

Supplementary Table S1. Association analysis of STDR

Nearest Gene(s)	SNP	Position	A1	A2	MAF		OR(95%CI)	P-value*	q-value
					Non-STDR	STDR			
<i>COL5A1</i>	<u>rs59126004</u> <sup>‡</sup>	9:137674341	C	T	0.17	0.14	0.84 (0.71-0.98)	0.034	0.798
<i>IGSF21-KLHDC7A</i>	<u>rs3007729</u>	1:18795255	T	C	0.32	0.30	0.87 (0.77-0.99)	0.034	0.798
<i>CREB5</i>	<u>rs11765845</u>	7:28391142	A	G	0.29	0.28	0.87 (0.76-0.99)	0.036	0.798
<i>LOC728275-LOC728316</i>	<u>rs227455</u> <sup>†</sup>	6:165478051	C	T	0.48	0.47	0.89 (0.79-0.99)	0.048	0.798
<i>CCDC68-TCF4</i>	<u>rs12607567</u> <sup>†</sup>	18:52858659	G	A	0.47	0.45	0.89 (0.80-1.00)	0.064	0.798
<i>C6orf170</i>	<u>rs17083119</u> <sup>‡</sup>	6:121402110	G	A	0.12	0.10	0.84 (0.70-1.01)	0.077	0.798
<i>SLC25A32</i>	<u>rs3098241</u> <sup>‡</sup>	8:104425304	G	A	0.32	0.30	0.89 (0.79-1.01)	0.081	0.798
<i>GRIK2</i>	<u>rs2518344</u> <sup>†</sup>	6:101881867	A	G	0.10	0.11	1.14 (0.94-1.38)	0.164	0.892
<i>VSTM2B-POP4</i>	<u>rs10403021</u>	19:30079604	T	C	0.29	0.30	1.08 (0.95-1.22)	0.198	0.892
<i>COX5BL1-LOC441026</i>	<u>rs11736136</u> <sup>†</sup>	4:83018274	G	A	0.04	0.04	1.2 (0.89-1.60)	0.218	0.892
<i>NOX3-ARID1B</i>	<u>rs10499298</u>	6:156175762	T	C	0.06	0.05	0.85 (0.67-1.09)	0.221	0.892
<i>MALRD1</i>	<u>rs12267418</u>	10:19714554	A	G	0.01	0.02	1.34 (0.83-2.14)	0.225	0.892
<i>CNTN5</i>	<u>rs10501943</u> <sup>†</sup>	11:99946999	C	T	0.03	0.03	1.22 (0.87-1.71)	0.229	0.892
<i>KIAA0825</i>	<u>rs13163610</u> <sup>†</sup>	5:93548877	C	A	0.04	0.03	0.82 (0.58-1.14)	0.246	0.892
<i>MYTIL-LOC729897</i>	<u>rs10199521</u> <sup>†</sup>	2:2519513	T	C	0.35	0.36	1.06 (0.94-1.20)	0.276	0.892
<i>CEP135</i>	<u>rs4865047</u> <sup>†</sup>	4:56821806	T	C	0.22	0.23	1.07 (0.93-1.22)	0.323	0.892
<i>INSR</i>	<u>rs2115386</u> <sup>†</sup>	19:7196565	C	T	0.47	0.49	1.05 (0.94-1.18)	0.325	0.892
<i>ZNRF1</i>	<u>rs17684886</u> <sup>†</sup>	16:75086875	A	T	0.47	0.47	0.94 (0.84-1.06)	0.333	0.892
<i>COMMD6-LMO7</i>	<u>rs7986566</u>	13:76197931	C	T	0.32	0.31	0.94 (0.83-1.06)	0.336	0.892
<i>LOC729902-NPY2R</i>	<u>rs1902491</u> <sup>†</sup>	4:156055333	C	A	0.17	0.17	0.92 (0.79-1.08)	0.343	0.892
<i>TBC1D4</i>	<u>rs9565164</u>	13:76039376	C	T	0.29	0.29	0.95 (0.84-1.07)	0.416	0.892
<i>COMMD6</i>	<u>rs4643195</u>	13:76103840	G	A	0.30	0.29	0.95 (0.84-1.07)	0.418	0.892
<i>TNFSF18</i>	<u>rs1033465</u> <sup>‡</sup>	1:172987730	T	A	0.03	0.02	0.86 (0.60-1.23)	0.425	0.892
<i>UBE2E2</i>	<u>rs79941515</u> <sup>‡</sup>	3:23225738	T	C	0.18	0.17	0.94 (0.81-1.09)	0.426	0.892
<i>TBC1D4</i>	<u>rs7335576</u>	13:76043318	G	A	0.33	0.33	0.95 (0.84-1.07)	0.439	0.892

