Table S1. Summary of variation identified by *S1PR3* re-sequencing in European (ED) and African descent (AD) subjects.

SNP #	Position[a]	Location[b]	rs #	Flanking (5')	Flanking (3')	MAF in AD[c]	MAF in ED[c]	Val[d]
1	90794283	-1899T>G	**rs7022797**	GACAGGGATC	TTAGGGAAAC	0.39	0.31	‡
2	90794397	-1785G>C	**rs11137480**	ACTCCTCAGG	CCTCTGGGCT	0.39	0.31	‡
3	90794645	-1537C>A	rs117210461	TATTGTTATC	TGGTTGTGAC	0	0.04	‡
4	90794806-11	-1376_-1371dupAGTGCC	NA	CTACAGTGCC	GGAAGACTCC	0	0.12	-
5	90794814	-1368G>A	rs7022664	ACAGTGCCGG	AGACTCCACA	0.18	0.38	‡
6	90795129-30	-1053_-1052insGAATC	rs10648003	TTTGCACAAA	CTCAACTCTC	0.36	0.50	-
7	90795641	-541C>A	rs7048483	GGGACCCGCG	GGAAAAGGAA	0.04	0	‡
8	90796342	c.-236T>A	rs11795137	CCAGCCCATC	GGCATTCGAG	0	0.08	‡
9	90797066	c.-148+660A>G	**rs73654718**	GACACTCCCA	TGGTATATTT	0.19	0.08	‡
10	90797090	c.-148+684T>G	NA	TGTGGTGTTT	TATATTTGGA	0.04	0	-
11	90797181	c.-148+775G>T	rs73496033	GGGAGCTACA	GAACAGAGAG	0.04	0	‡
12	90797198	c.-148+792A>C	rs62551536	AGAGCTCTTT	GAAGGTTACT	0	0.08	‡
13	90797209	c.-148+803T>G	NA	GAAGGTTACT	TTAAATGGAG	0	0.04	-
14	90797298	c.-148+892T>C	rs73496035	AATCTGGACA	TAGAAGTCAC	0.04	0	‡
15	90797507	c.-148+1101C>T	rs59180453	GGTGATGGTG	GGGGCATGTG	0.04	0	‡
16	90797534	c.-148+1128C>T	rs7863572	TGTGTGTGTG	GCGCTTGAGG	0.43	0.46	‡
17	90797689	c.-148+1283C>T	**rs6559331**	CTTTGGGCCT	TGAAATCACT	0.37	0.29	‡
18	90797872	c.-148+1466dupA	**rs11398943**	CATATACAAA	GGGTAGAGAC	0.43	0.38	-
19	90798329	c.-148+1923T>A	rs79303380	CTCTGCCATA	GTTTTCTGCC	0.04	0	‡
20	90798448	c.-148+2042C>T	rs10867149	GTTAATAACA	GTTTCAGTTG	0.39	0.42	‡
21	90798465	c.-148+2059C>T	rs73496042	GTTGATGTTA	TGTTATAGCT	0.04	0	‡
22	90798974	c.-148+2568delC	NA	GACACCCCCC	TCCCCCAGCC	0	0.12	-
23	90799235	c.-148+2829C>T	rs41304228	AATCATTTAT	CTATGCTGTC	0	0.04	‡
24	90799458	c.-148+3052A>C	NA	CAGATAGCTC	TAATGTCCCA	0.04	0	-
25	90799625	c.-148+3219G>A	NA	ATTTCTCAGG	GAGCTGCATT	0.04	0	-
26	90800116	c.-148+3710C>T	rs73496046	GTAGAGAAAG	GAATCGCTAG	0.04	0	‡
27	90800363	c.-148+3957G>A	rs3934594	AGCTTAGTGA	GATGACATGA	0.25	0.46	‡
28	90800415	c.-148+4009T>G	**rs11137481**	AGAACTCAGG	AAGTTCAGAT	0.21	0.04	‡
29	90800633	c.-148+4227T>C	rs115138747	AGCATCTGTA	TGGTTAGAAG	0.04	0	‡
30	90800748	c.-148+4342A>G	NA	TAGTCTGCAA	AAGCCATATG	0.04	0	-
31	90800749	c.-148+4343G>A	**rs7045576**	AGTCTGCAAA	AGCCATATGT	0.07	0.42	‡
32	90801370-2	c.-147-4419_-147-4417delGTG	NA	GGGACAGGTG	ACTAGGAGGG	0	0.04	-
33	90801401	c.-147-4388G>C	**rs6559333**	AAGGCTGCAG	GTCCGGCCCA	0.25	0.08	‡
34	90802459	c.-147-3330G>A	rs7858626	GTATCCCAGC	ATCTGTAGGA	0.32	0.46	‡
35	90802700	c.-147-3089C>T	NA	GCAGAGCCCT	GCGGTCCCCA	0.04	0	-
36	90802703	c.-147-3086G>A	**rs7870888**	GAGCCCTCGC	GTCCCCATCA	0.04	0.12	‡
37	90802886	c.-147-2903T>C	**rs7038457**	ATTCTCCAGT	CCTGTTCACA	0.36	0.15	‡
38	90802906	c.-147-2883A>C	NA	AGATAAAGAA	GAAAGAAATA	0.04	0	-
39	90803463	c.-147-2326C>G	**rs58235552**	CAGGGGCTGG	ATGATTCCAG	0.21	0.12	‡
40	90803547	c.-147-2242G>A	NA	AATCAGAAAC	GTAGAGAGGG	0.04	0	-
41	90804006	c.-147-1783G>A	rs76590495	GGTTTCCAGA	CAACCAACAC	0.14	0	‡
42	90804199	c.-147-1590A>C	**rs73496049**	CCACCCAGGC	AGCCCTGGAT	0.11	0.04	‡
43	90804466-8	c.-147-1323_-147-1321dupGTG	NA	GGGTGCGGTG	TCTCATGCCT	0.04	0	-
44	90804595	c.-147-1194T>C	NA	AAATTAGCCA	GCATGGTGGC	0.11	0	-
45	90804777-81	c.-147-1012_-147-1008delAATAA	NA	AATAAAATAA	GTGAGTCCAC	0.11	0	-
46	90804984	c.-147-805C>T	rs116473341	TGCCACTTTT	TGTTGGCTCA	0.11	0	‡
47	90805081-4	c.-147-708-147-705delCCTT	NA	TCCTGTCCTT	TATCATCTGT	0.04	0	-
48	90805320-2	c.-147-469-147-467delTTC	NA	GTGCGGGATC	CCACGATGTC	0	0.19	-
49	90805677	c.-147-112A>C	rs41287345	TGACGTGGCT	GCCATCCCAG	0.04	0	‡
50	90805687	c.-147-102G>A	NA	AGCCATCCCA	TACTTCCACG	0.04	0	-
51	90806433	c.498C>T (p.Phe166Phe)	NA	TCATTGCCTT	ACGCTGGGCG	0.04	0	-
52	90806565	c.630C>G (p.Thr210Thr)	rs34962307	TCCTGGTGAC	ATCGTGATCC	0.11	0	‡
53	90806663	c.728G>A (p.Arg243Gln)	rs34075341	GCACTGCTGC	GACCGTGGTG	0.04	0.12	‡
54	90807075	c.*3G>A	NA	GCAACTGATC	TCTCCATGCG	0	0.04	-
55	90807194	c.*122G>A	**rs73496050**	AGCCTGCCCA	TGTGGATGTC	0.25	0	‡

