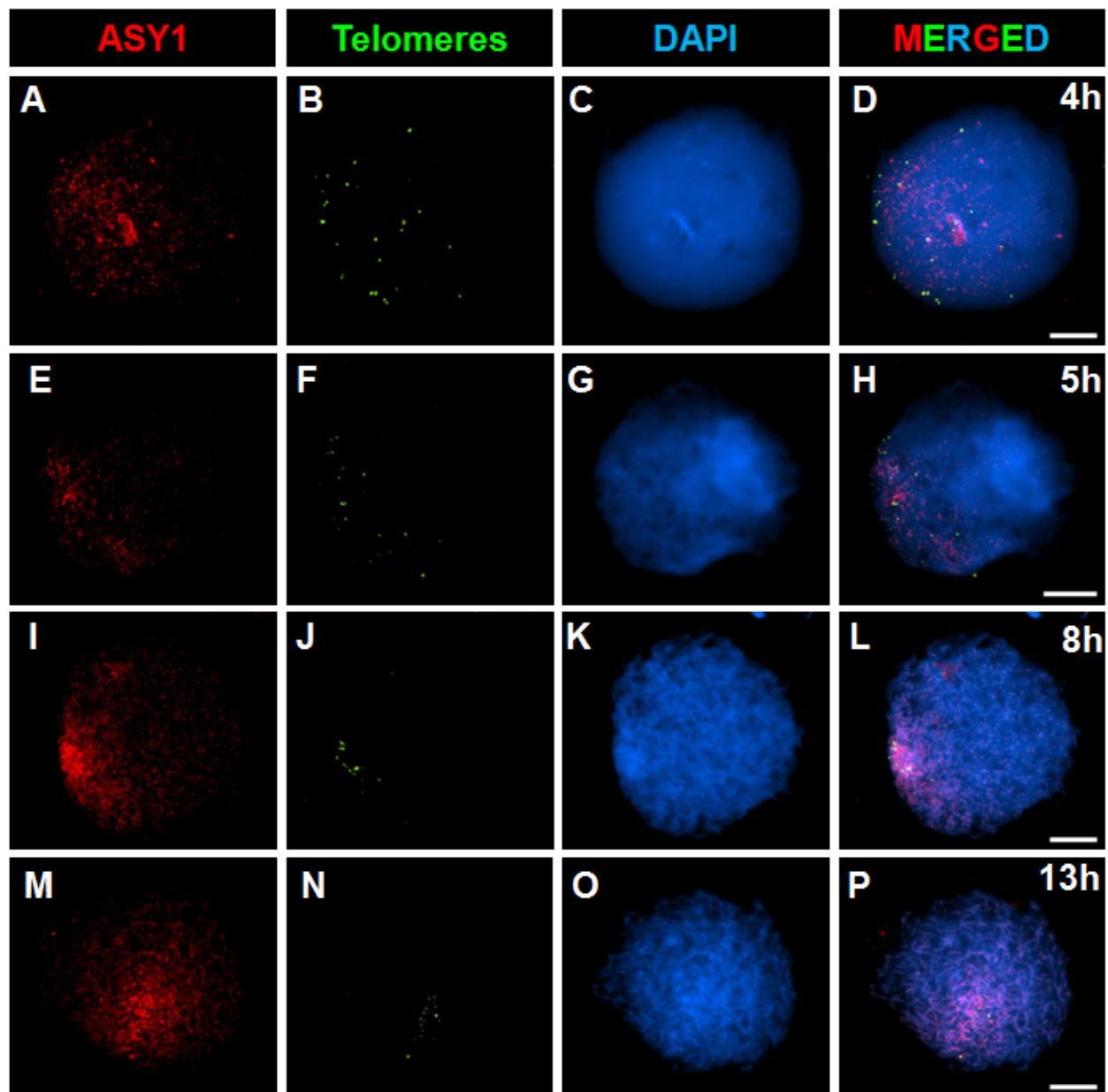


ASY1, positives = 436/605 (72%)		RAD51, positives = 317/343 (92%)	
AtASY1 HvASY1	MAQKLKEAITEQDSSLTRNLLRRAIFNISYIRGLFPEKVFNDSKVPALDMKIKKLM MAQKLKEAITEQDSSLTRNLLRRAIVNISYIRGLFPEKVFNDSKVPALMKIKKLM ****:*****:*****:*****:*****:*****:*****:*****:*****:*****:	AtRAD51 HvRAD51	MITIMEQRNNQNAVQQDDETE-QHGPFFVQLQLAGIASVDKKLRLDAGLCTVEGVAYTP MSSAAHQKA AAAAFVEEEAGEHGPFPIEHLQASGIAAVDVVKLKDAGLCTVESVAYSP *: : : * . : : * : * : * : * : * : * : * : * : * : * : * : * : * :
AtASY1 HvASY1	PMDAESRRLIDWMERKGVYDALQRKYLKTLMSICETVDGPMIEEYSFSFSYSDSDSQDV PMDFESRRLIDWMERKGVYDALQRKYLKTLFCICKEEGFSMIEEYAFSFSYFNTNGEZWV ****:*****:*****:*****:*****:*****:*****:*****:*****:*****:	AtRAD51 HvRAD51	RKDLLQIKGISEAKVDKIMAEASKVPLGFTSATQLHQAQRLIEIQTGTSRSRELDKLG RKDLLQIKGISEAKVDKIMAEASKVPLGFTSATQLHQAQRLIEIQTGTSRSRELDKLG *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:
AtASY1 HvASY1	MNINRTGNKKNGGIFN-STADTPNQMRSSACKMVRTLQVLMRTLDKMPDERTIVMKL MNINRTGNKKNGGIFN-STADTPNQMRSSACKMVRTLQVLMRTLDKMPDERTIVMKL ****:*****:*****:*****:*****:*****:*****:*****:*****:*****:	AtRAD51 HvRAD51	IETGSITELYGEFRSGKTLQLCILCVCITCQLPMDQGGGEGKAMYIDAEGTFRPQRLLQIAD IETGSITELYGEFRSGKTLQLCILCVCITCQLPMDQGGGEGKALYIDAEGTFRPQRLLQIAD *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:
AtASY1 HvASY1	YDVTIPPEVPPPFPGCTEDAEAQWWTNPLRMIGNVNSKHLVLTLLKVRVSVLDPCEDE YDVTIPPEVPPPFPGCTEDAEAQWWTNPLRMIGNVNSKHLVLTLLKVRVSVLDPCEDE ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtRAD51 HvRAD51	RFGLNGADVLENVAYARAYNTDHQSRLLLEAASMIMETRFLALIVDSTSATALYRTDFS RFGLNGADVLENVAYARAYNTDHQSRLLLEAASMIMETRFLALIVDSTSATALYRTDFS *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:
AtASY1 HvASY1	DDMQDDGK81GPDSVHDPSBDSSEISQTCQENFIVAVPEVKQDDGEVEDDNTDQP/ ANSDDDRMMLSLGRSEDDHDDFTDT-EVPRSEVDYRVVAPNDNGNRQSGTNSDEDETQAJ ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtRAD51 HvRAD51	ELSAQMHAKLFLRSLOKLADEFVGAVWLTINQVVAQVGDGSALFAGPKFPIGGNMIAHAT ELSAQMHAKLFLRSLOKLADEFVGAVWLTINQVVAQVGDGSALFAGPKFPIGGNMIAHAT *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:
AtASY1 HvASY1	ENEQCLARVKDWINSRHLTDILETLANFPDISIVLSEEIMDQVLTEGVLSKTKGKDMY HEELTQAQRVAKCSGDMGTVNADSNLPNVDIEMEDILERLLKGGLLSRAGKDGY ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtRAD51 HvRAD51	TTRALRKGRAEERICKVISSPCPLPEAERAFQISTEGVITDCRD TTRALRKGRAEERICKVISSPCPLPEAERAFQISTEGVITDCRD *****:*****:*****:*****:*****:*****:*****:*****:*****:*****:
AtASY1 HvASY1	KKRDTPESEFTFVKEEAD-GQISPGKSVAPEDLYM(KALYH83LPWVTVITLHNMLD VNKVIDSKTPYKKEVATHNVSPTEGTQNNDGDLIMYKALYH83LPWVTVITVAKLQGKLDG ****:***:***:***:***:***:***:***:***:***:***:***:***:***:		
AtASY1 HvASY1	EANQTAVRKLMRMTQEGYVEAASSNRLGKRVHSSLTEKKLNNEVRKVLATDDMDVDT EANQSTVRKLMRMTQEGYVEAASSNRLGKRVHSSLTEKKLNNEVRKVLATDDMDVDT ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	ALGLDTTYKQHYHLSAAAAATIKHIEAEKGIVVINTNHSLTVFNGSFDMHNIADTSVENLE ALGLDTTYKQHYHLSAAAAATIKHIESEKGIVVINTNHSLTVFNGSFDMHNIADTSVENLE *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtASY1 HvASY1	TINKINGPD-----AKVTADVSTCGGIHSIGSDFTIRTKGRSGGMQNGSVLSEQTISK TNARPAECORDHMETDQEMDKDGSTNTGRFSVQSDLTTRRELPGGGGGNNKDPRTF3 ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	LIDPFHINALLGTGSNKKRSLFQMFKTTKTAGGTRLRLRANLQLPKDIDETINTRLCLDELM IIDPLHTELWGSNKKRSLFQMFKTTKTAGGTRLRLRANLQLPKDIDETINTRLCLDELM *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtASY1 HvASY1	AGNTPISNKAQPAASRESPAVTHGGAVKAEATTNCQASQDSRGRKTSMVREPIPLQYSKRQ N-----REPATSLESGULGQTRKSLAGNESMCTPDKRTEKTSMVKEPILQQLVQRQ ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	SNEQLFGGLSQVLRKFPEETDRLVCHFCFKPKVKEAVIGFENTRKSQSNMIIILLKTA SNEQLFGGLSQVLRKFPEETDRLVCHFCFKPKVKEAVIGFENTRKSQSNMIIILLKTA *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtASY1 HvASY1	RSQAN KSVVQ	AtMSH4 HvMSH4	LDALPILAKVLDAKCFLLANLVNKYKSVCENDRYASIRKIGIVEDDVVLHARPVFARTQQ LDAPIFLSKVLYKGANSFLQNLQYOTICENPKYGSRMKRIKREVIDEYIHSRAPFVACTQQ *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
