

Supplementary table 1. Table detailing studies that contributed datasets to the SEAD			
Cohort	unrelated samples in Release	country	Depth
WBBC	4480	China	13.9x
SG10K	4563	Singapore	13.7x
GAsP	30	China	36x
	30	Japan	
	149	KOREA	
	97	Mongolia	
	464	India	
	91	Pakistan	
	25	India	
	8	Sri Lanka	
	64	Indonesia	
	48	Philippines	
	25	Vietnam	
1000G Phase 3 (EAS+SAS)	301	China	30x
	104	Japan	
	99	Vietnamese	
	86	Bengali	
	103	Gujarati	
	102	Telugu	
	96	Punjabi	
	102	Tamil	
Total	11067		

Supplementary table 2. Overview of populations included in HGDP dataset		
Regions	Populations	Samples
Africa	BantuKenya	11
Africa	BantuSouthAfrica	8
Africa	Biaka	22
Africa	Mandenka	22
Africa	Mbuti	13
Africa	San	6
Africa	Yoruba	22
America	Colombian	7
America	Karitiana	12
America	Maya	21
America	Pima	13
America	Surui	8
Central & South Asia	Balochi	24
Central & South Asia	Brahui	25
Central & South Asia	Burusho	24
Central & South Asia	Hazara	19
Central & South Asia	Kalash	22
Central & South Asia	Makrani	25
Central & South Asia	Pathan	24
Central & South Asia	Sindhi	24
Central & South Asia	Uygur	10
East Asia	Cambodian	9
East Asia	Dai	9
East Asia	Daur	9
East Asia	Han	33
East Asia	Hezhen	9
East Asia	Japanese	27
East Asia	Lahu	8
East Asia	Miao	10
East Asia	Mongolian	9
East Asia	Naxi	8
East Asia	NorthernHan	10
East Asia	Oroqen	9
East Asia	She	10
East Asia	Tu	10
East Asia	Tujia	9
East Asia	Xibo	9
East Asia	Yakut	25
East Asia	Yi	10
Europe	Adygei	16
Europe	Basque	23

Europe	BergamoItalian	12
Europe	French	28
Europe	Orcadian	15
Europe	Russian	25
Europe	Sardinian	28
Europe	Tuscan	8
Middle East	Bedouin	46
Middle East	Druze	42
Middle East	Mozabite	27
Middle East	Palestinian	46
Oceania	Bougainville	11
Oceania	PapuanHighlands	6
Oceania	PapuanSepik	7
Oceania	Papuan	4

Supplementary table 5. The mean concordance rate of 54 populations imputed by all five reference panels in HGDP by using Axiom array and Asian Screening Array

Array	Region	Population	GASP	1KGP	SG10K	WBBC	SEAD
Axiom array	Africa	BantuKenya	0.745212	0.901709	0.701731	0.70626	0.717113
	Africa	BantuSouthAfrica	0.71885	0.869909	0.677144	0.683038	0.690528
	Africa	Biaka	0.653808	0.747627	0.640343	0.654959	0.639565
	Africa	Mandenka	0.731148	0.899218	0.696001	0.699147	0.704245
	Africa	Mbuti	0.633953	0.701276	0.63044	0.646477	0.625459
	Africa	San	0.593141	0.619246	0.601963	0.621926	0.593906
	Africa	Yoruba	0.748443	0.927909	0.690683	0.696557	0.711421
	Middle East	Bedouin	0.906738	0.942689	0.917017	0.887566	0.917029
	Middle East	Druze	0.929379	0.9551	0.942822	0.908225	0.941869
	Middle East	Mozabite	0.873269	0.944205	0.872484	0.85074	0.875335
	Middle East	Palestinian	0.911662	0.947066	0.922124	0.89137	0.922018
	America	Colombian	0.935126	0.967418	0.949192	0.943532	0.949636
	America	Karitiana	0.938309	0.969673	0.951704	0.946572	0.951718
	America	Maya	0.931241	0.96543	0.944059	0.936565	0.94445
	America	Pima	0.934362	0.966679	0.948308	0.942936	0.948785
	America	Surui	0.938303	0.967669	0.952403	0.946094	0.951594
	Europe	Adygei	0.938403	0.959608	0.952492	0.918662	0.951911
	Europe	Basque	0.941828	0.976289	0.955098	0.918322	0.955067
	Europe	BergamoItalian	0.93864	0.966817	0.953688	0.915403	0.952852
	Europe	French	0.941884	0.970644	0.955455	0.917615	0.954828
	Europe	Orcadian	0.947475	0.97567	0.95879	0.920394	0.958886
	Europe	Russian	0.944228	0.970036	0.956892	0.923633	0.957109

	Europe	Sardinian	0.936399	0.96608	0.9503	0.913161	0.950083
	Europe	Tuscan	0.939367	0.965212	0.953674	0.916015	0.952115
	Oceania	Bougainville	0.927678	0.931624	0.939618	0.931286	0.938334
	Oceania	PapuanHighlands	0.920539	0.924658	0.926885	0.923682	0.929034
	Oceania	Papuan	0.920781	0.927049	0.929296	0.922254	0.93002
	Oceania	PapuanSepik	0.920717	0.925985	0.927597	0.923983	0.928949
	Central & South Asia	Balochi	0.934487	0.954665	0.947589	0.911187	0.947128
	Central & South Asia	Brahui	0.942831	0.954596	0.94921	0.911162	0.950841
	Central & South Asia	Burusho	0.941237	0.952962	0.9535	0.922991	0.953716
	Central & South Asia	Hazara	0.956582	0.95275	0.953592	0.936462	0.96195
	Central & South Asia	Kalash	0.943279	0.958472	0.957862	0.922504	0.955918
	Central & South Asia	Makrani	0.925865	0.952801	0.936829	0.901914	0.936249
	Central & South Asia	Pathan	0.946293	0.956898	0.9555	0.919314	0.956301
	Central & South Asia	Sindhi	0.936303	0.954418	0.945839	0.909197	0.94688
	Central & South Asia	Uygur	0.93946	0.952675	0.954515	0.937256	0.955397
	East Asia	Cambodian	0.932826	0.94693	0.958298	0.947053	0.954977
	East Asia	Dai	0.934952	0.953835	0.96145	0.957883	0.961525
	East Asia	Daur	0.941519	0.947635	0.953426	0.952989	0.955711
	East Asia	Han	0.934265	0.948994	0.962572	0.959153	0.960035
	East Asia	Hezhen	0.942966	0.94848	0.95403	0.954426	0.956937
	East Asia	Japanese	0.939274	0.949864	0.951823	0.95247	0.953869
	East Asia	Lahu	0.936476	0.950085	0.9599	0.956481	0.958413
	East Asia	Miao	0.93447	0.949634	0.960205	0.963041	0.961118
	East Asia	Mongolian	0.939665	0.94806	0.954357	0.952028	0.956261
	East Asia	Naxi	0.934458	0.945935	0.955385	0.954755	0.955259

