

Supplementary Tables

Supplementary Table 1. Sequence-based cumulative prediction for the potentially deleterious effects of the retrieved missense single nucleotide polymorphisms. Green and red colors refer to the neutral to deleterious SNPs respectively. The bold letters refer to the entirely deleterious consequences for these SNPs.

SNP	AA variant	SIFT	PolyPhen	REVEL	PROVEAN	PANTHER	SNAP2	PhD SNP	Mutation assessor	SUSPect	UMD-Predictor
rs894487373	L2Q	0.33	0.011	0.074	0.234	361	-56	7	0.404	77	100
rs1169388532	S3C	0.11	0.754	0.14	-1.069	324	-7	9	0.681	72	78
rs763961867	R5H	0.13	0.765	0.29	-1.715	455	70	7	0.519	81	87
rs1449103221	R5S	0.02	0.388	0.301	-1.760	455	69	7	0.725	83	100
rs1199313550	C8Y	0	0.994	0.43	-4.461	456	76	5	0.795	95	99
rs543191354	A9S	0.25	0.587	0.085	-0.870	455	18	3	0.725	89	66
rs1339670088	L10R	0	0.997	0.456	-2.848	456	77	5	0.765	92	99
rs35603672	A11V	0.33	0.007	0.017	-0.793	361	20	8	0.355	76	81
rs1250282492	L13P	0	0.997	0.604	-4.505	456	76	7	0.789	92	84
rs770602806	L13V	0.08	0.987	0.255	-1.553	456	4	2	0.789	91	54
rs778157951	S14P	0.23	0.638	0.199	-2.507	456	55	4	0.735	89	75
rs1165279234	I15M	0.03	0.152	0.078	-0.379	324	-4	5	0.35	91	60
rs1388517325	I15T	0.01	0.05	0.132	-2.035	324	35	4	0.35	92	22
rs1429304478	I15F	0.02	0.055	0.094	-1.686	324	-4	1	0.35	93	81
rs1444152903	V16A	1	0	0.119	0.162	176	-18	9	0.144	94	63
rs1473327564	V16F	0.09	0.105	0.157	-1.325	176	20	0	0.005	92	69
rs770130563	A18T	0.03	0.115	0.062	-1.104	455	32	6	0.627	93	75
rs146833076	C21Y	0.08	0	0.083	-1.479	6	49	2	0.112	95	42
rs1296332370	V22A	0.48	0.04	0.164	0.066	456	45	5	0.364	90	51
rs1203767986	V22L	0.6	0.001	0.035	-1.118	456	49	4	0.404	90	42
rs1291568665	T23A	0.14	0	0.046	-0.318	176	27	6	0.065	84	63
rs916710988	G24C	0.01	0.371	0.113	-0.464	176	49	2	0.112	72	81
rs1380116959	A25V	0.13	0.283	0.207	-1.436	456	9	2	0.769	79	63
rs867771684	A25S	0.08	0.423	0.141	-1.148	456	14	0	0.769	82	66
rs1230103434	P26L	0.13	0.476	0.248	-3.691	456	42	5	0.51	87	72
rs187722336	S27L	0.06	0.063	0.109	-1.288	324	25	3	0.444	73	90
rs187722336	S27W	0	0.828	0.239	-3.064	324	68	1	0.643	75	90
rs143908336	S27P	0.01	0.221	0.087	-1.516	324	68	2	0.643	69	87
rs750665235	R30G	0.01	0.001	0.219	-3.246	455	53	2	0.735	91	99
rs965410829	L31P	0.18	0.879	0.326	-1.630	455	70	2	0.735	94	84
rs764051709	R32H	0.04	0.994	0.261	-3.159	455	67	2	0.789	58	78
rs1325698850	R32G	0.01	0.993	0.349	-1.439	455	27	4	0.673	89	100
rs1390404178	Q33H	0.04	0.908	0.141	-0.459	456	76	7	0.714	85	78
rs1161858021	F34V	0.05	0.058	0.136	-1.191	455	41	5	0.561	88	69
rs1227313890	S38T	0.05	0.003	0.133	-0.787	456	15	9	0.359	85	75
rs1413312311	A43V	0.43	0.452	0.097	-0.727	456	-6	7	0.46	84	72
rs1413312311	A43E	0.94	0.59	0.096	-0.373	456	5	4	0.666	79	100
rs752479698	A43S	0.77	0.048	0.046	-0.653	456	-29	7	0.666	58	87
rs752479698	A43T	0.58	0.234	0.077	-3.182	456	1	7	0.666	61	96
rs867113930	Q46H	0.01	0.854	0.226	-3.869	456	61	4	0.795	73	100
rs1366311497	E47G	0	0.326	0.262	-2.820	456	66	1	0.725	76	100
rs1437560183	E47K	0.01	0.257	0.142	-2.820	456	66	1	0.725	69	84
rs1429193569	L48P	0.18	0.927	0.283	-3.101	456	64	4	0.666	89	93
rs764814996	A49V	0.36	0.079	0.104	-0.599	456	9	7	0.202	87	100
rs772647920	A49S	0.76	0.079	0.146	0.000	456	3	9	0.561	71	87
rs1341576465	Y51H	0.14	0.694	0.092	-0.652	456	66	5	0.687	78	87
rs1386131364	F52L	0.63	0.015	0.132	0.197	455	34	7	0.469	77	63
rs761483991	A54G	0.1	0.24	0.18	-2.200	456	45	6	0.702	81	75
rs1170033526	E55Q	0.16	0.709	0.106	-1.322	455	74	5	0.763	76	75
rs1158174810	E59K	0.24	0.257	0.158	-1.122	324	60	4	0.666	69	78
rs33934967	N61S	0.91	0	0.144	0.557	176	-26	10	0.002	74	47
rs33934967	N61T	0.51	0	0.153	0.295	176	-32	9	0.033	67	69
rs149673471	T63M	0.03	0.215	0.141	-1.214	455	20	9	0.098	75	93
rs747541189	T63A	0.74	0	0.137	-0.329	455	-16	9	0.439	63	78
rs745967614	A67V	0.51	0.02	0.177	-0.762	456	-12	9	0.458	83	78
rs757462006	E69Q	0.17	0.328	0.219	-0.852	456	16	9	0.643	72	72