ZYP1, positives = 282/431 (65%)		AtMSH4 HvMSH4	CFALKAGIDGFLDIARRTFCDSEIAHNLASKYKREEFNLPNLKLFPNRLRQGFFFRIPOKE CFALKAGIDGFLDIARRTFCDSEIAHNLASKYKREEFNLPNLKLFPNRLRQGFFFRIPOKE *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	MDTLESVRTSEDKGKESIJKLSSLEIESKOKYKEKLOADAQRQVGELETQKESESHOLQ -QKLLDEDSSLAEQNKEELLQKTLKLESDNQELLGRMQSVLDEKNSDAEHLSEIAKRDQQ ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	VQGKLPNKFQTVVKGKGNHICSSLELASLNRNKSAAEGCFIRTECTCLEAIMDAREDIS ITEKLPNKFQTVVKGKGNHICSSLELASLNRNKSAAEGCFIRTECTCLEAIMDAREDIS *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	ADLILAKEVNQLOTTIEEKGHLLQCNNEKNINQOIIKDKELLATACTLAEAKQYDLM VTDQEKGKISELRSVLDEKEOLYISSVEREKSLSKQLOIQAOSLAATECQLTEAKQHDLI ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	ALTLILAEVLCLLDIMIVNSFAHTISTKPVDRYSRPELTDSLGLAIDAGRPHILESHINDFV ILTLILAEVLCLLDIMIVNSFAHTISTKPVDRYSRPELTDSLGLAIDAGRPHILESHINDFV *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	LESKOILELRSHLKELQSNRQDAINEIRRKYDEVEKGHEINSEKVKVEKILKELSTKYDGL LOGKESKHLKELQSNRQDAINEIRRKYDEVEKGHEINSEKVKVEKILKELSTKYDGL *****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	SNSIFMESEATNMVVMGPNMSKGKSTYLLQVCLVLLQVLAQIGCYPAQFASLRVDRIFTM PNNIFLESEASNMVVLMGPNMSKGKSTYLLQVCLVLLQVLAQIGCYPAQFASLRVDRIFTM *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	SDCKEESKQRLITIIEQEHSSRLIINREEEHESKELNLIKAKYDQELRQNOIQAENELKERL LENKRESERCILRKEEHAANVARIQDNEKESTIRAHKEELQIRSQGENELKERL ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	GTMDELNSTNSTMTEMRETAFIMQNVTNRSLSIVMDDEL GTMDELNSTNSTMTEMRETAFIMQNVTNRSLSIVMDDEL *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	ALKSEHDAQLAKGFKCQYEDDCKKLQLEELLQKRRKEERQRALVOLQWKVMSDNPQEEQEVN LRLQHEAQIAQTKVNIRHEDDCQKLQDELELQKSRKEEKORALQJLQWVKGMEQSQVQDQEVN ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMSH4 HvMSH4	MLH1, Positives = 218/267 (82%)
AtZYP1b HvZYP1	SNKQYSHSSVVKVESLIGG-----NKGSEHITTEPFSVKAQVTVSVNLLKEATPNKGHSK SKGRRDPYVREKESQLOLPGPGPGETKRKNANISGVHISPISNVLRVKEAQSDVNPNSK ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMLH1 HvMLH1	LETVRNCITYGMADDVFALQVYNTHLYLANVNLSKELMYQQTLRRAFHNAIQLSDPAP FDIVTRNCITYGMADVFALQVYNTHLYLANVNLSKELMYQQTLRRAFHNAIQLSDPAP *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	VTHREYEVEITNNGRIPKRNKRTRQTTFMQEPQRTRLTFPKLMTPTIIAKETAMADHPHSA VTHREYEVEITANGKIKRTRKTKTSTVGMPEPNQMS-LQNTADKWDVTKTRVVAGSRRPFA ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMLH1 HvMLH1	LSELILLLAKKEEDLDPGNDTKD-DLKERAIAEMNTIELKEGAEMLEEYFSVHIDSSANLRL LLEILRMLAKD--DEMSDVMNEKEKLEIAEVNTIELKEAEMINEYFSIHHIDQGNPTR *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtZYP1b HvZYP1	NIGDLFSEGS NIGELFSEGS ****:*****	AtMLH1 HvMLH1	LFVILDQYTPDMRVPFLLCLGNDVWEDEKSCFGQVSAAGIGNFYAMHPPLLPNPSGDG LFVILDQYTPDMRVPFLLCLGNDVWEDEKSCFGQVSAAGIGNFYAMHPPLLPNPSGDG *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtMLH1 HvMLH1	IQFYSKRGESSQKEKSLSDELEGN--VDMEDNLQDQLLSDAEWAQREWISQHVLPFSMRFL IOLYKQKVKDCMGSAEQADNPLPSTDDEDIDQELLEAEAAWQREWISQHVLPFSMRFL ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMLH1 HvMLH1	IQFYSKRGESSQKEKSLSDELEGN--VDMEDNLQDQLLSDAEWAQREWISQHVLPFSMRFL IOLYKQKVKDCMGSAEQADNPLPSTDDEDIDQELLEAEAAWQREWISQHVLPFSMRFL *****:***:***:***:***:***:***:***:***:***:***:***:***:***:
AtMLH1 HvMLH1	KPPASMASNGTFVKVASLEKLYKIFERC KPPKSMATDGTGFVQIASLEKLYKIFERC ****:***:***:***:***:***:***:***:***:***:***:***:***:***:	AtMLH1 HvMLH1	KPPASMASNGTFVKVASLEKLYKIFERC KPPKSMATDGTGFVQIASLEKLYKIFERC *****:***:***:***:***:***:***:***:***:***:***:***:***:***:

