Table S2. Redundant requirement of *lag-2* and *apx-1* for germline proliferation

Background and phenotype*	RNAi†	%	*n*‡
Wild type	Control	–	307
0	–	0	–
1-10	–	0	–
11-40	–	0	–
>50, <200	–	0	–
Wild type	*apx-1*	–	94
0	–	0	–
1-10	–	0	–
11-40	–	0	–
>50, <200	–	16	–
lag-2(q420ts)	Control	–	50
0	–	35	–
1-10	–	0	–
11-40	–	6	–
>50, <200	–	39	–
lag-2(q420ts)	*apx-1*	–	26
0	–	58	–
1-10	–	0	–
11-40	–	8	–
>50, <200	–	38	–
apx-1(or3)	Control	–	40
0	–	0	–
1-10	–	0	–
11-40	–	0	–
>50, <200	–	5	–
apx-1(or3)	*lag-2*	–	42
0	–	38	–
1-10	–	29	–
11-40	–	14	–
>50, <200	–	17	–

*Gonad arms were classified by the number of nuclei in the proliferative zone (nuclei with non-meiotic morphology, distal to the transition zone). This table reports all classifications of defects observed in the experiment shown in Fig. 3E, which presents only the most severe class (the '0' class or 'Glp-1-like phenotype' in which all germ cells display a nuclear morphology consistent with meiotic prophase or gametogenesis). The last category includes gonad arms in which more than 50 but noticeably fewer than the normal ~200 were observed. Remaining gonad arms were normal.

†For the *apx-1(RNAi)* and controls, to avoid embryonic lethality, RNAi was performed as follows: after rearing strains at 15°C, synchronous L1 larvae were transferred to RNAi plates at 20°C and fixed and stained with DAPI ~50 hours later. For the *lag-2(RNAi)* and controls, conditions were the same except that L4 animals were placed on the appropriate RNAi bacteria, and removed after 1 day, after which the progeny were scored the next day. Control RNAi was the L4440 vector.

‡Number of gonad arms counted.