	East Asia	NorthernHan	0.936201	0.949074	0.956983	0.956883	0.955965
	East Asia	Oroqen	0.943365	0.947847	0.953298	0.952921	0.956418
	East Asia	She	0.93402	0.950393	0.967415	0.96243	0.964749
	East Asia	Tu	0.935976	0.947581	0.955491	0.953596	0.954986
	East Asia	Tujia	0.934503	0.94892	0.959525	0.960541	0.959454
	East Asia	Xibo	0.938369	0.949876	0.955089	0.952257	0.955915
	East Asia	Yakut	0.949326	0.950486	0.951362	0.94757	0.958566
	East Asia	Yi	0.936137	0.948786	0.95706	0.957673	0.95727
Asian Screening Array	Central & South Asia	Balochi	0.888971	0.920377	0.913352	0.857091	0.91679
	Central & South Asia	Brahui	0.900123	0.919495	0.913144	0.855906	0.922522
	Central & South Asia	Burusho	0.898865	0.920945	0.922093	0.876046	0.92576
	Central & South Asia	Hazara	0.930151	0.925077	0.927348	0.901805	0.944419
	Central & South Asia	Kalash	0.895991	0.925103	0.924323	0.874769	0.924743
	Central & South Asia	Makrani	0.875701	0.91709	0.898794	0.846653	0.901311
	Central & South Asia	Pathan	0.902428	0.923031	0.922252	0.868235	0.928475
	Central & South Asia	Sindhi	0.891373	0.92195	0.913891	0.855801	0.917639
	Central & South Asia	Uygur	0.901481	0.926189	0.927008	0.902052	0.93115
	East Asia	Cambodian	0.909048	0.927714	0.94518	0.930467	0.941422
	East Asia	Dai	0.911083	0.938043	0.950981	0.947423	0.951205
	East Asia	Daur	0.914891	0.928661	0.936794	0.936842	0.941581
	East Asia	Han	0.911076	0.932829	0.953233	0.949742	0.950683
	East Asia	Hezhen	0.920479	0.929067	0.939213	0.939841	0.944045
	East Asia	Japanese	0.917504	0.932834	0.937382	0.939742	0.941784

	East Asia	Lahu	0.915383	0.931484	0.947883	0.945062	0.945954
	East Asia	Miao	0.910663	0.932837	0.94832	0.953713	0.950916
	East Asia	Mongolian	0.914721	0.928887	0.939464	0.935809	0.942489
	East Asia	Naxi	0.909902	0.928906	0.942481	0.943873	0.942894
	East Asia	NorthernHan	0.912391	0.93128	0.945047	0.945005	0.945056
	East Asia	Oroqen	0.918212	0.929109	0.93699	0.938434	0.942731
	East Asia	She	0.912061	0.935321	0.958209	0.953458	0.956362
	East Asia	Tu	0.910826	0.927982	0.94141	0.939624	0.942062
	East Asia	Tujia	0.912054	0.931969	0.948034	0.951737	0.949094
	East Asia	Xibo	0.914492	0.930294	0.939242	0.936858	0.94193
	East Asia	Yakut	0.925187	0.929094	0.93166	0.92652	0.943476
	East Asia	Yi	0.912186	0.930283	0.943432	0.945965	0.944692

Supplementary table 7. The well imputed variants in 7 MAF bins when imputing GWAS catalog association sites in Asia studies						
	MafBin	GASP	1KGP	WBBC	SG10K	SEAD
rare	< 0.1%	8	8	16	20	37
	0.1-0.3%	8	10	31	26	28
	0.3-0.5%	1	8	12	8	11
	0.5-0.7%	7	9	23	17	20
	0.7-1%	9	20	29	36	37
low frequency	1-2%	36	56	85	84	94
	2-5%	126	213	236	258	262
common	5%-50%	2255	3505	3255	3945	3935

Supplementary table 8. The well-imputed variants imputed by five reference panels.						
	MafBin	GASP	1KG	WBBC	SG10K	SEAD
rare	< 0.1%	45622	130862	447705	552073	1172069
	0.1-0.3%	36363	112243	272060	306560	374099
	0.3-0.5%	22071	69189	119411	132377	159818
	0.5-0.7%	18606	56654	91220	100780	121834
	0.7-1%	30293	79368	111821	127276	152399
low	1-2%	183748	357938	378206	439066	486601
	2-5%	406492	761145	715693	843850	914303
common	> 5%	1801654	4187528	3357540	4395219	4766529
total		2401953	5583493	5326963	6725695	7976019

Supplementary table 9. The number of well-imputed variants in all shared sites in 7 MAF bins					
MafBin	GASP	1KG	WBBC	SG10K	SEAD
< 0.1%	15756	18912	37551	43803	50260
0.1-0.3%	20696	26343	46492	44505	49750
0.3-0.5%	9813	12920	17212	17405	18298
0.5-0.7%	7453	9472	11597	11769	12132
0.7-1%	14698	18444	21734	22228	22819
1-2%	154776	195490	213321	219720	223117
2-5%	366771	463888	498341	511974	515944

