

Figure S1. Multiple alignment of GASA gene family. (a) Multiple alignment of the conserved GASA domains in *P. euphratica* and *P. trichocarpa*; (b) Sequence logo of the conserved GASA domains *P. euphratica* and *P. trichocarpa*. Each stack represented the amino acids in their corresponding position.

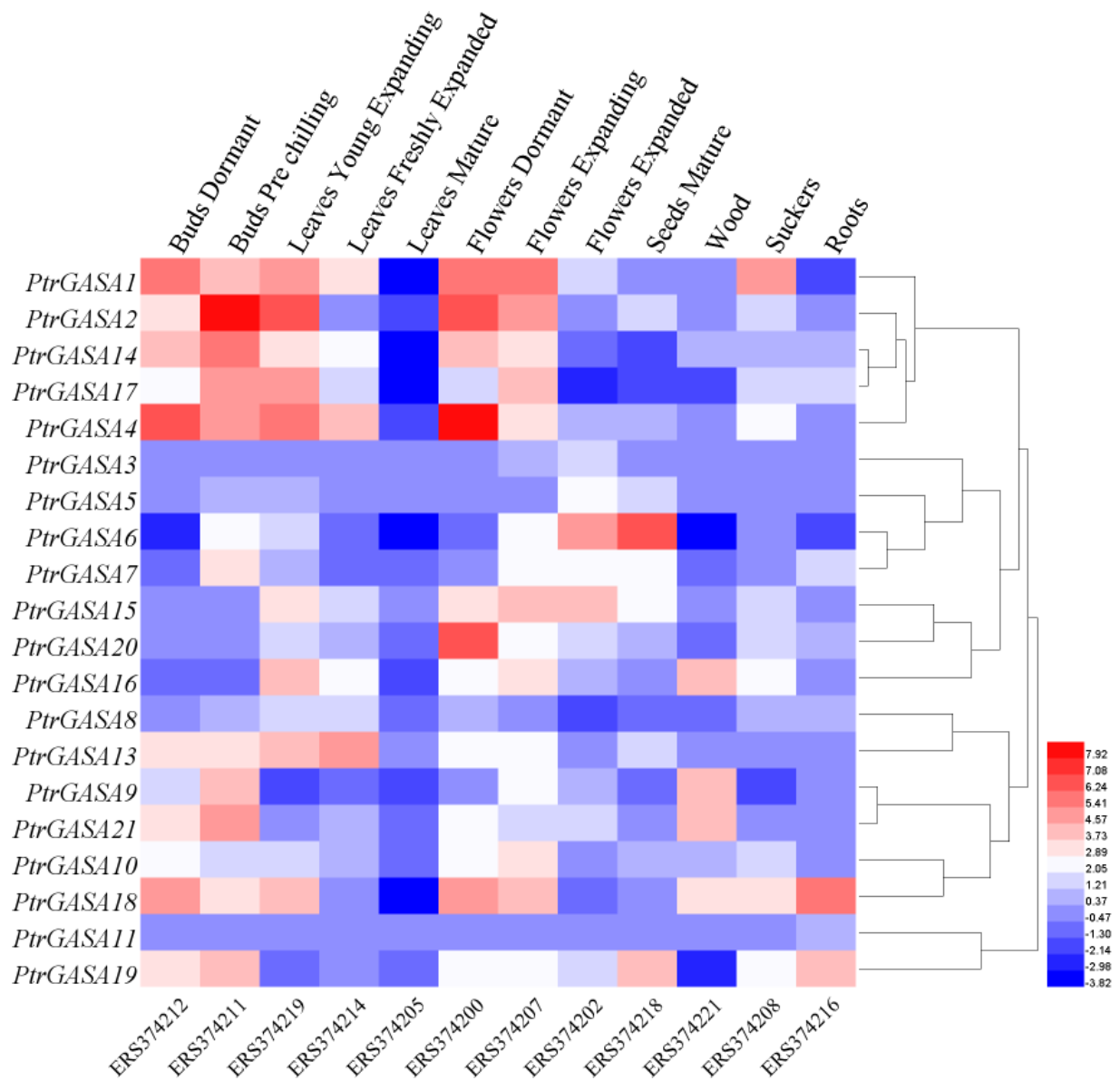


Figure S2. The *PtrGASAs* expression profiles in different tissues. Relative expression profiles are based the online PlantGenIE database.

