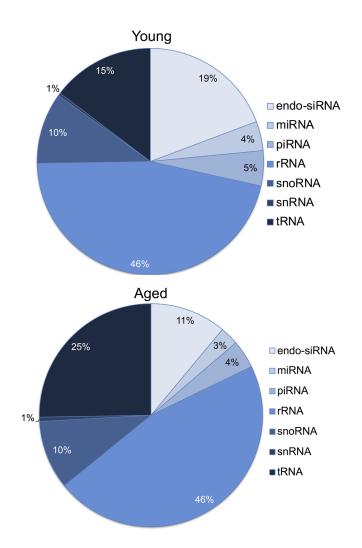
## **Supplementary Figures**



**Supplementary Figure S1. The small RNA signatures of young and aged oocytes.** Following filtering and normalisation, sncRNA reads were mapped to known and miRNA, endo-siRNA, piRNA, rRNA, snoRNA, snRNA, and tRNA fragments from RNAcentral. Pie chart was generated to illustrate the number of total sequences aligning to each small RNA category.

VTD01		2.0
KIFC1 KIFC5B	ATTCAAAAGTGGCGGGGTGTGGCCTGATTGGCCT GAAGTGCGTTGACTGCGCGGAGGTTGAAATTCAAAAGTGACTGGTGTGGCGGATTGGCTT	32 60
KIFCJB	******** * ******* * ******* *	00
KIFC1	GGCTCCTGGACAGCCTGGCTTCGGCGTTTTGCGGCGCGAGCCCTTGAGAG	82
KIFC5B	GGCCGATTGGCCTGGCGAATTGGCCTGGCTCCGACGTTTTGCGGCGCGAGCCCTTGAGAG	120
	*** * * ******	
KIFC1	GACGCGGGTCTCATCGTCCTGCCTGCCTGCCTTTGCACC-CTTTCTGTGCGGACCACCATG	141
KIFC5B	GACGCGGGTCTCGTCACCCTGCCTGCTGCCTTTGCATCCCTTCCTGTGCGGACCACCATG	180
	*********	
KIFC1	GACGTGCAGGCGCAGAGGCCACCTTTGTTGGAAGTGAAGAGGAACGTAGAACTGAAGGCA	
KIFC5B	GACGTGCAGGCGCAGAGAAAGGGAAGGGAAGGGAAGAGGAACGTAGAACTGAAGGCG	237
KIFC1		261
KIFCI KIFC5B		297
KIFCJD	******* *******************************	291
KIFC1	GACCAGATGGAGGATGCCTTGGAGCCTGCAAAGAAACGGACACGAGTCATGGGTGCAGTG	321
KIFC5B	GACCAGATGGAGGATGCCTTGGAGCCTGCAAAGAAACGGACACGAGTCATGGGTGCAGTG	357
	***************************************	
KIFC1	${\tt ACCAAAGTTGACACATCCCGTCCCAGAGGACCACTCCTCAGCACAGTGTCACAGACCCAG}$	381
KIFC5B	ACCAAAGTTGACACATCCCGTCCCAGAGGACCACTCCTCAGCACAGTGTCACAGACCCAG	417
	***************************************	
KIFC1	GGCCACACTGCAGCTCAGAAAGGCCCTAAGAAGACAGGACCTCGTGGGTGCTCTGCTATT	441
KIECOB	GGCCACAATGCAGCTCAGAAAGGCCCTAAGAAGACAGGACCTGGTGGGTG	477
KIFC1	GGTACAGTGCTGAGGAGCCAGAAGCCAGTTCCCGCTGCTCCTGCCCAGAAGCCTGGCACA	501
KIFC5B		
	***************************************	
KIFC1	${\tt TCCACTGCTCCTGTGGTGGTAGGGAAGAGAGCTGGCAAACGCCCTGCCTG$	561
KIFC5B		594
	***************************************	
KIFC1	GGCCAGTTGTGTGACCTCAATGAAGAGTTGAAACGCTATCGGGAGAAGACTCAAACGCTG	621
KIFC5B	GGCCAGTTGTGTGACCTCAATGAAGAGTTGAAACGCTATCGGGAGAAGACTGAAACGCTG	654
KIFC1	GAACTGGAGAACCGGGGTCTTCGGGAGCAACTCAGAGAGGTCCAGGAGCAGGCCACGACC	681
	GAACTGGAGAACCGGGGTCTTCGGGAGCAACTCAGAGAGGTCCAGGAGCAGGCCACGACC	714
1122 002	*****	/
KIFC1	CTGGGGACAGAGCGGAACACCCTGGAAGGGGAGCTGGCCAGTGTACGCAGCCGAGCTGAG	741
KIFC5B	${\tt CTGGGGACAGAGCGGAACACCCTGGAAGGGGAGCTGGCCAGTGTACGCAGCCGAGCTGAG}$	774
	***************************************	
KIFC1	CAGGACCAGCAGAGGCTGGAGACGCTGAGTGCCCGTGTCTTGGAGCTGGAGGAATGTCTG	
KIFC5B	CAGGACCAGCAGAGGCTGGAGACGCTGAGTGCCCGTGTCTTGGAGCTGGAGGAATGTCTG	834
KIFC1	GGTACCAGGGAAAGGCTGCTTCAGGAGCTTCAGGGAGAGCGGCTGCAATTGCAGGAGGAG	061
	GGTACCAGGGAAAGGCTGCTTCAGGAGCTTCAGGGAGAGCGGCTGCAATTGCAGGAGGAG	
KII COD	***************************************	FCO
KIFC1	CGGAGCACACTGAGCACCCAGCTGGAGGAGCAGGAGGAGGAGGAGGTTTCAGGCCACAGAAGCA	921
	CGGAGCACACTGAGCACCCAACTGGAGGAGCAGGAGGAGGAGGAGGTTTCAGGCCACAGAAGCA	
	***************************************	
KIFC1	${\tt GCTCTGTCAAGCAGCCAAGAAGAGGTGGTGTGTCTTCGGCAGAAGACTGAAGCCCAGGTG$	
KIFC5B	GCTCTGTCAAGCAGCCAAGAAGAGGTGGTGTGTCTTCGGCAGAAGACTGAAGCCCAGGTG	1014
WT DO1		1041
KIFC1 KIEC5B	ACCTTACTGGCTGAGCAAGGAGACCGGCTCTATGGGTTAGAGATGGAGCGGCGA <b>CGACTC</b> ACCTTACTGGCTGAGCAAGGAGACCGGCTCTATGGGTTAGAGATGGAGCGGCGGC <b>GACTC</b>	
NTE COD	ACCITACIONCIDACIANONONCODOCICIAIOGUIAGAGAIOGAGCOGCOGCOACIC	10/4

