



(12) **DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION**

(13) **A1**

(86) **Date de dépôt PCT/PCT Filing Date:** 2022/09/01
(87) **Date publication PCT/PCT Publication Date:** 2023/03/09
(85) **Entrée phase nationale/National Entry:** 2024/03/01
(86) **N° demande PCT/PCT Application No.:** US 2022/075807
(87) **N° publication PCT/PCT Publication No.:** 2023/034892
(30) **Priorité/Priority:** 2021/09/02 (US63/240,308)

(51) **Cl.Int./Int.Cl.** **G16B 25/10** (2019.01),
C12Q 1/6886 (2018.01), **G16H 50/20** (2018.01)
(71) **Demandeur/Applicant:**
UNIVERSITY OF UTAH RESEARCH FOUNDATION, US
(72) **Inventeurs/Inventors:**
JUDSON-TORRES, ROBERT L., US;
BELOTE, RACHEL, US
(74) **Agent:** ROBIC AGENCE PI S.E.C./ROBIC IP AGENCY
LP

(54) **Titre : EVALUATION DE LA REPONSE A LA THERAPIE DU MELANOME**
(54) **Title: ASSESSMENT OF MELANOMA THERAPY RESPONSE**

(57) **Abrégé/Abstract:**

Described herein are methods for stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis and optionally administering a treatment depending on the results. Embodiment described herein are methods for stratifying and evaluating melanoma treatment response in a subject based on single cell or bulk RNA sequencing, bulk transcriptome profiling and/or transcript counting and a two-step deconvolution analysis and optionally administering a treatment depending on the results.



Date Submitted: 2024/03/01

CA App. No.: 3230778

Abstract:

Described herein are methods for stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis and optionally administering a treatment depending on the results. Embodiment described herein are methods for stratifying and evaluating melanoma treatment response in a subject based on single cell or bulk RNA sequencing, bulk transcriptome profiling and/or transcript counting and a two-step deconvolution analysis and optionally administering a treatment depending on the results.

ASSESSMENT OF MELANOMA THERAPY RESPONSE

CROSS-REFERENCE TO RELATED APPLICATIONS

5 This application claims priority to U.S. Provisional Patent Application No. 63/240,308 filed on September 2, 2021, which is incorporated by reference herein in its entirety.

REFERENCE TO SEQUENCE LISTING

10 This application was filed with a Sequence Listing XML in ST.26 XML format accordance with 37 C.F.R. § 1.831 and PCT Rule 13~~ter~~. The Sequence Listing XML file submitted in the USPTO Patent Center, "026389-9325-WO01_sequence_listing_xml_24-AUG-2022.xml," was created on August 24, 2022, contains 3 sequences, has a file size of 3.92 Kbytes, and is incorporated by reference in its entirety into the specification.

TECHNICAL FIELD

15 Described herein are methods for stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis and optionally administering a treatment depending on the results. Embodiment described herein are methods for stratifying and evaluating melanoma treatment response in a subject based on single cell or bulk RNA sequencing, bulk transcriptome profiling
20 and/or transcript counting and a two-step deconvolution analysis and optionally administering a treatment depending on the results.

BACKGROUND

25 Epidermal melanocytes, the pigment producing cells of human skin, are responsible for skin tone and orchestrate the primary defense against ultraviolet (UV) radiation. Some anatomic site-specific differences in pigmentation are due to environmental factors, such as the tanning response to UV exposure. Others, like the hypopigmentation at volar sites (such as palms and soles), are present at birth. In adult skin, mesenchymal – melanocyte interactions are known to influence anatomic site-specific melanocyte survival and pigment production but melanocyte
30 intrinsic factors that contribute to site-specific specialization remain unclear.

Model organisms are powerful tools for investigating melanocyte development. In chick and mouse, a transient, multipotent neural crest cell population gives rise to committed immature melanocyte precursors, called melanoblasts, via two spatially and temporally distinct pathways. Such studies focus primarily on melanocytes in skin appendages (hair follicle, feather, and sweat

gland). However, despite constituting the predominate subtype in human skin, resident epidermal melanocytes have not been the subject of analogous investigations into developmental trajectories and anatomic-specializations.

Melanocytes can give rise to melanomas which present distinct phenotypic and genomic characteristics correlated with primary tumor location. Like many cancers, melanoma progression is coupled to dedifferentiation of the cell of origin. The aggressive nature of melanoma is proposed to be rooted in unique attributes of the melanocytic lineage. Decoding the transcriptome of epidermal melanocytes across the human body during development and in aged skin would provide insight into the precise origins of melanoma and the developmental programs reacquired during progression.

Single cell RNA sequencing (scRNA-seq) characterizes cell heterogeneity with unprecedented resolution. Pioneering studies of human skin with scRNA-seq focused on predominant cell types (keratinocytes, fibroblasts) from few and/or uniform samples and lacked substantial representation of rare cell types, including melanocytes. Consequently, the melanocytes captured were not characterized beyond inter-cell type comparisons. Additionally, single cell sequencing efforts for human fetal tissue have not included the melanocytic lineage.

What is needed is a cell atlas of human epidermal melanocytes during development and aging that captured diversity within and across anatomic locations, sex, and multiple skin tones. This will permit assessment of the response of melanoma cancers to various therapeutic agents.

SUMMARY

One embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from a subject; (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data; (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor sample into a specific melanoma cell subtype; and (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when the calculated total melanoma tumor expression of the second gene signature is below the critical threshold value, an effective

amount of an ICI treatment is administered to the subject; or when the calculated total melanoma tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18. In another aspect, when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma. In another aspect, when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14,

PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

Another embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from a subject; (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data; (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor into a specific melanoma cell subtype; (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; and (e) calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment; when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered

to the subject. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

Another embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using RNA hybridization, and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from the subject; (b) performing RNA hybridization of the melanoma tumor sample using a targeted RNA probe panel to obtain targeted transcript expression data; (c) on a processor, deconvoluting the targeted transcript expression data using a first gene signature from the targeted RNA probe panel to stratify the melanoma into a specific melanoma cell subtype; and (d) deconvoluting the targeted transcript expression data using a second gene signature from the targeted RNA probe panel to calculate an estimate of the total number of cells in the tumor sample that express the second gene signature; wherein when the calculated estimate of total tumor expression of the second gene signature reaches a critical threshold value, the tumor will not respond to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the melanoma tumor sample comprises one or more biopsy samples or one or more formalin fixed paraffin embedded (FFPE) tumor tissue samples from the subject. In another aspect, the targeted RNA probe panel comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18,

NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, 5 MOB1B, RPS24, UQCRRF5, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, 10 DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, 15 GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, and CYC1. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the method further comprises: 20 when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor 25 selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from 30 trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin,

carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof.

Another embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using bulk transcriptomic data and a two-step deconvolution analysis, the method comprising: (a) obtaining one or more melanoma tumor samples from a subject; (b) performing RNA sequencing of the one or more melanoma tumor samples and obtaining bulk transcriptomic data; (b) performing transcript counting on the bulk transcriptomic data to obtain transcript expression data; (c) on a processor, deconvoluting the transcript expression data using a first gene signature to stratify the melanoma into a specific melanoma cell subtype or origin; and (d) deconvoluting the transcript expression data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature or determine the cell differentiation state; wherein when the calculated estimate of total expression of the second gene signature reaches a critical threshold value, the melanoma will not respond to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when the calculated total tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or when the calculated total tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from

dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the first gene signature comprises

5 one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18. In another aspect, when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma. In

10 another aspect, the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5,

15 MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN,

20 NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1,

25 TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2,

30 TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

- 5 FIG. 1A–L show melanocyte transcriptomic profiles differ based on development and anatomic location. FIG. 1A shows fresh from healthy human skin single cell isolation, enrichment, and sequencing pipeline. FIG. 1B shows UMAP visualization of the 9,719 cells (7088 melanocytes, 1865 keratinocytes, 636 eccrine, 76 dendritic, 25 mast, and 29 T-cells) that passed quality control. Colored by cell types identified from Louvain clustering and candidate genes.
- 10 FIG. 1C shows a heat map showing the relative expression of top differentially expressed genes for 100 random selected cells from each cell-type cluster in FIG. 1B. FIG. 1D–H show UMAPs of all non-cycling melanocytes with Louvain clustering and demographic information overlays. Three low-resolution Louvain clusters correspond to developmental age: adult (cluster A), fetal (cluster B), and neonatal (cluster C). FIG. 1E shows the 11 high-resolution Louvain clusters (0–10) do
- 15 not correspond to sex (FIG. 1F), skin tone (FIG. 1G), or donor (FIG. 1H). FIG. 1I shows a dot plot of the mean expression and fraction of cells expressing the top 5 ranked genes (two-sided Wilcoxon Rank-sum) for each high-resolution Louvain cluster in FIG. 1E with a hierarchical clustering dendrogram. Using the average expression of the top 15 melanocyte specific principal components, high-resolution Louvain clusters were binned into four groups: m1 (fetal cluster 10),
- 20 m2 (fetal clusters 3,2,6), m3 (adult clusters 4,1,0,7,5), and m4 (neonatal (neo) clusters 9,8). FIG. 1J shows a dot plot showing group m1, from fetal hair-bearing non-volar cutaneous skin, expresses known melanocyte stem cell (MSC) markers. FIG. 1K–L show UMAP of all non-cycling melanocytes with developmental age (FIG. 1K) and fetal MSC annotation based on hierarchical clustering of high-resolution Louvain clusters in FIG. 1I and anatomic location overlay (FIG. 1L).
- 25 FIG. 2A–H show the characterization of divergent pigment developmental trajectories in volar and non-volar melanocytes. FIG. 2A shows a schematic illustrating cohort of donor-matched non-volar and volar skin. $n = 6$ donors and 17 total skin specimens. FIG. 2B shows raw and average normalized BSC values (FIG. 2C) of volar and non-volar cutaneous melanocytes prior to 18 weeks (pre-bifurcation) and at/after 18 weeks (post-bifurcation). Two-sided Wilcoxon Rank
- 30 Sum Test, Bonferroni multiple testing adjusted p-value: ns, p-value = 0.25; *p-value = 3.6×10^{-165} . Box: interquartile range with median, standard deviation, and outliers (grey circles). FIG. 2D shows Fontana Masson staining for melanin/melanosomes in fetal and adult non-volar and volar skin. Representative images from $n = 3$ for each age. Scale bars 50 μm . FIG. 2E shows increased pigment content coincides with upregulation of the pigment transcriptional program in

cutaneous melanocytes at 18 wks. Normalized mean expression of 170 pigment associated genes (thin lines) in volar (blue) and non-volar cutaneous (red) melanocytes. Thick lines: average expression of all pigment associated genes. FIG. 2F shows mean expression of the 14 pigment genes with significant differential expression between non-volar and volar melanocytes from both adult donors with color and size corresponding to fold change between sites. FIG. 2G shows the fold change in expression of the differentially expressed genes in FIG. 2F for each donor matched age. Lineage genes: melanocyte lineage specific genes. Bifurcation-associated: genes with significant differential expression coinciding with pigment bifurcation (between 12 f.w. and 18 f.w.). Post-bifurcation: genes with significant differential expression only in donor matched adult. Unpaired two-tailed t-test * p-value = 0.0278; ** p-value = 0.0013; *** p-value = 3.3×10^{-5} . Box: full range of data values (min to max) and mean. FIG. 2H shows a schematic summarizing the identification of pigment genes associated with intra-individual pigmentation divergence between non-volar cutaneous and volar melanocytes.

FIG. 3A–K show anatomic site-specific melanocyte sub-population enrichment arises during development and persists in adulthood. FIG. 3A shows a volcano plot of genes enriched (two-sided Wilcoxon Rank Sum Test, Benjamini-Hochberg multiple testing) in donor matched non-volar cutaneous vs volar melanocytes. See also Table 1. FIG. 3B shows top site-specific DEGs. FIG. 3C shows fraction of melanocytes with v-mel or c-mel signature in each skin specimen (n = 34) from all 22 donors. Box: 25%, 75%, and median. Two-sided Mann-Whitney U test with Bonferroni multiple testing correction, * p-value = 0.12, ** p-value palm: 0.0061, sole: 0.0058 ***p-value = 0.00021, ****p-value = 8.2×10^{-6} . FIG. 3D shows expression level of v-mel gene, *NTRK2*, and c-mel gene, *HPGD*, in all volar melanocytes (n = 1,634 cells) compared to all non-volar cutaneous melanocytes (n = 5,192 cells). Two-sided Mann-Whitney U test, ***p-value = 1.9×10^{-100} , ****p-value = 0. Interquartile range with median, standard deviation, and outliers (grey circles). FIG. 3E shows representative pseudo-colored fluorescent microscopy images from *NTRK2*, *HPGD*, and the melanocyte marker *DCT* (outlined in yellow) mRNA staining in adult volar and non-volar epidermis. Dashed line: epidermal-dermal junction. FIG. 3F shows quantification of *NTRK2* and *HPGD* foci in *DCT*+ melanocytes in volar (n = 44 cells) and non-volar cutaneous skin (n = 22) in FIG. 3E. Two-tailed unpaired t-test ***p-value = 5.5×10^{-6} , ****p-value = 4.1×10^{-7} ; box: 25%, 75%, median; whiskers: 10–90%, and outliers (grey circles). FIG. 3G shows the percent v-mel (*NTRK2* > *HPGD*) and c-mel (*HPGD* > *NTRK2*) at each site in FIG. 3E–F; ‡ two-tailed, two-sample Z-test for proportions, v-mel: z = 6.062, p-value = 1.8×10^{-11} , and c-mel: z = 7.885, p-value = 1.6×10^{-15} . FIG. 3H shows immunofluorescence co-staining of adult volar and non-volar skin cryo-sections with the c-mel marker *HPGD* (green) and melanocyte marker *KIT*

(magenta). Dashed line: epidermal-dermal junction. FIG. 3I shows percent HPGD positive melanocytes per donor volar and non-volar skin. Adult skin: A1046, n = 78 cells; A1038, n = 39 cells; A1018, n = 48 cells; A1026, n = 15 cells. Fetal skin: 9WK07, n = 41 cells; 16WK04, n = 10 cells. Two-tailed unpaired t-test, ** p-value = 0.001. FIG. 3J shows an illustration depicting the hypothesis that healthy melanocyte anatomic site-specific transcriptional programs are conserved in melanoma. FIG. 3K shows the ratio of the average expression of the top v-mel and c-mel genes in primary melanomas (acral: n = 15, non-acral cutaneous: n = 103), unpaired two-tailed t-test, ****p-value = 1.5×10^{-6} ; box: 25%, 75%, median; whiskers: 10–90%, and outliers (grey circles).

FIG. 4A–G show defining human specific melanocyte developmental transcriptomic programs. FIG. 4A shows a heatmap of the median Normalized Enrichment Scores (NES)s of GO-bp terms enriched at each developmental stage. FIG. 4B shows a schematic of the Developmental stage Melanocyte logistical regression model (DevMel LOGIT) used to generate and validate unique transcription profiles for each developmental stage of normal human melanocytes. The bottom of FIG 4B shows a heatmap of the relative expression (column z score) of genes in each DevMel program (prg). FIG. 4C–F show DevMel program expression is highly expressed by cells from all skin donors within each corresponding developmental stage. Program expression for each donor (black line, average) is the ratio of the mean expression of positively correlated genes and negatively correlated genes. Significant by one-sided Mann Whitney U test, MSC n = 3; FET n = 5; NEO n = 2; ADT n = 14 donors. FIG. 4C: prg[MSC]: MSC vs rest *** p-value = 0.0005; FIG. 4D: prg[FET]: FET vs rest **** p-value = 0.0001; FIG. 4E: prg[NEO]: FET vs rest ** p-value = 0.0072; FIG. 4F: prg[ADT]: ADT vs rest **** p-value = 5.1×10^{-7} .

FIG. 5A–J shown the evaluation of model mammalian melanocyte developmental program expression in human non-volar cutaneous melanocyte developmental groups. FIG. 5A shows a schematic summarizing human and corresponding mouse melanocyte development. In hair-bearing skin, both humans and mice develop follicular melanocytes (purple). Mice retain a dermal melanocyte population (blue) in fully developed skin, whereas humans develop resident epidermal melanocytes (red) within the skin at all anatomic locations. Pink bar indicates human fetal ages captured in this study's dataset. FIG. 5B–C show violin plots showing distribution of indicated transcriptional program expression scores for individual cells within each developmental group: ADT n = 3281, NEO n = 735, FET n = 1176, and MSC n = 63. Dashed line: mean expression. Program scores were generated from published signatures of: FIG. 5B shows mouse melanoblasts (cells committed to the melanocyte fate) **** p-value = 1.5×10^{-14} ; ** p-value = 1.0×10^{-8} ; *** p-value = 2.3×10^{-19} ; **** p-value = 5.9×10^{-28} ; mouse melanocytes, **** p-value = 2.8

$\times 10^{-13}$; melanocyte stem cells from mature hair follicles in adult mice, **** p-value = 4.5×10^{-38} . FIG. 5C shows *in vitro* stages of differentiation of human pluripotent stem cells to melanocytes, **** p-value = 2.8×10^{-25} . Significance determined by one-sided Man-Whitney U test, **** p-value < 1×10^{-7} . The variance (reported below the corresponding group for each violin plot) of the average program expression among donors within the MSC, FET, NEO, and ADT groups was low showing concordance across ages within each group. FIG. 5D–E show Venn diagrams showing the number of unique and overlapping genes of melanoblast-related gene signatures with the positive correlated component of the DevMel profiles prg[MSC] (FIG. 5D) and prg[FET] (FIG. 5E). FIG. 5F–G show Venn diagrams showing the number of unique and overlapping genes of differentiated melanocyte related gene signatures with the positively correlated component of the DevMel profiles prg[NEO] (FIG. 5GF) and prg[ADT] (FIG. 5G).

FIG. 6A–G show the identification of distinct patterns of developmental programs reacquired in metastasized melanomas. FIG. 6A shows DevMel LOGIT was used to classify individual melanoma cells by normal melanocyte developmental stages. Every melanoma cell (MAL) was categorized by the predominantly expressed developmental stage program. FIG. 6B shows individual tumors are a heterogeneous mix of malignant cells in different dedifferentiation states. Fraction of MAL^{ADT}, MAL^{NEO}, MAL^{FET} and MAL^{MSC} cells in each of the 14 tumors analyzed from Tirosh et al., *Science* 352(6282):189-196 (2016) and Jerby-Arnon et al., *Cell* 175(4) :984-997 (2018) in FIG. 6A. FIG. 6C shows Top: Workflow to generate gene set (511 unique genes) used to identify patterns associated with melanoma dedifferentiation. Bottom: Percent of genes across MAL groups that exhibit patterns consistent with dedifferentiation categories in (FIG 6 D, E, and G). FIG. 6D–G show dedifferentiation can occur through several categories of cancer-associated transcriptional reprogramming: FIG. 6D shows sequential dedifferentiation, a reverse stepwise unfolding of development; FIG. 6E shows direct dedifferentiation, direct reacquisition of programs from early developmental stages; FIG. 6F shows melanoma specific, acquisition of programs not associated with the stages of melanocyte development identified here. FIG. 6G shows normal adult developmental stage programs that are lost and earlier developmental stage programs that are not readopted in metastatic melanoma. Examples of each category are visualized as heatmaps of the relative expression (row z score). See Table 3 for complete gene lists.

FIG. 7A–F show the reacquisition of specific developmental programs in heterogeneous melanoma is prognostic. FIG. 7A shows the hierarchical clustering of TCGA SKCM tumors based on fractional composition of normal melanocyte developmental stages assigned using CIBERSORT (top) with clinicopathological features (bottom panels). FIG. 7B shows Kaplan Meier

curves (two-side, log-rank test) for each SKCM group from FIG. 7A. Enrichment for cells similar to ADT is associated with increased survival, whereas enrichment for NEO is associated with worse survival. FIG. 7C shows Kaplan Meier curve (two-side, log-rank test) showing enrichment of NEO fraction is associated with worse survival in second cohort (Lund University). FIG. 7D shows the fraction of MAL^{NEO} cells from the single cell tumors (untreated n = 7, resistant n = 7) from FIG. 5B correlates with post-ICI resistance. Unpaired one-sided t-test, ** p-value = 0.0099. Black bar: mean. FIG. 7E shows expression of the MAL^{NEO} signature (Top 100 DEGs, see Table 4) is significantly higher in tumors from patients exhibiting only partial (PR, n = 25) or no response (PD, n = 49) to anti-PD1 treatment compared to those that responded (CR, n = 14). Unpaired one-side t-test, * p-value = 0.018; Box: median, 25%, 75%; whiskers: min-max. FIG. 7F shows a schematic summarizing the decoding of melanoma dedifferentiation using human developmental programs. The left panel of FIG. 7F show that individual melanoma tumors are comprised of a heterogeneous mix of malignant cells expressing defined melanocyte developmental programs. The fraction of cells expressing each program within the tumor is predictive of overall survival and correlates to signatures of immune infiltration, evasion, and potential therapeutic options. The right panel of FIG. 7F shows that each melanoma cell can occupy a different degree of dedifferentiation defined by sequential dedifferentiation transcriptional programs. See FIG. 6 A–G and Table 3. The MSC- and adult-like programs are associated with previously described melanoma signatures whereas the fetal- and neonatal-like programs do not segregate with known melanoma signatures offering unique insight into previously uncharacterized melanoma transcriptional states (see FIG. 8). Melanoma specific genes: genes common to melanoma cells but not melanocytes, such as PRAME. Direct dedifferentiation genes: MSC or FET genes that can be expressed in melanoma cells regardless of the over-all differentiation state of the cell, such as *AXL*, *EGR1* and *HMGA2*.

FIG. 8A–H show the characterization of melanoma cells and tumors classified by *in situ* human melanocyte developmental programs. FIG. 8A–B show density plots showing the expression of the Widmer et al. invasive and proliferative programs (FIG. 8A) and the Tirosh et al (FIG. 8B). *AXL* and *MITF* programs for individual cells in MALADT, MALNEO, MALFET and MALMSC groups. FIG. 8C shows pairwise Fisher (one-sided) exact test showing negative log₁₀ adjusted (Bonferroni multiple testing) p-values for the gene set enrichment analysis conducted using gene signatures from Akbani et al., *Cell* 161: 1681-1696 (2015); Cirenajwis et al., *Oncotarget* 6: 12297-12309 (2015); and Tsoi et al., *Cancer Cell* 33: 890-904.e5 (2018). Significant enrichment determined as adjusted p-value < 0.05. FIG. 8D shows a heatmap illustrating the relative expression levels (row z score) of WNT5A high, TP53 high slow cycling

cell associated genes in each normal melanocyte and MAL developmental group. FIG. 8E shows a heatmap illustrating the relative expression levels (row z score) of the four minimal residual disease states identified by Rambow et al., *Cell* 174: 843-855.e19 (2018) in each normal melanocyte and MAL developmental group. FIG. 8F shows pairwise Fisher (one-sided) exact test showing negative log₁₀ adjusted (Bonferroni multiple testing) p-values for clinicopathological feature and transcriptional categorization within each SKCM group (SKCMADT, SKCMNEO, SKCMFET, SKCMMSC). There is little to no difference in the enrichment of pigment level, mutation category, or tissue origin between SKCM groups in FIG 7. FIG. 8G shows a heatmap illustrating the relative expression levels (row z-score) of immune infiltration program, immune evasion program and FDA-approved therapeutic targets in SKCM groups. FIG. 8H shows the MALNEO signature is enriched for genes down regulated in tumors that respond to Nivolumab treatment (green text). Pairwise Fisher (one-sided) exact test showing negative log₁₀ adjusted (Bonferroni multiple testing) p-values for the gene set enrichment analysis conducted using previously identified prognostic signatures (Table 4).

FIG. 9 shows a scheme for the discovery of two types of melanocytes in adult human skin affected by AM was used to develop classifier that determines the melanocyte cell of origin for individual AM tumors.

FIG. 10 shows a scheme for deconvolving melanoma tumors using healthy melanocyte developmental states identified a dedifferentiated state (neonatal) that was resistant to ICI (anti-PD1) and stratified tumors based on response to anti-PD1 therapy.

FIG. 11A shows one-step deconvolution to estimate percent of ICI-R melanoma cells does not predict response in AM. FIG. 11B shows that the TD-IR method uses a two-step deconvolution to (1) classify tumors as cAM or vAM prior to (2) estimating the percent ICI-R. When the TD-IR method is applied to pretreated AM tumor transcriptomic data the resulting single value score is predictive of anti-PD1 response.

FIG. 12A shows pooling of melanocyte specific RNAscope probes into a melanocyte cocktail provides robust cell-type(state) specific staining in FFPE sections. FIG. 12B shows exemplary RNAscope cocktails for classifying AM by cell of origin and ICI-R cell state.

FIG. 13 shows the sensitivity of NanoString probes are determined using sections from FFPE embedded cell pellets comprising different ratios of cAM/vAM/ ICI-R cells mixed with non-cAM/vAM/ICI-R melanocytes.

DETAILED DESCRIPTION

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art. For example, any nomenclatures used in connection with, and techniques of biochemistry, molecular biology, immunology, microbiology, genetics, cell and tissue culture, and protein and nucleic acid chemistry described herein are well known and commonly used in the art. In case of conflict, the present disclosure, including definitions, will control. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can be used in practice or testing of the embodiments and aspects described herein.

As used herein, the terms “amino acid,” “nucleotide,” “polynucleotide,” “vector,” “polypeptide,” and “protein” have their common meanings as would be understood by a biochemist of ordinary skill in the art. Standard single letter nucleotides (A, C, G, T, U) and standard single letter amino acids (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, or Y) are used herein.

As used herein, the terms such as “include,” “including,” “contain,” “containing,” “having,” and the like mean “comprising.” The present disclosure also contemplates other embodiments “comprising,” “consisting of,” and “consisting essentially of,” the embodiments or elements presented herein, whether explicitly set forth or not.

As used herein, the term “a,” “an,” “the” and similar terms used in the context of the disclosure (especially in the context of the claims) are to be construed to cover both the singular and plural unless otherwise indicated herein or clearly contradicted by the context. In addition, “a,” “an,” or “the” means “one or more” unless otherwise specified.

As used herein, the term “or” can be conjunctive or disjunctive.

As used herein, the term “substantially” means to a great or significant extent, but not completely.

As used herein, the term “about” or “approximately” as applied to one or more values of interest, refers to a value that is similar to a stated reference value, or within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, such as the limitations of the measurement system. In one aspect, the term “about” refers to any values, including both integers and fractional components that are within a variation of up to $\pm 10\%$ of the value modified by the term “about.” Alternatively, “about” can mean within 3 or more standard deviations, per the practice in the art. Alternatively, such as with respect to biological systems or processes, the term “about” can mean

within an order of magnitude, in some embodiments within 5-fold, and in some embodiments within 2-fold, of a value. As used herein, the symbol “~” means “about” or “approximately.”

All ranges disclosed herein include both end points as discrete values as well as all integers and fractions specified within the range. For example, a range of 0.1–2.0 includes 0.1,
5 0.2, 0.3, 0.4 . . . 2.0. If the end points are modified by the term “about,” the range specified is expanded by a variation of up to $\pm 10\%$ of any value within the range or within 3 or more standard deviations, including the end points.

As used herein, the terms “active ingredient” or “active pharmaceutical ingredient” refer to a pharmaceutical agent, active ingredient, compound, or substance, compositions, or mixtures
10 thereof, that provide a pharmacological, often beneficial, effect.

As used herein, the terms “control,” or “reference” are used herein interchangeably. A “reference” or “control” level may be a predetermined value or range, which is employed as a baseline or benchmark against which to assess a measured result. “Control” also refers to control experiments or control cells.

As used herein, the term “dose” denotes any form of an active ingredient formulation or composition, including cells, that contains an amount sufficient to initiate or produce a therapeutic effect with at least one or more administrations. “Formulation” and “composition” are used
15 interchangeably herein.

As used herein, the term “prophylaxis” refers to preventing or reducing the progression of a disorder, either to a statistically significant degree or to a degree detectable by a person of
20 ordinary skill in the art.

As used herein, the terms “effective amount” or “therapeutically effective amount,” refers to a substantially non-toxic, but sufficient amount of an action, agent, composition, or cell(s) being administered to a subject that will prevent, treat, or ameliorate to some extent one or more of the
25 symptoms of the disease or condition being experienced or that the subject is susceptible to contracting. The result can be the reduction or alleviation of the signs, symptoms, or causes of a disease, or any other desired alteration of a biological system. An effective amount may be based on factors individual to each subject, including, but not limited to, the subject’s age, size, type or extent of disease, stage of the disease, route of administration, the type or extent of supplemental
30 therapy used, ongoing disease process, and type of treatment desired.

As used herein, the term “subject” refers to an animal. Typically, the subject is a mammal. A subject also refers to primates (e.g., humans, male or female; infant, adolescent, or adult), non-human primates, rats, mice, rabbits, pigs, cows, sheep, goats, horses, dogs, cats, fish, birds, and the like. In one embodiment, the subject is a primate. In one embodiment, the subject is a human.

As used herein, a subject is “in need of treatment” if such subject would benefit biologically, medically, or in quality of life from such treatment. A subject in need of treatment does not necessarily present symptoms, particular in the case of preventative or prophylaxis treatments.

As used herein, the terms “inhibit,” “inhibition,” or “inhibiting” refer to the reduction or suppression of a given biological process, condition, symptom, disorder, or disease, or a significant decrease in the baseline activity of a biological activity or process.

As used herein, “treatment” or “treating” refers to prophylaxis of, preventing, suppressing, repressing, reversing, alleviating, ameliorating, or inhibiting the progress of biological process including a disorder or disease, or completely eliminating a disease. A treatment may be either performed in an acute or chronic way. The term “treatment” also refers to reducing the severity of a disease or symptoms associated with such disease prior to affliction with the disease. “Repressing” or “ameliorating” a disease, disorder, or the symptoms thereof involves administering a cell, composition, or compound described herein to a subject after clinical appearance of such disease, disorder, or its symptoms. “Prophylaxis of” or “preventing” a disease, disorder, or the symptoms thereof involves administering a cell, composition, or compound described herein to a subject prior to onset of the disease, disorder, or the symptoms thereof. “Suppressing” a disease or disorder involves administering a cell, composition, or compound described herein to a subject after induction of the disease or disorder thereof but before its clinical appearance or symptoms thereof have manifest.

As used herein, “bulk transcriptomic data” refers to mRNA transcript data obtained using any technology for assessing average mRNA transcript levels of a mass, group, or population of cells averaged together. For example, “bulk transcriptomic data” could refer to mRNA transcript levels for the entire mixture of cells isolated from a tumor. Typically, such data would include RNA sequencing (RNAseq) and transcript counting (e.g., using NanoString as described herein).

As used herein, “transcript counting” refers to assessing the number of sequences or hybridization probes mapped to each gene as a measure of gene expression. For example, NanoString as described herein provides a hybridization-based technology that permits targeted transcript counting, without amplification and produces highly reproducible gene expression patterns.

As used herein, “immune checkpoint inhibitors” (ICIs) are compounds activate the antitumor immune response by interrupting co-inhibitory signaling pathways and promote immune-mediated elimination of tumor cells. Immune checkpoint inhibitors (ICIs) are approved to treat a variety of cancers, including: breast cancer, bladder cancer, cervical cancer, colon cancer, head and neck cancer, Hodgkin lymphoma, liver cancer, lung cancer, renal cell cancer,

skin cancer, including melanoma, stomach cancer, rectal cancer, or any solid tumor that is not able to repair DNA errors occurring during DNA replication. Typical immune checkpoint inhibitors categorized by their targets. PD-1 inhibitors are monoclonal antibodies that target PD-1. Exemplary approved drugs include: Pembrolizumab (Keytruda®), Nivolumab (Opdivo®), and Cemiplimab (Libtayo®). D-L1 inhibitors are monoclonal antibodies that target PD-L1. Exemplary approved drugs include Atezolizumab (Tecentriq®), Avelumab (Bavencio®), and Durvalumab (Imfinzi®). LAG-3 inhibitors are monoclonal antibodies that target LAG-3. Relatlimab is often coadministered with given along with the PD-1 inhibitor Nivolumab (Opdivo®) in a combination therapeutic known as Opdualag® (nivolumab and relatlimab-rmbw). Opdualag is effective against melanoma and other cancers.

As used herein, “non-immune checkpoint inhibitor therapies” (non-ICI therapy) are cancer or melanoma treatments or therapies not involving immune checkpoint inhibitors. Typical therapies include one or more of surgical excision of the tumor; PARP inhibitors including olaparib (Lynparza®), niraparib (Zejula®), rucaparib (Rubraca®), talazoparib (Talzenna®); BRAF inhibitors including dabrafenib (Tafinlar®), encorafenib (Braftovi®), Vemurafenib (Zelboraf®), combinations of vemurafenib and atezolizumab (Tecentriq®); MEK inhibitors including: trametinib (Mekinist), cobimetinib (Cotellic), and binimetinib (Mektovi); KIT inhibitors including: dasatinib (Sprycel®), imatinib (Gleevec®), and nilotinib (Tasigna®); tumor-agnostic treatments: larotrectinib (Vitrakvi®) and entrectinib (Rozlytrek®); CTLA-4 inhibitors including ipilimumab (Yervoy®); interleukin-2 (IL-2, Proleukin); interferon alfa-2b (Intron A®) or pegylated interferon alfa-2b (Sylatron®); combinations of BRAF inhibitors and MEK inhibitors; chemotherapies including dacarbazine (DTIC®), temozolomide (Temodar®), cisplatin, carboplatin, fotemustine (Muphoran®), iomustine (Gleostine®), docetaxel (Taxotere®), paclitaxel (Taxol®), vinblastine, or combinations such as paclitaxel plus carboplatin or cisplatin plus vinblastine and dacarbazine; or combinations thereof.

In humans, epidermal melanocytes are responsible for skin pigmentation, defense against ultraviolet radiation, and the deadliest common skin cancer, melanoma. While there is substantial overlap in melanocyte, development pathways between different model organisms, species dependent differences are frequent and the conservation of these processes in human skin remains unresolved. Here, a single-cell enrichment and RNA-sequencing pipeline was used to study human epidermal melanocytes directly from skin, capturing transcriptomes across different anatomic sites, developmental age, sexes, and multiple skin tones. The study uncovered subpopulations of melanocytes exhibiting anatomic site-specific enrichment that occurs during gestation and persists through adulthood. The transcriptional signature of the volar-enriched

subpopulation is retained in acral melanomas. In addition, human melanocyte differentiation transcriptional programs were identified that are distinct from gene signatures generated from model systems. Finally, these programs were used to define patterns of dedifferentiation that are predictive of melanoma prognosis and response to immune checkpoint inhibitor therapy.

5 One embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from a subject; (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data; (c) on a processor, deconvoluting the scRNA-seq sequence data using a first
10 gene signature to stratify the melanoma tumor sample into a specific melanoma cell subtype; and (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond
15 to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when the calculated total melanoma tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or when the calculated total melanoma tumor expression of the second gene signature is above the critical threshold value, an effective
20 amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the ICI
25 treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or
30 combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b,

pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18. In another aspect, when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma. In another aspect, when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

Another embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from a subject; (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data; (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor into a specific melanoma cell subtype; (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; and (e) calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value; wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment; when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

Another embodiment described herein is a method of stratifying and evaluating melanoma

treatment response in a subject using RNA hybridization, and a two-step deconvolution analysis, the method comprising: (a) obtaining a melanoma tumor sample from the subject; (b) performing RNA hybridization of the melanoma tumor sample using a targeted RNA probe panel to obtain targeted transcript expression data; (c) on a processor, deconvoluting the targeted transcript expression data using a first gene signature from the targeted RNA probe panel to stratify the melanoma into a specific melanoma cell subtype; and (d) deconvoluting the targeted transcript expression data using a second gene signature from the targeted RNA probe panel to calculate an estimate of the total number of cells in the tumor sample that express the second gene signature; wherein when the calculated estimate of total tumor expression of the second gene signature reaches a critical threshold value, the tumor will not respond to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the melanoma tumor sample comprises one or more biopsy samples or one or more formalin fixed paraffin embedded (FFPE) tumor tissue samples from the subject. In another aspect, the targeted RNA probe panel comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, and CYC1. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR)

score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the method further comprises: when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount
5 of an ICI treatment is administered to the subject; or when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof; a LAG-3 inhibitor
10 selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof; a KIT inhibitor selected from
15 dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;
20 surgical excision; or combinations thereof.

Another embodiment described herein is a method of stratifying and evaluating melanoma treatment response in a subject using bulk transcriptomic data and a two-step deconvolution analysis, the method comprising: (a) obtaining one or more melanoma tumor samples from a subject; (b) performing RNA sequencing of the one or more melanoma tumor samples and
25 obtaining bulk transcriptomic data; (b) performing transcript counting on the bulk transcriptomic data to obtain transcript expression data; (c) on a processor, deconvoluting the transcript expression data using a first gene signature to stratify the melanoma into a specific melanoma cell subtype or origin; and (d) deconvoluting the transcript expression data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that
30 express the second gene signature or determine the cell differentiation state; wherein when the calculated estimate of total expression of the second gene signature reaches a critical threshold value, the melanoma will not respond to immune checkpoint inhibition (ICI) treatment. In one aspect, the melanoma is acral melanoma (AM). In another aspect, the method further comprises: when the calculated total tumor expression of the second gene signature is below the critical

threshold value, an effective amount of an ICI treatment is administered to the subject; or when the calculated total tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject. In another aspect, the method further comprises: calculating a transcriptomic deconvolution-based

5 predictor of ICI resistance (TD-IR) score value; wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment. In another aspect, the ICI treatment comprises: a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof; a PD-L1 inhibitor selected from atezolizumab, avelumab,

10 durvalumab, or combinations thereof; a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof. In another aspect, the alternative non-ICI therapy comprises: a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof; a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof; a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or

15 combinations thereof; a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof; a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof; a CTLA-4 inhibitor selected from ipilimumab; aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof; a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel,

20 vinblastine, or combinations thereof; surgical excision; or combinations thereof. In another aspect, the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5,

25 APCDD1, LINC00462, or GALNT18. In another aspect, when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma. In another aspect, the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified

30 as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma. In another aspect, the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14,

PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1,
5 KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1,
10 SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME,
15 RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

It will be apparent to one of ordinary skill in the relevant art that suitable modifications and adaptations to the compositions, formulations, methods, processes, and applications described herein can be made without departing from the scope of any embodiments or aspects thereof.

20 The compositions and methods provided are exemplary and are not intended to limit the scope of any of the specified embodiments. All of the various embodiments, aspects, and options disclosed herein can be combined in any variations or iterations. The scope of the compositions, formulations, methods, and processes described herein include all actual or potential combinations of embodiments, aspects, options, examples, and preferences herein described.

25 The exemplary compositions and formulations described herein may omit any component, substitute any component disclosed herein, or include any component disclosed elsewhere herein. The ratios of the mass of any component of any of the compositions or formulations disclosed herein to the mass of any other component in the formulation or to the total mass of the other components in the formulation are hereby disclosed as if they were expressly disclosed.

30 Should the meaning of any terms in any of the patents or publications incorporated by reference conflict with the meaning of the terms used in this disclosure, the meanings of the terms or phrases in this disclosure are controlling. Furthermore, the foregoing discussion discloses and describes merely exemplary embodiments. All patents and publications cited herein are incorporated by reference herein for the specific teachings thereof.

Various embodiments and aspects of the inventions described herein are summarized by the following clauses:

Clause 1. A method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising:

- (a) obtaining a melanoma tumor sample from a subject;
- (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data;
- (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor sample into a specific melanoma cell subtype; and
- (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature;

wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment.

Clause 2. The method of clause 1, wherein the melanoma is acral melanoma (AM).

Clause 3. The method of clause 1 or 2, further comprising:

when the calculated total melanoma tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or

when the calculated total melanoma tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject.

Clause 4. The method of any one of clauses 1–3, further comprising:

calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;

wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or

wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.

Clause 5. The method of any one of clauses 1–4, wherein the ICI treatment comprises:

a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;

a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;

5 a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.

Clause 6. The method of any one of clauses 1–5, wherein the alternative non-ICI therapy comprises:

10 a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;

a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;

a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;

a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;

15 a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;

a CTLA-4 inhibitor selected from ipilimumab;

aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;

20 a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;

surgical excision; or

combinations thereof.

25 Clause 7. The method of any one of clauses 1–6, wherein the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

30 Clause 8. The method of any one of clauses 1–7, wherein the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18.

Clause 9. The method of any one of clauses 1–8, wherein when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma.

Clause 10. The method of any one of clauses 1–9, wherein when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

5 Clause 11. The method of any one of clauses 1–10, wherein the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1,
10 ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17,
15 TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRRF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1,
20 SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITS2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2,
25 RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

Clause 12. A method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis,
30 the method comprising:
(a) obtaining a melanoma tumor sample from a subject;
(b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data;

- (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor into a specific melanoma cell subtype;
- (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; and
- (e) calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;

wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment;

when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or

when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.

Clause 13. The method of clause 12, wherein the melanoma is acral melanoma (AM).

Clause 14. The method of clause 12 or 13, further comprising:

when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or

when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject.

Clause 15. The method of any one of clauses 12–14, wherein the ICI treatment comprises:

a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;

a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;

a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.

Clause 16. The method of any one of clauses 12–15, wherein the alternative non-ICI therapy comprises:

a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;

a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;

a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;

a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
 a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
 a CTLA-4 inhibitor selected from ipilimumab;
 aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or
 5 combinations thereof;
 a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin,
 carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or
 combinations thereof;
 surgical excision; or
 10 combinations thereof.

Clause 17. The method of any one of clauses 12–16, wherein the specific melanoma cell
 subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-
 derived melanoma.

Clause 18. A method of stratifying and evaluating melanoma treatment response in a subject
 15 using RNA hybridization, and a two-step deconvolution analysis, the method comprising:

- (a) obtaining a melanoma tumor sample from the subject;
- (b) performing RNA hybridization of the melanoma tumor sample using a targeted
 RNA probe panel to obtain targeted transcript expression data;
- (c) on a processor, deconvoluting the targeted transcript expression data using a first
 20 gene signature from the targeted RNA probe panel to stratify the melanoma into a
 specific melanoma cell subtype; and
- (d) deconvoluting the targeted transcript expression data using a second gene
 signature from the targeted RNA probe panel to calculate an estimate of the total
 number of cells in the tumor sample that express the second gene signature;

25 wherein when the calculated estimate of total tumor expression of the second gene
 signature reaches a critical threshold value, the tumor will not respond to immune
 checkpoint inhibition (ICI) treatment.

Clause 19. The method of clause 18, wherein the melanoma is acral melanoma (AM).

Clause 20. The method of clause 18 or 19, wherein the melanoma tumor sample comprises
 30 one or more biopsy samples or one or more formalin fixed paraffin embedded (FFPE)
 tumor tissue samples from the subject.

Clause 21. The method of any one of clauses 18–20, wherein the targeted RNA probe panel
 comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5,
 CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5,

MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRFS1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, and CYC1.

Clause 22. The method of any one of clauses 18–21, further comprising:

calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;

wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or

wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.

Clause 23. The method of any one of clauses 18–22, further comprising:

when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or

when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject.

Clause 24. The method of any one of clauses 18–23, wherein the ICI treatment comprises:

a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;

a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;

5 a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.

Clause 25. The method of any one of clauses 18–24, wherein the alternative non-ICI therapy comprises:

10 a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;

a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;

a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;

a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;

15 a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;

a CTLA-4 inhibitor selected from ipilimumab;

aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;

20 a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;

surgical excision; or

combinations thereof.

Clause 26. A method of stratifying and evaluating melanoma treatment response in a subject
25 using bulk transcriptomic data and a two-step deconvolution analysis, the method comprising:

(a) obtaining one or more melanoma tumor samples from a subject;

(b) performing RNA sequencing of the one or more melanoma tumor samples and obtaining bulk transcriptomic data;

30 (b) performing transcript counting on the bulk transcriptomic data to obtain transcript expression data;

(c) on a processor, deconvoluting the transcript expression data using a first gene signature to stratify the melanoma into a specific melanoma cell subtype or origin; and

(d) deconvoluting the transcript expression data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature or determine the cell differentiation state; wherein when the calculated estimate of total expression of the second gene signature reaches a critical threshold value, the melanoma will not respond to immune checkpoint inhibition (ICI) treatment.

Clause 27. The method of clause 26, wherein the melanoma is acral melanoma (AM).

Clause 28. The method of clause 26 or 27, further comprising:

when the calculated total tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or

when the calculated total tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject.

Clause 29. The method of any one of clauses 26–28, further comprising:

calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;

wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or

wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.

Clause 30. The method of any one of clauses 26–29, wherein the ICI treatment comprises:

a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;

a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;

a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.

Clause 31. The method of any one of clauses 26–30, wherein the alternative non-ICI therapy comprises:

a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;

a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;

a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;
 a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
 a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
 a CTLA-4 inhibitor selected from ipilimumab;

5 aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;

a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;

10 surgical excision; or combinations thereof.

Clause 32. The method of any one of clauses 26–31, wherein the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

15 Clause 33. The method of any one of clauses 26–32, wherein the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18.

Clause 34. The method of any one of clauses 26–33, wherein when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma.

Clause 35. The method any one of clauses 26–34, wherein when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.

Clause 36. The method of any one of clauses 26–35, wherein the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1,

NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRFS1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

EXAMPLES

Example 1

Human Subject Details

All skin was collected from surgical discards with informed consent and approval from the UCSF Institutional Review Board. The research conducted using human tissue is compliant with all relevant ethical regulations regarding human patients. All ages, races/ethnicities, and sexes were included in the eligibility criteria for this study. Participants were not compensated for their participation. Adult tissue was obtained from surgical remnants of healthy skin taken for reconstructive surgery or from amputations with healthy skin. Neonatal foreskins were obtained after routine circumcision. Anonymous fetal specimens were obtained from elective terminations and fetal age (stated as fetal weeks) was estimated by heel-toe length. When possible, fetal sex was determined by visual inspection using a dissecting microscope. All samples were collected in cold CO₂ Independent Media (Gibco—Thermo Fisher Scientific) or Medium 154 (Gibco) with 1× Antibiotic-Antimycotic (Gibco) at 4 °C until dissociation. Human melanoma data were obtained from previous studies: the TCGA Research Network; Lund University (GSE65904); Translational Genomics Research Institute (dbGAP phs001036.v1.p1); and Broad Institute (GSE72056, GSE115978).

Skin Sample Preparation

Tissue dissociation was started the same day as sample acquisition. For adult and neonatal skin, the epidermis was enzymatically dissociated from the dermis with a dispase, neutral protease, grade II (Roche–Sigma-Aldrich), incubation for 14 hours at 4 °C. Epidermal sheets were manually separated from the dermis, finely minced, and incubated with 0.5% trypsin (Gibco) for 3 minutes at 37 °C. After manual trituration, trypsin was deactivated using ice cold soybean trypsin inhibitor (Gibco), then diluted 2:3 in ice cold Hanks' balanced salt solution, no Mg^{2+} , no Ca^{2+} (Gibco). The dissociated cell suspension was centrifuged at $500 \times g$, 4°C, for 4 minutes, resuspended in FACS buffer (0.1% bovine serum albumin (Sigma) and 25 mM Hepes (Gibco) in Dulbecco's phosphate-buffered saline (DPBS; Gibco) and strained with a 70 μm filter to achieve a single cell suspension. For fetal tissue, the developing epidermis was manually removed from the dermis following a 20–30-minute incubation with 10 mM EDTA (Invitrogen), DPBS at 37 °C. The resulting epidermal layer was incubated with 0.5% trypsin (Gibco) for 1 min at 37 °C and manually trituated. Trypsin was deactivated using ice cold soybean trypsin inhibitor (Gibco), then diluted 2:3 in ice cold Hanks' balanced salt solution (Gibco). The dissociated cell suspension was centrifuged at $500 \times g$, 4 °C, for 4 minutes, resuspended in FACS buffer, and strained with a 70 μm filter to achieve a single cell suspension.

FACS Analysis and Single Cell Sorting

Single cell suspensions were counted, diluted to 1×10^6 cells/100 μL with ice cold FACS buffer containing dye conjugated antibodies (anti-KIT (104D2), 15 ng/100 μL (CD11705, Thermo Fisher Scientific), anti-ITGA6 (GoH3), 15 ng/100 μL (12-0495-82, Thermo Fisher Scientific) and CD11c, 1:20 dilution (46-0116-41, Thermo Fisher Scientific)) and incubated on ice for 25 minutes. Cells were washed one time with 10 $\times$ volume of FACS buffer, centrifuged for 2 minutes at 500g, resuspended in 30 ng/mL Dapi (D3571, Molecular Probes), FACS buffer. Resuspended cells were strained through a 35 μm nylon mesh filter and kept on ice until sorted.

Single cells were sorted into 384-well plates using the "Ultra purity" setting on a SH800S (Sony) sorter. For a typical sort, a tube containing 0.3–1 mL the pre-stained cell suspension was vortexed gently and loaded onto the FACS machine. A small number of cells were flowed at low pressure to check cell concentration and the amount of debris. Then the pressure was adjusted, flow was paused, the first destination plate was unsealed and loaded. Single cells were sorted into plates by gating to exclude dead/dying cells (DAPI+) and doublets. The majority of the plate contained melanocytes (CD11c-/KIT+) with 4–5 columns of basal keratinocytes (CD11c-/KIT-/ITGA6+) and other triple negative cells such as suprabasal keratinocytes (CD11c-/KIT-/ITGA6-).

Immediately, after sorting, plates were sealed with a pre-labeled aluminum seal, centrifuged at 4 °C and flash frozen on dry ice, before storage at -80 °C for later use.

Lysis Plate Preparation

- 5 Lysis plates were created by dispensing 0.4 µL lysis buffer (0.5U Recombinant RNase Inhibitor (Takara Bio, 2313B), 0.0625% Triton™ X-100 (Sigma, 93443-100ML), 3.125 mM dNTP mix (Thermo Fisher, R0193), 3.125 µM Oligo-dT30VN (commercially available from IDT, 5'-AAGCAGTGGTATCAACGCAGAGTACT₃₀VN-3'; SEQ ID NO: 1) and 1:600,000 ERCC RNA spike-in mix (Thermo Fisher, 4456740)) into 384-well hard-shell PCR plates (Biorad HSP3901) using a Tempest liquid handler (Formulatrix). All plates were then spun down for 1 minute at 3220 × g and flash frozen on dry ice. Plates were stored at -80 °C until used for sorting.

cDNA Synthesis and Library Preparation

- 15 cDNA synthesis was performed using the Smart-seq2 protocol. Briefly, 384-well plates containing single-cell lysates were thawed on ice followed by first strand synthesis. 0.6 µL of reaction mix (16.7 U/µL SMARTScribe Reverse Transcriptase (Takara Bio, 639538), 1.67 U/µL Recombinant RNase Inhibitor (Takara Bio, 2313B), 1.67× First-Strand Buffer (Takara Bio, 639538), 1.67 µM TSO (commercially available from Exiqon, 5'-AAGCAGTGGTATCAACGCAGACTACATrGrG+G-3'; SEQ ID NO: 2), 8.33 mM DTT (Bioworld, 40420001-1), 1.67 M Betaine (Sigma, B0300-5VL), and 10 mM MgCl₂ (Sigma, M1028-10X1ML)) was added to each well using a Tempest liquid handler or Mosquito (TTP Labtech). Reverse transcription was carried out by incubating wells on a ProFlex 2 × 384 thermal-cycler (Thermo Fisher) at 42 °C for 90 min and stopped by heating at 70 °C for 5 min. Subsequently, 1.5 µL of PCR mix (1.67× KAPA HiFi HotStart ReadyMix (Kapa Biosystems, KK2602), 0.17 µM IS PCR primer (commercially available from IDT, 5'-AAGCAGTGGTATCAACGCAGAGT-3'; SEQ ID NO: 3), and 0.038 U/µL Lambda Exonuclease (NEB, M0262L)) was added to each well with a Mantis liquid handler (Formulatrix) or Mosquito, and second strand synthesis was performed on a ProFlex 2 × 384 thermal-cycler by using the following program: 37 °C for 30 minutes; 95 °C for 3 minutes; 23 cycles of: 98 °C for 20 seconds, 67 °C for 15 seconds, and 72 °C for 4 minutes; and 72 °C for 5 minutes. The amplified product was diluted with a ratio of 1 part cDNA to 10 parts 10 mM Tris-HCl (Thermo Fisher, 15568025). 0.6 µL of diluted product was transferred to a new 384-well plate using the Viaflow 384 channel pipette (Integra). Illumina sequencing libraries were prepared as follows. Briefly, tagmentation was carried out on double-stranded cDNA using the Nextera XT Library Sample Preparation kit (Illumina, FC-131-1096). Each well was mixed with

0.8 μ L Nextera tagmentation DNA buffer (Illumina) and 0.4 μ L Tn5 enzyme (Illumina), then incubated at 55°C for 10 min. The reaction was stopped by adding 0.4 μ L “Neutralize Tagment Buffer” (Illumina) and spinning at room temperature in a centrifuge at 3220 $\times$ g for 5 min. Indexing PCR reactions were performed by adding 0.4 μ L of 5 μ M i5 indexing primer, 0.4 μ L of 5 μ M i7 indexing primer, and 1.2 μ L of Nextera NPM mix (Illumina). All reagents were dispensed with the Mantis or Mosquito liquid handlers. PCR amplification was carried out on a ProFlex 2 $\times$ 384 thermal cycler using the following program: 72 °C for 3 minutes; 95 °C for 30 seconds; 12 cycles of: 95 °C for 10 seconds, 55 °C for 30 seconds, and 72 °C for 1 minute; and 72 °C for 5 minutes. Library pooling, quality control, and sequencing. Following library preparation, wells of each library plate were pooled using a Mosquito liquid handler. Pooling was followed by two purifications using 0.7 $\times$ AMPure beads (Fisher, A63881). Library quality was assessed using capillary electrophoresis on a Fragment Analyzer (Agilent) or Tapestation (Agilent), and libraries were quantified by qPCR (Kapa Biosystems, KK4923) on a CFX96 Touch Real-Time PCR Detection System (Biorad). Plate pools were normalized to 2 nM and equal volumes from library plates were mixed together to make the sequencing sample pool.

Sequencing Libraries From 384-Well Plates

Libraries were sequenced on the NextSeq or NovaSeq 6000 Sequencing System (Illumina) using 2 $\times$ 100bp paired-end reads and 2 $\times$ 8bp or 2 $\times$ 12 bp index reads. NextSeq runs used high output kits, whereas NovaSeq runs used either a 200- or 300-cycle kit (Illumina, 20012860). PhiX control library was spiked in at 1%.

Single-Cell Transcriptomic Processing and Analysis

Single cell RNAseq analysis was conducted in Jupyter (4.4.0)/Jupyter lab(2.1.0)/Python (3.7.3) using: Pandas(1.0.3), *numpy* (1.18.2), *scanpy.api* (1.4.4.post1), *anndata* (0.6.22rc1), *plotnine* (0.6.0), *scipy* (1.4.1), *more_itertools* (8.2.0), *tqdm* (4.45.0), *sklearn* (0.22.2.post1), *lifelines* (0.24.3), *matplotlib* (3.0.3). Single cell reads were mapped to the human reference hg38 containing ERCC sequences using *STAR* aligner. *HTSeq* was used to create gene count tables. These count tables were compiled and processed using *Scanpy*. Low-quality cells were filtered based on the following criteria: number of genes < 500 or number of reads < 50,000. Each gene in the transcriptome exhibited read counts in at least 3 cells. Cells exhibiting > 2-fold higher number of genes than average were labeled as putative doublets and removed. Iterative Louvain clustering yielded cell type-specific clusters, which were annotated using published marker genes based on inter-cluster differential expression analysis (two-sided Mann Whitney U test, Benjamini-

Hochberg FDR < 5%). Briefly, Louvain clustering was performed on the k-nearest neighbor graph in principle component space of scaled highly variable genes. Cells were visualized using 2-dimensional UMAP embeddings. Cell cycle status was inferred by the mean ranked expression of marker genes, referred to as the cell cycle program score. Cells below the 95th-percentile of the cell cycle program score were labeled non-cycling; conversely, cells equal to or greater than 95th-percentile of the cell cycle program score were labeled cycling. In order to control for variance introduced by disproportionate populations of cycling cells across groups, non-cycling cells were considered for all downstream analyses. Thus, derivation of the four melanocyte developmental groups, anatomic site-specific analyses, and human melanocyte differentiation programs analyses were conducted on non-cycling cells.

Data and code availability: The resulting scRNA-seq data generated for this study available under accession number GSE151091 and code used to annotate and analyze the data can be found at: github.com/czbiohub/human_melanocytes.

Melanocyte Specific Louvain Clustering

Louvain clustering on melanocytes was performed on the melanocyte only k-nearest neighbor graph in principle component space of scaled highly variable genes. Low-resolution clustering (FIG. 1D) was achieved using resolution = 0.1. High-resolution Louvain clustering (FIG. 1E) was achieved independently of the low-resolution Louvain clustering using resolution = 0.9.

Identification Of Four Melanocyte Developmental Stages

Differential gene expression analysis (Wilcoxon Rank-sum) of the high-resolution Louvain clusters indicated high similarity between clusters within each developmental age group (consistent with the low-resolution clustering), with the exception of fetal cluster 10. Unsupervised hierarchical clustering was employed to group the high-resolution clusters according to the median values of the first 15 PCs. PCs were chosen according to the elbow point in the variance explained PC plot. Cells were binned according to high-resolution Louvain clustering groups (0-10). For each group of cells, the median of individual PCs was computed, resulting in a matrix consisting of 11 high-resolution Louvain clustering groups by 15 median PCs. This matrix was mean-centered and scaled to unit variance before performing hierarchical clustering using Ward's criterion method. The four hierarchical clustering groups were established independent of the low-resolution Louvain clusters. However, as expected, they were consistent with the three low resolution Louvain clusters while revealing a small distinct group of fetal cells enriched for

melanocyte stem cell markers. Thus, both independent methods revealed this forth cluster ("cluster 10" or "m4 cluster") as a distinct group of cells ultimately defined as MSCs.

Backscatter Analysis

- 5 Normalized FACS backscatter (BSC) was computed as the ratio of mean non-volar cutaneous cell BSC over mean volar cell BSC for each multi-site donor matched pair.

Fontana-Masson Staining

- 10 Fontana-Masson staining was performed on fixed frozen sections, from patient matched volar and non-volar cutaneous skin, using the Fontana-Masson Stain Kit (ab150669, Abcam) following the manufacturer's protocol.

Identification of Pigment Bifurcation and Post-Bifurcation Genes

- 15 Pigment associated genes identified by Baxter et al. were filtered for genes associated with a human phenotype and mean ranked expression greater than the 10th-percentile across each age of donor matched melanocytes. Baxter et al., *Pigment Cell and Melanoma Research* 32: 348-358 (2019). Next, the differentially expressed pigment genes between adult donor matched volar and non-volar melanocytes were identified (Mann-Whitney U test). Genes that were differentially expressed in both donors were further investigated for divergent expression in the fetal donor matched volar / non-volar melanocytes. Genes coinciding with pigment bifurcation were identified as differentially expressed between volar and non-volar melanocytes at 18wks and/or 12wks with a greater than or equal to 1.3-fold higher expression in non-volar melanocytes. The remaining genes were categorized at post-bifurcation.

25 Percent v-mel and c-mel

- Top-10 cutaneous and top-10 volar DEGs were identified from the site-enriched genes based on highest median per-patient log-fold-change between cutaneous and volar samples. Individual cells were classified as v-mel if 4 or more top-10 volar DEGs exhibited non-zero expression AND fewer than 4 top-10 cutaneous DEGs exhibited non-zero expression. 30 Conversely, individual cells were classified as c-mel if 4 or more top-10 cutaneous DEGs exhibited non-zero expression AND fewer than 4 top-10 volar DEGs exhibited non-zero expression. Percent v-mel and c-mel were then calculated for each skin specimen of unique anatomic location from each individual patient.

To determine the percent of HPGD positive melanocytes in tissue sections, melanocytes (TYRP1+ cells) were manually counted. Fraction of cells was determined by the number of HPGD+ TYRP1+ cells divided by the total number of TYRP1+ cells from each fixed frozen section. To quantify the number of NTRK2 and HPGD foci per DCT+ cells from the RNAscope data, images were processed to correct for Opal 570 (HPGD) bleed-through into the Opal 620 (NTRK2) channel. After bleed-through correction, DCT and associated dapi signal was used to define the area of DCT+ cells. Then, NTRK2 and HPGD foci within DCT+ cells were counted manually. All Image analysis was performed in *Fiji* with statistical analysis performed in OriginPro and GraphPad Prism.

Immunofluorescence

Skin samples were fixed in 4% paraformaldehyde (Electron Microscopy Sciences) at 4 °C overnight, washed with cold DPBS prior to paraffin or OCT embedding. Fixed frozen skin sections were incubated in blocking buffer: 2.5% donkey serum, 2.5% goat serum (Jackson ImmunoResearch Laboratories), 1% bovine serum albumin (Sigma-Aldrich), and 0.1% Triton X-100 (Sigma-Aldrich) for 1–2 hours at room temperature. The following primary antibodies were used at the indicated concentration in blocking buffer overnight at 4°C: mouse monoclonal anti-TYRP1 1:200 (TA99, ab3312, Abcam), mouse monoclonal anti-KIT 1:100 (MA1-10072, Invitrogen–Thermo Fisher Scientific), rabbit polyclonal anti-HPGD 1:100 (HPA005679, Sigma-Aldrich). Secondary antibodies against mouse IgG Alexa Fluor 488(A21202,Thermo Fisher Scientific), or rabbit IgG conjugated to Dylight 594 (SA5-10040,Thermo Fisher Scientific) were used at a 1:1,000 dilution for 1–2 h at room temperature followed by Dapi, 1:1000 (Molecular Probes) for 1 minute. Sections were mounted in VECTASHIELD Vibrance (Vector Laboratories) prior to imaging.

Immunofluorescence images were acquired using Nikon NIS-Elements multi-platform acquisition software (5.30.01) on a fully automated Nikon Ti-E inverted microscope with an Apo TIRF, 60x, 1.49 NA, oil objective (Nikon) and a Clara CCD camera (Andor). All Image analysis was performed in *Fiji* with statistical analysis performed in OriginPro and GraphPad Prism.

Multiplex RNA-FISH

Multiplex RNA-FISH was employed using the RNAscope Multiplex Fluorescent V2 assay (Bio-technie, cat. No. 323110) kit according to manufacturer's protocol on 10 µM FFPE tissue sections. Tissues were stained using probes purchased from ACD for *HPGD* (Channel 1, cat. no. 583651), *NTRK2* (Channel 2, cat. no. 402621-C2), *DCT* (Channel 3, cat. no. 494361-C3) and

TSA Opal 570 (Channel 1, Akoya Biosciences, cat. No. FP1488001KT), TSA Opal 620 (Channel 2, Akoya Biosciences, cat. No. FP1488001KT) and TSA Opal 690 (Channel 3, Akoya Biosciences, cat. No. FP1497001KT). TSA was used at a 1:1500 dilution. Cells were counterstained with DAPI and mounted with Prolong Gold Antifade Mountant (Thermo Fisher, P36930). Tissues were imaged using a Leica DMI8 microscope.

Melanoma v-mel:c-mel Score

Average log2 normalized expression of the top 100 volar enriched and top 100 cutaneous enriched genes was calculated for each primary tumor from SKCM TCGA and dbGAP phs001036.v1.p1. a v-mel:c-mel ratio was then calculated for each tumor by dividing the v-mel score (average expression) by the c-mel score. Tumors were then grouped by reported anatomic subtype: acral (n = 13 dbGAP phs001036.v1.p1, n = 2 SKCM) and non-acral cutaneous (n = 103 SKCM).

Diffusion Pseudotime

Diffusion pseudotime analysis on all non-cycling melanocyte cells was performed using the “*scanpy.tl.dpt*” function. The pseudotime reference root cell was chosen from the youngest sample (9.5 f.w.). The diffusion map was computed from an n = 30 neighborhood graph with a Gaussian kernel.

Developmental Group GSEA Analyses

Gene set enrichment analyses for GO-biological processes (GO-bp) and previously identified neonatal foreskin and adult non-volar melanocyte cell-type DEG lists were conducted using the top differentially expressed genes (Mann-Whitney U test, Benjamini-Hochberg FDR < 5%) between developmental group in GSEA4.1.0 using the GSEAPreranked tool with the weighted enrichment statistic, max size of 500 and min size of 10. Significantly enriched biological processes between temporally adjacent developmental groups (FET vs MSC, NEO vs FET and NEO vs ADT) were determined by grouping the top 50 GO-bp terms (top 50 terms with FDR q-value <0.250) for each developmental group in each pairwise comparison based on common biological themes. The above identified biological processes were then assessed for enrichment across all the human developmental stages using the differentially expressed genes for a) each developmental group compared to ADT and b) each developmental group compared to MSC and then calculating the median normalized enrichment score (for all GO-bp terms with an FDR q-value <0.250) for each common biological theme (FIG. 4A).

DevMel Program Biological Pathway Analysis

PercayAI (v4.0, build 21) was used to identify relevant biological processes and pathways represented by the positive correlated genes within each DevMel program. The *PercayAI* software extracts all abstracts from PubMed that reference entities (genes) of interest (or their synonyms), using contextual language processing and a biological language dictionary that is not restricted to fixed pathway and ontology knowledge bases. Conditional probability analysis is utilized to compute the statistical enrichment of biological concepts (processes/pathways) over those that occur by random sampling. Related concepts built from the list of differentially expressed entities are further clustered into higher-level themes (e.g., biological pathways/processes, cell types and structures, etc.). Within the *PercayAI* software platform, scoring of gene, concept, and overall theme enrichment is accomplished using a multi-component function referred to as the Normalized Enrichment Score (NES). The first component utilizes an empirical p-value derived from several thousand random entity lists of comparable size to the users input entity list to define the rarity of a given entity-concept event. The second component, effectively representing the fold enrichment, is based on the ratio of the concept enrichment score to the mean of that concept's enrichment score across the set of randomized entity data. The top themes (chosen using the following settings: scale factor = 5, visible theme threshold = 7, connector threshold = 70) were manually reviewed for quality control to ensure concepts within themes were based on key words linked to biological processes and pathways.

Single Cell Developmental Stage Melanocyte (DevMel) Logistic Regression Model

Input data was composed of single cell transcriptomes from the following 4 non-volar cutaneous groups: MSC, FET, NEO, and ADT. The input examples were randomly sampled, and the number of examples was balanced among all labels. The combination of normal and melanoma transcriptomes was used to scale and center the data. The input data was split into testing and training partitions at a ratio 33:67. Elasticnet regularization was implemented with an l1 ratio = 0.8. Single cell transcriptomes were evaluated by the model to yield a developmental stage label.

Data and code availability: The code for the logistical regression model can be found at: github.com/danledinh/human_melanocytes.

Model Systems Melanocyte Program Scores

For each individual cell, the program score is the mean normalized expression for all genes in the indicated published gene signature.

Classification of Genes in Melanoma Dedifferentiation Categories

5 Genes involved in melanoma dedifferentiation were identified from the normal melanocyte developmental programs (Logistic regression variables: [MSC]prg, [FET]prg, [NEO]prg, and [ADT]prg) and the top-100 differentially expressed genes for each DevMel melanoma cell population (MAL^[MSC] vs rest, etc...). To identify transcriptional programs associated with patterns of dedifferentiation, the mean ranked expression pattern of each gene was compared (1) across
10 four normal melanocyte DevMel groups (MSC, FET, NEO, and ADT) and/or (2) across the four melanoma DevMel-based groups (MAL^[MSC] MAL^[FET] MAL^[NEO] MAL^[ADT]), and (3) between the normal melanocyte groups and the melanoma groups. Genes were then grouped into the following de-differentiation pathways based on the following expressing patterns:

15 *Direct Dedifferentiation*

Met both of the following two criteria: (1) mean expression for MAL^[MSC], MAL^[FET], MAL^[NEO], and MAL^[ADT] was greater than or equal to 4-fold the mean expression of MSC, FET, and NEO and (2) mean expression of ADT was less than the mean expression of MSC, FET, and NEO.

20 *Sequential Dedifferentiation*

The DevMel stage with the highest mean expression in the normal melanocyte group was also the DevMel stage with the highest mean expression of the MAL^[DevMel] melanoma groups. Ex: MSC group has the highest expression of WNT5A compared all the normal melanocyte DevMel groups and MAL^[MSC] also has the highest expression of WNT5A compared to the other MAL^[DevMel]
25 melanoma groups.

Normal-Specific

Met all of the following criteria: (1) mean expression in each MAL^[DevMel] melanoma group was less than the corresponding normal melanocyte DevMel group, and (2) the mean expression
30 was in the bottom 10th percentile for all MAL^[DevMel] melanoma groups, and (3) the mean expression was in the top 15th-percentile for all normal melanocyte DevMel groups. Genes were then further classified into the following two groups:

Down Regulated

Met all of the following criteria: (1) mean expression in each MAL^[DevMel] melanoma group was less than or equal to the mean expression of MSC, FET, and NEO normal melanocyte groups, and (2) mean expression of the ADT normal melanocyte group was greater than 1.5-fold mean expression of MSC, FET, and NEO normal melanocyte groups.

5

Not-Readopted

Met all of the following criteria: (1) mean expression in each MAL^[DevMel] was less than or equal to the mean expression of the ADT normal melanocyte group, and (2) mean expression in the MSC, FET, and NEO normal melanocyte groups were greater than 1.5-fold the mean expression of the ADT normal melanocyte group.

10

Melanoma-Specific (identified from full transcriptomes of normal and malignant cells)

Met all of the following criteria: (1) The mean expression for each MAL^[DevMel] melanoma group was greater than the corresponding normal melanocyte DevMel group, and (2) the mean expression was in the top 40th-percentile for each MAL^[DevMel] melanoma group, and (3) the mean expression was in the bottom 10th percentile for all normal melanocyte DevMel groups.

15

Bulk Tumor Deconvolution

Bulk mRNAseq analysis was conducted in Python(3.7.3) using: *Pandas* (1.0.3), *numpy* (1.18.2), *scanpy.api* (1.4.4.post1), *anndata* (0.6.22rc1), *plotnine* (0.6.0), *scipy* (1.4.1), *more_itertools* (8.2.0), *tqdm* (4.45.0), *sklearn* (0.22.2.post1), *lifelines* (0.24.3), *matplotlib* (3.0.3), and *CIBERSORT* (1.06). *CIBERSORT* was used to deconvolve bulk RNA-seq from the SKCM-TCGA (<https://www.cancer.gov/tcga>) as well as the LUND dataset (GSE65904) cohorts. As input, *CIBERSORT* requires cell type-labeled transcriptomes to estimate the proportion of each cell type in a bulk RNA-seq sample. Here, trimmed both single cell and bulk RNA-seq transcriptomes to include only genes that are shared in both datasets. Adopting a k-fold cross-validation approach, 10 sets of single cell input transcriptomes from normal melanocytes were prepared across 4 developmental stages: MSC, FET, NEO, and ADT (balanced cell counts across all labels). Each input transcriptome set was used to devolve the SKCM-TCGA or LUND bulk RNA-seq samples, yielding 10 estimates of cell proportion. For each individual sample in the SKCM-TCGA or LUND dataset, the label means were used as the final estimate of label proportion. Hierarchical clustering was used to group SKCM-TCGA samples based on similar label proportions. One-sided Fisher Exact test was used to determine significant enrichment between two gene lists. The

20

25

30

lifelines python package (10.5281/zenodo.3833188) was used to create Kaplan-Meier survival plots and perform logrank tests using curated SKCM-TCGA metadata.

Multi-Site scRNA-seq of Normal Human Melanocytes

5 scRNA-seq was performed on 34 healthy skin specimens across multiple anatomic locations (leg, arm, foreskin, palm and sole) from 22 donors aged 9.5 fetal weeks (f.w.) to 81 years (FIG. 1A) representing multiple skin tones and sexes. Each epidermis was enzymatically removed from the dermis and dissociated into a single cell suspension. Since melanocytes comprise a small fraction of the total epidermal cell mass, FACS was used to increase the capture rate of KIT+ melanocytes within the basal layer (FIG. 1A). Sorted cells were processed using the Smartseq2 scRNA-seq protocol. After quality control and iterative Louvain clustering, differential expression was used to annotate 9,719 cells into the following cell-types: melanocytes, keratinocytes, eccrine sweat gland cells, and three immune cell populations (FIG. 1B–C. Gene expression within the melanocyte cluster presented agreement with differentially expressed genes (DEG)s from melanocyte clusters identified in previous fresh from human skin sequencing studies. Individual cells were designated as cycling or non-cycling based on expression of established marker genes. To investigate heterogeneity within melanocytes, Louvain clustering was performed on melanocytes alone. Low-resolution Louvain clustering yielded three major clusters (clusters A–C) that aligned with the three developmental ages collected in this study (cluster A: 97.5% adult, cluster B: 99.5% fetal, cluster C: 93.2% neonatal, FIG. 1D. High-resolution Louvain clustering was then performed. The resulting 11 high-resolution clusters (0–10, FIG. 1E), individually, did not correspond to skin tone, sex, or donor (FIG. 1F–H). Differential gene expression analysis of the high-resolution clusters indicated high similarity between clusters within each developmental age group, with the notable exception of fetal cluster 10 (FIG. 1I). Consistent with this observation, unsupervised hierarchical clustering using principal components binned the high-resolution clusters into four groups: m1, one fetal cluster (10); m2, the remaining fetal clusters (2, 3, 6); m3, encompassing all adult clusters (0, 1, 4, 5, 7); and m4, both neonatal clusters (8, 9) (FIG. 1I). Two of the top 5 ranked genes for the m1 group had known associations with stem- and progenitor- cell function (*TC4F* and *CXCL14*) (FIG. 1I). Established melanocyte stem cell (MSC) signatures were assessed and high expression in the m1 group was identified (FIG. 1J), indicating the melanocytes captured from this cohort encompass four developmental groups: adult, neonatal, fetal and MSC (FIG. 1K). Additionally, evaluation of anatomic location presented volar vs non-volar site as another possible source of heterogeneity within the adult and fetal groups (FIG. 1L).

Site-Specific Pigment Associated Transcriptional Programs

Hypopigmentation of palms and soles is present in neonates and continues through adulthood, indicating that site-specific pigmentation occurs during development, but the genes that regulate intra-individual pigmentation variation are poorly understood. Since anatomic location was a possible source of melanocyte heterogeneity (FIG. 1L), this study sought to identify the genes associated with differential pigmentation. As part of the single cell isolation pipeline, FACS back-scatter (BSC) measurements were indexed for individual cells (FIG. 1A). BSC values are an established correlate of relative pigmentation and pigment organelle (melanosome) content. Using BSC, relative pigmentation between donor-matched volar and non-volar melanocytes was queried (FIG. 2A). At 10 and 12 f.w., there were no detectable differences in BSC (FIG. 2B–C). In contrast, a striking increase in BSC was observed within the non-volar cutaneous-derived melanocytes at 18 f.w. and adulthood (FIG. 2B–C). Additionally, fetal skin presented an increase in Fontana-Masson staining at 18.5 f.w. in non-volar cutaneous skin with no evidence of staining in donor-matched volar skin (FIG. 2D). These observations are consistent with previous reports and indicate that the site-specific bifurcation of melanocyte pigmentation occurs between 12 and 18 f.w.

To identify genes correlated with intra-individual pigmentation, age-dependent expression of known pigment genes between donor-matched volar and non-volar cutaneous melanocytes were analyzed. Although an overall increase in the relative expression of pigment-associated genes in non-volar cutaneous melanocytes was observed compared to volar melanocytes after 12 f.w. (FIG. 2E, bold red line), the expression patterns of individual pigment-associated genes were varied (FIG. 2E, thin red lines). Pigment-associated genes were grouped based upon three expression patterns – lineage genes: melanocytic lineage specific genes highly expressed in volar and non-volar cutaneous melanocytes, bifurcation genes: upregulated in non-volar cutaneous melanocytes in concordance with pigment bifurcation at 12 f.w. - 18 f.w., and post-bifurcation genes: upregulated in adult non-volar cutaneous melanocytes (FIG. 2F–G). Lineage genes included melanocyte differentiation genes and master regulators of melanin production (*SOX10*, *PAX3*, *MITF*, *DCT*, *TYRP1*, *TYR*, *PMEL*) whereas bifurcation genes and post-bifurcation genes were involved in melanosome biogenesis and function (*SLC45A2*, *TPCN2*, *OCA2*, *RAB27A*, *AP3D1*, *ADAM10*, *TRAPPC6A*, *SLC24A5*, *ATOX1*) and/or pigment signaling pathways/UV response (*MC1R*, *GNAS*, *DSTYK*) (FIG. 2H). Further supporting these finding, allelic variation and/or differential expression of several bifurcation and post-bifurcation genes, such as *MFSD12*, are known to regulate skin pigmentation variation between individuals. This approach pinpointed

pigment genes with differential expression correlated to intra-individual pigment variation (FIG. 2H).

Anatomic Site-Enriched Melanocyte Sub-Populations

5 The anatomic location of skin influences melanocyte survival and function but it remains unclear how site-specific specialization arises during melanocyte maturation. To broaden the understanding of melanocyte intrinsic differences during development between anatomic sites, donor matched volar and non-volar cutaneous specimens that spanned 10 f.w. to 77 years, sexes, and skin tone were examined for transcriptional programs that distinguished volar vs non-volar cutaneous melanocytes across developmental ages (n = 6 donors, n = 17 skin specimens, FIG. 10 2A). Differential gene expression analysis (Mann-Whitney U test, Benjamini-Hochberg FDR < 5%) revealed 2,042 transcripts with site-specific expression in both fetal and adult donors (FIG. 3A, Table 1). Volar melanocytes presented increased expression of *NTRK2*, *ID2* and *ID3* – genes previously associated with a subset of melanomas and/or silenced in non-volar cutaneous melanocytes. As expected from the above analyses, non-volar melanocytes expressed genes involved in pigmentation. Using binary expression of the top 10 volar and non-volar cutaneous genes (FIG. 3B), individual cells were classified from the full cohort (n = 22 donors, n = 34 skin specimens) as volar-like (v-mel) and non-volar cutaneous-like (c-mel). While v-mels and c-mels were present in all anatomic locations for both adult and fetal skin (FIG. 3C), v-mels were enriched in volar skin (mean: 94% ± 5% s.d. volar sites, ~7% ± 5 % non-volar sites) and c-mels were enriched in non-volar cutaneous skin (mean: ~89% ± 9% non-volar sites, 5% ± 5% volar sites). The presence of melanocytes with a c-mel signature in volar sites and melanocytes with the v-mel signature in cutaneous sites indicated: (1) two distinct sub-populations of epidermal melanocytes exist in human skin with anatomic site-specific enrichment, and (2) enrichment occurs during and persists after skin development. This discovery was validated via RNA FISH and immunofluorescence using the v-mel and c-mel signature genes that presented a striking level of inverse expression between volar and non-volar cutaneous melanocytes across all donor-matched skin: *NTRK2* and *HPGD*, respectively (FIG. 3D–I). These observations further suggest the previously reported site specific mesenchymal–melanocyte interactions that drive the epidermal phenotype in fully-developed skin, provide more permissive, but non-exclusive, conditions for one melanocyte subpopulation over another.

Approximately 4% of primary cutaneous melanomas (CM), called acral melanomas (AM), arise from volar regions. The disease-specific death rate from AM is more than twice as high as that of CM in general. While AMs are, on average, diagnosed at more advanced stages and

deeper Breslow depth, partially explaining the increased morbidity, when adjusted for Breslow depth and stage, AMs still have worse outcomes suggestive of a biologic etiology for this discrepancy. To determine whether AM may arise from v-mels (FIG. 3J), publicly available datasets were accessed to compare expression of v-mel to c-mel signatures in 103 primary non-acral CMs and 15 primary AMs. The v-mel signature was significantly elevated in the AM cohort (FIG. 3K, unpaired, two tailed t-test, p -value < 0.0001), suggesting that AMs retain v-mel transcriptional programs and are therefore possibly derived from v-mels.

Human-Specific Melanocyte Differentiation Programs

The transcriptional programs that changed with non-volar cutaneous melanocyte development were assessed. Diffusion pseudotime analysis, pairwise differential gene expression, and gene set enrichment analysis for Gene Ontology Biological Process (GO-bp) terms identified neonatal melanocytes (NEO) as an intermediate transcriptional state between fetal (FET) and adult (ADT) (FIG. 4A). Comparison to previously published transcriptomes of neonatal and adult human melanocytes demonstrated significant enrichment with the NEO (normalized enrichment score (NES) = -1.81 for Cheng et al., *Cell Reports* 25, 871–883 (2018) neonatal foreskin, FDR q -value = 0.00) and ADT (normalized enrichment score (NES) = 3.15 for Cheng et al. (2018) adult non-volar, FDR q -value = 0.00) programs, respectively, further supporting this distinction. Melanocyte stem cells (MSC)s were enriched for terms associated with extracellular matrix (ECM) assembly and morphogenesis, development, and differentiation – the latter of which remained significant but trended downward in FET and NEO (FIG. 4A). In contrast, genes associated with immunity, inflammation, organelle maturation and pigmentation presented increasingly significant enrichment with each consecutive developmental group. Together, these data suggest the four main developmental groups represent distinct developmental stages along a differentiation trajectory. These analyses did not reveal significant further transcriptional changes associated with donor age in adult melanocytes.

To identify gene signatures that best distinguished each human melanocyte developmental group from each other, a regularized logistic regression model was trained using the single cell transcriptomes from 66% of the dataset representing the four developmental stages (FIG. 4B). The resultant Developmental stage Melanocyte (DevMel) model demonstrated excellent classification accuracy when tested on the holdout set, with $f1$ -scores ranging from 0.93–1.00 (Table 2). Elastic net regularization yielded genes that collectively constituted developmental stage-specific expression programs: prg[MSC], prg[FET], prg[NEO] and prg[ADT] (FIG. 4B–F and Table 2). Each program is a relatively small (45–69 genes) expression program unique to the

associated developmental group. Small gene sets are not amenable to reliable GO analyses, so an augmented artificial intelligence approach was employed to identify biological processes associated with each program (see methods). The prg[MSC] was again associated with ECM assembly, as well as neural crest cell fate specification, IGF signaling and a stem cell associated WNT-TCF-LEF-Beta-catenin program; prg[FET] with MAPK, PI3K and NF κ B signaling and chromatin remodeling; and prg[ADT] with inflammation, skin epidermis, and cell polarity. The prg[NEO], in particular, was least associated with unique known biological processes, potentially reflective of its intermediated status between FET and ADT.

While there is substantial overlap in melanocyte development pathways between different model organisms, there are known species dependent differences and conservation of these processes in human skin remains unresolved. To benchmark human melanocyte development against known mammalian developmental systems, the expression of the gene signatures previously defined during mouse melanocyte development (FIG. 5A) and *in vitro* differentiation of human embryonic stem (ES) cells into mature melanocytes were assessed within ADT, NEO, FET and MSC non-volar cutaneous skin. Both the Sennet et al. E14.5 mouse melanoblast signature and the Rezza et al. P4 & P5 mouse melanocyte signature were more highly expressed in the FET, NEO and ADT melanocytes compared to MSCs (p-value < 1×10^{-12} , FIG. 5B). In these studies, melanocytic cells were isolated using LEF1 and KIT expression, and the gene signatures were derived from the comparison of melanocytic cells to other skin cells. In mice, LEF1 is a marker of differentiated (and differentiating) melanocytes and is not expressed in MSC. Thus, the resulting gene signatures represent a general melanocytic cell-type specific program, exclusive of MSCs, at each mouse developmental time point. The observed low program expression in the human MSC group defined in the current study is therefore consistent with the experimental design for the Sennet and Rezza studies (FIG. 5B). Rezza et al., *Cell Reports* 14, 3001-3018 (2016); Sennett et al., *Dev. Cell* 34, 577-591 (2015). In contrast, the Marie et al. melanoblast signature was most highly expressed in MSC (> 1.5-fold change when compared to each other group, p-value < 1×10^{-7} , FIG. 5B). Marie et al., *Nature Comm.* 11, 1-18 (2020). Unlike the Sennet et al. melanoblast signature, the Marie et al. melanoblast signature was derived from the comparison of DCT+ melanoblasts at E15.5 & E17.5 to P1 & P7 melanocytes and is therefore a melanoblast specific signature. DCT is expressed in differentiated (and differentiating) melanocytes as well as MSCs. Consistent with this finding, the CD34+ mouse hair follicle melanocyte stem cell gene set was most highly expressed in MSC (p-value = 5.4×10^{-38} , FIG. 5B).

Mouse hair follicle morphogenesis occurs around E14 and is completed postnatally by P8 as a fully mature hair-bearing follicle in anagen phase. In humans, hair follicle formation is reported to start around 10 f.w. with mature hair follicles appearing around 20 f.w. depending on anatomic location and study. The fetal skin specimens in the dataset coincide with the onset and later stages of human hair follicle development, which would encompass morphological stages that resemble mouse hair follicle development at E15.5 and E17.5 from Marie et al. (FIG. 5A). Unlike mice, human hair-bearing skin contains both hair follicle-associated and epidermal-associated melanocytes. Therefore, it is reasonable that the mouse melanoblast-specific program from Marie et al. is most highly expressed in a subset of the human fetal melanocytes that express known follicular-associated gene signatures (FIG. 1J and FIG. 5B). Together, these data suggest the human MSCs are melanoblasts that give rise to follicular and perhaps also epidermal melanocytes.

Of the *in vitro* differentiation programs, the mature differentiated melanocyte program was expressed across all developmental groups with the highest expression in FET, NEO and ADT groups compared to MSC (p-value $< 1 \times 10^{-14}$, FIG. 5C). These observations suggest that *in vitro* generation of melanocytes from pluripotent stem cells does not distinguish between differentiating, young and aged melanocytes. Differentiation protocols that better distinguish the *in vivo* profiles reported here, especially accounting for the effect of the aged adult developmental state, would be a valuable tool for the field.

Comparison of DevMel program genes to those identified in mouse or in human *in vitro* differentiation yielded sparse overlap (FIG. 5D–G), indicating that this approach revealed previously unidentified programs specific to human fetal, neonatal, and adult skin. The study therefore sought to determine whether profiles unique to human *in vivo* development could provide insight into melanoma dedifferentiation and aggression.

Reacquisition Of Developmental Programs During Tumorigenesis

Melanoma progression often coincides with the loss of melanocyte differentiation markers and upregulation of genes associated with earlier stages of development. This process is broadly described as dedifferentiation. Given the substantial cell-to-cell intra-tumor heterogeneity of melanoma, it was reasoned that single cells within a tumor might occupy various stages of dedifferentiation and that the proportion of cells in each state potentially influences overall patient outcome. To assess tumor heterogeneity, published single-cell malignant melanoma samples were classified using the DevMel model. Each melanoma cell was classified by the similarity of its transcriptome to the human development-associated programs, resulting in four groups of

melanoma cells – MAL^{MSC}, MAL^{FET}, MAL^{NEO}, and MAL^{ADT} (FIG. 6A). Inter- and intra-tumor heterogeneity was observed in the representation of each melanoma group (FIG. 6B), indicating tumors are composed of a mix of dedifferentiated states.

Previous reports have used bulk-tumor transcriptional signatures to classify cohorts of melanomas - most notably, the TCGA cohort can be classified as “immune,” “keratin,” or “MITF-low;” and the Cirenajwis et al. cohort as “Immune,” “Normal-like,” “Pigmented,” or “Proliferative,” Cirenajwis et al., *Oncotarget* 6: 12297-12309 (2015). Others have classified tumors based upon profiling of *in vitro* differentiation of human stem cells into melanocytes, resulting in signatures for “undifferentiated,” “neural crest like,” “transition,” and “melanocytic.” It was determined how the signatures derived from human melanocyte development corresponded with published melanoma states and signatures. Similar to the analysis of model system developmental programs, the MAL^{MSC} melanoma cells corresponded with previously identified stem cell-like transcriptional states (FIG. 8A–E). Significant enrichment was observed between the MAL^{ADT} group and the Cirenajwis et al. “normal-like” signature, consistent with these cells retaining a substantial component of the differentiated melanocyte program. Surprisingly, neither the MAL^{FET} nor the MAL^{NEO} group exclusively segregated with previously defined signatures. For example, the MAL^{FET} group was significantly enriched for both the TCGA immune and MITF-low signatures, whereas the MAL^{NEO} group was not enriched for any previously defined signatures. These observations suggest that categorization of malignant melanoma cells by the human developmental stage categories defined here represents a different classification system, with the MAL^{MSC} and MAL^{ADT} groups reasonably aligned with previously reported MITF-low/stem cell and normal melanocytes, respectively, and the MAL^{FET} and MAL^{NEO} groups representing previously unreported signatures. Thus, it was reasoned that classification of melanoma cells by human developmental programs might offer further insight toward understanding dedifferentiation in melanoma.

To better define the course of dedifferentiation during melanoma progression, differential gene expression patterns were identified across each of the four MAL groups that were consistent with different forms of cellular reprogramming: (1) a retrograde unfolding of the differentiation cascade (sequential dedifferentiation). (2) direct reprogramming to a more pluripotent stage (direct dedifferentiation), or (3) the acquisition of a melanoma-specific program (FIG. 6C–G). Of 511 total unique genes, inclusive of DevMel model variables and MAL group top differentially expressed genes (Table 3), 45% exhibited expression patterns consistent with sequential dedifferentiation, in which the relative expression across healthy melanocyte developmental groups was conserved among MAL groups (FIG. 5D). 3.1% of genes exhibited a direct

dedifferentiation pattern, indicating that expression of these genes may be a prerequisite for disease progression and metastasis (FIG. 5E). Supporting this interpretation, this small set of genes includes known markers of aggressive melanoma such as AXL and HMGA2. Similarly, recently identified therapeutic resistance programs were evident in both the MSC healthy and MAL^{MSC} populations (FIG. 8D–E). Genes expressed in healthy melanocyte groups were identified that were down-regulated in all melanoma groups (FIG. 5G), thus characterizing aspects of normal melanocyte expression that are either non-essential or potentially inhibitory to melanoma progression and/or metastasis. Although no significant enrichment was observed for the *in vitro* differentiation based gene signatures from Tsoi et al. in any of the MAL groups (FIG. 8C), the analyses suggest that sequential dedifferentiation, which recapitulates the ordered cascade of differentiation in reverse (FIG. 5B), is predominant in melanoma progression. Tsoi et al., *Cancer Cell* 33(5): 890-904 (2018). This discovery mirrors the findings of Tsoi et al. which show that development of therapeutic resistance in melanoma traverses a sequential dedifferentiation trajectory.

Finally, 52 highly expressed genes in melanoma were absent from each of the healthy melanocyte developmental groups (FIG. 5F and Table 3). Among the top differentially expressed genes was the melanoma-associated antigen PRAME, further supporting its use as a melanoma molecular diagnostic. Other of these “melanoma specific” genes might be important for melanoma progression such as the MTRNR2L family of transcripts, which encode for short peptides with anti-apoptotic activity, and were highly and exclusively expressed in all melanoma groups.

Developmental Stage Programs Correlate with Patient Survival

To determine whether gene expression programs characteristic of different human developmental ages offer prognostic value, *CIBERSORT* was applied to estimate the fraction of melanoma cells similar to ADT, NEO, FET, MSC for all skin cutaneous melanoma (SKCM) tumor samples from The Cancer Genome Atlas (TCGA). Similar to the single cell melanoma dataset (FIG. 6B), inter-tumor heterogeneity was observed in the fractional representation of the four developmental groups (FIG. 7A). Hierarchical clustering of SKCM label distributions classified tumor samples according to the observed predominant developmental group: SKCM^{ADT}, SKCM^{NEO}, SKCM^{FET}, SKCM^{MSC}. Neither genetic driver nor tumor site correlated with the developmental group classification of the tumor (FIG. 6A; FIG. 8F).

Using developmentally-defined subclasses of melanoma tumors, the correlation of bulk tumor differentiation status was evaluated with patient outcome. As expected, the most

differentiated group (SKCM^{ADT}) exhibited best median overall survival (FIG. 7B, SKCM^{ADT} = 11.0 yr vs rest = 5.3 yr). Surprisingly, the most dedifferentiated groups (SKCM^{FET}, SKCM^{MSC}) were not associated with worse outcomes; rather, the intermediately differentiated group (SKCM^{NEO}) exhibited the shortest median overall survival (SKCM^{NEO} = 4.2 yr vs rest = 8.2 yr). To validate this observation, specimens from the Lund University dataset were developmentally-classified and again found that tumors comprised of predominantly NEO-like cells (LUND^{NEO}) were associated with worse outcomes (FIG. 7C, LUND^{NEO} = 1.21 yr vs rest = 3.43 yr). To better understand this unexpected finding, the expression of transcriptional programs associated with clinical response to therapeutics were evaluated. Indeed, SKCM^{NEO} tumors expressed higher levels of transcripts associated with immune resistance (p-value = 1.6×10^{-2} , SKCM^{NEO} vs rest) and a dearth in immune infiltration signatures (p-value = 5.5×10^{-4} , SKCM^{NEO} vs rest) as well as FDA-approved therapeutic targets (p-value = 1.6×10^{-5} , SKCM^{NEO} vs rest) (FIG. 8G). The SKCM^{MSC} tumor group was unique in its increased expression of FDA-approved therapeutic targets (p-value = 4.6×10^{-21} , SKCM^{MSC} vs rest) in agreement with previous studies of stem-like melanoma cells. The MAL^{NEO} signature presented virtually no enrichment for previously published prognostic signatures, with the striking exception of genes that are poorly expressed in tumors that respond to the immune checkpoint inhibitor (ICI), nivolumab (FIG. 8H, Table 4). Consistent with this finding, the fraction of MAL^{NEO} cells within a melanoma was a strong predictor of ICI-resistant versus treatment naïve tumors (FIG. 7D, unpaired one-sided t-test, p-value = 0.0099) and, importantly, the MAL^{NEO} signature was significantly more expressed in tumors exhibiting only partial or no response to ICI therapy as compared to full response (FIG. 7E, unpaired, one-sided t-test p-value = 0.018).

Taken together, classification using human epidermal melanocyte developmental stage signatures revealed that at least four states of dedifferentiation constitute individual tumors (FIG. 7F). The proportion of melanocytes that have readopted a neonatal-like signature is associated with worse prognosis and higher likelihood of resistance to ICI therapy, demonstrating that while some amount of dedifferentiation is associated with worse prognosis, overall survival, immune evasion, and immune resistance are not linearly correlated with dedifferentiation (FIG. 7F).

This study has provided a fresh-from-skin human epidermal melanocyte dataset that encompasses human development, sex and diverse race/ethnicities and includes multiple donor-matched anatomic locations. These findings deliver a unique perspective on human melanocyte biology through the characterization of distinct transcriptional programs specific to development and function. Thus, the transcriptional programs identified here are valuable for understanding the diversity and malignant transformation of human melanocytes.

An additional population of epidermal melanocytes was identified that appear early during human development. It is possible epidermal v-mels are hypopigmented descendants of previously defined sweat gland stem cells. It is also possible that v-mels derive from Schwann-cell derived melanoblasts which undergo a distinct lineage specification pathway. Having identified genes in each subtype that are conserved through fetal development to adulthood, markers that permit exploration of these hypotheses in future studies have been identified. As the predominant class of melanocytes in volar regions, it was speculated these v-mels could represent a distinct cell of origin of acral melanomas and demonstrated that the v-mel signature was significantly elevated in primary AMs compared to other primary cutaneous melanomas (FIG. 3J–K). Since AM is associated with poor therapeutic response and overall survival, assessing whether the v-mel origin confers therapeutic vulnerabilities unique to AMs could be clinically valuable.

By characterizing melanoma dedifferentiation using human-specific developmental programs, this work sheds light on the relationships among developmental stages, tumor characteristics, and melanoma cell transcriptional states (FIG. 6 and FIG. 7). For example, with 63 years as the average age of melanoma diagnosis, the *in situ* adult melanocyte transcriptome provides a relevant basis for interrogating disease etiology and progression. Moreover, these analyses identified the transcriptional state associated with neonatal melanocytes correlated to worst overall survival and predicted response to immune checkpoint inhibitors. One limitation of the cohort is the neonatal samples are limited to a single anatomic location (foreskin). The pseudotime analysis and the frequency of observed sequential dedifferentiation in melanoma both support the hypothesis that neonatal melanocytes represent an intermediate developmental stage, but the contribution of the foreskin tissue environment on the transcriptional programs cannot ruled out. Indeed, foreskin is established as immunologically hyperactive, it is therefore possible that foreskin melanocytes evolved to express more immune-evasive programs. Regardless, the discovery of the prognostic value of this expression program could prove clinically valuable in the *a priori* prediction of therapeutic response to immune checkpoint inhibition. Due to tissue availability and ease of culture, the neonatal melanocyte transcriptome is often considered the baseline “normal differentiated program” for comparison to melanoma transcriptomes. This technical artifact can explain why this program has been previously underappreciated. Melanoma-specific genes directly acquired in all stages of dedifferentiation were identified (FIG. 6G, FIG. 7G, Table 3), suggesting that these genes may undergo positive selection during early metastatic dissemination. Along with the widely-accepted diagnostic melanoma biomarker PRAME and an established marker of invasion AXL, additional melanoma-

associated genes were identified. Further investigation into the mechanistic roles of these gene sets could reveal previously uncharacterized drivers of melanoma metastasis.

