

Table A. List of 93 SNPs and genes associated with biological processes.

SSC	SNP marker	Variant	Position	P<	A1	F_A1 DUROC	F_A1 YBH	A2	Annotated genes	Biological process
1	DIAS0004572	rs328115005	144135159	4.59E-24	A	1	0.0777	G	VPS39	intracellular protein transport
2	DRGA0017468	rs713429023	28427108	3.54E-29	T	1	0.0529	G	PDHX	acetyl-CoA biosynthetic process
2	MARC0028771	rs81223208	28699945	4.37E-33	A	1	0.0385	G	EHF	epithelial cell differentiation
3	WU_10.2_3	rs325133759	12957980	1.21E-50	G	1	0.0000	T	VCF	
3	ALGA0018879	rs81370102	50192060	2.40E-21	G	1	0.0962	A	SLC5A7	neuromuscular synaptic transmission
3	ASGA0097352	rs81317284	50726908	9.93E-23	T	1	0.0865	C	ST6GAL2	carbohydrate metabolic process
4	INRA0015919	rs326729657	107586557	3.54E-29	G	1	0.0529	A	ARNT	embryonic placenta development
6	ALGA0116528	rs81346062	72847504	5.10E-27	T	1	0.0625	C	CAMK2N1	
6	ALGA0109523	rs81337627	85299522	1.62E-20	A	1	0.1019	G	GRIK3	G-protein coupled glutamate receptor
6	ALGA0036047	rs81389915	88054224	4.77E-26	A	1	0.0673	G	MACF1	membrane protein transport
6	SIRI0000176	rs329679425	88136526	4.77E-26	G	1	0.0673	A	MACF1	membrane protein transport
6	ALGA0036052	rs81389921	88163612	4.77E-26	G	1	0.0673	T	MACF1	membrane protein transport
6	MARC0008963	rs81251860	88243944	4.77E-26	G	1	0.0673	A	MACF1	membrane protein transport
6	ASGA0028956	rs81389936	88264983	4.77E-26	C	1	0.0673	T	MACF1	membrane protein transport
6	ASGA0028958	rs81389948	88285881	4.77E-26	T	1	0.0673	G	MACF1	membrane protein transport
6	ALGA0036062	rs81389955	88312799	4.77E-26	C	1	0.0673	T	MACF1	membrane protein transport
6	ALGA0036064	rs81389959	88334239	4.77E-26	C	1	0.0673	T	MACF1	membrane protein transport
6	MARC0076965	rs81262099	88357843	4.77E-26	G	1	0.0673	A	MACF1	membrane protein transport
6	DIAS0002485	rs81211910	88384679	4.77E-26	C	1	0.0673	A	MACF1	membrane protein transport
6	ASGA0028971	rs81389986	88445968	5.27E-34	T	1	0.0343	G	BMP8B	bone morphogenetic protein family
6	ALGA0036086	rs81390019	88484410	1.11E-31	A	1	0.0433	G	PABPC4	nucleic acid binding
6	H3GA0018528	rs81390069	88586835	1.11E-31	G	1	0.0433	A	HPCAL4	calcium channel regulator activity, increased mean corpuscular volume
6	ALGA0036101	rs81390070	88600864	1.11E-31	C	1	0.0433	A	HPCAL4	calcium channel regulator activity, increased mean corpuscular volume
6	ALGA0036113	rs81390112	88789277	1.11E-31	G	1	0.0433	A	TRIT1	tRNA processing
6	ASGA0029025	rs81390137	88943854	4.37E-33	T	1	0.0385	C	MFSD2A	fatty acid transport, lipid transport across blood brain barrier
6	MARC0015713	rs81285728	89573648	4.37E-33	C	1	0.0385	T	MC2R	melanocortin receptor activity
6	ASGA0097503	rs81317489	89640457	2.48E-42	T	1	0.0144	C	MC2R	melanocortin receptor activity