<i>MRPL14</i>	<u>rs713050</u> <sup>†</sup>	6:44200107	G	T	0.05	0.05	0.90 (0.68-1.17)	0.443	0.892
<i>TNFRSF13B-MPRIP</i>	rs11867934	17:16933404	T	C	0.12	0.12	1.06 (0.89-1.26)	0.452	0.892
<i>API5</i>	rs899036	11:41682910	G	T	0.08	0.09	1.07 (0.88-1.31)	0.460	0.892
<i>ARHGAP22</i>	rs4838605 <sup>†</sup>	10:49699957	C	T	0.10	0.10	1.07 (0.88-1.29)	0.466	0.892
<i>RASL11A</i>	<u>rs1333347</u> <sup>‡</sup>	13:27900204	T	C	0.14	0.15	1.05 (0.90-1.24)	0.492	0.892
<i>AKT3-ZNF238</i>	rs10927101	1:244173872	C	A	0.29	0.30	1.04 (0.92-1.18)	0.502	0.892
<i>BFSP2</i>	rs1197310 <sup>†</sup>	3:133128224	T	A	0.48	0.49	1.03 (0.92-1.16)	0.512	0.892
<i>MYSM1</i>	rs2811893	1:59162148	C	T	0.34	0.35	1.04 (0.92-1.17)	0.516	0.892
<i>EDIL3</i>	rs1445754 <sup>†</sup>	5:83575631	T	A	0.05	0.06	1.08 (0.84-1.39)	0.517	0.892
<i>LINC01249</i>	rs699549	2:4705263	T	C	0.24	0.23	0.95 (0.83-1.09)	0.519	0.892
<i>FMN1</i>	rs10519765 <sup>†</sup>	15:32993421	A	G	0.11	0.10	0.94 (0.78-1.13)	0.530	0.892
<i>MALRD1</i>	<u>rs17670074</u> <sup>†</sup>	10:19705383	C	A	0.35	0.34	0.96 (0.85-1.08)	0.539	0.892
<i>HS6ST3</i>	rs16953072 <sup>†</sup>	13:96950313	T	G	0.05	0.05	0.92 (0.70-1.20)	0.541	0.892
<i>KRT18P34-VEPH1</i>	rs9866141 <sup>†</sup>	3:156950579	T	C	0.08	0.09	1.05 (0.86-1.29)	0.569	0.892
<i>TNFSF4-LOC730070</i>	rs1342038	1:173301516	G	A	0.42	0.41	0.96 (0.86-1.08)	0.599	0.892
<i>TMEM217</i>	<u>rs1224329</u>	6:37288215	G	A	0.11	0.11	0.95 (0.79-1.14)	0.600	0.892
<i>LINC00511</i>	<u>rs759563</u> <sup>‡</sup>	17:70370888	T	C	0.30	0.30	0.96 (0.85-1.09)	0.601	0.892
<i>CAMK4</i>	rs2300782 <sup>†</sup>	5:110788785	T	C	0.40	0.41	1.03 (0.91-1.15)	0.612	0.892
<i>KIFC3</i>	<u>rs247040</u> <sup>‡</sup>	16:57877310	C	T	0.09	0.09	0.95 (0.77-1.15)	0.613	0.892
<i>COLEC12</i>	rs599019	18:294495	C	A	0.47	0.47	1.03 (0.91-1.15)	0.615	0.892
<i>C5orf36</i>	rs17376456 <sup>†</sup>	5:93557702	G	A	0.05	0.04	0.93 (0.70-1.23)	0.645	0.892
<i>PACRG</i>	<u>rs2294458</u> <sup>‡</sup>	6:163666336	G	T	0.24	0.24	1.03 (0.90-1.17)	0.654	0.892
<i>AKT3-ZNF238</i>	<u>rs479338</u>	1:244159143	G	A	0.28	0.26	0.97 (0.85-1.10)	0.660	0.892
<i>ZWINT-MRPS35P3</i>	rs4462262	10:59189178	T	C	0.05	0.06	1.05 (0.82-1.35)	0.667	0.892
<i>FABP3P2-TNFSF11</i>	<u>rs4941432</u>	13:43098347	A	G	0.24	0.23	0.97 (0.85-1.11)	0.670	0.892
<i>SCYLIBP1</i>	rs6427247 <sup>†</sup>	1:170380480	G	A	0.25	0.26	1.02 (0.90-1.16)	0.693	0.892
<i>PLXDC2-NEBL</i>	rs12219125 <sup>†</sup>	10:20593087	T	G	0.10	0.11	1.03 (0.86-1.24)	0.698	0.892
<i>CDC42BPA</i>	<u>rs2953655</u> <sup>‡</sup>	1:227554171	T	C	0.21	0.20	0.97 (0.84-1.12)	0.711	0.892

