

Figure S1. The conservative motif analysis of the *VvSAUR* family. The distribution of motifs in the *VvSAUR* family is represented by rectangles of different colors.

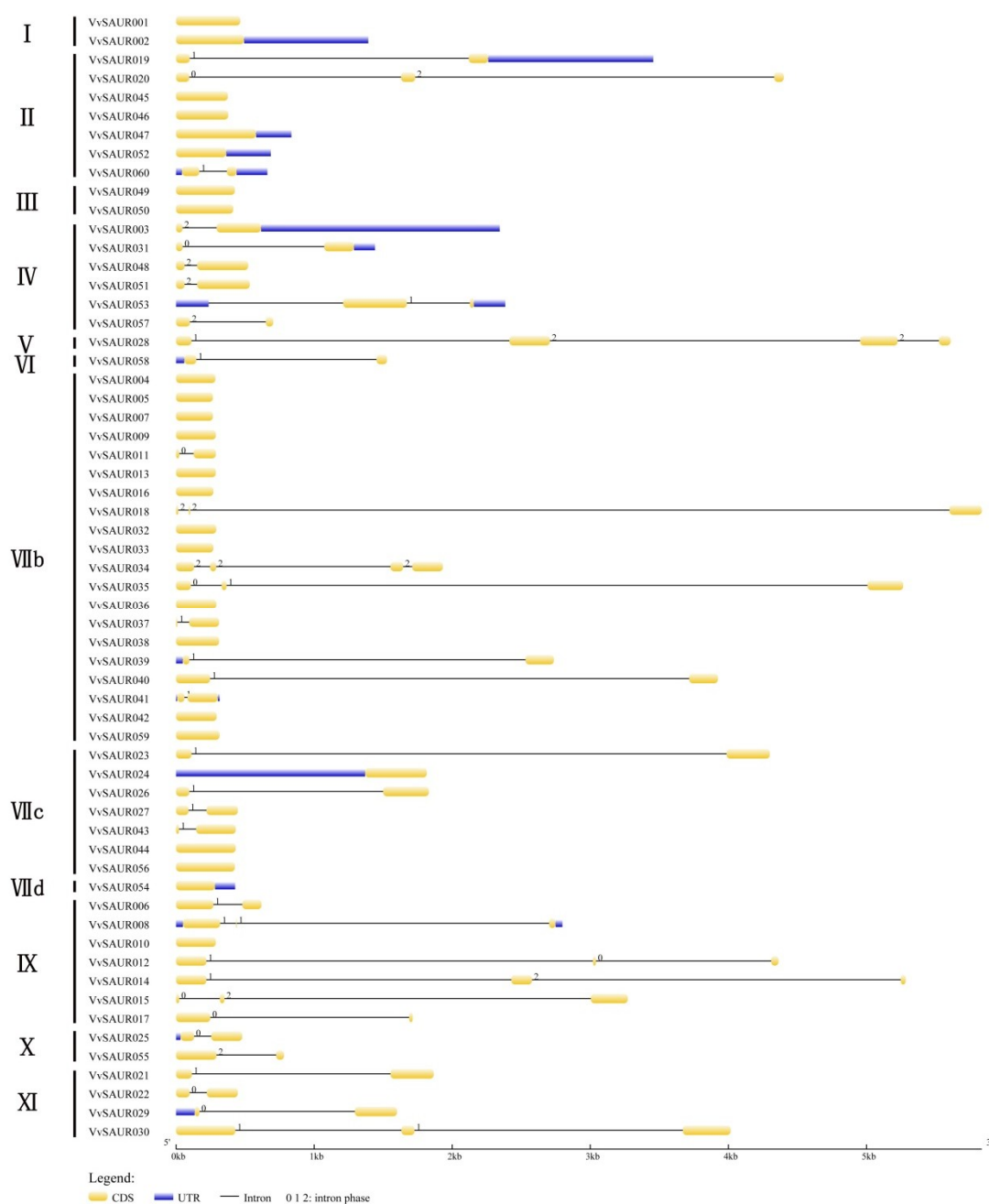


Figure S2. The structural features of the *VvSAUR* family. The blue rectangles represent untranslated regions (UTRs). The yellow round-cornered rectangles represent exons. The black lines represent introns. The number above the lines represents the intron phase.

