Supplemental Table 3. *PDE11A* coding variants identified as non-significantly associated with testicular germ cell tumors

Chr	**Position**	**Variant**	**rs #**	**Amino Acid Change**	**CADDscore**	**Total Affected, n=217** **n (MAF)** **p-value**	**Unaffected, n=335** **n (MAF)**	**Familial Affected, n=101** **n (MAF)** **p-value**	**Sporadic Affected, n=72** **n (MAF)** **p-value**	**Bilateral Affected, n=44** **n (MAF)** **p-value**
2	178937010	c.155G>C	rs77972073	p.R52T*	7.15	1 (0.002) 1.0	1 (0.001)	0 1.0	1 (0.007) 0.32	0 1.0
2	178936614	c.551G>A	rs6433711	p.R184Q	8.87	0 1.0	1 (0.001)	0 1.0	0 1.0	0 1.0
2	178936330	c.835C>G	N/A	p.Q279E	20.7	0 1.0	1 (0.001)	0 1.0	0 1.0	0 1.0
2	178936272	c.893A>G	rs78328794	p.N298S	21.4	1 (0.002) 1.0	**2 (0.001)**	1 (0.005) 0.41	0 1.0	0 1.0
2	178879055	c.1045G>A	rs77477862	p.A349T*	12.87	1 (0.002) 1.0	2 (0.003)	1 (0.005) 0.55	0 1.0	0 1.0
2	178879181	c.919C>T	rs76308115	p.R307X*	34	2 (0.005) 0.71	5 (0.007)	1 (0.005) 1.0	0 0.59	1 (0.011) 0.52
2	178681638	c.1655T>C	rs138427178	p.I552T	19.5	0 0.52	2 (0.003)	0 1.0	0 1.0	0 1.0
2	178681585	c.1708T>C	rs149795546	p.S570P	21.4	1 (0.002) 1.0	1 (0.001)	1 (0.005) 0.41	0 1.0	0 1.0
2	178592864	c.1825G>A	rs77934668	p.D609N*	13.98	1 (0.002) 1.0	1 (0.001)	0 1.0	1 (0.007) 0.32	0 1.0
2	178592758	c.1931A>G	N/A	p.Y644C	20.2	0 1.0	1 (0.001)	0 1.0	0 1.0	0 1.0
2	178565913	c.2180A>G	rs17400325	p.Y727C*	21.6	24 (0.055) 0.13	24 (0.036)	10 (0.050) 0.41	9 (0.063) 0.16	5 (0.057) 0.37
2	178545566	c.2411G>T	rs75127279	p.R804H*	23.6	7 (0.016) 0.82	13 (0.019)	4 (0.020) 1.0	1 (0.007) 0.48	2 (0.023) 0.69
2	178528641	c.2599C>G	rs61306957	p.R867G*	10.44	7 (0.016) 1.0	12 (0.018)	4 (0.020) 0.77	1 (0.007) 0.48	2 (0.023) 0.67
2	178528608	c.2632A>G	rs74357545	p.M878V*	12.34	4 (0.009) 0.43	11 (0.016)	1 (0.005) 0.31	2 (0.014) 1.0	1 (0.011) 1.0

Previously reported in Horvath et al. (Horvath et al. 2009); MAF: Minor allele frequency; CADD = Combined Annotation-Dependent Depletion score (Kircher et al. 2014).N/A: not available