



Supplemental Materials for The draft transcriptome of *Arctostaphylos glauca*: de novo assembly and analysis, Senn et al 2026

Table S1. Full BLAST results from NCBI core nucleotide collection for the transcripts of interest

qseqid	sseqid	pid ent	len gt h	mis matc h	qst art	qe n d	ssta rt	send	eval ue	bits cor e	Gene_Name
TRINITY_DN4 933_c0_g1_i4	OZ2286 08.1	10 0	77	0	32 80	33 56	5951 2040	5951 1964	3.48 E- 31	143	Calluna vulgaris genome assembly, chromosome: 5
TRINITY_DN3 406_c0_g1_i1	MZ7791 11.1	10 0	42	0	1	42	1764 97	1765 38	3.57 E- 12	78. 7	Arctostaphylos glauca isolate Glendora Ridge Rd-6 mitochondrion, partial genome
TRINITY_DN6 89_c0_g1_i6	OZ2286 05.1	10 0	28	0	20 43	20 70	5165 9897	5165 9924	0.00 3	52. 8	Calluna vulgaris genome assembly, chromosome: 2
TRINITY_DN9 05_c0_g2_i2	KF0244 64.1	46 8	79	1	1	79	20	97	E- 29	134	Arbutus unedo clone 99638 microsatellite sequence
TRINITY_DN3 508_c0_g1_i14	OZ2245 85.1	40 3	77	2	11 41	12 17	5864 2342	5864 2266	E- 28	132	Calluna vulgaris genome assembly, chromosome: 6
TRINITY_DN2 250_c0_g1_i20	OZ2286 10.1	36 8	76	2	10 68	11 43	4564 3751	4564 3826	E- 27	130	Calluna vulgaris genome assembly, chromosome: 7
TRINITY_DN1 626_c0_g2_i1	OZ2245 83.1	14 3	35	1	25 4	28 8	3580 5475	3580 5441	E- 07	60. 2	Calluna vulgaris genome assembly, chromosome: 2
TRINITY_DN1 290_c0_g1_i8	OZ2286 07.1	10 1	69	2	13 58	14 26	5106 6366	5106 6298	E- 23	117	Calluna vulgaris genome assembly, chromosome: 4
TRINITY_DN6 89_c0_g4_i1	OZ2286 06.1	96. 97	33	0	18 65	18 97	3953 3242	3953 3211	015 3	54. 7	Calluna vulgaris genome assembly, chromosome: 3
TRINITY_DN9 66_c0_g1_i9	OZ2286 04.1	87 5	96	3	11 05	12 00	6297 1672	6297 1767	5.1E -37	161	Calluna vulgaris genome assembly, chromosome: 1
TRINITY_DN9 66_c0_g1_i11	OZ2245 80.1	87 5	96	3	11 05	12 00	6238 9299	6238 9394	E- 37	161	Calluna vulgaris genome assembly, chromosome: 1



