

Additional File 4: Annotation of KA/KS ratio in *Coffea* spp. contigs.

A): Annotation of Top 20 *C. arabica* contigs with highest and lowest KA/KS ratio

High KA/KS						
Sequence	KS	KA	KA/KS	Firts Hit (BlastX-NR)	E-value	Annotation
Contig9578	0.004	0.0094	2.0952	emb CAO71103.1 unnamed protein product [<i>Vitis vinifera</i>]	2.00E-62	Major intrinsic protein (MIP) superfamily
Contig4156	0.003	0.0064	2.0936	ref NP_568215.2 SNG2 (Sinapylglucose accumulator 2)[<i>Arabidopsis thaliana</i>]	1.00E-133	Serine carboxypeptidase-like
Contig1735	0.006	0.0127	2.0609	gb ABK94488.1 unknown [<i>Populus trichocarpa</i>]	5.00E-81	Glutathione peroxidase
Contig12903	0.006	0.0113	1.8721	emb CAA46808.1 Rieske FeS [<i>Nicotiana tabacum</i>]	1.00E-103	Cytochrome b6-f complex iron-sulfur
Contig15568	0.002	0.0037	1.8685	emb CAO45533.1 unnamed protein product [<i>Vitis vinifera</i>]	0.00E+00	Leucine-rich repeat transmembrane protein kinase
Contig6193	0.018	0.0341	1.8471	gb ABK91930.1 Mal d 1 isoallergen [<i>Malus x domestica</i>]	7.00E-45	Major allergen Mal d/ PR10-like proteins
Contig9214	0.006	0.0102	1.8168	emb CAO65210.1 unnamed protein product [<i>Vitis vinifera</i>]	5.00E-57	Jasmonate ZIM-domain protein 1
Contig5255	0.009	0.0158	1.7112	gb ABK91930.1 Mal d 1 isoallergen [<i>Malus x domestica</i>]	1.00E-44	Major allergen Mal d/PR10-like proteins
Contig10695	0.022	0.0349	1.5664	gb AAX49391.1 OLE-3 [<i>Coffea canephora</i>]	4.00E-61	Oleosin
Contig17112	0.003	0.0052	1.5054	emb CAO40012.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-152	Beta-glucosidase
Contig2205	0.004	0.0064	1.4983	gb AAP42136.1 erg-1 [<i>Solanum tuberosum</i>]	1.00E-121	Phosphate-responsive protein (phi-1)
Contig1918	0.008	0.012	1.4876	emb CAO45507.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-69	Protein phosphatase 2C-like protein
Contig82	0.008	0.0116	1.4828	emb CAO17977.1 unnamed protein product [<i>Vitis vinifera</i>]	8.00E-71	Vegetative storage protein
Contig7582	0.013	0.0189	1.4709	emb CAO40168.1 unnamed protein product [<i>Vitis vinifera</i>]	8.00E-52	PII protein
Contig2035	0.004	0.0059	1.4164	gb AAP40022.1 callus-expressing factor [<i>Nicotiana tabacum</i>]	1.00E-97	Ethylene-responsive element binding protein ERF2
Contig2469	0.007	0.0092	1.3556	dbj BAB09523.1 unnamed protein product [<i>Arabidopsis thaliana</i>]	5.00E-58	Cytochrome b5 domain-containing protein
Contig2994	0.008	0.0102	1.3395	gb ABK92934.1 unknown [<i>Populus trichocarpa</i>]	4.00E-82	Coated vesicle membrane protein
Contig2672	0.006	0.0076	1.3247	gb ABK92454.1 unknown [<i>Populus trichocarpa</i>]	3.00E-98	5'-Methylthioadenosine Nucleosidase
Contig8174	0.004	0.0055	1.3046	dbj BAA03526.1 F1-ATPase gamma subunit [<i>Ipomoea batatas</i>]	1.00E-137	F1-ATPase gamma subunit
Contig16950	0.02	0.0263	1.2831	gb ABG73415.1 chloroplast pigment-binding protein CP29 [<i>Nicotiana tabacum</i>]	1.00E-92	Chlorophyll A-B binding protein CP29
Low KA/KS						
Sequence	KS	KA	KA/KS	Firts Hit (BlastX-NR)	E-value	Annotation
Contig6524	0.057	0.0017	0.0298	dbj BAD10939.1 14-3-3 protein [<i>Nicotiana tabacum</i>]	9.00E-133	14-4-3 protein
Contig2240	0.027	0.001	0.0354	gb EAZ34301.1 hypothetical protein OsJ_017784 [<i>Oryza sativa</i> (japonica cultivar-group)]	0.00E+00	Tubulin beta-2 chain
Contig15974	0.028	0.001	0.036	emb CAO23450.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-172	Male sterility protein 2/ acyl CoA reductase
Contig5581	0.025	0.0009	0.0363	emb CAO15686.1 unnamed protein product [<i>Vitis vinifera</i>]	0.00E+00	Rubisco activase
Contig15938	0.028	0.0011	0.038	emb CAA81527.1 S-adenosyl-L-homocysteine hydrolase [<i>Catharanthus roseus</i>]	0	S-adenosyl-L-homocysteine hydrolase
Contig4350	0.038	0.0015	0.0406	emb CAO44494.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-134	Light-harvesting complex II protein 5
Contig13838	0.021	0.0009	0.0411	emb CAO66235.1 unnamed protein product [<i>Vitis vinifera</i>]	0.00E+00	Catalase
Contig5884	0.047	0.002	0.0415	gb AAD56018.1 60S ribosomal protein L10 [<i>Vitis riparia</i>]	1.00E-123	60S ribosomal protein L10
Contig2627	0.065	0.0027	0.0416	gb AAS48586.1 eukaryotic initiation factor 5A2 [<i>Capsicum annuum</i>]	2.00E-72	Eukaryotic translation initiation factor 5
Contig11187	0.016	0.0006	0.0417	emb CAA42660.1 luminal binding protein (BiP) [<i>Nicotiana tabacum</i>]	0	Luminal-binding protein
Contig3104	0.033	0.0014	0.0433	gb EAO4358.1 hypothetical protein Osl_025590 [<i>Oryza sativa</i> (indica cultivar-group)]	1.00E-107	Putative secretory carrier-associated membrane protein 1
Contig6370	0.039	0.0017	0.0441	emb CAN79984.1 hypothetical protein [<i>Vitis vinifera</i>]	1.00E-124	LHCA4 (Photosystem I light harvesting complex gene 4)

