

**Supplementary Table S1.** Pathways shared between all patient groups in the MEN1 pituitary analysis. P-values for the pathway in each group are stated. Genes with non-neutral variants for each patient group are listed. Genes that repeatedly contributed to the identification of pathways are mentioned on a shaded background. In brackets, the frequencies of variant alleles [GnomAD, non-Finnish European population] identified in the genes are presented.

Pathway - identifier			
	Family A	Patient X5	Patient X15
Alzheimer's disease - WP5124			
	P=0.0335	P=0.0671	P=0.1524
	<i>KIF5C</i> (0.0018)	<i>APOE</i> (0.0767)	<i>CACNA1F</i> (0.0247)
	<i>LRP1</i> (unknown)	<i>ATP2A3</i> (0.0020)	<i>CACNA1S</i> (0.1294)
		<i>LRP5</i> (0.0522)	
		<i>CACNA1S</i> (0.1294, 3.52E-5, 0.0502)	
Brain-Derived Neurotrophic Factor (BDNF) signaling pathway - WP2380			
	P=0.1453	P=0.2016	P=0.5212
	<i>NGF</i> (5.74E-4)	<i>ACACB</i> (0.0631)	<i>DLG1</i> (0.0514)
Burn wound healing - WP5055			
	P=1.97E-4	P=0.0219	P=0.0159
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)
	<i>MMP1</i> (3.88E-5)		<i>TNC</i> (2.56E-3)
Ciliary landscape - WP4352			
	P=0.2057	P=0.3434	P=0.0232
	<i>USH1C</i> (0.000*)	<i>CDH23</i> (6.41E-4)	<i>EXOC2</i> (0.1016)
			<i>LZTFL1</i> (0.0830)
*detected only in the Latino/Admixed American population			
Development of ureteric collection system - WP5053			
	P=0.0622	P=2.36E-5	P=1.31E-5
	<i>FREM2</i> (0.0499)	<i>FRAS1</i> (0.0201)	<i>BMPRI1A</i> (8.79E-6)
		<i>FREM1</i> (0.2456)	<i>FREM1</i> (0.2456)
		<i>GPC3</i> (unknown)	<i>GLI3</i> (0.0502)
		<i>PBX1</i> (0.2192)	<i>PBX1</i> (0.2192)
DNA IR-damage and cellular response via ATR - WP4016			
	P=0.0845	P=0.3740	P=0.0644
	<i>FANCI</i> (1.08E-3)	<i>FANCA</i> (3.88E-3)	<i>FANCI</i> (0.0833)
			<i>HERC2</i> (5.06E-3)
DNA repair pathways, full network - WP4946			
	P=0.1207	P=0.0311	P=0.1217
	<i>FANCI</i> (1.08E-3)	<i>FANCA</i> (3.88E-3)	<i>FANCI</i> (0.0833)
		<i>PARP2</i> (0.0247)	<i>POLL</i> (0.2233)
		<i>POLE</i> (0.0144)	
Focal Adhesion - WP306			

	P=0.1934	P=2.06E-5	P=8.46E-6	
	<i>COL1A1</i> (5.06E-3)	<i>FLNB</i> (0.2467, 0.2472)	<i>COL4A4</i> (0.4798)	
		<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)	
		<i>LAMC2</i> (0.0868)	<i>LAMA1</i> (6.25E-3)	
		<i>MET</i> (0.0118)	<i>LAMC2</i> (0.0868)	
		<i>THBS1</i> (8.28E-4)	<i>MET</i> (0.0118)	
		<i>TLN2</i> (4.12E-3)	<i>RELN</i> (0.0160)	
			<i>TNC</i> (2.56E-3)	
Focal Adhesion-PI3K-Akt-mTOR-signaling pathway - WP3932				
	P=0.0420	P=3.70E-4	P=4.53E-7	
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>COL4A4</i> (0.4798)	
	<i>NGF</i> (5.74E-4)	<i>LAMC2</i> (0.0868)	<i>FN1</i> (3.10E-5)	
		<i>MET</i> (0.0118)	<i>HIF1A</i> (0.1049)	
		<i>TBC1D1</i> (0.0133)	<i>LAMA1</i> (6.25E-3)	
		<i>THBS1</i> (8.28E-4)	<i>LAMC2</i> (0.0868)	
