

	CLL	BPLL	sMZL	LPD	SLL	HCL	HCLv	IL	Ctrl	Total
Total	34	6	5	3	1	3	1	2	23	78
CD19+ 3' scRNA-seq	28	5	5	1	1	1	0	1	4	46
CD19+ 5' scRNA-seq	13	5	3	2	0	3	1	2	10	39
CD19+ DNA WES	13	2	3	0	1	1	0	1	0	21
CD34+ 5' scRNA-seq	2	1	1	0	0	0	0	0	10	14
Multiple samples per individual	5	0	2	0	0	0	0	0	0	7

CLL: Chronic Lymphocytic Leukemia
BPLL: B-Prolymphocytic Leukemia
MZL: Marginal Zone Lymphoma
SLL: Small Lymphocytic Leukemia
Ctrl: Control
IL: Intermittent Lymphocytosis
scRNA-seq: Single-cell RNA-sequencing
WES: Whole Exome sequencing

[illegible]

Up-regulated aged-HCL vs aged

ADAMTS19
ARMH1
BX284613.2
CCDC88A
CKLF
CPVL
GALNTL6
HCST
HOPX
IL1R2
MEIKIN
MYF6
PSD3
RFTN1
RGS13
S100A4
SGK1
SNTG1
SORL1
TACC1
TCL1A
TIMP1

Down-regulated aged-HCL vs aged

ALOX5
COBLL1
CXXC5
FAM30A
GNG7
NIBAN3
PPP1R14A
TCF4

Sex_chr	Cell cycle	Ig	Ribosomal	HLA	Stress	Platelet	Erythrocyte	Illumina/Ultima_diff
AMELY	DNAJB1	IGHA1	B2M	HLA-A	DUSP1	PF4	HBA1	AC000093.1
AZFa	HSPA1A	IGHA2	EEF1A1	HLA-B	DUSP2	PF4V1	HBA2	AC002464.1
AZFb	HSPA1B	IGHD	HIST1H4C	HLA-C	FOS	PPBP	HBB	AC004556.1
AZFc	HSPA6	IGHD1-1	NEAT1	HLA-DMA	FOSB		HBG2	AC005726.5
BPY2	HSPB1	IGHD1-14	TMSB4X	HLA-DMB	HSP90AA1			AC005921.2
CDY1	MCM4	IGHD1-20	RPL10	HLA-DOA	HSP90AB1			AC006064.4
CDY2	MKI67	IGHD1-26	RPL10A	HLA-DOB	HSP90B1			AC007014.1
CYorf15	PCNA	IGHD1-7	RPL10L	HLA-DPA1	HSPA5			AC007952.4
DAZ1	STMN1	IGHD1OR15-1A	RPL11	HLA-DPB1	HSPA8			AC008035.1
DAZ2	TOP2A	IGHD1OR15-1B	RPL12	HLA-DQA1	HSPD1			AC010642.2
DAZ3	UBE2C	IGHD2-15	RPL13	HLA-DQA2	HSPE1			AC010880.1
DAZ4		IGHD2-2	RPL13A	HLA-DQB1	HSPH1			AC010883.1
DDX3Y		IGHD2-21	RPL14	HLA-DQB1-AS1	IER2			AC012306.2
EIF1AY		IGHD2-8	RPL15	HLA-DQB2	IFI27			AC015849.3
HSFY1		IGHD2OR15-2A	RPL17	HLA-DRA	IFI30			AC016735.1
HSFY2		IGHD2OR15-2B	RPL18	HLA-DRB1	IFI35			AC020656.1
KDM5D		IGHD3-10	RPL18A	HLA-DRB5	IFI44L			AC020910.4
NLGN4Y		IGHD3-16	RPL19	HLA-E	IFI6			AC025171.3
PCDH11Y		IGHD3-22	RPL21	HLA-F	IFIH1			AC068491.3
PRKY		IGHD3-3	RPL22	HLA-G	IFIT1			AC073896.3
PRY		IGHD3-9	RPL22L1		IFIT2			AC074032.1
PRY2		IGHD3OR15-3A	RPL23		IFIT3			AC074183.1
RBMY1A1		IGHD3OR15-3B	RPL23A		IFIT5			AC087190.1
RPS4Y1		IGHD4-11	RPL24		IFITM2			AC091057.6
RPS4Y2		IGHD4-17	RPL26		IFITM3			AC092069.1
SRY		IGHD4-23	RPL26L1		ISG15			AC092171.3
TB4Y		IGHD4-4	RPL27		ISG20			AC093495.1
TBL1Y		IGHD4OR15-4A	RPL27A		JUN			AC104532.2
TGIF2LY		IGHD4OR15-4B	RPL28		JUNB			AC108047.1
TMSB4Y		IGHD5-12	RPL29		JUND			AC109597.2
TSPY1		IGHD5-18	RPL3		MX1			AC127521.1
TSPY2		IGHD5-24	RPL30		MX2			AC132192.1
TXLNGY		IGHD5-5	RPL31		TRIM22			ACOT2
USP9Y		IGHD5OR15-5A	RPL32		ZFP36			AD000090.1
UTY		IGHD5OR15-5B	RPL34					ADSL
VCY		IGHD6-13	RPL34-AS1					AF127577.1
VCY1		IGHD6-19	RPL35					AKT1
VCY2		IGHD6-25	RPL35A					AL022238.2
XIST		IGHD6-6	RPL36					AL049840.1
XKRY		IGHD7-27	RPL36A					AL121944.1
ZFY		IGHE	RPL36AL					AL133453.1

