Supplementary Table 1. Protein coding genes located in 1 Mb windows across each of the 14 AA GWAS loci. A list of the single most signficant SNPs at each of the 14 GWAS loci (Table 1) was uploaded to Biomart in Ensembl to identify 225 protein coding SNPs, listed here. For three of the genes (SOWAHA, TEX40, PMEL), alternative gene names are sometimes used in public databases. Therefore, these alternative names were included in the uploaded gene list (rows 230-233), in addition to the official gene name. Gene positions are from build Hg38. Columns A-F(black header) list information retrieved from BIOMART. Columns G-K (gray header) report summary of results from this study. Indirect indicates that the protein is connected to the network by an intermediary protein (i.e. a protein not at an AA GWAS loci). Direct indicates that there is evidence the protein directly interacts with a protein from another AA GWAS loci.

GWAS Locus	Gene Name	Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	DAVID recognized (1=yes)	Count of DAVID Pathways	Count of DAVID GO terms	DAPPLE results	Count of Analyses with positive results
1p13.2	MAGI3	ENSG00000081026	1	113390749	113685923	1			indirect	1
1p13.2	PHTF1	ENSG00000116793	1	113696831	113759489	1				0
1p13.2	RSBN1	ENSG00000081019	1	113761832	113812476	1			direct	1
1p13.2	PTPN22	ENSG00000134242	1	113813811	113871759	1		11	indirect	2
1p13.2	BCL2L15	ENSG00000188761	1	113878168	113887547	1				0
1p13.2	AP4B1	ENSG00000134262	1	113894748	113905201	1			direct	1
1p13.2	DCLRE1B	ENSG00000118655	1	113905141	113914086	1			indirect	1
1p13.2	HIPK1	ENSG00000163349	1	113929192	113977804	1		2	indirect	2
1p13.2	OLFML3	ENSG00000116774	1	113979391	113982254	1			indirect	1
1p13.2	SYT6	ENSG00000134207	1	114089291	114153919	1		1	indirect	2
2q13	AC108938.5	ENSG00000257207	2	110402934	110473075	0				0
2q13	LIMS3L	ENSG00000256671	2	110465051	110472934	0				0
2q13	RGPD6	ENSG00000183054	2	110513812	110577185	1			indirect	1
2q13	BUB1	ENSG00000169679	2	110637698	110678114	1		1	direct	2
2q13	ACOXL	ENSG00000153093	2	110732573	111118222	1				0
2q13	BCL2L11	ENSG00000153094	2	111119378	111168447	1		5	indirect	2
2q33.2	ABI2	ENSG00000138443	2	203328219	203447723	1			direct	1
2q33.2	RAPH1	ENSG00000173166	2	203394345	203535410	1			indirect	1
2q33.2	CD28	ENSG00000178562	2	203706475	203738912	1	15	39	indirect	3
2q33.2	CTLA4	ENSG00000163599	2	203867786	203873960	1	4	13	indirect	3
2q33.2	ICOS	ENSG00000163600	2	203936748	203961577	1	5	1		2
4q27	KIAA1109	ENSG00000138688	4	122152333	122362758	1			indirect	1
4q27	ADAD1	ENSG00000164113	4	122378966	122429802	1		6		1
4q27	IL2	ENSG00000109471	4	122451470	122456725	1	15	64	direct	3
4q27	IL21	ENSG00000138684	4	122612628	122621069	1	1	31	direct	3
4q27	BBS12	ENSG00000181004	4	122732702	122744943	1				0
4q27	FGF2	ENSG00000138685	4	122826708	122898236	1		15	indirect	2
4q27	NUDT6	ENSG00000170917	4	122888697	122922968	1			indirect	1
4q27	SPATA5	ENSG00000145375	4	122923074	123319450	1		2	indirect	2
5q31.1	P4HA2	ENSG00000072682	5	132191838	132295315	1			indirect	1
5q31.1	PDLIM4	ENSG00000131435	5	132257671	132273454	1			indirect	1
5q31.1	SLC22A4	ENSG00000197208	5	132294443	132344206	1			indirect	1
5q31.1	SLC22A5	ENSG00000197375	5	132369752	132395614	1			indirect	1
5q31.1	C5orf56	ENSG00000197536	5	132410636	132476044	1				0
5q31.1	IRF1	ENSG00000125347	5	132481609	132490798	1		18	indirect	2