Supplementary table 10. The mean R-square of shared sites in 7 MAF bins					
MafBin	GASP	1KG	WBBC	SG10K	SEAD
< 0.1%	0.267948	0.325562	0.425817	0.460316	0.478538
0.1-0.3%	0.424904	0.547426	0.630506	0.644247	0.659188
0.3-0.5%	0.601361	0.705777	0.759449	0.772925	0.785043
0.5-0.7%	0.699688	0.785714	0.834238	0.844929	0.854634
0.7-1%	0.727684	0.807526	0.849029	0.859154	0.867694
1-2%	0.728542	0.837935	0.857633	0.875119	0.879197
2-5%	0.72247	0.825218	0.841977	0.859391	0.860301

Supplementary table 12. 2kb-slide window of STAAR-O analysis results (Grey markers: P-meta < 1e-4 and P-cohort1 / P-cohort2 < 5e-2).									
				Cohort1 (N=2,332)		Cohort2 (N=3,037)		Combined (N=5,369)	
Phenotype	CHR	Start	End	#SNV	P (STAAR-O)	#SNV	P (STAAR-O)	#SNV	P (STAAR-O)
Hip-BMD	3	7823859	7825858	4	1.05E-05	3	4.52E-02	3	3.37E-05
Hip-BMD	3	7824859	7826858	2	8.90E-06	2	3.52E-02	2	2.61E-05
Hip-BMD	5	148948778	148950777	5	1.80E-02	4	2.65E-05	4	1.35E-05
Hip-BMD	8	49873459	49875458	2	1.42E-03	2	1.25E-05	2	7.25E-08
Hip-BMD	8	49874459	49876458	2	1.26E-03	3	1.21E-05	3	5.08E-08
Hip-BMD	8	49877459	49879458	3	2.13E-03	5	8.56E-06	5	4.55E-08
Hip-BMD	8	49878459	49880458	3	1.68E-03	5	9.79E-06	5	7.22E-08
Hip-BMD	8	49879459	49881458	5	1.50E-02	7	2.57E-05	7	2.85E-07
Hip-BMD	8	49892459	49894458	2	1.30E-03	4	5.25E-06	4	2.25E-08
Hip-BMD	8	49893459	49895458	2	2.02E-03	3	9.92E-06	3	4.70E-08
Hip-BMD	8	49895459	49897458	2	1.60E-03	3	8.81E-06	3	3.86E-08
Hip-BMD	8	49896459	49898458	3	1.27E-03	3	9.84E-05	3	8.81E-07
Hip-BMD	8	49897459	49899458	2	1.30E-03	2	5.39E-05	2	5.40E-07
Hip-BMD	8	49898459	49900458	2	1.61E-03	5	2.10E-06	5	1.08E-08
Hip-BMD	8	49902459	49904458	2	2.78E-03	3	3.58E-06	3	2.00E-08
Hip-BMD	8	49908459	49910458	3	1.56E-02	4	6.88E-06	4	1.56E-07
Hip-BMD	8	49909459	49911458	3	3.85E-02	7	2.74E-06	7	4.36E-08
Hip-BMD	8	49910459	49912458	3	4.03E-02	7	2.75E-06	7	4.58E-08
Hip-BMD	8	49911459	49913458	4	2.56E-02	4	5.88E-06	5	2.12E-07
Hip-BMD	8	49917459	49919458	4	1.88E-02	5	1.84E-06	5	1.21E-07
Hip-BMD	8	49919459	49921458	3	4.51E-03	4	6.29E-06	4	1.07E-07
Hip-BMD	8	49920459	49922458	5	7.92E-03	6	1.24E-05	6	2.53E-07

[illegible]

Supplementary table 13. Gene-centric noncoding analysis of STAAR-O analysis results (P-meta < 1e-4).

				Combined (N=5,369)	
Phenotype	CHR	Gene	Category	#SNV	P (STAAR-O)
Hip-BMD	8	SNTG1	UTR	17	9.72E-08
Hip-BMD	8	SNTG1	upstream	3	2.39E-07
Hip-BMD	20	POLR3F	downstream	2	4.44E-05
Hip-BMD	8	SNTG1	promoter_CAGE	6	4.72E-08
Hip-BMD	12	CD9	promoter_CAGE	4	3.80E-06
Hip-BMD	8	SNTG1	promoter_DHS	9	7.13E-08
Hip-BMD	12	CD9	promoter_DHS	12	3.45E-06
Hip-BMD	12	CD9	enhancer_CAGE	12	1.93E-05
Hip-BMD	8	SNTG1	enhancer_DHS	16	1.67E-07
Hip-BMD	12	CD9	enhancer_DHS	100	7.58E-05
Hip-BMD	15	MEGF11	enhancer_DHS	14	7.90E-05
FN-BMD	8	SNTG1	UTR	6	2.42E-05
FN-BMD	8	SNTG1	upstream	3	1.70E-05
FN-BMD	10	GJD4	downstream	3	8.65E-05
FN-BMD	8	SNTG1	promoter_CAGE	6	5.43E-06
FN-BMD	8	SNTG1	promoter_DHS	9	6.96E-06
FN-BMD	8	SNTG1	enhancer_DHS	9	3.95E-05
FN-BMD	19	ETFB	enhancer_DHS	8	7.79E-05