56	90807340	c.*268C>T	rs117135373	ATCCTAGACA	CCTCCCTGTT	0	0.12	‡
57	90807402	c.*330G>A	rs41287349	GACCCTCTCC	TGTGCCTCTG	0.39	0	‡
58	90807494	c.*422G>A	NA	ATGTTACACA	AATTTGTGTT	0.07	0	-
59	90807509	c.*437G>T	NA	TGTGTTGCAG	TGTTTGCCAT	0.04	0	-
60	90807692	c.*620C>T	rs41287351	TTCAAATTCC	CAAAAAGGCT	0	0.12	‡
61	90807922	c.*850A>G	rs7853537	AAGCAGAAGC	GACGGCTGGC	0.25	0.15	‡
62	90807919-24	c.*847_*852dupAGCAGA	NA	CAGAAGCAGA	CGGCTGGCCT	0.04	0	-
63	90807926	c.*854G>A	rs7865415	AGAAGCAGAC	GCTGGCCTGG	0.14	0	‡
64	90808344	c.*1272A>G	rs41287355	TTCCCCAAGG	TTGTACGTAT	0.04	0	‡
65	90808518	c.*1446C>T	rs117145268	GAGCATTTGC	TGAATAAAAC	0	0.12	‡
66	90808722	c.*1650delC	NA	AGATCTTCCC	AGGAGCATTT	0.04	0	-
67	90808951	c.*1879T>C	NA	CTGGCCAACA	AGTGAAATCC	0.18	0	-
68	90809094	c.*2022A>G	rs1129925	AGATCGCACC	CTGCACTCCA	0.29	0.42	‡
69	90809249	c.*2177T>C	rs77515659	ATCTGTGTTA	AGTTATGAGT	0.11	0	‡
70	90809604	c.*2532C>T	**rs1867**	AAGCCCTAAC	TTGAAGTTTG	0.04	0.15	‡
71	90809871	*126A>G	rs114837647	CAGGAATTAA	CCACATTCAG	0.11	0	‡
72	90809944	*199G>A	**rs9314668**	TTAATGAAGC	TCTGTGCCTT	0.04	0.15	‡
73	90810315	*570dupT	NA	AAGGTGAGTT	CTCTAGGAGT	0.04	0	-
74	90810497	*752A>G	NA	CCATCATCCA	ATGAAAGATA	0.04	0	-
75	90811017	*1272A>G	**rs7865979**	AGAGTGAAGG	ATCCCTGTGG	0.07	0.42	‡
76	90811043	*1298G>A	NA	TCAAAAGGGA	GAGGGAATTT	0.04	0	-
77	90811081	*1336C>G	rs118017965	CTGCTGTATT	TCAAATCTCC	0	0.12	‡
78	90811225	*1480G>A	rs76432254	AGAAAGTGGT	AATTGGCAAT	0.04	0	‡
79	90811237	*1492C>T	NA	ATTGGCAATA	GCCAAGACAT	0.04	0	-
80	90811270	*1525dupT	NA	AATTCTTTTT	GTTTCACAAA	0.04	0	-

[a]Position in chromosome 9 according to NCBI build 36
[b]With respect to reference sequence NM_005226.2
[c]Minor allele frequency in re-sequencing
[d]Validation status: frequency available, ‡; unknown or by 2-hit as in dbSNP build 135
Selected SNPs for genotyping are underlined and in bold