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5q31.1	IL5	ENSG00000113525	5	132541444	132556838	1	14	34	direct	3
5q31.1	RAD50	ENSG00000113522	5	132556019	132646344	1		2	indirect	2
5q31.1	IL13	ENSG00000169194	5	132656263	132661110	1	5	23	direct	3
5q31.1	IL4	ENSG00000113520	5	132673986	132682676	1	16	53	direct	3
5q31.1	KIF3A	ENSG00000131437	5	132692628	132737638	1			indirect	1
5q31.1	CCNI2	ENSG00000205089	5	132747445	132754403	1				0
5q31.1	SEPT8	ENSG00000164402	5	132750817	132807241	1			indirect	1
5q31.1	SOWAHA	ENSG00000198944	5	132813587	132816797	0				0
5q31.1	SHROOM1	ENSG00000164403	5	132822141	132830898	1			direct	1
5q31.1	GDF9	ENSG00000164404	5	132861181	132866884	1		3	indirect	2
5q31.1	UQCRQ	ENSG00000164405	5	132866560	132868031	1			indirect	1
5q31.1	LEAP2	ENSG00000164406	5	132872322	132875046	1				0
5q31.1	AFF4	ENSG00000072364	5	132875379	132963634	1		6	indirect	2
5q31.1	ZCCHC10	ENSG00000155329	5	132996985	133026604	1			indirect	1
5q31.1	HSPA4	ENSG00000170606	5	133051962	133106449	1	1		direct	2
6p21.32	NOTCH4	ENSG00000204301	6	32194843	32224067	1		12	indirect	2
6p21.32	C6orf10	ENSG00000204296	6	32288526	32371912	1				0
6p21.32	BTNL2	ENSG00000204290	6	32393963	32407128	1				0
6p21.32	HLA-DRA	ENSG00000204287	6	32439842	32445046	1	19	9	direct	3
6p21.32	HLA-DRB5	ENSG00000198502	6	32517343	32530287	1	11	3	direct	3
6p21.32	HLA-DRB1	ENSG00000196126	6	32552990	32589848	1	19	3	direct	3
6p21.32	HLA-DQA1	ENSG00000196735	6	32628179	32647062	1	10	3	direct	3
6p21.32	HLA-DQB1	ENSG00000179344	6	32659467	32668383	1	10	3	direct	3
6p21.32	HLA-DQA2	ENSG00000237541	6	32741342	32747215	1	10	3	direct	3
6p21.32	HLA-DQB2	ENSG00000232629	6	32756098	32763534	1				0
6p21.32	HLA-DOB	ENSG00000241106	6	32812763	32817048	1	10	3	direct	3
6p21.32	TAP2	ENSG00000250264	6	32813767	32838822	1	3	9	direct	3
6p21.32	PSMB8	ENSG00000204264	6	32840717	32844703	1		8	direct	2
6p21.32	PSMB9	ENSG00000240065	6	32844136	32859585	1		8		1
6p21.32	TAP1	ENSG00000168394	6	32845209	32853978	1	3	1	direct	3
6p21.32	HLA-DMB	ENSG00000242574	6	32934629	32941070	1	10	3	direct	3
6p21.32	XXbac-BPG181M17.5	ENSG00000248993	6	32937364	32953122	0				0
6p21.32	HLA-DMA	ENSG00000204257	6	32948613	32969094	1	10	33	direct	3
6p21.32	BRD2	ENSG00000204256	6	32968660	32981505	1		2	indirect	2
6p21.32	HLA-DOA	ENSG00000204252	6	33004178	33009612	1	10	14	direct	3
6p21.32	HLA-DPA1	ENSG00000231389	6	33064569	33080775	1	10	3		2
6p21.32	HLA-DPB1	ENSG00000223865	6	33075926	33087201	1	10	3	indirect	3
6p21.32	COL11A2	ENSG00000204248	6	33162681	33192499	1			indirect	1
6p21.32	RXRB	ENSG00000204231	6	33193588	33200688	1		7	indirect	2
6p21.32	SLC39A7	ENSG00000112473	6	33200445	33204439	1			indirect	1
6p21.32	HSD17B8	ENSG00000204228	6	33204642	33206831	1				0

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6q25.1	PPIL4	ENSG00000131013	6	149504733	149546038	1		1	indirect	2
6q25.1	GINM1	ENSG00000055211	6	149566294	149591748	0				0
6q25.1	KATNA1	ENSG00000186625	6	149594873	149648972	1		1	indirect	2
6q25.1	LATS1	ENSG00000131023	6	149658153	149718256	1		1	indirect	2
6q25.1	AL358852.1	ENSG00000278899	6	149717621	149718888	0				0
6q25.1	NUP43	ENSG00000120253	6	149724315	149749665	1		1	indirect	2
6q25.1	PCMT1	ENSG00000120265	6	149749443	149811420	1			indirect	1
6q25.1	LRP11	ENSG00000120256	6	149818798	149864026	1			indirect	1
6q25.1	RAET1E	ENSG00000164520	6	149883375	149898102	1		2	indirect	2
6q25.1	RAET1G	ENSG00000203722	6	149916878	149923121	1		2	direct	2
6q25.1	ULBP2	ENSG00000131015	6	149942000	149949235	1		6	indirect	2
6q25.1	ULBP1	ENSG00000111981	6	149964007	149973710	1		6	direct	2
6q25.1	RAET1L	ENSG00000155918	6	150018334	150025532	1		2		1
6q25.1	ULBP3	ENSG00000131019	6	150063150	150069095	1		6	indirect	2
6q25.1	PPP1R14C	ENSG00000198729	6	150143076	150250357	1				0
6q25.1	IYD	ENSG00000009765	6	150368892	150405969	1				0
9q31.1	NR4A3	ENSG00000119508	9	99821855	99866891	1		7	indirect	2
9q31.1	STX17	ENSG00000136874	9	99906633	99970341	1				0
9q31.1	ERP44	ENSG00000023318	9	99979179	100099040	1		1	direct	2
9q31.1	INVS	ENSG00000119509	9	100099256	100301000	1			indirect	1
9q31.1	TEX10	ENSG00000136891	9	100302077	100352939	1			indirect	1
10p15.1	ASB13	ENSG00000196372	10	5638867	5666595	1			indirect	1
10p15.1	FAM208B	ENSG00000108021	10	5684838	5763740	0				0
10p15.1	GDI2	ENSG00000057608	10	5765223	5842132	1			indirect	1
10p15.1	ANKRD16	ENSG00000134461	10	5861617	5889906	1				0
10p15.1	FBXO18	ENSG00000134452	10	5890203	5937594	1			indirect	1
10p15.1	IL15RA	ENSG00000134470	10	5937569	5978187	1	2		direct	2
10p15.1	IL2RA	ENSG00000134460	10	6010689	6062325	1	4	29	direct	3
10p15.1	RBM17	ENSG00000134453	10	6088987	6117457	1			direct	1
10p15.1	PFKFB3	ENSG00000170525	10	6144934	6235545	1			indirect	1
10p15.1	PRKCQ	ENSG00000065675	10	6427143	6580301	1	1	25	indirect	3
11q13	MARK2	ENSG00000072518	11	63838928	63911019	1			indirect	1
11q13	RCOR2	ENSG00000167771	11	63911221	63916844	1			indirect	1
11q13	NAA40	ENSG00000110583	11	63938959	63957328	1				0
11q13	COX8A	ENSG00000176340	11	63974607	63976543	1				0
11q13	AP000721.4	ENSG00000256100	11	63974620	63988346	0				0
11q13	OTUB1	ENSG00000167770	11	63985853	64001811	1		1	indirect	2
11q13	MACROD1	ENSG00000133315	11	63998558	64166106	1				0
11q13	FLRT1	ENSG00000126500	11	64103188	64119173	1				0
11q13	STIP1	ENSG00000168439	11	64185272	64204543	1			direct	1
11q13	FERMT3	ENSG00000149781	11	64206678	64223886	1				0