Supplementary table 14.Candidate genes list with confidence level A and B

Gene	CHR	Individual analysis (meta)											Sliding window (combined)				confidence	
		SNP	POS	Effect allele	MAF	Imputed R ²	Hip			FN			top region	Hip		FN		
							Beta	Se	P-value	Beta	Se	P-value		cluster number	P-value	cluster number	P-value	level
SNTG1	8	rs60103302 (rs61260287, rs60600379, rs57319781)	49899672	T	0.0091	0.9159	- 0.0508	0.0093	4.79E- 08	- 0.0411	0.009	4.85E- 06	49898459- 49900458	73	1.08E- 08	16	2.36E- 06	A
CPT2	1	rs199952566	53174688	T	0.0016	0.5760	-	-	-	0.1059	0.0229	3.95E- 06	53174053- 53176052	-	-	1	7.50E- 05	A
GRM7	3	rs538143187	7825275	G	0.0077	0.6354	-0.05	0.0105	1.73E- 06	-	-	-	7823859- 7825858	3	2.61E- 05	-	-	A
LINC00407	13	rs183265631	44698306	C	0.0063	0.5606	-	-	-	0.0477	0.0107	8.87E- 06	44696646- 44699645	-	-	2	2.88E- 05	A
C4BPA	1	rs55867570	207113036	A	0.0033	0.6391	0.0727	0.0159	4.66E- 06	0.0684	0.0153	7.55E- 06	-	-	-	-	-	B
LINC02572	2	rs141957142	129784869	T	0.0059	0.5163	0.0547	0.0118	3.78E- 06	0.0535	0.0114	2.63E- 06	-	-	-	-	-	B
LINC00461	5	rs185331344	88645590	A	0.0027	0.6892	0.0763	0.0177	1.67E- 05	0.0793	0.0171	3.34E- 06	-	-	-	-	-	B
SH3TC2	5	-	-	-	-	-	-	-	-	-	-	-	148948778- 148950777	1	1.35E- 05	2	1.79E- 07	B
ADIG	20	-	-	-	-	-	-	-	-	-	-	-	38586971- 38588970	1	1.02E- 05	1	2.01E- 05	B

MORC2	22	rs149352690	30929488	A	0.0018	0.8285	0.0868	0.0204	2.07E-05	0.0948	0.0197	1.41E-06	-	-	-	-	-	B
-------	----	-------------	----------	---	--------	--------	--------	--------	----------	--------	--------	----------	---	---	---	---	---	---

Supplementary table 15. Protein-protein interaction score between 7 novel genes and known GWS BMD-related genes.				
Novel_gene	Known_gene	Ensembl_ID_1	Ensembl_ID_2	combined_score
<i>ADIG</i>	<i>PPARG</i>	ENSP00000440331	ENSP00000287820	0.625
<i>C4BPA</i>	<i>VTN</i>	ENSP00000356037	ENSP00000226218	0.482
<i>C4BPA</i>	<i>ITIH4</i>	ENSP00000356037	ENSP00000266041	0.422
<i>C4BPA</i>	<i>HSPA4</i>	ENSP00000356037	ENSP00000302961	0.437
<i>C4BPA</i>	<i>MBL2</i>	ENSP00000356037	ENSP00000363079	0.4
<i>C4BPA</i>	<i>SERPINC1</i>	ENSP00000356037	ENSP00000356671	0.467
<i>CPT2</i>	<i>SMARCD3</i>	ENSP00000360541	ENSP00000262188	0.427
<i>CPT2</i>	<i>CREBBP</i>	ENSP00000360541	ENSP00000262367	0.432
<i>CPT2</i>	<i>SLC27A5</i>	ENSP00000360541	ENSP00000263093	0.492
<i>CPT2</i>	<i>PPARG</i>	ENSP00000360541	ENSP00000287820	0.548
<i>CPT2</i>	<i>PPARD</i>	ENSP00000360541	ENSP00000310928	0.511
<i>CPT2</i>	<i>ETFA</i>	ENSP00000360541	ENSP00000452762	0.522
<i>GRM7</i>	<i>THRB</i>	ENSP00000350348	ENSP00000379904	0.57
<i>MORC2</i>	<i>FOXK1</i>	ENSP00000380763	ENSP00000328720	0.486
<i>SH3TC2</i>	<i>TRIM2</i>	ENSP00000423660	ENSP00000339659	0.421
<i>SH3TC2</i>	<i>LITAF</i>	ENSP00000423660	ENSP00000459533	0.709
<i>SNTG1</i>	<i>SSPN</i>	ENSP00000493900	ENSP00000242729	0.771
<i>SNTG1</i>	<i>SGCA</i>	ENSP00000493900	ENSP00000262018	0.785
<i>SNTG1</i>	<i>SYN3</i>	ENSP00000493900	ENSP00000351614	0.624
<i>SNTG1</i>	<i>SYN2</i>	ENSP00000493900	ENSP00000480050	0.618

Novel_gene: level-A and -B suggestive genes reported in this study; **Known_gene**: previously reported BMD-related genes in Morris et al. (2019); **combined_score**: the likelihood of an interaction being true based on the available evidence in STRING database.

Supplementary table 16. FDR-corrected functional enrichment analysis of novel candidate and known GWS BMD-related genes. (STRING database)							
#category	term ID	term description	observed gene count	background gene count	strength	false discovery rate	matching proteins in your network (labels)
GO Process	GO:0006631	Fatty acid metabolic process	6	325	1.15	0.0493	SLC27A5,PPARG,PPARD,CPT2,MORC2,ETFA
GO Process	GO:0015908	Fatty acid transport	4	75	1.61	0.0493	SLC27A5,PPARG,PPARD,CPT2
GO Process	GO:0019395	Fatty acid oxidation	4	85	1.55	0.0493	PPARG,PPARD,CPT2,ETFA
GO Process	GO:0032787	Monocarboxylic acid metabolic process	7	502	1.02	0.0493	SLC27A5,PPARG,PPARD,FOXK1,CPT2,MORC2,ETFA
GO Function	GO:0001221	Transcription coregulator binding	5	114	1.52	0.0022	SMARCD3,CREBBP,PPARG,PPARD,THRB
GO Component	GO:0016010	Dystrophin-associated glycoprotein complex	3	17	2.13	0.0047	SSPN,SGCA,SENTG1
GO Component	GO:0072562	Blood microparticle	4	118	1.41	0.0128	VTN,ITIH4,C4BPA,SERPINC1
STRING clusters	CL:28700	Dystrophin-associated	3	14	2.21	0.0062	SSPN,SGCA,SENTG1

