

## SUPPLEMENTARY TABLES S1-S4; S8-S9

**Table S1. Summary of samples and mapping statistics.**

Sample name	No. of nucelli sections	Total reads	Mapped reads	Mapped reads [%]	Unique reads [%]	Counted reads [%]
ES517_1	211	66,245,546	64,378,845	97.2	95.0	85.5
ES517_2	90	70,248,191	68,712,897	97.8	95.7	85.3
B12-1578_1	158	28,396,884	27,595,928	97.2	93.9	81.2
B12-1578_2	142	62,426,422	60,849,184	97.5	94.4	83.5
B12-1599	198	99,921,406	96,830,008	96.9	94.2	83.5
B12-1524	226	58,993,566	57,517,841	97.5	95.5	86.1
B12-558	209	60,961,974	59,919,196	98.3	96.0	86.8
LTM_1	204	57,922,925	57,255,354	98.8	97.5	88.3
LTM_2	38	61,563,456	60,484,970	98.2	96.7	86.4

Number of pooled nucellus sections used as input for extraction of total RNA per sample are given. For each RNA-Seq library total number of raw reads and reads mapped to the reference genome of *B. stricta* (Lee et al., 2017) are listed, as well as percentages of mapped, unique and counted reads mapped to exon. Reads mapped to exons using STAR were counted with featureCounts (Dobin et al., 2013; Liao et al., 2014). Percentages refer to raw read numbers.

**Table S2: Cloning of constructs for *in situ* probes.**

Gene locus	primer F	primer R
Bostr.3279s0010	5'-CTCAAAGCAACTCGGAGAAAG-3'	5'-TTAAACCTTCAATTGACTAGTGGG-3'
Bostr.7867s1023	5'-AACGCTAGTAAGGGTGTGTCA-3'	5'-ACTACCCATTTACGACGCTTC-3'
Bostr.7867s1594	5'-CTTCCCAAGGCTAGTTAATCCTG-3'	5'-CGTTTGGATCTTGTGAGCAAG-3'
Bostr.13129s0275	5'-ATTTTTGGAGGGACAGAATACC-3'	5'-CCTCAACCTACTCTTACATCAC-3'

List of gene loci and primers used for cloning of constructs for *in situ* hybridisations.

**Table S3. Gene ontology analysis.**

<b>GO ID</b>	<b>Term</b>	<b>Annotated</b>	<b>Significant</b>	<b>Expected</b>	<b>P Value</b>
GO:0006412	translation	421	351	201	< 1e-30
GO:0015031	protein transport	174	139	83.07	6.80E-15
GO:0051649	establishment of localization in cell	164	128	78.3	9.00E-13
GO:0006457	protein folding	90	75	42.97	2.10E-12
GO:0006396	RNA processing	178	127	84.98	6.70E-08
GO:0006164	purine nucleotide biosynthetic process	78	59	37.24	4.90E-07
GO:0042254	ribosome biogenesis	47	38	22.44	1.10E-06
GO:0019752	carboxylic acid metabolic process	349	241	166.63	2.30E-06
GO:1901566	organonitrogen compound biosynthetic process	739	566	352.83	4.10E-06
GO:0019359	nicotinamide nucleotide biosynthetic process	46	37	21.96	5.00E-06
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	64	48	30.56	7.60E-06
GO:0006511	ubiquitin-dependent protein catabolic process	70	51	33.42	1.60E-05
GO:0015991	ATP hydrolysis coupled proton transport	29	25	13.85	1.90E-05
GO:0000413	protein peptidyl-prolyl isomerization	32	27	15.28	1.90E-05
GO:0006399	tRNA metabolic process	102	70	48.7	3.00E-05
GO:0016192	vesicle-mediated transport	128	85	61.11	3.80E-05
GO:0071824	protein-DNA complex subunit organization	23	20	10.98	0.00011
GO:0009166	nucleotide catabolic process	40	31	19.1	0.00011
GO:0070925	organelle assembly	20	18	9.55	0.00018
GO:0009451	RNA modification	39	30	18.62	0.00022
GO:0016053	organic acid biosynthetic process	185	123	88.33	0.00037
GO:0051188	cofactor biosynthetic process	113	84	53.95	0.00068
GO:0008610	lipid biosynthetic process	145	93	69.23	0.00079
GO:0045454	cell redox homeostasis	108	68	51.56	0.00097
GO:0006289	nucleotide-excision repair	19	16	9.07	0.00117
GO:0031668	cellular response to extracellular stimulus	9	9	4.3	0.00269