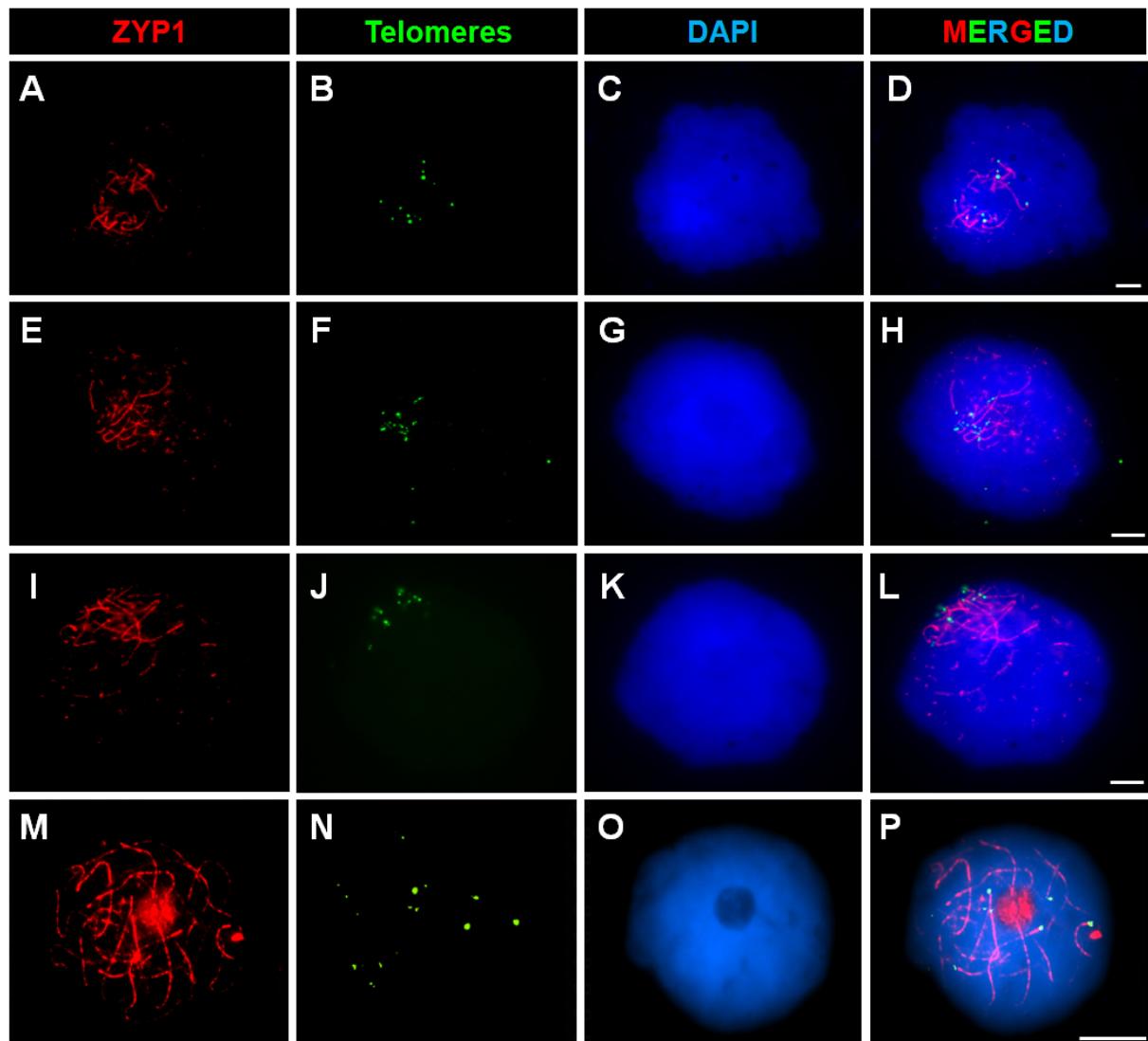
Supplemental Figure 1 *Arabidopsis* and barley meiotic protein ClustalW alignments

The regions of *Arabidopsis* proteins used for raising the antibodies are aligned against the homologous regions in the barley proteins. * denotes identical amino acids; : denotes similar amino acids.



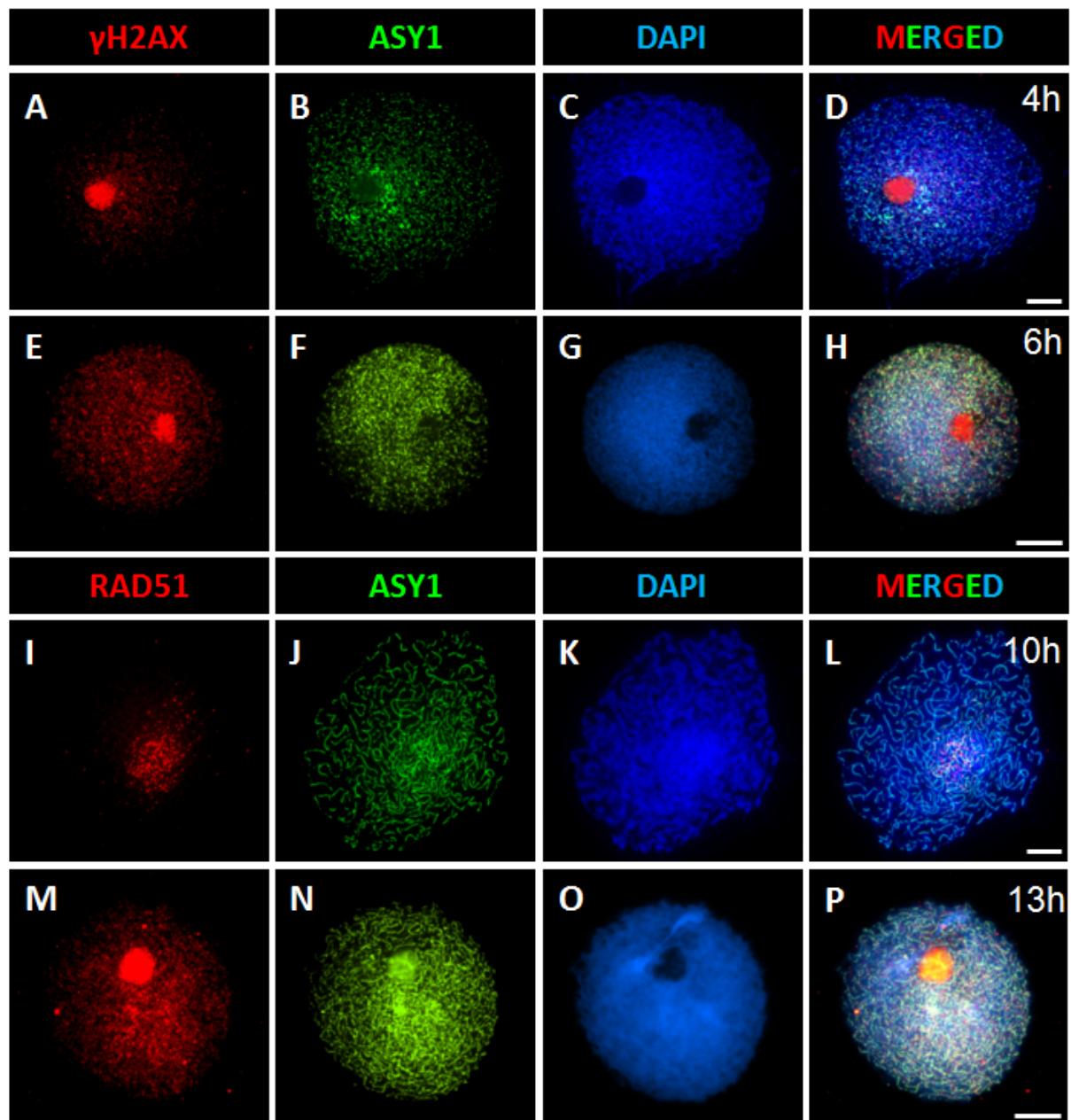
Supplemental Figure 2 Axis morphogenesis in relation to telomere clustering (unmerged images from Figure 2).

