

Supplementary Materials: Patterns of Spontaneous Nucleotide Substitutions in Grape Processed Pseudogenes

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Table S1 List of processed pseudogenes analyzed in this study. The Chr = scaffold molecule as in the gff file. The third and fourth columns reports the genomic coordinate of pseudogenes in the strand reported in column two.

Chr	Strand	Start	End	Pater_Locus	Ks	Ka	Ka/Ks
chr1	+	2327664	2327885	VIT_02s0025g01220.t01	0.086	0.024	0.279
chr1	-	7000737	7000385	VIT_04s0044g01670.t01	0.058	0.058	0.997
chr1	+	8290661	8290940	VIT_16s0039g00310.t01	0.215	0.088	0.411
chr1	+	9159921	9160172	VIT_07s0031g02750.t01	0.188	0.078	0.417
chr1	-	10322391	10322107	VIT_17s0000g05880.t01	0.073	0.034	0.462
chr1	+	10386156	10386805	VIT_09s0002g07880.t01	0.108	0.094	0.868
chr1	-	11696981	11696732	VIT_15s0046g02390.t01	0.103	0.034	0.330
chr1	+	16287427	16287651	VIT_09s0054g00930.t01	0.197	0.071	0.361
chr1	+	16288202	16288474	VIT_06s0004g01890.t01	1.921	0.457	0.238
chr1	+	16288487	16288771	VIT_02s0025g03430.t01	0.250	0.089	0.354
chr1	-	16330445	16329881	VIT_01s0026g00220.t01	0.353	0.148	0.420
chr1	-	19076741	19076487	VIT_18s0001g12840.t01	0.223	0.138	0.618
chr1	-	20813538	20813318	VIT_14s0128g00220.t01	0.069	0.040	0.584
chr1	-	22005427	22004952	VIT_11s0016g02830.t01	0.115	0.125	1.089
chr2	+	9393975	9394172	VIT_18s0001g11380.t01	0.100	0.070	0.696
chr2	-	9996801	9996301	VIT_02s0025g02400.t01	0.157	0.090	0.575
chr2	+	10259562	10259894	VIT_15s0046g02460.t01	0.053	0.033	0.619
chr2	-	12703945	12703578	VIT_14s0128g00750.t01	0.157	0.089	0.568
chr2	-	13091639	13091284	VIT_15s0021g02730.t01	0.246	0.059	0.240
chr2	+	13241432	13242044	VIT_14s0006g02490.t01	0.076	0.064	0.852
chr2	-	13551306	13550827	VIT_07s0031g03110.t01	0.265	0.110	0.416
chr2	-	14154406	14154115	VIT_12s0059g01430.t01	0.148	0.089	0.601
chr2	-	15413296	15412778	VIT_06s0004g02480.t01	0.113	0.079	0.704
chr2	-	15461674	15461239	VIT_07s0191g00090.t01	0.333	0.176	0.530
chr2	+	16133979	16134165	VIT_09s0054g00890.t01	0.223	0.082	0.367
chr2	-	16262802	16261664	VIT_14s0083g00200.t01	0.101	0.036	0.359
chr2	-	16443598	16443062	VIT_14s0171g00520.t01	0.126	0.062	0.490
chr2	-	16647976	16647688	VIT_17s0000g07680.t01	0.092	0.063	0.680
chr2	+	17533033	17533239	VIT_14s0108g01680.t01	0.562	0.224	0.399
chr3	+	795950	796168	VIT_07s0005g05610.t01	0.110	0.099	0.898
chr3	-	4438235	4438065	VIT_08s0056g00440.t01	0.106	0.041	0.384
chr3	+	4780007	4780260	VIT_14s0066g00920.t01	0.094	0.051	0.545
chr3	-	7774472	7773884	VIT_11s0016g02430.t01	0.108	0.082	0.763

