

SUPPLEMENTARY FILE 1

Gymnosperm species

Taxus chinensis

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * Tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 461.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.62633	-0.65638	-0.01874	0.54624	2.75311

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.3826	0.6186
Residual		0.5987	0.7737
Number of obs:	172	groups:	Sample, 86

Fixed effects:

	Estimate	Std. Error	df	t value	Pr(> t)	
(Intercept)	1.2046	0.3133	137.1481	3.845	0.000184	***
GenesLAR2	0.871	0.346	79	2.517	0.013851	*
TissueBud and Leave	1.2824	1.039	137.1481	1.234	0.219219	
TissueCambial meristem	-1.1068	0.4242	137.1481	-2.61	0.010074	*
TissueCell line	-0.4101	0.4102	137.1481	-1	0.319115	
TissueCone	0.9612	0.5116	137.1481	1.879	0.062373	.
TissueLeaf	0.8637	0.3531	137.1481	2.446	0.015698	*
TissueRoot	0.4388	0.5116	137.1481	0.858	0.392537	
GenesLAR2:TissueBud and leave	1.5703	1.1477	79	1.368	0.175117	
GenesLAR2:TissueCambial meristem	3.9742	0.4685	79	8.482	9.98E-13	***
GenesLAR2:TissueCell line	3.3827	0.4531	79	7.466	9.48E-11	***
GenesLAR2:TissueCone	1.3847	0.5651	79	2.451	0.016475	*
GenesLAR2:TissueLeaf	0.9309	0.39	79	2.387	0.019378	*
GenesLAR2:TissueRoot	0.7534	0.5651	79	1.333	0.186281	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 1S. Estimated marginal means and pairwise comparison for the species *Taxus chinensis*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
Tissue = Bark: Genes emmean SE df lower.CL upper.CL LAR1 1.2046 0.313 137 0.585 1.824 LAR2 2.0756 0.313 137 1.456 2.695 Tissue = Bud and leave: Genes emmean SE df lower.CL upper.CL LAR1 2.4869 0.991 137 0.528 4.446 LAR2 4.9282 0.991 137 2.969 6.887 Tissue = Cambial meristem: Genes emmean SE df lower.CL upper.CL LAR1 0.0977 0.286 137 -0.468 0.663 LAR2 4.9430 0.286 137 4.378 5.508 Tissue = Cell line: Genes emmean SE df lower.CL upper.CL LAR1 0.7944 0.265 137 0.271 1.318 LAR2 5.0482 0.265 137 4.525 5.572 Tissue = Cone: Genes emmean SE df lower.CL upper.CL LAR1 2.1658 0.404 137 1.366 2.965 LAR2 4.4215 0.404 137 3.622 5.221 Tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 2.0683 0.163 137 1.746 2.390 LAR2 3.8702 0.163 137 3.548 4.192 Tissue = Root: Genes emmean SE df lower.CL upper.CL LAR1 1.6433 0.404 137 0.844 2.443 LAR2 3.2678 0.404 137 2.468 4.067	Tissue = Bark: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.871 0.346 79 -2.517 0.0139 Tissue = Bud and leave: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -2.441 1.090 79 -2.231 0.0285 Tissue = Cambial meristem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -4.845 0.316 79 -15.339 <.0001 Tissue = Cell line: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -4.254 0.292 79 -14.545 <.0001 Tissue = Cone: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -2.256 0.447 79 -5.050 <.0001 Tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.802 0.180 79 -10.017 <.0001 Tissue = Root: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.624 0.447 79 -3.636 0.0005

Ginkgo biloba

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 2493.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1077	-0.5304	-0.0785	0.4852	4.7825

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.3123	0.5588
Residual		0.5487	0.7407
Number of obs:	954	groups:	Sample, 477

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	2.7967	0.3507	820.112	7.975	5.12E-15	***
GenesLAR2	-0.2512	0.3959	464	-0.634	0.526149	
tissueCalli	-0.784	0.405	820.112	-1.936	0.053211	.
tissueCambium	-1.9581	0.4676	820.112	-4.188	3.13E-05	***
tissueFlower	-1.0843	0.4103	820.112	-2.643	0.008373	**
tissueFruit	-1.4112	0.4676	820.112	-3.018	0.002624	**
tissueKernel	-2.6392	0.4802	820.112	-5.496	5.20E-08	***
tissueLeaf	-0.182	0.3543	820.112	-0.514	0.607551	
tissueOvule	-0.0745	0.3986	820.112	-0.187	0.851769	
tissueRoot	-1.576	0.5162	820.112	-3.053	0.00234	**
tissueSeedling leaves	-0.7702	0.4676	820.112	-1.647	0.099897	.
tissueSeedling stem	-2.1762	0.6403	820.112	-3.399	0.00071	***
tissueStem	0.2434	0.4247	820.112	0.573	0.566711	
tissueTesta	-2.4819	0.6403	820.112	-3.876	0.000115	***
GenesLAR2:tissueCalli	1.6212	0.4572	464	3.546	0.000431	***
GenesLAR2:tissueCambium	0.6589	0.5279	464	1.248	0.212642	
GenesLAR2:tissueFlower	1.637	0.4632	464	3.534	0.00045	***
GenesLAR2:tissueFruit	0.9921	0.5279	464	1.879	0.060836	.
GenesLAR2:tissueKernel	0.6385	0.5422	464	1.178	0.239495	
GenesLAR2:tissueLeaf	-1.2138	0.4	464	-3.035	0.002541	**
GenesLAR2:tissueOvule	0.1129	0.45	464	0.251	0.802091	
GenesLAR2:tissueRoot	1.5588	0.5828	464	2.675	0.007746	**
GenesLAR2:tissueSeedling leaves	-0.1148	0.5279	464	-0.217	0.82798	

<i>GenesLAR2:tissueSeedling stem</i>	2.3996	0.7229	464	3.32	0.000973	***
<i>GenesLAR2:tissueStem</i>	-1.4876	0.4795	464	-3.102	0.002036	**
<i>GenesLAR2:tissueTesta</i>	0.3654	0.7229	464	0.505	0.61349	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 2S. Estimated marginal means and pairwise comparison for the species *Ginkgo biloba*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Buds: Genes emmean SE df lower.CL upper.CL LAR1 2.797 0.351 820 2.108 3.485 LAR2 2.546 0.351 820 1.857 3.234	tissue = Buds: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.251 0.3960 464 0.634 0.5261
tissue = Calli: Genes emmean SE df lower.CL upper.CL LAR1 2.013 0.202 820 1.615 2.410 LAR2 3.383 0.202 820 2.985 3.780	tissue = Calli: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.370 0.2290 464 -5.993 <.0001
tissue = Cambium: Genes emmean SE df lower.CL upper.CL LAR1 0.839 0.309 820 0.232 1.446 LAR2 1.246 0.309 820 0.639 1.853	tissue = Cambium: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.408 0.3490 464 -1.168 0.2436
tissue = Flower: Genes emmean SE df lower.CL upper.CL LAR1 1.712 0.213 820 1.295 2.130 LAR2 3.098 0.213 820 2.680 3.516	tissue = Flower: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.386 0.2400 464 -5.766 <.0001
tissue = Fruit: Genes emmean SE df lower.CL upper.CL LAR1 1.386 0.309 820 0.778 1.993 LAR2 2.127 0.309 820 1.519 2.734	tissue = Fruit: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.741 0.3490 464 -2.122 0.0344
tissue = Kernel: Genes emmean SE df lower.CL upper.CL LAR1 0.158 0.328 820 -0.486 0.802 LAR2 0.545 0.328 820 -0.099 1.189	tissue = Kernel: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.387 0.3700 464 -1.046 0.2962
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 2.615 0.050 820 2.517 2.713 LAR2 1.150 0.050 820 1.052 1.248	tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.465 0.0565 464 25.938 <.0001
tissue = Ovule: Genes emmean SE df lower.CL upper.CL LAR1 2.722 0.189 820 2.350 3.094 LAR2 2.584 0.189 820 2.212 2.956	tissue = Ovule: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.138 0.2140 464 0.647 0.5180
	tissue = Root: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.308 0.4280 464 -3.058 0.0024
	tissue = Seedling leaves: contrast estimate SE df t.ratio p.value

tissue = Root: Genes emmean SE df lower.CL upper.CL LAR1 1.221 0.379 820 0.477 1.964 LAR2 2.528 0.379 820 1.785 3.272 tissue = Seedling leaves: Genes emmean SE df lower.CL upper.CL LAR1 2.027 0.309 820 1.419 2.634 LAR2 1.661 0.309 820 1.053 2.268 tissue = Seedling stem: Genes emmean SE df lower.CL upper.CL LAR1 0.621 0.536 820 -0.431 1.672 LAR2 2.769 0.536 820 1.717 3.821 tissue = Stem: Genes emmean SE df lower.CL upper.CL LAR1 3.040 0.240 820 2.570 3.510 LAR2 1.301 0.240 820 0.831 1.772 tissue = Testa: Genes emmean SE df lower.CL upper.CL LAR1 0.315 0.536 820 -0.737 1.366 LAR2 0.429 0.536 820 -0.623 1.481	LAR1 - LAR2 0.366 0.3490 464 1.048 0.2952 tissue = Seedling stem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -2.148 0.6050 464 -3.552 0.0004 tissue = Stem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.739 0.2700 464 6.429 <.0001 tissue = Testa: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.114 0.6050 464 -0.189 0.8503 Degrees-of-freedom method: kenward-roger Confidence level used: 0.95
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Pinus pinaster

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 613.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.67838	-0.36856	-0.00996	0.24	2.29392

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.8802	0.9382
Residual	0.3831	0.619	
Number of obs:	224	groups:	Sample, 112

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)
(Intercept)	0.10854	0.32446	142.72131	0.335	0.73847
GenesLAR2	3.68975	0.2527	106	14.601	< 2E-016 ***
TissueRoot	2.47978	0.36276	142.72131	6.836	2.19E-10 ***
Tissueshoot	1.11747	0.40336	142.72131	2.77	0.00634 **
TissueSomatic embryo	-0.03068	0.49562	142.72131	-0.062	0.95073
TissueStem	-0.03791	0.45886	142.72131	-0.083	0.93427
TissueZygotic embryo	-0.10689	0.49562	142.72131	-0.216	0.82956
GenesLAR2:TissueRoot	-2.65545	0.28253	106	-9.399	1.27E-15 ***
GenesLAR2:Tissueshoot	-1.29568	0.31415	106	-4.124	7.41E-05 ***
GenesLAR2:TissueSomatic embryo	-2.42709	0.386	106	-6.288	7.33E-09 ***
GenesLAR2:TissueStem	0.85597	0.35737	106	2.395	0.01837 *
GenesLAR2:TissueZygotic embryo	-3.45121	0.386	106	-8.941	1.35E-14 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 3S. Estimated marginal means and pairwise comparison for the species *Pinus pinaster*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

Estimated Marginal Means	Contrasts
Tissue = Needles: Genes emmean SE df lower.CL upper.CL LAR1 0.10854 0.324 143 -0.533 0.750 LAR2 3.79830 0.324 143 3.157 4.440	Tissue = Needles: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -3.690 0.253 106 -14.601 <.0001
Tissue = Root: Genes emmean SE df lower.CL upper.CL LAR1 2.58832 0.162 143 2.268 2.909 LAR2 3.62263 0.162 143 3.302 3.943	Tissue = Root: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.034 0.126 106 -8.186 <.0001
Tissue = shoot: Genes emmean SE df lower.CL upper.CL LAR1 1.22601 0.240 143 0.752 1.700 LAR2 3.62009 0.240 143 3.146 4.094	Tissue = shoot: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -2.394 0.187 106 -12.828 <.0001
Tissue = Somatic embryo: Genes emmean SE df lower.CL upper.CL LAR1 0.07787 0.375 143 -0.663 0.818 LAR2 1.34053 0.375 143 0.600 2.081	Tissue = Somatic embryo: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.263 0.292 106 -4.327 <.0001
Tissue = Stem: Genes emmean SE df lower.CL upper.CL LAR1 0.07063 0.324 143 -0.571 0.712 LAR2 4.61635 0.324 143 3.975 5.258	Tissue = Stem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -4.546 0.253 106 -17.989 <.0001
Tissue = Zygotic embryo: Genes emmean SE df lower.CL upper.CL LAR1 0.00166 0.375 143 -0.739 0.742 LAR2 0.24020 0.375 143 -0.500 0.981	Tissue = Zygotic embryo: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.239 0.292 106 -0.818 0.4155
	Degrees-of-freedom method: kenward-roger Confidence level used: 0.95

Picea sitchensis

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 308.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.8217	-0.41947	-0.00553	0.41571	2.8217

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.1518	0.3897
Residual		0.2081	0.4561
Number of obs:	178	groups:	Sample, 89

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	4.87926	0.59992	139.22303	8.133	2.07E-13	***
GenesLAR2	-0.37136	0.64509	82	-0.576	0.566413	
tissueCortex	-1.7998	0.61636	139.22303	-2.92	0.004083	**
tissueEndosperm	-3.28643	0.73474	139.22303	-4.473	1.59E-05	***
tissueNeedle	0.35175	0.73474	139.22303	0.479	0.632872	
tissueSclereid	-2.19898	0.61636	139.22303	-3.568	0.000494	***
tissueShoot tip	-1.30728	0.61229	139.22303	-2.135	0.034505	*
tissueStem	-0.87324	0.61229	139.22303	-1.426	0.156051	
GenesLAR2:tissueCortex	-0.46952	0.66277	82	-0.708	0.48069	
GenesLAR2:tissueEndosperm	-0.99933	0.79007	82	-1.265	0.209507	
GenesLAR2:tissueNeedle	-2.84911	0.79007	82	-3.606	0.000533	***
GenesLAR2:tissueSclereid	0.62355	0.66277	82	0.941	0.349556	
GenesLAR2:tissueShoot tip	1.11278	0.6584	82	1.69	0.094798	
GenesLAR2:tissueStem	-0.03206	0.6584	82	-0.049	0.961284	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 4S. Estimated marginal means and pairwise comparison for the species *Picea sitchensis*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

Estimated Marginal Means	Contrasts
tissue = Bark:	tissue = Bark:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 4.879 0.600 139 3.693 6.07	LAR1 - LAR2 0.371 0.645 82 0.576 0.5664

LAR2 4.508 0.600 139 3.322 5.69	
tissue = Cortex:	tissue = Cortex:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 3.079 0.141 139 2.800 3.36	LAR1 - LAR2 0.841 0.152 82 5.530 <.0001
LAR2 2.239 0.141 139 1.959 2.52	
tissue = Endosperm:	tissue = Endosperm:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 1.593 0.424 139 0.754 2.43	LAR1 - LAR2 1.371 0.456 82 3.005 0.0035
LAR2 0.222 0.424 139 -0.617 1.06	
tissue = Needle:	tissue = Needle:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 5.231 0.424 139 4.392 6.07	LAR1 - LAR2 3.220 0.456 82 7.060 <.0001
LAR2 2.011 0.424 139 1.172 2.85	
tissue = Sclereid:	tissue = Sclereid:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 2.680 0.141 139 2.401 2.96	LAR1 - LAR2 -0.252 0.152 82 -1.659 0.1010
LAR2 2.932 0.141 139 2.653 3.21	
tissue = Shoot tip:	tissue = Shoot tip:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 3.572 0.122 139 3.330 3.81	LAR1 - LAR2 -0.741 0.132 82 -5.631 <.0001
LAR2 4.313 0.122 139 4.071 4.56	
tissue = Stem:	tissue = Stem:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 4.006 0.122 139 3.764 4.25	LAR1 - LAR2 0.403 0.132 82 3.064 0.0030
LAR2 3.603 0.122 139 3.360 3.84	
	Degrees-of-freedom method: kenward-roger
	Confidence level used: 0.95

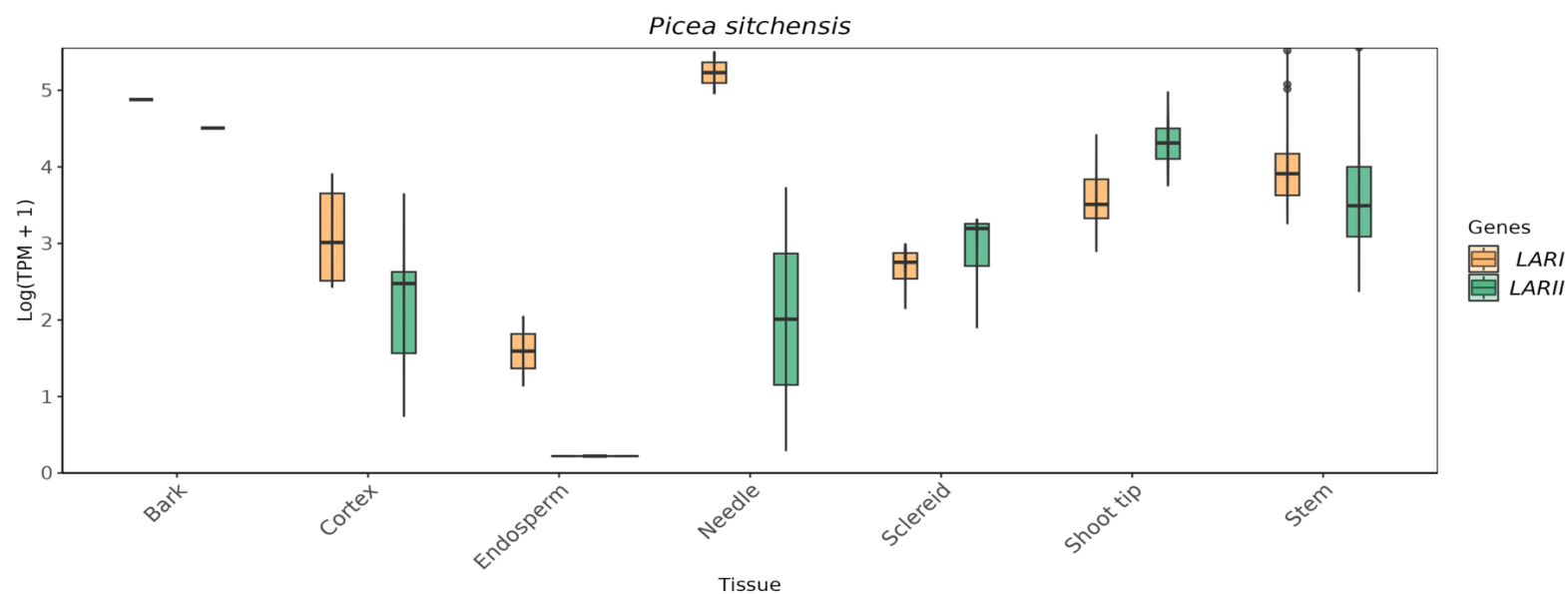


Figure 1S. Comparison of the expression of *LARI* (orange) and *LARII* (green) genes in the species *Picea sitchensis*

Thuja plicata

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 296.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.1305	-0.2767	-0.0173	0.2678	5.7278

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.007017	0.08377
Residual	0.075059	0.27397	
Number of obs:	664	groups:	Sample, 83

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	4.34E-14	7.40E-02	6.01E+02	0	1	
GenesLAR1b	-3.39E-14	1.00E-01	5.53E+02	0	1	
GenesLAR1c	4.66E-02	1.00E-01	5.53E+02	0.466	0.64142	
GenesLAR1d	7.15E-02	1.00E-01	5.53E+02	0.715	0.47484	
GenesLAR1e	-3.49E-14	1.00E-01	5.53E+02	0	1	
GenesLAR1f	5.63E-03	1.00E-01	5.53E+02	0.056	0.95515	
GenesLAR2a	3.26E+00	1.00E-01	5.53E+02	32.538	< 2.00E-16	***
GenesLAR2b	1.61E+00	1.00E-01	5.53E+02	16.057	< 2.00E-16	***
tissueFoliage	8.01E-04	8.97E-02	6.01E+02	0.009	0.99288	
tissueWhole seedling	6.07E-01	1.03E-01	6.01E+02	5.89	6.42E-09	***
tissueWood core	-4.50E-14	9.79E-02	6.01E+02	0	1	
GenesLAR1b:tissueFoliage	3.27E-04	1.21E-01	5.53E+02	0.003	0.99785	
GenesLAR1c:tissueFoliage	8.89E-01	1.21E-01	5.53E+02	7.334	8.02E-13	***
GenesLAR1d:tissueFoliage	7.64E-01	1.21E-01	5.53E+02	6.304	5.93E-10	***
GenesLAR1e:tissueFoliage	1.87E-02	1.21E-01	5.53E+02	0.154	0.87756	
GenesLAR1f:tissueFoliage	5.98E-02	1.21E-01	5.53E+02	0.494	0.62182	
GenesLAR2a:tissueFoliage	8.04E-01	1.21E-01	5.53E+02	6.628	8.08E-11	***
GenesLAR2b:tissueFoliage	2.30E+00	1.21E-01	5.53E+02	18.937	< 2.00E-16	***
GenesLAR1b:tissueWhole seedling	-6.04E-01	1.39E-01	5.53E+02	-4.335	1.73E-05	***
GenesLAR1c:tissueWhole seedling	3.10E-01	1.39E-01	5.53E+02	2.223	0.02664	*
GenesLAR1d:tissueWhole seedling	-2.18E-01	1.39E-01	5.53E+02	-1.566	0.118	
GenesLAR1e:tissueWhole seedling	2.37E-01	1.39E-01	5.53E+02	1.7	0.08969	.
GenesLAR1f:tissueWhole seedling	4.30E-01	1.39E-01	5.53E+02	3.087	0.00212	**
GenesLAR2a:tissueWhole seedling	-1.93E+00	1.39E-01	5.53E+02	-13.838	< 2.00E-16	***
GenesLAR2b:tissueWhole seedling	6.23E-01	1.39E-01	5.53E+02	4.47	9.49E-06	***
GenesLAR1b:tissueWood core	3.55E-14	1.32E-01	5.53E+02	0	1	
GenesLAR1c:tissueWood core	-4.66E-02	1.32E-01	5.53E+02	-0.352	0.72479	
GenesLAR1d:tissueWood core	-1.59E-02	1.32E-01	5.53E+02	-0.12	0.90469	
GenesLAR1e:tissueWood core	2.95E-03	1.32E-01	5.53E+02	0.022	0.98223	
GenesLAR1f:tissueWood core	-3.51E-03	1.32E-01	5.53E+02	-0.027	0.97886	
GenesLAR2a:tissueWood core	-1.69E+00	1.32E-01	5.53E+02	-12.752	< 2.00E-16	***
GenesLAR2b:tissueWood core	3.33E-01	1.32E-01	5.53E+02	2.518	0.0121	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 5S. Estimated marginal means and pairwise comparison for the species *Thuja plicata*. Degrees-of-freedom method: kenward-roge. P value adjustment: bonferroni method for 28 tests.