As a marker for chromosome axis formation, ASY1 foci (red) are initially observed adjacent to the telomeres (green) (A-H) and as the ASY1 signal progressively linearises (I) the telomeres cluster into a 'bouquet' (J), which persists through leptotene (M-P). Bar, 10 μ M.



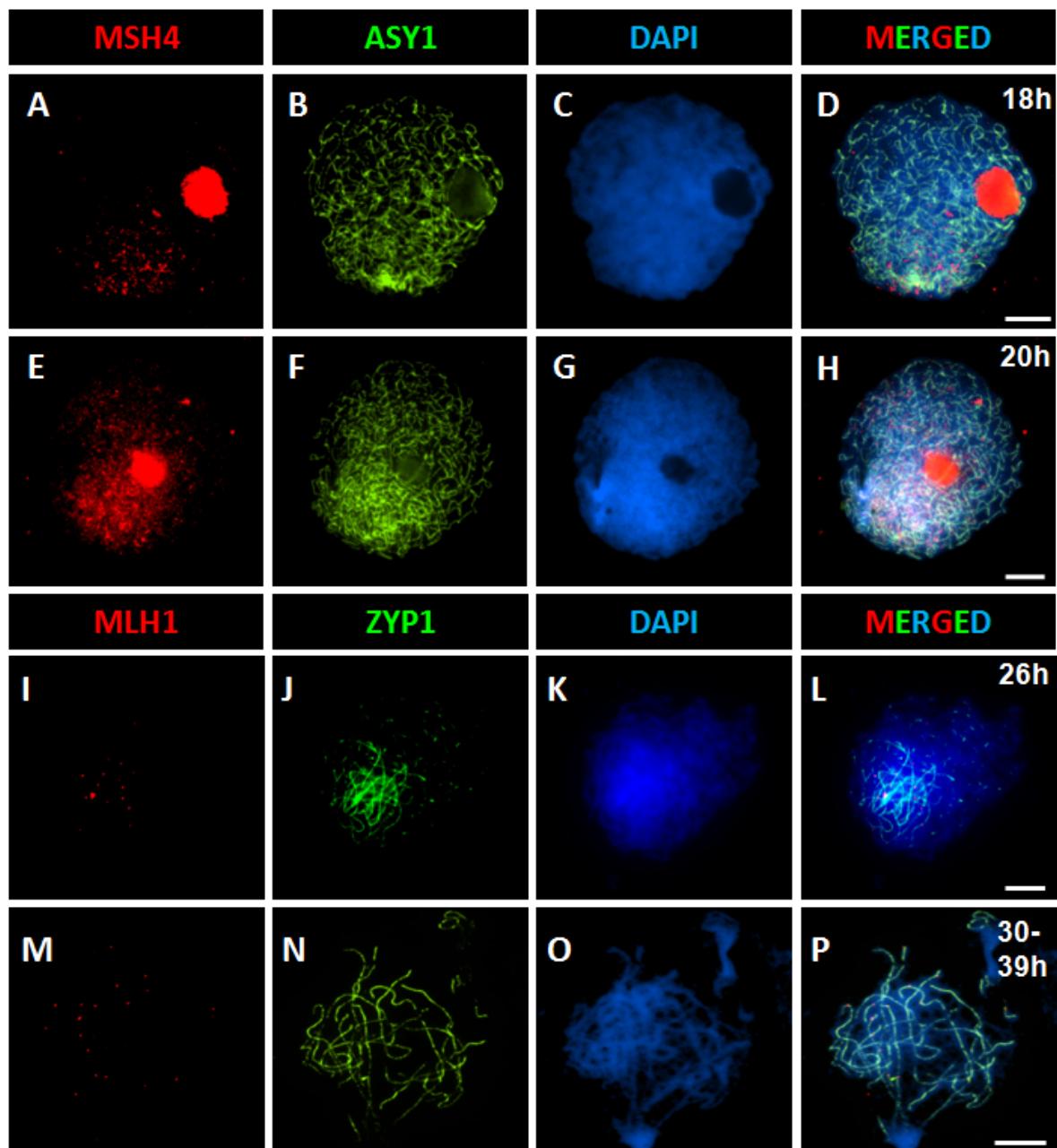
Supplemental Figure 3 Chromosome synapsis initiates from sub-telomeric regions (unmerged images from Figure 2)

As a marker for chromosome synapsis, ZYP1 stretches (red) are initially observed adjacent to the telomeres (green) (A-H). As the ZYP1 signal extends from the sub-telomeric regions, further synapsis initiation sites are observed in the interstitial regions (I-L) until synapsis is complete (M-P). Bar, 10 μ M.