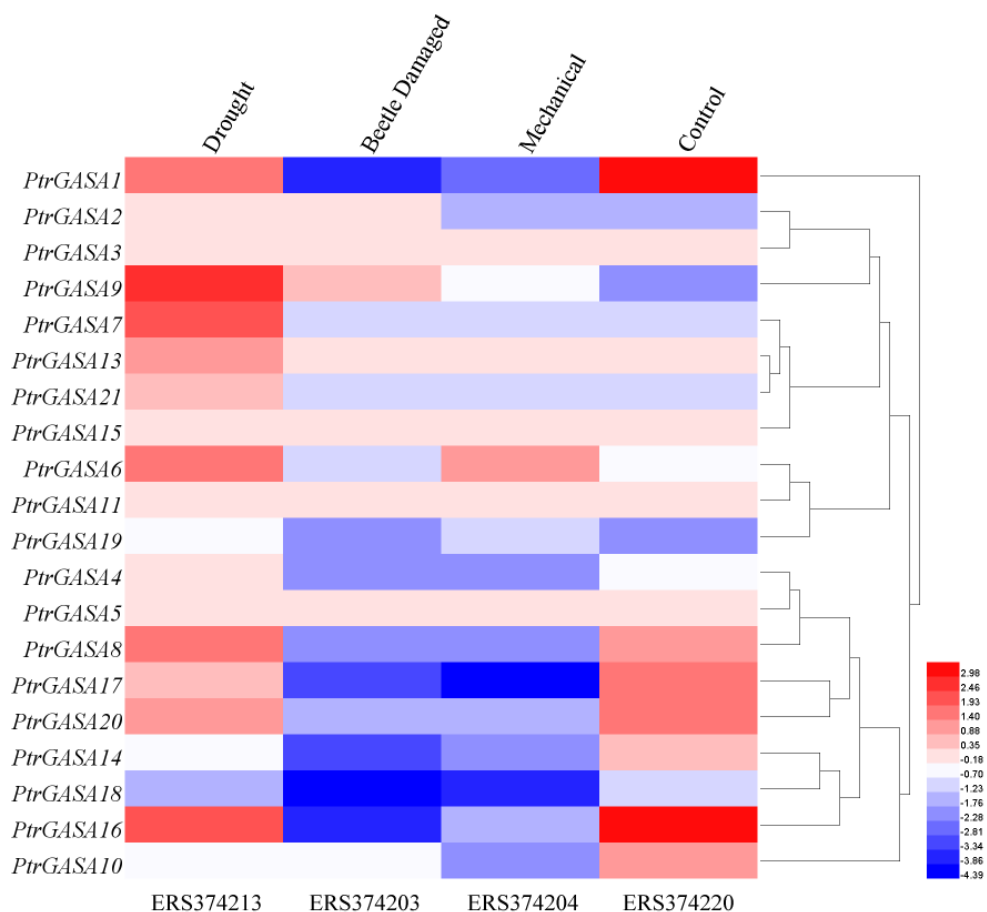


Figure S3. The *PtrGASAs* expression profiles respond to stresses. Relative expression profiles are based on the online PlantGenIE database.

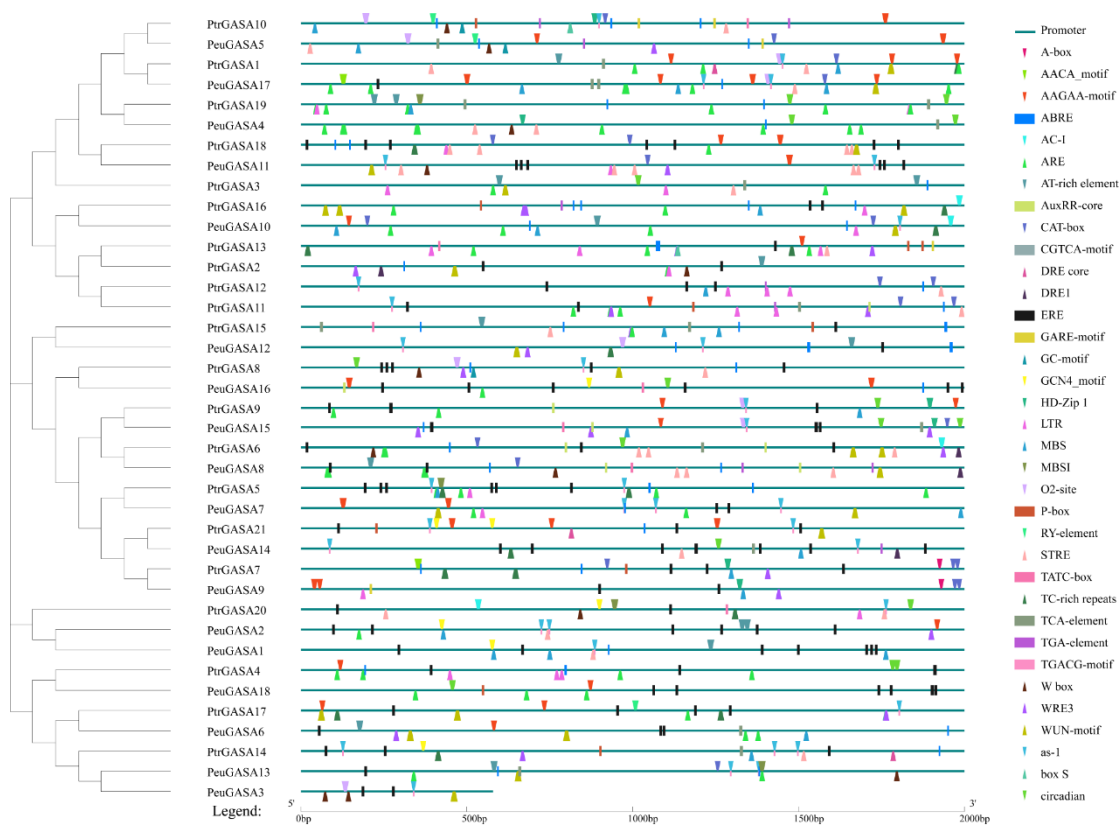


Figure S4. The position of the *cis*-acting elements on the promoter region of *GASAs*.