6	DIAS0001681	rs341367004	89654568	2.48E-42	A	1	0.0144	G	RNMT	cellular response to leukemia inhibitory factor
6	ASGA0106427	rs81306790	89661963	2.48E-42	C	1	0.0144	T	RNMT	cellular response to leukemia inhibitory factor
6	H3GA0052949	rs81336360	89936198	2.48E-42	A	1	0.0144	G	CEP192	
6	MARC0032131	rs81226716	90705621	1.47E-20	T	1	0.1000	G	MPPE1	glycosylphosphatidylinositol (GPI) anchor biosynthetic process
6	ASGA0098169	rs81318326	90750373	3.87E-25	C	1	0.0721	T	IMPA2	inositol phosphate dephosphorylation, a growth factor for animals
6	DIAS0000866	rs339432830	96522899	3.54E-29	A	1	0.0529	G	MYOM1	striated muscle myosin thick filament assembly
6	M1GA0026030	rs81475823	96767590	2.48E-42	G	1	0.0144	A	PTPN2	insulin receptor signaling pathway, T cell differentiation0
7	H3GA0020592	rs80793059	31714979	5.10E-27	A	1	0.0625	C	GCLC	Cysteine Y glutamate metabolic process
7	ASGA0032342	rs80830437	33558872	2.40E-21	G	1	0.0962	A	DST	cytoskeleton organization, assembly of hemidesmosomes, contact between the basal surface of epithelial cells and the underlying basal lamina
7	ALGA0041905	rs81398013	55580590	1.11E-31	T	1	0.0433	C	IL6	chemotaxis, Pro Interleukin 16
7	MARC0030885	rs80837723	55598505	4.37E-33	T	1	0.0385	C	IL6	chemotaxis, Pro Interleukin 16
7	MARC0074526	rs80805016	55634091	4.37E-33	A	1	0.0385	G	IL6	chemotaxis, Pro Interleukin 16
7	H3GA0021713	rs80976160	55660752	2.61E-34	A	1	0.0340	G	IL6	chemotaxis, Pro Interleukin 16
7	M1GA0010388	rs80849899	55681553	4.37E-33	G	1	0.0385	A	IL6	chemotaxis, Pro Interleukin 16
7	DIAS0000025	rs342597254	56526714	5.80E-36	A	1	0.0291	G	ADAMTSL3	proteolysis, protein metabolic process
7	MARC0060380	rs80868794	56611249	4.77E-26	T	1	0.0673	C	ADAMTSL3	proteolysis, protein metabolic process
7	H3GA0021773	rs80837023	56626692	8.20E-26	A	1	0.0680	G	ADAMTSL3	proteolysis, protein metabolic process
7	H3GA0021777	rs80951652	56662624	5.10E-27	C	1	0.0625	T	ADAMTSL3	proteolysis, protein metabolic process
7	ASGA0034116	rs80816179	57335680	3.87E-25	A	1	0.0721	G	TM6SF1	lysosomal membrane
7	M1GA0010414	rs80986501	57520911	4.10E-40	A	1	0.0192	G	HOMER2	calcium-mediated signaling using intracellular calcium source, regulation of G-protein coupled receptor protein signaling pathway

7	ALGA0042092	rs80845345	57561137	4.10E-40	C	1	0.0192	A	HOMER2	calcium-mediated signaling using intracellular calcium source, regulation of G-protein coupled receptor protein signaling pathway
7	ALGA0042123	rs81398046	57840044	4.10E-40	T	1	0.0192	G	CPEB1	regulation of meiotic cell cycle process involved in oocyte maturation
7	INRA0026053	rs331746636	57940346	4.10E-40	C	1	0.0192	T	PDE8A	cellular response to epidermal growth factor stimulus
7	MARC0027851	rs81222725	57982718	4.10E-40	A	1	0.0192	G	PDE8A	cellular response to epidermal growth factor stimulus
7	ASGA0034157	rs81398056	58003125	4.10E-40	T	1	0.0192	C	PDE8A	cellular response to epidermal growth factor stimulus
7	ALGA0042155	rs80850402	58558358	4.77E-26	T	1	0.0673	C	UNC45A	chaperone-mediated protein folding, protein folding
7	WU_10.2_7	rs325625775	67341839	4.17E-20	A	1	0.1058	G	FOXA1	response to estradiol, lung epithelial cell differentiation
8	ASGA0087368	rs81476832	130997013	9.93E-23	T	1	0.0865	C	TSPAN5	protein maturation
9	ASGA0105200	rs81305287	9811957	9.93E-23	T	1	0.0865	C	PRRC2C	hematopoietic progenitor cell differentiation
12	MARC0075799	rs81261131	14161646	5.11E-22	A	1	0.0914	G	PITPNC1	phospholipid transport
13	H3GA0037403	rs81448371	146920356	5.11E-22	G	1	0.0914	A	PDIA5	protein folding, oxidation-reduction process
14	ALGA0078977	rs81451083	81274878	1.29E-34	A	1	0.0337	G	MICU1	mitochondrial calcium ion transport
14	DIAS0003048	rs327184000	81902429	1.29E-34	G	1	0.0337	A	P4HA1	embryonic growth retardation, decreased embryo size
14	DIAS0001052	rs339061874	82287949	1.73E-28	G	1	0.0516	A	CFAP70	protein binding
14	DIAS0004516	rs328957349	82633976	1.76E-21	A	1	0.0918	C	CHCHD1	zinc finger SWIM-type containing 8, fucosyltransferase 11
14	ALGA0079038	rs81451108	82694745	1.75E-23	A	1	0.0817	G	CAMK2G	calcium ion transport, protein serine/threonine kinase activity
14	ALGA0079042	rs80785304	82922948	2.40E-21	C	1	0.0962	T	VCL	morphogenesis and desarrollo of an epithelium
14	INRA0045033	rs345768654	82923849	2.40E-21	T	1	0.0962	G	VCL	morphogenesis and desarrollo of an epithelium
14	INRA0045038	rs345309524	83128477	1.04E-20	T	1	0.1010	C	ADK	AMP biosynthetic process, Metabolism of nucleotides