rs757462006	E69K	0.04	0.156	0.17	-1.185	456	47	8	0.643	76	78
rs749502183	P70H	0.21	0.174	0.083	-0.972	176	-13	10	0.339	75	84
rs1432148122	P70T	0.65	0.011	0.073	-0.259	176	-15	10	0.339	69	81
rs915781109	D72Y	0.01	0.754	0.191	-3.990	456	67	7	0.64	74	99
rs754797232	L73M	0.39	0.092	0.095	-0.475	456	22	10	0.404	85	60
rs376379180	S74F	0	0.451	0.165	-3.290	176	58	8	0.307	69	81
rs200885816	S74P	0.09	0.003	0.035	-1.085	176	16	7	0.683	57	75
rs758278952	A76P	0.18	0.136	0.079	-0.771	176	56	6	0.364	66	60
rs35517186	E78K	0.08	0.257	0.138	-1.955	456	69	7	0.69	76	66
rs776344515	D80H	0.01	0.444	0.191	-2.593	455	57	8	0.572	70	84
rs201328656	M82I	0.15	0	0.148	0.027	324	29	9	0.281	82	60
rs150548817	Q87H	0	0.06	0.095	-1.655	324	34	8	0.281	79	67
rs1432256919	Q87R	0	0.007	0.151	-0.723	324	44	7	0.281	61	69
rs775949412	R88G	0	0.987	0.395	-4.821	456	76	4	0.795	84	100
rs1471784893	N91D	0.58	0.099	0.152	-0.550	455	57	8	0.575	69	60
rs772737037	S92P	0.37	0.278	0.129	-0.607	455	10	6	0.542	51	75
rs1396406322	N93K	0.18	0	0.139	-1.027	361	36	7	0.281	81	87
rs746348246	P94L	0.01	0.997	0.326	-2.952	456	55	6	0.735	80	87
rs771028983	A95V	0.32	0.003	0.112	-0.778	361	-4	9	0.288	64	81
rs1361731371	M96I	0.19	0.003	0.159	-0.293	324	51	8	0.263	71	66
rs375199307	M96V	0.11	0.005	0.072	-0.833	324	51	8	0.212	77	60
rs749537579	R99P	0.15	0.999	0.705	-6.618	456	72	4	0.709	85	99
rs749537579	R99Q	0.02	0.997	0.602	-3.894	456	68	3	0.709	77	78
rs778060901	G104S	0.01	0.999	0.579	-4.032	456	69	4	0.694	91	84
rs769850019	K106R	0.09	0.994	0.366	-2.756	456	67	1	0.709	95	72
rs746825485	N107S	0.01	0.301	0.276	-4.951	456	61	2	0.668	89	84
rs1290802184	T114I	0	0.998	0.677	-5.592	456	70	2	0.709	92	87
rs961702090	S115T	0.01	0.992	0.608	-2.856	456	72	6	0.694	86	72



neutral

moderate

deleterious

Supplementary Table 2. Cumulative structure-based predictions for the possible deleterious consequences of the retrieved missense single nucleotide polymorphisms of SST protein. The green and red colors refer to the non-deleterious and deleterious consequences, respectively. The bold letters refer to the entirely deleterious effect of a particular SNP. All prediction values were calculated using DDG values, which presented to indicate free energy change upon mutation.