patient	SAMPLE	sample_g	CHR	POS	REF	DEPTH	R	ALT	ALT_REAL	VAR	AF_B	AF_nont	Func.refG	Gene.refL	functional	variant_id	
T20	T20 b	mature B	11	60710040	G	530	527	A	3	0.006	0.42	0.42	enonic	MS4A8	FALSE	3	
T20	T20 b	CL	CLP	11	60710040	G	798	452	A	366	0.434	0.42	enonic	MS4A8	FALSE	3	
T20	T20 b	CL	CLP	11	60710040	G	103	99	A	4	0.039	0.42	enonic	MS4A8	FALSE	3	
T20	T20 b	mature myeloid	11	60710040	G	107	105	A	1	0.009	0.42	0.42	enonic	MS4A8	FALSE	3	
T20	T20 b	Pro B	11	60710040	G	614	414	A	200	0.326	0.42	0.42	enonic	MS4A8	FALSE	3	
T29	T29 b	mature myeloid	10	77030803	C	232	224	T	8	0.034	0.407	0.086	enonic	KCNMA1	FALSE	30	
T29	T29 b	Pro B	10	77030803	C	376	374	T	2	0.005	0.407	0.086	enonic	KCNMA1	FALSE	30	
T29	T29 b	mature myeloid	11	1.126E+08	c	37	31	T	6	0.162	0.551	0.183	enonic	PATE1	FALSE	35	
T29	T29 b	Pro B	11	1.126E+08	c	167	162	T	35	0.21	0.551	0.183	enonic	PATE1	FALSE	35	
T29	T29 b	mature myeloid	8	1.338E+08	A	43	42	G	1	0.021	0.33	0.049	enonic	COL22A1	FALSE	38	
T29	T29 b	Pro B	8	1.338E+08	A	366	355	G	11	0.03	0.33	0.049	enonic	COL22A1	FALSE	38	
T58	T58	CLP	CLP	1	1.17273397	G	113	120	C	3	0.024	0.457	0.457	enonic	PAD3	FALSE	49
T58	T58	CLP	CLP	1	1.17273397	G	172	145	C	27	0.157	0.457	0.457	enonic	PAD3	FALSE	49
T42	T42	CLP	CLP	9	1.021E+08	A	242	186	G	56	0.231	0.571	0.06	enonic	RMF20	FALSE	57
T42	T42	CLP	CLP	9	1.021E+08	A	55	54	G	1	0.038	0.571	0.06	enonic	RMF20	FALSE	57
T42	T42	Myel	myeloid	9	1.021E+08	A	56	48	G	8	0.143	0.571	0.06	enonic	RMF20	FALSE	57
T42	T42	Pro B	9	1.021E+08	A	396	394	G	2	0.005	0.571	0.06	enonic	RMF20	FALSE	57	
T58	T58	Myel	myeloid	1	1.17273397	G	33	32	C	1	0.03	0.457	0.457	enonic	PAD3	FALSE	49
T58	T58	Pro B	1	1.17273397	G	88	45	C	43	0.489	0.457	0.457	enonic	PAD3	FALSE	49	
T42	T42	CLP	CLP	7	1.031E+08	T	465	386	C	79	0.17	0.321	0.061	enonic	SLC26A5	FALSE	58
T42	T42	Myel	myeloid	7	1.031E+08	T	182	179	C	3	0.016	0.321	0.061	enonic	SLC26A5	FALSE	58
T42	T42	Pro B	7	1.031E+08	T	414	325	C	89	0.215	0.321	0.061	enonic	SLC26A5	FALSE	58	
T42	T42	CLP	CLP	12	1.046E+08	C	150	147	A	3	0.02	0.372	0.064	enonic	HCFC2	FALSE	59
T42	T42	Pro B	12	1.046E+08	C	181	91	A	90	0.497	0.372	0.064	enonic	HCFC2	FALSE	59	
T42	T42	CLP	CLP	3	1.715E+08	T	348	282	C	66	0.19	0.462	0.103	enonic	EIF5A2	FALSE	82
T42	T42	Myel	myeloid	3	1.715E+08	T	72	70	C	2	0.028	0.462	0.103	enonic	EIF5A2	FALSE	82
T57	T57 b	mature B	3	1.511E+08	T	1752	591	G	1161	0.663	0.506	0.159	enonic	MED12L	FALSE	83	
T55	T55	CLP	CLP	6	24566603	G	729	728	A	1	0.001	0.293	0.293	enonic	KIAA0319	FALSE	97