chr3	-	7891323	7889076	VIT_19s0015g01380.t01	0.081	0.053	0.659
chr3	+	9755048	9755753	VIT_13s0067g00600.t01	0.088	0.038	0.434
chr3	-	15254133	15253715	VIT_18s0122g00140.t01	0.178	0.082	0.462
chr3	-	18274928	18274722	VIT_12s0028g03140.t01	0.127	0.063	0.492
chr3	+	18635932	18636465	VIT_07s0129g00250.t01	0.128	0.092	0.719
chr3	-	18900724	18900278	VIT_18s0117g00150.t01	0.180	0.042	0.231
chr4	+	17193	17423	VIT_04s0023g03620.t01	0.181	0.095	0.525
chr4	+	1894345	1894656	VIT_01s0010g03370.t01	0.136	0.084	0.618
chr4	-	7585623	7585366	VIT_11s0016g05020.t01	0.169	0.067	0.397
chr4	+	8177119	8177482	VIT_07s0151g00430.t01	0.197	0.106	0.539
chr4	-	8217298	8217041	VIT_03s0017g01760.t01	0.080	0.039	0.494
chr4	-	8400113	8399700	VIT_13s0106g00490.t01	0.077	0.046	0.588
chr4	+	8963333	8964656	VIT_06s0061g01180.t01	0.085	0.035	0.416
chr4	-	9473168	9472775	VIT_18s0001g09100.t01	0.219	0.122	0.558
chr4	-	15596174	15595845	VIT_17s0000g00280.t01	0.123	0.068	0.557
chr4	-	15678559	15678395	VIT_09s0002g00880.t01	0.176	0.058	0.331
chr4	+	16138021	16138395	VIT_14s0081g00490.t01	0.241	0.122	0.508
chr4	+	16919673	16919852	VIT_04s0008g03120.t01	0.215	0.110	0.510
chr4	-	17750766	17750583	VIT_17s0000g03760.t01	0.091	0.067	0.735
chr4	-	17909593	17909288	VIT_18s0001g07800.t01	0.197	0.095	0.480
chr5	+	2068481	2068705	VIT_08s0056g01710.t01	0.060	0.068	1.126
chr5	+	5787293	5787514	VIT_19s0085g00690.t01	0.117	0.065	0.555
chr5	-	7057315	7056828	VIT_14s0068g01890.t01	0.076	0.039	0.517
chr5	-	9734355	9734028	VIT_07s0031g00320.t01	0.069	0.038	0.545
chr5	-	10380383	10378921	VIT_09s0002g03490.t01	0.123	0.064	0.519
chr5	-	11007512	11007093	VIT_06s0080g00800.t01	0.183	0.086	0.471
chr5	+	13494965	13495168	VIT_18s0001g07220.t01	0.215	0.085	0.393
chr5	+	15356424	15356888	VIT_07s0031g02400.t01	0.084	0.040	0.469
chr5	-	17217482	17217163	VIT_08s0007g05370.t01	0.381	0.127	0.332
chr5	-	23991801	23991619	VIT_04s0008g00800.t01	0.297	0.099	0.332
chr5	+	24041027	24041338	VIT_09s0002g00610.t01	0.182	0.087	0.476
chr5	+	24042046	24042255	VIT_16s0022g02110.t01	0.234	0.113	0.485
chr6	+	6977317	6977520	VIT_07s0104g01240.t01	0.131	0.071	0.544
chr6	+	8005933	8006481	VIT_02s0025g03950.t01	0.080	0.056	0.698
chr6	+	8524048	8524272	VIT_10s0003g05840.t01	0.129	0.059	0.459
chr6	+	12127219	12127431	VIT_08s0040g00230.t01	0.191	0.099	0.519
chr6	-	12575700	12574868	VIT_11s0037g00230.t01	0.091	0.053	0.583
chr6	+	12793918	12794186	VIT_14s0083g00540.t01	0.237	0.123	0.519
chr6	+	13291786	13292154	VIT_02s0025g04100.t01	0.242	0.178	0.736
chr6	+	14584009	14584244	VIT_11s0016g00100.t01	0.185	0.087	0.469