Supplementary Figure S2 (Part 1). mRNA sequence alignment of Kifc1 and Kicf5b. Location of siRNA targeting sites, 5' and 3' untranslated regions are as marked.

## RNA9867

KIFC1	<b>CACAACCAGCTGCA</b> GGAACTGAAGGGCAATATCCGGGTGTTCTGCCGCGTGCGCCCTGTC	1101	
KIFC5B	<b>CACAACCAGCTGCA</b> GGAACTGAAGGGCAATATCCGGGTGTTCTGCCGCGTGCGCCCTGTC **********	1134	
KIFC1	CTCGAAGGGGAATCCACTCCATCTCCTGGCTTCCTCGTGTTTCCTCCTGGCCCTGCTGGA	1161	
KIFC5B	CTCGAAGGGGAATCCACTCCATCTCCTGGCTTCCTCGTGTTTCCTCCTGGCCCTGCA	1194	
KIFC1	CCCTCTGATCCCCCGACGGGCCTTAGCCTCTCACGATCTGATGATCGGCGCTCCACCCTG	1221	
KIFC5B	CCCTCTGATCGCCCGACGGGCCTTAGCCTCTCACGATCTGATGATCGGCGCTCCACCCTG	1254	
KIFC1	ACTGGGGCCCCGGCCCCACTGTCCGCCATGATTTCTCCTTTGATCGGGTGTTCCCGCCG	1281	
KIFC5B	ACTGGGGGCCCCGGCACCCACTGTCCGCCATGATTTCTCCTTTGATCGGGTGTTCCCGCCG ***********************	1314	
KIFC1	GGAAGCAAGCAGGAGGAAGTGTTTGAGGAGATCGCCATGCTTGTCCAGTCAGCACTGGAT	1341	
KIFC5B	GGAAGCAAGCAGGAGGAAGTGTTTGAGGAGATCGCCATGCTTGTCCAGTCAGCACTAGAT **********************************	1374	
KIFC1	GGCTACCCTGTGTGCATTTTTGCCTATGGACAGACAGGCAGTGGCAAGACCTTCACTATG	1401	
KIFC5B	GGCTACCCTGTGTGCATTTTTGCCTATGGACAGACAGGCAGTGGCAAGACCTTCACTATG	1434	
KIFC1	GAAGGAGGGCCTAGGGGAGACCCCCCAATTGGAAGGGCTGATCCCTCGGGCCATGCGGCAT	1461	
KIFC5B	GAAGGAGGGCCTAGGGGAGACCCCCCAATTGGCAGGGCTGATCCCTCGGGCCATGCGGCAT ************************************	1494	
KIFC1	CTGTTCTCTGTGGCCCAGGAGATGAGCGGCCAGGGCTGGACATACAGTTTTGTGGCGAGT	1521	
KIFC5B	CTGTTCTCTGTGGCCCAGGAGATGAGCGGCCAGGGCTGGACATACAGTTTTGTGGCGAGT ***********************************	1554	
KIFC1	TACGTAGAGATCTACAATGAGACCGTTCGAGACCCTGCTAGCTA	1581	RNA9878
KIFC5B	TACGTAGAGATCTACAATGAGACCGTTCGAGACCC <b>TGCTAGCTACTGGGCCCCGCAA</b> GGGA	1614	<u>RNA9879</u>
KIFC1	CAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1641	
	CAAGGGGGGGGAGTGTGAGATCCGTCGGGCAAGCCCAGGAAGTGAGGAGCTTACTGTCACC CAAGGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC ***********		
	CAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1674	
KIFC5B KIFC1	CAAGGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC	1674 1701	
KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734	
KIFC5B KIFC1 KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761	
KIFC5B KIFC1 KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794	
KIFC5B KIFC1 KIFC5B KIFC1 KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821	
KIFC5B KIFC1 KIFC5B KIFC1 KIFC1 KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881	
KIFC5B KIFC1 KIFC5B KIFC1 KIFC1 KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881	
KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881 1914	
KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881 1914	
KIFC5B KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881 1914 1941 1974	
KIFC5B KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC1	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1794 1821 1854 1881 1914 1941 1974 2001	
KIFC5B KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1821 1854 1881 1914 1914 1974 2001 2034 2061	
KIFC5B KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1821 1854 1881 1914 1914 1974 2001 2034 2061	
KIFC5B KIFC1 KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1821 1854 1881 1914 1914 1974 2001 2034 2061 2094	
KIFC5B KIFC1 KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B KIFC1 KIFC5B	CAAGGGGGCGAGTGCGAGATCCGTCGGGGCAAGCCCAGGGAGTGAGGAGCTTACTGTCACC **********************************	1674 1701 1734 1761 1821 1854 1881 1914 1914 1974 2001 2001 2034 2061 2094 2121	