No.	Variant ID	mutation	I-Mutant2	MAESTRO	STRUM	Mupro	iStable	CUPSAT	DynaMut	mCSM	SDM	DUET
1.	rs894487373	L2Q	-1.51	1.165	-0.63	-1	-1.02	-3.27	0.064	-0.904	-0.71	-0.829
2.	rs1169388532	S3C	-0.98	0.573	0.02	-0.26	-0.59	-0.43	0.831	-0.428	0.82	-0.004
3.	rs763961867	R5H	-1.17	0.211	-0.03	-1	-1.07	0.62	-0.324	-0.779	0.17	-0.93
4.	rs1449103221	R5S	-0.85	0.969	-0.52	-1	-0.86	0.33	-0.063	-0.779	-0.82	-0.93
5.	rs1199313550	C8Y	-0.26	-0.283	-0.89	0.36	0.16	2.98	0.271	-0.373	0.06	-0.152
6.	rs543191354	A9S	-0.58	-0.272	-0.64	Unknown	-0.19	0.87	-0.108	-0.5	-0.39	-0.302
7.	rs1339670088	L10R	-1.12	-0.764	-0.68	-2.42	-1.24	-0.38	-0.076	0.248	-0.46	0.341
8.	rs35603672	A11V	-0.09	0.150	-0.19	0.89	0.11	-0.04	-0.17	-0.254	-0.84	-0.098
9.	rs1250282492	L13P	-1.81	1.913	-1.81	-1	-2.27	-1.44	-1.588	-1.494	-2.23	-1.853
10.	rs770602806	L13V	-1.32	1.037	-0.69	-0.75	-1.27	-0.96	-0.122	-1.494	-0.67	-1.345
11.	rs778157951	S14P	-0.37	1.257	-0.73	-0.79	-0.39	-1	0.411	-0.144	-1.62	-0.025
12.	rs1165279234	I15M	-1.16	-0.159	-0.36	-1.05	-0.88	-0.38	-0.225	-0.458	-0.11	-0.258
13.	rs1388517325	I15T	-1.98	1.435	-1.52	-0.75	-1.27	-1.97	-0.356	-1.233	-1.5	-1.256
14.	rs1429304478	I15F	-0.98	0.235	-0.59	-1.20	-0.76	-1.98	-0.046	-0.85	-0.3	-0.827
15.	rs1444152903	V16A	-1.51	1.191	-0.88	-0.81	-1.26	-1.81	-0.91	-1.484	-1.16	-1.621
16.	rs1473327564	V16F	-1.23	0.590	-0.44	-1	-1.01	-1	0.978	-1.098	-0.46	-1.226
17.	rs770130563	A18T	-0.87	0.601	-0.92	-1	-0.82	0.69	-0.188	-1.343	-0.38	-1.12
18.	rs146833076	C21Y	-0.34	1.245	-1.46	-0.08	-0.49	-2.37	1.562	-0.949	-1.22	-1.143
19.	rs1296332370	V22A	-0.79	1.166	-0.72	-0.55	-0.70	-1.04	-0.549	-0.684	-0.26	-0.584
20.	rs1203767986	V22L	-0.59	0.809	-0.29	0.24	-0.56	-0.52	-0.442	-0.437	0.06	-0.227
21.	rs1291568665	T23A	-0.21	-0.184	0.03	-0.75	-0.003	-2.94	0.449	-0.195	0.98	0.247
22.	rs916710988	G24C	-1.42	0.898	-0.77	-0.24	-0.70	1.06	-0.253	-0.894	0.36	-0.685
23.	rs1380116959	A25V	0.07	0.119	-0.53	-0.36	-0.18	-0.38	0.753	-0.625	0.7	-0.163
24.	rs867771684	A25S	-0.55	0.976	-0.64	-1	-0.25	-0.23	-0.077	-0.983	-0.58	-0.967
25.	rs1230103434	P26L	-0.24	-1.422	-0.37	0.26	-0.46	-1.54	1.682	-0.614	2.37	0.26
26.	rs187722336	S27L	-0.01	-0.452	-1.25	0.07	-0.29	-2.95	1.456	0.457	0.81	0.928
27.	rs187722336	S27W	-0.28	-0.138	-1.12	0.04	0.49	-1.25	1.851	-0.85	0.06	-0.814
28.	rs143908336	S27P	-0.75	1.331	-1.2	0.13	-0.86	-0.8	1.312	0.167	-0.77	0.129
29.	rs750665235	R30G	-1.41	1.646	-1.6	-1	-1.69	-2	-1.652	-1.979	-1.39	-2.157
30.	rs965410829	L31P	-1.95	4.130	-2.33	-1	-2.52	-6.82	-2.112	-1.916	-4.41	-2.61
31.	rs764051709	R32H	-1.34	0.746	-0.22	-0.35	-1.10	-0.87	0.343	-1.435	0.26	-1.198
32.	rs1325698850	R32G	-1.40	1.220	-1.04	-0.66	-1.27	-2.01	-1.34	-1.194	-1.03	-1.278
33.	rs1390404178	Q33H	-1.01	0.649	0.01	-0.31	-0.47	0.34	0.27	-1.029	0.06	-0.832
34.	rs1161858021	F34V	-0.83	2.185	-1.49	-1	-0.92	-0.51	-1.82	-2.242	-2.51	-2.541
35.	rs1227313890	S38T	-0.07	0.151	-0.65	1	-0.002	0.55	0.819	-0.505	0.2	-0.217
36.	rs1413312311	A43V	0.27	0.393	-0.49	0.38	-0.32	-0.75	0.074	-0.316	-0.99	-0.357
37.	rs1413312311	A43E	-0.54	1.255	-0.45	-0.07	-0.33	-0.62	0.163	-0.567	-1.89	-0.726
38.	rs752479698	A43S	-0.87	0.936	-0.82	-0.79	-0.57	0.23	0.482	-0.39	-1.93	-0.533
39.	rs752479698	A43T	-0.76	0.803	-0.75	-0.76	-0.47	-0.69	-0.126	-0.473	-2.03	-0.639