Contig12505	0.023	0.001	0.045	gb ABV80356.1 phosphoenolpyruvate carboxylase [<i>Gossypium hirsutum</i>]	0	Phosphoenolpyruvate carboxylase
Contig6753	0.057	0.0025	0.0451	emb CAO66090.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-64	Iron-sulfur cluster assembly complex protein
Contig1269	0.018	0.0008	0.0456	gb ABP98813.1 chloroplast biotin carboxylase [<i>Gossypium hirsutum</i>]	0.00E+00	Biotin carboxylase
Contig8981	0.023	0.001	0.0458	emb CAO22101.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-173	60S ribosomal protein L4/L1
Contig4659	0.024	0.0011	0.0465	emb CAN80621.1 hypothetical protein [<i>Vitis vinifera</i>]	1.00E-139	Beta-1.3-glucanase
Contig9099	0.031	0.0015	0.0475	ref NP_177596.1 NRP1 (NAP1-RELATED PROTEIN 1) [<i>Arabidopsis thaliana</i>]	1.00E-90	NRP1 (Nap1-related protein 1)
Contig4086	0.014	0.0007	0.0476	emb CAO61278.1 unnamed protein product [<i>Vitis vinifera</i>]	0	Leucine Rich Repeat family protein
Contig3271	0.041	0.002	0.0484	emb CAO71073.1 unnamed protein product [<i>Vitis vinifera</i>]	1.00E-81	Glutamate binding protein

ID: Contig number; KS: rate of synonymous substitutions, KA: rate of non-synonymous substitutions; KA/KS: KA to KS ratio; First Hit (BLASTX-NR): Most similar sequence in GenBank; E-value: E-value of most similar sequence; Annotation: automatic annotation based in AutoFACT results.