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11q13	TRPT1	ENSG00000149743	11	64223799	64226254	1			indirect	1
11q13	NUDT22	ENSG00000149761	11	64225941	64230686	1				0
11q13	DNAJC4	ENSG00000110011	11	64230278	64234286	1		1		1
11q13	VEGFB	ENSG00000173511	11	64234538	64238793	1		3	indirect	2
11q13	FKBP2	ENSG00000173486	11	64241003	64244132	1		1	indirect	2
11q13	PPP1R14B	ENSG00000173457	11	64244480	64246941	1			indirect	1
11q13	PLCB3	ENSG00000149782	11	64251523	64269150	1			indirect	1
11q13	BAD	ENSG00000002330	11	64269830	64284704	1		16	indirect	2
11q13	GPR137	ENSG00000173264	11	64270062	64289500	1				0
11q13	KCNK4	ENSG00000182450	11	64291302	64300031	1				0
11q13	TEX40	ENSG00000219435	11	64300446	64304770	0				0
11q13	ESRRA	ENSG00000173153	11	64305572	64316743	1		8	indirect	2
11q13	TRMT112	ENSG00000173113	11	64316460	64318084	1				0
11q13	PRDX5	ENSG00000126432	11	64318088	64321811	1			indirect	1
11q13	CCDC88B	ENSG00000168071	11	64340223	64357534	1			indirect	1
11q13	RPS6KA4	ENSG00000162302	11	64359148	64372215	1			indirect	1
11q13	SLC22A11	ENSG00000168065	11	64555626	64572875	1			indirect	1
11q13	SLC22A12	ENSG00000197891	11	64590641	64602353	1			indirect	1
11q13	NRXN2	ENSG00000110076	11	64606174	64723188	1	1		indirect	2
11q13	RASGRP2	ENSG00000068831	11	64726911	64745456	1		1	indirect	2
11q13	PYGM	ENSG00000068976	11	64746389	64760297	1			indirect	1
11q13	SF1	ENSG00000168066	11	64764606	64778786	1		3	direct	2
11q13	MAP4K2	ENSG00000168067	11	64788818	64803241	1		1	indirect	2
11q13	MEN1	ENSG00000133895	11	64803510	64811294	1		19	indirect	2
11q13	CDC42BPG	ENSG00000171219	11	64823387	64844569	1			direct	1
11q13.5	UVRAG	ENSG00000198382	11	75815167	76143195	1				0
11q13.5	WNT11	ENSG00000085741	11	76186325	76210736	1			indirect	1
11q13.5	PRKRIR	ENSG00000137492	11	76349956	76380971	1		1	indirect	2
11q13.5	RP11-111M22.2	ENSG00000179240	11	76381313	76414619	0				0
11q13.5	C11orf30	ENSG00000158636	11	76444923	76553025	1			indirect	1
11q13.5	LRRC32	ENSG00000137507	11	76657524	76670747	1				0
11q13.5	TSKU	ENSG00000182704	11	76782251	76798154	1			indirect	1
11q13.5	ACER3	ENSG00000078124	11	76860867	77026797	1				0
11q13.5	B3GNT6	ENSG00000198488	11	77034398	77041973	1				0
11q13.5	CAPN5	ENSG00000149260	11	77066932	77126155	1			indirect	1
12q13	OR10P1	ENSG00000175398	12	55636860	55637854	1				0
12q13	METTL7B	ENSG00000170439	12	55681546	55684611	1				0
12q13	ITGA7	ENSG00000135424	12	55684568	55716043	1			indirect	1
12q13	RP11-644F5.10	ENSG00000258311	12	55716036	55724703	0				0
12q13	BLOC1S1	ENSG00000135441	12	55716037	55720087	1			indirect	1
12q13	RDH5	ENSG00000135437	12	55720367	55724705	1				0

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12q13	CD63	ENSG00000135404	12	55725323	55729707	1			direct	1
12q13	GDF11	ENSG00000135414	12	55743280	55757278	1		1	indirect	2
12q13	SARNP	ENSG00000205323	12	55752463	55817756	1		1	indirect	2
12q13	RP11-762I7.5	ENSG00000257390	12	55757275	55827546	0				0
12q13	ORMDL2	ENSG00000123353	12	55817919	55821879	1				0
12q13	DNAJC14	ENSG00000135392	12	55820960	55830824	1		1	indirect	2
12q13	MMP19	ENSG00000123342	12	55835433	55842966	1				0
12q13	WIBG	ENSG00000170473	12	55901413	55932618	1		7		1
12q13	DGKA	ENSG00000065357	12	55927319	55954027	1			indirect	1
12q13	PMEL	ENSG00000185664	12	55954105	55973317	0				0
12q13	CDK2	ENSG00000123374	12	55966769	55972784	1		8	direct	2
12q13	RAB5B	ENSG00000111540	12	55973913	55996683	1			indirect	1
12q13	SUOX	ENSG00000139531	12	55997180	56006641	1				0
12q13	IKZF4	ENSG00000123411	12	56007659	56038435	1			indirect	1
12q13	RPS26	ENSG00000197728	12	56041853	56044675	1			indirect	1
12q13	ERBB3	ENSG00000065361	12	56079857	56103505	1		1	direct	2
12q13	RP11-603J24.9	ENSG00000257411	12	56101331	56109289	0				0
12q13	PA2G4	ENSG00000170515	12	56104319	56113907	1		2	direct	2
12q13	RPL41	ENSG00000229117	12	56116586	56117943	1				0
12q13	ZC3H10	ENSG00000135482	12	56118159	56127514	1			indirect	1
12q13	ESYT1	ENSG00000139641	12	56118250	56144671	1				0
12q13	MYL6B	ENSG00000196465	12	56152256	56159647	1			indirect	1
12q13	MYL6	ENSG00000092841	12	56158161	56163496	1			indirect	1
12q13	SMARCC2	ENSG00000139613	12	56162983	56189567	1		7	direct	2
12q13	RNF41	ENSG00000181852	12	56202175	56221933	1			direct	1
12q13	NABP2	ENSG00000139579	12	56222015	56229854	0				0
12q13	SLC39A5	ENSG00000139540	12	56230049	56237846	1				0
12q13	ANKRD52	ENSG00000139645	12	56237807	56258391	1				0
12q13	COQ10A	ENSG00000135469	12	56266858	56270966	1			indirect	1
12q13	CS	ENSG00000062485	12	56271699	56300392	1			indirect	1
12q13	RP11-977G19.10	ENSG00000144785	12	56285916	56316059	0				0
12q13	CNPY2	ENSG00000257727	12	56309842	56316336	1			indirect	1
12q13	PAN2	ENSG00000135473	12	56316223	56334053	1			direct	1
12q13	IL23A	ENSG00000110944	12	56334174	56340410	1	1	5	direct	3
12q13	STAT2	ENSG00000170581	12	56341597	56360155	1	1		direct	2
12q13	APOF	ENSG00000175336	12	56360569	56362823	1			indirect	1
12q13	TIMELESS	ENSG00000111602	12	56416373	56449403	1		2	indirect	2
12q13	MIP	ENSG00000135517	12	56449502	56469166	1			indirect	1
12q13	SPRYD4	ENSG00000176422	12	56468567	56479707	1			indirect	1
12q13	GLS2	ENSG00000135423	12	56470944	56488414	1			indirect	1
12q13	RBMS2	ENSG00000076067	12	56521929	56596196	1				0