chr6	+	14584565	14584723	VIT_16s0050g02670.t01	0.217	0.133	0.613
chr6	-	14918428	14918022	VIT_03s0038g03940.t01	0.409	0.190	0.464
chr6	-	15495004	15494807	VIT_19s0015g01940.t01	0.328	0.051	0.156

chr6	+	16425154	16425438	VIT_08s0056g00210.t01	0.256	0.144	0.561
chr6	+	16425664	16426035	VIT_08s0007g02160.t01	0.060	0.082	1.367
chr6	+	16529988	16530357	VIT_10s0003g01530.t01	0.092	0.060	0.644
chr6	-	16990580	16990139	VIT_03s0038g02760.t01	0.112	0.098	0.869
chr7	+	3173761	3174497	VIT_05s0020g04480.t01	0.108	0.051	0.473
chr7	-	5238575	5237912	VIT_16s0022g00750.t01	0.125	0.056	0.447
chr7	+	5667540	5667766	VIT_18s0089g00910.t01	0.121	0.065	0.540
chr7	-	5818987	5818735	VIT_16s0050g00160.t01	0.112	0.044	0.395
chr7	-	6306530	6306131	VIT_14s0068g01100.t01	0.378	0.154	0.408
chr7	-	11553769	11553542	VIT_09s0002g02500.t01	0.258	0.111	0.431
chr7	-	12726209	12725974	VIT_10s0116g00970.t01	0.108	0.009	0.080
chr7	+	13704778	13705191	VIT_17s0053g00780.t01	0.168	0.123	0.731
chr7	-	18625648	18625104	VIT_06s0004g00470.t01	0.736	0.159	0.216
chr7	+	19908351	19908757	VIT_06s0004g02140.t01	0.216	0.150	0.693
chr8	+	538476	538877	VIT_03s0038g00220.t01	0.141	0.061	0.433
chr8	-	585610	585243	VIT_08s0040g01640.t01	0.165	0.108	0.653
chr8	-	1594534	1594244	VIT_11s0016g00360.t01	0.486	0.222	0.458
chr8	+	2312555	2313159	VIT_14s0171g00350.t01	0.389	0.151	0.388
chr8	-	4699635	4699142	VIT_18s0001g00500.t01	0.175	0.141	0.804
chr8	-	5391404	5391195	VIT_19s0014g02750.t01	0.239	0.135	0.563
chr8	+	5576114	5576719	VIT_13s0064g00730.t01	0.037	0.061	1.661
chr8	-	7079786	7079577	VIT_02s0025g02440.t01	0.173	0.103	0.595
chr8	-	7101719	7101426	VIT_10s0003g01150.t01	0.106	0.049	0.462
chr8	+	7679411	7680519	VIT_07s0005g01280.t01	0.130	0.078	0.600
chr8	+	10893882	10894164	VIT_19s0085g01020.t01	0.083	0.023	0.274
chr8	+	11833874	11834158	VIT_14s0060g02200.t01	0.164	0.153	0.937
chr8	-	16747781	16747563	VIT_03s0180g00270.t01	0.148	0.046	0.312
chr8	-	19258507	19258262	VIT_00s0199g00110.t01	0.202	0.088	0.436
chr9	-	949555	948852	VIT_17s0000g07470.t01	0.358	0.185	0.518
chr9	-	949965	949737	VIT_12s0057g01220.t01	0.060	0.040	0.675
chr9	+	1728372	1728772	VIT_01s0011g03350.t01	0.207	0.084	0.409
chr9	-	6822176	6821881	VIT_03s0097g00550.t01	0.100	0.033	0.332
chr9	-	11547707	11547327	VIT_05s0062g01190.t01	0.077	0.025	0.323
chr9	+	12347624	12348129	VIT_03s0038g00700.t01	0.117	0.064	0.542
chr9	-	14430966	14430213	VIT_07s0005g03100.t01	0.103	0.081	0.792
chr9	-	14770403	14770217	VIT_19s0014g01390.t01	0.247	0.140	0.565
chr9	-	15089712	15089032	VIT_14s0171g00480.t01	0.235	0.074	0.314