40.	rs867113930	Q46H	-0.35	0.487	-0.23	0.28	0.26	-0.64	-0.135	-0.062	-0.24	0.0
41.	rs1366311497	E47G	-0.90	2.169	-1.51	-1	-1.25	-1.38	-0.014	-1.133	-0.37	-1.158
42.	rs1437560183	E47K	-0.84	1.063	-1.05	-1	-0.84	1.39	-0.336	-0.45	-0.54	-0.308
43.	rs1429193569	L48P	-1.83	3.968	-2.21	-1	-2.04	2.21	-1.057	-0.897	-2.87	-1.255
44.	rs764814996	A49V	0.14	-0.342	-0.51	-0.43	-0.19	0.76	0.587	0.026	-0.61	0.302
45.	rs772647920	A49S	-0.79	1.601	-0.89	-1	-0.98	-0.48	0.395	-1.52	-2.37	-1.649
46.	rs1341576465	Y51H	-0.87	1.490	-0.59	-0.27	-1.27	-0.78	-0.247	-0.742	-0.3	-0.432
47.	rs1386131364	F52L	-0.53	0.627	-0.71	0.003	-0.24	-2.62	-0.136	-0.767	-1.53	-0.83
48.	rs761483991	A54G	-0.98	1.629	-1.11	0.89	-1.21	-1.79	-0.609	-0.718	-1.58	-0.743
49.	rs1170033526	E55Q	-0.81	-0.325	-0.71	-0.204	-0.66	-0.68	-0.237	-1.142	-0.69	-0.989
50.	rs1158174810	E59K	-1.04	-0.582	-0.22	-0.34	-0.73	0.08	-0.041	0.028	-0.59	0.26
51.	rs33934967	N61S	-0.23	0.721	-0.59	-0.27	-0.54	0.41	-0.232	-0.26	-0.51	-0.051
52.	rs33934967	N61T	-0.12	1.021	-0.36	-0.72	-0.27	0.22	0.152	-0.15	0.29	0.259
53.	rs149673471	T63M	-0.10	-0.35	-0.25	-0.76	0.26	-3.89	0.144	-0.119	0.01	-0.117
54.	rs747541189	T63A	-0.08	-0.12	-0.17	-1	-0.24	0.49	0.034	-0.16	0.32	0.079
55.	rs745967614	A67V	0.15	-0.21	-0.03	-0.29	-0.13	-0.63	0.754	-0.634	0.44	-0.226
56.	rs757462006	E69Q	-0.42	-0.26	-0.03	-0.408	-0.11	-0.41	-0.64	-0.407	-0.93	-0.386
57.	rs757462006	E69K	-0.96	0.105	-0.6	-0.32	-0.55	0.13	-0.207	-0.01	-0.58	0.149
58.	rs749502183	P70H	-0.90	-0.26	-0.09	-1	-0.56	-0.71	0.592	-0.388	1.12	0.078
59.	rs1432148122	P70T	-0.90	1.346	0.1	-1	-0.61	-1.21	-0.149	-0.648	0.35	-0.162
60.	rs915781109	D72Y	0.12	1.055	-0.24	-0.35	0.46	-1.31	0.496	-0.237	0.26	-0.059
61.	rs754797232	L73M	-0.94	-0.78	-0.79	-0.51	-0.83	-0.75	-0.354	-0.721	-0.96	-0.749
62.	rs376379180	S74F	0.35	0.487	-0.3	-0.03	0.61	0.01	1.815	-0.855	0.8	-0.482
