

Table S1. List of significantly up- and downregulated transcripts in ALMS and BBS.

upregulated in ALMS (FC > 1.5)	upregulated in BBS (FC > 1.5)	downregulated in ALMS (FC < 0.67)	downregulated in BBS (FC < 0.67)
<i>TRIM4</i>	<i>TRIM4</i>	<i>ZIC1</i>	<i>PTH1R</i>
<i>HIST1H3C</i>	<i>HIST1H3C</i>	<i>PTH1R</i>	<i>ZIC1</i>
<i>CCDC152</i>	<i>CCDC152</i>	<i>STMN2</i>	<i>PAX7</i>
<i>CTCF</i>	<i>HIST1H4L</i>	<i>PAX7</i>	<i>STMN2</i>
<i>HIST1H4L</i>	<i>ZNF558</i>	<i>CNTFR</i>	<i>SCGB3A2</i>
<i>ZNF558</i>	<i>TEK</i>	<i>FOXA1</i>	<i>CRIL</i>
<i>HTR7</i>	<i>HMOX1</i>	<i>SCGB3A2</i>	<i>MECOM</i>
<i>SGIP1</i>	<i>HTR7</i>	<i>OLIG3</i>	<i>CNTFR</i>
<i>VSIG1</i>	<i>SGIP1</i>	<i>PAX6</i>	<i>HAPLN1</i>
<i>IFNA16</i>	<i>VSIG1</i>	<i>RSPO3</i>	<i>DPP6</i>
<i>ENPEP</i>		<i>PITX2</i>	<i>RSPO3</i>
		<i>SLITRK2</i>	<i>PAX6</i>
		<i>MECOM</i>	<i>GTF2A1L</i>
		<i>NPFFR2</i>	<i>FOXA1</i>
		<i>DKK1</i>	<i>TBX1</i>
		<i>CRIL</i>	<i>OLIG3</i>
		<i>HAPLN1</i>	<i>PITX2</i>
		<i>SCNN1G</i>	<i>LOC101927668</i>
		<i>SCD5</i>	<i>SCD5</i>
		<i>TBX1</i>	<i>TENM1</i>
		<i>SP8</i>	<i>TFAP2C</i>
		<i>TFAP2C</i>	<i>SP8</i>
		<i>ARSE</i>	<i>ARSE</i>
		<i>SLC16A12</i>	<i>CACNA2D3</i>
		<i>TMEM88</i>	<i>TMEM88</i>
		<i>CHRNA3</i>	<i>NRG3</i>
		<i>LOXL3</i>	<i>SCNN1G</i>
		<i>SORBS2</i>	<i>NTRK3</i>

		<i>DMBX1</i> <i>DLL1</i> <i>ROR2</i> <i>CHRNA4</i> <i>TMEM51</i> <i>TMEM150C</i> <i>ZADH2</i>	<i>MCOLN3</i> <i>GABRB2</i> <i>NR5A2</i> <i>NPFFR2</i> <i>SORBS2</i> <i>ADGRA2</i> <i>DLL1</i> <i>VIPR2</i> <i>CHRNA3</i> <i>ZFHX4</i> <i>DMBX1</i> <i>SEZ6</i> <i>POTEF</i>
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Table S2. List of significantly up- and downregulated proteins in ALMS and BBS.

upregulated in ALMS (FC > 1.5)	upregulated in BBS (FC > 1.5)	downregulated in ALMS (FC < 0.67)	downregulated in BBS (FC < 0.67)
CRYZ	CRYZ	MYH14	IFITM3
CGREF1	DYNC2LI1	HSD11B2	GPC4
CDC25C	NAB2	TMEM63A	MBP
FAH	APOBEC3B	ALMS1	CLN8
ASAH1	LGALS1	GALNT3	SOX3
HSBP1	FABP7	IFITM3	
CDKN2AIPNL	SELENBP1	ITPR2	
AGGF1	FHL1	ZSCAN10	
C9orf64	HEBP1	GPC4	
TCEAL5	KIF17	METTL7A	
NAB2	TRIM5	ARRB1	
ARHGAP8	DERA	POU5F1	
	SCRN2	CD9	
	DDAH2		
	CYBA		
	DMXL2		

Table S3. List of reactome pathways significantly up- and down-regulated by both proteomic and transcriptomic analysis in ALMS and BBS syndromes. P-proteomics; T- transcriptomics.