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Cambium:	tissue = Cambium:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1a 0.000000 0.0740 601 -0.1453 0.145	LAR1a - LAR1b 0.000000 0.1000 553 0.000 1.0000
LAR1b 0.000000 0.0740 601 -0.1453 0.145	LAR1a - LAR1c -0.046616 0.1000 553 -0.466 1.0000
LAR1c 0.046616 0.0740 601 -0.0987 0.192	LAR1a - LAR1d -0.071541 0.1000 553 -0.715 1.0000
LAR1d 0.071541 0.0740 601 -0.0737 0.217	LAR1a - LAR1e 0.000000 0.1000 553 0.000 1.0000
LAR1e 0.000000 0.0740 601 -0.1453 0.145	LAR1a - LAR1f -0.005629 0.1000 553 -0.056 1.0000
LAR1f 0.005629 0.0740 601 -0.1396 0.151	LAR1a - LAR2a -3.255100 0.1000 553 -32.538 <.0001
LAR2a 3.255100 0.0740 601 3.1098 3.400	LAR1a - LAR2b -1.606325 0.1000 553 -16.057 <.0001
LAR2b 1.606325 0.0740 601 1.4611 1.752	LAR1b - LAR1c -0.046616 0.1000 553 -0.466 1.0000
	LAR1b - LAR1d -0.071541 0.1000 553 -0.715 1.0000
tissue = Foliage:	LAR1b - LAR1e 0.000000 0.1000 553 0.000 1.0000
Genes emmean SE df lower.CL upper.CL	LAR1b - LAR1f -0.005629 0.1000 553 -0.056 1.0000
LAR1a 0.000801 0.0506 601 -0.0987 0.100	LAR1b - LAR2a -3.255100 0.1000 553 -32.538 <.0001
LAR1b 0.001128 0.0506 601 -0.0983 0.101	LAR1b - LAR2b -1.606325 0.1000 553 -16.057 <.0001
LAR1c 0.936533 0.0506 601 0.8371 1.036	LAR1c - LAR1d -0.024924 0.1000 553 -0.249 1.0000
LAR1d 0.836638 0.0506 601 0.7372 0.936	LAR1c - LAR1e 0.046616 0.1000 553 0.466 1.0000
LAR1e 0.019487 0.0506 601 -0.0800 0.119	LAR1c - LAR1f 0.040988 0.1000 553 0.410 1.0000
LAR1f 0.066268 0.0506 601 -0.0332 0.166	LAR1c - LAR2a -3.208484 0.1000 553 -32.072 <.0001
LAR2a 4.059520 0.0506 601 3.9601 4.159	LAR1c - LAR2b -1.559709 0.1000 553 -15.591 <.0001
LAR2b 3.903093 0.0506 601 3.8036 4.003	LAR1d - LAR1e 0.071541 0.1000 553 0.715 1.0000
tissue = Whole seedling:	LAR1d - LAR1f 0.065912 0.1000 553 0.659 1.0000
Genes emmean SE df lower.CL upper.CL	LAR1d - LAR2a -3.183560 0.1000 553 -31.823 <.0001
LAR1a 0.606477 0.0716 601 0.4658 0.747	LAR1d - LAR2b -1.534785 0.1000 553 -15.342 <.0001
LAR1b 0.002840 0.0716 601 -0.1378 0.144	LAR1e - LAR1f -0.005629 0.1000 553 -0.056 1.0000
LAR1c 0.962611 0.0716 601 0.8219 1.103	LAR1e - LAR2a -3.255100 0.1000 553 -32.538 <.0001
LAR1d 0.460002 0.0716 601 0.3193 0.601	LAR1e - LAR2b -1.606325 0.1000 553 -16.057 <.0001
LAR1e 0.843202 0.0716 601 0.7025 0.984	LAR1f - LAR2a -3.249472 0.1000 553 -32.482 <.0001
LAR1f 1.041985 0.0716 601 0.9013 1.183	LAR1f - LAR2b -1.600697 0.1000 553 -16.001 <.0001
LAR2a 1.934677 0.0716 601 1.7940 2.075	LAR2a - LAR2b 1.648775 0.1000 553 16.481 <.0001
LAR2b 2.835261 0.0716 601 2.6946 2.976	tissue = Foliage:
tissue = Wood core:	contrast estimate SE df t.ratio p.value
Genes emmean SE df lower.CL upper.CL	LAR1a - LAR1b -0.000327 0.0685 553 -0.005 1.0000
LAR1a 0.000000 0.0641 601 -0.1258 0.126	LAR1a - LAR1c -0.935732 0.0685 553 -13.662 <.0001
LAR1b 0.000000 0.0641 601 -0.1258 0.126	LAR1a - LAR1d -0.835837 0.0685 553 -12.203 <.0001
LAR1c 0.000000 0.0641 601 -0.1258 0.126	LAR1a - LAR1e -0.018687 0.0685 553 -0.273 1.0000
LAR1d 0.055687 0.0641 601 -0.0701 0.181	LAR1a - LAR1f -0.065467 0.0685 553 -0.956 1.0000
LAR1e 0.002949 0.0641 601 -0.1229 0.129	LAR1a - LAR2a -4.058719 0.0685 553 -59.258 <.0001
LAR1f 0.002121 0.0641 601 -0.1237 0.128	LAR1a - LAR2b -3.902292 0.0685 553 -56.974 <.0001
LAR2a 1.567546 0.0641 601 1.4417 1.693	LAR1b - LAR1c -0.935405 0.0685 553 -13.657 <.0001
LAR2b 1.939493 0.0641 601 1.8137 2.065	LAR1b - LAR1d -0.835510 0.0685 553 -12.199 <.0001
	LAR1b - LAR1e -0.018359 0.0685 553 -0.268 1.0000
	LAR1b - LAR1f -0.065140 0.0685 553 -0.951 1.0000
	LAR1b - LAR2a -4.058392 0.0685 553 -59.253 <.0001

	LAR1b - LAR2b -3.901965 0.0685 553 -56.969 <.0001
	LAR1c - LAR1d 0.099896 0.0685 553 1.458 1.0000
	LAR1c - LAR1e 0.917046 0.0685 553 13.389 <.0001
	LAR1c - LAR1f 0.870265 0.0685 553 12.706 <.0001
	LAR1c - LAR2a -3.122987 0.0685 553 -45.596 <.0001
	LAR1c - LAR2b -2.966560 0.0685 553 -43.312 <.0001
	LAR1d - LAR1e 0.817150 0.0685 553 11.931 <.0001
	LAR1d - LAR1f 0.770370 0.0685 553 11.248 <.0001
	LAR1d - LAR2a -3.222882 0.0685 553 -47.055 <.0001
	LAR1d - LAR2b -3.066455 0.0685 553 -44.771 <.0001
	LAR1e - LAR1f -0.046780 0.0685 553 -0.683 1.0000
	LAR1e - LAR2a -4.040033 0.0685 553 -58.985 <.0001
	LAR1e - LAR2b -3.883605 0.0685 553 -56.701 <.0001
	LAR1f - LAR2a -3.993252 0.0685 553 -58.302 <.0001
	LAR1f - LAR2b -3.836825 0.0685 553 -56.018 <.0001
	LAR2a - LAR2b 0.156427 0.0685 553 2.284 0.6372
	tissue = Whole seedling:
	contrast estimate SE df t.ratio p.value
	LAR1a - LAR1b 0.603637 0.0969 553 6.232 <.0001
	LAR1a - LAR1c -0.356133 0.0969 553 -3.677 0.0073
	LAR1a - LAR1d 0.146475 0.0969 553 1.512 1.0000
	LAR1a - LAR1e -0.236725 0.0969 553 -2.444 0.4155
	LAR1a - LAR1f -0.435508 0.0969 553 -4.496 0.0002
	LAR1a - LAR2a -1.328200 0.0969 553 -13.712 <.0001
	LAR1a - LAR2b -2.228784 0.0969 553 -23.010 <.0001
	LAR1b - LAR1c -0.959770 0.0969 553 -9.909 <.0001
	LAR1b - LAR1d -0.457162 0.0969 553 -4.720 0.0001
	LAR1b - LAR1e -0.840362 0.0969 553 -8.676 <.0001
	LAR1b - LAR1f -1.039144 0.0969 553 -10.728 <.0001
	LAR1b - LAR2a -1.931837 0.0969 553 -19.944 <.0001
	LAR1b - LAR2b -2.832421 0.0969 553 -29.242 <.0001
	LAR1c - LAR1d 0.502608 0.0969 553 5.189 <.0001
	LAR1c - LAR1e 0.119408 0.0969 553 1.233 1.0000
	LAR1c - LAR1f -0.079374 0.0969 553 -0.819 1.0000
	LAR1c - LAR2a -0.972066 0.0969 553 -10.035 <.0001
	LAR1c - LAR2b -1.872651 0.0969 553 -19.333 <.0001
	LAR1d - LAR1e -0.383200 0.0969 553 -3.956 0.0024
	LAR1d - LAR1f -0.581983 0.0969 553 -6.008 <.0001
	LAR1d - LAR2a -1.474675 0.0969 553 -15.224 <.0001
	LAR1d - LAR2b -2.375259 0.0969 553 -24.522 <.0001
	LAR1e - LAR1f -0.198783 0.0969 553 -2.052 1.0000
	LAR1e - LAR2a -1.091475 0.0969 553 -11.268 <.0001
	LAR1e - LAR2b -1.992059 0.0969 553 -20.566 <.0001
	LAR1f - LAR2a -0.892692 0.0969 553 -9.216 <.0001
	LAR1f - LAR2b -1.793277 0.0969 553 -18.514 <.0001
	LAR2a - LAR2b -0.900584 0.0969 553 -9.298 <.0001
	tissue = Wood core:
	contrast estimate SE df t.ratio p.value

	LAR1a - LAR1b	0.000000	0.0866	553	0.000	1.0000
	LAR1a - LAR1c	0.000000	0.0866	553	0.000	1.0000
	LAR1a - LAR1d	-0.055687	0.0866	553	-0.643	1.0000
	LAR1a - LAR1e	-0.002949	0.0866	553	-0.034	1.0000
	LAR1a - LAR1f	-0.002121	0.0866	553	-0.024	1.0000
	LAR1a - LAR2a	-1.567546	0.0866	553	-18.093	<.0001
	LAR1a - LAR2b	-1.939493	0.0866	553	-22.386	<.0001
	LAR1b - LAR1c	0.000000	0.0866	553	0.000	1.0000
	LAR1b - LAR1d	-0.055687	0.0866	553	-0.643	1.0000
	LAR1b - LAR1e	-0.002949	0.0866	553	-0.034	1.0000
	LAR1b - LAR1f	-0.002121	0.0866	553	-0.024	1.0000
	LAR1b - LAR2a	-1.567546	0.0866	553	-18.093	<.0001
	LAR1b - LAR2b	-1.939493	0.0866	553	-22.386	<.0001
	LAR1c - LAR1d	-0.055687	0.0866	553	-0.643	1.0000
	LAR1c - LAR1e	-0.002949	0.0866	553	-0.034	1.0000
	LAR1c - LAR1f	-0.002121	0.0866	553	-0.024	1.0000
	LAR1c - LAR2a	-1.567546	0.0866	553	-18.093	<.0001
	LAR1c - LAR2b	-1.939493	0.0866	553	-22.386	<.0001
	LAR1d - LAR1e	0.052738	0.0866	553	0.609	1.0000
	LAR1d - LAR1f	0.053566	0.0866	553	0.618	1.0000
	LAR1d - LAR2a	-1.511859	0.0866	553	-17.451	<.0001
	LAR1d - LAR2b	-1.883806	0.0866	553	-21.744	<.0001
	LAR1e - LAR1f	0.000828	0.0866	553	0.010	1.0000
	LAR1e - LAR2a	-1.564597	0.0866	553	-18.059	<.0001
	LAR1e - LAR2b	-1.936544	0.0866	553	-22.352	<.0001
	LAR1f - LAR2a	-1.565425	0.0866	553	-18.069	<.0001
	LAR1f - LAR2b	-1.937372	0.0866	553	-22.362	<.0001
	LAR2a - LAR2b	-0.371947	0.0866	553	-4.293	0.0006

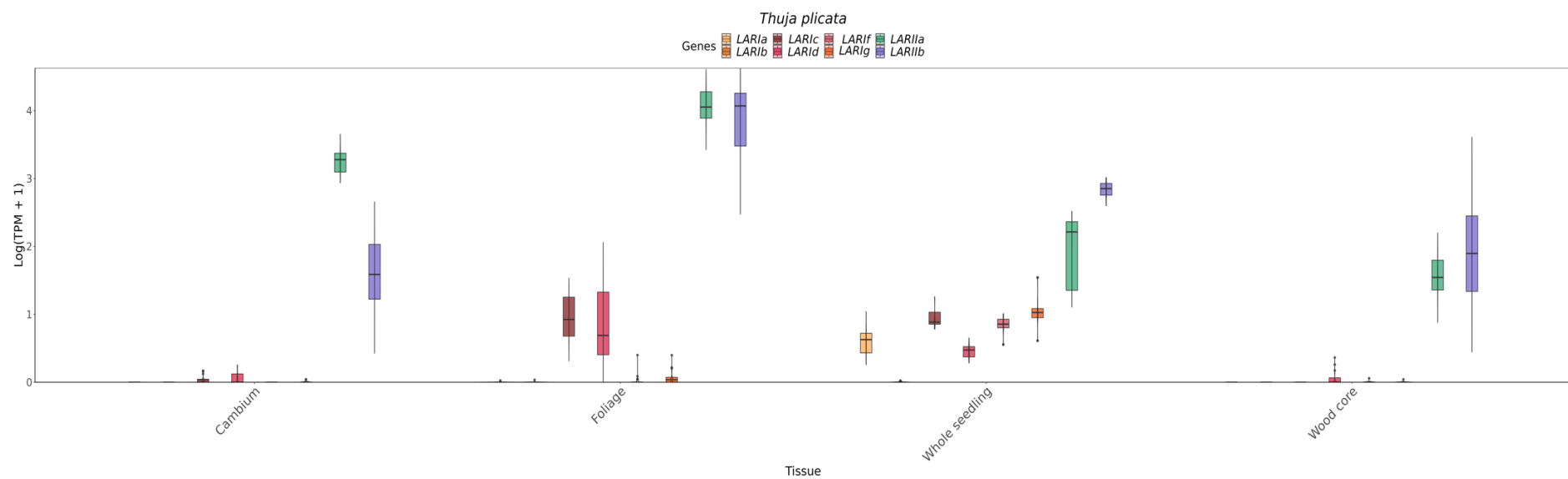


Figure 2S. Comparison of the expression of *LARla* (yellow), *LARlb* (coral), *LARlc* (brown), *LARld* (pink), *LARlf* (red), *LARlg* (orange), *LARIIa* (green) and *LARIIb* (lila) genes in the species *Thuja plicata*.

Dicotyledon species

Vitis vinifera

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 2277.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.52487	-0.66092	-0.08172	0.50523	3.04447

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.3433	0.5859
Residual	1.4538	1.2058	
Number of obs:	674	groups:	Sample, 337

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	1.49268	0.10374	630.97507	14.389	< 2E-016	***
GenesLAR2	0.7286	0.13195	326.99998	5.522	6.85E-08	***
tissueCallus	-1.46912	0.67827	630.97507	-2.166	0.03069	*
tissueFlower	1.5704	0.40065	630.97507	3.92	9.84E-05	***
tissueGrapevine	2.32336	0.40065	630.97507	5.799	1.06E-08	***
tissueInflorescence	0.97675	0.40065	630.97507	2.438	0.01505	*
tissueLeaf	0.31846	0.16696	630.97507	1.907	0.05693	.
tissueOvule	2.23736	0.45874	630.97507	4.877	1.36E-06	***
tissuePlant	0.82036	0.55703	630.97507	1.473	0.14132	
tissueSeedling	2.26516	0.95359	630.97507	2.375	0.01783	*
tissueStem	0.79727	0.48519	630.97507	1.643	0.10084	
GenesLAR2:tissueCallus	-0.7298	0.86275	326.99998	-0.846	0.39822	
GenesLAR2:tissueFlower	-0.8013	0.50963	326.99998	-1.572	0.11684	
GenesLAR2:tissueGrapevine	-0.9581	0.50963	326.99998	-1.88	0.061	.
GenesLAR2:tissueInflorescence	-0.61914	0.50963	326.99998	-1.215	0.22528	
GenesLAR2:tissueLeaf	0.67119	0.21238	326.99998	3.16	0.00172	**
GenesLAR2:tissueOvule	-0.47409	0.58351	326.99998	-0.812	0.41711	
GenesLAR2:tissuePlant	-1.02363	0.70854	326.99998	-1.445	0.1495	

GenesLAR2:tissueSeedling	-2.09943	1.21296	326.99998	-1.731	0.08442	.
GenesLAR2:tissueStem	0.07115	0.61715	326.99998	0.115	0.90829	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 6S. Estimated marginal means and pairwise comparison for the species *Vitis vinifera*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

Estimated Marginal Means	Contrasts
tissue = Berry: Genes emmean SE df lower.CL upper.CL LAR1 1.4927 0.104 631 1.289 1.70 LAR2 2.2213 0.104 631 2.018 2.42	tissue = Berry: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.72860 0.132 327 -5.522 <.0001
tissue = Callus: Genes emmean SE df lower.CL upper.CL LAR1 0.0236 0.670 631 -1.293 1.34 LAR2 0.0224 0.670 631 -1.294 1.34	tissue = Callus: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.00121 0.853 327 0.001 0.9989
tissue = Flower: Genes emmean SE df lower.CL upper.CL LAR1 3.0631 0.387 631 2.303 3.82 LAR2 2.9904 0.387 631 2.230 3.75	tissue = Flower: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.07270 0.492 327 0.148 0.8827
tissue = Grapevine: Genes emmean SE df lower.CL upper.CL LAR1 3.8160 0.387 631 3.056 4.58 LAR2 3.5865 0.387 631 2.827 4.35	tissue = Grapevine: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.22951 0.492 327 0.466 0.6414
tissue = Inflorescence: Genes emmean SE df lower.CL upper.CL LAR1 2.4694 0.387 631 1.709 3.23 LAR2 2.5789 0.387 631 1.819 3.34	tissue = Inflorescence: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.10946 0.492 327 -0.222 0.8242
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 1.8111 0.131 631 1.554 2.07 LAR2 3.2109 0.131 631 2.954 3.47	tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.39979 0.166 327 -8.412 <.0001
tissue = Ovule: Genes emmean SE df lower.CL upper.CL LAR1 3.7300 0.447 631 2.853 4.61 LAR2 3.9845 0.447 631 3.107 4.86	tissue = Ovule: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.25451 0.568 327 -0.448 0.6546
tissue = Plant: Genes emmean SE df lower.CL upper.CL LAR1 2.3130 0.547 631 1.238 3.39 LAR2 2.0180 0.547 631 0.943 3.09	tissue = Plant: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.29504 0.696 327 0.424 0.6720
tissue = Seedling:	tissue = Seedling: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.37084 1.210 327 1.137 0.2564
	tissue = Stem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.79975 0.603 327 -1.327 0.1856
	Degrees-of-freedom method: kenward-roger