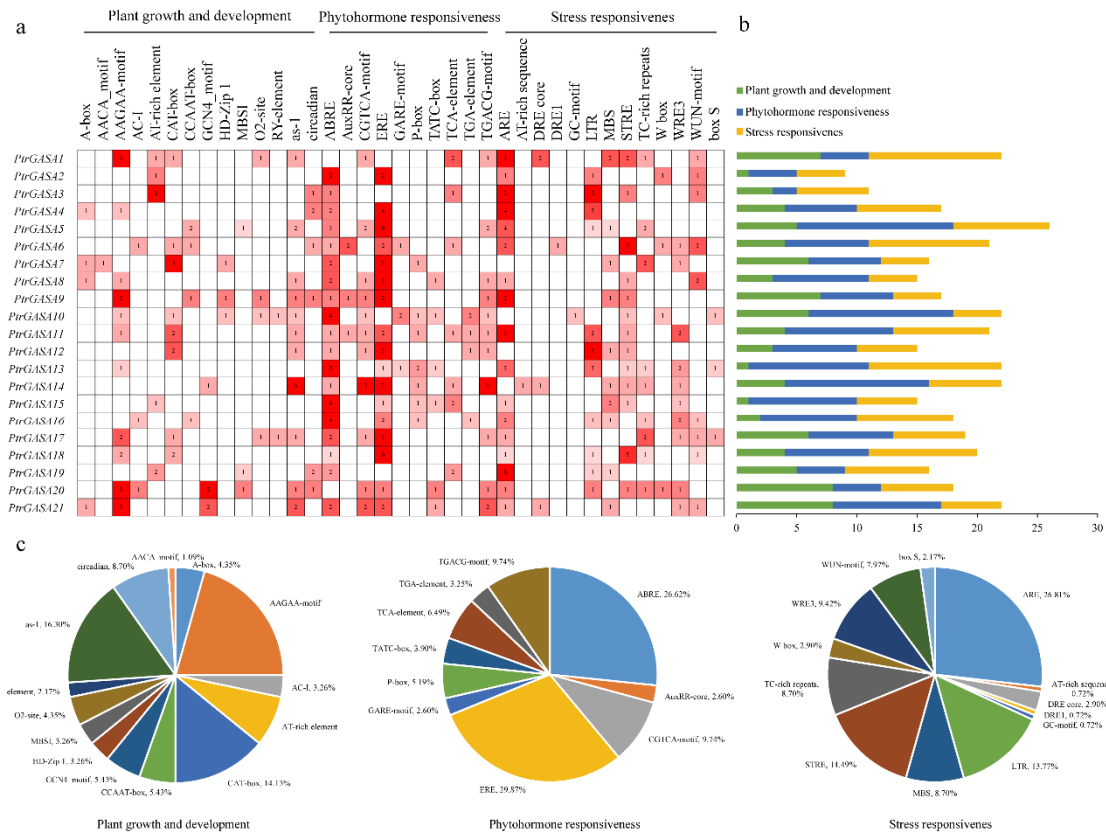


Figure S5. The *cis*-acting elements of *PtrGASA* genes. (a) Numbers and gradient red colors indicate the number of *cis*-acting elements; (b) Color-coded histograms indicate the number of *cis*-acting elements of genes in each category; (c) Pie charts show the proportion of different *cis*-acting elements in each category.

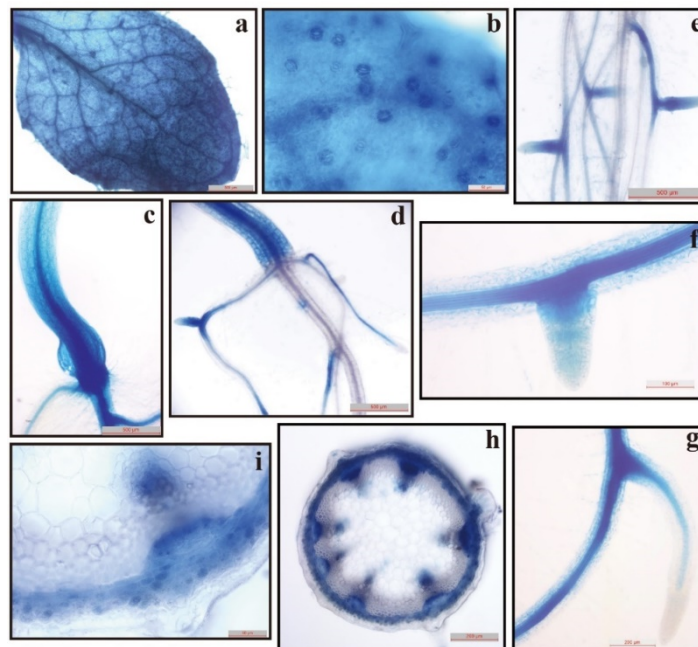


Figure S6. Transgenic *Arabidopsis* tissue under a microscope. (a) Leaf; (b) stoma; (c-g) hypocotyls and roots; (h,i) Stem crosscutting.