Table 1. Differentially expressed genes between donor-matched volar and non-volar cutaneous melanocytes in FIG. 3. Differentially expressed genes were determined by Two-sided Wilcoxon Rank Sum Test. Adjusted p-value computed using Benjamini-Hochberg multiple testing procedure.									
2,042 site-enriched Non-volar Cutaneous vs Volar DE genes from FIG. 3A									
Volar melanocyte enriched genes (ordered by adj p-value)									
gene	log2 fold change	p-value	adj p-value	neg log10(adj p-value)	gene	log2 fold change	p-value	adj p-value	neg log10(adj p-value)
NTRK2	-3.754142284	6.0618E-117	1.4848E-112	111.8283411	MILR1	-1.915088654	0.000230505	0.003987284	2.399322812
ID2	-3.118757248	7.3139E-114	8.9573E-110	109.0478211	REC8	-0.483075172	0.000250983	0.004320157	2.364500478
ID3	-5.690807819	1.8069E-100	1.4753E-96	95.8311202	POLH	-0.671879053	0.00025536	0.004386244	2.357907191
RAB3B	-2.387235165	7.54019E-47	8.79473E-44	43.05577743	RASSF1	-0.513198197	0.000284417	0.004847961	2.314440919
NAV2	-1.751379967	2.37292E-35	1.38387E-32	31.85890558	GABBR1	-0.532790005	0.000296878	0.005039315	2.297628512
MEG3	-2.796798229	3.07647E-29	1.17742E-26	25.92906722	RCC1	-0.853792727	0.000298043	0.00505558	2.296228999
IGDCC4	-1.539427519	1.78188E-28	6.41843E-26	25.19257112	TPD52	-0.492767602	0.000299608	0.005075111	2.294554451
PDLIM3	-1.612020731	6.19953E-27	1.92217E-24	23.71620878	BTG1	-0.407893956	0.000301619	0.005105643	2.291949539
FRZB	-1.646557808	1.34414E-25	3.50248E-23	22.45562373	BAZ2B	-0.533544838	0.00031108	0.005247661	2.280034191
PHACTR3	-1.470532894	7.049E-25	1.76182E-22	21.75403896	CFAP61	-1.924341798	0.000315875	0.005317551	2.274288376
CDR1	-1.032910705	1.3114E-22	2.67679E-20	19.57238491	BRD2	-0.437898695	0.000329578	0.005525457	2.257631822
MIR3654	-0.924516261	1.63998E-22	3.29259E-20	19.48246274	CDK12	-0.473014653	0.000329827	0.005525836	2.257602028
PDLIM4	-1.470458388	7.73993E-21	1.29851E-18	17.88655592	FBXO9	-0.50252986	0.000334136	0.005586569	2.252854857
PHGDH	-1.276817083	1.00025E-17	1.2069E-15	14.91832984	CTGF	-0.960378349	0.000350917	0.005831321	2.234233071
NES	-1.352597833	2.85687E-17	3.28527E-15	14.48342937	TULP2	-0.907613456	0.000354464	0.005878297	2.2307485
UACA	-1.034484386	3.68537E-17	4.16104E-15	14.38079777	CCND2	-1.739438057	0.000365307	0.006025474	2.220008765
EIF5AL1	-1.093874812	6.40036E-17	7.03006E-15	14.15304085	MRPS25	-0.48961851	0.000374311	0.006140904	2.211767676
SHC4	-1.831962585	3.49658E-16	3.56855E-14	13.44750809	MGRN1	-0.600480974	0.000374847	0.006145582	2.211436962

PTN	- 1.602055 55	3.01005 E-15	2.85768 E-13	12.54398 693	DLGAP1	- 0.827429 175	0.000425 877	0.006903 656	2.160920 852
TOX3	- 1.691528 678	3.84395 E-15	3.57999 E-13	12.44611 824	GSTM1	- 2.121361 017	0.000442 87	0.007146 025	2.145935 49
DAAM1	- 1.109912 515	5.98286 E-15	5.42756 E-13	12.26539 513	SPDYE6	- 0.695437 849	0.000450 701	0.007234 258	2.140605 98
LOC28445 4	- 1.213872 91	8.93756 E-15	7.81845 E-13	12.10687 917	LDB1	- 0.582141 876	0.000470 401	0.007496 42	2.125146 108
CECR2	- 1.307452 559	1.11969 E-13	8.847E- 12	11.05320 419	PDLIM7	- 0.555002 63	0.000480 093	0.007631 023	2.117417 22
ARID5A	- 1.309638 143	4.36493 E-13	3.11705 E-11	10.50625 683	CDK2	- 0.477404 356	0.000506 735	0.008028 438	2.095368 922
RUNX3	- 0.877994 716	6.86589 E-13	4.76411 E-11	10.32201 809	C5orf45	- 0.813335 001	0.000516 337	0.008143 689	2.089178 82
SLC12A5	- 1.706906 08	1.0757E- 12	7.29867 E-11	10.13675 644	UST	- 0.571886 778	0.000523 076	0.008228 782	2.084664 417
CREB5	- 0.968270 242	1.15405 E-12	7.78711 E-11	10.10862 374	CREBBP	- 0.440704 614	0.000528 288	0.008294 799	2.081194 157
IGFBP3	- 1.045001 268	3.24344 E-12	2.06662 E-10	9.684739 789	ZKSCAN1	- 0.465340 495	0.000530 477	0.008323 829	2.079676 85
HIST1H1E	- 0.909290 969	6.55059 E-12	4.01125 E-10	9.396719 976	ARHGAP2 4	- 0.506841 421	0.000540 726	0.008452 173	2.073031 637
ERBB3	- 0.917368 829	6.82942 E-12	4.16119 E-10	9.380782 58	PXMP4	- 0.583741 486	0.000591 83	0.009174 86	2.037400 571
FAM210B	- 0.871610 045	7.57578 E-12	4.54807 E-10	9.342172 899	HSPB2	- 0.531414 628	0.000605 254	0.009353 364	2.029032 15
TXNIP	- 0.860300 303	4.33145 E-11	2.37348 E-09	8.624614 925	BID	- 0.678387 821	0.000674 465	0.010323 091	1.986190 24
PLAT	- 1.019935 846	5.26297 E-11	2.85834 E-09	8.543886 335	LOC10192 7481	- 1.164224 505	0.000676 727	0.010340 458	1.985460 216
KIAA1683	- 1.209673 762	1.1385E- 10	5.97138 E-09	8.223925 331	ZSWIM4	- 1.092056 274	0.000680 255	0.010374 948	1.984014 051
LINC0047 3	- 1.922710 896	1.58793 E-10	8.18839 E-09	8.086801 734	PHF23	- 0.494915 485	0.000686 337	0.010448 188	1.980959 01
CXXC5	- 0.940584 302	3.5077E- 10	1.71835 E-08	7.764887 888	TBC1D7	- 0.520888 388	0.000703 376	0.010661 193	1.972194 213
KCNQ1OT 1	- 1.014119 387	5.78022 E-10	2.71748 E-08	7.565833 652	GABPB1- AS1	- 0.512583 017	0.000717 554	0.010849 238	1.964600 767
TUBB2B	- 0.821122 766	5.85632 E-10	2.74273 E-08	7.561817 072	MYCBP2	- 0.444684 952	0.000719 222	0.010867 511	1.963869 903
TTYH1	- 1.230690 241	9.3237E- 10	4.23701 E-08	7.372940 889	MED15	- 0.457610 13	0.000748 485	0.011261 298	1.948411 557
ANK2	- 0.817035 079	1.10343 E-09	4.98661 E-08	7.302194 728	CCT5	- 0.443800 718	0.000749 152	0.011264 408	1.948291 61
ATP10A	- 0.775570 571	1.30535 E-09	5.82391 E-08	7.234785 35	SMOX	- 0.583074 51	0.000781 159	0.011681 14	1.932514 787

DCLK1	- 1.574236 512	1.76998 E-09	7.81152 E-08	7.107264 536	PPIP5K2	- 0.444087 595	0.000823 705	0.012279 875	1.910806 06
LOC10019 0986	- 0.646294 057	2.84269 E-09	1.21942 E-07	6.913847 124	RAB22A	- 0.432175 994	0.000828 574	0.012344 943	1.908510 897
PHACTR1	- 0.800598 741	3.49783 E-09	1.47972 E-07	6.829820 437	HEXIM1	- 0.397823 662	0.000838 342	0.012460 162	1.904476 304
GLCCI1	- 0.903584 361	8.73357 E-09	3.51265 E-07	6.454365 739	IFFO2	- 1.111767 173	0.000840 566	0.012485 635	1.903589 349
FJX1	- 1.343385 22	1.35162 E-08	5.26338 E-07	6.278735 367	ADARB1	- 0.424865 156	0.000860 522	0.012751 141	1.894450 959
CDH19	- 0.714088 798	2.62708 E-08	9.85416 E-07	6.006380 188	CECR1	- 0.886685 908	0.000874 327	0.012924 416	1.888589 084
BMPR1B	- 0.762638 211	2.65854 E-08	9.95693 E-07	6.001874 589	SPINT2	- 1.828564 048	0.000884 231	0.013031 496	1.885005 709
IGF2BP3	- 1.123615 265	3.09079 E-08	1.14359 E-06	5.941729 146	IRX5	- 0.494660 467	0.000897 651	0.013207 758	1.879170 903
NR4A3	- 1.113756 299	3.42846 E-08	1.25902 E-06	5.899967 15	FHL1	- 0.461762 488	0.000929 23	0.013629 082	1.865533 386
SEMA6A	- 0.677349 985	3.5274E- 08	1.29148 E-06	5.888911 77	DBNDD1	- 0.566572 726	0.000935 822	0.013717 542	1.862723 702
TRIO	- 0.768395 305	4.76421 E-08	1.71862 E-06	5.764819 115	TRIM27	- 0.496750 176	0.000941 247	0.013778 77	1.860789 539
NRP2	- 1.247081 518	5.56544 E-08	1.98717 E-06	5.701764 962	CGN	- 1.103968 859	0.000944 714	0.013806 577	1.859913 967
NEDD4L	- 0.779282 808	7.39636 E-08	2.57339 E-06	5.589494 749	ADGRG6	- 0.728225 589	0.000971 014	0.014165 591	1.848765 292
VNT4	- 1.060254 097	7.61719 E-08	2.63897 E-06	5.578565 065	PCF11	- 0.427823 395	0.000983 301	0.014327 769	1.843821 437
POTEM	- 2.180957 079	8.02417 E-08	2.76433 E-06	5.558409 504	CDK15	- 0.541725 755	0.001006 085	0.014624 948	1.834905 678
LOC10193 0452	- 0.767530 62	1.39367 E-07	4.65709 E-06	5.331885 434	MCHR1	- 0.527775 466	0.001060 832	0.015329 807	1.814463 324
RAB6B	- 0.802143 812	1.48199 E-07	4.93875 E-06	5.306383 07	HNRNPAB	- 0.353627 503	0.001087 782	0.015654 6	1.805358 018
CTSH	- 0.838142 276	1.522E- 07	5.06505 E-06	5.295416 075	RASSF8	- 0.440227 3	0.001164 624	0.016682 048	1.777750 629
SYT17	- 1.624316 216	2.3863E- 07	7.6807E- 06	5.114599 267	HRK	- 0.479664 654	0.001180 785	0.016893 785	1.772273 04
MIA	- 0.658910 453	2.61287 E-07	8.38789 E-06	5.076347 217	STOX2	- 0.482516 289	0.001182 82	0.016913 016	1.771778 928
AMOTL1	- 0.813666 88	2.78676 E-07	8.86479 E-06	5.052331 593	LDLRAD3	- 0.426682 949	0.001200 177	0.017121 226	1.766465 133
LINC0063 2	- 0.811102 152	3.4611E- 07	1.09107 E-05	4.962146 696	EIF4G3	- 0.408019 96	0.001256 252	0.017796 78	1.749658 577
KLHL24	- 0.672709 584	5.91357 E-07	1.79488 E-05	4.745963 892	ANKRD44- IT1	- 0.461289 287	0.001360 508	0.019118 927	1.718536 49

MYC	- 0.730143 487	9.47784 E-07	2.78692 E-05	4.554875 696	PLK2	- 0.486807 287	0.001408 623	0.019715 891	1.705183 59
ENC1	- 1.312815 905	1.34786 E-06	3.84337 E-05	4.415287 309	DDIT4	- 0.524279 058	0.001412 616	0.019760 487	1.704202 365
ZNF608	- 0.917593 718	1.52493 E-06	4.3032E- 05	4.366208 724	NAB2	- 0.551342 607	0.001418 625	0.019833 217	1.702606 845
SOBP	- 1.174356 341	2.33231 E-06	6.29852 E-05	4.200761 577	GNL3	- 0.457763 195	0.001430 309	0.019955 532	1.699936 696
SNTB2	- 0.718637 288	2.36878 E-06	6.38996 E-05	4.194502 047	DLGAP4	- 0.451495 916	0.001482 614	0.020561 134	1.686952 932
BACH1	- 0.741264 88	2.41373 E-06	6.48977 E-05	4.187770 667	FRMD4B	- 0.577405 989	0.001491 248	0.020656 332	1.684946 804
IRX3	- 0.877258 003	2.51052 E-06	6.71317 E-05	4.173072 251	KIF21A	- 0.433043 897	0.001533 913	0.021167 131	1.674337 996
CSNK2B	- 0.365997 672	2.74397 E-06	7.32943 E-05	4.134929 521	LRRN4CL	- 0.478344 798	0.001553 873	0.021370 338	1.670188 61
DENND2A	- 0.970220 387	2.88662 E-06	7.69368 E-05	4.113866 129	CDIP1	- 0.586156 309	0.001558 594	0.021411 221	1.669358 574
FMNL2	- 0.848814 726	3.09759 E-06	8.19356 E-05	4.086527 566	CAMSAP2	- 0.556104 779	0.001559 557	0.021412 445	1.669333 748
BANP	- 0.802499 89	3.35108 E-06	8.78814 E-05	4.056102 989	WDR46	- 0.579849 482	0.001579 736	0.021665 208	1.664237 133
CHP1	- 0.162610 397	3.44472 E-06	9.01442 E-05	4.045062 211	CHST2	- 0.933671 594	0.001582 486	0.021690 778	1.663724 861
ZNF429	- 0.786960 9	3.52913 E-06	9.22546 E-05	4.035012 015	HN1	- 0.479145 765	0.001598 99	0.021880 253	1.659947 654
LOC38990 6	- 1.091573 715	3.7587E- 06	9.7838E- 05	4.009492 593	FOXK1	- 0.459331 453	0.001672 289	0.022811 91	1.641838 345
CSGALNA CT1	- 1.370385 528	3.9718E- 06	0.000102 947	3.987385 093	NOP58	- 0.448678 046	0.001672 662	0.022811 91	1.641838 345
CTBP2	- 0.522060 99	5.48286 E-06	0.000137 741	3.860937 78	ZNF814	- 0.349755 406	0.001712 996	0.023297 131	1.632697 552
MYLIP	- 0.661476 552	5.55912 E-06	0.000139 228	3.856272 714	RNF41	- 0.495777 637	0.001720 46	0.023373 987	1.631267 199
LINC0051 8	- 0.736257 374	5.5946E- 06	0.000139 974	3.853954 017	SNHG3	- 0.423139 095	0.001728 146	0.023464 088	1.629596 315
CHD1	- 0.586650 491	6.77846 E-06	0.000165 866	3.780243 189	ZFC3H1	- 0.502495 468	0.001757 936	0.023789 439	1.623615 803
PPP1R10	- 0.649186 611	7.35214 E-06	0.000178 654	3.747986 974	KLHL6	- 1.532083 273	0.001764 991	0.023832 237	1.622835 195
OPN3	- 0.598926 663	9.41352 E-06	0.000223 859	3.650025 454	PCCB	- 0.523212 433	0.001785 914	0.024084 305	1.618265 873
POLR2A	- 0.476708 978	9.71862 E-06	0.000230 89	3.636594 131	SESN3	- 0.343697 339	0.001786 608	0.024084 305	1.618265 873
CTSC	- 0.605605 066	1.06201 E-05	0.000250 607	3.601007 376	IMPDH2	- 0.450109 422	0.001843 815	0.024760 096	1.606247 677

PSAT1	- 0.578512 132	1.07734 E-05	0.000253 246	3.596457 229	NOP14	- 0.538847 208	0.001868 903	0.025006 583	1.601945 652
PEAK1	- 0.736703 396	1.13281 E-05	0.000265 776	3.575484 584	LINC0100 4	- 0.750608 683	0.001871 077	0.025016 463	1.601774 093
RASIP1	- 1.189228 892	1.1853E- 05	0.000277 559	3.556645 278	LMCD1	- 0.497713 119	0.001937 594	0.025807 199	1.588259 134
WIPI1	- 0.633573 592	1.75472 E-05	0.000395 038	3.403360 719	LMO4	- 0.343154 43	0.001965 042	0.026115 979	1.583093 685
BCL2	- 0.548934 46	1.79577 E-05	0.000403 908	3.393717 14	SETD2	- 0.421881 348	0.002049 542	0.027112 592	1.566828 954
FADS1	- 0.561894 119	1.96181 E-05	0.000438 435	3.358094 301	RC3H1	- 0.406871 885	0.002049 993	0.027112 592	1.566828 954
TSPAN14	- 0.582472 086	2.06375 E-05	0.000459 541	3.337675 782	IGF2BP1	- 0.773612 142	0.002058 23	0.027206 84	1.565321 895
NRIP1	- 0.614210 427	2.22747 E-05	0.000492 86	3.307276 454	FNBP1L	- 0.466912 508	0.002083 008	0.027489 874	1.560827 249
DAB2	- 0.665398 24	2.40752 E-05	0.000530 78	3.275085 26	VHL	- 0.445543 11	0.002091 023	0.027568 96	1.559579 61
ZNF276	- 0.567812 324	2.42435 E-05	0.000534 01	3.272450 648	CDK6	- 0.385241 359	0.002096 075	0.027604 339	1.559022 651
ORA12	- 0.686376 274	2.61078 E-05	0.000568 43	3.245323 181	TFRC	- 0.676267 922	0.002172 023	0.028479 253	1.545471 41
TTN	- 0.929804 564	2.76918 E-05	0.000598 661	3.222819 238	E4F1	- 0.576384 068	0.002192 059	0.028697 112	1.542161 814
TOB2	- 0.563909 054	2.82439 E-05	0.000607 913	3.216158 365	JMY	- 0.549129 188	0.002218 553	0.029012 937	1.537408 311
CKS2	- 0.530575 454	2.95787 E-05	0.000635 527	3.196865 975	LINC0100 0	- 0.448901 206	0.002270 319	0.029610 858	1.528549 01
PART1	- 0.585063 338	3.08515 E-05	0.000659 403	3.180848 917	SOX12	- 0.835556 686	0.002309 082	0.030025 417	1.522510 957
CIRH1A	- 0.706342 28	3.21854 E-05	0.000686 715	3.163223 325	BOK	- 0.593950 57	0.002364 575	0.030646 049	1.513625 51
LOC72839 2	- 1.114708 9	3.29916 E-05	0.000702 081	3.153612 535	FAM210A	- 0.518214 941	0.002447 388	0.031633 947	1.499846 619
LOC10050 5938	- 1.422665 238	3.92821 E-05	0.000820 968	3.085673 527	LOC10012 6784	- 1.240818 024	0.002601 911	0.033419 617	1.475998 534
BOP1	- 0.766389 728	4.31102 E-05	0.000891 843	3.049711 72	KDM5B	- 0.462473 303	0.002649 807	0.033967 216	1.468940 052
ANKRD44	- 0.582318 068	4.43391 E-05	0.000914 177	3.038969 731	ACVR2B	- 0.504360 676	0.002774 207	0.035408 428	1.450893 359
SERTAD1	- 0.698935 449	5.17339 E-05	0.001046 822	2.980127 05	MRAS	- 0.453637 511	0.002839 221	0.036107 937	1.442397 33
NID1	- 0.597748 458	5.4009E- 05	0.001089 701	2.962692 632	NCS1	- 0.661911 011	0.002884 309	0.036605 315	1.436455 856
LRP6	- 0.522486 329	5.54763 E-05	0.001115 63	2.952479 703	LOC10574 7689	- 0.924577 296	0.002895 875	0.036695 07	1.435392 278

PRICKLE1	- 1.495618 582	5.63513 E-05	0.001132 295	2.946040 228	PAX8-AS1	- 0.598881 483	0.002908 26	0.036794 894	1.434212 448
HIST1H1D	- 1.286005 497	5.67838 E-05	0.001139 117	2.943431 791	LYPD1	- 0.386095 554	0.002907 174	0.036794 894	1.434212 448
SENP6	- 0.601767 957	6.53928 E-05	0.001294 851	2.887780 312	DHX33	- 0.354392 052	0.003009 089	0.038011 664	1.420083 113
ID1	- 2.443848 61	7.56247 E-05	0.001470 121	2.832646 987	BMPR2	- 0.318912 804	0.003109 468	0.038938 295	1.409623 072
NR4A2	- 0.500067 77	7.63317 E-05	0.001481 512	2.829294 963	WDR74	- 0.594340 622	0.003151 602	0.039385 378	1.404664 985
LDB3	- 0.802973 986	8.21827 E-05	0.001585 025	2.799963 789	THSD7A	- 0.777302 563	0.003153 772	0.039392 403	1.404587 525
NR2F2	- 0.570629 954	8.28458 E-05	0.001595 303	2.797156 935	ZNF195	- 0.489423 782	0.003180 597	0.039686 981	1.401351 939
NLN	- 0.594447 315	0.000101 11	0.001906 528	2.719756 921	CARHSP1	- 0.395971 119	0.003234 016	0.040230 573	1.395443 777
FBXO17	- 0.595686 913	0.000105 884	0.001990 422	2.701054 894	PPARGC1 B	- 0.579691 708	0.003355 842	0.041535 111	1.381584 621
RSRP1	- 0.606843 889	0.000106 92	0.002008 355	2.697159 434	GOLIM4	- 0.373602 271	0.003375 156	0.041710 928	1.379750 145
ID4	- 0.545931 28	0.000113 78	0.002117 73	2.674129 431	PYCR1	- 0.647311 985	0.003412 113	0.042103 928	1.375677 383
MYO9B	- 0.505093 813	0.000117 639	0.002176 316	2.662278 043	DMXL2	- 0.574098 11	0.003482 015	0.042836 999	1.368180 959
SOX2	- 3.345513 344	0.000124 455	0.002281 744	2.641733 038	CHD8	- 0.441651 225	0.003510 265	0.043162 862	1.364889 765
SLC10A1	- 1.008467 793	0.000130 547	0.002389 852	2.621629 055	XIAP	- 0.422707 021	0.003609 656	0.044296 055	1.353634 954
PAMR1	- 0.511576 355	0.000132 563	0.002423 136	2.615622 124	RGS10	- 0.306042 314	0.003616 083	0.044352 693	1.353080 002
WIP12	- 0.576881 826	0.000135 342	0.002468 4	2.607584 511	ENOSF1	- 0.404787 689	0.003625 173	0.044441 932	1.352207 073
PRPF8	- 0.484960 914	0.000139 442	0.002541 289	2.594945 996	OSBP	- 0.458655 208	0.003643 986	0.044650 228	1.350176 323
PDE8A	- 0.517045 498	0.000142 695	0.002592 855	2.586221 728	SELO	- 0.566946 089	0.003664 612	0.044876 826	1.347977 868
GFOD2	- 0.735636 413	0.000151 785	0.002741 765	2.561969 826	TOB1	- 0.382177 025	0.003727 71	0.045516 713	1.341829 108
BCHE	- 0.575244 129	0.000152 958	0.002760 911	2.558947 646	GOLGA3	- 0.451195 419	0.003776 024	0.045992 011	1.337317 603
KLF13	- 0.399398 565	0.000166 465	0.002982 738	2.525384 893	TCEAL7	- 0.802196 622	0.003837 866	0.046560 021	1.331986 83
CRLF3	- 0.682515 323	0.000171 122	0.003057 236	2.514671 073	NECAB2	- 1.256868 005	0.003849 062	0.046629	1.331343 895
GIT2	- 0.501495 779	0.000171 94	0.003069 609	2.512916 872	SFSWAP	- 0.359725 833	0.003861 895	0.046738 228	1.330327 753

SYT11	- 0.471145 779	0.000176 338	0.003129 873	2.504473 271	DUSP16	- 0.444329 172	0.003966 786	0.047894 32	1.319715 991
ATM	- 0.448352 098	0.000204 908	0.003592 709	2.444578 004	LIMS1	- 0.407905 877	0.003967 403	0.047894 32	1.319715 991
SQLE	- 0.507528 722	0.000211 126	0.003691 164	2.432836 666	FAM212A	- 0.432342 947	0.003973 581	0.047945 271	1.319254 226
PRR14L	- 0.529761 672	0.000215 666	0.003754 452	2.425453 433	TMEM164	- 0.484485 03	0.004062 677	0.048923 905	1.310478 886
NT5DC2	- 0.599480 212	0.000217 843	0.003784 295	2.422014 999	TRABD	- 0.388524 652	0.004123 433	0.049582 415	1.304672 321
TIMP3	- 0.803760 767	0.000223 896	0.003876 193	2.411594 558	DARS2	- 0.654618 859	0.004148 437	0.049785 313	1.302898 76
Non-volar cutaneous melanocyte enriched genes (ordered by adj p-value)									
gene	log2 fold chage	p-value	adj p- value	neg log10(adj p-value)	gene	log2 fold chage	p-value	adj p- value	neg log10(adj p-value)
AKAP12	2.699370 384	9.46219 E-85	5.79417 E-81	80.23700 882	RUNX2	1.118347 764	4.65509 E-06	0.000118 526	3.926187 523
MCOLN3	2.833744 526	2.33043 E-82	1.14163 E-78	77.94247 443	TRAPPC6 A	0.616699 755	4.69528 E-06	0.000119 425	3.922905 173
ASAH1	1.898617 983	3.00869 E-76	1.22825 E-72	71.91071 352	RPS6	0.163113 698	4.72693 E-06	0.000120 105	3.920437 814
SLITRK2	2.027208 567	1.05148 E-73	3.67929 E-70	69.43423 586	PRKACB	0.715507 805	4.8469E- 06	0.000123 026	3.910003 391
IFITM3	2.069860 458	1.67316 E-71	5.12281 E-68	67.29049 201	NGFRAP1	0.551466 346	4.87915 E-06	0.000123 716	3.907572 89
APOE	2.012315 035	7.66686 E-71	2.08658 E-67	66.68056 517	TMEM248	0.529887 08	5.0294E- 06	0.000127 394	3.894850 86
APCDD1	2.503547 43	2.56261 E-67	6.27685 E-64	63.20225 852	RAB6A	0.500867 665	5.10319 E-06	0.000129 13	3.888974 017
CST3	1.767636 18	9.00599 E-64	2.00539 E-60	59.69780 134	CLPTM1	0.615574 181	5.21846 E-06	0.000131 91	3.879721 565
SEMA5A	2.578830 957	8.59542 E-62	1.75447 E-58	57.75585 437	CNAS	0.335209 876	5.22943 E-06	0.000132 051	3.879257 37
LGI3	2.409373 76	3.1473E- 60	5.92999 E-57	56.22694 595	ABLIM1	1.204136 848	5.29079 E-06	0.000133 463	3.874638 836
HPGD	2.589627 504	1.77195 E-57	3.10016 E-54	53.50861 605	DSTYK	0.516884 863	5.33042 E-06	0.000134 324	3.871844 931
HLA-C	2.514072 895	8.54598 E-54	1.3955E- 50	49.85526 956	RHOBTB3	0.449962 467	5.37117 E-06	0.000135 212	3.868984 108
S100A6	1.612758 279	1.19085 E-50	1.82305 E-47	46.73920 224	ATP2C1	0.803516 15	5.47903 E-06	0.000137 741	3.860937 78
CALM1	0.955999 255	6.16728 E-50	8.88596 E-47	46.05129 562	RPL32	0.181783 408	5.49607 E-06	0.000137 931	3.860337 905
HLA-A	1.768987 179	8.28804 E-50	1.12782 E-46	45.94776 105	ROBO1	0.570848 763	5.55051 E-06	0.000139 155	3.856502 326
CD99	1.023284 674	5.00759 E-49	6.45557 E-46	45.19006 532	RNF13	0.602058 768	5.67191 E-06	0.000141 763	3.848436 928
CD59	0.904966 891	5.66713 E-49	6.94053 E-46	45.15860 738	MRPL53	0.537935 197	5.67983 E-06	0.000141 816	3.848273 906
GMPR	1.911767 364	1.15917 E-46	1.29058 E-43	42.88921 655	ALG14	0.917375 922	5.81114 E-06	0.000144 947	3.838790 631
VAMP8	1.845114 35	3.5539E- 46	3.78475 E-43	42.42196 289	SLC25A3	0.440015 107	5.85721 E-06	0.000145 948	3.835802 966
PSAP	1.161190 629	4.02854 E-46	4.11146 E-43	42.38600 372	TRIM47	1.069660 306	5.87083 E-06	0.000145 99	3.835677 166
GSTP1	1.082921 386	5.66959 E-46	5.55484 E-43	42.25532 847	ATPIF1	0.454298 139	5.87083 E-06	0.000145 99	3.835677 166
EMP1	1.647157 192	9.92185 E-44	9.34715 E-41	40.02932 1	GBA	0.672983 05	5.87947 E-06	0.000146 056	3.835479 177

S100A10	0.941818 833	1.30788 E-43	1.18649 E-40	39.92573 614	TFAP2B	0.526278 913	5.89815 E-06	0.000146 372	3.834541 364
KIF1A	3.677368 402	1.63038 E-43	1.42623 E-40	39.84581 077	IDI2-AS1	0.742687 285	5.94489 E-06	0.000147 383	3.831553 646
ANXA2	0.793747 187	7.9711E- 43	6.73256 E-40	39.17182 003	RPL17	0.268229 842	5.99383 E-06	0.000148 446	3.828432 303
MLANA	0.887632 787	3.6701E- 42	2.99652 E-39	38.52338 307	EEF1A1	0.215667 71	6.05906 E-06	0.000149 91	3.824170 329
CISD1	1.459638 119	5.81089 E-41	4.59135 E-38	37.33805 947	CLTB	0.612687 886	6.10418 E-06	0.000150 874	3.821386 595
PPIA	0.935300 708	1.62419 E-40	1.24321 E-37	36.90545 418	OLMALIN C	1.010815 859	6.12923 E-06	0.000151 34	3.820046 134
RAB2A	1.314177 632	8.00067 E-40	5.93844 E-37	36.22632 762	PELI1	0.793637 514	6.23522 E-06	0.000153 802	3.813037 641
ABCA1	2.152475 834	3.52145 E-39	2.5369E- 36	35.59569 741	ATP1A1	0.586060 345	6.25982 E-06	0.000154 254	3.811764 97
DBI	1.116612 196	3.06471 E-38	2.14477 E-35	34.66861 859	ZDHHC2	1.071432 352	6.3459E- 06	0.000156 218	3.806269 885
STXBP6	1.739797 592	2.0595E- 36	1.40126 E-33	32.85348 111	C12orf57	0.452799 588	6.42172 E-06	0.000157 925	3.801548 001
ARL6IP5	1.220052 719	2.29528 E-36	1.51948 E-33	32.81830 566	SNHG18	1.417284 846	6.45996 E-06	0.000158 706	3.799405 743
CDC42	0.849657 595	2.46582 E-36	1.58942 E-33	32.79876 178	S100A11	0.569003 701	6.50392 E-06	0.000159 467	3.797330 509
SCD	1.657971 382	9.85905 E-36	6.19199 E-33	32.20816 997	ANXA4	0.551753 938	6.50342 E-06	0.000159 467	3.797330 509
HLA-H	1.625596 285	1.60064 E-35	9.80154 E-33	32.00870 559	H2AFV	0.582843 9	6.52098 E-06	0.000159 725	3.796627 193
NUCKS1	0.873907 804	1.87603 E-35	1.12077 E-32	31.95048 509	OSBPL1A	0.534100 354	6.88563 E-06	0.000168 32	3.773864 028
HMGB1	0.840564 966	6.54562 E-35	3.72857 E-32	31.42845 816	CCDC53	0.696893 215	6.92917 E-06	0.000169 215	3.771560 067
ENPP2	1.690974 116	1.75084 E-34	9.7466E- 32	31.01114 665	GUSB	0.645039 558	6.95798 E-06	0.000169 75	3.770190 729
SAT1	1.017593 622	2.85559 E-34	1.55433 E-31	30.80845 737	RABIF	0.726716 399	6.9853E- 06	0.000170 247	3.768921 376
PHPT1	1.295602 441	6.82435 E-34	3.63382 E-31	30.43963 692	ESRP1	0.649079 442	7.05919 E-06	0.000171 877	3.764783 494
SLC1A4	1.714347 124	7.11524 E-34	3.7081E- 31	30.43084 875	PFKM	0.705948 234	7.15796 E-06	0.000174 108	3.759180 721
B2M	1.079897 523	9.06545 E-34	4.62602 E-31	30.33479 209	EMC2	0.651475 906	7.37981 E-06	0.000179 149	3.746786 56
CDC42EP 3	0.870583 653	1.31501 E-33	6.57346 E-31	30.18220 606	COL4A1	0.959004 7	7.43714 E-06	0.000180 362	3.743855 655
IFITM2	1.556226 85	5.51423 E-33	2.70131 E-30	29.56842 523	RPN1	0.521993 697	7.46625 E-06	0.000180 71	3.743018 031
CALD1	1.063532 829	6.93923 E-33	3.33274 E-30	29.47719 921	C8orf59	0.489566 684	7.46225 E-06	0.000180 71	3.743018 031
ATP1B1	1.973482 847	8.53945 E-33	4.02241 E-30	29.39551 398	FAH	1.289369 226	7.61871 E-06	0.000184 218	3.734668 36
MLEC	1.288105 965	8.90238 E-33	4.11424 E-30	29.38571 005	HNRNPH2	0.778444 171	7.73382 E-06	0.000186 817	3.728584 45
TIMP1	1.904671 788	4.53171 E-32	2.05555 E-29	28.68707 198	ANP32B	0.469415 933	7.80272 E-06	0.000188 295	3.725160 267
ATP5E	1.008920 789	4.78847 E-32	2.07856 E-29	28.68223 72	RALBP1	0.552542 269	7.87221 E-06	0.000189 785	3.721737 162
ANXA5	0.978220 284	4.70375 E-32	2.07856 E-29	28.68223 72	TOMM5	0.512061 536	7.98793 E-06	0.000192 386	3.715827 186
CAV1	0.933490 217	4.83702 E-32	2.07856 E-29	28.68223 72	C19orf71	0.739407 42	8.01971 E-06	0.000192 961	3.714529 399
TJP1	1.374222 875	1.53824 E-31	6.49615 E-29	28.18734 401	EFNA5	0.789746 046	8.54564 E-06	0.000205 414	3.687369 953
ADI1	1.555323 601	2.32053 E-31	9.63373 E-29	28.01620 565	UGCG	0.571954 191	8.55736 E-06	0.000205 494	3.687200 702
GAS7	1.757321 477	4.34674 E-31	1.77448 E-28	27.75092 81	RAP2B	0.433253 556	8.60047 E-06	0.000206 327	3.685444 039
APOD	1.807666 302	1.46984 E-30	5.90201 E-28	27.22899 983	TREX1	0.826975 048	8.62932 E-06	0.000206 817	3.684414 641

PTGDS	2.127863 884	3.87051 E-30	1.5291E- 27	26.81556 348	VDAC2	0.448020 518	8.64181 E-06	0.000206 913	3.684211 343
CD82	1.738316 894	1.25782 E-29	4.89031 E-27	26.31066 403	GPX1	0.439471 215	8.76697 E-06	0.000209 705	3.678390 56
VAMP5	1.459658 027	6.10148 E-29	2.29922 E-26	25.63841 856	GSTO1	0.477269 739	8.78366 E-06	0.000209 899	3.677988 694
SH3BGRL 3	1.098842 263	1.0872E- 28	4.03483 E-26	25.39417 472	NBPF1	0.673107 922	8.99651 E-06	0.000214 776	3.668013 407
REXO2	1.374169 111	1.5788E- 28	5.77179 E-26	25.23868 914	UQCRH	0.422556 4	9.14045 E-06	0.000218	3.661543 086
TPPP3	1.690592 289	2.27022 E-28	8.05895 E-26	25.09372 173	POP4	0.784631 968	9.22689 E-06	0.000219 848	3.657878 192
PRKCDBP	1.687404 037	3.01605 E-28	1.05536 E-25	24.97659 938	TMEM261	0.587527 514	9.38359 E-06	0.000223 364	3.650986 673
TYRP1	1.289903 283	4.10722 E-28	1.41693 E-25	24.84865 072	RCBTB2	0.991737 485	9.85119 E-06	0.000233 813	3.631131 256
CSTB	1.047525 644	4.22038 E-28	1.43575 E-25	24.84292 163	KDELR2	0.599416 673	1.01821 E-05	0.000241 434	3.617202 261
LGALS3B P	1.202749 133	2.68357 E-27	9.00428 E-25	24.04555 092	WBP5	0.506096 721	1.03184 E-05	0.000244 428	3.611849 238
SOD1	0.936190 724	3.01127 E-27	9.96731 E-25	24.00142 216	RAD23B	0.615690 112	1.03519 E-05	0.000244 986	3.610859 067
ACP5	1.904941 559	3.2691E- 27	1.06765 E-24	23.97157 312	NCSTN	0.713413 417	1.04272 E-05	0.000246 478	3.608222 582
NDUFA1	0.965797 782	4.03743 E-27	1.30122 E-24	23.88564 878	RPS15A	0.243689 03	1.04351 E-05	0.000246 478	3.608222 582
NPC2	0.848909 14	5.03338 E-27	1.60114 E-24	23.79557 119	KIT	0.072548 807	1.06643 E-05	0.000251 406	3.599624 482
COX8A	0.991601 944	5.99213 E-27	1.88168 E-24	23.72545 331	SNF8	0.588225 126	1.06771 E-05	0.000251 467	3.599518 384
H3F3AP4	0.858687 878	6.8109E- 27	2.08533 E-24	23.68082 609	TIMP2	0.341778 815	1.07644 E-05	0.000253 246	3.596457 229
LAMTOR5	1.101730 585	8.63705 E-27	2.57995 E-24	23.58838 857	PYGL	1.933088 303	1.10486 E-05	0.000259 468	3.585915 873
SRP14	0.762441 456	8.61267 E-27	2.57995 E-24	23.58838 857	ARL6IP1	0.443365 693	1.16737 E-05	0.000273 623	3.562847 434
LGALS1	0.677863 419	1.52678 E-26	4.50567 E-24	23.34624 072	PKM	0.450106 412	1.1877E- 05	0.000277 856	3.556180 455
HLA-B	2.144397 736	1.62796 E-26	4.6912E- 24	23.32871 61	OSTM1	0.514372 826	1.19943 E-05	0.000280 332	3.552327 448
LY6E	1.655328 87	1.6123E- 26	4.6912E- 24	23.32871 61	PRDX5	0.415558 398	1.20105 E-05	0.000280 443	3.552155 414
EID1	0.754281 223	1.69778 E-26	4.83551 E-24	23.31555 778	CPEB4	0.643920 839	1.21974 E-05	0.000284 536	3.545862 61
PARK7	1.082201 719	2.3516E- 26	6.62069 E-24	23.17909 691	MRPL57	0.479111 999	1.22285 E-05	0.000284 991	3.545169 564
PFN1	0.796626 091	4.29993 E-26	1.19685 E-23	22.92196 18	TOMM22	0.532216 668	1.24307 E-05	0.000289 428	3.538458 753
IGFBP7	1.089352 965	6.63297 E-26	1.82548 E-23	22.73862 248	RPS18	0.192804 843	1.27682 E-05	0.000297 004	3.527237 531
PPP1CB	1.036500 096	7.2493E- 26	1.95126 E-23	22.70968 571	CRTAP	0.434522 39	1.27969 E-05	0.000297 389	3.526675 515
AHNAK	0.999482 095	7.23297 E-26	1.95126 E-23	22.70968 571	EIF2S2	0.490307 748	1.28737 E-05	0.000298 889	3.524489 838
MAL	1.371539 593	7.60211 E-26	2.02398 E-23	22.69379 384	PSMB7	0.515392 184	1.30042 E-05	0.000301 634	3.520519 589
VEPH1	1.468867 54	1.29922 E-25	3.42183 E-23	22.46574 173	PRDX4	0.460111 946	1.31429 E-05	0.000304 562	3.516323 94
TSPO	0.825918 555	1.62087 E-25	4.17911 E-23	22.37891 633	TALDO1	0.379667 64	1.32929 E-05	0.000307 747	3.511805 975
MFSD12	1.178993 106	1.75386 E-25	4.4749E- 23	22.34921 658	KBTBD2	0.662996 471	1.34205 E-05	0.000310 407	3.508067 824
DMKN	2.301013 947	4.93609 E-25	1.24644 E-22	21.90432 873	ERGIC3	0.464884 43	1.35553 E-05	0.000313 23	3.504136 781
NDUFA4	0.854060 471	1.57879 E-24	3.90614 E-22	21.40825 174	VPS37B	0.873410 94	1.36232 E-05	0.000314 206	3.502785 709
PSMB4	0.787421 882	2.4586E- 24	6.0221E- 22	21.22025 231	SNRPF	0.483279 228	1.3612E- 05	0.000314 206	3.502785 709

SKP1	0.689387 739	2.51922 E-24	6.10949 E-22	21.21399 523	ADAM10	0.496815 711	1.38608 E-05	0.000319 385	3.495685 245
COX6A1	0.857328 117	3.28436 E-24	7.88698 E-22	21.10308 941	TRAM1	0.542603 076	1.39447 E-05	0.000321 016	3.493473 269
PRSS23	1.795303 226	4.1983E- 24	9.98379 E-22	21.00070 454	PCBP1	0.366541 445	1.40113 E-05	0.000322 247	3.491811 373
COMT	1.001740 932	5.492E- 24	1.29347 E-21	20.88824 279	SZRD1	0.593736 41	1.4156E- 05	0.000325 269	3.487757 354
MYEOV2	0.990652 919	1.20808 E-23	2.81817 E-21	20.55003 242	ATP5D	0.484262 079	1.46682 E-05	0.000336 723	3.472726 953
COL4A2	1.409939 17	1.27545 E-23	2.94725 E-21	20.53058 346	TMTC2	0.914530 396	1.47283 E-05	0.000337 785	3.471359 123
GNG2	1.278660 092	1.77865 E-23	4.0716E- 21	20.39023 456	TOMM7	0.324899 942	1.4782E- 05	0.000338 7	3.470184 796
DAD1	0.865105 867	1.97418 E-23	4.47736 E-21	20.34897 755	ASB11	0.954565 048	1.52897 E-05	0.000349 353	3.456735 968
NDUFA13	0.932585 597	2.78002 E-23	6.24714 E-21	20.20431 898	ORMDL2	0.637868 404	1.52829 E-05	0.000349 353	3.456735 968
RPL23	0.668311 417	2.8917E- 23	6.43902 E-21	20.19118 045	SRPK2	0.516653 24	1.52784 E-05	0.000349 353	3.456735 968
ITM2B	0.664394 2	3.56028 E-23	7.85634 E-21	20.10477 969	MYO1D	0.762114 227	1.53636 E-05	0.000350 713	3.455047 656
PRELP	1.005093 336	3.84874 E-23	8.41706 E-21	20.07483 944	FAM96B	0.483148 724	1.54951 E-05	0.000353 387	3.451749 927
NENF	1.195331 573	5.17129 E-23	1.12093 E-20	19.95042 001	GAS5	0.414231 628	1.56277 E-05	0.000356 079	3.448453 293
SSR4	0.831053 674	6.17063 E-23	1.32582 E-20	19.87751 549	EZR	0.591603 279	1.58082 E-05	0.000359 856	3.443871 372
SLC45A2	1.557040 691	9.10268 E-23	1.93879 E-20	19.71246 874	ADD3	0.606239 736	1.58691 E-05	0.000360 909	3.442602 772
TMBIM6	0.891980 529	9.24403 E-23	1.95192 E-20	19.70953 688	HSP90AB 1	0.365408 54	1.62578 E-05	0.000369 404	3.432498 213
VMP1	1.161426 187	1.00148 E-22	2.09661 E-20	19.67848 302	POMC	1.059912 443	1.62939 E-05	0.000369 539	3.432339 802
CRYL1	1.256764 531	1.1037E- 22	2.29102 E-20	19.63997 188	NFIC	0.649380 207	1.62806 E-05	0.000369 539	3.432339 802
GNPMB	1.022765 875	1.30043 E-22	2.6767E- 20	19.57240 058	YIF1A	0.573261 142	1.6382E- 05	0.000371 195	3.430397 872
LINC0046 2	3.379219 532	1.34119 E-22	2.71498 E-20	19.56623 395	IAH1	0.524902 463	1.64208 E-05	0.000371 73	3.429772 176
TMSB10	0.701115 787	2.0881E- 22	4.15821 E-20	19.38109 347	XRN2	0.581026 256	1.68124 E-05	0.000380 243	3.419939 079
COX4I1	0.718603 432	2.54851 E-22	5.03413 E-20	19.29807 595	OS9	0.490287 066	1.69445 E-05	0.000382 876	3.416941 674
CFL1	0.560776 83	2.62447 E-22	5.1427E- 20	19.28880 848	L1CAM	0.504581 928	1.71343 E-05	0.000386 809	3.412503 414
FTL	0.578958 273	3.65412 E-22	7.10349 E-20	19.14852 802	MAPRE1	0.578903 854	1.71571 E-05	0.000386 966	3.412326 869
BSG	0.731443 644	4.19986 E-22	8.10012 E-20	19.09150 877	MICAL1	0.760659 993	1.73748 E-05	0.000391 516	3.407250 387
SKAP2	2.200052 023	5.5686E- 22	1.0656E- 19	18.97240 459	PSMD7	0.525504 231	1.82346 E-05	0.000409 761	3.387469 398
TMEM147	0.959870 815	5.74601 E-22	1.09103 E-19	18.96216 353	FCGRT	0.390538 871	1.83665 E-05	0.000412 346	3.384737 861
GAPDH	0.858291 924	6.63563 E-22	1.25025 E-19	18.90300 179	EIF2AK4	0.577619 433	1.86508 E-05	0.000418 346	3.378464 56
TMBIM4	0.980383 813	7.83714 E-22	1.46537 E-19	18.83405 383	RAB1B	0.467691 749	1.90649 E-05	0.000427 241	3.369326 58
MGST3	0.920697 987	1.02223 E-21	1.88588 E-19	18.72448 566	TMEM120 A	0.576262 057	1.92363 E-05	0.000430 689	3.365835 856
FTH1	0.482964 933	1.02401 E-21	1.88588 E-19	18.72448 566	COA4	0.615577 757	1.95449 E-05	0.000437 198	3.359321 408
PCSK2	0.973265 409	1.13648 E-21	2.07739 E-19	18.68248 297	CAP1	0.480936 587	1.98814 E-05	0.000443 916	3.352698 916
PLP1	0.899620 533	1.39406 E-21	2.52934 E-19	18.59699 359	LINC0068 1	1.557628 751	2.04258 E-05	0.000455 655	3.341363 909
HIGD2A	1.080669 522	1.47593 E-21	2.65819 E-19	18.57541 398	RPL5	0.184221 923	2.05787 E-05	0.000458 649	3.338519 295

HINT1	0.790259 242	2.08429 E-21	3.72646 E-19	18.42870 299	PPIE	0.684673 19	2.08711 E-05	0.000464 321	3.333181 56
TXN	0.875577 569	2.2822E- 21	4.05075 E-19	18.39246 497	FRG1	0.633555 055	2.15746 E-05	0.000479 101	3.319572 496
RNASEK	0.785449 445	2.73761 E-21	4.82411 E-19	18.31658 277	DNAJC3	0.374100 536	2.15715 E-05	0.000479 101	3.319572 496
TMEM59	0.616931 379	3.38428 E-21	5.92103 E-19	18.22760 24	RPL22	0.388623 536	2.16235 E-05	0.000479 751	3.318983 82
CBR1	1.154143 691	4.0704E- 21	7.07096 E-19	18.15052 18	EEF1B2	0.306186 676	2.1731E- 05	0.000481 701	3.317222 814
SERF2	0.631174 088	4.24799 E-21	7.32749 E-19	18.13504 504	EEA1	0.393598 408	2.2039E- 05	0.000488 085	3.311504 307
RPS11	0.375319 69	5.1069E- 21	8.74744 E-19	18.05811 905	SUPT4H1	0.499374 896	2.24195 E-05	0.000495 618	3.304853 242
POLR2L	0.952073 395	5.27147 E-21	8.96663 E-19	18.04737 086	SNRPD3	0.482543 677	2.36026 E-05	0.000521 301	3.282911 659
ZFYVE21	1.144884 348	6.9781E- 21	1.17877 E-18	17.92857 141	EDNRB	0.389129 281	2.40402 E-05	0.000530 488	3.275324 589
TYR	0.841504 514	8.2968E- 21	1.38246 E-18	17.85934 72	VTI1B	0.549896 359	2.45211 E-05	0.000539 64	3.267895 538
RAC1	0.733914 554	1.03543 E-20	1.71364 E-18	17.76608 057	ANKS1B	1.294572 353	2.45977 E-05	0.000540 84	3.266931 546
RPS25	0.526731 908	1.09388 E-20	1.79822 E-18	17.74515 67	EIF4EBP1	0.563168 824	2.46959 E-05	0.000542 513	3.265589 637
ATP6V0E1	0.958368 123	1.28912 E-20	2.10505 E-18	17.67673 743	SF3B6	0.450958 58	2.49297 E-05	0.000547 158	3.261887 464
SEPT7	0.866448 7	1.30108 E-20	2.11051 E-18	17.67561 25	UBE2B	0.353586 882	2.51219 E-05	0.000550 882	3.258941 685
UQCQRQ	0.814134 598	1.61722 E-20	2.60606 E-18	17.58401 521	PSMB9	2.537453 413	2.51747 E-05	0.000551 439	3.258502 521
UBB	0.574596 882	2.07603 E-20	3.32355 E-18	17.47839 742	CHD1L	0.693206 549	2.52148 E-05	0.000551 439	3.258502 521
ATOX1	0.916679 502	2.17625 E-20	3.46136 E-18	17.46075 304	NAMPT	0.649378 121	2.51947 E-05	0.000551 439	3.258502 521
GNG5	0.934737 027	2.2017E- 20	3.47925 E-18	17.45851 374	RAB9A	0.511231 661	2.5479E- 05	0.000556 721	3.254362 69
RABAC1	1.019441 485	2.23462 E-20	3.50863 E-18	17.45486 187	RER1	0.530742 884	2.55492 E-05	0.000557 756	3.253555 582
SYNGR1	0.956699 789	3.09303 E-20	4.82552 E-18	17.31645 613	CHCHD10	0.581996 5	2.56641 E-05	0.000559 765	3.251994 147
RPS27L	1.041485 31	3.41287 E-20	5.29081 E-18	17.27647 816	GTF2H5	0.491772 532	2.57813 E-05	0.000561 822	3.250401 379
CD63	0.643839 24	3.82015 E-20	5.88495 E-18	17.23025 717	CHPF	0.555068 672	2.63847 E-05	0.000573 949	3.241126 565
AHNAK2	2.164326 191	3.95968 E-20	6.06178 E-18	17.21739 974	GLG1	0.368060 172	2.64878 E-05	0.000575 681	3.239817 799
H3F3A	0.681281 149	5.74761 E-20	8.74422 E-18	17.05827 881	EPHX1	0.934535 921	2.68325 E-05	0.000582 138	3.234973 878
NSMF	1.230613 947	7.34299 E-20	1.11024 E-17	16.95458 251	CYB5R1	0.532831 252	2.68266 E-05	0.000582 138	3.234973 878
MYL12B	0.918736 696	7.6379E- 20	1.14775 E-17	16.94015 399	TGFBR3	0.943657 696	2.7105E- 05	0.000587 53	3.230970 063
NDUFB11	1.020690 322	8.30823 E-20	1.24086 E-17	16.90627 548	MAP3K3	0.723381 579	2.715E- 05	0.000587 985	3.230633 495
GPM6B	0.772643 805	9.84885 E-20	1.46205 E-17	16.83503 889	ZDHHC7	0.809713 84	2.75325 E-05	0.000595 744	3.224940 458
ATP6V0E2	1.319425 344	1.33178 E-19	1.9651E- 17	16.70661 628	NPM1	0.449071 586	2.77597 E-05	0.000599 6	3.222138 098
RAB27A	1.194572 926	1.39092 E-19	2.04007 E-17	16.69035 569	TOLLIP	0.594495 773	2.78519 E-05	0.000601 061	3.221081 196
OAZ1	0.686629 772	1.45308 E-19	2.11856 E-17	16.67395 916	COMMD3	0.638926 268	2.79222 E-05	0.000602 049	3.220368 392
SH3BGRL	1.158374 429	1.93746 E-19	2.80805 E-17	16.55159 489	YWHAH	0.496766 061	2.80513 E-05	0.000604 299	3.218748 092
HLA-DPA1	1.970546 126	1.96863 E-19	2.83645 E-17	16.54722 477	GCSH	0.463813 752	2.83376 E-05	0.000609 395	3.215101 344
RPS20	0.534705 162	2.40686 E-19	3.44758 E-17	16.46248 542	PDZRN3	0.661841 869	2.96894 E-05	0.000637 347	3.195624 381

TPP1	0.896618 187	2.73804 E-19	3.89916 E-17	16.40902 909	ZNHIT1	0.474387 139	2.98262 E-05	0.000639 722	3.194008 468
C4orf3	0.917157 71	2.95874 E-19	4.1891E- 17	16.37787 89	KRT10	0.401700 109	3.0482E- 05	0.000653 216	3.184943 193
TMA7	0.699146 748	3.05151 E-19	4.29561 E-17	16.36697 522	ABCG1	2.525199 175	3.07345 E-05	0.000658 051	3.181740 766
NDUFB1	0.802649 319	3.31381 E-19	4.6382E- 17	16.33365 091	CCSER2	0.655194 581	3.08117 E-05	0.000659 128	3.181030 279
H2AFJ	0.965035 617	3.47835 E-19	4.84084 E-17	16.31507 936	NDUFV2	0.438857 526	3.18874 E-05	0.000680 949	3.166885 137
LAMTOR4	0.830777 824	3.52556 E-19	4.87882 E-17	16.31168 525	ADAM17	0.465740 561	3.24049 E-05	0.000690 796	3.160650 139
HSPB1	0.464148 283	3.83373 E-19	5.27548 E-17	16.27773 834	EEF1G	0.145939 738	3.28974 E-05	0.000700 686	3.154476 48
CHCHD2	0.785480 678	4.31646 E-19	5.90655 E-17	16.22866 593	ACSS1	1.053247 809	3.30364 E-05	0.000702 11	3.153594 858
NDUFA6	0.921058 893	4.41123 E-19	6.00271 E-17	16.22165 289	LSM3	0.511060 476	3.306E- 05	0.000702 11	3.153594 858
HMG3	0.992473 245	4.70043 E-19	6.3609E- 17	16.19648 147	GSTK1	0.486371 726	3.30789 E-05	0.000702 11	3.153594 858
SNHG6	0.825036 049	5.00391 E-19	6.73438 E-17	16.17170 237	EPB41L3	0.756706 178	3.31641 E-05	0.000703 309	3.152854 048
SCARB1	1.053153 515	6.9483E- 19	9.30009 E-17	16.03151 27	S100A4	1.496086 359	3.34161 E-05	0.000707 53	3.150255 33
OCA2	1.731920 958	7.11668 E-19	9.47369 E-17	16.02348 081	COPE	0.472071 648	3.34209 E-05	0.000707 53	3.150255 33
OST4	0.760849 535	7.20925 E-19	9.54505 E-17	16.02022 201	PDE4B	1.155525 923	3.39693 E-05	0.000718 518	3.143562 362
WDR63	3.063688 04	9.02394 E-19	1.18835 E-16	15.92505 702	TXNDC17	0.464057 326	3.4396E- 05	0.000726 916	3.138516 023
GABARAP	0.595390 856	1.14127 E-18	1.49489 E-16	15.82539 185	NEAT1	0.021474 367	3.45927 E-05	0.000730 443	3.136413 438
RPL15	0.482807 785	1.18941 E-18	1.54965 E-16	15.80976 599	MTDH	0.340117 037	3.48054 E-05	0.000734 302	3.134125 537
HSP90AA 1	0.579884 887	1.48913 E-18	1.92988 E-16	15.71446 909	PDAP1	0.387150 526	3.48725 E-05	0.000735 889	3.133663 829
XRCC5	0.881445 646	2.2679E- 18	2.92368 E-16	15.53406 994	TMEM179 B	0.487425 238	3.55091 E-05	0.000747 859	3.126180 392
CHCHD6	0.938161 612	2.52892 E-18	3.24311 E-16	15.48903 797	FAM200B	0.556892 812	3.55496 E-05	0.000748 068	3.126058 967
FBLN7	1.612652 779	2.74445 E-18	3.50117 E-16	15.45578 63	KIFAP3	0.709772 766	3.68287 E-05	0.000774 32	3.111079 718
COX6C	0.782659 054	3.60306 E-18	4.57271 E-16	15.33982 592	MT1G	1.614374 28	3.71071 E-05	0.000779 504	3.108181 577
MT1F	1.466759 92	3.74418 E-18	4.72732 E-16	15.32538 522	DCK	1.269013 405	3.8065E- 05	0.000798 94	3.097485 737
POMP	0.891595 662	5.43292 E-18	6.8243E- 16	15.16594 169	ACTR1A	0.536726 654	3.84203 E-05	0.000805 708	3.093822 489
NDUFB4	0.810926 02	5.4696E- 18	6.83532 E-16	15.16524 09	RPL26	0.182495 385	3.86936 E-05	0.000810 746	3.091115 107
PIR	1.287799 001	5.49786 E-18	6.83576 E-16	15.16521 29	KTN1	0.399337 59	3.90435 E-05	0.000817 377	3.087577 662
SOX4	0.581649 363	6.55784 E-18	8.11251 E-16	15.09084 484	CTSS	2.371190 548	3.91848 E-05	0.000819 635	3.086379 525
MBP	1.045734 286	7.621E- 18	9.38034 E-16	15.02778 136	PEA15	0.608195 961	3.93712 E-05	0.000822 13	3.085059 622
CTNNAL1	1.428975 105	7.78346 E-18	9.53241 E-16	15.02079 733	ACTG1	0.399410 754	4.0009E- 05	0.000834 737	3.078450 546
CYSTM1	0.934885 621	7.85254 E-18	9.56915 E-16	15.01912 645	PMF1	0.525518 06	4.01963 E-05	0.000837 93	3.076792 204
LAMTOR2	0.990105 271	8.36159 E-18	1.01391 E-15	14.99400 265	LIMA1	0.471411 824	4.02874 E-05	0.000839 115	3.076178 507
DSTN	0.814635 932	1.43257 E-17	1.72007 E-15	14.76445 402	MSX1	2.116905 928	4.06135 E-05	0.000845 189	3.073046 09
SNRPD2	0.687391 639	1.51246 E-17	1.80713 E-15	14.74300 967	MAP6	1.254459 143	4.17159 E-05	0.000867 393	3.061784 13
CEP72	1.660027 623	1.66204 E-17	1.97622 E-15	14.70416 474	CMC2	0.463078 529	4.18221 E-05	0.000868 863	3.061048 701

FAM124A	1.633755 803	1.75356 E-17	2.07496 E-15	14.68299 106	TCTN2	0.593632 102	4.19107 E-05	0.000869 967	3.060497 061
UQCR11	0.732141 495	1.84587 E-17	2.17369 E-15	14.66280 284	PHLDA1	0.424866 17	4.25035 E-05	0.000881 524	3.054765 853
EMX2	2.300971 508	1.87364 E-17	2.19584 E-15	14.65840 016	SLC19A2	0.665811 002	4.28315 E-05	0.000887 576	3.051794 582
MAP1B	1.140796 542	2.34884 E-17	2.73964 E-15	14.56230 633	A1BG	0.467788 815	4.29525 E-05	0.000889 33	3.050936 914
PTTG1IP	0.743923 068	2.51574 E-17	2.92041 E-15	14.53455 666	TMSB4X	0.534632 862	4.31497 E-05	0.000891 907	3.049680 377
CALM2	0.603281 319	2.80452 E-17	3.24028 E-15	14.48941 684	MIR4458H G	0.600424 945	4.34396 E-05	0.000897 142	3.047138 888
PSMB1	0.830644 488	2.91589 E-17	3.33747 E-15	14.47658 285	PPP1CA	0.554171 622	4.35714 E-05	0.000899 106	3.046189 072
ATP5O	0.974675 357	3.28738 E-17	3.74517 E-15	14.42652 84	PPT1	0.594768 822	4.45268 E-05	0.000917 274	3.037501 073
GPR143	0.777115 405	3.6864E- 17	4.16104 E-15	14.38079 777	FLNA	0.551986 039	4.47907 E-05	0.000921 936	3.035299 15
EDF1	0.748168 051	4.34027 E-17	4.87663 E-15	14.31187 997	CAPN1	0.612809 837	4.48569 E-05	0.000922 524	3.035022 315
GTF2F2	1.190070 033	4.88261 E-17	5.46094 E-15	14.26273 245	COTL1	0.619974 732	4.54124 E-05	0.000933 165	3.030041 749
SNCA	0.759882 092	5.57232 E-17	6.20401 E-15	14.20732 722	SEZ6L2	1.567870 975	4.57874 E-05	0.000940 082	3.026834 276
TP11	0.920636 535	6.1329E- 17	6.79725 E-15	14.16766 653	NAPA	0.475968 003	4.62953 E-05	0.000949 713	3.022407 801
USMG5	0.770136 178	6.35617 E-17	7.01298 E-15	14.15409 768	POLR2F	0.375527 263	4.72872 E-05	0.000969 249	3.013564 487
ATP6V0B	0.948582 113	7.1184E- 17	7.78384 E-15	14.10880 603	TMED2	0.509700 954	4.8046E- 05	0.000983 979	3.007014 003
BACE2	0.717782 736	9.31425 E-17	1.01397 E-14	13.99397 493	C7orf50	0.565492 451	4.81776 E-05	0.000985 849	3.006189 722
HEXA	0.961841 762	1.01057 E-16	1.09526 E-14	13.96048 348	SDHD	0.455037 892	4.84586 E-05	0.000990 772	3.004026 235
SON	0.676162 422	1.0308E- 16	1.11226 E-14	13.95379 193	SLC16A10	0.977722 347	4.85776 E-05	0.000992 376	3.003323 583
KRTCAP2	0.801041 007	1.06409 E-16	1.14315 E-14	13.94189 567	GAS6	0.371127 576	4.88574 E-05	0.000997 261	3.001190 996
DPP6	2.027810 812	1.2029E- 16	1.28663 E-14	13.89054 507	RPS4X	0.103819 363	4.92042 E-05	0.001003 504	2.998481 101
RPL27	0.510710 12	1.23504 E-16	1.31526 E-14	13.88098 719	HOXB7	0.755761 087	4.94182 E-05	0.001007 03	2.996957 551
CTSA	1.054712 892	1.26907 E-16	1.34565 E-14	13.87106 771	GRAMD3	0.707031 786	4.96853 E-05	0.001011 63	2.994978 241
MYL6	0.598981 023	1.55635 E-16	1.64315 E-14	13.78432 189	COPRS	0.540202 379	5.01533 E-05	0.001020 311	2.991267 643
COX5B	0.731863 081	1.57434 E-16	1.65502 E-14	13.78119 791	PARP14	0.749527 812	5.08737 E-05	0.001033 252	2.985793 945
NFATC2	1.491753 101	1.91354 E-16	2.003E- 14	13.69831 887	DGUOK	0.507428 944	5.08453 E-05	0.001033 252	2.985793 945
KLF6	0.704577 506	2.07104 E-16	2.15864 E-14	13.66581 977	TIMM13	0.510233 462	5.10982 E-05	0.001036 951	2.984241 825
PSME1	1.013999 462	2.40695 E-16	2.49813 E-14	13.60238 48	SNU13	0.416409 343	5.13523 E-05	0.001041 245	2.982447 131
ARPC3	0.842056 513	2.55914 E-16	2.64488 E-14	13.57759 383	TTC1	0.531439 245	5.15104 E-05	0.001043 586	2.981471 682
RNF145	0.770240 664	2.89372 E-16	2.9781E- 14	13.52606 096	GJA1	2.001495 838	5.17556 E-05	0.001046 822	2.980127 05
ROPN1B	1.104176 641	3.18261 E-16	3.26171 E-14	13.48655 449	VPS28	0.418588 728	5.27549 E-05	0.001066 154	2.972180 159
TSPAN4	1.030030 727	5.94933 E-16	6.04659 E-14	13.21848 954	SLC18B1	0.830502 629	5.28359 E-05	0.001066 911	2.971871 846
COX7B	0.811161 518	6.95333 E-16	7.03781 E-14	13.15256 272	SEC61A1	0.602198 005	5.46485 E-05	0.001101 697	2.957938 024
COX6B1	0.709402 8	7.09632 E-16	7.15297 E-14	13.14551 363	C19orf53	0.392784 774	5.4862E- 05	0.001105 091	2.956602 035
RNF7	0.811091 602	8.67333 E-16	8.70674 E-14	13.06014 42	ASNA1	0.500286 937	5.49729 E-05	0.001106 414	2.956082 295

C11orf31	0.785324 395	1.10524 E-15	1.10497 E-13	12.95664 892	MCUR1	0.592690 825	5.66143 E-05	0.001136 649	2.944373 771
TCEB2	0.651867 39	1.32251 E-15	1.31681 E-13	12.88047 617	SRSF5	0.312133 849	5.77945 E-05	0.001158 443	2.936125 355
ATP5L	0.728517 592	1.37838 E-15	1.36689 E-13	12.86426 783	COX7A2L	0.378592 67	5.78948 E-05	0.001159 506	2.935726 861
LRRC16A	1.378694 415	1.4877E- 15	1.46935 E-13	12.83287 608	LOC65434 2	0.544074 357	5.80478 E-05	0.001161 619	2.934936 261
SET	0.564666 927	1.58299 E-15	1.55717 E-13	12.80766 274	BCL6	0.580954 194	5.82981 E-05	0.001165 676	2.933422 203
COX17	0.870893 657	1.71732 E-15	1.68256 E-13	12.77403 015	RPL7	0.106590 442	5.88875 E-05	0.001176 501	2.929407 83
IFI27	1.841121 316	1.72687 E-15	1.66518 E-13	12.77335 363	SRPR	0.577966 69	5.90838 E-05	0.001179 462	2.928316 228
NINJ1	1.014419 556	1.80524 E-15	1.75466 E-13	12.75580 587	SLC39A11	1.043327 332	5.92479 E-05	0.001181 774	2.927465 48
MYDGF	0.950088 084	1.8555E- 15	1.79639 E-13	12.74560 044	FGD5-AS1	0.451381 445	6.08749 E-05	0.001213 238	2.916053 836
ATRAID	0.807048 261	1.97784 E-15	1.90729 E-13	12.71958 328	FRG2DP	2.401662 35	6.10818 E-05	0.001215 383	2.915286 793
ANXA2P2	0.512970 865	2.22623 E-15	2.1384E- 13	12.66991 062	KIAA1715	0.562832 534	6.10437 E-05	0.001215 383	2.915286 793
IFITM1	1.860036 135	2.2754E- 15	2.17709 E-13	12.66212 28	CRISPLD2	2.072827 339	6.18302 E-05	0.001228 814	2.910513 789
RPL21	0.452848 881	2.88907 E-15	2.75349 E-13	12.56011 594	TDRD7	0.912105 143	6.18901 E-05	0.001228 814	2.910513 789
NDUFC1	0.785579 741	3.6071E- 15	3.41128 E-13	12.46708 24	PDCD6	0.447008 938	6.19073 E-05	0.001228 814	2.910513 789
AHR	0.983914 316	3.64119 E-15	3.43028 E-13	12.46467 081	AMFR	0.634195 089	6.23283 E-05	0.001236 169	2.907922 063
NSG1	0.518368 304	3.68424 E-15	3.45754 E-13	12.46123 233	CIB1	0.622575 7	6.48581 E-05	0.001285 303	2.890994 347
LINC0086 9	1.136823 773	3.76793 E-15	3.52259 E-13	12.45313 824	HTATIP2	1.060834 05	6.72808 E-05	0.001331 16	2.875769 85
TMEM14C	0.760088 98	4.19446 E-15	3.89163 E-13	12.40986 84	FGFBP2	1.900160 432	6.78904 E-05	0.001341 053	2.872553 902
BRI3	0.613031 089	4.66965 E-15	4.31616 E-13	12.36490 211	CKAP4	0.672939 301	6.78904 E-05	0.001341 053	2.872553 902
STOM	1.231079 817	4.87385 E-15	4.48797 E-13	12.34795 021	CORO2B	0.846568 406	6.84251 E-05	0.001349 439	2.869846 682
SEPW1	0.551917 97	5.02963 E-15	4.61407 E-13	12.33591 535	NDUFB5	0.444406 629	6.83968 E-05	0.001349 439	2.869846 682
HP1BP3	0.784286 559	5.21262 E-15	4.7641E- 13	12.32201 919	C18orf32	0.472491 652	6.85759 E-05	0.001351 325	2.869240 085
ZNF706	0.811532 259	5.34147 E-15	4.86372 E-13	12.31303 183	ARGLU1	0.332099 319	6.96499 E-05	0.001371 387	2.862839 899
YWHAE	0.531483 412	6.01864 E-15	5.43988 E-13	12.26441 106	BOC	1.126646 042	7.01978 E-05	0.001381 063	2.859786 431
RRAS	1.247763 634	6.1352E- 15	5.5046E- 13	12.25927 434	GTF2A2	0.508305 788	7.08663 E-05	0.001393 033	2.856038 652
RPS12	0.417209 536	6.1352E- 15	5.5046E- 13	12.25927 434	SDF4	0.443287 641	7.09199 E-05	0.001393 033	2.856038 652
APOA1BP	0.984113 395	7.27144 E-15	6.50024 E-13	12.18707 059	MEA1	0.489862 293	7.15066 E-05	0.001403 431	2.852808 8
MALAT1	0.296129 793	7.30063 E-15	6.5026E- 13	12.18691 288	CALM3	0.447917 104	7.23655 E-05	0.001419 151	2.847971 405
PTRF	1.372162 938	7.57835 E-15	6.72551 E-13	12.17227 473	CYFIP1	0.619206 846	7.28485 E-05	0.001427 481	2.845429 807
HSBP1	0.869912 803	7.78967 E-15	6.88809 E-13	12.16190 102	LINC0113 8	0.776723 683	7.34905 E-05	0.001438 911	2.841966 18
NDUFB8	0.712562 859	7.84517 E-15	6.91222 E-13	12.16038 265	RPL35A	0.152758 226	7.4006E- 05	0.001447 846	2.839277 666
PAG1	0.704228 997	8.08047 E-15	7.09402 E-13	12.14910 766	BAX	0.524325 49	7.41278 E-05	0.001449 071	2.838910 332
RPL27A	0.372294 545	9.08145 E-15	7.91605 E-13	12.10149 142	HES6	0.687318 623	7.42396 E-05	0.001450 099	2.838602 285
GLUL	1.130079 508	9.22643 E-15	8.0139E- 13	12.09615 584	TRIM9	2.857247 829	7.45606 E-05	0.001454 051	2.837420 395

MSANTD3	1.044047 952	9.50121 E-15	8.22342 E-13	12.08494 759	NT5C3A	0.538684 011	7.45504 E-05	0.001454 051	2.837420 395
TGFBI	3.234729 528	9.7376E- 15	8.39833 E-13	12.07580 686	EBP	0.606148 064	7.46833 E-05	0.001455 284	2.837052 247
LRRFIP2	1.134467 84	1.04055 E-14	8.94291 E-13	12.04852 135	SH3GLB1	0.431151 301	7.515E- 05	0.001463 215	2.834691 749
NDUFA11	0.665408 432	1.07493 E-14	9.20605 E-13	12.03592 681	RPS2	0.128720 686	7.5449E- 05	0.001467 869	2.833312 701
SEC61B	0.790967 107	1.08924 E-14	9.29612 E-13	12.03169 806	AP3M2	0.486658 394	7.61856 E-05	0.001479 849	2.829782 464
COX5A	0.842416 465	1.11171 E-14	9.4549E- 13	12.02434 313	HIPK1	0.694231 331	7.65303 E-05	0.001484 191	2.828510 268
NDUFB7	0.725215 435	1.42774 E-14	1.21007 E-12	11.91718 891	AP2B1	0.472168 326	7.85223 E-05	0.001521 618	2.817694 497
KIAA0930	0.998934 09	1.45278 E-14	1.22705 E-12	11.91113 863	AURKAIP1	0.387147 963	7.892E- 05	0.001528 117	2.815843 507
OLFM1	1.327364 445	1.56031 E-14	1.31334 E-12	11.88162 134	CHURC1	0.408841 282	7.94497 E-05	0.001537 158	2.813281 465
CRIP2	1.101250 768	1.65993 E-14	1.39241 E-12	11.85623 325	KIF5B	0.389677 703	7.96832 E-05	0.001540 459	2.812349 97
FBXO32	0.990670 204	1.82038 E-14	1.52179 E-12	11.81764 506	PTRHD1	0.535453 439	8.04534 E-05	0.001554 121	2.808515 18
TSPAN10	1.066144 109	1.8633E- 14	1.55237 E-12	11.80900 532	FDFT1	0.282441 378	8.1519E- 05	0.001573 464	2.803143 072
ITGB1BP1	0.936465 323	2.15806 E-14	1.79184 E-12	11.74669 965	STX8	0.676751 375	8.23452 E-05	0.001586 91	2.799447 704
ASPA	1.114335 418	2.38168 E-14	1.97084 E-12	11.70534 835	CANX	0.361062 676	8.40613 E-05	0.001617 438	2.791172 389
RPS7	0.471603 215	4.14187 E-14	3.41585 E-12	11.46650 06	EHD4	0.677356 243	8.45028 E-05	0.001624 656	2.789238 532
GPX4	0.744344 115	4.50027 E-14	3.69898 E-12	11.43191 768	ARL4C	1.223694 801	8.54795 E-05	0.001642 144	2.784588 666
PPIB	0.736930 966	4.52121 E-14	3.70377 E-12	11.43135 656	CES1	1.697817 922	8.60156 E-05	0.001651 149	2.782213 694
EIF3K	0.857389 808	4.91924 E-14	4.00305 E-12	11.39760 893	FAM127A	0.527288 973	8.61267 E-05	0.001651 988	2.781993 231
COX7C	0.656610 847	4.91369 E-14	4.00305 E-12	11.39760 893	CAPZA1	0.409783 304	8.64081 E-05	0.001656 087	2.780916 897
TRPM4	1.357009 768	5.16416 E-14	4.18844 E-12	11.37794 739	MT1E	0.758553 326	8.87865 E-05	0.001700 341	2.769464 069
UQCR10	0.772781 432	5.50235 E-14	4.448E- 12	11.35183 502	PLA2G4C	1.262204 528	8.93119 E-05	0.001709 067	2.767240 962
H3F3B	0.291507 214	6.04592 E-14	4.87134 E-12	11.31235 136	EFNB2	0.966145 575	9.10353 E-05	0.001740 152	2.759412 703
S100A13	0.900659 204	6.10432 E-14	4.90227 E-12	11.30960 299	TRAPPC5	0.434509 516	9.10784 E-05	0.001740 152	2.759412 703
LIMD2	0.897961 259	7.08409 E-14	5.67052 E-12	11.24637 74	ZC3H15	0.528942 585	9.15981 E-05	0.001748 716	2.757280 641
PEBP1	0.564732 194	8.16818 E-14	6.51699 E-12	11.18595 315	PITHD1	0.462939 709	9.26332 E-05	0.001767 101	2.752738 742
BCAN	0.749105 275	8.55325 E-14	6.80205 E-12	11.16735 999	SEC31A	0.537380 338	9.32179 E-05	0.001776 871	2.750344 051
RDX	0.971986 89	8.67188 E-14	6.87408 E-12	11.16278 533	DDX5	0.295726 627	9.3578E- 05	0.001782 348	2.749007 426
MITF	0.583578 289	1.14133 E-13	8.98901 E-12	11.04628 794	BZW1	0.616345 644	9.3749E- 05	0.001784 219	2.748551 961
DYNLL1	0.757417 798	1.17291 E-13	9.20807 E-12	11.03583 139	SEMA3C	0.378002 495	9.45831 E-05	0.001798 694	2.745042 694
ARSB	1.009860 516	1.21925 E-13	9.52264 E-12	11.02124 257	CYTH3	0.397750 586	9.50766 E-05	0.001806 676	2.743119 664
NFIB	0.932283 878	1.22075 E-13	9.52264 E-12	11.02124 257	SNRPE	0.415916 383	9.56823 E-05	0.001816 777	2.740698 28
NME2	0.660222 59	1.25944 E-13	9.79325 E-12	11.00907 298	SEC11A	0.423288 703	9.63893 E-05	0.001828 783	2.737837 724
LINC0131 4	1.852920 532	1.27538 E-13	9.88579 E-12	11.00498 853	SIRPA	0.633098 423	9.78313 E-05	0.001852 838	2.732162 514
TMEM50A	0.761584 52	1.33981 E-13	1.03525 E-11	10.98495 657	SLC35B2	0.404316 574	9.77785 E-05	0.001852 838	2.732162 514

YWHAB	0.733088 195	1.35474 E-13	1.04349 E-11	10.98151 102	CLCN7	0.393751 472	9.78841 E-05	0.001852 838	2.732162 514
POLR2G	0.849233 389	1.40415 E-13	1.07816 E-11	10.96731 754	TMEM219	0.366783 053	9.83407 E-05	0.001860 045	2.730476 577
BRK1	0.711579 204	1.44694 E-13	1.10754 E-11	10.95563 99	CAPN2	0.505916 655	9.90462 E-05	0.001871 943	2.727707 451
NDUFB2	0.788868 546	1.66915 E-13	1.27365 E-11	10.89494 919	TRIM8	0.634671 211	0.000100 377	0.001895 627	2.722247 04
PRNP	1.370777 845	1.82609 E-13	1.38908 E-11	10.85727 4	TBC1D16	0.409138 411	0.000100 804	0.001902 223	2.720738 679
NDUFB6	0.754124 045	1.84678 E-13	1.40047 E-11	10.85372 676	LRRC2	1.900245 667	0.000101 937	0.001920 644	2.716553 073
CTSK	1.379814 625	1.95663 E-13	1.47919 E-11	10.82997 667	PAPSS1	0.717161 953	0.000104 176	0.001961 325	2.707450 391
TAPBP	0.888468 385	1.96527 E-13	1.48115 E-11	10.82940 223	RBM39	0.304089 099	0.000105 515	0.001985 005	2.702238 504
UBL5	0.618393 719	1.9737E- 13	1.48294 E-11	10.82887 694	SBDS	0.372636 616	0.000107 337	0.002014 645	2.695801 55
WSB2	0.873756 766	2.02084 E-13	1.51372 E-11	10.81995 567	MXD3	0.542868 197	0.000107 669	0.002019 326	2.694793 497
ATP5G3	0.822960 734	2.19566 E-13	1.63965 E-11	10.78524 967	HDDC2	0.445139 557	0.000108 328	0.002030 139	2.692474 305
PARVA	0.870565 951	2.26342 E-13	1.68511 E-11	10.77337 138	TGFBR2	0.735537 589	0.000108 627	0.002034 173	2.691612 082
C6orf1	0.859267 652	2.27783 E-13	1.6907E- 11	10.77193 362	SRGAP2B	0.390785 456	0.000110 789	0.002073 076	2.683384 847
SLIRP	0.658799 648	2.43852 E-13	1.8045E- 11	10.74364 225	EXOC2	0.712153 256	0.000111 758	0.002088 016	2.680266 282
SLC24A5	0.826314 688	2.45971 E-13	1.8147E- 11	10.74119 464	JMJD8	0.507090 688	0.000111 713	0.002088 016	2.680266 282
C3orf70	1.031989 455	2.57373 E-13	1.89312 E-11	10.72282 193	AGTRAP	0.633523 226	0.000113 279	0.002113 217	2.675055 976
YWHAZ	0.746937 096	2.58315 E-13	1.89436 E-11	10.72253 785	RPSA	0.156427 011	0.000113 211	0.002113 217	2.675055 976
LINC0142 0	0.884212 136	2.68019 E-13	1.95966 E-11	10.70782 015	NANS	0.595627 069	0.000113 514	0.002115 94	2.674496 587
B4GALT1	0.941307 008	2.75455 E-13	2.00804 E-11	10.69722 83	GNAI1	0.471438 557	0.000113 598	0.002115 94	2.674496 587
WDR83OS	0.773307 86	2.98024 E-13	2.16611 E-11	10.66431 861	NARS	0.496550 769	0.000114 735	0.002133 887	2.670828 609
PSMB6	0.798742 354	3.28922 E-13	2.38361 E-11	10.62276 447	CYR61	1.206548 095	0.000115 204	0.002139 644	2.669658 407
UBE2L3	0.810989 201	3.7113E- 13	2.68155 E-11	10.57161 363	APOBEC3 C	0.558024 108	0.000115 22	0.002139 644	2.669658 407
DKK3	2.125280 38	3.89192 E-13	2.80378 E-11	10.55225 552	TMTC1	3.938338 041	0.000115 605	0.002145 181	2.668536 091
SLC25A4	0.822105 527	3.99242 E-13	2.86775 E-11	10.54245 815	ASB9	0.979350 567	0.000116 552	0.002160 432	2.665459 405
RPL12	0.388610 542	4.05022 E-13	2.90077 E-11	10.53748 726	MREG	0.669823 825	0.000116 676	0.002160 432	2.665459 405
TTYH3	0.894651 413	4.46933 E-13	3.18232 E-11	10.49725 657	C7orf73	0.378016 919	0.000116 692	0.002160 432	2.665459 405
PSMB2	0.869120 717	5.11584 E-13	3.6321E- 11	10.43984 212	UPP1	0.574083 09	0.000118 15	0.002184 131	2.660721 333
NEDD8	0.709221 005	5.40799 E-13	3.81739 E-11	10.41823 391	NBPF8	0.362063 408	0.000118 379	0.002186 713	2.660208 306
ST13	0.674700 022	5.40604 E-13	3.81739 E-11	10.41823 391	RAB32	0.537716 568	0.000120 426	0.002222 851	2.653089 662
SERPINB6	0.914572 954	5.77373 E-13	4.06384 E-11	10.39106 34	ATP6V1E1	0.472015 917	0.000120 869	0.002229 337	2.651824 25
COPS8	0.824326 813	5.87787 E-13	4.1135E- 11	10.38578 815	FLII	0.654322 386	0.000121 151	0.002232 863	2.651137 879
FKBP9	0.587365 448	5.86871 E-13	4.1135E- 11	10.38578 815	MAF	0.463726 044	0.000121 596	0.002239 378	2.649872 521
TTC3	0.693936 706	6.61824 E-13	4.61844 E-11	10.33550 491	PGGT1B	0.676456 988	0.000121 864	0.002242 622	2.649243 885
FAM114A1	1.117810 965	6.64205 E-13	4.62188 E-11	10.33518 092	TBL1XR1	0.534770 548	0.000122 384	0.002250 515	2.647718 177

TSC22D3	1.021483 898	7.3835E- 13	5.1088E- 11	10.29168 136	IL6ST	0.666593 015	0.000122 695	0.002254 526	2.646944 764
PTMA	0.365496 367	7.83023 E-13	5.40264 E-11	10.26739 436	PARVB	0.530256 689	0.000123 137	0.002260 953	2.645708 5
RPS13	0.454698 056	9.30794 E-13	6.40417 E-11	10.19353 687	FUNDC2	0.486482 292	0.000123 572	0.002267 247	2.644501 231
CRYM	1.117062 211	9.42715 E-13	6.46803 E-11	10.18922 809	MRPL54	0.595739 186	0.000128 134	0.002347 424	2.629408 509
RBX1	0.723724 723	9.50821 E-13	6.50542 E-11	10.18672 453	IFIT5	1.089094 52	0.000132 142	0.002417 239	2.616680 403
TXNDC5	1.332899 928	9.8335E- 13	6.70924 E-11	10.17332 644	TXNDC12	0.473647 892	0.000133 33	0.002435 337	2.613440 968
TBCA	0.757002 234	9.94041 E-13	6.76334 E-11	10.16983 867	EPAS1	1.156666 431	0.000133 578	0.002438 043	2.612958 633
GNPTAB	0.808806 896	1.13251 E-12	7.66287 E-11	10.11560 827	CISD3	0.478044 301	0.000139 608	0.002542 423	2.594752 156
DNAJC13	0.991593 122	1.29138 E-12	8.68983 E-11	10.06098 888	PSMB5	0.424723 327	0.000140 962	0.002565 169	2.590883 977
ARL2	0.664188 683	1.30905 E-12	8.76063 E-11	10.05746 462	TIMMDC1	0.540030 36	0.000141 512	0.002573 276	2.589513 574
RPS28	0.386180 103	1.30843 E-12	8.76063 E-11	10.05746 462	WDR13	0.521604 836	0.000145 702	0.002645 529	2.577487 445
ECM1	1.056805 611	1.33199 E-12	8.88986 E-11	10.05110 498	RTF1	0.433546 543	0.000146 25	0.002653 525	2.576176 855
GALNT18	2.455232 62	1.47379 E-12	9.80954 E-11	10.00835 117	ADGRA3	0.763312 28	0.000147 218	0.002669 098	2.573635 426
NDUFS7	0.739266 515	1.53932 E-12	1.02179 E-10	9.990638 103	CADPS	0.846083 283	0.000147 529	0.002672 755	2.573040 838
RPS8	0.423106 045	1.56087 E-12	1.0333E- 10	9.985775 514	NAPG	0.701556 385	0.000148 582	0.002689 853	2.570271 512
GRN	0.651506 126	1.57491 E-12	1.03978 E-10	9.983059 693	DNAJC15	0.360297 71	0.000148 739	0.002690 7	2.570134 648
SUB1	0.764939 725	1.75352 E-12	1.15459 E-10	9.937572 962	CABLES1	0.463192 582	0.000149 958	0.002710 761	2.566908 81
LRPAP1	0.742829 621	1.97383 E-12	1.29617 E-10	9.887338 816	TNIP1	0.742573 142	0.000153 079	0.002761 056	2.558924 849
NDUFA7	0.776345 253	2.00392 E-12	1.31241 E-10	9.881931 966	PSMA2	0.407117 903	0.000153 684	0.002769 93	2.557531 181
SAR1A	0.677712 381	2.25317 E-12	1.47171 E-10	9.832177 88	SOAT1	0.495386 153	0.000154 942	0.002790 545	2.554310 956
ATP5J	0.735955 834	2.30542 E-12	1.50183 E-10	9.823378 703	DTX3L	1.031688 333	0.000156 702	0.002820 18	2.549723 104
NDUFB10	0.756456 673	2.35692 E-12	1.53131 E-10	9.814936 163	RPL8	0.113135 353	0.000157 032	0.002824 038	2.549129 504
CTNNA1	0.780731 738	2.4135E- 12	1.56392 E-10	9.805784 285	RTTN	0.580073 178	0.000159 619	0.002868 461	2.542351 068
MRPL33	0.695313 692	2.47315 E-12	1.59834 E-10	9.796329 772	LPP	0.424522 4	0.000159 755	0.002868 803	2.542299 234
SNW1	0.859416 187	2.65097 E-12	1.70876 E-10	9.767318 913	TCN2	0.833893 299	0.000164 839	0.002957 924	2.529013 031
ABCA5	1.237149 239	2.93069 E-12	1.8841E- 10	9.724895 316	MRPS24	0.423728 913	0.000165 195	0.002962 151	2.528392 786
PFDN5	0.536692 381	3.07458 E-12	1.97144 E-10	9.705217 167	NAP1L4	0.440535 128	0.000166 913	0.002988 564	2.524537 414
UQCC2	0.928892 553	3.09107 E-12	1.97683 E-10	9.704029 602	TFAP2A	0.245466 962	0.000170 152	0.003044 347	2.516505 841
RPL13A	0.324521 899	3.24834 E-12	2.06662 E-10	9.684739 789	HNMT	0.408183 634	0.000170 899	0.003055 472	2.514921 646
SPECC1	2.320668 459	3.34092 E-12	2.12001 E-10	9.673661 238	TMEM141	0.561117 411	0.000172 356	0.003074 794	2.512183 91
UBA52	0.500758 588	3.50209 E-12	2.21654 E-10	9.654323 519	HABP4	0.452160 954	0.000172 886	0.003082	2.511167 316
RPL10	0.373298 109	3.58635 E-12	2.25898 E-10	9.646086 755	RPL37	0.195185 751	0.000173 18	0.003084 991	2.510746 098
RPL23A	0.296635 747	3.58759 E-12	2.25898 E-10	9.646086 755	ATP6V0A1	0.663006 723	0.000173 383	0.003086 373	2.510551 52
C4orf48	0.552130 342	3.60427 E-12	2.26367 E-10	9.645187 826	BCAP29	0.561958 194	0.000173 768	0.003090 984	2.509903 197

PLS3	0.955374 181	3.75911 E-12	2.35488 E-10	9.628031 852	LNP1	0.594593 108	0.000175 833	0.003125 434	2.505089 644
PSMB8	2.112588 882	4.09004 E-12	2.55565 E-10	9.592499 29	HIGD1A	0.391730 964	0.000176 189	0.003129 489	2.504526 636
MINOS1	0.666468 024	4.28308 E-12	2.66946 E-10	9.573576 398	MEF2C	0.449040 443	0.000177 041	0.003138 822	2.503233 264
HMG2	0.736269 355	4.6559E- 12	2.89446 E-10	9.538432 451	ZC3H4	0.357115	0.000177 099	0.003138 822	2.503233 264
EMP3	0.492562 92	4.93272 E-12	3.05879 E-10	9.514450 613	FAM3C	0.590757 37	0.000179 025	0.003170 671	2.498848 794
PON2	0.757967 83	5.08326 E-12	3.14418 E-10	9.502492 99	ST5	0.543210 03	0.000182 58	0.003231 302	2.490622 419
ABCB5	2.197893 143	5.57073 E-12	3.43701 E-10	9.463818 813	TCEAL8	0.422591 865	0.000184 575	0.003264 241	2.486217 806
BANF1	0.652234 137	5.93129 E-12	3.65028 E-10	9.437674 035	MSRA	0.551275 849	0.000189 521	0.003349 307	2.475045 042
LRRC75A- AS1	0.503461 957	6.32267 E-12	3.88139 E-10	9.411012 769	PSMD10	0.438784 987	0.000190 929	0.003371 753	2.472144 271
MORF4L1	0.705899 06	6.77491 E-12	4.13827 E-10	9.383181 161	ZNF428	0.473082 84	0.000191 463	0.003378 739	2.471245 348
C14orf2	0.710772 514	6.95643 E-12	4.22806 E-10	9.373859 088	TUBB6	0.546634 436	0.000192 597	0.003396 299	2.468994 023
NDUFC2	0.605518 699	7.06713 E-12	4.28471 E-10	9.368078 483	SDC2	0.658910 871	0.000194 593	0.003429 031	2.464828 625
RPL36AL	0.516065 359	7.13047 E-12	4.31243 E-10	9.365277 449	GRINA	0.408472 151	0.000195 174	0.003436 798	2.463845 965
DUT	0.762745 857	7.15825 E-12	4.31857 E-10	9.364659 707	CSPG4	0.648697 734	0.000195 579	0.003441 459	2.463257 346
ABR	0.941336 215	7.21743 E-12	4.34358 E-10	9.362152 337	PPFIBP2	1.031066 537	0.000195 795	0.003442 78	2.463090 763
GUK1	0.678512 752	7.92438 E-12	4.74572 E-10	9.323698 25	GLRX5	0.441764 265	0.000200 491	0.003522 824	2.453109 082
RPL18	0.325358 45	8.15925 E-12	4.87446 E-10	9.312073 668	ADAP1	1.040561 08	0.000203 733	0.003574 659	2.446765 384
CTSD	0.413331 032	8.36558 E-12	4.98556 E-10	9.302285 823	BBS5	0.519138 515	0.000203 588	0.003574 659	2.446765 384
PRDX2	0.784907 103	8.7637E- 12	5.21015 E-10	9.283149 89	SAP30	0.427205 95	0.000205 491	0.003600 361	2.443653 943
TMEM205	0.905851 543	9.10234 E-12	5.39837 E-10	9.267737 09	LRRC8D	0.824615 777	0.000210 935	0.003690 466	2.432918 797
RPLP1	0.295068 562	9.3405E- 12	5.52624 E-10	9.257570 295	RAPH1	0.558872 521	0.000210 922	0.003690 466	2.432918 797
GNPTG	0.834547 102	1.03041 E-11	6.08166 E-10	9.215977 617	TMEM64	1.266702 652	0.000211 699	0.003698 537	2.431969 981
RPL41	0.340564 042	1.09365 E-11	6.4394E- 10	9.191154 382	THUMPDI	0.546757 46	0.000212 314	0.003706 643	2.431019 251
SSR2	0.720680 118	1.09788 E-11	6.44877 E-10	9.190522 897	MICA	1.430611 014	0.000212 602	0.003709 022	2.430740 583
PRELID1	0.766710 877	1.1256E- 11	6.59579 E-10	9.180733 186	BCAP31	0.369226 992	0.000213 839	0.003727 95	2.428529 9
ALX1	0.989362 061	1.14593 E-11	6.6989E- 10	9.173996 463	INSR	0.419311 285	0.000214 737	0.003740 938	2.427019 524
RPS26	0.442385 733	1.38422 E-11	8.07266 E-10	9.092983 365	DTX4	1.169619 322	0.000216 264	0.003759 522	2.424867 316
POLR2E	0.799014 33	1.45498 E-11	8.46513 E-10	9.072366 533	UQCRLH	0.475858 659	0.000216 166	0.003759 522	2.424867 316
ATP5I	0.523076 057	1.48999 E-11	8.64829 E-10	9.063069 722	SFXN3	0.539713 323	0.000222 047	0.003854 58	2.414022 963
QPCT	0.395058 602	1.51402 E-11	8.76697 E-10	9.057150 455	C17orf49	0.454065 084	0.000223 005	0.003868 48	2.412459 611
GRB2	0.729496 121	1.53617 E-11	8.87428 E-10	9.051866 761	UBXN4	0.441596 359	0.000223 479	0.003873 953	2.411845 703
ITGB1	0.754933 655	1.5952E- 11	9.1936E- 10	9.036514 368	BMP1	0.850818 038	0.000223 925	0.003876 193	2.411594 558
ATP5H	0.675718 904	1.6492E- 11	9.48251 E-10	9.023076 598	RPL13	0.110551 044	0.000233 691	0.004039 534	2.393668 693
JUN	0.941374 898	1.65533 E-11	9.49547 E-10	9.022483 571	BNIP2	0.569132 328	0.000235 314	0.004064 726	2.390968 773

RMND5A	0.794564 009	1.66935 E-11	9.55349 E-10	9.019837 874	ZSWIM7	0.585825 086	0.000239 204	0.004129 01	2.384154 016
RPL24	0.384114 712	1.89916 E-11	1.08434 E-09	8.964835 866	NDFIP1	0.461331 01	0.000244 183	0.004211 983	2.375513 411
PSMA7	0.717040 062	1.90599 E-11	1.0857E- 09	8.964289 13	PNRC1	0.284688 652	0.000247 324	0.004263 163	2.370268 017
RAN	0.752148 092	2.05844 E-11	1.16982 E-09	8.931879 909	SNRPB2	0.470882 118	0.000248 861	0.004286 642	2.367882 822
HNRNPH1	0.408778 787	2.15987 E-11	1.22462 E-09	8.911997 042	VAMP3	0.398044 288	0.000253 656	0.004363 092	2.360205 667
RPS16	0.338685 93	2.22903 E-11	1.26092 E-09	8.899313 093	PDS5B	0.533208 907	0.000255 278	0.004386 244	2.357907 191
NDUFB9	0.694542 706	2.25105 E-11	1.27044 E-09	8.896045 316	LSM1	0.507180 274	0.000257 337	0.004417 108	2.354862 003
IFI27L2	0.640802 205	2.31918 E-11	1.30588 E-09	8.884095 849	VIMP	0.421383 291	0.000259 031	0.004439 968	2.352620 184
ATP5G2	0.606312 096	2.44813 E-11	1.37533 E-09	8.861592 251	LSM4	0.382922 232	0.000258 866	0.004439 968	2.352620 184
MOB3B	1.290115 833	2.52069 E-11	1.41285 E-09	8.849903 04	ZFAS1	0.335448 593	0.000266 269	0.004560 838	2.340955 362
ATP6V1G 1	0.620355 308	2.62353 E-11	1.46714 E-09	8.833528 195	SLC7A5	0.581118 286	0.000266 829	0.004567 224	2.340347 645
LINC0062 3	1.536426 425	2.82029 E-11	1.57358 E-09	8.803110 549	DDX17	0.319777 161	0.000273 054	0.004670 523	2.330634 47
PSMB3	0.743638 277	3.03383 E-11	1.68888 E-09	8.772401 258	EPS15	0.443231 046	0.000278 655	0.004762 998	2.322119 623
CD44	0.300985 187	3.1414E- 11	1.7448E- 09	8.758255 354	RPS27	0.146370 471	0.000281 674	0.004811 244	2.317742 586
MYEF2	0.747854 769	3.23401 E-11	1.79217 E-09	8.746621 707	ARPP19	0.366247 147	0.000282 21	0.004813 685	2.317522 322
CCDC80	0.829238 236	3.28494 E-11	1.81628 E-09	8.740816 156	TMED4	0.339955 121	0.000282 067	0.004813 685	2.317522 322
PLOD3	0.764856 339	3.79228 E-11	2.09208 E-09	8.679422 654	FBLN1	0.836228 967	0.000286 641	0.004882 464	2.311360 966
GAPDHS	1.393696 666	3.88684 E-11	2.13942 E-09	8.669703 175	JTB	0.358362 585	0.000291 598	0.004963 44	2.304217 184
TM9SF2	0.930609 167	4.05109 E-11	2.22483 E-09	8.652703 356	TMCO3	0.746726 811	0.000291 819	0.004963 758	2.304189 37
BTF3	0.461730 897	4.91776 E-11	2.68874 E-09	8.570451 386	LINC0098 7	0.642604 709	0.000292 428	0.004970 673	2.303584 782
RAB7A	0.543390 036	5.05687 E-11	2.75864 E-09	8.559304 83	PSMD4	0.351861 864	0.000294 227	0.004997 773	2.301223 439
RPL34	0.302993 238	5.11999 E-11	2.78687 E-09	8.554883 668	SMC3	0.374514 103	0.000298 551	0.005060 701	2.295789 299
OSBPL9	0.813868 403	5.42766 E-11	2.94127 E-09	8.531465 721	POMGNT1	0.637447 655	0.000304 026	0.005142 829	2.288797 884
TMEM140	1.578589 32	5.46168 E-11	2.95317 E-09	8.529711 983	ANAPC11	0.454937 786	0.000307 728	0.005201 86	2.283841 347
PRPF6	0.854774 833	5.66029 E-11	3.05381 E-09	8.515157 385	MIR3074	0.397342 443	0.000310 083	0.005238 049	2.280830 44
TRPM1	0.720565 975	5.70135 E-11	3.06921 E-09	8.512973 883	WTAP	0.398579 121	0.000310 493	0.005241 367	2.280555 46
ATP5C1	0.641188 979	5.96172 E-11	3.20233 E-09	8.494533 315	SP100	0.493695 885	0.000313 045	0.005277 169	2.277598 992
ADCY2	1.407117 605	6.02532 E-11	3.22941 E-09	8.490876 625	TSPAN5	1.822309 971	0.000314 605	0.005299 824	2.275738 545
NDUFA12	0.701633 513	6.31462 E-11	3.37708 E-09	8.471458 813	MRPL27	0.515141 189	0.000317 069	0.005333 991	2.272947 708
RPL19	0.295767 784	6.62327 E-11	3.53443 E-09	8.451680 639	NRXN3	0.582901 18	0.000323 084	0.005431 455	2.265083 844
CLEC12B	1.310696 125	7.36926 E-11	3.92397 E-09	8.406274 043	QKI	0.383665 532	0.000325 242	0.005463 984	2.262490 606
SERINC1	0.643859 208	7.63462 E-11	4.05645 E-09	8.391853 775	BSCL2	0.433433 861	0.000327 455	0.005497 385	2.259843 88
RTFDC1	0.721319 199	8.21327 E-11	4.35445 E-09	8.361066 2	POP5	0.648589 551	0.000328 938	0.005518 497	2.258179 16
RPS24	0.430135 608	8.33639 E-11	4.41019 E-09	8.355543 031	TMEM106 C	0.632210 493	0.000331 673	0.005552 971	2.255474 585