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12q24.12	CUX2	ENSG00000111249	12	111034024	111350554	1			indirect	1
12q24.12	FAM109A	ENSG00000198324	12	111360651	111369121	1			direct	1
12q24.12	SH2B3	ENSG00000111252	12	111405948	111451623	1		3	direct	2
12q24.12	ATXN2	ENSG00000204842	12	111452214	111599676	1		2	direct	2
12q24.12	BRAP	ENSG00000089234	12	111642146	111685986	1			indirect	1
12q24.12	ACAD10	ENSG00000111271	12	111686056	111757107	1				0
12q24.12	RP11-162P23.2	ENSG00000257767	12	111753890	111791418	0				0
12q24.12	ALDH2	ENSG00000111275	12	111766887	111809985	1			indirect	1
12q24.12	MAPKAPK5	ENSG00000089022	12	111841978	111896539	1			indirect	1
12q24.12	TMEM116	ENSG00000198270	12	111931282	112013185	1				0
12q24.12	ERP29	ENSG00000089248	12	112013316	112023451	1		1	indirect	2
12q24.12	NAA25	ENSG00000111300	12	112026689	112109022	1				0
16p13.13	TEKT5	ENSG00000153060	16	10627501	10694945	1				0
16p13.13	NUBP1	ENSG00000103274	16	10743786	10769351	1				0
16p13.13	TVP23A	ENSG00000166676	16	10760919	10818794	0				0
16p13.13	CIITA	ENSG00000179583	16	10877198	10932281	1	2	8	indirect	3
16p13.13	DEXI	ENSG00000182108	16	10928891	10942460	1				0
16p13.13	CLEC16A	ENSG00000038532	16	10944488	11182189	1				0
16p13.13	RMI2	ENSG00000175643	16	11249619	11351762	0				0
16p13.13	SOCS1	ENSG00000185338	16	11254405	11256179	1	1	4	direct	3
16p13.13	TNP2	ENSG00000178279	16	11267748	11269533	1		3		1
16p13.13	PRM3	ENSG00000178257	16	11273218	11273641	1		3		1
16p13.13	PRM2	ENSG00000122304	16	11275639	11276480	1		7		1
16p13.13	PRM1	ENSG00000175646	16	11280836	11281350	1		8		1
16p13.13	CTD-3088G3.8	ENSG00000188897	16	11359845	11523588	0				0
16p13.13	LITAF	ENSG00000189067	16	11547722	11636381	1			indirect	1
5q31.1	ANKRD43	alt SOWAHA	5	132813587	132816797	1				0
11q13	TRAAK	alt TEX40	11	64300446	64304770	0				0
12q13	SILV	alt PMEL	12	55954105	55973317	1				0

Supplementary Table 2. Pathways that are significantly enriched by genes in AA GWAS loci (p<0.05). Protein-coding genes located at GWAS loci were uploaded to the Database for Annotation, Visualization and Integrated Discovery (DAVID). Pathway analysis in the on-line computer program identified 27 pathways in Biocarta and KEGG that are enriched with AA GWAS genes. This evidence is being driven by 31 genes from eight loci.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa04672:Intestinal immune network for IgA production	18	8.70	3.89E-19	HLA-DQB1, IL4, IL5, HLA-DRB1, HLA-DMB, HLA-DQA2, HLA-DMA, HLA-DQA1, ICOS, HLA-DRB5, IL15RA, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, IL2, HLA-DRA	85	49	5085	21.97599	4.36E-17	4.36E-17	4.41E-16
KEGG_PATHWAY	hsa05330:Allograft rejection	16	7.73	2.10E-18	HLA-DQB1, IL4, IL5, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, HLA-DRA, IL2	85	36	5085	26.588235	2.35E-16	1.18E-16	2.38E-15
KEGG_PATHWAY	hsa05310:Asthma	15	7.25	2.29E-18	HLA-DQB1, IL4, IL5, HLA-DRB1, IL13, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA	85	29	5085	30.943205	2.57E-16	8.57E-17	2.60E-15
KEGG_PATHWAY	hsa05320:Autoimmune thyroid disease	17	8.21	3.06E-17	HLA-DQB1, IL4, IL5, HLA-DRB1, CTLA4, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, IL2, HLA-DRA	85	51	5085	19.941176	3.42E-15	8.56E-16	3.47E-14
KEGG_PATHWAY	hsa05332:Graft-versus-host disease	14	6.76	1.51E-14	HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA, IL2, CD28	85	39	5085	21.475113	1.69E-12	3.38E-13	1.71E-11
KEGG_PATHWAY	hsa04940:Type I diabetes mellitus	14	6.76	4.54E-14	HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA, IL2, CD28	85	42	5085	19.941176	5.09E-12	8.48E-13	5.15E-11
KEGG_PATHWAY	hsa04612:Antigen processing and presentation	16	7.73	2.55E-12	CIITA, HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, TAP2, TAP1, HLA-DRB5, HSPA4, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA	85	83	5085	11.532247	2.85E-10	4.07E-11	2.89E-09