Table S1. The position of *GASA* gene family in *Populus*.

Gene	Gene Name	Position
LOC105108948	<i>PeuGASA1</i>	NW_011500085.1 (253260..255106, complement)
LOC105118698	<i>PeuGASA2</i>	NW_011501980.1 (1939..3437, complement)
LOC105120240	<i>PeuGASA3</i>	NW_011505596.1 (579..1520)
LOC105123460	<i>PeuGASA4</i>	NW_011499856.1 (2422403..2423496, complement)
LOC105127637	<i>PeuGASA5</i>	NW_011499872.1 (1730061..1731124, complement)
LOC105128593	<i>PeuGASA6</i>	NW_011499877.1 (999727..1000813,complement)
LOC105128863	<i>PeuGASA7</i>	NW_011499878.1 (1475944..1477033, complement)
LOC105128865	<i>PeuGASA8</i>	NW_011499878.1 (1472235..1473361, complement)
LOC105128866	<i>PeuGASA9</i>	NW_011499878.1 (1469630..1470495, complement)
LOC105128880	<i>PeuGASA10</i>	NW_011499846.1 (516539..517398)
LOC105133442	<i>PeuGASA11</i>	NW_011499907.1 (13672..14941)
LOC105135117	<i>PeuGASA12</i>	NW_011499921.1 (212676..214532, complement)
LOC105139569	<i>PeuGASA13</i>	NW_011499976.1 (560472..561432, complement)
LOC105140101	<i>PeuGASA14</i>	NW_011499986.1 (190386..191299)
LOC105140102	<i>PeuGASA15</i>	NW_011499986.1 (204050..205174)
LOC105140103	<i>PeuGASA16</i>	NW_011499986.1 (208383..209439)
LOC105140300	<i>PeuGASA17</i>	NW_011499990.1 (62980..63949, complement)
LOC105141680	<i>PeuGASA18</i>	NW_011500016.1 (91069..92453, complement)
GWHGAAYU001570	<i>PeuGASA19</i>	GWHAAAYU00000002 (26615279..26616111)

Gene Locus	Gene Name	Position	Homologous Gene
Potri.001G254100	<i>PtrGASA1</i>	Chr01:26388610..26389799 reverse	<i>PeuGASA17</i>
Potri.001G297700	<i>PtrGASA2</i>	Chr01:30205607..30206690 forward	<i>PeuGASA19</i>
Potri.001G315500	<i>PtrGASA3</i>	Chr01:32117807..32119314 reverse	No
Potri.001G350600	<i>PtrGASA4</i>	Chr01:35731577..35732904 forward	<i>PeuGASA18</i>
Potri.002G022500	<i>PtrGASA5</i>	Chr02:1361599..1362424 forward	<i>PeuGASA7</i>
Potri.002G022600	<i>PtrGASA6</i>	Chr02:1364982..1366298 forward	<i>PeuGASA8</i>
Potri.002G022700	<i>PtrGASA7</i>	Chr02:1368371..1369242 forward	<i>PeuGASA9</i>
Potri.005G239000	<i>PtrGASA8</i>	Chr05:24568559..24569894 reverse	<i>PeuGASA16</i>
Potri.005G239100	<i>PtrGASA9</i>	Chr05:24571982..24573134 reverse	<i>PeuGASA15</i>
Potri.006G044400	<i>PtrGASA10</i>	Chr06:3162131..3163068 reverse	<i>PeuGASA5</i>
Potri.007G051300	<i>PtrGASA11</i>	Chr07:5014100..5015000 reverse	No
Potri.007G051400	<i>PtrGASA12</i>	Chr07:5029280..5029709 reverse	No
Potri.009G092600	<i>PtrGASA13</i>	Chr09:8437317..8438127 forward	No
Potri.012G076700	<i>PtrGASA14</i>	Chr12:10207178..10208272 forward	<i>PeuGASA3/13</i>
Potri.013G113400	<i>PtrGASA15</i>	Chr13:12673726..12675596 reverse	<i>PeuGASA12</i>
Potri.014G020100	<i>PtrGASA16</i>	Chr14:1815675..1816439 forward	<i>PeuGASA10</i>
Potri.015G071500	<i>PtrGASA17</i>	Chr15:9609662..9611128 forward	<i>PeuGASA6</i>
Potri.017G083000	<i>PtrGASA18</i>	Chr17:9992148..9993493 forward	<i>PeuGASA11</i>
Potri.017G124200	<i>PtrGASA19</i>	Chr17:13635455..13636699 reverse	<i>PeuGASA4</i>
Potri.019G083900	<i>PtrGASA20</i>	Chr19:11678588..11680344 forward	<i>PeuGASA1/2</i>
Potri.T155100	<i>PtrGASA21</i>	scaffold_621:5902..7033 reverse	<i>PeuGASA14</i>

Table S2. Physicochemical properties and subcellular localization prediction of GASAs in *Populus*.

