

**Supplemental Table S1. Genes studied**

Gene	Chr.	Start (bp)	Size (kb)	GeneID	RefSeq	Description	Sub-Pathway	Genotyping reference (see footnotes)	N SNPs	N PCs	% Variation from PC
<i>ACVR2B</i>	3	38,470,794	38.8	93	NM_001106.3	activin A receptor, type IIB	Induction	1	19	5	93.5%
<i>AGTR1</i>	3	149,898,348	45.1	185	NM_000685.4	angiotensin II receptor, type 1	Induction	1	35	8	90.7%
<i>CCL11</i>	17	29,636,800	2.5	6356	NM_002986.2	chemokine (C-C motif) ligand 11	Trafficking	1	14	6	95.4%
<i>CCL17</i>	16	55,996,180	11.3	6361	NM_002987.2	chemokine (C-C motif) ligand 17	Trafficking	1	9	6	97.9%
<i>CCL19</i>	9	34,679,567	1.7	6363	NM_006274.2	chemokine (C-C motif) ligand 19	Trafficking	1	9	3	95.7%
<i>CCL2</i>	17	29,606,409	1.9	6347	NM_002982.3	chemokine (C-C motif) ligand 2	Trafficking	1	12	5	93.2%
<i>CCL20</i>	2	228,386,814	3.7	6364	NM_004591.1	chemokine (C-C motif) ligand 20	Trafficking	1	3	2	96.1%
<i>CCL22</i>	16	55,950,219	7.4	6367	NM_002990.3	chemokine (C-C motif) ligand 22	Trafficking	1	9	3	95.0%
<i>CCL3</i>	17	31,439,715	1.9	6348	NM_002983.2	chemokine (C-C motif) ligand 3	Trafficking	1	9	3	95.2%
<i>CCL4</i>	17	31,455,333	1.8	6351	NM_002984.2	chemokine (C-C motif) ligand 4	Trafficking	1	8	5	97.8%
<i>CCL5</i>	17	31,222,608	8.9	6352	NM_002985.2	chemokine (C-C motif) ligand 5	Trafficking	1	4	2	93.9%
<i>CCR4</i>	3	32,968,070	3.3	1233	NM_005508.4	chemokine (C-C motif) receptor 4	Trafficking	1	4	2	94.4%
<i>CCR6</i>	6	167,445,285	27.3	1235	NM_004367.5	chemokine (C-C motif) receptor 6	Trafficking	1	39	13	91.3%
<i>CCR7</i>	17	35,963,547	11.7	1236	NM_001838.2	chemokine (C-C motif) receptor 7	Trafficking	1	8	7	95.7%
<i>CCR8</i>	3	39,346,219	4.9	1237	NM_005201.2	chemokine (C-C motif) receptor 8	Trafficking	1	4	3	99.0%

<i>CD274</i>	9	5,440,559	17.9	29126	NM_014143.2	CD274 molecule	Suppressive Function	1	29	9	91.8%
<i>CD28</i>	2	204,571,198	31.4	940	NM_006139.1	CD28 molecule	Induction	2	4	4	100.0%
<i>CD46</i>	1	205,992,025	43.5	4179	NM_002389.3	CD46 molecule, complement regulatory protein	Induction	1	17	6	94.4%
<i>CD80</i>	3	120,725,830	35.3	941	NM_005191.3	CD80 molecule	Induction	1	50	11	90.2%
<i>CD86</i>	3	123,256,911	65.8	942	NM_175862.3	CD86 molecule	Induction	1	42	11	90.6%
<i>CTLA4</i>	2	204,732,,509	6.2	1493	NM_005214.3	cytotoxic T-lymphocyte-associated protein 4	Induction	2	7	3	90.3%
<i>CXCL10</i>	4	77,161,295	2.4	3627	NM_001565.2	chemokine (C-X-C motif) ligand 10	Trafficking	1	8	5	99.8%
<i>CXCL13</i>	4	78,651,931	100.1	10563	NM_006419.1	chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	Trafficking	1	23	9	91.4%
<i>CXCR5</i>	11	118,259,777	12.4	643	NM_001716.2	chemokine (C-X-C motif) receptor 5	Trafficking	1	16	7	92.1%
<i>DUSP4</i>	8	29,249,530	14.6	1846	NM_001394.5	dual specificity phosphatase 4	ND	1	14	3	90.4%
<i>EGR2</i>	10	64,241,763	4.4	1959	NM_000399.2	early growth response 2 (Krox-20 homolog, Drosophila)	Suppressive Function	1	8	3	96.3%
<i>FOXP3</i>	X	49,106,897	14.4	50943	NM_014009.2	forkhead box P3	Suppressive Function	2	4	2	98.8%
<i>GPR83</i>	11	93,750,131	23.9	10888	NM_016540.2	G protein-coupled receptor 83	Induction	1	21	4	92.0%
<i>IDO1</i>	8	39,771,328	14.6	3620	NM_002164.4	indoleamine 2,3-dioxygenase 1	Induction	1 & 2	17	6	93.8%
<i>IKZF2</i>	2	213,572,653	151.9	22807	NM_001079526.1	IKAROS family zinc finger 2 (Helios)	ND	1	54	12	90.8%
<i>IKZF4</i>	12	54,700,956	17.5	64375	NM_022465.3	IKAROS family	Induction	1	5	3	99.2%