T55	T55	CLP	CLP	6	24566603	G	27	26	A	1	0.037	0.293	0.293	enonic	KIAA0319	FALSE	97
T55	T55	Myel	myeloid	6	24566603	G	470	435	A	35	0.074	0.293	0.293	enonic	KIAA0319	FALSE	97
T55	T55	CLP	CLP	6	65407074	T	447	442	C	5	0.011	0.3	0.633	enonic	EYS	FALSE	104
T55	T55	Myel	myeloid	6	65407074	T	626	593	C	33	0.053	0.633	0.633	enonic	EYS	FALSE	104
T55	T55	non	mature n	6	65407074	T	503	497	C	6	0.012	0.633	0.633	enonic	EYS	FALSE	104
T55	T55	CLP	CLP	6	68993916	A	1195	1126	G	69	0.058	0.385	0.385	enonic	ADGRB3	FALSE	105
T55	T55	CLP	CLP	6	68993916	A	71	66	G	5	0.07	0.385	0.385	enonic	ADGRB3	FALSE	105
T55	T55	Myel	myeloid	6	68993916	A	1589	1489	G	100	0.063	0.385	0.385	enonic	ADGRB3	FALSE	105
T55	T55	Pro B	6	68993916	A	1976	145	G	1831	0.927	0.385	0.385	enonic	ADGRB3	FALSE	105	
T55	T55	non	mature n	6	68993916	A	1537	1514	G	3	0.002	0.385	0.385	enonic	ADGRB3	FALSE	105
T55	T55	CLP	CLP	11	77280978	C	743	720	A	23	0.031	0.403	0.403	enonic	GDPR4	FALSE	107
T55	T55	Myel	myeloid	11	77280978	C	774	719	A	55	0.071	0.403	0.403	enonic	GDPR4	FALSE	107
T55	T55	Pro B	11	77280978	C	87	86	A	1	0.011	0.403	0.403	enonic	GDPR4	FALSE	107	
T57	T57	CLP	CLP	3	1.511E+08	T	723	704	C	19	0.026	0.505	0.159	enonic	MED12L	FALSE	83
T57	T57	CLP	CLP	3	1.511E+08	T	2070	1973	G	97	0.047	0.505	0.159	enonic	MED12L	FALSE	83
T57	T57	Myel	myeloid	3	1.511E+08	T	1793	1493	G	308	0.167	0.505	0.159	enonic	MED12L	FALSE	83
T57	T57	Pro B	3	1.511E+08	T	467	69	G	398	0.852	0.505	0.159	enonic	MED12L	FALSE	83	
T55	T55	CLP	CLP	14	87947802	T	1250	1183	G	66	0.053	0.352	0.352	ignoring	GALC	FALSE	108
T55	T55	Myel	myeloid	14	87947802	T	945	898	G	47	0.05	0.352	0.352	ignoring	GALC	FALSE	108
T55	T55	Pro B	14	87947802	T	113	108	G	5	0.044	0.352	0.352	ignoring	GALC	FALSE	108	
T55	T55	non	mature n	14	87947802	T	1166	1002	A	73	0.063	0.352	0.352	ignoring	GALC	FALSE	108
T55	T55	CLP	CLP	15	92967324	C	513	503	A	10	0.039	0.384	0.384	ignoring	CHD2	TRUE	110
T55	T55	Myel	myeloid	15	92967324	C	555	527	A	28	0.05	0.384	0.384	ignoring	CHD2	TRUE	110
T57	T57 b	mature B	3	1.791E+08	T	1343	604	A	739	0.55	0.468	0.186	enonic	PK3CA	FALSE	111	
T57	T57	CLP	CLP	3	1.791E+08	T	866	764	A	102	0.118	0.468	0.186	enonic	PK3CA	FALSE	111
T57	T57	CLP	CLP	3	1.791E+08	T	1612	1502	A	20	0.012	0.468	0.186	enonic	PK3CA	FALSE	111
T55	T55	CLP	CLP	X	1.11E+08	G	1440	1426	T	14	0.01	0.491	0.491	enonic	LHPFL1	FALSE	112
T55	T55	Myel	myeloid	X	1.11E+08	G	1302	1246	T	56	0.043	0.491	0.491	enonic	LHPFL1	FALSE	112
T55	T55	non	mature n	X	1.11E+08	G	1397	1395	T	2	0.001	0.491	0.491	enonic	LHPFL1	FALSE	112
T55	T55	CLP	CLP	4	1.251E+08	G	1119	1113	A	6	0.005	0.289	0.289	enonic	FAT4	TRUE	117