			<i>MET</i> (0.0118)	
			<i>RELN</i> (0.0160)	
			<i>TNC</i> (2.56E-3)	
Hepatitis C and Hepatocellular Carcinoma - WP3646				
	P=0.0530	P=0.2510	P=0.2254	
	<i>MMP1</i> (3.88E-5)	<i>CXCR1</i> (7.38E-4)	<i>HIF1A</i> (0.1049)	
Hypothesized Pathways in Pathogenesis of Cardiovascular Disease - WP3668				
	P=0.0269	P=0.1345	P=0.1199	
	<i>LTBP1</i> (0.0184)	<i>FBN2</i> (1.68E-3)	<i>FBN2</i> (3.15E-3)	
IL-18 signaling pathway - WP4754				
	P=0.0033	P=0.0217	P=0.4074	
	<i>COL1A1</i> (5.06E-3)	<i>ACACB</i> (0.0631)	<i>FN1</i> (3.10E-5)	
	<i>MMP1</i> (3.88E-5)	<i>ACADS</i> (0.0442)		
	<i>PTPRZ1</i> (6.48E-5)	<i>FN1</i> (4.34E-3)		
		<i>HADH</i> (8.16E-3)		
Inflammatory Response Pathway - WP453				
	P=0.0332	P=2.99E-5	P=5.27E-4	
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)	
		<i>LAMC2</i> (0.0868)	<i>LAMC2</i> (0.0868)	
		<i>THBS1</i> (8.28E-4)		
Malignant_pleural_mesothelioma - WP5087				
	P=0.0765	P=0.0032	P=1.94E-6	
	<i>NGF</i> (5.74E-4)	<i>COL4A3</i> (0.4822)	<i>CDH20</i> (0.1372)	
	<i>SOST</i> (1.40E-4)	<i>EZH2</i> (0.0798)	<i>COL4A3</i> (0.4822)	
		<i>FN1</i> (4.34E-3)	<i>COL4A4</i> (0.4798)	
		<i>LAMC2</i> (0.0868)	<i>FN1</i> (3.10E-5)	
		<i>LRP5</i> (0.0522)	<i>HIF1A</i> (0.1049)	

		<i>MET</i> (0.0118)	<i>LAMA1</i> (6.25E-3)
		<i>SELE</i> (0.1051)	<i>LAMC2</i> (0.0868)
			<i>MET</i> (0.0118)
			<i>TERT</i> (0.0301)
MAPK Signaling Pathway - WP382			
	P=0.2364	P=0.1712	P=0.3587
	<i>NGF</i> (5.74E-4)	<i>CACNA1S</i> (0.1294, 3.52E-5, 0.0502)	<i>CACNA1F</i> (0.0247)
		<i>FLNB</i> (0.2467, 0.2472)	<i>CACNA1S</i> (0.1294)
		<i>HSPA1L</i> (0.000*)	
*detected only in the Asian population			
Metapathway biotransformation Phase I and II - WP702			
	P=0.1836	P=1.36E-5	P=0.0154
	<i>CHST12</i> (8.94E-6)	<i>CHST5</i> (0.2044)	<i>AKR7A2</i> (0.0915)
		<i>CYP27A1</i> (0.0224)	<i>EPHX2</i> (0.0991)
		<i>CYP2C18</i> (0.1461)	<i>FMO2</i> (0.0869)
		<i>CYP4F2</i> (0.2866)	<i>GSTO2</i> (3.10E-4)
		<i>EPHX2</i> (0.0991)	
		<i>FMO2</i> (0.0869)	
		<i>FMO5</i> (0.0109)	
		<i>MGST1</i> (1.64E-4)	
miR-509-3p alteration of YAP1/ECM axis - WP3967			
	P=0.0194	P=0.0988	P=0.0878
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)
Nanoparticle-mediated activation of receptor signaling - WP2643			
	P=0.0300	P=0.1494	P=0.1333
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)
Nephrotic syndrome - WP4758			
	P=0.0489	P=0.0290	P=0.0231
	<i>ARHGAP24</i> (2.64E-5)	<i>COL4A3</i> (0.4822)	<i>COL4A3</i> (0.4822)
		<i>CUBN</i> (0.0384)	<i>COL4A4</i> (0.4798)
Neural Crest Differentiation - WP2064			
	P=0.1032	P=0.4392	P=0.0925
	<i>GFAP</i> (8.34E-3)	<i>GFAP</i> (0.0296)	<i>NOTCH3</i> (0.0168)
Neuroinflammation and glutamatergic signaling - WP5083			
	P=0.0102	P=0.1932	P=0.0351
	<i>GFAP</i> (8.34E-3)	<i>DLAT</i> (0.3569)	<i>SHMT1</i> (1.20E-3)