Genes emmean SE df lower.CL upper.CL	
LAR1 3.7578 0.948 631 1.896 5.62	
LAR2 2.3870 0.948 631 0.526 4.25	
tissue = Stem:	
Genes emmean SE df lower.CL upper.CL	
LAR1 2.2900 0.474 631 1.359 3.22	
LAR2 3.0897 0.474 631 2.159 4.02	
Degrees-of-freedom method: kenward-roger	
Confidence level used: 0.95	

Theobroma cacao

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 2160.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.41237	-0.50204	0.01226	0.51105	1.94826

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	1.2945	1.1378
Residual		0.4684	0.6844
Number of obs:	716	groups:	Sample, 358

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	3.92368	0.22443	454.78463	17.483	<2E-016	***
GenesLAR2	-0.99649	0.16361	350.00001	-6.091	2.96E-09	***
tissueInflorescence	0.53744	0.47609	454.78463	1.129	0.25955	
tissueLeaf	-0.96882	0.23975	454.78463	-4.041	6.25E-05	***
tissueMix-leaf-flower	0.31182	0.37218	454.78463	0.838	0.40257	
tissuePistil	0.1097	0.47609	454.78463	0.23	0.81788	
tissuePod	-2.65025	0.44416	454.78463	-5.967	4.87E-09	***
tissueSeedling	-0.05375	0.47609	454.78463	-0.113	0.91015	
tissueYoung red leaves	-0.45728	0.43126	454.78463	-1.06	0.28955	
GenesLAR2:tissueInflorescence	0.25293	0.34706	350.00001	0.729	0.46662	
GenesLAR2:tissueLeaf	0.57051	0.17477	350.00001	3.264	0.00121	**

<i>GenesLAR2:tissueMix-leaf-flower</i>	0.37982	0.27131	350.00001	1.4	0.16242	
<i>GenesLAR2:tissuePistil</i>	2.27943	0.34706	350.00001	6.568	1.85E-10	***
<i>GenesLAR2:tissuePod</i>	3.70218	0.32379	350.00001	11.434	<2E-016	***
<i>GenesLAR2:tissueSeedling</i>	0.27493	0.34706	350.00001	0.792	0.42881	
<i>GenesLAR2:tissueYoung red leaves</i>	-0.08063	0.31438	350.00001	-0.256	0.79774	

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Table 7S. Estimated marginal means and pairwise comparison for the species *Theobroma cacao*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Cells: Genes emmean SE df lower.CL upper.CL LAR1 3.92 0.2240 455 3.48 4.36 LAR2 2.93 0.2240 455 2.49 3.37	tissue = Cells: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.996 0.1640 350 6.091 <.0001
tissue = Inflorescence: Genes emmean SE df lower.CL upper.CL LAR1 4.46 0.4200 455 3.64 5.29 LAR2 3.72 0.4200 455 2.89 4.54	tissue = Inflorescence: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.744 0.3060 350 2.429 0.0156
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 2.95 0.0843 455 2.79 3.12 LAR2 2.53 0.0843 455 2.36 2.69	tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.426 0.0615 350 6.931 <.0001
tissue = Mix-leaf-flower: Genes emmean SE df lower.CL upper.CL LAR1 4.24 0.2970 455 3.65 4.82 LAR2 3.62 0.2970 455 3.04 4.20	tissue = Mix-leaf-flower: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.617 0.2160 350 2.849 0.0046
tissue = Pistil: Genes emmean SE df lower.CL upper.CL LAR1 4.03 0.4200 455 3.21 4.86 LAR2 5.32 0.4200 455 4.49 6.14	tissue = Pistil: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.283 0.3060 350 -4.192 <.0001
tissue = Pod: Genes emmean SE df lower.CL upper.CL LAR1 1.27 0.3830 455 0.52 2.03 LAR2 3.98 0.3830 455 3.23 4.73	tissue = Pod: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -2.706 0.2790 350 -9.684 <.0001
tissue = Seedling: Genes emmean SE df lower.CL upper.CL LAR1 3.87 0.4200 455 3.04 4.70 LAR2 3.15 0.4200 455 2.32 3.97	tissue = Seedling: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.722 0.3060 350 2.357 0.0190
tissue = Young red leaves: Genes emmean SE df lower.CL upper.CL LAR1 3.47 0.3680 455 2.74 4.19 LAR2 2.39 0.3680 455 1.67 3.11	tissue = Young red leaves: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.077 0.2680 350 4.012 0.0001
	Degrees-of-freedom method: kenward-roger Confidence level used: 0.95

Moringa oleifera

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 221.1

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.90128	-0.47035	-0.05556	0.55924	2.55943

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.1212	0.3482
Residual		0.6087	0.7802
Number of obs:	92	groups:	Sample, 46

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	2.48954	0.3488	77.85264	7.137	4.35E-10	***
GenesLAR2	0.18026	0.45046	40	0.4	0.69116	
tissueFlower	-2.03704	0.60414	77.85264	-3.372	0.00117	**
tissueLeaf	-2.03072	0.39166	77.85264	-5.185	1.66E-06	***
tissuePod	-2.31756	0.6976	77.85264	-3.322	0.00136	**
tissueRoot	0.71184	0.46142	77.85264	1.543	0.12696	
tissueStem	0.3158	0.5515	77.85264	0.573	0.56855	
GenesLAR2:tissueFlower	0.57236	0.78022	40	0.734	0.46748	
GenesLAR2:tissueLeaf	1.10037	0.50581	40	2.175	0.03556	*
GenesLAR2:tissuePod	0.02109	0.90092	40	0.023	0.98144	
GenesLAR2:tissueRoot	1.10062	0.5959	40	1.847	0.07216	.
GenesLAR2:tissueStem	1.47121	0.71224	40	2.066	0.04538	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 8S. Estimated marginal means and pairwise comparison for the species *Moringa oleifera*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95.

Estimated Marginal Means	Contrasts
tissue = Callus:	tissue = Callus:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 2.490 0.349 77.8 1.795 3.184	LAR1 - LAR2 -0.180 0.450 40 -0.400 0.6912
LAR2 2.670 0.349 77.8 1.975 3.364	tissue = Flower:
tissue = Flower:	contrast estimate SE df t.ratio p.value
Genes emmean SE df lower.CL upper.CL	LAR1 - LAR2 -0.753 0.637 40 -1.181 0.2444
LAR1 0.453 0.493 77.8 -0.530 1.435	tissue = Leaf:

LAR2	1.205	0.493	77.8	0.223	2.187	contrast	estimate	SE	df	t.ratio	p.value
tissue = Leaf:						LAR1 - LAR2	-1.281	0.230	40	-5.566	<.0001
Genes emmean	SE	df	lower.CL	upper.CL		tissue = Pod:					
LAR1	0.459	0.178	77.8	0.104	0.813	contrast	estimate	SE	df	t.ratio	p.value
LAR2	1.739	0.178	77.8	1.385	2.094	LAR1 - LAR2	-0.201	0.780	40	-0.258	0.7977
tissue = Pod:						tissue = Root:					
Genes emmean	SE	df	lower.CL	upper.CL		contrast	estimate	SE	df	t.ratio	p.value
LAR1	0.172	0.604	77.8	-1.031	1.375	LAR1 - LAR2	-1.281	0.390	40	-3.283	0.0021
LAR2	0.373	0.604	77.8	-0.829	1.576	tissue = Stem:					
tissue = Root:						contrast	estimate	SE	df	t.ratio	p.value
Genes emmean	SE	df	lower.CL	upper.CL		LAR1 - LAR2	-1.651	0.552	40	-2.993	0.0047
LAR1	3.201	0.302	77.8	2.600	3.803						
LAR2	4.482	0.302	77.8	3.881	5.084						
tissue = Stem:											
Genes emmean	SE	df	lower.CL	upper.CL							
LAR1	2.805	0.427	77.8	1.955	3.656						
LAR2	4.457	0.427	77.8	3.606	5.307						

Degrees-of-freedom method: kenward-roger
Confidence level used: 0.95

Gossypium hirsutum

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 10769.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.7343	-0.5257	-0.0146	0.4647	4.155

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.8483	0.921
Residual		0.4139	0.6433
Number of obs:	4316	groups:	Sample, 1079

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	2.47E+00	1.26E-01	1.78E+03	19.695	<2E-016	***
GenesLAR1b	5.01E-01	1.02E-01	3.14E+03	4.924	8.92E-07	***
GenesLAR2a	-1.14E+00	1.02E-01	3.14E+03	-11.196	<2E-016	***
GenesLAR2b	-5.02E-02	1.02E-01	3.14E+03	-0.493	0.622041	

tissueBinucleate	-5.22E-01	4.76E-01	1.78E+03	-1.097	0.272634	
tissueBoll	1.06E-01	8.04E-01	1.78E+03	0.132	0.894907	
tissueBoll-Shell	1.94E+00	1.13E+00	1.78E+03	1.717	0.0862	.
tissueBracts	2.27E+00	1.13E+00	1.78E+03	2.01	0.044592	*
tissueBud	1.27E+00	2.93E-01	1.78E+03	4.325	1.61E-05	***
tissueCallus	-4.69E-01	3.48E-01	1.78E+03	-1.349	0.177454	
tissueCalycle	2.82E+00	1.13E+00	1.78E+03	2.491	0.012836	*
tissueCalyxs	6.93E-01	1.13E+00	1.78E+03	0.613	0.539894	
tissueCell	-1.34E+00	4.76E-01	1.78E+03	-2.825	0.004784	**
tissueCorollas	-1.98E+00	1.13E+00	1.78E+03	-1.751	0.080116	.
tissueCotyledon	1.64E+00	2.09E-01	1.78E+03	7.846	7.36E-15	***
tissueEpidermal cells	1.66E-01	5.18E-01	1.78E+03	0.32	0.748766	
tissueFiber	-4.90E-01	1.51E-01	1.78E+03	-3.246	0.001193	**
tissueFlower	-7.94E-01	6.61E-01	1.78E+03	-1.202	0.229578	
tissueGynoecium	6.15E-01	8.04E-01	1.78E+03	0.765	0.444663	
tissueHypocotyl	5.00E-01	3.36E-01	1.78E+03	1.489	0.136794	
tissueJunction	2.22E+00	5.18E-01	1.78E+03	4.279	1.97E-05	***
tissueLeaf	2.01E+00	1.47E-01	1.78E+03	13.692	<2E-016	***
tissueMature seed	-2.47E+00	8.04E-01	1.78E+03	-3.076	0.002131	**
tissueMeristem	1.82E+00	8.04E-01	1.78E+03	2.259	0.02403	*
tissueOvule	7.61E-01	1.58E-01	1.78E+03	4.823	1.53E-06	***
tissuePetal	-2.34E-01	3.36E-01	1.78E+03	-0.695	0.487099	
tissuePollen	-2.47E+00	4.76E-01	1.78E+03	-5.202	2.20E-07	***
tissueProtoplasts	-2.02E+00	4.76E-01	1.78E+03	-4.244	2.31E-05	***
tissueRoots	5.12E-01	1.49E-01	1.78E+03	3.441	0.000592	***
tissueSeed	-8.33E-01	3.36E-01	1.78E+03	-2.48	0.013241	*
tissueSeedlings	-5.21E-02	4.76E-01	1.78E+03	-0.11	0.912698	
tissueShoot Apical	1.93E+00	2.54E-01	1.78E+03	7.603	4.66E-14	***
tissueStamen	-2.56E-01	1.13E+00	1.78E+03	-0.226	0.82108	
tissueStem	1.53E+00	1.95E-01	1.78E+03	7.835	8.01E-15	***
tissueTetrads	-9.47E-03	4.76E-01	1.78E+03	-0.02	0.984118	
tissueTorus	3.71E+00	1.13E+00	1.78E+03	3.285	0.001039	**
tissueUninucleate	3.42E-01	4.76E-01	1.78E+03	0.719	0.472033	
GenesLAR1b:tissueBinucleate	-1.04E+00	3.85E-01	3.14E+03	-2.695	0.007079	**
GenesLAR2a:tissueBinucleate	-6.32E-01	3.85E-01	3.14E+03	-1.641	0.100989	
GenesLAR2b:tissueBinucleate	-1.25E+00	3.85E-01	3.14E+03	-3.246	0.001183	**
GenesLAR1b:tissueBoll	7.23E-01	6.51E-01	3.14E+03	1.11	0.267139	
GenesLAR2a:tissueBoll	6.87E-01	6.51E-01	3.14E+03	1.055	0.291578	
GenesLAR2b:tissueBoll	1.93E+00	6.51E-01	3.14E+03	2.959	0.003114	**
GenesLAR1b:tissueBoll-Shell	1.33E-01	9.16E-01	3.14E+03	0.145	0.884668	
GenesLAR2a:tissueBoll-Shell	-2.67E-02	9.16E-01	3.14E+03	-0.029	0.976767	
GenesLAR2b:tissueBoll-Shell	5.83E-03	9.16E-01	3.14E+03	0.006	0.99492	
GenesLAR1b:tissueBracts	-2.22E+00	9.16E-01	3.14E+03	-2.429	0.015199	*
GenesLAR2a:tissueBracts	-2.54E+00	9.16E-01	3.14E+03	-2.776	0.005531	**
GenesLAR2b:tissueBracts	7.59E-01	9.16E-01	3.14E+03	0.829	0.407374	

<i>GenesLAR1b:tissueBud</i>	6.53E-02	2.37E-01	3.14E+03	0.275	0.783215	
<i>GenesLAR2a:tissueBud</i>	-1.15E-02	2.37E-01	3.14E+03	-0.049	0.96123	
<i>GenesLAR2b:tissueBud</i>	-1.37E-01	2.37E-01	3.14E+03	-0.576	0.56447	
<i>GenesLAR1b:tissueCallus</i>	2.86E-01	2.82E-01	3.14E+03	1.014	0.310522	
<i>GenesLAR2a:tissueCallus</i>	6.34E-01	2.82E-01	3.14E+03	2.253	0.02435	*
<i>GenesLAR2b:tissueCallus</i>	1.41E-01	2.82E-01	3.14E+03	0.501	0.616634	
<i>GenesLAR1b:tissueCalyx</i>	-1.82E+00	9.16E-01	3.14E+03	-1.991	0.046587	*
<i>GenesLAR2a:tissueCalyx</i>	-1.25E+00	9.16E-01	3.14E+03	-1.367	0.171628	
<i>GenesLAR2b:tissueCalyx</i>	1.30E+00	9.16E-01	3.14E+03	1.42	0.155711	
<i>GenesLAR1b:tissueCalyxs</i>	-1.31E+00	9.16E-01	3.14E+03	-1.43	0.152906	
<i>GenesLAR2a:tissueCalyxs</i>	-1.59E+00	9.16E-01	3.14E+03	-1.733	0.083138	.
<i>GenesLAR2b:tissueCalyxs</i>	4.93E-01	9.16E-01	3.14E+03	0.539	0.590062	
<i>GenesLAR1b:tissueCell</i>	3.62E-01	3.85E-01	3.14E+03	0.941	0.346686	
<i>GenesLAR2a:tissueCell</i>	5.99E-01	3.85E-01	3.14E+03	1.556	0.119817	
<i>GenesLAR2b:tissueCell</i>	-9.67E-02	3.85E-01	3.14E+03	-0.251	0.801669	
<i>GenesLAR1b:tissueCorollas</i>	-6.59E-01	9.16E-01	3.14E+03	-0.72	0.471676	
<i>GenesLAR2a:tissueCorollas</i>	6.78E-01	9.16E-01	3.14E+03	0.741	0.458873	
<i>GenesLAR2b:tissueCorollas</i>	8.56E-01	9.16E-01	3.14E+03	0.935	0.34961	
<i>GenesLAR1b:tissueCotyledon</i>	-6.54E-01	1.70E-01	3.14E+03	-3.858	0.000117	***
<i>GenesLAR2a:tissueCotyledon</i>	-2.31E+00	1.70E-01	3.14E+03	-13.629	<2E-016	***
<i>GenesLAR2b:tissueCotyledon</i>	-1.52E+00	1.70E-01	3.14E+03	-8.945	<2E-016	***
<i>GenesLAR1b:tissueEpidermal Cells</i>	6.13E-01	4.19E-01	3.14E+03	1.462	0.143956	
<i>GenesLAR2a:tissueEpidermal Cells</i>	4.13E-01	4.19E-01	3.14E+03	0.985	0.324945	
<i>GenesLAR2b:tissueEpidermal Cells</i>	1.87E+00	4.19E-01	3.14E+03	4.455	8.67E-06	***
<i>GenesLAR1b:tissueFiber</i>	5.86E-01	1.22E-01	3.14E+03	4.794	1.71E-06	***
<i>GenesLAR2a:tissueFiber</i>	7.86E-01	1.22E-01	3.14E+03	6.431	1.46E-10	***
<i>GenesLAR2b:tissueFiber</i>	1.51E+00	1.22E-01	3.14E+03	12.387	<2E-016	***
<i>GenesLAR1b:tissueFlower</i>	-4.75E-01	5.35E-01	3.14E+03	-0.888	0.374655	
<i>GenesLAR2a:tissueFlower</i>	4.51E-01	5.35E-01	3.14E+03	0.842	0.399598	
<i>GenesLAR2b:tissueFlower</i>	1.25E+00	5.35E-01	3.14E+03	2.343	0.019213	*
<i>GenesLAR1b:tissueGynoecium</i>	-3.98E-01	6.51E-01	3.14E+03	-0.611	0.541297	
<i>GenesLAR2a:tissueGynoecium</i>	-6.34E-01	6.51E-01	3.14E+03	-0.973	0.330457	
<i>GenesLAR2b:tissueGynoecium</i>	1.11E+00	6.51E-01	3.14E+03	1.704	0.088439	.
<i>GenesLAR1b:tissueHypocotyl</i>	2.60E-01	2.72E-01	3.14E+03	0.957	0.338762	
<i>GenesLAR2a:tissueHypocotyl</i>	1.53E+00	2.72E-01	3.14E+03	5.612	2.17E-08	***
<i>GenesLAR2b:tissueHypocotyl</i>	5.38E-01	2.72E-01	3.14E+03	1.979	0.047912	*
<i>GenesLAR1b:tissueJunction</i>	-2.95E-01	4.19E-01	3.14E+03	-0.704	0.481244	
<i>GenesLAR2a:tissueJunction</i>	-1.48E+00	4.19E-01	3.14E+03	-3.517	0.000443	***
<i>GenesLAR2b:tissueJunction</i>	-5.70E-01	4.19E-01	3.14E+03	-1.359	0.174102	
<i>GenesLAR1b:tissueLeaf</i>	-3.63E-01	1.19E-01	3.14E+03	-3.045	0.002348	**
<i>GenesLAR2a:tissueLeaf</i>	-2.15E+00	1.19E-01	3.14E+03	-18.021	<2E-016	***
<i>GenesLAR2b:tissueLeaf</i>	-1.04E+00	1.19E-01	3.14E+03	-8.724	<2E-016	***
<i>GenesLAR1b:tissueMature Seed</i>	-5.01E-01	6.51E-01	3.14E+03	-0.769	0.44195	
<i>GenesLAR2a:tissueMature Seed</i>	1.21E+00	6.51E-01	3.14E+03	1.865	0.062339	
<i>GenesLAR2b:tissueMature Seed</i>	5.02E-02	6.51E-01	3.14E+03	0.077	0.938633	