Table S1. Details of the *VvSAUR* family. The gene locus is available in the National Center for Biotechnology Information Database. Mw, molecular weight; PI, isoelectric point.

Gene locus	Gene symbol	ORF length(bp)	No. of aa	Mw	PI	Chr.	Location	Orientation	Group
GSVIVG01 000929001	VvSAUR00 1	465	155	17397.04	9.62	1	22022632- 22023096	forward	I
GSVIVG01 001263001	VvSAUR00 2	492	164	19012.29	10.62	2	4821803- 4823194	reverse	I
GSVIVG01 024152001	VvSAUR00 3	369	123	13585.51	5.61	3	736293- 738636	forward	IV
GSVIVG01 024138001	VvSAUR00 4	285	95	10554.18	6.56	3	858886- 859170	reverse	VIIb
GSVIVG01 024136001	VvSAUR00 5	267	89	9522.85	5.71	3	864608- 864874	forward	VIIb
GSVIVG01 024135001	VvSAUR00 6	411	137	15518.07	8.88	3	866406- 867024	forward	IX
GSVIVG01 024134001	VvSAUR00 7	267	89	9536.88	5.71	3	867890- 868156	forward	VIIb
GSVIVG01 024133001	VvSAUR00 8	324	108	12260.50	8.91	3	869578- 872375	forward	IX
GSVIVG01 024131001	VvSAUR00 9	288	96	10559.18	6.82	3	883689- 883976	reverse	VIIb
GSVIVG01 024130001	VvSAUR01 0	288	96	10767.51	6.95	3	885397- 885684	reverse	IX
GSVIVG01 024129001	VvSAUR01 1	186	62	6807.89	4.70	3	888666- 888953	forward	VIIb
GSVIVG01 024128001	VvSAUR01 2	297	99	11306.30	9.63	3	890779- 895141	reverse	IX
GSVIVG01 024127001	VvSAUR01 3	288	96	10496.09	6.55	3	897891- 898178	forward	VIIb
GSVIVG01 024126001	VvSAUR01 4	408	136	15613.93	9.22	3	898286- 903569	reverse	IX
GSVIVG01 024125001	VvSAUR01 5	327	109	11939.88	6.89	3	905892- 909162	forward	IX
GSVIVG01 024123001	VvSAUR01 6	270	90	9743.06	4.97	3	915230- 915499	reverse	VIIb
GSVIVG01 024122001	VvSAUR01 7	276	92	10479.22	9.51	3	915998- 917711	reverse	IX
GSVIVG01 024120001	VvSAUR01 8	264	88	9643.04	5.60	3	922119- 927953	forward	VIIb
GSVIVG01 023917001	VvSAUR01 9	240	80	9292.95	11.33	3	2502521- 2505976	forward	II
GSVIVG01 023916001	VvSAUR02 0	270	90	10507.66	12.02	3	2508656- 2513056	forward	II
GSVIVG01 023915001	VvSAUR02 1	429	143	16365.33	9.27	3	2513557- 2515422	forward	XI
GSVIVG01 023913001	VvSAUR02 2	324	108	12236.35	8.68	3	2518586- 2519032	forward	XI
GSVIVG01 023912001	VvSAUR02 3	426	142	16204.15	9.65	3	2520298- 2524597	forward	VIIc
GSVIVG01 023911001	VvSAUR02 4	447	149	17029.75	9.03	3	2525431- 2527246	reverse	VIIc
GSVIVG01 023910001	VvSAUR02 5	324	108	12071.35	9.62	3	2528389- 2528867	forward	X
GSVIVG01 023909001	VvSAUR02 6	429	143	16236.16	9.35	3	2530531- 2532361	forward	VIIc
GSVIVG01 023908001	VvSAUR02 7	318	106	12068.19	9.51	3	2533266- 2533712	reverse	VIIc