chr9	-	19131784	19131302	VIT_07s0031g01350.t01	0.202	0.082	0.404
chr9	-	21290329	21289946	VIT_14s0060g01100.t01	0.095	0.062	0.652
chr10	-	3334304	3333994	VIT_04s0044g01700.t01	0.094	0.038	0.408
chr10	+	7059964	7060308	VIT_00s0337g00090.t01	0.208	0.099	0.477
chr10	+	8662033	8662223	VIT_08s0007g08180.t01	0.123	0.048	0.391
chr10	-	9615244	9614278	VIT_13s0019g02940.t01	0.893	0.239	0.268

chr10	-	10082102	10081892	VIT_17s0000g02860.t01	0.240	0.131	0.545
chr10	+	12255214	12256352	VIT_07s0104g00390.t01	0.072	0.065	0.908
chr10	+	12572411	12573150	VIT_07s0141g00830.t01	0.151	0.069	0.456
chr10	-	13032052	13031669	VIT_14s0066g02550.t01	0.094	0.074	0.783
chr10	-	13150171	13149762	VIT_09s0002g00790.t01	0.198	0.072	0.362
chr10	-	13769377	13769071	VIT_18s0122g00620.t01	0.084	0.039	0.457
chr10	+	14164681	14165488	VIT_03s0017g00830.t01	0.190	0.075	0.393
chr10	+	15062723	15063349	VIT_04s0008g06580.t01	0.109	0.057	0.523
chr10	+	16274206	16274565	VIT_14s0083g00940.t01	0.426	0.156	0.367
chr10	+	18011992	18012930	VIT_04s0023g03360.t01	0.285	0.146	0.513
chr10	+	18112962	18113747	VIT_09s0002g07880.t01	0.831	0.156	0.187
chr11	+	19099	19362	VIT_18s0001g03060.t01	0.183	0.107	0.584
chr11	-	5658226	5657984	VIT_02s0012g00900.t01	0.019	0.054	2.846
chr11	+	6699547	6700074	VIT_07s0005g04550.t01	0.079	0.052	0.658
chr11	-	7547788	7547422	VIT_08s0007g07850.t01	0.202	0.115	0.566
chr11	+	9403822	9404319	VIT_13s0019g00590.t01	0.284	0.096	0.337
chr11	+	11682130	11682723	VIT_08s0040g00910.t01	0.089	0.078	0.872
chr11	+	13565919	13566101	VIT_01s0011g02820.t01	0.164	0.174	1.061
chr11	+	14561049	14561306	VIT_16s0013g01530.t01	0.404	0.132	0.327
chr11	-	14626771	14626439	VIT_03s0038g04460.t01	0.201	0.084	0.417
chr12	+	2167301	2167623	VIT_11s0037g00070.t01	0.208	0.156	0.753
chr12	-	2250272	2250048	VIT_03s0038g00800.t01	0.249	0.070	0.283
chr12	-	2489186	2488571	VIT_01s0011g01590.t01	0.137	0.082	0.598
chr12	-	6501649	6501229	VIT_06s0009g00960.t01	0.121	0.057	0.473
chr12	-	7704446	7703709	VIT_18s0001g09990.t01	0.469	0.232	0.494
chr12	-	9044921	9044101	VIT_18s0001g10090.t01	0.176	0.129	0.733
chr12	-	9114872	9114609	VIT_01s0026g02170.t01	0.133	0.067	0.502
chr12	+	9452257	9452619	VIT_14s0030g00710.t01	0.073	0.074	1.003
chr12	+	9814719	9815220	VIT_18s0001g12300.t01	0.092	0.052	0.567
chr12	+	12319442	12319699	VIT_06s0004g01200.t01	0.108	0.035	0.327
chr12	-	12490210	12489745	VIT_16s0098g01160.t01	0.205	0.108	0.529
chr12	-	12539860	12539336	VIT_13s0073g00610.t01	0.106	0.057	0.540
chr12	+	15644704	15644925	VIT_19s0090g01250.t01	0.266	0.094	0.354
chr12	-	15725032	15724800	VIT_14s0006g00960.t01	0.194	0.092	0.471