TRINITY_DN9	OZ2245	96.49			13	14	4049	4049	4.78		
66_c0_g1_i7	82.1	1	57	2	90	46	1335	1279	E-17	95.3	Calluna vulgaris genome assembly, chromosome: 3
TRINITY_DN2	KF0241	96.10			19	20			6.21		
450_c0_g1_i2	52.1	4	77	1	44	18	1	77	E-26	124	Arbutus unedo clone 63033 microsatellite sequence
TRINITY_DN3	OZ2286	95.52			68	75	2461	2461	4.67		
121_c0_g1_i2	11.1	2	67	3	7	3	8673	8739	E-21	108	Calluna vulgaris genome assembly, chromosome: 8
TRINITY_DN3	XM_058	95.45			34	41			1.51		PREDICTED: Rhododendron vialii protein transport protein sec31-like
683_c0_g1_i3	364102.1	5	66	3	9	4	116	181	E-20	106	(LOC131330492), mRNA
TRINITY_DN1	OZ2286	95.45			80	86	4880	4880	1.47		
0367_c0_g1_i1	09.1	5	66	3	4	9	8345	8410	E-20	106	Calluna vulgaris genome assembly, chromosome: 6
TRINITY_DN0	OZ2245	95.23	12		67	80	6447	6448	1.07		
_c0_g1_i9	86.1	8	6	6	6	1	62	87	E-48	200	Calluna vulgaris genome assembly, chromosome: 7
TRINITY_DN1	OZ2245	94.76	17		96	11	2297	2297	1.71		
55_c0_g1_i11	81.1	7	2	9	3	34	7434	7263	E-69	268	Calluna vulgaris genome assembly, chromosome: 4
TRINITY_DN2	XR_009	94.11			46	52			1.93		PREDICTED: Rhododendron vialii uncharacterized LOC131303166
304_c0_g1_i1	191913.1	8	68	3	0	7	563	629	E-19	102	(LOC131303166), ncRNA
TRINITY_DN5	XM_058	93.65			34	40			2.57		PREDICTED: Rhododendron vialii uncharacterized LOC131308357
073_c0_g1_i6	335277.1	1	63	4	5	7	1058	1120	E-17	95.3	(LOC131308357), mRNA
TRINITY_DN1	OZ2245	93.93	11		11	12	1301	1301	9.66		
473_c0_g1_i20	84.1	22	8	8	22	39	6807	6924	E-41	174	Calluna vulgaris genome assembly, chromosome: 5
TRINITY_DN1	XM_058	93.02			14	15			1.35		PREDICTED: Rhododendron vialii cytochrome P450 736A117-like
448_c0_g1_i1	371471.1	3	43	3	71	13	1328	1370	E-07	63.9	(LOC131335912), transcript variant X3, mRNA
TRINITY_DN1	PQ5370	92.03	11		23	34	3271	3272	3.19		
68_c0_g1_i9	97.1	5	3	8	4	6	49	60	E-36	158	Rhododendron vialii mitochondrion, complete genome
TRINITY_DN1	MT3276	91.45	19		48	68			3.38		
731_c0_g1_i4	89.1	7	9	17	3	1	555	357	E-71	274	Arbutus unedo clone AU88GT16 microsatellite sequence
TRINITY_DN3	AY1237	91.91	16		54	70			1.44		
35_c0_g1_i5	65.1	25	0	14	9	8	11	170	E-54	219	Vaccinium myrtillus chalcone synthase (chs) mRNA, partial cds



TRINITY_DN4 01_c0_g1_i3	MK9908 22.1	91. 07 1	56	3	20 80	21 35	5179 48	5180 01	7.52 E- 11	75	Monotropa hypopitys chromosome 1 mitochondrion, complete sequence
TRINITY_DN3 663_c0_g1_i1	XM_058 348024.1	90. 95 5	15 81	137	30 3	18 80	953	2530	0	212 2	PREDICTED: Rhododendron vialii 3-ketoacyl-CoA synthase 11-like (LOC131318190), mRNA
TRINITY_DN7 8_c0_g1_i2	AB2895 94.1	90. 62 5	48 0	45	32 8	80 7	1	480	1.4E -180	638	Rhododendron x pulchrum RpF3H mRNA for flavanone 3-hydroxylase, partial cds
TRINITY_DN4 481_c0_g1_i3	XM_058 370819.1	90. 54 1	74	5	13 14	13 85	1512	1585	E- 18	97. 1	PREDICTED: Rhododendron vialii caffeoylshikimate esterase (LOC131335458), mRNA
TRINITY_DN4 014_c0_g1_i2	KJ83074 8.1	90. 50 3	10 74	99	25 8	13 28	1113	40	0	141 5	Vaccinium corymbosum O-methyltransferase mRNA, complete cds
TRINITY_DN5 073_c0_g1_i14	XM_058 335270.1	90. 37 7	23 9	19	23 66	26 04	1532	1298	E- 82	311	PREDICTED: Rhododendron vialii jasmonate-induced oxygenase 2-like (LOC131308351), mRNA
TRINITY_DN1 468_c0_g1_i6	XM_058 349111.1	90 90	80	5	70 6	78 2	1093	1172	E- 19	100	PREDICTED: Rhododendron vialii glycine-rich cell wall structural protein 1.8-like (LOC131319014), mRNA
TRINITY_DN2 195_c0_g1_i8	XM_058 352597.1	89. 88 89	75 1	72	74 1	74 9	1019	271	0	963	PREDICTED: Rhododendron vialii tryptophan synthase beta chain 1 (LOC131321704), mRNA
TRINITY_DN3 947_c0_g1_i2	XM_058 328933.1	89. 75 89	16 99	166	33 5	20 32	1758	67	0	216 7	PREDICTED: Rhododendron vialii bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic-like (LOC131302366), transcript variant X2, mRNA
TRINITY_DN4 942_c1_g1_i1	XM_058 326189.1	89. 89 89	15 19	147	22 4	17 38	1532	19	0	193 2	PREDICTED: Rhododendron vialii 3-ketoacyl-CoA thiolase 2, peroxisomal-like (LOC131300387), mRNA
TRINITY_DN3 35_c0_g2_i1	MW358 095.1	89. 72 8	99 3	100	29 9	12 90	1049	2040	0	126 7	Rhododendron x hybridum chalcone synthase (CHS) gene, complete cds
TRINITY_DN1 078_c0_g2_i1	ON2609 05.1	89. 65 4	21 07	216	18 7	22 92	37	2142	0	268 2	Vaccinium corymbosum phenylalanine ammonia-lyase (PALd) mRNA, complete cds
TRINITY_DN4 358_c0_g1_i4	XM_058 346074.1	89. 48 5	46 6	49	52 7	99 2	188	653	3.7E -166	590	PREDICTED: Rhododendron vialii cyanate hydratase (LOC131316642), transcript variant X1, mRNA
TRINITY_DN4 48_c0_g1_i8	XM_058 340875.1	89. 13 9	26 7	27	17 4	43 9	35	300	E- 88	331	PREDICTED: Rhododendron vialii protein PYRICULARIA ORYZAE RESISTANCE 21-like (LOC131312870), transcript variant X3, mRNA
TRINITY_DN1 078_c0_g1_i1	MW735 988.1	88. 88 77	21 55	231	17 7	23 30	1	2145	0	262 8	Rhododendron fortunei phenylalanine ammonia lyase (PAL) gene, complete cds