	<i>NGF</i> (5.74E-4)	<i>GFAP</i> (0.0296)	
Pathways in clear cell renal cell carcinoma - WP4018			
	P=0.0875	P=0.0847	P=9.17E-4
	<i>GPI</i> (0.0215)	<i>ACACB</i> (0.0631)	<i>HIF1A</i> (0.1049)

		<i>ZEB1</i> (3.32E-3)	<i>PGM1</i> (0.1898)	
			<i>SHMT1</i> (1.20E-3)	
PI3K-Akt Signaling Pathway - WP4172				
	P=0.0518	P=1.59E-4	P=2.23E-8	
	<i>COL1A1</i> (5.06E-3)	<i>COL4A3</i> (0.4822)	<i>COL4A3</i> (0.4822)	
	<i>NGF</i> (5.74E-4)	<i>COL6A3</i> (0.0883)	<i>COL4A4</i> (0.4798)	
		<i>FN1</i> (4.34E-3)	<i>COL6A3</i> (0.0883)	
		<i>LAMC2</i> (0.0868)	<i>COL9A2</i> (3.87E-3)	
		<i>MET</i> (0.0118)	<i>FN1</i> (3.10E-5)	
		<i>PCK1</i> (0.1216)	<i>G6PC2</i> (8.59E-3)	
		<i>THBS1</i> (8.28E-4)	<i>LAMA1</i> (6.25E-3)	
			<i>LAMC2</i> (0.0868)	
			<i>MET</i> (0.0118)	
			<i>RELN</i> (0.0160)	
			<i>TNC</i> (2.56E-3)	
PPAR signaling pathway - WP3942				
	P=0.0714	P=0.0072	P=0.2935	
	<i>MMP1</i> (3.88E-5)	<i>APOA5</i> (0.0637)	<i>ACADL</i> (0.0307)	
		<i>CYP27A1</i> (0.0224)		
		<i>PCK1</i> (0.1216)		
Prader-Willi and Angelman syndrome - WP3998				
	P=0.0704	P=0.0572	P=0.0049	
	<i>NGF</i> (5.74E-4)	<i>CDC6</i> (0.0604)	<i>HERC2</i> (5.06E-3)	
		<i>KISS1</i> (0.0379)	<i>OCA2</i> (0.0650)	
Senescence and Autophagy in Cancer - WP615				
	P=0.1101	P=0.1268	P=0.4214	
	<i>COL1A1</i> (5.06E-3)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)	
		<i>THBS1</i> (8.28E-4)		
Statin inhibition of cholesterol production - WP430				
	P=0.0311	P=6.17E-4	P=0.1377	
	<i>LRP1</i> (unknown)	<i>APOA5</i> (0.0637)	<i>APOB</i> (0.2156)	
		<i>APOE</i> (0.0767)		
		<i>LCAT</i> (0.0284)		
Sudden Infant Death Syndrome (SIDS) Susceptibility Pathways - WP706				
	P=0.1656	P=0.2481	P=0.2074	
	<i>NGF</i> (5.74E-4)	<i>CHAT</i> (0.0650)	<i>HIF1A</i> (0.1049)	
		<i>PBX1</i> (0.2192)	<i>PBX1</i> (0.2192)	
TGF-beta Signaling Pathway - WP366				
	P=0.1340	P=0.0073	P=0.0048	
	<i>MMP1</i> (3.88E-5)	<i>FN1</i> (4.34E-3)	<i>FN1</i> (3.10E-5)	
		<i>MET</i> (0.0118)	<i>MET</i> (0.0118)	
		<i>THBS1</i> (8.28E-4)	<i>TERT</i> (0.0301)	
		<i>ZEB1</i> (3.32E-3)	<i>TNC</i> (2.56E-3)	

VEGFA-VEGFR2 signaling pathway - WP3888				
	P=0.3781		P=0.1072	
	<i>PTPRZ1</i>	(6.48E-5)	<i>ACACB</i>	(0.0631)
			<i>FLNB</i>	(0.2467, 0.2472)
			<i>FN1</i>	(4.34E-3)
			<i>SELE</i>	(0.1051)
	P=0.1814		<i>FN1</i>	(3.10E-5)
			<i>TKT</i>	(7.45E-3)
			<i>TRAF3IP2</i>	(1.22E-3)

**Supplementary Table S2.** Pathways shared between all patient groups in the MEN1 adrenal analysis. P-values for the pathway in each group are stated. Genes with non-neutral variants for each patient group are listed. Genes that repeatedly contributed to the identification of pathways are mentioned on a shaded background. In brackets, the frequencies of variant alleles [GnomAD, non-Finnish European population] identified in the genes are presented.