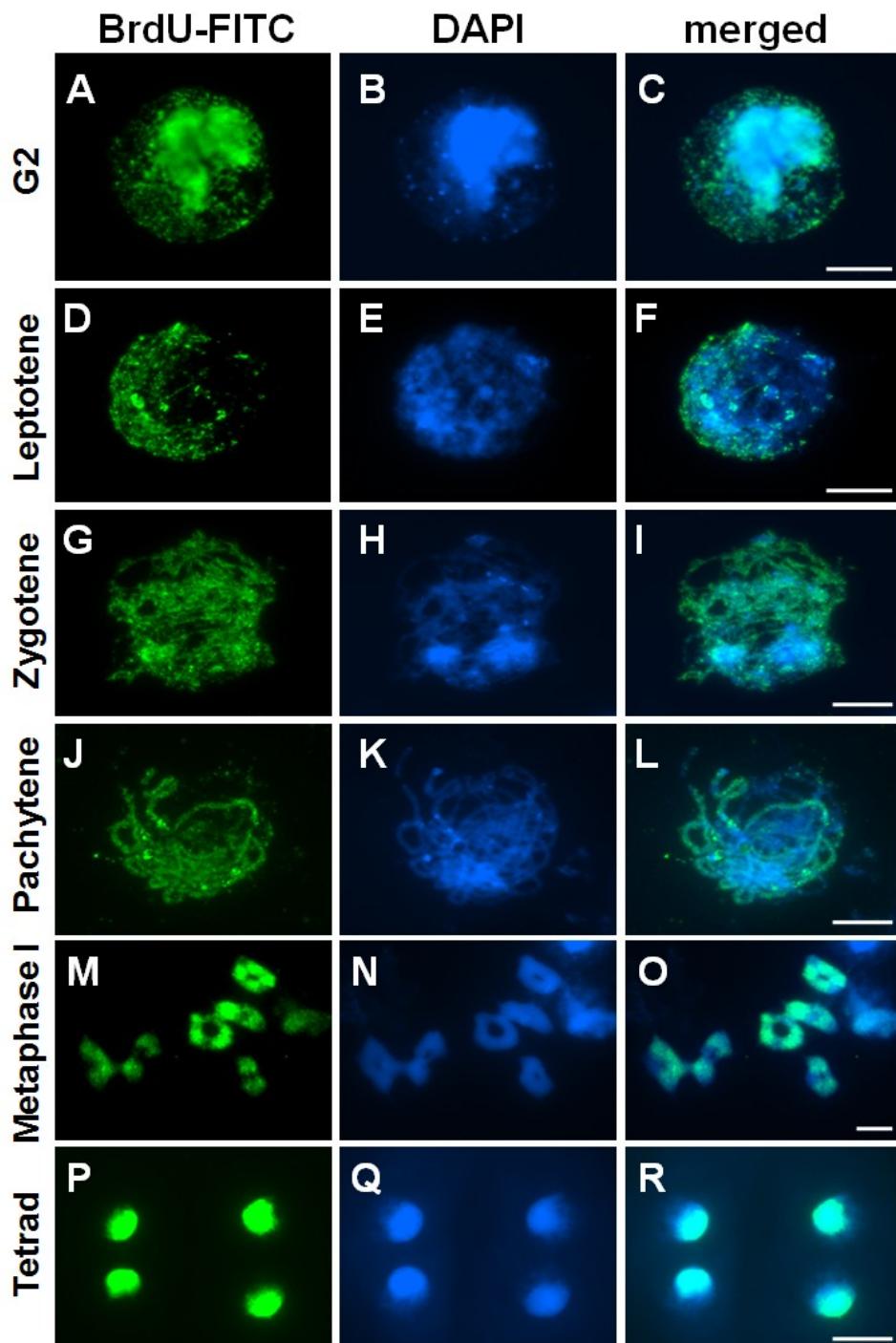
Supplemental Figure 4 Axis morphogenesis in relation to early recombination markers (unmerged images from Figure 2).

Markers for recombination (γ H2AX, **A-D**; RAD51, **I-L**) are initially observed as a cluster in the distal regions (corresponding to the most intense region of ASY1 staining) where axis morphogenesis is most advanced and later throughout the nucleus (γ H2AX, **E-H**; RAD51, **M-P**). Note: the intense 'ball like' structure is the nucleolus. Bar, 10 μ M.



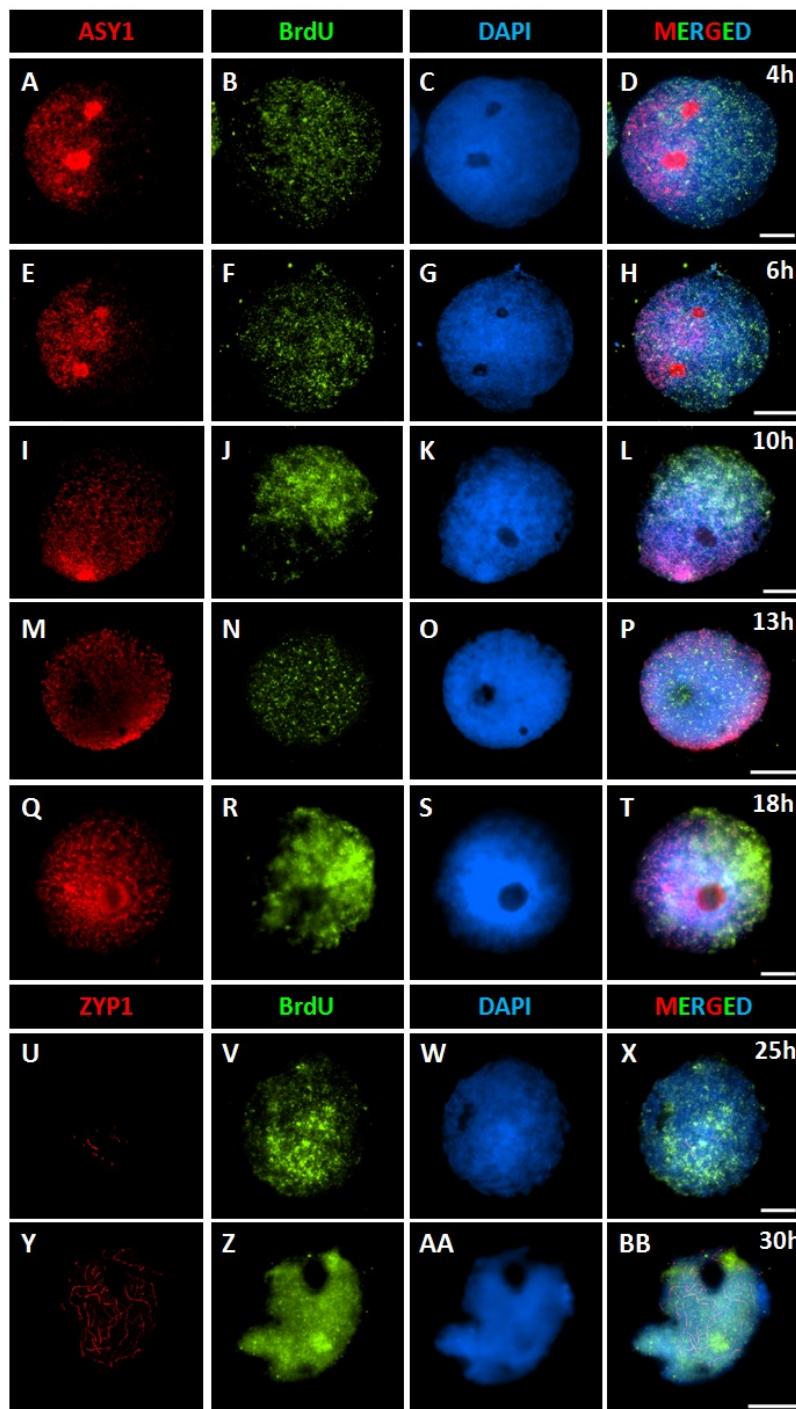
Supplemental Figure 5 Axis morphogenesis in relation to late recombination markers (unmerged from Figure 2)

MSH4 is initially observed as a cluster of foci in the distal regions (**A-D**) and later throughout the nucleus (**E-H**). MLH1 is initially observed contiguous with synapsis in the distal regions (**I-L**) and later still appears to be in these regions (**M-P**). Note: the intense 'ball like' structure is the nucleolus. Bar, 10 μ M.



