

Table S2. Gene sets with significant $diffSSMD = SSMD_{EUR} - SSMD_{YRI}$.

	MSigDB gene set	# of genes	# of genes used in SSMD	Observed SSMD
diffSSMD_{obs} > diffSSMD_{rand}				
	PHOTORECEPTOR_CELL_MAINTENANCE	10	8	13282.27
	NIELSEN_MALIGNANT_FIBROUS_HISTIOCYTOMA_UP	18	12	8588.03
	WALLACE_PROSTATE_CANCER_DN	6	4	5203.44
	BERGER_MBD2_TARGETS	7	2	1003.57
diffSSMD_{obs} < diffSSMD_{rand}				
	GOLGI_MEMBRANE	45	43	12167.03
	VESICLE_COAT	16	15	4060.43
	INTEGRAL_TO_GOLGI_MEMBRANE	10	10	2876.98
	KINESIN_COMPLEX	14	13	3482.33
	GOLGI_APPARATUS_PART	100	94	26243.37
	ENDOCYTIC_VESICLE	14	11	3066.16
	COATED_VESICLE_MEMBRANE	17	15	4060.43
	TRANSPORT_VESICLE	33	28	7491.02
	INTEGRAL_TO_ORGANELLE_MEMBRANE	50	48	14317.3
	MEMBRANE_COAT	17	16	4325.21
	TRANS_GOLGI_NETWORK	21	19	4744.92
	GOLGI_ASSOCIATED_VESICLE	29	26	7170.73
	INTRINSIC_TO_GOLGI_MEMBRANE	15	15	4531.93
	COATED_MEMBRANE	17	16	4325.21
	TRANS_GOLGI_NETWORK_TRANSPORT_VESICLE	13	12	2874.72
	PHOSPHOLIPID_BIOSYNTHETIC_PROCESS	39	38	9697.56
	GLYCEROPHOSPHOLIPID_BIOSYNTHETIC_PROCESS	30	29	7703.07
	GLYCOLIPID_METABOLIC_PROCESS	16	15	2599
	VIRAL_GENOME_REPLICATION	21	18	4830.73
	PATTERN_SPECIFICATION_PROCESS	31	20	4631.62
	RESPONSE_TO_TOXIN	10	7	270.64
	VIRAL_INFECTIOUS_CYCLE	32	26	7117.43
	VIRAL_REPRODUCTIVE_PROCESS	36	30	8402.15
	POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	14	14	4122.54
	MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS	49	47	10606.59
	RAS_PROTEIN_SIGNAL_TRANSDUCTION	66	61	9605.12
	GLYCOSPHINGOLIPID_METABOLIC_PROCESS	12	11	1131.99
	NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	17	15	3907.94
	GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	46	44	10876.91
	ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CELL_POLARITY	19	13	3864.83
	INACTIVATION_OF_MAPK_ACTIVITY	14	12	3095.47
	SPHINGOLIPID_BIOSYNTHETIC_PROCESS	10	9	926
	REGULATION_OF_RAS_GTPASE_ACTIVITY	11	11	3108
	ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	122	91	28148.17
	SUGAR_BINDING	34	16	4145.68
	SPECIFIC_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	35	31	7741.1
	SULFOTRANSFERASE_ACTIVITY	28	20	5935.63
	OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	12	12	3329.06
	NEUROPEPTIDE_BINDING	23	8	1173.58
	NEUROPEPTIDE_RECEPTOR_ACTIVITY	22	8	1173.58
	NEUTRAL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	12	7	1776.72
	PEPTIDE_BINDING	85	51	16039.52
	ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY	16	15	2975.02
	NF_KAPPAB_BINDING	11	11	2975.53
	ACTIN_FILAMENT_BINDING	25	25	6998.07
	TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	20	17	5162.21
	TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	32	24	6177.74
	CARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	44	27	7153.4
	GALACTOSYLTRANSFERASE_ACTIVITY	16	14	3551.61
	AAGWWRNYGGC_UNKNOWN	119	107	28387.78
	AGCYRWTTTC_UNKNOWN	122	87	16729.68
	ATGGYGGA_UNKNOWN	102	92	28125.28
	CCTNTMAGA_UNKNOWN	127	102	32811.66
	ACTACCT,MIR-196A,MIR-196B	145	113	31626.25
	KMCATNNWGGA_UNKNOWN	90	77	21122.92

RRCCGTTA_UNKNOWN	87	74	23615.87
SNACANNYSYAGA_UNKNOWN	90	79	19106.18
TGTYNNNNRGCARM_UNKNOWN	86	68	23086.7
TNCATNTCCYR_UNKNOWN	131	117	33594.9
MORF_TERF2IP	112	110	32561.32
MORF_PAPSS1	101	100	29472.36
MORF_RUNX1	150	117	34955.63
MORF_SS18	61	59	17950.71
GCM_ERBB2IP	64	61	19546.33
GCM_BMPR2	84	80	22228.1
GNF2_ATM	30	28	8025.4
GNF2_CASP4	24	24	6469.52
GNF2_MSN	24	24	6571.8
GNF2_PAK2	28	28	7839.01
GNF2_PTPN4	51	40	6740.23
GNF2_PTPRC	68	67	20342.76
GNF2_RAP1B	36	36	10316.35
GNF2_SNRK	28	27	7832.82
GNF2_STAT6	79	79	23979.37
KEGG_GLYCOLYSIS_GLUONEOGENESIS	62	53	15518.48
KEGG_FATTY_ACID_METABOLISM	42	33	8919.33
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	77	64	19703.59
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	26	21	5234.08
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES	14	12	1593.52
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	15	14	2324.53
KEGG_PROPANOATE_METABOLISM	33	31	8209.5
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	22	22	5115.46
KEGG_PROSTATE_CANCER	89	83	22999.38
BIOCARTA_BLYMPHOCYTE_PATHWAY	11	11	2853.81
BIOCARTA_IL4_PATHWAY	11	11	2993.47
BIOCARTA_MCALPAIN_PATHWAY	25	23	7087.18
BIOCARTA_PPARA_PATHWAY	58	48	5427.65
BIOCARTA_P38MAPK_PATHWAY	40	39	11738.56
BIOCARTA_PML_PATHWAY	17	16	4053.62
BIOCARTA_TEL_PATHWAY	18	18	6510.63
BIOCARTA_ACTINY_PATHWAY	20	19	5278.7
chr1p11	11	4	720.08
chr8p23	201	39	13126.04
chr9q32	45	26	6788.69
chrXq13	102	43	12290.93
chr9p22	61	18	3732.1
chr2q35	66	44	10933.41
MODULE_89	14	13	3134.48
MODULE_90	17	15	3334.59
MODULE_168	22	22	5893.79
MODULE_182	101	88	26595.14
MODULE_189	23	22	5163.49
MODULE_203	16	14	3340.15
MODULE_235	81	70	16624.16
MODULE_239	120	114	32611.37
MODULE_261	101	91	27362.39
MODULE_432	15	14	3771.95
MODULE_464	14	13	3639.27
MODULE_519	15	13	3244.43
MODULE_543	17	13	3082.26
MODULE_552	18	18	4693.43
PID_TELOMERASEPATHWAY	68	67	19612.91
PID_HEDGEHOG_GLIPATHWAY	48	46	12508.48
PID_TGFBRPATHWAY	55	50	14630.74
REACTOME_GLYCOGEN_BREAKDOWN_GLYCOGENOLYSIS	18	15	3997.26
REACTOME_PYRIMIDINE_CATABOLISM	12	9	549.45
REACTOME_TETRAHYDROBIOPTERIN_BH4_SYNTHESIS_RECYCLING_SALVAGE_AND_REGULATION	13	11	3080.34
REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS	17	15	4213.4
REACTOME_ALPHA_LINOLENIC_ACID_ALA_METABOLISM	12	11	1871.36

REACTOME_ELEVATION_OF_CYTOSOLIC_CA2_LEVELS	10	5	1053.85