<i>GenesLAR1b:tissueMeristem</i>	-2.00E-01	6.51E-01	3.14E+03	-0.308	0.758303	
<i>GenesLAR2a:tissueMeristem</i>	-1.19E+00	6.51E-01	3.14E+03	-1.83	0.067272	.
<i>GenesLAR2b:tissueMeristem</i>	5.35E-01	6.51E-01	3.14E+03	0.822	0.411118	
<i>GenesLAR1b:tissueOvule</i>	4.61E-01	1.28E-01	3.14E+03	3.602	0.00032	***
<i>GenesLAR2a:tissueOvule</i>	2.90E-01	1.28E-01	3.14E+03	2.266	0.023514	*
<i>GenesLAR2b:tissueOvule</i>	2.73E-01	1.28E-01	3.14E+03	2.138	0.032556	*
<i>GenesLAR1b:tissuePetal</i>	8.95E-01	2.72E-01	3.14E+03	3.288	0.001018	**
<i>GenesLAR2a:tissuePetal</i>	-1.02E+00	2.72E-01	3.14E+03	-3.731	0.000194	***
<i>GenesLAR2b:tissuePetal</i>	-4.60E-01	2.72E-01	3.14E+03	-1.69	0.0912	.
<i>GenesLAR1b:tissuePollen</i>	-5.01E-01	3.85E-01	3.14E+03	-1.301	0.193489	
<i>GenesLAR2a:tissuePollen</i>	1.15E+00	3.85E-01	3.14E+03	2.989	0.002825	**
<i>GenesLAR2b:tissuePollen</i>	5.02E-02	3.85E-01	3.14E+03	0.13	0.8964	
<i>GenesLAR1b:tissueProtoplasts</i>	3.20E-02	3.85E-01	3.14E+03	0.083	0.933774	
<i>GenesLAR2a:tissueProtoplasts</i>	6.86E-01	3.85E-01	3.14E+03	1.782	0.074806	.
<i>GenesLAR2b:tissueProtoplasts</i>	5.03E-01	3.85E-01	3.14E+03	1.307	0.1912	
<i>GenesLAR1b:tissueRoots</i>	2.42E-01	1.21E-01	3.14E+03	2.006	0.044918	*
<i>GenesLAR2a:tissueRoots</i>	-2.85E-01	1.21E-01	3.14E+03	-2.366	0.01806	*
<i>GenesLAR2b:tissueRoots</i>	-6.33E-01	1.21E-01	3.14E+03	-5.248	1.64E-07	***
<i>GenesLAR1b:tissueSeed</i>	3.71E-02	2.72E-01	3.14E+03	0.136	0.891652	
<i>GenesLAR2a:tissueSeed</i>	4.35E-01	2.72E-01	3.14E+03	1.597	0.110266	
<i>GenesLAR2b:tissueSeed</i>	-4.78E-01	2.72E-01	3.14E+03	-1.756	0.079215	.
<i>GenesLAR1b:tissueSeedlings</i>	-1.39E-01	3.85E-01	3.14E+03	-0.362	0.717453	
<i>GenesLAR2a:tissueSeedlings</i>	-1.09E+00	3.85E-01	3.14E+03	-2.833	0.004636	**
<i>GenesLAR2b:tissueSeedlings</i>	-1.89E+00	3.85E-01	3.14E+03	-4.916	9.31E-07	***
<i>GenesLAR1b:tissueShoot Apical</i>	1.48E-01	2.05E-01	3.14E+03	0.72	0.471878	
<i>GenesLAR2a:tissueShoot Apical</i>	-8.26E-01	2.05E-01	3.14E+03	-4.019	5.97E-05	***
<i>GenesLAR2b:tissueShoot Apical</i>	-3.14E-01	2.05E-01	3.14E+03	-1.529	0.126367	
<i>GenesLAR1b:tissueStamen</i>	-6.84E-02	9.16E-01	3.14E+03	-0.075	0.940462	
<i>GenesLAR2a:tissueStamen</i>	-8.93E-01	9.16E-01	3.14E+03	-0.975	0.329537	
<i>GenesLAR2b:tissueStamen</i>	-1.75E+00	9.16E-01	3.14E+03	-1.916	0.055438	.
<i>GenesLAR1b:tissueStem</i>	-7.41E-02	1.58E-01	3.14E+03	-0.47	0.638608	
<i>GenesLAR2a:tissueStem</i>	-1.26E+00	1.58E-01	3.14E+03	-7.964	2.31E-15	***
<i>GenesLAR2b:tissueStem</i>	-5.18E-01	1.58E-01	3.14E+03	-3.283	0.001038	**
<i>GenesLAR1b:tissueTetrads</i>	1.56E-01	3.85E-01	3.14E+03	0.405	0.68521	
<i>GenesLAR2a:tissueTetrads</i>	-2.04E-01	3.85E-01	3.14E+03	-0.531	0.59561	
<i>GenesLAR2b:tissueTetrads</i>	-7.22E-01	3.85E-01	3.14E+03	-1.875	0.060919	.
<i>GenesLAR1b:tissueTorus</i>	-3.43E-01	9.16E-01	3.14E+03	-0.374	0.708182	
<i>GenesLAR2a:tissueTorus</i>	-1.70E+00	9.16E-01	3.14E+03	-1.852	0.064133	.
<i>GenesLAR2b:tissueTorus</i>	-1.65E+00	9.16E-01	3.14E+03	-1.806	0.071054	.
<i>GenesLAR1b:tissueUninucleate</i>	1.73E-01	3.85E-01	3.14E+03	0.45	0.65248	
<i>GenesLAR2a:tissueUninucleate</i>	-1.32E-01	3.85E-01	3.14E+03	-0.344	0.731145	
<i>GenesLAR2b:tissueUninucleate</i>	-5.43E-01	3.85E-01	3.14E+03	-1.411	0.158378	

Table 9S. Estimated marginal means and pairwise comparison for the species *Gossypium hirsutum*. Degrees-of-freedom method: asymptotic. P value adjustment: bonferroni method for 6 tests

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Anther: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.47375 0.1260 Inf 2.2276 2.720 LAR1b 2.97461 0.1260 Inf 2.7284 3.221 LAR2a 1.33492 0.1260 Inf 1.0887 1.581 LAR2b 2.42360 0.1260 Inf 2.1774 2.670	tissue = Anther: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.5009 0.1020 Inf -4.924 <.0001 LAR1a - LAR2a 1.1388 0.1020 Inf 11.196 <.0001 LAR1a - LAR2b 0.0501 0.1020 Inf 0.493 1.0000 LAR1b - LAR2a 1.6397 0.1020 Inf 16.120 <.0001 LAR1b - LAR2b 0.5510 0.1020 Inf 5.417 <.0001 LAR2a - LAR2b -1.0887 0.1020 Inf -10.703 <.0001
tissue = Binucleate: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 1.95192 0.4590 Inf 1.0530 2.851 LAR1b 1.41500 0.4590 Inf 0.5161 2.314 LAR2a 0.18132 0.4590 Inf -0.7176 1.080 LAR2b 0.65175 0.4590 Inf -0.2472 1.551	tissue = Binucleate: contrast estimate SE df z.ratio p.value LAR1a - LAR1b 0.5369 0.3710 Inf 1.446 0.8897 LAR1a - LAR2a 1.7706 0.3710 Inf 4.767 <.0001 LAR1a - LAR2b 1.3002 0.3710 Inf 3.501 0.0028 LAR1b - LAR2a 1.2337 0.3710 Inf 3.322 0.0054 LAR1b - LAR2b 0.7632 0.3710 Inf 2.055 0.2393 LAR2a - LAR2b -0.4704 0.3710 Inf -1.267 1.0000
tissue = Boll: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.58000 0.7940 Inf 1.0230 4.137 LAR1b 3.80374 0.7940 Inf 2.2468 5.361 LAR2a 2.12821 0.7940 Inf 0.5712 3.685 LAR2b 4.45679 0.7940 Inf 2.8998 6.014	tissue = Boll: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -1.2237 0.6430 Inf -1.902 0.3429 LAR1a - LAR2a 0.4518 0.6430 Inf 0.702 1.0000 LAR1a - LAR2b -1.8768 0.6430 Inf -2.917 0.0212 LAR1b - LAR2a 1.6755 0.6430 Inf 2.604 0.0552 LAR1b - LAR2b -0.6530 0.6430 Inf -1.015 1.0000 LAR2a - LAR2b -2.3286 0.6430 Inf -3.620 0.0018
tissue = Boll-Shell: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 4.41443 1.1200 Inf 2.2125 6.616 LAR1b 5.04809 1.1200 Inf 2.8462 7.250 LAR2a 3.24894 1.1200 Inf 1.0470 5.451 LAR2b 4.37011 1.1200 Inf 2.1682 6.572	tissue = Boll-Shell: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.6337 0.9100 Inf -0.696 1.0000 LAR1a - LAR2a 1.1655 0.9100 Inf 1.281 1.0000 LAR1a - LAR2b 0.0443 0.9100 Inf 0.049 1.0000 LAR1b - LAR2a 1.7991 0.9100 Inf 1.978 0.2879 LAR1b - LAR2b 0.6780 0.9100 Inf 0.745 1.0000 LAR2a - LAR2b -1.1212 0.9100 Inf -1.232 1.0000
tissue = Bracts: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 4.74583 1.1200 Inf 2.5439 6.948 LAR1b 3.02310 1.1200 Inf 0.8212 5.225 LAR2a 1.06540 1.1200 Inf -1.1365 3.267 LAR2b 5.45426 1.1200 Inf 3.2524 7.656	tissue = Bracts: contrast estimate SE df z.ratio p.value LAR1a - LAR1b 1.7227 0.9100 Inf 1.894 0.3497 LAR1a - LAR2a 3.6804 0.9100 Inf 4.045 0.0003 LAR1a - LAR2b -0.7084 0.9100 Inf -0.779 1.0000 LAR1b - LAR2a 1.9577 0.9100 Inf 2.152 0.1885 LAR1b - LAR2b -2.4312 0.9100 Inf -2.672 0.0452 LAR2a - LAR2b -4.3889 0.9100 Inf -4.824 <.0001
tissue = Bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 3.74127 0.2650 Inf 3.2223 4.260 LAR1b 4.30744 0.2650 Inf 3.7884 4.826 LAR2a 2.59091 0.2650 Inf 2.0719 3.110 LAR2b 3.55435 0.2650 Inf 3.0354 4.073	tissue = Bud:
tissue = Callus: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.00453 0.3240 Inf 1.3689 2.640 LAR1b 2.79106 0.3240 Inf 2.1554 3.427	

LAR2a 1.50015 0.3240 Inf 0.8645 2.136	contrast estimate SE df z.ratio p.value
LAR2b 2.09539 0.3240 Inf 1.4598 2.731	LAR1a - LAR1b -0.5662 0.2140 Inf -2.640 0.0497
tissue = Calyces:	LAR1a - LAR2a 1.1504 0.2140 Inf 5.364 <.0001
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b 0.1869 0.2140 Inf 0.872 1.0000
LAR1a 5.28946 1.1200 Inf 3.0876 7.491	LAR1b - LAR2a 1.7165 0.2140 Inf 8.005 <.0001
LAR1b 3.96780 1.1200 Inf 1.7659 6.170	LAR1b - LAR2b 0.7531 0.2140 Inf 3.512 0.0027
LAR2a 2.89892 1.1200 Inf 0.6970 5.101	LAR2a - LAR2b -0.9634 0.2140 Inf -4.493 <.0001
LAR2b 6.53925 1.1200 Inf 4.3373 8.741	tissue = Callus:
tissue = Calyxes:	contrast estimate SE df z.ratio p.value
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR1b -0.7865 0.2630 Inf -2.995 0.0165
LAR1a 3.16681 1.1200 Inf 0.9649 5.369	LAR1a - LAR2a 0.5044 0.2630 Inf 1.920 0.3288
LAR1b 2.35885 1.1200 Inf 0.1569 4.561	LAR1a - LAR2b -0.0909 0.2630 Inf -0.346 1.0000
LAR2a 0.44121 1.1200 Inf -1.7607 2.643	LAR1b - LAR2a 1.2909 0.2630 Inf 4.915 <.0001
LAR2b 3.60991 1.1200 Inf 1.4080 5.812	LAR1b - LAR2b 0.6957 0.2630 Inf 2.649 0.0485
tissue = Cell:	LAR2a - LAR2b -0.5952 0.2630 Inf -2.266 0.1405
Genes emmean SE df asymp.LCL asymp.UCL	tissue = Calycle:
LAR1a 1.13046 0.4590 Inf 0.2315 2.029	contrast estimate SE df z.ratio p.value
LAR1b 1.99376 0.4590 Inf 1.0948 2.893	LAR1a - LAR1b 1.3217 0.9100 Inf 1.453 0.8778
LAR2a 0.59083 0.4590 Inf -0.3081 1.490	LAR1a - LAR2a 2.3905 0.9100 Inf 2.628 0.0516
LAR2b 0.98357 0.4590 Inf 0.0846 1.882	LAR1a - LAR2b -1.2498 0.9100 Inf -1.374 1.0000
tissue = Corollas:	LAR1b - LAR2a 1.0689 0.9100 Inf 1.175 1.0000
Genes emmean SE df asymp.LCL asymp.UCL	LAR1b - LAR2b -2.5714 0.9100 Inf -2.826 0.0282
LAR1a 0.49433 1.1200 Inf -1.7076 2.696	LAR2a - LAR2b -3.6403 0.9100 Inf -4.001 0.0004
LAR1b 0.33621 1.1200 Inf -1.8657 2.538	tissue = Calyxes:
LAR2a 0.03368 1.1200 Inf -2.1682 2.236	contrast estimate SE df z.ratio p.value
LAR2b 1.30058 1.1200 Inf -0.9013 3.502	LAR1a - LAR1b 0.8080 0.9100 Inf 0.888 1.0000
tissue = Cotyledon:	LAR1a - LAR2a 2.7256 0.9100 Inf 2.996 0.0164
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b -0.4431 0.9100 Inf -0.487 1.0000
LAR1a 4.11625 0.1670 Inf 3.7880 4.444	LAR1b - LAR2a 1.9176 0.9100 Inf 2.108 0.2103
LAR1b 3.96312 0.1670 Inf 3.6349 4.291	LAR1b - LAR2b -1.2511 0.9100 Inf -1.375 1.0000
LAR2a 0.66690 0.1670 Inf 0.3387 0.995	LAR2a - LAR2b -3.1687 0.9100 Inf -3.483 0.0030
LAR2b 2.54959 0.1670 Inf 2.2214 2.878	tissue = Cell:
tissue = Epidermal Cells:	contrast estimate SE df z.ratio p.value
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR1b -0.8633 0.3710 Inf -2.324 0.1206
LAR1a 2.63963 0.5020 Inf 1.6549 3.624	LAR1a - LAR2a 0.5396 0.3710 Inf 1.453 0.8776
LAR1b 3.75347 0.5020 Inf 2.7687 4.738	LAR1a - LAR2b 0.1469 0.3710 Inf 0.395 1.0000
LAR2a 1.91370 0.5020 Inf 0.9290 2.898	LAR1b - LAR2a 1.4029 0.3710 Inf 3.777 0.0010
LAR2b 4.45801 0.5020 Inf 3.4733 5.443	LAR1b - LAR2b 1.0102 0.3710 Inf 2.720 0.0392
tissue = Fiber:	LAR2a - LAR2b -0.3927 0.3710 Inf -1.057 1.0000
Genes emmean SE df asymp.LCL asymp.UCL	tissue = Corollas:
LAR1a 1.98378 0.0837 Inf 1.8197 2.148	contrast estimate SE df z.ratio p.value
	LAR1a - LAR1b 0.1581 0.9100 Inf 0.174 1.0000
	LAR1a - LAR2a 0.4607 0.9100 Inf 0.506 1.0000

LAR1b 3.07076 0.0837 Inf 2.9066 3.235	LAR1a - LAR2b -0.8063 0.9100 Inf -0.886 1.0000
LAR2a 1.63119 0.0837 Inf 1.4671 1.795	LAR1b - LAR2a 0.3025 0.9100 Inf 0.333 1.0000
LAR2b 3.44798 0.0837 Inf 3.2839 3.612	LAR1b - LAR2b -0.9644 0.9100 Inf -1.060 1.0000
tissue = Flower:	LAR2a - LAR2b -1.2669 0.9100 Inf -1.393 0.9826
Genes emmean SE df asymp.LCL asymp.UCL	tissue = Cotyledon:
LAR1a 1.67972 0.6490 Inf 0.4084 2.951	contrast estimate SE df z.ratio p.value
LAR1b 1.70552 0.6490 Inf 0.4342 2.977	LAR1a - LAR1b 0.1531 0.1360 Inf 1.129 1.0000
LAR2a 0.99163 0.6490 Inf -0.2796 2.263	LAR1a - LAR2a 3.4494 0.1360 Inf 25.433 <.0001
LAR2b 2.88291 0.6490 Inf 1.6116 4.154	LAR1a - LAR2b 1.5667 0.1360 Inf 11.552 <.0001
tissue = Gynoecium:	LAR1b - LAR2a 3.2962 0.1360 Inf 24.304 <.0001
Genes emmean SE df asymp.LCL asymp.UCL	LAR1b - LAR2b 1.4135 0.1360 Inf 10.422 <.0001
LAR1a 3.08862 0.7940 Inf 1.5316 4.646	LAR2a - LAR2b -1.8827 0.1360 Inf -13.882 <.0001
LAR1b 3.19158 0.7940 Inf 1.6346 4.749	tissue = Epidermal Cells:
LAR2a 1.31584 0.7940 Inf -0.2411 2.873	contrast estimate SE df z.ratio p.value
LAR2b 4.14845 0.7940 Inf 2.5915 5.705	LAR1a - LAR1b -1.1138 0.4070 Inf -2.738 0.0371
tissue = Hypocotyl:	LAR1a - LAR2a 0.7259 0.4070 Inf 1.784 0.4464
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b -1.8184 0.4070 Inf -4.469 <.0001
LAR1a 2.97381 0.3120 Inf 2.3631 3.585	LAR1b - LAR2a 1.8398 0.4070 Inf 4.522 <.0001
LAR1b 3.73497 0.3120 Inf 3.1243 4.346	LAR1b - LAR2b -0.7045 0.4070 Inf -1.732 0.5001
LAR2a 3.36181 0.3120 Inf 2.7511 3.973	LAR2a - LAR2b -2.5443 0.4070 Inf -6.253 <.0001
LAR2b 3.46205 0.3120 Inf 2.8514 4.073	tissue = Fiber:
tissue = Junction:	contrast estimate SE df z.ratio p.value
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR1b -1.0870 0.0678 Inf -16.029 <.0001
LAR1a 4.68992 0.5020 Inf 3.7052 5.675	LAR1a - LAR2a 0.3526 0.0678 Inf 5.200 <.0001
LAR1b 4.89537 0.5020 Inf 3.9106 5.880	LAR1a - LAR2b -1.4642 0.0678 Inf -21.592 <.0001
LAR2a 2.07620 0.5020 Inf 1.0915 3.061	LAR1b - LAR2a 1.4396 0.0678 Inf 21.229 <.0001
LAR2b 4.06963 0.5020 Inf 3.0849 5.054	LAR1b - LAR2b -0.3772 0.0678 Inf -5.563 <.0001
tissue = Leaf:	LAR2a - LAR2b -1.8168 0.0678 Inf -26.792 <.0001
Genes emmean SE df asymp.LCL asymp.UCL	tissue = Flower:
LAR1a 4.48691 0.0764 Inf 4.3371 4.637	contrast estimate SE df z.ratio p.value
LAR1b 4.62522 0.0764 Inf 4.4754 4.775	LAR1a - LAR1b -0.0258 0.5250 Inf -0.049 1.0000
LAR2a 1.20225 0.0764 Inf 1.0524 1.352	LAR1a - LAR2a 0.6881 0.5250 Inf 1.310 1.0000
LAR2b 3.39796 0.0764 Inf 3.2481 3.548	LAR1a - LAR2b -1.2032 0.5250 Inf -2.291 0.1319
tissue = Mature Seed:	LAR1b - LAR2a 0.7139 0.5250 Inf 1.359 1.0000
Genes emmean SE df asymp.LCL asymp.UCL	LAR1b - LAR2b -1.1774 0.5250 Inf -2.242 0.1500
LAR1a 0.00000 0.7940 Inf -1.5570 1.557	LAR2a - LAR2b -1.8913 0.5250 Inf -3.601 0.0019
LAR1b 0.00000 0.7940 Inf -1.5570 1.557	tissue = Gynoecium:
LAR2a 0.07557 0.7940 Inf -1.4814 1.633	contrast estimate SE df z.ratio p.value
LAR2b 0.00000 0.7940 Inf -1.5570 1.557	LAR1a - LAR1b -0.1030 0.6430 Inf -0.160 1.0000
tissue = Meristem:	LAR1a - LAR2a 1.7728 0.6430 Inf 2.756 0.0351
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b -1.0598 0.6430 Inf -1.647 0.5968
	LAR1b - LAR2a 1.8757 0.6430 Inf 2.916 0.0213
	LAR1b - LAR2b -0.9569 0.6430 Inf -1.487 0.8215