B) Annotation of Top 20 *C. canephora* contigs with highest and lowest KA/KS ratio

High KA/KS						
Sequence	KS	KA	KA/KS	Firts Hit (BlastX-NR)	E-value	Annotation
Contig2864	0.0069	0.00905	1.30796	gb AAT40548.1 Putative vicilin, identical [Solanum demissum]	1.00E-151	Vicilin/ globulin
Contig386	0.0047	0.0061	1.2914	gb AAL35365.1 ascorbate peroxidase [Capsicum annuum]	1.00E-134	Ascorbate peroxidase
Contig3937	0.0061	0.00749	1.23655	gb ABK93197.1 unknown [Populus trichocarpa]	3.00E-54	Membrane steroid-binding protein
Contig2694	0.0163	0.01959	1.20048	gb AAF31403.1 putative glycine-rich RNA binding protein 3 [Catharanthus roseus]	3.00E-38	Glycine-rich RNA binding protein-like
Contig1112	0.0038	0.00446	1.18711	gb ABK95575.1 unknown [Populus trichocarpa]	1.00E-170	Aminopeptidase N
Contig3653	0.0039	0.00446	1.13298	gb AAQ94896.1 putative N-methyltransferase [Coffea canephora]	0.00E+00	Dimethylxanthine Methyltransferase
Contig6678	0.0032	0.00362	1.13002	gb AAL37719.1 AF413204_1 beta-mannosidase [Solanum lycopersicum]	0	Beta-mannosidase enzyme
Contig175	0.0029	0.00311	1.07339	emb CAO24398.1 unnamed protein product [Vitis vinifera]	1.00E-123	Fasciclin-like arabinogalactan protein
Contig5988	0.0099	0.01001	1.00908	—		No Hits Found
Contig2645	0.003	0.00292	0.97927	dbj BAA22813.1 CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]	1.00E-166	Nucleoid DNA-binding protein cnd41-like protein
Contig3544	0.0033	0.00308	0.94748	emb CAN68737.1 hypothetical protein [Vitis vinifera]	1.00E-107	7S globulin 2 precursor small subunit
Contig4994	0.007	0.00628	0.89978	emb CAO65935.1 unnamed protein product [Vitis vinifera]	1.00E-94	Beta-adaptin
Contig1021	0.0089	0.00779	0.87871	gb ABB13620.1 USP-like protein [Astragalus sinicus]	3.00E-58	Universal stress protein family protein
Contig1581	0.0184	0.01616	0.87812	emb CAN65185.1 hypothetical protein [Vitis vinifera]	3.00E-57	Small heat-shock protein
Contig409	0.01	0.00857	0.8546	emb CAO40936.1 unnamed protein product [Vitis vinifera]	7.00E-48	Bet v I allergen family protein/ PR10-like proteins
Contig1866	0.0102	0.00853	0.83941	emb CAO40936.1 unnamed protein product [Vitis vinifera]	2.00E-49	Bet v I allergen family protein/ PR10-like proteins
Contig8158	0.0034	0.00282	0.82975	gb ABK94910.1 unknown [Populus trichocarpa]	1.00E-111	E3 ubiquitin-protein ligase PRT1
Contig1010	0.0049	0.00405	0.8204	gb AAP03998.1 EIL2 [Nicotiana tabacum]	0.00E+00	Ethylene-insensitive3-like1
Contig3075	0.007	0.00475	0.67981	emb CAO15071.1 unnamed protein product [Vitis vinifera]	8.00E-38	Zinc finger (AN1-like) family protein
Contig3473	0.0082	0.0055	0.67422	gb AAM63420.1 unknown [Arabidopsis thaliana]	4.00E-43	MD-2-related lipid recognition domain-containing protein
Low KA/KS						
Sequence	KS	KA	KA/KS	Firts Hit (BlastX-NR)	E-value	Annotation
Contig5300	0.0428	0.00179	0.04179	gb ABK96261.1 unknown [Populus trichocarpa x Populus deltoides]	1.00E-125	Peroxisomal membrane protein-related
Contig3566	0.0238	0.00118	0.04963	emb CAO24361.1 unnamed protein product [Vitis vinifera]	0.00E+00	Methionine aminopeptidase
Contig8165	0.017	0.00086	0.05052	gb ABB87123.1 aspartic protease precursor-like [Solanum tuberosum]	9.00E-133	Aspartic proteinase
Contig4689	0.0509	0.00277	0.05441	gb ABQ11264.1 mago nashi-like protein 1 [Physalis pubescens]	2.00E-76	Mago Nashi like protein
Contig8253	0.035	0.00205	0.05867	emb CAO40052.1 unnamed protein product [Vitis vinifera]	6.00E-90	60S ribosomal protein L19
Contig6691	0.0181	0.00112	0.06173	dbj BAA05641.1 chalcone synthase [Camellia sinensis]	0.00E+00	Chalcone synthase
Contig7328	0.024	0.00165	0.06904	emb CAO61870.1 unnamed protein product [Vitis vinifera]	1.00E-62	Chloroplast photosystem II 22 kDa
Contig3171	0.0154	0.00114	0.07425	emb CAI47559.1 alpha galactosidase [Coffea arabica]	0.00E+00	Alpha galactosidase
Contig8251	0.0125	0.00095	0.07596	gb AAL99198.1 UTP:alpha-D-glucose-1-phosphate uridylyltransferase [Solanum tuberosum]	0.00E+00	UTP:alpha-D-glucose-1-phosphate uridylyltransferase
Contig3901	0.015	0.00115	0.07662	gb ABF61806.1 alcohol dehydrogenase [Dimocarpus longan]	0.00E+00	Alcohol dehydrogenase
Contig944	0.0187	0.00144	0.07722	emb CAO70082.1 unnamed protein product [Vitis vinifera]	8.00E-72	Nodulin MtN3 family protein
Contig8189	0.0477	0.00387	0.08126	dbj BAA34348.1 elongation factor-1 alpha [Nicotiana paniculata]	0.00E+00	Elongation factor-1 alpha
Contig3388	0.0215	0.0018	0.084	emb CAO70406.1 unnamed protein product [Vitis vinifera]	1.00E-37	Putative AP2/EREBP transcription factor