63.	rs200885816	S74P	0.11	2.172	-0.52	-0.38	-0.11	0.06	0.161	-0.167	-0.96	-0.119
64.	rs758278952	A76P	-0.51	0.048	-0.92	0.63	-0.72	-0.85	-0.771	-0.538	-3.0	-0.898
65.	rs35517186	E78K	-0.38	0.417	-0.77	-0.003	-0.03	-0.24	-0.55	-0.029	-0.98	0.177
66.	rs776344515	D80H	-0.38	-0.18	-1.08	-0.003	-0.03	-2.83	1.571	-0.917	1.06	-0.435
67.	rs201328656	M82I	-0.66	1.047	-0.17	-0.26	0.147	0.82	-0.307	-0.521	0.08	0.029
68.	rs150548817	Q87H	-1.12	1.563	-1.2	-0.42	-0.85	0.83	-0.723	-2.168	0.25	-1.868
69.	rs1432256919	Q87R	-0.66	0.953	-1.23	-0.308	-0.56	-1.19	-1.069	-1.517	-1.76	-1.561
70.	rs775949412	R88G	-0.89	0.427	-0.8	-1	-0.55	0.06	-0.579	-0.816	-0.17	-0.795
71.	rs1471784893	N91D	-0.07	0.400	-0.19	-0.189	-0.07	-0.41	-0.046	-1.447	0.07	-1.065
72.	rs772737037	S92P	0.08	0.431	-0.06	0.69	-0.23	-0.02	-0.196	-0.227	-0.39	-0.096
73.	rs1396406322	N93K	-1.08	-0.36	-0.7	-0.844	-0.86	-0.69	0.897	-0.324	-0.35	-0.188
74.	rs746348246	P94L	-0.08	-0.09	-0.35	0.61	0.09	2.39	0.21	-0.508	0.84	-0.105
75.	rs771028983	A95V	-0.31	1.514	-0.64	-0.26	-0.30	0.47	-0.084	-0.636	-0.21	-0.454
76.	rs1361731371	M96I	-0.79	1.672	-0.49	-0.96	-0.77	-0.19	0.451	-0.607	-0.17	-0.12
77.	rs375199307	M96V	-0.82	1.431	-0.63	-0.76	-0.79	-1.19	0.424	-0.952	-0.12	-0.474
78.	rs749537579	R99P	-0.67	0.052	-0.32	-0.08	-0.91	0.33	-0.014	-0.481	-0.96	-0.567
79.	rs749537579	R99Q	-0.70	0.542	0.22	-0.208	-0.76	-0.58	-0.155	-0.711	-0.15	-0.441
80.	rs778060901	G104S	-0.84	0.950	-1.68	-1	-0.71	-1.48	-0.518	-1.152	-3.08	-1.489
81.	rs769850019	K106R	-0.89	0.697	-1.72	-0.15	-0.78	-1.4	1.733	-1.093	-0.68	-1.126
82.	rs746825485	N107S	-0.92	-0.41	-0.64	-0.61	-1.04	0.82	0.079	-1.046	-0.73	-1.055
83.	rs1290802184	T114I	-0.16	-0.00	-0.6	-0.33	0.144	0.4	-0.013	-0.3	0.46	-0.031
84.	rs961702090	S115T	0.23	-0.58	-0.26	0.15	0.02	-0.42	0.548	-0.107	0.83	0.306