LAR1a 4.29025 0.7940 Inf 2.7333 5.847	LAR2a - LAR2b -2.8326 0.6430 Inf -4.403 0.0001
LAR1b 4.59068 0.7940 Inf 3.0337 6.148	tissue = Hypocotyl:
LAR2a 1.95921 0.7940 Inf 0.4022 3.516	contrast estimate SE df z.ratio p.value
LAR2b 4.77550 0.7940 Inf 3.2185 6.332	LAR1a - LAR1b -0.7612 0.2520 Inf -3.017 0.0153
tissue = Ovule:	LAR1a - LAR2a -0.3880 0.2520 Inf -1.538 0.7448
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b -0.4882 0.2520 Inf -1.935 0.3180
LAR1a 3.23517 0.0956 Inf 3.0477 3.423	LAR1b - LAR2a 0.3732 0.2520 Inf 1.479 0.8351
LAR1b 4.19656 0.0956 Inf 4.0091 4.384	LAR1b - LAR2b 0.2729 0.2520 Inf 1.082 1.0000
LAR2a 2.38605 0.0956 Inf 2.1986 2.573	LAR2a - LAR2b -0.1002 0.2520 Inf -0.397 1.0000
LAR2b 3.45841 0.0956 Inf 3.2710 3.646	tissue = Junction:
tissue = Petal:	contrast estimate SE df z.ratio p.value
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR1b -0.2054 0.4070 Inf -0.505 1.0000
LAR1a 2.24024 0.3120 Inf 1.6295 2.851	LAR1a - LAR2a 2.6137 0.4070 Inf 6.424 <.0001
LAR1b 3.63577 0.3120 Inf 3.0251 4.246	LAR1a - LAR2b 0.6203 0.4070 Inf 1.525 0.7642
LAR2a 0.08645 0.3120 Inf -0.5242 0.697	LAR1b - LAR2a 2.8192 0.4070 Inf 6.929 <.0001
LAR2b 1.73041 0.3120 Inf 1.1197 2.341	LAR1b - LAR2b 0.8257 0.4070 Inf 2.029 0.2545
tissue = Pollen:	LAR2a - LAR2b -1.9934 0.4070 Inf -4.899 <.0001
Genes emmean SE df asymp.LCL asymp.UCL	tissue = Leaf:
LAR1a 0.00000 0.4590 Inf -0.8989 0.899	contrast estimate SE df z.ratio p.value
LAR1b 0.00000 0.4590 Inf -0.8989 0.899	LAR1a - LAR1b -0.1383 0.0619 Inf -2.234 0.1528
LAR2a 0.01204 0.4590 Inf -0.8869 0.911	LAR1a - LAR2a 3.2847 0.0619 Inf 53.061 <.0001
LAR2b 0.00000 0.4590 Inf -0.8989 0.899	LAR1a - LAR2b 1.0889 0.0619 Inf 17.591 <.0001
tissue = Protoplasts:	LAR1b - LAR2a 3.4230 0.0619 Inf 55.295 <.0001
Genes emmean SE df asymp.LCL asymp.UCL	LAR1b - LAR2b 1.2273 0.0619 Inf 19.825 <.0001
LAR1a 0.45580 0.4590 Inf -0.4431 1.355	LAR2a - LAR2b -2.1957 0.0619 Inf -35.470 <.0001
LAR1b 0.98866 0.4590 Inf 0.0897 1.888	tissue = Mature Seed:
LAR2a 0.00331 0.4590 Inf -0.8956 0.902	contrast estimate SE df z.ratio p.value
LAR2b 0.90909 0.4590 Inf 0.0102 1.808	LAR1a - LAR1b 0.0000 0.6430 Inf 0.000 1.0000
tissue = Roots:	LAR1a - LAR2a -0.0756 0.6430 Inf -0.117 1.0000
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR2b 0.0000 0.6430 Inf 0.000 1.0000
LAR1a 2.98593 0.0798 Inf 2.8295 3.142	LAR1b - LAR2a -0.0756 0.6430 Inf -0.117 1.0000
LAR1b 3.72860 0.0798 Inf 3.5721 3.885	LAR1b - LAR2b 0.0000 0.6430 Inf 0.000 1.0000
LAR2a 1.56199 0.0798 Inf 1.4055 1.718	LAR2a - LAR2b 0.0756 0.6430 Inf 0.117 1.0000
LAR2b 2.30328 0.0798 Inf 2.1468 2.460	tissue = Meristem:
tissue = Seed:	contrast estimate SE df z.ratio p.value
Genes emmean SE df asymp.LCL asymp.UCL	LAR1a - LAR1b -0.3004 0.6430 Inf -0.467 1.0000
LAR1a 1.64069 0.3120 Inf 1.0300 2.251	LAR1a - LAR2a 2.3310 0.6430 Inf 3.623 0.0017
LAR1b 2.17861 0.3120 Inf 1.5679 2.789	LAR1a - LAR2b -0.4853 0.6430 Inf -0.754 1.0000
LAR2a 0.93647 0.3120 Inf 0.3258 1.547	LAR1b - LAR2a 2.6315 0.6430 Inf 4.090 0.0003
LAR2b 1.11285 0.3120 Inf 0.5021 1.724	LAR1b - LAR2b -0.1848 0.6430 Inf -0.287 1.0000
tissue = Seedlings:	LAR2a - LAR2b -2.8163 0.6430 Inf -4.378 0.0001
	tissue = Ovule:

Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.42161 0.4590 Inf 1.5227 3.321 LAR1b 2.78310 0.4590 Inf 1.8842 3.682 LAR2a 0.19167 0.4590 Inf -0.7072 1.091 LAR2b 0.47849 0.4590 Inf -0.4204 1.377 tissue = Shoot Apical: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 4.40200 0.2200 Inf 3.9702 4.834 LAR1b 5.05063 0.2200 Inf 4.6188 5.482 LAR2a 2.43764 0.2200 Inf 2.0058 2.869 LAR2b 4.03782 0.2200 Inf 3.6060 4.470 tissue = Stamen: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.21806 1.1200 Inf 0.0162 4.420 LAR1b 2.65053 1.1200 Inf 0.4486 4.852 LAR2a 0.18648 1.1200 Inf -2.0154 2.388 LAR2b 0.41376 1.1200 Inf -1.7881 2.616 tissue = Stem: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 3.99944 0.1490 Inf 3.7078 4.291 LAR1b 4.42623 0.1490 Inf 4.1346 4.718 LAR2a 1.60470 0.1490 Inf 1.3131 1.896 LAR2b 3.43154 0.1490 Inf 3.1399 3.723 tissue = Tetrads: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.46428 0.4590 Inf 1.5654 3.363 LAR1b 3.12126 0.4590 Inf 2.2223 4.020 LAR2a 1.12105 0.4590 Inf 0.2221 2.020 LAR2b 1.69217 0.4590 Inf 0.7932 2.591 tissue = Torus: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 6.18732 1.1200 Inf 3.9854 8.389 LAR1b 6.34549 1.1200 Inf 4.1436 8.547 LAR2a 3.35315 1.1200 Inf 1.1512 5.555 LAR2b 4.48408 1.1200 Inf 2.2822 6.686 tissue = Uninucleate: Genes emmean SE df asymp.LCL asymp.UCL LAR1a 2.81581 0.4590 Inf 1.9169 3.715 LAR1b 3.49010 0.4590 Inf 2.5912 4.389 LAR2a 1.54465 0.4590 Inf 0.6457 2.444 LAR2b 2.22234 0.4590 Inf 1.3234 3.121	contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.9614 0.0774 Inf -12.414 <.0001 LAR1a - LAR2a 0.8491 0.0774 Inf 10.964 <.0001 LAR1a - LAR2b -0.2232 0.0774 Inf -2.883 0.0237 LAR1b - LAR2a 1.8105 0.0774 Inf 23.378 <.0001 LAR1b - LAR2b 0.7382 0.0774 Inf 9.531 <.0001 LAR2a - LAR2b -1.0724 0.0774 Inf -13.846 <.0001 tissue = Petal: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -1.3955 0.2520 Inf -5.531 <.0001 LAR1a - LAR2a 2.1538 0.2520 Inf 8.536 <.0001 LAR1a - LAR2b 0.5098 0.2520 Inf 2.020 0.2600 LAR1b - LAR2a 3.5493 0.2520 Inf 14.066 <.0001 LAR1b - LAR2b 1.9054 0.2520 Inf 7.551 <.0001 LAR2a - LAR2b -1.6440 0.2520 Inf -6.515 <.0001 tissue = Pollen: contrast estimate SE df z.ratio p.value LAR1a - LAR1b 0.0000 0.3710 Inf 0.000 1.0000 LAR1a - LAR2a -0.0120 0.3710 Inf -0.032 1.0000 LAR1a - LAR2b 0.0000 0.3710 Inf 0.000 1.0000 LAR1b - LAR2a -0.0120 0.3710 Inf -0.032 1.0000 LAR1b - LAR2b 0.0000 0.3710 Inf 0.000 1.0000 LAR2a - LAR2b 0.0120 0.3710 Inf 0.032 1.0000 tissue = Protoplasts: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.5329 0.3710 Inf -1.435 0.9083 LAR1a - LAR2a 0.4525 0.3710 Inf 1.218 1.0000 LAR1a - LAR2b -0.4533 0.3710 Inf -1.220 1.0000 LAR1b - LAR2a 0.9853 0.3710 Inf 2.653 0.0479 LAR1b - LAR2b 0.0796 0.3710 Inf 0.214 1.0000 LAR2a - LAR2b -0.9058 0.3710 Inf -2.439 0.0884 tissue = Roots: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.7427 0.0647 Inf -11.486 <.0001 LAR1a - LAR2a 1.4239 0.0647 Inf 22.023 <.0001 LAR1a - LAR2b 0.6827 0.0647 Inf 10.558 <.0001 LAR1b - LAR2a 2.1666 0.0647 Inf 33.510 <.0001 LAR1b - LAR2b 1.4253 0.0647 Inf 22.045 <.0001 LAR2a - LAR2b -0.7413 0.0647 Inf -11.465 <.0001 tissue = Seed: contrast estimate SE df z.ratio p.value LAR1a - LAR1b -0.5379 0.2520 Inf -2.132 0.1981 LAR1a - LAR2a 0.7042 0.2520 Inf 2.791 0.0315
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Degrees-of-freedom method: asymptotic Confidence level used: 0.95	LAR1a - LAR2b					
	0.5278 0.2520 Inf 2.092 0.2187					
	LAR1b - LAR2a					
	1.2421 0.2520 Inf 4.923 <.0001					
	LAR1b - LAR2b					
	1.0658 0.2520 Inf 4.224 0.0001					
	LAR2a - LAR2b					
	-0.1764 0.2520 Inf -0.699 1.0000					
	tissue = Seedlings:					
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.3615	0.3710	Inf	-0.973	1.0000
	LAR1a - LAR2a	2.2299	0.3710	Inf	6.004	<.0001
	LAR1a - LAR2b	1.9431	0.3710	Inf	5.232	<.0001
	LAR1b - LAR2a	2.5914	0.3710	Inf	6.977	<.0001
	LAR1b - LAR2b	2.3046	0.3710	Inf	6.205	<.0001
	LAR2a - LAR2b	-0.2868	0.3710	Inf	-0.772	1.0000
	tissue = Shoot Apical:					
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.6486	0.1780	Inf	-3.635	0.0017
	LAR1a - LAR2a	1.9644	0.1780	Inf	11.009	<.0001
	LAR1a - LAR2b	0.3642	0.1780	Inf	2.041	0.2475
	LAR1b - LAR2a	2.6130	0.1780	Inf	14.645	<.0001
	LAR1b - LAR2b	1.0128	0.1780	Inf	5.676	<.0001
	LAR2a - LAR2b	-1.6002	0.1780	Inf	-8.968	<.0001
	tissue = Stamen:					
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.4325	0.9100	Inf	-0.475	1.0000
	LAR1a - LAR2a	2.0316	0.9100	Inf	2.233	0.1533
	LAR1a - LAR2b	1.8043	0.9100	Inf	1.983	0.2841
	LAR1b - LAR2a	2.4641	0.9100	Inf	2.708	0.0406
	LAR1b - LAR2b	2.2368	0.9100	Inf	2.459	0.0837
	LAR2a - LAR2b	-0.2273	0.9100	Inf	-0.250	1.0000
	tissue = Stem:					
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.4268	0.1210	Inf	-3.542	0.0024
	LAR1a - LAR2a	2.3947	0.1210	Inf	19.873	<.0001
	LAR1a - LAR2b	0.5679	0.1210	Inf	4.713	<.0001
	LAR1b - LAR2a	2.8215	0.1210	Inf	23.414	<.0001
	LAR1b - LAR2b	0.9947	0.1210	Inf	8.254	<.0001
	LAR2a - LAR2b	-1.8268	0.1210	Inf	-15.160	<.0001
	tissue = Tetrads:					
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.6570	0.3710	Inf	-1.769	0.4615
	LAR1a - LAR2a	1.3432	0.3710	Inf	3.616	0.0018
	LAR1a - LAR2b	0.7721	0.3710	Inf	2.079	0.2258
	LAR1b - LAR2a	2.0002	0.3710	Inf	5.385	<.0001
	LAR1b - LAR2b	1.4291	0.3710	Inf	3.848	0.0007

	LAR2a - LAR2b	-0.5711	0.3710	Inf	-1.538	0.7448
tissue = Torus:						
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.1582	0.9100	Inf	-0.174	1.0000
	LAR1a - LAR2a	2.8342	0.9100	Inf	3.115	0.0110
	LAR1a - LAR2b	1.7032	0.9100	Inf	1.872	0.3671
	LAR1b - LAR2a	2.9923	0.9100	Inf	3.289	0.0060
	LAR1b - LAR2b	1.8614	0.9100	Inf	2.046	0.2446
	LAR2a - LAR2b	-1.1309	0.9100	Inf	-1.243	1.0000
tissue = Uninucleate:						
	contrast	estimate	SE	df	z.ratio	p.value
	LAR1a - LAR1b	-0.6743	0.3710	Inf	-1.815	0.4167
	LAR1a - LAR2a	1.2712	0.3710	Inf	3.422	0.0037
	LAR1a - LAR2b	0.5935	0.3710	Inf	1.598	0.6605
	LAR1b - LAR2a	1.9454	0.3710	Inf	5.238	<.0001
	LAR1b - LAR2b	1.2678	0.3710	Inf	3.413	0.0039
	LAR2a - LAR2b	-0.6777	0.3710	Inf	-1.825	0.4084

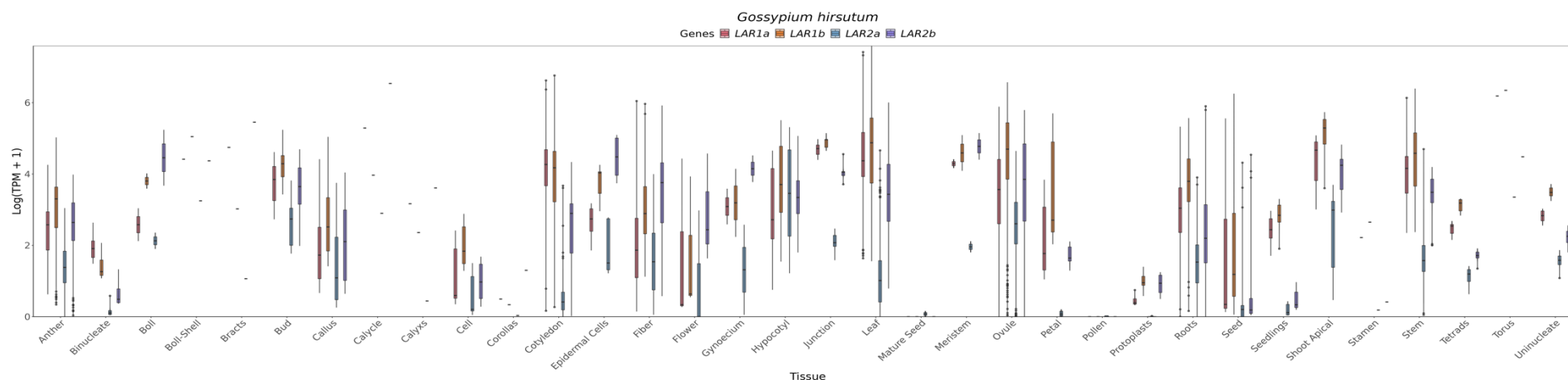


Figure 3S. Comparison of the expression of *LAR1a* (red), *LAR1b* (yellow), *LAR2a* (blue) and *LAR2b* (purple) genes in the species *Gossypium hirsutum*.

Actinidia chinensis

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 2095.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.1345	-0.4801	-0.0858	0.3651	5.7218

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.09163	0.3027
Residual		0.34866	0.5905
Number of obs:	1080	groups:	Sample, 270

Fixed effects:

	Estimate	Std. Error	df	T value	Pr(> t)	
(Intercept)	3.62247	0.16589	881.46223	21.837	<2E-016	***
GenesLAR1b	-3.53968	0.20876	747	-16.955	<2E-016	***
GenesLAR1c	-2.12177	0.20876	747	-10.164	<2E-016	***
GenesLAR2	-0.7778	0.20876	747	-3.726	0.000209	***
tissueAxillary bud	1.64506	0.26748	881.46223	6.15	1.17E-09	***
tissueCane	1.32631	0.68397	881.46223	1.939	0.052802	.
tissueFlesh	-2.35286	0.19854	881.46223	-11.851	<2E-016	***
tissueFloral bud	-0.40476	0.27648	881.46223	-1.464	0.143556	
tissueFlower	0.83305	0.68397	881.46223	1.218	0.223559	
tissueFlower bud	0.97416	0.68397	881.46223	1.424	0.154719	
tissueFruit	-2.41667	0.17931	881.46223	-13.477	<2E-016	***
tissueFull fruit	-2.83403	0.31765	881.46223	-8.922	<2E-016	***
tissueImmature fruit	-1.50145	0.49766	881.46223	-3.017	0.002626	**
tissueLeaf	0.47633	0.20795	881.46223	2.291	0.022223	*
tissueLeaf blade	0.37852	0.21416	881.46223	1.767	0.077495	.
tissueMature fruit	-1.30208	0.41747	881.46223	-3.119	0.001874	**
tissuePlant root	0.14609	0.27648	881.46223	0.528	0.597351	
tissuePulp	-2.10614	0.31765	881.46223	-6.63	5.83E-11	***
tissueRipe fruit	-2.0808	0.41747	881.46223	-4.984	7.49E-07	***
tissueRoot	-0.95254	0.2534	881.46223	-3.759	0.000182	***
tissueShoot	2.0984	0.68397	881.46223	3.068	0.002221	**
tissueStem	-1.17261	0.49766	881.46223	-2.356	0.018679	*

tissueTerminal bud	1.63388	0.41747	881.46223	3.914	9.79E-05	***
tissueYoung leaves	0.7751	0.68397	881.46223	1.133	0.257422	
GenesLAR1b:tissueAxillary bud	-1.59738	0.33662	747	-4.745	2.49E-06	***
GenesLAR1c:tissueAxillary bud	-0.83576	0.33662	747	-2.483	0.013255	*
GenesLAR2:tissueAxillary bud	-0.23178	0.33662	747	-0.689	0.491329	
GenesLAR1b:tissueCane	0.07015	0.86075	747	0.081	0.935068	
GenesLAR1c:tissueCane	0.16149	0.86075	747	0.188	0.851226	
GenesLAR2:tissueCane	0.09901	0.86075	747	0.115	0.908456	
GenesLAR1b:tissueFlesh	2.28408	0.24986	747	9.142	<2E-016	***
GenesLAR1c:tissueFlesh	1.36766	0.24986	747	5.474	6.02E-08	***
GenesLAR2:tissueFlesh	0.28253	0.24986	747	1.131	0.258521	
GenesLAR1b:tissueFloral bud	0.79027	0.34794	747	2.271	0.023414	*
GenesLAR1c:tissueFloral bud	1.55397	0.34794	747	4.466	9.19E-06	***
GenesLAR2:tissueFloral bud	0.41707	0.34794	747	1.199	0.231032	
GenesLAR1b:tissueFlower	-0.32613	0.86075	747	-0.379	0.704881	
GenesLAR1c:tissueFlower	1.68435	0.86075	747	1.957	0.05074	.
GenesLAR2:tissueFlower	0.23481	0.86075	747	0.273	0.785084	
GenesLAR1b:tissueFlower bud	-0.92048	0.86075	747	-1.069	0.285241	
GenesLAR1c:tissueFlower bud	1.72006	0.86075	747	1.998	0.046045	*
GenesLAR2:tissueFlower bud	-0.1377	0.86075	747	-0.16	0.872943	
GenesLAR1b:tissueFruit	2.51757	0.22566	747	11.156	<2E-016	***
GenesLAR1c:tissueFruit	1.31038	0.22566	747	5.807	9.41E-09	***
GenesLAR2:tissueFruit	0.7733	0.22566	747	3.427	0.000644	***
GenesLAR1b:tissueFull fruit	2.75124	0.39975	747	6.882	1.25E-11	***
GenesLAR1c:tissueFull fruit	3.68874	0.39975	747	9.228	<2E-016	***
GenesLAR2:tissueFull fruit	1.14855	0.39975	747	2.873	0.004179	**
GenesLAR1b:tissueImmature fruit	1.41865	0.62629	747	2.265	0.023788	*
GenesLAR1c:tissueImmature fruit	3.00364	0.62629	747	4.796	1.96E-06	***
GenesLAR2:tissueImmature fruit	0.42284	0.62629	747	0.675	0.499789	
GenesLAR1b:tissueLeaf	-0.3111	0.2617	747	-1.189	0.23491	
GenesLAR1c:tissueLeaf	0.47117	0.2617	747	1.8	0.072197	.
GenesLAR2:tissueLeaf	-0.43898	0.2617	747	-1.677	0.093881	.
GenesLAR1b:tissueLeaf blade	-0.39489	0.26951	747	-1.465	0.143283	
GenesLAR1c:tissueLeaf blade	0.2207	0.26951	747	0.819	0.413123	
GenesLAR2:tissueLeaf blade	-1.45963	0.26951	747	-5.416	8.23E-08	***
GenesLAR1b:tissueMature fruit	1.22347	0.52538	747	2.329	0.020139	*
GenesLAR1c:tissueMature fruit	1.19436	0.52538	747	2.273	0.023289	*
GenesLAR2:tissueMature fruit	0.55707	0.52538	747	1.06	0.289344	
GenesLAR1b:tissuePlant root	1.22912	0.34794	747	3.533	0.000437	***
GenesLAR1c:tissuePlant root	0.22126	0.34794	747	0.636	0.525019	
GenesLAR2:tissuePlant root	-0.6733	0.34794	747	-1.935	0.053354	.
GenesLAR1b:tissuePulp	2.02335	0.39975	747	5.062	5.24E-07	***
GenesLAR1c:tissuePulp	1.00726	0.39975	747	2.52	0.011953	*
GenesLAR2:tissuePulp	-0.27943	0.39975	747	-0.699	0.484761	
GenesLAR1b:tissueRipe fruit	2.00368	0.52538	747	3.814	0.000148	***
GenesLAR1c:tissueRipe fruit	0.60233	0.52538	747	1.146	0.251964	