GSVIVG01 023907001	VvSAUR02 8	765	255	28965.02	9.41	3	2536206- 2541814	forward	V
GSVIVG01 023881001	VvSAUR02 9	342	114	12891.88	5.48	3	2749512- 2751111	reverse	XI
GSVIVG01 023880001	VvSAUR03 0	873	291	32880.35	5.63	3	2751841- 2755856	reverse	XI
GSVIVG01 023879001	VvSAUR03 1	264	88	9888.54	10.23	3	2757523- 2758963	forward	IV
GSVIVG01 019106001	VvSAUR03 2	291	97	10860.46	7.82	4	16733927- 16734217	reverse	VIIb
GSVIVG01 019105001	VvSAUR03 3	270	90	9990.55	8.64	4	16735502- 16735771	reverse	VIIb
GSVIVG01 019103001	VvSAUR03 4	492	164	18532.53	8.54	4	16738840- 16740771	reverse	VIIb
GSVIVG01 019101001	VvSAUR03 5	405	135	15287.92	9.67	4	16744811- 16750076	reverse	VIIb
GSVIVG01 019099001	VvSAUR03 6	291	97	10809.53	7.84	4	16755874- 16756164	reverse	VIIb
GSVIVG01 019097001	VvSAUR03 7	228	76	8361.52	6.26	4	16763888- 16764199	reverse	VIIb
GSVIVG01 019096001	VvSAUR03 8	312	104	11472.27	9.25	4	16765755- 16766066	reverse	VIIb
GSVIVG01 019095001	VvSAUR03 9	255	85	9441.86	7.95	4	16767618- 16770353	reverse	VIIb
GSVIVG01 019094001	VvSAUR04 0	456	152	16871.48	8.89	4	16772358- 16776281	reverse	VIIb
GSVIVG01 019093001	VvSAUR04 1	273	91	10019.53	6.25	4	16779757- 16780072	reverse	VIIb
GSVIVG01 019092001	VvSAUR04 2	294	98	10962.60	6.16	4	16782060- 16782353	reverse	VIIb
GSVIVG01 031508001	VvSAUR04 3	309	103	11635.28	5.76	6	17809104- 17809535	forward	VIIc
GSVIVG01 031507001	VvSAUR04 4	432	144	16135.55	6.83	6	17828336- 17828767	forward	VIIc
GSVIVG01 025708001	VvSAUR04 5	375	125	14244.64	8.84	8	12797230- 12797604	forward	II
GSVIVG01 033868001	VvSAUR04 6	378	126	13881.91	6.29	8	17142119- 17142496	reverse	II
GSVIVG01 016698001	VvSAUR04 7	579	193	21144.01	6.21	9	445796- 446630	forward	II
GSVIVG01 029567001	VvSAUR04 8	432	144	16284.00	6.10	9	21457323- 21457844	forward	IV
GSVIVG01 029566001	VvSAUR04 9	426	142	16737.43	9.37	9	21482997- 21483422	reverse	III
GSVIVG01 029559001	VvSAUR05 0	414	138	16094.85	9.30	9	21569331- 21569744	forward	III
GSVIVG01 029558001	VvSAUR05 1	444	148	16771.60	6.43	9	21572109- 21572642	reverse	IV
GSVIVG01 015021001	VvSAUR05 2	363	121	13265.03	5.60	11	516935- 517620	forward	II
GSVIVG01 015023001	VvSAUR05 3	492	164	18227.53	5.22	11	528067- 530450	reverse	IV
GSVIVG01 020838001	VvSAUR05 4	282	94	10594.48	9.23	12	1253357- 1253784	reverse	VIIId
GSVIVG01 038622001	VvSAUR05 5	351	117	13282.46	6.06	16	21394851- 21395632	reverse	X
GSVIVG01 008695001	VvSAUR05 6	426	142	15802.62	9.83	18	1262260- 1262685	forward	VIIc

GSVIVG01 VvSAUR05 009870001 7	156	52	6102.37	11.79	18	11959701- 11960404	forward	IV
GSVIVG01 VvSAUR05 009872001 8	165	55	5987.21	10.31	18	11986451- 11987978	reverse	VI
GSVIVG01 VvSAUR05 009875001 9	315	105	11720.72	8.85	18	12002966- 12003280	forward	VIIb
GSVIVG01 VvSAUR06 036807001 0	198	66	7502.57	10.03	19	22279115- 22279775	forward	II

Table S2. Normal expression sequences of 10 motifs identified. Sites represent the time of motif appeared.