14	ALGA0079049	rs80889570	83379418	1.04E-20	T	1	0.1010	G	ADK	AMP biosynthetic process, Metabolism of nucleotides
14	H3GA0041058	rs80895748	83426816	1.04E-20	A	1	0.1010	G	ADK	AMP biosynthetic process, Metabolism of nucleotides
14	ASGA0064611	rs80897302	83799407	1.11E-31	T	1	0.0433	C	DUSP13	protein dephosphorylation
15	MARC0052627	rs81241812	52530188	4.64E-28	T	1	0.0577	G	ACSL1	long-chain fatty acid metabolic process, lipid biosynthetic process
15	Affx-114689732		62926906	1.11E-31	G	1	0.0433	A	CTLA4	lymphocyte associated antigen 4 CTLA 4 CD152 antigen
15	ASGA0070241	rs80949190	114183041	2.22E-30	A	1	0.0481	G	SATB2	embryonic skeletal system morphogenesis, osteoblast development
15	WU_10.2_15	rs338906811	116371556	3.16E-41	T	1	0.0149	C	ALS2CR12	
15	WU_10.2_15	rs343808632	116389325	2.48E-42	T	1	0.0144	C	TRAK2	anterograde dendritic transport of mitochondrion
18	H3GA0050399	rs81471732	14334075	2.22E-30	C	1	0.0481	T	SLC13A4	transporter activity
18	WU_10.2_18	rs322407819	23034512	1.04E-20	G	1	0.1010	A	GRM8	regulation of synaptic transmission, glutamatergic
X	WU_10.2_X	rs328334089	99650421	1.61E-22	G	1	0.0419	A	IL1RAPL2	cytokine-mediated signaling pathway, interleukin-1, Type II, blocking receptor activity
X	WU_10.2_X	rs327024720	99740050	1.61E-22	C	1	0.0419	A	IL1RAPL2	cytokine-mediated signaling pathway, interleukin-1, Type II, blocking receptor activity
X	WU_10.2_X	rs336767148	99921032	1.61E-22	T	1	0.0419	G	IL1RAPL2	cytokine-mediated signaling pathway, interleukin-1, Type II, blocking receptor activity
X	WU_10.2_X	rs326399484	140512948	3.69E-40	C	1	0.0052	T	VMA21	arrangement and bonding together of a vacuolar proton-transporting V-type ATPase complex
X	SIRI0000378	rs337683495	140634325	3.92E-36	A	1	0.0105	G	PASD1	regulation of transcription, DNA-templated
X	H3GA0052122	rs81473903	140667871	3.92E-36	G	1	0.0105	A	PASD1	regulation of transcription, DNA-templated
X	ASGA0081587	rs81473906	140694550	3.92E-36	T	1	0.0105	C	PASD1	regulation of transcription, DNA-templated
X	WU_10.2_X	rs330548482	141025364	1.61E-32	C	1	0.0159	A	GABRA3	gamma aminobutyric acid
X	WU_10.2_X	rs322056532	141073615	7.74E-33	C	1	0.0157	A	GABRA3	receptor subunit alpha 3

X	WU_10.2_X	rs325753884	141104407	8.76E-36	C	1	0.0106	T	GABRA3	gamma aminobutyric acid
X	ASGA0081595	rs80918182	141319763	7.74E-33	T	1	0.0157	G	GABRQ	receptor subunit alpha 3
X	H3GA0052129	rs80784223	141412550	7.74E-33	G	1	0.0157	A	ZNF185	gamma-aminobutyric acid receptor subunit alpha3
X	ALGA0100286	rs80910586	141433236	7.74E-33	A	1	0.0157	G	ZNF185	ion transmembrane transport
X	WU_10.2_X	rs327444342	141487498	7.74E-33	C	1	0.0157	T	nucleus	zinc ion binding
X	WU_10.2_X	rs322147119	141930278	7.74E-33	A	1	0.0157	G	FAM58A	zinc ion binding
X	H3GA0052154	rs81474001	142922072	9.12E-26	T	1	0.0314	C	VBP1	spermatid development, spermiogenesis
X	M1GA0023917	rs81474003	143013614	9.12E-26	G	1	0.0314	T	BRCC3	protein serine/threonine kinase regulator activity

A1 allele MAF. A2 alternate allele. F_A1 A1 allele frequency. YBH Yucatan black hairless.