chr12	+	15800563	15801027	VIT_09s0002g00840.t01	0.311	0.176	0.565
chr12	+	16951867	16952147	VIT_13s0074g00710.t01	0.160	0.101	0.630
chr12	-	19283643	19282964	VIT_07s0104g01320.t01	0.059	0.043	0.734
chr12	+	20511279	20511629	VIT_11s0206g00130.t01	0.167	0.109	0.650
chr12	-	21293158	21292486	VIT_07s0005g03830.t01	0.068	0.024	0.349
chr12	+	22373362	22373661	VIT_08s0007g04380.t01	0.269	0.077	0.287
chr13	+	892112	892372	VIT_12s0059g02310.t01	5.881	0.339	0.058
chr13	-	3763570	3763004	VIT_04s0008g03170.t01	0.076	0.018	0.236
chr13	-	4921986	4921260	VIT_01s0011g03220.t01	0.225	0.094	0.417

chr13	+	7730680	7730946	VIT_06s0004g03600.t01	0.089	0.084	0.937
chr13	+	7731550	7732401	VIT_11s0016g00420.t01	0.149	0.050	0.338
chr13	-	10051420	10051214	VIT_04s0079g00160.t01	0.196	0.066	0.339
chr13	-	10078897	10078259	VIT_19s0014g01010.t01	0.119	0.051	0.427
chr13	-	11500140	11499789	VIT_04s0008g03750.t01	0.285	0.066	0.230
chr13	-	13527104	13526793	VIT_13s0064g01510.t01	0.203	0.049	0.240
chr13	+	13718916	13719269	VIT_09s0002g03380.t01	0.113	0.066	0.586
chr13	-	16523492	16523207	VIT_09s0002g01610.t01	0.170	0.086	0.506
chr13	+	17966805	17968031	VIT_02s0012g01240.t01	0.094	0.069	0.734
chr13	-	19970472	19970215	VIT_17s0000g02570.t01	0.089	0.058	0.653
chr13	+	22571692	22572171	VIT_08s0058g00490.t01	0.219	0.137	0.622
chr14	+	739517	740098	VIT_07s0104g00540.t01	0.150	0.062	0.415
chr14	+	740128	740427	VIT_05s0020g00410.t01	0.145	0.072	0.498
chr14	+	3525711	3526016	VIT_04s0023g01280.t01	0.132	0.021	0.158
chr14	-	3776832	3776177	VIT_11s0016g03540.t01	0.100	0.033	0.327
chr14	-	5522017	5521827	VIT_04s0023g01650.t01	0.267	0.113	0.422
chr14	+	5526617	5527413	VIT_08s0007g01790.t01	0.115	0.075	0.655
chr14	+	5980244	5980915	VIT_06s0004g00950.t01	0.083	0.033	0.401
chr14	+	5983353	5983732	VIT_19s0090g01570.t01	0.087	0.052	0.597
chr14	+	7237811	7238443	VIT_16s0100g00670.t01	0.170	0.075	0.442
chr14	-	12099208	12098960	VIT_07s0005g00690.t01	0.465	0.131	0.281
chr14	+	13346501	13346782	VIT_05s0020g02210.t01	0.268	0.068	0.252
chr14	+	13823423	13823734	VIT_18s0122g00550.t01	0.271	0.121	0.445
chr14	-	14413670	14413324	VIT_07s0005g05160.t01	0.187	0.155	0.824
chr14	-	14579777	14579048	VIT_07s0005g05520.t01	0.130	0.089	0.685
chr14	+	14887132	14887496	VIT_05s0062g00130.t01	nan	0.293	nan
chr14	+	14945857	14946100	VIT_01s0026g02280.t01	0.143	0.136	0.954
chr14	-	15468211	15467938	VIT_01s0011g04360.t01	0.119	0.073	0.613
chr14	+	16031309	16032164	VIT_15s0045g00500.t01	0.048	0.036	0.746
chr14	+	16350117	16350482	VIT_07s0031g01470.t01	0.099	0.103	1.039