Gene Name	Formula	Molecular Weight	Theoretical pI	Instability Index (II)	Aliphatic Index	GRAVY	Localization Predicted
<i>PeuGASA1</i>	C ₅₂₁ H ₈₅₀ N ₁₅₂ O ₁₄₇ S ₁₄	12,184.32	9.47	54.87	71.91	-0.224	extr: 13, vacu: 1
<i>PeuGASA2</i>	C ₅₂₁ H ₈₅₀ N ₁₅₂ O ₁₄₇ S ₁₄	12,184.32	9.47	54.87	71.91	-0.224	extr: 13, vacu: 1
<i>PeuGASA3</i>	C ₄₉₄ H ₈₃₀ N ₁₅₆ O ₁₅₀ S ₁₇	11,900	8.88	40.03	75.96	-0.073	extr: 11, vacu: 3 chlo: 6, extr: 5, cyto: 1, mito: 1, E.R.: 1
<i>PeuGASA4</i>	C ₄₆₁ H ₇₄₆ N ₁₃₀ O ₁₂₇ S ₁₄	10,590.63	9.2	40.4	71.89	-0.109	extr: 9, vacu: 3, chlo: 1, golg: 1
<i>PeuGASA5</i>	C ₅₅₂ H ₈₉₀ N ₁₅₈ O ₁₅₉ S ₁₄	12,732.94	9.36	56.2	61.38	-0.397	extr: 8, vacu: 6 cyto: 4, extr: 3, nucl: 2, vacu: 2, chlo: 1, mito: 1, E.R.: 1
<i>PeuGASA6</i>	C ₅₁₈ H ₈₅₇ N ₁₅₉ O ₁₅₁ S ₁₇	12,273.5	8.88	30.55	80.09	0.134	extr: 12, mito: 1, vacu: 1
<i>PeuGASA7</i>	C ₅₂₅ H ₈₈₄ N ₁₅₈ O ₁₆₁ S ₁₅	12,466.66	9.2	41.33	81.86	0.074	extr: 12, chlo: 1, vacu: 1
<i>PeuGASA8</i>	C ₄₄₈ H ₇₃₅ N ₁₃₉ O ₁₃₄ S ₁₄	10,661.45	9.04	53.61	69.12	0.012	extr: 10, vacu: 2, golg: 2
<i>PeuGASA9</i>	C ₄₄₀ H ₇₄₅ N ₁₄₁ O ₁₃₅ S ₁₃	10,587.4	9.16	43	84.16	0.023	extr: 7, vacu: 5, chlo: 1, cyto: 1
<i>PeuGASA10</i>	C ₄₁₇ H ₆₇₁ N ₁₁₃ O ₁₁₇ S ₁₅	9620.5	9.01	25.79	60.91	0.03	extr: 12, cyto: 1, vacu: 1
<i>PeuGASA11</i>	C ₅₂₁ H ₈₁₈ N ₁₅₂ O ₁₃₅ S ₁₅	11,852.06	9.59	43.65	55.19	-0.286	extr: 11, vacu: 3 extr: 6, chlo: 3, vacu: 3, cyto: 1, E.R.: 1
<i>PeuGASA12</i>	C ₄₁₇ H ₆₈₁ N ₁₂₇ O ₁₂₆ S ₁₇	10,034.79	8.6	53.7	63.3	-0.127	extr: 12, vacu: 2
<i>PeuGASA13</i>	C ₄₉₄ H ₈₃₀ N ₁₅₆ O ₁₅₀ S ₁₇	11,900	8.88	40.03	75.96	-0.073	extr: 12, cyto: 1, vacu: 1
<i>PeuGASA14</i>	C ₄₅₅ H ₇₆₆ N ₁₄₂ O ₁₃₇ S ₁₄	10,866.8	9.16	41.78	82.43	0.122	extr: 9, vacu: 3, chlo: 1, golg: 1
<i>PeuGASA15</i>	C ₄₄₄ H ₇₃₇ N ₁₃₅ O ₁₄₀ S ₁₅	10,687.4	8.61	59.73	73.82	0.092	extr: 12, vacu: 1, golg: 1 chlo: 4, extr:
<i>PeuGASA16</i>	C ₄₃₉ H ₇₁₄ N ₁₃₀ O ₁₂₉ S ₁₅	10,358.19	8	37.72	88.57	0.356	4,vacu: 3, cyto: 2, nucl: 1
<i>PeuGASA17</i>	C ₅₃₀ H ₈₅₇ N ₁₅₅ O ₁₄₉ S ₁₅	12,265.48	9.48	49.68	61.42	-0.262	extr: 9, chlo: 3, vacu: 2
<i>PeuGASA18</i>	C ₁₀₆₃ H ₁₇₀₄ N ₂₈₀ O ₂₈₄ S ₁₉	23,560.07	9.76	81.44	52.16	-0.441	chlo: 4, extr: 3, vacu: 3, cyto: 2, nucl: 1, plas: 1
<i>PeuGASA19</i>	C ₄₂₁ H ₆₇₇ N ₁₁₉ O ₁₁₉ S ₁₅	9790.63	9.12	33.52	56.59	-0.205	extr: 13, vacu: 1 chlo: 6, nucl: 2, plas: 2, cyto: 1, mito: 1, vacu: 1, E.R.: 1
<i>PtrGASA1</i>	C ₅₅₄ H ₈₉₆ N ₁₆₂ O ₁₅₅ S ₁₅	12,787.1	9.54	41.77	64.27	-0.223	extr: 12, mito: 1, E.R.: 1
<i>PtrGASA2</i>	C ₄₂₂ H ₆₇₉ N ₁₁₉ O ₁₁₉ S ₁₅	9804.66	9.12	37.23	56.59	-0.203	extr: 13, vacu: 1 chlo: 6, nucl: 2, plas: 2, cyto: 1, mito: 1, vacu: 1, E.R.: 1
<i>PtrGASA3</i>	C ₄₄₁ H ₇₀₃ N ₁₁₉ O ₁₃₆ S ₁₅	10,329.05	7.96	52.4	61.04	-0.014	extr: 12, mito: 1, E.R.: 1
<i>PtrGASA4</i>	C ₉₁₁ H ₁₄₆₉ N ₂₄₇ O ₂₄₇ S ₁₉	20,443.33	9.73	71.58	49.95	-0.442	extr: 13, vacu: 1 chlo: 6, nucl: 2, plas: 2, cyto: 1, mito: 1, vacu: 1, E.R.: 1
<i>PtrGASA5</i>	C ₅₁₈ H ₈₇₁ N ₁₅₇ O ₁₆₁ S ₁₅	12,355.47	9.11	44.96	76.95	-0.015	extr: 12, mito: 1, E.R.: 1
<i>PtrGASA6</i>	C ₄₅₉ H ₇₅₆ N ₁₄₀ O ₁₃₆ S ₁₄	10,860.75	9.03	55.53	73.11	0.042	extr: 12, mito: 1, E.R.: 1