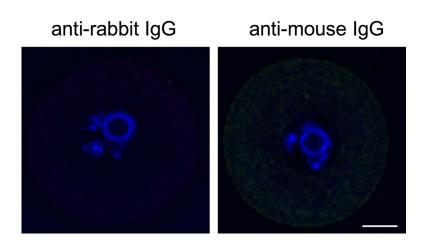
Supplementary Figure S2 (Part 2). mRNA sequence alignment of Kifc1 and Kicf5b. Location of siRNA targeting sites, 5' and 3' untranslated regions are as marked.

	2181 2211
	2237 2267
	2297 2320
	2330 2380
** * ***** ** **** *****	2300
KIFC1	2330
KIFC5B TTTGCCTGAGTGTATATGCATGCACCATGTGCATGTCTCCTGCTCCAGTGAGTTCAGAAC	2440
KIFC1	2330
	2500
KIFC1	2330
KIFC5B <mark>AGTCAGTGCTCTTAACCGCCCAGCCATCTTCCCAGCCCGGCCCTTGTTACAGCTCTAAAC</mark>	2560
	2330
KIFC5B <mark>GGTTTTATTAACTTAACGGTTTTAGCTGCCAAAGGAAGGTATTGTAAATAAA</mark>	2620
KIFC1 2330 KIFC5B GCACGTA 2627	
3' UTR	

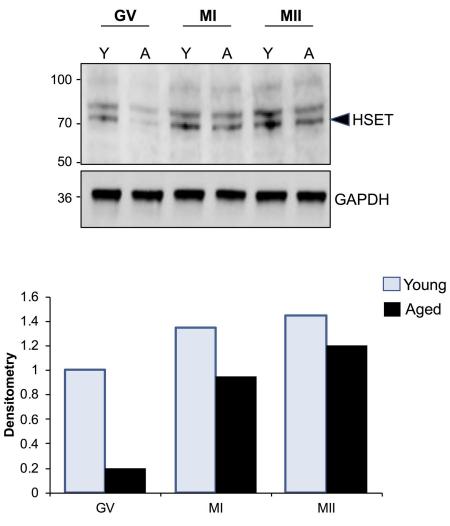
Supplementary Figure S2 (Part 3). mRNA sequence alignment of Kifc1 and Kicf5b. Location of siRNA targeting sites, 5' and 3' untranslated regions are as marked.