		glycoprotein complex					
STRING clusters	CL:9988	Mixed, incl. Regulation of cholesterol storage, and Carnitine metabolism	3	35	1.81	0.0271	PPARG,PPARD, CPT2
KEGG	hsa03320	PPAR signaling pathway	4	75	1.61	0.0011	SLC27A5,PPARG,PPARD, CPT2
KEGG	hsa04610	Complement and coagulation cascades	4	82	1.57	0.0011	VTN, C4BPA ,SERPINC1,MBL2
Reactome	HSA-166658	Complement cascade	3	59	1.59	0.0414	VTN, C4BPA ,MBL2
Reactome	HSA-1989781	PPARA activates gene expression	4	117	1.41	0.0414	SMARCD3,CREBBP,PPARG, CPT2
Reactome	HSA-556833	Metabolism of lipids	7	739	0.86	0.0414	SMARCD3,CREBBP,SLC27A5,PPARG,PPARD, CPT2 , MORC2
WikiPathways	WP3942	PPAR signaling pathway	4	67	1.66	0.0017	SLC27A5,PPARG,PPARD, CPT2
Monarch	EFO:0009270	Heel bone mineral density	16	878	1.14	1.18E-11	VTN,SSPN,SGCA,SMARCD3,CREBBP,SLC27A5,ITIH4,PPARG,HSPA4,PPARD,SYN3,SERPINC1,THRB,ETFA,LITAF,SYN2

Monarch	EFO:0004512	Bone measurement	17	2295	0.75	4.72E-07	VTN,SSPN,SGCA,SMARCD3,CREBBP,SLC27A5,ITIH4,PPARG,HSPA4,PPARD,TRIM2,SYN3,SERPINC1,THRB,ETFA,LITAF,SYN2
Monarch	EFO:0004747	Protein measurement	19	5856	0.39	0.0158	VTN,SSPN,SMARCD3,CREBBP,SLC27A5,ITIH4,PPARG,PPARD,FOXK1,TRIM2, GRM7 ,SYN3, C4BPA , CPT2 ,MBL2,THRB,LITAF,SYN2, SNTG1
Monarch	HP:0003130	Abnormal peripheral myelination	4	99	1.49	0.0195	TRIM2, MORC2 , SH3TC2 ,LITAF
Monarch	HP:0011805	Abnormal skeletal muscle morphology	10	1537	0.69	0.0246	SGCA,CREBBP,PPARG,TRIM2, GRM7 , CPT2 , MORC2 , SH3TC2 ,ETFA,LITAF
TISSUES	BTO:0000392	Plasma cell	5	171	1.35	0.0073	VTN,ITIH4, C4BPA ,SERPINC1,MBL2
TISSUES	BTO:0000141	Bone marrow	6	528	0.93	0.0337	VTN,ITIH4,PPARG, C4BPA ,SERPINC1,MBL2
COMPAR TMENTS	GOCC:0016010	Dystrophin-associated glycoprotein complex	3	20	2.06	0.0081	SSPN,SGCA, SNTG1
COMPAR TMENTS	GOCC:0072562	Blood microparticle	4	118	1.41	0.0144	VTN,ITIH4, C4BPA ,SERPINC1
COMPAR TMENTS	GOCC:0016013	Syntrophin complex	2	8	2.28	0.043	SSPN, SNTG1

UniProt Keywords	KW- 0144	Charcot-Marie- Tooth disease	4	55	1.74	0.00069	TRIM2, MORC2 , SH3TC2 ,LITAF
---------------------	-------------	---------------------------------	---	----	------	---------	--

Variant (VCF)	rsID	Chr	Position	WBBC AF	TOPMed Bravo AF	ALL 1000G AF	AFR 1000G AF	AMR 1000G AF	EAS 1000G AF	EUR 1000G AF	SAS 1000G AF	Total GNOMAD AF	AMI GNOMAD AF	OTH GNOMAD AF	AFR GNOMAD AF	SAS GNOMAD AF	ASJ GNOMAD AF	FIN GNOMAD AF	AMR GNOMAD AF	NFE GNOMAD AF	EAS GNOMAD AF
1- 53174688- G-T	rs199952566	1	53174688	0.0016	0.03238	NA	NA	NA	NA	NA	NA	0.04857	0.05090	0.04964	0.01512	0.07143	0.04374	0.06716	0.04627	0.06736	0.00220
1- 207113036- C-A	rs55867570	1	207113036	0.0033	0.03489	0.0347	0.0030	0.0994	0.0030	0.0249	0.0746	0.03280	0.00444	0.03482	0.00921	0.07566	0.02505	0.01929	0.08430	0.03967	0.00192
2- 129784869- C-T	rs141957142	2	129784869	0.0059	0.00057	0.0022	NA	NA	0.0099	0.0010	NA	0.00194	NA	0.00046	NA	0.00164	NA	0.02250	NA	0.00025	0.00670
3-7825275- A-G	rs538143187	3	7825275	0.0077	0.00051	0.0018	NA	NA	0.0079	NA	0.0010	0.00022	NA	0.00093	NA	0.00165	NA	NA	NA	0.00002	0.00766
5- 88573589- C-T	rs557762331	5	88573589	0.0022	0.00025	0.0002	0.0008	NA	NA	NA	NA	0.00033	NA	0.00093	0.00081	NA	NA	0.00086	NA	0.00003	NA
5- 88645590- G-A	rs185331344	5	88645590	0.0027	0.00008	0.0004	NA	NA	0.0020	NA	NA	0.00003	NA	NA	NA	NA	NA	NA	NA	NA	0.00128
5- 148949166- T-G	rs555552329	5	148949166	0.0012	0.00014	0.0004	NA	NA	0.0020	NA	NA	0.00006	NA	NA	NA	0.00033	NA	NA	NA	NA	0.00223