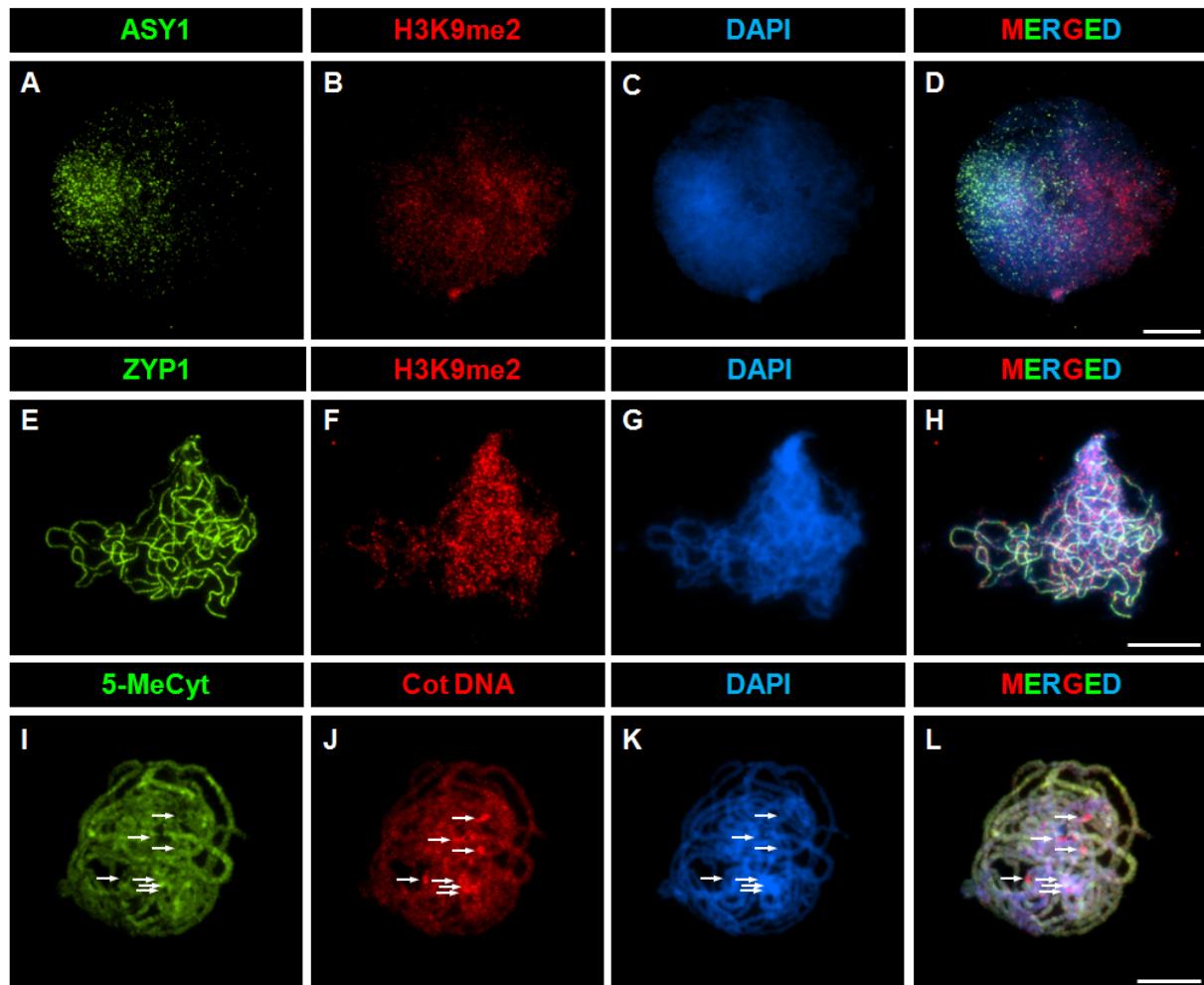
Supplemental Figure 6 A cytological meiotic time-course

5-bromo-2'-deoxyuridine(BrdU) is incorporated into newly synthesised DNA during pre-meiotic S-phase and detected with an anti-BrdU antibody labelled with FITC (green). Leptotene nuclei with labelled BrdU were observed after 13h (D-F), followed by zygotene at 25h (G-I), pachytene 30h (J-L), metaphase I 40h (M-O) and tetrad 43h (P-R). Nuclei were counterstained with DAPI (blue). Bar, 10 μ M.



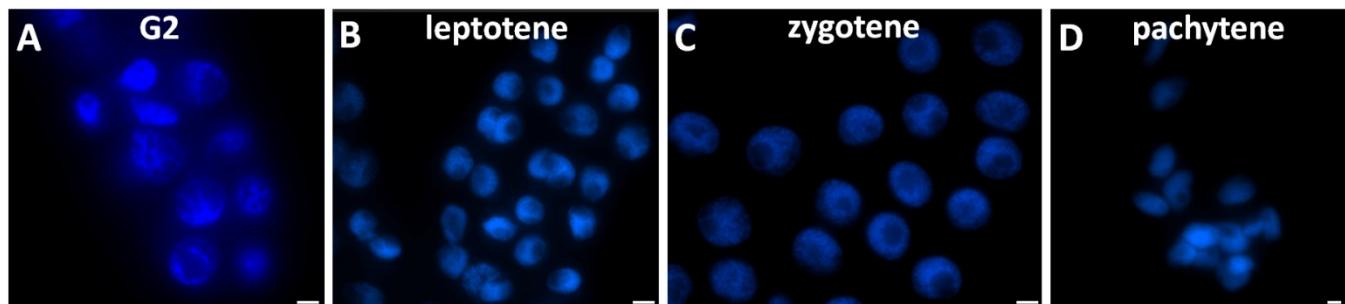
Supplemental Figure 7 An immunological time-course of barley meiotic prophase I

5-bromo-2'-deoxyuridine (BrdU) is incorporated into newly synthesised DNA during pre-meiotic S-phase and detected with an anti-BrdU antibody labelled with FITC (green). By dual labelling with markers for chromosome axis formation (ASY1, red) (**A-T**) and synapsis (ZYP1, red) (**U, BB**) the duration of meiotic stages can be determined. Bar, 10µM.



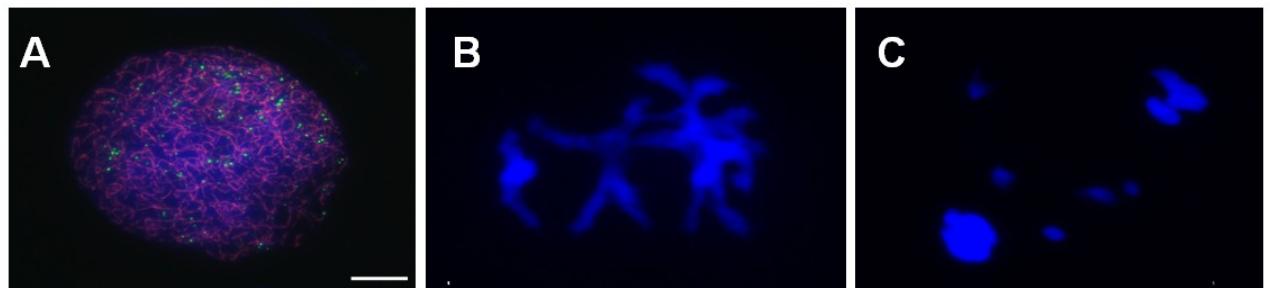
Supplemental Figure 8 Heterochromatin, methylated DNA and repetitive Cot DNA, are abundant throughout the barley chromosomes

The heterochromatin mark histone 3 lysine 9 dimethylation (H3K9me3) (**B,F**) occurs throughout the nucleus during prophase I but appears less abundant in the chromosome distal regions where ASY1 is loading (**A, D**). The methylated DNA nucleoside 5-methyl cytidine (5-MeCyt) is also abundant throughout the chromosomes during pachytene (**I**) along with fluorescence *in situ* hybridization of barley repeat sequence Cot DNA (**J**), DAPI (**K**) and merged (**L**), showing centromeres with white arrows. Bar, 10 μ M.