TRINITY_DN1	XM_058	88.43	99		47	14				119	PREDICTED: Rhododendron vialii 2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic-like (LOC131322104), transcript variant X2, mRNA
756_c0_g1_i3	353265.1	1	4	112	8	69	472	1464	0	5	
TRINITY_DN3	XM_058	88.20	20		24	22				238	PREDICTED: Rhododendron vialii heat shock cognate 70 kDa protein 2-like (LOC131318808), mRNA
48_c0_g1_i1	348784.1	6	01	235	1	40	220	2220	0	6	
TRINITY_DN1	XM_058	88.17	88		31	12				105	PREDICTED: Rhododendron vialii protein HEAT-STRESS-ASSOCIATED 32 (LOC131311405), mRNA
311_c0_g1_i5	338857.1	6	8	101	4	00	972	88	0	5	
TRINITY_DN6	XM_058	88.02	21		25	23				249	PREDICTED: Rhododendron vialii phenylalanine ammonia-lyase-like (LOC131318698), mRNA
767_c0_g1_i7	348634.1	7	13	243	3	60	322	2429	0	2	
TRINITY_DN1	XM_058	88.01	11		26	13				131	PREDICTED: Rhododendron vialii anthocyanidin reductase ((2S)-flavan-3-ol-forming) (LOC131313714), mRNA
494_c0_g1_i1	342174.1	4	18	127	5	79	1414	301	0	5	
TRINITY_DN6	OK6244	87.83	78		78						Vaccinium dunalianum phenylalanin ammonia-lyase 3 (PAL3) mRNA, complete cds
767_c0_g1_i8	54.1	6	1	93	2	1	1555	2334	0	915	
TRINITY_DN4	XM_058	87.66	12		12					146	PREDICTED: Rhododendron vialii butanoate--CoA ligase AAE1-like (LOC131303765), mRNA
01_c0_g1_i7	330760.1	8	65	145	1	62	719	1975	0	1	
TRINITY_DN1	XM_058	87.26	99		44	14				113	PREDICTED: Rhododendron vialii vestitone reductase-like (LOC131324828), transcript variant X1, mRNA
039_c0_g1_i1	356975.1	2	7	125	0	35	998	3	0	6	
TRINITY_DN1	XM_058	87.20	80		40	12					PREDICTED: Rhododendron vialii jasmonate-induced oxygenase 2-like (LOC131326023), mRNA
418_c0_g1_i6	358565.1	5	5	101	7	10	1318	515	0	915	
TRINITY_DN1	XM_058	87.20	11		14	12				124	PREDICTED: Rhododendron vialii trans-resveratrol di-O-methyltransferase-like (LOC131314185), mRNA
268_c0_g1_i1	342680.1	5	02	131	6	47	171	1262	0	5	
TRINITY_DN4	XM_058	86.98	18		18					206	PREDICTED: Rhododendron vialii berberine bridge enzyme-like 15 (LOC131312968), mRNA
868_c0_g1_i1	341007.1	7	52	216	3	37	1844	1	0	1	
TRINITY_DN1	XM_058	86.96	97		27	12				108	PREDICTED: Rhododendron vialii cytochrome P450 71A1-like (LOC131312986), transcript variant X2, mRNA
251_c0_g1_i2	341023.1	1	4	118	3	43	1101	134	0	6	
TRINITY_DN1	XM_058	86.44	11		18	12				121	PREDICTED: Rhododendron vialii xyloglucan O-acetyltransferase 1 (LOC131310296), mRNA
894_c0_g1_i4	337239.1	1	21	140	7	95	1487	367	0	8	
TRINITY_DN1	XM_058	86.29	46		22	68			3.3E		PREDICTED: Rhododendron vialii cell number regulator 2-like (LOC131301855), mRNA
000_c0_g1_i5	328336.1	6	7	62	2	7	201	666	-141	507	

