



Box	Gene symbol	The Populus genome v1.1
(A) ABA biosynthesis [43, 44, 109]	<i>DXS</i>	gw1.171.35.1 / gw1.III.2599.1
	<i>MCS</i>	gw1.I.8813.1*
	<i>GPPS/GPS1</i>	eugene3.00101320*
	<i>PSD</i>	fgenes4_pm.C_LG_II000277*
	<i>PSY</i>	gw1.44.342.1*
	<i>BETA-OHASE</i>	estExt_fgenes4_pg.C_440224* / estExt_Genewise1_v1.C_17880001
	<i>LYC</i>	grail3.0066009001
	<i>NCED</i>	eugene3.00110845* / gw1.146.74.1 / gw1.VI.2099.1
	<i>ABA2</i>	eugene3.00010285* / eugene3.00160678 / eugene3.00061405*
	<i>ZEP</i>	gw1.VII.2982.1* / eugene3.00160678
<i>AAO</i>	eugene3.00102359	
(B) ABA-mediated signalling pathway [45- 49, 51]	<i>RD26</i>	fgenes4_pg.C_scaffold_107000083 / estExt_Genewise1_v1.C_LG_XI3994
	<i>DREB1(-A,-D)</i>	gw1.I.9165.1 / fgenes4_pg.C_LG_XII001200
	<i>MYC2</i>	eugene3.00021640
	<i>ABRE binding factors</i>	eugene3.00021164 / grail3.0040023201* / fgenes4_pg.C_LG_IX000628 / gw1.130.194.1 / grail3.0003013801*
	<i>OST1/SNRK2-6</i>	estExt_fgenes4_pg.C_1300020*
<i>PYL</i>	fgenes4_pg.C_scaffold_118000009 / estExt_fgenes4_pm.C_LG_II0464 / gw1.VI.730.1 / gw1.X.1600.1 / gw1.XVI.3905.1	
(C) Response to ABA stimulus [48, 50, 51, 53, 55-60, 88]	<i>NF-YA</i>	grail3.0024038301
	<i>ATHB12</i>	eugene3.00140486*
	<i>Zat10/STZ</i>	estExt_Genewise1_v1.C_LG_XIV0633 / gw1.II.2573.1 / gw1.I.4086.1
	<i>AZF2</i>	eugene3.00090763
	<i>GBF3</i>	gw1.XIV.1557.1*
	<i>RC12</i>	eugene3.00080380 / eugene3.01310022 / eugene3.00130015
	<i>COR413-PMs</i>	estExt_Genewise1_v1.C_LG_IV0366 / estExt_fgenes4_pm.C_LG_IX0279
	<i>REM</i>	gw1.VI.1266.1 / gw1.XVI.1724.1
<i>RD22</i>	gw1.801.1.1 / gw1.XIX.246.1	
(D) Negative regulation of ABA-mediated signalling pathway [42, 46- 48, 51, 68, 111-113]	<i>ABF</i>	eugene3.00170499 / eugene3.00170500 / eugene3.00080900
	<i>ERD15</i>	estExt_fgenes4_pg.C_LG_III1639
	<i>ABR1</i>	fgenes4_pg.C_LG_V001123 / grail3.0003056501
	<i>ATHB6</i>	estExt_Genewise1_v1.C_LG_V4715 / gw1.VII.1686.1* / estExt_fgenes4_pm.C_LG_II0461* / estExt_Genewise1_v1.C_LG_V2675*
	<i>PP2C</i>	gw1.XII.1331.1* / gw1.211.9.1* / fgenes4_pm.C_LG_XII000477 / estExt_Genewise1_v1.C_LG_VIII0367* / grail3.0022022401* / fgenes4_pg.C_LG_IX001205* / gw1.I.1127.1
<i>Dead-box RNA Helicase</i>	estExt_fgenes4_pg.C_LG_II1544 / estExt_Genewise1_v1.C_LG_XIV1670 / gw1.XIV.1672.1	
(E) ABA-independent signalling pathway [47, 49, 52, 54, 56]	<i>DREB2A</i>	eugene3.00101772
	<i>ZAT12</i>	eugene3.00091367 / estExt_Genewise1_v1.C_LG_I1393
	<i>NF-YB</i>	gw1.XIV.2649.1
	<i>JAR1</i>	estExt_fgenes4_pg.C_LG_II1531*
(F) [91, 92]	<i>ESKIMO1</i>	gw1.VIII.1375.1 / gw1.X.1696.1
(G) [110]	<i>XERICO</i>	estExt_Genewise1_v1.C_LG_XIV3857*
(H) Detoxification Cell rescue [23, 76 -86, 88]	<i>sHSP</i>	estExt_Genewise1_v1.C_LG_XIX2021 / grail3.0023024001 / grail3.0066002801 / eugene3.00080557 / estExt_Genewise1_v1.C_LG_IX3982 / eugene3.00011624 / gw1.I.502.1 / grail3.0022018701 / eugene3.00012051
	<i>MT</i>	eugene3.01070053 / eugene3.00110909 / eugene3.00060718 / gw1.I.1300.1 / eugene3.01200081 / eugene3.00060718 /
	<i>TIL</i>	estExt_fgenes4_pg.C_2080003
	<i>Catalase</i>	estExt_Genewise1_v1.C_LG_XVIII3
	<i>GST</i>	estExt_fgenes4_pm.C_LG_V0695
	<i>SOD</i>	eugene3.00020134 / gw1.X.2945.1 / gw1.VIII.2464.1 / estExt_fgenes4_pg.C_8990003 / grail3.0094003001 /
	<i>Lactoylglutathione lyase</i>	estExt_fgenes4_pg.C_LG_VIII1530 / grail3.0036009801 / estExt_Genewise1_v1.C_860293 / gw1.942.4.1 / eugene3.00161127 / fgenes4_pg.C_scaffold_3983000002 / gw1.7940.4.1
	<i>GPX</i>	gw1.XV.2559.1
	<i>APX</i>	estExt_Genewise1_v1.C_570289 / estExt_Genewise1_v1.C_LG_IV1582
	<i>SEN1</i>	estExt_Genewise1_v1.C_LG_I8960
	<i>GoIS</i>	estExt_fgenes4_pg.C_570071 / eugene3.00090344
	<i>DIN10</i>	estExt_fgenes4_pg.C_570018
	<i>SIP1</i>	estExt_fgenes4_pm.C_LG_II0906 / fgenes4_pm.C_LG_X000590 / gw1.131.196.1 / fgenes4_pm.C_LG_VIII000417 /
	<i>AtSIP1</i>	estExt_fgenes4_pm.C_LG_XIII0025 / gw1.XIII.547.1
	<i>AtSIP2</i>	fgenes4_pg.C_LG_VI000475 / grail3.4045000202
	<i>STS</i>	eugene3.00640058 / fgenes4_pm.C_LG_VII000086
<i>AOX</i>	eugene3.01400033	
<i>SAG21</i>	estExt_Genewise1_v1.C_LG_XVI1715 / eugene3.00060481 / eugene3.00150654	
<i>HSPRO2</i>	eugene3.00140639	
	gw1.XII.484.1	
	estExt_Genewise1_v1.C_LG_II1841	
	estExt_fgenes4_pm.C_LG_X0749 / gw1.VIII.884.1	

\* : Gene models listed in ABA biosynthesis, ABA transcription factor or ABA signal transduction in poplar [38]  
[ ] : supporting literature