<i>PtrGASA7</i>	C ₄₄₀ H ₇₄₄ N ₁₄₂ O ₁₃₅ S ₁₃	10,600.4	9.16	48.37	83.17	0.026	vacu: 1
<i>PtrGASA8</i>	C ₄₃₇ H ₇₀₆ N ₁₂₈ O ₁₃₁ S ₁₅	10,330.09	8.00	36.62	80.61	0.317	extr: 13, vacu: 1
<i>PtrGASA9</i>	C ₄₆₃ H ₇₅₄ N ₁₃₈ O ₁₃₉ S ₁₄	10,926.76	8.66	55.04	75.92	0.147	extr: 12, cyto: 1, vacu: 1
<i>PtrGASA10</i>	C ₅₅₁ H ₈₈₆ N ₁₅₈ O ₁₅₉ S ₁₄	12,716.9	9.36	57.86	58.02	-0.443	extr: 12, mito: 1, vacu: 1
<i>PtrGASA11</i>	C ₄₉₃ H ₇₈₀ N ₁₃₀ O ₁₃₇ S ₁₄	11,169.25	9.05	47.3	67.94	-0.015	extr: 8, vacu: 4, golg: 2
<i>PtrGASA12</i>	C ₄₉₃ H ₇₈₀ N ₁₃₀ O ₁₃₇ S ₁₄	11,169.25	9.05	47.3	67.94	-0.015	extr: 7, chlo: 4, vacu: 3
<i>PtrGASA13</i>	C ₄₂₉ H ₆₉₂ N ₁₂₀ O ₁₂₁ S ₁₅	9947.85	9.11	34.21	55.96	-0.245	extr: 7, chlo: 4, vacu: 3
<i>PtrGASA14</i>	C ₄₉₆ H ₈₃₂ N ₁₅₄ O ₁₅₀ S ₁₈	11,930.08	8.75	36.72	77.71	-0.012	extr: 9, cyto: 3, chlo: 1, E.R.: 1
<i>PtrGASA15</i>	C ₄₁₅ H ₆₈₉ N ₁₃₁ O ₁₂₄ S ₁₇	10,042.86	8.97	49.23	60.11	-0.221	extr: 10, vacu: 3, chlo: 1
<i>PtrGASA16</i>	C ₄₁₇ H ₆₇₁ N ₁₁₃ O ₁₁₇ S ₁₆	9652.56	9.01	27.19	57.61	0.003	extr: 12, cyto: 1, vacu: 1
<i>PtrGASA17</i>	C ₄₉₀ H ₈₂₂ N ₁₅₄ O ₁₄₇ S ₁₇	11,767.88	8.88	35.07	79.45	0.081	extr: 11, golg: 2, vacu: 1
<i>PtrGASA18</i>	C ₅₂₄ H ₈₂₂ N ₁₅₀ O ₁₃₇ S ₁₅	11,896.11	9.54	42.59	54.67	-0.305	extr: 11, vacu: 3
<i>PtrGASA19</i>	C ₄₅₀ H ₇₂₇ N ₁₂₉ O ₁₂₅ S ₁₅	10,425.41	9.14	42.88	68.17	-0.13	extr: 8, vacu: 4, chlo: 1, cyto: 1
<i>PtrGASA20</i>	C ₅₂₁ H ₈₅₀ N ₁₆₂ O ₁₄₇ S ₁₄	12,184.32	9.47	54.87	71.91	-0.244	chlo: 6, extr: 5, cyto: 1, mito: 1, E.R.: 1
<i>PtrGASA21</i>	C ₄₆₃ H ₇₇₆ N ₁₄₂ O ₁₃₄ S ₁₄	10,924.97	9.36	45.95	82.43	0.131	extr: 13, vacu: 1
							extr: 6, chlo: 3, vacu: 3, cyto: 1, E.R.: 1