TRINITY_DN1_563_c0_g1_i6	XM_058335292.1	86.24	92		17	10					PREDICTED: Rhododendron vialii 2-hydroxyisoflavanone dehydratase-like (LOC131308379), mRNA
TRINITY_DN1_555_c0_g1_i2	XM_058324387.1	85.98	94		50	14				101	PREDICTED: Rhododendron vialii 2-methylene-furan-3-one reductase-like (LOC131298887), mRNA
TRINITY_DN2_642_c0_g1_i3	XM_058370921.1	85.96	12		19	13				126	PREDICTED: Rhododendron vialii ethylene-responsive transcription factor RAP2-12-like (LOC131335522), transcript variant X3, mRNA
TRINITY_DN2_642_c0_g1_i4	XM_058370920.1	85.71	12		19	13				124	PREDICTED: Rhododendron vialii ethylene-responsive transcription factor RAP2-12-like (LOC131335522), transcript variant X2, mRNA
TRINITY_DN1_0539_c1_g1_i1	XM_058363428.1	85.61	98		42	14				103	PREDICTED: Rhododendron vialii flavonol synthase/flavanone 3-hydroxylase-like (LOC131329984), mRNA
TRINITY_DN1_133_c0_g1_i1	XM_058370895.1	85.32	10		11	11				109	PREDICTED: Rhododendron vialii hydroxyphenylpyruvate reductase (LOC131335507), mRNA
TRINITY_DN1_104_c0_g1_i7	XM_058341352.1	85.29	10		21	13				111	PREDICTED: Rhododendron vialii uncharacterized LOC131313185 (LOC131313185), mRNA
TRINITY_DN4_853_c0_g1_i8	XM_058326354.1	85.15	48		51	99			7.1E		PREDICTED: Rhododendron vialii small heat shock protein, chloroplastic-like (LOC131300481), transcript variant X1, mRNA
TRINITY_DN1_442_c0_g1_i12	MH321460.1	84.11	47		19	66			9.8E		Vaccinium corymbosum chalcone synthase (CHS) mRNA, partial cds
TRINITY_DN2_237_c0_g1_i8	AM392497.1	84.49	32		54	87			-136	488	Rhododendron noriakianum partial cpsHSP gene for chloroplast small heat shock protein
TRINITY_DN2_237_c0_g1_i7	AM392492.1	84.49	32		53	86			E-	326	Rhododendron kanahirai partial cpsHSP gene for chloroplast small heat shock protein
TRINITY_DN7_00_c2_g1_i1	XM_058346429.1	83.25	20		52	72			87		PREDICTED: Rhododendron vialii 18.1 kDa class I heat shock protein-like (LOC131316907), mRNA
TRINITY_DN3_31_c0_g1_i2	XM_058326945.1	83.17	12		23	15			45	187	PREDICTED: Rhododendron vialii chitinase-like protein 1 (LOC131300915), transcript variant X1, mRNA
TRINITY_DN7_390_c0_g1_i1	XM_058345313.1	83.01	47		37	83			E-		PREDICTED: Rhododendron vialii pathogenesis-related genes transcriptional activator PTI5-like (LOC131316045), mRNA