**Table S3 continued.**

<b>GO ID</b>	<b>Term</b>	<b>Annotated</b>	<b>Significant</b>	<b>Expected</b>	<b>P value</b>
GO:0007264	small GTPase mediated signal transduction	45	32	21.48	0.003
GO:0045333	cellular respiration	24	21	11.46	0.00366
GO:0045047	protein targeting to ER	16	14	7.64	0.00379
GO:0006839	mitochondrial transport	14	12	6.68	0.00398
GO:0006366	transcription by RNA polymerase II	38	27	18.14	0.00458
GO:0008202	steroid metabolic process	27	20	12.89	0.00494
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	7	7	3.34	0.00564
GO:0006505	GPI anchor metabolic process	16	13	7.64	0.00649
GO:0051603	proteolysis involved in cellular protein catabolic process	83	62	39.63	0.0107
GO:0044272	sulfur compound biosynthetic process	25	20	11.94	0.01113

Biological processes identified to be upregulated based on 10,526 genes consistently expressed in all samples included in this study compared to all genes with annotations for biological processes in the *B. stricta* reference genome (Lee et al., 2017). *P* value < 0.01 regarded as significant, *p* value 0.011 as near significant.

**Table S4. Expression of selected meiotic genes, core cell cycle regulators, *APOLLO* and *KNUCKLES*.**

<b>Gene locus</b>	<b>LTM</b>	<b>B12-558</b>	<b>B12-1524</b>	<b>B12-1599</b>	<b>B12-1578</b>	<b>ES517</b>
<b>Bostr.0124s0185</b>	1225.05	160.43	203.72	748.14	431.45	230.54
<b>Bostr.0556s0453</b>	479.46	234.48	1.22	216.23	602.05	62.83
<b>Bostr.0597s0018</b>	136.43	207.74	331.81	0.00	11.06	51.82
<b>Bostr.10058s0011</b>	3053.89	1465.47	1471.19	841.18	1695.23	1435.10
<b>Bostr.13129s0420</b>	5686.27	538.88	0.00	7635.39	1728.39	64.77
<b>Bostr.13671s0113</b>	127.10	686.97	858.81	696.81	754.56	516.00
<b>Bostr.15774s0011</b>	11.60	113.12	134.19	62.88	21.15	43.08
<b>Bostr.15774s0271</b>	88.34	30.85	0.00	111.00	16.32	73.62
<b>Bostr.18351s0222</b>	1.96	1738.00	651.42	143.72	60.52	1377.07
<b>Bostr.19424s0371</b>	65.84	1022.23	709.98	62.88	481.80	201.60
<b>Bostr.19424s0607</b>	4.42	665.38	674.60	455.56	420.54	369.49
<b>Bostr.20129s0174</b>	962.98	471.01	1806.66	1656.05	1082.09	1167.64
<b>Bostr.20903s0038</b>	2356.10	2276.88	407.44	2319.49	5738.78	2438.16
<b>Bostr.21532s0001</b>	756.29	552.25	414.76	1008.00	481.60	681.40
<b>Bostr.23794s0493</b>	0.00	583.10	994.21	279.75	258.18	627.91
<b>Bostr.25463s0397</b>	1661.00	1712.29	2844.79	1484.73	1426.04	2390.44
<b>Bostr.26527s0097</b>	1005.39	76.10	8575.86	1601.51	1905.57	2250.15
<b>Bostr.26833s0466</b>	75.02	305.44	1049.11	447.86	90.45	390.07
<b>Bostr.26959s0167</b>	393.43	879.28	329.37	482.51	637.98	604.75
<b>Bostr.27991s0220</b>	3405.54	12216.37	9944.58	3243.44	1990.95	8749.18
<b>Bostr.2902s0137</b>	0.00	0.00	18.30	0.00	5.84	9.47
<b>Bostr.29223s0135</b>	723.56	489.52	303.75	289.37	274.55	517.70
<b>Bostr.3288s0084</b>	526.59	316.75	997.87	1394.26	1000.95	1251.94
<b>Bostr.3640s0094</b>	0.00	2693.38	4479.45	87.26	21.58	2910.28
<b>Bostr.3750s0001</b>	0.00	81.24	35.38	69.94	123.44	43.27
<b>Bostr.5325s0089</b>	124.65	448.38	506.26	45.56	167.56	340.87