Table S3. Subcellular localization and prediction of potential cleavage sites of GASAs in *Populus*.

Gene Name	Len	cTP	mTP	SP	other	Loc	RC	TPle
<i>PeuGASA1</i>	110	0.037	0.014	0.973	0.025	S	1	20
<i>PeuGASA2</i>	110	0.037	0.014	0.973	0.025	S	1	20
<i>PeuGASA3</i>	109	0.075	0.03	0.793	0.073	S	2	21
<i>PeuGASA4</i>	95	0.035	0.028	0.971	0.005	S	1	24
<i>PeuGASA5</i>	116	0.014	0.03	0.946	0.015	S	1	25
<i>PeuGASA6</i>	113	0.01	0.038	0.946	0.044	S	1	21
<i>PeuGASA7</i>	118	0.005	0.082	0.375	0.678	—	4	-
<i>PeuGASA8</i>	102	0.111	0.003	0.937	0.008	S	1	24
<i>PeuGASA9</i>	101	0.084	0.004	0.948	0.012	S	1	23
<i>PeuGASA10</i>	88	0.011	0.015	0.995	0.024	S	1	25
<i>PeuGASA11</i>	106	0.092	0.035	0.501	0.017	S	2	24
<i>PeuGASA12</i>	91	0.015	0.004	0.982	0.052	S	1	28
<i>PeuGASA13</i>	109	0.075	0.03	0.793	0.073	S	2	21
<i>PeuGASA14</i>	103	0.039	0.006	0.96	0.017	S	1	23
<i>PeuGASA15</i>	102	0.076	0.003	0.968	0.015	S	1	24
<i>PeuGASA16</i>	98	0.042	0.011	0.95	0.022	S	1	22
<i>PeuGASA17</i>	113	0.02	0.066	0.844	0.014	S	2	24
<i>PeuGASA18</i>	222	0.017	0.017	0.723	0.114	S	2	20
<i>PeuGASA19</i>	88	0.09	0.051	0.948	0.017	S	1	25

<i>PtrGASA1</i>	117	0.031	0.025	0.903	0.018	S	1	24
<i>PtrGASA2</i>	88	0.073	0.045	0.957	0.02	S	1	25
<i>PtrGASA3</i>	96	0.018	0.017	0.987	0.021	S	1	27
<i>PtrGASA4</i>	191	0.017	0.018	0.763	0.097	S	2	20
<i>PtrGASA5</i>	118	0.011	0.059	0.293	0.64	—	4	-
<i>PtrGASA6</i>	103	0.056	0.002	0.963	0.017	S	1	24
<i>PtrGASA7</i>	101	0.073	0.005	0.956	0.014	S	1	23
<i>PtrGASA8</i>	98	0.052	0.011	0.95	0.019	S	1	22
<i>PtrGASA9</i>	103	0.032	0.003	0.979	0.018	S	1	24
<i>PtrGASA10</i>	116	0.014	0.028	0.95	0.015	S	1	25
<i>PtrGASA11</i>	102	0.055	0.098	0.946	0.003	S	1	25
<i>PtrGASA12</i>	102	0.055	0.098	0.946	0.003	S	1	25
<i>PtrGASA13</i>	89	0.041	0.057	0.972	0.013	S	1	26
<i>PtrGASA14</i>	109	0.035	0.021	0.913	0.063	S	1	21
<i>PtrGASA15</i>	91	0.11	0.005	0.855	0.049	S	2	28
<i>PtrGASA16</i>	88	0.011	0.016	0.995	0.025	S	1	25
<i>PtrGASA17</i>	109	0.025	0.017	0.94	0.044	S	1	21
<i>PtrGASA18</i>	107	0.075	0.022	0.751	0.013	S	2	24
<i>PtrGASA19</i>	97	0.04	0.024	0.971	0.008	S	1	29
<i>PtrGASA20</i>	110	0.037	0.014	0.973	0.025	S	1	25
<i>PtrGASA21</i>	103	0.044	0.005	0.97	0.015	S	1	23

Table S4. The gene-specific primers for qRT-PCR.

