



Supplementary Table 3. Characteristic of the two testis associated motifs TA1 and TA2 and their associated retrogenes. gene name, strand orientation, start position, P value as calculated by MEME, and expression information for the gene are given. Start position is reported in bold when the motif is part of a most conserved region as annotated in the UCSC Genome Browser. CDS: motif hits within a coding region.

Motif Logo	Gene Name	Strand	Start Location (Based on the TSS)	P value	cDNA/EST hits
	<i>CG17268</i>	-	-269 CDS	3.04E-07	AT LP
	<i>CG4264</i>	+	-964	4.51E-07	RH GM LD AT SD GH LP RE EN
	<i>CG9582</i>	-	-386	4.51E-07	AT
	<i>CG18290</i>	+	-799	5.73E-07	RE AT LP RH GH EC LD HL GM EK
	<i>CG17645</i>	+	81 CDS	7.17E-07	GH AT
	<i>CG31003</i>	-	-438	1.16E-06	AT GH
	<i>CG7768</i>	+	-694	1.16E-06	GM AT EC
	<i>CG5648</i>	+	-853	1.32E-06	AT
	<i>CG7542</i>	+	-833 CDS	1.41E-06	AT
	<i>CG4264</i>	+	1622 CDS	1.74E-06	RH GM LD AT SD GH LP RE EN
	<i>CG6255</i>	-	-388	1.86E-06	GH AT UT
	<i>CG2830</i>	-	113 CDS	2.23E-06	GH AT
	<i>CG5409</i>	+	-696	2.52E-06	EC AT
	<i>CG4264</i>	+	1741 CDS	2.52E-06	RH GM LD AT SD GH LP RE EN
	<i>CG9582</i>	+	-555	2.93E-06	AT
	<i>CG9573</i>	+	-34	3.08E-06	RE AT LP GH
	<i>CG14508</i>	+	-562	3.33E-06	AT
<i>CG4701</i>	-	-722	7.37E-06	AT	
	<i>CG31003</i>	+	-372	6.83E-08	AT GH
	<i>CG6050</i>	-	-683	6.83E-08	RH GM AT SD LP UT RE GH LD EK CK
	<i>CG17268</i>	+	-282 CDS	4.45E-07	AT LP
	<i>CG16988</i>	-	-772 CDS	4.45E-07	LD AT EK
	<i>CG12334</i>	+	-397	4.45E-07	AT EK EC
	<i>CG9582</i>	-	68 CDS	4.45E-07	AT
	<i>CG9436</i>	+	102	4.90E-07	LD AT SD RH RE GH EN EK
	<i>CG4706</i>	-	-449	9.47E-07	AT
	<i>CG2830</i>	+	-243	1.05E-06	GH AT
	<i>CG2512</i>	-	-901	3.14E-06	SD AT LD GH LP UT GM RH RE HL EK EC