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa05416:Viral myocarditis	13	6.28	1.08E-09	HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, HLA-DRA	85	71	5085	10.953604	1.21E-07	1.51E-08	1.22E-06
KEGG_PATHWAY	hsa04514:Cell adhesion molecules (CAMs)	16	7.73	2.38E-09	HLA-DQB1, NRXN2, HLA-DRB1, CTLA4, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, ICOS, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, HLA-DRA	85	132	5085	7.2513369	2.67E-07	2.97E-08	2.70E-06
KEGG_PATHWAY	hsa05322:Systemic lupus erythematosus	13	6.28	5.36E-08	HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, HLA-DQA1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, HLA-DRA	85	99	5085	7.855615	6.00E-06	6.00E-07	6.07E-05
BIOCARTA	h_ctla4Pathway:The Co-Stimulatory Signal During T-cell Activation	6	2.90	1.27E-05	HLA-DRB1, ICOS, CTLA4, HLA-DRA, CD28, IL2	27	19	1437	16.807018	7.87E-04	7.87E-04	0.0128108
BIOCARTA	h_th1th2Pathway:Th1/Th2 Differentiation	6	2.90	1.67E-05	IL4, IL2RA, HLA-DRB1, HLA-DRA, CD28, IL2	27	20	1437	15.966667	0.0010361	5.18E-04	0.0168713
BIOCARTA	h_asbcellPathway:Antigen Dependent B Cell Activation	5	2.42	3.79E-05	IL4, HLA-DRB1, HLA-DRA, CD28, IL2	27	12	1437	22.175926	0.0023463	7.83E-04	0.038228
BIOCARTA	h_inflamPathway:Cytokines and Inflammatory Response	6	2.90	6.59E-05	IL4, IL5, HLA-DRB1, IL13, HLA-DRA, IL2	27	26	1437	12.282051	0.0040759	0.0010205	0.0664552
BIOCARTA	h_mhcPathway:Antigen Processing and Presentation	4	1.93	5.81E-04	HLA-DRB1, TAP2, TAP1, HLA-DRA	27	10	1437	21.288889	0.0353834	0.007179	0.5846416
BIOCARTA	h_il5Pathway:IL 5 Signaling Pathway	4	1.93	5.81E-04	IL4, IL5, HLA-DRB1, HLA-DRA	27	10	1437	21.288889	0.0353834	0.007179	0.5846416
KEGG_PATHWAY	hsa04630:Jak-STAT signaling pathway	10	4.83	9.38E-04	IL4, IL5, IL23A, IL2RA, SOCS1, IL15RA, IL13, IL21, STAT2, IL2	85	155	5085	3.8595825	0.0998058	0.0095131	1.0585524
BIOCARTA	h_tob1Pathway:Role of Tob in T-cell activation	4	1.93	0.002	IL4, IL2RA, CD28, IL2	27	14	1437	15.206349	0.0989364	0.0172134	1.6813924
BIOCARTA	h_cytokinePathway:Cytokine Network	4	1.93	0.005	IL4, IL5, IL13, IL2	27	20	1437	10.644444	0.2621369	0.0424986	4.8276216
BIOCARTA	h_bbcellPathway:Bystander B Cell Activation	3	1.45	0.008	HLA-DRB1, HLA-DRA, CD28	27	8	1437	19.958333	0.4015723	0.062165	8.0175349
BIOCARTA	h_eosinophilsPathway:The Role of Eosinophils in the Chemokine Network of Allergy	3	1.45	0.008	IL5, HLA-DRB1, HLA-DRA	27	8	1437	19.958333	0.4015723	0.062165	8.0175349
KEGG_PATHWAY	hsa04660:T cell receptor signaling pathway	7	3.38	0.008	IL4, PRKCQ, IL5, ICOS, CTLA4, CD28, IL2	85	108	5085	3.877451	0.6151393	0.0764892	9.21218
BIOCARTA	h_nktPathway:Selective expression of chemokine receptors during T-cell polarization	4	1.93	0.009	IL4, IL5, CD28, IL2	27	25	1437	8.5155556	0.4394231	0.0622856	8.9905866
BIOCARTA	h_GATA3pathway:GATA3 participate in activating the Th2 cytokine genes expression	3	1.45	0.013	IL4, IL5, IL13	27	10	1437	15.966667	0.5546599	0.0777064	12.336479

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	6	2.90	0.013	IL4, IL5, IL2RA, HLA-DRB1, HLA-DRB5, HLA-DRA	85	86	5085	4.1737346	0.7781832	0.1093812	14.136904
KEGG_PATHWAY	hsa05340:Primary immunodeficiency	4	1.93	0.019	CIITA, TAP2, ICOS, TAP1	85	35	5085	6.8369748	0.8892836	0.1454659	19.968232
BIOCARTA	h_stemPathway:Regulation of hematopoiesis by cytokines	3	1.45	0.029	IL4, IL5, IL2	27	15	1437	10.644444	0.8346624	0.1509312	25.393385

Supplementary Table 3. Gene Ontlology Terms representing biological processes that are significantly enriched by genes in AA GWAS loci (p<0.05). Protein-coding genes located at GWAS loci were uploaded to the Database for Annotation, Visualization and Integrated Discovery (DAVID). Gene ontology (GO) term enrichment analysis identified 81 biological processes enriched with AA GWAS genes. This evidence is being driven by 83 genes from 14 GWAS loci. Some genes are assigned to multiple GO terms, as summarized in Supplementary Table 1, column 9.