REACTOME_METABOLISM_OF_NUCLEOTIDES	72	66	18322.99
REACTOME_SPHINGOLIPID_METABOLISM	69	59	18781.85
REACTOME_RECYCLING_PATHWAY_OF_L1	27	26	7619.25
REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSMINATION	17	16	4254.72
REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION	33	29	7564.11
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION	14	10	2384.54
REACTOME_KINESINS	24	22	5924.76
REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI	18	14	3433.84
REACTOME_CHOLESTEROL_BIOSYNTHESIS	24	21	5678.3
REACTOME_PYRIMIDINE_METABOLISM	24	21	3657.69
ZHONG_RESPONSE_TO_AZACITIDINE_AND_TSA_DN	70	65	19101
LIU_VMYB_TARGETS_UP	127	113	32555.06
NEWMAN_ERCC6_TARGETS_UP	26	21	6248.71
RODRIGUES_DCC_TARGETS_DN	121	112	35789.78
VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN	138	93	16508
TIEN_INTESTINE_PROBIOTICS_2HR_DN	88	85	22303.09
KIM_WT1_TARGETS_8HR_DN	129	103	31243.64
LAU_APOPTOSIS_CDKN2A_DN	5	4	973.36
CASTELLANO_HRAS_TARGETS_DN	6	6	957.56
CASTELLANO_HRAS_AND_NRAS_TARGETS_DN	8	7	1114.4
WANG_BARRETTES_ESOPHAGUS_UP	51	37	10187.32
LUCAS_HNF4A_TARGETS_UP	58	49	9702.12
KLEIN_TARGETS_OF_BCR_ABL1_FUSION	45	40	11652.34
IWANAGA_E2F1_TARGETS_NOT_INDUCED_BY_SERUM	6	6	1392.35
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29	11	4	1207.76
MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_18	8	5	1279.71
BOWIE_RESPONSE_TO_TAMOXIFEN	18	18	-1176.29
DAUER_STAT3_TARGETS_DN	50	48	10800.47
KORKOLA_TERATOMA	39	27	7927.57
TERAMOTO_OPN_TARGETS_CLUSTER_3	5	4	1049.74
TERAMOTO_OPN_TARGETS_CLUSTER_5	7	7	1684.51
HEIDENBLAD_AMPLICON_12P11_12_DN	30	20	4203.83
MURATA_VIRULENCE_OF_H_PILORI	24	20	5763.69
MAINA_VHL_TARGETS_DN	18	14	2702.83
THEODOROU_MAMMARY_TUMORIGENESIS	31	15	3597.49
KAUFFMANN_MELANOMA_RELAPSE_UP	61	59	16517.77
GROSS_ELK3_TARGETS_DN	32	25	7547.74
SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX6_DN	5	2	443.28
COURTOIS_SENESCENCE_TRIGGERS	6	6	1479.96
RICKMAN_HEAD_AND_NECK_CANCER_D	37	21	7500.37
MORI_LARGE_PRE_BII_LYMPHOCYTE_DN	58	56	16464.52
MORI_MATURE_B_LYMPHOCYTE_UP	90	86	26604.64
NIKOLSKY_BREAST_CANCER_1Q32_AMPLICON	13	12	3293.55
BYSTRYKH_SCP2_QTL	6	4	619.58
KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN	58	55	15315.08
PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP	19	18	4654.95
SHIPP_DLCL_VS_FOLLICULAR_LYMPHOMA_DN	45	40	9414.39
REN_BOUND_BY_E2F	61	61	18365.62
GALINDO_IMMUNE_RESPONSE_TO_ENTEROTOXIN	85	81	26394.45
FAELT_B_CLL_WITH_VH_REARRANGEMENTS_UP	48	48	12734.2
NEMETH_INFLAMMATORY_RESPONSE_LPS_UP	88	82	24735.13
XU_RESPONSE_TO_TRETINOIN_UP	16	14	3396.55
GREENBAUM_E2A_TARGETS_UP	33	32	8452.65
ZHANG_RESPONSE_TO_CANTHARIDIN_UP	19	17	4657.55
BROWNE_INTERFERON_RESPONSIVE_GENES	68	64	13894.72