						zinc finger 4 (Eos)					
<i>IL10</i>	1	206,940,948	4.9	3586	NM_000572.2	interleukin 10	Induction	2	3	3	100.0%
<i>IL10RA</i>	11	117,857,106	15.1	3587	NM_001558.2	interleukin 10 receptor, alpha	Induction	2	15	3	93.1%
<i>IL10RB</i>	21	33,560,542	30.8	3588	NM_000628.3	interleukin 10 receptor, beta	Induction	1	26	8	91.3%
<i>IL15</i>	4	142,557,754	96.9	3600	NM_000585.2	interleukin 15	Induction	2	7	5	99.9%
<i>IL15RA</i>	10	6,034,340	25.8	3601	NM_172200.1	interleukin 15 receptor, alpha	Induction	1	32	9	91.2%
<i>IL17RA</i>	22	17,565,849	25.6	23765	NM_014339.4	interleukin 17 receptor A	ND	2	21	8	92.2%
<i>IL23A</i>	12	56,732,663	1.5	51561	NM_016584.2	interleukin 23, alpha subunit p19	ND	2	1	1	100.0%
<i>IL23R</i>	1	67,632,169	93.5	149233	NM_144701.2	interleukin 23 receptor	ND	2	59	7	92.8%
<i>IL2RA</i>	10	6,052,657	51.7	3559	NM_000417.1	interleukin 2 receptor, alpha	ND	2	54	10	90.9%
<i>IL2RB</i>	22	35,851,824	24.1	3560	NM_000878.2	interleukin 2 receptor, beta	Induction	1	33	11	91.1%
<i>IL6</i>	7	22,766,766	4.9	3569	NM_000600.2	interleukin 6 (interferon, beta 2)	Induction	2	1	1	100.0%
<i>IL6R</i>	1	154,377,669	62.5	3570	NM_000565.2	interleukin 6 receptor	Induction	2	32	4	91.5%
<i>IL6ST</i>	5	55,272,451	54.1	3572	NM_002184.2	interleukin 6 signal transducer (gp130, oncostatin M receptor)	Induction	1	8	3	91.7%
<i>IL8</i>	4	74,606,275	3.2	3576	NM_000584.2	interleukin 8	Trafficking	2	3	2	98.2%
<i>IL9</i>	5	135,255,834	3.6	3578	NM_000590.1	interleukin 9	Suppressive Function	1	11	5	92.3%
<i>INHBA</i>	7	41,695,126	14.1	3624	NM_002192.2	inhibin, beta A	Induction	1	9	4	92.5%
<i>INHBB</i>	2	120,820,189	5.7	3625	NM_002193.2	inhibin, beta B	Induction	1	12	7	94.1%
<i>IRF4</i>	6	336,760	19.4	3662	NM_002460.1	interferon regulatory factor 4	ND	1	23	7	91.1%
<i>ITGAE</i>	17	3,564,668	86.6	3682	NM_002208.4	integrin, alpha E	Trafficking	1	60	18	90.8%