COL6A2	0.871650 398	9.17539 E-11	4.84358 E-09	8.314833 715	HLA-C	2.267853 26	0.000332 798	0.005568	2.254300 778
SERPINE2	0.875655 651	9.25627 E-11	4.87577 E-09	8.311957 122	ANKRD40	0.342999 756	0.000335 017	0.005597 474	2.252007 951
HLA-E	0.705374 599	9.66497 E-11	5.08013 E-09	8.294125 482	APOLD1	1.567027 569	0.000335 921	0.005608 751	2.251133 823
ETFB	0.772463 918	1.17795 E-10	6.16509 E-09	8.210060 397	POLR2I	0.408921 808	0.000336 806	0.005619 7	2.250286 906
SF3B5	0.705650 926	1.20672 E-10	6.30221 E-09	8.200507 439	PGRMC2	0.503021 598	0.000346 276	0.005773 777	2.238539 984
RPL30	0.314372 987	1.22439 E-10	6.38088 E-09	8.195119 168	ETFA	0.433319 718	0.000346 883	0.005779 961	2.238075 084
RGL1	1.960083 961	1.24579 E-10	6.47865 E-09	8.188515 747	ARRDC3	0.750768 721	0.000349 211	0.005814 8	2.235465 255
CDH1	0.605099 201	1.25373 E-10	6.5061E- 09	8.186679 428	SNURF	0.409648 359	0.000349 56	0.005816 663	2.235326 082
GTF3C6	0.781549 275	1.35842 E-10	7.03448 E-09	8.152767 809	INPP4B	0.347926 348	0.000349 888	0.005818 166	2.235213 879
TAX1BP1	0.697759 569	1.45876 E-10	7.53814 E-09	8.122736 02	CAPN3	0.171938 032	0.000353 138	0.005864 252	2.231787 363
RPS15	0.280946 553	1.60536 E-10	8.26086 E-09	8.082974 482	DPM3	0.402705 103	0.000354 022	0.005874 937	2.230996 764
FAU	0.446727 753	1.64922 E-10	8.46878 E-09	8.072178 915	TMCO1	0.424786 985	0.000357 263	0.005920 709	2.227626 313
LPPR4	1.349840 879	1.72016 E-10	8.81457 E-09	8.054799	SNX3	0.262625 009	0.000358 313	0.005934 085	2.226646 229
NDUFAB1	0.714878 142	1.8316E- 10	9.36602 E-09	8.028444 77	MX2	1.536661 983	0.000361 095	0.005973 581	2.223765 207
TMEM14B	0.733836 412	1.89276 E-10	9.65859 E-09	8.015086 101	SGK1	0.451893 628	0.000361 185	0.005973 581	2.223765 207
PSMD9	0.801653 385	1.92798 E-10	9.81787 E-09	8.007982 523	TSEN15	0.682245 374	0.000362 065	0.005981 917	2.223159 621
MDH1	0.693605 959	1.95009 E-10	9.90983 E-09	8.003933 622	WDR61	0.450386 524	0.000362 178	0.005981 917	2.223159 621
TAX1BP3	0.621565 998	1.98149 E-10	1.00486 E-08	7.997895 443	ICAM1	1.242388 01	0.000362 471	0.005982 734	2.223100 325
SAP18	0.603723 586	2.00483 E-10	1.0146E- 08	7.993707 232	CDC42BP A	0.742003 083	0.000367 041	0.006049 702	2.218266 005
SEC11C	0.759819 686	2.02349 E-10	1.02192 E-08	7.990581 669	TSN	0.461002 231	0.000367 27	0.006049 702	2.218266 005
TECR	0.687431 157	2.02953 E-10	1.02286 E-08	7.990181 965	SUPT16H	0.387697 518	0.000367 934	0.006056 568	2.217773 372
TRMT112	0.578607 857	2.04296 E-10	1.02752 E-08	7.988209 168	MAD2L2	0.587536 156	0.000369 22	0.006073 649	2.216550 318
YWHAQ	0.579188 168	2.25834 E-10	1.13352 E-08	7.945570 696	RPL6	0.211419 657	0.000370 717	0.006094 189	2.215084 046
MIEN1	0.760342 36	2.31145 E-10	1.1578E- 08	7.936365 039	RAB1A	0.323273 42	0.000371 086	0.006096 172	2.214942 792
SERPINB1	1.051168 561	2.43473 E-10	1.21707 E-08	7.914685 684	CYCS	0.402787 775	0.000373 404	0.006130 125	2.212530 679
ATP1B3	0.629047 871	2.62983 E-10	1.31192 E-08	7.882093 959	NOL7	0.373892 754	0.000379 303	0.006214 474	2.206595 612
DTYMK	0.967122 197	2.75303 E-10	1.37041 E-08	7.863150 305	TXN2	0.455533 236	0.000379 822	0.006218 82	2.206292 043
COMMD6	0.568412 483	2.75827 E-10	1.37041 E-08	7.863150 305	UBE2H	0.507721 424	0.000387 256	0.006336 298	2.198164 393
MT2A	0.898296 416	2.86457 E-10	1.42034 E-08	7.847608 084	CNIH1	0.471934 527	0.000390 732	0.006388 916	2.194572 841
NDUFS5	0.565566 361	2.9802E- 10	1.47469 E-08	7.831299 861	NUTM2A- AS1	0.482429 206	0.000391 776	0.006400 221	2.193805 052
SPRY1	1.623767 018	3.23312 E-10	1.59458 E-08	7.797354 328	AP1G1	0.347509 265	0.000391 946	0.006400 221	2.193805 052
DNAJC8	0.668618 5	3.23551 E-10	1.59458 E-08	7.797354 328	NEO1	0.557470 322	0.000395 904	0.006459 039	2.189832 103
WLS	0.921645 88	3.32526 E-10	1.63552 E-08	7.786343 724	CBX6	0.268816 918	0.000396 076	0.006459 039	2.189832 103
HMCN1	1.902261 615	3.34245 E-10	1.64068 E-08	7.784976 193	CCNDBP1	0.402900 13	0.000397 971	0.006485 622	2.188048 372

AP2S1	0.750058 472	3.55146 E-10	1.73286 E-08	7.761237 63	LMBRD1	0.570271 134	0.000398 365	0.006487 739	2.187906 602
TLE1	0.747913 659	3.55108 E-10	1.73286 E-08	7.761237 63	TAP1	0.931718 528	0.000403 132	0.006556 644	2.183318 418
DPYSL2	0.804835 379	3.70106 E-10	1.80226 E-08	7.744181 938	PTBP1	0.580061 674	0.000402 882	0.006556 644	2.183318 418
ANXA2P1	0.825463 116	3.71078 E-10	1.80341 E-08	7.743905 136	SYPL1	0.609084 487	0.000403 956	0.006565 695	2.182719 316
MT1M	1.448841 214	3.89909 E-10	1.89117 E-08	7.723268 299	GSTM2	0.669403 136	0.000408 835	0.006640 594	2.177793 085
CTSB	0.510485 291	4.10015 E-10	1.98476 E-08	7.702291 326	FKBP9P1	0.435956 299	0.000413 156	0.006706 329	2.173515 124
MRPL51	0.678442 478	4.10831 E-10	1.98479 E-08	7.702284 961	NRDE2	0.591873 884	0.000421 9	0.006843 725	2.164707 424
RPL31	0.348705 888	4.16328 E-10	2.00739 E-08	7.697367 891	PTK7	0.733278 513	0.000426 771	0.006913 577	2.160297 216
STAT2	0.458592 266	4.58258 E-10	2.20522 E-08	7.656548 44	ATG14	0.651173 234	0.000427 904	0.006927 357	2.159432 434
NDUFS4	0.723379 076	4.59791 E-10	2.20826 E-08	7.655949 887	WBSCR22	0.473588 258	0.000429 464	0.006948 016	2.158139 171
CDS2	0.719959 14	4.63502 E-10	2.22172 E-08	7.653309 747	PIN1	0.372850 686	0.000430 206	0.006955 428	2.157676 132
TPT1	0.382009 178	4.64422 E-10	2.22179 E-08	7.653297 53	BCAS3	1.110972 881	0.000433 507	0.007004 172	2.154643 204
EIF1	0.317461 61	4.7234E- 10	2.25526 E-08	7.646803 065	RAB4B	0.651771 367	0.000435 22	0.007027 212	2.153216 954
COL27A1	0.971150 577	4.84212 E-10	2.30745 E-08	7.636868 018	LTBR	0.479951 65	0.000443 416	0.007150 114	2.145687 007
SRPX	0.804776 788	4.94052 E-10	2.34977 E-08	7.628974 434	CD81	0.358287 305	0.000445 603	0.007180 665	2.143835 32
AP1S2	0.425751 388	4.99176 E-10	2.36954 E-08	7.625336 517	PARP9	1.909301 043	0.000446 399	0.007184 032	2.143631 714
PET100	0.571542 084	5.05982 E-10	2.3972E- 08	7.620295 708	RNF213	0.449580 759	0.000446 152	0.007184 032	2.143631 714
ETHE1	0.975715 22	5.08147 E-10	2.40281 E-08	7.619280 34	MFAP3L	0.789176 643	0.000447 856	0.007202 754	2.142501 425
NUCB1	0.701004 088	5.11759 E-10	2.41522 E-08	7.617042 463	SCAMP3	0.463671 088	0.000449 042	0.007217 084	2.141638 257
RNF130	0.739968 002	5.48934 E-10	2.58569 E-08	7.587423 436	TMEM255 A	1.810063 362	0.000450 646	0.007234 258	2.140605 98
SFTPC	1.846952 677	5.82601 E-10	2.73376 E-08	7.563239 855	BAD	0.422875 464	0.000454 875	0.007296 463	2.136887 597
CD55	1.361979 246	6.05025 E-10	2.82815 E-08	7.548498 226	SCIN	3.090935 946	0.000457 312	0.007325 959	2.135135 5
GLMP	0.763043 761	6.53916 E-10	3.05086 E-08	7.515577 459	ANXA7	0.531219 542	0.000457 227	0.007325 959	2.135135 5
SELK	0.704958 737	6.63529 E-10	3.08982 E-08	7.510066 255	RPS19	0.078740 746	0.000460 41	0.007370 779	2.132486 609
RPL9	0.305623 293	6.7656E- 10	3.14453 E-08	7.502444 442	ATF6B	0.621507 585	0.000460 976	0.007375 012	2.132237 268
CTNNB1	0.608740 628	6.93344 E-10	3.21643 E-08	7.492625 248	C5orf15	0.656372 607	0.000462 222	0.007390 126	2.131348 176
AK2	0.763328 016	7.18653 E-10	3.32754 E-08	7.477876 434	GALK1	0.528114 08	0.000463 358	0.007401 351	2.130689 027
SPAG7	0.837044 954	7.39884 E-10	3.41938 E-08	7.466052 804	AIMP1	0.478464 186	0.000463 529	0.007401 351	2.130689 027
MYO10	0.478778 422	7.73757 E-10	3.56919 E-08	7.447430 14	CNPY2	0.369750 708	0.000465 323	0.007425 168	2.129293 687
ZEB2	0.589832 902	7.99862 E-10	3.68267 E-08	7.433836 856	FAM198B	1.248951 077	0.000466 81	0.007444 036	2.128191 537
TRAPPC1	0.597944 796	8.15415 E-10	3.74724 E-08	7.426289 061	STAT3	0.555426 18	0.000472 944	0.007532 053	2.123086 633
TMEM258	0.474837 601	8.51954 E-10	3.90782 E-08	7.408065 531	S100A1	0.792594 075	0.000474 163	0.007546 551	2.122251 471
NDUFA2	0.662420 392	8.77556 E-10	4.01773 E-08	7.396019 241	IRF1	1.130978 703	0.000477 222	0.007590 305	2.119740 801
RPS14	0.255933 702	9.11738 E-10	4.16644 E-08	7.380234 87	LMAN1	0.614187 658	0.000482 774	0.007668 66	2.115280 506

RND3	0.747841 895	9.24841 E-10	4.21845 E-08	7.374847 432	SMIM7	0.452709 436	0.000489 852	0.007776 046	2.109241 167
RPS29	0.400920 391	9.28074 E-10	4.22532 E-08	7.374139 958	POLR2K	0.503406 346	0.000497 3	0.007889 161	2.102969 177
GADD45G IP1	0.709824 681	1.07812 E-09	4.89028 E-08	7.310666 129	ESYT2	0.556663 334	0.000499 582	0.007920 237	2.101261 799
COLGALT 1	0.810695 231	1.09433 E-09	4.95464 E-08	7.304987 768	P4HA2	0.521531 701	0.000507 725	0.008038 92	2.094802 295
RPL14	0.290335 268	1.10761 E-09	4.99628 E-08	7.301353 33	KANK2	1.031996 25	0.000508 53	0.008046 473	2.094394 466
KIAA1456	0.983334 124	1.12001 E-09	5.04294 E-08	7.297316 233	UFSP2	0.438294 291	0.000509 772	0.008060 911	2.093615 885
KCNE4	1.418795 943	1.14452 E-09	5.14385 E-08	7.288711 57	RRAGD	0.460464 776	0.000512 919	0.008105 45	2.091222 861
ROMO1	0.550616 324	1.22823 E-09	5.50994 E-08	7.258852 759	PCMTD2	0.497438 252	0.000513 451	0.008108 619	2.091053 109
PLA2G16	1.156492 949	1.24702 E-09	5.58401 E-08	7.253053 986	SELT	0.392944 276	0.000515 771	0.008140 007	2.089375 215
PFDN1	0.811592 4	1.25902 E-09	5.62744 E-08	7.249688 882	RNF181	0.324664 891	0.000519 743	0.008192 146	2.086602 32
NOP10	0.642263 174	1.36564 E-09	6.08183 E-08	7.215965 602	STT3A	0.426453 65	0.000521 423	0.008212 552	2.085521 885
HEBP1	0.776765 406	1.46789 E-09	6.52532 E-08	7.185398 408	MARCKS	0.201730 579	0.000521 709	0.008212 552	2.085521 885
LINC0099 8	0.683173 299	1.47177 E-09	6.5307E- 08	7.185040 336	RPL36A	0.244550 452	0.000525 628	0.008263 625	2.082829 399
PRKDC	0.686728 537	1.51339 E-09	6.70325 E-08	7.173714 68	DCTN3	0.414965 421	0.000527 967	0.008294 799	2.081194 157
CDH3	0.428084 522	1.67041 E-09	7.38538 E-08	7.131626 863	MRPS15	0.468171 03	0.000532 059	0.008343 314	2.078661 394
WFS1	1.021361 828	1.77948 E-09	7.83931 E-08	7.105722 372	TAOK3	0.430815 637	0.000533 743	0.008364 368	2.077566 848
SDHB	0.684752 226	1.79011 E-09	7.87198 E-08	7.103916 085	TMED7	0.648157 597	0.000534 327	0.008368 168	2.077369 593
S100B	0.875911 832	1.80298 E-09	7.91439 E-08	7.101582 815	SEC14L1	0.724489 212	0.000536 083	0.008390 304	2.076222 323
TCEAL4	0.662527 978	1.84699 E-09	8.09304 E-08	7.091888 096	MEGF6	1.281494 975	0.000540 595	0.008452 173	2.073031 637
MRPL41	0.672435 582	1.88632 E-09	8.25065 E-08	7.083511 81	NCL	0.434315 771	0.000542 798	0.008479 149	2.071647 74
FBXL5	0.967761 099	1.89547 E-09	8.27589 E-08	7.082185 332	DAG1	0.414707 005	0.000543 557	0.008485 582	2.071318 351
APLP2	0.697575 867	1.91294 E-09	8.33728 E-08	7.078975 766	CPEB2	0.490182 102	0.000548 792	0.008561 862	2.067431 787
ST8SIA6	1.215541 124	1.93913 E-09	8.43644 E-08	7.073840 698	B3GNT2	0.865657 628	0.000555 184	0.008656 072	2.062679 147
FAM46A	1.135538 22	2.08361 E-09	9.04891 E-08	7.043403 502	ZBED5- AS1	0.958973 527	0.000570 381	0.008887 354	2.051227 526
SUMO2	0.544288 278	2.18657 E-09	9.47927 E-08	7.023225 211	IFI16	0.354881 227	0.000574 223	0.008941 528	2.048588 24
CBX3	0.689852 893	2.35792 E-09	1.0204E- 07	6.991227 715	WASH7P	0.458838 105	0.000578 823	0.009007 433	2.045398 957
CLU	1.658089 757	2.40372 E-09	1.03839 E-07	6.983638 955	TMEM185 A	0.568716 109	0.000582 929	0.009065 57	2.042604 875
SNRPG	0.591850 579	2.54945 E-09	1.09941 E-07	6.958841 836	ETS1	0.376926 422	0.000585 859	0.009105 344	2.040703 636
USP22	0.541697 86	2.66356 E-09	1.1466E- 07	6.940589 842	SRI	0.367246 181	0.000587 701	0.009128 183	2.039615 662
MRPL20	0.704763 889	2.82968 E-09	1.21597 E-07	6.915078 559	CAST	0.392394 125	0.000588 802	0.009139 485	2.039078 28
SH3BP4	1.003214 359	2.87978 E-09	1.23317 E-07	6.908976 831	PIGT	0.401897 788	0.000591 508	0.009174 86	2.037400 571
GSN	0.599892 676	3.01185 E-09	1.28748 E-07	6.890261 005	FSTL4	2.570472 956	0.000593 224	0.009190 657	2.036653 452
DAZAP2	0.433351 904	3.16773 E-09	1.35175 E-07	6.869104 571	BTF3L4	0.485920 34	0.000594 191	0.009199 82	2.036220 688
LAMP2	0.614622 951	3.19112 E-09	1.35936 E-07	6.866664 508	BLVRA	0.467644 542	0.000598 002	0.009252 971	2.033718 8

HSPE1	0.543538 034	3.23682 E-09	1.37643 E-07	6.861244 82	EFHD1	2.315544 367	0.000602 67	0.009319 315	2.030615 986
GABARAP L2	0.576479 912	3.25294 E-09	1.38089 E-07	6.859839 84	DEK	0.431543 38	0.000613 916	0.009481 25	2.023134 387
RPL35	0.329265 505	3.41517 E-09	1.44725 E-07	6.839455 418	MYADM	0.424624 711	0.000614 989	0.009491 827	2.022650 167
HLA-F	1.515982 866	3.61274 E-09	1.5257E- 07	6.816531 617	COPS6	0.379299 045	0.000618 105	0.009533 914	2.020728 774
CAP2	2.086347 342	3.75356 E-09	1.58244 E-07	6.800673 338	THYN1	0.663065 91	0.000620 601	0.009566 389	2.019251 98
KLF9	1.283636 689	3.82974 E-09	1.61178 E-07	6.792693 532	KCNN3	0.900473 356	0.000629 921	0.009703 957	2.013051 15
SEC61G	0.567168 593	4.35542 E-09	1.82987 E-07	6.737579 048	RAP1GAP	0.847214 282	0.000634 364	0.009760 114	2.010545 128
ADGRG1	0.465326 995	4.58534 E-09	1.92317 E-07	6.715981 728	HSPA8	0.377990 097	0.000634 211	0.009760 114	2.010545 128
LDHB	0.780707 717	4.59438 E-09	1.92323 E-07	6.715969 599	ANAPC16	0.347303 212	0.000640 909	0.009853 17	2.006424 038
CPQ	0.603915 334	4.60117 E-09	1.92323 E-07	6.715969 599	HNRNPL	0.220828 697	0.000641 216	0.009853 17	2.006424 038
44076	0.681917 429	4.61796 E-09	1.92696 E-07	6.715127 801	OXCT1	0.626751 9	0.000646 275	0.009924 678	2.003283 593
RPLP0	0.390155 524	4.64441 E-09	1.9347E- 07	6.713387 001	RPS9	0.163317 993	0.000657 055	0.010083 898	1.996371 568
IRS2	0.526293 099	4.69312 E-09	1.95167 E-07	6.709593 495	VLDLR	1.195731 997	0.000663 817	0.010181 302	1.992196 676
SLC6A15	0.894570 649	4.70746 E-09	1.95432 E-07	6.709005 21	GPC1	0.656397 104	0.000669 322	0.010259 304	1.988882 12
MFGE8	0.724413 455	4.80432 E-09	1.99115 E-07	6.700895 871	ASXL1	0.441753 924	0.000673 82	0.010321 798	1.986244 624
COMMD1	0.827085 316	4.87332 E-09	2.01633 E-07	6.695437 347	PRKD1	0.611034 214	0.000674 748	0.010323 091	1.986190 24
ESYT1	0.923043 668	4.93842 E-09	2.03983 E-07	6.690406 809	ATG4B	0.507546 902	0.000676 565	0.010340 458	1.985460 216
GNG11	0.753622 115	5.39724 E-09	2.22559 E-07	6.652554 864	CBR3	0.681693 137	0.000678 509	0.010361 225	1.984588 885
TMEM98	0.824052 334	5.70277 E-09	2.34762 E-07	6.629371 776	FAM189A2	0.723243 415	0.000678 996	0.010362 199	1.984548 092
ISCU	0.686388 314	5.87325 E-09	2.41375 E-07	6.617307 946	HSPA12A	0.588326 156	0.000682 209	0.010398 272	1.983038 846
RBM8A	0.643823 743	6.16024 E-09	2.52745 E-07	6.597316 79	NFU1	0.566298 962	0.000682 902	0.010402 364	1.982867 945
NARF	0.761276 484	6.52101 E-09	2.671E- 07	6.573326 285	CCDC107	0.523123 145	0.000688 142	0.010469 169	1.980087 803
ATP5J2	0.577804 565	6.64815 E-09	2.71853 E-07	6.565666 097	SEMA6D	0.738139 153	0.000689 088	0.010477 047	1.979761 099
TCEA1	0.633507 848	6.74936 E-09	2.75531 E-07	6.559828 959	CCL2	3.439841 986	0.000696 489	0.010576 437	1.975660 6
SSNA1	0.711164 892	6.76187 E-09	2.75583 E-07	6.559748 046	AKR1B1	0.397513 777	0.000696 406	0.010576 437	1.975660 6
PLBD2	1.018955 112	6.93667 E-09	2.82237 E-07	6.549385 645	CCDC25	0.585574 627	0.000699 361	0.010613 476	1.974142 353
UFC1	0.712689 161	6.9651E- 09	2.82924 E-07	6.548330 297	MAPKAP1	0.500307 5	0.000702 831	0.010659 529	1.972261 966
AMOTL2	1.183326 602	7.20504 E-09	2.92186 E-07	6.534340 767	SUMO1	0.306208 76	0.000707 707	0.010720 209	1.969796 761
RNF144B	0.825903 416	7.2585E- 09	2.93867 E-07	6.531848 682	IQCK	0.381798 536	0.000712 36	0.010784 022	1.967219 229
ARNT2	0.769370 019	7.47477 E-09	3.02124 E-07	6.519814 789	HIBCH	0.436185 36	0.000715 549	0.010825 604	1.965547 844
ILVBL	0.664249 361	7.72201 E-09	3.11603 E-07	6.506398 447	COA6	0.550274 551	0.000719 65	0.010867 511	1.963869 903
DYNC112	0.609551 847	8.32162 E-09	3.35246 E-07	6.474635 931	UBQLN2	0.697792 053	0.000725 195	0.010944 501	1.960804 048
PSME2	0.870562 136	8.78527 E-09	3.52765 E-07	6.452515 046	CDC25B	0.540728 152	0.000730 997	0.011025 271	1.957610 745
MESDC2	0.747751 176	9.17507 E-09	3.67814 E-07	6.434372 28	LGALS3	0.201724 812	0.000731 997	0.011033 562	1.957284 263

PSMA6	0.639119 446	9.23198 E-09	3.6949E- 07	6.432396 898	PBXIP1	0.515148 818	0.000741 012	0.011162 58	1.952235 431
GOLM1	0.850989 461	9.2543E- 09	3.6978E- 07	6.432057 016	BCL10	0.472834 498	0.000746 4	0.011236 827	1.949356 31
CORO1C	0.738921 523	9.33691 E-09	3.72119 E-07	6.429318 573	SMC6	0.441757 202	0.000749 73	0.011266 186	1.948223 07
CDV3	0.632633 626	9.34323 E-09	3.72119 E-07	6.429318 573	ATAD1	0.686810 732	0.000757 599	0.011377 45	1.943955 047
ZFP36L1	0.513053 119	9.53369 E-09	3.79088 E-07	6.421260 185	CSRP2	2.057490 11	0.000761 246	0.011425 217	1.942135 531
PTEN	0.614432 216	9.79572 E-09	3.88876 E-07	6.410189 267	SCAND1	0.372254 997	0.000765	0.011474 53	1.940265 095
LEF1	0.859762 728	9.84877 E-09	3.90349 E-07	6.408546 952	MRPS36	0.394344 956	0.000770 869	0.011555 482	1.937211 922
CTSO	1.242852 926	9.86588 E-09	3.90395 E-07	6.408495 25	WWC3	0.557444 93	0.000771 508	0.011557 994	1.937117 53
ALDOA	0.422914 386	1.06122 E-08	4.19252 E-07	6.377524 793	ACADS	0.552390 635	0.000773 933	0.011587 239	1.936020 043
ATP5F1	0.640120 506	1.07365 E-08	4.23479 E-07	6.373168 291	PDIA6	0.476896 465	0.000781 113	0.011681 14	1.932514 787
SPTBN1	0.404987 723	1.09514 E-08	4.31258 E-07	6.365262 445	ARHGAP3 1	1.101248 503	0.000796 834	0.011908 262	1.924151 634
RPL38	0.324875 504	1.19813 E-08	4.7106E- 07	6.326923 77	DNM2	0.482607 037	0.000800 75	0.011959 498	1.922287 053
ZCRB1	0.785244 882	1.20829 E-08	4.74291 E-07	6.323955 324	MAFIP	1.129866 838	0.000818 767	0.012221 125	1.912888 802
ECH1	0.693313 658	1.22861 E-08	4.81497 E-07	6.317406 645	PQLC2L	2.463640 213	0.000823 171	0.012279 389	1.910823 251
C9orf3	0.390638 351	1.27135 E-08	4.97452 E-07	6.303248 769	CLNS1A	0.413777 888	0.000829 453	0.012350 53	1.908314 408
GDI2	0.620795 131	1.30576 E-08	5.101E- 07	6.292344 83	PQLC3	0.423848 987	0.000835 435	0.012432 041	1.905457 569
PHB	0.647751 51	1.31504 E-08	5.12906 E-07	6.289962 464	MMGT1	0.658735 871	0.000838 243	0.012460 162	1.904476 304
NDUFS8	0.628571 093	1.35524 E-08	5.26911 E-07	6.278263 028	CAPZB	0.326253 474	0.000849 765	0.012614 629	1.899125 52
CUTA	0.481335 044	1.3697E- 08	5.31685 E-07	6.274345 247	MRPS7	0.421972 215	0.000851 766	0.012636 679	1.898367 061
PCBD1	0.795430 779	1.39678 E-08	5.41341 E-07	6.266528 959	WASH2P	0.478009 88	0.000853 972	0.012661 744	1.897506 484
MME	1.368176 818	1.47246 E-08	5.69772 E-07	6.244299 203	DYNLT1	0.412087 56	0.000864 018	0.012795 195	1.892953 089
HSBP1L1	1.032973 409	1.49353 E-08	5.77011 E-07	6.238816 084	PPP1R15 A	0.408996 314	0.000868 444	0.012852 969	1.890996 533
DECR1	0.681937 337	1.54667 E-08	5.96599 E-07	6.224317 287	INPP5K	0.508225 799	0.000869 873	0.012866 343	1.890544 866
BIRC3	2.196219 921	1.61525 E-08	6.21099 E-07	6.206838 89	PAQR8	0.680358 291	0.000877 205	0.012959 138	1.887423 886
SPSB1	1.286089 897	1.6151E- 08	6.21099 E-07	6.206838 89	SDC4	0.787303 686	0.000881 435	0.013005 941	1.885858 215
PAFAH1B 2	0.791041 255	1.62852 E-08	6.25218 E-07	6.203968 838	PLA2G15	0.603113 532	0.000881 331	0.013005 941	1.885858 215
TMED9	0.683480 918	1.6974E- 08	6.50642 E-07	6.186657 621	ACSL1	0.851944 625	0.000882 935	0.013020 239	1.885381 059
WASF2	0.552489 46	1.75373 E-08	6.71186 E-07	6.173156 85	GMFG	1.788087 368	0.000884 905	0.013033 592	1.884935 863
PSMD1	0.728985 25	1.76508 E-08	6.74476 E-07	6.171033 487	UQCRRF51	0.295044 81	0.000897 808	0.013207 758	1.879170 903
HERC2	0.956747 353	1.78427 E-08	6.80746 E-07	6.167015 163	STMN1	0.208255 261	0.000903 452	0.013282 804	1.876710 231
ARSA	0.853154 182	1.95278 E-08	7.4388E- 07	6.128497 3	ACOT7	0.426820 338	0.000909 075	0.013357 462	1.874276 065
IFNGR2	0.648304 641	1.99401 E-08	7.58407 E-07	6.120097 836	MAGOH	0.463456 392	0.000918 752	0.013491 558	1.869937 899
CTSZ	0.672708 452	2.02784 E-08	7.70075 E-07	6.113466 935	ADK	0.629167 02	0.000924 248	0.013564 123	1.867608 278
H2AFZ	0.480883 539	2.08374 E-08	7.90081 E-07	6.102328 401	C21orf33	0.387183 16	0.000936 587	0.013720 551	1.862628 46

NAP1L1	0.380236 477	2.23814 E-08	8.47309 E-07	6.071958 161	APH1B	0.611713 409	0.000941 686	0.013778 77	1.860789 539
GNB1	0.464463 174	2.25379 E-08	8.51919 E-07	6.069601 878	RAB18	0.451515 526	0.000942 676	0.013785 02	1.860592 599
CNPY3	0.737265 944	2.2779E- 08	8.59705 E-07	6.065650 438	MYO1E	0.475840 032	0.000955 633	0.013957 827	1.855182 188
TMEM230	0.595962 405	2.32381 E-08	8.75683 E-07	6.057653 258	RASGEF1 B	0.362987 25	0.000962 678	0.014052 345	1.852251 195
HPS4	0.851876 438	2.37865 E-08	8.94973 E-07	6.048189 934	PPM1B	0.649869 323	0.000977 937	0.014258 083	1.845938 872
ECHS1	0.626672 745	2.43293 E-08	9.13989 E-07	6.039059 004	ESD	0.286255 36	0.000985 764	0.014355 119	1.842993 203
BICC1	1.683460 593	2.66503 E-08	9.96598 E-07	6.001479 906	BMP7	1.007565 498	0.000992 668	0.014447 069	1.840220 267
SGCE	0.698387 444	2.77533 E-08	1.03469 E-06	5.985191 52	SLCO4A1	0.501950 145	0.001001 361	0.014564 929	1.836691 617
CTTN	0.445470 333	2.77377 E-08	1.03469 E-06	5.985191 52	TMEM184 B	0.493982 494	0.001013 885	0.014729 598	1.831809 094
NDUFA3	0.499722 004	2.83623 E-08	1.05579 E-06	5.976424 059	ARHGEF4 0	0.492768 347	0.001017 304	0.014770 512	1.830604 454
LIPA	1.340698 242	2.93908 E-08	1.09241 E-06	5.961613 736	NIPA2	0.524401 963	0.001025 661	0.014883 025	1.827308 799
SLCO4A1- AS1	0.757601 619	3.03052 E-08	1.12299 E-06	5.949625 039	KIAA0556	1.039207 339	0.001039 911	0.015071 946	1.821830 683
TXNL4A	0.589421 868	3.02769 E-08	1.12299 E-06	5.949625 039	CD99L2	0.725026 369	0.001039 851	0.015071 946	1.821830 683
TJP2	1.141427 755	3.10582 E-08	1.1474E- 06	5.940284 075	ITGA3	0.786168 933	0.001044 198	0.015125 121	1.820301 138
ZNF652	0.682116 985	3.11046 E-08	1.1474E- 06	5.940284 075	ARHGEF9	0.737133 92	0.001046 438	0.015148 613	1.819627 14
FIS1	0.729519 188	3.38598 E-08	1.24716 E-06	5.904076 939	SNRPC	0.413831 383	0.001056 911	0.015291 181	1.815558 973
DDT	0.677693 963	3.41954 E-08	1.25763 E-06	5.900446 657	LPCAT1	0.769713 998	0.001060 525	0.015329 807	1.814463 324
NHP2	0.633412 54	3.52543 E-08	1.29148 E-06	5.888911 77	IFT81	0.610623 419	0.001072 429	0.015488 259	1.809997 391
CHST9	1.477501 154	3.72673 E-08	1.36243 E-06	5.865686 69	ANKRD28	0.525986 91	0.001078 272	0.015554 296	1.808149 632
CAV2	0.617839 813	3.7751E- 08	1.37805 E-06	5.860734 646	C11orf73	0.471376 836	0.001078 21	0.015554 296	1.808149 632
NDUFB3	0.572153 151	4.02135 E-08	1.46576 E-06	5.833937 906	TMEM54	1.530860 186	0.001081 954	0.015598 226	1.806924 792
RETSAT	0.599687 934	4.29067 E-08	1.5616E- 06	5.806430 353	UBA6	0.431570 59	0.001084 395	0.015615 026	1.806457 278
EMC4	0.604271 829	4.30138 E-08	1.56318 E-06	5.805991 929	GTF3A	0.390459 09	0.001084 081	0.015615 026	1.806457 278
RPS17	0.412584 215	4.41486 E-08	1.60204 E-06	5.795326 708	SDCBP	0.455851 257	0.001089 165	0.015665 297	1.805061 367
NOTCH2N L	0.783808 231	4.53877 E-08	1.64457 E-06	5.783948 528	GALE	0.488427 043	0.001102 256	0.015844 28	1.800127 484
FXVD3	1.437506 795	4.5952E- 08	1.66179 E-06	5.779424 966	SLC35A5	0.761637 151	0.001107 993	0.015917 405	1.798127 72
RAB13	0.697258 949	4.59986 E-08	1.66179 E-06	5.779424 966	RTN4	0.400013 238	0.001124 139	0.016139 894	1.792099 311
TMED10	0.578586 817	4.78752 E-08	1.72449 E-06	5.763338 725	CTSF	0.173648 223	0.001128 031	0.016186 282	1.790852 895
COX7A2	0.511314 034	4.88411 E-08	1.7567E- 06	5.755302 164	ALDH1B1	1.124852 896	0.001163 621	0.016677 43	1.777870 867
LAMTOR1	0.571969 867	5.28388 E-08	1.8977E- 06	5.721771 903	CBFB	0.549068 809	0.001163 621	0.016677 43	1.777870 867
MZT2B	0.519026 816	5.31013 E-08	1.90434 E-06	5.720255 576	FAM126A	0.375172 168	0.001167 437	0.016712 574	1.776956 659
RPL10A	0.341183 871	5.36401 E-08	1.92085 E-06	5.716506 951	EIF4B	0.211700 261	0.001186 082	0.016949 768	1.770836 243
HPS1	0.670031 786	5.5466E- 08	1.98333 E-06	5.702604 213	NTPCR	0.605081 26	0.001193 658	0.017048 083	1.768324 437
MTUS1	0.932735 205	5.75783 E-08	2.05287 E-06	5.687638 355	OR7A5	1.484264 016	0.001195 713	0.017067 484	1.767830 498

MTHFD1L	0.816458 106	5.84598 E-08	2.08127 E-06	5.681671 224	SCARB2	0.387297 899	0.001205 9	0.017192 85	1.764652 123
IFIT3	1.049758 911	5.90188 E-08	2.09812 E-06	5.678169 383	ELOVL5	0.567289 948	0.001213 593	0.017282 406	1.762395 785
ADAM9	0.928937 078	5.93327 E-08	2.10623 E-06	5.676495 049	DIP2C	0.406671 137	0.001213 106	0.017282 406	1.762395 785
FKBP2	0.553104 937	6.04776 E-08	2.14376 E-06	5.668824 076	RPS18P9	0.231293 768	0.001217 212	0.017323 876	1.761354 934
PEPD	0.671213 925	6.13236 E-08	2.17061 E-06	5.663418 904	EIF3H	0.255139 947	0.001218 607	0.017333 654	1.761109 876
GANAB	0.659878 075	6.44523 E-08	2.27806 E-06	5.642435 199	TRAPPC4	0.477441 072	0.001222 8	0.017383 2	1.759870 263
SMDT1	0.594753 146	6.47647 E-08	2.2658E- 06	5.640961 617	PRDX1	0.263645 262	0.001231 719	0.017499 836	1.756966 014
UBE2I	0.581882 119	6.56388 E-08	2.31332 E-06	5.635764 585	ANXA1	0.628599 226	0.001234 893	0.017534 77	1.756099 923
COX14	0.644691 825	6.68586 E-08	2.35292 E-06	5.628392 192	NAA20	0.341873 854	0.001239 209	0.017585 853	1.754836 55
TOMM6	0.574760 795	7.00305 E-08	2.46102 E-06	5.608885 711	SOD2	0.560766 757	0.001247 24	0.017689 576	1.752282 571
PYCARD	1.521375 179	7.05036 E-08	2.47409 E-06	5.606584 223	RNASE4	0.697884 977	0.001249 737	0.017714 737	1.751665 285
NSRP1	0.657296 479	7.08315 E-08	2.48204 E-06	5.605191 055	CAPRIN1	0.525518 239	0.001260 132	0.017841 435	1.748570 223
MBNL2	0.709334 135	7.15762 E-08	2.50455 E-06	5.601269 546	TRAF3	0.877681 792	0.001272 784	0.018010 157	1.744482 509
MYL12A	0.653023 601	7.17783 E-08	2.50804 E-06	5.600665 313	C11orf58	0.268485 367	0.001274 456	0.018023 397	1.744163 35
BLOC1S1	0.557074 308	7.23812 E-08	2.5255E- 06	5.597651 904	SRSF1	0.476376 355	0.001298 071	0.018346 771	1.736440 355
LOC10124 3545	0.361014 187	7.31616 E-08	2.5491E- 06	5.593612 433	MAFF	0.733260 214	0.001304 075	0.018420 997	1.734686 86
CHMP2A	0.604333 639	7.41722 E-08	2.57698 E-06	5.588888 258	MRPL14	0.418225 288	0.001320 661	0.018644 538	1.729448 385
VKORC1	0.641132 116	7.44895 E-08	2.58434 E-06	5.587649 9	PLA2G7	0.970813 394	0.001322 541	0.018660 323	1.729080 847
SCUBE2	1.640160 561	7.68941 E-08	2.66023 E-06	5.575080 339	SCCPDH	0.551659 226	0.001328 12	0.018722 802	1.727629 161
RPS10	0.273107 35	7.71177 E-08	2.6642E- 06	5.574432 463	AHCYL1	0.359017 611	0.001328 498	0.018722 802	1.727629 161
SMPD1	0.951208 472	7.98284 E-08	2.75397 E-06	5.560041 413	FAM160B1	0.675868 511	0.001332 811	0.018772 79	1.726471 177
ATP6V1B2	0.732837 141	8.31564 E-08	2.86072 E-06	5.543524 555	RN7SK	0.347018 152	0.001341 172	0.018879 694	1.724005 045
RAB30	0.888944 268	8.48666 E-08	2.91546 E-06	5.535293 078	SMUG1	0.580817 759	0.001346 135	0.018938 676	1.722650 395
NDUFS6	0.588175 714	8.59168 E-08	2.9474E- 06	5.530560 626	KXD1	0.392245 531	0.001350 808	0.018993 511	1.721394 738
DNPH1	0.619629 8	8.65013 E-08	2.96023 E-06	5.528673 823	DPY30	0.444095 105	0.001371 595	0.019263 672	1.715260 924
MRPS21	0.550809 801	8.65325 E-08	2.96023 E-06	5.528673 823	DNAJC1	0.361051 887	0.001377 677	0.019338 008	1.713588 269
HADHA	0.620715 141	8.87898 E-08	3.03322 E-06	5.518096 437	MVP	0.510506 69	0.001379 867	0.019357 647	1.713147 432
GYPC	0.532649 696	8.89583 E-08	3.03474 E-06	5.517878 039	SARNP	0.423430 741	0.001383 078	0.019391 597	1.712386 412
UTRN	1.141355 395	9.37804 E-08	3.1948E- 06	5.495556 905	PRDX3	0.346877 962	0.001388 971	0.019463 08	1.710788 423
EIF4G2	0.492413 908	9.39497 E-08	3.19612 E-06	5.495377 412	PRKCH	1.153917 074	0.001406 153	0.019692 567	1.705697 667
EPS8	0.678442 24	9.6559E- 08	3.28033 E-06	5.484082 63	FEM1B	0.467718 035	0.001422	0.019869 065	1.701822 58
ATP6V1F	0.591918 707	9.97398 E-08	3.38369 E-06	5.470608 827	SMARCA2	0.422211 617	0.001428 773	0.019952 317	1.700006 668
TRAK2	0.592544 675	1.02791 E-07	3.48038 E-06	5.458373 692	BBX	0.387924 224	0.001430 633	0.019955 532	1.699936 696
RPLP2	0.243088 096	1.02874 E-07	3.48038 E-06	5.458373 692	LOC10099 6447	0.411565 363	0.001434 521	0.019998 378	1.699005 218

KIAA1033	0.969338 059	1.03105 E-07	3.4834E- 06	5.457997 162	CD47	0.340240 628	0.001451 072	0.020206 122	1.694517 027
CCDC124	0.617655 396	1.03896 E-07	3.50527 E-06	5.455278 004	TOMM20	0.321881 95	0.001450 253	0.020206 122	1.694517 027
MATN2	1.387170 076	1.04158 E-07	3.50927 E-06	5.454783 059	PCNP	0.415438 294	0.001452 959	0.020220 894	1.694199 644
APRT	0.571416 02	1.05599 E-07	3.55295 E-06	5.449410 571	SNRNP27	0.473485 529	0.001460 527	0.020314 678	1.692190 061
NAA38	0.588605 762	1.06189 E-07	3.56789 E-06	5.447588 476	PKHD1	0.952828 765	0.001463 994	0.020351 345	1.691406 878
IRF2BPL	0.596535 683	1.2731E- 07	4.27169 E-06	5.369400 107	TMOD1	0.560194 552	0.001464 903	0.020352 435	1.691383 626
RAB14	0.689265 966	1.28245 E-07	4.29719 E-06	5.366815 68	GSTM3	0.566012 502	0.001466 144	0.020358 126	1.691262 197
CYB561A3	0.524803 936	1.38033 E-07	4.61883 E-06	5.335468 251	TRIM5	0.761355 221	0.001467 717	0.020368 422	1.691042 612
SPATS2L	0.507076 085	1.46354 E-07	4.88391 E-06	5.311232 703	SMPDL3A	0.650407 195	0.001483 283	0.020561 134	1.686952 932
BLVRB	0.560459 673	1.52402 E-07	5.06505 E-06	5.295416 075	HIPK2	0.400419 444	0.001491 837	0.020656 332	1.684946 804
ARPC5	0.485333 353	1.52904 E-07	5.07483 E-06	5.294578 875	ABCC2	0.446914 554	0.001494 361	0.020679 883	1.684457 919
44077	0.860058 367	1.5618E- 07	5.17656 E-06	5.285958 998	MTHFS	0.464651 227	0.001503 906	0.020799 928	1.681938 16
SLC35F6	0.586712 778	1.59171 E-07	5.26857 E-06	5.278306 958	ZSCAN16- AS1	0.440720 767	0.001516 833	0.020966 883	1.678466 137
SHFM1	0.477551 43	1.59878 E-07	5.28483 E-06	5.276969 114	GATM	1.006914 377	0.001527 283	0.021099 422	1.675729 443
TFF3	1.549136 877	1.62261 E-07	5.35637 E-06	5.271129 582	F8A1	0.581438 601	0.001532 361	0.021157 633	1.674532 927
BNIP3L	0.704238 832	1.68035 E-07	5.5395E- 06	5.256529 588	SRSF6	0.645352 304	0.001540 136	0.021241 038	1.672824 26
SIGIRR	0.613581 419	1.724E- 07	5.67575 E-06	5.245976 483	METRNL	0.411207 438	0.001542 562	0.021262 529	1.672385 079
AEBP1	0.617488 146	1.72888 E-07	5.68419 E-06	5.245331 464	RALA	0.449469 358	0.001543 95	0.021269 692	1.672238 791
ATP6V0D1	0.645439 506	1.78348 E-07	5.85585 E-06	5.232409 717	HMGH5	1.231239 557	0.001547 425	0.021297 205	1.671677 391
WSCD1	1.416603 804	1.843E- 07	6.04317 E-06	5.218735 057	C6orf48	0.274605 632	0.001547 686	0.021297 205	1.671677 391
OPTN	0.583661 973	1.89774 E-07	6.21433 E-06	5.206605 722	PHYH	0.817574 024	0.001555 445	0.021379 956	1.669993 202
TBCB	0.596639 454	1.90897 E-07	6.24277 E-06	5.204622 41	UGT2B7	6.278800 488	0.001567 988	0.021516 129	1.667235 862
LOC72973 2	0.539223 373	1.95456 E-07	6.38333 E-06	5.194952 779	FXD5	0.412808 567	0.001590 317	0.021785 919	1.661824 115
HES4	0.542455 733	1.96387 E-07	6.4052E- 06	5.193467 319	PIP4K2C	0.633575 261	0.001598 542	0.021880 253	1.659947 654
CYGB	1.035890 579	2.02243 E-07	6.58741 E-06	5.181285 464	MRPL43	0.409499 317	0.001618 096	0.022129 342	1.655031 501
SEL1L	0.668210 626	2.06155 E-07	6.70593 E-06	5.173541 145	KLF2	0.627043 843	0.001631 103	0.022289 821	1.651893 425
GHITM	0.581679 583	2.10141 E-07	6.82651 E-06	5.165801 409	TM9SF3	0.425929 606	0.001631 651	0.022289 821	1.651893 425
NSMCE1	0.711767 852	2.15388 E-07	6.9877E- 06	5.155665 519	NQO1	0.852332 056	0.001648 164	0.022502 86	1.647762 273
C14orf166	0.549316 585	2.19874 E-07	7.12379 E-06	5.147289 173	EVA1A	1.363569 736	0.001691 067	0.023050 075	1.637327 655
COA3	0.637836 695	2.20956 E-07	7.14939 E-06	5.145731 124	SEC24C	0.590666 354	0.001699 201	0.023148 064	1.635485 327
ASAP2	0.655915 022	2.27238 E-07	7.34298 E-06	5.134127 603	DUSP23	0.514520 347	0.001710 897	0.023294 442	1.632747 681
CRABP1	1.115592 837	2.32348 E-07	7.4982E- 06	5.125043 004	CREBL2	0.647610 724	0.001711 946	0.023295 784	1.632722 677
ABHD2	0.711188 972	2.33632 E-07	7.52973 E-06	5.123220 661	ANP32E	0.417618 632	0.001720 556	0.023373 987	1.631267 199
ARPC2	0.566159 964	2.58545 E-07	8.31077 E-06	5.080358 914	YIPF2	0.567141 593	0.001733 063	0.023517 805	1.628603 218

RPS23	0.197833 583	2.62062 E-07	8.40177 E-06	5.075629 037	MRPL55	0.451234 788	0.001735 574	0.023538 843	1.628214 885
CYB5A	0.838325 143	2.64172 E-07	8.45833 E-06	5.072715 293	DMD	0.581283 569	0.001739 735	0.023582 216	1.627415 395
SKA2	0.690693 855	2.65487 E-07	8.48934 E-06	5.071125 89	LOC40004 3	1.078658 104	0.001743 225	0.023616 459	1.626785 21
FRMD6	1.161721 826	2.67041 E-07	8.5279E- 06	5.069157 84	DYNC1LI1	0.527909 16	0.001751 492	0.023715 339	1.624970 661
CYBA	0.445435 137	2.76358 E-07	8.81396 E-06	5.054828 684	CD79B	0.633413 196	0.001759 404	0.023796 152	1.623493 275
CLIC4	0.648869 514	2.77805 E-07	8.84857 E-06	5.053127 06	GULP1	0.438257 515	0.001764 009	0.023832 124	1.622837 254
LINC0157 8	0.560521 543	2.81061 E-07	8.92906 E-06	5.049194 165	CAPZA2	0.418174 654	0.001763 813	0.023832 124	1.622837 254
VPS29	0.520443 678	2.84255 E-07	9.01884 E-06	5.044849 157	SNX7	0.521920 502	0.001766 66	0.023841 636	1.622663 952
APBA2	0.817653 716	2.96304 E-07	9.38898 E-06	5.027381 609	NBAT1	0.443475 693	0.001793 27	0.024160 817	1.616888 388
POLR2J	0.567241 371	3.04698 E-07	9.64246 E-06	5.015812 002	SLC16A4	0.837427 855	0.001809 975	0.024372 479	1.613100 299
SEC62	0.468506 604	3.4092E- 07	1.07748 E-05	4.967589 925	MIR21	1.491248 727	0.001830 474	0.024634 964	1.608448 07
LAMC1	0.777239 978	3.44292 E-07	1.08674 E-05	4.963874 523	RELB	0.964757 621	0.001831 591	0.024636 458	1.608421 73
DLC1	0.670153 201	3.48509 E-07	1.09722 E-05	4.959706 4	BHLHE41	0.661944 389	0.001833 827	0.024652 99	1.608130 401
PRR13	0.627445 996	3.82628 E-07	1.20309 E-05	4.919700 433	TSC22D2	0.262163 877	0.001839 223	0.024711 967	1.607092 682
C1orf122	0.569933 176	3.83485 E-07	1.20424 E-05	4.919286 266	ACOT1	0.388247 55	0.001850 263	0.024833 067	1.604969 642
NFIA	0.643778 682	3.894E- 07	1.22125 E-05	4.913194 992	AKIP1	0.631985 545	0.001853 546	0.024844 558	1.604768 718
EMP2	1.414267 302	3.93404 E-07	1.23223 E-05	4.909308 445	LRP10	0.543503 106	0.001853 444	0.024844 558	1.604768 718
ARL6IP4	0.489957 392	3.95811 E-07	1.23819 E-05	4.907213 785	SF3B1	0.336248 755	0.001854 162	0.024844 558	1.604768 718
TAF7	0.520955 682	4.04611 E-07	1.2641E- 05	4.898219 051	SNRPB	0.231769 323	0.001865 905	0.024988 234	1.602264 43
HEYL	1.657332 659	4.05654 E-07	1.26574 E-05	4.897654 1	JOSD2	0.372889 787	0.001869 317	0.025006 583	1.601945 652
EMC3	0.653958 678	4.20249 E-07	1.30962 E-05	4.882855 865	NEK9	0.450864 375	0.001891 164	0.025271 236	1.597373 518
SNAPIN	0.750937 462	4.21838 E-07	1.3129E- 05	4.881769 738	PSMC3	0.335276 484	0.001892 838	0.025279 815	1.597226 104
RPS3A	0.157440 186	4.23359 E-07	1.31596 E-05	4.880757 582	TAF9B	0.972216 249	0.001923 631	0.025677 067	1.590454 587
CBX5	0.671901 405	4.35612 E-07	1.35233 E-05	4.868917 942	DDX1	0.441210 032	0.001924 8	0.025678 676	1.590427 366
GNG10	0.571611 047	4.43475 E-07	1.375E- 05	4.861697 821	ARNT	0.521976 769	0.001933 001	0.025760 023	1.589053 76
RPL37A	0.191981 241	4.69178 E-07	1.45285 E-05	4.837779 023	NMT1	0.323164 016	0.001932 147	0.025760 023	1.589053 76
HOTAIRM 1	3.226736 069	4.70904 E-07	1.45489 E-05	4.837169 602	GAMT	0.662066 102	0.001948 854	0.025943 055	1.585978 882
PEG3	1.116071 224	4.71025 E-07	1.45489 E-05	4.837169 602	GNB2	0.368202 955	0.001950 252	0.025947 566	1.585903 383
TIMM8B	0.534235 716	4.75835 E-07	1.4679E- 05	4.833304 35	TTC27	1.066931 367	0.001959 633	0.026058 219	1.584055 275
FAM177A1	0.596907 079	4.84233 E-07	1.49192 E-05	4.826253 225	MARCKSL 1	0.019618 055	0.001988 243	0.026409 988	1.578231 804
B3GLCT	0.920603 871	5.06353 E-07	1.55812 E-05	4.807400 028	NT5C	0.422322 452	0.001997 461	0.026518 055	1.576458 341
TCERG1L	1.376517 296	5.11859 E-07	1.57308 E-05	4.803248 226	MX1	1.221611 619	0.001998 781	0.026521 205	1.576406 741
SSR3	0.629820 704	5.12731 E-07	1.57379 E-05	4.803053 268	MAP3K1	0.458415 598	0.002015 35	0.026726 576	1.573056 683
SCP2	0.530862 868	5.25453 E-07	1.61082 E-05	4.792952 925	METTL9	0.406113 267	0.002024 795	0.026837 299	1.571261 189

MRPL34	0.610886 157	5.31205 E-07	1.62642 E-05	4.788768 354	KIAA1549 L	0.683491 588	0.002036 294	0.026964 985	1.569199 812
PKIG	0.761800 766	5.3374E- 07	1.63214 E-05	4.787243 059	PTP4A2	0.317894 071	0.002036 63	0.026964 985	1.569199 812
CLIC1	0.510033 071	5.70773 E-07	1.74321 E-05	4.758651 346	DLST	0.497977 555	0.002063 435	0.027260 943	1.564459 121
C7orf55	0.621402 442	5.72858 E-07	1.7474E- 05	4.757608 784	MBNL1	0.389479 488	0.002072 291	0.027363 172	1.562833 554
PMM1	0.786223 948	5.78324 E-07	1.76187 E-05	4.754025 173	IFI27L1	0.521007 836	0.002091 252	0.027568 96	1.559579 61
ANAPC13	0.664336 264	5.85425 E-07	1.77908 E-05	4.749803 803	RPF1	0.473244 876	0.002096 19	0.027604 339	1.559022 651
FSTL1	0.645989 895	5.85128 E-07	1.77908 E-05	4.749803 803	LRRK2	2.980920 315	0.002097 915	0.027612 209	1.556898 85
SVIP	0.772621 93	6.02171 E-07	1.82319 E-05	4.739169 111	ST3GAL5	0.392668 456	0.002120 341	0.027892 396	1.554514 175
MYO5A	0.359496 981	6.02171 E-07	1.82319 E-05	4.739169 111	43896	0.309723 228	0.002146 745	0.028224 563	1.549372 779
VAT1	0.313799 381	6.07135 E-07	1.83595 E-05	4.736140 165	ATP6V1A	0.546720 564	0.002159 114	0.028371 959	1.547110 675
USP13	0.887583 435	6.17495 E-07	1.86497 E-05	4.729327 904	IFI35	1.492541 194	0.002164 435	0.028426 631	1.546274 615
HSPB11	0.732304 573	6.23739 E-07	1.88151 E-05	4.725493 094	TMEM30A	0.652688 384	0.002167 278	0.028448 713	1.545937 381
ERH	0.479883 85	6.26487 E-07	1.88748 E-05	4.724118 536	SPPL3	0.408428 46	0.002173 092	0.028479 253	1.545471 41
CSRP1	0.516811 43	6.27653 E-07	1.88867 E-05	4.723844 801	HNRNPA1 P10	0.231057 435	0.002172 617	0.028479 253	1.545471 41
RELL1	0.857942 224	6.46215 E-07	1.93975 E-05	4.712253 121	FUCA2	0.416654 021	0.002180 47	0.028560 662	1.544231 735
FAM53B	0.770201 743	6.45725 E-07	1.93975 E-05	4.712253 121	CHI3L2	2.776178 837	0.002204 547	0.028845 179	1.539926 768
LAPTM4A	0.276757 836	6.61445 E-07	1.98304 E-05	4.702668 694	HSF2	0.835441 947	0.002224 858	0.029079 862	1.536407 66
ERP29	0.579482 317	6.66935 E-07	1.99706 E-05	4.699609 97	RPL11	0.069800 943	0.002234 955	0.029196 262	1.534672 754
ENPP1	1.316067 815	6.9593E- 07	2.08133 E-05	4.681658 319	MRPS14	0.503073 454	0.002247 789	0.029348 268	1.532417 526
SUCLG1	0.619225 621	7.10551 E-07	2.1206E- 05	4.673541 998	VPS13C	0.394675 493	0.002255 03	0.029427 126	1.531252 149
BUD31	0.586570 978	7.1079E- 07	2.1206E- 05	4.673541 998	DHX30	0.465827 793	0.002277 006	0.029682 275	1.527502 814
COL6A1	0.745697 081	7.11688 E-07	2.12069 E-05	4.673522 541	CYC1	0.435717 493	0.002282 966	0.029744 133	1.526598 691
CDC42SE 2	0.730081 26	7.31961 E-07	2.17845 E-05	4.661852 356	PICALM	0.540448 427	0.002306 32	0.030019 741	1.522593 065
COPZ1	0.570719 957	7.53169 E-07	2.23885 E-05	4.649975 261	SUN1	0.538053 334	0.002306 571	0.030019 741	1.522593 065
CSDE1	0.621261 656	7.79596 E-07	2.3146E- 05	4.635524 501	SRD5A3	0.648735 225	0.002309 459	0.030025 417	1.522510 957
LOC10309 1866	1.496359 468	7.86819 E-07	2.33321 E-05	4.632045 24	CYB5B	0.393265 545	0.002329 64	0.030271 72	1.518962 906
FAM111A	0.929202 676	8.12748 E-07	2.40719 E-05	4.618489 91	ELMSAN1	0.386649 638	0.002347 94	0.030493 344	1.515794 949
ATAD3C	0.557803 75	8.40412 E-07	2.48612 E-05	4.604478 61	AEBP2	0.709119 32	0.002353 43	0.030548 45	1.515010 827
ITM2C	0.583308 399	9.07824 E-07	2.6823E- 05	4.571492 98	PPP6R3	0.323021 084	0.002359 445	0.030610 297	1.514132 456
ACTB	0.362627 536	9.18942 E-07	2.71187 E-05	4.566730 462	HS6ST2	1.486431 003	0.002364 703	0.030646 049	1.513625 51
C9orf16	0.583729 208	9.26941 E-07	2.73219 E-05	4.563489 426	FBXO25	0.471825 54	0.002392 841	0.030994 316	1.508717 949
MDK	1.207130 194	9.43769 E-07	2.77845 E-05	4.556198 134	FOXN3	0.458620 31	0.002410 158	0.031202 123	1.505815 858
ZFAND5	0.432817 787	9.6113E- 07	2.82277 E-05	4.549324 084	CCPG1	0.536913 157	0.002429 037	0.031429 915	1.502656 788
TP53TG1	0.838454 783	9.70289 E-07	2.84626 E-05	4.545725 578	C19orf24	0.395685 494	0.002439 716	0.031551 421	1.500981 073

EIF4EBP2	0.611932 755	1.00118 E-06	2.93336 E-05	4.532634 384	SURF4	0.412420 511	0.002449 111	0.031639 519	1.499770 133
EIF2S3	0.398995 519	1.00318 E-06	2.9357E- 05	4.532287 622	YIF1B	0.387237 102	0.002455 083	0.031699 951	1.498941 406
MZT2A	0.600753 725	1.01466 E-06	2.96222 E-05	4.528382 271	GNA12	0.665707 529	0.002472 545	0.031908 591	1.496092 376
RWDD1	0.532901 943	1.01432 E-06	2.96222 E-05	4.528382 271	PPM1A	0.415445 209	0.002493 217	0.032158 427	1.492705 199
SHISA4	0.904652 774	1.06671 E-06	3.11048 E-05	4.507173 25	PRELID2	1.035774 112	0.002539 966	0.032744 176	1.484865 934
HIATL1	0.678709 984	1.06866 E-06	3.11245 E-05	4.506898 062	GPAT4	0.404110 909	0.002547 79	0.032827 752	1.483758 852
HEBP2	0.666354 418	1.07034 E-06	3.11365 E-05	4.506730 289	LOC10192 7204	2.032190 8	0.002556 324	0.032920 4	1.482534 89
UQCRB	0.476218 82	1.07568 E-06	3.12546 E-05	4.505086 453	SMIM12	0.442536 324	0.002562 811	0.032986 599	1.481662 461
AK1	0.703350 902	1.09283 E-06	3.17154 E-05	4.498730 181	CD151	0.378201 485	0.002570 283	0.033065 396	1.480626 272
TRIB1	1.153262 973	1.12393 E-06	3.25792 E-05	4.487059 136	FAAP20	0.335085 392	0.002582 224	0.033201 571	1.478841 372
THRAP3	0.582136 989	1.1422E- 06	3.30697 E-05	4.480569 38	MRPS33	0.488050 103	0.002595 753	0.033358 012	1.476799 842
PDCD5	0.563004 315	1.15435 E-06	3.3382E- 05	4.476487 635	ZCCHC24	0.632993 579	0.002630 213	0.033765 429	1.471527 732
CD164	0.740198 91	1.16662 E-06	3.36971 E-05	4.472407 122	RPL4	0.207107 097	0.002638 006	0.033847 734	1.470470 396
ALKBH5	0.802211 165	1.1699E- 06	3.37521 E-05	4.471699 265	PPP3CA	0.350260 198	0.002650 092	0.033967 216	1.468940 052
DYNLRB1	0.445166 588	1.20072 E-06	3.46006 E-05	4.460916 548	SORT1	0.370125 771	0.002678 872	0.034318 147	1.464476 17
SLC25A1	0.608487 904	1.21607 E-06	3.50018 E-05	4.455909 744	NAGLU	0.398744 792	0.002693 297	0.034484 902	1.462371 005
NDUFA8	0.580642 819	1.22554 E-06	3.52328 E-05	4.453053 298	KAT2B	0.782295 108	0.002695 901	0.034500 209	1.462178 278
MAP1LC3 B	0.474357 158	1.29699 E-06	3.72432 E-05	4.428953 117	RNH1	0.388496 369	0.002732 453	0.034949 71	1.456556 422
EMX2OS	2.436973 81	1.29934 E-06	3.7267E- 05	4.428675 897	RAB3D	0.592091 68	0.002744 639	0.035087 255	1.454850 611
HMGB2	0.855986 059	1.30416 E-06	3.73614 E-05	4.427576 46	NUBP1	0.622347 474	0.002764 121	0.035299 471	1.452231 808
SMIM3	1.702076 077	1.32371 E-06	3.78774 E-05	4.421619 953	DAZAP1	0.452167 124	0.002763 529	0.035299 471	1.452231 808
LOC28378 8	0.921700 776	1.34399 E-06	3.83681 E-05	4.416030 259	GALT	0.586820 722	0.002775 544	0.035408 428	1.450893 359
ENY2	0.574177 384	1.34388 E-06	3.83681 E-05	4.416030 259	FTCDNL1	0.668071 628	0.002779 411	0.035439 3	1.450514 861
SRRM1	0.470174 789	1.35954 E-06	3.87216 E-05	4.412046 943	PABPC1	0.134751 782	0.002789 548	0.035550 043	1.449159 874
MARVELD 1	0.767415 941	1.38762 E-06	3.94753 E-05	4.403674 033	HNRNPR	0.291469 574	0.002792 087	0.035563 901	1.448990 602
NACA	0.305664 033	1.41997 E-06	4.03489 E-05	4.394167 985	SH3D19	0.493059 903	0.002799 718	0.035642 565	1.448031 052
HMG20B	0.606040 835	1.44451 E-06	4.09985 E-05	4.387231 972	CASP1	3.093244 791	0.002833 612	0.036055 319	1.443030 655
ATP5G1	0.512618 959	1.45555 E-06	4.12642 E-05	4.384426 074	COL1A2	0.497699 916	0.002841 346	0.036116 211	1.442297 82
MMP14	0.612986 326	1.4626E- 06	4.14162 E-05	4.382829 782	ZNF106	0.250707 746	0.002842 865	0.036116 774	1.442291 048
REEP5	0.488979 369	1.48699 E-06	4.20582 E-05	4.376149 288	ADGRA2	0.625886 917	0.002871 098	0.036456 539	1.438224 568
MLLT3	1.012093 067	1.5202E- 06	4.2948E- 05	4.367057 558	GADD45A	0.526783 049	0.002892 015	0.036684 111	1.435522 005
PSMA4	0.481881 32	1.55083 E-06	4.37123 E-05	4.359396 092	LOC65351 3	0.883711 517	0.002895 412	0.036695 07	1.435392 278
SPARC	1.060105 085	1.59475 E-06	4.48988 E-05	4.347765 592	EFEMP2	0.843316 615	0.002908 105	0.036794 894	1.434212 448
PTP4A1	0.730869 174	1.60795 E-06	4.52184 E-05	4.344684 756	PCDH7	0.373351 157	0.002979 303	0.037674 261	1.423955 257

SPCS1	0.482046 902	1.67486 E-06	4.70459 E-05	4.327478 443	SERINC5	0.482226 193	0.002999 024	0.037904 069	1.421314 169
AKR1A1	0.656924 665	1.68608 E-06	4.72797 E-05	4.325324 901	PLXND1	0.683725 119	0.003010 849	0.038014 299	1.420053 014
PTPRM	0.642086 685	1.68705 E-06	4.72797 E-05	4.325324 901	PLXNB1	0.522469 521	0.003015 655	0.038055 365	1.419584 105
GNAL	1.137399 793	1.69448 E-06	4.73836 E-05	4.324372 322	ELAVL1	0.432554 901	0.003028 345	0.038195 825	1.417984 109
VPS35	0.613831 282	1.69462 E-06	4.73836 E-05	4.324372 322	ZHX1	0.325101 823	0.003034 144	0.038249 269	1.417376 861
SPG20	0.685614 407	1.72173 E-06	4.80868 E-05	4.317973 735	MTCH2	0.358595 192	0.003041 73	0.038319 718	1.416577 692
GREB1	1.142894 387	1.72608 E-06	4.81534 E-05	4.317373 068	PRKAR1A	0.291071 832	0.003042 862	0.038319 718	1.416577 692
DGCR6	0.651177 108	1.72861 E-06	4.81691 E-05	4.317231 329	CTHRC1	1.216300 726	0.003061 015	0.038528 519	1.414217 683
RPL7A	0.217803 985	1.73185 E-06	4.82045 E-05	4.316912 386	FAM127C	0.380423 516	0.003067 522	0.038590 594	1.413518 541
HSD17B14	0.810159 087	1.74259 E-06	4.84484 E-05	4.314720 467	CSRNP3	0.832820 177	0.003076 327	0.038681 493	1.412496 767
TPCN2	0.623597 383	1.77116 E-06	4.9187E- 05	4.308150 038	TNFAIP3	0.510048 568	0.003078 94	0.038694 488	1.412350 892
ARF5	0.516981 959	1.77953 E-06	4.93634 E-05	4.306594 694	GPI	0.458107 591	0.003083 354	0.038710 243	1.412174 1
IFI6	1.131512 523	1.78359 E-06	4.94199 E-05	4.306097 96	LAMP1	0.444698 751	0.003082 373	0.038710 243	1.412174 1
TMX1	0.780679 524	1.7862E- 06	4.94363 E-05	4.305953 68	OSBPL8	0.279816 508	0.003092 037	0.038799 357	1.411175 471
FCRLA	0.936919 749	1.7907E- 06	4.95051 E-05	4.305350 112	LSM5	0.434334 01	0.003094 99	0.038816 535	1.410983 232
RHOB	0.673812 032	1.87719 E-06	5.18375 E-05	4.285355 884	MAP3K13	0.448903 59	0.003104 361	0.038894 226	1.410114 863
CLTA	0.527830 482	1.90927 E-06	5.2664E- 05	4.278485 831	UBE2V2	0.368304 61	0.003104 032	0.038894 226	1.410114 863
ATP5EP2	0.571646 273	1.94377 E-06	5.35552 E-05	4.271198	FEM1A	0.665272 295	0.003124 835	0.039110 734	1.407704 03
PDZD11	0.707202 017	1.99817 E-06	5.49923 E-05	4.259697 745	FBXW11	0.471875 548	0.003127 651	0.039125 993	1.407534 623
DDR2	1.021381 855	2.00871 E-06	5.52202 E-05	4.257901 722	BIN3	0.656350 017	0.003138 442	0.039240 937	1.406260 634
FTH1P3	0.327163 07	2.02502 E-06	5.56063 E-05	4.254876 38	FAM134A	0.299172 193	0.003156 446	0.039405 697	1.404440 981
TM7SF3	0.505150 199	2.05653 E-06	5.64083 E-05	4.248657 236	GFM1	0.626196 504	0.003189 528	0.039778 161	1.400355 297
ARPC1B	0.578877 628	2.06285 E-06	5.6501E- 05	4.247944 24	CHRM1	0.497038 126	0.003192 06	0.039789 478	1.400231 755
SMARCB1	0.519715 369	2.06452 E-06	5.6501E- 05	4.247944 24	ADNP	0.397857 726	0.003194 932	0.039805 017	1.400062 182
COX16	0.552364 051	2.07104 E-06	5.6616E- 05	4.247060 69	C9orf89	0.463349 402	0.003215 27	0.040019 809	1.397724 993
ARHGAP1	0.520226 181	2.08699 E-06	5.69886 E-05	4.244212 25	EIF3I	0.316451 013	0.003215 44	0.040019 809	1.397724 993
BROX	0.756592 274	2.13643 E-06	5.82736 E-05	4.234528 358	CCDC115	0.425923 645	0.003252 691	0.040442 34	1.393163 728
FKBP3	0.556350 47	2.14403 E-06	5.84158 E-05	4.233469 837	FAM161A	0.584655 821	0.003263 874	0.040560 792	1.391893 576
APOL2	1.100778 341	2.15182 E-06	5.85631 E-05	4.232375 96	SAT2	0.360063 672	0.003285 478	0.040808 563	1.389248 698
NDUFAF3	0.502129 793	2.16715 E-06	5.89148 E-05	4.229775 584	RAB21	0.454829 901	0.003293 982	0.040893 456	1.388346 188
HOXD- AS2	1.182919 383	2.22755 E-06	6.04895 E-05	4.218320 218	RAP1GDS 1	0.369626 164	0.003295 894	0.040896 463	1.388314 255
PKNOX2	0.933417 618	2.26335 E-06	6.13937 E-05	4.211876 178	DUSP22	0.450679 511	0.003303 203	0.040966 404	1.387572 161
ERLEC1	0.663175 762	2.26955 E-06	6.14939 E-05	4.211168 115	LACTB	0.568296 194	0.003324 167	0.041205 544	1.385044 345
COP22	1.170683 861	2.30768 E-06	6.24577 E-05	4.204413 706	HIVEP3	2.307512 522	0.003343 139	0.041419 752	1.382792 509

SELM	1.076600 79	2.31325 E-06	6.25396 E-05	4.203845 236	BOLA3	0.431530 237	0.003347 016	0.041446 817	1.382508 814
RHOA	0.333084 881	2.38808 E-06	6.43494 E-05	4.191455 591	IDH1	0.592092 335	0.003360 439	0.041571 012	1.381209 4
EIF6	0.546013 534	2.40947 E-06	6.48543 E-05	4.188060 968	PPDPF	0.382709 444	0.003372 669	0.041701 242	1.379851 015
SLC44A1	0.604143 739	2.44199 E-06	6.55856 E-05	4.183191 371	GAA	0.667565 286	0.003379 6	0.041728 138	1.379570 994
RPL29	0.267658 293	2.48648 E-06	6.67073 E-05	4.175826 828	EAPP	0.342848 45	0.003379 955	0.041728 138	1.379570 994
EVA1B	0.631518 245	2.49407 E-06	6.68377 E-05	4.174978 636	CCL28	0.634943 128	0.003426 675	0.042262 322	1.374046 649
ALDH6A1	0.663765 013	2.49787 E-06	6.68664 E-05	4.174791 789	DOCK10	0.569732 726	0.003429 738	0.042278 814	1.373877 202
ARPC4	0.499104 619	2.84185 E-06	7.5826E- 05	4.120181 991	MRPL9	0.391307 741	0.003454 879	0.042567 306	1.370923 839
CS	0.542897 105	2.89884 E-06	7.71785 E-05	4.112503 466	SEPT11	0.387691 23	0.003463 781	0.042655 536	1.370024 594
CELF2	0.457038 82	2.92088 E-06	7.76807 E-05	4.109686 941	LSM12	0.382030 01	0.003480 37	0.042836 999	1.368180 959
CAMTA1	0.493004 918	2.93113 E-06	7.7869E- 05	4.108635 559	PTPRN2	0.817936 897	0.003521 881	0.043283 976	1.363672 856
MPV17	0.583896 22	2.99556 E-06	7.94944 E-05	4.099663 686	SSBP3	0.477746 844	0.003523 729	0.043284 959	1.363662 993
FARP2	0.742182 076	3.02768 E-06	8.02598 E-05	4.095502 152	SPCS2	0.324290 901	0.003609 279	0.044296 055	1.353634 954
CHMP1B	0.566385 269	3.08604 E-06	8.17182 E-05	4.087681 163	MRPS28	0.464301 765	0.003666 144	0.044876 826	1.347977 868
PXN	0.562960 863	3.11363 E-06	8.22712 E-05	4.084752 352	ARPIN	0.514118 254	0.003671 319	0.044917 723	1.347582 265
CALU	0.552352 667	3.14022 E-06	8.28214 E-05	4.081857 429	KEAP1	0.628715 277	0.003694 784	0.045182 252	1.345032 13
SEC22B	0.525937 319	3.14122 E-06	8.28214 E-05	4.081857 429	RQCD1	0.258359 76	0.003708 697	0.045329 752	1.343616 659
RHEB	0.515273 213	3.17534 E-06	8.3631E- 05	4.077632 823	RPS5	0.001271 536	0.003712 182	0.045349 725	1.343425 346
RPS21	0.296932 012	3.1857E- 06	8.38136 E-05	4.076685 509	ZNF702P	1.392593 98	0.003739 784	0.045641 393	1.340641 113
TANGO2	0.790221 989	3.27153 E-06	8.59795 E-05	4.065604 992	LPAR6	0.601944 029	0.003754 046	0.045792 635	1.339204 365
APP	0.640009 165	3.28714 E-06	8.62971 E-05	4.064003 974	TMEM167 A	0.423893 303	0.003764 824	0.045901 249	1.338175 497
NONO	0.457201 421	3.439E- 06	9.00907 E-05	4.045319 902	QRICH1	0.498756 528	0.003773 074	0.045978 941	1.337441 037
MLIP	3.438048 601	3.64304 E-06	9.51196 E-05	4.021729 94	HINT2	0.467810 363	0.003791 596	0.046158 73	1.335746 151
POLE4	0.825977 206	3.6465E- 06	9.51196 E-05	4.021729 94	LGALS7B	1.066919 088	0.003814 568	0.046393 247	1.333545 227
MAGEH1	0.599603 951	3.67192 E-06	9.56809 E-05	4.019174 596	THNSL2	0.668342 888	0.003817 548	0.046393 247	1.333545 227
ARMC9	0.685960 114	3.77504 E-06	9.81589 E-05	4.008070 129	STRA13	0.381086 618	0.003820 331	0.046393 247	1.333545 227
CHADL	1.334148 765	3.81182 E-06	9.90103 E-05	4.004319 407	URM1	0.368006 617	0.003817 349	0.046393 247	1.333545 227
WASH3P	0.656000 912	3.8532E- 06	9.99791 E-05	4.000090 828	MPC1	0.284850 359	0.003818 939	0.046393 247	1.333545 227
HNRNPC	0.401104 569	4.04113 E-06	0.000104 634	3.980328 688	CWC15	0.323568 761	0.003826 898	0.046449 967	1.333014 587
OSTC	0.524619 758	4.05896 E-06	0.000104 984	3.978875 298	ARL3	0.421635 24	0.003843 26	0.046602 387	1.331591 842
PTPMT1	0.672026 157	4.06631 E-06	0.000105 063	3.978548 377	PMP22	0.128996 819	0.003849 263	0.046629 000	1.331343 895
EXT2	0.892300 487	4.12748 E-06	0.000106 532	3.972521 423	KIAA0513	1.398183 346	0.003862 096	0.046738 228	1.330327 753
GNB2L1	0.162897 84	4.15415 E-06	0.000107 107	3.970181 346	SEC23A	0.548068 702	0.003915 851	0.047365 362	1.324539 138
RPS27A	0.108491 771	4.2004E- 06	0.000108 186	3.965829 731	HM13	0.345783 412	0.003941 551	0.047652 686	1.321912 615

ATP6V1D	0.552772 045	4.2615E- 06	0.000109 624	3.960095 686	ARHGEF6	1.491312 265	0.003963 289	0.047891 865	1.319738 25
QDPR	0.497434 944	4.26518 E-06	0.000109 624	3.960095 686	FN1	0.467027 009	0.004006 263	0.048315 811	1.315910 728
UNC93B1	0.694101 214	4.2759E- 06	0.000109 784	3.959460 87	IL34	2.281309 128	0.004018 113	0.048434 876	1.314841 806
DHRS7	0.438496 56	4.29035 E-06	0.000110 04	3.958450 969	SSH1	0.506762 445	0.004034 799	0.048612 081	1.313255 787
CASP4	0.779087 543	4.32549 E-06	0.000110 744	3.955681 17	ABCA2	0.641017 556	0.004094 118	0.049278 289	1.307344 382
UBE4A	0.579939 842	4.32684 E-06	0.000110 744	3.955681 17	WBP11	0.367152 512	0.004098 567	0.049307 607	1.307086 072
STX7	0.476404 876	4.37185 E-06	0.000111 779	3.951640 731	CDCA7L	0.770933 807	0.004132 821	0.049670 906	1.303897 917
BST1	0.960110 962	4.57712 E-06	0.000116 905	3.932166 652	SMG1P2	0.602243 245	0.004142 227	0.049735 151	1.303336 559
MGP	1.894036 293	4.58608 E-06	0.000117 012	3.931769 996	ZNF749	0.404445 171	0.004141 157	0.049735 151	1.303336 559
YPEL5	0.652892 59	4.62534 E-06	0.000117 891	3.928520 096	SUN2	0.566820 92	0.004154 227	0.049830 379	1.302505 808

Table 2: DevMel classifier performance and program genes from FIG. 4B-C.

prg[NEO]						
			Average expression in each developmental group			
gene	correlation	correlation coefficient	MSC	FET	NEO	ADT
SLCO4A1	positive	0.090387866	1.2641387	2.2223482	4.4089575	2.9625027
MAD1L1	positive	0.088423595	1.574745	2.4751017	3.734714	2.4787169
ZNF330	positive	0.082257025	1.4132726	2.2405398	2.908652	1.4611392
ARSI	positive	0.080429129	0.45168975	0.32408157	1.913959	0.8914525
BECN1	positive	0.071492493	1.1748694	1.7884659	3.2874742	1.8919536
HPSE2	positive	0.068503164	0.08345231	0.32956576	0.36913574	0.019688668
SERPINF1	positive	0.065788649	4.8836894	6.648149	6.917258	0.51705354
RAB38	positive	0.057122298	1.5772153	4.2450595	5.9825363	3.1496892
YIPF1	positive	0.056810245	0.8221121	0.91739696	1.6859776	0.6793742
MICAL2	positive	0.053889818	0.055973977	0.23363082	0.6947131	0.18538292
CRYM	positive	0.045158569	1.5019817	2.1356192	4.3455877	3.3008857
SPG21	positive	0.039370753	2.4692748	2.7790964	4.120765	2.6216724
AIG1	positive	0.03902632	0.8168259	1.0098033	2.6221852	2.12121
TMEM204	positive	0.03674816	1.6701108	2.921409	3.8727286	1.953419
OSGEP	positive	0.033427302	0.9557276	1.2769252	1.6479856	0.65386707
PKIG	positive	0.032207351	1.548999	2.218216	2.5356324	1.4581879
XPNPEP1	positive	0.032172151	1.3597461	1.963225	2.756986	0.8228575
PNP	positive	0.031229842	0.59185636	1.2257788	0.8961103	0.35904828
MDH1	positive	0.029996442	3.651967	4.0780215	5.0006723	3.1776147
LOC100506207	positive	0.029380322	0.05932809	0.07873423	0.14590637	0.08275345
TMEM192	positive	0.028370077	0.9477396	1.5735964	2.2449844	1.407366
EDNRB	positive	0.026418285	2.7628288	5.784856	6.4040513	4.214343
TBC1D22A	positive	0.025291344	0.58803004	0.9796431	1.603178	0.80322593
SNAP29	positive	0.024973786	1.549973	1.7450494	2.1002898	1.0529053
ATPAF2	positive	0.023587655	0.7748545	1.0627764	1.2049105	0.5101456
PIGF	positive	0.021800861	1.2482812	1.3904904	2.333466	0.9272668
SMIM10	positive	0.020101931	0.07572515	0.72577757	1.076914	1.0465267
RASSF3	positive	0.020095265	1.4990807	2.636765	3.3724935	1.1099204
SURF1	positive	0.019730411	0.9887694	2.2500045	3.0078278	1.9837278
CA14	positive	0.019581549	1.5182956	4.2730937	5.2114754	2.786004
PSMC2	positive	0.018524449	2.3387544	2.5367527	3.2294247	1.8619167
OGFRL1	positive	0.015771769	0.29537252	0.24070978	0.23712452	0.20464727
CHAF1A	positive	0.014102879	0.5736362	0.5822738	0.6266711	0.3423366
TMEM120A	positive	0.013812479	1.1263111	2.714449	3.186496	2.2905407
C3orf79	positive	0.013760562	1.4406384	4.0078783	4.3267064	0.6375698
ALDH9A1	positive	0.013119848	1.695161	1.8958144	2.7588363	0.9460103
TM2D3	positive	0.012048749	2.0711215	1.5586205	2.470953	1.3085501
NIT2	positive	0.012037567	1.4372725	2.274058	2.948152	1.2818611
MFF	positive	0.011782891	2.2005944	2.5820446	3.6633673	1.8016573
SEC11C	positive	0.011070455	1.7599106	3.025719	4.482602	2.413646

WDSUB1	positive	0.010225798	0.51219493	0.9197637	1.0488262	0.43562293
SWI5	positive	0.008850762	0.8228434	1.1968639	1.7355535	0.78589004
LOC100128239	positive	0.007376726	0.05231487	0.061804365	0.2155686	0.048798792
CIDEA	positive	0.007167832	0	0.002457799	0.15804134	0.03021288
SRA1	positive	0.006507153	2.0325682	1.9060123	2.996753	1.5445827
CDSN	positive	0.005387611	0	0.002998606	0.017288228	0.035618667
PTN	positive	0.005049676	1.2579261	0.8591071	1.7545797	0.64777094
POLR3C	positive	0.003192311	1.1535691	1.0163639	1.4843215	0.6954018
HSD3B7	positive	0.001688014	0.33113748	0.57711715	0.75472283	0.28170633
PRMT2	positive	0.000903664	3.6686363	4.337189	5.0091147	3.184627
RSU1	positive	0.000878775	2.8472228	3.101452	4.2101083	2.657136
CXorf65	positive	0.000235604	0.066014014	0.19770019	0.2718642	0.06323015
PIGH	positive	0.00012663	1.2143983	1.1305461	2.4842274	1.4027914
TMEM47	negative	-0.000138397	0.69669145	0.067746066	0.01837892	1.41113984
COL4A1	negative	-0.000919739	3.5493493	0.9515583	0.08015933	0.5023679
GADD45B	negative	-0.003297595	2.5731995	1.2874947	0.070805416	0.553457
ZNF292	negative	-0.003308671	2.7704186	1.5917178	1.297286	1.192457
DUSP1	negative	-0.004282618	3.3223352	2.9337955	0.6719816	0.38588747
ZNF611	negative	-0.005172588	0.9284777	0.435658	0.40290838	0.30054748
LGALS7B	negative	-0.006083135	0.22598274	0.17045487	0.2373416	0.6022198
CRABP1	negative	-0.010406487	3.9758992	0.15768035	0.35247055	4.6406727
GIGYF1	negative	-0.011564057	2.5608938	2.1389678	1.2187794	1.5760902
NOTCH2NL	negative	-0.01182266	1.9714447	2.5837905	1.1206172	1.4002622
S100A6	negative	-0.019262059	4.9298663	3.5497944	2.7664566	5.426575
KIF1A	negative	-0.020587912	1.215462	0.9164256	0.24859013	1.746996
CLU	negative	-0.024498215	0.092144996	0.047891695	0.025947277	4.33635
COL1A2	negative	-0.04516096	7.69115	4.45441	0.6376246	0.38812172
FOS	negative	-0.050811801	5.7766986	6.3614197	2.3022602	1.8408839
LYPD1	negative	-0.08372236	1.1204109	3.3728514	0.007065248	0.004874161

Table 3. Melanoma dedifferentiation analysis gene set from FIG. 6C–G.

All 511 genes in dedifferentiation analysis.

source: gene was identified via melanoma group differential expression analysis (diff_exp), DevMel logistical regression analysis (logit) or by both methods (both).

pattern: type of dedifferentiation pattern

gene	source	pattern	gene	source	pattern
DUSP6	diff_exp	direct	TMEM120A	logit	sequential
EGR1	diff_exp	direct	TMEM192	logit	sequential
HMG2	diff_exp	direct	TMEM204	logit	sequential
KRT18	diff_exp	direct	VNT5A	logit	sequential
NT5DC3	diff_exp	direct	XPBPEP1	logit	sequential
PCOLCE	diff_exp	direct	YIPF1	logit	sequential
SERPING1	diff_exp	direct	ZNF330	logit	sequential
AXL	logit	direct	ZNF517	logit	sequential
CYR61	logit	direct	APOE	both	no_pattern
DHRS3	logit	direct	FOS	both	no_pattern
DUSP1	logit	direct	TIMP3	both	no_pattern
IER2	logit	direct	ADRBK2	diff_exp	no_pattern
MGP	logit	direct	AEBP1	diff_exp	no_pattern
MOXD1	logit	direct	ANXA1	diff_exp	no_pattern
PSAT1	logit	direct	APOC2	diff_exp	no_pattern
RAB3B	logit	direct	ASAP1	diff_exp	no_pattern
CHADL	logit	down regulated	ATP1A1	diff_exp	no_pattern
CRABP1	logit	down regulated	ATP5B	diff_exp	no_pattern
EMX2	logit	down regulated	ATP5G2	diff_exp	no_pattern
KIF1A	logit	down regulated	BRIX1	diff_exp	no_pattern
KRT1	logit	down regulated	BZW2	diff_exp	no_pattern
MAP6	logit	down regulated	C1QBP	diff_exp	no_pattern
POU3F3	logit	down regulated	CALU	diff_exp	no_pattern
SEPT4	logit	down regulated	CCT2	diff_exp	no_pattern
SFTPC	logit	down regulated	CD47	diff_exp	no_pattern
TMEM47	logit	down regulated	CD58	diff_exp	no_pattern
TRIM29	logit	down regulated	CD63	diff_exp	no_pattern
C3orf79	logit	not_readopted	CD68	diff_exp	no_pattern
COL21A1	logit	not_readopted	CDH19	diff_exp	no_pattern

COL23A1	logit	not_readopted		CHCHD2	diff_exp	no_pattern
COL5A1	logit	not_readopted		CNRIP1	diff_exp	no_pattern
LIMS2	logit	not_readopted		CS	diff_exp	no_pattern
PAMR1	logit	not_readopted		CSNK2B	diff_exp	no_pattern
RADIL	logit	not_readopted		CTSB	diff_exp	no_pattern
APOD	both	sequential		DDX5	diff_exp	no_pattern
ARHGDIB	both	sequential		EEA1	diff_exp	no_pattern
CA14	both	sequential		EEF1B2	diff_exp	no_pattern
CAPG	both	sequential		EEF1D	diff_exp	no_pattern
COL1A1	both	sequential		EGFL3	diff_exp	no_pattern
COL1A2	both	sequential		EIF2S3	diff_exp	no_pattern
FXYD3	both	sequential		EIF3E	diff_exp	no_pattern
HLA-B	both	sequential		EIF3K	diff_exp	no_pattern
ID3	both	sequential		EIF3M	diff_exp	no_pattern
IFI27	both	sequential		EMP1	diff_exp	no_pattern
LGALS3	both	sequential		ESRP1	diff_exp	no_pattern
MAD1L1	both	sequential		FAM178B	diff_exp	no_pattern
MT2A	both	sequential		FARSA	diff_exp	no_pattern
NGFRAP1	both	sequential		FBXO32	diff_exp	no_pattern
NREP	both	sequential		FLNA	diff_exp	no_pattern
RAB38	both	sequential		FOXRED2	diff_exp	no_pattern
RASSF3	both	sequential		GAS5	diff_exp	no_pattern
S100A6	both	sequential		GNB2L1	diff_exp	no_pattern
SERPINF1	both	sequential		GPM6B	diff_exp	no_pattern
TCF4	both	sequential		GNPMB	diff_exp	no_pattern
TSC22D3	both	sequential		GRN	diff_exp	no_pattern
A2M	diff_exp	sequential		HLA-G	diff_exp	no_pattern
ABR	diff_exp	sequential		HMGB1	diff_exp	no_pattern
ACP5	diff_exp	sequential		HN1	diff_exp	no_pattern
ADSL	diff_exp	sequential		IGFBP7	diff_exp	no_pattern
AHCY	diff_exp	sequential		ILF2	diff_exp	no_pattern
AHNAK	diff_exp	sequential		IMPDH2	diff_exp	no_pattern
ATP1B1	diff_exp	sequential		ITGB3	diff_exp	no_pattern
B2M	diff_exp	sequential		ITGB8	diff_exp	no_pattern
BCAN	diff_exp	sequential		JUN	diff_exp	no_pattern
BTF3	diff_exp	sequential		KCNAB2	diff_exp	no_pattern
C12orf57	diff_exp	sequential		KIF17	diff_exp	no_pattern
C19orf53	diff_exp	sequential		KLHDC8B	diff_exp	no_pattern
CAV1	diff_exp	sequential		LAMP2	diff_exp	no_pattern
CCT3	diff_exp	sequential		LDHB	diff_exp	no_pattern
CD151	diff_exp	sequential		LGALS1	diff_exp	no_pattern
CD59	diff_exp	sequential		LGALS3BP	diff_exp	no_pattern
CHP1	diff_exp	sequential		LRPAP1	diff_exp	no_pattern
CSPG4	diff_exp	sequential		MAGEA4	diff_exp	no_pattern
CST3	diff_exp	sequential		MARCKS	diff_exp	no_pattern
CTSD	diff_exp	sequential		MDH2	diff_exp	no_pattern
CYC1	diff_exp	sequential		MID1	diff_exp	no_pattern
DAG1	diff_exp	sequential		MTRNR2L1	diff_exp	no_pattern
DCI	diff_exp	sequential		MTRNR2L3	diff_exp	no_pattern
DUSP4	diff_exp	sequential		MTRNR2L6	diff_exp	no_pattern
EEF1A1	diff_exp	sequential		MTRNR2L8	diff_exp	no_pattern
EEF1G	diff_exp	sequential		MYL6	diff_exp	no_pattern
EIF3G	diff_exp	sequential		NAP1L1	diff_exp	no_pattern
EIF3H	diff_exp	sequential		NDUFS5	diff_exp	no_pattern
EIF3L	diff_exp	sequential		NEAT1	diff_exp	no_pattern
EIF4EBP2	diff_exp	sequential		NF2	diff_exp	no_pattern
ERRF1	diff_exp	sequential		NME1	diff_exp	no_pattern
FAM174B	diff_exp	sequential		NPM1	diff_exp	no_pattern
FAU	diff_exp	sequential		NR4A1	diff_exp	no_pattern
FBL	diff_exp	sequential		NSG1	diff_exp	no_pattern
GAA	diff_exp	sequential		NUDT1	diff_exp	no_pattern
GALE	diff_exp	sequential		OXA1L	diff_exp	no_pattern
GLOD4	diff_exp	sequential		PABPC1	diff_exp	no_pattern
GPC3	diff_exp	sequential		PERP	diff_exp	no_pattern
GPI	diff_exp	sequential		PFN1	diff_exp	no_pattern
GPR155	diff_exp	sequential		PGAM1	diff_exp	no_pattern

GSN	diff_exp	sequential		PKM	diff_exp	no_pattern
GSTO1	diff_exp	sequential		PKNOX2	diff_exp	no_pattern
H3F3A	diff_exp	sequential		PLTP	diff_exp	no_pattern
HLA-A	diff_exp	sequential		POLR2l	diff_exp	no_pattern
HLA-C	diff_exp	sequential		PPA1	diff_exp	no_pattern
HLA-E	diff_exp	sequential		PPIA	diff_exp	no_pattern
HLA-F	diff_exp	sequential		PRDX2	diff_exp	no_pattern
HLA-H	diff_exp	sequential		PSMB6	diff_exp	no_pattern
HNRNPA1	diff_exp	sequential		PTP4A3	diff_exp	no_pattern
HNRNPA1P10	diff_exp	sequential		RPL10	diff_exp	no_pattern
IDH2	diff_exp	sequential		RPL10A	diff_exp	no_pattern
IFI6	diff_exp	sequential		RPL11	diff_exp	no_pattern
IGF2BP1	diff_exp	sequential		RPL12	diff_exp	no_pattern
ITGA3	diff_exp	sequential		RPL13A	diff_exp	no_pattern
LHFPL3-AS1	diff_exp	sequential		RPL13AP5	diff_exp	no_pattern
LSM7	diff_exp	sequential		RPL14	diff_exp	no_pattern
MATN2	diff_exp	sequential		RPL17	diff_exp	no_pattern
MFGE8	diff_exp	sequential		RPL18A	diff_exp	no_pattern
MIA	diff_exp	sequential		RPL19	diff_exp	no_pattern
MOB3B	diff_exp	sequential		RPL22	diff_exp	no_pattern
NACA	diff_exp	sequential		RPL26	diff_exp	no_pattern
NENF	diff_exp	sequential		RPL27	diff_exp	no_pattern
NOP56	diff_exp	sequential		RPL28	diff_exp	no_pattern
NPC1	diff_exp	sequential		RPL29	diff_exp	no_pattern
NPC2	diff_exp	sequential		RPL3	diff_exp	no_pattern
NPL	diff_exp	sequential		RPL39	diff_exp	no_pattern
OLA1	diff_exp	sequential		RPL6	diff_exp	no_pattern
PDE4DIP	diff_exp	sequential		RPL7A	diff_exp	no_pattern
PFDN5	diff_exp	sequential		RPL8	diff_exp	no_pattern
PIH1D1	diff_exp	sequential		RPL9	diff_exp	no_pattern
PPP1CB	diff_exp	sequential		RPLP0	diff_exp	no_pattern
PPP2R1A	diff_exp	sequential		RPLP1	diff_exp	no_pattern
PRMT1	diff_exp	sequential		RPLP2	diff_exp	no_pattern
PROS1	diff_exp	sequential		RPS10	diff_exp	no_pattern
PSAP	diff_exp	sequential		RPS12	diff_exp	no_pattern
PTMA	diff_exp	sequential		RPS16	diff_exp	no_pattern
RPL13	diff_exp	sequential		RPS17	diff_exp	no_pattern
RPL15	diff_exp	sequential		RPS19	diff_exp	no_pattern
RPL18	diff_exp	sequential		RPS21	diff_exp	no_pattern
RPL21	diff_exp	sequential		RPS25	diff_exp	no_pattern
RPL21P28	diff_exp	sequential		RPS28	diff_exp	no_pattern
RPL24	diff_exp	sequential		RPS3	diff_exp	no_pattern
RPL27A	diff_exp	sequential		RPS3A	diff_exp	no_pattern
RPL30	diff_exp	sequential		RPS4X	diff_exp	no_pattern
RPL31	diff_exp	sequential		RPS6	diff_exp	no_pattern
RPL32	diff_exp	sequential		RPS7	diff_exp	no_pattern
RPL35A	diff_exp	sequential		RPS9	diff_exp	no_pattern
RPL36	diff_exp	sequential		RPSA	diff_exp	no_pattern
RPL36A	diff_exp	sequential		S100B	diff_exp	no_pattern
RPL37	diff_exp	sequential		SAE1	diff_exp	no_pattern
RPL4	diff_exp	sequential		SCARB2	diff_exp	no_pattern
RPL41	diff_exp	sequential		SCCPDH	diff_exp	no_pattern
RPL7	diff_exp	sequential		SCD	diff_exp	no_pattern
RPS11	diff_exp	sequential		SCIN	diff_exp	no_pattern
RPS13	diff_exp	sequential		SDC3	diff_exp	no_pattern
RPS14	diff_exp	sequential		SERPINA3	diff_exp	no_pattern
RPS15	diff_exp	sequential		SET	diff_exp	no_pattern
RPS15A	diff_exp	sequential		SGK1	diff_exp	no_pattern
RPS18	diff_exp	sequential		SLC25A6	diff_exp	no_pattern
RPS20	diff_exp	sequential		SLC26A2	diff_exp	no_pattern
RPS23	diff_exp	sequential		SLC5A3	diff_exp	no_pattern
RPS24	diff_exp	sequential		SNAI2	diff_exp	no_pattern
RPS27	diff_exp	sequential		SNHG6	diff_exp	no_pattern
RPS27A	diff_exp	sequential		SNRPD1	diff_exp	no_pattern
RPS5	diff_exp	sequential		SNRPD2	diff_exp	no_pattern
RPS8	diff_exp	sequential		SNRPF	diff_exp	no_pattern

S100A1	diff_exp	sequential		SORD	diff_exp	no_pattern
S100A13	diff_exp	sequential		SQSTM1	diff_exp	no_pattern
SAMM50	diff_exp	sequential		SS18L1	diff_exp	no_pattern
SERPINE2	diff_exp	sequential		STOML2	diff_exp	no_pattern
SLC25A5	diff_exp	sequential		TIMP1	diff_exp	no_pattern
SMC4	diff_exp	sequential		TNFRSF14	diff_exp	no_pattern
SNRPE	diff_exp	sequential		TP11	diff_exp	no_pattern
SOAT1	diff_exp	sequential		TRMT112	diff_exp	no_pattern
SOX4	diff_exp	sequential		TUBB	diff_exp	no_pattern
SSBP1	diff_exp	sequential		TUBB4A	diff_exp	no_pattern
SSR2	diff_exp	sequential		TXNDC17	diff_exp	no_pattern
TAPBP	diff_exp	sequential		TYR	diff_exp	no_pattern
TIMM50	diff_exp	sequential		UBA52	diff_exp	no_pattern
TIMP2	diff_exp	sequential		UBC	diff_exp	no_pattern
TM4SF1	diff_exp	sequential		UBL5	diff_exp	no_pattern
TMC6	diff_exp	sequential		UQCRH	diff_exp	no_pattern
TP53	diff_exp	sequential		ABCG1	logit	no_pattern
TPM2	diff_exp	sequential		ADAT2	logit	no_pattern
TPM4	diff_exp	sequential		AFF3	logit	no_pattern
TPP1	diff_exp	sequential		ANK2	logit	no_pattern
TRPM1	diff_exp	sequential		ARSI	logit	no_pattern
U2AF1	diff_exp	sequential		ASXL1	logit	no_pattern
UQCRFS1	diff_exp	sequential		ATPAF2	logit	no_pattern
ZNF749	diff_exp	sequential		CCBE1	logit	no_pattern
AIG1	logit	sequential		CCND1	logit	no_pattern
ALDH9A1	logit	sequential		CCND2	logit	no_pattern
AMFR	logit	sequential		CD36	logit	no_pattern
AUTS2	logit	sequential		CDSN	logit	no_pattern
BDH1	logit	sequential		CEBPD	logit	no_pattern
BECN1	logit	sequential		CELF6	logit	no_pattern
BEX5	logit	sequential		CES1	logit	no_pattern
C14orf132	logit	sequential		CHAF1A	logit	no_pattern
CCDC3	logit	sequential		CHCHD3	logit	no_pattern
CD248	logit	sequential		CHD3	logit	no_pattern
CIDEA	logit	sequential		COL12A1	logit	no_pattern
CLDN11	logit	sequential		CRMP1	logit	no_pattern
CLU	logit	sequential		CRYM	logit	no_pattern
COL3A1	logit	sequential		CXorf65	logit	no_pattern
COL4A1	logit	sequential		FAM126A	logit	no_pattern
CXCL14	logit	sequential		FAM183A	logit	no_pattern
DAZAP2	logit	sequential		FSTL4	logit	no_pattern
DCN	logit	sequential		FUT11	logit	no_pattern
DNAJA1	logit	sequential		GADD45B	logit	no_pattern
EDNRB	logit	sequential		GBX2	logit	no_pattern
FBN1	logit	sequential		GIGYF1	logit	no_pattern
GAPDHS	logit	sequential		GTPBP2	logit	no_pattern
GFRA1	logit	sequential		HPSE2	logit	no_pattern
GPX1	logit	sequential		HSPB3	logit	no_pattern
HSD3B7	logit	sequential		IQGAP2	logit	no_pattern
IGFBP3	logit	sequential		ITGB5	logit	no_pattern
IGFBP5	logit	sequential		KLHL24	logit	no_pattern
ITPA	logit	sequential		LDHA	logit	no_pattern
KIAA1549L	logit	sequential		LGALS7B	logit	no_pattern
KRT13	logit	sequential		LOC100506207	logit	no_pattern
LAMTOR5	logit	sequential		LUM	logit	no_pattern
LOC100128239	logit	sequential		LYPD1	logit	no_pattern
LOC400043	logit	sequential		MEST	logit	no_pattern
LOXL2	logit	sequential		MICAL3	logit	no_pattern
LRRN4CL	logit	sequential		MLANA	logit	no_pattern
MARCH9	logit	sequential		MSX1	logit	no_pattern
MDH1	logit	sequential		NCKAP5	logit	no_pattern
MEG3	logit	sequential		NDRG2	logit	no_pattern
MFAP4	logit	sequential		NID1	logit	no_pattern
MFF	logit	sequential		NOTCH2NL	logit	no_pattern
MICAL2	logit	sequential		PIGF	logit	no_pattern
MIR205HG	logit	sequential		PIGH	logit	no_pattern