Table S4 continued						
<b>Bostr.6864s0034</b>	103.06	120.32	70.75	193.13	181.22	74.15
<b>Bostr.6864s0235</b>	77.55	5151.26	1335.78	424.76	212.85	2567.26
<b>Bostr.7128s0171</b>	1.47	2060.92	978.36	232.91	59.65	1346.42
<b>Bostr.7305s0036</b>	0.00	46.28	21.96	300.28	162.88	152.58
<b>Bostr.7867s0762</b>	2251.41	636.58	627.03	1870.35	391.29	843.53
<b>Bostr.7867s1410</b>	1715.22	963.61	927.12	710.28	438.96	878.70

Normalized mean read counts of selected meiotic genes, core cell cycle genes, *APOLLO* (Bostr.3288s0084) and *KNUCKLES* (Bostr.2902s0137).

**Table S8. Table of common, differentially expressed genes between apomictic and sexual nucelli.**

Gene locus	GO term	<i>A. thaliana</i> gene locus	<i>A. thaliana</i> gene name	<i>A. thaliana</i> gene/ protein description
Bostr.0556s0720	NA	AT3G44220	NA	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein
Bostr.13129s0275	NA	NA	NA	NA
Bostr.19424s0775	NA	NA	NA	NA
Bostr.3279s0010	GO:0010468, GO:0005777	AT4G30760	NA	Putative endonuclease or glycosyl hydrolase
Bostr.3288s0214	GO:0033177, GO:0015991, GO:0015078	AT1G19910	ATVHA-C2, AVA-2PE, AVA-P2	ATPase, F0/V0 complex, subunit C protein
Bostr.3359s0099	GO:0005515	AT3G57590	NA	F-box and associated interaction domains-containing protein
Bostr.7867s0569	GO:0046872	AT4G27470	ATRMA3, RMA3	RING membrane-anchor 3

All 7 identified differentially expressed genes (DEGs) are upregulated in apomictic accessions and listed with information on *B. stricta* gene locus, GO terms and *Arabidopsis thaliana* (*A. thaliana*) homologues based on genome annotations by Lee et al. (2017). DEGs identified consistently in both analyses are highlighted in grey. NA = no information available.

**Table S9: List of candidate genes, homologues of which are differentially expressed in *Hieracium praealtum* cells and tissue types (Juranić et al., 2018).**

<i>A. thaliana</i> gene locus	aposporous initial cell <i>versus</i> somatic cells	aposporous initial cells <i>versus</i> early gametophyte
AT1G19910	yes	no
AT4G00740	yes	no
AT4G00620	yes	yes
AT5G54510	yes	yes
AT5G08430	yes	yes
AT1G67800	yes	no
AT4G26830	yes	yes
AT1G26570	yes	yes
AT2G17820	yes	yes
AT4G37330	yes	yes
AT3G54700	yes	yes
AT5G55240	yes	yes
AT3G53750	yes	yes

Yes = indicates differential expression in between the aposporous initial cell and somatic cells of the ovule or young gametophyte. No = indicates no differential expression.

## REFERENCES

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