Pathway – identifier				
	Family A	Family C	Patient X11	Patient X15
Selenium micronutrient network - WP15				
	P= 0.1513	P= 0.1657	P= 0.3389	P= 0.3188
	<i>APOB</i> (0.0350)	<i>SELP</i> (0.000*)	<i>TXNRD2</i> (0.3430)	<i>TXNRD2</i> (0.3430)
		<i>TXNRD2</i> (0.3430)		
* identified only in the African/African American population				
MicroRNAs in cardiomyocyte hypertrophy - WP1544				
	P= 0.1594	P= 0.1744	P= 0.0097	P= 0.3339
	<i>NRG1</i> (2.32E-5)	<i>NRG1</i> (0.0441)	<i>FZD1</i> (1.30E-4)	<i>NRG1</i> (0.0208)
Neural crest differentiation - WP2064				
	P= 0.0157	P= 0.1899	P= 0.3821	P= 0.0735
	<i>MPZ</i> (0.0316)	<i>COL11A2</i> (1.09E-4)	<i>TCF7L1</i> (0.0595)	<i>NOTCH3</i> (0.0168)
	<i>NOTCH3</i> (6.62E-5)			
Arrhythmogenic right ventricular cardiomyopathy - WP2118				
	P= 0.0088	P= 0.1443	P=4.54E-4	P= 0.0045
	<i>CACNB2</i> (0.1800)	<i>DSP</i> (1.77E-3)	<i>ACTN2</i> (8.21E-4)	<i>ACTN2</i> (3.26E-4)
	<i>ITGB4</i> (2.25E-4)		<i>CACNA1S</i> (8.79E-6)	<i>CACNA1F</i> (0.0247)
			<i>SGCG</i> (0.1305)	<i>SGCG</i> (0.1305)
			<i>TCF7L1</i> (0.0595)	
Primary focal segmental glomerulosclerosis FSGS - WP2572				
	P= 0.0084	P= 0.1407	P= 0.0051	P= 0.0411
	<i>DNM1</i> (4.86E-3)	<i>COL4A4</i> (0.0367)	<i>CR1</i> (0.0282)	<i>AGRN</i> (2.05E-3)
	<i>ITGB4</i> (2.25E-4)		<i>JAG1</i> (0.0673)	<i>COL4A4</i> (0.4798)
			<i>LAMA5</i> (0.0186, 0.0904)	
Cardiac Hypertrophic Response - WP2795				
	P= 0.0978	P= 0.1075	P= 0.2288	P= 0.2142
	<i>NRG1</i> (2.32E-5)	<i>NRG1</i> (0.0441)	<i>CDK7</i> (0.0245)	<i>NRG1</i> (0.0208)
Ectoderm differentiation - WP2858				
	P= 0.0290	P= 0.2539	P= 0.4880	P= 0.0035
	<i>SIX6</i> (4.88E-3)	<i>PTPRB</i> (unknown)	<i>TCF7L1</i> (0.0595)	<i>BMPR1A</i> (8.79E-6)
				<i>EDA2R</i> (8.99E-3)
				<i>GLI3</i> (0.0502)
				<i>ZFHX4</i> (7.37E-3)
Apoptosis-related network due to altered Notch3 in ovarian cancer - WP2864				
	P= 0.0961	P= 0.1056	P= 0.0021	P= 0.0234

	<i>NRG1</i> (2.32E-5)	<i>NRG1</i> (0.0441)	<i>ABL1</i> (7.61E-3)	<i>NRG1</i> (0.0208)
			<i>NQO1</i> (0.1886)	
			<i>TNFRSF10B</i> (0.0706)	
Vitamin D Receptor Pathway - WP2877				
	P= 0.2963	P= 0.3216	P= 0.0592	P= 0.1977
