG8412	RE17513	0.0	10.0	13.3	76.7	30	266.7	A
CG17221	RH24774	69.2	7.7	23.1	0.0	26	53.9	B
CG13176	RH05781	75.0	3.6	21.4	0.0	28	46.4	C
CG9296	RE06748	10.7	35.7	42.9	10.7	28	153.6	A
Hrb87F	GH05625	76.7	0.0	23.3	0.0	86	46.6	C
CG12253	LD32974	97.6	2.4	0.0	0.0	41	2.4	D
CG15579	Genomic PCR	97.1	2.9	0.0	0.0	34	2.9	D
CG13879	Genomic PCR	70.4	18.5	0.0	11.1	27	51.8	B
CG1234	LD35257	71.9	18.8	9.4	0.0	32	37.6	C
Itp-r83A	Genomic PCR	70.6	8.8	8.8	11.8	34	61.8	B
CG3983	AT23067	20.0	26.7	23.3	30.0	30	163.3	A
CG6083	AT02556	97.2	2.8	0.0	0.0	36	2.8	D
PP2A-B'	LD29902	38.9	0.0	19.4	41.7	36	163.9	A
Sema-1a	RE36155	41.2	8.8	11.8	38.2	34	147.0	A
elk	HL01061	56.7	0.0	43.3	0.0	30	86.6	B
Atg5	LD34980	94.1	5.9	0.0	0.0	34	5.9	D
CG4853	GH27815	92.9	0.0	0.0	7.1	28	21.3	C

Table 3. Summary of *in situ* hybridization

RN-tre	LD31492	66.7	0.0	33.3	0.0	96	99.9	B
Pkn	RH55776	7.7	0.0	11.5	80.8	26	265.4	A
CG10948	RE29010	81.0	0.0	19.0	0.0	58	38.0	C
Nep1	GH03315	50.0	0.0	36.7	13.3	60	113.3	A
CG5669	LD04007	58.8	0.0	11.8	29.4	34	111.8	A
CG10880	LD25288	94.1	5.9	0.0	0.0	34	5.9	D
CG13213	SD01170	40.9	0.0	59.1	0.0	22	118.2	A
CG10083	SD28142	100.0	0.0	0.0	0.0	32	0.0	D
CG14483	Genomic PCR	93.8	6.3	0.0	0.0	32	6.3	D
Rpb11	GM15177	92.6	0.0	7.4	0.0	54	14.8	D
Dp1	SD20908	58.6	0.0	35.7	5.7	70	88.5	B
mod(mdg4)	SD03001	57.9	0.0	42.1	0.0	76	84.2	B
CG5384	LD26251	43.3	16.7	10.0	30.0	30	126.7	A
tra2	RH39422	64.8	0.0	35.2	0.0	88	70.4	B
usp	LD09973	72.7	0.0	27.3	0.0	22	54.6	B
fra	RE61427	42.3	38.5	11.5	7.7	26	84.6	B
CG7328	RE49431	60.0	0.0	40.0	0.0	30	80.0	B
CG3305	RE72002	71.4	21.4	3.6	3.6	28	39.4	C
CG13004	AT03755	92.9	7.1	0.0	0.0	28	7.1	D
CG2915	SD12095	36.7	10.0	53.3	0.0	30	116.6	A
CG9839	LD40589	100.0	0.0	0.0	0.0	30	0.0	D
CG4287	GH08991	81.8	18.2	0.0	0.0	22	18.2	D
apt	LD45581	86.8	0.0	13.2	0.0	76	26.4	C
PHDP	RE20490	78.6	10.7	3.6	7.1	28	39.2	C
CG12252	SD01014	100.0	0.0	0.0	0.0	26	0.0	D

CG9248	Genomic PCR	75.0	22.5	2.5	0.0	40	27.5	C
Sara	LD33044	93.3	0.0	6.7	0.0	30	13.4	D

***Probe: cDNA clones used to generate complementary RNA probes for *in situ* hybridization. For genes with no EST clone, DNA template for *in vitro* transcription was directly generated by PCR from the genomic sequence (Genomic PCR). Existence-uncertain genes (CG14350 and CG16803) were not tested and excluded from the list. Kif3C was tested with a full-length EST clone.**

† Percent distribution of signal intensities in MBs. Hybridization signals in MBs are scanned by confocal microscopy and categorized into four grades: (-), no signal; (±), weak; (+), moderate; (++), strong. Right and left hemispheres are independently assessed. Note that hybridization signals were amplified with tyramin and exhibited variation among brains.

‡To evaluate expression levels and reflect the variation in signal intensities among samples, points were given based on signal intensities: zero for (-), one for (±), two for (+), and three for (++). Total point was calculated as the sum of (point x % value). Expression level of each gene was then ranked in four groups according to its total point. Rank A, ≥100; rank B, 50.0-99.9; rank C, 20.0-49.9; and rank D, 0-19.9. Because of signal variation, weak-to-moderate signals were occasionally detected even for D-rank genes. Conversely, negative brains were observed for A-rank genes at varying percentages.