Motif	Sequences	Sites	Length(aa)
Motif1	[KR][KR]RF[VM][VI]P[IL][S VE]YL[NKS][HN][PN][SI]F[Q R][NEKA]L[LF][SER][QME][AS]EEE[FY]GF[DNQ][HQS][P E][GM][GP]	48	34
Motif2	[PTSA][ASKT][NDVE][VA][P D]KG[HY][FLV][AVP]VYVG[ED]	57	15
Motif3	GLTIPC[KTREN]E[ED][AT]F[IL][DN][LV][TA][SC][RSQ]L[NQS][ASC]S	22	21
Motif4	MI[SN][PA]KKLI[KR]MAR[K EN]WQ[KR][MY]AA[ILM][R GK]RKRI[SI][LS][PQ]R	12	29
Motif5	I[TI]LP[CYF]D[SAL][VFA][F T][ML][EDQ]Y[IAVM][IVL][PSF][LFM][IV][QG][RQ][GH][VM][AS][KE][DE][LIVM]E[K R]AL[LI][MFVTI] S[ILV][AVG][TYS][STD][RN TQC][CS][SL][SLQC][SLF]	9	41
Motif6	M[GAS][IFN][RHA][LF][PQD][SRGL][IMV][IVLG][PQN]A K[QK][IVF][LVPF][RKQ]	16	16
Motif7	[TKVQ][ILV]P[CS][EDRV][V EISP][EVST][EFV][FMLIA][E KRQ][YKER][IVL][LY][KSG] [LMEV]	24	15
Motif8	[SFI][HQC]Q[EG][QH][MTSN I][NGS][ESQH][QRP]LL[LVF] C[ASGR][YFC]	9	15
Motif9	F[KQE]MSEEE[FY]G[LI][PQ] [SR][DTN]GP	5	15
Motif10	NAEKEMIGCCSSSDCELT- PSHHPQMC	2	26

Table S3. The orthologous *SAUR* genes in grape, *Arabidopsis* and tomato genome.

SAUR Name1	SAUR Name2
VvSAUR002	AtSAUR045
VvSAUR003	AtSAUR004
VvSAUR003	AtSAUR018
VvSAUR003	AtSAUR067
VvSAUR021	AtSAUR006
VvSAUR021	AtSAUR007
VvSAUR021	AtSAUR008
VvSAUR021	AtSAUR009
VvSAUR021	AtSAUR012
VvSAUR021	AtSAUR013
VvSAUR021	AtSAUR076
VvSAUR023	AtSAUR006
VvSAUR023	AtSAUR007
VvSAUR023	AtSAUR008
VvSAUR023	AtSAUR009
VvSAUR023	AtSAUR012
VvSAUR023	AtSAUR013
VvSAUR023	AtSAUR076
VvSAUR032	AtSAUR059
VvSAUR033	AtSAUR059
VvSAUR036	AtSAUR059
VvSAUR037	AtSAUR068
VvSAUR037	AtSAUR069
VvSAUR037	AtSAUR070
VvSAUR037	AtSAUR071
VvSAUR037	AtSAUR072
VvSAUR037	AtSAUR073
VvSAUR039	AtSAUR023
VvSAUR041	AtSAUR058
VvSAUR043	AtSAUR027
VvSAUR044	AtSAUR027
VvSAUR045	AtSAUR030
VvSAUR046	AtSAUR029
VvSAUR048	AtSAUR026
VvSAUR049	AtSAUR041
VvSAUR050	AtSAUR041
VvSAUR051	AtSAUR026
VvSAUR052	AtSAUR002
VvSAUR052	AtSAUR075
VvSAUR053	AtSAUR042
VvSAUR055	AtSAUR032
VvSAUR001	SISAUR062
VvSAUR002	SISAUR071
VvSAUR003	SISAUR003
VvSAUR018	SISAUR101
VvSAUR021	SISAUR047
VvSAUR024	SISAUR044
VvSAUR036	SISAUR084
VvSAUR041	SISAUR028
VvSAUR043	SISAUR063
VvSAUR044	SISAUR063
VvSAUR045	SISAUR072
VvSAUR046	SISAUR086
VvSAUR048	SISAUR041
VvSAUR051	SISAUR041