	<i>STEAP4</i> (0.1942)	<i>KNG1</i> (0.1109)	<i>KL</i> (0.1526)	<i>HIF1A</i> (0.1049)
			<i>NOX1</i> (0.0272)	<i>KNG1</i> (0.1109)
			<i>STEAP4</i> (0.1942)	
NRF2 pathway - WP2884				
	P= 0.0294	P= 0.0352	P= 0.0047	P= 0.4650
	<i>EPHA3</i> (1.87E-3)	<i>NRG1</i> (0.0441)	<i>NQO1</i> (0.1886)	<i>NRG1</i> (0.0208)
	<i>NRG1</i> (2.32E-5)	<i>SLC5A2</i> (1.55E-5)	<i>SLC2A6</i> (0.0872)	
			<i>SLC39A13</i> (3.65E-3)	
			<i>SLC39A4</i> (1.50E-3)	
miRNA targets in ECM and membrane receptors - WP2911				
	P= 0.0592	P= 0.0021	P= 0.1427	P= 0.1331
	<i>LAMA4</i> (0.0645)	<i>COL5A1</i> (1.04E-3)	<i>COL5A1</i> (0.0468)	<i>FN1</i> (3.10E-5)
		<i>COL6A2</i> (3.15E-5)		
Focal adhesion - WP306				
	P= 5.59E-4	P= 0.0084	P= 0.0153	P= 2.66E-4
	<i>ITGB4</i> (2.25E-4)	<i>COL4A4</i> (0.0367)	<i>FLNA</i> (3.97E-3)	<i>COL4A4</i> (0.4798)
	<i>LAMA4</i> (0.0645)	<i>COL6A2</i> (3.15E-5)	<i>FLNC</i> (9.68E-3)	<i>FN1</i> (3.10E-5)
	<i>THBS4</i> (0.2203)	<i>TNC</i> (7.08E-3)	<i>LAMA5</i> (0.0186, 0.0904)	<i>LAMA1</i> (0.0101)
			<i>RELN</i> (0.0158)	<i>RELN</i> (0.0160)
				<i>TNC</i> (2.56E-3)
TGF-beta signaling pathway - WP366				
	P= 0.2227	P= 0.0316	P= 0.4704	P= 0.0029
	<i>ITGB4</i> (2.25E-4)	<i>TGIF1</i> (0.0568)	<i>TRAP1</i> (0.1837)	<i>FN1</i> (3.10E-5)
		<i>TNC</i> (7.08E-3)		<i>TERT</i> (0.0301)
				<i>TNC</i> (2.56E-3)
				<i>TRAP1</i> (0.1837)
Striated muscle contraction - WP383				
	P= 0.0699	P= 0.0769	P= 0.0144	P= 6.52E-4
	<i>NEB</i> (3.59E-4)	<i>MYBPC1</i> (0.1563)	<i>ACTN2</i> (8.21E-4)	<i>ACTN2</i> (3.26E-4)
			<i>TTN</i> (4.96E-5)	<i>NEB</i> (0.3281)
				<i>TTN</i> (0.3075)
MYD88 distinct input-output pathway - WP3877				
	P= 0.0337	P= 0.0372	P= 0.0829	P= 0.0772
	<i>TLR10</i> (0.3691)	<i>TLR10</i> (0.3691)	<i>TLR10</i> (0.3691)	<i>TLR10</i> (0.3691)
VEGFA-VEGFR2 signaling pathway - WP3888				
	P= 0.2002	P= 0.2317	P= 0.0052	P= 0.3046

	<i>ACACB</i> (0.1943)	<i>TRAF3IP2</i> (0.0740)	<i>ABL1</i> (7.61E-3)	<i>FN1</i> (3.10E-5)
	<i>EPB41</i> (0.0492, 7.66E-3)		<i>BIN1</i> (0.0156)	<i>TKT</i> (7.45E-3)
			<i>JAG1</i> (0.0673)	<i>TRAF3IP2</i> (1.22E-3)
			<i>KL</i> (0.1526)	