MMP2	logit	sequential		PKIG	logit	no_pattern
MT1M	logit	sequential		PLAT	logit	no_pattern
MT1X	logit	sequential		PNP	logit	no_pattern
NIT2	logit	sequential		PRKCE	logit	no_pattern
NKAPP1	logit	sequential		PTGDS	logit	no_pattern
OGFRL1	logit	sequential		PTN	logit	no_pattern
OLFML3	logit	sequential		RASGEF1C	logit	no_pattern
OSGEP	logit	sequential		RIC3	logit	no_pattern
OSR2	logit	sequential		SEC11C	logit	no_pattern
PHB	logit	sequential		SEMA4D	logit	no_pattern
PITHD1	logit	sequential		SESN3	logit	no_pattern
PLAU	logit	sequential		SH3PXD2A	logit	no_pattern
POLR3C	logit	sequential		SLCO4A1	logit	no_pattern
PPAP2B	logit	sequential		SPTSSA	logit	no_pattern
PRMT2	logit	sequential		SRA1	logit	no_pattern
PSMC2	logit	sequential		SURF1	logit	no_pattern
RSU1	logit	sequential		SWI5	logit	no_pattern
SH3BGRL	logit	sequential		TBX15	logit	no_pattern
SMIM10	logit	sequential		TMSB4X	logit	no_pattern
SNAP29	logit	sequential		TULP2	logit	no_pattern
SOX2	logit	sequential		TWIST2	logit	no_pattern
SPECC1	logit	sequential		TXNDC15	logit	no_pattern
SPG21	logit	sequential		WDSUB1	logit	no_pattern
SUSD3	logit	sequential		WIF1	logit	no_pattern
SYK	logit	sequential		WSCD1	logit	no_pattern
TBC1D22A	logit	sequential		ZNF292	logit	no_pattern
TGFB1	logit	sequential		ZNF582	logit	no_pattern
THY1	logit	sequential		ZNF611	logit	no_pattern
TM2D3	logit	sequential				

52 melanoma specific genes. Subsequent tabs/sheets have more information on each dedifferentiation pattern

gene	pattern
TMEM212	melanoma specific
MTRNR2L10	melanoma specific
MTRNR2L6	melanoma specific
MIR4461	melanoma specific
MTRNR2L4	melanoma specific
EIF3C	melanoma specific
MTRNR2L1	melanoma specific
MTRNR2L3	melanoma specific
DDX39B	melanoma specific
MTRNR2L2	melanoma specific
SHISA9	melanoma specific
SPC25	melanoma specific
MTRNR2L8	melanoma specific
PRAME	melanoma specific
HNRNPA1P10	melanoma specific
U2AF1	melanoma specific
BST2	melanoma specific
ASTN2	melanoma specific
UGDH-AS1	melanoma specific
RPL21P28	melanoma specific
UBE2V1	melanoma specific
ORC4	melanoma specific
PET100	melanoma specific
CCNG1	melanoma specific
SNHG8	melanoma specific
METTL21A	melanoma specific
CBX3	melanoma specific
HIST1H2BK	melanoma specific
SRSF1	melanoma specific
UTP11L	melanoma specific
H3F3AP4	melanoma specific
DDT	melanoma specific
SHC1	melanoma specific
MRPS6	melanoma specific

RPL13AP5						melanoma specific			
MRPS24						melanoma specific			
SEC61G						melanoma specific			
SLIRP						melanoma specific			
IVNS1ABP						melanoma specific			
RPS29						melanoma specific			
UBAP2L						melanoma specific			
TSNAX						melanoma specific			
SNHG6						melanoma specific			
BZW1						melanoma specific			
PFDN2						melanoma specific			
NDUFB3						melanoma specific			
PDCD5						melanoma specific			
FAM96B						melanoma specific			
LSM3						melanoma specific			
ROMO1						melanoma specific			
TBCA						melanoma specific			
UXT						melanoma specific			
NEO									
		relative expression (z-score of rank mean)				relative expression (z-score of rank mean)			
		normal melanocytes				melanoma			
type	gene	MSC	FET	NEO	ADT	MAL_M SC	MAL_FE T	MAL_NE O	MAL_A DT
full_s eq	DAZAP2	- 1.18588 8712	- 0.468149 963	0.884384 853	0.7696538 22	- 1.13797 136	- 0.517567 516	1.010444 786	0.64509 409
full_s eq	GAPDHS	- 0.96252 6958	- 0.740975 338	1.043502 768	0.6599995 28	- 1.19178 0115	- 0.412809 502	1.049169 832	0.55541 9784
full_s eq	LHFPL3- AS1	- 1.34546 6334	- 0.170739 255	0.832697 553	0.6835080 37	- 0.97017 5463	- 0.391612 944	1.380238 554	- 0.01845 0146
full_s eq	SPG21	- 0.78455 7454	- 0.532908 3	1.443787 123	- 0.1263213 69	- 0.56275 4887	- 0.522257 705	1.496950 549	- 0.41193 7957
full_s eq	TBC1D22A	- 1.09225 3982	- 0.272970 341	1.315284 947	0.0499393 75	- 1.04643 6931	- 0.622761 864	1.083622 59	0.58557 6205
full_s eq	TMEM192	- 1.14346 1446	- 0.266539 881	1.265090 185	0.1449111 42	- 1.27382 1593	- 0.300643 546	0.941378 231	0.63308 6908
full_s eq	SH3BGRL	- 0.00490 6542	- 1.394233 178	0.896158	0.5029817 21	- 0.65569 7952	- 1.048261 505	0.950643 538	0.75331 592
full_s eq	ABR	- 1.24827 4643	0.155848 716	1.186847 177	- 0.0944212 5	- 0.83646 7297	- 0.081938 497	1.426641 252	- 0.50823 5459
full_s eq	BCAN	- 1.32770 7642	0.315554 455	1.065268 316	0.0531151 29	- 1.02956 8156	0.319404 168	1.245532 426	- 0.53536 8438
full_s eq	CA14	- 1.10878 7186	0.197794 115	1.266827 01	- 0.3558339 39	- 0.90508 7914	- 0.007456 413	1.395524 977	- 0.48298 065
full_s eq	FAM174B	- 0.92759 0307	0.804701 905	0.922977 8	- 0.8000893 98	- 1.05967 5872	0.225290 927	1.276911 01	- 0.44252 6064
full_s eq	LRRN4CL	- 0.85869 8523	0.458008 291	1.193468 704	- 0.7927784 72	- 1.33728 5705	0.224996 631	1.076937 186	0.03535 1888
full_s eq	NPL	- 0.70523 9094	- 0.098025 55	1.443364 477	- 0.6400998 34	- 0.60733 6324	- 0.286981 197	1.483711 332	- 0.58939 3812
full_s eq	TRPM1	- 1.26021 2523	0.647644 875	0.940634 26	- 0.3280666 12	- 1.11816 8938	0.089522 787	1.292984 569	- 0.26433 8419

full_s eq	ZNF749	- 0.78722 9167	- 0.336089 816	1.466201 117	- 0.3428821 33	- 0.78282 6612	0.194230 41	1.337426 64	- 0.74883 0438
full_s eq	TM2D3	0.29436 5733	- 1.057501 847	1.248704 233	- 0.4855681 18	0.47963 7707	- 1.451600 649	0.794564 721	0.17739 8221
full_s eq	RASSF3	- 0.68111 7389	0.204124 803	1.329516 733	- 0.8525241 48	- 0.73682 6984	0.157969 146	1.353523 263	- 0.77466 5425
full_s eq	EIF3L	0.48403 9818	0.361578 133	0.644297 357	- 1.4899153 08	0.70951 3803	- 0.624579 427	0.982931 217	- 1.06786 5593
full_s eq	NOP56	0.30698 0883	0.225858 424	0.898224 465	- 1.4310637 72	0.10205 0941	- 0.118372 361	1.227882 071	- 1.21156 065
full_s eq	TIMM50	0.62791 5975	0.087624 29	0.724367 7	- 1.4399079 65	0.09216 1075	- 0.005363 326	1.178834 868	- 1.26563 2618
max_ seq	BDH1	- 1.05137 7355	- 0.327433 226	1.336256 831	0.0425537 49	0.67965 3151	- 1.351181 973	0.829172 655	- 0.15764 3833
max_ seq	BECN1	- 1.01476 8858	- 0.443869 291	1.324890 897	0.1337472 51	- 0.73986 3565	- 0.980814 975	0.931881 471	0.78879 7069
max_ seq	CIDEA	- 0.76589 8216	- 0.661316 657	1.405557 238	0.0216576 35	- 0.55870 8742	0.123873 048	1.352750 171	- 0.91791 4476
max_ seq	DCT	- 1.40210 0891	- 0.010389 704	0.841227 342	0.5712632 52	- 1.16156 0263	0.308038 469	1.198654 779	- 0.34513 2985
max_ seq	GLOD4	- 0.93242 3751	- 0.244487 383	1.418591 688	- 0.2416805 54	0.50560 5767	- 0.520863 873	1.119597 404	- 1.10433 9299
max_ seq	LOC10012 8239	- 0.78177 9442	- 0.359744 808	1.467385 17	- 0.3258609 2	- 1.35912 2574	0.717424 44	0.785714 507	- 0.14401 6373
max_ seq	MAD1L1	- 1.27957 6057	- 0.221151 38	1.056701 573	0.4440258 63	- 0.18172 3113	- 0.996607 034	1.389015 11	- 0.21068 4963
max_ seq	PITHD1	- 1.08152 3843	- 0.551722 738	1.126591 837	0.5066547 44	- 0.59990 4382	- 0.731980 084	1.446122 268	- 0.11423 7802
max_ seq	RSU1	- 0.65348 0409	- 0.509212 485	1.486260 426	- 0.3235675 32	0.46963 0412	- 0.591084 463	1.161338 421	- 1.03988 4371
max_ seq	TMEM120A	- 1.46818 972	0.246324 753	0.747435 348	0.4744296 2	- 0.50263 0228	- 1.046794 072	1.249700 146	0.29972 4155
max_ seq	YIPF1	- 0.58047 3973	- 0.463518 824	1.497506 467	- 0.4535136 7	0.00790 1981	- 0.813498 724	1.410902 288	- 0.58950 1584
max_ seq	ACP5	- 1.06603 3642	0.524690 336	1.119714 066	- 0.5783707 6	- 1.13525 6907	- 0.159403 708	1.298371 458	- 0.00371 0843
max_ seq	CYC1	- 1.20232 5152	0.394202 507	1.136347 983	- 0.3282253 38	0.09461 5849	0.181009 748	1.070553 573	- 1.34617 9171
max_ seq	EDNRB	- 1.11650 433	0.365562 994	1.193341 481	- 0.4424001 45	- 1.29143 7365	- 0.012069 393	1.142914 72	0.16059 2038
max_ seq	GALE	- 1.17137 2214	0.759215 416	0.901255 525	- 0.4890987 28	- 0.65562 153	- 0.422357 603	1.490502 824	- 0.41252 3691
max_ seq	GPI	- 1.04664 9233	0.466988 893	1.161163 545	- 0.5815032 05	- 0.00458 1086	0.180139 954	1.127152 283	- 1.30271 1151
max_ seq	GSTO1	- 1.00028 8989	0.170113 727	1.316721 641	- 0.4865463 79	0.50455 7122	- 1.004563 459	1.147575 226	- 0.64756 8889

max_ seq	LAMTOR5	- 1.14326 2916	0.826016 247	0.851560 684	- 0.5343140 15	0.44307 961	- 1.498794 405	0.531660 493	0.52405 4301
max_ seq	MFF	- 0.61244 9935	- 0.297915 55	1.485175 156	- 0.5748096 71	0.34725 3073	- 0.905821 53	1.254708 059	- 0.69613 9601
max_ seq	MICAL2	- 0.90289 2535	- 0.214765 797	1.428909 809	- 0.3112514 76	0.17983 1964	- 0.704598 071	1.342547 923	- 0.81778 1816
max_ seq	MOB3B	- 0.86243 9448	0.092870 169	1.372573 811	- 0.6030045 31	- 0.37592 9249	- 0.083928 213	1.401657 968	- 0.94180 0507
max_ seq	POLR3C	- 0.66541 1437	- 0.369535 717	1.488327 111	- 0.4533799 57	0.83052 5926	- 0.498753 803	0.835721 387	- 1.16749 3509
max_ seq	RAB38	- 0.95591 4532	- 0.117810 382	1.401705 08	- 0.3279801 66	- 1.12223 951	- 0.331375 367	1.262657 578	0.19095 7299
max_ seq	SLC25A5	- 0.95784 2536	0.519278 34	1.145758 866	- 0.7071946 7	0.28840 5146	- 0.159811 548	1.136331 075	- 1.26492 4673
max_ seq	SOAT1	- 0.89118 3942	0.115200 179	1.360474 452	- 0.5844906 89	- 0.90686 3132	- 0.267965 925	1.428747 36	- 0.25391 8303
max_ seq	TMEM204	- 0.99411 207	- 0.039354 619	1.375850 83	- 0.3423841 41	- 0.15060 9172	- 0.243377 012	1.388729 63	- 0.99474 3446
max_ seq	UQCRCF5	- 0.88301 0168	0.475678 479	1.181178 881	- 0.7738471 92	- 0.28699 8638	0.164081 48	1.262115 636	- 1.13919 8478
max_ seq	ZNF330	- 0.91825 8934	- 0.027804 435	1.397290 711	- 0.4512273 42	- 0.81034 4027	- 0.542690 568	1.429338 059	- 0.07630 3464
max_ seq	NENF	0.57163 4256	- 1.462759 305	0.706826 344	0.1842987 04	- 0.94913 6737	- 0.264153 126	1.410798 659	- 0.19750 8795
max_ seq	ADSL	- 0.60287 7048	0.688394 617	0.996230 024	- 1.0817475 93	0.07311 4259	- 0.044598 927	1.208905 994	- 1.23742 1326
max_ seq	AHCY	0.36919 8053	0.437618 684	0.679805 844	- 1.4866225 81	0.49020 0814	- 0.154621 883	0.989683 78	- 1.32526 271
max_ seq	ALDH9A1	- 0.50280 1875	0.111978 687	1.348294 864	- 0.9574716 75	- 0.75830 2506	- 0.019486 76	1.418972 18	- 0.64118 2914
max_ seq	CCT3	- 0.38810 5377	0.360291 908	1.179920 706	- 1.1521072 37	0.60994 0782	- 0.224169 201	0.925888 216	- 1.31165 9797
max_ seq	CHP1	- 0.56991 8301	0.348774 548	1.235093 367	- 1.0139496 14	- 0.82891 7775	0.260568 894	1.304833 284	- 0.73648 4403
max_ seq	DNAJA1	0.32641 0082	0.521423 597	0.639606 296	- 1.4874399 74	0.74986 8573	- 0.786887 006	0.971877 136	- 0.93485 8703
max_ seq	EIF3H	0.30492 6235	0.443108 642	0.728456 288	- 1.4764911 65	0.46568 9488	- 0.053741 23	0.954929 505	- 1.36687 7763
max_ seq	GPX1	- 0.85885 3055	0.859212 482	0.872782 278	- 0.8731417 05	0.64905 4486	- 1.425443 868	0.738514 415	0.03787 4967
max_ seq	HSD3B7	- 0.60945 3959	0.185347 759	1.331043 503	- 0.9069373 04	- 0.82926 129	- 0.799506 211	1.230721 201	0.39804 63
max_ seq	ITPA	- 0.49180 6299	0.756547 915	0.904624 311	- 1.1693659 28	0.17826 4196	- 0.153313 046	1.200868 092	- 1.22581 9241
max_ seq	MDH1	- 0.52198 5049	- 0.392847 509	1.495381 389	- 0.5805488 31	- 0.44652 868	- 1.059385 845	1.274696 897	0.23121 7628

max_ seq	NIT2	- 0.69385 3422	0.075392 207	1.386643 32	- 0.7681821 06	- 0.26684 2495	- 0.865219 779	1.443358 704	- 0.31129 643
max_ seq	OSGEP	- 0.67689 0598	- 0.058057 026	1.432456 088	- 0.6975084 63	- 0.11067 5375	- 0.972542 707	1.394612 833	- 0.31139 475
max_ seq	PHB	- 0.28751 77	0.727108 779	0.850724 483	- 1.2903155 62	0.06348 7828	- 0.937692 817	1.368387 707	- 0.49418 2718
max_ seq	PPP2R1A	- 0.75679 2312	0.729438 119	0.987024 748	- 0.9596705 55	0.44546 7491	- 0.299158 75	1.089033 143	- 1.23534 1884
max_ seq	PRMT2	- 0.71718 783	0.206552 988	1.330632 144	- 0.8199973 03	- 1.17872 9215	- 0.479820 755	0.879152 236	0.77939 7734
max_ seq	PSMC2	- 0.53358 6863	- 0.323004 886	1.487559 343	- 0.6309675 94	0.67541 2059	- 1.367809 169	0.811606 842	- 0.11920 9732
max_ seq	SAMM50	- 0.52359 1428	- 0.422759 322	1.497708 61	0.5513578 61	- 0.08894 8927	- 0.364247 298	1.400633 586	- 0.94743 7361
max_ seq	SERPINF1	- 0.00227 2055	0.589767 297	0.819714 108	- 1.4072093 5	0.24890 3954	- 0.234265 861	0.934518 785	- 1.41768 8601
max_ seq	TMC6	- 0.79925 1165	0.482158 291	1.177969 561	- 0.8608766 87	- 0.72671 7754	- 0.205730 438	1.464929 878	- 0.53248 1687
max_ seq	XPNPEP1	- 0.74810 328	0.344155 438	1.260348 049	- 0.8564002 06	- 0.08769 9455	- 0.720486 063	1.440101 138	- 0.63191 5621
max_ seq	EEF1A1	0.35221 4988	- 0.408484 934	1.191642 924	- 1.1353729 79	0.72630 6555	- 1.300297 36	0.842410 941	- 0.26842 0136
max_ seq	SNAP29	0.55544 5472	0.060032 448	0.809952 835	- 1.4254307 55	- 1.19527 4337	0.019890 445	1.251077 197	- 0.07569 3305

Table 4. MALDevMel enriched genes and gene lists from FIG. 8C, G-H. Differentially expressed genes were determined by Two-sided Wilcoxon Rank Sum Test. Adjusted p-value computed using Benjamini-Hochberg multiple testing

Genes upregulated in MAL_NEO compared to rest of MAL groups

gene	logfol dchan ge	pval s_a dj	gene	logfol dchan ge	pvals _adj	gene	logfol dchan ge	pvals _adj	gene	logfol dchan ge	pvals _adj
SERPI NF1	4.9932 37	1.05 004 E-72	EXOC6	1.0273 753	4.748 94E- 07	COTL1	0.7078 207	0.000 23779 7	ZNF34 6	0.3867 1035	0.005 60084
PABPC 1	1.4770 935	4.07 258 E-50	RAD50	0.6040 2215	4.773 83E- 07	RARS	0.6663 8744	0.000 23785 7	TMEM 144	1.2119 049	0.005 61027 8
DCT	4.3615 58	1.90 234 E-47	FRMD4 B	1.1913 458	4.789 55E- 07	PATZ1	0.7964 412	0.000 23839 4	PMPC B	0.4740 0528	0.005 61781 1
TIMM5 0	2.2546 065	6.63 636 E-44	C10orf7 6	0.6018 952	4.877 62E- 07	INTS4	0.6460 5004	0.000 23898 3	PRKC A	0.1127 5025	0.005 62521 6
CA14	3.0168 433	8.54 592 E-40	PHC1	0.6281 601	4.892 31E- 07	CDAN1	0.2312 2744	0.000 24033 9	DPM2	0.4800 1775	0.005 62604
SCD	2.4233 62	1.83 385 E-39	ARPC1 A	1.0393 581	4.916 57E- 07	ATP6V OD1	0.7670 744	0.000 24149 7	KIAA20 26	0.1488 4436	0.005 63359 3
RPS19	1.8123 778	4.99 667 E-38	PDZRN 3	1.2931 554	4.945 07E- 07	FBXO2 2	0.5861 248	0.000 24199	NDUF A8	0.7160 7715	0.005 64404 5
RPL29	1.3152 49	4.43 932 E-37	SMARC C1	0.5960 095	4.968 21E- 07	GTF2H 1	0.5295 4686	0.000 24313 4	RPUS D4	0.4021 0626	0.005 66017

C17orf76-AS1	2.2633824	5.16619E-37	CRELD2	1.1421188	4.9887E-07	C9orf72	0.7952383	0.000243579	CTR9	0.46758485	0.00566017
BCAN	3.055299	8.16218E-37	CDS2	0.64481163	4.9954E-07	MRPL28	0.7758654	0.000245303	SSTR2	0.61892486	0.005664864
TRPM1	2.6077154	1.20004E-35	AK3	0.5488157	5.03968E-07	CLP1	0.9187167	0.000248008	CYB5A	0.5893577	0.005672465
KIF17	2.547519	5.10735E-35	TMEM165	0.9960775	5.05485E-07	UTP6	0.59848946	0.000250772	TMEM25	1.4717149	0.005675232
RPS24	1.3673493	4.45449E-34	THAP9-AS1	0.7266423	5.14359E-07	ZNF446	0.8128664	0.000251123	TMTC3	0.06458122	0.005687694
RPL28	1.3948458	1.1329E-33	CCT6A	0.9529907	5.1705E-07	RAB11FIP2	0.6871822	0.000251261	EDC3	0.26907957	0.005715755
ADRBK2	1.4972956	1.2389E-33	MRPL45	0.9010318	5.17889E-07	CCDC58	0.35267478	0.000251346	ST3GAL3	0.3570663	0.005748701
KCNA B2	2.1000416	3.12254E-33	NKIRAS2	0.75091773	5.19447E-07	DHRS4	0.61167526	0.000253305	LYSMD4	1.2798384	0.005804514
PFN1	1.3591379	3.85214E-33	PMS2P1	0.71415675	5.19857E-07	RENB P	1.1141849	0.000254469	PIGW	0.22865053	0.005817237
TMC6	2.3626826	1.87919E-32	EXOC1	0.8923078	5.22432E-07	NEK5	0.31084585	0.000254933	NFATC1	0.7409362	0.005824033
NENF	2.3568993	2.04185E-32	DCUN1D5	0.30153832	5.26765E-07	RLF	0.3363122	0.000255019	GAS8	0.28457308	0.005824884
ACP5	2.7189853	6.95157E-32	ZNF518A	0.9937619	5.29812E-07	PPID	0.48550284	0.000256634	BROX	0.41888216	0.005829703
RPLP0	1.3337592	8.75021E-32	FSCN1	0.82145774	5.34944E-07	AARS D1	0.63686574	0.000256634	SMARCD1	0.42864498	0.00583552
RPS6	1.3269582	2.20846E-31	RAB5C	0.73942333	5.37889E-07	RHOG	0.79227597	0.000256634	GNG10	0.60945517	0.005850014
GAS5	2.07283	3.87466E-31	TRUB1	1.1435124	5.42025E-07	SHPK	0.5530312	0.000256667	SNUP N	0.48708588	0.005852861
RPL13AP5	1.5734402	5.35045E-31	NUCKS1	0.5653603	5.44988E-07	TLCD1	1.4828973	0.000257244	PRKACB	0.32452998	0.005856705
SNAI2	2.5798244	6.92092E-31	PRKDC	0.6402711	5.46324E-07	PIN1	0.6605195	0.000260072	C18orf56	1.3710518	0.005870251
FAM174B	2.2155108	7.46431E-31	FARSA	1.082976	5.52983E-07	TBXA2R	0.27765468	0.000261298	UBL7	0.674087	0.005875105
RASSF3	1.2727015	3.21356E-30	FKRP	0.841667	5.64375E-07	ANKS6	0.5548058	0.000261441	MLL4	0.66289145	0.005889973
PTP4A3	2.497336	5.22417E-30	BCL2L1	0.7872485	5.73458E-07	H2AFY	0.48085195	0.000261917	UFL1	0.30795798	0.00589785
RPS7	1.2569237	5.53995E-30	PIH1D1	0.9258179	5.76927E-07	RNF4	0.5811294	0.000262506	TSPAN9	0.36039752	0.005901723
GPM6B	2.2160745	8.35276E-30	ZHX1	0.7194651	5.77203E-07	LOC595101	0.53110015	0.000264716	BRD8	0.3499636	0.005931615
FOXR ED2	1.684949	4.9492E-29	PPIL2	0.58239084	5.77203E-07	VRK2	0.64070755	0.000264861	FIGN	0.39962006	0.005957738

SOAT1	1.7153 088	4.94 92E- 29	ICMT	0.5578 9536	5.802 14E- 07	C11orf 70	0.0567 12184	0.000 26714 6	COPS7 A	0.5598 9325	0.005 96468 6
RPS16	1.3649 871	1.02 208 E-28	PLIN2	0.9405 383	5.882 24E- 07	HES2	0.4322 3614	0.000 26791 6	PSMB6	0.9093 1696	0.005 96555 7
PKNO X2	1.7719 697	5.19 508 E-28	GNAL	0.6518 6274	5.882 24E- 07	B3GAL NT1	0.8871 954	0.000 26846	GGPS 1	0.2262 4263	0.005 97048 4
RPL18	1.3628 294	1.12 65E- 27	FAM198 B	1.4925 305	5.921 06E- 07	SLC39 A9	0.4828 0907	0.000 26906 2	TMEM 64	0.3150 1994	0.005 97947 6
EIF4A1	1.5431 958	1.53 604 E-27	NOB1	0.9565 738	5.981 51E- 07	TMEM 189	0.5037 64	0.000 26932 4	ST3GA L1	0.1814 3994	0.005 98238 2
RPS27	0.9855 995	1.76 975 E-27	BANP	0.8548 973	6.020 76E- 07	SLC25 A19	0.9981 983	0.000 27015 6	BUD13	0.7071 883	0.005 98325 6
NOP56	1.8435 454	2.41 099 E-27	EID2B	0.4808 2367	6.035 49E- 07	ZC3H7 B	0.4228 0445	0.000 27110 6	PHF8	0.3096 597	0.005 99531 9
CHP1	1.2333 44	2.46 476 E-27	LRAT	1.0567 288	6.092 04E- 07	ANKR D32	0.6031 002	0.000 27165 6	PTMA	0.2262 5369	0.006 02448 1
TNFRS F14	2.0868 564	2.46 476 E-27	UQCRB	0.4659 0903	6.096 87E- 07	SSNA1	0.6572 709	0.000 27432 1	GAPV D1	0.1489 3256	0.006 02843
UQCR FS1	2.1952 944	3.12 019 E-27	FAM222 B	0.7597 491	6.100 02E- 07	C1orf3 5	0.5856 6463	0.000 27482	TKTL1	1.4343 877	0.006 05288 9
KLHDC 8B	2.2562 94	1.17 305 E-26	C17orf1 03	0.3294 71	6.104 86E- 07	SGSM 3	0.5679 212	0.000 27483 1	ZNF3	0.5179 154	0.006 06802 4
RPS9	1.0238 451	1.96 977 E-26	GCN1L 1	0.5520 5715	6.184 12E- 07	FBXO1 7	0.5052 481	0.000 27483 1	SNX32	1.7692 441	0.006 07303
SCIN	2.8699 81	2.68 472 E-26	NUBP2	1.0314 504	6.247 18E- 07	CRYZ	0.6424 467	0.000 27504	PRKA CA	0.4191 6874	0.006 09957 8
RPL4	0.9612 4005	2.74 016 E-26	IGHMB P2	0.9425 247	6.248 69E- 07	MIR18 1A2HG	1.4825 237	0.000 27536 5	SMAR CAD1	0.4047 767	0.006 13217 7
ASAP1	1.3114 85	3.10 441 E-26	ZNF518 B	0.8595 4005	6.390 54E- 07	GOLP H3L	0.7023 818	0.000 27709 2	CNPY3	0.5362 9756	0.006 13619 2
RAB38	2.2830 32	3.29 041 E-26	PAG1	0.7572 7415	6.390 54E- 07	DPM1	0.7141 2313	0.000 27900 5	ACAC B	0.0784 0544	0.006 15270 5
AHCY	2.0247 157	3.80 727 E-26	HNRPD L	0.7029 047	6.390 54E- 07	KIAA14 32	0.7449 5834	0.000 27921 7	FAM21 4B	0.6283 879	0.006 15673 2
LOC10 013344 5	1.7879 609	5.67 093 E-26	WDR75	0.8107 6854	6.393 85E- 07	AQP4- AS1	0.0288 95244	0.000 28129 8	TMEM 214	0.3124 2055	0.006 16284 9
CCT3	1.5656 347	6.87 453 E-26	KIAA01 96	0.6266 0104	6.487 43E- 07	CUBN	0.3840 313	0.000 28129 8	RAB2A	0.4797 5934	0.006 16583 7
RPS11	1.2937 845	7.12 199 E-26	ZBTB40	0.5881 537	6.510 44E- 07	EPN1	0.4671 361	0.000 28353 8	PPP2R 2D	0.9334 883	0.006 17614 5
GPI	1.6534 74	8.53 165 E-26	TRAF3I P2	0.4766 2205	6.592 99E- 07	ISOC2	0.7244 495	0.000 28363 4	ZSCAN 22	0.1993 5052	0.006 17913 9
RPL8	1.1438 296	9.01 651 E-26	CBX5	0.6079 53	6.594 59E- 07	GTPBP 8	0.7968 9205	0.000 28378 9	TYW5	0.0898 5625	0.006 19142
C1QBP	2.2327 676	1.35 287 E-25	ZNF790 -AS1	1.0712 54	6.597 81E- 07	UST	0.1557 9657	0.000 28388 4	GAL3S T4	0.1030 0357	0.006 19218

TUBB4 A	2.6409 42	1.50 694 E-25	MRPS1 1	0.9463 4324	6.597 81E- 07	ZNF27 4	0.8765 215	0.000 2853	LOC10 050568 7	0.2646 095	0.006 19218
PLTP	2.1910 825	2.22 205 E-25	C19orf2 5	0.8039 543	6.861 39E- 07	TMTC4	0.8411 696	0.000 28549 3	SPATS 2	0.2472 5066	0.006 20988 2
SS18L 1	1.6894 603	2.49 136 E-25	CCNF	0.9525 166	6.904 58E- 07	POP4	0.5717 206	0.000 28549 3	ASPM	0.7061 438	0.006 23275 8
SORD	1.7535 323	5.93 004 E-25	ZBTB8 OS	0.8588 657	6.949 95E- 07	NFU1	0.6822 976	0.000 28607 1	LOC15 0776	0.2892 4137	0.006 24528 2
RPS17 L	0.9169 573	5.93 004 E-25	NBPF1	0.3989 643	7.054 85E- 07	EPB41 L4A	0.8726 6177	0.000 28640 9	ECI2	0.5703 439	0.006 24725 1
RPS17	0.9169 573	5.93 004 E-25	SURF2	1.0239 604	7.054 85E- 07	RNF11 5	0.6091 54	0.000 28771 5	MSAN TD4	0.3582 2532	0.006 25662 5
MARC KS	1.2647 879	7.33 919 E-25	LUST	0.5768 675	7.216 81E- 07	SSSCA 1	0.6367 9034	0.000 29030 9	COA5	0.3455 87	0.006 26692 7
RPS4X	0.9399 8635	3.58 791 E-24	GIPC1	0.8515 646	7.396 53E- 07	RMND 1	0.5474 0006	0.000 29163 2	TSFM	0.4282 849	0.006 26692 7
ESRP1	2.0238 092	4.76 897 E-24	GALNT 18	2.1497 326	7.584 49E- 07	NCOA 2	0.5373 1465	0.000 29265 3	NPHP4	0.4361 8926	0.006 29226 8
NF2	1.1871 82	4.87 099 E-24	CROCC	0.5886 96	7.584 49E- 07	HHLA3	0.2535 5375	0.000 29275 2	PRPSA P1	0.3634 1232	0.006 30688 7
CNRIP 1	2.2585 275	4.95 775 E-24	HMBS	1.0836 414	7.781 33E- 07	ZNRD1	0.7013 682	0.000 29278 9	MERT K	1.2972 305	0.006 30688 7
OXA1L	1.8294 839	5.83 134 E-24	PEX11A	0.9107 48	7.813 04E- 07	U2SUR P	0.3707 9874	0.000 29307 2	LOC28 3585	0.1048 7416	0.006 31527 6
NPL	2.1170 392	6.28 17E- 24	AP3M1	0.5682 8576	7.885 67E- 07	CUTA	0.7253 154	0.000 29354 2	TTI1	0.3135 7348	0.006 34893 4
LHFPL 3-AS1	2.9002 924	7.61 502 E-24	ZFYVE1 6	0.5495 5834	7.904 84E- 07	PSMC 6	0.6458 2145	0.000 29448 2	SLC38 A9	0.5926 6865	0.006 35386 1
CD68	1.8744 749	8.58 449 E-24	CWF19 L1	0.5376 4254	7.908 93E- 07	FAM10 2A	0.5494 8354	0.000 29451 9	PRSS3 3	2.0581 758	0.006 35386 1
SAE1	1.8725 004	1.46 562 E-23	DDT	0.8878 769	7.938 99E- 07	TAF2	0.4962 9146	0.000 29523 9	L3MBT L1	0.6304 5496	0.006 35386 1
MID1	2.0847 409	1.86 169 E-23	PSMC1	0.9375 807	8.034 42E- 07	COX10 -AS1	0.2264 1063	0.000 29583 6	BRPF3	0.3781 9242	0.006 37521 5
ZNF74 9	1.5363 317	1.87 32E- 23	PPFIBP 2	1.0620 967	8.034 42E- 07	HNRN PA1L2	0.4350 0376	0.000 29643 4	TBC1D 13	0.6306 721	0.006 39217
PPP2R 1A	1.6789 838	1.96 163 E-23	CLN6	0.8052 726	8.051 75E- 07	WDR2 4	0.6776 009	0.000 30048 8	ATXN7 L2	0.8499 752	0.006 39217
RPS8	0.9207 014	1.97 628 E-23	YARS	0.7907 411	8.097 78E- 07	ZNF38 4	0.5444 7067	0.000 30395 6	FAM20 0A	0.4474 2396	0.006 39418 3
GSTO1	1.8520 924	2.10 478 E-23	TSPAN 14	0.7713 678	8.104 19E- 07	LY86- AS1	0.4456 599	0.000 30399 4	GTSE1	0.5386 9134	0.006 39835 6
SAMM 50	1.7988 638	2.10 478 E-23	TMEM1 68	0.8203 361	8.214 98E- 07	RIN3	0.7615 683	0.000 30486 4	WDR4 5B	0.3701 504	0.006 40793 8
EIF3K	2.0324 342	2.10 478 E-23	PLCB4	1.0783 652	8.214 98E- 07	HN1L	0.4424 2114	0.000 30506 9	COPS3	0.5591 724	0.006 43054 4

SNHG6	1.868701	2.10478E-23	BNIP2	0.8134605	8.30028E-07	LAPTM4B	0.5272409	0.00030566	ZNF678	0.5002233	0.006447781
FAM178B	1.77855	2.9775E-23	SF3B2	0.7104331	8.31365E-07	HSF1	0.5441	0.00030566	CARS	0.4297722	0.006467241
RPL6	1.0374544	2.9939E-23	OLA1	0.66110224	8.31797E-07	CCT5	0.7005977	0.000306019	STK3	0.39380017	0.006499894
TP53	1.5220754	3.08603E-23	CNTLN	0.43618405	8.39972E-07	MRPL42	0.5036687	0.000306315	MDN1	0.11623077	0.006502886
IDH2	2.066723	3.38605E-23	MCM3AP	0.55185056	8.41096E-07	TSEN54	0.55359346	0.00030807	ADAMTS7	1.2285048	0.006502886
SLC25A5	1.5623211	3.38605E-23	ERCC2	1.0980902	8.41533E-07	NKIRAS1	0.5054932	0.000308835	CWF19L2	0.035594143	0.00652235
RPS5	1.5625103	5.43E-23	MTSS1L	0.7967436	8.43348E-07	GSE1	0.335427	0.000308835	LOC389634	1.0340954	0.006523301
MOB3B	1.9657133	6.00663E-23	PRKAR1B	0.89663255	8.56728E-07	RBM27	0.30309445	0.000309003	NUDT8	0.89303553	0.006533054
MAD1L1	1.6609297	6.00663E-23	TASP1	0.8102557	8.56728E-07	ACP1	0.7435208	0.000309497	MRPL55	0.7097252	0.00654157
IMPDH2	1.7756917	6.00663E-23	C10orf118	0.4981388	8.57874E-07	RNF144B	0.4219376	0.000309641	FBXL4	0.1234223	0.006549141
BZW2	1.8954881	8.08185E-23	PRSS21	3.0848598	8.62066E-07	CCDC144A	0.66424084	0.000310135	CT49	0.6674941	0.00655893
GLOD4	1.7151943	1.0647E-22	DPCD	1.1187634	8.76946E-07	BABAM1	0.7464264	0.000313839	MAPK12	1.1235336	0.006559887
ADSL	1.9364839	1.1342E-22	POLR3E	0.82520044	8.79075E-07	BTBD7	0.20621213	0.000314604	UCA1	0.7996554	0.006581427
GALE	1.9373039	1.19122E-22	LOC284581	0.4795695	8.86495E-07	SIRT6	0.7227519	0.000314815	TAOK2	0.23800391	0.006581427
EIF2S3	1.3998122	1.36118E-22	RAB32	1.1659971	8.8766E-07	CCNB2	1.2583257	0.000314815	FIS1	0.7415657	0.006584605
ABR	1.6884952	1.90909E-22	SYNPO	1.0893025	8.8766E-07	DNAJC8	0.748202	0.000315358	SPCS2	0.55371404	0.006588746
PPA1	1.9970354	2.4764E-22	NRBF2	0.8233838	8.95861E-07	RECQL	0.3492747	0.000315358	VDAC1	0.66830367	0.006588746
ILF2	1.8700619	2.52843E-22	EXOC3	0.9443912	8.97303E-07	HDAC4	0.494586	0.000315861	GLYR1	0.1518465	0.006591927
EIF3L	1.4480551	2.70838E-22	PTPN14	0.5030877	8.9997E-07	ZNF440	0.2697694	0.000318293	C11orf82	1.1595792	0.006592889
EIF4EBP2	1.161519	3.18598E-22	LOC100131096	0.45696026	9.03625E-07	ATG16L2	1.1495674	0.000318641	ZBTB10	0.47879988	0.006619431
RPL13A	1.5419121	6.45382E-22	ABI1	0.70375985	9.12981E-07	SEC11A	0.686194	0.000319056	USP2	1.1428809	0.006624707
CS	1.4410021	7.03529E-22	URB2	1.019021	9.19429E-07	MASTL	0.4718275	0.000319056	BOLA1	0.57576793	0.006624707
EGFL8	2.5306191	8.36848E-22	ZNF410	0.7228844	9.24165E-07	LOC100130370	0.40898728	0.000319365	EXOC6B	0.599106	0.006626789

PRDX3	1.7506 256	9.49 225 E-22	S100PB P	0.4809 0595	9.279 16E- 07	PIP4K2 B	0.5627 1553	0.000 32014 2	TRIM6 8	0.3294 92	0.006 62887 2
GSTP1	1.3304 653	1.17 442 E-21	PARP2	1.1490 626	9.284 01E- 07	GNAI3	0.5684 9974	0.000 32035 8	C4orf4 6	0.3519 5306	0.006 62984
CYP51 A1	1.3197 622	1.19 571 E-21	TGDS	0.9020 9705	9.336 88E- 07	PNKP	0.7842 982	0.000 32091	TTC37	0.1004 21	0.006 63527 3
HPS4	1.4951 177	1.21 504 E-21	PARVA	0.5962 159	9.428 15E- 07	ST20	0.6776 1177	0.000 32091	ZCCH C10	0.5053 184	0.006 68666 5
PAFAH 1B3	2.0179 596	1.37 514 E-21	NELFC D	0.9584 945	9.428 15E- 07	RFWD 2	0.6097 1	0.000 32193 4	ZNHIT 2	0.6808 121	0.006 69311 7
TULP4	1.3052 988	1.51 511 E-21	PLCB2	1.8283 519	9.448 27E- 07	NMB	1.0246 868	0.000 32193 4	SIPA1L 2	0.2679 117	0.006 69957 5
ATP5A 1	1.4909 66	1.82 293 E-21	SCAP	0.7275 3	9.448 27E- 07	SHISA 2	0.3768 9418	0.000 32244 7	FLJ253 63	0.0081 81858	0.006 69957 5
SNHG 16	1.1941 8	1.93 22E- 21	EIF2S2	0.7258 009	9.577 06E- 07	PCBP1	0.5671 493	0.000 32431 6	MCM8	0.6277 339	0.006 72183 8
REV3L	1.1748 437	2.06 943 E-21	FARP1	0.7794 841	9.634 17E- 07	DPH2	0.6947 629	0.000 32462 9	GJB2	2.1900 208	0.006 72507 9
YWHA Z	0.9403 5554	2.76 02E- 21	HDGF	0.7519 366	9.649 5E-07	ABCC2	1.1079 868	0.000 32535 1	RPL35 A	0.3651 3472	0.006 73737 4
GPR14 3	1.8431 433	2.99 695 E-21	MTERF D1	0.9738 278	9.649 5E-07	MCM1 0	0.7973 15	0.000 32595 3	FAM17 3B	0.0440 08438	0.006 74628 7
BANC R	2.0898 807	3.09 021 E-21	EPS15	0.7330 3604	9.785 9E-07	UGDH	0.5298 411	0.000 32595 3	MTMR 14	0.3455 6374	0.006 79017 6
RPS3	1.0063 79	3.22 276 E-21	PWP2	0.8639 256	9.785 9E-07	RPS20	0.3186 876	0.000 32595 3	HELZ2	0.1384 3372	0.006 81973 1
USP22	1.2714 279	3.27 792 E-21	COX15	0.4163 0685	9.820 25E- 07	KLF12	0.4090 7457	0.000 32681 4	EIF4G 3	0.2429 5244	0.006 84366
PRAM E	1.5701 514	3.33 747 E-21	RPL22L 1	0.7029 695	9.862 73E- 07	TIMM9	0.6090 5594	0.000 32985	C1QTN F3	0.3407 3266	0.006 84580 5
RPSA	0.9831 066	5.46 113 E-21	TAF11	0.6937 9807	9.910 76E- 07	FBXL1 5	0.5461 78	0.000 32985	CCDC 77	0.6256 7097	0.006 86160 3
RPL18 A	1.4029 37	5.89 604 E-21	SYAP1	0.6200 662	9.932 08E- 07	SMC5	0.2627 7882	0.000 33037 5	PLEKH G2	0.1598 3634	0.006 86160 3
TUFM	1.6547 658	6.56 101 E-21	PPP2R 5D	0.8062 6047	1.003 19E- 06	COMT	0.7675 084	0.000 33135 9	TM2D3	0.5204 204	0.006 86836 2
TRA2A	1.5646 719	7.50 644 E-21	PRPF40 A	0.6277 499	1.009 98E- 06	RPRD1 B	0.3703 346	0.000 33137 5	LOC28 6467	0.1642 7222	0.006 89129
METTL 9	1.6120 61	1.18 109 E-20	VCL	0.7883 561	1.018 2E-06	CISD1	0.5234 091	0.000 33137 5	EHMT2	0.3882 202	0.006 92225 5
SMS	1.7002 423	1.28 088 E-20	DDX10	0.8237 063	1.023 15E- 06	ZNF54 4	0.3714 0092	0.000 33155 6	OCEL1	0.5982 5665	0.006 94851 1
TRIB2	1.4415 39	1.54 733 E-20	EXOGE	0.3601 3672	1.024 24E- 06	IK	0.6695 7474	0.000 33215 4	MPHO SPH8	0.2165 4767	0.006 94985 2
APP	1.6011 953	1.59 018 E-20	TBP	0.6005 1394	1.027 82E- 06	EXOS C7	0.7098 625	0.000 33247 4	NIPSN AP3A	0.5097 556	0.006 97186

RPL11	0.8567 6026	1.72 597 E-20		DLD	0.8037 92	1.035 62E- 06		UQCR C1	0.9978 369	0.000 33356		RGL2	0.2107 7977	0.006 97287 5
RPL21	3.1682 74	2.21 981 E-20		LSMD1	0.7233 3837	1.044 31E- 06		TOP3B	0.5384 7355	0.000 33423 1		C1orf5 1	0.9621 317	0.006 98324 2
SKAP2	1.5385 8	2.38 463 E-20		WDR74	0.9827 448	1.058 5E-06		FAM15 3C	0.0053 28791	0.000 33539 3		DNAJC 30	0.3007 8527	0.006 98777
C1orf1 98	1.3860 836	2.40 749 E-20		44446	0.7169 3695	1.064 21E- 06		BMPR 1A	0.8930 318	0.000 33620 7		C12orf 76	0.4157 7804	0.007 00402
WSB2	1.2752 829	2.45 89E- 20		MARCK SL1	0.9249 625	1.066 78E- 06		LINC00 477	0.4101 7872	0.000 33699 7		ARG2	0.4767 8348	0.007 01780 1
RPL3	0.7168 6274	2.47 671 E-20		DKFZp6 86O132 7	0.8985 4246	1.072 84E- 06		ADNP2	1.0093 008	0.000 33774 5		STK16	0.4877 117	0.007 01780 1
SF3B4	1.2582 308	4.27 359 E-20		ST6GA LNAC3	1.3572 377	1.076 01E- 06		CNST	0.4113 9588	0.000 33792 9		C1orf7 4	1.0556 656	0.007 01882 3
KIAA00 20	1.3316 151	5.93 052 E-20		SSBP3	0.8147 3386	1.076 58E- 06		FDX1L	0.8039 774	0.000 33924 5		KIAA17 31	0.0041 67877	0.007 02102
XPNP P1	1.6361 142	6.47 155 E-20		ACOX1	0.4926 7697	1.094 44E- 06		EHHA DH	0.1084 4173	0.000 33928 8		BTBD1	0.5383 385	0.007 02439 4
MRPS 16	1.2053 376	6.71 742 E-20		IWS1	0.8216 6773	1.095 01E- 06		PAK1	0.7528 548	0.000 33961 6		CCNI	0.4723 5745	0.007 03954 4
TPCN2	1.7517 785	7.11 689 E-20		RRP12	0.9100 8395	1.096 48E- 06		FBXO2 1	0.4334 68	0.000 34069 7		FAM20 7A	0.6592 344	0.007 04056 9
PI4KB	1.4379 435	7.81 745 E-20		HSD3B 7	0.5525 132	1.100 91E- 06		SUPT2 0H	0.4249 7635	0.000 34069 7		LIMD1	0.2267 4748	0.007 04395 2
HSPA8	0.9328 129	8.96 801 E-20		RFK	0.5969 29	1.106 26E- 06		KDM3 A	0.4213 0306	0.000 34102 5		BRD1	0.3599 6515	0.007 04497 8
NDST1	1.4439 476	9.22 123 E-20		METTL 5	0.9407 2163	1.111 03E- 06		MTMR 2	0.4276 1013	0.000 34363		WDR4 1	0.2861 897	0.007 05056 9
TTYH3	1.5114 995	1.00 32E- 19		HKR1	0.7488 349	1.127 31E- 06		FIP1L1	0.5333 452	0.000 34363		MED28	0.5283 6674	0.007 06916 6
NAPRT 1	1.8237 065	1.03 303 E-19		APC	0.5073 04	1.151 23E- 06		RAB20	1.2821 954	0.000 34381 8		MRPL1 8	0.6046 123	0.007 07256 2
ZNF33 0	1.6783 754	1.05 325 E-19		PMS2P 4	0.7482 6443	1.154 63E- 06		MIA3	0.3240 851	0.000 34443 6		PSMD 14	0.6623 5507	0.007 08646 8
MAZ	1.2879 483	1.23 706 E-19		IPO13	1.0531 936	1.172 16E- 06		DHX15	0.6700 5146	0.000 34448 1		FAM18 8A	0.7025 145	0.007 08868 7
UBL3	1.5054 482	1.26 975 E-19		NSUN5 P1	0.5397 838	1.180 06E- 06		SLC37 A4	0.9197 862	0.000 34514 5		ABRA CL	0.4136 3445	0.007 12522 5
ITPKB	1.4863 359	1.28 497 E-19		TCERG 1	0.6402 951	1.187 37E- 06		C10orf 88	0.9438 1136	0.000 34648 7		MRPL1 4	0.6925 1966	0.007 14415 5
OBSC N	1.3561 561	1.42 201 E-19		CD2BP 2	0.6441 987	1.188 64E- 06		SNX4	0.5860 267	0.000 34686 6		ACP6	0.5068 8154	0.007 15714 9
EIF3D	1.4930 276	1.64 457 E-19		LRRC2 8	0.9347 186	1.192 79E- 06		RCBTB 2	0.7578 273	0.000 34686 6		NISCH	0.3008 69	0.007 16178 1
PPM1 H	1.5763 603	1.89 889 E-19		LINC00 439	0.9166 0565	1.198 25E- 06		LOC10 028704 2	0.2151 6034	0.000 34698 3		CEP25 0	0.2743 1062	0.007 16730 5

GABA RAP	1.1681 566	2.30 935 E-19		SRD5A 3	0.8073 066	1.208 59E- 06		BCAS4	1.1503 575	0.000 34862 3		SMAR CA1	0.2393 2846	0.007 21279 6
TSPAN 10	2.0655 854	2.34 272 E-19		SRGAP 1	0.5284 6813	1.218 68E- 06		YEATS 4	0.6542 485	0.000 351		VTI1A	0.2027 4065	0.007 21625 6
RSL1D 1	1.0563 59	3.20 589 E-19		METTL 10	0.8185 635	1.228 54E- 06		LOC10 050612 3	0.1589 0647	0.000 35251		ZSCAN 2	0.2369 5923	0.007 22092 3
EEF2	1.3253 703	3.24 917 E-19		PLP1	0.8999 51	1.246 15E- 06		FAR2	0.7556 751	0.000 35262 9		PIBF1	0.3146 033	0.007 25929 5
C1orf8 5	1.5456 499	3.69 244 E-19		EIF2B3	0.9340 949	1.263 65E- 06		DR1	0.5038 4605	0.000 35286 8		ZNF91	0.0467 1344	0.007 28325 4
HADH B	1.6258 421	3.88 477 E-19		FAM212 A	1.7868 636	1.268 04E- 06		CDC5L	0.4054 9812	0.000 35286 8		PPM1 D	0.1034 59746	0.007 29161 1
RPL10 A	0.8788 381	4.29 414 E-19		TSN	0.8055 5516	1.270 08E- 06		CCSA P	0.1692 5389	0.000 35357 5		ZNF85	0.4860 9388	0.007 31948 6
QARS	1.5095 48	4.59 396 E-19		MRPS1 4	0.7424 7223	1.277 25E- 06		PANK1	0.1768 6978	0.000 35494 8		CDK2A P2	0.5876 367	0.007 32665 8
UBAP2 L	1.3846 632	4.59 396 E-19		FAM21 B	0.7066 753	1.280 67E- 06		MTPA P	0.3796 141	0.000 35603		KIF2C	0.8788 732	0.007 33016 8
CLCN5	1.1128 309	4.59 404 E-19		GYG2	0.9827 586	1.283 05E- 06		RNF25	0.8121 3284	0.000 35637 3		ZNF22 7	0.5947 4367	0.007 34469 5
FTL	0.9564 364	4.86 043 E-19		HCFC1	0.5783 53	1.283 05E- 06		CXXC1	0.5849 063	0.000 35907		INTS8	0.2832 8133	0.007 34698 8
ZFP10 6	1.1835 11	4.94 978 E-19		DCUN1 D1	0.6728 958	1.283 05E- 06		BLOC1 S6	0.4386 639	0.000 36141 1		TRIM2	0.2969 0006	0.007 35770 7
RPL26	1.0417 194	6.24 18E- 19		SIN3B	0.5872 754	1.296 19E- 06		GOLG A7	0.6692 014	0.000 36236 1		WRAP 53	0.8066 3574	0.007 35770 7
SMIM1 5	1.3830 6	8.27 957 E-19		RANBP 10	0.7444 2285	1.296 53E- 06		RHOT2	0.6286 453	0.000 36718 3		KIF13A	0.3036 649	0.007 37212 7
MSTO 1	1.513	8.97 468 E-19		SPDYE 8P	0.5999 0525	1.303 84E- 06		DUSP2 2	0.6816 4444	0.000 36738 3		VPS54	0.5443 8794	0.007 38042
DLL3	2.0907 133	1.23 57E- 18		PUF60	1.0509 573	1.315 05E- 06		LSM10	0.7586 721	0.000 36750 7		ZNF56 7	0.6196 563	0.007 38272 4
LIMD2	0.9784 3176	1.54 473 E-18		RANGR F	1.0093 777	1.316 1E-06		IRF2B P2	0.3461 5344	0.000 36809		ANKR D26	0.0418 34265	0.007 39118 5
PAICS	1.5675 36	1.62 064 E-18		TXNDC 17	0.7140 6794	1.330 98E- 06		SLC24 A4	0.5008 729	0.000 36890 3		HERC2 P10	0.7150 52	0.007 42435 3
RAB6B	1.8389 091	1.82 217 E-18		PAF1	0.7466 867	1.330 98E- 06		PKD1P 1	0.2755 6732	0.000 36910 4		SLC36 A1	0.5032 635	0.007 43022 4
RPL41	0.5740 5716	1.91 25E- 18		PTOV1- AS1	0.2571 8078	1.330 98E- 06		MEF2D	0.4561 4338	0.000 37115		MIIP	0.4257 0496	0.007 43022 4
RPS12	0.7072 6454	1.93 574 E-18		UBE2C	1.1398 761	1.375 18E- 06		PYCR2	0.4514 688	0.000 37143		PARP3	0.4601 0366	0.007 44477 5
CECR5	1.6564 658	1.95 692 E-18		BPNT1	0.5492 736	1.382 19E- 06		SRRD	0.7993 262	0.000 37155 5		IDI1	0.5010 6984	0.007 44585 8
RPS15	1.0349 993	2.24 153 E-18		RASA3	0.7025 863	1.400 79E- 06		STARD 13	0.4903 098	0.000 37160 3		FBXL1 2	0.3772 849	0.007 46432 2

P2RX7	1.3709 153	2.37 422 E-18	E2F3	1.0764 371	1.405 66E- 06	ZNF55 9	0.7787 7593	0.000 37188 3	ATG16 L1	0.4557 678	0.007 46525 1
FXYD5	1.8134 081	2.71 378 E-18	ITGAE	0.4818 0944	1.406 03E- 06	CROC CP2	0.6155 7865	0.000 37472	WDPC P	0.0914 4125	0.007 46525 1
DDX39 B	1.3009 882	3.16 581 E-18	SNRPA 1	0.8786 89	1.418 11E- 06	EPB41	0.4051 1537	0.000 37523 6	EID2	0.3996 524	0.007 46758
RGS12	1.2998 537	3.38 502 E-18	VAPB	0.4644 1582	1.433 34E- 06	RCL1	0.7778 932	0.000 37650 3	C9orf1 23	0.2738 171	0.007 48858 5
RPS15 A	0.8634 042	4.52 317 E-18	RMND5 A	0.4846 3634	1.442 56E- 06	NCKA P5L	0.4678 4478	0.000 37741 2	IGFBP 4	0.9236 694	0.007 48967 5
FAM12 6A	1.3625 453	4.81 557 E-18	GPN1	0.9880 409	1.444 49E- 06	NOL10	0.4686 2972	0.000 37848	PTCH D4	0.2134 0607	0.007 49138 7
WDR8 1	1.6037 195	4.82 935 E-18	SNAPC 3	0.4426 6272	1.446 8E-06	CNOT2	0.4760 4057	0.000 37892 2	BTRC	0.4607 7564	0.007 49138 7
RUUBL 2	1.7320 86	6.71 515 E-18	TMEM2 54	0.8787 8823	1.451 44E- 06	DDA1	0.1865 7659	0.000 38007 3	COL11 A2	0.6317 049	0.007 50121 1
SRCA P	1.0545 28	7.01 473 E-18	C17orf5 8	0.9798 0607	1.462 73E- 06	UBOX5	0.3760 1882	0.000 38127 7	RHOB TB1	0.8945 1325	0.007 50480 1
EEF1G	0.9892 5585	7.01 473 E-18	HOXA5	1.7567 79	1.472 52E- 06	C12orf 52	0.7345 2157	0.000 38172 2	C10orf 35	1.4844 519	0.007 56213 1
MAP1L C3A	1.4533 904	8.18 112 E-18	HECTD 3	0.8915 1484	1.491 11E- 06	DNM1L	0.3475 4226	0.000 38327 7	METTL 12	0.2934 937	0.007 57833 7
ALDH1 B1	1.2310 492	8.20 542 E-18	GHITM	0.9761 845	1.491 91E- 06	FADS1	0.4182 9127	0.000 38483 9	TMEM 115	0.5139 5243	0.007 62873
PPP5C	1.3325 665	8.65 E-18	EXOSC 3	0.8334 782	1.493 5E-06	PSEN2	0.6516 3666	0.000 38536 8	HSPBA P1	0.4400 104	0.007 63237 4
EDNR B	1.6154 726	8.65 E-18	PRPF4	0.6851 8066	1.507 11E- 06	TRMT1 0B	0.1492 9157	0.000 38824 3	KPNB1	0.3157 3495	0.007 63824 2
RPL17	0.7992 215	8.93 744 E-18	DHX33	0.3263 6	1.507 11E- 06	CHFR	0.6716 6907	0.000 38877 6	ROBO 3	0.5095 44	0.007 63824 2
CDKN2 A	2.2412 555	9.44 422 E-18	SLC39A 1	0.9722 11	1.507 51E- 06	PI15	1.0874 262	0.000 38963 2	GPX7	0.7398 5445	0.007 63935 3
NHEJ1	1.4838 881	9.96 609 E-18	STEAP 1	1.3782 257	1.518 E-06	HMGH 4	0.6720 0905	0.000 39148 3	AP3S1	0.6278 5363	0.007 65189 6
SNHG 15	1.7390 565	1.05 213 E-17	ZSWIM 8	0.7744 544	1.533 46E- 06	GPKO W	0.1408 5211	0.000 39148 3	C4orf2 7	0.4045 331	0.007 67703 8
WDR1 2	1.5633 91	1.17 05E- 17	GALNT 1	0.3794 0863	1.545 77E- 06	CRND E	0.6087 535	0.000 39454 2	SPIN4	1.3442 99	0.007 69730 2
AEN	1.5470 423	1.26 076 E-17	NDUFS 1	0.7256 497	1.548 66E- 06	MED4	0.5057 9685	0.000 39639 3	RNF20	0.3524 182	0.007 70481 3
SLC45 A2	1.9899 346	1.35 426 E-17	SLC25A 32	0.6226 493	1.548 66E- 06	SNOR D76	1.7552 718	0.000 39685 5	MORC 2-AS1	0.4015 7902	0.007 70977 2
RPL35	0.7008 17	1.47 426 E-17	CDCA7 L	1.3275 464	1.573 2E-06	SLC50 A1	0.4625 4453	0.000 39707 1	RIMKL A	0.0614 346	0.007 72626 7
C1orf4 3	1.3137 906	1.65 275 E-17	POPDC 3	0.9345 238	1.573 2E-06	TRMT1	0.6132 24	0.000 40042	NDUF S4	0.5983 366	0.007 73878 1

NDUF S2	1.5983 849	1.80 773 E-17		CBLL1	0.7692 527	1.587 94E- 06		PHYH	0.8739 2116	0.000 40088 6		UBAC2	0.4382 3394	0.007 74231 6
TYRP1	2.8456 04	1.87 425 E-17		DSG2	0.6073 3837	1.615 22E- 06		AP1G2	0.4190 2015	0.000 40110 4		LOC96 610	0.1742 5191	0.007 76788 9
RPS18	0.8839 341	2.17 602 E-17		ABT1	0.8483 5225	1.626 01E- 06		SPESP 1	1.2338 417	0.000 40140 5		ELAVL 1	0.3067 3462	0.007 77030 7
RPL36	1.1909 131	2.18 501 E-17		DIP2A	0.5288 197	1.630 34E- 06		CD320	0.8444 137	0.000 40604 4		TEAD1	0.2712 2697	0.007 77659 5
SLC25 A3	1.0551 683	2.48 672 E-17		DDX59	0.8185 38	1.641 22E- 06		USP54	0.3003 058	0.000 40912 6		GORA SP1	0.4557 8244	0.007 77805 2
VANGL 2	1.7326 217	2.77 738 E-17		TTC4	0.8862 285	1.645 6E-06		CC2D1 B	0.3239 4102	0.000 41036 4		USP8	0.2695 1352	0.007 80567 4
PDCD1 1	1.1695 18	2.96 188 E-17		PAM	1.4138 454	1.650 42E- 06		RPS10 - NUDT3	0.2554 101	0.000 41271		POLR3 GL	0.5353 06	0.007 80567 4
DAP3	1.4289 392	2.96 188 E-17		MCM6	0.9472 533	1.650 42E- 06		RBM23	0.6380 763	0.000 41378 7		LOC64 5513	0.3111 9037	0.007 81846 6
EEF1A 1	0.6683 643	3.24 373 E-17		ULK3	0.9132 138	1.651 31E- 06		PRR14 L	0.2841 871	0.000 41392 6		SPATC 1L	0.6414 215	0.007 8209
UCK2	1.1164 464	3.29 652 E-17		GTPBP 3	0.4552 511	1.664 1E-06		HNRN PA3	0.4639 915	0.000 41809 8		SCLT1	0.5766 42	0.007 83371 5
RPS10	0.8957 8134	3.57 813 E-17		PPP1R 12B	0.4810 6357	1.664 1E-06		POLR2 M	0.4283 6976	0.000 41858 4		KLHL1 8	0.6013 7135	0.007 85305 3
SSR2	1.4435 607	3.58 063 E-17		EMC6	0.9310 5114	1.667 2E-06		ZNF43 1	0.0453 3551	0.000 42088 8		RBM19	0.2512 7822	0.007 86331
HNRN PC	1.0212 173	3.84 705 E-17		ASB9	1.2500 592	1.675 65E- 06		TRAPP C6B	0.4489 1477	0.000 42111 6		FAM10 5A	0.1137 2442	0.007 88908 6
HMG2 0A	1.2937 242	4.07 879 E-17		CCDC7 4A	2.4322 46	1.702 58E- 06		C14orf 142	0.7263 3046	0.000 42256 2		NRSN2	0.3688 1897	0.007 88908 6
RPL12	0.7626 6694	4.25 07E- 17		IL11RA	1.0629 244	1.724 89E- 06		CTBS	0.5393 204	0.000 42296 5		BRE	0.4716 875	0.007 89415 5
NOP2	1.5333 383	4.45 328 E-17		SHQ1	0.7377 462	1.725 81E- 06		FAM16 8A	0.3965 966	0.000 42328 2		C16orf 95	0.9504 902	0.007 90707 9
RCHY1	1.1738 905	4.50 802 E-17		NOP10	1.0325 469	1.726 28E- 06		PARL	0.7530 777	0.000 42394 8		TBC1D 9B	0.3144 213	0.007 93052 1
GALNT 2	1.2891 084	4.53 545 E-17		LOC285 033	0.5741 945	1.729 04E- 06		XXYL T1	0.7332 362	0.000 42409 1		PHIP	0.2817 581	0.007 94087
MYO5 A	1.0525 825	5.60 283 E-17		MAU2	0.5817 113	1.735 49E- 06		NUP93	0.6154 864	0.000 42423 4		TTC21 A	0.5966 715	0.007 94728 4
RPL37 A	0.7095 295	6.50 544 E-17		FAM32 A	1.0489 243	1.735 49E- 06		TSSC4	0.6703 1246	0.000 42586 5		SLC2A 10	0.2510 277	0.007 95633 7
RQCD 1	1.2714 312	6.50 544 E-17		MAML1	0.9283	1.750 3E-06		CLN3	0.6223 67	0.000 42662 2		TROA P	0.9761 756	0.007 97331 2
RPL31	0.7664 481	8.16 678 E-17		GTF2E1	0.4150 9926	1.764 78E- 06		LOC15 2217	0.7327 521	0.000 42667 8		TCF19	0.8907 029	0.007 98487 2
TSTA3	1.5219 445	8.20 601 E-17		ARHGA P35	0.6461 2305	1.769 E-06		LGI4	0.9372 5	0.000 43046 3		ALG2	0.3973 048	0.008 00984 8

GPAT CH4	1.3619 831	8.29 612 E-17	RRAGC	0.4523 0532	1.779 84E- 06	MARS 2	0.9951 995	0.000 43247 3	GZMM	1.6400 149	0.008 02294 5
YY1AP 1	1.3085 543	8.38 367 E-17	UBXN2 A	0.6756 499	1.779 86E- 06	FABP3	1.0275 667	0.000 43580 1	TLE1	0.3546 4302	0.008 02676 5
SLC25 A44	1.4407 662	8.72 368 E-17	UBE2D 4	0.5211 867	1.792 18E- 06	PRKC SH	0.4619 6604	0.000 43912	PROS ER2- AS1	0.0880 0444	0.008 03058 7
TTC39 A	2.0115 97	9.45 364 E-17	DZIP1	0.4777 356	1.826 24E- 06	TIMM2 1	0.7126 104	0.000 43912	RWDD 3	0.5364 209	0.008 03441
THEM4	0.8959 4173	9.45 364 E-17	ZNF581	1.1099 159	1.833 04E- 06	OXLD1	0.6714 737	0.000 43999 1	CHMP 1A	0.4125 26	0.008 05286 8
KIRRE L	1.4129 268	9.81 966 E-17	KIF11	0.3545 916	1.834 03E- 06	ZNF61 1	0.4312 3353	0.000 44140 7	RPS14	0.2485 8405	0.008 07237 5
HAGH L	1.8041 626	1.13 228 E-16	SUGT1	0.7687 0966	1.834 03E- 06	MLH1	0.6581 514	0.000 44164 6	SLC18 A2	1.1701 008	0.008 13196 9
CDC42 EP1	1.7771 724	1.36 495 E-16	MRPS9	1.0260 855	1.836 48E- 06	TPST1	0.3866 375	0.000 44261 2	ATP5S	0.2159 2708	0.008 13196 9
SRP14	1.1384 493	1.52 071 E-16	ABHD1 4A	0.9617 355	1.838 44E- 06	MGST 2	0.8745 988	0.000 44330 7	TUB	0.7697 337	0.008 16782
NOLC1	1.2316 265	1.80 756 E-16	SMAP1	0.5577 68	1.840 4E-06	GMNN	0.8102 0176	0.000 44592 2	ZNF64 4	0.2792 6868	0.008 21633 8
TUBB	1.2900 04	1.81 637 E-16	MAPK11 P1L	0.5404 446	1.843 34E- 06	NAPEP LD	0.3246 6224	0.000 44671 4	TSR2	0.5163 226	0.008 22024 3
DDX21	1.0263 484	2.00 897 E-16	COX20	0.6828 383	1.849 24E- 06	NFRKB	0.3716 2492	0.000 44971 7	NCS1	0.6099 383	0.008 25677 8
HNRN PUL1	0.8908 143	2.18 592 E-16	SAFB2	0.6717 8166	1.856 61E- 06	RASG RP4	0.0471 28662	0.000 44996	DHRS7 B	0.5265 81	0.008 27160 8
FAM53 B	1.4619 02	2.21 281 E-16	DROSH A	0.4619 051	1.863 52E- 06	MRPL1 0	0.6570 0024	0.000 45057 4	KBTBD 2	0.1928 36	0.008 28099 7
PYGL	1.7138 95	2.23 139 E-16	SGK3	0.6817 369	1.864 03E- 06	COMM D8	0.7526 949	0.000 45128 1	CTNN BL1	0.4595 672	0.008 29980 4
CCT4	1.5418 782	2.34 115 E-16	WDR82	0.4463 4813	1.869 5E-06	EEF2K	0.3535 25	0.000 45236	CMTM 6	0.3543 9393	0.008 30237 6
ENOS F1	0.8759 226	2.49 354 E-16	TRMT6	1.0004 864	1.869 5E-06	SNOR D80	1.5403 174	0.000 45260 5	TDP1	0.4363 875	0.008 30494 9
RPL37	0.7700 0725	2.62 281 E-16	NMRAL 1	0.8285 4164	1.886 92E- 06	C19orf 35	0.0066 8466	0.000 45275 7	SLC9A 3R1	0.5945 3166	0.008 30889 2
COX6B 1	1.3487 247	2.67 349 E-16	RPE	0.7699 075	1.888 94E- 06	CASP6	0.3305 506	0.000 45337 4	NUSA P1	0.8389 899	0.008 33066 9
CCNB1 IP1	1.6603 248	2.82 535 E-16	SERPIN H1	0.9160 3196	1.897 47E- 06	HOXC 9	0.7701 778	0.000 45483 1	RBM28	0.2802 9338	0.008 33599 7
FBL	1.5909 128	2.90 479 E-16	MPRIIP	0.2329 079	1.897 99E- 06	ARFRP 1	0.5322 9797	0.000 45526 4	SNX33	0.6670 8684	0.008 36318 3
GNB2L 1	0.9307 4524	2.96 221 E-16	RWDD1	0.8382 1756	1.898 53E- 06	USPL1	0.6060 736	0.000 45569 7	NCAP H2	0.4046 2884	0.008 38647 2
CPSF1	1.0793 723	3.00 655 E-16	MED19	0.7625 99	1.898 53E- 06	PTRH1	0.7775 1553	0.000 45856 9	RNF21 9	0.3636 1837	0.008 40151 3

TSR1	1.1277 523	3.10 975 E-16	VPS28	1.0960 836	1.908 67E- 06	MED25	0.4808 34	0.000 45859 6	LOC28 5000	0.9960 435	0.008 42351 1
SETDB 1	1.2613 009	3.21 191 E-16	USP39	0.8833 163	1.911 22E- 06	PRKA R2A	0.5950 257	0.000 45918 7	TXLNG	0.3884 6552	0.008 42473 1
PEPD	1.5689 926	3.35 507 E-16	C2orf88	0.9629 919	1.914 78E- 06	FBXO9	0.1191 8597	0.000 46018 9	EXTL2	0.3364 7785	0.008 43011 5
ISYNA 1	1.4431 341	3.55 75E- 16	LRRN4 CL	0.7064 1935	1.943 87E- 06	ALK	1.3268 08	0.000 46223 5	LINC00 476	0.1101 9325	0.008 43689
COPA	1.1672 865	3.96 39E- 16	PAR-SN	0.6635 598	1.962 48E- 06	ITFG2	0.5352 6425	0.000 46365	HSD17 B7P2	0.0621 8642	0.008 45201 4
PQBP1	1.5185 07	3.98 019 E-16	RMDN3	0.7824 585	1.965 09E- 06	FAM63 A	0.5512 4414	0.000 46365	ATF7	0.3241 4228	0.008 45463
ATP5B	1.2859 535	4.58 635 E-16	ANKFY 1	0.6162 422	1.968 24E- 06	MAD2L 1	0.9131 8685	0.000 46365	CSRP2	0.7767 704	0.008 50609 4
ZBED3 -AS1	2.9992 902	4.60 174 E-16	ZNF480	0.3333 6303	1.968 26E- 06	LAMT OR3	0.3918 5825	0.000 46409 2	IFFO1	0.3325 73	0.008 52693 9
RPL30	0.7316 41	4.60 543 E-16	AKR7A 2	0.7608 214	1.978 19E- 06	BRMS 1	0.6419 9775	0.000 46481 9	HERC1	0.1317 4498	0.008 54344 5
POLR1 D	1.6579 156	4.69 052 E-16	STK24	0.7062 291	1.996 58E- 06	LRRC4 7	0.3243 687	0.000 46665 8	SLC26 A6	0.4802 2354	0.008 54468 2
LYPLA 1	1.3693 916	5.17 58E- 16	AP1S2	0.8510 3244	2.012 49E- 06	RASSF 1	0.5905 814	0.000 46940 3	DYM	0.3220 9972	0.008 57124 7
LZTS2	1.4199 854	5.18 451 E-16	ANGEL 2	0.4447 336	2.020 5E-06	PLEKH B2	0.5209 7917	0.000 46975 3	SCN8A	1.1678 21	0.008 57812 6
PLEKH J1	1.5947 064	6.14 649 E-16	TTC19	0.5343 576	2.035 51E- 06	LTBR4	0.2762 3186	0.000 47029 6	ETS2	0.7595 0074	0.008 58077 7
LMCD1	1.8142 28	6.79 743 E-16	PIK3R3	0.8716 7007	2.043 61E- 06	RNF14 1	0.3496 9166	0.000 47128 7	MOSP D3	0.4879 3942	0.008 59014 9
ALDH1 8A1	1.4167 343	7.16 467 E-16	PDLIM7	0.7750 068	2.063 13E- 06	RRM2	0.6470 7214	0.000 47144 6	TRIM4 6	1.4834 161	0.008 60269 6
WASH 1	1.1225 293	7.17 082 E-16	ZNF880	0.8477 89	2.065 88E- 06	CERKL	1.4933 789	0.000 47373 2	SRSF3	0.6079 2655	0.008 61384 3
RPL13	0.6524 236	7.24 126 E-16	IDE	0.7784 27	2.068 09E- 06	PRIM2	0.5888 931	0.000 47418 3	SGK19 6	0.4682 4598	0.008 61509
MPZL1	1.2751 448	7.30 316 E-16	RNMTL 1	1.0676 414	2.074 68E- 06	SIRT3	0.2329 7942	0.000 47434 3	PRKY	0.2644 8646	0.008 61633 7
GATA D2A	0.9466 6564	8.13 677 E-16	LTBP4	0.7935 2623	2.084 67E- 06	HSBP1 L1	0.6849 293	0.000 47440 5	EAF1	0.0867 0827	0.008 65162 7
WASH 2P	0.9225 9306	8.30 82E- 16	UVRAG	0.8309 1235	2.084 67E- 06	TMEM 141	0.5557 9215	0.000 47485 6	ZBTB1 7	0.4669 3176	0.008 66835 5
RNF2	1.1170 307	8.30 82E- 16	SNORA 70	1.3354 545	2.084 67E- 06	SRPR B	0.5838 069	0.000 47628 1	MRPL1 7	0.3931 7513	0.008 69081 8
BCCIP	1.4148 864	8.76 002 E-16	PRR14	0.9659 545	2.101 8E-06	RBMX	0.8348 355	0.000 47722 1	ASH1L -AS1	0.3052 053	0.008 69635 8
RPL36 A	0.7787 6544	9.02 007 E-16	KIF3A	0.4332 3952	2.101 84E- 06	SIPA1L 3	0.8099 122	0.000 47787	FOXJ3	0.2600 1114	0.008 74611 5

CCT2	1.5725 16	1.01 449 E-15	GTF2H 2D	0.7865 0266	2.107 42E- 06	TUBA3 FP	0.2007 3445	0.000 47891 2	TCEB1	0.3843 7423	0.008 75168 7
CDH3	1.7702 986	1.20 97E- 15	EFCAB 2	0.3970 619	2.111 34E- 06	PLXNA 1	0.4008 7044	0.000 47917 1	PUS3	0.7260 218	0.008 75726 2
UBA52	1.0153 921	1.45 88E- 15	PABPC 4	0.6857 123	2.113 64E- 06	CHCH D4	0.8115 8864	0.000 47952 8	GMPP A	0.4053 0446	0.008 76284
SUCL G2	1.3775 02	1.52 536 E-15	KCNJ13	0.8905 148	2.114 79E- 06	SDHD	0.7339 5133	0.000 47995	TNFAI P2	0.5987 8474	0.008 77273 8
GPR89 A	1.3854 978	1.78 154 E-15	PAK1IP 1	0.8600 4627	2.134 97E- 06	NAA16	0.3460 1605	0.000 48105 9	44447	0.2688 253	0.008 78408 6
KLHL9	1.3846 745	1.81 995 E-15	DYNC1I 2	0.4605 0766	2.141 2E-06	PITPN B	0.6168 243	0.000 48105 9	VRK1	0.6615 5136	0.008 78968
VDAC2	1.5908 885	1.81 995 E-15	TP53I3	1.2180 699	2.152 54E- 06	NDUF AF7	0.2932 0282	0.000 48141 8	EGFL7	0.9325 981	0.008 80070 9
HSPA2	1.9735 177	1.93 571 E-15	GTF3A	1.1013 631	2.155 42E- 06	AQP6	0.0794 2233	0.000 48194	SLC2A 1	0.6313 298	0.008 80342 6
SLC19 A1	1.3194 92	1.99 103 E-15	RNF44	0.7444 41	2.177 12E- 06	COX19	0.2064 6116	0.000 48194	APBB3	0.2194 2706	0.008 80903 2
AFG3L 2	1.1712 917	1.99 97E- 15	TMEM1 83B	0.8292 074	2.183 47E- 06	POLG2	0.5693 6723	0.000 48220 1	PPAN	0.6231 4653	0.008 82025 4
LINC00 662	0.8721 5143	2.09 941 E-15	ZMAT3	0.3899 4518	2.184 66E- 06	LYRM2	0.2945 0616	0.000 48582 4	ACAD S	0.4977 5895	0.008 82025 4
ILVBL	1.5377 74	2.28 936 E-15	NOC4L	0.9553 158	2.200 27E- 06	C16orf 80	0.7264 173	0.000 48747 9	MAN2 A1	0.6128 026	0.008 83004 2
PRCC	0.9465 6545	2.37 343 E-15	AASDH	0.9180 0606	2.223 58E- 06	KIF20B	0.5871 6375	0.000 48764 3	TUT1	0.4452 6803	0.008 84435 8
ARHG AP4	1.8118 917	2.40 479 E-15	ATIC	1.0467 994	2.231 82E- 06	COQ3	1.1438 069	0.000 48940 4	SS18L 2	0.4669 4	0.008 84981 9
CINP	1.5988 017	2.47 858 E-15	THUMP D3	0.5300 1887	2.234 21E- 06	DGCR 6L	0.7855 6544	0.000 48966 9	ARMC X5- GPRA SP2	0.7917 2957	0.008 84981 9
MICAL 1	1.4025 055	2.66 881 E-15	WIPF3	0.3816 6207	2.262 62E- 06	TIMMD C1	0.7180 603	0.000 49053 4	RRM2 B	0.3844 04	0.008 85545 3
GALT	1.4345 373	2.68 836 E-15	COPS8	0.8883 17	2.265 64E- 06	MAST2	0.3981 8636	0.000 4907	DDX20	0.5185 594	0.008 87562 1
SCAM P3	1.4112 239	2.71 937 E-15	MEF2B NB	0.6895 7233	2.268 66E- 06	TUBA1 A	0.8371 746	0.000 49076 5	CFL1P 1	0.1080 8803	0.008 88188 3
WDR6	1.1881 061	2.76 567 E-15	CSNK2 A1	0.7253 748	2.313 24E- 06	KIAA04 08	0.1661 3673	0.000 49488 4	NUP18 8	0.1720 7049	0.008 88188 3
SETDB 2	1.0980 233	2.98 293 E-15	MTX2	0.9058 461	2.316 93E- 06	TMEM 167A	0.4106 645	0.000 49488 4	PPA2	0.2828 31	0.008 88188 3
FES	1.8897 954	3.05 019 E-15	BTF3L4	0.6320 372	2.329 17E- 06	NFATC 3	0.4971 9593	0.000 49596	PIK3R 2	0.1552 584	0.008 97640 5
C22orf 29	0.9827 8546	3.24 673 E-15	URI1	0.6854 0955	2.371 83E- 06	SLC7A 6	0.1859 5928	0.000 49622 8	PUM2	0.1711 4612	0.008 98064 3

SOX4	1.1470 406	3.24 673 E-15	MYO19	0.6496 899	2.378 73E- 06	TECPR 1	0.1750 8098	0.000 49812	C20orf 194	0.2402 0064	0.008 98341 3
CTSK	2.0418 55	3.31 029 E-15	PPDPF	0.5004 3344	2.395 05E- 06	XPO4	0.3998 855	0.000 49838 9	IPO7	0.3155 493	0.009 00531 9
PHB2	1.4575 746	3.32 368 E-15	KLHDC 3	0.9458 614	2.399 5E-06	NAA20	0.8402 332	0.000 49906 6	LIN28A	0.1555 5757	0.009 01087 4
ZNF14 6	1.2274 264	3.49 149 E-15	NR2F2	0.7425 6516	2.407 11E- 06	MX2	0.7664 948	0.000 50093 2	WDYH V1	0.5497 803	0.009 04170 9
CHCH D6	1.3479 503	3.80 384 E-15	C16orf8 9	1.3040 226	2.413 48E- 06	RBMS 1	0.4579 9002	0.000 50093 2	TRMT1 1	0.3229 072	0.009 05024 4
NDUF A3	1.4878 757	3.87 343 E-15	DNMT1	0.5564 1764	2.420 5E-06	PAIP1	0.5276 5954	0.000 50130 5	RNF16 9	0.1897 3596	0.009 05024 4
IDH3A	1.3319 203	4.00 185 E-15	ZDHHC 11	1.7516 104	2.456 34E- 06	CDK7	0.6600 13	0.000 50137 2	SECIS BP2	0.2098 0114	0.009 05895 8
TRUB2	1.5774 869	4.03 814 E-15	MGC27 52	0.3850 359	2.482 96E- 06	SPRY D4	0.3013 643	0.000 50557 5	EDEM 2	0.3858 5576	0.009 06471 4
POLR3 C	1.4168 736	4.44 806 E-15	MCRS1	0.7855 5596	2.511 79E- 06	SWSA P1	0.2446 3995	0.000 50560 7	C14orf 93	0.7560 8027	0.009 06602 7
C11orf 24	1.4325 162	4.57 45E- 15	EBNA1 BP2	0.9895 262	2.511 84E- 06	ACAD VL	0.5394 7157	0.000 50560 7	DCXR	0.6476 6896	0.009 07327 1
IPO9	0.8573 903	4.86 244 E-15	LENG8	0.5154 038	2.527 07E- 06	PCBD1	0.6379 3683	0.000 50577 7	TTPAL	0.0869 5073	0.009 11603 9
ZFAS1	1.3500 79	4.94 923 E-15	COX7A 2L	0.9444 463	2.549 76E- 06	RFX7	0.3432 0402	0.000 50636 1	ZNF58 5A	0.4270 422	0.009 13226 8
ZCCH C9	1.2067 9	5.11 083 E-15	ZNF273	0.1920 9838	2.549 76E- 06	UBE2V 2	0.6921 199	0.000 50642 8	SDHB	0.8044 6863	0.009 15899
TRIM2 8	1.1553 061	5.76 871 E-15	APOA1 BP	0.9231 1496	2.571 25E- 06	DNM1 P35	0.1611 9091	0.000 50752 9	THEM6	0.5909 266	0.009 16031 5
TROV E2	1.3540 554	5.84 02E- 15	CIC	0.3879 853	2.571 31E- 06	SF3A3	0.7073 162	0.000 50842 4	NME7	0.4049 8093	0.009 18711 2
RPS28	0.9126 8826	5.98 85E- 15	RANBP 1	1.0042 049	2.593 71E- 06	ZNF27 6	0.0679 182	0.000 50856	SLMAP	0.2843 0438	0.009 20345 6
HNRN PF	1.3926 666	6.70 499 E-15	LIPA	0.9242 2086	2.607 37E- 06	LOC20 2181	0.5778 7246	0.000 50856	LINC00 641	0.0543 18633	0.009 20779 3
SLC5A 4	2.7282 388	6.82 722 E-15	GIN51	0.7579 302	2.612 89E- 06	CDK5R AP1	0.6184 623	0.000 50952 6	PTPN3	0.0695 76286	0.009 21196 1
PIP4K2 A	1.1515 472	7.10 455 E-15	ESRG	0.5191 969	2.615 E-06	IP6K1	0.5561 456	0.000 51160 2	PCED1 A	0.3650 0117	0.009 21196 1
GNPD A1	1.4051 727	8.96 227 E-15	TYSND 1	0.7782 5886	2.621 9E-06	ZNF79	1.2092 481	0.000 51160 2	NDUF B7	0.7768 4796	0.009 22516 2
RPL14	0.7238 382	9.11 761 E-15	SETMA R	0.4268 9416	2.676 65E- 06	ANAP C1	0.2600 6824	0.000 51160 2	PKMY T1	0.9603 803	0.009 22516 2
MTHF D1	1.3414 73	1.17 479 E-14	FBXW4	1.1287 831	2.689 32E- 06	LINC00 620	0.0053 35482	0.000 51278 2	LSM5	0.2599 2298	0.009 22632 6
LSM14 A	1.0176 215	1.22 315 E-14	FAM114 A2	0.8622 862	2.694 3E-06	XRRA1	0.5473 2627	0.000 51278 2	MAPK7	0.3835 8217	0.009 22632 6

LOC38 8796	1.3138 323	1.23 619 E-14	ATP5G 3	0.6464 931	2.697 18E- 06	FXYD7	2.4876 373	0.000 51347 8	BRF1	0.2301 6356	0.009 25010 7
SUPT5 H	1.1231 506	1.37 636 E-14	PIAS4	0.9967 5536	2.719 87E- 06	PFDN4	0.4558 6744	0.000 51943 1	RNPE PL1	0.5156 864	0.009 26655 3
LOC10 013224 7	1.1697 716	1.55 359 E-14	LIMA1	0.8235 228	2.721 36E- 06	NSUN2	0.4381 2504	0.000 52161 7	HACL1	0.5260 313	0.009 26940 7
HADH A	1.2895 776	1.63 379 E-14	COG8	0.7568 09	2.728 54E- 06	ZBTB1	0.6510 2774	0.000 52264 3	LOC28 3143	1.2639 449	0.009 29497 6
SPG20	1.0663 084	1.78 981 E-14	RAB3G AP2	0.4172 2214	2.737 88E- 06	CCDC 114	0.0417 2406	0.000 52683 6	FAM13 4A	0.1355 3762	0.009 30845 9
NIP7	1.0986 999	1.80 447 E-14	ATAD3 A	0.6365 8196	2.740 09E- 06	PI4KA P1	0.3418 755	0.000 52969 7	NDUF S3	0.6887 4794	0.009 32617 6
SNHG 5	1.2714 92	1.87 683 E-14	LOC100 288778	0.4666 0173	2.743 73E- 06	CCDC 50	0.5400 0413	0.000 53063	POLD3	0.5566 0224	0.009 35019 2
KIAA12 11	1.3563 745	1.92 696 E-14	PDHA1	0.7204 795	2.745 95E- 06	PHF14	0.2562 2153	0.000 53167 2	SULT1 C4	0.9169 5166	0.009 36832 7
HIST3 H2A	1.4275 537	2.03 602 E-14	ZNF780 A	0.4914 8998	2.747 45E- 06	OPRK1	0.3693 1866	0.000 53267 9	VASH1	0.2886 4396	0.009 37273 7
FAM45 A	1.4727 566	2.19 609 E-14	HHLA2	0.1890 6672	2.748 96E- 06	MGA	0.2967 3725	0.000 53524 4	CD302	0.4618 089	0.009 38003 4
METTL 13	1.2686 888	2.19 719 E-14	CERS6	1.0147 15	2.764 85E- 06	GAB1	0.3393 2865	0.000 53847 6	MYO1 E	0.2267 066	0.009 38139 2
VPS26 A	1.2133 503	2.27 775 E-14	TADA1	0.9158 8783	2.773 59E- 06	CCT8	0.8051 3275	0.000 54481 2	MBNL2	0.2394 2158	0.009 38274 9
ISG20L 2	1.1388 953	2.42 418 E-14	RABL2 B	0.6511 992	2.822 54E- 06	SLC25 A24	0.4172 801	0.000 5454	CXorf2 3	0.2054 2032	0.009 39941
HDGF RP3	1.4686 797	2.55 994 E-14	VWA9	0.7808 2997	2.860 37E- 06	PLSCR 3	0.7290 042	0.000 54654 3	LOC10 050737 7	1.5160 795	0.009 40672 8
FGD1	1.3200 495	2.60 706 E-14	KPNA2	1.1166 344	2.873 89E- 06	HSDL1	0.4495 9813	0.000 54654 3	SLC25 A30	0.4675 783	0.009 40672 8
TIMM1 7B	1.3104 908	2.68 729 E-14	TP53BP 2	0.5620 1494	2.893 49E- 06	MCU	1.1395 843	0.000 54717 1	LMAN2 L	0.5869 89	0.009 41729
SMND C1	1.1089 73	3.10 191 E-14	STRAP	1.0352 44	2.903 38E- 06	KIAA13 24L	0.4347 4507	0.000 54768 8	YTHD C2	0.2407 6223	0.009 43707 9
POLR2 D	1.2861 328	3.28 954 E-14	SELEN BP1	1.1444 612	2.915 58E- 06	MRPL3 2	0.7379 9217	0.000 54850 2	ZDHH C8	0.6218 027	0.009 43998 3
GBAS	1.3119 73	3.39 185 E-14	NFX1	0.5968 8926	2.942 34E- 06	ZNF22 6	0.6016 518	0.000 55043 1	RPAP3	0.3723 926	0.009 44288 7
RPLP1	0.4846 8754	3.70 703 E-14	SDAD1	0.6755 492	3.007 42E- 06	P4HA1	0.5941 399	0.000 55281 5	ARL2B P	0.4646 8002	0.009 49015 2
EEF1B 2	1.0300 751	4.13 214 E-14	ZGPAT	0.9005 166	3.007 5E-06	FLJ304 03	0.0764 14764	0.000 55674 7	POGL UT1	0.4161 7545	0.009 49908 1
ADCK3	1.4114 106	4.78 089 E-14	CES2	0.5297 328	3.019 34E- 06	CNOT1 0	0.4240 4786	0.000 55881 7	ZNF14 2	0.3135 123	0.009 53763 1
ARHG EF1	1.0524 01	5.18 266 E-14	PTBP2	0.3433 8874	3.028 07E- 06	MTL5	0.2634 997	0.000 55881 7	EFHD2	0.3824 045	0.009 54815 5

CCNG1	1.4901537	5.18373E-14	ERLIN1	0.91442287	3.03366E-06	LOC644961	0.26939267	0.000560592	PTOV1	0.21246007	0.009548155
SMCR7L	1.0728886	5.445E-14	MICU1	0.77334833	3.04243E-06	BAG5	0.21846032	0.000561576	FOXK2	0.18248834	0.009568194
FABP5	1.5463823	5.52036E-14	USB1	0.8217596	3.05917E-06	PCDHGA12	0.97478694	0.000561765	HCN3	1.0515953	0.009597459
PGAM4	1.7590581	5.58565E-14	MRPL34	0.924084	3.1162E-06	HAUS1	0.62605923	0.000561954	ATAD2	0.86518645	0.009618983
DDX50	1.1838949	6.17052E-14	EPB41L4A-AS1	0.81253654	3.1171E-06	UBAP1	0.3939296	0.000564423	RAB14	0.18523893	0.009665478
TTLL4	1.0199727	6.63689E-14	DHX30	0.6741269	3.13098E-06	MAGOH	0.6055626	0.000567591	ATM	0.14183833	0.009665478
SPG21	1.439938	6.86665E-14	CYB5B	0.5192946	3.14736E-06	AMACR	0.5854045	0.000572625	CPNE7	1.3961015	0.009701141
DCTN5	0.84385085	6.86665E-14	CLIP3	1.1541024	3.16055E-06	PUS7	0.40516877	0.000572934	AGAP1	0.32639116	0.009701141
CALM3	1.0031812	7.01142E-14	LIN54	0.37557274	3.17379E-06	DAZAP1	0.35965264	0.000574596	TCFL5	1.3917886	0.009714985
ACAT1	1.3174812	8.14079E-14	HUS1	0.569781	3.19371E-06	C5orf63	1.5347631	0.000574596	PITPNM1	0.6922695	0.009714985
TARS2	1.0372641	8.30877E-14	GBAP1	0.7537686	3.22043E-06	BRCA2	0.7687033	0.000574905	MYH14	0.82599574	0.009724282
PRMT7	1.3274492	8.55761E-14	PABPC3	1.1982741	3.25157E-06	CDH6	0.23210056	0.000575215	ZFYVE9	0.81998885	0.00974624
TIMM22	1.4730712	8.69628E-14	CCS	0.9085861	3.2975E-06	BTG3	0.6235347	0.000577389	TRIB3	0.68889713	0.009769654
LDB3	1.338086	8.71591E-14	DPF2	0.804873	3.30273E-06	RAB3A	1.0124253	0.0005777	MED11	0.69932187	0.009809024
MTAP	0.9792609	8.96271E-14	VLDLR	1.0009634	3.30282E-06	DZIP3	0.1495203	0.000580469	STXBP3	0.3002447	0.009827791
INPP4B	1.4055736	9.55701E-14	YWHAB	0.6581668	3.3175E-06	TEAD2	0.8525269	0.000582152	C1orf159	0.291875	0.009827791
BFAR	1.0918003	9.81183E-14	HEATR1	0.57390994	3.31759E-06	ZNF576	0.86627924	0.000582152	PTPDC1	0.8210554	0.009830805
TBRG4	1.420308	1.05226E-13	CCDC171	1.1928911	3.34271E-06	APOO	0.6712684	0.000583407	ZNF497	0.17205568	0.009835417
MIR4461	2.0905893	1.05226E-13	PNRC2	0.86714995	3.34541E-06	FKBP1A	0.6113673	0.000587702	ZNF605	0.30300575	0.009852632
DNMT3A	1.136066	1.09432E-13	EMC2	0.88329214	3.36288E-06	SNAPC2	0.66075486	0.000588494	ARHGEF2	0.17520398	0.009852632
SRM	1.3238746	1.16759E-13	C20orf112	0.6381485	3.39018E-06	ADNP	0.3851375	0.000593143	THRAP3	0.41801405	0.009855654
CCDC144C	1.647167	1.20101E-13	RAB3B	0.28600165	3.39018E-06	CSTF3	0.61518776	0.000596342	LIG3	0.30979434	0.009871476
TRIM63	1.435717	1.21516E-13	B3GALT	0.82029176	3.39995E-06	NSUN4	0.16369814	0.000597868	RP9	0.2731365	0.00988091

SIGMA R1	1.4369 969	1.22 901 E-13	MPP7	0.3498 1984	3.439 88E- 06	CLNS1 A	0.7662 812	0.000 60012 2	EXOS C10	0.4754 374	0.009 88233 9
CRISP LD1	1.5016 665	1.23 668 E-13	MAGI2- AS3	0.5482 8846	3.447 12E- 06	TRIO	0.2531 412	0.000 60173 7	CHSY1	0.0857 4306	0.009 90765 7
RPL7A	0.7562 907	1.32 505 E-13	ARSB	0.4409 806	3.461 52E- 06	MYL9	0.8114 853	0.000 60173 7	STAU1	0.4421 5533	0.009 93142 4
MET	1.1024 193	1.51 55E- 13	PHF20L 1	0.6978 129	3.462 52E- 06	STK25	0.5340 7615	0.000 60177 8	TAF6	0.2370 2362	0.009 93769
AVL9	1.2158 407	1.51 55E- 13	SH3PX D2B	0.7759 415	3.465 32E- 06	CD79B	1.4348 26	0.000 60234 5	BAG3	0.3509 046	0.009 95847
NARS2	1.3565 582	1.61 585 E-13	SUPV3 L1	0.8763 2227	3.506 89E- 06	PRPF8	0.4501 3514	0.000 60327 6	A1BG	0.2443 9114	0.009 99511 7
SRSF7	1.1524 453	1.67 102 E-13	PXK	0.9626 854	3.562 74E- 06	TOR2A	0.9618 009	0.000 60673 1	MLL	0.1788 541	0.009 99656 2
PFDN2	1.3878 196	1.70 194 E-13	FLYWC H1	0.6931 465	3.572 99E- 06	RUFY1	0.7164 784	0.000 60762 8	TBL1X	0.5580 9337	0.010 05645 3
GRWD 1	1.1301 931	1.83 508 E-13	SNAP4 7	0.8235 8724	3.613 94E- 06	SNRN P70	0.4611 0234	0.000 60762 8	WDR9 0	0.4214 3413	0.010 05790 5
TMEM 204	2.5623 136	1.90 134 E-13	TCEAL8	0.9057 985	3.647 92E- 06	RPSAP 9	0.1650 7256	0.000 60865	LOC14 8709	0.1468 6416	0.010 06750 1
MMS1 9	1.2712 047	2.14 87E- 13	SOGA1	0.6068 656	3.650 87E- 06	SAMD 4B	0.3510 365	0.000 60865	RPAP2	0.4433 215	0.010 09506
RPL10	0.6862 957	2.20 881 E-13	UTS2D	0.2841 5313	3.670 83E- 06	C15orf 38	0.4406 837	0.000 60995 9	LRP6	0.1949 832	0.010 11105 4
MRPL3 7	1.4458 843	2.20 881 E-13	KCTD2 1	0.7880 379	3.677 58E- 06	ADRB K1	0.3997 6233	0.000 61139 4	AMOT	0.7368 322	0.010 14856 4
PYCA RD	1.9805 158	2.44 937 E-13	YWHAE	0.6265 214	3.688 16E- 06	HARS	0.6652 3874	0.000 61382	HSD17 B11	0.5277 55	0.010 26369 4
DARS	1.3457 128	2.47 613 E-13	ARHGA P39	0.8102 2894	3.690 18E- 06	CCDC 167	0.6656 6426	0.000 61452 1	FSTL1	0.5616 551	0.010 28177
SHMT2	1.4637 899	2.47 999 E-13	SHOC2	0.7165 4576	3.693 28E- 06	OSTF1	0.6023 767	0.000 61534 7	NDOR 1	0.1939 5809	0.010 28491 2
LAMT OR1	1.3180 462	2.57 415 E-13	NAT9	0.8564 3095	3.693 28E- 06	QTRT1	0.6052 252	0.000 61642 2	PPAR D	0.1242 1812	0.010 28639 4
R3HC C1L	1.0281 934	2.60 836 E-13	C2orf47	0.9079 2704	3.693 4E-06	GUCD 1	0.2889 9822	0.000 61820 4	LINC00 518	0.4120 8917	0.010 35788 8
TRIM2 7	1.1938 953	2.62 057 E-13	GNPNA T1	0.4886 8588	3.705 93E- 06	INO80 E	0.4043 7758	0.000 61820 4	GUSB P4	0.5926 107	0.010 36738 1
MTG1	1.1716 692	2.76 58E- 13	SEC31 A	0.7278 607	3.709 88E- 06	NKAP	0.5529 5974	0.000 61853 6	SLC43 A1	0.6487 9245	0.010 37706 4
CTPS1	1.3868 127	2.84 853 E-13	AIFM2	0.3265 4983	3.737 86E- 06	RIOK3	0.4197 477	0.000 62332 5	RABL6	0.1008 14156	0.010 38340 3
TSNAX	1.1143 714	2.87 411 E-13	CCDC8 6	0.8407 825	3.758 28E- 06	HTRA3	2.6834 059	0.000 62416 2	FAM89 A	0.7984 667	0.010 39495 9
RPS27 A	0.5578 743	2.94 748 E-13	NGRN	0.9651 6013	3.791 5E-06	SNHG 9	0.5847 338	0.000 62462 3	MPDZ	0.3123 6872	0.010 39813 4