<i>GenesLAR2:tissueRipe fruit</i>	0.53542	0.52538	747	1.019	0.308476	
<i>GenesLAR1b:tissueRoot</i>	1.85218	0.31889	747	5.808	9.34E-09	***
<i>GenesLAR1c:tissueRoot</i>	1.00611	0.31889	747	3.155	0.001669	**
<i>GenesLAR2:tissueRoot</i>	0.44656	0.31889	747	1.4	0.161824	
<i>GenesLAR1b:tissueShoot</i>	-0.27922	0.86075	747	-0.324	0.745731	
<i>GenesLAR1c:tissueShoot</i>	-0.13677	0.86075	747	-0.159	0.87379	
<i>GenesLAR2:tissueShoot</i>	-0.94476	0.86075	747	-1.098	0.272737	
<i>GenesLAR1b:tissueStem</i>	1.10002	0.62629	747	1.756	0.07943	.
<i>GenesLAR1c:tissueStem</i>	0.04657	0.62629	747	0.074	0.94074	
<i>GenesLAR2:tissueStem</i>	0.55313	0.62629	747	0.883	0.377417	
<i>GenesLAR1b:tissueTerminal bud</i>	-1.07634	0.52538	747	-2.049	0.04084	*
<i>GenesLAR1c:tissueTerminal bud</i>	1.01347	0.52538	747	1.929	0.054105	.
<i>GenesLAR2:tissueTerminal bud</i>	-0.30105	0.52538	747	-0.573	0.566803	
<i>GenesLAR1b:tissueYoung leaves</i>	-0.10578	0.86075	747	-0.123	0.902225	
<i>GenesLAR1c:tissueYoung leaves</i>	1.27785	0.86075	747	1.485	0.138079	
<i>GenesLAR2:tissueYoung leaves</i>	-1.30573	0.86075	747	-1.517	0.1297	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 10S. Estimated marginal means and pairwise comparison for the species *Actinidia chinensis*. Degrees-of-freedom method: asymptotic

P value adjustment: bonferroni method for 6 tests

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = All plant: Genes emmean SE df lower.CL upper.CL LAR1a 3.62247 0.1660 881 3.29689 3.948 LAR1b 0.08279 0.1660 881 -0.24278 0.408 LAR1c 1.50070 0.1660 881 1.17512 1.826 LAR2 2.84467 0.1660 881 2.51910 3.170	tissue = All plant: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 3.53968 0.2090 747 16.955 <.0001 LAR1a - LAR1c 2.12177 0.2090 747 10.164 <.0001 LAR1a - LAR2 0.77780 0.2090 747 3.726 0.0013 LAR1b - LAR1c -1.41790 0.2090 747 -6.792 <.0001 LAR1b - LAR2 -2.76188 0.2090 747 -13.230 <.0001 LAR1c - LAR2 -1.34398 0.2090 747 -6.438 <.0001
tissue = Axillary bud: Genes emmean SE df lower.CL upper.CL LAR1a 5.26753 0.2100 881 4.85570 5.679 LAR1b 0.13048 0.2100 881 -0.28135 0.542 LAR1c 2.31000 0.2100 881 1.89817 2.722 LAR2 4.25796 0.2100 881 3.84613 4.670	tissue = Axillary bud: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 5.13705 0.2640 747 19.454 <.0001 LAR1a - LAR1c 2.95753 0.2640 747 11.200 <.0001 LAR1a - LAR2 1.00957 0.2640 747 3.823 0.0009 LAR1b - LAR1c -2.17952 0.2640 747 -8.254 <.0001 LAR1b - LAR2 -4.12748 0.2640 747 -15.630 <.0001 LAR1c - LAR2 -1.94796 0.2640 747 -7.377 <.0001
tissue = Cane: Genes emmean SE df lower.CL upper.CL LAR1a 4.94878 0.6640 881 3.64647 6.251 LAR1b 1.47925 0.6640 881 0.17694 2.782 LAR1c 2.98850 0.6640 881 1.68619 4.291 LAR2 4.26999 0.6640 881 2.96768 5.572	tissue = Cane: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 3.46953 0.8350 747 4.155 0.0002 LAR1a - LAR1c 1.96028 0.8350 747 2.347 0.1150 LAR1a - LAR2 0.67879 0.8350 747 0.813 1.0000 LAR1b - LAR1c -1.50925 0.8350 747 -1.807 0.4266 LAR1b - LAR2 -2.79074 0.8350 747 -3.342 0.0052 LAR1c - LAR2 -1.28149 0.8350 747 -1.535 0.7518
tissue = Flesh: Genes emmean SE df lower.CL upper.CL LAR1a 1.26961 0.1090 881 1.05551 1.484 LAR1b 0.01401 0.1090 881 -0.20009 0.228 LAR1c 0.51550 0.1090 881 0.30140 0.730	

LAR2 0.77434 0.1090 881 0.56024 0.988	tissue = Flesh: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 1.25560 0.1370 747 9.146 <.0001 LAR1a - LAR1c 0.75411 0.1370 747 5.493 <.0001 LAR1a - LAR2 0.49527 0.1370 747 3.608 0.0020 LAR1b - LAR1c -0.50149 0.1370 747 -3.653 0.0017 LAR1b - LAR2 -0.76033 0.1370 747 -5.538 <.0001 LAR1c - LAR2 -0.25884 0.1370 747 -1.885 0.3585
tissue = Floral bud: Genes emmean SE df lower.CL upper.CL LAR1a 3.21771 0.2210 881 2.78361 3.652 LAR1b 0.46831 0.2210 881 0.03420 0.902 LAR1c 2.64991 0.2210 881 2.21580 3.084 LAR2 2.85698 0.2210 881 2.42288 3.291	tissue = Floral bud: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 2.74941 0.2780 747 9.877 <.0001 LAR1a - LAR1c 0.56781 0.2780 747 2.040 0.2503 LAR1a - LAR2 0.36073 0.2780 747 1.296 1.0000 LAR1b - LAR1c -2.18160 0.2780 747 -7.838 <.0001 LAR1b - LAR2 -2.38868 0.2780 747 -8.582 <.0001 LAR1c - LAR2 -0.20708 0.2780 747 -0.744 1.0000
tissue = Flower: Genes emmean SE df lower.CL upper.CL LAR1a 4.45552 0.6640 881 3.15321 5.758 LAR1b 0.58972 0.6640 881 -0.71259 1.892 LAR1c 4.01810 0.6640 881 2.71579 5.320 LAR2 3.91254 0.6640 881 2.61023 5.215	tissue = Flower: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 3.86580 0.8350 747 4.629 <.0001 LAR1a - LAR1c 0.43743 0.8350 747 0.524 1.0000 LAR1a - LAR2 0.54299 0.8350 747 0.650 1.0000 LAR1b - LAR1c -3.42838 0.8350 747 -4.106 0.0003 LAR1b - LAR2 -3.32282 0.8350 747 -3.979 0.0005 LAR1c - LAR2 0.10556 0.8350 747 0.126 1.0000
tissue = Flower bud: Genes emmean SE df lower.CL upper.CL LAR1a 4.59663 0.6640 881 3.29432 5.899 LAR1b 0.13647 0.6640 881 -1.16584 1.439 LAR1c 4.19491 0.6640 881 2.89260 5.497 LAR2 3.68113 0.6640 881 2.37882 4.983	tissue = Flower bud: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 4.46016 0.8350 747 5.341 <.0001 LAR1a - LAR1c 0.40172 0.8350 747 0.481 1.0000 LAR1a - LAR2 0.91550 0.8350 747 1.096 1.0000 LAR1b - LAR1c -4.05844 0.8350 747 -4.860 <.0001 LAR1b - LAR2 -3.54466 0.8350 747 -4.245 0.0001 LAR1c - LAR2 0.51378 0.8350 747 0.615 1.0000
tissue = Fruit: Genes emmean SE df lower.CL upper.CL LAR1a 1.20580 0.0681 881 1.07219 1.339 LAR1b 0.18369 0.0681 881 0.05008 0.317 LAR1c 0.39441 0.0681 881 0.26079 0.528 LAR2 1.20131 0.0681 881 1.06769 1.335	tissue = Fruit: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 1.02211 0.0857 747 11.930 <.0001 LAR1a - LAR1c 0.81139 0.0857 747 9.471 <.0001 LAR1a - LAR2 0.00449 0.0857 747 0.052 1.0000 LAR1b - LAR1c -0.21072 0.0857 747 -2.459 0.0848 LAR1b - LAR2 -1.01761 0.0857 747 -11.878 <.0001 LAR1c - LAR2 -0.80690 0.0857 747 -9.418 <.0001
tissue = Full fruit: Genes emmean SE df lower.CL upper.CL LAR1a 0.78844 0.2710 881 0.25677 1.320 LAR1b 0.00000 0.2710 881 -0.53167 0.532 LAR1c 2.35541 0.2710 881 1.82374 2.887 LAR2 1.15919 0.2710 881 0.62753 1.691	tissue = Full fruit: contrast estimate SE df t.ratio p.value
tissue = Immature fruit: Genes emmean SE df lower.CL upper.CL LAR1a 2.12102 0.4690 881 1.20015 3.042 LAR1b 0.00000 0.4690 881 -0.92087 0.921 LAR1c 3.00289 0.4690 881 2.08202 3.924 LAR2 1.76607 0.4690 881 0.84519 2.687	
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1a 4.09880 0.1250 881 3.85268 4.345 LAR1b 0.24802 0.1250 881 0.00191 0.494	

LAR1c 2.44819 0.1250 881 2.20208 2.694	LAR1a - LAR1b 0.78844 0.3410 747 2.313 0.1260
LAR2 2.88202 0.1250 881 2.63591 3.128	LAR1a - LAR1c -1.56696 0.3410 747 -4.596 <.0001
tissue = Leaf blade:	LAR1a - LAR2 -0.37075 0.3410 747 -1.088 1.0000
Genes emmean SE df lower.CL upper.CL	LAR1b - LAR1c -2.35541 0.3410 747 -6.909 <.0001
LAR1a 4.00099 0.1350 881 3.73516 4.267	LAR1b - LAR2 -1.15919 0.3410 747 -3.400 0.0043
LAR1b 0.06642 0.1350 881 -0.19942 0.332	LAR1c - LAR2 1.19621 0.3410 747 3.509 0.0029
LAR1c 2.09991 0.1350 881 1.83408 2.366	tissue = Immature fruit:
LAR2 1.76356 0.1350 881 1.49773 2.029	contrast estimate SE df t.ratio p.value
tissue = Mature fruit:	LAR1a - LAR1b 2.12102 0.5900 747 3.592 0.0021
Genes emmean SE df lower.CL upper.CL	LAR1a - LAR1c -0.88187 0.5900 747 -1.493 0.8144
LAR1a 2.32039 0.3830 881 1.56850 3.072	LAR1a - LAR2 0.35496 0.5900 747 0.601 1.0000
LAR1b 0.00418 0.3830 881 -0.74771 0.756	LAR1b - LAR1c -3.00289 0.5900 747 -5.086 <.0001
LAR1c 1.39297 0.3830 881 0.64108 2.145	LAR1b - LAR2 -1.76607 0.5900 747 -2.991 0.0172
LAR2 2.09966 0.3830 881 1.34777 2.852	LAR1c - LAR2 1.23683 0.5900 747 2.095 0.2192
tissue = Plant root:	tissue = Leaf:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1a 3.76856 0.2210 881 3.33446 4.203	LAR1a - LAR1b 3.85078 0.1580 747 24.401 <.0001
LAR1b 1.45801 0.2210 881 1.02391 1.892	LAR1a - LAR1c 1.65061 0.1580 747 10.459 <.0001
LAR1c 1.86805 0.2210 881 1.43395 2.302	LAR1a - LAR2 1.21677 0.1580 747 7.710 <.0001
LAR2 2.31746 0.2210 881 1.88336 2.752	LAR1b - LAR1c -2.20017 0.1580 747 -13.942 <.0001
tissue = Pulp:	LAR1b - LAR2 -2.63400 0.1580 747 -16.691 <.0001
Genes emmean SE df lower.CL upper.CL	LAR1c - LAR2 -0.43383 0.1580 747 -2.749 0.0367
LAR1a 1.51633 0.2710 881 0.98466 2.048	tissue = Leaf blade:
LAR1b 0.00000 0.2710 881 -0.53167 0.532	contrast estimate SE df t.ratio p.value
LAR1c 0.40181 0.2710 881 -0.12985 0.933	LAR1a - LAR1b 3.93457 0.1700 747 23.083 <.0001
LAR2 0.45910 0.2710 881 -0.07257 0.991	LAR1a - LAR1c 1.90108 0.1700 747 11.153 <.0001
tissue = Ripe fruit:	LAR1a - LAR2 2.23743 0.1700 747 13.126 <.0001
Genes emmean SE df lower.CL upper.CL	LAR1b - LAR1c -2.03349 0.1700 747 -11.930 <.0001
LAR1a 1.54167 0.3830 881 0.78978 2.294	LAR1b - LAR2 -1.69714 0.1700 747 -9.957 <.0001
LAR1b 0.00568 0.3830 881 -0.74621 0.758	LAR1c - LAR2 0.33635 0.1700 747 1.973 0.2930
LAR1c 0.02223 0.3830 881 -0.72966 0.774	tissue = Mature fruit:
LAR2 1.29929 0.3830 881 0.54741 2.051	contrast estimate SE df t.ratio p.value
tissue = Root:	LAR1a - LAR1b 2.31621 0.4820 747 4.804 <.0001
Genes emmean SE df lower.CL upper.CL	LAR1a - LAR1c 0.92742 0.4820 747 1.924 0.3287
LAR1a 2.66993 0.1920 881 2.29398 3.046	LAR1a - LAR2 0.22073 0.4820 747 0.458 1.0000
LAR1b 0.98243 0.1920 881 0.60648 1.358	LAR1b - LAR1c -1.38879 0.4820 747 -2.881 0.0245
LAR1c 1.55426 0.1920 881 1.17831 1.930	LAR1b - LAR2 -2.09548 0.4820 747 -4.346 0.0001
LAR2 2.33869 0.1920 881 1.96274 2.715	LAR1c - LAR2 -0.70669 0.4820 747 -1.466 0.8588
tissue = Shoot:	tissue = Plant root:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1a 5.72087 0.6640 881 4.41856 7.023	LAR1a - LAR1b 2.31055 0.2780 747 8.301 <.0001
	LAR1a - LAR1c 1.90051 0.2780 747 6.828 <.0001
	LAR1a - LAR2 1.45110 0.2780 747 5.213 <.0001

LAR1b 1.90197 0.6640 881 0.59966 3.204 LAR1c 3.46232 0.6640 881 2.16001 4.765 LAR2 3.99832 0.6640 881 2.69601 5.301 tissue = Stem: Genes emmean SE df lower.CL upper.CL LAR1a 2.44986 0.4690 881 1.52899 3.371 LAR1b 0.01020 0.4690 881 -0.91067 0.931 LAR1c 0.37466 0.4690 881 -0.54621 1.296 LAR2 2.22520 0.4690 881 1.30433 3.146 tissue = Terminal bud: Genes emmean SE df lower.CL upper.CL LAR1a 5.25635 0.3830 881 4.50446 6.008 LAR1b 0.64033 0.3830 881 -0.11156 1.392 LAR1c 4.14805 0.3830 881 3.39616 4.900 LAR2 4.17750 0.3830 881 3.42561 4.929 tissue = Young leaves: Genes emmean SE df lower.CL upper.CL LAR1a 4.39757 0.6640 881 3.09525 5.700 LAR1b 0.75211 0.6640 881 -0.55020 2.054 LAR1c 3.55364 0.6640 881 2.25133 4.856 LAR2 2.31404 0.6640 881 1.01173 3.616 Degrees-of-freedom method: kenward-roger Confidence level used: 0.95	LAR1b - LAR1c -0.41004 0.2780 747 -1.473 0.8469 LAR1b - LAR2 -0.85945 0.2780 747 -3.088 0.0126 LAR1c - LAR2 -0.44941 0.2780 747 -1.615 0.6410 tissue = Pulp: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 1.51633 0.3410 747 4.448 0.0001 LAR1a - LAR1c 1.11451 0.3410 747 3.269 0.0068 LAR1a - LAR2 1.05723 0.3410 747 3.101 0.0120 LAR1b - LAR1c -0.40181 0.3410 747 -1.179 1.0000 LAR1b - LAR2 -0.45910 0.3410 747 -1.347 1.0000 LAR1c - LAR2 -0.05728 0.3410 747 -0.168 1.0000 tissue = Ripe fruit: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 1.53599 0.4820 747 3.186 0.0090 LAR1a - LAR1c 1.51944 0.4820 747 3.152 0.0101 LAR1a - LAR2 0.24238 0.4820 747 0.503 1.0000 LAR1b - LAR1c -0.01655 0.4820 747 -0.034 1.0000 LAR1b - LAR2 -1.29362 0.4820 747 -2.683 0.0447 LAR1c - LAR2 -1.27706 0.4820 747 -2.649 0.0495 tissue = Root: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 1.68750 0.2410 747 7.000 <.0001 LAR1a - LAR1c 1.11567 0.2410 747 4.628 <.0001 LAR1a - LAR2 0.33124 0.2410 747 1.374 1.0000 LAR1b - LAR1c -0.57183 0.2410 747 -2.372 0.1076 LAR1b - LAR2 -1.35626 0.2410 747 -5.626 <.0001 LAR1c - LAR2 -0.78443 0.2410 747 -3.254 0.0071 tissue = Shoot: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 3.81890 0.8350 747 4.573 <.0001 LAR1a - LAR1c 2.25855 0.8350 747 2.705 0.0420 LAR1a - LAR2 1.72255 0.8350 747 2.063 0.2369 LAR1b - LAR1c -1.56035 0.8350 747 -1.869 0.3725 LAR1b - LAR2 -2.09634 0.8350 747 -2.510 0.0736 LAR1c - LAR2 -0.53599 0.8350 747 -0.642 1.0000 tissue = Stem: contrast estimate SE df t.ratio p.value LAR1a - LAR1b 2.43966 0.5900 747 4.132 0.0002 LAR1a - LAR1c 2.07520 0.5900 747 3.514 0.0028 LAR1a - LAR2 0.22466 0.5900 747 0.380 1.0000 LAR1b - LAR1c -0.36446 0.5900 747 -0.617 1.0000 LAR1b - LAR2 -2.21500 0.5900 747 -3.751 0.0011 LAR1c - LAR2 -1.85054 0.5900 747 -3.134 0.0108
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		tissue = Terminal bud:				
		contrast	estimate	SE	df	t.ratio p.value
		LAR1a - LAR1b	4.61602	0.4820	747	9.574 <.0001
		LAR1a - LAR1c	1.10831	0.4820	747	2.299 0.1307
		LAR1a - LAR2	1.07885	0.4820	747	2.238 0.1532
		LAR1b - LAR1c	-3.50771	0.4820	747	-7.276 <.0001
		LAR1b - LAR2	-3.53717	0.4820	747	-7.337 <.0001
		LAR1c - LAR2	-0.02945	0.4820	747	-0.061 1.0000
		tissue = Young leaves:				
		contrast	estimate	SE	df	t.ratio p.value
		LAR1a - LAR1b	3.64546	0.8350	747	4.366 0.0001
		LAR1a - LAR1c	0.84392	0.8350	747	1.011 1.0000
		LAR1a - LAR2	2.08353	0.8350	747	2.495 0.0768
		LAR1b - LAR1c	-2.80153	0.8350	747	-3.355 0.0050
		LAR1b - LAR2	-1.56193	0.8350	747	-1.870 0.3709
		LAR1c - LAR2	1.23961	0.8350	747	1.484 0.8287

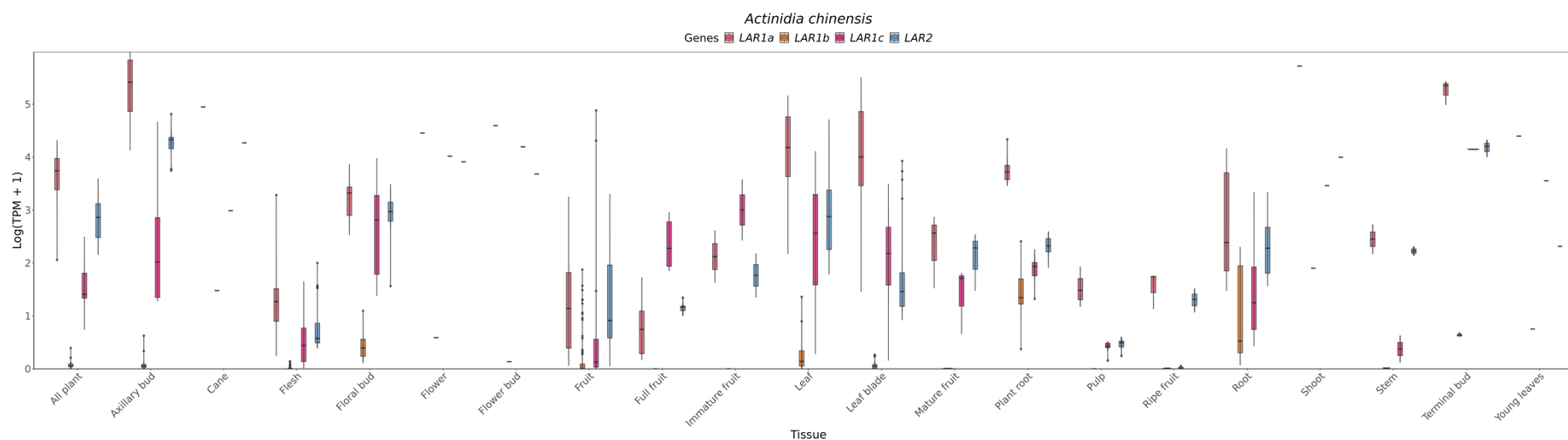


Figure 4S. Comparison of the expression of *LAR1a* (red), *LAR1b* (orange), *LAR1c* (pink) and *LAR2a* (blue) genes in the species *Actinidia chinensis*.