5- 148949664- T-A	rs200698141	5	148949664	0.0011	0.00003	NA	NA	NA	NA	NA	NA	0.00001	NA	NA	NA	NA	NA	NA	NA	NA	0.00064
5- 148950564- T-G	rs1752901948	5	148950564	0.0030	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
5- 148950586- G-A	rs182981414	5	148950586	0.0038	0.00024	0.0016	0.0008	NA	0.0060	NA	0.0010	0.00017	NA	0.00093	0.00010	0.00230	NA	NA	0.00015	0.00008	0.00160
8- 49874999- T-C	rs113710708	8	49874999	0.0045	0.00363	0.0056	0.0106	0.0014	0.0089	0.0020	0.0020	0.00327	0.00111	0.00372	0.00645	0.00066	0.00451	0.00010	0.00088	0.00226	0.00415
8- 49876358- G-A	rs185528914	8	49876358	0.0090	0.03572	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03278	0.00111	0.02742	0.09955	0.00099	0.00452	0.00010	0.01620	0.00287	0.00926
8- 49877049- C-T	rs113405654	8	49877049	0.0090	0.03575	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03264	0.00111	0.02742	0.09927	0.00099	0.00451	0.00010	0.01612	0.00282	0.00926
8- 49877219- GT-G	rs554772392	8	49877219	0.0045	0.00177	0.0032	NA	0.0043	0.0089	0.0020	0.0020	0.00149	0.00112	0.00189	0.00057	0.00069	0.00454	NA	0.00067	0.00223	0.00417
8- 49877603- G-T	rs374703333	8	49877603	0.0090	0.03566	0.0361	0.1059	0.0187	0.0238	0.0020	0.0020	0.03270	0.00111	0.02744	0.09951	0.00099	0.00451	0.00010	0.01598	0.00282	0.00925

8- 49878192- A-T	rs149975084	8	49878192	0.0090	0.03575	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03276	0.00111	0.02752	0.09968	0.00099	0.00452	0.00010	0.01606	0.00282	0.00929
8- 49879187- G-C	rs57405249	8	49879187	0.0045	0.00380	0.0056	0.0106	0.0014	0.0089	0.0020	0.0020	0.00350	0.00111	0.00466	0.00700	0.00066	0.00452	0.00010	0.00103	0.00234	0.00415
8- 49879944- T-C	rs77180384	8	49879944	0.0090	0.03574	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03278	0.00111	0.02742	0.09963	0.00099	0.00452	0.00010	0.01610	0.00282	0.00925
8- 49880246- G-A	rs112039318	8	49880246	0.0090	0.03574	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03276	0.00111	0.02747	0.09959	0.00099	0.00451	0.00010	0.01612	0.00282	0.00926
8- 49880773- C-T	rs185021562	8	49880773	0.0045	0.00367	0.0056	0.0106	0.0014	0.0089	0.0020	0.0020	0.00330	0.00111	0.00372	0.00644	0.00066	0.00452	0.00010	0.00088	0.00232	0.00415
8- 49882468- T-G	rs73584719	8	49882468	0.0090	0.03574	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03273	0.00111	0.02744	0.09952	0.00099	0.00452	0.00010	0.01604	0.00279	0.00925
8- 49882732- A-C	rs111939102	8	49882732	0.0090	0.03572	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.04448	0.00170	0.03694	0.12019	0.00152	0.00626	0.00017	0.02256	0.00398	0.01426
8- 49883179- G-A	rs73584721	8	49883179	0.0090	0.03579	0.0365	0.1074	0.0187	0.0238	0.0020	0.0020	0.03291	0.00111	0.02749	0.10006	0.00098	0.00452	0.00010	0.01616	0.00284	0.00926

8- 49884471- ATTT-A	rs58529870	8	49884471	0.0090	0.06058	NA	NA	NA	NA	NA	NA	0.03457	0.00112	0.03051	0.10580	0.00201	0.00455	0.00011	0.01678	0.00287	0.00935
8- 49885623- T-C	rs73676063	8	49885623	0.0090	0.03575	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03274	0.00111	0.02742	0.09954	0.00098	0.00451	0.00010	0.01605	0.00282	0.00927
8- 49885624- G-C	rs73676064	8	49885624	0.0090	0.03575	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03278	0.00111	0.02744	0.09969	0.00098	0.00451	0.00010	0.01609	0.00282	0.00928
8- 49885841- A-G	rs73584722	8	49885841	0.0090	0.03576	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03277	0.00111	0.02744	0.09963	0.00098	0.00452	0.00010	0.01600	0.00282	0.00928
8- 49885892- C-T	rs73584723	8	49885892	0.0090	0.03531	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03247	0.00111	0.02698	0.09880	0.00099	0.00452	0.00010	0.01585	0.00277	0.00927
8- 49886287- G-A	rs57382502	8	49886287	0.0090	0.03576	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.04315	0.00147	0.03856	0.10746	0.00168	0.00610	0.00018	0.02511	0.00392	0.01249
8- 49887564- CTTTTT- C	rs370905249	8	49887564	0.0045	0.00223	NA	NA	NA	NA	NA	NA	0.00355	0.00181	0.00321	0.00318	0.00263	0.00678	NA	0.00182	0.00380	0.00998
8- 49888081- G-C	rs58826965	8	49888081	0.0045	0.00587	0.0066	0.0144	0.0014	0.0089	0.0020	0.0020	0.00523	0.00111	0.00465	0.01289	0.00066	0.00452	0.00010	0.00140	0.00226	0.00416