UPF3A	0.9421 027	3.07 354 E-13	FAM104 B	0.7966 4534	3.806 32E- 06	TMEM 39B	0.6241 325	0.000 62613 4	H2AFZ	0.5239 368	0.010 40802 5
RRS1	1.4065 427	3.36 875 E-13	PRR5	0.8559 108	3.833 15E- 06	VN1R2	0.2029 8067	0.000 62613 4	TRNT1	0.2815 352	0.010 41120 4
BAX	1.1980 873	3.36 875 E-13	ZNF512	0.8165 6414	3.833 15E- 06	IFT52	0.7271 3643	0.000 62836 3	DEF6	1.2588 936	0.010 41942 6
MYBB P1A	1.1957 812	3.37 285 E-13	NACA	0.4464 1134	3.834 27E- 06	RPL19	0.2561 0694	0.000 63097 9	RBM12 B-AS1	0.8253 3777	0.010 43775
ARPC5	1.1977 361	3.42 16E- 13	ZNF552	0.9746 3644	3.847 27E- 06	C14orf 178	0.1708 9638	0.000 63106 4	PPIL6	0.0229 94198	0.010 46098 4
SHKBP 1	1.3790 375	3.54 715 E-13	XRCC1	0.8597	3.859 31E- 06	HBS1L	0.3698 019	0.000 63292 8	NOST RIN	2.1322 265	0.010 50287 3
TMEM 55A	1.2339 615	3.54 715 E-13	GYG1	0.8793 216	3.878 38E- 06	ZC3HA V1L	0.2183 3487	0.000 63365	BCL2A 1	0.7711 934	0.010 51267 4
RPP25	1.5398 225	4.01 346 E-13	SLC41A 1	0.7406 373	3.905 58E- 06	FAM76 A	0.1219 34935	0.000 63501	NDUF B9	0.7472 9836	0.010 52775 4
RPL39	0.8140 6575	4.23 765 E-13	TOMM4 0	0.7382 927	3.915 78E- 06	ETV1	0.5274 356	0.000 63880 5	PDCL	0.1913 2674	0.010 53436 2
FASTK D2	0.8683 7184	4.63 162 E-13	HELLS	1.2317 309	3.927 17E- 06	TCN2	0.9275 128	0.000 64172	GEMIN 5	0.4490 3147	0.010 56988 6
RPA1	1.1658 19	4.76 415 E-13	SURF6	0.8177 9456	3.965 9E-06	ZNF52 7	0.0881 97716	0.000 64193 5	TAF9	0.7369 624	0.010 59015 6
SYNC RIP	1.0627 056	4.76 415 E-13	TSC2	0.5554 264	3.967 06E- 06	FLYW CH2	0.5639 8803	0.000 64331 2	TMEM 48	0.4617 238	0.010 5968
IL6R	0.9943 4173	4.91 886 E-13	WDR26	0.4533 3967	3.980 5E-06	ADA	1.2653 879	0.000 64581 5	NAPG	0.2445 6057	0.010 60173 9
TFIP11	1.2226 466	4.94 205 E-13	RBM5	0.6704 3555	4.023 88E- 06	ANKR D30BL	0.2635 9355	0.000 64581 5	RBM48	0.2172 2932	0.010 62377 6
WAPA L	0.8466 762	5.06 931 E-13	RIOK1	0.7982 8805	4.048 04E- 06	ABCD3	0.4208 6586	0.000 64629 2	SIMC1	0.6151 1445	0.010 64071 3
MRPL4 4	1.1467 471	5.37 819 E-13	PITRM1	0.6750 491	4.049 23E- 06	COQ5	0.7139 3687	0.000 64702 8	ZNF26	0.3030 568	0.010 65252 9
GNL3L	0.6860 849	5.57 448 E-13	NDUFA 13	0.9662 969	4.053 55E- 06	RAI14	0.3083 5962	0.000 64733 4	NUF2	0.9136 2584	0.010 67809 7
TIMM1 7A	1.3576 809	5.57 448 E-13	ZNF672	0.8856 769	4.069 36E- 06	STRN3	0.3266 0967	0.000 64733 4	OSBPL 8	0.2183 1208	0.010 68135 2
NR2C1	0.9863 706	5.91 818 E-13	KDEL 1	0.7897 617	4.085 23E- 06	EDEM 3	0.2659 896	0.000 65145 9	NOP14	0.4549 4312	0.010 69130 6
ATP5D	1.3450 178	6.03 087 E-13	KPNA3	0.8089 5776	4.104 32E- 06	KTI12	0.7221 6845	0.000 65298 6	CDCA8	0.8664 9096	0.010 72195
UROS	1.3544 53	6.31 718 E-13	STON2	0.1779 3255	4.180 18E- 06	STRAD A	0.3940 3275	0.000 65307 5	ZDBF2	0.1954 4959	0.010 75458 7
RAC3	1.5460 919	6.37 862 E-13	KLHL6	0.1208 9547	4.246 32E- 06	GEMIN 8	0.4117 5082	0.000 65644 5	YJEFN 3	0.8671 4524	0.010 76824 9
TOP1 MT	1.3157 69	6.54 483 E-13	JRK	0.4230 0054	4.302 41E- 06	CAMS AP2	0.2065 0434	0.000 65653 9	MTO1	0.5257 5094	0.010 82342 5

SPDYE 5	0.7952 095	6.64 392 E-13	ADK	0.7580 6534	4.304 78E- 06	PRRC1	0.3456 8545	0.000 65653 9	ARHG DIB	0.8273 995	0.010 86506 7
MORF 4L1	1.0750 368	6.76 513 E-13	WDR35	0.7633 365	4.313 94E- 06	SEC24 B-AS1	0.0206 4959	0.000 65676	MKS1	0.4773 5745	0.010 88198 2
TPP2	0.7528 328	6.85 969 E-13	RRP1	0.7742 724	4.334 07E- 06	HGS	0.6357 611	0.000 65777 1	UBE2Q 1	0.3574 173	0.010 89404 1
MAP3K 13	0.9080 094	7.26 848 E-13	TMEM5 3	0.4259 1876	4.344 25E- 06	TADA2 B	0.1848 5047	0.000 65838 8	CUL3	0.0415 813	0.010 92872 1
MRPS 21	1.0948 908	7.34 479 E-13	H1F0	0.7742 6183	4.345 53E- 06	CORO 2B	0.9172 796	0.000 66121 7	MBD1	0.3189 0878	0.010 93731 4
RINL	0.6456 3555	7.35 154 E-13	TMEM2 51	0.9609 085	4.354 62E- 06	TPMT	0.3410 1796	0.000 66121 7	OTUD6 B	0.4112 379	0.010 96878 3
RPL22	0.8590 559	7.35 553 E-13	PCCB	0.9103 2946	4.414 35E- 06	LLPH	0.4149 434	0.000 66121 7	STIP1	0.5885 242	0.010 97388
EXOS C4	1.4915 665	7.44 416 E-13	FAM168 B	0.5437 6227	4.429 25E- 06	SMA4	0.1856 3639	0.000 66121 7	EFCAB 5	0.3156 3884	0.010 98074 3
TPM3	0.7351 0337	7.58 991 E-13	AARS2	0.4297 9077	4.439 65E- 06	TOMM 40L	0.7587 198	0.000 6625	SULT1 C2	0.3745 289	0.011 00172 6
MCC	0.8903 962	7.93 704 E-13	ZNF586	0.9771 987	4.443 24E- 06	ZNF54 3	0.3962 6107	0.000 66352	ZMPST E24	0.3549 8518	0.011 02060 5
FUS	0.8430 2646	8.67 069 E-13	SSBP4	0.9389 01	4.505 29E- 06	HIATL1	0.3911 39	0.000 66467 5	ESRR A	0.3380 711	0.011 03811 5
RBM12	0.7830 5966	8.79 504 E-13	PART1	0.0700 3537	4.519 51E- 06	NUDT1 6	0.5849 266	0.000 66569 8	RACG AP1	0.6978 217	0.011 04324 3
EIF3A	0.9878 9513	9.53 758 E-13	POLR1 B	0.6257 989	4.524 32E- 06	SRPK1	0.5151 228	0.000 66708 1	RBM17	0.2843 6044	0.011 15856 8
MRPL1 2	1.3351 558	9.66 686 E-13	MOSPD 1	0.8981 193	4.530 3E-06	C17orf 70	0.5645 0963	0.000 66953 7	PDCD6	0.6564 3734	0.011 18702 7
SDCB P	0.9757 397	9.67 971 E-13	MSH6	0.6112 3204	4.592 35E- 06	LNX1	1.7073 323	0.000 67150 8	SPRY D3	0.4928 015	0.011 21016 3
MTHF S	1.0947 375	9.80 352 E-13	ARHGE F7	0.4617 0244	4.662 37E- 06	C3orf3 8	0.5642 0004	0.000 67213 7	SRR	0.6686 637	0.011 24774 5
SEC24 C	1.0695 899	1.01 189 E-12	LOC100 132832	0.4728 9723	4.700 86E- 06	GBA2	0.5803 765	0.000 67803 7	SERPI NG1	0.2283 5302	0.011 27260 8
MPDU 1	1.2215 967	1.02 444 E-12	DECR2	0.9003 342	4.756 65E- 06	C11orf 49	0.5826 3355	0.000 67812 9	ZNF28 0A	1.4008 563	0.011 27964
NOP16	1.4096 624	1.08 824 E-12	MGRN1	0.6157 669	4.848 86E- 06	MZT2A	0.6275 5543	0.000 67985 1	GSS	0.4810 2236	0.011 28486 9
GTF3C 6	1.3458 478	1.09 923 E-12	POLR3 B	1.0089 229	4.873 87E- 06	44444	0.9211 64	0.000 68048 8	RAB24	0.4283 194	0.011 38061 2
GNL2	1.2359 158	1.10 782 E-12	ANKRD 12	0.4412 2544	4.907 78E- 06	NRIP1	0.4225 6594	0.000 68262 5	ZBTB2 4	0.3139 9122	0.011 38061 2
RPAIN	1.0782 744	1.14 903 E-12	C10orf2	1.4540 108	4.944 83E- 06	FSTL5	1.1896 893	0.000 68449 5	MCOL N2	0.1020 89055	0.011 40718 1
SMG5	0.9317 683	1.19 175 E-12	LOC440 354	0.6347 29	4.945 03E- 06	MRGP RX3	1.5194 985	0.000 69022	LDHB	0.4932 459	0.011 42890 1

EML4	0.8452 6545	1.21 017 E-12	ZNF692	0.7769 663	4.975 6E-06	WDHD 1	0.9469 6057	0.000 69197 1	AJUBA	0.0250 09895	0.011 47264 6
IPO4	1.2227 603	1.30 745 E-12	TARBP 1	0.8035 2825	4.979 62E- 06	PPIAL4 G	0.3787 2314	0.000 69358 8	INTS4L 2	0.5319 0315	0.011 47409 4
CD81	1.1553 06	1.31 815 E-12	IREB2	0.3459 148	4.996 36E- 06	YAF2	0.1758 422	0.000 69479 2	PASK	0.8244 77	0.011 47409 4
BCL7A	1.2746 671	1.40 025 E-12	PTBP1	0.7468 022	5.009 32E- 06	DGKE	0.1313 114	0.000 69595 3	ST13	0.4387 2714	0.011 49225 5
TBC1D 16	0.9056 73	1.45 162 E-12	TCF12	0.6921 262	5.073 8E-06	TGIF2	0.4614 8172	0.000 69604 8	CC2D2 A	0.1954 9362	0.011 50676 5
MLLT1	0.9924 1436	1.50 824 E-12	TSPAN 4	0.8570 219	5.090 85E- 06	CISH	1.5046 462	0.000 69753 5	THAP3	0.4502 7292	0.011 51945
UFC1	1.2976 983	1.52 843 E-12	MTHFR	0.3168 047	5.091 06E- 06	IAH1	0.7045 4603	0.000 70243 2	DFFB	0.1233 1568	0.011 53399
C16orf 88	1.0062 616	1.52 997 E-12	RNF123	0.5103 7264	5.099 07E- 06	KIAA14 67	0.2649 164	0.000 70252 8	EPOR	0.3801 1664	0.011 53709 7
ETS1	0.9500 9446	1.66 606 E-12	FAM178 A	0.6515 69	5.099 28E- 06	CIDEB	1.2301 711	0.000 70318 6	RAD54 L2	0.2897 0832	0.011 53709 7
YTHDF 3	0.9689 488	1.69 936 E-12	C15orf6 1	0.6848 766	5.158 3E-06	RNF11 3A	0.7131 878	0.000 70342 2	MPI	0.3954 39	0.011 53709 7
RPL9	0.5686 5984	1.73 528 E-12	SFR1	0.5784 7446	5.163 77E- 06	PHB	0.7475 877	0.000 70548 6	SMIM1 1	0.2061 8159	0.011 55719 5
RPS21	0.8848 8775	1.80 008 E-12	SMIM7	0.7803 652	5.165 31E- 06	TMED5	0.3285 7022	0.000 70558 3	TUBA8	1.9519 501	0.011 55884 8
BPHL	1.1764 526	1.94 221 E-12	SC5DL	0.4395 683	5.198 52E- 06	MRO	0.0315 89583	0.000 71232 5	KIAA15 24	0.6652 751	0.011 56750 6
TUBG CP2	1.1246 095	1.96 028 E-12	LOC100 128881	1.4427 041	5.205 37E- 06	DUSP1 1	0.5865 925	0.000 72004 1	STK17 A	0.5750 8	0.011 56750 6
STT3A	1.2056 005	1.99 022 E-12	KCNN2	0.6427 513	5.209 57E- 06	USP49	0.2078 8677	0.000 72128 8	BTN2A 3P	0.1121 5308	0.011 56750 6
NR2F6	1.5018 033	2.01 552 E-12	BIVM	0.3663 8013	5.280 56E- 06	LRSA M1	0.3577 259	0.000 72426 7	SMTN	0.3335 768	0.011 57470 7
UQCR C2	1.3602 647	2.35 845 E-12	BTAF1	0.4973 91	5.282 13E- 06	MRS2	0.4217 7907	0.000 72566 5	NASP	0.4432 9658	0.011 57636 4
ITPA	1.3047 011	2.36 266 E-12	ELMO2	0.6844 158	5.336 39E- 06	HIP1R	0.6685 6927	0.000 72677 7	EML2	0.4915 1906	0.011 59837 5
NSL1	0.6389 6537	2.85 387 E-12	STAG3 L4	0.7255 4106	5.413 17E- 06	ZNF25 0	0.2086 239	0.000 72818	DERL1	0.4310 649	0.011 60188 8
DEDD	1.0523 423	2.96 399 E-12	RALB	0.8393 528	5.478 71E- 06	TRIM3 7	0.4302 0576	0.000 72857	MLF11 P	0.5982 61	0.011 61633 2
NCBP1	0.8706 994	2.98 81E- 12	MMS22 L	0.3111 9147	5.495 68E- 06	MRPS 17	0.6219 527	0.000 73055 8	DHRS X	0.3882 1077	0.011 64027
MAST3	0.7512 601	3.00 57E- 12	DHRS2	1.4311 553	5.529 53E- 06	PTPLA D1	0.6993 687	0.000 73065 7	HINT2	0.4618 8897	0.011 64379 4
MMAC HC	0.7529 287	3.05 163 E-12	RPL23A P82	0.4728 719	5.565 E-06	LZTR1	0.6791 365	0.000 73104 8	MANB A	0.4040 2636	0.011 65847 8

TRAPP C1	1.0085 956	3.21 073 E-12	ZNF140	0.9434 969	5.577 98E- 06	SLC39 A11	0.5084 5176	0.000 73187 7	NRN1	0.4870 4594	0.011 66573
USE1	1.2823 396	3.42 721 E-12	RASIP1	1.0985 986	5.635 66E- 06	EZH2	0.6026 79	0.000 73398 3	ASB13	0.4965 02	0.011 67671 2
EIF1A X	0.9185 9	3.45 506 E-12	SUPT7L	0.4906 5933	5.635 66E- 06	ANP32 A	0.2737 1508	0.000 73398 3	TRAF3	1.0001 625	0.011 68564 8
APH1A	1.1147 891	3.76 057 E-12	LACTB2	0.8377 6546	5.635 66E- 06	ITGB1 BP1	0.6132 862	0.000 73398 3	CEP17 0B	0.5759 3536	0.011 70205 5
CRYL1	1.4882 585	3.83 202 E-12	YTHDC 1	0.4413 8208	5.644 5E-06	PHKG1	0.2790 0985	0.000 7354	ZNFX1	0.0205 85971	0.011 70205 5
LOC72 8190	0.9617 9926	3.90 193 E-12	RNASE H2B	0.8362 4345	5.680 94E- 06	PLAC4	0.4814 2943	0.000 73902	RHPN2	0.1045 18674	0.011 70559 8
PEX19	1.1270 479	3.93 652 E-12	FLJ360 00	0.9964 887	5.681 19E- 06	SENP6	0.1671 5324	0.000 74409	DDB2	0.3831 405	0.011 72035 3
MKI67I P	1.2288 995	3.95 384 E-12	ARID3B	1.1693 662	5.704 56E- 06	NARG 2	0.0940 81536	0.000 74533 1	PLEKH G4	0.3959 418	0.011 72951 1
C19orf 48	1.4437 742	4.04 088 E-12	SACS	0.6398 291	5.726 82E- 06	KRI1	0.2855 907	0.000 74533 1	IGF2B P1	0.6421 138	0.011 74242 1
FKBP4	1.1010 85	4.09 484 E-12	NOL12	0.4098 7128	5.738 72E- 06	SMG9	0.3250 579	0.000 74676 8	AGO1	0.2259 4221	0.011 76096 7
VNK3	1.0595 698	4.12 049 E-12	MARS	0.7975 4454	5.785 74E- 06	GPCP D1	0.4542 2596	0.000 74701 9	RSBN1 L-AS1	0.2066 6015	0.011 78310 5
ALDH3 A2	0.8910 249	4.19 098 E-12	RABEP K	0.9800 62	5.786 01E- 06	HDAC7	0.5604 612	0.000 74741 8	MLLT1 1	0.4741 3656	0.011 78667 1
C20orf 27	1.0895 972	4.67 988 E-12	GAREM L	0.4043 077	5.900 32E- 06	LENG1	0.7205 0834	0.000 74975 3	CALM1	0.4702 296	0.011 80151 8
VPS72	1.2275 904	4.84 637 E-12	ZFYVE1 9	0.8921 5285	5.906 58E- 06	FAM12 0C	0.4791 311	0.000 74985 6	RPL34	0.3183 3744	0.011 82937 9
GYS1	1.0667 409	4.89 65E- 12	C1QTN F6	0.5278 1814	5.932 34E- 06	KRR1	0.3847 8944	0.000 75095 6	SLC6A 15	0.2984 4055	0.011 82937 9
MDH2	1.3007 907	4.90 902 E-12	DSCR3	0.6238 4194	5.973 33E- 06	SLC5A 10	1.1250 68	0.000 75095 6	RFX3	0.7332 97	0.011 85182 5
SNRN P40	1.3301 884	5.00 201 E-12	MAN2A 2	0.5960 157	6.039 E-06	PTPR G-AS1	0.1534 1914	0.000 75165 7	FAM12 0A	0.2411 6568	0.011 85729 9
NUP62	1.0500 511	5.43 165 E-12	PTPRF	0.9804 748	6.048 46E- 06	CNTR OB	0.5100 922	0.000 75745 6	SLC46 A1	0.5346 3495	0.011 87411 8
NCL	0.7734 7755	5.43 556 E-12	ADHFE 1	1.0376 794	6.054 87E- 06	ZNF18 1	0.7346 8906	0.000 75876 4	ACAD9	0.3399 4755	0.011 88527 9
SH3PX D2A	0.9654 832	5.68 481 E-12	CNOT8	0.7387 9224	6.059 75E- 06	LOC10 065277 2	0.1594 3061	0.000 75901 9	RAB12	0.3434 541	0.011 89834 4
TMEM 70	1.1710 474	5.76 044 E-12	PPARG C1B	0.8848 5986	6.075 39E- 06	YTHDF 1	0.5254 5285	0.000 75987 7	HOGA 1	0.0134 22023	0.011 93420 1
HMOX 2	1.2673 781	5.84 566 E-12	HSPA1 2A	0.4513 9694	6.092 61E- 06	BMS1	0.2245 1584	0.000 76119	KIAA11 61	0.1642 4115	0.011 93571 7
GGH	1.4715 025	5.89 089 E-12	AP2S1	0.9314 967	6.133 11E- 06	CES1	2.7452 967	0.000 76159 7	MORC 3	0.1720 5653	0.011 93571 7

RNF167	1.0459 962	6.00 883 E-12	STXBP1	0.8360 4455	6.144 27E- 06	ECHDC2	0.6835 452	0.000 76792 5	TSHZ1	0.3769 148	0.011 94483 8
RUSC1	1.2399 246	6.18 785 E-12	GOT1	0.9727 548	6.163 24E- 06	SYT14L	2.0845 568	0.000 76818 3	ANKRD30B	1.2310 939	0.011 96938 7
CHD1L	1.1011 697	6.47 337 E-12	DDX54	0.7306 1967	6.179 14E- 06	CHCHD10	0.9790 6536	0.000 76996 7	ZNF337	0.3144 7408	0.011 98253 6
TFCP2	1.3344 347	6.49 718 E-12	HNRNPM	0.9566 8256	6.248 57E- 06	TRAPPC12	0.5796 6155	0.000 77007 3	L3HYPDH	0.3912 9147	0.012 02435 9
DDX39A	1.4453 456	6.54 503 E-12	NUFIP1	0.8719 8424	6.298 33E- 06	ZDHH C16	0.7799 02	0.000 77033 1	TICAM1	0.7266 6174	0.012 03545 6
FTSJ3	1.0946 895	6.69 549 E-12	MRPL38	0.7779 241	6.303 41E- 06	TSNARE1	0.8008 6994	0.000 77135 5	TMEM189-UBE2V1	0.6281 0767	0.012 03545 6
PGAM1	1.4706 194	7.28 1E- 12	JMJD4	0.9385 2216	6.324 45E- 06	MGEA5	0.2733 803	0.000 77253 3	44256	1.8517 138	0.012 05422 9
MPHOSPH10	1.0711 896	7.51 933 E-12	UGP2	0.8753 959	6.350 37E- 06	NANOS1	0.2228 0657	0.000 77817 4	OGFOD2	0.3446 7828	0.012 08435 9
HRNR	1.2240 399	7.72 56E- 12	FLJ31306	0.4357 5442	6.384 77E- 06	GLMN	0.6820 842	0.000 77982 5	ADCK4	0.3912 7448	0.012 09185 5
ZNF362	0.9118 718	7.74 577 E-12	FAM127C	0.7727 817	6.391 53E- 06	HMGXB4	0.4635 5015	0.000 78014 7	NEK2	0.1571 7211	0.012 12997 2
NNT	0.9844 377	7.74 577 E-12	HCG18	0.2431 2074	6.399 92E- 06	POLR2H	0.6937 9455	0.000 78014 7	DCUN1D2	0.0532 0981	0.012 20886
PTRHD1	1.3759 575	8.06 372 E-12	PRRC2A	0.4287 5174	6.452 16E- 06	ZDHH C9	0.573	0.000 78014 7	GNB1L	0.5858 28	0.012 22030 6
THOC5	1.1505 822	8.19 155 E-12	ANKLE1	0.4433 7326	6.472 05E- 06	TRMT2A	0.5072 4995	0.000 78361 7	REXO1	0.4823 3497	0.012 22787 7
APEX1	1.3865 318	8.65 283 E-12	GTPBP4	0.7959 2216	6.487 09E- 06	ALG12	0.5209 33	0.000 78434 6	TXNDC12	0.4432 0285	0.012 24128 4
SYTL2	1.7043 254	8.80 912 E-12	DHX9	0.7187 9125	6.489 05E- 06	KARS	0.7346 978	0.000 78678 9	N6AMT2	0.6864 3886	0.012 25275 8
WDR5	1.0968 074	8.98 782 E-12	PRPF39	0.5510 901	6.576 75E- 06	UFM1	0.4820 1048	0.000 78783 3	SDCCAG3	0.6220 785	0.012 25431 6
DHRS4-AS1	0.8341 031	9.70 02E- 12	PRKXP1	0.4468 1463	6.708 07E- 06	ZDHH C15	0.1519 4589	0.000 79375	C16orf91	0.4084 259	0.012 25801 5
NOL6	1.0806 606	9.97 316 E-12	C12orf43	0.4981 3947	6.708 39E- 06	SHE	0.2546 0142	0.000 79480 3	ALDH3B2	0.7058 6485	0.012 27886 1
TDRD7	1.5964 83	9.98 103 E-12	MAP4K4	0.3568 7676	6.720 58E- 06	SUV420H1	0.5776 608	0.000 79738 6	INVS	0.3111 2015	0.012 29036 7
BCKDHA	1.2885 015	1.11 144 E-11	ZC3H12B	0.1970 0994	6.731 08E- 06	C20orf96	0.4894 149	0.000 79934 4	TBC1D14	0.2384 8608	0.012 30774 2
NAPA	1.1450 38	1.12 694 E-11	PTP4A1	0.7978 493	6.794 48E- 06	HSPH1	0.5368 2923	0.000 79992 9	ADAMTSL5	0.3079 7657	0.012 31517 2
PTPLA	1.4072 937	1.23 908 E-11	SH3BP2	0.3343 661	6.806 81E- 06	ZNF529	0.2433 9926	0.000 80004	USP51	0.7689 85	0.012 35411 9

PNPLA3	1.1872301	1.23908E-11	ACO2	0.9216018	6.86398E-06	EIF3B	0.36831236	0.000802798	ANAPC10	0.35517243	0.012377077
BNIP3	1.2962544	1.25044E-11	CYBAS C3	0.75841177	6.86778E-06	SEPHS2	0.6612122	0.000803386	PPP1R3C	2.1264222	0.012396529
IDH3B	1.310444	1.28401E-11	TUBG1	0.85025674	6.88718E-06	SCO2	0.6651256	0.000806904	ACOT8	0.41157162	0.012429795
TUBA1B	1.1022774	1.28784E-11	PCTP	0.9452628	6.9625E-06	VPS33B	0.5933563	0.000809909	CDCA5	0.8120752	0.012431572
VPS36	0.8938355	1.33489E-11	PRKAG1	0.90355647	6.98919E-06	TPM3P9	0.054140802	0.000809909	EMD	0.2300462	0.012510437
RPL5	0.723892	1.36526E-11	LOC92249	0.80797845	7.02304E-06	IFIT1	0.5306698	0.000810342	EGLN3	1.3053488	0.01252214
RIT1	0.93771017	1.36983E-11	CWC22	0.5799649	7.05955E-06	MCMD C2	0.14541985	0.000811095	MRPL43	0.5675921	0.012525913
TOR3A	1.3054363	1.4072E-11	PFKFB2	0.9269702	7.05955E-06	ZC3HC1	0.632002	0.000812812	TEX101	0.00181203	0.012559298
YDJC	1.3577039	1.4617E-11	GMPR	0.7998096	7.05955E-06	CEP68	0.22760741	0.000814533	GRK5	1.0982953	0.012588978
DCAF13	1.2548944	1.49668E-11	LOC100271836	0.78454715	7.14746E-06	LPPR2	0.50412315	0.000814807	DHDD S	0.37268272	0.012648704
GART	1.0700693	1.50224E-11	ZNF507	0.4688481	7.15142E-06	LRRC42	0.6455783	0.000815403	SEPHS1	0.57720375	0.012650509
ATP7A	0.85736763	1.61039E-11	PIK3CD	0.52978224	7.21319E-06	AAAS	0.5692825	0.000821337	PTPN1	0.2888832	0.012657735
METTL16	0.80416137	1.61365E-11	SLC6A17	1.318999	7.27363E-06	ZNF271	0.19243194	0.000821613	MUTY H	0.43472698	0.012657735
C3orf14	1.4985203	1.61365E-11	THOC6	0.8541941	7.36041E-06	USO1	0.5161925	0.000824002	DPYSL4	1.6534219	0.012717761
ATP11A	1.2951267	1.62726E-11	PLAA	0.7901834	7.37004E-06	CSNK1G1	0.091767825	0.000827377	MPP6	1.3422763	0.012751608
UBIAD1	0.8971509	1.65504E-11	PSENE N	0.91112787	7.37042E-06	COPZ1	0.758224	0.000832078	ZNF707	0.5991381	0.012815691
HMG N1	1.1880448	1.65504E-11	PAPSS1	0.8206486	7.4284E-06	DPY19L2	1.4553931	0.000833508	PIGA	0.6636792	0.012821571
CSK	1.2255445	1.65504E-11	TCEB3	0.7133218	7.46056E-06	MRPL22	0.37585238	0.000836424	ANKR D65	0.45590484	0.012833537
HNRNPA1	1.0625536	1.67743E-11	AZIN1	0.70613694	7.4797E-06	LCMT2	0.9541667	0.000837366	USP48	0.33389187	0.012851605
SAFB	1.0302978	1.67946E-11	C9orf114	0.6601673	7.4876E-06	BEND3P3	0.40938026	0.000840859	DDI2	0.5835954	0.012922462
RPS23	0.5265005	1.68029E-11	UBAP2	0.59783596	7.52001E-06	CLASP2	0.31701437	0.000841473	DNAJC4	0.41007444	0.012928386
ARMC1	1.0287769	1.68112E-11	C1orf109	0.78302014	7.61534E-06	MKL2	0.537845	0.000842039	LOC729683	0.11071068	0.012954754
SSU72	1.1965593	1.72732E-11	LOC550112	0.28463978	7.63486E-06	AKAP10	0.53499115	0.000846651	ENOX2	0.031451713	0.012987119

TNS1	1.4064 006	1.73 628 E-11	PNPLA 4	0.4375 085	7.708 37E- 06	SHMT1	0.5814 033	0.000 85426 1	ZNF30	1.4567 513	0.013 02592 4
RPL32	0.5525 642	1.78 103 E-11	C2orf44	0.9307 365	7.726 19E- 06	THAP7	0.5540 313	0.000 85618 3	NCCRP1	0.0322 6064	0.013 08505 6
MMP17	1.3393 426	1.78 103 E-11	UHMK1	0.5167 661	7.749 87E- 06	NSMAF	0.2860 8137	0.000 85810 9	TMEM183A	0.8451 159	0.013 08691 9
FAM210A	0.7848 21	1.83 323 E-11	MRPL30	0.4547 277	7.76E -06	ARL16	0.4958 9434	0.000 85948 1	MYRF	1.3581 434	0.013 16309 6
EIF3E	1.1531 041	1.83 405 E-11	SMC6	0.6267 14	7.821 34E- 06	NHLRC3	0.4411 889	0.000 85948 1	XRCC3	0.3429 7448	0.013 21445 8
PES1	0.8833 2427	1.83 405 E-11	NAGK	0.7958 92	7.845 31E- 06	44445	0.7005 2654	0.000 85960 1	DMAP1	0.4537 1467	0.013 23280 6
44450	0.8692 8415	1.83 405 E-11	PEAK1	0.2942 1502	7.845 73E- 06	ISG20	0.9356 25	0.000 86396 2	ANXA11	0.4310 2333	0.013 25138
ARAP1	0.8280 596	1.83 962 E-11	DNAJC18	0.5029 5705	7.850 08E- 06	LOC400657	0.0768 3575	0.000 86476 3	ZNF251	0.5959 794	0.013 27395 6
PDCD5	1.4011 129	1.84 123 E-11	TPM4	0.8226 7576	7.975 35E- 06	PSMF1	0.5339 7423	0.000 86863 6	TSACC	1.0750 872	0.013 27584 5
NDUFB8	1.4313 183	1.95 1E- 11	ELOF1	0.8635 611	8.015 81E- 06	KANSL3	0.3159 5272	0.000 86961 2	AIF1L	0.3776 6427	0.013 28610 1
SLC1A4	1.3311 489	1.99 234 E-11	ERF	0.8609 254	8.062 52E- 06	PREB	0.5821 192	0.000 87041 8	IVD	0.2805 5832	0.013 28968
FLAD1	1.1177 883	2.00 701 E-11	PPP3R1	0.8312 628	8.085 18E- 06	FAM50A	0.5035 57	0.000 87122 4	BEX2	1.3406 848	0.013 28968
GCNT2	0.9019 198	2.01 962 E-11	CCDC8	0.8407 268	8.201 74E- 06	FAM133B	0.5960 243	0.000 87443 6	IFIT5	0.4744 8453	0.013 29575 9
LDB1	1.2516 624	2.04 327 E-11	SNAPIN	0.8226 205	8.212 44E- 06	IGBP1	0.6986 793	0.000 87457 9	CCDC169	2.2809 92	0.013 30961 9
LOC10190986	1.0589 269	2.04 839 E-11	SQLE	0.8309 725	8.241 68E- 06	FNIP2	0.6860 4964	0.000 87457 9	DOT1L	0.3400 2036	0.013 30961 9
PCNA	1.3981 571	2.04 839 E-11	PRADC1	1.0321 765	8.246 25E- 06	FBXW8	0.5392 1574	0.000 87457 9	WDR55	0.2899 4402	0.013 35349 2
RPS29	0.9027 7016	2.14 487 E-11	TRIP6	0.5284 952	8.284 34E- 06	ESCO1	0.3406 4576	0.000 87457 9	TBCCD1	0.2747 24	0.013 35539 3
SLC5A6	1.2698 373	2.14 526 E-11	GRPEL1	0.7540 2695	8.303 46E- 06	ENY2	0.4652 1726	0.000 87642 3	SAP130	0.3761 075	0.013 39518 6
TIMM8B	1.1578 397	2.14 719 E-11	COX11	0.7153 407	8.446 67E- 06	MEAF6	0.3688 9032	0.000 87948	SACM1L	0.2736 033	0.013 39709 3
DPP9	0.7187 9727	2.16 611 E-11	TOM1	0.8301 561	8.470 38E- 06	FBXW5	0.6337 002	0.000 88445 7	OLFM1	2.9738 35	0.013 41587 6
PRRC2C	0.6922 736	2.20 842 E-11	PWP1	0.8446 5265	8.477 19E- 06	HDAC8	0.5001 552	0.000 88674 2	IQCH-AS1	0.0983 77086	0.013 42814 2
ESD	1.4461 59	2.22 789 E-11	MED9	0.9181 7653	8.515 85E- 06	MRPL52	0.4379 6533	0.000 88738 8	DTX2P1- UPK3BP1- PMS2P11	0.2607 0294	0.013 43005 4

ECD	1.2892 475	2.23 631 E-11	TMEM1 38	0.7445 992	8.524 83E- 06	RPS25	0.3984 7502	0.000 88855 9	CD3EA P	0.1296 4477	0.013 43810 5
VPS53	0.7402 004	2.31 486 E-11	LOC100 128682	0.9312 2417	8.598 45E- 06	WASF 1	0.7631 0235	0.000 89710 1	BLM	0.7391 0165	0.013 43810 5
KBTBD 6	0.7678 0444	2.34 362 E-11	SNORD 47	1.7256 17	8.629 99E- 06	SCYL2	0.3588 311	0.000 89969 6	BCL2L 2- PABPN 1	0.1942 9342	0.013 49084 2
AKT1S 1	1.1582 545	2.53 294 E-11	CHMP3	0.6427 91	8.629 99E- 06	SNX18	0.3543 3567	0.000 90206 9	TRIM6 5	0.1369 9424	0.013 54589 4
LAMT OR2	1.2315 849	2.82 039 E-11	CSPP1	0.4982 1553	8.629 99E- 06	CUL5	0.3439 4747	0.000 90414 4	VCP	0.5501 13	0.013 57766 2
PSMG 1	1.3500 952	2.82 397 E-11	PEX16	0.7746 085	8.645 56E- 06	HSPD1	0.5790 4685	0.000 90907 4	RAP1B	0.5452 919	0.013 63068 9
RPL13 AP3	0.7049 83	2.89 169 E-11	COPS4	0.8704 795	8.648 69E- 06	ZNF52 6	0.2196 9004	0.000 91027 2	AURK AIP1	0.6211 899	0.013 63262 6
SIRT2	1.1616 269	2.92 02E- 11	DCP1B	0.9673 266	8.648 69E- 06	SUOX	0.7405 491	0.000 91249 2	LOC10 065299 9	0.2542 7324	0.013 64741 9
NOA1	1.4169 805	2.93 643 E-11	MED16	0.7210 082	8.660 47E- 06	SNRP B2	0.5085 664	0.000 91249 2	KIAA11 91	0.3687 595	0.013 67919 7
GTF2H 2	0.8064 633	2.93 808 E-11	LNX2	0.4096 1447	8.712 97E- 06	HUNK	0.0222 40298	0.000 91297 7	KIAA10 33	0.2346 2807	0.013 70909 4
ZFYVE 21	1.4059 027	2.98 082 E-11	MCTP1	1.4324 279	8.713 47E- 06	TSC1	0.2288 0189	0.000 91364 2	TRAPP C2P1	0.5097 513	0.013 72786 2
HSD17 B14	1.7618 53	2.98 782 E-11	C21orf3 3	0.7740 6174	8.793 56E- 06	DYRK1 A	0.2134 4616	0.000 91376 9	LOC10 013077 6	0.4726 6072	0.013 74449 9
ECH1	1.3921 402	2.99 656 E-11	RCC2	0.5252 779	8.793 56E- 06	SOST DC1	1.6705 114	0.000 91617 7	TRNA U1AP	0.3488 9248	0.013 74449 9
C10orf 90	1.4081 469	2.99 656 E-11	RPAP1	0.7061 6144	8.793 56E- 06	HSD11 B1L	0.8744 704	0.000 92364 7	ABCC1 0	0.2898 54	0.013 76588 1
EXTL1	1.2025 124	3.06 184 E-11	RUFY3	0.6795 019	8.899 93E- 06	DTX2	0.5833 224	0.000 92395 7	CADM 1	0.3882 846	0.013 80244 2
CECR7	0.7429 0013	3.07 779 E-11	CDYL	0.4430 3718	8.915 98E- 06	SUGP2	0.2527 8464	0.000 92888 3	RLIM	0.1952 238	0.013 80440 4
DPP7	1.1987 042	3.15 825 E-11	NFYA	0.5278 478	8.981 16E- 06	MYO10	0.4483 5448	0.000 92888 3	USP1	0.2585 4728	0.013 83651 2
IFI16	0.9612 7963	3.16 979 E-11	FKBP7	0.4701 0988	8.988 39E- 06	LOC64 3837	0.5781 234	0.000 92955 9	TMEM 218	0.3964 493	0.013 86631
BAHC C1	0.6854 219	3.16 979 E-11	DNPH1	1.0657 072	8.988 91E- 06	RRN3P 3	0.3279 582	0.000 93224 2	HRSP1 2	0.5647 9394	0.013 86631
PRMT5	1.2200 69	3.24 34E- 11	MS4A7	0.4102 1648	9.113 42E- 06	DHOD H	0.2007 5075	0.000 93781 2	KHDR BS1	0.2830 3394	0.013 86631
B4GAL T3	1.0961 558	3.26 494 E-11	COL4A 3BP	0.5886 6143	9.143 5E-06	CASP7	0.7730 126	0.000 93812 7	VILL	0.5799 413	0.013 90508 6
NME4	1.1432 805	3.28 081 E-11	FLII	0.6816 5225	9.144 03E- 06	PYCRL	0.3902 235	0.000 94230 7	SETD5 -AS1	0.1251 122	0.014 00485 4

TRAP1	1.2972 14	3.35 576 E-11	CACYB P	0.7627 284	9.167 36E- 06	FOX M1	0.7830 581	0.000 94299 2	NUBPL	0.1072 3846	0.014 01342 6
USP21	1.0816 139	3.41 056 E-11	OR7E1 56P	0.4428 831	9.170 17E- 06	PYRO XD2	0.8080 3186	0.000 94423 2	RPP40	0.6751 542	0.014 16278
C1orf1 51- NBL1	1.1259 803	3.42 957 E-11	PIAS3	0.6992 6393	9.179 85E- 06	ORC1	0.5666 968	0.000 94565 8	PRPF1 9	0.2840 3822	0.014 16478 8
TMEM 33	0.8252 914	3.45 971 E-11	SDHAF 1	0.9275 1074	9.198 68E- 06	C6orf1	0.6080 208	0.000 94653 1	RAB4B	0.9430 461	0.014 18897 8
WDFY 2	1.1094 866	3.46 423 E-11	RSL24D 1	0.8245 019	9.201 51E- 06	SUMO 1P3	0.3710 8395	0.000 94907 4	POLR2 K	0.5768 2675	0.014 19078 1
ACBD6	1.2015 067	3.63 538 E-11	JOSD2	0.7678 425	9.218 65E- 06	THAP1	0.8001 892	0.000 94939 2	GPAT CH3	0.5032 012	0.014 21480 4
DMKN	1.4211 007	3.64 273 E-11	BOP1	0.8448 6896	9.218 65E- 06	HEMK 1	0.3289 4045	0.000 95045 4	RPS6K A5	0.2549 025	0.014 24129 8
LOC64 6762	0.8264 1673	3.64 623 E-11	DET1	0.9562 9084	9.251 92E- 06	C8orf7 6	0.6393 077	0.000 95239 5	MIS18 BP1	0.3375 368	0.014 28548 4
MRPL9	1.2752 459	3.65 421 E-11	C2orf43	0.7942 446	9.251 92E- 06	LOC72 8554	0.5157 1107	0.000 95620 7	PTTG1	0.5453 08	0.014 31209 7
NRAS	0.8735 9846	3.65 421 E-11	TECPR 2	0.5272 7324	9.312 51E- 06	CERK	0.2288 0591	0.000 96468 3	BCAS2	0.4591 478	0.014 3186
TMEM 147	1.3784 3	3.65 421 E-11	CEP95	0.6480 9114	9.322 34E- 06	HSPA9	0.6313 9623	0.000 96576 1	DBF4	0.2641 376	0.014 32734 6
PLEKH H1	0.7374 158	3.66 131 E-11	APOLD 1	1.1123 242	9.364 73E- 06	DPY19 L3	0.3950 3703	0.000 96603 1	RPA2	0.5641 0164	0.014 32916 8
RPS3A	0.5342 802	3.66 131 E-11	UBE2G 2	0.6526 059	9.407 87E- 06	NUDT5	0.6357 9977	0.000 96603 1	PMS2P 3	0.2315 9626	0.014 32916 8
HPS1	1.0817 738	3.70 269 E-11	DERL2	0.7889 375	9.413 12E- 06	IP6K2	0.6480 671	0.000 96616 6	SULT1 A1	0.7023 448	0.014 35074 6
PRPF3 1	1.2080 157	3.79 523 E-11	SLC43A 3	0.9321 9024	9.439 47E- 06	OBSL1	0.2421 8658	0.000 96630 1	TIPIN	0.7918 485	0.014 35074 6
CDC16	1.2897 289	3.84 763 E-11	ALKBH 4	0.3823 4785	9.510 69E- 06	ISY1	0.2721 6372	0.000 96676 1	POLE	0.4251 3257	0.014 35074 6
BLOC1 S3	0.7136 264	3.92 009 E-11	B9D1	0.8461 9284	9.544 42E- 06	LASP1	0.4176 977	0.000 96676 1	DLEU2 L	0.6644 989	0.014 35726 7
TXLNA	1.0048 33	4.00 663 E-11	ZNF419	0.7736 609	9.569 33E- 06	UQCC	0.6213 8665	0.000 96916 6	PRKRI R	0.5964 9235	0.014 36603 5
ZNF54 9	0.9608 9095	4.04 329 E-11	PGS1	0.7991 697	9.581 81E- 06	RBM7	0.4718 6965	0.000 97252 5	DLGAP 1	0.4071 6988	0.014 37480 8
RBFO X2	0.8814 3635	4.06 733 E-11	BRCA1	0.3946 7463	9.582 39E- 06	FAM63 B	0.3220 1457	0.000 97279 8	FAM45 B	1.6867 464	0.014 45297 3
PLGRK T	1.3275 616	4.11 325 E-11	SMYD5	0.7725 25	9.719 61E- 06	PRMT3	0.4103 5703	0.000 97279 8	TNRC6 A	0.0222 47272	0.014 53626 6
YTHDF 2	1.2476 811	4.11 701 E-11	KCTD1 2	0.8809 6154	9.844 05E- 06	CARD1 4	0.6465 7426	0.000 97312 4	CXorf3 8	0.1323 0532	0.014 54286 3
TIMM4 4	0.9578 252	4.11 701 E-11	CDT1	0.1312 8814	9.859 33E- 06	RGS10	0.8531 2474	0.000 97345 1	RNF20 7	0.1127 76935	0.014 55173 3

TRAF7	0.7408 8484	4.11 963 E-11		SMPD2	1.2805 56	9.864 83E- 06		BCL9	0.4147 408	0.000 97491 9		ANKM Y1	0.2343 7369	0.014 56907 2
EIF3I	1.1794 871	4.14 123 E-11		OLFML 2A	0.0322 95298	1.000 1E-05		OSBPL 10	0.9039 69	0.000 97843 5		CCNYL 1	0.1601 9237	0.014 60071 4
POLR2 E	1.0130 435	4.16 416 E-11		TYRO3	0.8647 714	1.001 15E- 05		ISOC1	0.6749 4375	0.000 97895 4		PLXNB 1	0.1935 7291	0.014 60278 3
PTRH2	1.2864 828	4.16 416 E-11		PTPN23	0.4861 69	1.001 71E- 05		METTL 21D	1.0625 533	0.000 98062 2		POTEE	0.5502 552	0.014 61168 7
MLAN A	1.2658 86	4.17 126 E-11		C18orf2 1	0.8635 8154	1.002 27E- 05		PRRT3 -AS1	0.9523 524	0.000 98646 4		NPR2	1.0830 972	0.014 61831 7
G3BP2	1.1284 549	4.33 305 E-11		BLCAP	0.7921 103	1.006 32E- 05		SMAR CE1	0.5694 307	0.000 98726 5		TMEM 184B	0.2757 1243	0.014 65462 3
EGLN2	1.1854 205	4.36 016 E-11		TGFBR AP1	1.2293 278	1.006 88E- 05		SETD6	0.6365 125	0.000 98726 5		PHKA2	0.3022 07	0.014 67249 4
SFXN3	0.8669 867	4.37 996 E-11		KIF22	0.7757 6596	1.008 69E- 05		KIAA11 43	0.2497 7246	0.000 99930 5		UQCR 11	0.4723 7155	0.014 67249 4
MCF2L	1.3431 724	4.44 664 E-11		ZNF585 B	0.4017 0234	1.008 75E- 05		COA1	0.4720 062	0.001 00056 1		HIC2	0.5131 053	0.014 73770 6
SUCL G1	1.2111 906	4.48 736 E-11		ZNF473	1.1318 926	1.009 82E- 05		CENP W	0.9926 064	0.001 00435 9		ANKR D13D	0.4776 832	0.014 73770 6
FBLN1	1.3306 372	4.58 304 E-11		SLC39A 3	0.8163 6196	1.013 89E- 05		ARCNI	0.4223 5512	0.001 00935		AIDA	0.3239 046	0.014 73770 6
ATXN1 0	1.1240 182	4.71 712 E-11		MTR	0.3480 5262	1.013 96E- 05		PSMD 10	0.6551 1805	0.001 00935		ACVR1 B	0.7972 2357	0.014 73770 6
SNRN P27	1.0950 309	4.72 189 E-11		DNASE 1	0.1706 6997	1.026 73E- 05		SRGA P2C	0.4203 5118	0.001 01022 4		CTIF	0.2884 0348	0.014 75567
TMEM 206	1.3489 764	4.93 928 E-11		ARHGE F39	0.3004 1167	1.034 71E- 05		RNF6	0.5174 942	0.001 01115 4		MPV17 L2	0.4351 5882	0.014 78516 5
CDCA7	1.4835 886	4.96 345 E-11		MAGED 4	1.2793 841	1.040 94E- 05		KIF4A	1.1253 408	0.001 01954 6		LAMA1	0.4506 7897	0.014 81030 7
GMPR 2	1.2774 285	4.96 5E- 11		TONSL	0.4636 7562	1.041 26E- 05		KIAA16 09	0.2118 025	0.001 02048 3		CCDC 106	0.5057 802	0.014 82625 1
GALC	1.8729 728	5.07 068 E-11		SLC25A 43	0.6966 5396	1.051 69E- 05		TRIM1 6L	0.1827 855	0.001 02122 3		DEPD C1B	0.9183 9105	0.014 83990 1
PITHD 1	1.1369 832	5.07 228 E-11		LOC339 975	0.2060 3897	1.063 01E- 05		C15orf 41	0.7750 2096	0.001 02176 4		MCOL N1	0.2707 601	0.014 84852 3
NOC3L	0.9563 951	5.27 371 E-11		C11orf9 2	0.0550 45072	1.067 29E- 05		MIDN	0.1879 1147	0.001 02190 8		RAB2B	0.1114 81324	0.014 87376 2
NUDT1 4	1.3311 676	5.44 481 E-11		ZNF460	0.7513 371	1.071 59E- 05		CLN8	0.2672 8693	0.001 02304 7		SSRP1	0.3326 567	0.014 89187 8
PAX3	1.2194 217	5.54 689 E-11		FAM189 B	0.9438 3854	1.074 05E- 05		SREBF 1	0.4839 9267	0.001 02958 2		MGAT 2	0.6410 283	0.014 90326 3
AP1M1	1.1772 764	5.68 067 E-11		SLC25A 17	0.7452 2287	1.076 51E- 05		PP708 0	0.7462 253	0.001 03193 3		GORA SP2	0.4471 4785	0.014 92141 3
TMEM 180	1.1347 793	5.72 853 E-11		MAGED 4B	1.3581 516	1.080 04E- 05		CBFA2 T2	0.2096 713	0.001 03288 1		TNIP3	0.0175 74487	0.014 93049 6

PRKD3	0.8571 494	5.94 32E- 11	IARS	0.7076 077	1.083 12E- 05	COIL	0.3965 6702	0.001 03881 3	UBA6	0.3372 9786	0.014 95353 4
DLAT	1.1058 22	6.02 272 E-11	ZNF470	0.2628 2895	1.085 34E- 05	TRIM1 1	0.6222 746	0.001 03881 3	HSF2	0.4463 5814	0.014 96729
SNRP A	0.9922 4967	6.03 948 E-11	SNX6	0.6765 62	1.097 81E- 05	BRCC3	0.4928 4562	0.001 04077 8	COPS2	0.2216 6891	0.014 97406 9
TDG	0.9153 079	6.26 12E- 11	NEK8	0.0860 9634	1.100 06E- 05	DUT	0.5673 246	0.001 04695 6	N4BP2 L2	0.3879 6887	0.014 97831 5
EEF1D	0.9282 289	6.44 337 E-11	PEX2	0.5403 6677	1.100 94E- 05	WDR1 8	0.6142 696	0.001 04695 6	FAM16 7B	0.4365 6123	0.014 97831 5
CYC1	1.5655 866	6.47 035 E-11	CLTA	1.0111 403	1.101 56E- 05	TMEM 223	0.6790 766	0.001 05004 7	CAP1	0.4790 0718	0.015 00608 6
MED29	0.8383 47	6.47 93E- 11	PGBD2	1.2626 278	1.101 9E-05	SMAR CA5	0.3014 0725	0.001 05101 1	ABCB7	0.4624 8865	0.015 00821 4
TATDN 1	1.2636 234	6.77 818 E-11	UTP15	0.4301 6258	1.111 82E- 05	EEF1E 1	0.6776 4425	0.001 05259	MTA3	0.2651 598	0.015 01501
NSUN5	1.0214 07	7.00 676 E-11	IFT74	0.8382 863	1.116 29E- 05	LOC10 012857 3	0.2981 328	0.001 05314 7	MNS1	0.6533 816	0.015 03349 1
XYLB	1.1363 814	7.01 402 E-11	RAD23 B	0.4101 8304	1.118 57E- 05	RAD17	0.2792 9887	0.001 05554 8	DHX29	0.1518 282	0.015 08436 8
TRABD	0.9559 349	7.06 305 E-11	ZNF511	0.9998 989	1.123 9E-05	MFSD5	0.6520 6033	0.001 05939 4	CTSH	0.6172 7977	0.015 18485 1
PDHB	1.3618 178	7.06 305 E-11	BLVRB	0.9910 579	1.127 31E- 05	WDR2 0	0.5398 1465	0.001 06257 6	MVB12 B	0.8355 532	0.015 23660 5
ZCCH C17	1.1407 851	7.31 904 E-11	CENPH	0.5771 324	1.129 05E- 05	DHRS4 L2	0.3655 1335	0.001 06417 1	C19orf 47	0.7784 8226	0.015 27428 7
NPM3	1.5319 676	7.34 203 E-11	CTNS	0.5596 0935	1.132 19E- 05	MRPS 22	0.6058 5725	0.001 06556 1	MICAL L1	0.5194 825	0.015 28830 9
MYH10	0.9906 0786	7.53 663 E-11	CHMP2 B	0.7067 5933	1.134 51E- 05	PARP1	0.5590 368	0.001 06571 2	CBX1	0.2955 3297	0.015 36160 4
DTNB	1.1747 807	7.62 384 E-11	DARS2	0.7003 797	1.138 22E- 05	ZKSCA N7	0.0264 4825	0.001 06772 5	RNAS EK	0.6058 0885	0.015 36160 4
HIF1A N	0.7875 312	7.62 65E- 11	AKIRIN 1	0.6741 425	1.138 58E- 05	RRAG B	0.6988 51	0.001 07286	REV1	0.4017 451	0.015 36854 4
CCAR1	0.9766 931	7.68 79E- 11	MARVE LD1	0.9230 08	1.141 19E- 05	USP45	0.5230 7165	0.001 07545 5	NELFB	0.4017 7846	0.015 45176 5
DNAJC 11	1.0977 669	7.88 053 E-11	CNNM1	0.8991 2885	1.150 87E- 05	SNHG 4	0.2295 3553	0.001 07581 5	SH3GL 1	0.2803 6076	0.015 45853
NINL	1.0333 258	8.19 976 E-11	XPO1	0.4546 9174	1.152 37E- 05	LOC28 3683	0.0537 2292	0.001 07868 3	GCSH P3	0.9253 999	0.015 45853
ATP8B 2	0.7312 113	8.20 837 E-11	FAIM	0.3679 4093	1.158 14E- 05	FBXO1 0	0.8249 5844	0.001 08344 8	CISD2	0.2206 5574	0.015 46790 7
PLD6	1.3552 66	8.32 641 E-11	LDLRA D3	0.7670 781	1.166 52E- 05	GARN L3	0.8775 038	0.001 08675 6	CCDC 18	0.4273 0713	0.015 48625 7
TUBB6	1.2789 156	8.60 928 E-11	TDRD3	0.7580 764	1.169 48E- 05	INO80	0.7260 536	0.001 09091 9	SLC2A 11	0.1250 7111	0.015 48625 7

ACAA2	1.2926 904	8.73 906 E-11	TBRG1	0.3645 268	1.172 15E- 05	SNHG 1	0.6635 927	0.001 09213	TSPYL 1	0.3145 709	0.015 48625 7
XRCC5	1.0321 577	8.88 951 E-11	CHIC2	0.9932 9686	1.174 25E- 05	BVES	0.2470 8334	0.001 09228 4	DGCR 2	0.3708 4737	0.015 50285 7
ALAS1	1.1499 312	8.88 951 E-11	C12orf5	0.4479 5746	1.178 68E- 05	CEP85	0.5201 9876	0.001 09243 8	C7orf5 0	0.4799 563	0.015 51706 8
EPS15 L1	0.7571 193	8.88 951 E-11	XPR1	0.3718 2114	1.180 79E- 05	ZNF58 7	0.2619 4528	0.001 09832 3	FAS	0.7304 5236	0.015 55495 2
MRPS 2	1.2497 342	8.92 37E- 11	MCM7	0.8350 474	1.181 75E- 05	ATG5	0.4804 1543	0.001 09948 4	GTF3C 5	0.4302 598	0.015 55694 2
HEATR 2	1.0472 653	9.15 944 E-11	CDK10	0.7786 464	1.186 78E- 05	RNF38	0.4125 1513	0.001 10262 4	FBXO4 2	0.4275 5777	0.015 57119 9
ADAR	0.8767 2436	9.75 693 E-11	SNX27	0.5331 8006	1.187 45E- 05	YIF1A	0.7704 1405	0.001 10278	LOC10 012925 0	0.5824 319	0.015 61687 6
PVT1	0.8035 155	9.81 842 E-11	FANCF	0.5911 049	1.188 78E- 05	ZNF20 5-AS1	0.0114 97824	0.001 10357 7	ENO3	1.0283 778	0.015 65034 4
PGLS	1.2942 747	9.87 327 E-11	QRICH1	0.6011 862	1.190 03E- 05	INTS5	0.8008 701	0.001 10602 8	C14orf 119	0.3204 4566	0.015 70573 8
THAP4	1.1526 56	9.89 433 E-11	SUPT4 H1	0.7696 847	1.193 63E- 05	PELO	0.6631 736	0.001 10602 8	ELP2	0.3799 4173	0.015 78772 8
KIAA17 37	0.7354 3894	9.89 433 E-11	STX12	0.6245 05	1.193 71E- 05	RABG EF1	0.3976 3415	0.001 10639 8	MPLKI P	0.5405 898	0.015 83642 3
URM1	0.7157 094	1.00 571 E-10	ERCC1	0.7093 9326	1.205 39E- 05	FLJ419 41	0.0393 5884	0.001 10858 2	USMG 5	0.5991 5864	0.015 89016 6
ETNK2	1.4152 215	1.03 76E- 10	FDXAC B1	0.4262 409	1.207 26E- 05	TMEM 192	0.3759 776	0.001 10858 2	NIF3L1	0.5111 986	0.015 91207 3
CABLE S1	1.0765 17	1.06 236 E-10	BAK1	0.7225 3555	1.212 18E- 05	TSC22 D2	0.3191 4666	0.001 11427 4	SLC41 A3	0.4285 665	0.015 94139 5
ANP32 E	1.0101 403	1.08 023 E-10	ABCC5	0.5992 5205	1.214 14E- 05	TPR	0.3335 3662	0.001 11647 4	FZR1	0.0976 48144	0.015 95350 3
STRAD B	1.2109 668	1.08 289 E-10	MTRF1 L	0.6260 55	1.214 14E- 05	PNPT1	0.3295 4326	0.001 11647 4	MON1 A	0.5133 6086	0.016 00964 6
NDUF V1	1.2766 967	1.08 706 E-10	PCMTD 2	0.5858 375	1.215 12E- 05	C5orf2 8	0.3228 4826	0.001 11647 4	RMND 5B	0.2886 766	0.016 00964 6
RPS6K B2	0.9907 3225	1.09 692 E-10	QTRTD 1	0.3757 4735	1.220 9E-05	ITSN1	0.4616 1935	0.001 11749 6	ZNF32 9	0.0399 89986	0.016 05647 7
ELAC2	1.0743 779	1.09 697 E-10	SRRT	0.5873 0173	1.223 39E- 05	SPPL2 B	0.3771 1388	0.001 11802 9	C16orf 55	0.0270 0477	0.016 06844 7
RPF2	1.2133 638	1.10 999 E-10	ASCC1	0.6121 978	1.223 77E- 05	DNAJC 14	0.2295 1554	0.001 12262 2	SF3B1 4	0.6496 4724	0.016 0705
NHLR C2	0.7823 7796	1.12 472 E-10	HIBADH	0.8136 035	1.224 16E- 05	TEX11	0.3419 1063	0.001 12262 2	HOXA7	1.9554 125	0.016 11933 5
RPL38	0.5017 8695	1.12 516 E-10	FAM213 A	0.7169 7545	1.224 55E- 05	RAB4A	0.5148 3905	0.001 12299 8	NXN	0.0869 83524	0.016 11933 5
CEBPZ	0.8734 1964	1.14 291 E-10	MYD88	0.7989 3893	1.226 44E- 05	ULK2	0.2141 287	0.001 12424 4	SNRN P48	0.3654 8448	0.016 11933 5

ABCE1	0.9247 457	1.14 291 E-10	TOR1AI P1	0.4825 9163	1.230 15E- 05	PTPRJ	0.2567 872	0.001 12739 2	USP12	0.2979 0306	0.016 19641 1
UCHL5	1.0022 389	1.16 328 E-10	TOPOR S	0.7471 863	1.230 54E- 05	TAF1L	0.0798 0975	0.001 12809	GMEB 1	0.0396 68605	0.016 23621 7
KHSR P	0.6559 0143	1.16 576 E-10	UBE2J2	0.6843 207	1.238 21E- 05	DCAF8	0.4502 5566	0.001 12809	CPSF6	0.2410 2049	0.016 25103 2
DDX27	0.9881 976	1.22 025 E-10	EIF4E	0.6595 8065	1.241 34E- 05	SBDSP 1	0.4208 3514	0.001 13349 6	GATC	0.1244 41534	0.016 26084 3
LOC61 3037	0.8814 614	1.22 025 E-10	RDH13	1.1743 621	1.242 35E- 05	PALB2	0.5831 4615	0.001 13541 1	CYGB	0.7917 6	0.016 28069 8
WDR3	0.8930 213	1.25 275 E-10	DCTN2	0.8908 518	1.243 66E- 05	ZMYM 5	0.1685 3443	0.001 13557 2	FAM10 4A	0.3761 0573	0.016 28299 3
WDR4 6	1.1076 521	1.28 92E- 10	ASB4	0.3400 8995	1.251 41E- 05	PLRG1	0.5336 792	0.001 13902 9	CEP89	0.4132 2502	0.016 33032 4
FEN1	1.3328 639	1.32 852 E-10	GPRC5 B	0.9492 766	1.252 11E- 05	CYB5R 2	1.5837 16	0.001 14227 6	IGFBP 5	0.6594 3044	0.016 37042 5
HNRN PL	0.6141 8235	1.32 859 E-10	ZNF689	1.0581 632	1.252 29E- 05	NUP16 0	0.4819 1285	0.001 14752 4	OBFC1	0.1822 0586	0.016 41061 5
ITM2C	1.1617 124	1.35 036 E-10	MRPS3 1	0.7987 4635	1.254 63E- 05	GAMT	0.4340 037	0.001 14923 9	RGS14	0.5727 917	0.016 45089 3
RBM34	0.8414 035	1.38 291 E-10	GPR18 0	0.5088 5755	1.254 63E- 05	SPIRE 1	0.4988 9934	0.001 15295 8	SHB	0.6209 933	0.016 46842
GPR89 B	1.1702 47	1.40 361 E-10	BOLA3- AS1	0.4259 431	1.261 2E-05	KIAA10 24	1.8540 326	0.001 15356 6	VPS13 C	0.0979 12095	0.016 57481 3
EPS8	0.9625 065	1.42 561 E-10	WDR61	0.9889 307	1.262 84E- 05	ATAD3 C	0.0051 88969	0.001 15886 3	UFD1L	0.5023 8156	0.016 65106
CAD	0.8864 779	1.44 108 E-10	BCL2L1 2	0.6725 1736	1.266 35E- 05	METTL 1	0.6927 17	0.001 15902 7	CDC42 EP3	0.4059 7865	0.016 65106
SEMA6 A	0.8651 836	1.46 516 E-10	PATL1	0.3427 066	1.270 27E- 05	PLK1S 1	0.4998 019	0.001 17307 8	VWA2	0.0025 25972	0.016 66342 9
ANKR D10	0.9747 022	1.60 48E- 10	TMEM6 9	0.7131 8674	1.270 67E- 05	LINC00 221	0.2576 9544	0.001 17307 8	FAM83 D	1.0940 603	0.016 67089 9
AGPS	0.8991 442	1.60 48E- 10	CDPF1	1.0417 851	1.298 82E- 05	KIF14	0.2369 1268	0.001 17408 9	RAB36	0.1480 6046	0.016 68607
SNHG 8	1.2840 865	1.60 48E- 10	CSTF1	0.8601 531	1.299 55E- 05	LOC49 4141	0.1243 5391	0.001 17408 9	TOP1	0.1722 8168	0.016 71343 8
DAB2	1.0821 974	1.66 207 E-10	CCNC	0.8032 0865	1.310 29E- 05	C14orf 169	0.6258 3613	0.001 17532 8	CPT1C	0.6404 6043	0.016 71343 8
DDX6	0.8429 761	1.70 549 E-10	SRP9	0.8760 853	1.319 09E- 05	SV2A	1.0177 388	0.001 17730 9	CTNN D1	0.3468 3028	0.016 71343 8
BOLA3	1.1982 532	1.73 39E- 10	MVB12 A	0.6322 638	1.319 83E- 05	SLC35 C2	0.6142 142	0.001 17747 6	ZSCAN 9	0.6323 8925	0.016 72864 4
NOX4	0.9405 605	1.86 599 E-10	NEK4	0.5703 395	1.323 17E- 05	CUL7	0.4070 1792	0.001 17877 9	TSG10 1	0.6471 497	0.016 74643 7
PPT2- EGFL8	1.0332 422	1.90 092 E-10	NUTF2	0.9948 0903	1.327 16E- 05	TCAIM	0.5954 1315	0.001 18967 1	CABIN 1	0.1940 8245	0.016 75394 2

LY6K	1.7264 749	1.93 467 E-10		SNRK	0.7062 8995	1.341 31E- 05		MTCH 2	0.6334 727	0.001 19443 2		SMAD 9	0.2321 2688	0.016 76123 2
PMPC A	1.2134 651	1.93 467 E-10		ANKZF 1	0.7559 004	1.347 01E- 05		ZNF10 7	0.0900 47434	0.001 19759 6		APIP	0.2891 178	0.016 79173 6
MAPR E2	0.9209 135	1.94 012 E-10		MTA2	0.5838 8025	1.355 71E- 05		PSMB4	0.5011 8	0.001 19902 9		RARG	0.5600 15	0.016 79926
TIMM1 3	1.0708 095	1.94 56E- 10		OSGEP	0.9787 0326	1.361 13E- 05		CHD7	0.3852 858	0.001 19902 9		TMEM 67	0.0436 7755	0.016 86865 4
MEGF 8	0.6902 2167	1.95 309 E-10		TP53BP 1	0.5053 4546	1.363 89E- 05		NUP35	0.5072 1	0.001 19902 9		MAP7 D2	1.2960 16	0.016 87339 8
MFF	1.1062 462	2.01 631 E-10		ZNF234	0.3977 598	1.374 04E- 05		TBC1D 20	0.2347 1524	0.001 20631 5		TSEN3 4	0.2801 009	0.016 89133
DDX46	0.6674 572	2.06 544 E-10		UTP20	0.3884 627	1.375 49E- 05		CDK11 A	0.3085 3897	0.001 20741 5		BCAT1	0.7355 9535	0.016 94805
SLC18 B1	1.4423 625	2.07 057 E-10		SLC35E 2B	0.5241 927	1.394 9E-05		ACOT7	0.6993 009	0.001 20949 6		ABCD4	0.2278 1764	0.017 00255 1
STK32 A	1.2380 122	2.09 064 E-10		CCDC5 1	0.9399 7395	1.409 06E- 05		HDAC5	0.3507 3218	0.001 20949 6		TMEM 60	0.4443 9757	0.017 01799 4
PET11 7	1.2151 424	2.13 937 E-10		NP1P	0.5787 673	1.414 33E- 05		LOC10 018894 7	0.1874 5588	0.001 20949 6		DHRS1 3	0.7420 105	0.017 09081 9
GNL3	1.2353 324	2.17 859 E-10		PPM1F	0.5166 853	1.416 51E- 05		CYB5R L	0.7325 3125	0.001 20949 6		MGC1 6275	0.4811 4076	0.017 12208 4
RCC1	1.2458 841	2.18 549 E-10		YARS2	0.3228 4525	1.419 84E- 05		E4F1	0.6502 3816	0.001 21013 4		ZRANB 1	0.5055 291	0.017 12974 1
ENOP H1	1.1807 76	2.26 533 E-10		WDFY1	0.6673 0887	1.419 84E- 05		NEDD4 L	0.1311 8885	0.001 21350 9		GMIP	0.6946 575	0.017 14003
PPAT	1.1604 028	2.27 328 E-10		TMEM7 9	0.8584 7765	1.424 92E- 05		KIAA03 91	0.6149 989	0.001 21595 7		CYB5R 1	0.5465 9444	0.017 19200 4
ZNF74	0.7780 9775	2.29 529 E-10		C5orf30	0.8862 719	1.441 58E- 05		EIF6	0.8645 5446	0.001 21595 7		PSMD 6	0.6110 1985	0.017 19705 4
PHLDB 1	1.1082 191	2.29 865 E-10		HSPA1 4	0.9115 146	1.441 58E- 05		C3orf1 7	0.4463 9468	0.001 22340 1		MAGE A2	0.4101 5136	0.017 20715 8
BNC2	0.8605 634	2.33 12E- 10		TAF1B	0.6728 832	1.447 33E- 05		RPS13	0.2992 2652	0.001 22923 2		ZNF42 0	0.6878 436	0.017 26240 5
PDE4D	0.6205 0784	2.37 792 E-10		CENPM	1.3098 348	1.452 75E- 05		TMLHE	0.3811 7227	0.001 23746 5		IL16	0.2805 5006	0.017 27541 3
MRPL4	1.0659 838	2.42 886 E-10		VPS18	0.7124 3286	1.455 81E- 05		MTER F	0.8563 492	0.001 24503 2		NDUF B1	0.5445 524	0.017 28048 6
COMM D5	1.2440 57	2.44 07E- 10		LTBR	0.8242 982	1.461 25E- 05		ZNF63 9	0.1537 2798	0.001 24993 7		PHKG2	0.0560 05403	0.017 29593 4
ZFP36 L1	0.9603 5236	2.50 369 E-10		MLL2	0.2952 4204	1.465 29E- 05		CLUH	0.3483 4656	0.001 24993 7		DOLK	0.4567 094	0.017 35918 7
NT5DC 2	1.2540 836	2.50 369 E-10		ZNF773	0.3746 1787	1.477 97E- 05		SMAD 5	0.2602 0622	0.001 25059 4		PCGF6	0.7284 0536	0.017 40154 4
RRP15	0.6461 484	2.50 369 E-10		EIF1AD	0.4541 44	1.479 16E- 05		WBP1L	0.6168 068	0.001 25077 2		ZNF39 7	0.4594 5555	0.017 57773 4

UBA2	0.7495 8897	2.63 784 E-10	TAX1B P3	0.7691 991	1.486 14E- 05	KAT5	0.4987 9423	0.001 25407 5	ZNF77 0	0.2550 7024	0.017 61787 7
EPRS	1.0039 76	2.63 784 E-10	ZNF662	0.3884 0955	1.488 43E- 05	GPSM 1	0.7969 7555	0.001 25901 3	HERC4	0.2604 484	0.017 62573 3
ALKBH 7	1.0931 436	2.66 062 E-10	HSBP1	0.6819 7685	1.492 9E-05	LRRFI P1	0.3582 8346	0.001 26524 6	CNTRL	0.4171 437	0.017 67677 9
POLR3 A	0.8080 483	2.70 279 E-10	DOCK1	0.5813 0217	1.494 11E- 05	CASP8 AP2	0.3734 797	0.001 26542 6	WDR6 7	0.7164 936	0.017 70606 8
TRMT5	0.7155 569	2.71 689 E-10	STON1	0.3851 6498	1.504 82E- 05	PI4KA	0.2887 917	0.001 26925 2	TFB1M	0.3456 8062	0.017 74105
NTHL1	1.2905 643	2.73 046 E-10	PMS2P 5	0.4416 7098	1.506 03E- 05	ASB8	0.3087 6943	0.001 27186 9	HNRN PA1P1 0	0.6438 0527	0.017 80304 1
RPL7	0.6888 881	2.73 046 E-10	QRSL1	0.3566 902	1.510 56E- 05	HOXC 10	0.4567 9644	0.001 27375 8	TRAPP C8	0.1311 4527	0.017 83547 1
CYP7B 1	1.7348 754	2.76 058 E-10	RNF111	0.2542 9398	1.519 9E-05	ACSB G1	1.3852 835	0.001 27491 6	ZNF35 0	0.8551 578	0.017 87840 9
RAB7L 1	0.7995 3676	2.79 766 E-10	THUMP D2	0.6088 777	1.533 4E-05	ZNF33 3	0.1903 3045	0.001 27680 9	PKD1L 1	1.3435 235	0.017 91096 2
NUDC D3	0.8280 771	2.93 33E- 10	PCNXL 3	0.7944 615	1.545 89E- 05	DDX31	0.6448 225	0.001 28017 7	STK32 C	1.3646 28	0.017 92965
ACTR1 A	1.0053 842	2.99 692 E-10	NUPL2	0.7040 7873	1.558 48E- 05	NCALD	0.6958 746	0.001 28232 3	TCEAL 1	0.4927 4758	0.017 94036 9
TTYH2	1.0290 635	3.01 153 E-10	HLX	1.4980 065	1.559 35E- 05	UMPS	0.2898 6546	0.001 28792 3	LOC28 4757	0.4786 617	0.018 01970 1
FH	1.2032 83	3.04 47E- 10	APBB1	0.8114 0447	1.561 75E- 05	NDUF AF1	0.3297 1653	0.001 28878 3	RNF19 B	0.4010 029	0.018 07911 1
MECR	0.9363 095	3.06 161 E-10	PDHX	0.6793 085	1.573 31E- 05	SCRIB	0.5797 9906	0.001 28878 3	ZNF23 6	0.2728 8938	0.018 07911 1
SLC25 A6	0.6485 073	3.08 488 E-10	ACOT1	0.8216 025	1.578 03E- 05	CCT6P 3	0.4899 4282	0.001 29038 4	ARID3 A	0.9638 0544	0.018 09542 9
PSMD 4	1.2866 951	3.09 364 E-10	HDAC1	0.8397 65	1.587 39E- 05	TWIST NB	0.4079 1628	0.001 29038 4	ARMC 8	0.2126 8846	0.018 10071 7
ADSS	1.0606 922	3.11 82E- 10	UHRF1	1.0779 032	1.587 9E-05	METTL 20	0.0734 29205	0.001 29353 8	POLA2	0.6395 455	0.018 16406 3
NLN	0.7301 245	3.29 081 E-10	TET1	0.7838 8786	1.589 18E- 05	PDE12	0.2930 7875	0.001 29421 7	NOP14 -AS1	0.6329 789	0.018 17213 9
CHTO P	1.0167 994	3.30 281 E-10	ZFX	0.3936 024	1.609 51E- 05	NSMF	0.4740 0135	0.001 29899 1	CDAD C1	0.4699 0258	0.018 19962 2
ZCCH C3	0.9181 4536	3.30 281 E-10	OGG1	0.7595 007	1.609 64E- 05	PPIL1	0.6591 69	0.001 29899 1	C9orf6 9	0.5947 682	0.018 21048 7
TRAK2	0.9318 3726	3.32 116 E-10	GPSM3	0.5592 4875	1.611 72E- 05	RPP38	0.4778 2606	0.001 30715 9	FOXR ED1	0.2837 8415	0.018 26559 5
YIF1B	1.0196 247	3.34 864 E-10	SMARC B1	0.6749 7844	1.616 55E- 05	LINC00 310	0.0518 82934	0.001 30803 1	ZNF14 3	0.4918 647	0.018 33155
LOC37 5295	1.3998 669	3.41 993 E-10	PSTPIP 2	0.3079 1205	1.625 34E- 05	UBE2L 3	0.5600 572	0.001 30940 5	ZMYM 3	0.0220 0383	0.018 36763 7

SERBP1	0.7961883	3.53181E-10	DAPK1	0.5553489	1.62704E-05	PRIM1	0.804624	0.001312286	IGDCC4	1.0881517	0.018389786
RIMKL B	0.6925092	3.61667E-10	CCDC28B	0.90930223	1.62848E-05	PIAS2	0.25014806	0.001313729	DEK	0.3586672	0.018411726
TARS	1.0879767	3.68858E-10	MELK	1.2197086	1.62848E-05	CDC40	0.23482238	0.001314104	RBM45	0.6029638	0.018453335
PPP6R1	1.1894952	3.71404E-10	ACBD5	0.34791854	1.70256E-05	FGD6	0.5157292	0.001314291	LOC10130357	0.36301294	0.018469956
POLR1A	0.8644284	3.85216E-10	TAF1C	0.6252744	1.70365E-05	R3HDM4	0.67060655	0.001320398	NDUF B10	0.7187017	0.018477923
HAUS5	0.6014289	4.0946E-10	RNF144A-AS1	0.3016856	1.70365E-05	CERS6-AS1	1.5315001	0.001320398	TMEM160	0.3405012	0.018477923
LSM7	1.4484695	4.11174E-10	TMEM173	0.77309674	1.70626E-05	MESDC2	0.43301803	0.001323491	STX8	0.44775498	0.018539393
PCID2	1.1229569	4.1345E-10	C11orf57	0.64347386	1.72607E-05	ST6GALNAC4	0.8588095	0.001323933	ADAM12	0.8961189	0.018547621
GGA1	0.8995033	4.17981E-10	SLC7A2	1.973502	1.72607E-05	NCOR2	0.27442378	0.001324122	IRF3	0.322506	0.018561495
CCDC43	1.0908504	4.18463E-10	MZT1	0.7170609	1.72648E-05	ADARB1	0.55256027	0.001326338	SLC3A2	0.65482706	0.018566909
TRAK1	0.78489274	4.2762E-10	KIF2A	0.49841747	1.72648E-05	AMMECR1L	0.4861169	0.001327288	GRINA	0.23839359	0.018577972
EIF2S1	0.88799727	4.34779E-10	ADD3	0.7246797	1.72648E-05	METR N	0.6580716	0.001327986	ANP32B	0.4454498	0.018586215
NPIPL3	0.9162915	4.40787E-10	RNF138	0.7478923	1.728E-05	FOXK1	0.24339518	0.001331988	AP5B1	0.06856168	0.018644942
SCO1	1.3142617	4.40787E-10	OTUD7B	0.75253147	1.728E-05	RAE1	0.5808761	0.001332688	PPM1A	0.10838427	0.01871828
GLUD1	0.9419546	4.43227E-10	LHFPL5	0.17276011	1.73527E-05	ASF1B	1.1786702	0.001333133	TRIOBP	0.107994236	0.018780466
PPIE	0.95363224	4.48832E-10	CENPC1	0.7190016	1.7413E-05	KRBA1	0.5406008	0.001351205	GINS2	0.61640793	0.01878879
SLC25A13	0.8580746	4.51619E-10	ZNF292	0.49046823	1.7482E-05	E2F6	0.67041135	0.001353205	TRMT1L	0.27366567	0.018822355
RRP9	1.182791	4.63265E-10	REEP3	0.29498082	1.74847E-05	HARS2	0.56284267	0.001360131	IFT81	0.21216106	0.018822355
NCOA4	1.0816562	4.63265E-10	MRT04	0.48727232	1.74847E-05	ZBTB9	0.5884701	0.001360845	CEP192	0.1810289	0.018850717
AK1	0.66137743	4.63337E-10	44260	0.61724544	1.7554E-05	ZSWIM1	0.33593178	0.001365461	LOC441155	0.05381197	0.018864796
TYMS	1.3881396	4.86394E-10	PAQR7	0.420739	1.77219E-05	TRIT1	0.58651304	0.001366698	ANKRD36B	0.19351147	0.018878885
PFAS	0.6827101	4.99009E-10	KIT	2.5560722	1.77576E-05	TRMT61B	0.54393464	0.001368198	ATP5F1	0.6103369	0.018913062
MITF	1.1496682	5.05306E-10	FANCD2	0.13317607	1.77633E-05	GID8	0.43026066	0.001368393	C14orf166	0.57186186	0.018938673

SET	0.9126 158	5.19 442 E-10	GTF2H 2B	0.4176 8783	1.788 55E- 05	TRMT6 1A	0.6420 4067	0.001 36982 9	C16orf 13	0.5514 6515	0.018 99886 6
CHD3	0.8624 2145	5.23 011 E-10	TCF20	0.7661 042	1.810 89E- 05	INTS9	0.5221 213	0.001 36982 9	USP31	0.2273 2937	0.019 03612 5
LYPLA L1	0.9178 042	5.33 159 E-10	SKA2	0.5342 5044	1.830 84E- 05	RNF12 2	0.8879 8016	0.001 37788 5	GUSB P1	0.3917 4163	0.019 12485 4
SFXN1	0.7627 0497	5.50 075 E-10	PTGFR N	0.5767 194	1.842 97E- 05	GORA B	0.6551 6764	0.001 38248 9	NIPAL 2	0.7071 034	0.019 12485 4
SCAR B1	1.0318 352	5.52 743 E-10	NDUFS 8	0.9305 02	1.853 38E- 05	UBE2O	0.2956 7894	0.001 38295	RNF21 4	0.1536 015	0.019 13621 5
DUSP1 2	1.2124 035	5.59 145 E-10	DNAJA 2	0.6249 0404	1.860 26E- 05	CKS1B	0.7327 5036	0.001 38882 7	HECT D2	0.7335 258	0.019 18510 2
SNX5	0.9501 143	5.62 42E- 10	FHIT	0.9142 8965	1.860 85E- 05	LOC10 050659 9	0.0658 0062	0.001 39087 9	TRAIP	0.9425 1645	0.019 19940 4
IARS2	0.9922 224	5.76 578 E-10	UNC13 B	0.9415 4865	1.869 11E- 05	DES12	0.4774 0442	0.001 39825 1	TMEM 234	0.5014 8726	0.019 23677 8
NFYC	0.9094 0773	5.93 257 E-10	FAM106 A	0.2260 324	1.883 9E-05	PTBP3	0.3270 8552	0.001 40338 7	MEST	0.8830 5336	0.019 28321 1
LSM4	1.1624 392	5.98 921 E-10	NPFFR 2	0.2881 8002	1.896 83E- 05	AQR	0.4669 7974	0.001 40338 7	CDC45	1.1011 461	0.019 29173 6
SAT2	1.0626 986	6.11 021 E-10	PGGT1 B	0.5213 374	1.903 4E-05	GCDH	0.6020 515	0.001 40338 7	TRERF 1	0.6639 574	0.019 30026 4
MYC	1.2660 818	6.11 021 E-10	BRD7	0.5287 525	1.910 6E-05	SKIV2L	0.4986 5952	0.001 40733 4	MAL	1.0260 917	0.019 35562 2
DPAG T1	1.2074 88	6.19 43E- 10	INPP5K	0.7637 3583	1.939 07E- 05	PSMC 5	0.8086 382	0.001 40887 5	ZNF79 0	0.6546 6845	0.019 42581 4
LSS	1.1153 355	6.27 636 E-10	LRRC1 4	0.7749 379	1.947 19E- 05	BMS1P 4	0.1660 5842	0.001 41203	NDUF A9	0.5081 276	0.019 43097 8
ECHS1	1.2076 036	6.37 756 E-10	PARN	0.5895 8656	1.948 28E- 05	PBDC1	0.5967 603	0.001 41216 5	HPDL	0.9672 6465	0.019 43097 8
IMPAC T	0.8158 563	6.45 128 E-10	MRPL2	0.7498 275	1.956 44E- 05	CDK1	1.0005 844	0.001 42722 4	MPPE1	0.1312 1209	0.019 43097 8
EIF3J	0.9179 7316	6.63 306 E-10	HIGD1A	0.6670 1967	1.989 39E- 05	CSNK1 E	0.2949 235	0.001 42899	LRRC2 7	0.1096 6662	0.019 43908 8
ARF6	0.8282 203	6.86 305 E-10	PHF20	0.3718 56	1.992 43E- 05	CRIP1	1.6010 255	0.001 42899	CSRP2 BP	0.3773 558	0.019 43908 8
MSAN TD3	1.0595 01	7.01 179 E-10	VPS11	0.7212 798	2.015 75E- 05	LOC72 9609	0.0761 63076	0.001 43164 3	NCKA P5	0.8033 742	0.019 44767 6
MLPH	1.0995 947	7.16 606 E-10	APEX2	0.8169 037	2.019 31E- 05	UTP11 L	0.4526 724	0.001 43293 7	RNF13 9	0.6698 789	0.019 47688
NTPC R	1.1151 167	7.25 833 E-10	ACACA	0.4160 4757	2.034 1E-05	CYTL1	1.5416 617	0.001 43641 5	RNF13 0	0.4322 211	0.019 51792 6
GEMIN 7	1.1870 316	7.26 819 E-10	LRPPR C	0.5468 132	2.035 73E- 05	WASF 2	0.4186 5292	0.001 43908	ZNF26 6	0.1037 75285	0.019 53245 1
GLO1	1.1647 11	7.31 307 E-10	LOC284 578	0.1021 8703	2.044 08E- 05	MRPL4 7	0.6192 411	0.001 44031 3	LRCH3	0.2696 0936	0.019 55289 8

GAB2	1.0561 094	7.32 548 E-10	MIOS	1.0981 138	2.044 08E- 05	KIAA16 14	0.1777 2894	0.001 44031 3	ASF1A	0.4954 3414	0.019 55857 5
C8orf3 3	0.9523 217	7.46 918 E-10	RFX5	0.6855 886	2.044 08E- 05	KLHL7	0.5922 0004	0.001 44737 9	HDDC 2	0.4886 1903	0.019 60842 6
FAM98 A	1.0343 833	7.50 285 E-10	ZNF696	0.1357 458	2.051 63E- 05	FADD	0.3866 6403	0.001 44841 1	MOAP 1	0.2636 0703	0.019 61115 3
POLR3 G	1.0758 17	7.81 135 E-10	CTSL2	0.2514 5856	2.062 18E- 05	SDF2L 1	0.6727 9124	0.001 46091 6	CETN3	0.3104 0287	0.019 62550 5
TELO2	0.9225 7345	8.07 324 E-10	OSBPL 9	0.6615 576	2.068 31E- 05	NADK	0.5612 798	0.001 46140 2	TRAPP C13	0.1788 626	0.019 64603 9
QPCT	1.4589 316	8.09 886 E-10	TP73- AS1	0.1977 541	2.082 45E- 05	PRRC2 B	0.2794 5963	0.001 46647 7	HSD17 B10	0.5875 683	0.019 69859 4
PPP2R 3C	1.1592 219	8.14 611 E-10	MGME1	0.6733 2685	2.095 67E- 05	UBA3	0.5291 1884	0.001 46835 8	ACVR2 A	0.3169 976	0.019 76321
PHF23	1.2795 48	8.19 521 E-10	ZFYVE2 6	0.4557 4123	2.125 41E- 05	PCBP1 -AS1	0.6692 113	0.001 47163 8	HNRN PAB	0.2362 0573	0.019 76321
NOSIP	1.1992 965	8.19 521 E-10	OIP5- AS1	0.4788 5856	2.129 85E- 05	SMEK1	0.4854 2967	0.001 47912 7	VTA1	0.3820 7218	0.019 76894 4
RMDN 1	0.7780 977	8.21 308 E-10	CAP2	1.3305 732	2.150 05E- 05	WRAP 73	0.5057 4744	0.001 48158 6	DHTK D1	0.0480 24923	0.019 84645 4
SMG7	0.7957 817	8.24 463 E-10	FAM69 C	2.3823 128	2.153 33E- 05	WDR9 1	0.3061 3106	0.001 48884 1	SCYL3	0.3598 3136	0.019 86419 8
PDXD C1	0.9618 668	8.40 599 E-10	TEX30	0.8913 3805	2.172 36E- 05	FANCI	0.7910 0233	0.001 49188	HK2	0.0437 96193	0.019 89325 1
MLXIP	0.8354 184	8.41 877 E-10	C17orf8 0	0.6619 9493	2.183 51E- 05	KIAA07 54	0.0320 17138	0.001 49655 6	BACE1 -AS	0.0756 5246	0.019 89325 1
CUL4A	0.8136 336	8.62 044 E-10	XRCC6	0.7273 9613	2.186 83E- 05	SRGA P2	0.2315 6887	0.001 49904 2	MARK 4	0.5550 816	0.019 89325 1
CTSC	0.8158 276	8.77 45E- 10	F2R	0.6366 2493	2.192 44E- 05	CBWD 3	0.4563 6177	0.001 50253	ARFIP 2	0.1753 348	0.019 93784 9
COG2	1.0370 327	8.87 244 E-10	MLLT4- AS1	0.9109 536	2.192 44E- 05	TMCO 6	0.8303 996	0.001 50274 5	RIC8B	0.2719 5457	0.020 07289 4
CCDC 124	1.0360 564	8.88 008 E-10	RBM26	0.3516 3385	2.194 2E-05	COQ9	0.6291 9915	0.001 50381 5	NSA2	0.4333 1152	0.020 19962 5
TFAM	0.5522 611	9.00 592 E-10	LINC00 652	0.0787 7943	2.240 62E- 05	PLCD1	0.9440 365	0.001 51059 8	SLC30 A9	0.2812 8284	0.020 25045 5
PTDSS 1	1.1570 103	9.02 56E- 10	LOC100 507117	0.2271 449	2.251 57E- 05	TPM2	0.7152 307	0.001 51303 6	ACTL6 A	0.5473 4004	0.020 26547
G3BP1	1.0521 603	9.10 225 E-10	AGBL5	0.8027 623	2.263 65E- 05	MDGA 2	1.3921 695	0.001 52295 6	FANCE	0.8670 4963	0.020 29271 2
POLR2 I	1.0870 676	9.23 728 E-10	PLEKH A1	0.2653 34	2.271 44E- 05	BRAT1	0.4176 1768	0.001 52432 8	TOP2A	0.7282 649	0.020 50046 8
ZNF70 4	0.5961 627	9.26 665 E-10	ICAM4	0.4587 9567	2.279 44E- 05	RAD21	0.3272 9855	0.001 52447 6	RECQ L4	0.7179 477	0.020 54010 1
BCOR	1.1779 792	9.31 454 E-10	THUMP D1	0.5623 245	2.282 35E- 05	INCEN P	0.8195 9176	0.001 52447 6	KATNB 1	0.4260 2882	0.020 60791

TMEM161A	1.205652	9.53722E-10	LOC100505876	0.38998604	2.28856E-05	USP28	0.46511093	0.001528381	ENTPD5	0.93348616	0.020610764
CLCN7	0.9201709	9.55809E-10	NAP1L4	0.7616099	2.29973E-05	FAM20B	0.113574594	0.001539339	MRPL20	0.6283633	0.020631974
ALKBH2	1.2959516	9.64556E-10	ZNF561	0.39841765	2.30433E-05	PHACTR1	0.4836398	0.001544155	BSDC1	0.2942675	0.020631974
HELZ	0.66669375	9.6986E-10	PMS2	0.57807595	2.31446E-05	H3F3AP4	0.6702657	0.001544155	WRNIP1	0.14382109	0.020678292
DIEXF	0.68646634	9.81642E-10	PRR3	0.75877	2.32854E-05	AKAP1	0.43815923	0.001545545	PDCD7	0.11383819	0.020699809
NARS	1.1140763	9.96514E-10	COMM2	0.35857773	2.32985E-05	CLN5	0.46945208	0.001547743	STXBP5	0.19856821	0.020739787
ACOT2	1.1271528	9.97054E-10	CACUL1	0.4595869	2.33004E-05	C9orf41	1.0781956	0.001547743	SAYSD1	0.40997684	0.02076136
LUZP1	0.7207525	1.01049E-09	RPUSD1	0.88320065	2.33861E-05	ZNHIT6	0.30698255	0.001548258	NCAM2	1.5521085	0.020789198
ABCF1	0.8732791	1.02928E-09	CPNE1	0.85684454	2.35471E-05	HNRNPA2B1	0.5228857	0.001550753	PTCD2	0.5512807	0.02083583
DUSP3	0.9538343	1.02928E-09	ALS2CL	0.8597314	2.37355E-05	ANKRD49	0.6473663	0.001553839	KPNA1	0.2329823	0.020860625
TIAL1	0.62751675	1.03335E-09	MDM4	0.4381157	2.37508E-05	DCP1A	0.30217236	0.001553839	PHTF2	0.36736912	0.020891716
PINX1	1.461218	1.03335E-09	DNAJC9	0.9850901	2.37755E-05	ZNF670-ZNF695	0.34169057	0.001561128	PELP1	0.18582764	0.020935166
VPS16	1.1856738	1.03335E-09	GRAMD1A	0.7955531	2.39963E-05	ASB1	0.57055354	0.001561942	SARNP	0.51411897	0.020938062
SPDYE3	0.7710866	1.05627E-09	EMG1	0.8450252	2.41651E-05	PLSCR1	0.63491714	0.001565712	UBA1	0.55808866	0.020956675
SNAP29	0.72720206	1.08063E-09	CPM	0.54802054	2.42018E-05	ZNF84	0.16680863	0.001575729	BRD9	0.008692611	0.020978451
ZNF326	0.9385799	1.08943E-09	FAM69B	1.1083199	2.42038E-05	HOME3	0.3463207	0.001577742	DPH5	0.1887897	0.020987404
GTF2F1	0.9421066	1.10482E-09	POR	0.7891559	2.42637E-05	TIMM10B	0.44324178	0.00158933	PAPD4	0.20231165	0.021006057
MUM1	0.81056446	1.11528E-09	HYLS1	0.42484823	2.43063E-05	HEATR5A	0.20922282	0.001592416	SLTM	0.26011643	0.021034187
EI24	0.9634794	1.12794E-09	HS1BP3	0.7945517	2.43084E-05	PGAP2	0.54024667	0.001592944	RNF121	0.319298	0.021046319
RC3H1	0.6641144	1.12794E-09	FLJ35282	0.06734989	2.4322E-05	DAZAP2	0.6450992	0.001597688	PHF3	0.26735196	0.021046319
AKT2	0.5756431	1.2067E-09	DDX41	0.85263205	2.45515E-05	MAP7D1	0.5238836	0.001599426	TTPA	0.76920575	0.021058703
PSMC4	1.2207077	1.24108E-09	FAM86C1	0.9731633	2.4632E-05	ZNF430	0.13570252	0.001604188	DCAF17	0.17802452	0.021137536

ACY1	1.2130 564	1.24 218 E-09	THOC1	0.6668 2273	2.463 2E-05	PRR13	0.7020 174	0.001 61717 6	KIAA02 26	0.0154 41174	0.021 16265 1
TARBP 2	1.0602 657	1.25 638 E-09	TPX2	1.1733 183	2.472 24E- 05	LRR3 9	1.7843 604	0.001 61763 9	META P1	0.2273 9604	0.021 17509 5
RAB8A	1.0528 785	1.26 079 E-09	CTSF	0.7619 801	2.474 81E- 05	KLRG1	0.7633 9084	0.001 62329 6	FAM81 A	2.2756 941	0.021 18437 1
SDHC	0.9314 7284	1.31 85E- 09	GDAP1	1.1694 305	2.482 7E-05	GPR12 5	0.5531 762	0.001 62628 4	CYB56 1D2	0.5104 807	0.021 25014 8
RAP2B	0.7353 592	1.33 88E- 09	NBN	0.5263 065	2.487 06E- 05	ASXL1	0.3024 9122	0.001 62651 7	PXN	0.3453 65	0.021 25014 8
TRAF5	0.7134 87	1.34 513 E-09	CSTF2	0.9005 012	2.500 35E- 05	SUFU	0.8280 9883	0.001 63644	PRKC B	1.5055 223	0.021 25308 7
AGPAT 6	0.8397 2377	1.34 513 E-09	TRIM14	0.4239 0844	2.506 75E- 05	RPL17- C18orf 32	0.7316 686	0.001 64967 1	ELOVL 6	0.9092 806	0.021 28126 7
SRP72	1.0687 914	1.36 762 E-09	NHLRC 1	0.9778 4764	2.529 77E- 05	OIP5	1.3206 694	0.001 65177 2	PRAF2	0.4057 47	0.021 28739 8
MRPL2 4	1.1298 013	1.38 007 E-09	TMEM6 8	0.4585 5933	2.551 17E- 05	SMAR CD2	0.4544 6092	0.001 65480 9	PISD	0.2738 6537	0.021 3031
GLT25 D1	0.9071 9306	1.40 773 E-09	KCNQ5	1.6983 595	2.562 96E- 05	RAP2C	0.4123 7384	0.001 65660 4	MAP3K 12	0.4607 4525	0.021 37609 8
ECHD C1	0.9646 414	1.45 277 E-09	LOC100 506548	0.4121 6227	2.595 95E- 05	SFXN2	0.4157 5438	0.001 66183 8	BCL11 A	0.7659 258	0.021 38865 6
HMCN 1	0.9815 372	1.45 692 E-09	CHKB	0.9108 6316	2.631 62E- 05	ODF2	0.4220 2434	0.001 66238 9	NPDC1	0.3428 9548	0.021 39136 9
CUED C2	1.2434 427	1.45 869 E-09	AHRR	0.7003 103	2.632 47E- 05	FBXO2 2-AS1	0.5011 854	0.001 66952 2	AARS	0.4469 7633	0.021 43550 5
GRHP R	1.1589 133	1.45 904 E-09	ZWILC H	1.1677 334	2.649 65E- 05	SNHG 7	0.2061 1244	0.001 67062 9	RBM12 B	0.2758 3686	0.021 45130 5
CRK	0.6859 6464	1.47 856 E-09	ZNF791	0.5950 1654	2.653 03E- 05	TTF1	0.3055 9757	0.001 67062 9	KAT6B	0.1166 06474	0.021 45748 2
SEC23 IP	0.7036 543	1.51 062 E-09	ZC3H13	0.5536 445	2.656 42E- 05	ANKR D13C	0.2596 8274	0.001 67212 6	RIN2	0.4658 0717	0.021 47602 5
OAT	1.2403 307	1.55 483 E-09	LPGAT 1	0.1801 12	2.656 65E- 05	KANK1	0.3740 414	0.001 67330 9	EEF1E 1- MUTE D	0.5849 432	0.021 50077 5
ATAD3 B	0.9180 753	1.55 483 E-09	ASNSD 1	0.7505 6386	2.658 77E- 05	MPHO SPH6	0.6558 2603	0.001 67883 3	YBEY	0.3341 646	0.021 50077 5
GALM	0.8599 518	1.56 028 E-09	C10orf3 2	0.4327 477	2.676 12E- 05	PMM2	0.3894 311	0.001 67883 3	TPI1	0.5597 506	0.021 50077 5
DCLRE 1C	0.8496 073	1.56 576 E-09	PAPL	0.0674 4969	2.676 35E- 05	UBR1	0.3229 0843	0.001 68556 5	RAB8B	0.2949 279	0.021 51662
POLD2	1.2397 075	1.57 369 E-09	EBP	0.8134 2506	2.682 78E- 05	MYO5 C	0.2880 9333	0.001 68770 9	FLRT1	0.9192 1425	0.021 56099 4
TBCE	1.0559 337	1.57 369 E-09	TRIM16	0.4251 3594	2.682 78E- 05	F3	0.0655 4091	0.001 69208	SLC4A 2	0.1674 858	0.021 56099 4