Eucalyptus grandis

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 961.9

Scaled residuals:

Min	1Q	Median	3Q	Max
-4.069	-0.3202	0	0.3451	2.2926

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.1334	0.3652
Residual		0.4166	0.6454
Number of obs:	447	groups:	Sample, 149

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	3.171845	0.370792	367.738584	8.554	3.25E-16	***
GenesLAR2a	-3.137178	0.456381	274.000003	-6.874	4.21E-11	***
GenesLAR2b	-2.928155	0.456381	274.000003	-6.416	6.12E-10	***
tissueControl root	0.945845	0.403093	367.738583	2.346	0.019482	*
tissueEctomycorrhiza	0.622535	0.424017	367.738583	1.468	0.142909	
tissueFruit bud	1.434466	0.829116	367.738581	1.73	0.084449	.
tissueLeaf	1.115323	0.829116	367.738581	1.345	0.179391	
tissueLeaf adult	1.233245	0.566394	367.738582	2.177	0.030089	*
tissueLeaf and twigs	-0.834142	0.428153	367.738583	-1.948	0.052148	.
tissueLeaf juvenile	0.863925	0.566394	367.738582	1.525	0.128042	
tissueLeaf midrib	-0.219222	0.47869	367.738582	-0.458	0.647251	
tissueMixed	0.643171	0.64223	367.738581	1.001	0.31726	
tissueStem	1.495982	0.381542	367.738583	3.921	0.000105	***
tissueXylem	0.252605	0.420438	367.738583	0.601	0.548335	
GenesLAR2a:tissueControl root	1.091958	0.496139	274.000003	2.201	0.028576	*
GenesLAR2b:tissueControl root	1.324942	0.496139	274.000003	2.671	0.008026	**
GenesLAR2a:tissueEctomycorrhiza	0.761166	0.521892	274.000003	1.458	0.145855	
GenesLAR2b:tissueEctomycorrhiza	0.806413	0.521892	274.000003	1.545	0.123458	
GenesLAR2a:tissueFruit bud	0.918013	1.020499	274.000003	0.9	0.369138	
GenesLAR2b:tissueFruit bud	1.039574	1.020499	274.000003	1.019	0.309248	
GenesLAR2a:tissueLeaf	-1.11748	1.020499	274.000003	-1.095	0.274464	
GenesLAR2b:tissueLeaf	0.831917	1.020499	274.000003	0.815	0.415663	

GenesLAR2a:tissueLeaf adult	-1.267912	0.697134	274.000003	-1.819	0.070041	.
GenesLAR2b:tissueLeaf adult	-0.917419	0.697134	274.000003	-1.316	0.189278	
GenesLAR2a:tissueLeaf and twigs	0.918518	0.526984	274.000003	1.743	0.08246	.
GenesLAR2b:tissueLeaf and twigs	0.608164	0.526984	274.000003	1.154	0.249486	
GenesLAR2a:tissueLeaf juvenile	-0.599881	0.697134	274.000003	-0.86	0.390268	
GenesLAR2b:tissueLeaf juvenile	-0.869701	0.697134	274.000003	-1.248	0.213265	
GenesLAR2a:tissueLeaf midrib	1.724201	0.589186	274.000003	2.926	0.003716	**
GenesLAR2b:tissueLeaf midrib	1.663536	0.589186	274.000003	2.823	0.005099	**
GenesLAR2a:tissueMixed	-0.429915	0.790475	274.000003	-0.544	0.586974	
GenesLAR2b:tissueMixed	-0.838613	0.790475	274.000003	-1.061	0.289671	
GenesLAR2a:tissueStem	-0.190143	0.469612	274.000003	-0.405	0.685872	
GenesLAR2b:tissueStem	2.046957	0.469612	274.000003	4.359	1.85E-05	***
GenesLAR2a:tissueXylem	0.001223	0.517488	274.000003	0.002	0.998115	
GenesLAR2b:tissueXylem	-0.226549	0.517488	274.000003	-0.438	0.661887	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 11S. Estimated marginal means and pairwise comparison for the species *Eucalyptus grandis*. Degrees-of-freedom method: asymptotic
P value adjustment: bonferroni method for 3 tests.

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Cambium: Genes emmean SE df lower.CL upper.CL LAR1 3.1718 0.3710 368 2.443 3.901 LAR2a 0.0347 0.3710 368 -0.694 0.764 LAR2b 0.2437 0.3710 368 -0.485 0.973	tissue = Cambium: contrast estimate SE df t.ratio p.value LAR1 - LAR2a 3.1372 0.456 274 6.874 <.0001 LAR1 - LAR2b 2.9282 0.456 274 6.416 <.0001 LAR2a - LAR2b -0.2090 0.456 274 -0.458 1.0000
tissue = Control root: Genes emmean SE df lower.CL upper.CL LAR1 4.1177 0.1580 368 3.807 4.429 LAR2a 2.0725 0.1580 368 1.762 2.383 LAR2b 2.5145 0.1580 368 2.204 2.825	tissue = Control root: contrast estimate SE df t.ratio p.value LAR1 - LAR2a 2.0452 0.195 274 10.510 <.0001 LAR1 - LAR2b 1.6032 0.195 274 8.238 <.0001 LAR2a - LAR2b -0.4420 0.195 274 -2.271 0.0717
tissue = Ectomycorrhiza: Genes emmean SE df lower.CL upper.CL LAR1 3.7944 0.2060 368 3.390 4.199 LAR2a 1.4184 0.2060 368 1.014 1.823 LAR2b 1.6726 0.2060 368 1.268 2.077	tissue = Ectomycorrhiza: contrast estimate SE df t.ratio p.value LAR1 - LAR2a 2.3760 0.253 274 9.386 <.0001 LAR1 - LAR2b 2.1217 0.253 274 8.381 <.0001 LAR2a - LAR2b -0.2543 0.253 274 -1.004 0.9482
tissue = Fruit bud: Genes emmean SE df lower.CL upper.CL LAR1 4.6063 0.7420 368 3.148 6.065 LAR2a 2.3871 0.7420 368 0.929 3.845 LAR2b 2.7177 0.7420 368 1.259 4.176	tissue = Fruit bud: contrast estimate SE df t.ratio p.value LAR1 - LAR2a 2.2192 0.913 274 2.431 0.0471 LAR1 - LAR2b 1.8886 0.913 274 2.069 0.1184 LAR2a - LAR2b -0.3306 0.913 274 -0.362 1.0000
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 4.2872 0.7420 368 2.829 5.745 LAR2a 0.0325 0.7420 368 -1.426 1.491	tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2a 4.2547 0.913 274 4.661 <.0001 LAR1 - LAR2b 2.0962 0.913 274 2.297 0.0672

LAR2b 2.1909 0.7420 368 0.733 3.649	LAR2a - LAR2b -2.1584 0.913 274 -2.365 0.0562
tissue = Leaf adult:	tissue = Leaf adult:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 4.4051 0.4280 368 3.563 5.247	LAR1 - LAR2a 4.4051 0.527 274 8.359 <.0001
LAR2a 0.0000 0.4280 368 -0.842 0.842	LAR1 - LAR2b 3.8456 0.527 274 7.297 <.0001
LAR2b 0.5595 0.4280 368 -0.282 1.401	LAR2a - LAR2b -0.5595 0.527 274 -1.062 0.8679
tissue = Leaf and twigs:	tissue = Leaf and twigs:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 2.3377 0.2140 368 1.917 2.759	LAR1 - LAR2a 2.2187 0.263 274 8.420 <.0001
LAR2a 0.1190 0.2140 368 -0.302 0.540	LAR1 - LAR2b 2.3200 0.263 274 8.805 <.0001
LAR2b 0.0177 0.2140 368 -0.403 0.439	LAR2a - LAR2b 0.1013 0.263 274 0.385 1.0000
tissue = Leaf juvenile:	tissue = Leaf juvenile:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 4.0358 0.4280 368 3.194 4.878	LAR1 - LAR2a 3.7371 0.527 274 7.091 <.0001
LAR2a 0.2987 0.4280 368 -0.543 1.141	LAR1 - LAR2b 3.7979 0.527 274 7.207 <.0001
LAR2b 0.2379 0.4280 368 -0.604 1.080	LAR2a - LAR2b 0.0608 0.527 274 0.115 1.0000
tissue = Leaf midrib:	tissue = Leaf midrib:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 2.9526 0.3030 368 2.357 3.548	LAR1 - LAR2a 1.4130 0.373 274 3.792 0.0006
LAR2a 1.5396 0.3030 368 0.944 2.135	LAR1 - LAR2b 1.2646 0.373 274 3.394 0.0024
LAR2b 1.6880 0.3030 368 1.093 2.283	LAR2a - LAR2b -0.1484 0.373 274 -0.398 1.0000
tissue = Mixed:	tissue = Mixed:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 3.8150 0.5240 368 2.784 4.846	LAR1 - LAR2a 3.5671 0.645 274 5.527 <.0001
LAR2a 0.2479 0.5240 368 -0.783 1.279	LAR1 - LAR2b 3.7668 0.645 274 5.836 <.0001
LAR2b 0.0482 0.5240 368 -0.983 1.079	LAR2a - LAR2b 0.1997 0.645 274 0.309 1.0000
tissue = Stem:	tissue = Stem:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 4.6678 0.0899 368 4.491 4.845	LAR1 - LAR2a 3.3273 0.111 274 30.060 <.0001
LAR2a 1.3405 0.0899 368 1.164 1.517	LAR1 - LAR2b 0.8812 0.111 274 7.961 <.0001
LAR2b 3.7866 0.0899 368 3.610 3.963	LAR2a - LAR2b -2.4461 0.111 274 -22.099 <.0001
tissue = Xylem:	tissue = Xylem:
Genes emmean SE df lower.CL upper.CL	contrast estimate SE df t.ratio p.value
LAR1 3.4244 0.1980 368 3.035 3.814	LAR1 - LAR2a 3.1360 0.244 274 12.855 <.0001
LAR2a 0.2885 0.1980 368 -0.101 0.678	LAR1 - LAR2b 3.1547 0.244 274 12.932 <.0001
LAR2b 0.2697 0.1980 368 -0.120 0.659	LAR2a - LAR2b 0.0187 0.244 274 0.077 1.0000
Degrees-of-freedom method: kenward-roger	Degrees-of-freedom method: kenward-roger
Confidence level used: 0.95	P value adjustment: bonferroni method for 3 tests

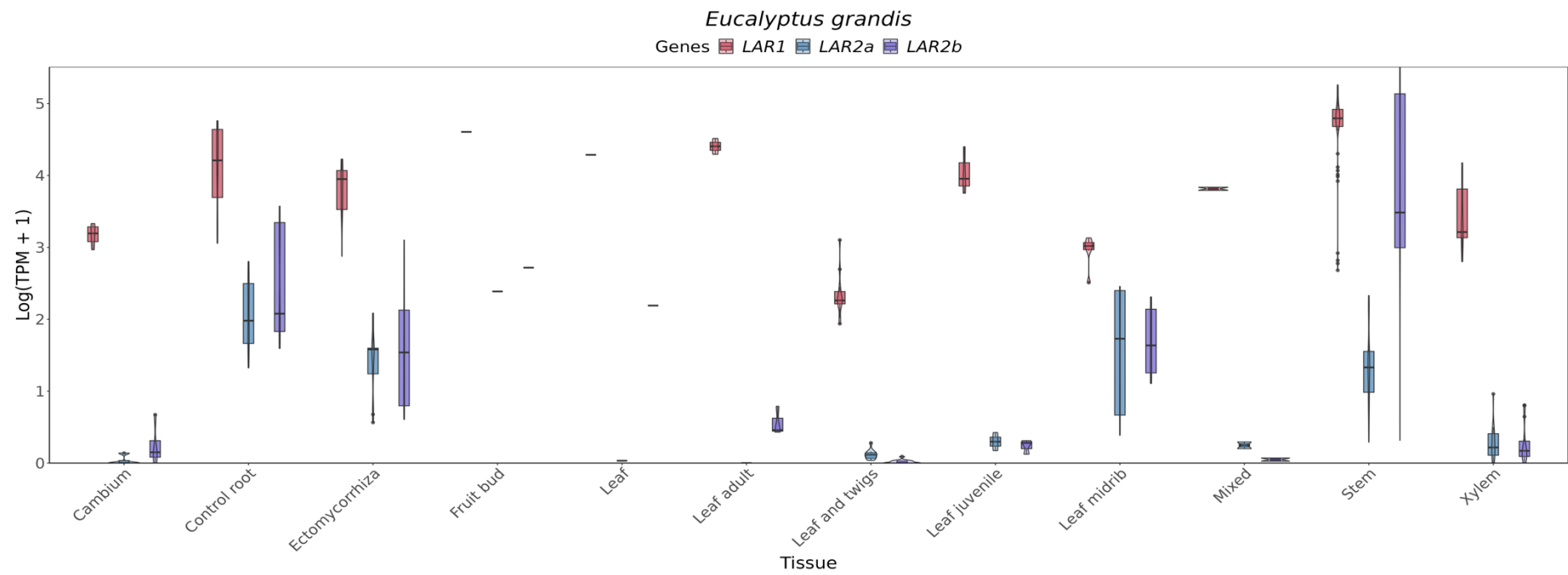


Figure 5S. Comparison of the expression of *LAR1a* (red), *LAR2a* (blue), and *LAR2b* (purple) genes in the species *Eucalyptus grandis*.

Populus trichocarpa

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 7655.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-5.2516	-0.3877	0.0057	0.3673	5.5306

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.5646	0.7514
Residual	0.1486	0.3855	
Number of obs:	3804	groups:	Sample, 1902

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	3.78672	0.59715	2316.32522	6.341	2.73E-10	***
GenesLAR2	-0.34828	0.38548	1884.00007	-0.904	0.366366	
tissueFlower	0.90106	0.6313	2316.32672	1.427	0.153623	
tissueInternode	-2.706	0.63838	2316.327	-4.239	2.33E-05	***
tissueLate-dormant-bud	-3.00948	0.77091	2316.33092	-3.904	9.74E-05	***
tissueLeaf	-0.36786	0.59823	2316.32527	-0.615	0.538678	
tissueMature-leaf	-1.5384	0.66017	2316.32781	-2.33	0.019876	*
tissueOpen-bud	-1.26494	0.84449	2316.33234	-1.498	0.134305	
tissuePredormant-bud	1.19204	0.70655	2316.32929	1.687	0.091716	.
tissueRoot	0.1208	0.59817	2316.32526	0.202	0.839977	
tissueSeedling	-1.07962	0.77091	2316.33092	-1.4	0.161514	
tissueShoot-apex	-2.1454	0.77091	2316.33092	-2.783	0.005431	**
tissueStem	-1.63536	0.64499	2316.32725	-2.535	0.011295	*
tissueSwelling-bud	-0.73183	0.77091	2316.33092	-0.949	0.342569	
tissueVascular leaf	-0.58716	0.6237	2316.3264	-0.941	0.346588	
tissueWhole root system	-1.55354	0.64499	2316.32725	-2.409	0.016091	*
tissueXylem	-3.40956	0.59807	2316.32526	-5.701	1.34E-08	***
tissueYoung-leaf	1.04921	0.64499	2316.32725	1.627	0.103938	
tissueYoung-stem	-0.37613	0.73135	2316.32997	-0.514	0.607095	
GenesLAR2:tissueFlower	-1.93239	0.40752	1884.00007	-4.742	2.28E-06	***
GenesLAR2:tissueInternode	-0.60867	0.41209	1884.00007	-1.477	0.139837	
GenesLAR2:tissueLate-dormant-bud	0.09812	0.49765	1884.00008	0.197	0.843723	
GenesLAR2:tissueLeaf	-0.25688	0.38618	1884.00007	-0.665	0.506014	

GenesLAR2:tissueMature-leaf	-0.52891	0.42616	1884.00007	-1.241	0.214721	
GenesLAR2:tissueOpen-bud	-0.63687	0.54514	1884.00009	-1.168	0.242849	
GenesLAR2:tissuePredormant-bud	0.1435	0.4561	1884.00008	0.315	0.75308	
GenesLAR2:tissueRoot	-0.55091	0.38614	1884.00007	-1.427	0.153822	
GenesLAR2:tissueSeedling	-1.07131	0.49765	1884.00008	-2.153	0.031464	*
GenesLAR2:tissueShoot-apex	-0.63473	0.49765	1884.00008	-1.275	0.202303	
GenesLAR2:tissueStem	-0.95	0.41636	1884.00007	-2.282	0.02262	*
GenesLAR2:tissueSwelling-bud	-0.77742	0.49765	1884.00008	-1.562	0.11841	
GenesLAR2:tissueVascular leaf	-1.44616	0.40262	1884.00007	-3.592	0.000337	***
GenesLAR2:tissueWhole root system	0.80384	0.41636	1884.00007	1.931	0.053678	.
GenesLAR2:tissueXylem	0.20509	0.38607	1884.00007	0.531	0.595319	
GenesLAR2:tissueYoung-leaf	-0.2396	0.41636	1884.00007	-0.575	0.565056	
GenesLAR2:tissueYoung-stem	-0.81694	0.47211	1884.00008	-1.73	0.083722	.