<i>ARL4C-SH3BP4</i>	rs2380261 <sup>†</sup>	2:235641180	A	C	0.46	0.45	1.02 (0.91-1.14)	0.719	0.892
<i>PPAR11</i>	<u>rs17836475<sup>‡</sup></u>	12:4073544	C	G	0.31	0.30	0.97 (0.86-1.10)	0.722	0.892
<i>FSTL5</i>	rs4470583 <sup>†</sup>	4:162250932	A	G	0.07	0.07	1.04 (0.83-1.30)	0.724	0.892
<i>AKAP11-FABP3P2</i>	<u>rs117850847</u>	13:42909215	A	C	0.06	0.06	0.96 (0.75-1.22)	0.750	0.908
<i>RP1-90L14.1</i>	<u>rs9362054<sup>†</sup></u>	6:85178268	T	C	0.30	0.31	1.01 (0.89-1.15)	0.795	0.936
<i>LRP2-BBS5</i>	rs1399634	2:170244607	A	T	0.37	0.37	0.98 (0.87-1.10)	0.809	0.936
<i>LEKRI-CCN1</i>	rs13064954 <sup>‡</sup>	3:156854742	A	G	0.09	0.09	1.02 (0.84-1.24)	0.833	0.936
<i>ARHGAP22</i>	rs11101357 <sup>†</sup>	10:49723300	A	G	0.10	0.10	1.01 (0.84-1.23)	0.847	0.936
<i>GRIK2</i>	<u>rs487083<sup>†</sup></u>	6:102133625	G	T	0.05	0.05	1.02 (0.79-1.32)	0.863	0.936
<i>AKT3-ZNF238</i>	rs476141	1:244176424	T	G	0.20	0.20	0.98 (0.85-1.14)	0.868	0.936
<i>TINAG</i>	rs6909083 <sup>‡</sup>	6:54182303	T	C	0.25	0.25	0.98 (0.86-1.12)	0.868	0.936
<i>GRB2</i>	<u>rs9896052<sup>†</sup></u>	17:73418862	C	A	0.43	0.43	1.00 (0.89-1.13)	0.891	0.946
<i>MYTIL-LOC729897</i>	<u>rs2668843</u>	2:2521301	A	G	0.20	0.19	0.99 (0.86-1.14)	0.911	0.952
<i>LOC729200-MAP3K7IP2</i>	rs7772697	6:149435111	C	T	0.19	0.19	1.00 (0.86-1.16)	0.954	0.972
<i>KIAA1804-KCNK1</i>	rs6662352 <sup>†</sup>	1:233642172	T	G	0.34	0.35	1.00 (0.89-1.13)	0.958	0.972
<i>HNMT</i>	rs763970	2:138636133	A	C	0.31	0.31	1.00 (0.88-1.13)	0.976	0.976

A1, minor allele; A2, major allele; MAF, minor allele frequency; OR, odds ratio. SNPs ranked by the P-value. Chromosomal position corresponds to human reference genome hg19. OR corresponds to the minor allele. \*Adjusted for age, sex, BMI, duration of diabetes, the presence of HT and HbA1c. <sup>†</sup>Direction of effect consistent with the original report. <sup>‡</sup>Direction of effect not available in the original report. SNPs not examined in the previous study<sup>1</sup> are underlined.