FAM19 5B	1.1066 116	1.60 723 E-09	NUMB	0.5900 842	2.682 78E- 05	ALG1	0.3258 001	0.001 69614 2	HOOK 2	0.4644 124	0.021 57042 8
HMGA 1	0.8712 865	1.61 13E- 09	WDR77	0.7723 406	2.693 87E- 05	BTF3	0.4055 2422	0.001 69670 4	TMOD 3	0.1332 6217	0.021 59205 7
MRPS 26	1.1978 308	1.69 509 E-09	ATP5SL	0.8804 65	2.717 89E- 05	NFKBI B	0.2152 043	0.001 70077 7	MND1	0.7314 1223	0.021 59205 7
ABCB6	1.1429 863	1.69 993 E-09	RGS20	0.7157 8234	2.720 7E-05	NCAP D2	0.3426 4696	0.001 70742 3	PCSK7	0.3457 626	0.021 60796 3
KCTD1 5	1.0645 066	1.72 037 E-09	CRTC1	0.2371 3925	2.750 82E- 05	WDR4 8	0.4946 127	0.001 71055 6	PPP1R 16A	0.3368 0698	0.021 62064 8
ATAD1	1.0412 539	1.73 259 E-09	NCOA5	0.6649 68	2.751 06E- 05	COQ2	1.1710 591	0.001 71337 3	PLA2G 4C	1.1642 438	0.021 66545 6
MPV17	1.3298 894	1.73 866 E-09	ELK4	0.3601 324	2.753 26E- 05	LOC14 8413	0.6486 475	0.001 72394 3	NDUF B11	0.5515 812	0.021 67493 3
CEP17 0	0.8134 3085	1.80 884 E-09	TANC2	0.4983 76	2.755 29E- 05	NEK6	0.5769 9776	0.001 72451 4	LIPT1	0.3476 7473	0.021 74906 2
DUS3L	1.1210 762	1.83 222 E-09	GLTSC R2	0.6736 6767	2.755 29E- 05	DNAJC 15	0.4877 8892	0.001 72864 9	RPL36 AL	0.4619 3898	0.021 76507 2
SCNM 1	1.1035 749	1.85 362 E-09	CDC42	0.6755 9654	2.755 29E- 05	BSCL2	0.6193 177	0.001 72987	FMN1	0.2133 4398	0.021 77458 8
PPIA	0.5076 2105	1.95 033 E-09	AMOTL 2	0.7291 845	2.760 59E- 05	KDM6 A	0.4584 2475	0.001 73466 8	TBC1D 10B	0.2998 584	0.021 77760 2
PSME3	0.9561 3486	1.95 399 E-09	GALK2	0.5262 1925	2.764 77E- 05	SCFD1	0.5338 7356	0.001 73484	RFNG	0.3368 3696	0.021 79037 6
RPS19 BP1	1.1232 412	1.96 083 E-09	PGAP1	0.3775 9468	2.768 95E- 05	SLC25 A22	0.4525 1468	0.001 73484	MRPS 30	0.4385 884	0.021 79990 3
NIPA2	0.9602 1515	1.96 515 E-09	FAM57 A	1.1384 78	2.790 3E-05	HHAT	0.6049 071	0.001 73574	LOC10 012798 3	0.6309 685	0.021 80292 1
GK	1.3117 907	1.99 647 E-09	CIZ1	0.5594 613	2.811 14E- 05	NUP85	0.3730 7835	0.001 74022 7	PMS2L 2	0.2466 8725	0.021 81245 2
PRPSA P2	1.1105 281	2.04 874 E-09	VPS37B	0.3932 156	2.813 63E- 05	GPAA1	0.6010 1366	0.001 74113	ANKR A2	0.4102 8	0.021 89632 7
CAMT A2	0.7051 094	2.13 733 E-09	IGFBPL 1	0.5360 1366	2.832 62E- 05	MUL1	0.5657 447	0.001 74301 3	FCGR T	0.4731 0665	0.021 97440 8
RBFA	0.7110 1874	2.14 758 E-09	ARNT	0.5445 967	2.838 25E- 05	USP7	0.1861 6028	0.001 74326 3	DNMB P	0.8235 7794	0.021 98728 7
HNRN PD	0.6891 1904	2.15 44E- 09	MAPKB P1	0.3814 3155	2.839 85E- 05	SLC25 A12	0.4498 2013	0.001 74678 5	PPP4R 1	0.3622 0694	0.021 99361
TOMM 22	1.1456 077	2.21 428 E-09	FAM69 A	0.7425 537	2.842 12E- 05	KIAA15 86	0.3690 8534	0.001 75261 2	ACER3	0.4150 528	0.022 00250 8
NONO	0.8773 3227	2.27 947 E-09	MRPS1 8A	0.7729 409	2.851 14E- 05	RP1- 177G6. 2	0.3489 4675	0.001 75845 8	ABCC1	0.5050 2986	0.022 00250 8
ZCCH C7	0.8888 875	2.28 36E- 09	PKD1	0.1302 6156	2.866 98E- 05	PRKD2	1.0227 649	0.001 76266 9	SIK2	0.2186 494	0.022 04121 4
PKN1	0.7685 632	2.28 36E- 09	PLEKH O2	0.6982 4904	2.878 12E- 05	UHRF1 BP1	0.2118 2373	0.001 76284 5	SMYD 3	0.2932 7586	0.022 04121 4

CLPP	1.2639 912	2.31 838 E-09	GAPDH S	0.9877 9666	2.881 79E- 05	CDC37	0.8198 8686	0.001 76284 5	PAXBP 1	0.2434 541	0.022 04121 4
MRRF	1.1022 493	2.33 854 E-09	CLDN1	2.6627 462	2.908 78E- 05	EIF3H	0.5741 79	0.001 76309 8	CCDC 125	0.1558 6516	0.022 09691 8
ZNF56 6	0.6240 2564	2.34 671 E-09	ALDH16 A1	0.6808 6624	2.914 56E- 05	RANB P9	0.3080 5445	0.001 76897 5	M6PR	0.5112 8376	0.022 11645 6
POLR1 E	1.2335 416	2.39 94E- 09	KDM4A	0.6488 048	2.932 81E- 05	RAF1	0.5129 74	0.001 77147 3	NBPF1 1	0.1218 4675	0.022 15227 6
LEO1	1.1118 977	2.40 857 E-09	LRWD1	0.8425 31	2.933 07E- 05	CDC42 EP4	0.4335 9885	0.001 77147 3	FEM1A	0.3022 6496	0.022 28753 8
EIF4B	0.9214 904	2.40 92E- 09	PRPF38 A	0.6278 9094	2.951 44E- 05	METTL 22	0.6450 908	0.001 77904 2	NBPF2 4	0.1391 0349	0.022 28753 8
ZNF68 7	1.0837 733	2.43 17E- 09	C2orf69	0.5882 0266	2.969 91E- 05	SYT11	0.2255 2903	0.001 78730 9	MAP4K 1	0.6410 072	0.022 30698 7
MRPS 18B	1.1216 007	2.43 785 E-09	PRTG	0.8687 1	2.979 32E- 05	STX17	0.0891 7182	0.001 80260 3	LOC10 049940 5	0.4606 4982	0.022 36947 3
MCCC 2	0.7137 333	2.44 308 E-09	ACTR8	0.5963 2295	2.987 35E- 05	MYL6B	0.4972 689	0.001 80514 5	LRRC5 7	0.1922 3703	0.022 41232 9
MRPS 24	1.2550 683	2.44 308 E-09	RELA	0.5423 8874	2.997 52E- 05	TMEM 164	0.5728 3497	0.001 80540 4	ZNF55 0	0.6372 6497	0.022 43211 5
C1orf1 31	0.9396 2395	2.44 453 E-09	GOLGA 3	0.3445 8438	3.009 42E- 05	MTBP	0.4801 4554	0.001 80836 7	CCDC 101	0.6066 569	0.022 43521 7
SMU1	0.6465 484	2.45 217 E-09	LRRC4 1	0.7759 6927	3.038 28E- 05	EIF5A	0.6691 6513	0.001 80930 3	FGL2	0.1832 8893	0.022 45836 3
RNF40	0.7399 0715	2.45 217 E-09	TEX10	0.6215 535	3.090 22E- 05	MCAT	0.7624 2274	0.001 81023 9	EPHA2	0.9286 7774	0.022 48153 1
C9orf1 42	1.0668 036	2.45 917 E-09	RPP30	0.4211 88	3.126 73E- 05	TRAF2	0.5122 5287	0.001 81253 2	AATF	0.4441 461	0.022 56817 7
CNPP D1	1.0037 509	2.50 036 E-09	SLK	0.4688 9582	3.126 73E- 05	STAT6	0.4514 0737	0.001 81652 4	MAF1	0.4969 399	0.022 58472 7
VEPH1	1.4270 75	2.50 036 E-09	NXT1	0.7731 401	3.133 2E-05	SLC7A 6OS	0.6149 3534	0.001 81916 4	GTPBP 1	0.2270 2156	0.022 59120 7
ISG15	1.5329 988	2.53 757 E-09	UBL4A	0.8270 4186	3.185 66E- 05	MTSS1	0.2993 3092	0.001 82487 5	NUS1	0.3363 5753	0.022 62795 1
DCTPP 1	1.1669 793	2.54 318 E-09	MDH1	0.9120 1484	3.186 7E-05	CHD8	0.2934 7226	0.001 82718 4	MEGF 10	1.3026 348	0.022 65464 2
PAN3	0.6986 2163	2.54 552 E-09	ARID1B	0.2076 4516	3.204 6E-05	RCBTB 1	0.3874 8538	0.001 83181 2	FTO	0.1499 8864	0.022 67461 9
AIFM1	0.7795 367	2.55 856 E-09	UAP1	0.6702 6347	3.204 6E-05	ZNF61 8	0.4357 697	0.001 83602 9	IGF2R	0.1151 2862	0.022 67775 1
DCAF7	0.8658 248	2.60 835 E-09	SMPD4	0.5258 335	3.209 71E- 05	DLST	0.2756 3998	0.001 83602 9	SRD5A 1	0.4874 6845	0.022 77836 4
ATP5G 2	0.5959 1115	2.62 244 E-09	PTTG1I P	0.6836 175	3.209 71E- 05	ZBTB4 8	0.4032 4324	0.001 84316 5	DNPE P	0.0502 49737	0.022 78828
BMP7	0.5064 992	2.62 244 E-09	NUP54	0.7393 533	3.223 65E- 05	AMDH D2	0.4366 566	0.001 84722	EXTL3	0.3901 737	0.022 81513 9

FHL2	1.2412 854	2.62 74E- 09	ELP5	0.5684 2107	3.241 46E- 05	TUBG CP3	0.4519 903	0.001 84817 6	CCDC 23	0.3932 086	0.022 83863 5
POLR3 K	1.2203 659	2.75 183 E-09	PTK7	0.6786 12	3.249 4E-05	DISC1	0.3522 4286	0.001 85085 9	MTHF D1L	0.2276 1524	0.022 91313 2
NANP	1.1277 558	2.78 106 E-09	ZMYM2	0.4490 2658	3.252 76E- 05	SHRO OM3	0.0226 05281	0.001 85573	AUTS2	0.6031 0256	0.022 95010 1
HN1	1.1016 978	2.81 241 E-09	ATE1	0.7202 227	3.260 72E- 05	SNOR A67	1.3659 245	0.001 85573	AKAP8	0.2224 9614	0.022 95010 1
MTIF3	1.0089 964	2.81 772 E-09	EHMT1	0.5899 555	3.262 56E- 05	DDX12 P	0.5400 1206	0.001 85957 3	MXRA 7	0.2057 2609	0.023 02834
CDC6	0.9934 474	2.86 691 E-09	ANKS4 B	0.1086 53255	3.277 49E- 05	TET2	0.0713 69596	0.001 86088 3	FNIP1	0.1760 6543	0.023 04519
ARMC 6	1.1982 886	2.95 748 E-09	POLR2 B	0.6275 543	3.296 66E- 05	CASP1 0	0.0460 76372	0.001 86358 3	KIAA07 53	0.5525 9407	0.023 08601 5
GARS	1.1149 759	2.96 973 E-09	SLMO2	0.6310 294	3.296 66E- 05	LOC73 0183	0.9371 6717	0.001 88404 4	KANSL 2	0.3228 1888	0.023 09947 6
HAS2	1.4910 998	2.98 576 E-09	LOC100 288637	0.2652 2192	3.302 4E-05	GXYLT 1	0.1603 7591	0.001 88951 1	MTMR 6	0.3768 1684	0.023 12642
RBBP4	0.7558 486	2.98 576 E-09	TBL3	0.8095 9797	3.302 7E-05	CT64	0.0132 50005	0.001 90285 9	BLOC1 S5	0.3480 8204	0.023 22191 5
C17orf 85	0.5890 3605	3.03 88E- 09	LOC400 043	1.0962 827	3.310 78E- 05	CTPS2	0.5753 968	0.001 90774 7	DCTN4	0.2933 079	0.023 23889 1
SYMP K	0.8398 281	3.09 176 E-09	CCDC1 48	0.1748 8447	3.311 99E- 05	ANKR D40	0.3423 4953	0.001 90837 7	PPP1R 37	0.7908 697	0.023 28002 1
ASCC2	0.9037 43	3.09 562 E-09	UBE2V 1	0.6787 4986	3.311 99E- 05	C16orf 59	1.2658 638	0.001 91248 5	NCAP G	0.7564 651	0.023 31085
FAM65 A	0.9113 053	3.14 442 E-09	ZNF761	0.2861 8488	3.314 64E- 05	GYPC	0.5432 801	0.001 91248 5	NFATC 4	0.5961 3395	0.023 36939 9
MKL1	0.8705 6994	3.19 918 E-09	TUBA1 C	0.8814 6335	3.318 06E- 05	KIF26B	0.9044 2103	0.001 91418 5	CLK3	0.4098 5206	0.023 42089 4
SMC3	0.8100 818	3.20 627 E-09	FBXW2	0.2627 596	3.324 62E- 05	UBE2R 2	0.4618 1017	0.001 91481 7	ADAL	0.0505 39106	0.023 45536 3
PPP2R 5C	0.9074 583	3.23 816 E-09	TBC1D 7	0.8825 7253	3.340 61E- 05	RBM14	0.4062 9503	0.001 91973 4	SLC27 A1	0.2147 4375	0.023 54882 4
C19orf 60	1.1063 645	3.33 803 E-09	C19orf1 2	0.3285 0978	3.360 93E- 05	SNHG 11	0.6405 886	0.001 92494	SLC38 A6	0.2154 6659	0.023 62537 9
POLL	1.1581 198	3.35 292 E-09	HAT1	0.8057 415	3.367 57E- 05	CDC23	0.5027 677	0.001 92916 3	SLC39 A4	0.2796 9584	0.023 70215 5
TRIAP 1	1.2363 561	3.35 712 E-09	AMZ2P 1	0.4174 8118	3.380 1E-05	44441	0.6152 2985	0.001 93015 9	CTTNB P2NL	0.3593 819	0.023 74727 6
ALDH1 L2	0.7443 536	3.37 21E- 09	GM2A	0.6291 309	3.383 59E- 05	HCCS	0.6660 5926	0.001 95703	CDC42 SE1	0.3240 036	0.023 74727 6
ANKR D36	0.7307 839	3.45 606 E-09	UCK1	0.8632 418	3.386 29E- 05	TBK1	0.3592 1034	0.001 95703	SPIN2 B	0.3607 2007	0.023 76107 9
RBM4	1.1338 065	3.47 139 E-09	EPB41L 1	0.9979 046	3.403 68E- 05	DBR1	0.2558 8658	0.001 95803 9	CAPN S1	0.2849 1914	0.023 81686 2

TP53R K	0.8253 1697	3.47 139 E-09	CLOCK	0.9480 9747	3.408 E-05	RPS6K A4	1.0525 082	0.001 9616	METTL 2A	0.2677 5438	0.023 98920 6
RUVBL 1	1.2236 519	3.48 243 E-09	MTIF2	0.4948 588	3.459 96E- 05	USP46	0.0242 59694	0.001 96188 3	CCDC 112	0.3594 167	0.024 00313 4
KRTAP 19-1	4.0434 117	3.52 151 E-09	XG	1.0527 169	3.489 66E- 05	FTSJ1	0.4534 4526	0.001 96792 6	E2F7	0.8204 7105	0.024 04166 2
SNX2	1.1175 911	3.56 444 E-09	VAR52	0.4610 02	3.493 26E- 05	MED22	0.5960 443	0.001 98399 8	LINC00 189	0.1119 8179	0.024 19758 8
RPLP2	0.5361 6416	3.65 061 E-09	TATDN 3	0.5207 519	3.524 06E- 05	C11orf 30	0.7036 628	0.001 98871 1	USP32 P1	0.0937 02845	0.024 20397 2
POM12 1C	0.6093 796	3.65 631 E-09	MC1R	0.8979 935	3.549 11E- 05	MINOS 1	0.3576 6298	0.001 98973 6	SCML2	0.1911 8266	0.024 22873 5
NOS3	0.8851 15	3.65 631 E-09	CYTH2	0.3989 5186	3.549 11E- 05	SLC2A 6	0.3713 9282	0.002 00522 8	RER1	0.4575 6528	0.024 32467 7
NDUF AF6	0.9497 338	3.71 98E- 09	HCG11	0.4199 3383	3.550 28E- 05	SPRY D7	0.2017 202	0.002 00841 2	HEATR 6	0.1352 1814	0.024 36391 7
BCS1L	1.0769 149	3.90 315 E-09	ATP5O	0.9657 239	3.553 94E- 05	TVP23 B	0.5542 2544	0.002 01504 8	TACC3	0.8852 2935	0.024 37085
NDUF AB1	1.2695 042	3.94 183 E-09	FAM35 A	1.0962 138	3.565 13E- 05	44448	0.2959 2395	0.002 01571 1	FAM21 0B	0.2124 643	0.024 58345 6
LAMC1	0.6992 291	3.94 806 E-09	MAP3K 9	0.1275 498	3.590 97E- 05	NAA40	0.1902 0909	0.002 02603 9	KIAA03 17	0.1684 231	0.024 58656 3
PSPC1	0.9773 1584	4.11 617 E-09	AAGAB	0.6948 285	3.590 97E- 05	HSCB	0.2901 369	0.002 03142 8	PRKCI	0.0826 05556	0.024 58656 3
NUDC D1	0.8945 2624	4.13 712 E-09	RHBDF 2	0.6280 54	3.609 88E- 05	YWHA H	0.5105 907	0.002 03142 8	DHX57	0.4108 0713	0.024 58967 2
ACTG1	0.5794 422	4.26 535 E-09	DTNA	1.2851 684	3.631 78E- 05	ZDHH C3	0.2354 667	0.002 03804 9	PLIN3	0.2403 4815	0.024 66559 3
MRPL1 5	1.1059 322	4.31 577 E-09	AKAP11	0.5690 4685	3.631 78E- 05	EIF4E BP3	0.6988 304	0.002 03804 9	PKDC C	1.0103 67	0.024 74146 4
CDK4	1.0533 764	4.34 186 E-09	PVR	0.1273 7726	3.637 23E- 05	TWF2	0.6076 8247	0.002 03976 9	GNG7	0.2897 5424	0.024 78130 1
MTX1	1.0034 238	4.34 319 E-09	LOC100 506421	0.3372 692	3.645 25E- 05	GCSH	0.5792 2894	0.002 04498 4	FUBP3	0.3240 1025	0.024 90796 2
FAM96 A	1.1647 07	4.34 591 E-09	LINC00 094	0.2520 9773	3.658 43E- 05	LETMD 1	0.5587 911	0.002 04565 7	PRELI D1	0.6468 149	0.024 96271 8
KIAA01 01	0.8135 296	4.39 029 E-09	SARS2	0.7943 5277	3.675 09E- 05	APOOL	0.2969 9853	0.002 05042 1	ARID4 A	0.1474 856	0.025 17964 1
IFRD2	1.1184 155	4.48 326 E-09	DDX1	0.7633 638	3.678 02E- 05	ZNF78 8	0.0413 94304	0.002 05519 6	CSRNP P3	0.1830 2388	0.025 22751 5
HMGB 1	0.7913 206	4.50 606 E-09	AFMID	0.4670 7028	3.681 82E- 05	ZSCAN 25	0.5112 407	0.002 05959 9	TACC2	0.6884 349	0.025 29005 8
PDS5B	0.6387 924	4.54 482 E-09	UPK3B	0.2705 2358	3.683 89E- 05	BCYR N1	0.5364 3024	0.002 05959 9	NCOA 6	0.0607 1361	0.025 29005 8
TAF1D	0.8690 9884	4.62 482 E-09	PPHLN 1	0.6213 144	3.731 3E-05	EPS8L 2	0.6566 3564	0.002 06371 5	C16orf 70	0.5327 739	0.025 38998 6

TRMT1 OC	1.0382 756	4.62 773 E-09	ANXA5	0.4857 811	3.739 52E- 05	CNOT1 1	0.6097 6785	0.002 07005 1	NSD1	0.1262 2611	0.025 44541 6
PSMA7	0.9323 434	4.67 938 E-09	ATP13A 1	0.5768 1656	3.747 24E- 05	RFC2	0.3547 689	0.002 07005 1	PRC1	0.5729 523	0.025 48625 7
RNPS1	1.0774 953	4.70 018 E-09	HOXA1 0	1.1538 71	3.747 24E- 05	PPWD 1	0.4109 7003	0.002 07188 3	HOXA4	2.3071 83	0.025 48946 3
FAM20 4A	0.6696 144	4.71 959 E-09	SLC7A1	0.5916 7576	3.789 91E- 05	RNF10	0.4727 7096	0.002 07602 1	CDC20	0.8109 6375	0.025 48946 3
TUBG CP5	0.8613 2634	4.73 755 E-09	RAPGE F1	0.3678 835	3.790 27E- 05	NFATC 2IP	0.1340 0418	0.002 08595 1	ACTR5	0.3232 0434	0.025 58231 7
IFI30	1.4407 456	4.73 755 E-09	CYP27 A1	0.8240 2426	3.799 51E- 05	LOC10 013106 7	0.1004 22196	0.002 08779 6	STRA1 3	0.6135 618	0.025 78835 2
WASH 7P	0.6967 4915	4.73 755 E-09	SPRTN	0.7651 2593	3.813 22E- 05	ACTB	0.3896 3094	0.002 09265 2	METTL 14	0.1701 9516	0.025 79564 1
KLHL1 2	0.9228 4775	4.87 002 E-09	ZNF92	0.4858 9203	3.834 15E- 05	PILRB	0.3643 4546	0.002 10607 1	SNRP D3	0.4906 791	0.025 79915 2
SBNO1	0.6897 3434	4.97 607 E-09	ZC3H7 A	0.4607 4003	3.880 49E- 05	NEK3	0.6232 423	0.002 10667 7	TTC9C	0.4229 6255	0.025 85158 6
INTS3	0.6830 219	5.02 04E- 09	RBBP9	0.3176 3658	3.884 49E- 05	CPSF3 L	0.4715 9487	0.002 11830 9	LOC64 2846	0.1441 2606	0.025 87025 9
RABEP 1	0.6540 77	5.02 04E- 09	ORC3	0.5751 648	3.887 95E- 05	ZNF39 4	0.2508 1202	0.002 11939 7	LOC10 050573 8	0.2065 6806	0.025 88515 2
HYOU 1	0.6181 45	5.08 118 E-09	SMC1A	0.4717 4916	3.887 95E- 05	ST7L	0.3915 3028	0.002 1314	CXorf2 1	0.0535 8559	0.025 89246 7
NOP58	1.0164 481	5.18 024 E-09	FAM175 B	0.9577 671	3.891 96E- 05	ANKR D44	0.4707 0417	0.002 13753 5	CKMT2	1.5188 853	0.025 91822
PPRC1	1.0942 365	5.23 131 E-09	ZBED4	0.8509 595	3.913 3E-05	IRS1	0.7012 3714	0.002 13902 7	SRBD1	0.2828 3516	0.025 96680 1
MIPEP	1.0411 302	5.24 625 E-09	ZNF551	0.3909 3107	3.930 15E- 05	SMAR CAL1	0.3831 8342	0.002 14646	EXOS C9	0.3484 8493	0.025 98935 3
MBD6	0.7550 02	5.28 959 E-09	U2AF1L 4	0.7560 7455	3.937 88E- 05	MGAT 5B	1.2698 712	0.002 15144 3	PET10 0	0.6223 108	0.026 01493 2
MCM4	0.9578 0987	5.32 658 E-09	SYF2	0.6124 3737	3.970 56E- 05	SDHA	0.5464 0883	0.002 15144 3	DDTL	0.6498 7123	0.026 01493 2
ATXN2 L	0.6971 447	5.32 658 E-09	MRPS2 3	0.8040 584	3.974 65E- 05	NMD3	0.5347 595	0.002 16890 1	TRIM6	0.1539 7976	0.026 01493 2
SGPL1	0.7166 4006	5.43 203 E-09	GTF3C 2	0.6614 0544	4.010 43E- 05	PCYT2	0.6219 226	0.002 17001 3	PARS2	0.8169 8537	0.026 04895 7
PLEKH F2	1.1509 316	5.43 551 E-09	SLC25A 26	0.4914 6825	4.038 04E- 05	BRD3	0.3127 2376	0.002 17955 5	NAAA	0.1097 07355	0.026 13241 2
KIAA09 07	0.6278 924	5.45 276 E-09	NAE1	0.7619 3315	4.123 09E- 05	MTER FD3	0.7215 718	0.002 18027	KRTCA P2	0.4424 8658	0.026 15891 9
AIMP2	1.1723 899	5.51 344 E-09	SEH1L	0.6109 329	4.143 13E- 05	C9orf7 8	0.4871 7913	0.002 18622 2	EFHA1	0.3385 057	0.026 18162
MGC5 7346	0.7458 05	5.53 268 E-09	PNN	0.5512 4617	4.150 29E- 05	RAVE R1	0.4447 014	0.002 19664	PPIAP 30	0.4513 9956	0.026 27233 3

MRPS31P5	0.80808926	5.56956E-09	TXNL4B	0.39691663	4.15553E-05	CLPTM1	0.49548703	0.002197766	RBM15B	0.25978348	0.026272333
CEP135	0.9746641	5.65467E-09	RANBP17	0.81063396	4.16756E-05	LOC10131089	0.068331055	0.002200109	ELK1	0.14002326	0.026272333
MYCBP2	0.61147887	5.77376E-09	MRPS18C	0.6664985	4.18254E-05	C19orf55	0.69675213	0.002203266	SLC35B2	0.5550586	0.026272333
CHMP5	1.0080669	5.77747E-09	ADPRHL2	0.8259636	4.18392E-05	CARHSP1	0.085856326	0.002204713	FSTL4	1.8773373	0.026325889
FRA10AC1	0.39048156	5.98543E-09	ATG9A	0.7081823	4.19643E-05	RAD51	0.9183085	0.002205843	NABP2	0.25548252	0.026433292
BCAS3	0.8808771	5.98543E-09	SPAG7	0.8430864	4.19879E-05	SOCS6	0.4695441	0.002211859	FBXO11	0.043791126	0.026525584
U2AF2	0.5084883	6.1306E-09	COMTD1	1.4547616	4.20996E-05	GCAT	0.41866237	0.002212585	GTF2H3	0.1656145	0.026529189
FIBP	1.1597058	6.15779E-09	DDX19B	0.74512005	4.21625E-05	FAM86B1	0.8024499	0.002215759	ATG4C	0.4899874	0.026563809
RRP1B	0.7863595	6.15789E-09	BAAT	1.9965804	4.2196E-05	DSCC1	0.9336647	0.002220574	RHOBTB3	0.2055311	0.026575179
DMXL1	0.70849305	6.2341E-09	DPP3	0.8326864	4.23674E-05	KIAA1429	0.4469822	0.002221302	ALG13	0.09680033	0.026617353
SLC24A5	1.2695807	6.23421E-09	ACLY	0.685795	4.24899E-05	MYEF2	0.20137031	0.002225308	ARL14EP	0.24915615	0.026702419
DCK	1.2748634	6.32925E-09	ARFGAP1	0.6032521	4.322E-05	TUBGCP4	0.20657115	0.002235487	RTF1	0.15039827	0.026702419
OVCA2	1.0157379	6.45013E-09	DNAJB12	0.5241787	4.32845E-05	PGBD1	0.8172724	0.002252241	ST6GAL1	0.27338716	0.026737239
LYPLA2	1.1512693	6.55869E-09	CCNJ	0.91013414	4.36017E-05	BIRC5	0.84242105	0.002255884	ZNF710	0.61740273	0.026748675
UTP3	1.1877844	6.57328E-09	PPP1CC	0.75731224	4.3854E-05	LRRC3	0.29277858	0.002262027	ZNF75A	0.43472832	0.026752039
BAG1	0.36675853	6.65034E-09	LOC100130691	0.2454665	4.38787E-05	DHFR	0.5117427	0.002263601	SCP2	0.51854706	0.026752039
RAP1GAP	1.5808489	7.00432E-09	CRYM-AS1	0.031366285	4.50164E-05	WBG	0.6314046	0.00226476	CFH	1.310398	0.026763482
PMF1	1.0446268	7.0641E-09	TMPO	0.50710654	4.51865E-05	SLC25A1	0.61100286	0.002272832	UBP1	0.41529337	0.026848423
SNRPF	1.0120302	7.10428E-09	SRSF1	0.5549012	4.51865E-05	POSTN	1.0269961	0.002281954	PACS2	0.12949473	0.026879492
TMOD2	0.8741692	7.1402E-09	SERPINB9	0.7528661	4.51865E-05	NSMCE1	0.65892416	0.002290926	HAUS2	0.06821199	0.026922365
ADAM15	1.0097857	7.15832E-09	USP24	0.33735374	4.52539E-05	SLC15A4	0.509841	0.002293783	PACSN3	0.64531285	0.026945386
XRN2	0.9209107	7.22166E-09	UBE2M	0.8939565	4.54776E-05	SPDYE2	0.20357253	0.002294352	EIF4ENIF1	0.3348488	0.027086301
TCEANC2	0.68046755	7.24908E-09	DNTTIP2	0.65860593	4.54776E-05	SPDYE2L	0.20357253	0.002294352	ABHD14A-ACY1	1.0796372	0.027093924

NRP2	0.9399 264	7.32 468 E-09	PSAT1	1.0482 687	4.547 76E- 05	MED8	0.6044 881	0.002 29435 2	CMTM 7	0.4466 6946	0.027 10549 7
CCT7	1.1438 491	7.33 657 E-09	APOPT 1	0.4677 55	4.568 29E- 05	NAA15	0.3604 1978	0.002 30778 9	EMC9	0.4994 998	0.027 15579 1
TCTN3	1.1352 872	7.36 695 E-09	PSIMCT -1	0.8647 2976	4.593 62E- 05	POLR2 C	0.4857 0597	0.002 31193 9	ARHG AP10	0.6061 795	0.027 15579 1
MINPP 1	1.1189 897	7.36 695 E-09	THAP6	0.3308 8356	4.653 E-05	RDH11	0.5993 936	0.002 31354 6	PPP1R 21	0.1118 592	0.027 15947 7
RAN	0.7654 97	7.37 41E- 09	KLHL20	0.6351 902	4.688 07E- 05	RNFT1	0.5756 897	0.002 32666 1	CCDC 107	0.3957 4444	0.027 16712 1
TMEM 177	1.2781 35	7.39 748 E-09	ATP5J2 -PTCD1	0.7675 0815	4.738 74E- 05	HNRN PKP3	0.3580 27	0.002 33512 5	GMPP B	0.5470 841	0.027 20221
WDR4 3	0.6740 455	7.96 048 E-09	CAMK2 D	0.4696 5155	4.801 49E- 05	FAT3	0.0324 3977	0.002 33588 9	YY1	0.1816 5818	0.027 20590 4
SPDYE 1	0.5386 73	8.07 865 E-09	TCEA1	0.6693 7256	4.816 42E- 05	DSN1	0.4549 8648	0.002 36189 6	ZCCH C8	0.0460 58036	0.027 20959 9
UBLCP 1	0.9701 845	8.09 915 E-09	CENPL	0.4504 8195	4.831 4E-05	RTN4I P1	0.1314 6245	0.002 36995	RALGA PB	0.3067 721	0.027 2162
OLIG1	2.5221 765	8.09 941 E-09	ZNF24	0.4807 0621	4.882 41E- 05	ZWINT	0.8044 797	0.002 37725 3	WBP11	0.2553 5122	0.027 2162
PRDM 2	0.5859 392	8.16 836 E-09	DEGS1	0.7424 61	4.886 1E-05	TMEM 186	0.7389 323	0.002 38021 1	HMOX 1	0.7830 3087	0.027 2162
USF2	0.9639 5296	8.25 077 E-09	NSUN5 P2	0.5174 887	4.886 1E-05	ZNF10 0	0.0778 34226	0.002 38701 1	IST1	0.3833 7475	0.027 2162
PYCR1	1.0924 586	8.25 105 E-09	COG1	0.7235 0127	4.886 1E-05	LOC10 012825 2	1.0313 114	0.002 38701 1	RAB40 C	0.8411 5213	0.027 26695 6
DIABL O	1.0101 653	8.29 79E- 09	ACN9	0.5965 136	4.901 29E- 05	HMG2 0B	0.6123 8956	0.002 39085 6	DCLK1	1.1968 653	0.027 2786
POLDI P3	0.9469 187	8.33 198 E-09	CRKL	0.5089 9065	4.928 86E- 05	PCBP2	0.4556 4732	0.002 39242	USP5	0.1906 0755	0.027 34139 2
KIAA09 30	0.5629 102	8.48 997 E-09	UBQLN 4	0.4757 819	4.993 53E- 05	MLLT1 0	0.2753 6628	0.002 39652 3	HNRPL L	0.1527 0561	0.027 34139 2
MRPS 12	1.1958 286	8.49 293 E-09	ZNF280 B	0.5048 1826	5.000 94E- 05	PARPB P	1.0360 447	0.002 39652 3	TMC8	1.1383 97	0.027 36102 5
WAC- AS1	0.5480 447	8.94 287 E-09	MRPL4 6	0.7972 808	5.067 68E- 05	MRPL1	0.4781 603	0.002 40072 7	GABP A	0.2484 2803	0.027 46016 3
SCML4	0.5059 976	8.97 395 E-09	CDC42 BPA	0.5216 727	5.111 63E- 05	MICAL 3	0.1907 3007	0.002 40072 7	C21orf 2	0.3198 491	0.027 61173 9
MRPL1 9	0.5948 8076	9.02 765 E-09	TUFT1	0.4220 593	5.112 13E- 05	SNRP B	0.6847 607	0.002 40151 2	KIFC3	0.2926 8202	0.027 75949
EIF3G	1.4268 057	9.07 034 E-09	MRPL1 3	0.8278 4814	5.114 99E- 05	KLF16	0.5040 2963	0.002 40449 9	TM9SF 2	0.4289 0677	0.027 77938 8
MGST 3	0.8563 94	9.19 104 E-09	CCT6P 1	0.5827 9693	5.142 03E- 05	HIBCH	0.4333 6922	0.002 40616 6	MST1R	1.6581 962	0.027 79095 9
SKP2	0.6901 6206	9.19 143 E-09	CDK20	0.9555 346	5.152 03E- 05	ERAL1	0.6687 17	0.002 41745 8	TOR1A IP2	0.2374 6835	0.027 81491 6

ZFH3	0.6092 0614	9.29 555 E-09	TRAPP C2L	0.9210 343	5.169 2E-05	ZNF21 1	1.0274 215	0.002 41824 8	PPIB	0.5899 834	0.027 83458 3
GLUL	1.1313 407	9.31 916 E-09	NCSTN	0.7600 3635	5.173 8E-05	SLC35 B4	0.1575 6312	0.002 41903 9	CHST1 0	0.5242 8013	0.027 86639 7
MED17	0.7617 569	9.34 866 E-09	GPHN	0.3637 109	5.176 69E- 05	FUZ	0.4211 1033	0.002 42594 4	PFKM	0.3724 513	0.027 88205 2
CENPF	0.9516 153	9.40 166 E-09	ASB11	0.1963 4372	5.186 76E- 05	ASAH1	0.6159 532	0.002 42594 4	GTF2A 1	0.2911 5242	0.027 90581 5
CRTC3	0.8573 955	9.56 498 E-09	PRDM1 5	1.3650 51	5.190 87E- 05	THOP1	0.3778 64	0.002 43073 7	CALML 4	0.3992 4356	0.027 90581 5
ASUN	1.0095 742	9.56 589 E-09	RNF8	0.3229 4932	5.197 37E- 05	JAGN1	0.5761 0595	0.002 43420 2	C21orf 58	0.0429 05178	0.027 90960 2
NBPF1 5	0.7745 722	9.63 511 E-09	ZNF772	0.2015 3451	5.229 12E- 05	USP35	1.3653 053	0.002 44338 1	PTPN4	0.0976 2446	0.027 92959 7
TRIM3 2	1.2833 277	9.64 759 E-09	C6orf20 3	0.7631 1076	5.236 88E- 05	RB1CC 1	0.2683 9063	0.002 45672 6	SOCS4	0.1634 2172	0.027 93744 1
EIF2D	1.0493 64	9.67 914 E-09	UNG	0.7640 693	5.390 33E- 05	IQCC	0.0218 52616	0.002 47049 5	PMS2 CL	0.5625 079	0.027 94123 3
TSTD1	2.7002 058	9.67 914 E-09	COLEC 11	1.8581 232	5.393 34E- 05	PLD2	0.7765 228	0.002 47049 5	LOC10 050647 4	0.5036 911	0.027 96098 7
DGCR 14	0.9465 173	9.67 914 E-09	FEM1B	0.7032 594	5.403 81E- 05	ADI1	0.5678 013	0.002 47175 4	CIRBP	0.4774 467	0.028 06151 9
RREB1	0.6443 9845	9.70 68E- 09	MLF2	0.7712 6306	5.550 26E- 05	ZFP90	0.0717 7055	0.002 47256 1	TTC28- AS1	0.1013 2231	0.028 07346 8
MRP63	0.6627 519	9.76 844 E-09	SHCBP 1	0.5787 9734	5.561 02E- 05	SMG8	0.4986 606	0.002 48187 4	NDUF AF5	0.3797 5407	0.028 12921
ARRB1	0.7427 293	9.76 844 E-09	VPS45	0.5466 878	5.573 09E- 05	SLC7A 5P1	0.9341 646	0.002 50134 5	RABG GTB	0.5017 245	0.028 12921
IDH1	1.0647 503	9.79 332 E-09	SNRPD 1	0.7379 1546	5.639 32E- 05	SLC38 A8	3.5178 607	0.002 51819 9	TTLL1	0.3842 9657	0.028 13710 8
PSMD 8	1.0868 429	1.01 221 E-08	SCFD2	0.8777 719	5.737 81E- 05	SAR1A	0.4881 748	0.002 52500 3	ADAM TS4	0.1614 7573	0.028 26711 8
GRSF1	0.8802 0843	1.01 826 E-08	RBM3	0.4804 6985	5.743 64E- 05	WTAP	0.3819 593	0.002 52711 2	DHPS	0.4996 2047	0.028 35297 9
NID1	0.7133 903	1.05 248 E-08	NUMBL	0.3363 2925	5.787 68E- 05	ANKR D53	2.0646 36	0.002 52978 2	MAP3K 3	0.1385 5684	0.028 44292 6
HSF4	0.9355 37	1.05 843 E-08	UBE2N	0.6950 156	5.787 68E- 05	HOXB1 3	1.1717 062	0.002 53328	RAD51 AP1	1.0102 149	0.028 61609 2
LOC10 029414 5	0.9489 488	1.05 948 E-08	NOL11	0.7111 7586	5.794 9E-05	MRPS 7	0.6538 348	0.002 53456 9	ADAM 33	0.5710 1655	0.028 63159 7
RPRD2	0.6336 6836	1.06 449 E-08	TMEM5	0.5798 865	5.808 02E- 05	ZNF76 4	0.1875 6779	0.002 53539 6	LTN1	0.2010 6658	0.028 63159 7
TCEA3	1.6455 119	1.07 651 E-08	ZNF22	0.7983 721	5.808 02E- 05	ZNF78 6	0.4627 889	0.002 54307 3	C19orf 43	0.2175 9698	0.028 63159 7
ANAP C5	1.1045 703	1.08 732 E-08	XPO6	0.4825 4368	5.808 6E-05	FYTTD 1	0.4614 1592	0.002 54307 3	ZW10	0.4953 5584	0.028 66448 8

COA6	1.0643 642	1.08 941 E-08	DNAJC 17	0.8483 194	5.853 3E-05	CREB1	0.1192 00446	0.002 54658 9	LRR1	0.6944 672	0.028 71401 9
USP3	0.5922 604	1.09 354 E-08	YLPM1	0.3470 566	5.853 88E- 05	CTNN B1	0.5149 414	0.002 54834 9	RPL13 AP6	0.1832 7105	0.028 71790 7
CA5BP 1	1.0084 946	1.10 007 E-08	DIP2B	0.4203 109	5.858 49E- 05	LPCAT 3	0.3053 8625	0.002 55011	DNA2	0.9165 843	0.028 75062 1
DDX55	0.7433 108	1.11 733 E-08	TRA2B	0.5793 0523	5.859 08E- 05	OAF	0.7904 6017	0.002 55047 7	NAA50	0.2028 5632	0.028 75062 1
BOLA2	0.6310 455	1.12 512 E-08	ME2	0.4580 9487	5.893 92E- 05	ATPAF 2	0.5479 5605	0.002 55084 5	STK36	0.2525 935	0.028 80444 7
BOLA2 B	0.6310 455	1.12 512 E-08	HAUS6	0.5532 2295	5.893 92E- 05	PFN2	0.6260 385	0.002 55167 7	ANGEL 1	0.3102 678	0.028 84141 8
MKKS	0.7363 322	1.13 852 E-08	FAM21 C	0.4313 4448	5.906 68E- 05	POLR2 L	0.5662 6284	0.002 56490 6	DGCR 8	0.1971 1378	0.028 85783 3
META P2	0.8156 9546	1.13 973 E-08	GCFC2	0.5331 879	5.926 25E- 05	COMM D9	0.3278 3017	0.002 56490 6	ALKBH 6	0.4709 4363	0.028 88677 9
TOMM 20	0.8623 5327	1.13 973 E-08	ZNF7	0.7895 781	5.947 24E- 05	ZNF28 OD	0.4521 1217	0.002 56490 6	RANB P6	0.6112 431	0.028 89486 5
ANKR D39	1.2267 026	1.14 689 E-08	ACSF3	0.8255 99	5.977 88E- 05	ZNF28 OC	0.1647 5585	0.002 56892	RAB28	0.2165 2564	0.028 91966 4
SCMH 1	0.8017 1967	1.18 928 E-08	TRIM26	0.7799 224	5.981 22E- 05	HMGB 3	0.5277 3017	0.002 56892	MBOA T7	0.1759 2072	0.028 93612
UROD	1.1471 205	1.19 268 E-08	MCM2	0.8063 6704	6.012 02E- 05	LMNB1	0.6737 8604	0.002 57622 2	ORC2	0.2517 1754	0.028 96932
LOC10 012859 3	0.3547 972	1.19 645 E-08	GALNT 3	0.9704 0415	6.029 77E- 05	ZNF93	0.9105 8135	0.002 57659 4	TCHP	0.3358 72	0.028 98998 8
VPS4B	0.6954 554	1.20 003 E-08	USP4	0.4883 0664	6.038 66E- 05	ATP5E P2	0.2839 438	0.002 58119 3	LTA4H	0.4149 766	0.029 04840 3
SNRN P25	1.1571 875	1.20 003 E-08	C12orf1 0	0.8309 742	6.050 34E- 05	SAP25	1.7652 792	0.002 58344 6	VAMP3	0.4375 495	0.029 06912 1
MRPS 15	1.1570 284	1.21 845 E-08	WDR89	0.5230 109	6.050 95E- 05	LINC00 668	1.0568 006	0.002 58523 1	TRIP13	0.1141 34006	0.029 20266 2
POP1	1.2133 256	1.24 251 E-08	KIAA01 95	0.4529 1644	6.080 54E- 05	SPATA 2	0.5054 729	0.002 59409 2	ZNF8	0.9219 088	0.029 23164 9
SFXN4	1.2237 587	1.24 49E- 08	UAP1L1	0.4523 6844	6.080 54E- 05	GLE1	0.2762 241	0.002 59777 4	SLC27 A4	0.9503 346	0.029 23164 9
APTX	1.0782 176	1.24 816 E-08	PPP4C	0.6735 6503	6.086 73E- 05	C16orf 87	0.5965 6876	0.002 59956 8	STK40	0.4771 583	0.029 27359 4
MOCS 3	0.6326 547	1.25 095 E-08	SRSF10	0.5955 9685	6.105 47E- 05	NUDC	0.6357 3104	0.002 60126 5	KANK3	0.4701 5607	0.029 29022 9
POLR MT	0.9432 498	1.26 895 E-08	FBXO2 8	0.4384 861	6.110 28E- 05	HEATR 3	0.2236 297	0.002 60780 3	PTK6	0.0570 41906	0.029 31955 8
DDX56	1.0371 356	1.28 086 E-08	SIKE1	0.3123 073	6.124 89E- 05	MPP3	1.5601 256	0.002 61150 4	FAHD2 CP	0.3533 5413	0.029 37432 2
TPM1	1.0620 828	1.30 774 E-08	AP1B1	0.5860 794	6.129 72E- 05	CHEK2	0.7071 1076	0.002 62025 1	PRMT1 0	0.4526 2167	0.029 37829 3

LCOR	0.8418 8277	1.30 783 E-08	GTF2F2	0.6789 9686	6.135 95E- 05	SNRN P35	0.4672 6814	0.002 62025 1	PDLIM 1	0.4177 7217	0.029 39445 3
BCKD K	1.0558 158	1.35 602 E-08	TMEM9	0.8456 769	6.200 03E- 05	FBXO3 8	0.3367 0822	0.002 62281 6	MAPK APK5- AS1	0.3019 634	0.029 43660 4
ANXA6	0.9450 211	1.35 653 E-08	CENPT	0.4339 198	6.206 33E- 05	ZNF76 5	0.0012 97718	0.002 62281 6	RPL23 AP7	0.1706 7084	0.029 55965
YIPF1	1.0986 39	1.35 999 E-08	DPP8	0.4923 7612	6.215 48E- 05	YME1L 1	0.3157 179	0.002 62281 6	TMEM 91	0.7757 761	0.029 57137 2
GPR19	2.3714 664	1.37 189 E-08	CLK2	0.6490 1954	6.263 64E- 05	ANKR D27	0.3927 3152	0.002 63026 3	HIRA	0.5804 2747	0.029 57137 2
PPIF	1.0303 297	1.37 601 E-08	UBQLN 2	0.5639 736	6.272 87E- 05	MAP3K 7	0.4282 9683	0.002 63437 4	PARK7	0.5907 8795	0.029 57137 2
ZSWIM 7	0.6964 1083	1.37 601 E-08	MYO1B	0.5730 2856	6.305 12E- 05	FAN1	0.3767 7956	0.002 63513 5	PUS1	0.7827 818	0.029 58389 4
NUP88	1.1283 058	1.37 601 E-08	DNAH1 4	0.5325 114	6.349 75E- 05	BECN1	0.6740 404	0.002 63599 5	ZNF53 0	0.0718 5369	0.029 58789 4
VPS33 A	0.6458 1805	1.37 761 E-08	ICT1	0.8438 725	6.349 75E- 05	CENP B	0.4191 442	0.002 64021 4	POLE4	0.4237 6792	0.029 63429 6
C19orf 70	0.9766 5215	1.37 761 E-08	GLS	0.3782 2077	6.350 4E-05	ATG12	0.3376 2932	0.002 64347 7	AFF1	0.1338 0866	0.029 72380 3
RHBD D3	1.0167 578	1.37 857 E-08	SOX10	0.5821 74	6.351 05E- 05	PJA1	0.5460 266	0.002 64434	ARHG AP5- AS1	0.2101 3908	0.029 77923 2
PDK3	0.6824 0225	1.38 507 E-08	TMEM8 7A	0.6136 4263	6.351 7E-05	LOC15 8435	0.1274 0661	0.002 66275 2	TEN1	0.3770 8429	0.029 83904 6
DCAF1 2	0.8643 665	1.38 518 E-08	CBY1	0.7221 337	6.391 62E- 05	ZBTB4 1	0.3939 966	0.002 66410 5	LOC73 0102	0.3497 3514	0.029 87316
FASTK D1	0.8969 41	1.38 743 E-08	MRPL3	0.8631 8433	6.396 65E- 05	OTUD3	0.1232 2504	0.002 66497 4	CEBP G	0.2962 062	0.029 87719 4
SUPT1 6H	0.7927 022	1.38 926 E-08	SAP18	0.6385 2227	6.432 44E- 05	LSG1	0.3459 6863	0.002 66875 1	DEPD C5	0.1503 4316	0.029 91081 5
GOT2	1.0573 976	1.39 078 E-08	HYPK	0.6574 431	6.443 38E- 05	RAI1	0.2628 4724	0.002 68128 3	AURK B	0.8412 8404	0.029 95309 1
REXO2	1.0868 942	1.39 078 E-08	ZNF664	0.5796 484	6.464 65E- 05	RAMP 2	0.9652 951	0.002 68498 2	ACAD8	0.4407 6404	0.029 98248
GPX1	0.9062 926	1.39 402 E-08	PNMAL 1	0.4185 822	6.468 27E- 05	SPIRE 2	0.0937 16465	0.002 68858 7	ZNF68 4	0.8770 203	0.029 98248
NTAN1	1.1631 495	1.39 402 E-08	EXOSC 8	0.6451 5	6.520 77E- 05	CEP16 4	0.2280 0612	0.002 69093	ARFG AP2	0.3054 407	0.030 10293 2
IMMT	0.9825 181	1.41 273 E-08	DHX34	0.5889 711	6.643 62E- 05	SLC39 A10	0.3919 194	0.002 69474 1	TESK2	0.7631 188	0.030 15464 7
EPN2	0.6608 9326	1.43 181 E-08	NEFH	1.5509 679	6.643 62E- 05	CRCP	0.2262 0778	0.002 69904 7	GYG2 P1	0.0413 08086	0.030 17579 9
PLCG1	0.7226 4194	1.43 181 E-08	CYB561 D1	0.0811 07885	6.660 97E- 05	TUBG2	0.2952 4085	0.002 70718 7	ANKD D1A	0.0433 2396	0.030 29667
CBWD 1	0.8258 648	1.44 878 E-08	ARIH2	0.5435 1294	6.672 28E- 05	INTS2	0.0889 2256	0.002 70993 7	TMX3	0.2464 152	0.030 30075 9

MAGE D1	1.0334 42	1.49 511 E-08	SRRM1	0.4645 2993	6.735 55E- 05	ENTPD 7	0.3052 3995	0.002 71131 3	USP42	0.3352 3756	0.030 32200 3
HSD17 B7	0.8670 827	1.50 123 E-08	ZSCAN 21	0.8629 713	6.744 61E- 05	RGS19	0.9005 787	0.002 71416 6	RSBN1 L	0.0311 24532	0.030 32200 3
PA2G4	0.9362 3817	1.51 016 E-08	RCN3	0.6753 934	6.744 61E- 05	C11orf 83	0.2518 5987	0.002 71554 5	ZNF32 4	0.7885 4513	0.030 36096 5
ILF3	0.9207 874	1.54 077 E-08	VAR5	0.6389 36	6.782 25E- 05	DTWD 1	0.3595 1	0.002 71889 5	CTDSP L2	0.2392 5328	0.030 41743 7
WASH 3P	0.7095 325	1.54 091 E-08	PRPF4 B	0.3006 9146	6.861 25E- 05	DDX23	0.4870 121	0.002 71929	TK1	0.7650 9166	0.030 53916 1
NUP13 3	0.9348 656	1.54 295 E-08	COX10	0.8491 338	6.945 15E- 05	GCLC	0.7909 056	0.002 72363 2	SLC2A 4RG	0.6037 844	0.030 56082
C9orf1 39	0.4165 5126	1.57 083 E-08	CENPJ	0.8493 657	6.952 18E- 05	ZNF58 4	0.9629 064	0.002 72600 4	CTDN EP1	0.2870 2268	0.030 57810 3
ANKR D52	0.6835 913	1.57 29E- 08	C12orf2 3	0.5431 4333	6.959 22E- 05	RFC4	0.8111 9627	0.002 72738 8	KIAA12 79	0.3455 399	0.030 62148 2
ZBED6	0.8840 001	1.57 305 E-08	MBD3	0.6796 6986	7.023 49E- 05	LAMA5	0.4449 862	0.002 72778 4	TTC28	0.0460 4904	0.030 67398 1
EIF2B4	1.0842 135	1.57 9E- 08	C2orf68	0.4239 4304	7.086 57E- 05	ZNF28 3	0.2367 838	0.002 73164 4	ECSIT	0.4767 3488	0.030 69132 1
PPP2R 1B	0.7414 353	1.58 595 E-08	KIAA17 04	0.7573 9425	7.088 91E- 05	MTF1	0.0388 32776	0.002 73650 1	ZNF55 5	0.0267 24573	0.030 69545 9
PPCS	0.9906 769	1.58 658 E-08	ZNF317	0.5350 937	7.138 09E- 05	HDAC1 0	0.5340 111	0.002 74623 9	PIIP5 K2	0.0993 5111	0.030 71695 1
FARSB	1.0303 934	1.59 455 E-08	NGLY1	0.6303 595	7.142 07E- 05	ZFP82	0.8452 5126	0.002 74623 9	IQGAP 3	0.5763 8425	0.030 74313
SNHG 3	0.9375 541	1.61 604 E-08	CBX8	0.8951 299	7.144 44E- 05	LRRFI P2	0.3371 266	0.002 75750 8	FLJ446 35	0.1110 7366	0.030 79113 3
MRPS 5	0.9474 922	1.63 164 E-08	ADPRM	1.0741 948	7.175 17E- 05	LIAS	0.0480 3353	0.002 75790 8	SEPT7 P2	0.0391 2904	0.030 81736 8
CTBP2	0.6728 679	1.64 789 E-08	ERI3	0.5675 814	7.175 17E- 05	POC1A	1.0804 402	0.002 76180 8	PPP6R 3	0.2942 9996	0.030 93216 5
PIR	1.2102 21	1.65 109 E-08	CDC25 B	0.5528 6926	7.249 55E- 05	LCMT1	0.5949 378	0.002 76821 9	HAUS3	0.1668 9497	0.030 9452
TIA1	0.7123 5085	1.66 821 E-08	CCSER 2	0.3804 9096	7.253 59E- 05	LOC64 4936	0.1410 163	0.002 77253 5	LOC10 024073 5	0.6259 072	0.030 98460 1
TIPRL	0.8361 758	1.67 452 E-08	CERS4	0.7732 3395	7.300 56E- 05	CBWD 2	0.4477 752	0.002 77544 9	FBXO3 4	0.5384 0894	0.030 99321 6
UBE2G 1	0.6428 1654	1.68 395 E-08	ABHD1 1	0.3968 184	7.309 6E-05	TFCP2 L1	2.1265 976	0.002 77786 3	RABA C1	0.6206 067	0.031 00627 4
ELP6	1.0492 748	1.69 603 E-08	FKBP1 AP1	0.5515 2196	7.340 25E- 05	IFIT3	0.1461 0773	0.002 78925 2	SLC39 A6	0.4374 008	0.031 01489 5
INTS7	0.6381 1463	1.70 141 E-08	DRG2	0.8081 7205	7.352 67E- 05	CLPB	0.6032 212	0.002 79066 7	ARPC4	0.5375 153	0.031 07243 6
C19orf 54	0.5770 65	1.70 419 E-08	TTL	0.0898 5418	7.377 57E- 05	CDCA2	0.9129 5624	0.002 79562 2	GPAT CH2L	0.3422 7607	0.031 08107 3

ZNF562	0.6077259	1.71116E-08	IBTK	0.4740237	7.42194E-05	C12orf4	0.64199144	0.002800585	UBN1	0.16502006	0.031165219
ANAPC13	1.135116	1.75325E-08	LARS	0.50030166	7.43449E-05	KBTBD7	0.9772398	0.002803526	VKORC1	0.6249046	0.031178078
MTRF1	0.7781613	1.75611E-08	MYO9B	0.39404595	7.44032E-05	ECT2L	0.004069156	0.00281919	LOC100505817	0.5217544	0.031204605
PPAP2C	2.358574	1.75845E-08	NAA60	0.5284752	7.46642E-05	ZNF519	0.5232889	0.002824702	LOC728323	0.28202644	0.03128931
HDAC2	0.7547584	1.79342E-08	LUC7L	0.5652433	7.47905E-05	CCP110	0.2693344	0.00283176	UBASH3B	0.63603264	0.031301951
RHOJ	0.7633507	1.80351E-08	PRRG1	0.5786541	7.53423E-05	LOC90784	0.2679578	0.002833707	ABHD5	0.2994892	0.031301951
BLOC1S2	0.6074125	1.80922E-08	GPS1	0.88267964	7.56235E-05	TMEM185B	0.2928685	0.002836168	ZNF621	0.04386697	0.031301951
ZNF197	0.8517431	1.81495E-08	TAF1A	0.4401354	7.582E-05	SPHK2	0.49619377	0.00284675	DEPD C7	1.27875	0.031306166
EIF4E2	1.0774661	1.81625E-08	C17orf49	0.758139	7.59732E-05	TAF1	0.24938884	0.00284675	RPGRIP1L	0.42359257	0.031341756
MRPL50	1.1428171	1.83937E-08	RNF34	0.677492	7.59732E-05	G2E3	0.36152005	0.002851282	CSNK2B	0.6128286	0.031345977
MYADM	0.8926605	1.85311E-08	ZNF557	0.44733888	7.61361E-05	ATAT1	0.3177243	0.002856853	LIX1L	0.19478515	0.031521035
CHAMP1	1.3282903	1.87955E-08	UQCRH	0.8713349	7.61773E-05	PARP16	0.6706313	0.002871134	ALDH4A1	0.511858	0.031611014
DKC1	1.0396743	1.88205E-08	TMEM38A	0.14626005	7.61773E-05	PRPF38B	0.36880758	0.002872588	NADSYN1	0.47436526	0.031714543
NDUFS7	1.2999194	1.90307E-08	AES	0.5755402	7.61773E-05	FUBP1	0.43151653	0.002878095	PEX14	0.28352967	0.031872942
HAX1	1.1625515	1.92629E-08	ZFP64	0.004305294	7.61853E-05	ZNF768	0.82143295	0.002882571	PGPEP1	0.16705208	0.031935899
FAM86A	1.0526968	1.95494E-08	ZMAT5	0.7063946	7.64177E-05	LBH	0.85413986	0.002887156	GMPS	0.37243494	0.031953868
DNAJA3	0.9792723	1.95635E-08	MBP	0.85197866	7.65296E-05	C15orf57	0.50611335	0.002887995	CTNNA2	1.5791153	0.031967284
POLR1C	1.0900111	1.9812E-08	ALS2C R11	1.3307809	7.68058E-05	DNAJB7	0.20451313	0.002891964	CDK19	0.15686421	0.032026378
EIF5AL1	0.40235233	1.98323E-08	ZNF593	0.84095615	7.71005E-05	U2AF1	0.6496788	0.002896359	LRCH1	0.16535984	0.032094726
TRO	1.3792286	2.0023E-08	SLC26A4	0.42551318	7.77387E-05	LARS2	0.6482984	0.002913552	HERC2 P7	0.11308116	0.032158342
UTP14A	0.9588864	2.00558E-08	TWF1	0.65409285	7.90399E-05	GATA D2B	0.17646384	0.002913873	TSC22 D4	0.05669151	0.032190192
CHERP	0.6294927	2.01438E-08	F5	0.3937655	7.97834E-05	CHTF18	0.630599	0.002915348	C8orf46	0.59499925	0.032437844
ALDH9A1	1.0825001	2.02076E-08	TOE1	0.82239646	8.01348E-05	GLRX2	0.5081855	0.002924095	MMP2	0.5916085	0.032460411

NKD1	0.2866 7566	2.03 273 E-08	ANKRD 45	0.3267 3255	8.024 22E- 05	INPP5 A	1.3414 89	0.002 92409 5	OTX1	1.0782 022	0.032 46041 1
LOC65 2276	0.4484 891	2.07 199 E-08	PRDM7	0.8080 009	8.024 22E- 05	KCNIP 2	1.4890 4	0.002 92610 3	SYS1	0.2450 6083	0.032 46476 1
RUSC2	0.9685 965	2.08 998 E-08	ATF5	0.2748 1627	8.025 06E- 05	CAPZA 1	0.6233 3536	0.002 92811 2	MAP1L C3C	0.0883 93696	0.032 58875 5
TRMT1 2	1.3685 583	2.09 66E- 08	PMEL	0.7056 346	8.034 97E- 05	META P1D	0.7338 7456	0.002 93699 7	C22orf 39	0.1257 7617	0.032 58875 5
TRAF4	0.5054 2134	2.14 007 E-08	KDM5B	0.4402 699	8.044 89E- 05	TP53I1 1	1.0439 974	0.002 93795 3	PSMA4	0.5546 805	0.032 66253 1
BIRC7	1.2421 241	2.15 536 E-08	C17orf5 1	0.7212 3826	8.100 38E- 05	LOC28 2997	0.0224 43417	0.002 95314 2	DNAJC 13	0.3087 1075	0.032 71809 8
IRAK1	0.6598 749	2.16 349 E-08	PTPRG	0.4142 818	8.114 04E- 05	LZIC	0.5096 0106	0.002 95676 6	TCF25	0.3629 9086	0.032 75016
FAM92 A1	1.0371 891	2.20 63E- 08	RFPL2	3.0998 993	8.162 62E- 05	CHM	0.1189 98155	0.002 95719 6	MKI67	0.5264 8926	0.032 75893 3
FDPS	1.1645 252	2.21 126 E-08	MRPL1 1	0.6237 577	8.220 74E- 05	KNSTR N	0.6695 619	0.002 95975 8	EEFSE C	0.3922 0506	0.032 75893 3
STARD 10	1.4121 931	2.24 064 E-08	RNMT	0.4130 375	8.256 9E-05	SSB	0.6370 4455	0.002 96392 3	EP400 NL	0.6025 713	0.032 81931 2
MMAD HC	1.2123 713	2.26 694 E-08	PI4KAP 2	0.5162 0865	8.309 04E- 05	GGA3	0.3390 6522	0.002 96702 5	NDUF AF4P1	0.5203 937	0.032 85173 8
RPL27 A	0.4523 2636	2.27 965 E-08	IQCK	0.6326 589	8.309 04E- 05	C12orf 77	0.0965 5158	0.002 99246 7	VAMP4	0.1350 6745	0.032 89272 6
IPO5	0.6763 819	2.33 745 E-08	SLC35A 4	0.7048 8125	8.326 68E- 05	LARP4 B	0.1711 1756	0.002 99451 9	DYRK1 B	0.3922 201	0.032 89272 6
ZNF53 6	1.8657 131	2.37 71E- 08	GIT2	0.6457 225	8.396 25E- 05	SPIN3	0.7391 1005	0.003 01031 2	MBIP	0.3633 8562	0.032 89272 6
MLST8	0.9786 5623	2.37 882 E-08	ALDH3 B1	0.5556 65	8.452 14E- 05	CCDC 138	0.9255 503	0.003 01779 8	PDRG 1	0.5100 797	0.032 94367 7
KAZN	0.8380 509	2.39 287 E-08	SLC25A 46	0.6399 8336	8.470 18E- 05	TMEM 117	0.5255 1556	0.003 02421 4	MAPK8 IP3	0.1058 13615	0.032 95718 8
PRKC D	0.9378 5095	2.39 825 E-08	CNIH	0.7930 87	8.476 81E- 05	GEMIN 6	0.6372 5084	0.003 02519 8	RPL23	0.3163 4635	0.033 11160 9
ZNF56 8	0.8798 202	2.43 402 E-08	ZNF556	0.8690 4943	8.490 07E- 05	HELQ	0.5172 656	0.003 02825 6	C10orf 32- AS3MT	0.3561 524	0.033 13487 1
H3F3A	1.7632 413	2.49 942 E-08	SPATS 2L	0.3048 6935	8.490 07E- 05	PIGB	0.1678 4528	0.003 03295 2	SWT1	0.2438 1807	0.033 25694 3
TTLL1 2	1.0815 798	2.50 883 E-08	FTSJ2	0.7616 766	8.570 58E- 05	RWDD 4	0.4777 6502	0.003 03295 2	FAM20 6A	0.3906 571	0.033 35572 2
SUCLA 2	1.0408 003	2.51 218 E-08	LBR	0.8149 956	8.573 42E- 05	MED6	0.2137 1275	0.003 04312 1	SEC61 A2	0.3600 4466	0.033 35990 7
ZNF58 7B	0.9259 404	2.62 168 E-08	RMI1	1.0524 999	8.584 9E-05	METTL 21A	0.2711 541	0.003 04411 1	ALDH2	1.7498 164	0.033 40675 2
C14orf 2	0.8391 187	2.62 168 E-08	MED27	0.8377 631	8.584 9E-05	RPS2	0.3525 6976	0.003 05222 4	RECQ L5	0.2025 9018	0.033 52494 5

CRTC2	0.8019 103	2.65 315 E-08	EMILIN 2	1.5124 612	8.614 83E- 05	MTER FD2	0.4781 3296	0.003 05541 2	VIPAS 39	0.3650 1375	0.033 55770 7
CHCH D1	0.9256 344	2.67 768 E-08	NSF	0.6882 6944	8.656 53E- 05	ZAK	0.0548 0705	0.003 05585 7	TYW1	0.2851 9762	0.033 56219 3
MRPL4 8	1.1384 494	2.69 704 E-08	ZNF668	1.1561 068	8.657 45E- 05	RIOK2	0.3478 866	0.003 05849 9	COX4I 1	0.3936 5783	0.033 58545 9
PNO1	0.7293 539	2.72 478 E-08	XPO5	0.3825 013	8.664 22E- 05	STXBP 2	0.6408 2456	0.003 05894 5	FNBP1	0.1003 2091	0.033 58545 9
GMFB	0.7925 0973	2.74 082 E-08	AZI1	0.7761 293	8.678 8E-05	PAFAH 1B2	0.4922 336	0.003 06104	TPRA1	0.3929 476	0.033 60424 7
SEMA4 C	0.8934 76	2.76 364 E-08	C15orf3 9	0.3314 7654	8.721 64E- 05	REEP6	0.8529 1934	0.003 06203 6	CCDC 59	0.2501 0565	0.033 70338 1
STAM BP	0.6921 1555	2.80 609 E-08	CIAPIN 1	0.7046 1065	8.721 64E- 05	PPM1K	0.2181 4172	0.003 06964 1	RCE1	0.4094 9333	0.033 80277 5
ICK	0.5284 269	2.85 815 E-08	AIMP1	0.5289 568	8.741 18E- 05	MAD2L 1BP	0.5617 07	0.003 07053 6	TLK2	0.1024 9241	0.033 80277 5
DECR1	1.0908 494	2.85 815 E-08	GEN1	0.4061 7394	8.778 42E- 05	AZI2	0.4759 8058	0.003 07053 6	SIVA1	0.5541 0945	0.033 94142 4
EARS2	1.1043 705	2.94 386 E-08	TRAPP C5	0.8451 926	8.778 42E- 05	NSMC E4A	0.7560 246	0.003 0857	XAB2	0.1260 7047	0.033 99408
LTV1	1.1232 758	2.98 539 E-08	HADH	0.6891 247	8.778 42E- 05	GNAO 1	1.7247 804	0.003 0857	OSGIN 1	0.8322 517	0.034 01279 4
SLC25 A11	1.0614 007	3.02 112 E-08	HNRNP K	0.5845 972	8.778 42E- 05	DUXA	0.1127 64694	0.003 0866	POLB	0.4522 249	0.034 02215 5
MLX	0.9385 755	3.02 41E- 08	HSPB6	1.9938 338	8.787 26E- 05	BUB1	0.9115 6644	0.003 0866	INCA1	0.1024 7566	0.034 12775 8
PDSS2	0.6700 496	3.02 41E- 08	ALS2	0.4112 9026	8.807 97E- 05	SYK	0.1980 2488	0.003 08926 8	PPP3C A	0.0940 1768	0.034 20002 5
SMAR CA4	0.6731 913	3.02 944 E-08	ZNF776	0.5230 358	8.822 79E- 05	RND2	0.3143 5847	0.003 10974 5	SRP19	0.3309 2272	0.034 20943 1
GGCT	1.1187 465	3.11 506 E-08	MOB1B	0.2757 4578	8.827 71E- 05	RPS15 AP10	0.0857 93614	0.003 11075 6	FAM14 9B1	0.2763 8575	0.034 23821 6
C9orf6 4	0.5433 1166	3.12 204 E-08	CCDC2 2	0.8654 194	8.846 52E- 05	AFF3	0.1510 335	0.003 11735 6	HES6	0.6527 916	0.034 42250 4
THOC7	1.0101 869	3.14 891 E-08	BCAT2	0.8397 7574	8.859 41E- 05	PITPN A-AS1	0.5902 302	0.003 13969 3	PQLC1	0.3564 3893	0.034 42709 3
TNKS2	0.7679 569	3.15 597 E-08	MOB4	0.3678 1478	8.860 37E- 05	NHSL1	0.3463 552	0.003 15856 8	PCOL CE	0.5435 8214	0.034 43140 5
PRPF6	0.8991 227	3.18 408 E-08	BTBD10	0.8035 443	8.937 25E- 05	PHLPP 1	0.3106 107	0.003 16469 4	TMEM 51	0.4391 1338	0.034 43140 5
TFAP2 A	0.7407 2766	3.19 988 E-08	TPT1	0.2995 425	8.976 41E- 05	LZTS1	0.4826 5144	0.003 17310 4	CYP4A 11	0.0209 4242	0.034 43572
SMIM4	0.9312 826	3.20 212 E-08	HINFP	0.9033 7694	9.008 62E- 05	GIGYF 2	0.3511 1427	0.003 17584 1	ZDHH C7	0.2769 2854	0.034 68403 7
SLX1A	0.8094 968	3.20 212 E-08	NCAPH	0.8578 311	9.010 59E- 05	ATOH8	1.2173 036	0.003 17744 1	SLC1A 5	0.3549 295	0.034 68865 8

SLX1B	0.8094 968	3.20 212 E-08	PEX11B	0.7370 3545	9.010 59E- 05	RUNX3	0.4537 6772	0.003 17904 3	RHO	0.8797 2444	0.034 71289 3
RBM10	0.8035 4214	3.22 967 E-08	PRPF3	0.5464 8715	9.056 15E- 05	TIMM8 A	0.7836 8783	0.003 19938 9	POU6F 1	0.0887 3535	0.034 72242 3
RRN3P 2	1.4031 755	3.25 156 E-08	SNAPC 5	0.6578 292	9.115 17E- 05	TSSC1	0.3856 1705	0.003 19938 9	C2orf4 9	0.3749 914	0.034 81545 7
PREX1	1.1515 453	3.30 031 E-08	FOPNL	0.4529 3468	9.134 58E- 05	TTC27	0.4957 87	0.003 21593 3	LRP5	0.4608 696	0.034 82501 2
TYK2	0.7600 036	3.33 916 E-08	TSTD2	0.4593 9627	9.141 72E- 05	RALBP 1	0.2708 143	0.003 22273 8	WDR4 5	0.3074 4573	0.034 86409 7
TP53IN P1	0.8109 947	3.35 875 E-08	DIS3	0.2548 3164	9.144 77E- 05	ITGB3 BP	0.4415 931	0.003 22320 7	CASC5	0.8991 7463	0.034 88323 4
DLEU1	1.3382 348	3.42 036 E-08	ALKBH 5	0.5500 3035	9.184 8E-05	PRDX6	0.5598 2965	0.003 22425 3	POFUT 1	0.1382 6992	0.034 88323 4
WDR7 3	0.9640 024	3.43 422 E-08	SPNS1	0.6733 366	9.214 67E- 05	SCAN D2P	0.1158 299	0.003 22529 9	ZNF50 3-AS2	1.6058 168	0.034 92730 6
DAGLA	2.1238 78	3.44 607 E-08	LOC100 129361	0.4675 5695	9.228 07E- 05	TMF1	0.2690 321	0.003 22807 8	RBM22	0.2242 1327	0.034 93688 9
CELSR 3	1.5840 485	3.47 253 E-08	THNSL 1	0.3846 1232	9.231 15E- 05	SBF1	0.0601 8192	0.003 23201 5	HNRN PUL2- BSCL2	0.5636 4155	0.034 94647 5
LMNB2	0.8689 1544	3.49 499 E-08	SMN1	0.7280 0106	9.238 37E- 05	XPC	0.3346 1162	0.003 23248 6	CYCS	0.3548 3867	0.035 02986 6
UBE3A	0.5648 8705	3.55 903 E-08	TMEM1 1	0.8200 194	9.310 02E- 05	PHF5A	0.5513 6216	0.003 23758 6	PLXNC 1	0.3533 5758	0.035 06915 3
KLHL8	0.5756 354	3.57 451 E-08	ERICH1	0.5702 852	9.384 29E- 05	BET1L	0.4282 0275	0.003 24955 2	POLA1	0.2688 3933	0.035 09362 1
PPOX	0.9606 977	3.64 544 E-08	ADRM1	0.8322 77	9.393 73E- 05	SNX30	0.3118 2086	0.003 24955 2	SOX12	0.0117 7846	0.035 21206 7
C10orf 137	1.2438 582	3.65 522 E-08	PAM16	0.6718 564	9.405 24E- 05	NPRL2	0.4848 7124	0.003 26214 2	AHSA1	0.5815 822	0.035 23137 4
SNX8	0.7768 9373	3.66 891 E-08	PIP4K2 C	0.5973 0923	9.405 24E- 05	RGMB	0.4701 26	0.003 26495	FAM12 7A	0.4890 4958	0.035 35520 9
LSM2	1.0421 698	3.71 202 E-08	CASP2	0.4671 3722	9.425 24E- 05	AMPD 2	0.5047 723	0.003 26600 9	C1orf5 0	0.3816 901	0.035 39481 6
AUNIP	0.7795 115	3.71 202 E-08	CLSPN	0.4238 776	9.434 72E- 05	DNAJC 3	0.3264 0633	0.003 27514 5	ANXA1 3	2.0574 856	0.035 42946 8
TRIM1 3	0.5470 2324	3.76 523 E-08	CHST9	1.3522 053	9.446 32E- 05	UEVLD	0.4407 886	0.003 28723 9	SKIV2L 2	0.1311 2861	0.035 43917 3
GSPT1	0.5158 508	3.81 804 E-08	MALL	0.2776 6782	9.472 77E- 05	MORN 4	0.1120 5677	0.003 28948	TBC1D 4	0.2365 3473	0.035 47358 3
NME6	0.7867 0955	3.83 463 E-08	TRMU	0.5257 304	9.501 4E-05	HMBO X1	0.5862 1	0.003 29455 6	FAM19 5A	0.3552 049	0.035 51330 6
HENM T1	1.7051 415	3.84 553 E-08	DPH3	0.4055 9635	9.506 71E- 05	ATG7	0.2574 9245	0.003 29455 6	AKR7L	0.3973 884	0.035 54305 4
DERA	1.0279 431	3.87 903 E-08	ATP8A2	1.7754 077	9.524 78E- 05	PKNO X1	0.1414 4771	0.003 30092 6	PEX26	0.1089 40765	0.035 60205 4

C5orf2 2	0.9735 8125	3.87 903 E-08	FDX1	0.7121 141	9.577 1E-05	APPL1	0.1263 0625	0.003 30886 2	PIGN	0.2722 4016	0.035 60205 4
MRPL2 1	1.1556 834	4.08 821 E-08	ACADM	0.5435 16	9.587 79E- 05	TCF3	0.4300 0352	0.003 31041 7	TAS2R 20	0.4153 7672	0.035 60651
PHLDB 2	1.7352 943	4.10 718 E-08	TSPAN 6	0.7158 01	9.587 39E- 05	GNAI1	0.5559 55	0.003 31267 4	TRIM5	0.1508 6676	0.035 68123 3
ATG4B	0.8266 604	4.11 269 E-08	ARHGA P17	0.5378 044	9.599 58E- 05	SP3	0.1379 2774	0.003 31304 9	DYDC2	0.0743 8534	0.035 68597 8
MTFP1	1.1875 484	4.14 167 E-08	ALG8	0.8063 924	9.604 94E- 05	LSM12	0.4686 339	0.003 31708 3	ZKSCA N5	0.3768 4038	0.035 85126 4
CDIP1	0.6653 6725	4.16 96E- 08	EIF3F	1.0009 818	9.625 35E- 05	ANAP C4	0.3750 7182	0.003 32764 8	PSRC1	0.4310 7033	0.035 85126 4
ZNF49 6	0.8780 673	4.19 52E- 08	BNIP1	0.0234 87652	9.704 18E- 05	EFEM P2	0.6266 546	0.003 34398 7	FAM64 A	0.8651 506	0.035 85602 9
RHOA	0.6960 909	4.22 349 E-08	D2HGD H	0.5610 3456	9.741 1E-05	GABP B1- AS1	0.2508 2523	0.003 34398 7	PTS	0.3699 4445	0.035 90089 9
RBM4 B	0.9337 568	4.23 421 E-08	LANCL2	0.7201 729	9.813 14E- 05	UBE4A	0.2916 6028	0.003 34805 6	MVK	0.7866 4476	0.035 90089 9
GPAT CH2	0.8622 8895	4.34 113 E-08	ZNF131	0.5770 868	9.814 24E- 05	UBE2D 1	0.6450 137	0.003 35740 6	KIN	0.0809 0562	0.035 9256
SCAF4	0.8671 821	4.35 735 E-08	MIS18A	0.8236 1937	9.837 27E- 05	PSMC 2	0.6284 3764	0.003 37891 4	TGFBR 1	0.1873 5619	0.035 9256
HJURP	0.6068 2094	4.41 56E- 08	L3MBTL 2	0.7142 3346	9.948 8E-05	CHCH D5	0.4898 3756	0.003 38000 9	TOM1L 2	0.1070 2826	0.035 94048 5
JAKM1 P2	0.4122 3833	4.52 562 E-08	MNF1	0.5550 3815	9.961 01E- 05	CHAF1 A	1.0252 943	0.003 38291 3	DBF4B	0.3334 588	0.035 95031 9
TFPT	0.7895 7635	4.53 71E- 08	GTSF1	1.3762 04	0.000 10090 7	METTL 18	0.8052 0296	0.003 38581 9	RBBP7	0.5617 1316	0.036 03046 3
MAPR E1	0.9938 454	4.59 289 E-08	FUOM	0.8328 496	0.000 10123 4	GBE1	0.4620 9383	0.003 39658 6	PIK3A P1	1.0075 992	0.036 03046 3
PRELP	0.5845 573	4.59 289 E-08	POP7	0.7812 177	0.000 10158 5	ADD1	0.4049 3488	0.003 40859 9	ZNF37 A	0.0145 43218	0.036 03046 3
HNRN PH3	0.9206 407	4.72 547 E-08	YAE1D 1	0.7820 064	0.000 10164 1	NCK2	0.4842 2495	0.003 41517 3	AP5M1	0.2769 3072	0.036 18244 4
FKBP1 1	1.1910 377	4.79 207 E-08	NGDN	0.8174 501	0.000 10178 9	ANLN	0.9090 551	0.003 42785 7	AADAT	0.8479 7806	0.036 23813 5
ILKAP	0.9394 2255	4.83 722 E-08	CORO1 B	0.6861 561	0.000 10186 8	RCOR 3	0.3030 3088	0.003 42885 6	MAGO HB	0.1869 6097	0.036 25794 7
POGK	0.7992 63	4.86 538 E-08	SPECC 1L	0.3881 135	0.000 10189 1	IFT172	0.6360 7246	0.003 43913 7	MED24	0.2733 0983	0.036 32904 5
QPRT	0.9577 839	4.88 352 E-08	TXNDC 9	0.7295 786	0.000 10215 2	RBMX 2	0.3045 9973	0.003 45128 9	C6orf4 7	0.3452 3416	0.036 34407 6
OAZ2	1.0710 675	4.95 23E- 08	RPP25L	0.9359 0343	0.000 10225 5	USP32 P2	0.5460 556	0.003 45978 6	SPAG5	0.8293 421	0.036 34834 4
IMP4	1.1574 746	4.96 189 E-08	C21orf9 1	0.8373 6455	0.000 10235 8	C3orf6 2	0.0312 41395	0.003 46090 5	CNOT3	0.2171 8192	0.036 34834 4

ZFAT	0.5981 8685	4.98 335 E-08	CPED 1	0.3282 5896	0.000 10377	LOC64 2852	0.5400 298	0.003 47610 6	CCRN 4L	0.1296 8028	0.036 35317 2
EXO5	0.8200 6073	5.09 879 E-08	HMHA1	0.4043 404	0.000 10418 6	ATP6V 1H	0.5744 547	0.003 47723 1	CDKN2 AIP	0.4018 5684	0.036 51631 1
CSE1L	0.8973 757	5.12 235 E-08	SREK11 P1	0.0727 9836	0.000 10418 6	C16orf 58	0.4212 722	0.003 50544 7	LOC72 9603	0.0094 05023	0.036 53141 1
LIG1	0.7485 51	5.15 366 E-08	LARP1	0.4138 752	0.000 10482 6	MAMS TR	1.0794 193	0.003 51344 2	NEIL1	1.2149 234	0.036 55164 7
ANXA7	1.0131 824	5.19 288 E-08	SCG3	0.7268 959	0.000 10493 1	EGLN1	0.2552 6032	0.003 51384	COPS7 B	0.3004 458	0.036 58645 9
ZBED1	0.7277 3665	5.23 083 E-08	SLC47A 1	0.4898 3142	0.000 10510 7	ZNF34 3	0.5552 0314	0.003 51384	ACVR2 B	0.2275 4672	0.036 58645 9
RPP21	1.0838 091	5.26 905 E-08	UBXN2 B	0.3116 3338	0.000 10601 1	ZNF57 3	0.0532 2448	0.003 51810 1	ZBTB4	0.3087 364	0.036 58645 9
PAK4	0.9567 208	5.29 653 E-08	MOSPD 2	0.8122 705	0.000 10604 7	KDM1 A	0.3411 2307	0.003 52162 8	SNX1	0.2483 8582	0.036 64269 2
ZNF59 2	0.8077 27	5.29 735 E-08	UTP23	0.3683 0676	0.000 10643 7	MTMR 3	0.3365 7	0.003 52162 8	RAB3G AP1	0.1376 9805	0.036 66812 7
GGA2	0.6807 9424	5.35 986 E-08	ZNF503 -AS1	1.6565 312	0.000 10666 2	C15orf 38- AP3S2	0.7052 571	0.003 53091 1	WDR7 0	0.2994 4667	0.036 68843
RRN3	0.7227 789	5.39 42E- 08	ACADS B	0.2971 768	0.000 10667 4	OSTC	0.7468 2677	0.003 53142 5	EDC4	0.2487 348	0.036 78088 9
CPSF3	1.0547 193	5.44 166 E-08	IMPA1	0.5116 643	0.000 10685 2	RPL23 AP32	0.8815 9853	0.003 54765 6	RGR	0.5066 572	0.036 87816 5
GLRX3	1.0431 585	5.45 382 E-08	SOX6	0.5078 2305	0.000 10695 9	CRTA C1	1.4910 908	0.003 55006 3	RSAD1	0.3283 2736	0.036 89312 1
PMVK	0.9233 8824	5.56 336 E-08	ZNF766	0.4916 687	0.000 10704 3	FAHD2 B	0.4605 836	0.003 55247 1	EED	0.3967 501	0.036 89312 1
FAM10 1B	0.7302 5435	5.56 336 E-08	PPP1C A	0.7724 812	0.000 10712 6	DUSP2 3	0.6297 265	0.003 55413 8	MMAA	0.5016 258	0.036 90808 4
PDCD4	0.7976 972	5.57 006 E-08	RPL7L1	0.6997 7486	0.000 10759 2	NT5C3	0.4257 2176	0.003 55654 9	MAP4K 3	0.2075 4497	0.036 93368
APEH	0.9583 9506	5.57 006 E-08	FOXO3 B	0.4584 0043	0.000 10834 8	FEZ1	0.1671 1767	0.003 57467 5	LOC10 028956 1	0.4417 428	0.036 99528 7
ZNF57 4	1.2560 191	5.59 908 E-08	NARF	0.7862 652	0.000 10857 7	TTC21 B	0.0041 02779	0.003 57773 4	ZRSR2	0.2738 9443	0.036 99528 7
TIMM2 3	0.9769 205	5.67 01E- 08	TSEN15	0.7135 706	0.000 10887 9	PGF	0.9572 5644	0.003 58513 2	SNX17	0.6005 5214	0.037 04687 9
FAM21 7B	0.5210 6774	5.67 1E- 08	AKAP6	1.1321 793	0.000 10901 2	CCDC 97	0.4812 0353	0.003 58756 3	ZC3H1 8	0.2394 9198	0.037 07228 5
RPP14	0.7198 6187	5.71 068 E-08	COMM D6	0.5189 0236	0.000 10907 3	MAGE A4	1.0768 204	0.003 59254 4	MED7	0.3875 2654	0.037 14997 5
ZNF34 5	0.7081 066	5.74 553 E-08	VCPIP1	0.3437 6243	0.000 10921 9	ZNF32 2	0.2309 489	0.003 60455 6	MAP2K 5	0.4719 485	0.037 26347 8
CIRH1 A	0.9288 039	5.75 496 E-08	LINC00 665	0.3416 8813	0.000 10921 9	SSH2	0.2420 1694	0.003 61788 7	DBP	0.6893 3547	0.037 32584 4

ZEB2	0.6756 155	5.76 1E- 08	BAP1	0.5611 922	0.000 11001	MSL3	0.5930 0995	0.003 61969 7	CD40	0.8480 121	0.037 36187 4
HNRN PR	0.9677 098	5.76 285 E-08	ZNF121	0.8461 1124	0.000 11090 5	METTL 3	0.4278 7233	0.003 62150 8	FAM86 EP	0.1945 6083	0.037 40289 3
CCL28	0.8227 4383	5.76 285 E-08	ALX1	0.8070 514	0.000 11120 1	DTX3	0.6267 1435	0.003 62332	LOC10 050620 7	0.1048 563	0.037 58064 2
TRAPP C4	0.9726 262	5.80 067 E-08	NCBP2	0.7676 1204	0.000 11120 1	ASCC3	0.1893 1173	0.003 63478 3	USP16	0.2541 6756	0.037 66452 9
ALG5	1.0730 752	5.82 916 E-08	MCM3	0.7805 655	0.000 11225 5	POU2F 1	0.0185 23348	0.003 63982 5	HDLBP	0.3883 469	0.037 67977 1
DNAJA 1	1.1377 294	5.87 689 E-08	EID1	0.8606 277	0.000 11226 8	RPL39 L	0.6066 688	0.003 64422 7	POLM	0.2134 3029	0.037 78996 7
MAP1S	1.0685 806	5.91 449 E-08	POLR3 H	0.5591 864	0.000 11245 5	HTR3B	0.0643 1211	0.003 65122 1	NT5C3 B	0.4123 1567	0.037 79997 3
CDKN2 B-AS1	0.2791 0885	5.98 764 E-08	ZC3H4	0.2222 1033	0.000 11249 3	MYLK	0.6781 811	0.003 65498 8	C12orf 45	0.4324 734	0.037 79997 3
SCRN1	1.4734 824	5.99 039 E-08	ALG11	0.7127 7374	0.000 11276 8	FAM10 3A1	0.5329 2876	0.003 65552 1	PLEKH M2	0.3148 6788	0.037 85254 5
NBL1	1.5030 098	6.00 38E- 08	IKZF5	0.6358 15	0.000 11377 3	BCL9L	0.6021 241	0.003 66047 4	NDUF A7	0.5536 978	0.037 90490 3
ZC2HC 1A	0.6453 533	6.13 863 E-08	RFPL1- AS1	0.1793 6906	0.000 11377 3	SDCC AG8	0.2925 6877	0.003 66100 8	LOC10 050586 5	0.4865 616	0.037 95174 7
RRAG D	0.8500 528	6.25 502 E-08	TXN2	0.8472 27	0.000 11391 2	NUDT2	0.5779 919	0.003 66673 3	HMGC R	0.3313 483	0.037 95174 7
GDPD 5	1.3176 46	6.28 755 E-08	ARHGA P42	0.4515 2	0.000 11415 2	PPIL4	0.3861 519	0.003 66921 6	MUS81	0.3467 2388	0.037 95174 7
RBM18	0.8186 921	6.36 144 E-08	ENG	0.7037 992	0.000 11445 7	LAMP1	0.3505 7873	0.003 67105 1	CDH15	1.1687 511	0.037 95677 1
SLC16 A1	0.7806 6176	6.37 377 E-08	AAR2	0.6637 488	0.000 11445 7	HIGD2 A	0.8174 304	0.003 68852 4	PKIB	0.8682 0453	0.038 04083 4
HSDL2	0.8791 4747	6.40 88E- 08	UCHL3	0.7685 1296	0.000 11454 6	TMCO 1	0.4898 9293	0.003 70399 2	C17orf 100	0.4336 1697	0.038 04083 4
NUPL1	0.5428 8524	6.57 987 E-08	CKAP2	0.7838 1115	0.000 11515 7	RTKL1	0.3062 7316	0.003 70649 8	BTBD2	0.2101 1111	0.038 05118 2
CRTAP	0.7418 161	6.61 991 E-08	SLC35A 1	0.6475 3324	0.000 11518 4	LGR4	0.9521 462	0.003 71557 4	PSME4	0.1677 1474	0.038 06684 5
XIST	0.9554 4076	6.66 216 E-08	ORC6	0.3956 3894	0.000 11518 4	ROGDI	0.7530 035	0.003 71940 3	PCGF1	0.2975 4028	0.038 14607 6
DRG1	1.1215 507	6.67 114 E-08	CLASR P	0.5015 323	0.000 11529 9	IER3IP 1	0.5689 528	0.003 71994 6	WBP1	0.3138 9824	0.038 15644 9
TOP3A	0.5214 661	6.70 185 E-08	DUSP7	0.7618 3075	0.000 11541 4	FAM84 B	0.0838 4265	0.003 72366 4	PGM3	0.1085 4381	0.038 2249
DIS3L	0.5849 725	6.79 649 E-08	RNF26	0.7990 138	0.000 11581 2	NUBP1	0.5864 149	0.003 72420 7	UBFD1	0.1465 7249	0.038 30976 1
RAB3D	0.5448 143	6.83 496 E-08	SHARPI N	0.6041 87	0.000 11684 2	CHMP 6	0.6085 43	0.003 72804 5	IDH3G	0.4278 9948	0.038 34663 1

DPH1	0.8691 803	6.93 144 E-08	POLDIP 2	0.6257 8714	0.000 11745 2	BAZ1A	0.3478 3003	0.003 76423 3	SCYL1	0.3401 535	0.038 37310 3
RABIF	0.6836 7624	6.93 466 E-08	PRMT6	0.8935 6494	0.000 11754 3	RSC1A 1	0.9226 012	0.003 77343 9	DDX11	0.1686 159	0.038 43708 7
DCTD	0.9438 5797	6.94 198 E-08	RARS2	0.6703 2117	0.000 11754 4	NPRL3	0.3935 535	0.003 77865 9	NDUF AF2	0.2954 261	0.038 48506 7
GPS2	0.9503 8044	6.98 213 E-08	C1orf23 3	2.1648 831	0.000 11754 4	AKR1A 1	0.5973 8624	0.003 78778	ZC3H1 1A	0.1788 9473	0.038 53227 7
FAM16 1A	0.5464 586	7.07 646 E-08	SNRPC	0.8994 72	0.000 11763 6	PRR19	1.1908 203	0.003 79502 8	GTF2H 4	0.6587 898	0.038 53227 7
BLZF1	0.5341 576	7.12 995 E-08	ZNF33A	0.2122 5105	0.000 11928 7	EOGT	0.1747 044	0.003 79759 2	PCMT D1	0.1353 9374	0.038 53227 7
GNPA T	0.9314 8625	7.15 219 E-08	JARID2	0.3408 516	0.000 12008 2	POLG	0.4047 8355	0.003 80485 8	MSH5	0.2148 2673	0.038 56933 7
ZC3H1 2C	1.0806 198	7.16 818 E-08	PCNP	0.6664 572	0.000 12114 9	MKRN 2	0.4725 9364	0.003 83034 5	EMCN	0.4433 5777	0.038 59594 5
AP2A1	0.5202 521	7.16 856 E-08	LOC100 144602	2.0843 47	0.000 12141 8	RTBD N	0.0099 86922	0.003 83157 9	ECI1	0.5776 0227	0.038 70308 4
SLC25 A15	0.5084 784	7.16 856 E-08	HK1	0.6690 787	0.000 12141 8	RBM6	0.4739 6168	0.003 83958 1	SLC2A 9	1.6026 437	0.038 70820 3
ERCC3	0.7133 7116	7.19 516 E-08	PPIH	0.7582 9583	0.000 12160 7	TAB1	0.2339 1043	0.003 84420 7	GPBP1 L1	0.0785 5936	0.038 81534 1
ANKR D54	0.8757 4285	7.31 378 E-08	TTF2	0.2364 3115	0.000 12160 7	TMEM 41A	0.2669 3523	0.003 85267 7	COX7B	0.6834 054	0.038 83641 8
C6orf4 8	1.2143 489	7.31 936 E-08	EXOSC 2	0.3582 5965	0.000 12170 2	THBS3	0.6850 0954	0.003 85267 7	MIPOL 1	0.2865 556	0.038 92273 8
AKT1	0.8838 3853	7.34 868 E-08	SHANK 2-AS3	0.1953 5725	0.000 12171 6	CBX2	0.6266 2274	0.003 85459 8	ATP2C 1	0.1838 5608	0.038 94956
KIFAP 3	0.8112 99	7.34 997 E-08	MAP2K 2	0.4857 9773	0.000 12189 1	LCLAT 1	0.2625 949	0.003 8572	POP5	0.3982 5302	0.038 99809 8
HMGX B3	0.7090 634	7.36 641 E-08	FOXN2	0.2425 5393	0.000 12374 9	UNC13 D	0.8053 9817	0.003 85844 2	TTK	0.9549 258	0.039 00325 2
ZNF25 2P	0.3087 733	7.42 641 E-08	PTEN	0.4971 1597	0.000 12455 7	DDX42	0.1837 1153	0.003 86581 5	DAK	0.1815 7372	0.039 01383 5
DDX19 A	0.7388 3265	7.53 766 E-08	NDEL1	0.7102 4054	0.000 12473 7	COQ4	0.3340 8257	0.003 86626	FAM13 8F	0.2078 2629	0.039 08934 9
ATF1	0.8297 252	7.62 272 E-08	TMED3	0.8868 478	0.000 12516 4	DDX58	0.0119 97225	0.003 87489 5	RYBP	0.1609 9104	0.039 12715 5
NDUF V3	0.6801 064	7.81 582 E-08	ZNF428	0.4321 1237	0.000 12587 1	KIAA14 30	0.2762 7808	0.003 88092 9	STK39	0.9496 4194	0.039 19768 3
C9orf9 1	0.4647 7154	7.83 558 E-08	ACO1	0.6074 104	0.000 12695 9	SFPQ	0.3087 568	0.003 89302 3	PACR GL	0.4723 0586	0.039 22985 2
CHML	0.5127 2255	7.87 617 E-08	PLD3	0.6850 352	0.000 12731	EIF2A K2	0.3187 2693	0.003 89359	TM9SF 4	0.2575 544	0.039 24049
GEMIN 4	1.1997 47	8.03 3E- 08	WIZ	0.8410 69	0.000 12833 8	ARIH1	0.2996 539	0.003 89690 4	PPT2	0.4057 441	0.039 47515 1

HSD17 B1	0.6746 345	8.03 3E- 08	ENO1	0.7495 346	0.000 12870 7	EXOC2	0.3299 887	0.003 90147 6	TMEM 194B	0.3361 5845	0.039 56820 5
DEF8	0.9985 3724	8.08 644 E-08	LAS1L	0.7049 8496	0.000 12870 7	GSTA4	0.5284 9776	0.003 90147 6	COQ7	0.1691 994	0.039 62814 4
PTCD3	0.6303 322	8.09 026 E-08	ARMCX 1	0.8324 348	0.000 12912 1	ADCY9	0.7015 347	0.003 90617 2	SMIM1	0.7076 6217	0.039 64437 9
RAB9A	0.9127 8535	8.13 93E- 08	PYGO2	0.4786 7164	0.000 12912 1	BRMS 1L	0.8639 104	0.003 91431 9	GALK1	0.4303 9823	0.039 64960 8
COA4	1.0392 623	8.16 466 E-08	SF3A2	0.6306 3914	0.000 12912 1	BPGM	0.6432 752	0.003 92374 5	TNFAI P1	0.3475 379	0.039 65483 8
RSU1	0.6220 599	8.25 032 E-08	TTC5	0.9324 977	0.000 12926 5	NARFL	0.3899 275	0.003 92431 7	LINC00 338	0.1936 4862	0.039 66006 9
NOC2L	0.9353 5185	8.25 907 E-08	ABHD1 0	0.6687 266	0.000 12939 3	ARRB2	0.6788 1984	0.003 93665 5	CSDA	0.0813 11844	0.039 72592
PROS ER1	1.0127 962	8.26 449 E-08	C6orf14 7	0.2790 9246	0.000 12969 4	TTN- AS1	0.3193 737	0.003 93849 7	TMA16	0.0863 76965	0.039 75874 4
SNRP E	0.8428 46	8.26 449 E-08	SMCR8	0.4307 3583	0.000 12996 6	LOC10 013087 2	0.0078 9233	0.003 93849 7	LOC65 0226	0.8484 88	0.039 91851
PKLR	2.6651 9	8.27 327 E-08	USP19	0.5466 464	0.000 13143 4	THAP8	0.8740 9896	0.003 93895 4	NEURL 4	0.3968 6668	0.040 05689 3
RPL13 AP20	0.6263 942	8.34 781 E-08	HSPBP 1	0.6466 2755	0.000 13217 4	INF2	0.3223 8594	0.003 96165 9	DHCR 7	0.8463 0746	0.040 08439 6
POM12 1	0.5706 567	8.40 33E- 08	EPT1	0.2700 2284	0.000 13274 3	IDI2- AS1	0.8793 9185	0.003 96921 4	NEK1	0.1873 3917	0.040 10607 6
ARNT2	0.9664 745	8.57 54E- 08	TMEM5 0B	0.4933 405	0.000 13275 8	RAD54 L	1.1091 844	0.003 96979 4	FREM1	1.7297 304	0.040 11692
HDHD 1	1.2435 932	8.67 795 E-08	LINC00 516	0.5082 875	0.000 13287 6	SLC30 A8	0.9087 113	0.003 97246 9	ARGL U1	0.3634 033	0.040 18343 3
NADK D1	0.5101 187	8.83 32E- 08	LOC101 101776	0.5082 875	0.000 13287 6	ZBTB4 4	0.0783 4857	0.003 97572 7	SLC35 E1	0.0572 36	0.040 25506 3
PGM2	0.9095 0906	8.88 404 E-08	ZC3H15	0.6384 475	0.000 13327 2	LINC00 847	0.5822 464	0.003 97700 7	GGAC T	1.0228 95	0.040 26036 4
MXI1	0.9051 2294	8.94 205 E-08	PCBP4	0.6808 39	0.000 13383 2	DCAF5	0.3949 079	0.003 98038 7	FAM21 A	0.5106 517	0.040 26566 6
NCLN	0.7254 825	8.94 205 E-08	NVL	0.5380 5697	0.000 13393 5	MED21	0.4978 2538	0.003 99218 5	EAPP	0.3507 983	0.040 26986 9
SUSD5	1.0130 986	9.02 51E- 08	MAN2B 1	0.6055 7926	0.000 13395 1	PAGR1	0.2736 4638	0.003 99347 1	PM20D 2	0.1826 3282	0.040 26986 9
PRUN E	1.0588 404	9.02 677 E-08	DSTYK	0.4025 1482	0.000 13494 1	IKBKE	0.6726 6196	0.003 99791 4	IPP	0.0443 01428	0.040 26986 9
KXD1	1.0031 45	9.02 845 E-08	NLE1	0.8472 8914	0.000 13641 7	ZHX3	0.0960 6709	0.003 99849 9	TMEM 222	0.3555 2925	0.040 29192
PEMT	1.0793 391	9.03 277 E-08	RPS26	0.6364 052	0.000 13697 3	COAS Y	0.4398 5212	0.004 00964 1	GTF2B	0.3910 0274	0.040 35309 4
HDHD 2	0.8622 039	9.15 4E- 08	SCN2B	0.0113 198	0.000 13769 8	HINT3	0.3389 269	0.004 01093 3	TBC1D 2B	0.2663 4336	0.040 39196 5