Contig4389	0.0238	0.00205	0.08607	gb AAO85557.1 photosystem I subunit XI [<i>Nicotiana attenuata</i>]	4.00E-84	Photosystem I subunit XI precursor
Contig1320	0.0157	0.00147	0.09373	emb CAO65178.1 unnamed protein product [<i>Vitis vinifera</i>]	2.00E-47	Zinc finger (C3HC4-type RING finger) family protein
Contig3416	0.024	0.00226	0.09405	gb AAM18501.1 N-methyltransferase [<i>Coffea arabica</i>]	0	3,7-dimethylxanthine N-methyltransferase
Contig6826	0.0122	0.00117	0.09613	dbj BAD34459.1 flavanone 3-hydroxylase [<i>Eustoma grandiflorum</i>]	0	Flavanone 3-hydroxylase
Contig2822	0.0087	0.00085	0.09744	gb AAC61844.1 tyrosine/dopa decarboxylase [<i>Papaver somniferum</i>]	0	Tyrosine decarboxylase
Contig1066	0.0089	0.00089	0.09935	emb CAN70603.1 hypothetical protein [<i>Vitis vinifera</i>]	0	Vacuolar-processing enzyme precursor (VPE)
Contig4399	0.017	0.00176	0.10343	emb CAN79985.1 hypothetical protein [<i>Vitis vinifera</i>]	1.00E-113	Alpha-expansin precursor

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