

**Supplementary table S1: Primer sequences and locations**

Gene	BS-seq (FF)	BS-seq (RV)	Location	Size	Start	Stop	TSS	TSS distance (5')	TSS distance (3')
<i>PIWIL1</i>	GTTTGCGGGGTAGTTAATGAG	ACCTAACACCTCAACCTAACCC	chr12:130,822,386-130,822,640	255	130,822,386	130,822,640	130822433	-47	207
<i>PIWIL2</i>	TATAGGGAATTTGTTGGAAAGG	CCCTACCAAAAATCTATCTCCT	chr8:22,132,691-22,133,201	511	22,132,691	22,133,201	22132810	-119	391
<i>TDRD1</i>	TTGGAAAAATTTGGAAGATTTT	ACAAAATCCAAATCTCCTCTC	chr10:115,938,773-115,939,337	565	115,938,773	115,939,337	115939029	-256	308
<i>TDRD9</i>	ATATATAGGGGTTGTTAYGGAA	TACACCTCCCTAACC	chr14:104,394,513-104,394,971	459	104,394,513	104,394,971	104394817	-304	154

Gene	Pyro-seq (FF)	Pyro-seq (RV)	Sequencing primer	Size	Start	TSS	TSS distance (5')
<i>PIWIL2</i>	ATGGGTTAATTAGATAGTTTGTGTTTGTGA	AACCCACATACTCCAAAACCAATTC	AATTAGATAGTTTGTGTTTGTGAA	106	22,132,759	22132810	-51
<i>TDRD1</i>	AAGGAATTTTTGAGTTTGAATTAGAGTA	ATACAAACCTCTCCCTCCCCTATA	TTGTAATTAGAGTATAAGTTGTTT	296	115,938,961	115939029	-68

BS-seq (bisulphite-sequencing), Pyro-seq (pyro-sequencing), FF (forward primer), RV (reverse primer), TSS (transcription start site)