#### Reference:

1. Cheung CY, Hui EY, Lee CH, et al. Impact of Genetic Loci Identified in Genome-Wide Association Studies on Diabetic Retinopathy in Chinese Patients With Type 2 Diabetes. *Invest Ophthalmol Vis Sci* 2016;57:5518-5524.

Supplementary Table S2. Association analysis of PDR

Nearest Gene(s)	SNP	Position	A1	A2	MAF		OR(95%CI)	P-value*	q-value
					Non-STDR	PDR			
<i>INSR</i>	rs2115386 <sup>†</sup>	19:7196565	C	T	0.47	0.52	1.25 (1.06-1.47)	5.65x10 <sup>-3</sup>	0.190
<i>UBE2E2</i>	rs79941515 <sup>‡</sup>	3:23225738	T	C	0.18	0.14	0.72 (0.57-0.91)	6.75x10 <sup>-3</sup>	0.190
<i>MYTIL-LOC729897</i>	rs10199521 <sup>†</sup>	2:2519513	T	C	0.35	0.39	1.24 (1.05-1.47)	8.93x10 <sup>-3</sup>	0.190
<i>COL5A1</i>	rs59126004 <sup>‡</sup>	9:137674341	C	T	0.17	0.13	0.73 (0.57-0.93)	0.011	0.190
<i>ZNRF1</i>	rs17684886 <sup>†</sup>	16:75086875	A	T	0.47	0.43	0.82 (0.69-0.97)	0.022	0.259
<i>IGSF21-KLHDC7A</i>	rs3007729	1:18795255	T	C	0.32	0.29	0.81 (0.67-0.97)	0.023	0.259
<i>AKAP11-FABP3P2</i>	rs117850847	13:42909215	A	C	0.06	0.04	0.65 (0.44-0.96)	0.030	0.259
<i>CCDC68-TCF4</i>	rs12607567 <sup>†</sup>	18:52858659	G	A	0.47	0.44	0.83 (0.70-0.98)	0.030	0.259
<i>KIAA0825</i>	rs13163610 <sup>†</sup>	5:93548877	C	A	0.04	0.02	0.62 (0.35-1.08)	0.092	0.705
<i>API5</i>	rs899036	11:41682910	G	T	0.08	0.10	1.25 (0.95-1.64)	0.109	0.752
<i>GRB2</i>	rs9896052	17:73418862	C	A	0.43	0.40	0.88 (0.75-1.04)	0.144	0.853
<i>FABP3P2-TNFSF11</i>	rs4941432	13:43098347	A	G	0.24	0.21	0.87 (0.71-1.05)	0.159	0.853
<i>C6orf170</i>	rs17083119 <sup>‡</sup>	6:121402110	G	A	0.12	0.10	0.82 (0.63-1.08)	0.165	0.853
<i>MYTIL-LOC729897</i>	rs2668843 <sup>†</sup>	2:2521301	A	G	0.20	0.21	1.14 (0.94-1.38)	0.180	0.853
<i>NOX3-ARID1B</i>	rs10499298	6:156175762	T	C	0.06	0.05	0.78 (0.55-1.12)	0.188	0.853
<i>GRIK2</i>	rs2518344 <sup>†</sup>	6:101881867	A	G	0.10	0.11	1.18 (0.90-1.54)	0.212	0.853
<i>COLEC12</i>	rs599019	18:294495	C	A	0.47	0.47	1.10 (0.93-1.30)	0.226	0.853
<i>TBC1D4</i>	rs7335576	13:76043318	G	A	0.33	0.32	0.90 (0.75-1.07)	0.233	0.853
<i>COMMD6-LMO7</i>	rs7986566	13:76197931	C	T	0.32	0.31	0.90 (0.75-1.07)	0.235	0.853
<i>CAMK4</i>	rs2300782	5:110788785	T	C	0.40	0.39	0.91 (0.77-1.07)	0.285	0.923
<i>SLC25A32</i>	rs3098241 <sup>‡</sup>	8:104425304	G	A	0.32	0.31	0.90 (0.76-1.08)	0.290	0.923
<i>KIAA1804-KCNK1</i>	rs6662352	1:233642172	T	G	0.34	0.33	0.91 (0.77-1.09)	0.338	0.923
<i>MYSM1</i>	rs2811893	1:59162148	C	T	0.34	0.36	1.08 (0.91-1.27)	0.369	0.923
<i>VSTM2B-POP4</i>	rs10403021	19:30079604	T	C	0.29	0.29	1.07 (0.90-1.28)	0.402	0.923
<i>LOC729902-NPY2R</i>	rs1902491 <sup>†</sup>	4:156055333	C	A	0.17	0.17	0.91 (0.73-1.13)	0.416	0.923