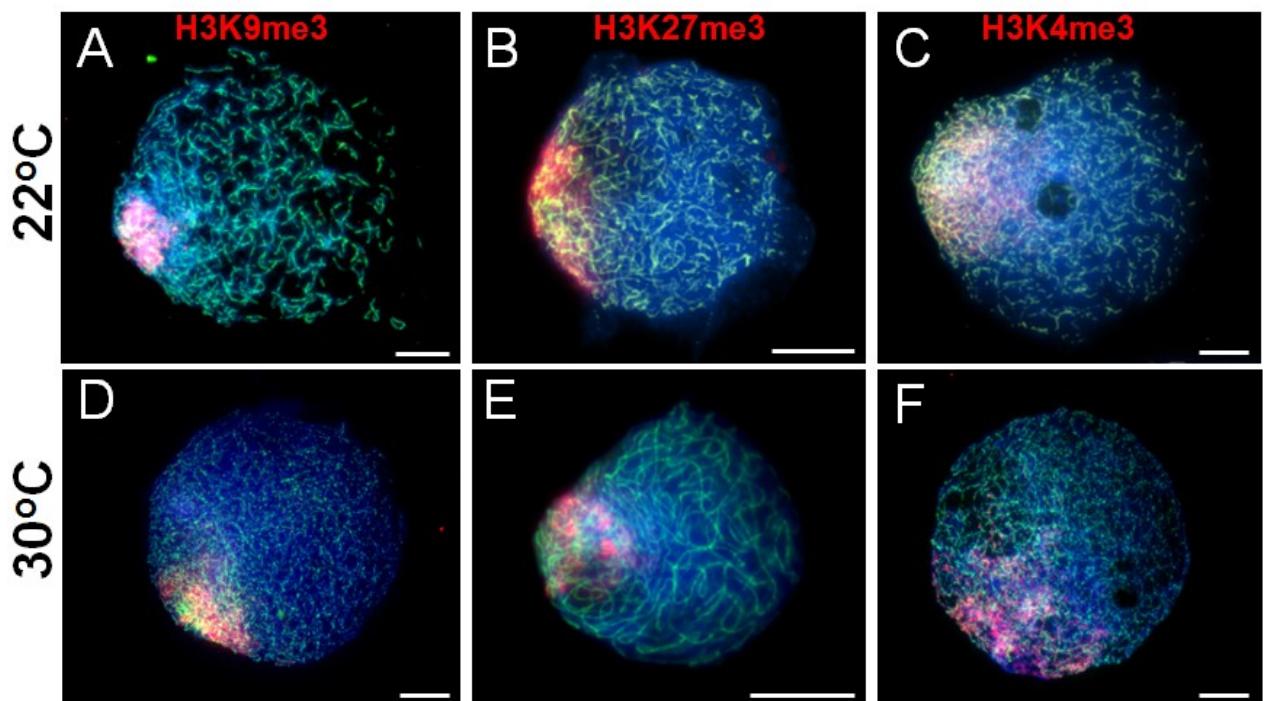
Supplemental Figure 9 Undigested meiocytes squeezed out of the anther locules shows that nuclear volume changes *in vivo*, but not as much as cell wall free nuclei.

Meiotic stages were determined by measuring anther lengths and sizes of nuclei by tracing round the DAPI (blue) stained areas. **A**, G2 = $485\mu\text{m}^2$ (n=45); **B**, leptotene = $479\mu\text{m}^2$ (n=45); **C**, zygotene = $449\mu\text{m}^2$ (n=45); **D**, pachytene = $283\mu\text{m}^2$ (n=45). Bar, 10 μM .



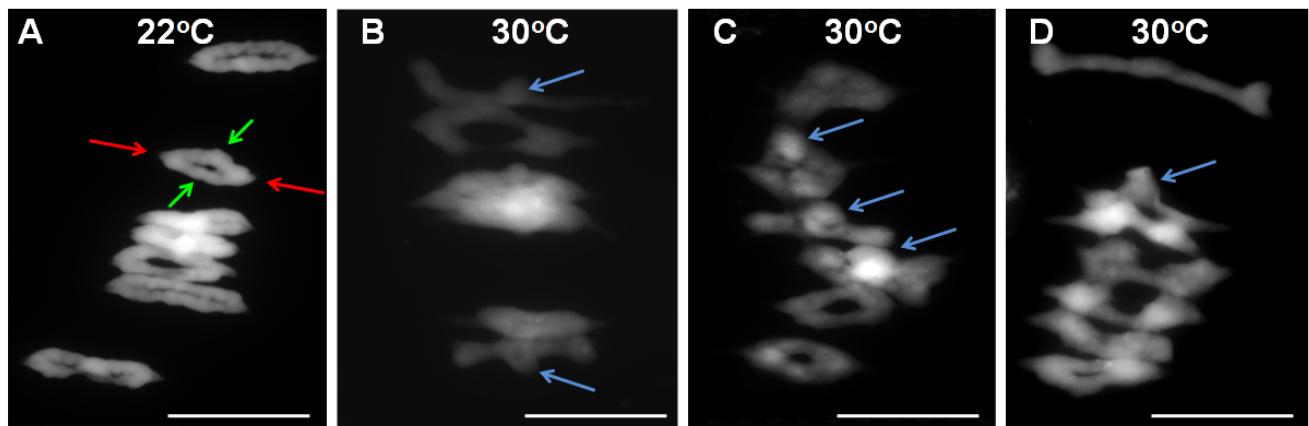
Supplemental Figure 10 Meiotic defects at 35°C

(A) In a mid-prophase I nucleus ZYP1 foci (green) are observed but do not elongate when ASY1 is linear (red). **(B)** Metaphase I chromosomes have unusual shapes that are agglomerated, leading to aberrant segregation **(C)**. Bar, 10 μ M.



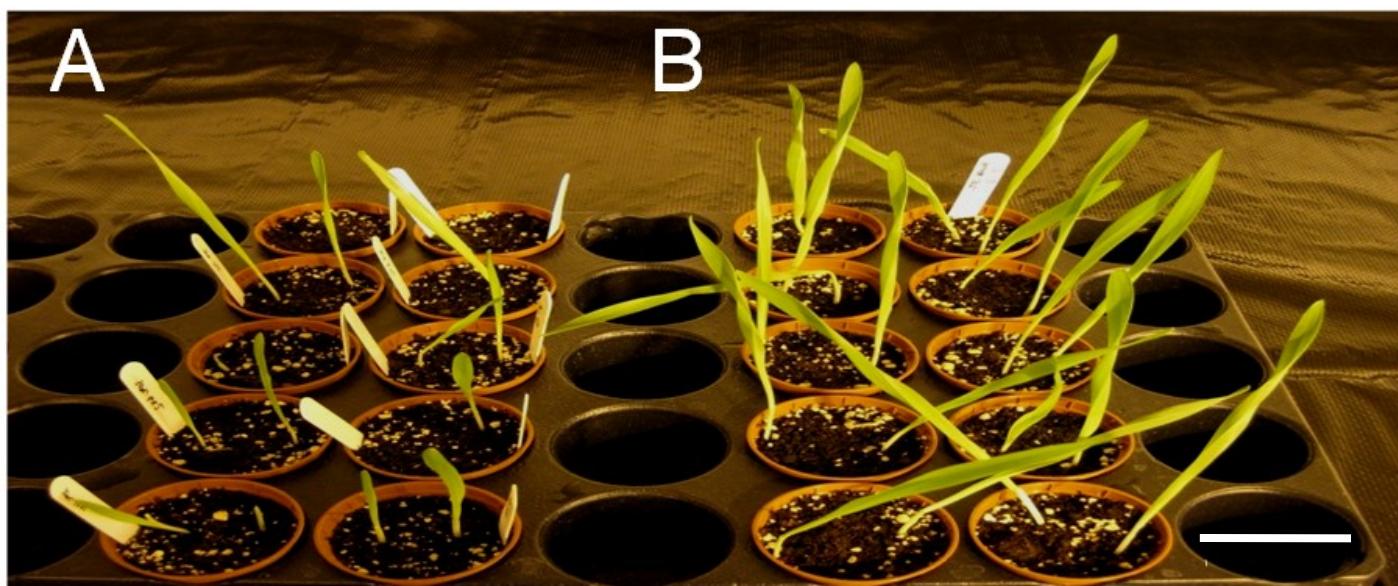
Supplemental Figure 11 Sub-telomeric euchromatic histone marks are indistinguishable at 22°C and 30°C