KIFC1 KIFC5B	MDVQAQRPPLLEVKRNVELKAALVKSSSRVPLSASRLKRGPDQMEDALEPAKKRTRVMGA MDVQAQRKG-REGKRNVELKAALVKSSSRLPLSASSLKRGPDQMEDALEPAKKRTRVMGA ****** * * **************************	
KIFC1 KIFC5B	VTKVDTSRPRGPLLSTVSQTQGHTAAQKGPKKTGPRGCSAIGTVLRSQKPVPAAPAQKPG VTKVDTSRPRGPLLSTVSQTQGHNAAQKGPKKTGPGGCSAVGTVLRSQKPAPAAPA-KPG ************************************	120 118
KIFC1 KIFC5B	TSTAPVVVGKRAGKRPAWDLKGQLCDLNEELKRYREKTQTLELENRGLREQLREVQEQAT TSTAPVVVGKRAGKRPAWDLKGQLCDLNEELKRYREKTETLELENRGLREQLREVQEQAT ************************************	180 178
KIFC1 KIFC5B	TLGTERNTLEGELASVRSRAEQDQQRLETLSARVLELEECLGTRERLLQELQGERLQLQE TLGTERNTLEGELASVRSRAEQDQQRLETLSARVLELEECLGTRERLLQELQGERLQLQE **********************************	240 238
KIFC1 KIFC5B	ERSTLSTQLEEQERRFQATEAALSSSQEEVVCLRQKTEAQVTLLAEQGDRLYGLEMERRR ERSTLSTQLEEQERRFQATEAALSSSQEEVVCLRQKTEAQVTLLAEQGDRLYGLEMERRR *********************************	300 298
KIFC1 KIFC5B	LHNQLQELKGNIRVFCRVRPVLEGESTPSPGFLVFPPGPAGPSDPPTGLSLSRSDDRRST LHNQLQELKGNIRVFCRVRPVLEGESTPSPGFLVFPPGPAGPSDRPTGLSLSRSDDRRST ***********************************	360 358
KIFC1 KIFC5B	LTGAPAPTVRHDFSFDRVFPPGSKQEEVFEEIAMLVQSALDGYPVCIFAYGQTGSGKTFT LTGAPAPTVRHDFSFDRVFPPGSKQEEVFEEIAMLVQSALDGYPVCIFAYGQTGSGKTFT ***********************************	420 418
KIFC1 KIFC5B	MEGGPRGDPQLEGLIPRAMRHLFSVAQEMSGQGWTYSFVASYVEIYNETVRDLLATGPRK MEGGPRGDPQLAGLIPRAMRHLFSVAQEMSGQGWTYSFVASYVEIYNETVRDLLATGPRK ********** **************************	480 478
KIFC1 KIFC5B	GQGGECEIRRASPGSEELTVTNARYVPVSCEKEVEALLHLAHQNRAVAHTAQNKRSSRSH GQGGECEIRRASPGSEELTVTNARYVPVSCEKEVEALLHLAHQNRAVAHTAQNKRSSRSH *****	540 538
KIFC1 KIFC5B	SVFQLQISGEHAARGLQCGAPLNLVDLAGSERLDPGLHLGPGERDRLRETQAINSSLSTL SVFQLQISGEHAARGLQCGAPLNLVDLAGSERLDPGLPLGPGERDRLRETQAINSSLSTL *********************************	600 598
KIFC1 KIFC5B	GLVIMALSNKESHVPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRFASK GLVIMALSNKESHVPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRFASK ************************************	
KIFC1 KIFC5B	VNQCVIGTAQANKK 674 VNQCVIGTAQANKK 672 ******	

Supplementary Figure S3. Protein sequence alignment of Kifc1 and Kicf5b.



**Supplementary Figure S4. Antibody specificity**. Primary antibodies were substituted with the appropriate concentration of either anti-rabbit (red) or anti-mouse (green) IgG in negative control groups for immunocytochemistry. Oocytes were counterstained with the nuclear stain Hoechst 33342 (blue) and viewed using confocal microscopy. Scale bar =  $20 \mu m$ .



**Supplementary Figure S5. Anti-HSET immunoblot in young and aged oocytes.** Immunoblotting with anti-HSET antibodies revealed a predominant band at the appropriate molecular weight of approximately 74 kDa in cell lysates prepared from isolated GV, MI and MII stage oocytes of young (Y) and aged (A) animals. Densitometric analysis of the labeling intensity of the HSET band relative to that of the GAPDH loading control, revealed an age-dependent decrease in the relative abundance of HSET in lysates of aged GV, MI and, to a lesser extent, MII stage oocytes. This experiment was repeated once with each lane being loaded with total protein lysates prepared from the equivalent of 100 oocytes (i.e. ~ 2  $\mu$ g protein / lane).