			<i>NCF2</i> (0.0487)	
			<i>SCUBE2</i> (0.0777)	
			<i>TKT</i> (1.19E-3)	
Amino acid metabolism - WP3925				
	P= 0.1594	P= 0.1744	P= 0.3547	P= 0.0623
	<i>HDC</i> (0.0273)	<i>IDH1</i> (0.0136)	<i>FAH</i> (0.0234)	<i>G6PC2</i> (8.59E-3)
				<i>HDC</i> (0.0273)
Focal adhesion-PI3K-Akt-mTOR-signaling pathway - WP3932				
	P= 2.37E-5	P= 4.32E-4	P= 0.0150	P= 6.32E-5
	<i>HSP90B1</i> (0.0176)	<i>COL11A2</i> (1.09E-4)	<i>COL5A1</i> (0.0468)	<i>COL4A4</i> (0.4798)
	<i>ITGAE</i> (0.0533)	<i>COL4A4</i> (0.0367)	<i>LAMA5</i> (0.0186, 0.0904)	<i>FN1</i> (3.10E-5)
	<i>ITGB4</i> (2.25E-4)	<i>COL5A1</i> (1.04E-3)	<i>NGF</i> (0.0172)	<i>HIF1A</i> (0.1049)
	<i>LAMA4</i> (0.0645)	<i>COL6A2</i> (3.15E-5)	<i>RELN</i> (0.0158)	<i>LAMA1</i> (0.0101)
	<i>THBS4</i> (0.2203)	<i>TNC</i> (7.08E-3)		<i>RELN</i> (0.0160)
				<i>TNC</i> (2.56E-3)
TYROBP Causal Network - WP3945				
	P= 0.1081	P= 0.0071	P= 0.2507	P= 0.2349
	<i>TCIRG1</i> (0.0616)	<i>TCIRG1</i> (1.71E-4)	<i>NCF2</i> (0.0487)	<i>DPYD</i> (0.1018)
PI3K-Akt signaling pathway - WP4172				
	P= 4.65E-4	P= 0.0056	P= 0.0235	P= 2.18E-5
	<i>HSP90B1</i> (0.0176)	<i>COL4A4</i> (0.0367)	<i>LAMA5</i> (0.0186, 0.0904)	<i>COL4A4</i> (0.4798)
	<i>ITGB4</i> (2.25E-4)	<i>COL6A2</i> (3.15E-5)	<i>NGF</i> (0.0172)	<i>COL9A2</i> (3.87E-3)
	<i>LAMA4</i> (0.0645)	<i>TNC</i> (7.08E-3)	<i>RELN</i> (0.0158)	<i>FN1</i> (3.10E-5)
	<i>THBS4</i> (0.2203)			<i>G6PC2</i> (8.59E-3)
				<i>LAMA1</i> (0.0101)
				<i>RELN</i> (0.0160)
				<i>TNC</i> (2.56E-3)
EMT in colorectal cancer - WP4239				
	P= 0.2632	P= 0.0448	P= 0.1792	P= 7.76E-4
	<i>NOTCH3</i> (6.62E-5)	<i>COL4A4</i> (0.0367)	<i>FZD1</i> (1.30E-4)	<i>CLDN20</i> (0.0154)
		<i>DSP</i> (1.77E-3)	<i>JAG1</i> (0.0673)	<i>COL4A4</i> (0.4798)
				<i>FN1</i> (3.10E-5)
				<i>HIF1A</i> (0.1049)
				<i>NOTCH3</i> (0.0168)
Ciliary landscape - WP4352				
	P= 0.3318	P= 0.3592	P= 0.0036	P= 0.2417
	<i>CDH23</i> (0.1719)	<i>BBS5</i> (1.49E-3)	<i>APC</i> (5.45E-5)	<i>CDH23</i> (0.2679)



			<i>BBS5</i> (8.68E-3)	<i>EXOC2</i> (0.1016)
			<i>CDH23</i> (0.0279, 0.2679)	
			<i>IFT122</i> (6.37E-3)	
GPCRs, Class A Rhodopsin-like - WP455				