						(antigen CD103)					
<i>KLF10</i>	8	103,730,188	6.9	7071	NM_005655.1	Kruppel-like factor 10	Induction	1	13	6	92.7%
<i>LAG3</i>	12	6,751,931	5.9	3902	NM_002286.4	lymphocyte-activation gene 3	Suppressive Function	1	10	6	93.5%
<i>LGALS1</i>	22	38,071,613	4.2	3956	NM_002305.3	lectin, galactoside-binding, soluble, 1	ND	2	3	1	92.6%
<i>LGALS9</i>	17	25,958,174	18.4	3965	NM_002308.3	lectin, galactoside-binding, soluble, 9	ND	2	11	2	92.5%
<i>LRRC32</i>	11	76,046,222	12.3	2615	NM_005512.1	leucine rich repeat containing 32	Suppressive Function	1	32	8	90.2%
<i>MAP3K8</i>	10	30,722,866	27.9	1326	NM_005204.2	mitogen-activated protein kinase kinase kinase 8	ND	2	6	2	94.3%
<i>MDFIC</i>	7	114,349,445	97.1	29969	NM_199072.3	MyoD family inhibitor domain containing	ND	1	45	10	90.5%
<i>NRP1</i>	10	33,506,432	157.4	8829	NM_003873.4	neuropilin 1	Suppressive Function	1	141	22	90.2%
<i>PDCD1</i>	2	242,440,711	9	5133	NM_005018.1	programmed cell death 1	Suppressive Function	1	9	4	95.9%
<i>PLAGL1</i>	6	144,303,130	124.3	5325	NM_001080951.1	pleiomorphic adenoma gene-like 1	ND	1	79	16	90.0%
<i>PRNP</i>	20	4,614,797	15.4	5621	NM_000311.3	prion protein (p27-30)	ND	1	19	7	92.8%
<i>RGS1</i>	1	190,811,480	4.3	5996	NM_002922.3	regulator of G-protein signaling 1	Trafficking	1	13	7	93.6%
<i>RGS16</i>	1	180,834,381	5.8	6004	NM_002928.3	regulator of G-protein signaling 16	ND	1	8	5	92.3%
<i>SH3BGRL2</i>	6	80,397,719	72.4	83699	NM_031469.2	SH3 domain binding glutamic acid-rich protein like 2	ND	1	42	9	91.4%
<i>SLC22A2</i>	6	160,557,780	42.2	6582	NM_003058.2	solute carrier	ND	1	27	7	92.4%

						family 22 (organic cation transporter), member 2					
<i>SMAD3</i>	15	65,145,249	129.3	4088	NM_005902.3	SMAD family member 3	Induction	1	95	22	90.2%
<i>SOCS2</i>	12	92,487,729	6.4	8835	NM_003877.3	suppressor of cytokine signaling 2	ND	1	8	3	96.3%
<i>STAT5A</i>	17	40,439,565	24.4	6776	NM_003152.2	signal transducer and activator of transcription 5A	ND	2	7	2	99.7%
<i>STAT5B</i>	17	40,351,195	77.2	6777	NM_012448.3	signal transducer and activator of transcription 5B	ND	2	16	3	93.7%
<i>TGFB1</i>	19	41,836,812	23	7040	NM_000660.3	transforming growth factor, beta 1	Induction	2	5	4	94.1%
<i>TGFB2</i>	1	218,519,391	98.6	7042	NM_003238.1	transforming growth factor, beta 2	Induction	2	57	9	91.4%
<i>TGFB3</i>	14	76,424,442	23.7	7043	NM_003239.1	transforming growth factor, beta 3	Induction	2	18	3	94.8%
<i>TGFBR1</i>	9	101,867,412	49.1	7046	NM_004612.2	transforming growth factor, beta receptor 1	Induction	2	39	4	93.4%
<i>TGFBR2</i>	3	30,647,994	87.6	7048	NM_003242.5	transforming growth factor, beta receptor II (70/80kDa)	Induction	2	112	15	90.8%
<i>TGFBR3</i>	1	92,145,900	205.9	7049	NM_003243.2	transforming growth factor, beta receptor III	Induction	2	255	14	90.2%
<i>TNFRSF18</i>	1	1,128,751	3.2	8784	NM_004195.2	tumor necrosis factor receptor superfamily,	Suppressive Function	1	5	3	94.4%

						member 18					
<i>TNFRSF4</i>	1	1,136,569	2.8	7293	NM_003327.2	tumor necrosis factor receptor superfamily, member 4	Suppressive Function	1	4	3	94.4%
<i>TNFRSF9</i>	1	7,902,494	21	3604	NM_001561.4	tumor necrosis factor receptor superfamily, member 9	Suppressive Function	1	8	5	94.3%