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0019882~antigen processing and presentation	21	10	9.70E-21	HLA-DQB1, HLA-DRB1, HLA-DMB, HLA-DMA, HLA-DQA2, PSMB8, HLA-DQA1, PSMB9, RAET1E, RAET1G, ULBP3, TAP2, ULBP1, ULBP2, RAET1L, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DOA, HLA-DOB, HLA-DRA	169	83	13528	20.25	1.21E-17	1.21E-17	1.58E-17
GO:0002504~antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	12	6	1.19E-13	HLA-DQB1, HLA-DRB1, HLA-DRB5, HLA-DPA1, HLA-DPB1, HLA-DMB, HLA-DOA, HLA-DQA2, HLA-DOB, HLA-DMA, HLA-DQA1, HLA-DRA	169	33	13528	29.11	1.48E-10	7.41E-11	1.93E-10
GO:0006955~immune response	34	16	1.67E-11	HLA-DQB1, HLA-DRB1, MAP4K2, IL13, HLA-DMB, HLA-DMA, RAET1E, IL23A, RAET1G, TAP2, ICOS, TAP1, RAET1L, HLA-DRB5, HLA-DPB1, HLA-DOA, HLA-DOB, CD28, CIITA, IL4, IL2RA, IL5, CTLA4, HLA-DQA2, PSMB8, HLA-DQA1, PSMB9, ULBP3, OTUB1, ULBP1, ULBP2, HLA-DPA1, IL2, HLA-DRA	169	690	13528	3.94	2.07E-08	6.92E-09	2.71E-08
GO:0051249~regulation of lymphocyte activation	12	6	2.30E-06	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, BAD, HLA-DOA, IL21, HLA-DMA, CD28, IL2	169	148	13528	6.49	0.0028605	7.16E-04	0.0037394
GO:0051251~positive regulation of lymphocyte activation	10	5	3.18E-06	IL4, PRKCQ, IL5, IL2RA, IL13, BAD, IL21, HLA-DMA, CD28, IL2	169	97	13528	8.25	0.0039477	7.91E-04	0.0051633
GO:0050671~positive regulation of lymphocyte proliferation	8	4	4.94E-06	IL4, PRKCQ, IL5, IL2RA, IL13, IL21, CD28, IL2	169	55	13528	11.64	0.006127	0.0010238	0.0080225
GO:0032946~positive regulation of mononuclear cell proliferation	8	4	5.59E-06	IL4, PRKCQ, IL5, IL2RA, IL13, IL21, CD28, IL2	169	56	13528	11.44	0.006927	9.93E-04	0.0090735
GO:0070665~positive regulation of leukocyte proliferation	8	4	5.59E-06	IL4, PRKCQ, IL5, IL2RA, IL13, IL21, CD28, IL2	169	56	13528	11.44	0.006927	9.93E-04	0.0090735
GO:0002696~positive regulation of leukocyte activation	10	5	6.64E-06	IL4, PRKCQ, IL5, IL2RA, IL13, BAD, IL21, HLA-DMA, CD28, IL2	169	106	13528	7.55	0.0082284	0.0010323	0.0107852
GO:0002694~regulation of leukocyte activation	12	6	6.99E-06	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, BAD, HLA-DOA, IL21, HLA-DMA, CD28, IL2	169	166	13528	5.79	0.0086601	9.66E-04	0.0113535
GO:0050670~regulation of lymphocyte proliferation	9	4	8.56E-06	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, IL21, CD28, IL2	169	83	13528	8.68	0.0105922	0.0010643	0.0138998
GO:0070663~regulation of leukocyte proliferation	9	4	9.36E-06	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, IL21, CD28, IL2	169	84	13528	8.58	0.011579	0.0010582	0.0152022
GO:0032944~regulation of mononuclear cell proliferation	9	4	9.36E-06	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, IL21, CD28, IL2	169	84	13528	8.58	0.011579	0.0010582	0.0152022
GO:0050867~positive regulation of cell activation	10	5	9.69E-06	IL4, PRKCQ, IL5, IL2RA, IL13, BAD, IL21, HLA-DMA, CD28, IL2	169	111	13528	7.21	0.011986	0.0010044	0.0157397
GO:0050865~regulation of cell activation	12	6	1.16E-05	IL4, PRKCQ, IL5, IL2RA, CTLA4, IL13, BAD, HLA-DOA, IL21, HLA-DMA, CD28, IL2	169	175	13528	5.49	0.0142763	0.0011055	0.0187688

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0050863~regulation of T cell activation	10	5	1.49E-05	IL4, PRKCQ, IL2RA, CTLA4, BAD, HLA-DOA, IL21, HLA-DMA, CD28, IL2	169	117	13528	6.84	0.0183262	0.0013203	0.024142
GO:0002684~positive regulation of immune system process	13	6	4.19E-05	IL4, PRKCQ, IL2RA, IL5, TAP2, PTPN22, IL13, BAD, IL21, HLA-DMA, CD28, IL2, HLA-DRA	169	238	13528	4.37	0.0507599	0.0034669	0.0679795
GO:0050870~positive regulation of T cell activation	8	4	4.28E-05	IL4, PRKCQ, IL2RA, BAD, IL21, HLA-DMA, CD28, IL2	169	76	13528	8.43	0.0518246	0.0033205	0.0694435
GO:0042102~positive regulation of T cell proliferation	6	3	1.14E-04	IL4, PRKCQ, IL2RA, IL21, CD28, IL2	169	39	13528	12.31	0.1320728	0.0082976	0.184735
GO:0042129~regulation of T cell proliferation	7	3	1.16E-04	IL4, PRKCQ, IL2RA, CTLA4, IL21, CD28, IL2	169	62	13528	9.04	0.1343948	0.0079861	0.1882256
GO:0045619~regulation of lymphocyte differentiation	7	3	1.27E-04	IL2RA, CTLA4, BAD, HLA-DOA, IL21, HLA-DMA, IL2	169	63	13528	8.89	0.1460619	0.0082759	0.2059052
GO:0002478~antigen processing and presentation of exogenous peptide antigen	4	2	2.88E-04	TAP2, HLA-DOA, HLA-DMA, HLA-DRA	169	11	13528	29.11	0.3015847	0.017787	0.4674644
GO:0045580~regulation of T cell differentiation	6	3	4.12E-04	IL2RA, CTLA4, BAD, HLA-DOA, HLA-DMA, IL2	169	51	13528	9.42	0.4010909	0.0241161	0.6669709
GO:0019884~antigen processing and presentation of exogenous antigen	4	2	6.19E-04	TAP2, HLA-DOA, HLA-DMA, HLA-DRA	169	14	13528	22.87	0.537239	0.0344185	1.0008235
GO:0050871~positive regulation of B cell activation	5	2	7.09E-04	IL4, IL5, IL13, BAD, IL2	169	33	13528	12.13	0.5861737	0.0376348	1.1451547
GO:0046649~lymphocyte activation	10	5	8.50E-04	IL4, IL23A, ULBP3, ULBP1, ULBP2, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	199	13528	4.02	0.6529586	0.0431382	1.3720154
GO:0045621~positive regulation of lymphocyte differentiation	5	2	8.90E-04	IL2RA, BAD, IL21, HLA-DMA, IL2	169	35	13528	11.44	0.6696188	0.0433334	1.4353358
GO:0042127~regulation of cell proliferation	21	10	1.81E-03	IL4, ESRRA, IL5, IL2RA, ERBB3, SF1, CTLA4, IL13, IL21, CDK2, MEN1, VEGFB, PRKCQ, TIMELESS, HIPK1, NOTCH4, GDF11, FGF2, PRKRIR, CD28, IL2	169	787	13528	2.14	0.895105	0.0830689	2.9005039
GO:0030890~positive regulation of B cell proliferation	4	2	1.84E-03	IL4, IL5, IL13, IL2	169	20	13528	16.01	0.8983392	0.0811853	2.9401918
GO:0030101~natural killer cell activation	4	2	2.12E-03	ULBP3, ULBP1, ULBP2, IL2	169	21	13528	15.25	0.9288769	0.0900859	3.3917541
GO:0045321~leukocyte activation	10	5	3.26E-03	IL4, IL23A, ULBP3, ULBP1, ULBP2, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	242	13528	3.31	0.9826891	0.1305344	5.1574764
GO:0050864~regulation of B cell activation	5	2	3.64E-03	IL4, IL5, IL13, BAD, IL2	169	51	13528	7.85	0.9893125	0.1404012	5.7526796
GO:0002495~antigen processing and presentation of peptide antigen via MHC class II	3	1	4.09E-03	HLA-DOA, HLA-DMA, HLA-DRA	169	8	13528	30.02	0.9938697	0.1515459	6.434047
GO:0019886~antigen processing and presentation of exogenous peptide antigen via MHC class II	3	1	4.09E-03	HLA-DOA, HLA-DMA, HLA-DRA	169	8	13528	30.02	0.9938697	0.1515459	6.434047
GO:0048610~reproductive cellular process	8	4	4.10E-03	ADAD1, AFF4, SF1, GDF9, SYT6, PRM1, PRM2, TNP2	169	162	13528	3.95	0.993976	0.1476434	6.4554076
GO:0030888~regulation of B cell proliferation	4	2	4.91E-03	IL4, IL5, IL13, IL2	169	28	13528	11.44	0.9977982	0.1692357	7.676423