DASU_IL6_SIGNALING_SCAR_UP	30	27	8056.83
CHIBA_RESPONSE_TO_TSA	50	42	12412.14
EHRlich_ICF_SYNDROM_DN	15	14	3931.79
WEIGEL_OXIDATIVE_STRESS_BY_HNE_AND_TBH	60	53	16019.48
ZHU_CMV_24_HR_UP	93	90	23697.2
NIELSEN_LEIOMYOSARCOMA_UP	18	14	-602.41
GENTILE_UV_RESPONSE_CLUSTER_D8	40	38	10431.4

GENTILE_RESPONSE_CLUSTER_D3	61	59	17748.07
TSENG_ADIPOGENIC_POTENTIAL_UP	30	22	6353.8
DURCHDEWALD_SKIN_CARCIANOGENESIS_UP	88	68	20112.66
GAVIN_FOXP3_TARGETS_CLUSTER_T4	94	88	27334.62
GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_DN	5	4	749.06
MCGOWAN_RSP6_TARGETS_DN	5	5	1094.58
MOSERLE_IFNA_RESPONSE	31	31	9180.06
BERNARD_PPAPDC1B_TARGETS_UP	40	35	10925.22
CHUNG_BLISTER_CYTOTOXICITY_DN	44	41	11565.73
SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN	7	4	1182.49
HUANG_DASATINIB_RESISTANCE_DN	69	59	12873.63
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	102	98	29003.88
MARTINELLI_IMMATURE_NEUTROPHIL_UP	11	3	372.46
HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP	70	63	19582.94
LEE_EARLY_T_LYMPHOCYTE_DN	57	51	15821.05
SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5	70	58	16674.65
FERRANDO_HOX11_NEIGHBORS	23	18	5263.15
ZHAN_EARLY_DIFFERENTIATION_GENES_DN	42	40	11082.27
MILI_PSEUDOPODIA	43	43	12697.83
IRITANI_MAD1_TARGETS_UP	13	9	1018.97
ZHAN_LATE_DIFFERENTIATION_GENES_DN	16	15	3173.69
BOYALT_LIVER_CANCER_SUBCLASS_G1_DN	40	37	11819.47
CHIANG_LIVER_CANCER_SUBCLASS_UNANNOTATED_UP	85	68	20471.15
MIKKELSEN_IPS_ICP_WITH_H3K27ME3	54	27	9328.12
MARSON_FOXP3_TARGETS_DN	54	49	14468.09
WINNEPENNINGKX_MELANOMA_METASTASIS_DN	46	26	-728.51
TSAI_DNAJB4_TARGETS_UP	13	12	3266.59
ZHAN_MULTIPLE_MYELOMA_CD1_DN	45	42	12073.8
KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN	46	43	10219.1
DAZARD_UV_RESPONSE_CLUSTER_G24	28	19	-944.96
RUAN_RESPONSE_TO_TROGLITAZONE_DN	19	14	3535.99
KIM_ALL_DISORDERS_DURATION_CORR_UP	9	7	1825.02
JOHNSTONE_PARVB_TARGETS_1_DN	63	50	6177.03
DELPUECH_FOXP3_TARGETS_UP	68	62	18823.22
KASLER_HDAC7_TARGETS_2_DN	32	30	8681.28
JUBAN_TARGETS_OF_SPI1_AND_FLI1_UP	115	107	32090.64
KOHOUTEK_CCNT2_TARGETS	58	39	11809.4
LE_NEURONAL_DIFFERENTIATION_DN	19	17	4403.91
HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_DN	25	23	6467.86
SMIRNOV_RESPONSE_TO_IR_2HR_DN	55	54	15749.72
BCAT_BILD_ET_AL_DN	46	44	13511.4
EIF4E_UP	100	79	24878.26
PDGF_ERK_DN.V1_DN	149	129	38457.45
HORTON_SREBF_TARGETS	25	23	6436.94
GSE15659_NAIVE_CD4_TCELL_VS_RESTING_TREG_UP	200	146	27222.29
GSE15659_NAIVE_CD4_TCELL_VS_ACTIVATED_TREG_UP	200	133	36038.03
GSE15659_RESTING_VS_ACTIVATED_TREG_UP	200	120	22963.11
GSE17974_IL4_AND_ANTI_IL12_VS_UNTREATED_1H_ACT_CD4_TCELL_UP	200	113	34236.76
GSE34205_HEALTHY_VS_RSV_INF_INFANT_PBMCDN	200	148	42489.3