<i>FSTL5</i>	rs4470583	4:162250932	A	G	0.07	0.07	0.87 (0.62-1.21)	0.419	0.923
<i>CEP135</i>	rs4865047 <sup>†</sup>	4:56821806	T	C	0.22	0.23	1.08 (0.88-1.31)	0.439	0.923
<i>COMMD6</i>	rs4643195	13:76103840	G	A	0.30	0.29	0.93 (0.78-1.11)	0.448	0.923
<i>LOC728275-LOC728316</i>	rs227455 <sup>†</sup>	6:165478051	C	T	0.48	0.48	0.94 (0.80-1.10)	0.453	0.923
<i>ARHGAP22</i>	rs11101357	10:49723300	A	G	0.10	0.09	0.89 (0.67-1.19)	0.454	0.923
<i>MALRD1</i>	rs12267418	10:19714554	A	G	0.01	0.01	1.28 (0.65-2.50)	0.465	0.923
<i>PPAR11</i>	rs17836475 <sup>‡</sup>	12:4073544	C	G	0.31	0.32	1.06 (0.89-1.26)	0.480	0.923
<i>AKT3-ZNF238</i>	rs10927101	1:244173872	C	A	0.29	0.30	1.05 (0.88-1.26)	0.527	0.923
<i>COX5BL1-LOC441026</i>	rs11736136 <sup>†</sup>	4:83018274	G	A	0.04	0.04	1.13 (0.76-1.70)	0.528	0.923
<i>TNFRSF13B-MPRIP</i>	rs11867934 <sup>†</sup>	17:16933404	T	C	0.12	0.11	0.92 (0.71-1.19)	0.538	0.923
<i>CNTN5</i>	rs10501943 <sup>†</sup>	11:99946999	C	T	0.03	0.03	1.16 (0.71-1.89)	0.542	0.923
<i>LINC00511</i>	rs759563 <sup>‡</sup>	17:70370888	T	C	0.30	0.31	0.94 (0.79-1.13)	0.555	0.923
<i>TNFSF4-LOC730070</i>	rs1342038 <sup>†</sup>	1:173301516	G	A	0.42	0.43	1.04 (0.89-1.23)	0.571	0.923
<i>Bfsp2</i>	rs1197310	3:133128224	T	A	0.48	0.48	0.95 (0.81-1.12)	0.597	0.923
<i>AKT3-ZNF238</i>	rs479338	1:244159143	G	A	0.28	0.25	0.95 (0.79-1.14)	0.611	0.923
<i>PACRG</i>	rs2294458 <sup>‡</sup>	6:163666336	G	T	0.24	0.23	1.05 (0.86-1.27)	0.614	0.923
<i>LOC729200-MAP3K7IP2</i>	rs7772697 <sup>†</sup>	6:149435111	C	T	0.19	0.18	0.94 (0.76-1.17)	0.622	0.923
<i>TBC1D4</i>	rs9565164	13:76039376	C	T	0.29	0.29	0.95 (0.80-1.14)	0.635	0.923
<i>LEKRI-CCN1</i>	rs13064954 <sup>‡</sup>	3:156854742	A	G	0.09	0.09	0.93 (0.70-1.24)	0.654	0.923
<i>RASL11A</i>	rs1333347 <sup>‡</sup>	13:27900204	T	C	0.14	0.16	1.05 (0.83-1.32)	0.662	0.923
<i>CREB5</i>	rs11765845	7:28391142	A	G	0.29	0.29	0.96 (0.80-1.15)	0.670	0.923
<i>GRIK2</i>	rs487083 <sup>†</sup>	6:102133625	G	T	0.05	0.06	1.07 (0.75-1.53)	0.688	0.923
<i>ZWINT-MRPS35P3</i>	rs4462262	10:59189178	T	C	0.05	0.06	1.07 (0.75-1.52)	0.697	0.923
<i>EDIL3</i>	rs1445754 <sup>†</sup>	5:83575631	T	A	0.05	0.06	1.06 (0.74-1.52)	0.715	0.923
<i>FMN1</i>	rs476141 <sup>†</sup>	15:32993421	A	G	0.11	0.10	0.95 (0.73-1.24)	0.737	0.923
<i>AKT3-ZNF238</i>	rs10519765 <sup>†</sup>	1:244176424	T	G	0.20	0.20	1.03 (0.84-1.26)	0.737	0.923
<i>KIFC3</i>	rs247040 <sup>‡</sup>	16:57877310	C	T	0.09	0.09	0.95 (0.72-1.25)	0.750	0.923
<i>ARL4C-SH3BP4</i>	rs2380261	2:235641180	A	C	0.46	0.43	0.97 (0.82-1.14)	0.752	0.923