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0048002~antigen processing and presentation of peptide antigen	4	2	4.91E-03	TAP2, HLA-DOA, HLA-DMA, HLA-DRA	169	28	13528	11.44	0.9977982	0.1692357	7.676423
GO:0048534~hemopoietic or lymphoid organ development	10	5	5.20E-03	MEN1, IL4, NOTCH4, IRF1, SH2B3, PTPN22, HLA-DMA, BCL2L11, CD28, IL2	169	260	13528	3.08	0.9984777	0.1737103	8.1201107
GO:0042104~positive regulation of activated T cell proliferation	3	1	5.21E-03	IL4, IL2RA, IL2	169	9	13528	26.68	0.9984973	0.1695007	8.1356443
GO:0008284~positive regulation of cell proliferation	13	6	5.55E-03	VEGFB, IL4, PRKCQ, IL2RA, IL5, HIPK1, NOTCH4, IL13, IL21, FGF2, CDK2, CD28, IL2	169	414	13528	2.51	0.9990213	0.1750903	8.6484701
GO:0045582~positive regulation of T cell differentiation	4	2	7.16E-03	IL2RA, BAD, HLA-DMA, IL2	169	32	13528	10.01	0.9998695	0.2147405	11.020133
GO:0010557~positive regulation of macromolecule biosynthetic process	17	8	7.41E-03	IL4, CIITA, ESRRA, IL5, RXRB, NR4A3, IL21, CDK2, MEN1, PRKCQ, WIBG, NOTCH4, SMARCC2, IRF1, FGF2, CD28, IL2	169	654	13528	2.08	0.9999036	0.2159942	11.370757
GO:0002520~immune system development	10	5	7.60E-03	MEN1, IL4, NOTCH4, IRF1, SH2B3, PTPN22, HLA-DMA, BCL2L11, CD28, IL2	169	276	13528	2.90	0.999924	0.2158876	11.645726
GO:0002697~regulation of immune effector process	6	3	8.46E-03	IL4, TAP2, IL13, IL21, CD28, IL2	169	101	13528	4.76	0.9999744	0.232254	12.89052
GO:0030217~T cell differentiation	5	2	8.63E-03	IRF1, PTPN22, HLA-DMA, CD28, IL2	169	65	13528	6.16	0.9999793	0.2312784	13.131522
GO:0032270~positive regulation of cellular protein metabolic process	9	4	8.66E-03	MEN1, IL4, IL5, WIBG, FGF2, PSMB8, PSMB9, CD28, IL2	169	233	13528	3.09	0.9999799	0.2270466	13.168311
GO:0030098~lymphocyte differentiation	6	3	9.17E-03	IL4, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	103	13528	4.66	0.9999895	0.2339595	13.895039
GO:0046006~regulation of activated T cell proliferation	3	1	9.32E-03	IL4, IL2RA, IL2	169	12	13528	20.01	0.9999913	0.2326855	14.112155
GO:0030097~hemopoiesis	9	4	9.44E-03	MEN1, IL4, NOTCH4, IRF1, SH2B3, PTPN22, HLA-DMA, CD28, IL2	169	236	13528	3.05	0.9999925	0.2307302	14.280537
GO:0001775~cell activation	10	5	9.68E-03	IL4, IL23A, ULBP3, ULBP1, ULBP2, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	287	13528	2.79	0.9999944	0.2312322	14.607042
GO:0046425~regulation of JAK-STAT cascade	4	2	9.95E-03	IL4, IL5, SOCS1, IL2	169	36	13528	8.89	0.999996	0.2324892	14.985069
GO:0051247~positive regulation of protein metabolic process	9	4	0.011	MEN1, IL4, IL5, WIBG, FGF2, PSMB8, PSMB9, CD28, IL2	169	243	13528	2.96	0.9999989	0.2490306	16.42697
GO:0031328~positive regulation of cellular biosynthetic process	17	8	0.011	IL4, CIITA, ESRRA, IL5, RXRB, NR4A3, IL21, CDK2, MEN1, PRKCQ, WIBG, NOTCH4, SMARCC2, IRF1, FGF2, CD28, IL2	169	685	13528	1.99	0.9999992	0.2495058	16.77253
GO:0009891~positive regulation of biosynthetic process	17	8	0.013	IL4, CIITA, ESRRA, IL5, RXRB, NR4A3, IL21, CDK2, MEN1, PRKCQ, WIBG, NOTCH4, SMARCC2, IRF1, FGF2, CD28, IL2	169	695	13528	1.96	0.9999999	0.2736695	18.836149
GO:0002700~regulation of production of molecular mediator of immune response	4	2	0.014	IL4, IL13, IL21, IL2	169	41	13528	7.81	1	0.2944572	20.721729
GO:0032268~regulation of cellular protein metabolic process	13	6	0.015	SARNP, MEN1, IL4, ATXN2, PA2G4, IL5, WIBG, SOCS1, FGF2, PSMB8, CD28, IL2, PSMB9	169	474	13528	2.20	1	0.3073774	22.065778