DIMT1	0.9180 8563	9.31 481 E-08	NQO1	0.5762 98	0.000 13961 6	LAP3	0.5513 9375	0.004 01575 1	PMS1	0.1813 1657	0.040 45887 4
RNPE P	0.9648 624	9.42 223 E-08	PTGDS	2.0293 229	0.000 13987 8	SNX20	0.1383 6043	0.004 02410 9	HIAT1	0.3164 5977	0.040 47541
SWAP 70	0.7274 951	9.42 223 E-08	MINA	0.5291 7445	0.000 14010 9	PROR SD1P	0.2699 336	0.004 02682	AMER 1	0.9895 235	0.040 57585 3
GFM2	0.8763 746	9.45 153 E-08	DTD2	0.2627 75	0.000 14049 4	KIAA01 46	0.3285 2527	0.004 04584 4	SF1	0.1719 9527	0.040 58653 9
ZNF28 6A	0.6277 283	9.45 607 E-08	TBC1D 22A	0.5469 223	0.000 14057 2	ARMC X5	0.5732 864	0.004 05200 5	FAM13 8A	0.1946 0325	0.040 58653 9
ZDHH C6	1.0972 103	9.54 836 E-08	RCCD1	0.9810 865	0.000 14086 6	COQ6	0.5214 1684	0.004 05200 5	ZNF21 9	0.4459 062	0.040 61436 3
RBM8 A	0.6078 917	9.54 836 E-08	UPF3B	0.5479 2184	0.000 14096 1	JAK2	0.8053 8166	0.004 07114	H2AFV	0.2623 5247	0.040 66470 7
ZNF42 6	0.7930 374	9.85 18E- 08	YBX1	0.6313 5374	0.000 14096 1	GADD 45GIP1	0.5443 592	0.004 07602 5	HDAC6	0.2896 2827	0.040 78275 5
USF1	1.1207 918	9.95 758 E-08	RIC8A	0.6502 073	0.000 14103 9	LOC10 050576 1	0.4179 0915	0.004 08509 6	NBPF7	0.0055 63724	0.040 81634 1
FAM13 6A	0.9719 927	9.97 108 E-08	GTF3C 3	0.6057 4406	0.000 14111 7	DDX3X	0.3623 673	0.004 08509 6	MAP3K 11	0.1817 6138	0.040 84995 2
VAMP2	0.6394 6193	1.00 459 E-07	CHRNA 7	0.8169 6165	0.000 14128 9	UCKL1	0.3340 561	0.004 09215	RBM25	0.2550 0336	0.040 91131 3
NUDT1 9	0.6782 3935	1.00 683 E-07	FXN	0.3764 564	0.000 14173 9	SENP1	0.4235 0516	0.004 11218	ATRN	0.1737 3277	0.040 92235 3
COPS5	1.0478 833	1.01 172 E-07	AURKA	0.8364 589	0.000 14175 6	C7orf1 3	1.0109 024	0.004 11783 3	PSKH1	0.5108 885	0.040 94444 3
PPP1R 7	0.9345 152	1.04 059 E-07	SOLH	0.7099 804	0.000 14363 3	C20orf 111	0.4834 7804	0.004 12204 8	GFM1	0.2373 756	0.040 98947 8
CBX6	1.0734 998	1.04 808 E-07	BAG6	0.3443 8938	0.000 14373	LOC10 050671 0	0.2563 7227	0.004 13133 4	ACAP2	0.0399 12846	0.041 10238 9
INPPL 1	0.6358 144	1.05 042 E-07	ACTR1 0	0.6040 438	0.000 14412 5	NAP1L 1	0.4114 5015	0.004 13556 1	OXSM	0.5823 7535	0.041 34698 5
MRPS 10	0.7665 6294	1.05 399 E-07	GAPDH	0.4243 3378	0.000 14423 6	RNF14 4A	0.1644 0332	0.004 13967 1	NPLO C4	0.0930 2753	0.041 36356
STOM L2	1.1243 829	1.05 665 E-07	HERPU D2	0.2686 126	0.000 14460 1	TRIM2 5	0.3764 2044	0.004 16198 1	CCNB1	0.5614 7015	0.041 36356
LRRC5 8	0.5557 47	1.05 931 E-07	RGL1	0.6621 877	0.000 14480 8	LARP4	0.3504 0745	0.004 18880 1	GPX8	0.0753 3577	0.041 39074 3
ZBTB4 5	1.0130 877	1.07 973 E-07	FASTK D5	0.9089 3614	0.000 14509 6	LOC40 1321	0.0680 87794	0.004 20988	NOD1	0.3240 7787	0.041 39074 3
THOC3	0.9821 422	1.08 686 E-07	NABP1	0.3969 7373	0.000 14528 9	TXNR D1	0.4369 7193	0.004 23167 4	HMGC S1	0.0119 60143	0.041 39074 3
PARVB	0.5594 564	1.08 707 E-07	ACAA1	0.7026 8846	0.000 14584 7	OSGE PL1	0.3440 747	0.004 23599 6	LD0C1 L	0.2433 6277	0.041 48198 5
OFD1	0.6789 3636	1.09 266 E-07	FKBP15	0.5801 8196	0.000 14634 4	COMM D7	0.5153 445	0.004 23809 7	SYNJ2 BP	0.1364 1512	0.041 50461 7

NOL8	0.6947 7344	1.09 542 E-07	SGSH	0.5213 189	0.000 14674 6	MVD	0.5116 684	0.004 24391	ZKSCA N8	0.1723 924	0.041 51007
WDR7 6	0.4672 9428	1.12 008 E-07	C8orf44	0.2659 4833	0.000 14705 2	CHAC1	1.3720 258	0.004 24601 4	GPC2	0.7766 767	0.041 52125 3
TMEM 220	0.4615 739	1.12 03E- 07	C16orf7 4	1.5231 85	0.000 14723	MINK1	0.1124 6783	0.004 24799 7	ZNF44 4	0.4593 8078	0.041 54390 4
EIF2A K4	0.3857 598	1.13 294 E-07	LEPR	0.0602 33407	0.000 14802 2	STX7	0.4706 0353	0.004 25221 2	RDX	0.2331 7945	0.041 57803 8
SMYD 2	1.0002 657	1.13 844 E-07	SFSWA P	0.3924 8362	0.000 14862 3	GID4	1.1850 121	0.004 25221 2	CNNM 3	0.0037 42871	0.041 62367 9
EIF5B	0.6147 787	1.14 296 E-07	ZZEF1	0.5796 751	0.000 14873 8	ZNF67 4-AS1	0.1977 3844	0.004 2609	GTF2I RD1	0.2717 7018	0.041 68086 1
DDX52	0.7354 102	1.18 607 E-07	SLC2A8	1.0138 911	0.000 14908 1	CDK16	0.3859 268	0.004 2609	DOCK 6	0.3254 2682	0.041 88772 6
TRAPP C3	1.0366 687	1.22 012 E-07	MZT2B	0.5340 5887	0.000 14922 9	SGTA	0.4776 5264	0.004 26276 8	C1orf5 4	0.7737 538	0.041 97992 3
KIAA15 49	0.2095 2208	1.22 106 E-07	LRP4- AS1	0.4144 9818	0.000 15019 5	ARFG EF2	0.1210 9223	0.004 26276 8	TPRKB	0.4470 9542	0.042 06650 2
PPM1 G	0.9955 811	1.22 733 E-07	ORAOV 1	0.4817 6	0.000 15047 6	VAC14	0.5502 3086	0.004 26786 6	TXND C5	0.3995 5917	0.042 21133 5
MKNK 1	0.9567 583	1.25 73E- 07	POLR3 F	0.7412 4664	0.000 15088 8	COL25 A1	1.8663 768	0.004 26923 7	DNM2	0.2021 9922	0.042 34494 5
SUGP1	0.7591 944	1.26 582 E-07	TBC1D 17	0.4483 0236	0.000 15169 9	ARID5 B	0.3791 8913	0.004 27422	ADC	0.2859 3555	0.042 40882 7
SRSF1 2	0.3658 0712	1.26 582 E-07	MGST1	1.5427 438	0.000 15278	AGPAT 5	0.2858 8027	0.004 27858 3	ASH1L	0.1519 1875	0.042 42605 6
HEBP1	1.0663 912	1.27 747 E-07	ADIPO R1	0.7908 385	0.000 15370 1	LOC44 1454	0.3124 398	0.004 28070 5	EIF4G 1	0.3074 1337	0.042 48975 9
GAS2L 3	1.1137 242	1.27 846 E-07	TAOK3	0.4960 8824	0.000 15467 9	RIPK2	0.4371 456	0.004 28807 2	CHRN E	2.6829 364	0.042 49532 1
TTC38	1.1147 673	1.27 871 E-07	ARV1	0.6560 4407	0.000 15473 1	SRSF4	0.5033 4024	0.004 29469 9	CPT1A	0.1710 8378	0.042 65260 1
STARD 3NL	1.0076 691	1.29 871 E-07	NIPSNA P1	0.6807 907	0.000 15573 4	CGNL1	0.0377 66475	0.004 30647 7	ARID1 A	0.0547 44825	0.042 65260 1
ANKR D17	0.5944 824	1.30 386 E-07	VPS35	0.6688 518	0.000 15599	HAUS4	0.4803 585	0.004 30647 7	RNGT T	0.2132 3153	0.042 68752 5
VRK3	1.0961 908	1.31 585 E-07	CYFIP1	0.4504 2711	0.000 15806 2	TRPV2	0.6005 374	0.004 30786	NUP37	0.5256 45	0.042 69311 1
PPFIA 3	1.5043 696	1.33 565 E-07	SULT1A 4	0.3373 659	0.000 15834	ARHG DIA	0.3409 5687	0.004 31225 5	PFDN6	0.3579 9366	0.042 75744 9
EIF2B1	1.0602 427	1.35 221 E-07	SULT1A 3	0.3373 659	0.000 15834	CDV3	0.2646 198	0.004 32395 6	PNPLA 6	0.1350 999	0.042 84542 4
EIF4A3	1.0914 164	1.36 227 E-07	KLHL30	0.3947 681	0.000 15873 9	SAAL1	0.5832 568	0.004 33139 1	CKB	0.6855 5856	0.042 92175 9
SPATA 20	0.9319 548	1.37 043 E-07	RFWD3	0.4180 4895	0.000 15955 5	RAP1G DS1	0.2183 3631	0.004 33202 5	SES3	0.1860 9834	0.042 92708 3

MRPL3 5	0.7548 9855	1.40 233 E-07	PHYHD 1	0.3630 6003	0.000 15960 8	CCDC 90B	0.4944 0965	0.004 33417 2	CYB5R 4	0.4668 1672	0.042 92708 3
TMEM 97	0.8735 3003	1.40 233 E-07	CPNE8	0.5376 285	0.000 15969 7	ABLM1 1	0.7912 279	0.004 36429 5	KIF15	0.7836 8396	0.043 06857 8
GREB1	0.5059 1075	1.40 233 E-07	PIK3R4	0.5209 28	0.000 15999 4	TUSC3	0.5812 8303	0.004 36722	ASB7	0.4828 3246	0.043 07420 6
ZNF28 1	0.8078 1454	1.40 735 E-07	PAAF1	0.6726 354	0.000 16001 3	LOC44 0288	0.0340 64926	0.004 38759 4	UNC11 9B	0.5530 1225	0.043 10351
GBF1	0.6562 771	1.40 735 E-07	SLC7A4	2.0811 4	0.000 16055 6	LOC10 050591 2	1.5434 46	0.004 38759 4	ZBED5	0.1557 0359	0.043 10914 3
NFS1	0.8125 9096	1.41 373 E-07	MAX	0.5077 2697	0.000 16064 5	FAM16 1B	0.0285 08622	0.004 39206 4	TBCC	0.2993 8155	0.043 11449 1
DDX49	1.0533 769	1.41 524 E-07	ZNF253	0.4612 4652	0.000 16245 6	ACD	0.4202 0023	0.004 39871 6	MAPK AP1	0.3434 4772	0.043 11449 1
ITGA4	1.8026 558	1.44 105 E-07	YEATS 2	0.3356 7193	0.000 16370 1	METTL 2B	0.2742 5352	0.004 39871 6	UBALD 1	0.5436 18	0.043 14974 5
KIAA01 41	0.6740 788	1.44 674 E-07	FAM86 C2P	1.0496 459	0.000 16382 7	TKT	0.5559 779	0.004 40012 7	NUDT3	0.3192 016	0.043 15538 5
CAMK K2	0.6784 8176	1.44 745 E-07	SMCR5	0.6254 097	0.000 16542 1	WBP4	0.3534 3954	0.004 40230 6	ZCCH C11	0.0135 57062	0.043 30884 3
SELRC 1	0.7356 986	1.45 318 E-07	ZNF259	0.6899 1774	0.000 16565 7	CAAP1	0.3651 2035	0.004 40513 1	CACN B3	0.6152 2067	0.043 32044 7
OSBPL 1A	0.6762 409	1.45 628 E-07	TMEM2 01	0.6822 17	0.000 16573 2	TPD52 L2	0.5902 2427	0.004 40513 1	SOCS7	0.0278 91738	0.043 35584 8
BBS4	0.8814 437	1.46 246 E-07	COX16	0.4823 6296	0.000 16573 2	DALRD 3	0.5256 7095	0.004 40654 5	CDK5R 1	0.5673 322	0.043 36066 2
SETD9	1.1667 547	1.48 941 E-07	ZNF134	0.8863 3615	0.000 16582 4	NR2C2 AP	0.4588 8036	0.004 42850 8	HDAC3	0.3447 4993	0.043 36066 2
RBBP5	0.5507 9114	1.49 314 E-07	C6orf13 6	0.8859 0264	0.000 16597 1	STAT5 A	0.5711 1144	0.004 44139 9	NDUF B6	0.4552 0493	0.043 48520 4
RUFY2	0.4477 56	1.49 905 E-07	MRPL3 9	0.6255 064	0.000 16597 1	PDCL3	0.5370 732	0.004 44139 9	PGAM 2	1.0902 607	0.043 48520 4
TFB2M	0.9318 892	1.49 935 E-07	LRR4 5	0.8218 4374	0.000 16655 3	CDKN3	1.0828 594	0.004 44502 3	NACA P1	0.2398 8008	0.043 55001
DENN D4B	0.6861 5675	1.50 268 E-07	NELFA	0.5011 676	0.000 16668 1	ZNF11 4	0.1575 3081	0.004 44502 3	APBA3	0.3965 0455	0.043 59155 3
PRMT1	0.9581 623	1.51 633 E-07	CHTF8	0.6150 737	0.000 16695 5	WDR6 2	1.0556 812	0.004 44555 1	FAM20 3A	0.5538 819	0.043 61490 3
TGS1	0.5756 155	1.51 633 E-07	PDPK1	0.4215 629	0.000 16728 5	CDCA4	0.4820 5492	0.004 45628 3	EIF1B	0.4673 3603	0.043 63854 8
FAHD1	0.8044 431	1.53 76E- 07	GTF2H 2C	0.3848 3602	0.000 16728 5	KEAP1	0.5243 627	0.004 45771 3	ZNF56 3	0.0274 25673	0.043 67417 6
MESD C1	0.7578 235	1.54 946 E-07	ALDH7 A1	0.3973 2596	0.000 16788 7	IQGAP 2	1.2463 1	0.004 46769 4	GFER	0.2193 897	0.043 78749 7
FBLN2	2.2358 34	1.56 095 E-07	MAPK1	0.4781 951	0.000 16823 6	SUV39 H2	0.1425 6512	0.004 47457 8	ANO10	0.2411 228	0.043 97358 2

ZMIZ1	0.5344 6186	1.57 693 E-07	DOCK7	0.3680 5516	0.000 16843 9	ASNA1	0.5231 673	0.004 47757 2	ABHD1 4B	0.4144 4206	0.044 03930 8
NIT1	0.6708 806	1.62 508 E-07	TAF12	0.7462 031	0.000 16864 2	LINC00 381	0.3998 8354	0.004 47888 4	SEN2	0.2346 4502	0.044 07522
EXOS C1	1.1109 642	1.63 149 E-07	MPC1	0.7233 2454	0.000 16932 2	PRH1- PRR4	0.2901 9567	0.004 48032 1	GLB1L	0.1238 8354	0.044 09908 1
HSPA4	0.8538 3755	1.67 308 E-07	URB1	0.2559 934	0.000 17043 2	SLC30 A5	0.1736 6228	0.004 49335 3	TIE1	1.4633 955	0.044 11087 3
WRB	0.9869 677	1.70 882 E-07	SMAD2	0.2952 0267	0.000 17110 2	CLCN6	0.1786 2716	0.004 50720 4	SDK2	0.6379 617	0.044 11634 4
FDXR	1.3671 317	1.71 064 E-07	KANK2	0.4520 8323	0.000 17138 3	UBR5	0.2341 0738	0.004 50720 4	PANK2	0.3817 1706	0.044 11634 4
CLPX	0.8093 1	1.71 788 E-07	TOMM5	0.8244 7124	0.000 17267 2	PDCD2 L	1.0575 29	0.004 51939 9	ZMYM 1	0.2533 6137	0.044 13418 3
RPUS D3	1.0452 073	1.74 503 E-07	FAM213 B	0.7306 8154	0.000 17291 7	DNAJB 13	0.2369 3138	0.004 55003 5	STAG3	0.6669 0487	0.044 15779 1
FBXO7	1.0776 892	1.75 19E- 07	E2F4	0.8381 2726	0.000 17316 3	ANKR D13B	0.5601 3256	0.004 55070 2	FAM83 H	0.2324 0362	0.044 18774
SNW1	0.8526 5356	1.76 89E- 07	EMC8	0.7951 554	0.000 17325 9	RAB1A	0.6076 694	0.004 55216	SUDS3	0.2314 2548	0.044 26586 1
CHEK1	0.3440 831	1.79 567 E-07	SH3GL B1	0.3542 4855	0.000 17361 8	SNX12	0.3347 9452	0.004 55678 7	IBA57	0.1461 3044	0.044 26586 1
GDE1	0.8635 1955	1.79 567 E-07	LOC285 762	0.0416 00775	0.000 17424 2	RNAS EH1	0.4958 9226	0.004 57852 1	DNMT 3B	0.7357 532	0.044 28981 4
C6orf2 11	0.9632 474	1.80 273 E-07	MSTO2 P	0.6616 081	0.000 17433 8	RAD54 B	0.2234 2749	0.004 57919 2	PEF1	0.4562 8655	0.044 29559 3
RGS3	1.1105 803	1.81 346 E-07	BANF1	0.6796 482	0.000 17443 5	C19orf 40	0.1231 347	0.004 58782 9	SLC35 B3	0.3221 1104	0.044 44677 1
CYB56 1	0.7050 3914	1.82 843 E-07	EBAG9	0.6710 9483	0.000 17475 8	FAM50 B	1.2985 616	0.004 58837 7	GMDS	0.4097 5136	0.044 47604 7
PUSL1	1.5679 483	1.83 247 E-07	RANBP 3	0.4234 4528	0.000 17512	NEK7	0.2286 7812	0.004 58837 7	ZNF58 9	0.5040 068	0.044 50618 6
EYA3	0.6092 289	1.84 971 E-07	C14orf1 05	0.0394 64537	0.000 17536 9	EIF4G 2	0.5392 157	0.004 60077 6	TMEM 256	0.3806 6596	0.044 51199 2
CDK2	0.9983 403	1.85 486 E-07	MRPS2 7	0.5757 7574	0.000 17565 7	LOC49 3754	0.0423 27538	0.004 60077 6	QSER1	0.0798 1891	0.044 56014 4
UNC45 A	0.8757 2235	1.85 844 E-07	RPS6K C1	0.4852 2052	0.000 17602	EMILIN 1	2.1205 778	0.004 60077 6	CACF D1	0.4781 3085	0.044 61471 9
POLD1	1.1165 16	1.87 431 E-07	TCOF1	0.5375 431	0.000 17615 6	DAPK3	0.3984 6155	0.004 60624 9	POMZ P3	0.1983 4448	0.044 61998 4
DVL2	0.7320 9244	1.89 084 E-07	RFXAN K	0.5566 7585	0.000 17629 2	ZNF30 2	0.4131 2137	0.004 61160 4	PDPR	0.0974 8437	0.044 61998 4
HDDC 3	1.0980 347	1.91 407 E-07	RGS16	1.0844 514	0.000 17639	C11orf 48	0.4073 4288	0.004 61228 1	NAB2	0.3507 3456	0.044 74793 5
FECH	0.5555 896	1.91 776 E-07	RANGA P1	0.5338 885	0.000 17690 8	MTMR 10	0.5570 5374	0.004 61295 8	SALL4	1.0322 448	0.044 90686 2

TACC1	0.7102 9913	1.92 86E- 07	ATAD2 B	0.5220 6755	0.000 17718 1	SEMA5 A	0.1957 112	0.004 63358 1	GRPEL 2	0.1948 2063	0.044 96794 6
STX6	0.9775 5766	1.93 232 E-07	COL22 A1	0.9675 7174	0.000 17747 1	SLBP	0.5609 7996	0.004 63562 3	PTK2	0.2008 7871	0.044 97380 5
SLC25 A16	1.4776 918	1.93 3E- 07	KIAA18 41	0.1178 9367	0.000 17810 8	ICAM3	0.6181 613	0.004 63562 3	ZNF72 0	0.3009 7595	0.044 97966 5
UBE2T	1.2771 65	1.93 3E- 07	MAPK6	0.6049 561	0.000 17846	ABHD8	0.8787 502	0.004 63562 3	TMEM 216	0.5131 7215	0.044 99753 2
MFAP1	0.9394 4657	1.93 3E- 07	DCDC2	0.1721 3875	0.000 17846	NT5C2	0.1952 5942	0.004 64758 3	HERC2 P9	0.1635 6844	0.045 13818 2
PSMG 3	1.0200 125	1.93 451 E-07	GUF1	0.4055 8714	0.000 17968 2	PIGC	0.5184 2165	0.004 65391 6	FAF2	0.2763 2	0.045 18692 5
HAUS7	1.1901 174	1.95 827 E-07	CCDC4 1	0.6112 7174	0.000 18044 4	ABL1	0.3051 6782	0.004 66592	LACE1	0.6249 82	0.045 23571 5
PLEKH G3	0.9590 8034	1.96 148 E-07	C10orf1 1	0.9365 8537	0.000 18073 9	SRP54	0.4627 3205	0.004 67053	STRIP 1	0.2604 2306	0.045 30954 5
ZNF19 5	0.4627 7538	1.96 526 E-07	TERF1	0.3490 3967	0.000 18076 1	ARPP1 9	0.3875 8472	0.004 67445 8	CHRM 1	2.5194 576	0.045 35872 9
NSMC E2	0.9897 137	1.96 681 E-07	ATN1	0.2597 305	0.000 18094	CTU2	0.5507 304	0.004 67826 5	CAPN2	0.3308 462	0.045 40176 9
PCIF1	0.9398 6005	1.97 004 E-07	OLAH	0.1014 0943	0.000 18324 9	PREP	0.3376 1686	0.004 6822	LIN37	0.6183 3775	0.045 43217 4
STRN4	0.7873 804	1.97 271 E-07	DAXX	0.6454 1745	0.000 18366 8	GPAT CH1	0.7761 744	0.004 71466 2	WLS	0.2963 163	0.045 43217 4
WDR1 1	0.7797 8534	2.02 329 E-07	ETFA	0.8263 928	0.000 18452 5	HEY1	0.5441 609	0.004 73381 1	CRLF3	0.0477 8453	0.045 44428 5
SLC37 A1	1.7176 845	2.03 24E- 07	KLHL29	0.9121 96	0.000 18518 6	TPRN	1.3111 35	0.004 73614 7	PDIA6	0.6160 679	0.045 47499 5
FAM12 0B	0.8765 058	2.04 155 E-07	TMEM1 20A	0.6966 4335	0.000 18551 2	KREM EN1	0.2731 9634	0.004 76634 9	HIST1 H2BK	0.4379 867	0.045 51729 9
FANC G	1.2666 574	2.07 957 E-07	HNRNP H2	0.5544 272	0.000 18551 2	MTHF D2	0.5118 458	0.004 76762 3	ALKBH 1	0.4601 8794	0.045 64125 3
BUB3	0.9590 09	2.14 666 E-07	RAB7A	0.5703 3795	0.000 18611 8	ATXN2	0.3426 3712	0.004 77799	NR1H2	0.3233 3064	0.045 68424 8
EIF3M	1.0774 609	2.16 677 E-07	SASH1	0.3166 7924	0.000 18686 6	DNAJC 16	0.1436 3043	0.004 77799	ACAT2	0.4106 2346	0.045 88948 6
FOCA D	0.7436 694	2.18 457 E-07	TRIP4	0.7029 791	0.000 18826 5	RPS6K B1	0.2455 2684	0.004 78067 4	JMJD7	0.2535 9035	0.045 93921 6
MAPK APK3	1.0361 823	2.20 314 E-07	ABCF2	0.5597 4054	0.000 18847 3	FLCN	0.2546 102	0.004 78067 4	STAM	0.2235 488	0.045 97021 7
SPR	1.0713 985	2.22 108 E-07	TFDP1	0.7640 038	0.000 18847 3	KDM1 B	0.4077 111	0.004 78067 4	ZSCAN 29	0.0683 82904	0.046 15144 7
C16orf 62	0.8093 996	2.27 782 E-07	RNF185	0.6254 109	0.000 18910 7	HIF3A	0.0572 9493	0.004 78386 1	LHPP	0.6534 2057	0.046 26374 9
CARK D	0.9435 522	2.28 155 E-07	LOC100 505776	0.0010 39125	0.000 18917 1	CARS2	0.6420 6004	0.004 78444 1	BBS9	0.0687 4971	0.046 26374 9

SNRP D2	1.0655 247	2.29 7E- 07		MED12	0.3307 838	0.000 18948		ETHE1	0.6121 573	0.004 79413 9		LPAR2	1.0634 844	0.046 38316 3
STARD 7	0.8163 7555	2.33 565 E-07		MAEA	0.6981 4605	0.000 19065		EMR2	0.1527 7433	0.004 80897 1		HIST2 H2BC	0.6061 8323	0.046 42073 3
WDR3 6	0.5331 012	2.49 047 E-07		STIL	0.3802 8768	0.000 19100 3		KPTN	0.8650 3375	0.004 82789 4		LPHN1	0.1798 7318	0.046 47039 5
PIPSL	0.5767 743	2.49 047 E-07		SETD8	0.3556 6422	0.000 19168 6		CSRN P2	0.6301 0705	0.004 82789 4		SYT14	0.6663 368	0.046 69772 5
TRPM6	0.4409 6452	2.50 303 E-07		POLE3	0.6603 965	0.000 19233		MSRB 1	0.7559 847	0.004 85346 9		RAD9A	0.3088 3858	0.046 80510 8
PRKC E	0.7231 7797	2.52 924 E-07		C15orf5 2	0.2107 9955	0.000 19473 6		NDUF A11	0.6315 875	0.004 85645		RNAS EL	0.3219 4975	0.046 86813 9
C7orf4 1	1.1234 889	2.54 848 E-07		RFC3	0.7384 615	0.000 19526 3		UQCR 10	0.5204 1084	0.004 85645		TMEM 63A	0.1950 9861	0.046 86813 9
PIK3C 2B	0.3095 5353	2.55 626 E-07		PARP1 0	0.6588 2	0.000 19600 3		PSMD 7	0.6081 638	0.004 86893 4		C20orf 26	2.1979 556	0.046 87364 6
NECA P2	0.8317 8204	2.57 133 E-07		ZNF461	0.4663 547	0.000 19759 4		RPRD1 A	0.2903 9314	0.004 88482 2		PIK3C B	0.0539 7103	0.046 87364 6
EXOS C5	1.0989 69	2.57 773 E-07		AP3D1	0.3196 2568	0.000 19825 7		GBA	0.5483 1195	0.004 88638 5		NHP2	0.6384 6403	0.046 89854 2
SIGIR R	0.8182 718	2.58 121 E-07		SMIM12	0.3659 968	0.000 19836 7		CYB5D 1	0.5019 758	0.004 90207 3		RHPN1 -AS1	0.2261 5881	0.046 93010 4
ADAM TS2	2.2034 132	2.58 616 E-07		NME2	0.5312 7694	0.000 19901 4		LOC64 2361	0.3266 7434	0.004 90207 3		DHRS1 2	0.5912 2366	0.046 94256 5
ANKR D46	1.3122 363	2.62 284 E-07		ADAT2	0.4686 8154	0.000 19925 2		PLXNA 2	0.8154 689	0.004 91963 4		ZNF28	0.2302 8684	0.047 01129 6
ARHG AP11A	0.5971 787	2.62 638 E-07		DCAF4	0.9875 767	0.000 19974 9		CMSS 1	0.4589 8828	0.004 91963 4		NUDC D2	0.3887 6823	0.047 03015 9
NDUF A10	0.6721 6396	2.64 335 E-07		SEC22 C	0.5520 702	0.000 19984		SPDYE 7P	0.3223 1227	0.004 93397		LOC10 013235 6	0.2563 6488	0.047 10651 9
MEIS1	0.8036 643	2.67 25E- 07		CDC73	0.5086 7164	0.000 19984		ARAF	0.4175 0124	0.004 95603 7		MSRB 2	0.3156 727	0.047 15071 5
HEATR 5B	0.5610 6246	2.67 989 E-07		CEP57	0.5212 9006	0.000 20001 8		ASPSC R1	0.4684 4643	0.004 96177 4		MYH13	0.6725 9824	0.047 15071 5
IMP3	1.0378 861	2.75 886 E-07		EPHA5	2.1200 3	0.000 20001 8		LDHAL 6A	0.3363 9362	0.004 96177 4		NUP98	0.1486 624	0.047 17519 3
MGAT 1	0.9340 0955	2.85 821 E-07		LOC389 906	1.3842 962	0.000 20105 9		WWP1	0.1600 134	0.004 99760 2		KLHL3 5	1.5804 954	0.047 17519 3
MRPS 35	0.9588 4794	2.85 821 E-07		FLG2	0.0176 926	0.000 20134 3		FAM21 6A	0.5618 618	0.004 99919 8		SLC40 A1	1.3728 577	0.047 17519 3
RBM42	0.7942 882	2.85 964 E-07		FABP7	1.4760 73	0.000 20158 5		CCDC 94	0.6292 1405	0.005 00252		LOXL1 -AS1	0.3590 313	0.047 17519 3
FAM17 5A	1.0746 298	2.87 808 E-07		VPS4A	0.6320 3055	0.000 20239 1		COMM D1	0.5186 112	0.005 01102 6		SPATA 2L	0.7682 2996	0.047 22585 3
NIT2	0.9704 5183	2.90 481 E-07		NREP	1.0289 08	0.000 20324 4		PPP6R 2	0.2150 4517	0.005 01781 5		SLC25 A20	0.5182 6656	0.047 28966 1

GON4L	0.5510 276	2.93 178 E-07	COMM D4	0.8139 307	0.000 20344 3	DCP2	0.0903 62094	0.005 01855 2	SHAN K3	0.9045 629	0.047 37922 7
ESF1	0.5030 365	2.95 567 E-07	KATNB L1	0.5037 821	0.000 20355 6	PDCD2	0.5260 2524	0.005 02015 5	CYP2U 1	0.6442 188	0.047 39179 7
BYSL	1.0048 703	3.02 967 E-07	SORBS 1	0.4091 862	0.000 2038	YKT6	0.3067 4595	0.005 03437 6	FAM19 3A	0.0939 6501	0.047 43007 8
SEC23 B	0.8634 742	3.07 503 E-07	LETM1	0.4013 392	0.000 20386 8	ZNF44 5	0.1736 2761	0.005 03437 6	ERCC6 L2	0.2297 5835	0.047 72576
C22orf 28	1.0761 061	3.09 22E- 07	IGSF11	0.5013 02	0.000 20446 4	ABL2	0.2935 69	0.005 03598 4	URGC P	0.2491 0337	0.047 78368 2
AASD HPPT	0.7778 7936	3.09 986 E-07	RNF216 P1	0.5987 507	0.000 20448 9	TAF7	0.5316 3797	0.005 04976 1	PSIP1	0.0401 34102	0.047 82223 7
MFN2	0.6229 2784	3.11 347 E-07	TOX4	0.4023 3713	0.000 20519 9	FAH	0.3752 858	0.005 08529 6	ZRANB 3	0.5270 805	0.047 88646
AK2	0.8598 1655	3.11 347 E-07	FADS2	0.8135 3366	0.000 20560 2	PTAR1	0.1419 0015	0.005 10170 2	ATXN7 L3B	0.3667 1305	0.047 96402 2
OCA2	1.7129 14	3.11 592 E-07	GPAM	0.8274 373	0.000 20627 2	CCDC 34	0.5239 037	0.005 10170 2	ZFP1	0.6573 801	0.047 98321 8
AKAP2	0.6919 973	3.14 125 E-07	LGALS L	1.1748 765	0.000 20638 6	RASA4	0.0544 7199	0.005 11036 3	RBBP8	0.1678 4632	0.048 00891 8
POLR2 A	0.6715 966	3.15 08E- 07	BTBD3	0.4921 3493	0.000 20679 2	EXOS C6	0.1639 4824	0.005 13227	UBXN1	0.5902 076	0.048 01513 4
NCOR 1	0.5823 783	3.17 285 E-07	ELL	0.7824 993	0.000 20679 2	CENP O	0.8107 3225	0.005 14628 9	HYAL1	1.5036 244	0.048 11890 7
GAR1	0.8225 47	3.18 518 E-07	TMEM1 9	0.2529 1106	0.000 20838 3	USP10	0.4220 182	0.005 15058 7	SH3YL 1	0.3348 8348	0.048 13815 8
STK38 L	1.2351 058	3.20 565 E-07	YOD1	0.8393 199	0.000 20838 3	PICAL M	0.2796 078	0.005 15577 6	ANKH D1- EIF4E BP3	0.2526 2868	0.048 15062
PIP5K1 A	0.7497 818	3.22 589 E-07	TNFRS F19	0.5121 931	0.000 20838 3	C1orf1 12	0.7340 562	0.005 15729	HECT D1	0.1004 4944	0.048 22827 1
MEMO 1	1.0022 343	3.26 583 E-07	DYX1C 1	0.1086 79764	0.000 20899 1	NUDT1 6L1	0.5629 213	0.005 15729	GAS2	1.8661 059	0.048 26685 7
MRPS 28	0.9479 0375	3.32 301 E-07	METTL 17	0.6830 7924	0.000 20901 7	TM9SF 3	0.0018 97405	0.005 16159 7	RAB1B	0.3638 2943	0.048 30519 3
MED20	0.9564 214	3.34 604 E-07	IP6K3	2.0534 387	0.000 20931 2	INE1	0.1651 3184	0.005 17302	EXO1	0.6485 916	0.048 38250 7
LSAMP	0.6877 1535	3.46 294 E-07	CCDC1 63P	0.1623 7497	0.000 21136 8	EHD4	0.4122 147	0.005 20500 6	FAM13 3DP	0.1669 097	0.048 41466 3
ENC1	1.2715 873	3.52 544 E-07	HNRNP H1	0.5250 2203	0.000 21157 5	BRAP	0.5092 528	0.005 20563 8	TACO1	0.4607 6265	0.048 42093 2
RTTN	0.9311 456	3.53 712 E-07	RNASE H2A	0.8783 855	0.000 21164 7	CHUK	1.2165 911	0.005 21625 4	EXOC5	0.2278 968	0.048 46648 3
IFT88	0.8030 3365	3.55 381 E-07	AP5S1	0.4328 9477	0.000 2119	ONEC UT1	1.7981 732	0.005 22778 8	BCL7C	0.7675 306	0.048 51862 5

NDUF AF4	0.7149 457	3.55 86E- 07		TMX1	0.4816 4004	0.000 21281 7		ISCA1	0.4069 9977	0.005 23574 6		RAP2A	0.1777 9824	0.048 52490 6
DCTN1	0.8005 065	3.62 378 E-07		HMG3	0.8082 1013	0.000 21281 7		SRP68	0.4917 6645	0.005 25801 4		TPGS2	0.3404 038	0.048 64933 2
MRPS 34	1.1055 993	3.63 273 E-07		TMEM2 46	1.6069 937	0.000 21311 7		AHCTF 1	0.2304 8635	0.005 25942 5		DGKZ	0.0487 50903	0.048 68191 8
MCMC P	0.6159 064	3.73 458 E-07		ANAPC 15	0.7780 796	0.000 21383		BACE1	0.4195 9965	0.005 25942 5		DES1	0.1656 3545	0.048 72768 1
TIMEL ESS	0.9077 1025	3.76 796 E-07		ZNF16	1.1834 406	0.000 21445 3		SLC35 G1	1.1112 564	0.005 25942 5		NET1	0.3632 1193	0.048 78006 7
DLG5	0.9717 419	3.77 514 E-07		ALG9	0.5974 7624	0.000 21637		LYAR	0.3473 639	0.005 26561 9		ZNF81 4	0.0791 31715	0.048 81931 9
CCDC 137	0.8231 539	3.80 354 E-07		RECK	0.7096 567	0.000 21721 3		EXOC8	0.4068 1228	0.005 28813 6		DFFA	0.2335 2411	0.048 83881 8
SYNG R1	1.0124 968	3.83 926 E-07		ZNF124	0.4206 097	0.000 21721 3		LAGE3	0.2721 5835	0.005 29708 7		TRAM1 L1	1.9536 455	0.048 85777 5
RPL36 A- HNRN PH2	0.9358 851	3.83 926 E-07		RPUSD 2	0.9104 0635	0.000 21821 9		GTPBP 10	0.0389 8525	0.005 30059 3		LPCAT 4	0.3059 2433	0.048 85777 5
SLC4A 1AP	0.7537 0055	3.94 631 E-07		AAMP	0.8649 2	0.000 21852 6		PTCSC 3	0.1019 67596	0.005 30228		POMC	0.5631 3604	0.048 91028 1
MCM5	1.1096 343	3.95 935 E-07		NAA25	0.5668 3916	0.000 21923 6		SAP30 BP	0.4392 833	0.005 30305 8		ZNF67 5	0.2698 7472	0.049 02894 3
NUDT1 5	0.5538 017	3.97 576 E-07		DGUOK	0.7601 4096	0.000 21923 6		SLC25 A23	0.6619 0034	0.005 30747 8		COMM D3- BMI1	0.2086 3147	0.049 03528 3
MRPL1 6	0.9379 7904	3.99 316 E-07		OR11A 1	0.1870 1327	0.000 22025		PUM1	0.2987 2945	0.005 31646		SPDL1	0.5006 5106	0.049 04824 1
DDX28	1.3531 691	3.99 316 E-07		DENR	0.4784 627	0.000 22079 7		CASP3	0.3741 5412	0.005 35922 3		HUWE 1	0.2195 7485	0.049 24626 4
B3GAL NT2	0.4445 938	4.00 077 E-07		MSH2	0.5691 742	0.000 22082 4		BRIX1	0.5945 9627	0.005 37920 5		NECA P1	0.3034 2862	0.049 28584 1
RTFDC 1	1.0634 643	4.01 399 E-07		FAIM3	1.0251 266	0.000 22213		UPRT	0.8996 7823	0.005 38183 8		SH3KB P1	0.2767 119	0.049 37173 2
NPAT	0.7280 0404	4.05 884 E-07		PRKRA	0.6472 222	0.000 22220 5		RPL27	0.3199 1538	0.005 39080 3		ENPP2	0.4186 3713	0.049 38476 7
TBCB	0.9802 087	4.07 679 E-07		CCNK	0.4925 9418	0.000 22534 1		A1BG- AS1	0.7839 14	0.005 41446 9		SLC25 A39	0.5347 427	0.049 39780 5
FGF13	1.7801 492	4.11 658 E-07		DYNC1 LI1	0.5371 398	0.000 22735 1		FAM49 B	0.4285 7572	0.005 42547 5		EIF4H	0.6665 1946	0.049 58396 5
LONP1	0.6781 4773	4.11 867 E-07		CEMP1	0.6179 257	0.000 22760 2		TRIM5 9	0.1991 1133	0.005 45781 8		PCK2	0.4259 4895	0.049 65720 6
RNLS	2.7679 21	4.12 652 E-07		SLC25A 51	0.4033 2952	0.000 22763		PSMD 1	0.5328 4127	0.005 46516 3		POMP	0.5144 432	0.049 70348 4
CDC12 3	1.0330 906	4.27 974 E-07		SGOL1	0.2993 3882	0.000 22843 7		DCUN 1D4	0.2795 64	0.005 46596 3		DTNBP 1	0.4363 9317	0.049 78357 9

ZC3H3	0.8160 2126	4.32 867 E-07		TCIRG1	0.6187 273	0.000 22851 4		DNAJC 2	0.3840 5234	0.005 48255 8		MED14	0.1523 7562	0.049 80956 4
ZFAND 1	0.8346 597	4.33 69E- 07		PNMA1	0.7376 7203	0.000 22986 3		MSI1	0.6722 083	0.005 48429 9		SLC52 A2	0.3807 664	0.049 80956 4
ANAP C7	0.8394 057	4.34 757 E-07		DTL	1.2278 926	0.000 23021 5		TSEN2	0.2115 6617	0.005 49261 6		UBE2F -SCLY	1.2507 169	0.049 81599 4
NBPF3	0.3809 9548	4.37 629 E-07		SCLY	0.7982 044	0.000 23021 5		BRIP1	0.0376 65073	0.005 50753 6		RPTO R	0.2518 6542	0.049 94971 5
CHKA	0.8413 042	4.37 974 E-07		ZNF548	0.4587 91	0.000 23058 8		LYSM D2	1.2409 658	0.005 51305 5		UPF1	0.1563 1709	0.049 96933 1
LINS	0.8723 08	4.39 663 E-07		RBP1	0.6401 607	0.000 23066 6		NUDT2 2	0.5284 902	0.005 51480 6		PRKX	0.1449 6046	0.049 96933 1
RPL15	0.3482 3257	4.43 554 E-07		WDR83	0.9125 4395	0.000 23089 2		SNN	0.7569 4	0.005 51750 1		MYL6	0.0556 6979	0.045 68424 8
WDR4	0.8532 374	4.48 246 E-07		NRG3	1.3236 904	0.000 23185 8		ATG10	0.1347 9058	0.005 52019 8		TMEM 59	0.0188 37657	0.005 83637 3
UGCG	0.9257 56	4.50 85E- 07		SLC31A 1	0.4653 6243	0.000 23367 4		NAV1	0.1627 2695	0.005 53329 4		MTRN R2L2	0.2547 141	0.005 42627 1
PBRM 1	0.5124 916	4.51 332 E-07		C19orf2 4	0.7427 914	0.000 23440 1		RFPL3 S	2.8062 913	0.005 53978 4		MTRN R2L8	0.1395 1954	0.000 20030 1
PIGM	0.7690 971	4.52 19E- 07		PAPOL G	0.2262 3034	0.000 23448 1		NUP21 4	0.2515 6242	0.005 55482 1		MTRN R2L10	0.0148 22896	0.000 18318 7
NPM1	0.4830 6182	4.55 197 E-07		TPT1- AS1	0.2999 5823	0.000 23486		WBSC R22	0.6745 7914	0.005 55753 5		MTRN R2L1	0.0082 6583	3.128 49E- 05
SOCS2	1.3506 18	4.55 683 E-07		ZNF839	0.0088 01705	0.000 23718 2		SREBF 2	0.2049 5689	0.005 57261 6				
ATP5L	0.7998 482	4.60 371 E-07		PAFAH 1B1	0.4436 3567	0.000 23756 5		DIDO1	0.3273 0576	0.005 58950 7				

Example 2

Acral melanoma (AM) is a deadly adult skin cancer that is the predominant cutaneous melanoma (CM) subtype in populations of African descent with the lowest disease specific survival rates in minority ethnic and racial populations (Hispanic, Asian, and African descent). The disease specific death rate from AM is more than twice as high than that of CM in general. When adjusted for stage, AM still has worse outcomes when compared to other forms of CM that predominately affect the white population. This has been postulated to be due to sociodemographic factors or delays in time to definitive treatment following initial diagnosis, though poorer response to adjuvant therapy would also suggest a biologic etiology for this discrepancy.

Recent research has discovered that AMs arise from a cell of origin distinct from other CMs. This observation suggests that the historic practice of either omitting AM or grouping AM

with other CMs for the purpose of biomarker and therapeutic development, as opposed to investigating AM as a distinct and unrelated cancer, is one cause of the response and survival disparities experienced by AM patients.

Immune checkpoint inhibitor (ICI) therapies have garnered unprecedented response rates in patients with advanced stage CM. However, while efficacious in most subtypes of melanoma, single agent ICIs demonstrate lower objective response rates (16–40%) and are less likely to achieve complete responses in AM patients. There are ongoing efforts to improve the therapeutic landscape for patients with advanced AM, with several eminent therapies on the horizon. However, the undeniable effectiveness of ICIs at the population level has made ICI therapy the standard of care for all CM, even when less efficacious for AM, specifically. Additionally, 40% of non-responding patients experience treatment-related adverse side effects despite experiencing no benefit from the treatment. Identifying AM patients who are more likely to respond to ICI would provide critical information for clinicians and permit precision implementation of the next generation front-line therapies awaiting FDA approval.

It is hypothesized that transcriptomic deconvolution will permit *a priori* stratification of AM by likelihood of ICI response. The feasibility studies support this hypothesis. The objectives are (i) to validate a CLIA compatible biomarker for predicting ICI response; and (iii) to test the biomarker on an independent validation set.

An additional objective is to stratify acral melanoma (AM) patients by likelihood of response to immune checkpoint inhibitors (ICI). First, a biomarker assay is developed and analytically validated using NanoString – a cost-effective approach that is amenable to clinical specimens, simple interpretation, and CLIA certification. Second, the biomarker assay will undergo additional clinical validation using an independent dataset.

Deconvolution-based Classifier that Stratifies AM by ICI Response

Using single cell RNA (scRNA) sequencing, over 9,000 cells were analyzed from 32 healthy skin specimens representing a diverse ethnic and racial cohort and discovered two distinct types of melanocytes (v-mels and c-mels), either of which can give rise to AM. A classifier was trained to deconvolute bulk transcriptomic data which successfully stratified AMs as v-mel derived (vAM) or c-mel derived (cAM) in three independent cohorts (FIG. 9). Utilizing scRNA-seq data of developing melanocytes and metastasized melanomas a classifier was similarly trained to deconvolute cutaneous melanoma (CM) bulk transcriptomic data and identify those tumors predominantly composed of dedifferentiated cells resistant to ICI (ICI-R). For non-AM CM, this classifier stratified tumors based upon ICI response (FIG. 10). Importantly, for AM, a two-step

deconvolution was required – first stratifying by cell of origin and then identifying predominant dedifferentiation state (FIG. 11). This approach resulted in perfect classification of the largest and only publicly available cohort of matched AM transcriptomes with ICI (anti-PD1) response. That this cohort comprises only ten patients is indicative of the degree to which the AM patient population is under-represented and under-studied. Seeking to adapt the classifier to NanoString technology, the classifier was refined to 200 highly expressed genes that comprise minimal signatures for identifying the cAM, vAM, and ICI-R states (Table 5). These signatures provide sufficient information for deconvolution and high accuracy classification. Conceptionally, the cAM and vAM signatures permit identification of cell of origin and the ICI-R signature then allows estimation of the percentage of cells that are resistant to ICI. This established analytic pipeline that converts the expression of 200 genes to a single value as the transcriptomic deconvolution-based predictor of ICI-R (TD-IR). This estimate, converted to a single positive or negative “TD-IR score” (FIG. 11), is the ultimate and only readout of the approach.

Table 5. TD-IR NanoString Custom Panel

SERPINF1	GPM6B	RPS17L	GAS5	CREBBP	MACF1	ZNF263	PEX10
PABPC1	FOXRED2	RPS17	RPL13AP5	MYCBP2	VPS13C	GGCT	NR2F6
DCT	SOAT1	MARCKS	SNAI2	HIVEP2	SYNE1	ZFAT	EXTL2
TIMM50	RPS16	RPS4X	FAM174B	NTRK2	NOTCH2	ARMC1	ZMYND19
CA14	PKNOX2	ESRP1	RASSF3	SNX29	DYSF	DUS4L	CDK12
SCD	RPL18	NF2	PTP4A3	VPS13D	NBEAL1	ZNHIT1	ZNF146
RPS19	EIF4A1	CNRIP1	RPS7	KMT2C	POLR3A	MRPL32	SRR
RPL29	RPS27	OXA1L	EIF2S3	WNK1	NBAS	SLC25A36	FNTA
BCAN	NOP56	NPL	ABR	KDM5A	RANBP2	SRM	COMMD5
TRPM1	CHP1	CD68	PPA1	HUWE1	KAT6B	TSNAX	ZNF24
KIF17	TNFRSF14	SAE1	CS	MYH9	TRAPPC10	CBX3	MOB1B
RPS24	UQCRRF51	MID1	EGFL8	EP300	REL	PLA2G12A	TOMM20
RPL28	KLHDC8B	ZNF749	GPI	CEP128	ATXN7	SRSF6	ARL10
ADRBK2	RPS9	PPP2R1A	RPL8	TRIP11	ANKRD11	MAD2L1BP	SHARPIN
KCNAB2	SCIN	RPS8	C1QBP	CHD8	STAT3	MED1	TIGD5
PFN1	RPL4	GSTO1	TUBB4A	HERC1	JMJD1C	NRSN2	C8orf33
TMC6	ASAP1	SAMM50	PLTP	SETX	FLNA	LSM7	COA5
NENF	RAB38	EIF3K	SS18L1	EGFR	DYNC1H1	TMEM128	TSPYL4
ACP5	AHCY	SNHG6	SORD	ASCC3	SPTAN1	TBRG4	ZNF517
RPLP0	CCT3	FAM178B	ILF2	BIRC6	ITSN2	TSTD2	ZNF121
RPS6	TP53	RPL6	EIF3L	ALMS1	ZNF407	MRPL15	SPIN3
EIF4EBP2	IDH2	MAD1L1	MLANA	ASH1L	PLEKHM1	SAT2	TRIM27
RPL13A	SLC25A5	IMPDH2	RPS11	BAZ2B	ERCC6	BOD1	TRIM13
PRAME	RPS5	BZW2	ADSL	NCOA3	PARG	PURB	TMEM231
MOB3B	GLOD4	GALE	PRDX3	MRPS21	NDUFA7	NDUFA3	CYC1

NanoString Platform

Assays performed on formalin fixed paraffin embedded (FFPE) tissue and that utilize a small number of sections are the most easily adopted clinical tests with regards to tissue

requirements. NanoString provides a hybridization-based technology that permits targeted transcript counting, without amplification, on the poor-quality RNA extracted from FFPE blocks. A custom NanoString nCounter RNA expression panel of 200 highly-expressed transcripts was designed. The expression values inform the TD-IR classifier, resulting in a single score
5 representing the presence of ICI-R resistant cells (henceforth referred to as the biomarker). Samples consist of 3–5 macrodissected 4 μ m formalin-fixed paraffin-embedded (FFPE) sections per specimen. The NanoString pipeline, inclusive of sectioning, macrodissection, RNA extraction, and transcript counting, has produced highly reproducible gene expression patterns. See e.g., Leal et al., *Neuropathology* 38(5):475-483 (2018); Veldman-Jones et al., *Cancer Res.* 75(13):
10 2587–2593 (2015), each of which are incorporated by reference for the teachings thereof.

RNAScope Platform

The TD-IR classifier is a bioinformatic method intended to deconvolute the noise introduced into bulk transcriptomic data by diverse cells of origin and tumor heterogeneity –
15 ultimately successful, because it accurately infers the percentage of ICI-R cells. As both a complementary method of validation for the approach and to directly confirm this mechanism, a single molecule RNA in-situ hybridization assay called RNAScope is used. Since RNAScope retains spatial and single cell resolution, thereby substantially reducing non-specific transcriptomic noise from other cell-types/states within the tumor, only 18 gene probes are
20 expected to be needed to determine the fraction of ICI-R cells. Previous work shows the combination of probes for a molecular signature into a single uni-colored “cocktail” permits a simplified and robust method for cell-type/state detection using total fluorescence intensity (FIG. 12A). Probes are pooled to generate a four-cocktail stain (FIG. 12B) for a 4 μ m FFPE section compatible with the Leica BOND Fully Automated ISH Staining System. The percent of ICI-R
25 cells are quantified relative to the total number of melanoma cells.

Statistical Methods

There are separate biomarker development and validation data sets. Once established, the biomarker is analyzed using the validation data set to avoid overfitting and bias that can result
30 from using the same data to both develop and validate the assay.

Receiver operator characteristic (ROC) curves and bootstrap confidence intervals are calculated on the development and validation sets using the *R* package *pROC*. An optimal binary classifier (Yes/No response to ICI) is constructed using the cases in the development set and evaluated on the validation set. For this application of TD-IR, the goal is to confidently identify

those AM patients who will not benefit from ICI, but it is also critical not to erroneously identify ICI responsive patients as ICI-R. Thus, the threshold is tuned to minimize the false negative rate and tolerate a modest number of false positive estimates by the model. For this reason, false negatives are weighted twice as heavily as false positive in construction of the optimal binary classifier.

Sample Size Justification

A variety of ICI-R predictive biomarkers based upon molecular profiling are currently in development, including measuring PD-L1 expression, mismatch repair deficiency, tumor mutation burden, tumor infiltrating lymphocyte load, and gene expression signatures. The best reported test characteristics achieve an area under the ROC curve (AUC) of 0.68–0.78 but are discouraged for use in clinical decision making by 2021 NCCN guidelines. Based upon these observations and modeling of clinical utility of melanoma biomarkers, the AUC must be at least 0.85 for the biomarker to be clinically useful. The achievable sample size for assay development is $N1 = 50$ and the sample size for assay validation is $N2 = 200$. The biomarker are adequately validated if the estimated AUC is 0.85 or higher, and the lower bound of a 95% one-sided confidence interval for the AUC is at least 0.80. The feasibility data (FIG. 11) completely separates cases from controls (AUC = 100%) so the true AUC of the biomarker is expected to be 90% or larger. Approximately 30% of AM patients respond to ICI (based upon reported 16–40% and observed rate in feasibility cohort) to estimate proportion in the sample size justification. To evaluate the performance with $N2 = 200$ samples in the validation set is simulated normally distributed data with various values of AUC. Table 6 presents the probability of adequately validating the biomarker for various values of the AUC. There is greater than 80% probability of validation (power) if the true AUC = 0.88. There is 5.0% probability of validation (Type I error) if the true AUC = 0.80.

Table 6. Validation Probability for Various AUC Values

True AUC	Probability the Biomarker is Validated*
75%	0.1%
80%	5.5%
85%	47.1%
86%	66.7%
87%	76.0%
88%	87.9%
89%	94.1%
90%	96.3%

95%

>99%

*The biomarker is considered adequately validated if the estimated AUC is at least 85% and the lower bound of a one-sided 95% confidence interval is at least 80%.

Conversion and Analytical Validation of NanoString Assay

An assay development cohort (N1) for 50 AM specimens, inclusive of ~30% ICI responsive patients, with sufficient archived material to obtain 3–5 4µm FFPE sections is assembled. RNA is extracted from macrodissected sections and subjected to NanoString assessment of the 200 gene panel to inform the TD-IR classifier. The ultimate read-out of the classifier (the biomarker) is a single score that infers percent of ICI-R tumor cells. AUC is calculated and a threshold value for the TD-IR score is determined.

The assay characteristics of the NanoString panel are determined using engineered cell lines with known gene expression levels. To determine the specificity of each probe, lines that are uniformly either cAM or vAM and either ICI-R or not are used. The top 15 genes shared in these signatures (cAM, vAM, ICI-R) are overexpressed in a non-expressing line (lentivirus) or knocked out in an expressing line (CRISPR) using established methods. Each pair of lines are fixed in formalin, embedded in paraffin (FFPE) and assessed via NanoString and RNAScope. If individual discrepancies with probe specificity are observed, new probes can be designed.

To determine the sensitivity of NanoString probes, limited dilution series of uniform cAM, vAM or ICI-R cells are mixed with non-cAM/vAM/ICI-R melanocytes and FFPE processed (FIG. 13). TD-IR is assessed in quadruplicate on different days, providing the full range of relative expression of each signature.

To assess precision (reproducibility), technical variability is assessed. The same sample is run 3 times in the same assay (intra-assay variability). In addition, the sample is analyzed on three different days with three different operators (inter-assay variability). Precision is considered sufficient if the coefficient of variance is <11% for all sources of technical variability.

To assess limit of detection, FFPE-derived RNA from benign tissue types where melanoma frequently spreads (lymph nodes, liver, brain, lung, bone, intestine, kidney, adrenal gland, healthy skin, muscle, and fat) are generated. TD-IR is measured for each pure sample and an equal-molar mix of each is used to create a limited dilution series of pure ICI-R cell RNA. The lowest dilution that provides TD-IR signal greater than 2 standard deviations from the full negative cohort is considered the LOD, will define a positive classification and will inform the minimal amount (percent) of tumor cells to detect true signal over the background noise from non-tumor tissue. Total RNA from the lowest detectable dilution will then undergo a second limiting dilution series in water to determine the minimal amount of total RNA required for the assay.

As a complementary validation, 20 specimens of N1 spanning both cAM and vAM and representing the full working range of TD-IR (as assessed above) will undergo RNAScope analysis to directly assess the concordance between bioinformatically inferred ICI-R content (TD-IR) and actual ICI-R content.

5

Clinical Validation of TD-IR Assay

In parallel, the larger N2 (200 specimens) cohort are assembled. The cohort is used for a retrospective study to determine if TD-IR reliably stratifies AM tumors into distinct responder vs non-responder groups in an independent cohort. The performance characteristics of the assay will define the potential utility for prospective clinical trials. Even if TD-IR does not perform sufficiently for trial incorporation, the assembled cohorts containing outcome, transcript data, and banked RNA are essential tools for investigating other candidate biomarkers aimed at addressing the disparities associated with the underrepresented and understudied AM population.

15

CLAIMS

What is claimed:

1. A method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising:
 - (a) obtaining a melanoma tumor sample from a subject;
 - (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data;
 - (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor sample into a specific melanoma cell subtype; and
 - (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature;wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment.
2. The method of claim 1, wherein the melanoma is acral melanoma (AM).
3. The method of claim 1, further comprising:

when the calculated total melanoma tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or

when the calculated total melanoma tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject.
4. The method of claim 1, further comprising:

calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;

wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or

wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.

5. The method of claim 3, wherein the ICI treatment comprises:
 - a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;
 - a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;
 - a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.
6. The method of claim 3, wherein the alternative non-ICI therapy comprises:
 - a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;
 - a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;
 - a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;
 - a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
 - a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
 - a CTLA-4 inhibitor selected from ipilimumab;
 - aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;
 - a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;
 - surgical excision; or combinations thereof.
7. The method of claim 1, wherein the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.
8. The method of claim 1, wherein the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4,

MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18.

9. The method of claim 8, wherein when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDCC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma.
10. The method of claim 8, wherein when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.
11. The method of claim 1, wherein the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRRF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

12. A method of stratifying and evaluating melanoma treatment response in a subject using single cell RNA sequencing (scRNA-seq) and a two-step deconvolution analysis, the method comprising:
- (a) obtaining a melanoma tumor sample from a subject;
 - (b) performing scRNA-seq of the melanoma tumor sample and obtaining scRNA-seq sequence data;
 - (c) on a processor, deconvoluting the scRNA-seq sequence data using a first gene signature to stratify the melanoma tumor into a specific melanoma cell subtype;
 - (d) deconvoluting the scRNA-seq sequence data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature; and
 - (e) calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;
- wherein when the calculated estimate of total melanoma tumor expression of the second gene signature reaches a critical threshold value, the melanoma tumor will not respond to immune checkpoint inhibition (ICI) treatment;
- when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or
- when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.
13. The method of claim 12, wherein the melanoma is acral melanoma (AM).
14. The method of claim 12, further comprising:
- when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or
- when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject.
15. The method of claim 14, wherein the ICI treatment comprises:
- a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;

- a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;
- a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.
16. The method of claim 14, wherein the alternative non-ICI therapy comprises:
- a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;
- a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;
- a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;
- a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
- a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
- a CTLA-4 inhibitor selected from ipilimumab;
- aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;
- a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;
- surgical excision; or
- combinations thereof.
17. The method of claim 12, wherein the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.
18. A method of stratifying and evaluating melanoma treatment response in a subject using RNA hybridization, and a two-step deconvolution analysis, the method comprising:
- obtaining a melanoma tumor sample from the subject;
 - performing RNA hybridization of the melanoma tumor sample using a targeted RNA probe panel to obtain targeted transcript expression data;
 - on a processor, deconvoluting the targeted transcript expression data using a first gene signature from the targeted RNA probe panel to stratify the melanoma into a specific melanoma cell subtype; and

- (d) deconvoluting the targeted transcript expression data using a second gene signature from the targeted RNA probe panel to calculate an estimate of the total number of cells in the tumor sample that express the second gene signature; wherein when the calculated estimate of total tumor expression of the second gene signature reaches a critical threshold value, the tumor will not respond to immune checkpoint inhibition (ICI) treatment.
19. The method of claim 18, wherein the melanoma is acral melanoma (AM).
20. The method of claim 18, wherein the melanoma tumor sample comprises one or more biopsy samples or one or more formalin fixed paraffin embedded (FFPE) tumor tissue samples from the subject.
21. The method of claim 18, wherein the targeted RNA probe panel comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6, ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6,

BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, and CYC1.

22. The method of claim 18, further comprising:
calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;
wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or
wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.
23. The method of claim 18, further comprising:
when it is determined that the melanoma tumor will respond to ICI treatment, an effective amount of an ICI treatment is administered to the subject; or
when it is determined that the melanoma tumor will not respond to ICI treatment, an effective amount of an alternative non-ICI therapy is administered to the subject.
24. The method of claim 23, wherein the ICI treatment comprises:
a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;
a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;
a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.
25. The method of claim 23, wherein the alternative non-ICI therapy comprises:
a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;
a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;
a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;
a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
a CTLA-4 inhibitor selected from ipilimumab;

aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;

a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;

surgical excision; or

combinations thereof.

26. A method of stratifying and evaluating melanoma treatment response in a subject using bulk transcriptomic data and a two-step deconvolution analysis, the method comprising:
- (a) obtaining one or more melanoma tumor samples from a subject;
 - (b) performing RNA sequencing of the one or more melanoma tumor samples and obtaining bulk transcriptomic data;
 - (b) performing transcript counting on the bulk transcriptomic data to obtain transcript expression data;
 - (c) on a processor, deconvoluting the transcript expression data using a first gene signature to stratify the melanoma into a specific melanoma cell subtype or origin; and
 - (d) deconvoluting the transcript expression data using a second gene signature to calculate an estimate of the total number of cells in the melanoma tumor sample that express the second gene signature or determine the cell differentiation state;
- wherein when the calculated estimate of total expression of the second gene signature reaches a critical threshold value, the melanoma will not respond to immune checkpoint inhibition (ICI) treatment.
27. The method of claim 26, wherein the melanoma is acral melanoma (AM).
28. The method of claim 26, further comprising:
- when the calculated total tumor expression of the second gene signature is below the critical threshold value, an effective amount of an ICI treatment is administered to the subject; or
- when the calculated total tumor expression of the second gene signature is above the critical threshold value, an effective amount of an alternative non-ICI therapy is administered to the subject.

29. The method of claim 26, further comprising:
calculating a transcriptomic deconvolution-based predictor of ICI resistance (TD-IR) score value;
wherein when the calculated TD-IR score value is positive, the melanoma tumor will not respond to ICI treatment; or
wherein when the calculated TD-IR score value is negative, the melanoma tumor will respond to ICI treatment.
30. The method of claim 28, wherein the ICI treatment comprises:
a PD-1 inhibitor selected from pembrolizumab, nivolumab, cemiplimab, or combinations thereof;
a PD-L1 inhibitor selected from atezolizumab, avelumab, durvalumab, or combinations thereof;
a LAG-3 inhibitor selected from relatlimab, relatlimab-RMBW, or combinations thereof; or combinations thereof.
31. The method of claim 28, wherein the alternative non-ICI therapy comprises:
a PARP inhibitor selected from olaparib, niraparib, rucaparib, talazoparib, or combinations thereof;
a BRAF inhibitor selected from dabrafenib, encorafenib, vemurafenib, or combinations thereof;
a MEK inhibitor selected from trametinib, cobimetinib, binimetinib, or combinations thereof;
a KIT inhibitor selected from dasatinib, imatinib, nilotinib, or combinations thereof;
a tumor-agnostic therapy selected from larotrectinib, entrectinib, or combinations thereof;
a CTLA-4 inhibitor selected from ipilimumab;
aldesleukin (Interleukin-2; IL-2), Interferon alfa-2b, pegylated Interferon alfa-2b, or combinations thereof;
a chemotherapeutic agent selected from dacarbazine, temozolomide, cisplatin, carboplatin, fotemustine, lomustine, docetaxel, paclitaxel, vinblastine, or combinations thereof;
surgical excision; or
combinations thereof.

32. The method of claim 26, wherein the specific melanoma cell subtype comprises volar-like (v-mel) or non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.
33. The method of claim 26, wherein the first gene signature comprises one or more genes selected from ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, PDLIM4, AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18.
34. The method of claim 33, wherein when the expression of one or more of ID3, NTRK2, ID2, LOC101930452, MEG3, LINC00473, RAB3B, IGDC4, MIA, or PDLIM4 is upregulated, the melanoma is stratified as a volar-like (v-mel) melanocyte-derived melanoma.
35. The method of claim 33, wherein when the expression of one or more of AKAP12, SLC45A2, HPGD, MCOLN3, RGL1, SEMA5A, ACP5, APCDD1, LINC00462, or GALNT18 is upregulated, the melanoma is stratified as a non-volar cutaneous-like (c-mel) melanocyte-derived melanoma.
36. The method of claim 26, wherein the second gene signature comprises one or more genes selected from SERPINF1, GPM6B, RPS17L, GAS5, CREBBP, MACF1, ZNF263, PEX10, PABPC1, FOXRED2, RPS17, RPL13AP5, MYCBP2, VPS13C, GGCT, NR2F6, DCT, SOAT1, MARCKS, SNAI2, HIVEP2, SYNE1, ZFAT, EXTL2, TIMM50, RPS16, RPS4X, FAM174B, NTRK2, NOTCH2, ARMC1, ZMYND19, CA14, PKNOX2, ESRP1, RASSF3, SNX29, DYSF, DUS4L, CDK12, SCD, RPL18, NF2, PTP4A3, VPS13D, NBEAL1, ZNHIT1, ZNF146, RPS19, EIF4A1, CNRIP1, RPS7, KMT2C, POLR3A, MRPL32, SRR, RPL29, RPS27, OXA1L, EIF2S3, WNK1, NBAS, SLC25A36, FNTA, BCAN, NOP56, NPL, ABR, KDM5A, RANBP2, SRM, COMMD5, TRPM1, CHP1, CD68, PPA1, HUWE1, KAT6B, TSNAX, ZNF24, KIF17, TNFRSF14, SAE1, CS, MYH9, TRAPPC10, CBX3, MOB1B, RPS24, UQCRCF1, MID1, EGFL8, EP300, REL, PLA2G12A, TOMM20, RPL28, KLHDC8B, ZNF749, GPI, CEP128, ATXN7, SRSF6, ARL10, ADRBK2, RPS9, PPP2R1A, RPL8, TRIP11, ANKRD11, MAD2L1BP, SHARPIN, KCNAB2, SCIN, RPS8, C1QBP, CHD8, STAT3, MED1, TIGD5, PFN1, RPL4, GSTO1, TUBB4A, HERC1, JMJD1C, NRSN2, C8orf33, TMC6, ASAP1, SAMM50, PLTP, SETX, FLNA, LSM7, COA5, NENF, RAB38, EIF3K, SS18L1, EGFR, DYNC1H1, TMEM128, TSPYL4, ACP5, AHCY, SNHG6, SORD, ASCC3, SPTAN1, TBRG4, ZNF517, RPLP0, CCT3, FAM178B, ILF2, BIRC6,

ITSN2, TSTD2, ZNF121, RPS6, TP53, RPL6, EIF3L, ALMS1, ZNF407, MRPL15, SPIN3, EIF4EBP2, IDH2, MAD1L1, MLANA, ASH1L, PLEKHM1, SAT2, TRIM27, RPL13A, SLC25A5, IMPDH2, RPS11, BAZ2B, ERCC6, BOD1, TRIM13, PRAME, RPS5, BZW2, ADSL, NCOA3, PARG, PURB, TMEM231, MOB3B, GLOD4, GALE, PRDX3, MRPS21, NDUFA7, NDUFA3, or CYC1.

FIG. 1A

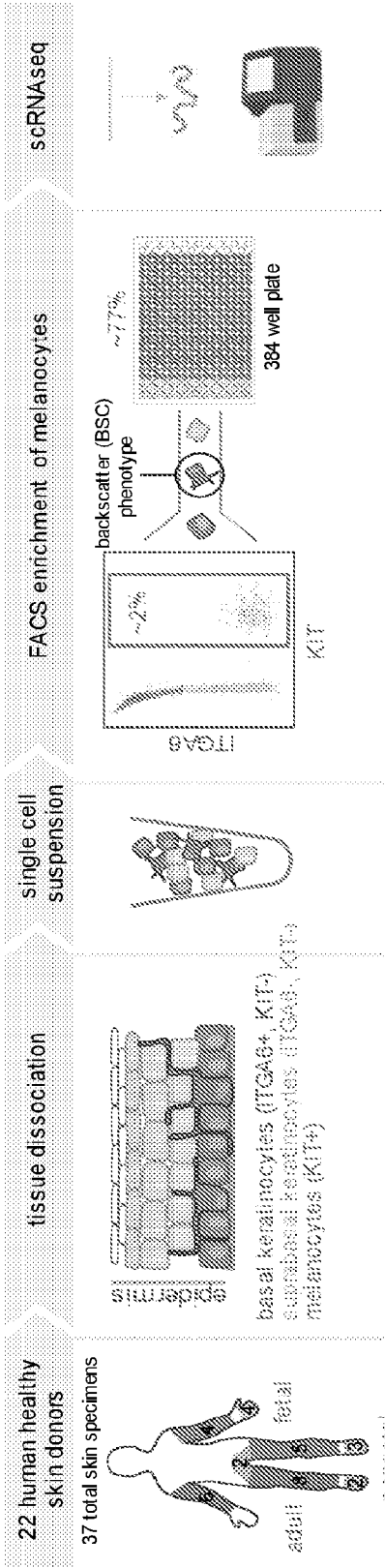


FIG. 1B

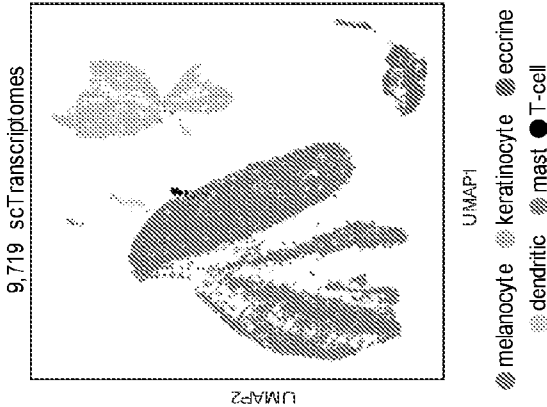


FIG. 1C

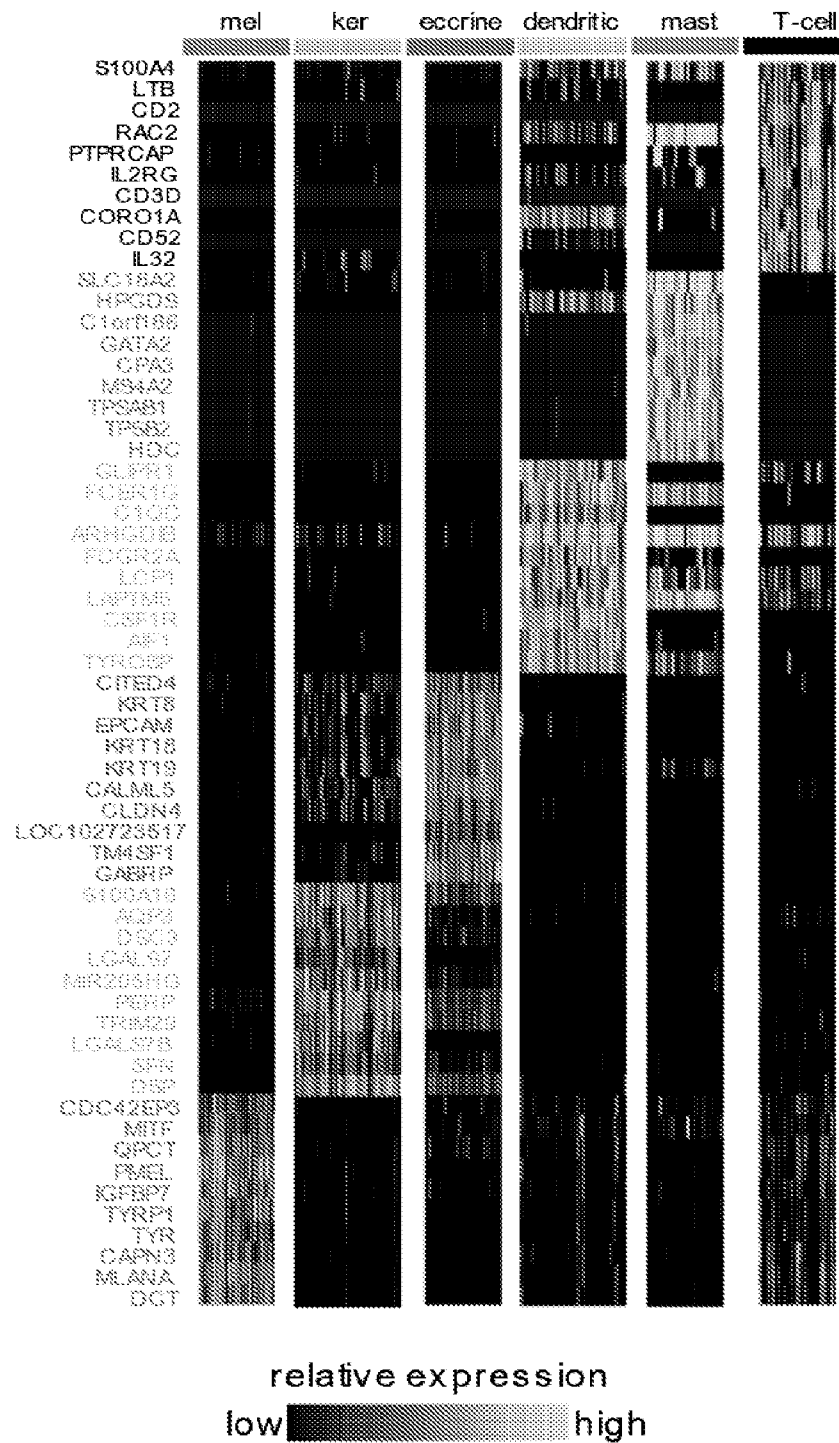


FIG. 1D

low-res Louvain clusters

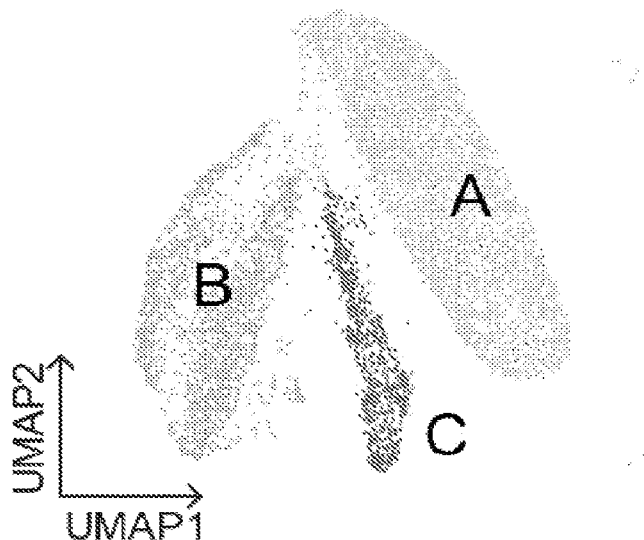


FIG. 1E

high-res Louvain clusters

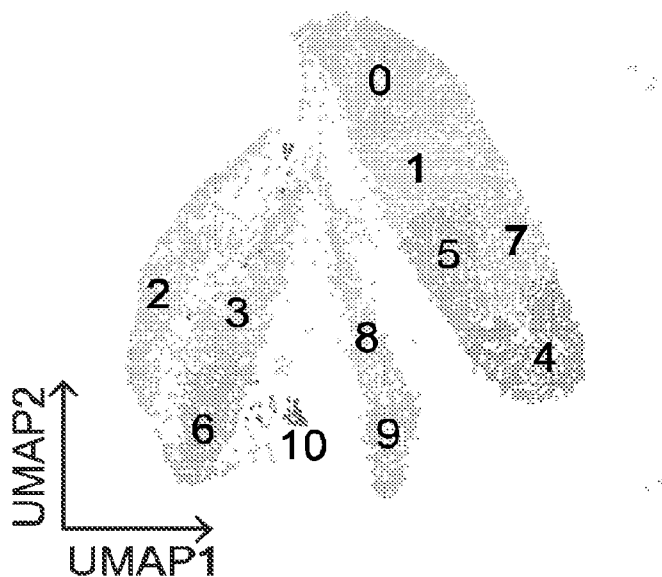


FIG. 1F

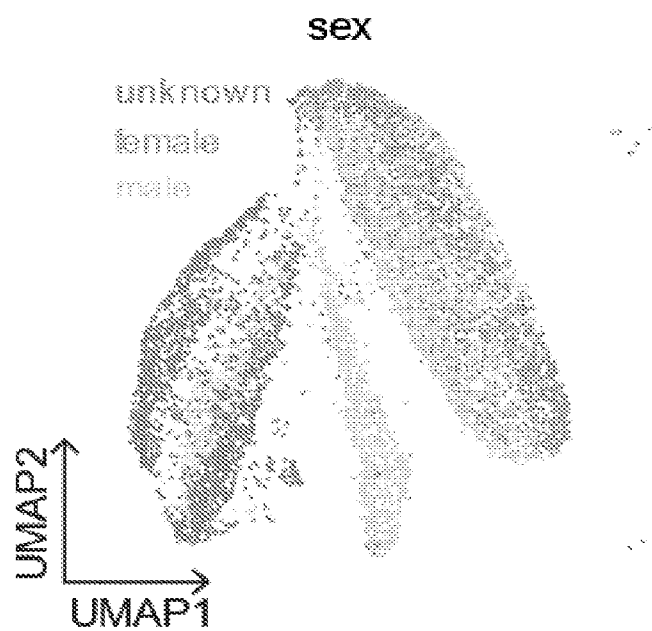


FIG. 1G

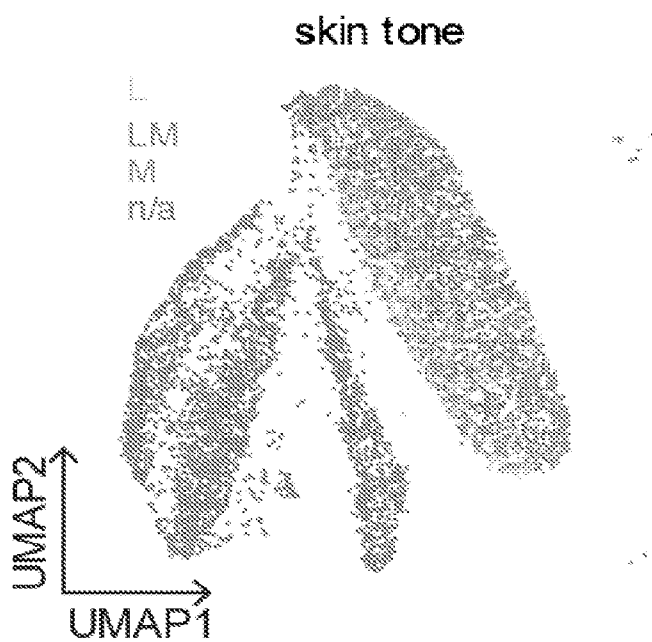


FIG. 1H

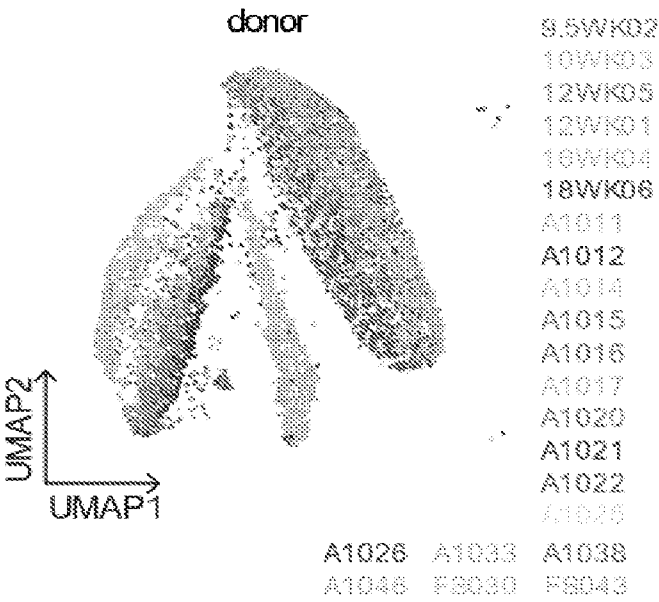


FIG. 1I

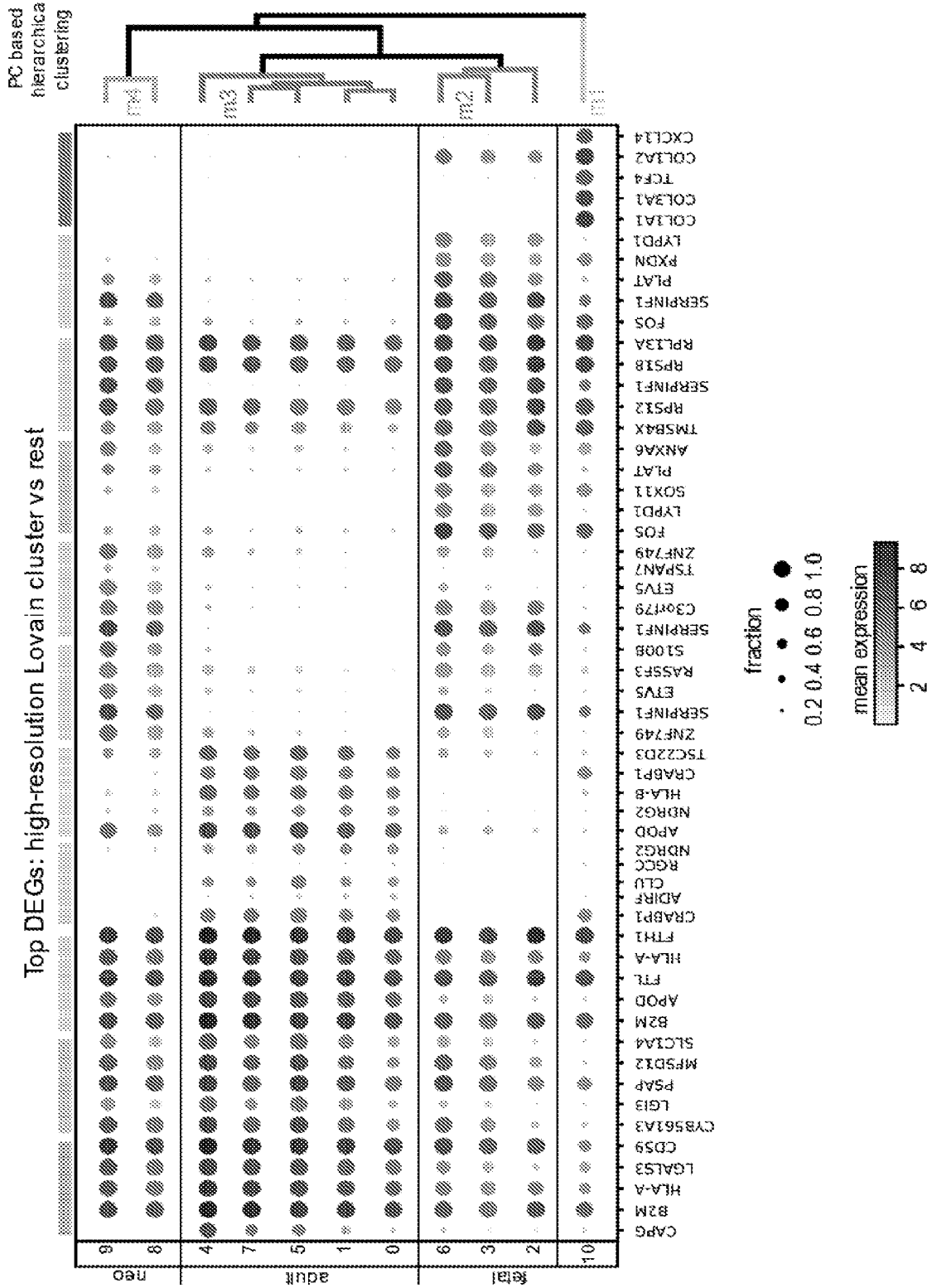


FIG. 1J

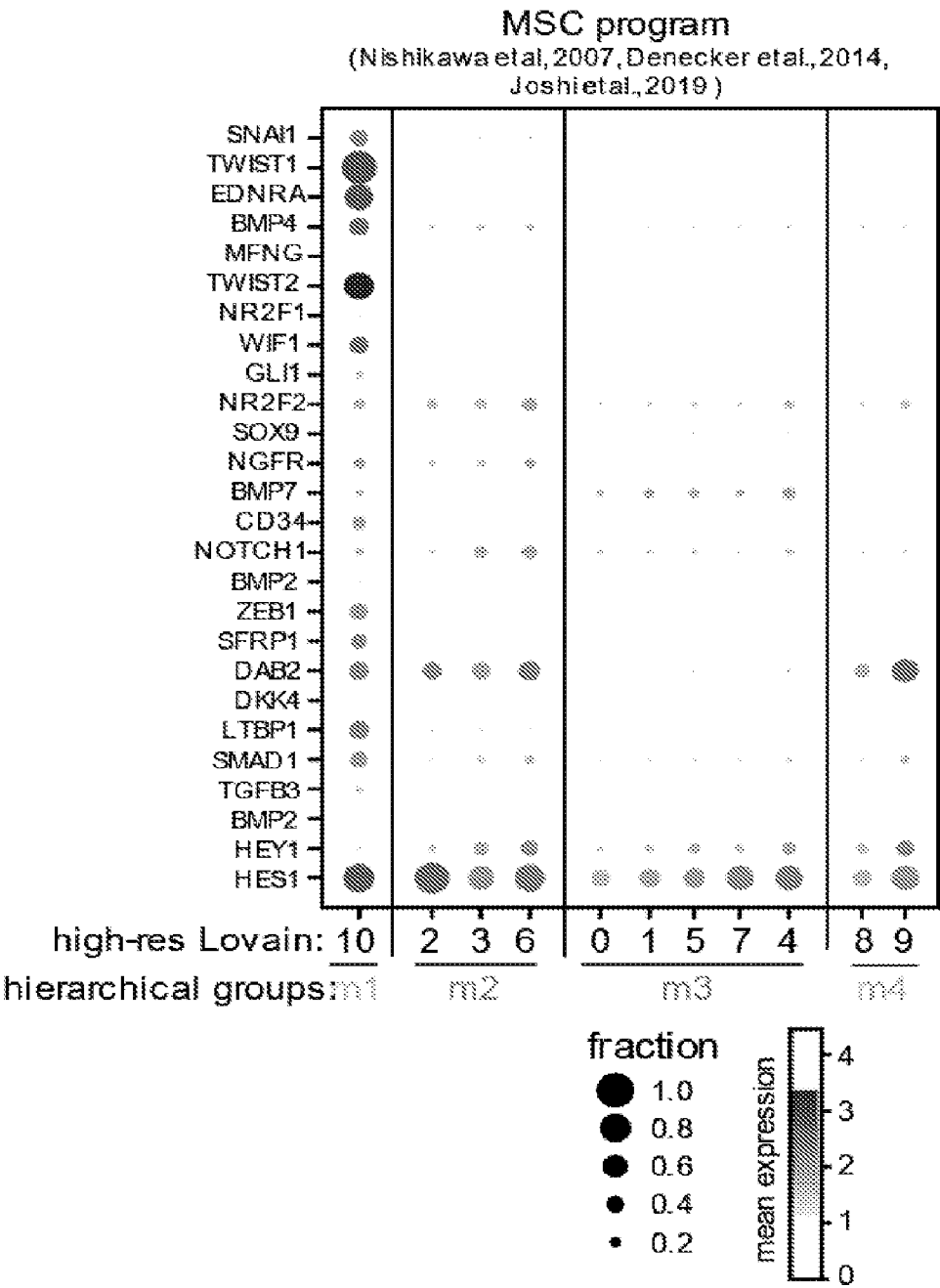


FIG. 1K

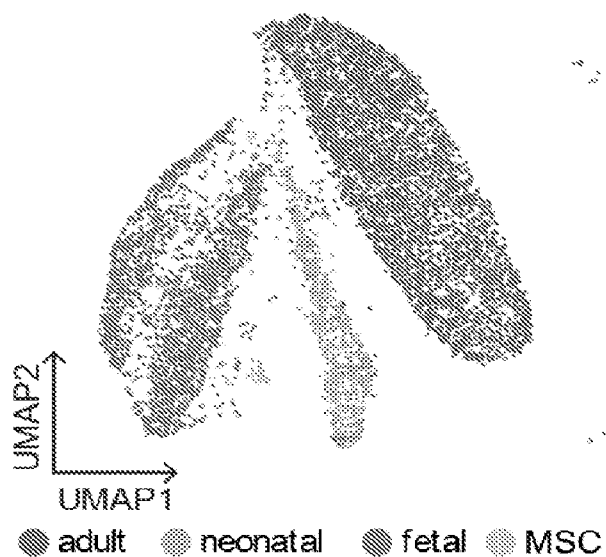


FIG. 1L

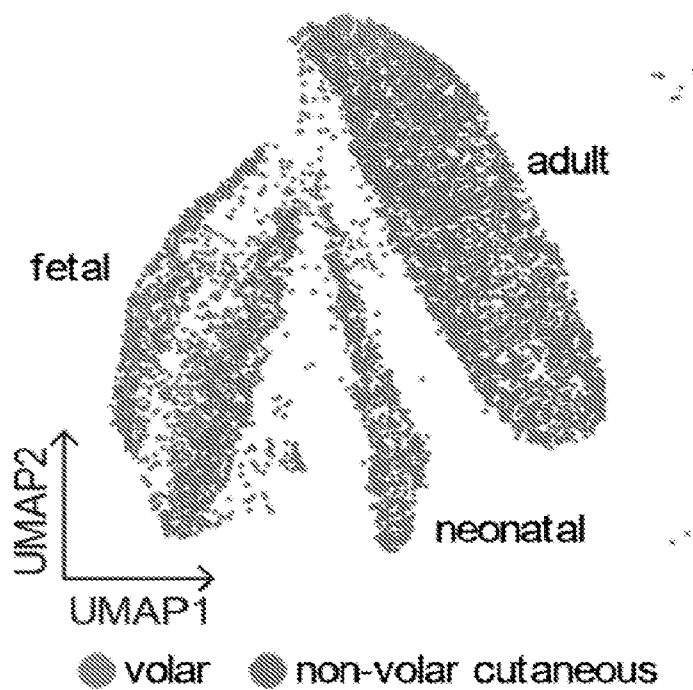


FIG. 2A

multi-site
donor matched skin
(n=20 skin specimens from 6 donors)

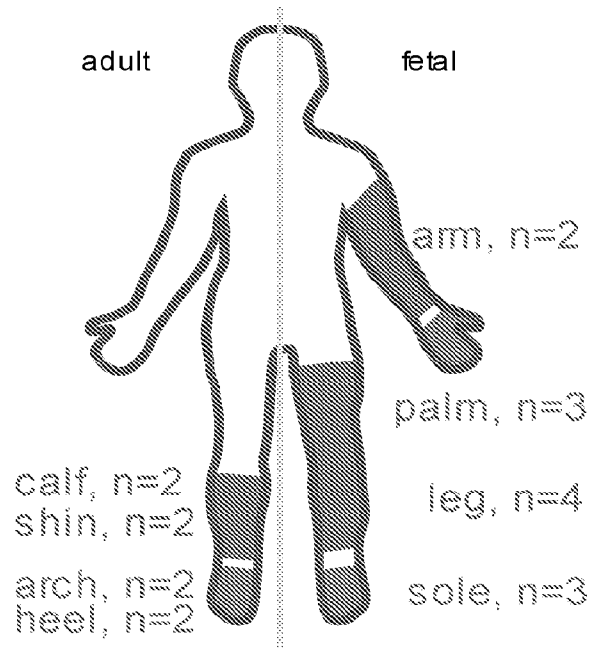
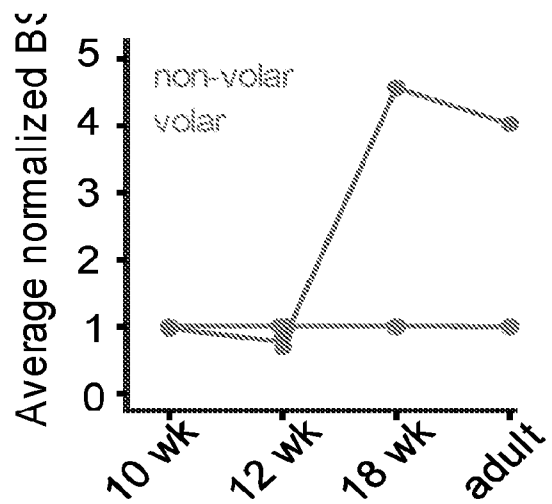
**FIG. 2B**