Histone 3 tri-methylated lysine 9 (H3K9me3) (**A,D**), histone 3 tri-methylated lysine 27 (H3K27me3) (**D,E**) and histone 3 tri-methylated lysine 4 (H3K4me3) (**C,F**) (red) immunolocalisation was indistinguishable between 22°C (**A,B,C**) and 30°C (**D,E,F**). Stages were identified with anti-ASY1 (green) counterstained with DAPI (blue). Bar, 10µM.



Supplemental Figure 12 Metaphase I chromosome spreads reveal increased interstitial chiasmata in plants grown at 30°C compared to 22°C

(A) At 22°C seven ring bivalents typically form with distal chiasmata (green arrows) and centromeres (red arrows) highlighted. (B,C,D) At 30°C, rod bivalents are more prevalent with increased interstitial chiasmata (blue arrows). Bar, 10µM.



Supplemental Figure 13 Post-meiotic fertility

Seeds collected from plants grown at 30°C were sown and 15/20 germinated (**A**) compared to the control where seeds were collected from plants grown at 22°C and 19/20 germinated (**B**). Bar, 5cm.

Gene name	cDNA fragment	Oligonucleotide	5'-Sequence-3'
RAD51	3'RACE	Rad51_F1	CCTTCAGAAATTAGCGGATGA
		Rad51_F2	ATTGGAGGGAACATCATGGCTCAC
	5'RACE	Rad51_R1	AGCCTTCCCTCACCAACACCTTG
		Rad51_R2	CTAGTGAACCCCAGTGGAACCAAC
	Full length	Rad51_FL_F1	AACCCCAAAACCGCCTCCCTGC
		Rad51_FL_F2	CGCCTCCCTGCTAGAGAAGAGAG
		Rad51_FL_R1	GGACCCAAGGAATATCGCTTCTAC
		Rad51_FL_R2	TCTTACGGAGGGCAAATTCCATC
DMC1	3'RACE	DMC1_F1	CGCATACACCTATGAGCACCAAGTAC
		DMC1_F2	TTGCTGAGGAGTTCAATGTTGCAG
	5'RACE	DMC1_R1	CAACACGGAATAGCGCAATCACAG
		DMC1_R2	AGCAGCCTCGCAGATCTTATCAAC
	Full length	DMC1_FL_F1	GAACGTCAGCGCCCCGTTCA
		DMC1_FL_F2	ATGGGCCTAGCTGGCAGCAGCAAAG
		DMC1_FL_R1	AAGCAAGAATCAAGAGACGGCGTA
		DMC1_FL_R2	AAGAGACGGCGTATTTCATTCTTC
MSH4	3'RACE	Msh4_F1	TTGAAGTACTCGAACCAAGGGGATG
		Msh4_F2	CAACCGTGAAGCATTGCAGGACCTC
	5'RACE	Msh4_R1	GTCCACTTCAGTATCGGACTCTG
		Msh4_R2	TTGCCTGCAGCGTAACTCTCCTT
	Full length	Msh4_FL_F1	CGCGCACACACCAGCTAGCAGC
		Msh4_FL_F2	CGTAGTTGCATCCTCCCAGGGTTC
		Msh4_FL_R1	GCTTGTACTTTAGGACATATCAC
		Msh4_FL_R2	CGCCACAACTTATGTGCCCCAG

MSH5	3'RACE	Msh5_F1	GGTTCTACTACCATACTCAAAAGACA
		Msh5_F2	TTACATCAAGTTGGAACAATGCTC
	5'RACE	Msh5_R1	TCACGTACAACGCTCTGCTGGTTC
		Msh5_R2	AATCATAATTGCAAAATGACTGATGG
	Full length	Msh5_FL_F1	GGACACTGACATGGACTGAAGGAG
		Msh5_FL_F2	ACATGGACTGAAGGAGTAGAAAAG
		Msh5_FL_R1	TGGATGGTCAAAACCGATTCTC
		Msh5_FL_R2	CCGATTCTCGTTGAATATGCTG
MLH1	3'RACE	Mlh1_F1	GTCCAGTCGCCATGAGCTGTTAC
		Mlh1_F2	GATCAGTACACTCCTGATATGGATC
	5'RACE	Mlh1_R1	GCAGCTGCTGCCGTTCTGAAGCAC
		Mlh1_R2	TGCAAACCGACTGATGAAGTCCAC
	Full length	Mlh1_FL_F1	TCCGCCCGGTCCCCAGACGC
		Mlh1_FL_F2	AGACGCGGCGCGGGGGCATG
		Mlh1_FL_R1	AGCAGAGCCAATCATTGTGCAT
		Mlh1_FL_R2	CAGGGCTGAGCTGGAGCCCAGC
ZYP1	3'RACE	Zyp1_F1	AATGGATCAGAGTTACAAGGAACAG
		Zyp1_F2	AGCTTCTAGGAAGAACATGCAGTCAG
	5'RACE	Zyp1_R1	TGTTGCTTTCTCAGCTTGGTATG
		Zyp1_R2	CTTCACCGAGGCCTGCTCCTGAC
	Full length	Zyp1_FL_F1	CCCTCTCCCCCTCCGCGTTCGTG
		Zyp1_FL_F2	GGCCTGGTGCTGCCGCCGTCGACG
		Zyp1_FL_R1	AACGACAGGAAACCTGAGATTCC
		Zyp1_FL_R2	CAAGACGGTATTGGCTGGGTGTG

ASY1	3'RACE	Asy1_F1	CTAATGATGCTAACAGTGACGATG
		Asy1_F2	TACTGGAAAGTTGATATCACTGAAG
	5'RACE	Asy1_R1	AACCTTGTAAACAGCATAACCAC
		Asy1_R2	TTGCTCCCTGTGCGACTCATGTT
	Full length	Asy1_FL_F1	CCCTCCCACGCGCACACACAGCAC
		Asy1_FL_F2	CACCAACCAGGGCGGGCAAAATGGTG
		Asy1_FL_R1	GCAGAAAATGACTTGCTCCGATTTC
		Asy1_FL_R2	AAATGACTTGCTCCGATTCACTAC

Supplemental Table 1: Primers used for cloning barley meiotic cDNAs

Two successive PCR reactions were carried out for each fragment. 1 µl of the barley inflorescence cDNA (see Material and Methods) was used as a template with the forward (F1) and reverse (R1) primers. 1 µl of this primary reaction was added in the secondary reaction with the corresponding nested primers indicated in **bold** (forward (F2) and reverse (R2)). The 3'RACE and 5'RACE oligonucleotides were used in combination with the GeneRacer 3' and 5' primers (Invitrogen), respectively. Oligonucleotides are shown 5'-3'.