8- 49888152- T-G	rs428507	8	49888152	0.0045	0.01542	0.0068	0.0151	0.0014	0.0089	0.0020	0.0020	0.00524	0.00111	0.00465	0.01297	0.00066	0.00452	0.00010	0.00140	0.00226	0.00416
8- 49888397- G-A	rs60042448	8	49888397	0.0090	0.03580	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03280	0.00111	0.02742	0.09973	0.00099	0.00452	0.00010	0.01612	0.00284	0.00927
8- 49888787- TA-T	rs1208385137	8	49888787	0.0090	0.03674	NA	NA	NA	NA	NA	NA	0.02889	0.00125	0.03121	0.08956	0.00136	0.00440	0.00021	0.01789	0.00289	0.00947
8- 49889490- A-T	rs73584728	8	49889490	0.0090	0.03577	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03278	0.00111	0.02700	0.09970	0.00098	0.00451	0.00010	0.01611	0.00280	0.00927
8- 49890023- A-G	rs73584729	8	49890023	0.0090	0.03576	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03168	0.00111	0.02573	0.09676	0.00099	0.00452	0.00010	0.01556	0.00279	0.00929
8- 49890519- C-CA	rs759038857	8	49890519	0.0079	0.03798	NA	NA	NA	NA	NA	NA	0.02295	0.00137	0.02151	0.07587	0.00072	0.00271	NA	0.00880	0.00234	0.00928
8- 49891087- C-T	rs111982554	8	49891087	0.0045	0.00587	0.0066	0.0144	0.0014	0.0089	0.0020	0.0020	0.00522	0.00111	0.00466	0.01287	0.00066	0.00452	0.00010	0.00139	0.00226	0.00416
8- 49892406- A-G	rs73584734	8	49892406	0.0090	0.03576	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03275	0.00111	0.02695	0.09954	0.00098	0.00452	0.00010	0.01593	0.00282	0.00928

8- 49892773- G-T	rs73676072	8	49892773	0.0090	0.03575	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03283	0.00111	0.02744	0.09970	0.00099	0.00452	0.00019	0.01615	0.00284	0.00927
8- 49892889- C-T	rs368588177	8	49892889	0.0045	0.00204	0.0032	0.0015	0.0014	0.0089	0.0020	0.0020	0.00175	0.00111	0.00186	0.00143	0.00066	0.00452	0.00010	0.00073	0.00225	0.00416
8- 49893243- G-A	rs73676073	8	49893243	0.0090	0.03576	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03274	0.00111	0.02698	0.09954	0.00099	0.00452	0.00010	0.01608	0.00282	0.00925
8- 49894015- A-C	rs113353857	8	49894015	0.0045	0.00362	0.0056	0.0106	0.0014	0.0089	0.0020	0.0020	0.00327	0.00111	0.00371	0.00645	0.00066	0.00452	0.00010	0.00088	0.00226	0.00416
8- 49894767- C-T	rs60295865	8	49894767	0.0090	0.03579	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03328	0.00112	0.02791	0.10077	0.00104	0.00454	0.00010	0.01663	0.00286	0.00933
8- 49896402- A-G	rs60356093	8	49896402	0.0090	0.03633	0.0365	0.1074	0.0187	0.0238	0.0020	0.0020	0.03338	0.00111	0.02739	0.10162	0.00098	0.00452	0.00010	0.01618	0.00282	0.00926
8- 49896752- G-A	rs59841322	8	49896752	0.0045	0.00215	0.0032	0.0015	0.0014	0.0089	0.0020	0.0020	0.00185	0.00111	0.00186	0.00176	0.00066	0.00451	0.00010	0.00073	0.00225	0.00415
8- 49897753- G-A	rs112543852	8	49897753	0.0045	0.00367	0.0056	0.0106	0.0014	0.0089	0.0020	0.0020	0.00332	0.00111	0.00373	0.00650	0.00066	0.00452	0.00010	0.00088	0.00232	0.00416

8- 49898509- C-T	rs111292084	8	49898509	0.0045	0.00585	0.0066	0.0144	0.0014	0.0089	0.0020	0.0020	0.00522	0.00111	0.00465	0.01285	0.00066	0.00451	0.00010	0.00139	0.00226	0.00416
8- 49899672- G-T	rs60103302	8	49899672	0.0091	0.03651	0.0369	0.1097	0.0173	0.0238	0.0020	0.0020	0.03330	0.00111	0.02793	0.10132	0.00099	0.00451	0.00010	0.01638	0.00282	0.00929
8- 49899678- A-C	rs61260287	8	49899678	0.0091	0.03651	0.0369	0.1097	0.0173	0.0238	0.0020	0.0020	0.03325	0.00111	0.02791	0.10116	0.00098	0.00451	0.00010	0.01627	0.00282	0.00927
8- 49899701- A-G	rs60600379	8	49899701	0.0091	0.03651	0.0371	0.1104	0.0173	0.0238	0.0020	0.0020	0.03325	0.00111	0.02791	0.10117	0.00098	0.00452	0.00010	0.01634	0.00282	0.00927
8- 49903401- A-T	rs57319781	8	49903401	0.0091	0.03572	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.09835	0.02083	0.08406	0.13208	0.00307	0.02698	0.00063	0.06564	0.02465	0.02031
8- 49903593- A-G	rs112423400	8	49903593	0.0045	0.00363	0.0058	0.0106	0.0014	0.0089	0.0020	0.0031	0.00326	0.00111	0.00372	0.00643	0.00066	0.00452	NA	0.00088	0.00226	0.00416
8- 49905890- G-A	rs58254228	8	49905890	0.0090	0.03572	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03277	0.00111	0.02698	0.09964	0.00099	0.00451	0.00010	0.01613	0.00282	0.00928
8- 49906635- C-T	rs73584754	8	49906635	0.0090	0.05095	0.0503	0.1558	0.0245	0.0238	0.0020	0.0031	0.04644	0.00111	0.03957	0.14243	0.00099	0.00602	0.00029	0.02195	0.00355	0.00960