<i>TINAG</i>	rs6909083 <sup>‡</sup>	6:54182303	T	C	0.25	0.25	1.03 (0.85-1.23)	0.752	0.923
<i>MALRD1</i>	<u>rs17670074</u> <sup>†</sup>	10:19705383	C	A	0.35	0.34	0.97 (0.82-1.15)	0.755	0.923
<i>CDC42BPA</i>	<u>rs2953655</u> <sup>‡</sup>	1:227554171	T	C	0.21	0.20	0.96 (0.79-1.18)	0.759	0.923
<i>RP1-90L14.1</i>	<u>rs9362054</u>	6:85178268	T	C	0.30	0.31	0.97 (0.81-1.16)	0.768	0.923
<i>SCYL1BP1</i>	rs6427247 <sup>†</sup>	1:170380480	G	A	0.25	0.25	1.02 (0.85-1.23)	0.776	0.923
<i>HNMT</i>	rs763970 <sup>†</sup>	2:138636133	A	C	0.31	0.31	0.98 (0.82-1.16)	0.847	0.952
<i>PLXDC2-NEBL</i>	rs12219125 <sup>†</sup>	10:20593087	T	G	0.10	0.11	1.02 (0.79-1.33)	0.849	0.952
<i>C5orf36</i>	rs17376456	5:93557702	G	A	0.05	0.04	1.03 (0.69-1.53)	0.869	0.952
<i>LINC01249</i>	rs699549 <sup>†</sup>	2:4705263	T	C	0.24	0.23	1.01 (0.83-1.23)	0.873	0.952
<i>TNFSF18</i>	<u>rs1033465</u> <sup>‡</sup>	1:172987730	T	A	0.03	0.03	1.04 (0.63-1.70)	0.878	0.952
<i>ARHGAP22</i>	rs4838605 <sup>†</sup>	10:49699957	C	T	0.10	0.09	1.02 (0.77-1.35)	0.884	0.952
<i>TMEM217</i>	<u>rs1224329</u>	6:37288215	G	A	0.11	0.11	0.98 (0.76-1.27)	0.899	0.952
<i>KRT18P34-VEPH1</i>	rs9866141	3:156950579	T	C	0.08	0.09	0.98 (0.74-1.30)	0.921	0.952
<i>LRP2-BBS5</i>	rs1399634	2:170244607	A	T	0.37	0.38	0.99 (0.84-1.17)	0.933	0.952
<i>MRPL14</i>	<u>rs713050</u> <sup>†</sup>	6:44200107	G	T	0.05	0.05	0.98 (0.68-1.42)	0.945	0.952
<i>HS6ST3</i>	rs16953072 <sup>†</sup>	13:96950313	T	G	0.05	0.05	0.98 (0.68-1.43)	0.952	0.952

A1, minor allele; A2, major allele; MAF, minor allele frequency; OR, odds ratio. SNPs ranked by the P-value. Chromosomal position corresponds to human reference genome hg19. OR corresponds to the minor allele. \*Adjusted for age, sex, BMI, duration of diabetes, the presence of HT and HbA1c. <sup>†</sup>Direction of effect consistent with the original report. <sup>‡</sup>Direction of effect not available in the original report. SNPs not examined in the previous study<sup>1</sup> are underlined.

#### Reference:

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