	P= 0.3928	P= 0.1046	P= 0.1310	P= 0.1113
	<i>MTNR1A</i> (0.0145)	<i>AVPR1A</i> (0.0126)	<i>ADRA1A</i> (0.0105)	<i>HTR1B</i> (0.0136)
			<i>MC1R</i> (0.0718)	<i>MC1R</i> (0.0797)
				<i>MTNR1B</i> (1.44E-3)
Small cell lung cancer - WP4658				
	P= 0.1658	P= 0.1813	P= 0.3670	P= 8.81E-4
	<i>LAMA4</i> (0.0645)	<i>COL4A4</i> (0.0367)	<i>LAMA5</i> (0.0186, 0.0904)	<i>COL4A4</i> (0.4798)
				<i>FN1</i> (3.10E-5)
				<i>LAMA1</i> (0.0101)
Male infertility - WP4673				
	P= 0.2374	P= 0.2586	P= 0.0312	P= 0.1320
	<i>APOB</i> (0.0350)	<i>PEMT</i> (1.05E-3)	<i>AHRR</i> (0.3994)	<i>AHRR</i> (0.3994)
			<i>AR</i> (2.48E-3)	<i>SHMT1</i> (1.20E-3)
			<i>NQO1</i> (0.1886)	
IL-18 signaling pathway - WP4754				
	P= 0.0962	P= 0.4392	P= 0.1452	P= 0.7066
	<i>ACACB</i> (0.1943)	<i>TRPM7</i> (0.000*)	<i>BIN1</i> (0.0156)	<i>FN1</i> (3.10E-5)
	<i>EPB41</i> (0.0492, 7.66E-3)		<i>NCF2</i> (0.0487)	
			<i>NOX1</i> (0.0272)	
* identified only in the African/African American population				
Proximal tubule transport - WP4917				
	P= 0.1013	P= 0.1112	P= 0.2362	P= 0.2211
	<i>ATP6V1B</i> <sub>1</sub> (0.0232)	<i>SLC5A2</i> (1.55E-5)	<i>ATP6V0A</i> <sub>4</sub> (7.12E-3, 0.0457)	<i>SLC7A9</i> (0.3356)
Malignant pleural mesothelioma - WP5087				
	P= 0.1906	P= 0.5886	P= 2.12E-4	P= 0.0029
	<i>ITGB4</i> (2.25E-4)	<i>COL4A4</i> (0.0367)	<i>APC</i> (5.45E-5)	<i>COL4A4</i> (0.4798)
	<i>LAMA4</i> (0.0645)		<i>CDK7</i> (0.0245)	<i>FN1</i> (3.10E-5)
			<i>FZD1</i> (1.30E-4)	<i>HIF1A</i> (0.1049)
			<i>LAMA5</i> (0.0186, 0.0904)	<i>LAMA1</i> (0.0101)
			<i>NGF</i> (0.0172)	<i>TERT</i> (0.0301)
			<i>TCF7L1</i> (0.0595)	
ErbB Signaling Pathway - WP673				
	P= 0.1578	P= 0.0155	P= 0.3516	P= 0.3309
	<i>NRG1</i> (2.32E-5)	<i>ERBB4</i> (unknown)	<i>ABL1</i> (7.61E-3)	<i>NRG1</i> (0.0208)
		<i>NRG1</i> (0.0441)		

Sudden Infant Death Syndrome (SIDS) susceptibility pathways - WP706				
	P= 0.2716	P= 0.0479	P= 0.0013	P= 0.5238
	<i>HSP90B1</i> (0.0176)	<i>NR3C1</i> (0.0266)	<i>AR</i> (2.48E-3)	<i>HIF1A</i> (0.1049)
			<i>MBD1</i> (0.2049)	
			<i>NGF</i> (0.0172)	
			<i>RET</i> (9.06E-4)	
			<i>TPH2</i> (1.48E-3)	