T55	T55	Myel	myeloid	4	1.251E+08	G	1065	1057	A	8	0.008	0.289	0.289	enonic	FAT4	TRUE	117
T55	T55	Pro B	4	1.251E+08	G	312	62	A	270	0.813	0.289	0.289	enonic	FAT4	TRUE	117	
T55	T55	non	mature n	4	1.251E+08	G	1290	1288	A	2	0.002	0.289	0.289	enonic	FAT4	TRUE	117
T55	T55	CLP	CLP	3	1.671E+08	C	668	663	A	5	0.007	0.494	0.494	enonic	WOR49	FALSE	118
T55	T55	Myel	myeloid	3	1.671E+08	C	803	765	A	38	0.047	0.494	0.494	enonic	WOR49	FALSE	118
T55	T55	non	mature n	3	1.671E+08	C	793	787	A	6	0.008	0.494	0.494	enonic	WOR49	FALSE	118
T55	T55	CLP	CLP	2	2.11E+08	C	959	987	C	9	0.008	0.336	0.336	enonic	UNC30	FALSE	119
T55	T55	Myel	myeloid	2	2.11E+08	C	794	777	C	17	0.021	0.336	0.336	enonic	UNC30	FALSE	119
T56	T56 b	mature B	16	15608289	A	519	488	C	31	0.06	0.253	0.253	ignoring	MARF1	FALSE	121	
T56	T56	CLP	CLP	16	15608289	A	723	698	C	34	0.046	0.253	0.253	ignoring	MARF1	FALSE	121
T56	T56	CLP	CLP	16	15608289	A	33	30	C	3	0.091	0.253	0.253	ignoring	MARF1	FALSE	121
T56	T56	Myel	myeloid	16	15608289	A	409	392	C	17	0.042	0.253	0.253	ignoring	MARF1	FALSE	121
T56	T56	non	mature n	16	15608289	A	448	428	C	20	0.045	0.253	0.253	ignoring	MARF1	FALSE	121
T56	T56 b	mature B	13	48307512	C	433	283	T	150	0.346	0.312	0.055	enonic	RB1	TRUE	123	
T56	T56	CLP	CLP	13	48307512	C	693	617	T	76	0.11	0.312	0.055	enonic	RB1	TRUE	123
T56	T56	Myel	myeloid	13	48307512	C	489	431	T	58	0.119	0.312	0.055	enonic	RB1	TRUE	123
T56	T56	Pro B	13	48307512	C	72	71	T	1	0.014	0.312	0.055	enonic	RB1	TRUE	123	
T56	T56 b	mature B	4	1.251E+08	T	1005	634	G	371	0.369	0.4	0.118	enonic	AMHR050	FALSE	127	
T56	T56	CLP	CLP	4	1.251E+08	T	1375	1150	G	225	0.164	0.4	0.118	enonic	AMHR050	FALSE	127
T56	T56	CLP	CLP	4	1.251E+08	T	44	31	G	13	0.295	0.4	0.118	enonic	AMHR050	FALSE	127
T56	T56	Myel	myeloid	4	1.251E+08	T	796	618	G	80	0.226	0.4	0.118	enonic	AMHR050	FALSE	127
T56	T56	non	mature n	4	1.251E+08	T	752	742	G	10	0.013	0.4	0.118	enonic	AMHR050	FALSE	127
T57	T57 b	mature B	15	42473311	T	887	863	G	524	0.951	0.455	0.167	enonic	ZNPF06	FALSE	135	
T57	T57	CLP	CLP	15	42473311	T	470	456	G	14	0.03	0.455	0.167	enonic	ZNPF06	FALSE	135
T57	T57	CLP	CLP	15	42473311	T	1207	1206	G	1	0.001	0.455	0.167	enonic	ZNPF06	FALSE	135
T57	T57	Myel	myeloid	15	42473311	T	664	607	G	57	0.086	0.455	0.167	enonic	ZNPF06	FALSE	135
T57	T57	Myel	myeloid	3	1.791E+08	T	782	679	A	103	0.132	0.468	0.186	enonic	PK3CA	FALSE	111
T57	T57	non	mature n	3	1.791E+08	T	430	429	A	1	0.002	0.468	0.186	enonic	PK3CA	FALSE	111
T57	T57	Pro B	3	1.791E+08	T	63	60	A	3	0.048	0.4						