VvSAUR052	SISAUR066
VvSAUR053	SISAUR065
VvSAUR054	SISAUR067
VvSAUR055	SISAUR036

Table S4. The paralogous *SAUR* genes in grape and *Arabidopsis* genome.

SAUR Name1	SAUR Name2
AtSAUR002	AtSAUR075
AtSAUR004	AtSAUR018
AtSAUR004	AtSAUR067
AtSAUR006	AtSAUR007
AtSAUR006	AtSAUR008
AtSAUR006	AtSAUR009
AtSAUR006	AtSAUR012
AtSAUR006	AtSAUR013
AtSAUR006	AtSAUR076
AtSAUR007	AtSAUR008
AtSAUR007	AtSAUR009
AtSAUR007	AtSAUR012
AtSAUR007	AtSAUR013
AtSAUR007	AtSAUR076
AtSAUR008	AtSAUR009
AtSAUR008	AtSAUR012
AtSAUR008	AtSAUR013
AtSAUR008	AtSAUR076
AtSAUR009	AtSAUR012
AtSAUR009	AtSAUR013
AtSAUR009	AtSAUR076
AtSAUR012	AtSAUR013
AtSAUR012	AtSAUR076
AtSAUR013	AtSAUR076
AtSAUR018	AtSAUR067
AtSAUR068	AtSAUR069
AtSAUR068	AtSAUR070
AtSAUR068	AtSAUR071
AtSAUR068	AtSAUR072
AtSAUR068	AtSAUR073
AtSAUR069	AtSAUR070
AtSAUR069	AtSAUR071
AtSAUR069	AtSAUR072
AtSAUR069	AtSAUR073
AtSAUR070	AtSAUR071
AtSAUR070	AtSAUR072
AtSAUR070	AtSAUR073
AtSAUR071	AtSAUR072
AtSAUR071	AtSAUR073
AtSAUR072	AtSAUR073
VvSAUR021	VvSAUR023
VvSAUR032	VvSAUR033
VvSAUR032	VvSAUR036
VvSAUR033	VvSAUR036
VvSAUR043	VvSAUR044
VvSAUR048	VvSAUR051
VvSAUR049	VvSAUR050

Table S5. List of primers used for qRT-PCR and construction of recombinant plasmid.

Gene name	Gene identifier	Forward primer (5'-3')	Reverse primer (5'-3')
VvSAUR041-pB221-GFP	GSVIVG01019093001	TCTAGAATGGG- TATTCGTTTGCCCTCA	GTCGACTTATGAGGCAC- TCAATTGAGA
VvSAUR041-3301	GSVIVG01019093001	CCATGGATGGG- TATTCGTTTGCCCTCA	AGATCTTTATGAGGCAC- TCAATTGAGA
VvSAUR041-pART-CAM-EGFP	GSVIVG01019093001	CTCGAGATGGG- TATTCGTTTGCCCTCA	GAATTCTTATGAGGCAC- TCAATTGAGA
VvSAUR041-qRT	GSVIVG01019093001	GCAG- TCTGTCCATATTAGAAG	GTTAGACCACCCA- TAGAATGA
SlActin	Q96483	TGTCCCTATCTAC- GAGGGTTATGC	AGTTAAATCACGACCAG- CAAGAT
AtUBQ3	AT5G03240	CGGAAAGAC- CATTACTCTGGA	CAAGTGTGCGAC- CATCCTCAA