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0010604~positive regulation of macromolecule metabolic process	19	9	0.020	IL4, CIITA, ESRRA, IL5, RXRB, NR4A3, IL21, CDK2, PSMB8, PSMB9, MEN1, PRKCQ, WIBG, NOTCH4, SMARCC2, IRF1, FGF2, CD28, IL2	169	857	13528	1.77	1	0.3770624	27.925025
GO:0042110~T cell activation	6	3	0.020	IL23A, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	126	13528	3.81	1	0.3782878	28.468331
GO:0042108~positive regulation of cytokine biosynthetic process	4	2	0.022	PRKCQ, IRF1, IL21, CD28	169	48	13528	6.67	1	0.3902356	29.894299
GO:0006457~protein folding	7	3	0.023	ERP44, DNAJC14, ERP29, PPIL4, DNAJC4, HLA-DMA, FKBP2	169	177	13528	3.17	1	0.4072063	31.768076
GO:0002521~leukocyte differentiation	6	3	0.024	IL4, IRF1, PTPN22, HLA-DMA, CD28, IL2	169	131	13528	3.67	1	0.407513	32.258331
GO:0045597~positive regulation of cell differentiation	8	4	0.024	MEN1, IL5, IL2RA, BAD, IL21, FGF2, HLA-DMA, IL2	169	229	13528	2.80	1	0.4099345	32.927909
GO:0040008~regulation of growth	10	5	0.027	MEN1, VEGFB, ATXN2, PRKCQ, SOCS1, RASGRP2, GDF9, FGF2, BCL2L11, IL2	169	341	13528	2.35	1	0.4335985	35.455312
GO:0031401~positive regulation of protein modification process	7	3	0.029	MEN1, IL4, IL5, FGF2, PSMB8, PSMB9, IL2	169	187	13528	3.00	1	0.4597863	38.264438
GO:0007286~spermatid development	4	2	0.029	ADAD1, AFF4, PRM1, PRM2	169	54	13528	5.93	1	0.4559265	38.410539
GO:0002706~regulation of lymphocyte mediated immunity	4	2	0.029	IL4, TAP2, IL21, IL2	169	54	13528	5.93	1	0.4559265	38.410539
GO:0048515~spermatid differentiation	4	2	0.034	ADAD1, AFF4, PRM1, PRM2	169	57	13528	5.62	1	0.4981003	42.760509
GO:0045893~positive regulation of transcription, DNA-dependent	12	6	0.036	MEN1, IL4, CIITA, ESRRA, IL5, RXRB, NOTCH4, SMARCC2, IRF1, NR4A3, FGF2, IL2	169	477	13528	2.01	1	0.5127574	44.639249
GO:0048585~negative regulation of response to stimulus	5	2	0.036	MEN1, IL2RA, SOCS1, CTLA4, IL2	169	100	13528	4.00	1	0.5087523	44.780048
GO:0046013~regulation of T cell homeostatic proliferation	2	1	0.037	IL2RA, IL2	169	3	13528	53.36	1	0.5120496	45.601796
GO:0007281~germ cell development	5	2	0.037	ADAD1, AFF4, GDF9, PRM1, PRM2	169	101	13528	3.96	1	0.5090473	45.823391
GO:0051254~positive regulation of RNA metabolic process	12	6	0.038	MEN1, IL4, CIITA, ESRRA, IL5, RXRB, NOTCH4, SMARCC2, IRF1, NR4A3, FGF2, IL2	169	481	13528	2.00	1	0.5093965	46.357578
GO:0030261~chromosome condensation	3	1	0.038	PRM3, PRM1, PRM2	169	25	13528	9.61	1	0.5091757	46.832695
GO:0007283~spermatogenesis	9	4	0.039	BRD2, PRM3, ADAD1, AFF4, PRM1, PRM2, SPATA5, BCL2L11, TNP2	169	308	13528	2.34	1	0.5072908	47.142165
GO:0048232~male gamete generation	9	4	0.039	BRD2, PRM3, ADAD1, AFF4, PRM1, PRM2, SPATA5, BCL2L11, TNP2	169	308	13528	2.34	1	0.5072908	47.142165
GO:0002703~regulation of leukocyte mediated immunity	4	2	0.040	IL4, TAP2, IL21, IL2	169	61	13528	5.25	1	0.5167141	48.544358
GO:0002637~regulation of immunoglobulin production	3	1	0.041	IL4, IL13, IL2	169	26	13528	9.24	1	0.519811	49.333255
GO:0000018~regulation of DNA recombination	3	1	0.041	IL4, RAD50, IL2	169	26	13528	9.24	1	0.519811	49.333255
GO:0046427~positive regulation of JAK-STAT cascade	3	1	0.041	IL4, IL5, IL2	169	26	13528	9.24	1	0.519811	49.333255

Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GO:0045941~positive regulation of transcription	13	6	0.049	CIITA, MEN1, IL4, ESRRA, IL5, RXRB, SMARCC2, NOTCH4, IRF1, NR4A3, FGF2, CDK2, IL2	169	564	13528	1.85	1	0.5773834	55.492532
GO:0022402~cell cycle process	13	6	0.049	MEN1, PA2G4, TIMELESS, KATNA1, SF1, BUB1, PRM1, NUP43, LATS1, RAD50, PSMB8, CDK2, PSMB9	169	565	13528	1.84	1	0.5764599	55.898506