chr14	+	18958359	18958752	VIT_12s0134g00460.t01	0.391	0.141	0.362
chr14	-	19335572	19334974	VIT_18s0001g08100.t01	0.042	0.031	0.747
chr14	+	19564809	19565262	VIT_11s0016g01730.t01	0.147	0.079	0.534
chr14	-	25070072	25069557	VIT_15s0046g01510.t01	0.151	0.043	0.287
chr15	-	1901312	1900969	VIT_03s0038g02660.t01	0.168	0.032	0.193
chr15	-	2339421	2338750	VIT_08s0007g07150.t01	0.115	0.073	0.635
chr15	-	2579127	2578721	VIT_04s0008g04820.t01	0.364	0.152	0.418
chr15	-	2593125	2592633	VIT_03s0063g00610.t01	0.100	0.072	0.715
chr15	-	9049023	9048841	VIT_09s0054g01120.t01	0.186	0.076	0.408
chr15	-	9409029	9408781	VIT_12s0059g00190.t01	0.168	0.060	0.356
chr15	-	9498318	9498120	VIT_07s0104g00230.t01	0.118	0.020	0.168
chr15	-	10302390	10302121	VIT_09s0002g01530.t01	0.165	0.062	0.373
chr15	-	13342756	13342345	VIT_06s0061g01450.t01	0.184	0.090	0.489

chr15	-	13613030	13612745	VIT_18s0001g10170.t01	0.161	0.089	0.553
chr15	-	13614464	13614085	VIT_00s0283g00020.t01	0.187	0.196	1.053
chr16	+	2024050	2024286	VIT_00s0630g00010.t01	0.017	0.022	1.307
chr16	-	3436664	3436423	VIT_18s0001g06770.t01	0.438	0.187	0.427
chr16	+	3555204	3555431	VIT_06s0080g00830.t01	0.181	0.130	0.717
chr16	+	3556334	3556558	VIT_18s0001g07280.t01	0.293	0.087	0.296
chr16	-	4581029	4580148	VIT_18s0001g07710.t01	0.112	0.082	0.729
chr16	-	4600561	4600258	VIT_04s0008g01430.t01	0.170	0.102	0.599
chr16	+	4813025	4813310	VIT_07s0151g00970.t01	0.097	0.061	0.627
chr16	+	4844126	4844560	VIT_17s0000g10430.t01	0.284	0.104	0.368
chr16	+	7379082	7379532	VIT_16s0022g01860.t01	0.114	0.070	0.618
chr16	-	8531644	8531099	VIT_10s0003g00500.t01	0.229	0.143	0.623
chr16	-	8729927	8729549	VIT_09s0018g01600.t01	0.248	0.098	0.397
chr16	+	8946329	8946761	VIT_18s0001g02510.t01	0.067	0.051	0.766
chr16	+	9455911	9456266	VIT_06s0009g03240.t01	0.161	0.072	0.446
chr16	+	11667983	11668231	VIT_11s0016g04200.t01	0.254	0.122	0.479
chr16	+	11935612	11936463	VIT_13s0019g03990.t01	0.143	0.110	0.766
chr16	-	11958872	11958453	VIT_03s0038g03100.t01	0.091	0.049	0.533
chr16	+	15375585	15375833	VIT_10s0092g00040.t01	0.088	0.041	0.463
chr16	+	15489458	15489706	VIT_18s0001g13950.t01	0.080	0.031	0.391
chr17	+	6119829	6120146	VIT_18s0089g00900.t01	0.076	0.064	0.839
chr17	+	14851837	14852100	VIT_08s0007g07220.t01	0.155	0.057	0.369
chr17	+	16520669	16521370	VVIT_04s0043g00220.t01	0.054	0.033	0.614
chr17	+	16957818	16958102	VIT_09s0002g00130.t01	0.181	0.108	0.593
chr18	-	1824482	1823905	VIT_08s0058g00730.t01	0.017	0.029	1.702
chr18	-	3316054	3315523	VIT_02s0025g00640.t01	0.168	0.078	0.466
chr18	-	8221944	8220844	VIT_12s0028g02240.t01	0.143	0.053	0.367