8-49909471-C-T	rs73584759	8	49909471	0.0090	0.03564	0.0363	0.1067	0.0187	0.0238	0.0020	0.0020	0.03269	0.00111	0.02742	0.09936	0.00098	0.00452	0.00010	0.01603	0.00280	0.00926
8-49910442-C-T	rs368874009	8	49910442	0.0035	0.00022	0.0012	NA	NA	0.0060	NA	NA	0.00009	NA	NA	0.00002	NA	NA	NA	NA	0.00002	0.00351
8-49910737-G-C	rs2306742	8	49910737	0.0090	0.03653	0.0371	0.1097	0.0187	0.0238	0.0020	0.0020	0.03328	0.00111	0.02791	0.10134	0.00099	0.00452	0.00010	0.01618	0.00280	0.00927
8-49911117-A-G	rs73584763	8	49911117	0.0091	0.05007	0.0515	0.1619	0.0216	0.0238	0.0020	0.0031	0.04595	0.00111	0.04050	0.14212	0.00164	0.00452	0.00010	0.02118	0.00287	0.00990
8-49911402-C-A	rs73584765	8	49911402	0.0091	0.05006	0.0515	0.1619	0.0216	0.0238	0.0020	0.0031	0.04585	0.00111	0.03972	0.14196	0.00165	0.00452	0.00010	0.02101	0.00288	0.00990
8-49911591-G-C	rs554851102	8	49911591	0.0035	0.00022	0.0012	NA	NA	0.0060	NA	NA	0.00009	NA	NA	0.00002	NA	NA	NA	NA	NA	0.00355
8-49911802-C-G	rs73584771	8	49911802	0.0091	0.05007	0.0515	0.1619	0.0216	0.0238	0.0020	0.0031	0.04587	0.00111	0.04043	0.14190	0.00164	0.00452	0.00010	0.02109	0.00288	0.00990
8-49914816-G-C	rs16913838	8	49914816	0.0090	0.03697	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03378	0.00111	0.02835	0.10291	0.00099	0.00451	0.00010	0.01636	0.00282	0.00925

8- 49917080- G-A	rs114269916	8	49917080	0.0044	0.00420	0.0064	0.0136	0.0014	0.0089	0.0020	0.0020	0.00375	0.00111	0.00420	0.00801	0.00099	0.00452	0.00010	0.00095	0.00226	0.00415
8- 49917532- G-A	rs111483692	8	49917532	0.0044	0.00648	0.0074	0.0174	0.0014	0.0089	0.0020	0.0020	0.00568	0.00111	0.00511	0.01445	0.00066	0.00451	0.00010	0.00147	0.00223	0.00415
8- 49919427- A-G	rs16913881	8	49919427	0.0090	0.03708	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03386	0.00111	0.02835	0.10319	0.00098	0.00452	0.00010	0.01649	0.00280	0.00926
8- 49921064- A-C	rs61374770	8	49921064	0.0090	0.03709	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03385	0.00111	0.02835	0.10314	0.00098	0.00451	0.00010	0.01651	0.00281	0.00926
8- 49921236- A-G	rs58740018	8	49921236	0.0044	0.00649	0.0074	0.0174	0.0014	0.0089	0.0020	0.0020	0.00571	0.00111	0.00513	0.01447	0.00066	0.00452	0.00010	0.00147	0.00226	0.00415
8- 49927998- G-A	rs188656392	8	49927998	0.0044	0.00636	0.0048	0.0008	0.0058	0.0089	0.0060	0.0041	0.00654	0.00111	0.00750	0.00124	0.00366	0.00784	0.00574	0.00774	0.01007	0.00448
8- 49929177- T-G	rs73569315	8	49929177	0.0090	0.03710	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03386	0.00111	0.02832	0.10317	0.00098	0.00451	0.00010	0.01655	0.00280	0.00926
8- 49929416- T-C	rs73569317	8	49929416	0.0090	0.03711	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03390	0.00111	0.02835	0.10328	0.00098	0.00452	0.00010	0.01655	0.00280	0.00925

8- 49929643- T-G	rs16913981	8	49929643	0.0090	0.03708	0.0379	0.1127	0.0187	0.0238	0.0020	0.0020	0.03388	0.00111	0.02835	0.10323	0.00099	0.00452	0.00010	0.01654	0.00280	0.00926
8- 49929720- A-AT	rs527259628	8	49929720	0.0090	0.00001	NA	NA	NA	NA	NA	NA	0.00003	NA	NA	NA	0.00033	NA	NA	NA	0.00005	NA
8- 49933239- C-T	rs80238025	8	49933239	0.0042	0.00212	0.0032	0.0015	0.0014	0.0089	0.0020	0.0020	0.00182	0.00111	0.00186	0.00155	0.00098	0.00452	0.00010	0.00073	0.00229	0.00415
8- 49935407- T-TC	rs1318388498	8	49935407	0.0089	0.03185	NA	NA	NA	NA	NA	NA	0.02879	0.00112	0.02548	0.08784	0.00101	0.00454	0.00010	0.01473	0.00267	0.00906
8- 49938358- T-C	rs78859218	8	49938358	0.0042	0.00356	0.0042	0.0053	0.0014	0.0089	0.0020	0.0020	0.00327	0.00111	0.00325	0.00647	0.00099	0.00451	0.00010	0.00081	0.00226	0.00415
8- 49942331- T-C	rs112548358	8	49942331	0.0042	0.00355	0.0042	0.0053	0.0014	0.0089	0.0020	0.0020	0.00327	0.00111	0.00325	0.00644	0.00099	0.00451	0.00010	0.00081	0.00226	0.00415
8- 49944791- G-GA	rs112235757	8	49944791	0.0042	0.00415	NA	NA	NA	NA	NA	NA	0.00455	0.00128	0.00399	0.00445	0.00327	0.00650	0.00526	0.00254	0.00414	0.02051
8- 49955987- T-C	rs113843753	8	49955987	0.0041	0.00410	0.0050	0.0083	0.0014	0.0089	0.0020	0.0020	0.00371	0.00111	0.00371	0.00789	0.00066	0.00451	0.00010	0.00088	0.00228	0.00447

[illegible]