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 12S. Estimated marginal means and pairwise comparison for the species *Populus trichocarpa*. Degrees-of-freedom method: asymptotic

<i>Estimated marginal means</i>	<i>Contrasts</i>
tissue = Early-dormant-bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1 3.787 0.5970 Inf 2.616 4.957 LAR2 3.438 0.5970 Inf 2.268 4.609	tissue = Early-dormant-bud: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.348 0.3850 Inf 0.904 0.3663
tissue = Flower: Genes emmean SE df asymp.LCL asymp.UCL LAR1 4.688 0.2050 Inf 4.286 5.089 LAR2 2.407 0.2050 Inf 2.006 2.809	tissue = Flower: contrast estimate SE df z.ratio p.value LAR1 - LAR2 2.281 0.1320 Inf 17.249 <.0001
tissue = Internode: Genes emmean SE df asymp.LCL asymp.UCL LAR1 1.081 0.2260 Inf 0.638 1.523 LAR2 0.124 0.2260 Inf -0.319 0.566	tissue = Internode: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.957 0.1460 Inf 6.568 <.0001
tissue = Late-dormant-bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1 0.777 0.4880 Inf -0.178 1.733 LAR2 0.527 0.4880 Inf -0.429 1.483	tissue = Late-dormant-bud: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.250 0.3150 Inf 0.795 0.4267
tissue = Leaf: Genes emmean SE df asymp.LCL asymp.UCL LAR1 3.419 0.0360 Inf 3.348 3.490 LAR2 2.814 0.0360 Inf 2.743 2.884	tissue = Leaf: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.605 0.0233 Inf 26.010 <.0001
tissue = Mature-leaf: Genes emmean SE df asymp.LCL asymp.UCL LAR1 2.248 0.2810 Inf 1.697 2.800 LAR2 1.371 0.2810 Inf 0.819 1.923	tissue = Mature-leaf: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.877 0.1820 Inf 4.827 <.0001
	tissue = Open-bud: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.985 0.3850 Inf 2.556 0.0106
	tissue = Predormant-bud: contrast estimate SE df z.ratio p.value

tissue = Open-bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1 2.522 0.5970 Inf 1.351 3.692 LAR2 1.537 0.5970 Inf 0.366 2.707 tissue = Predormant-bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1 4.979 0.3780 Inf 4.239 5.719 LAR2 4.774 0.3780 Inf 4.034 5.514 tissue = Root: Genes emmean SE df asymp.LCL asymp.UCL LAR1 3.908 0.0349 Inf 3.839 3.976 LAR2 3.008 0.0349 Inf 2.940 3.077 tissue = Seedling: Genes emmean SE df asymp.LCL asymp.UCL LAR1 2.707 0.4880 Inf 1.751 3.663 LAR2 1.288 0.4880 Inf 0.332 2.243 tissue = Shoot-apex: Genes emmean SE df asymp.LCL asymp.UCL LAR1 1.641 0.4880 Inf 0.686 2.597 LAR2 0.658 0.4880 Inf -0.297 1.614 tissue = Stem: Genes emmean SE df asymp.LCL asymp.UCL LAR1 2.151 0.2440 Inf 1.674 2.629 LAR2 0.853 0.2440 Inf 0.375 1.331 tissue = Swelling-bud: Genes emmean SE df asymp.LCL asymp.UCL LAR1 3.055 0.4880 Inf 2.099 4.011 LAR2 1.929 0.4880 Inf 0.974 2.885 tissue = Vascular leaf: Genes emmean SE df asymp.LCL asymp.UCL LAR1 3.200 0.1800 Inf 2.847 3.552 LAR2 1.405 0.1800 Inf 1.052 1.758 tissue = Whole root system: Genes emmean SE df asymp.LCL asymp.UCL LAR1 2.233 0.2440 Inf 1.755 2.711 LAR2 2.689 0.2440 Inf 2.211 3.167 tissue = Xylem: Genes emmean SE df asymp.LCL asymp.UCL LAR1 0.377 0.0332 Inf 0.312 0.442 LAR2 0.234 0.0332 Inf 0.169 0.299	LAR1 - LAR2 0.205 0.2440 Inf 0.840 0.4009 tissue = Root: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.899 0.0226 Inf 39.861 <.0001 tissue = Seedling: contrast estimate SE df z.ratio p.value LAR1 - LAR2 1.420 0.3150 Inf 4.510 <.0001 tissue = Shoot-apex: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.983 0.3150 Inf 3.123 0.0018 tissue = Stem: contrast estimate SE df z.ratio p.value LAR1 - LAR2 1.298 0.1570 Inf 8.250 <.0001 tissue = Swelling-bud: contrast estimate SE df z.ratio p.value LAR1 - LAR2 1.126 0.3150 Inf 3.577 0.0003 tissue = Vascular leaf: contrast estimate SE df z.ratio p.value LAR1 - LAR2 1.794 0.1160 Inf 15.439 <.0001 tissue = Whole root system: contrast estimate SE df z.ratio p.value LAR1 - LAR2 -0.456 0.1570 Inf -2.895 0.0038 tissue = Xylem: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.143 0.0214 Inf 6.676 <.0001 tissue = Young-leaf: contrast estimate SE df z.ratio p.value LAR1 - LAR2 0.588 0.1570 Inf 3.736 0.0002 tissue = Young-stem: contrast estimate SE df z.ratio p.value LAR1 - LAR2 1.165 0.2730 Inf 4.275 <.0001 Degrees-of-freedom method: asymptotic
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tissue = Young-leaf:					
Genes	emmean	SE	df	asympt.LCL	asympt.UCL
LAR1	4.836	0.2440	Inf	4.358	5.314
LAR2	4.248	0.2440	Inf	3.770	4.726
tissue = Young-stem:					
Genes	emmean	SE	df	asympt.LCL	asympt.UCL
LAR1	3.411	0.4220	Inf	2.583	4.238
LAR2	2.245	0.4220	Inf	1.418	3.073
Degrees-of-freedom method: asymptotic					
Confidence level used: 0.95					

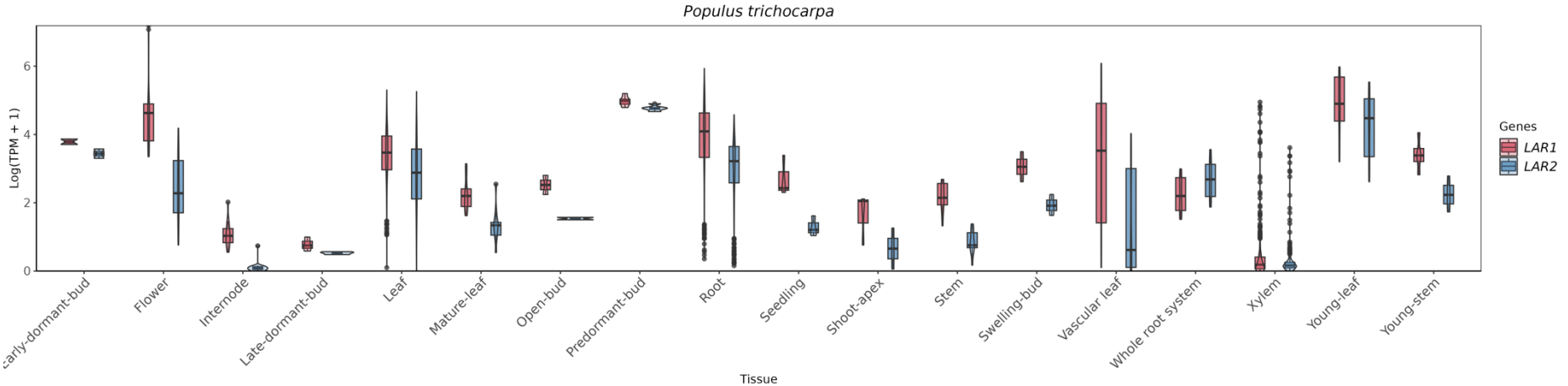


Figure 6S. Comparison of the expression of *LAR1* (red), and *LAR2* (blue) genes in the species *Populus trichocarpa*.

Carya illinoensis

Linear mixed model fit by REML. t-tests use Satterthwaite's method [`lmerModLmerTest`]

Formula: `TPM_log ~ Genes * tissue + (1 | Sample)`

Data: `data_long`

REML criterion at convergence: 7655.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.0486	-0.7132	-0.0787	0.5695	3.6612

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.002874	0.05361
Residual	0.438219	0.66198	
Number of obs:	178	groups:	Sample, 89

Fixed effects:

	<i>Estimate</i>	<i>Std. Error</i>	<i>df</i>	<i>T-value</i>	<i>Pr(> t)</i>	
(Intercept)	3.4887	0.1917	163.993	18.197	<2E-016	***
GenesLAR2	-0.7197	0.2703	82	-2.663	0.009317	**
tissuebud	-1.8182	0.3321	163.993	-5.475	1.61E-07	***
tissueembryo	-0.8942	0.2572	163.993	-3.476	0.000651	***
tissueflower	-1.9189	0.3834	163.993	-5.004	1.43E-06	***
tissueKernel	-1.4147	0.3834	163.993	-3.689	0.000305	***
tissueLeaf	-0.5105	0.2475	163.993	-2.062	0.040745	*
tissueseedling	-2.0248	0.2268	163.993	-8.926	8.53E-16	***
GenesLAR2:tissuebud	1.6143	0.4681	82	3.449	0.000892	***
GenesLAR2:tissueembryo	-1.374	0.3626	82	-3.789	0.000287	***
GenesLAR2:tissueflower	2.5682	0.5405	82	4.751	8.49E-06	***
GenesLAR2:tissueKernel	-0.7166	0.5405	82	-1.326	0.188606	
GenesLAR2:tissueLeaf	-0.9122	0.3489	82	-2.615	0.01063	*
enesLAR2:tissueseedling	0.791	0.3198	82	2.474	0.015432	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 13S. Estimated marginal means and pairwise comparison for the species *Carya illinoensis*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = Branch: Genes emmean SE df lower.CL upper.CL LAR1 3.489 0.192 164 3.1102 3.867 LAR2 2.769 0.192 164 2.3905 3.148	tissue = Branch: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.7197 0.270 82 2.663 0.0093
tissue = bud: Genes emmean SE df lower.CL upper.CL LAR1 1.671 0.271 164 1.1351 2.206 LAR2 2.565 0.271 164 2.0297 3.100	tissue = bud: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.8946 0.382 82 -2.341 0.0217
tissue = embryo: Genes emmean SE df lower.CL upper.CL LAR1 2.595 0.171 164 2.2559 2.933 LAR2 0.501 0.171 164 0.1622 0.839	tissue = embryo: contrast estimate SE df t.ratio p.value LAR1 - LAR2 2.0937 0.242 82 8.662 <.0001
tissue = flower: Genes emmean SE df lower.CL upper.CL LAR1 1.570 0.332 164 0.9142 2.226 LAR2 3.418 0.332 164 2.7626 4.074	tissue = flower: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -1.8485 0.468 82 -3.949 0.0002
tissue = Kernel: Genes emmean SE df lower.CL upper.CL LAR1 2.074 0.332 164 1.4184 2.730 LAR2 0.638 0.332 164 -0.0179 1.293	tissue = Kernel: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.4363 0.468 82 3.068 0.0029
tissue = Leaf: Genes emmean SE df lower.CL upper.CL LAR1 2.978 0.157 164 2.6692 3.287 LAR2 1.346 0.157 164 1.0373 1.655	tissue = Leaf: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.6319 0.221 82 7.396 <.0001
tissue = seedling: Genes emmean SE df lower.CL upper.CL LAR1 1.464 0.121 164 1.2245 1.703 LAR2 1.535 0.121 164 1.2959 1.775	tissue = seedling: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.0713 0.171 82 -0.417 0.6775
	Degrees-of-freedom method: kenward-roger Confidence level used: 0.95

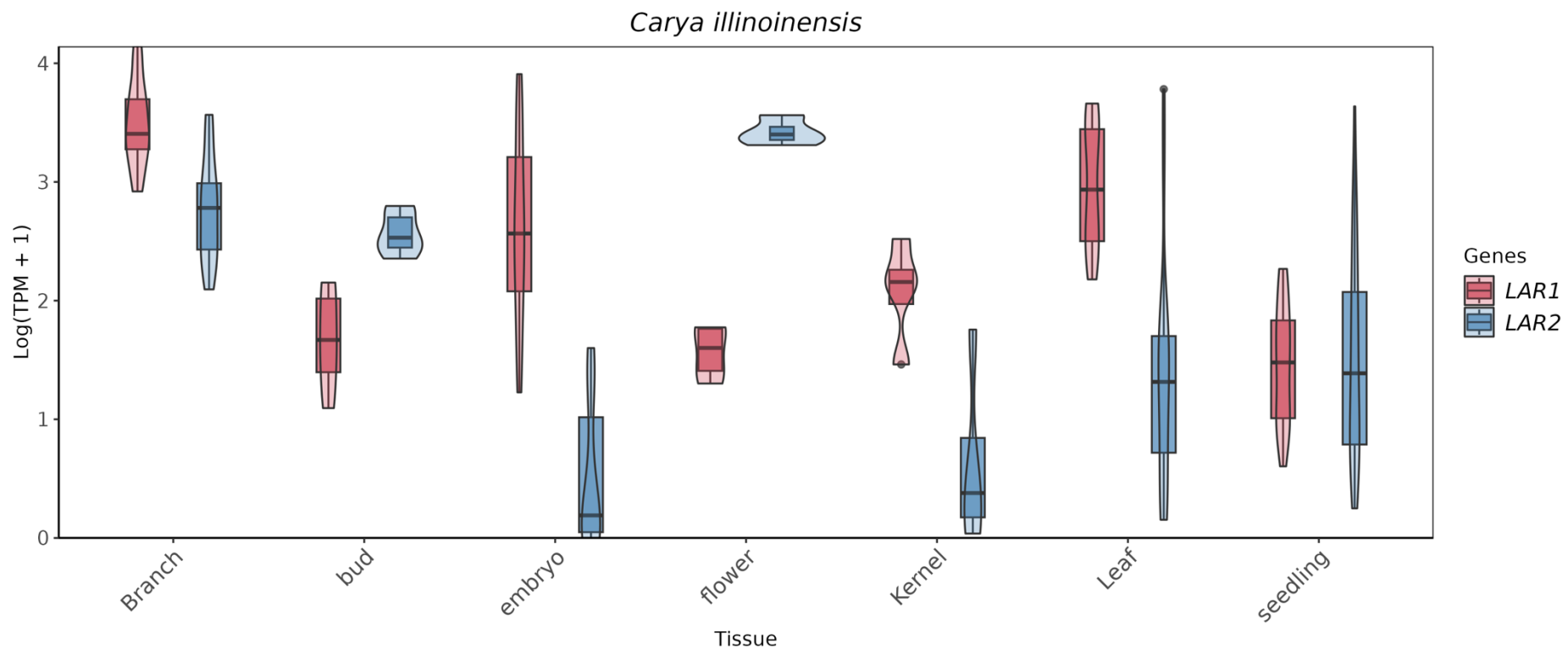


Figure 7S. Comparison of the expression of *LAR1* (red), and *LAR2* (blue) genes in the species *Carya illinoensis*.

Morella rubra

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: TPM_log ~ Genes * tissue + (1 | Sample)

Data: data_long

REML criterion at convergence: 638.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.5316	-0.5276	-0.1306	0.4559	5.5753

Random effects:

Groups	Name	Variance	Std.Dev.
Sample	(Intercept)	0.1621	0.4026
Residual		0.4913	0.7009
Number of obs:	272	groups:	Sample, 136

Fixed effects:

	Estimate	Std. Error	df	T-value	Pr(> t)	
(Intercept)	4.86342	0.80833	244.92727	6.017	6.45E-09	***
GenesLAR2	-0.38874	0.99127	130	-0.392	0.6956	
tissueflower	0.09484	0.88549	244.92727	0.107	0.9148	
tissuefruits	-2.07341	0.81262	244.92727	-2.552	0.0113	*
tissueleaves	0.29296	0.82014	244.92727	0.357	0.7212	
tissueroot	0.32799	1.14316	244.92727	0.287	0.7744	
tissuestem	-0.52627	1.14316	244.92727	-0.46	0.6457	
GenesLAR2:tissueflower	-0.47636	1.08589	130	-0.439	0.6616	
GenesLAR2:tissuefruits	-1.62229	0.99653	130	-1.628	0.106	
GenesLAR2:tissueleaves	-1.03024	1.00575	130	-1.024	0.3076	
GenesLAR2:tissueroot	-0.61444	1.40187	130	-0.438	0.6619	
GenesLAR2:tissuestem	1.19982	1.40187	130	0.856	0.3936	

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table 14S. Estimated marginal means and pairwise comparison for the species *Morella rubra*. Degrees-of-freedom method: kenward-roger. Confidence level used: 0.95

<i>Estimated Marginal Means</i>	<i>Contrasts</i>
tissue = bud: Genes emmean SE df lower.CL upper.CL LAR1 4.863 0.8080 245 3.271 6.456 LAR2 4.475 0.8080 245 2.883 6.067	tissue = bud: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.389 0.991 130 0.392 0.6956
tissue = flower: Genes emmean SE df lower.CL upper.CL LAR1 4.958 0.3610 245 4.246 5.670 LAR2 4.093 0.3610 245 3.381 4.805	tissue = flower: contrast estimate SE df t.ratio p.value LAR1 - LAR2 0.865 0.443 130 1.951 0.0532
tissue = fruits: Genes emmean SE df lower.CL upper.CL LAR1 2.790 0.0834 245 2.626 2.954 LAR2 0.779 0.0834 245 0.615 0.943	tissue = fruits: contrast estimate SE df t.ratio p.value LAR1 - LAR2 2.011 0.102 130 19.669 <.0001
tissue = leaves: Genes emmean SE df lower.CL upper.CL LAR1 5.156 0.1390 245 4.883 5.429 LAR2 3.737 0.1390 245 3.464 4.010	tissue = leaves: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.419 0.170 130 8.347 <.0001
tissue = root: Genes emmean SE df lower.CL upper.CL LAR1 5.191 0.8080 245 3.599 6.784 LAR2 4.188 0.8080 245 2.596 5.780	tissue = root: contrast estimate SE df t.ratio p.value LAR1 - LAR2 1.003 0.991 130 1.012 0.3134
tissue = stem: Genes emmean SE df lower.CL upper.CL LAR1 4.337 0.8080 245 2.745 5.929 LAR2 5.148 0.8080 245 3.556 6.740	tissue = stem: contrast estimate SE df t.ratio p.value LAR1 - LAR2 -0.811 0.991 130 -0.818 0.4147
Degrees-of-freedom method: kenward-roger Confidence level used: 0.95	Degrees-of-freedom method: kenward-roger

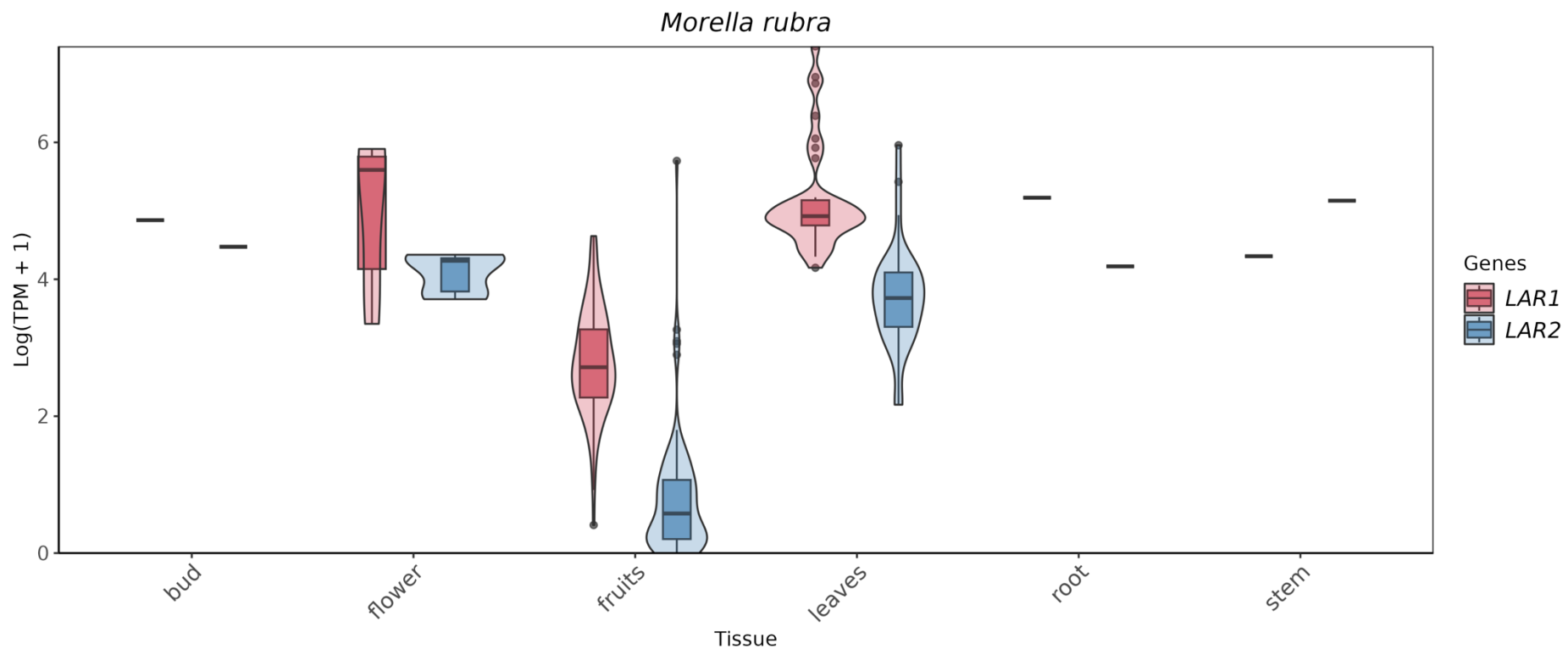


Figure 8S. Comparison of the expression of *LAR1* (red), and *LAR2* (blue) genes in the species *Morella rubra*.