TRINITY_DN2	XM_058	82.	84	47		20	68		3.7E			PREDICTED: Rhododendron vialii 18.5 kDa class I heat shock protein-like
93_c0_g1_i11	335467.1	5	8	73	8	0	644	171	-115	420		(LOC131308529), mRNA
TRINITY_DN2	FM1729	82.	78	39		23	62		5.11			Rhododendron rubropunctatum partial CTsHSP2 gene for cytosolic class I small
93_c0_g1_i14	31.1	5	5	64	7	9	393	1	E-	94	350	heat shock protein type 2
TRINITY_DN2	XM_058	82.	66	92		42	13					PREDICTED: Rhododendron vialii probable carboxylesterase 12
22_c0_g1_i2	360233.1	5	3	148	9	45	1051	135	0	808		(LOC131327195), mRNA
TRINITY_DN1	XM_058	81.	73	10		87	18					PREDICTED: Rhododendron vialii glucan endo-1,3-beta-glucosidase-like
685_c0_g1_i5	371778.1	1	40	169	5	94	101	1139	0	848		(LOC131336084), mRNA
TRINITY_DN1	XM_058	81.	51	93		25	11					PREDICTED: Rhododendron vialii 2-hydroxyisoflavanone dehydratase-like
5538_c0_g1_i3	360174.1	7	6	160	4	84	1017	90	0	758		(LOC131327152), mRNA
TRINITY_DN2	XM_058	80.	62	10		27	13					PREDICTED: Rhododendron vialii ethylene-responsive transcription factor 3
24_c0_g2_i1	354233.1	4	89	139	9	27	266	1322	0	776		(LOC131322774), mRNA
TRINITY_DN5	XM_058	78.	95	65		44	10		8E-			PREDICTED: Rhododendron vialii heavy metal-associated isoprenylated plant
55_c0_g1_i8	351969.1	5	1	100	9	70	1218	576	112	409		protein 3-like (LOC131321002), transcript variant X1, mRNA
TRINITY_DN5	XM_058	78.	17	67		44	11		2.2E			PREDICTED: Rhododendron vialii pathogenesis-related thaumatin-like protein
36_c0_g1_i4	367305.1	1	8	146	1	17	61	737	-118	431		3.5 (LOC131333007), mRNA
TRINITY_DN4	XM_058	78.	01	10		27	12		1.2E			PREDICTED: Rhododendron vialii heavy metal-associated isoprenylated plant
158_c0_g1_i2	367951.1	4	37	141	4	59	1005	5	-160	571		protein 39-like (LOC131333432), mRNA
TRINITY_DN6	KU5223	77.	24	31		34	65		1.14			Vaccinium corymbosum small heat shock protein HSP17.7 mRNA, complete
85_c0_g1_i4	04.1	4	2	63	3	3	166	470	E-	41	176	cds

Table S2. Full BLAST results for NCBI WGS collection for genes of interest

qseqid	sseqid	pid ent	len gth	mism atch	qst art	qe nd	sstart	send	evalu e	bitsc ore	Gene_Name
TRINITY_DN1448	JAHSPW0200				103	11	48021	48022	4.11e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6
_c0_g1_i1	00011.1	100	134	0	3	66	16	49	60	242	SCAF_11, whole genome shotgun sequence
TRINITY_DN1448	JAHSPW0200				103	11	48021	48022	3.66e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6
_c0_g1_i2	00011.1	100	134	0	3	66	16	49	60	242	SCAF_11, whole genome shotgun sequence
TRINITY_DN1448	JAHSPW0200				103	11	48021	48022	4.10e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6
_c0_g1_i6	00011.1	100	134	0	3	66	16	49	60	242	SCAF_11, whole genome shotgun sequence
TRINITY_DN3508	JAHSPW0200				163	18	22481	22481	1.01e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6
_c0_g1_i14	00012.1	100	257	0	5	91	239	495	126	464	SCAF_12, whole genome shotgun sequence
TRINITY_DN4853	JAHSPW0200					58	28386	28387			Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6
_c0_g1_i7	00013.1	21	580	8	1	0	744	323	0.0	1011	SCAF_13, whole genome shotgun sequence



