Table S1. Potential transcription factor binding sites (TFBSs) and interacting transcription factors (TFs) that respond to gibberellic acid (GA_3) signals found in *Salvia miltiorrhiza HMGR4* promoter sequence using PlantPan 2.0 tool.

TFBS motif and localisation[a,b,c]		TF family name	TF gene name and locus	processes in which TF is involved
AATTA 1268 **AATAT 1263**	AATAA 309 TTATT 475 ATATT 345; 631	AT-Hook	*AHL25;* At4g35390	negative regulation of GA_3-mediated signaling pathway; vegetative to reproductive phase transition of meristem
TATCT 186		MYB-related	*CCA1;* At2g46830	responded e.g. to GA_3; negative regulation of circadian rhythm; phytochrome regulation; long-day photoperiodism and flowering; regulation of protein homodimerization activity
ATATC 1166	**GATAT 1215**		*RVE8;* At3g09600	responded e.g. to GA_3; histone H3 acetylation; photoperiodism and flowering; positive regulation of circadian rhythm
			RVE4; At5g02840	responded e.g. to GA_3; regulation of circadian rhythm
ATAAT 309		Homeodomain; HD-ZIP	*ATHB-23;* At1g26960	induced by GA_3; lateral root development
CACAT 644	ACATG 644	bHLH	*PIF3;* At1g09530	regulation of GA_3-mediated, phytochrome and red/far-red light signaling pathways; de-etiolation; positive regulation of anthocyanin metabolic process
GGATC 220 TATCC 377 GGATA 392 GATAC 393 GATAA 439 **CGATG 1227** **AGATT 1405** CGATT 424; 1143 TATCG 448; 1169 CATCT 753; 872 **AATCA** 11; **1315** AATCG 75; 130 GATCG 101; 221	GGATG 962; 1178 ATATC 189; 1168 GTATC 376; 761 CTATC 447; 891 **GATAT** 769; **1217** AATCT 15; 197; 919 **AGATG** 120; 662; **1427** CATCC 141; 778; 999 TATCT 162; 190; 326 AATCC 179; 204; 548 **TGATA** 438; 768; **1216** **TTATC** 161; 325; 689; 860; **1226** **TATCA** 690; 762; 861; 892; **1213** TGATT 648; 1076; 1101; 1131; 1198	GATA	*GATA22;* At4g26150 *GATA21;* At5g56860	induced e.g. by GA_3; modulation of chloroplast development, growth and division in cytokinin-dependent manner; chlorophyll biosynthesis; regulation of sugar-sensing genes; circadian rhythm; regulation of germination, senescence, elongation growth and flowering time; influence leaf starch content
TTTTT 77; 78; 79; 80; 81; 82; 83; 84		MADS box;	*SOC1;*	up-regulated by GA_3; integration of signals from photoperiod,

		MIKC	At2g45660	vernalisation and autonomous floral induction pathways; when associated with AGL24, mediate effect of GA_3 on flowering under short-day conditions
AATGG 842 TTTTG 805 C**AAAA 1396**	ATTTCC 804; 801 **GGAAA 1364; 1362** TTTTT 77; 78; 79; 80; 81; 82; 83; 84		*AGL24;* At4g24540	up-regulated by GA_3; floral transition in response to vernalization; effect of GA_3 on flowering under short-day conditions; identity of floral meristem; inflorescence fate in apical meristems
AATGG 842 TTTCC 804; 801	**GGAAA 1364; 1362** TTTTT 77; 78; 79; 80; 81; 82; 83; 84	MADS box	*AGL71;* At5g51870	act through GA_3-dependent pathway; flowering time; flowering at shoot apical and axillary meristems
TTTTG 805 **CAAAA 1396**	TTTCC 804; 801 **GGAAA 1364; 1362** TTTTT 77; 78; 79; 80; 81; 82; 83; 84		*AGL72;* At5g51860	act through GA_3-dependent pathway; flowering time; flowering at shoot apical and axillary meristems
			AGL42; At5g62165	act through GA_3-dependent pathway; flowering time; flowering at shoot apical and axillary meristems; control of flower organ senescence and abscission; leaf senescence
CTAAT 42 CCCAT 139 GTTGG 389 CCAAC 530 AGTGG 592 TTTGG 811 CCTAT 890 ATGGG959 ATTGC 1039 CGAAT 1115 **ATTAG 1389** CCAAT 195; 202	ATCGG 102; 131 CCAAG 149; 213 AATGG 462; 847 ATTGA 766; 1099 CCATT 169; 266; 701 **CCACT** 144; 380; **1364** **TCAAT** 13; 1149; **1253** **ACAAT** 460; 800; **1247** ATTGT 599; 637; 1145; 1152 **CCAAA** 176; 534; **1261; 1396** C**AAAT** 177; 469; 897; 1107; 1161**;** **1262; 1313**	NF-YC	*NFYC3;* At1g54830	involved in GA_3- and abscisic acid-activated signaling pathway; long-day photoperiodism and flowering; positive regulation of photomorphogenesis; regulation of seed germination

[a] For TFBSs only most conserved positions within a matrix were listed. [b] Binding sites localised in proximal promoter region are in bold. [c] The transcription start site (TSS) is located at 1500 nucleotide of the studied promoter sequence.