1. Goode EL, Derycke M, Kalli KR, Oberg AL, Cunningham JM, Maurer MJ, et al. Inherited variants in regulatory T cell genes and outcome of ovarian cancer. *PLoS One*. 2013;8:e53903. 2. Charbonneau B, Moysich KB, Kalli KR, Oberg AL, Vierkant RA, Fogarty ZC, et al. Large-scale evaluation of common variation in regulatory T cell-related genes and ovarian cancer outcome. *Cancer Immunol Res*. 2014;2:332-40, ND=Not determined

**Supplemental Table S2: PC analysis p values examining gene level variation with T cell, Treg infiltration and accompanying ratios**

Gene	CD8 <sup>+</sup>	CD4 <sup>+</sup>	CD4 <sup>+</sup> CD25 <sup>+</sup> FOXP3 <sup>+</sup>	CD8 <sup>+</sup> / CD4 <sup>+</sup>	CD8 <sup>+</sup> / CD4 <sup>+</sup> CD25 <sup>+</sup> FOXP3 <sup>+</sup>	CD4 <sup>+</sup> / CD4 <sup>+</sup> CD25 <sup>+</sup> FOXP3 <sup>+</sup>
<i>ACVR2B</i>	0.906	0.958	0.595	0.809	0.950	0.455
<i>AGTR1</i>	0.731	0.224	0.067	0.439	0.591	0.362
<i>CCL11</i>	0.0086	0.033	0.143	0.206	0.706	0.940
<i>CCL17</i>	0.194	0.761	0.665	0.093	0.528	0.140
<i>CCL19</i>	0.028	0.052	0.755	0.520	0.048	0.113
<i>CCL2</i>	0.038	0.042	0.109	0.356	0.902	0.982
<i>CCL20</i>	0.277	0.120	0.612	0.238	0.996	0.641
<i>CCL22</i>	0.679	0.779	0.499	0.0058	0.765	0.772
<i>CCL3</i>	0.367	0.704	0.555	0.997	0.011	0.039
<i>CCL4</i>	0.674	0.789	0.689	0.997	0.094	0.033
<i>CCL5</i>	0.050	0.365	0.704	0.602	0.085	0.202
<i>CCR4</i>	0.366	0.500	0.299	0.159	0.203	0.737
<i>CCR6</i>	0.334	0.602	0.944	0.889	0.552	0.301
<i>CCR7</i>	0.878	0.989	0.818	0.776	0.996	0.490
<i>CCR8</i>	0.528	0.090	0.564	0.486	0.537	0.847
<i>CD274</i>	0.387	0.827	0.172	0.838	0.232	0.500
<i>CD28</i>	0.134	0.029	0.509	0.828	0.895	0.103
<i>CD46</i>	0.222	0.342	0.508	0.534	0.034	0.095
<i>CD80</i>	0.114	0.174	0.720	0.154	0.486	0.915
<i>CD86</i>	0.700	0.189	0.876	0.251	0.686	0.510
<i>CTLA4</i>	0.671	0.614	0.576	0.786	0.293	0.487
<i>CXCL10</i>	0.042	0.376	0.829	0.061	0.549	0.322
<i>CXCL13</i>	0.404	0.261	0.929	0.734	0.562	0.705
<i>CXCR5</i>	0.885	0.308	0.121	0.201	0.266	0.834
<i>DUSP4</i>	0.231	0.070	0.205	0.476	0.754	0.770
<i>EGR2</i>	0.821	0.347	0.146	0.423	0.422	0.063
<i>FOXP3</i>	0.312	0.968	0.277	0.193	0.227	0.422
<i>GPR83</i>	0.598	0.590	0.633	0.877	0.732	0.586