TRINITY_DN4853_c0_g1_i8	JAHSPW02000013.1	98.6	21	580	8	1	0	28386	28387	323	0.0	1011	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_13, whole genome shotgun sequence
TRINITY_DN4868_c0_g1_i1	JAHSPW02000001.1	99.4	218	04	2	13	1	23287	23285	430	0.0	3877	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_1, whole genome shotgun sequence
TRINITY_DN4868_c0_g1_i4	JAHSPW02000001.1	99.1	226	59	0	18	1	23287	23285	507	0.0	3987	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_1, whole genome shotgun sequence
TRINITY_DN607_c0_g2_i5	JAHSPX01000009.1		100	106	0		836	1	93031	93032	5.93e-	192	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0009, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i1	JAHSPW02000035.1	96.5	107	49	2	20	1	29301	29406	4	0.0	1769	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_35, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i1	JAHSPW02000035.1	96.5	107	49	2	21	1	29301	29406	4	0.0		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_35, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i2	JAHSPX01000004.1		112					11	13719	13730			Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i3	JAHSPW02000035.1	96.4	107	55	2	21	1	29301	29406	4	0.0		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_35, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i4	JAHSPW02000035.1	96.7	107	35	2	18	1	29301	29406	4	0.0		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_35, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i5	JAHSPX01000004.1	96.4					119	13	13731	13732	1.55e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i6	JAHSPX01000004.1	96.4	141	54			119	13	13731	13732	1.55e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i7	JAHSPX01000004.1	96.4					119	13	13731	13732	1.55e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i8	JAHSPW02000035.1	96.6	107	54	141	5	6	36	04	44	57		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN685_c0_g1_i9	JAHSPX01000004.1	96.5					121	13	13731	13732	1.18e-		Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0004, whole genome shotgun sequence
TRINITY_DN689_c0_g1_i2	JBHWAP010000063.1	28	144	5			1	54	01	44	58	238	Arbutus menziesii isolate PacificMadrone02 h2tg0000671_1, whole genome shotgun sequence
TRINITY_DN689_c0_g1_i3	JBHWAP010000063.1	100	96	0			1	96	4	9	40		Arbutus menziesii isolate PacificMadrone02 h2tg0000671_1, whole genome shotgun sequence
TRINITY_DN689_c0_g1_i6	JAHSPX01000014.1	100	96	0			1	96	4	9	40		Arbutus menziesii isolate PacificMadrone02 h2tg0000671_1, whole genome shotgun sequence
TRINITY_DN689_c0_g4_i1	JACYLG010002524.1	100	284	0			5	28	69	52	141	513	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0014, whole genome shotgun sequence
TRINITY_DN6977_c0_g1_i1	JAHSPX01000006.1	100	30	0			703	2	971	942	0.001		Rhododendron molle isolate GLZ1001 LG01, whole genome shotgun sequence
TRINITY_DN6977_c0_g3_i1	JAHSPX01000006.1	100	91	0			340	0	13167	13167	5.18e-	165	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0006, whole genome shotgun sequence
		100	98	0			1	98	13166	13166	7.21e-	178	Arctostaphylos glauca voucher Morrison 13 isolate GLNDR_RDG_Rd-6 SCAF_0006, whole genome shotgun sequence

Chunk 1. Source code to run Trinity assembly and salmon quantification

```
/local/cluster/trinity-2.13.2/opt/trinity-2.13.2/util/align_and_estimate_abundance.pl --transcripts Trinity.fasta --seqType fa --samples_file  
../././chaparral.txt --est_method salmon --trinity_mode --aln_method bowtie2 --thread_count 32 --prep_reference  
bash  
source /local/cluster/busco/activate.sh
```



```
busco --list -datasets
cd Trinity_busco_yerba/
busco -i Trinity.fasta -o Trinity_busco_yerba -l eudicots_odb10 -m transcriptome
```

```
SGE_Batch -q presley -c 'bash Trinotate_Pipeline.sh' -r -tri01
salmon index -t Trinity.fasta -I transcripts_index -k 31
salmon quant -i /path/to/transcripts_index -l A -1 /path/to/13BA_R1.fastq.gz -2 /path/to/13BA_R2.fastq.gz --validateMappings -o
/path/to/13BA_quant
salmon quant -i /path/to/salmon_index -l A -1 /path/to/14A_R1.fastq.gz -2 /path/to/14A_R2.fastq.gz --validateMappings -o /path/to/14A_quant
salmon quant -i /path/to/salmon_index -l A -1 /path/to/15A_R1.fastq.gz -2 /path/to/15A_R2.fastq.gz --validateMappings -o /path/to/15A_quant
#download quant.sf files from each resepective sample of interest
#download transcriptome
###See Deseq.R pipeline for DE analysis
```