Reactome Pathway	ALMS		BBS	
	P	T	P	T
RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	↓	↑	↓	↑
MITOCHONDRIAL_TRANSLATION TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM TRANSLATION			↓	↑
STABILIZATION_OF_P53 REGULATION_OF_PTEN_STABILITY_AND_ACTIVITY CROSS_PRESENTATION_OF_SOLUBLE_EXOGENOUS_ANTIGENS_ENDOSOMES_ DECTIN_1_MEDIATED_NONCANONICAL_NF_KB_SIGNALING DNA_REPLICATION G2_M_CHECKPOINTS ASSEMBLY_OF_THE_PRE_REPLICATIVE_COMPLEX DNA_REPLICATION_PRE_INITIATION	↑	↑	↑	↑
AUF1_HNRNP_D0_BINDS_AND_DESTABILIZES_MRNA REACTOME_APC_C_CDH1_MEDIATED_DEGRADATION_OF_CDC20_AND_OTHER_A PC_C_CDH1_TARGETED_PROTEINS_IN_LATE_MITOSIS_EARLY_G1 SWITCHING_OF_ORIGINS_TO_A_POST_REPLICATIVE_STATE METABOLISM_OF_POLYAMINES DNA_STRAND_ELONGATION DEGRADATION_OF_GLI1_BY_THE_PROTEASOME APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS ORC1_REMOVAL_FROM_CHROMATIN S_PHASE DEGRADATION_OF_DVL FCER1_MEDIATED_NF_KB_ACTIVATION NEGATIVE_REGULATION_OF_NOTCH4_SIGNALING DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR_ CELLULAR_RESPONSE_TO_HYPOXIA DEGRADATION_OF_AXIN CELL_CYCLE_CHECKPOINTS REGULATION_OF_RAS_BY_GAPS UCH_PROTEINASES REGULATION_OF_RUNX3_EXPRESSION_ANDACTIVITY MITOTIC_G1_PHASE_AND_G1_S_TRANSITION HIV_INFECTION REGULATION_OF_MRNA_STABILITY_BY_PROTEINS_THAT_BIND_AU_RICH_ELE MENTS HOST_INTERACTIONS_OF_HIV_FACTORS THE_ROLE_OF_GTSE1_IN_G2_M_PROGRESSION_AFTER_G2_CHECKPOINT G2_M_DNA_DAMAGE_CHECKPOIN G1_S_DNA_DAMAGE_CHECKPOINTS ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLAC EMENT_PATHWAY LAGGING_STRAND_SYNTHESIS PCNA_DEPENDENT_LONG_PATCH_BASE_EXCISION_REPAIR SEPARATION_OF_SISTER_CHROMATIDS CYCLIN_A_CDK2_ASSOCIATED_EVENTS_AT_S_PHASE_ENTRY SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR_ ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES DNA_REPAIR PROCESSIVE_SYNTHESIS_ON_THE_LAGGING_STRAND CELL_CYCLE_MITOTIC MISMATCH_REPAIR INTERLEUKIN_1_SIGNALING			↑	↑

MAPK6_MAPK4_SIGNALING				
TELOMERE_C_STRAND_LAGGING_STRAND_SYNTHESIS				
UB_SPECIFIC_PROCESSING_PROTEASES				
SCF_SKP2_MEDIATED_DEGRADATION_OF_P27_P21				
PROCESSING_OF_DNA_DOUBLE_STRAND_BREAK_ENDS				
DEGRADATION_OF_BETA_CATENIN_BY_THE_DESTRUCTION_COMPLEX				
GAP_FILLING_DNA_REPAIR_SYNTHESIS_AND_LIGATION_IN_GG_NER				
RECOGNITION_OF_DNA_DAMAGE_BY_PCNA_CONTAINING_REPLICATION_COMPLEX				
NUCLEOTIDE_SALVAGE				
METABOLISM_OF_NUCLEOTIDES				
DEUBIQUITINATION				
NEDDYLATION				
CLEC7A_DECTIN_1_SIGNALING				
RESOLUTION_OF_ABASIC_SITES_AP_SITES				
BUDDING_AND_MATURATION_OF_HIV_VIRION				
INTRAFLAGELLAR_TRANSPORT				
ENDOSOMAL_SORTING_COMPLEX_REQUIRED_FOR_TRANSPORT_ESCRT				
TRANSCRIPTIONAL_REGULATION_OF_PLURIPOTENT_STEM_CELLS	↓	↓	↓	↓
SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	↓	↓		
TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	↓	↓		
ION_TRANSPORT_BY_P_TYPE_ATPASES				
NCAM1_INTERACTIONS				
GLYCOSAMINOGLYCAN_METABOLISM				
CALNEXIN_CALRETICULIN_CYCLE				
SYNDECAN_INTERACTIONS				
TRANSPORT_OF_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS				
A_TETRASACCHARIDE_LINKER_SEQUENCE_IS_REQUIRED_FOR_GAG_SYNTHESIS				
CHONDROITIN_SULFATE_DERMATAN_SULFATE_METABOLISM			↓	↓
HEPARAN_SULFATE_HEPARIN_HS_GAG_METABOLISM				
ER_QUALITY_CONTROL_COMPARTMENT_ERQC				
DISEASES_ASSOCIATED_WITH_GLYCOSAMINOGLYCAN_METABOLISM				
N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE				
HS_GAG_DEGRADATION				
SYNTHESIS_OF_VERY_LONG_CHAIN_FATTY_ACYL_COAS				
DEFECTIVE_B4GALT7_CAUSES_EDS_PROGEROID_TYPE				
FATTY_ACYL_COA_BIOSYNTHESIS				
HS_GAG_BIOSYNTHESIS				