FIG. 2C

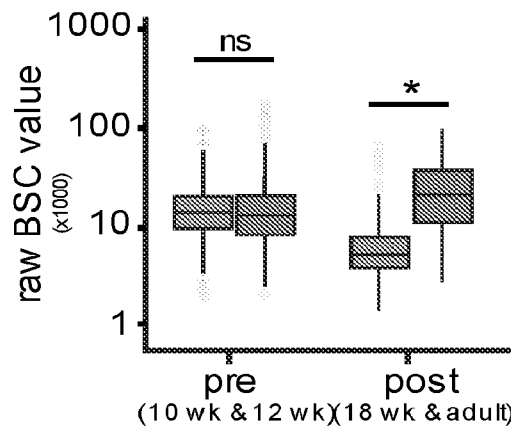


FIG. 2D

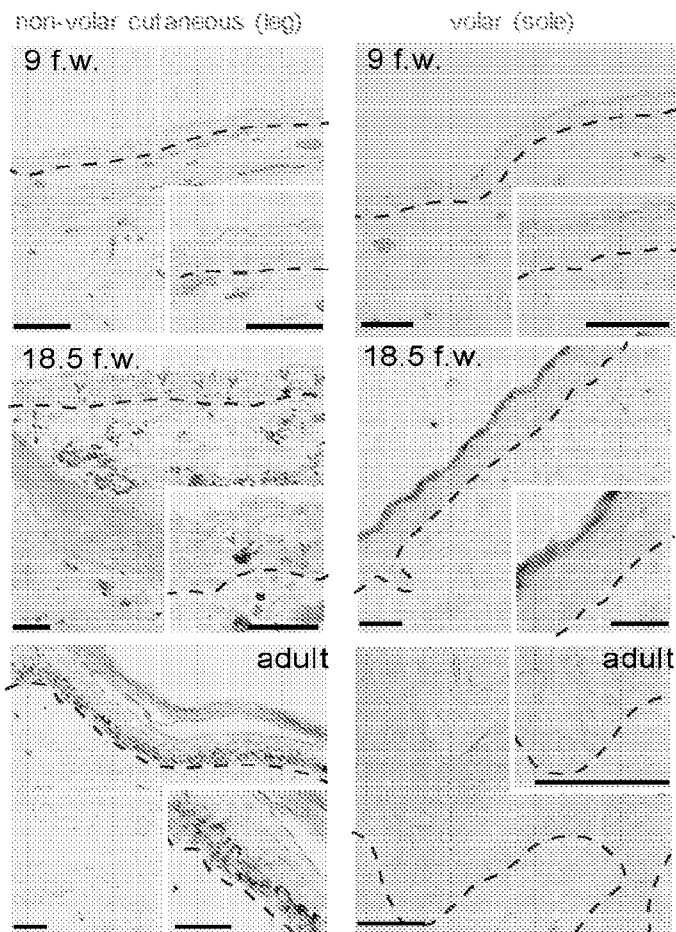


FIG. 2E

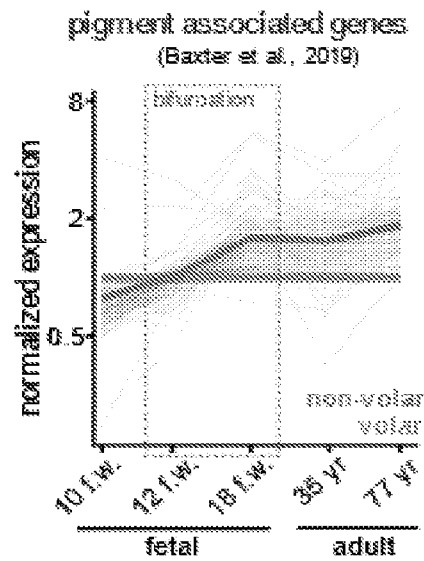


FIG. 2F

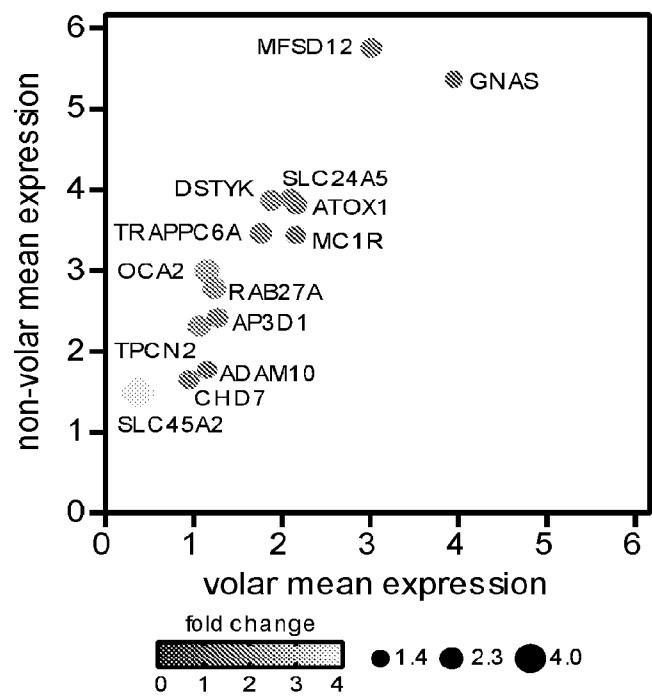


FIG. 2G

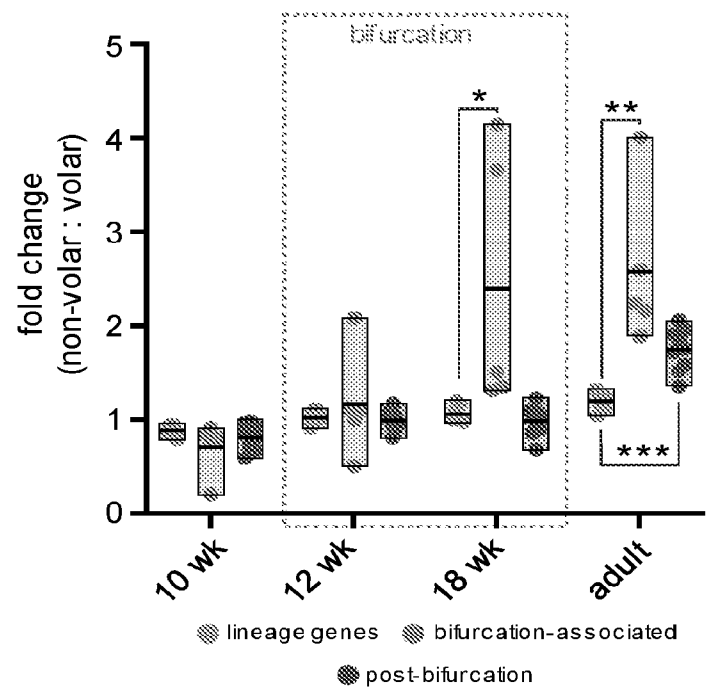


FIG. 2H

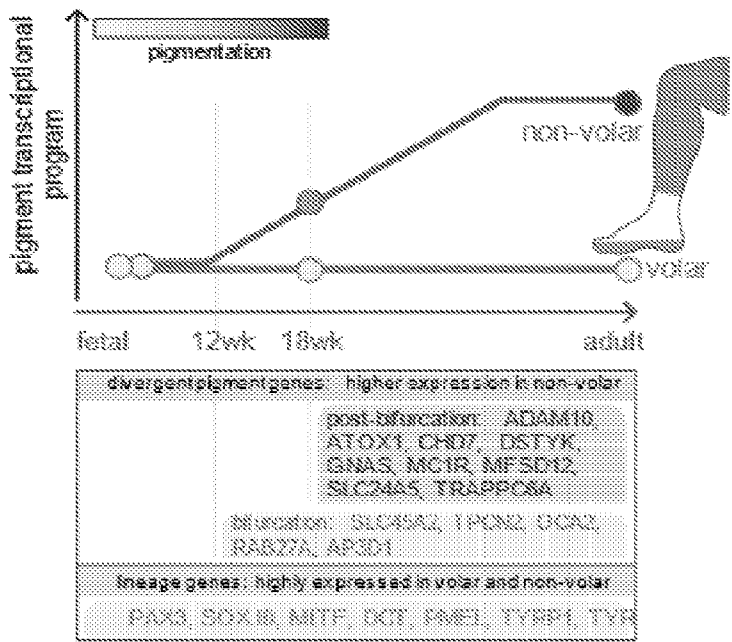


FIG. 3A

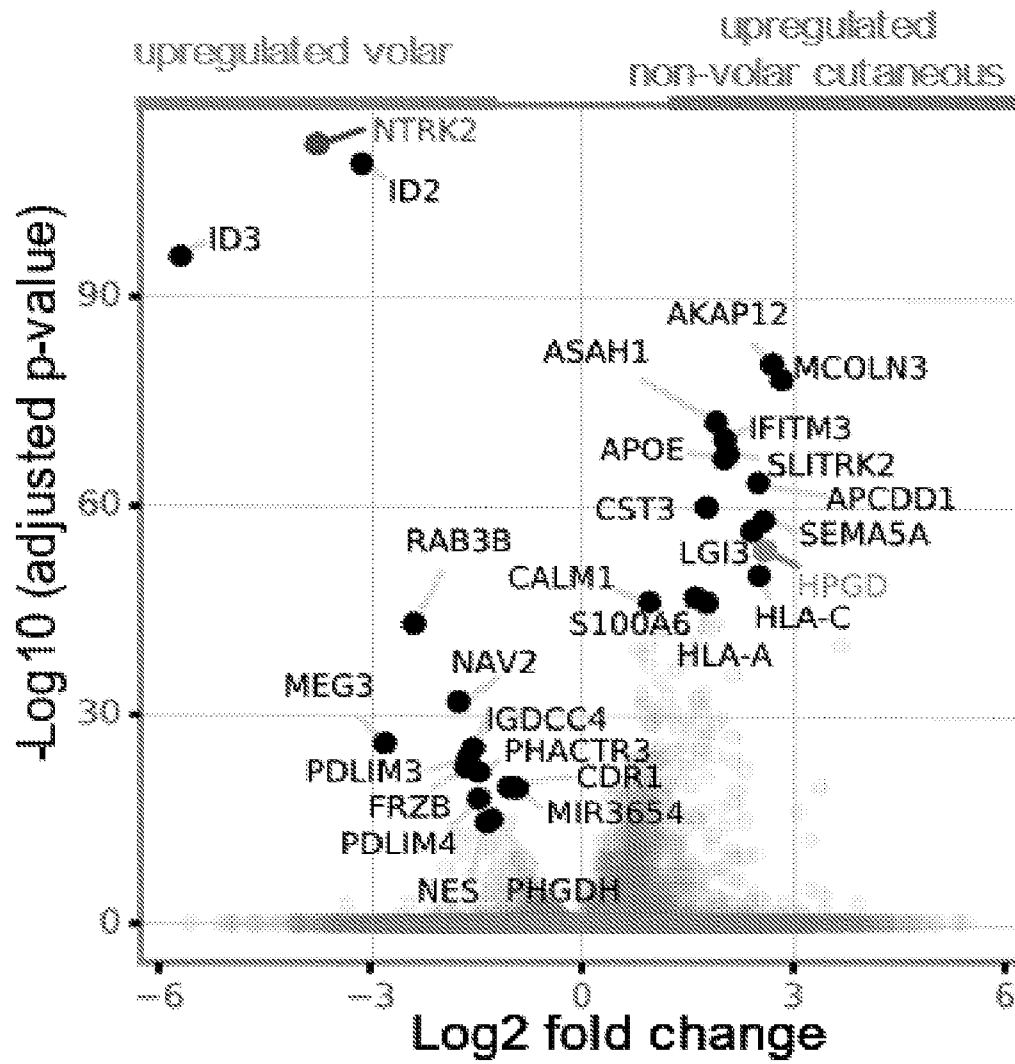


FIG. 3B

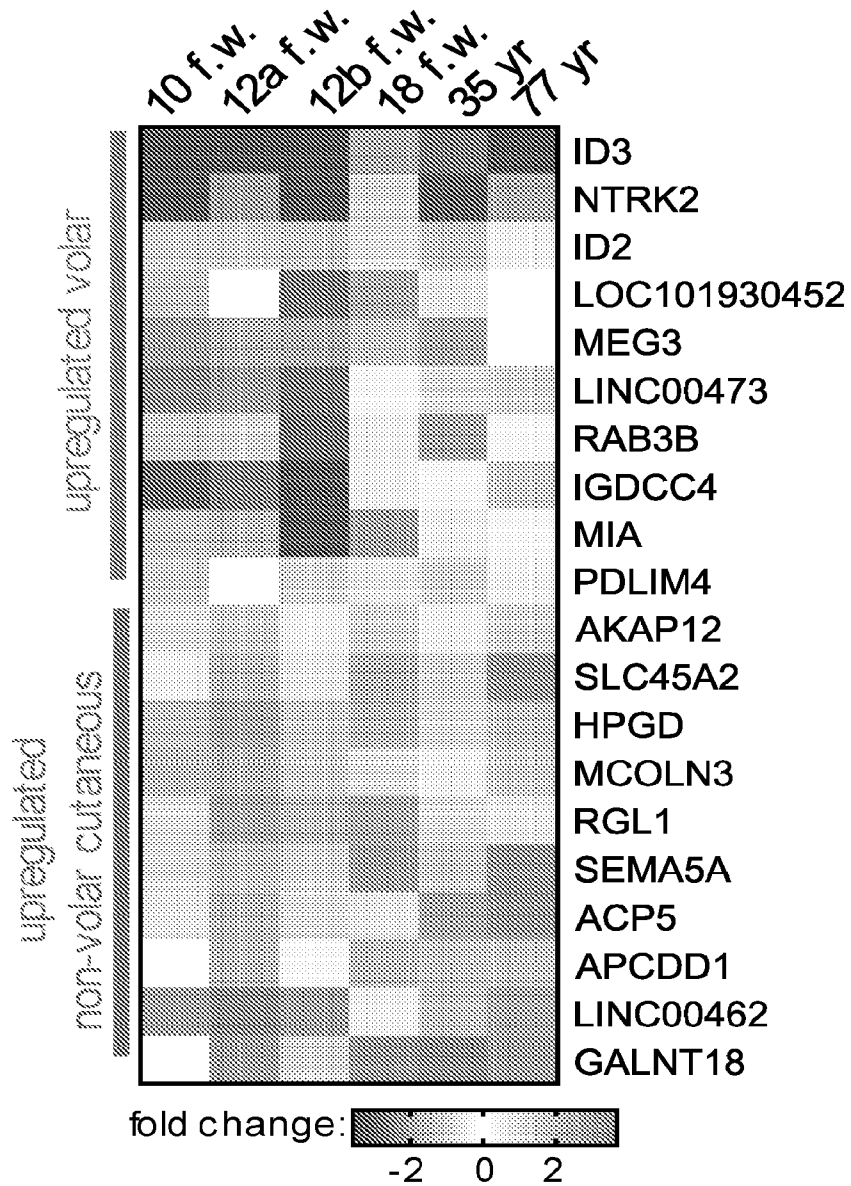


FIG. 3C

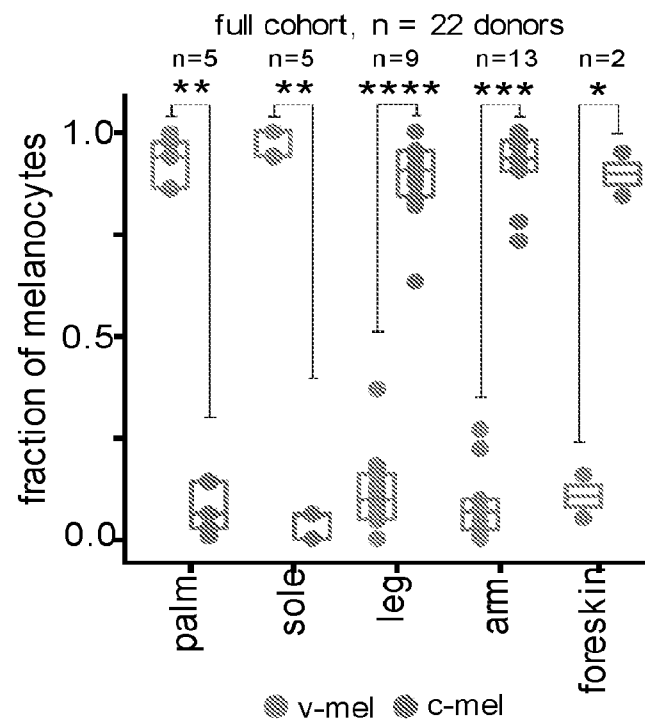


FIG. 3D

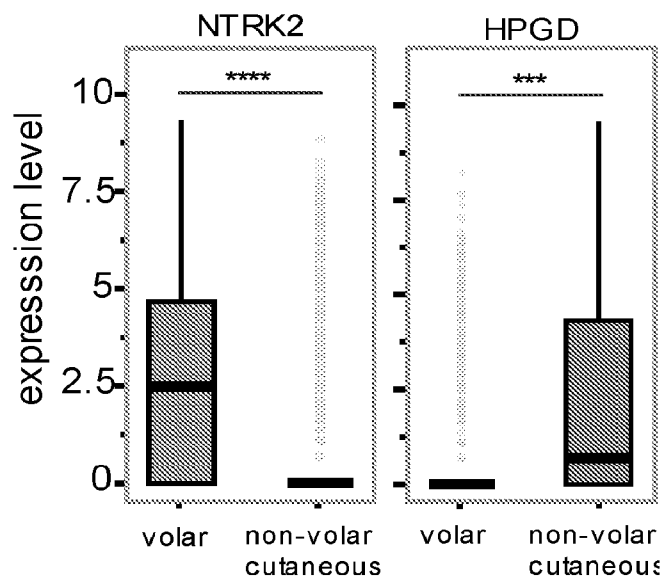


FIG. 3E

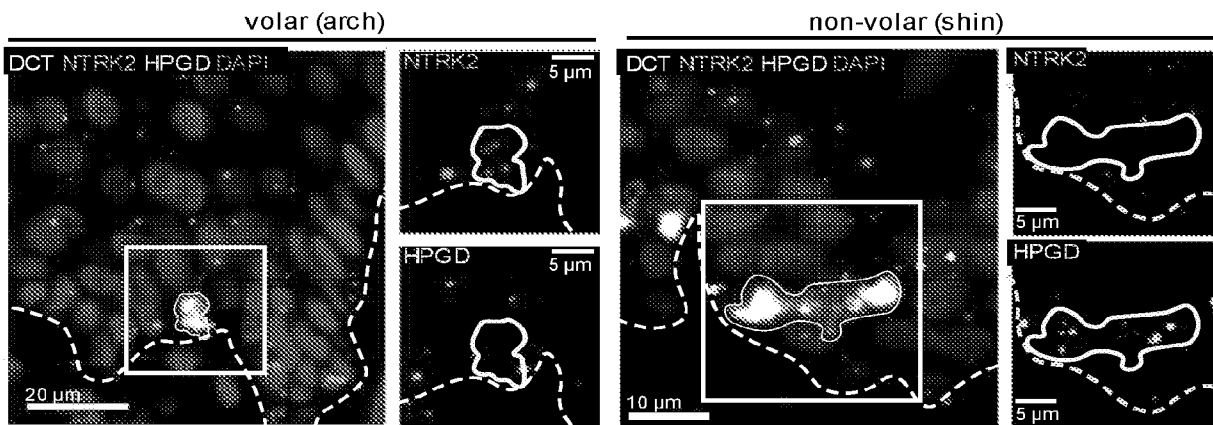


FIG. 3F

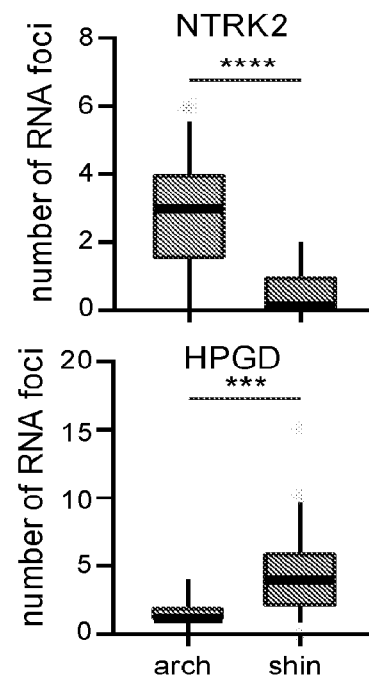


FIG. 3G

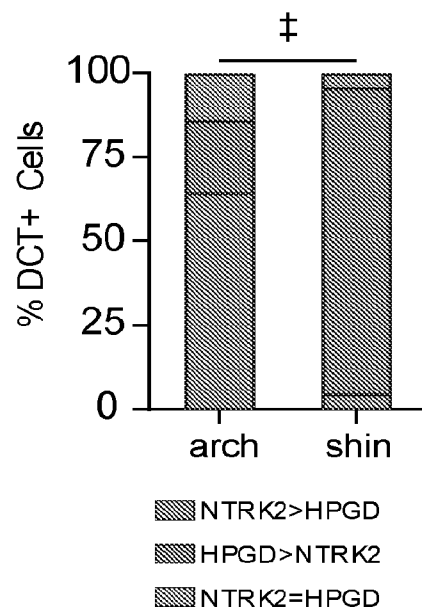


FIG. 3H

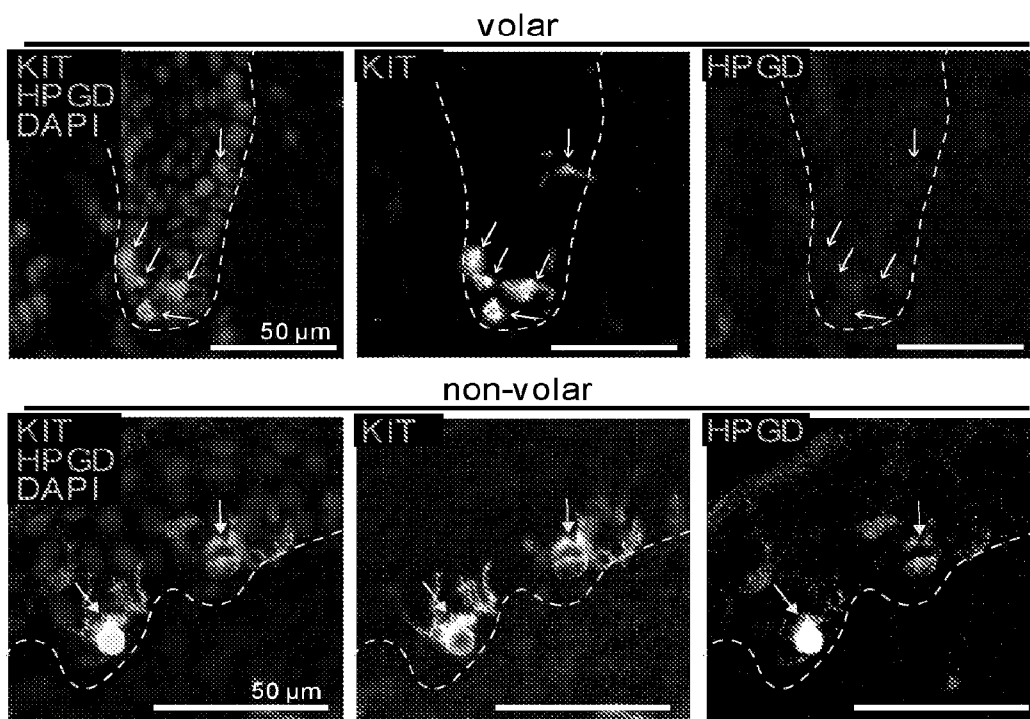


FIG. 3I

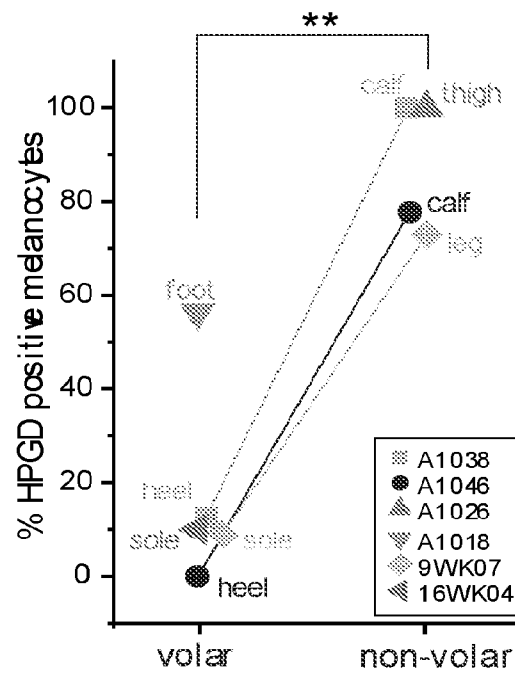


FIG. 3J

anatomic-site program conservation in melanoma?

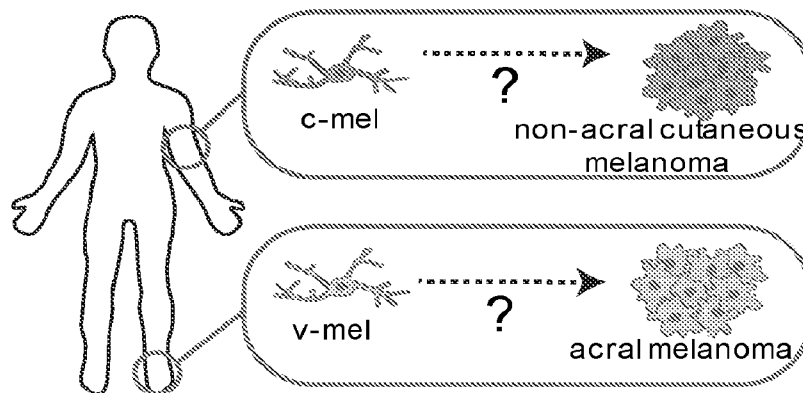


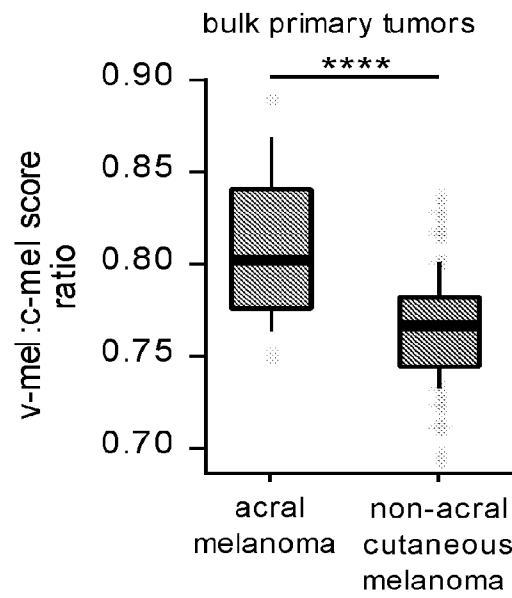
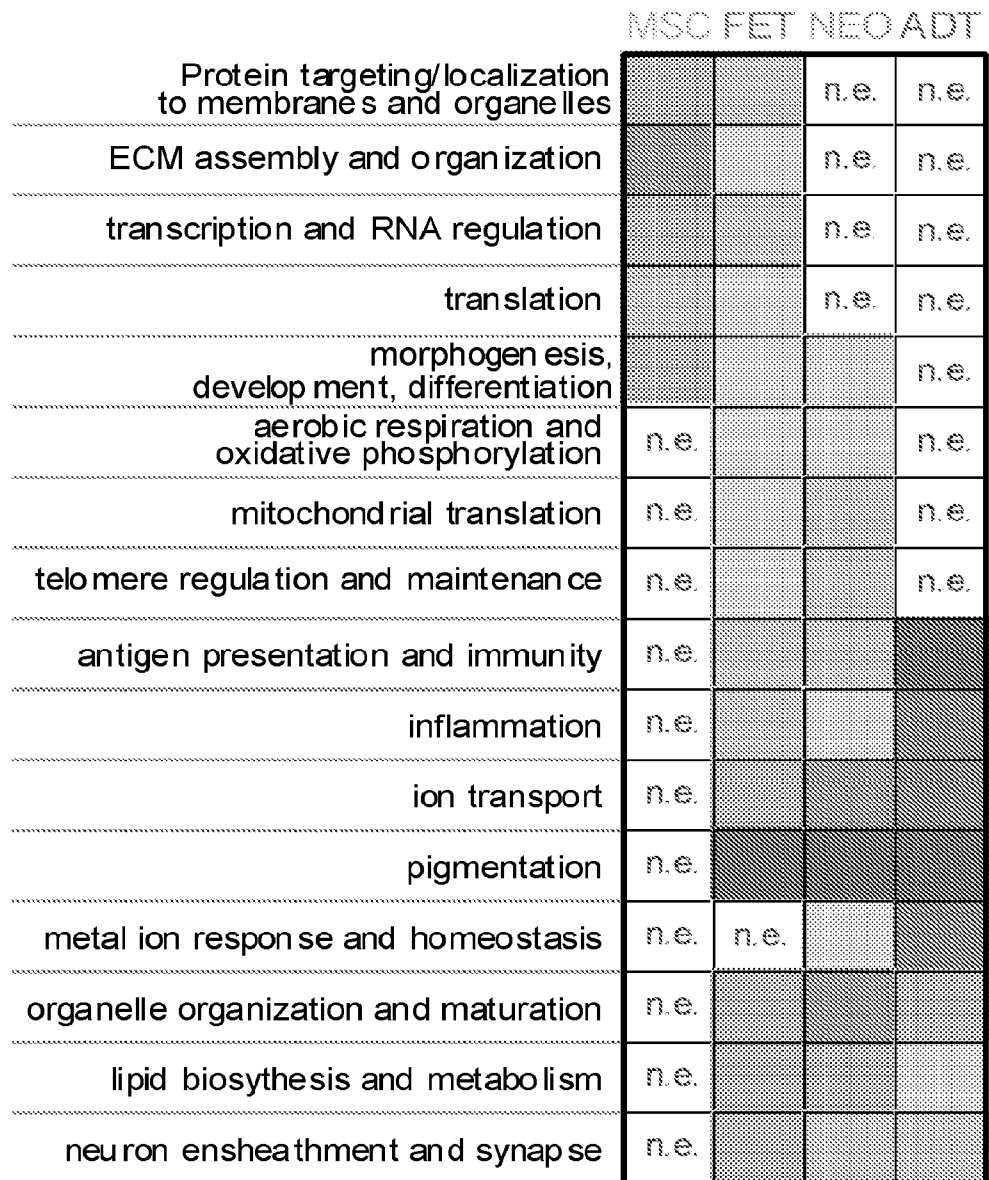
FIG. 3K

FIG. 4A



median [NES]
for GO-terms with FDR < 0.250

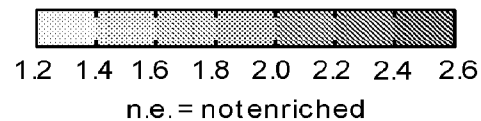


FIG. 4B

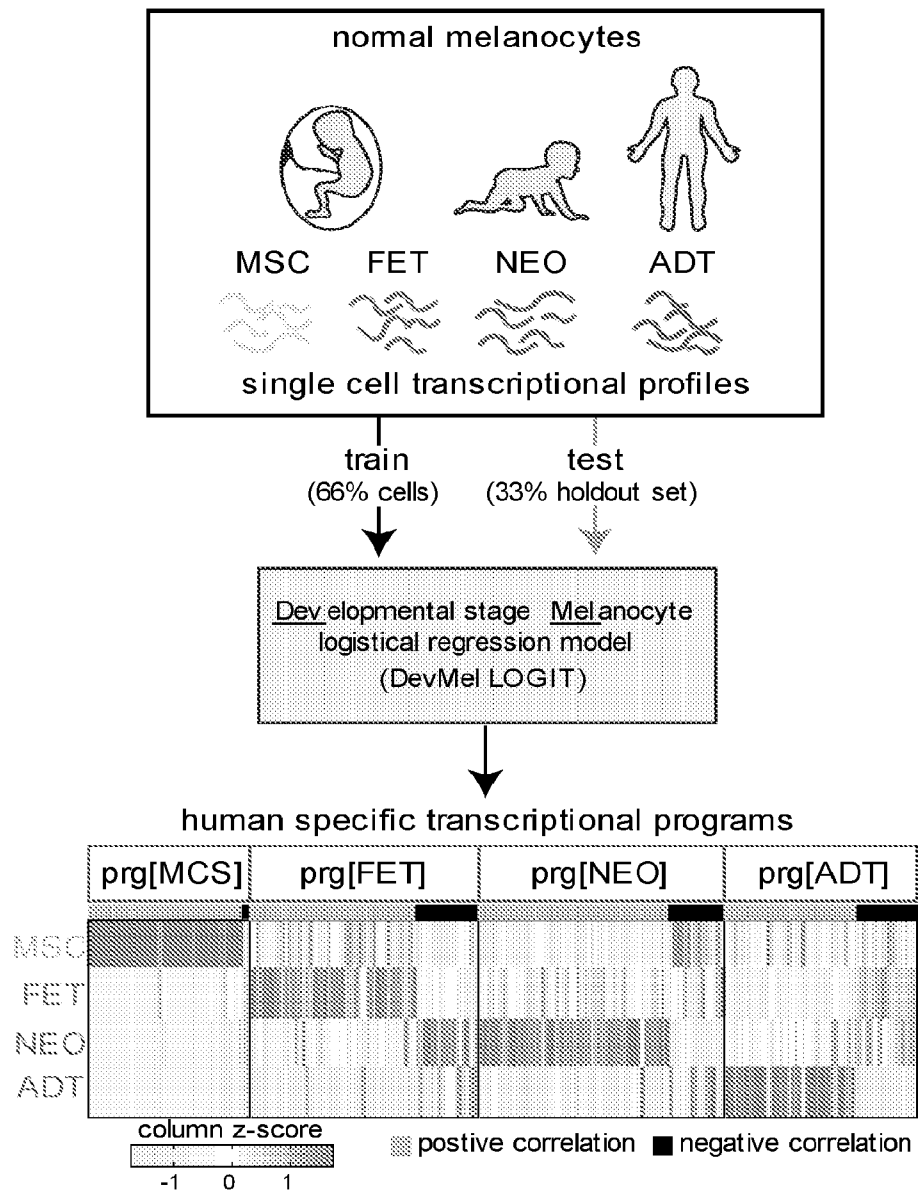


FIG. 4C

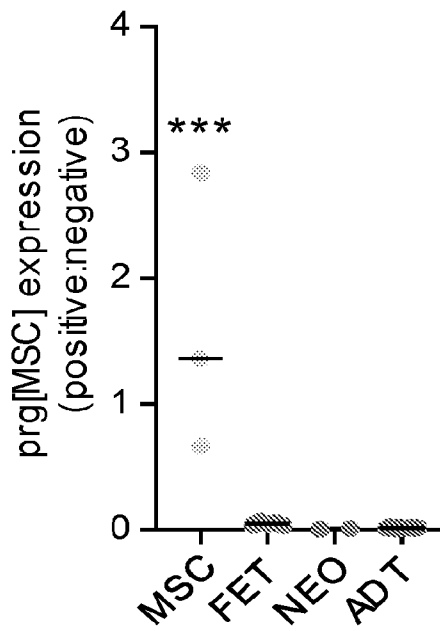


FIG. 4D

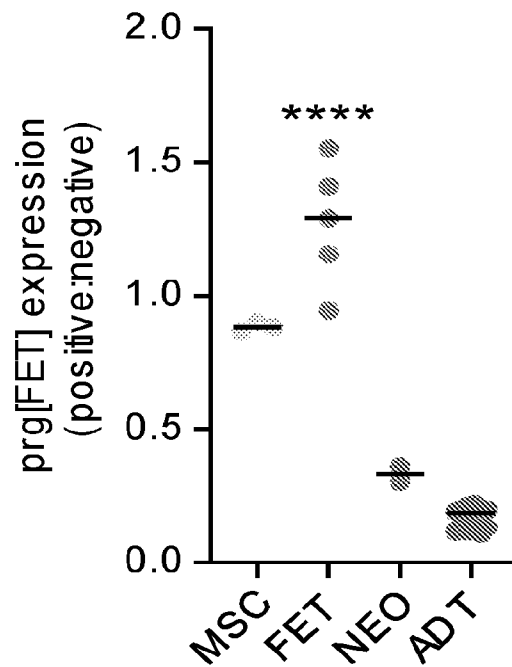


FIG. 4E

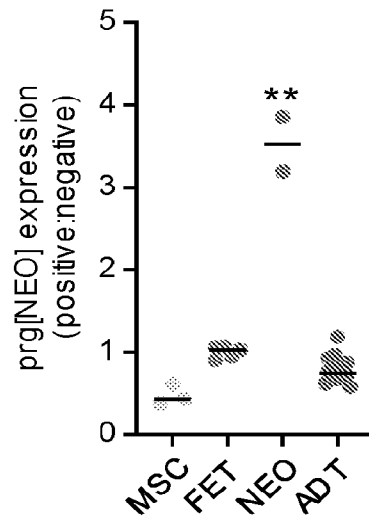


FIG. 4F

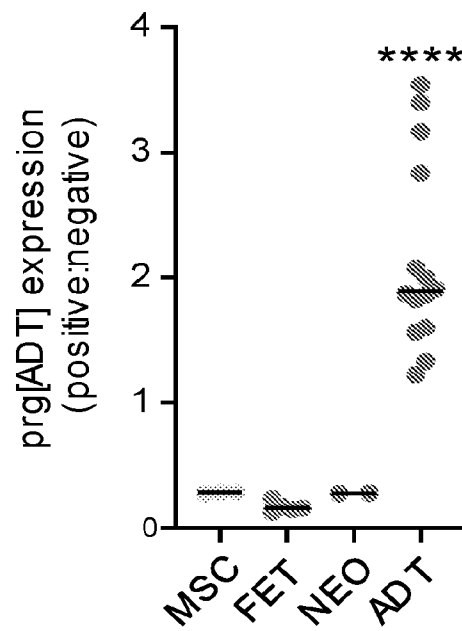


FIG. 5A

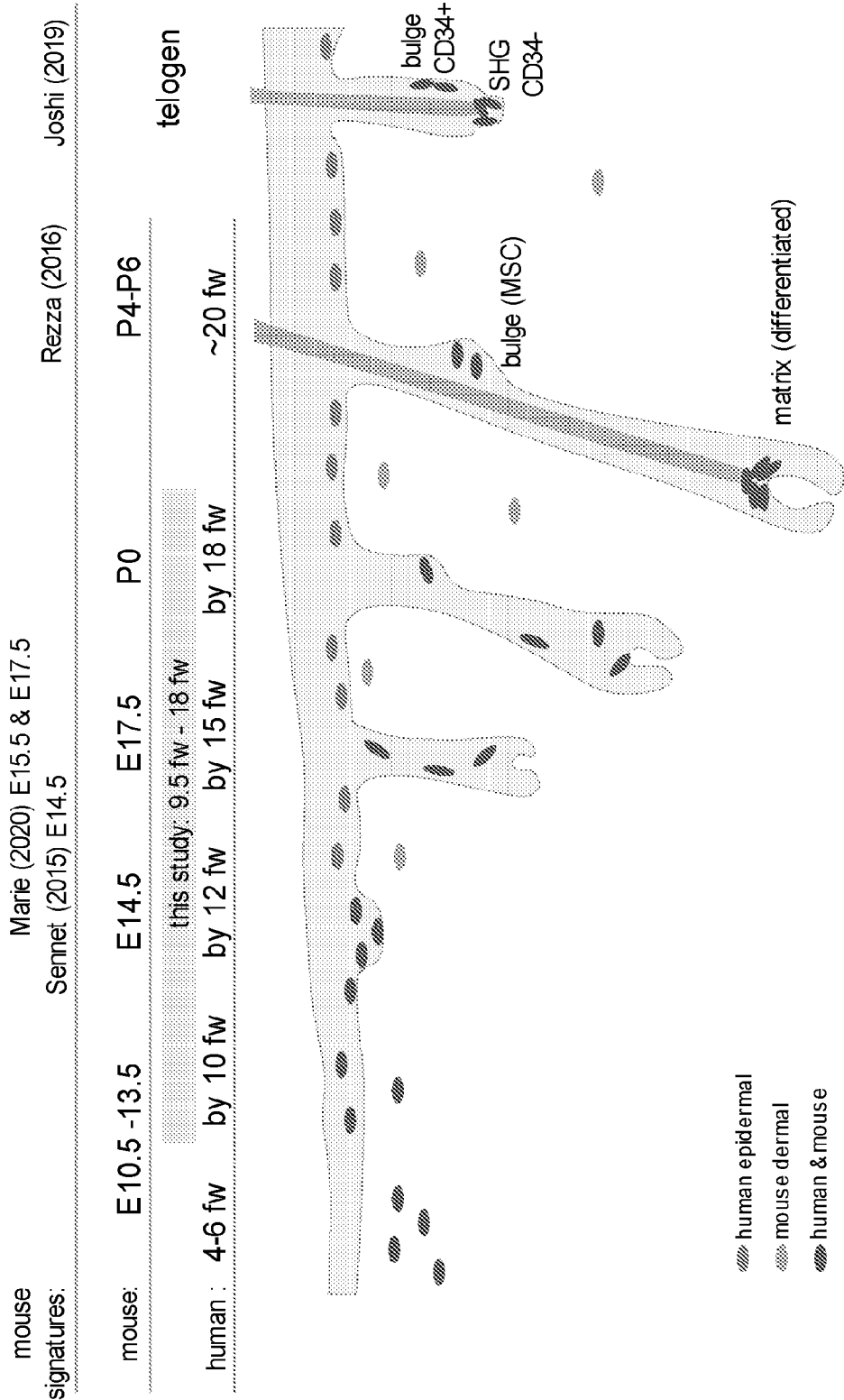


FIG. 5B

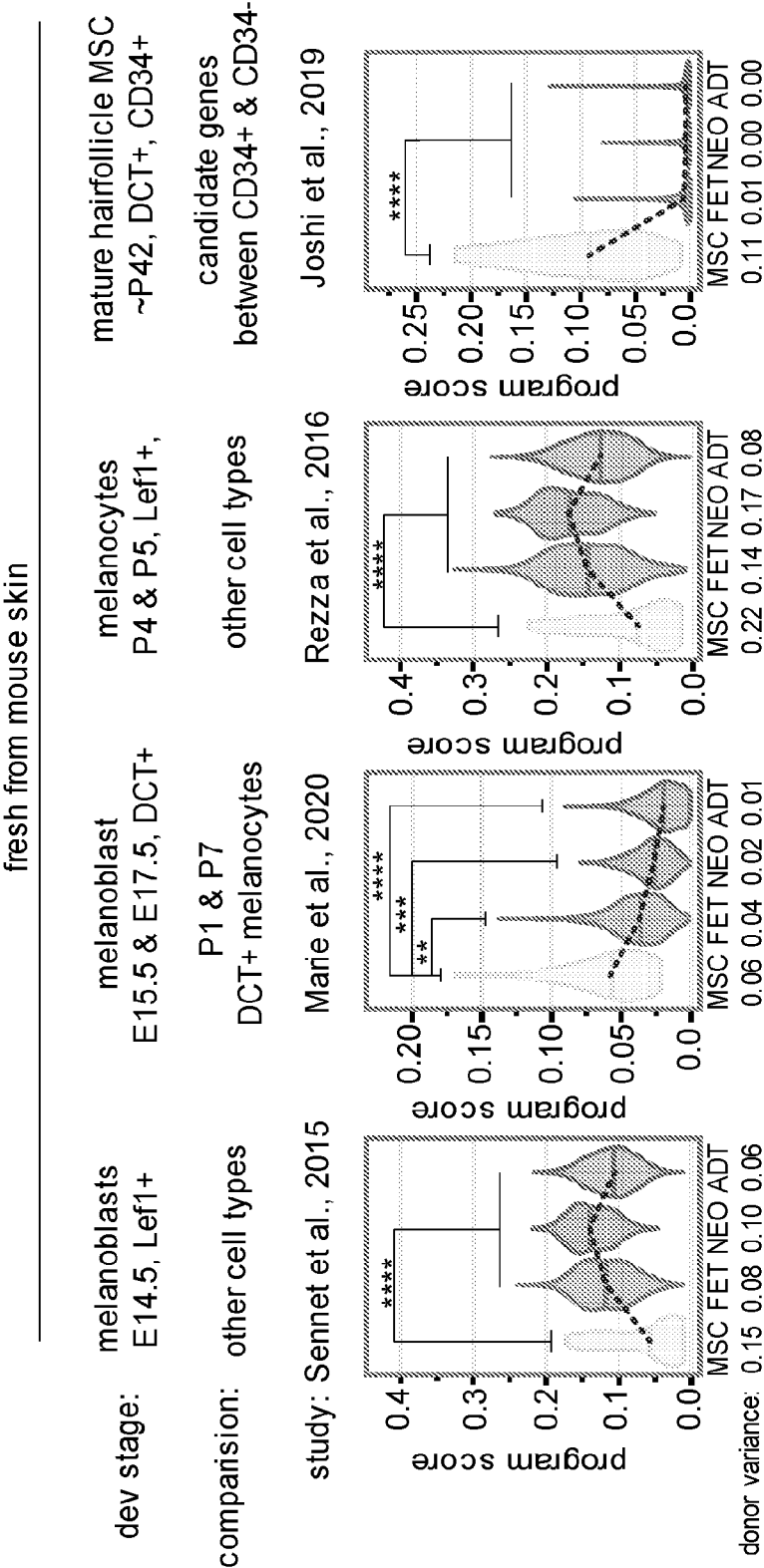


FIG. 5C

in vitro differentiation (Mica et al., 2013)

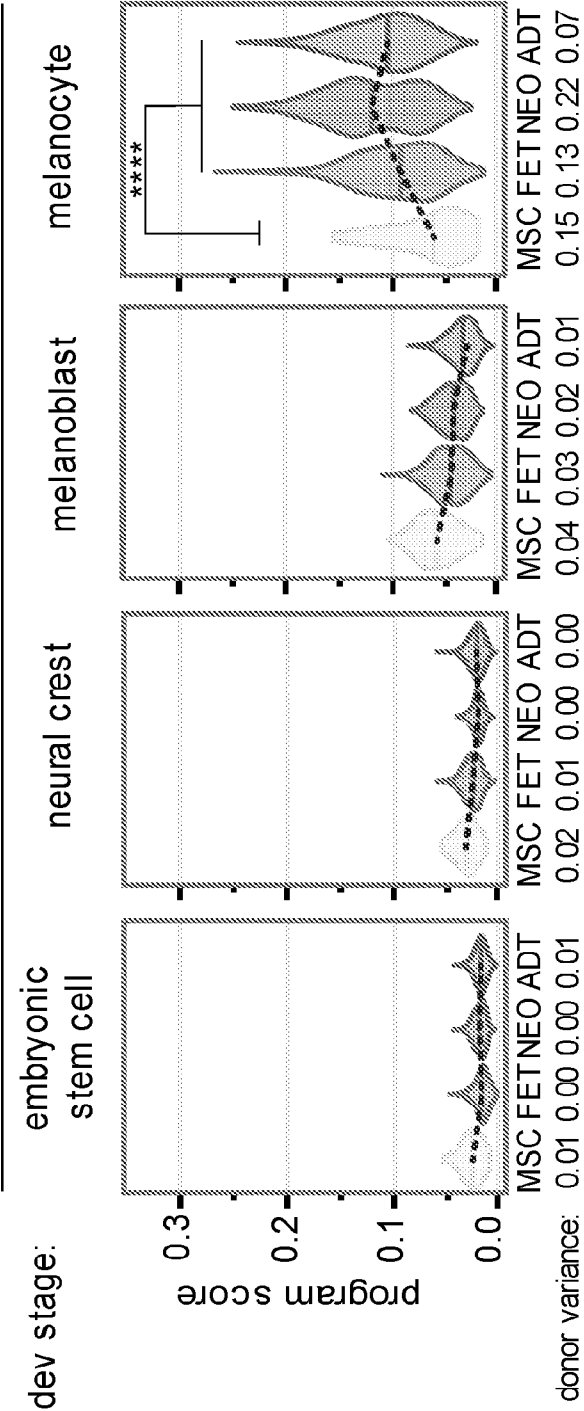


FIG. 5D

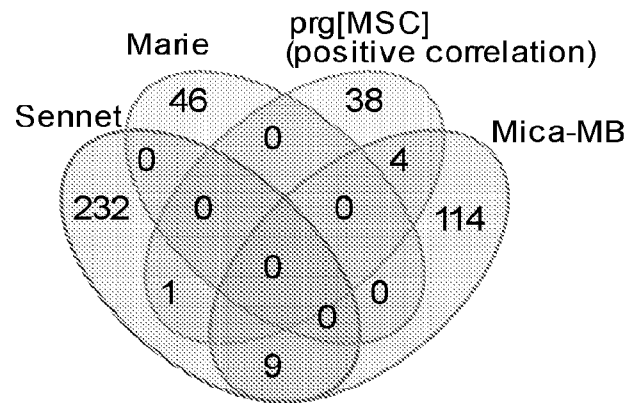


FIG. 5E

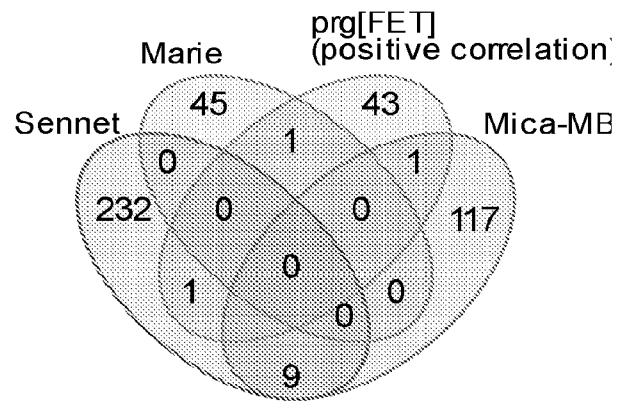


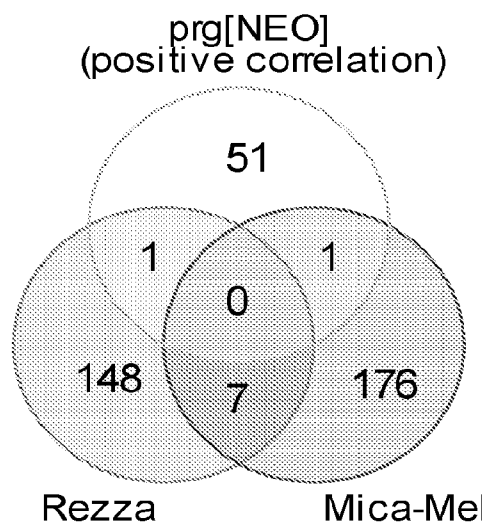
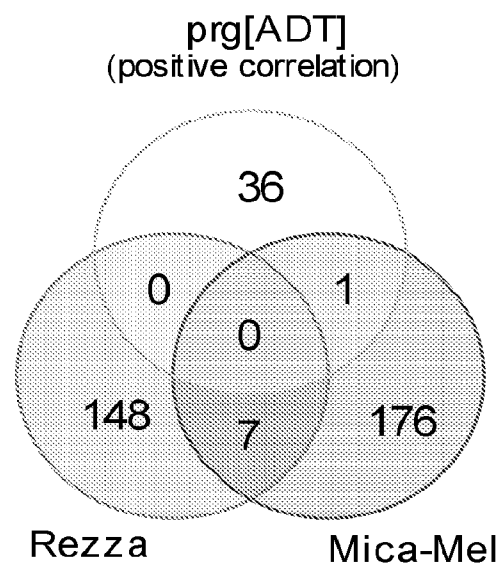
FIG. 5F**FIG. 5G**

FIG. 6A

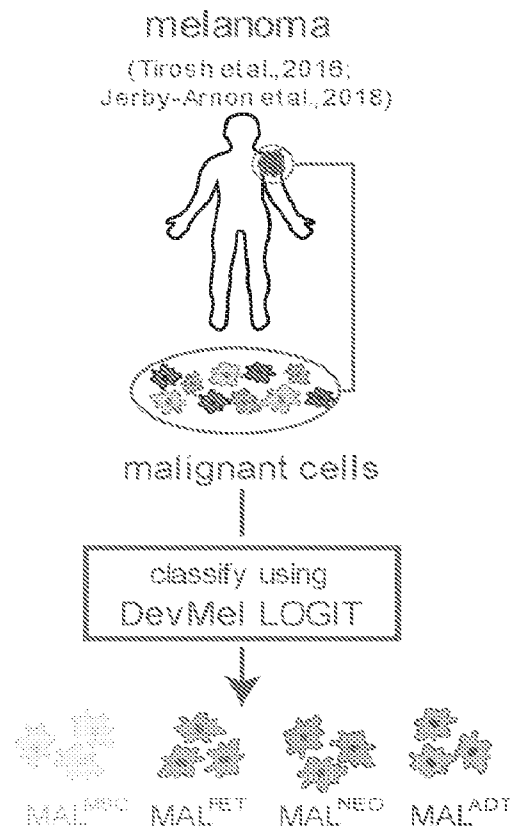


FIG. 6B

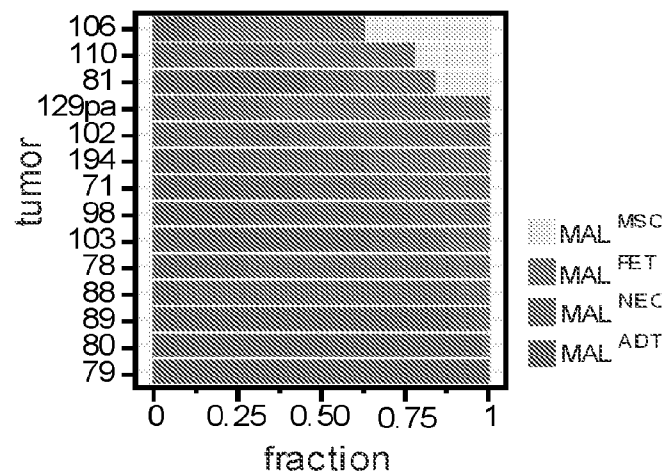


FIG. 6C

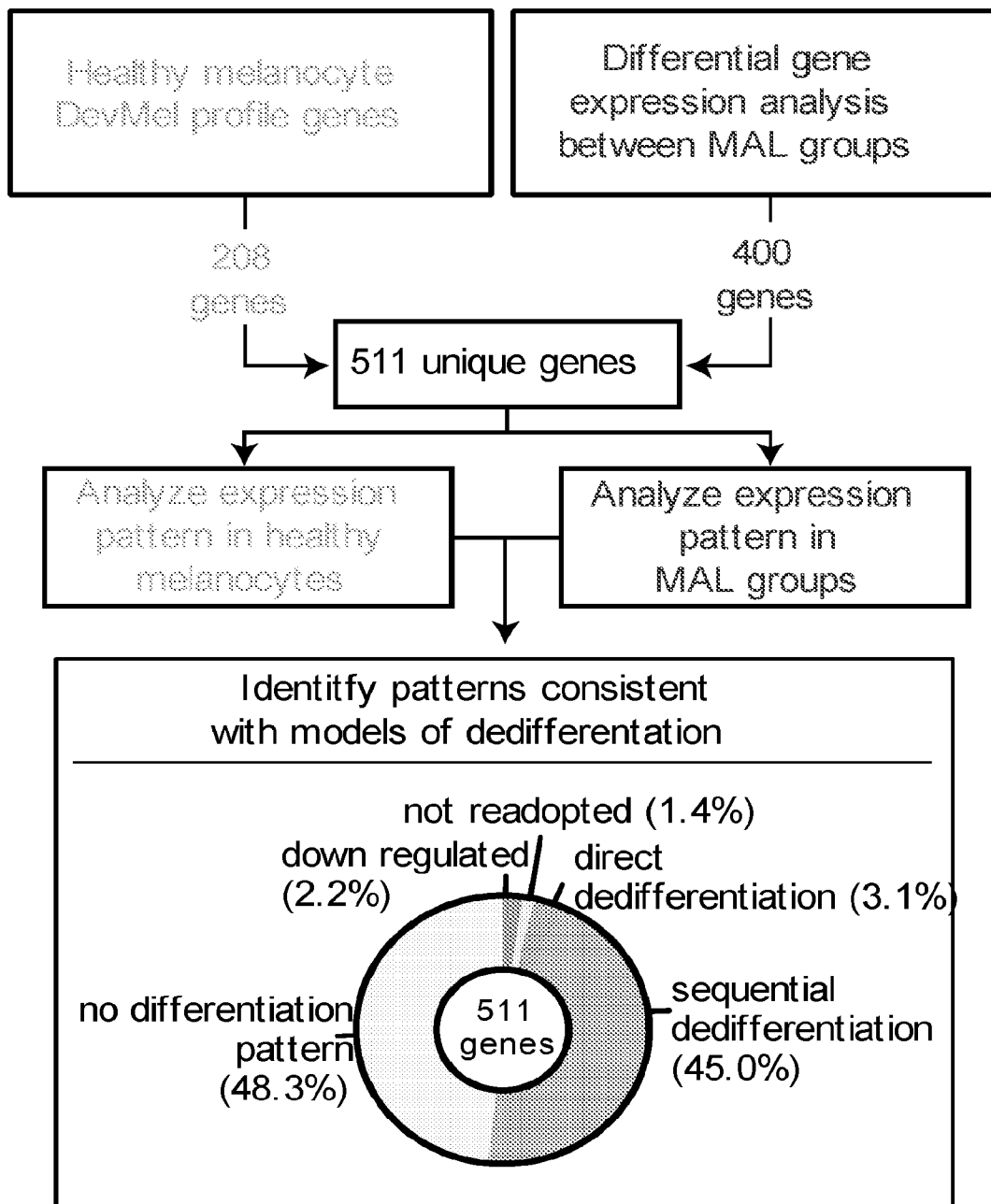


FIG. 6D

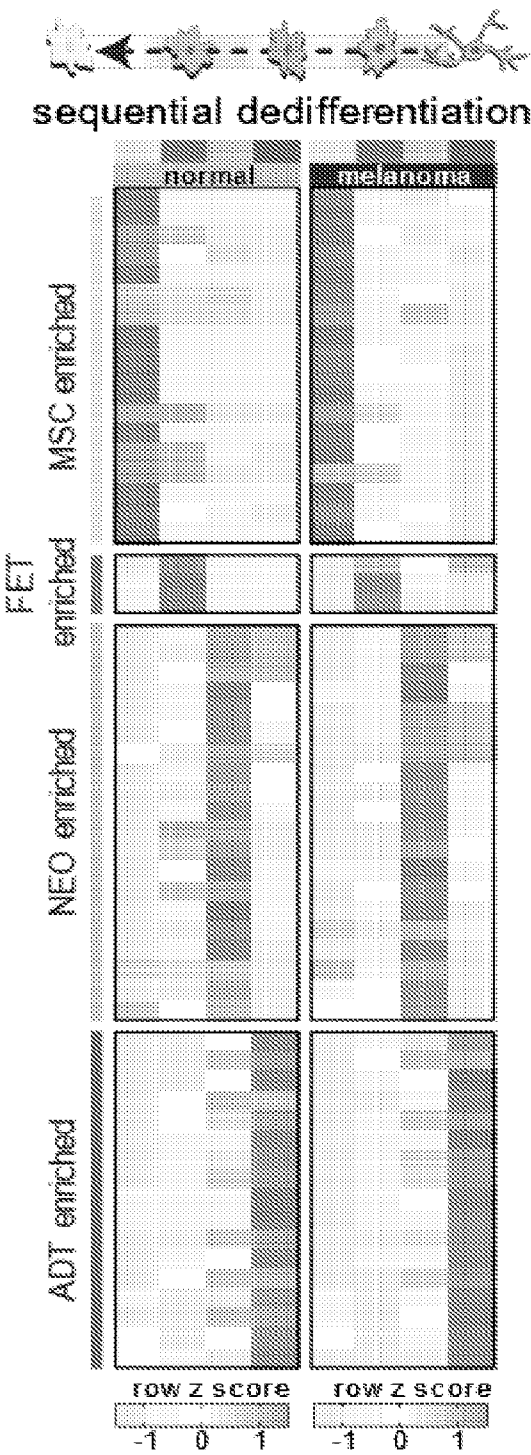


FIG.6E

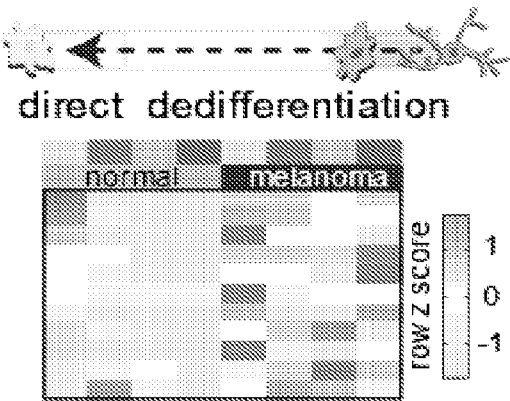


FIG. 6F

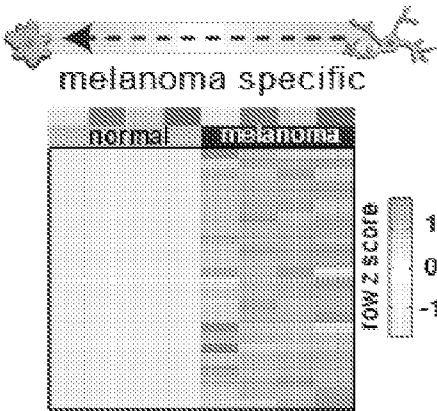


FIG. 6G

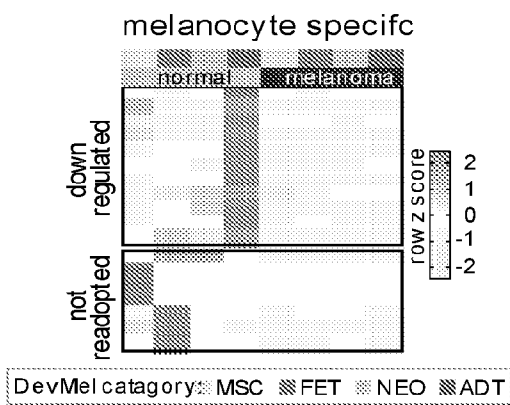


FIG. 7A

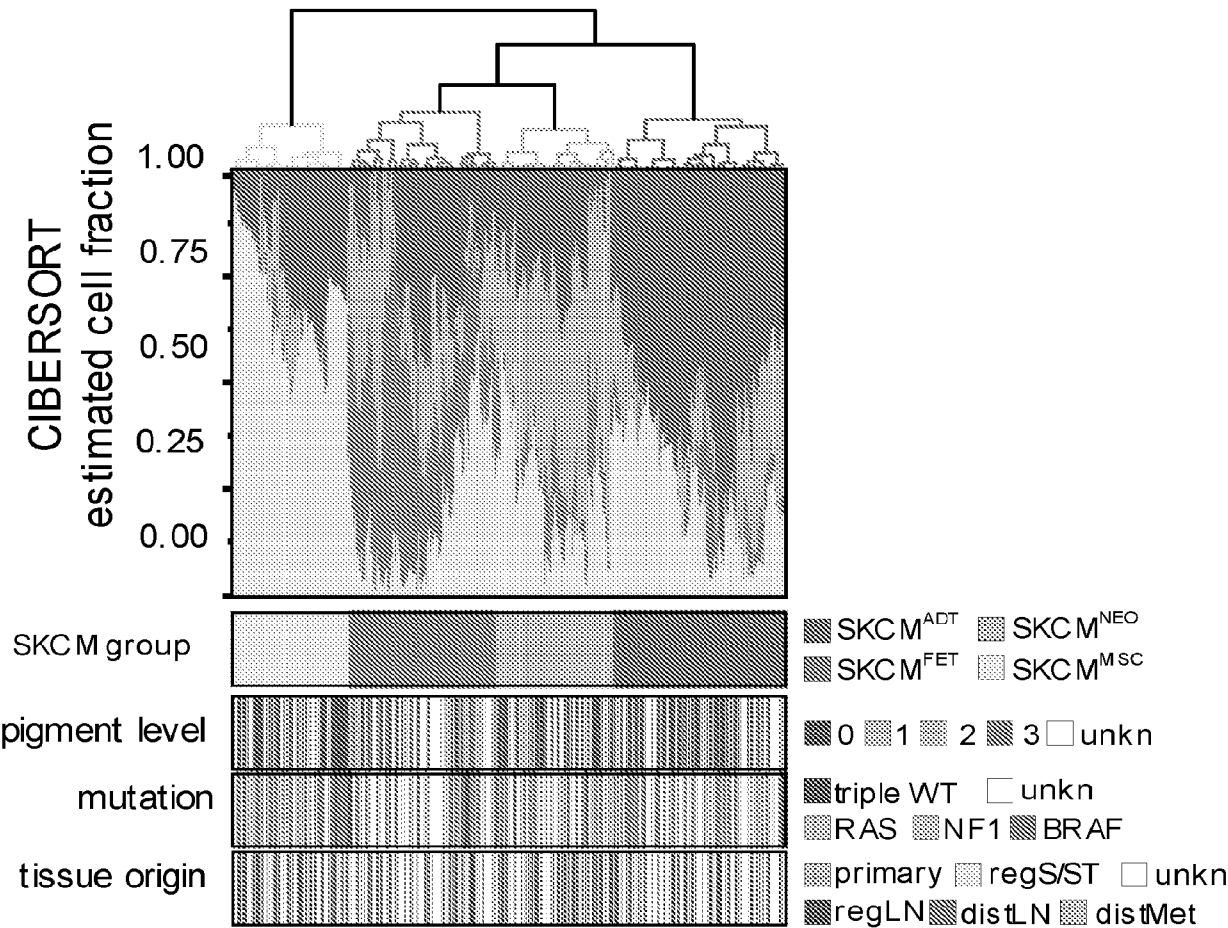


FIG. 7B

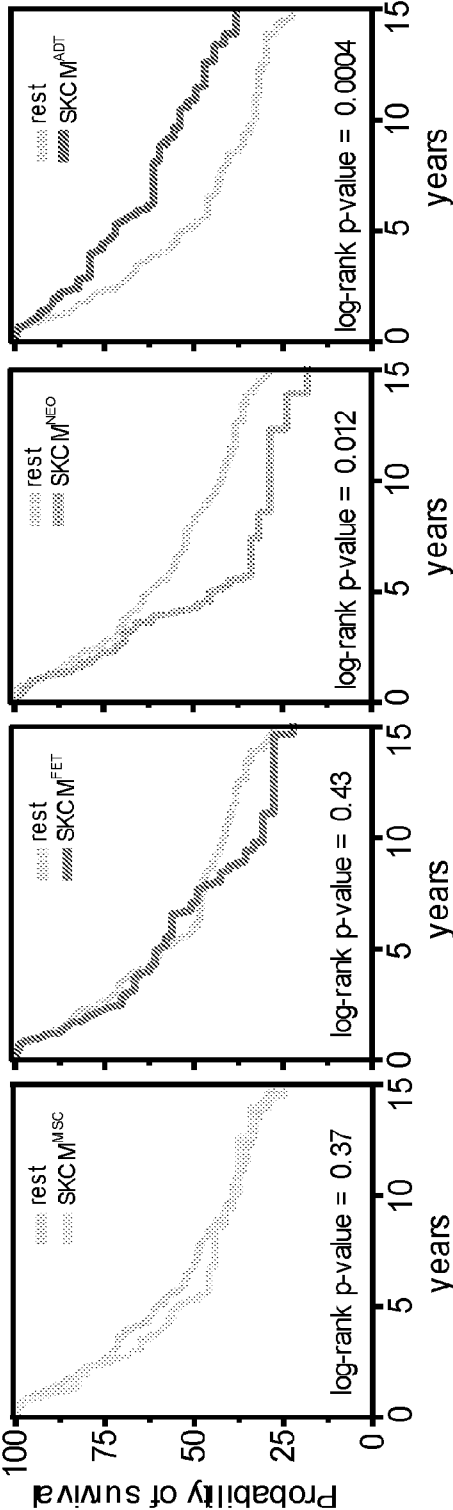


FIG. 7C

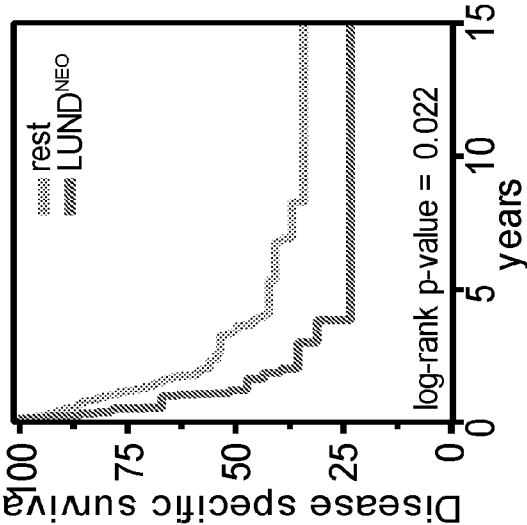


FIG. 7D

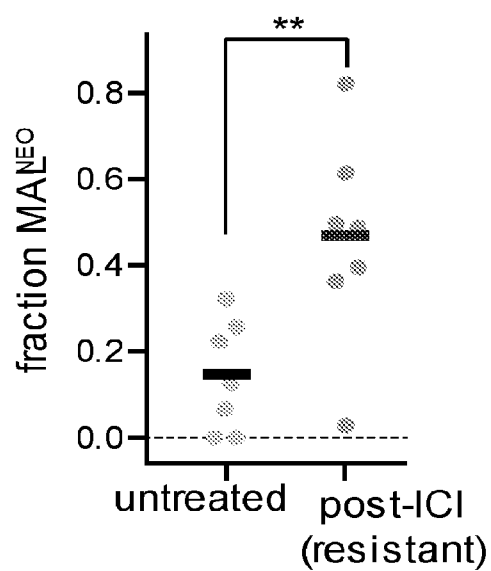


FIG. 7E

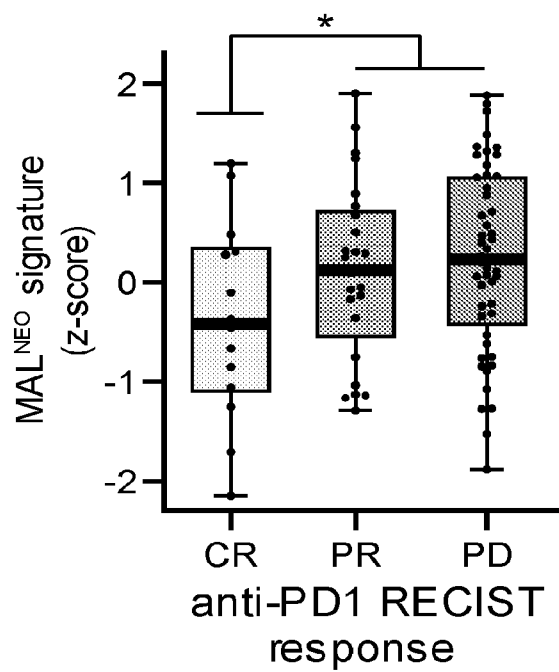


FIG. 7F

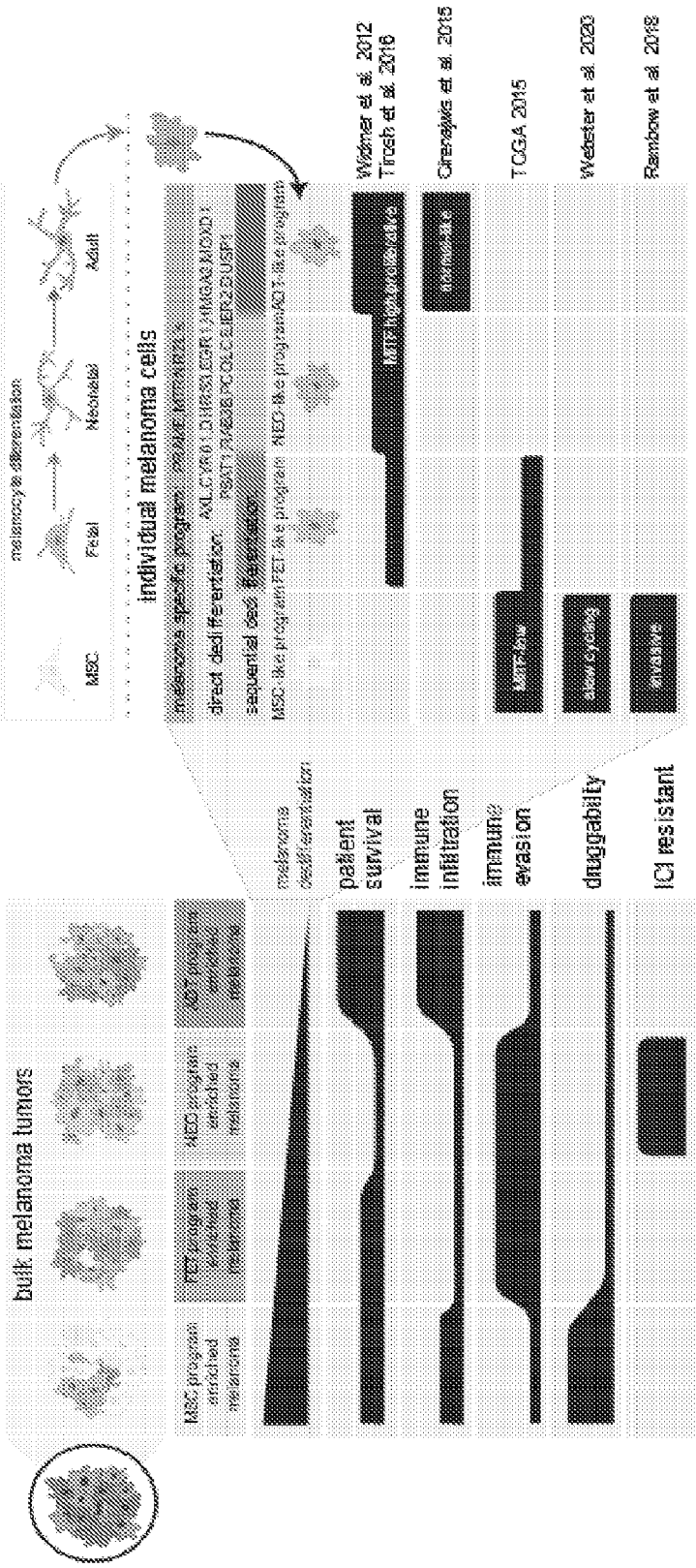


FIG. 8A

invasive - proliferative

(Widmer et al., 2012)

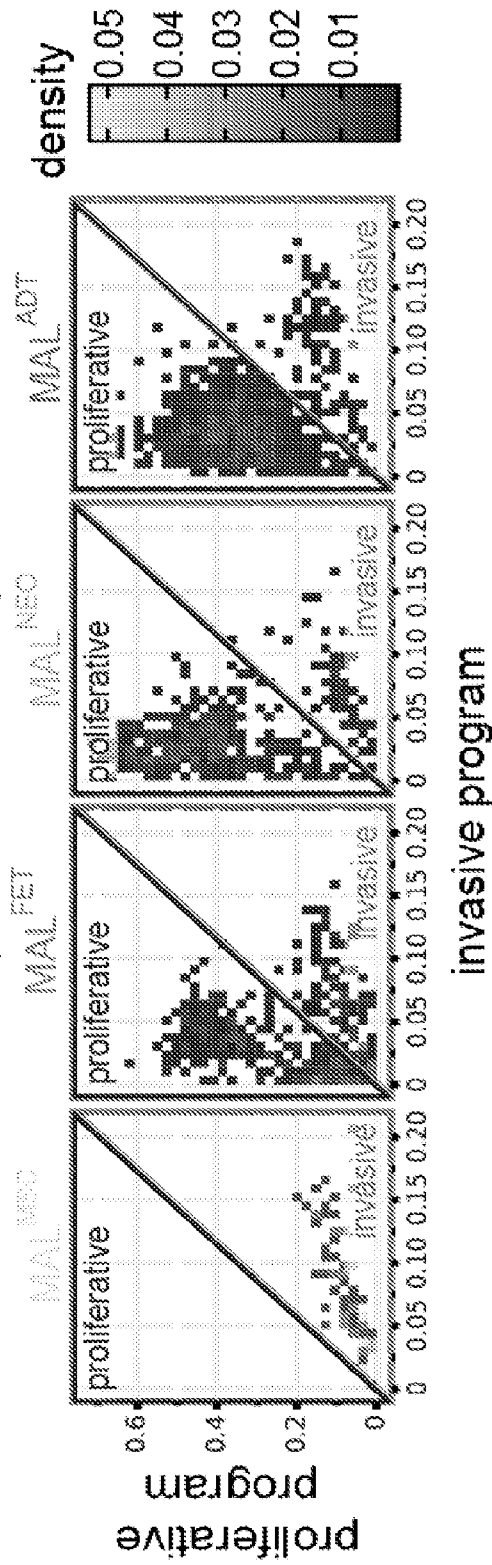


FIG. 8B

AXL - MITF

(Tirosh et al., 2016)

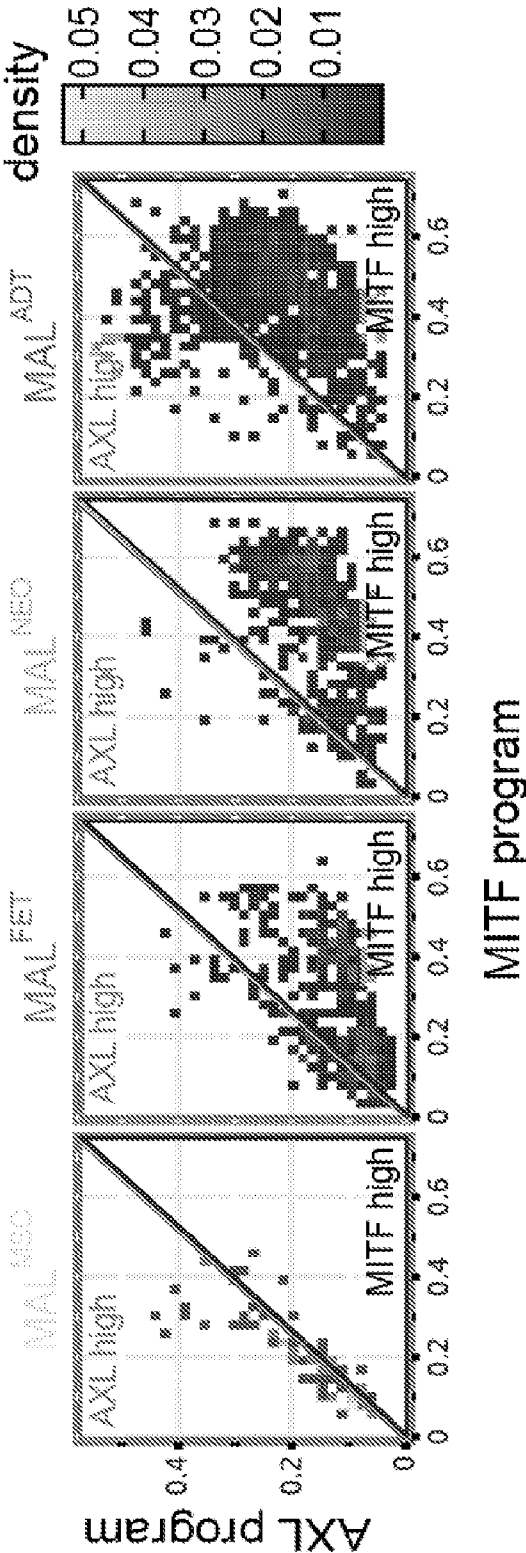
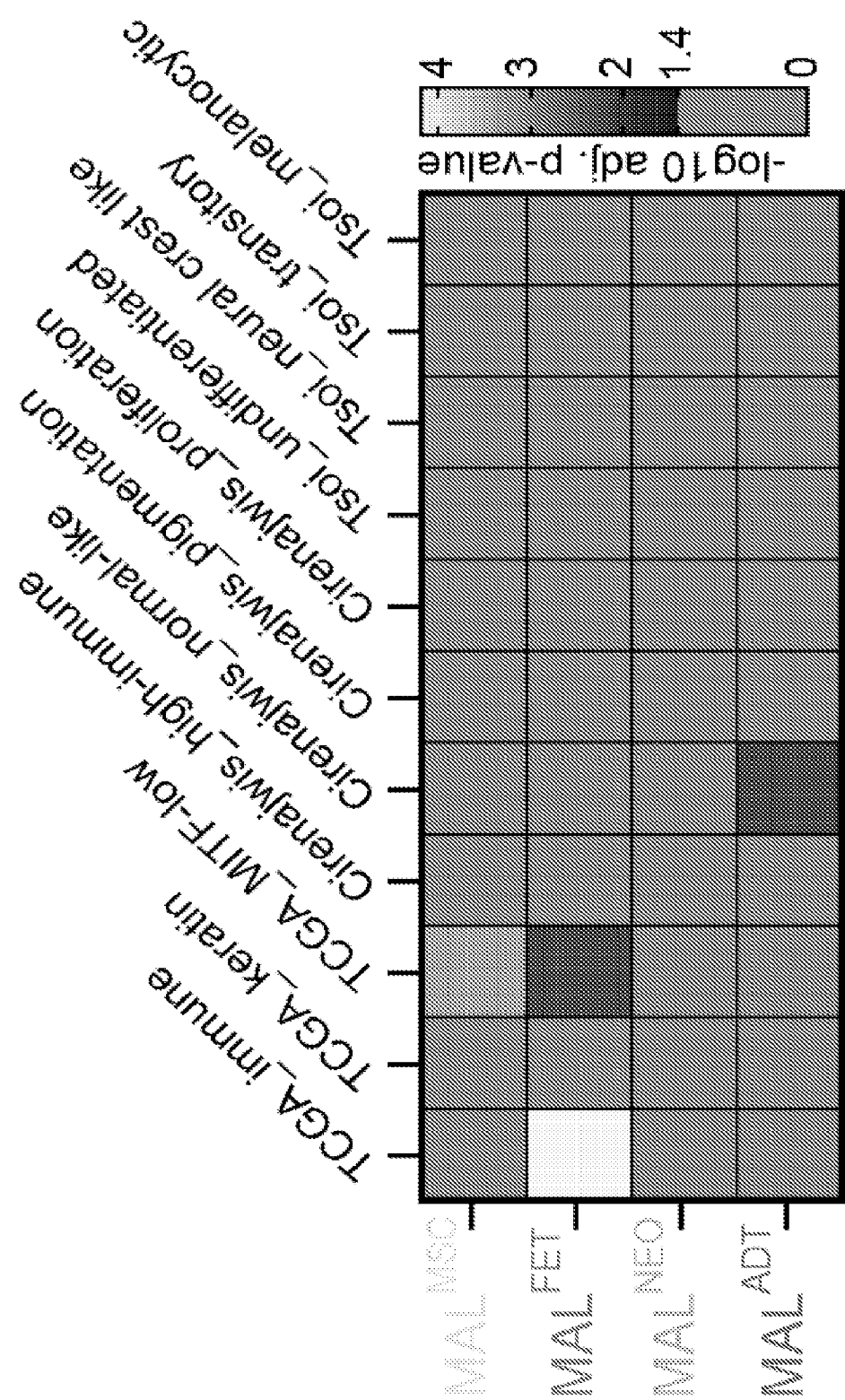


FIG. 8C



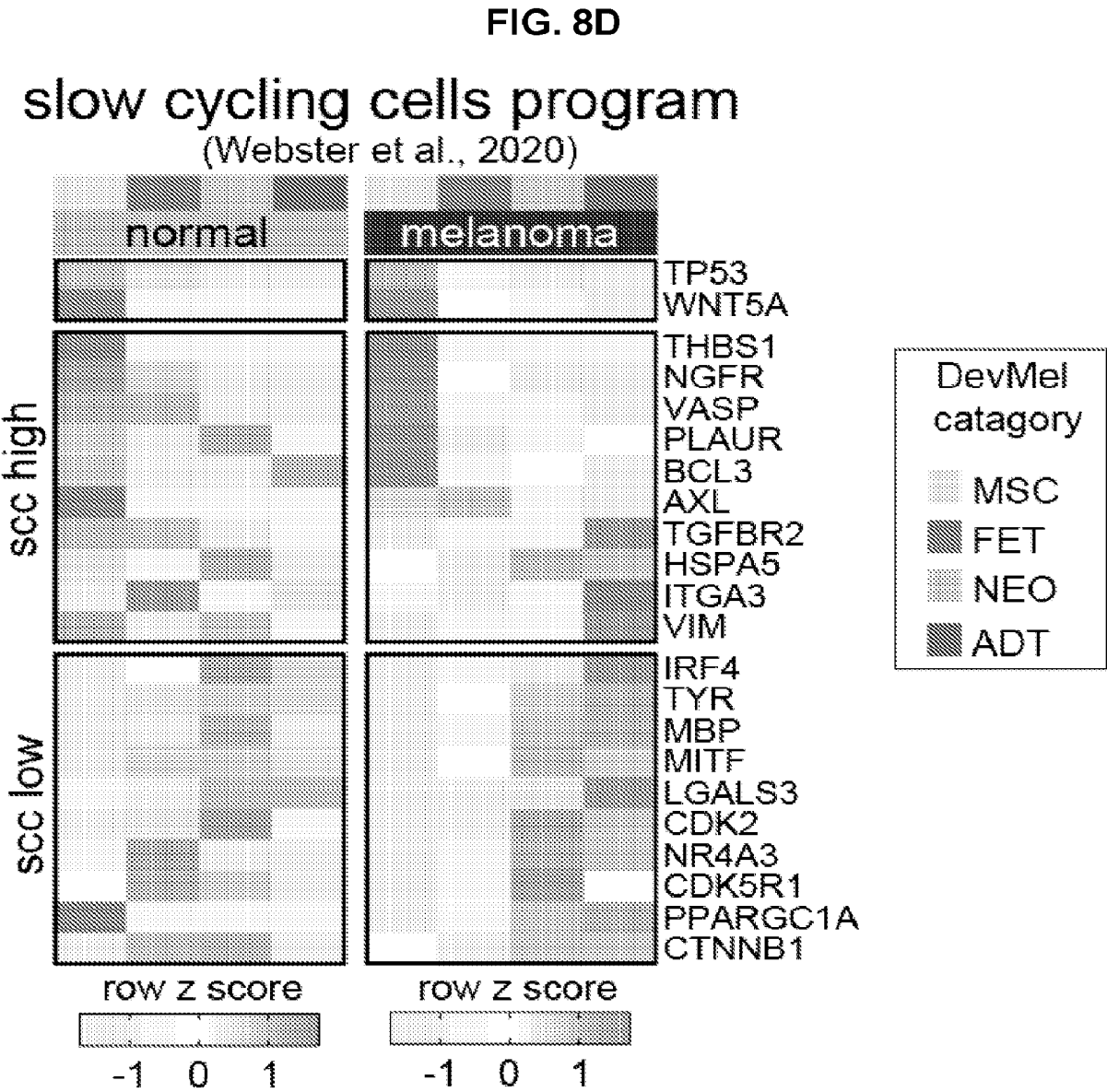


FIG. 8E

minimal residual disease states
(Rambow et al., 2018)

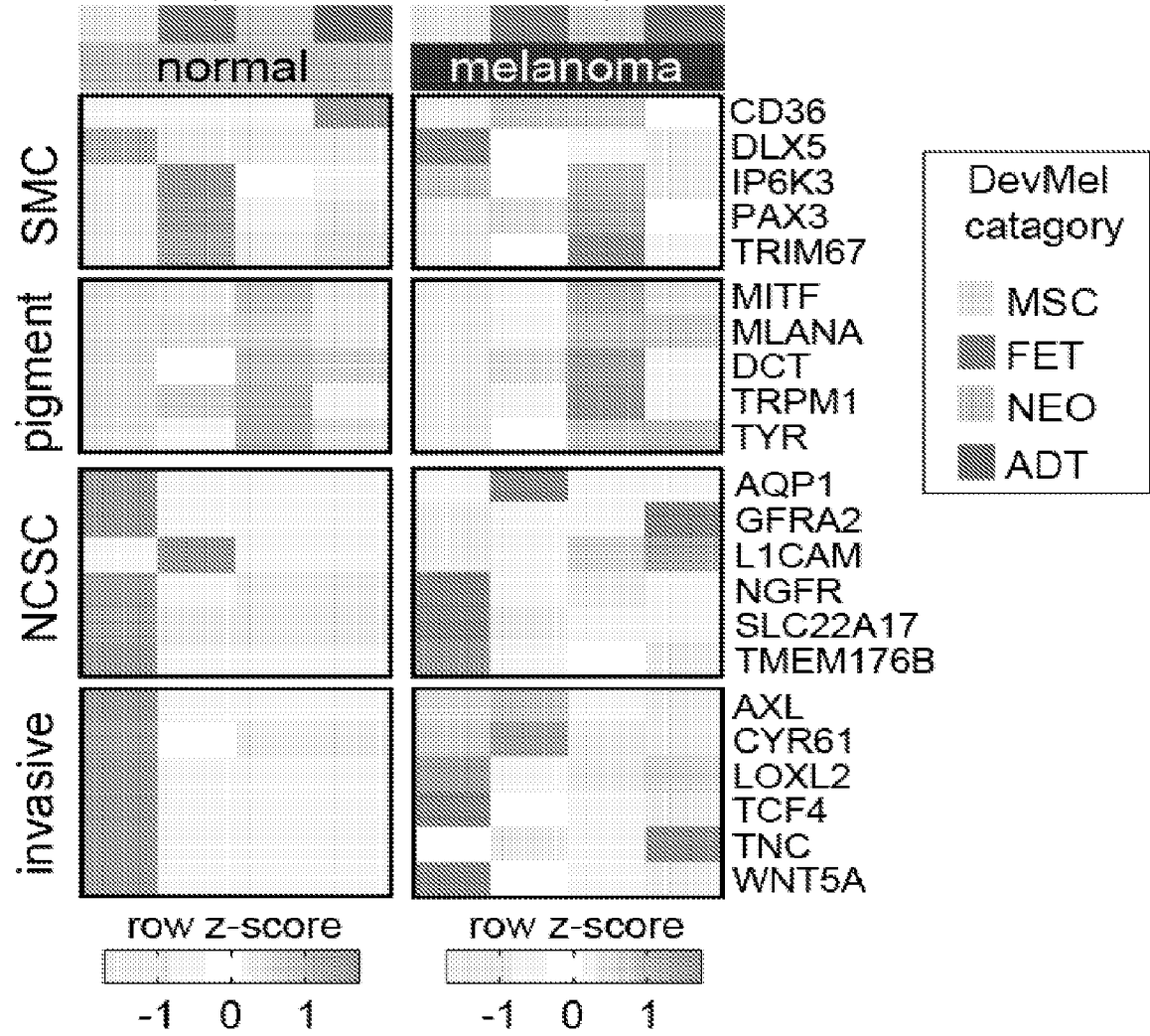


FIG. 8F

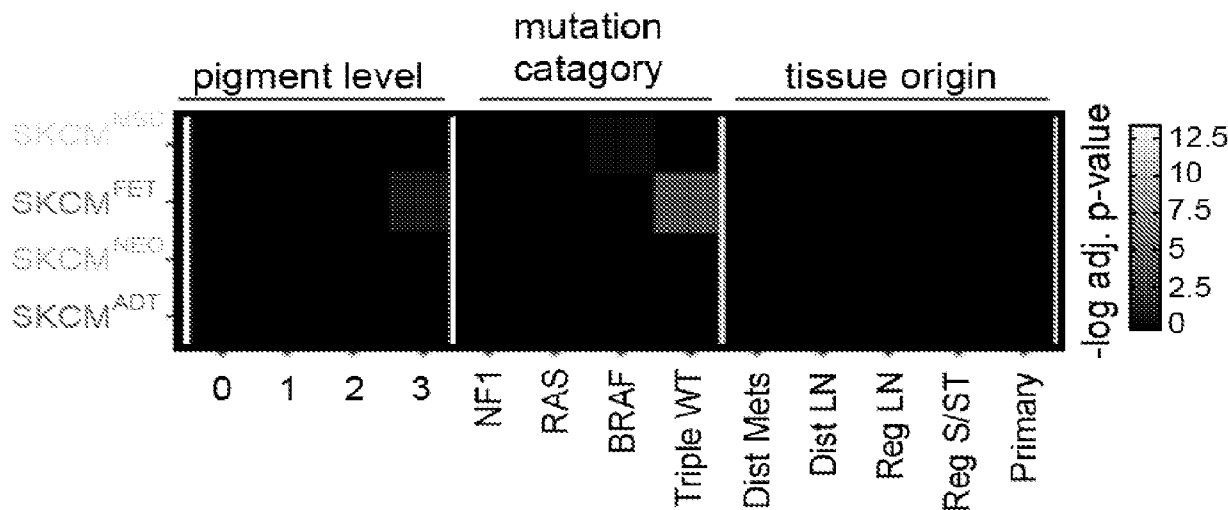


FIG. 8G

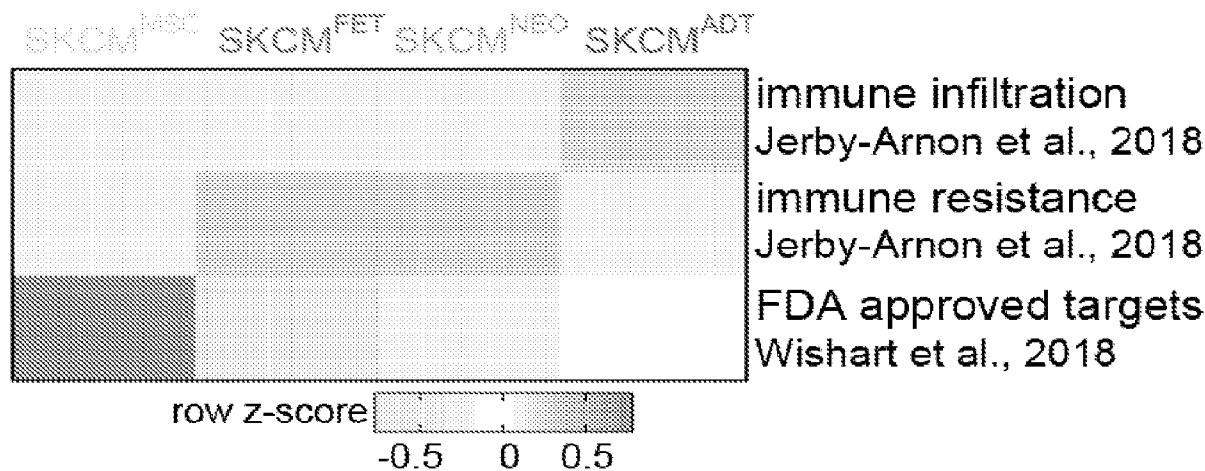


FIG. 9

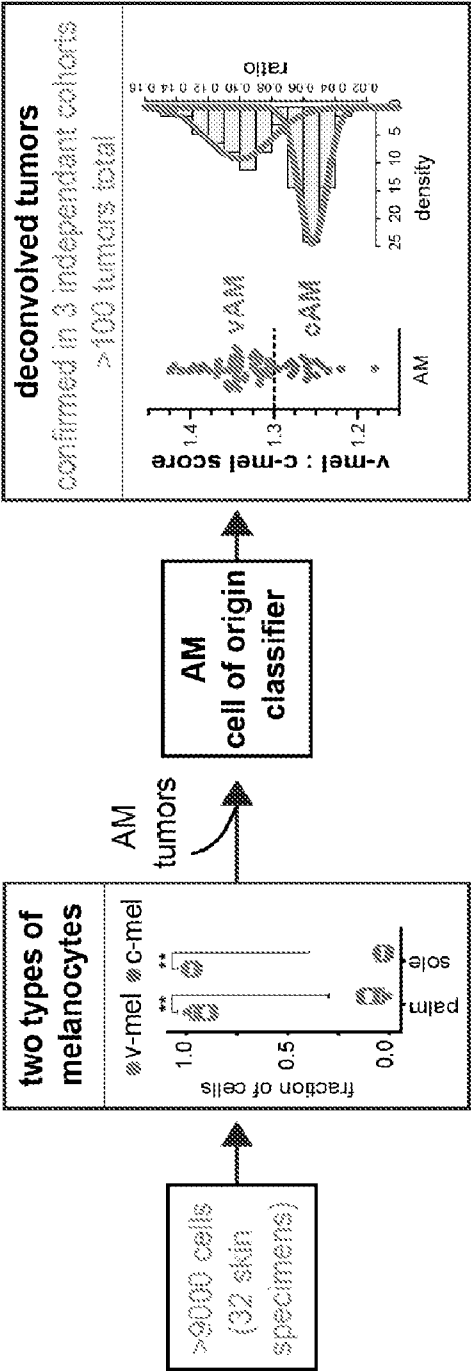


FIG. 10

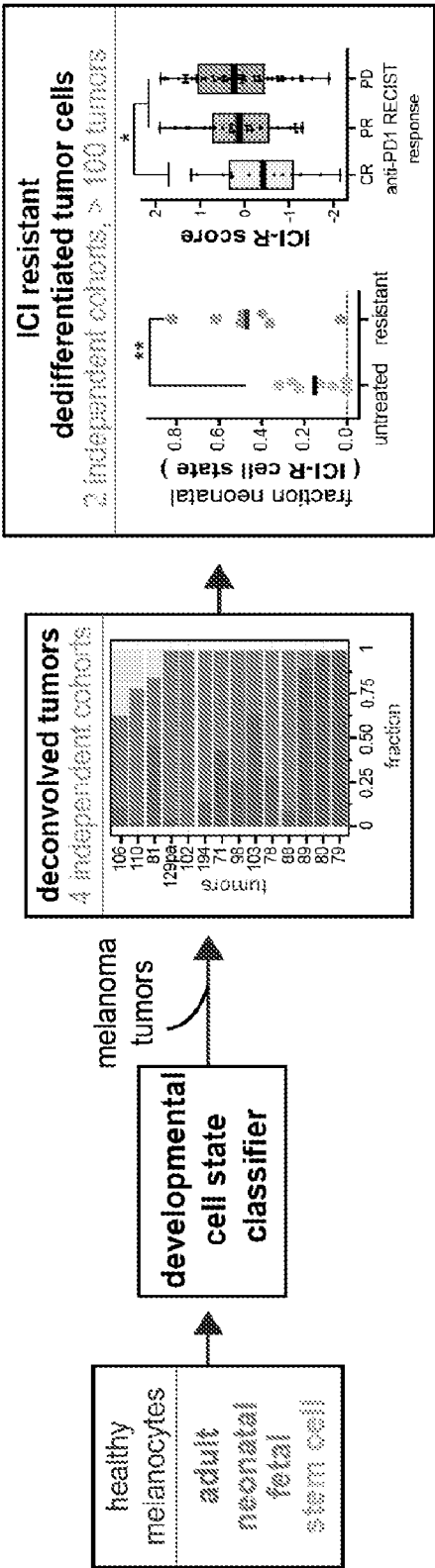


FIG. 11A

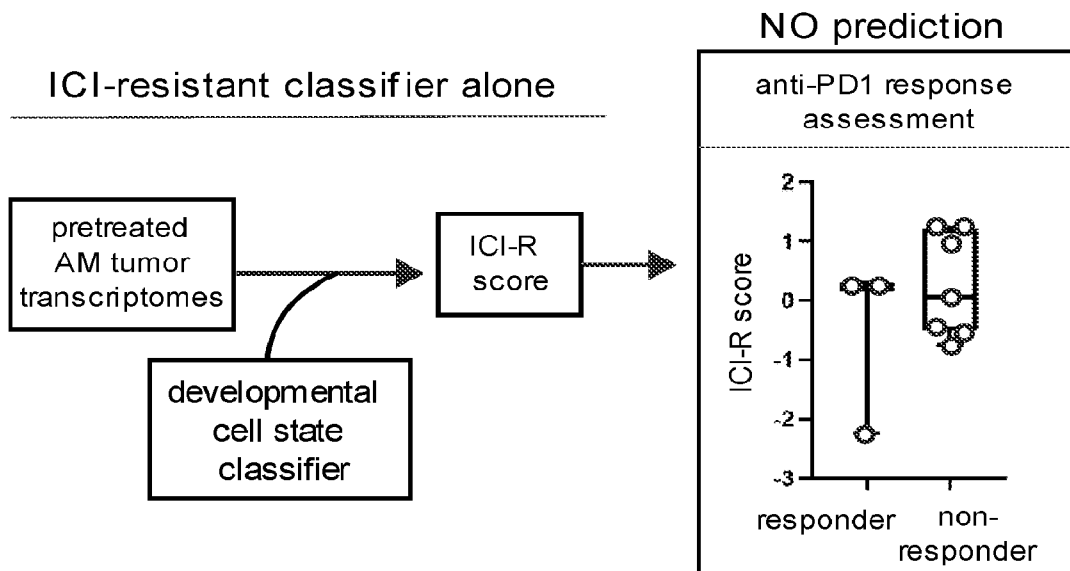


FIG. 11B

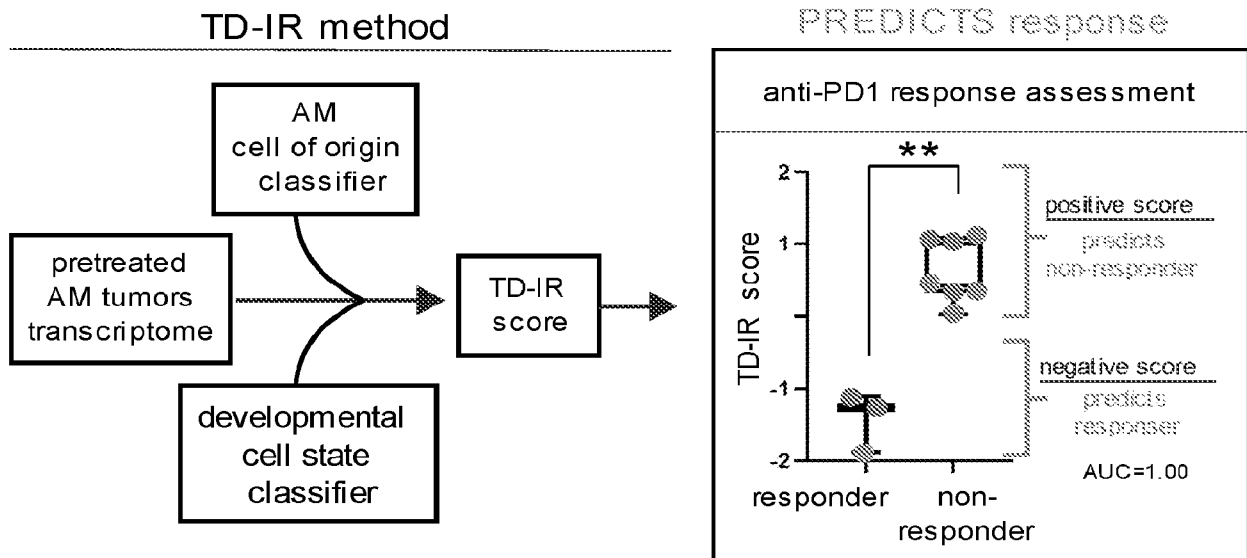
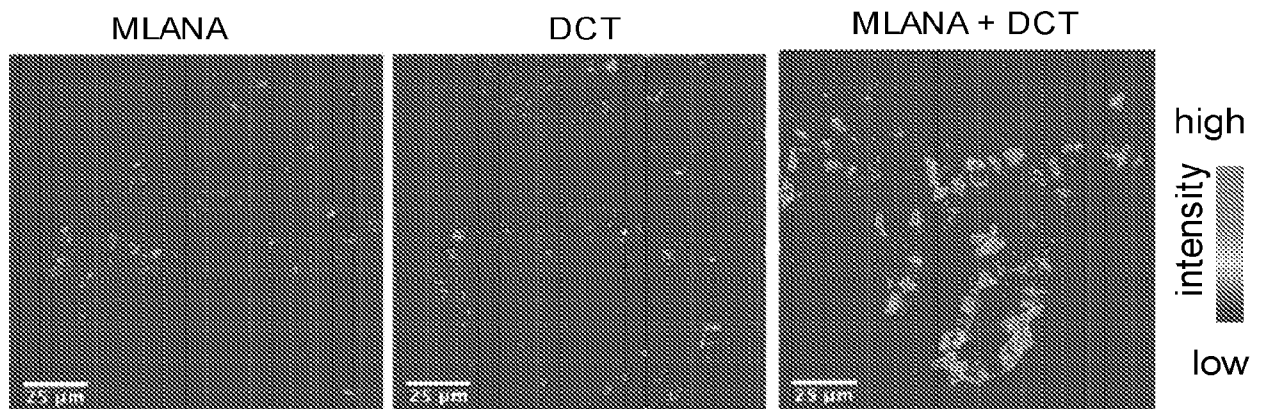


FIG. 12A**FIG. 12B**

4 cocktails RNAscope stain

color 1- vAM: (NTRK2, EGFR, NOTCH2)

color 2- cAM: (NDUFA3, CYC1, NDUFA7)

color 3- ICI-R: (SERPINF1, RAB38, TRPM1, FAM174B, CA14, TMC6)

color 4- pan-melanoma: (PRAME, MFAP4, DCT, MLANA, GPC3, S)

FIG. 13