chr18	-	11840526	11840234	VIT_11s0103g00550.t01	0.074	0.134	1.819
chr18	-	12773020	12772691	VIT_16s0100g00690.t01	0.306	0.173	0.565
chr18	+	13300722	13301659	VIT_04s0008g03110.t01	0.123	0.050	0.409
chr18	+	14275681	14276198	VIT_09s0002g01430.t01	0.183	0.097	0.531
chr18	+	18970374	18970625	VIT_14s0060g00970.t01	0.074	0.041	0.558
chr18	+	19249602	19250114	VIT_17s0000g08580.t01	0.186	0.106	0.569
chr18	-	20031108	20030734	VIT_12s0059g00200.t01	0.050	0.039	0.792
chr18	-	20702046	20701198	VIT_08s0007g00340.t01	0.037	0.030	0.833
chr18	+	22088371	22088925	VIT_05s0077g02140.t01	0.090	0.063	0.700
chr18	-	22332850	22332323	VIT_02s0154g00180.t01	0.092	0.067	0.724
chr18	+	22846414	22847323	VIT_03s0038g04500.t01	0.164	0.099	0.605
chr18	+	22932871	22933663	VIT_18s0001g10120.t01	0.176	0.095	0.542
chr18	-	23796070	23795686	VIT_19s0015g01830.t01	0.138	0.114	0.825
chr18	+	25751718	25752440	VIT_08s0007g07130.t01	0.108	0.067	0.625
chr18	-	27334486	27333982	VIT_08s0007g07200.t01	0.069	0.051	0.736
chr18	+	28018869	28019548	VIT_15s0045g01090.t01	0.132	0.048	0.366

chr18	-	28332343	28331961	VIT_19s0014g03960.t01	0.280	0.119	0.425
chr19	+	4028675	4029013	VIT_04s0023g01610.t01	0.105	0.074	0.707
chr19	+	9899872	9900317	VIT_14s0066g01430.t01	0.333	0.115	0.346
chr19	+	13249553	13250143	VIT_01s0026g02340.t01	0.087	0.045	0.514
chr19	+	15825052	15825349	VIT_12s0028g01550.t01	0.119	0.048	0.400
chr19	+	16715576	16715755	VIT_05s0049g01160.t01	0.073	0.077	1.049
chr19	+	18456141	18456419	VIT_02s0087g00050.t01	0.241	0.206	0.852
chr19	+	19776588	19777070	VIT_16s0039g01890.t01	0.124	0.060	0.487
chr19	+	20151928	20152361	VIT_01s0026g00920.t01	0.177	0.071	0.402
chr19	+	21999736	21999947	VIT_02s0025g02760.t01	0.208	0.155	0.746
chr19	+	22061066	22062073	VIT_19s0014g03080.t01	0.174	0.116	0.666

Table S2. Summary of nucleotide substitutions in grape processed pseudogenes. Non synonymous dataset

	Total	Unchanged		Deleted		Substituted		Transitions		Transversions		Rati o
A	26783	24925	93.06%	430	1.60%	1428	5.33%	864	60.50%	564	39.50%	1.53
G (all)	23517	20400	86.75%	402	1.71%	2715	11.54%	2095	77.16%	620	22.84%	3.38
CpG	1087	827	76.08%	18	1.65%	242	22.22%	198	81.82%	44	18.18%	4.50
non- CpG	22430	19573	87.20%%	384	1.71%	2473	10.07%	1897	76.68%	527	21.31%	3.29
C(all)	19110	16406	85.85%	298	1.55%	2406	12.59%	1870	77.72%	536	28.66%	3.49
Cpg	1087	862	79.30%	18	1.00%	223	20.51%	166	74.43%	41	24.70%	4.05
non CpG	18023	15544	86.58%	268	1.49%	2183	12.11%	1584	72.50%	455	20.84%	3.48
T	21876	20456	93.51%	312	1.42%	1108	5.06%	673	60.74%	435	39.26%	1.55