Chunk 2. Source code to calculate transcriptome summary statistics

```
nano stats.py
```

```
from Bio import SeqIO
from statistics import median
```

```
def get_contig_lengths(fasta_file):
    contig_lengths = []
    for record in SeqIO.parse(fasta_file, "fasta"):
        contig_lengths.append(len(record))
    return contig_lengths

def calculate_stats(contig_lengths):
    contig_lengths_sorted = sorted(contig_lengths, reverse=True)
    max_length = max(contig_lengths)
    total_length = sum(contig_lengths)
```



```
half_length = total_length / 2

# Calculate N50
current_length = 0
n50 = 0
for length in contig_lengths_sorted:
    current_length += length
    if current_length >= half_length:
        n50 = length
        break

# Calculate L50
l50 = contig_lengths_sorted.index(n50) + 1

# Calculate N80
n80_cutoff = total_length * 0.8
current_length = 0
n80 = 0
for length in contig_lengths_sorted:
    current_length += length
    if current_length >= n80_cutoff:
        n80 = length
        break

return max_length, l50, n50, n80

# Replace 'Trinity.fasta' with the path to your Trinity assembled transcriptome file
```



```
fasta_file = "Trinity.fasta"

contig_lengths = get_contig_lengths(fasta_file)
max_length, l50, n50, n80 = calculate_stats(contig_lengths)

print("Max Length:", max_length)
print("L50:", l50)
print("N50:", n50)
print("N80:", n80)
```

Chunk 3. Source code to concatenate and filter BLAST results

```
---
title: "Concatenate and filter BLAST results"
author: "Savanah Senn"
date: "2025-02-26"
---

```{r setup, include=FALSE}
knitr::opts_chunk$set(echo = TRUE)
library(tidyverse)
```

## R Markdown

```{r}
p1=read.csv("part 1.csv", header=FALSE)
p2=read.csv("part 2.csv", header=FALSE)
p3=read.csv("part 3.csv", header=FALSE)
p4=read.csv("part 4.csv", header=FALSE)
p5=read.csv("part 5.csv", header=FALSE)
```



```
p6=read.csv("part 6.csv", header=FALSE)
p7=read.csv("part 7.csv", header=FALSE)
p8=read.csv("part 8.csv", header=FALSE)
p9=read.csv("part 9.csv", header=FALSE)
p10=read.csv("part 10.csv", header=FALSE)
df=rbind(p1,p2,p3,p4,p5,p6,p7,p8,p9,p10)
df
names(df)=c("query.acc.ver", "subject.acc.ver", "pct.id", "align.length", "mismatches", "gap.opens", "q.start", "q.end", "s.start", "s.end","evaluate",
"bit.score")
df
df.filt=df %>%
 filter(pct.id >=80)
#df.filt=df.filt %>%
filter(align.length >=1000)

df.filt=df.filt %>% group_by(query.acc.ver) %>% slice(which.max(pct.id))
df.filt
Change filename for your family of plant
write.csv(df.filt, "LamiaceaeBLAST.csv")
dff=df.filt[,2]
write.csv(dff, "LamiaceaeENTREZ.csv")
'''
```

### **Tutorial 1. Tutorial to map transcripts from Trinity.fasta transcriptome assembly to closely related species**

Please download at the link: <https://drive.google.com/file/d/1j-dLWddt4JqkAZzM8P70Cl2yn4CxUfzC/view?usp=sharing>

### **Tutorial 2. Tutorial with teaching slides for group and individual activities related to RNAseq and the Phenylpropanoid pathway**

Please download at the link:

<https://docs.google.com/presentation/d/1XYl4bYxQ8FGWuxAlbQKFTTUyY37AjHxh/edit?usp=sharing&ouid=115463549975505016476&rtpof=true&sd=true>