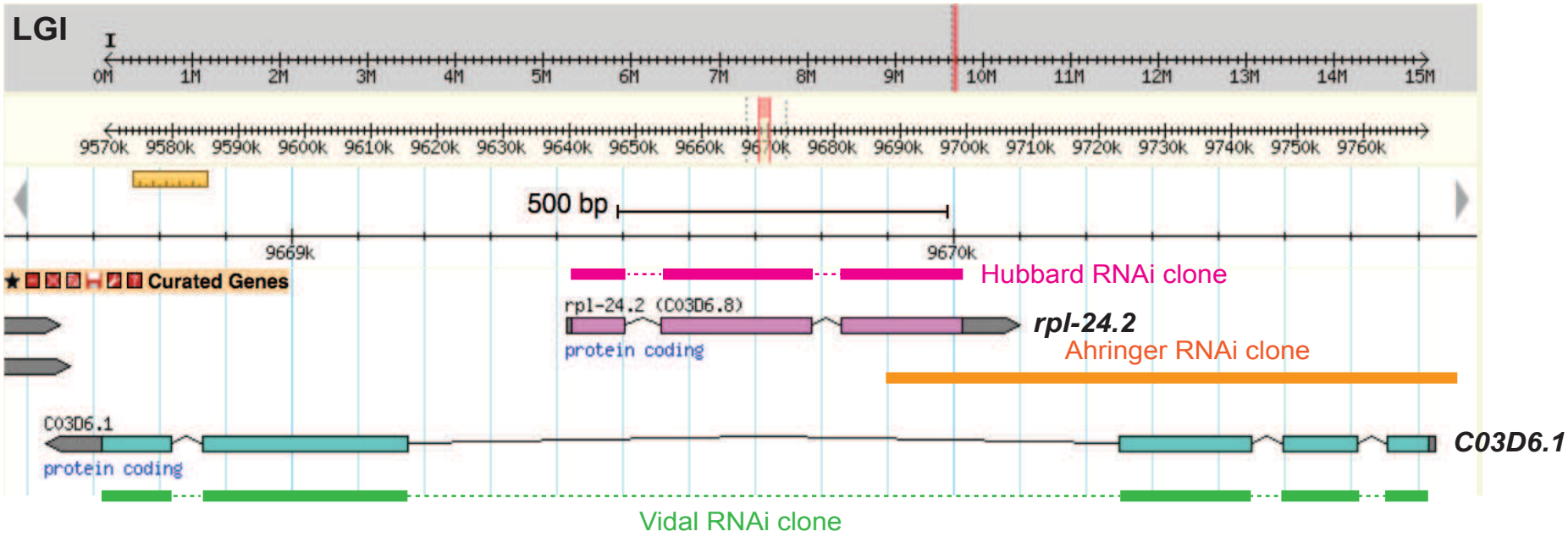

RNAi Clone				% of gonad arms				
Source	**ID**	**Target(s)**	**Type**	**No GSCs/ progenitors**	**Reduced pool**	**Normal pool**	**Other**	**n (gonad arms)**
Ahringer	sjj_C03D6.1	*rpl-24.2* *C03D6.1*	genomic	29	39.5	29	2.5	38
Vidal	mv_C03D6.1	*C03D6.1*	cDNA	7	88	4.3	0.7	148
Hubbard	pGC734	*rpl-24.2*	cDNA	31.6	54.1	1	13.2	154
Control	pL4440	-	empty	4.9	94.4	0.6	0	138

Figure S4. Separation of rpl-24.2 versus C03D6.1 RNAi.
The top panel shows the relevant region of LGI and the position of *rpl-24.2* within the second intron of C03D6.1, as well as the transcription orientation of each. The pink, orange and green lines represent the different RNAi clones used to target *rpl-24.2* and C03D6.1 (orange: genomic clone from the Ahringer library that was identified in the screen) or target mRNAs of the individual genes (pink: *rpl-24.2*-specific RNAi using Hubbard clone (pGC734); green: C03D6.1-specific RNAi using Vidal library clone). The table in the lower panel presents the results from each clone, with negative controls used. Data are represented as the percent of gonad arms that exhibit (1) no GSCs/progenitors, (2) a reduced progenitor pool, (3) a qualitatively normal progenitor pool, or (4) phenotypic abnormalities that precluded classification of the progenitor pool (Other). “n” represents the number of gonad arms assessed for each RNAi treatment. See Table S6 for statistical analysis.