Gene	Forward Primer	Reverse Primer
<i>PeuUBQ</i>	5'-AGACCTACACCAAGCCCAAGAAGAT-3'	5'-CCAGCACC GCACTCAGCATTAG-3'
<i>PeuGASA1/2</i>	5'-TAGCAACGCTGCAAATTCTCC-3'	5'-AGGCTTGCATAACATGGGCA-3'
<i>PeuGASA3/13</i>	5'-ATGGCAGTACGTTTCGTTCTT-3'	5'-ACGCACTTGCATCTCACACA-3'
<i>PeuGASA4</i>	5'-ATTCCCTCTTGCTGGTCCTT-3'	5'-CCATAAGTCCCAGGAGGAACAC-3'
<i>PeuGASA5</i>	5'-ACATCACAGAGGCTCCAACC-3'	5'-TCCCATAAGTTCCAGCAGGC-3'
<i>PeuGASA6</i>	5'-CAGCTTGTTGTGAGAGGTGG-3'	5'-CCATGGGTGGTCATGTCAGTA-3'
<i>PeuGASA7</i>	5'-CGCTTCGCTTGTCGTATCTC-3'	5'-TATCTAGGTTGCCGGAAGTGC-3'
<i>PeuGASA8</i>	5'-GTGAACTCGAATCTTGCTGCG-3'	5'-ATGGGTAGTCAAGCTGGCG-3'
<i>PeuGASA9</i>	5'-TGTGCTCCATCTTGCCGAAG-3'	5'-CACGAGTAGTCAAGGTGGCA-3'
<i>PeuGASA10</i>	5'-CACGAGTGCCCTTGCTACAG-3'	5'-CGGTGGCAACTACCGGAAT-3'
<i>PeuGASA11</i>	5'-TTGCCATTTCATGCTCCAA-3'	5'-TGTAAGCAAGGGCACACAGC-3'
<i>PeuGASA12</i>	5'-GGTCAGTGCCAAGACAACATT-3'	5'-GTTGGCATAGCAAGGACAGGT-3'
<i>PeuGASA14</i>	5'-CATCTCTCCTTGCTCCGC-3'	5'-CGGTAGTCATGCTGGCATAG-3'
<i>PeuGASA15</i>	5'-CTTCTTGTTCTCCAATTGCCG-3'	5'-GGCAAGCGTCATAGTTACCG-3'
<i>PeuGASA16</i>	5'-GCTGTCCTCCTGTAGGCAT-3'	5'-CCATAGCAGGGACACACGTC-3'
<i>PeuGASA17</i>	5'-ACAACGACAGGGCAACCAT-3'	5'-CAGTTGTTGTAGCAAGGGCA-3'
<i>PeuGASA18</i>	5'-GCTGTGTCTTATGCTGGT-3'	5'-AGGTGGTGTCTTAAGTGGTGG-3'
<i>PeuGASA19</i>	5'-GTTGCTGTGTTCCCTCCTCTT-3'	5'-AAGGGCACTCGTGCTTGTTTC-3'

Table S5. The gene-specific primers of *Peu*GASAs for PCR-amplified.

Gene Name	Forward Primer	Reverse Primer
<i>PeuGASA4</i>	5'-ATGGCTAGCCTCAGTCGCA-3'	5'-CAAGGGCACTTGGGTCTTCC-3'
<i>PeuGASA5</i>	5'-ATGTCGAGGAAGCCAAGCATTA-3'	5'-AAGGGCACTTGGGGCCTC-3'
<i>PeuGASA8</i>	5'-AAGGACACTTGCGTCTGCC-3'	5'-AAGGACACTTGCGTCTGCC-3'
<i>PeuGASA10</i>	5'-ATGAAGCCTGTTTTTGCAGCTATT-3'	5'-AAGGGCACTTCGGTTTGCC-3'
<i>PeuGASA11</i>	5'-ATGGCTAAGTTTGTGCTGTCTTC-3'	5'-AAGGGCACTTGGGCCCTC-3'
<i>PeuGASA15</i>	5'-ATGGCTATGATCACCAAGTTGCT-3'	5'-AAGGACACTTGCGTCTGCC-3'
<i>PeuGASA18</i>	5'-ATGGCTTTCAAAGCTGTGTGTC-3'	5'-AAGGGCACTTGGGCTTGTTG-3'
<i>PeuGASA17</i>	5'-ATGGGCAAATCAAGCATTGCC-3'	5'-AAGGGCATTGTTGGGCCCTC-3'
<i>PeuGASA15Pro</i>	<u>5'-GGATCCACGCGATTGTCTGGTTGGAAG-3'</u>	<u>5'-GAATTCCTGGGATGAACTAGGAAAGGGTC-3'</u>