<i>IDO1</i>	0.040	0.025	0.893	0.896	0.306	0.067
<i>IKZF2</i>	0.990	0.422	0.538	0.897	0.704	0.859
<i>IKZF4</i>	0.350	0.731	0.650	0.779	0.825	0.649
<i>IL10</i>	0.589	0.112	0.203	0.381	0.0073	0.010
<i>IL10RA</i>	0.373	0.327	0.621	0.360	0.533	0.812
<i>IL10RB</i>	0.405	0.706	0.998	0.403	0.664	0.474
<i>IL15</i>	0.529	0.586	0.299	0.346	0.364	0.946
<i>IL15RA</i>	0.352	0.403	0.021	0.882	0.075	0.319
<i>IL17RA</i>	0.771	0.944	0.635	0.126	0.483	0.895
<i>IL23A</i>	0.804	0.457	0.571	0.790	0.745	0.878
<i>IL23R</i>	0.679	0.775	0.440	0.011	0.090	0.481
<i>IL2RA</i>	0.842	0.399	0.570	0.416	0.549	0.833
<i>IL2RB</i>	0.244	0.073	0.860	0.158	0.945	0.841
<i>IL6</i>	0.366	0.126	0.395	0.467	0.791	0.546
<i>IL6R</i>	0.114	0.105	0.887	0.128	0.252	0.260
<i>IL6ST</i>	0.348	0.621	0.023	0.419	0.214	0.300
<i>IL8</i>	0.773	0.063	0.661	0.694	0.695	0.017
<i>IL9</i>	0.185	0.899	0.447	0.665	0.913	0.993
<i>INHBA</i>	0.091	0.209	0.496	0.219	0.057	0.312
<i>INHBB</i>	0.221	0.511	0.471	0.510	0.231	0.424
<i>IRF4</i>	0.257	0.676	0.680	0.994	0.312	0.093
<i>ITGAE</i>	0.862	0.929	0.709	0.382	0.297	0.179
<i>KLF10</i>	0.716	0.604	0.778	0.957	0.338	0.265
<i>LAG3</i>	0.933	0.799	0.905	0.480	0.964	0.913
<i>LGALS1</i>	0.095	0.694	0.561	0.098	0.240	0.931
<i>LGALS9</i>	0.136	0.199	0.733	0.902	0.886	0.747
<i>LRRC32</i>	0.016	0.742	0.995	0.332	0.111	0.838
<i>MAP3K8</i>	0.766	0.726	0.810	0.845	0.723	0.836
<i>MDFIC</i>	0.438	0.051	0.794	0.957	0.062	0.039
<i>NRP1</i>	0.820	0.916	0.446	0.152	0.214	0.631
<i>PDCD1</i>	0.821	0.683	0.968	0.540	0.484	0.352
<i>PLAGL1</i>	0.386	0.970	0.497	0.320	0.480	0.624

<i>PRNP</i>	0.575	0.908	0.577	0.628	0.590	0.091
<i>RGS1</i>	0.796	0.922	0.975	0.810	0.502	0.501
<i>RGS16</i>	0.456	0.914	0.441	0.825	0.374	0.289
<i>SH3BGRL2</i>	0.620	0.555	0.743	0.265	0.723	0.914
<i>SLC22A2</i>	0.036	0.267	0.844	0.915	0.302	0.170
<i>SMAD3</i>	0.428	0.733	0.837	0.479	0.608	0.803
<i>SOCS2</i>	0.504	0.738	0.671	0.563	0.706	0.943
<i>STAT5A</i>	0.443	0.630	0.279	0.914	0.282	0.628
<i>STAT5B</i>	0.688	0.230	0.493	0.720	0.566	0.618
<i>TGFB1</i>	0.535	0.140	0.759	0.544	0.831	0.656
<i>TGFB2</i>	0.581	0.904	0.184	0.831	0.666	0.255
<i>TGFB3</i>	0.516	0.947	0.349	0.966	0.774	0.379
<i>TGFBR1</i>	0.107	0.317	0.365	0.429	0.846	0.904
<i>TGFBR2</i>	0.890	0.332	0.134	0.678	0.391	0.184
<i>TGFBR3</i>	0.843	0.667	0.127	0.200	0.275	0.176
<i>TNFRSF18</i>	0.527	0.452	0.864	0.068	0.787	0.337
<i>TNFRSF4</i>	0.485	0.139	0.416	0.670	0.400	0.083
<i>TNFRSF9</i>	0.425	0.197	0.339	0.098	0.962	0.746