Markers used for annotation of BM cells

[illegible]

A1BG ADAR2 ARAP2 BACE2 CAMT1A CDK14 COQ2 DHX57 ERAD03 FDX1 GNG11 HOPX KCNA3 LINC00471 MAGEF1 MOGB8 NFATC3 PAPSS1 PCLB1 PSD3 ROX SCMH1 SLC25A1 SRA1 TASP1 TME8B0 UBE2E2 XRC4C
ABCA1 ADGRG5 ARF4 BACH1 CANX CDK17 CORO1A DIAPH1 ELAVS1 FER1 GNG2 HPD0 KCNMB LINC00476 MAGT1 MORC3 NFKB2 PARM1 PCLG1 PSMA4 REEP3 SCML4 SLC25A19 SRB01 TBC1D1 TMSB10 UBE2G1 XRN1
ABCA5 ADL1 ARFGAP3 BBAIP2L1 BACH2 CDK19 CORO1B DIAPH2 ELMF1 FERMT3 GNG7 HPGD KCNJ3 LINC00486 MAM12 MOSM0 NFKBIA PARN PCLG1 PSMA8 REEP5 SCNB18 SLC25A29 SREB2 TBC1D12 TM64 UBE2G1 XHRAL
ABCA6 ADK ARFGEF2 BANK1 CAPN2 CDKAL1 CORO7 DP2A EMB FG02 GNPTAB HS25T1 KCNJ1 LINC00841 MAN1A1 MPC1 NKBIE PARP3A PLD4 PSMB5 RELB SCPEP1 SLC25A42 SRM TBC1D22A TNFAIP8 UBE2J1 YAF2
ABCA9 ADTRP ARGLU1 BARK2 CAPN3 CDK11 COTL1 DP2B EMC2 FG04 GOLGABA HS017B12 KCTD7 LINC00861 MAN2A1 MPPE NIX1 PARP8 PLEC PSMC2 RELT SDOCA68 TBC1D23 TNFRSF13 UBE2O YAR5
ABCB10 AEBP1 ARHGAP11 BASP1 CAPN51 CDKN2A COX17 DPK1A EMC7 FG0Y GOLGABA HS017B12 KCTD7 LINC00861 MAN2A1 MPPE NIX1 PARP8 PLEC PSMC2 RELT SDOCA68 TBC1D32 TNFRSF17 UBE2Q YBEY
ABCB14 AFON ARHGAP12 BATF CAPZB CDKN2A COX41 DPK1A EM14 FGL2 GOLGB1 HS017B4 KDEL1 LINC00914 MAN2B1 MPPIP NKBIA PARP9 PLEK PSMD11 RELE SDF2L1 SLC1A11 SRPK2 TBC1D5 TNFRSF18 UBE2Z YBK1
ABCC1 AFPI ARHGAP1 BAK CAPN1 CDKN2A COX2 DPK1A EM15 FGR GOLGB1 HS017B4 KDEL1 LINC00924 MAN2A1 MPPI1 PARB8 PLEKHA1 PSMD3 REEP3 SCLD19 TNFRSF12 UBE2C YBK3
ABCC1 AF1F3 ARHGAP11 BAZ2B CARM1L1 CDV3 COX2A2 DSP1 ENDO01 FHIT GS0R2 HS12D KNMB LINC00944 MAP2 MNRP NPBRL PARVG PLEKHA2 PSME2 REKO2 SKL1 SLC3B2 SRM22 TBC1D0B TNFSF13 UBN2 YIPFA
ABHD17A AFG3L2 ARHGAP22 BB3C CARS2 CDVL COX7C DLEU1 FN1 FIGA GPAAL1 HSPA12A KNMC LINC01004 MAP2K5 MRP1L1 NIT2 PAT1 PLEKHA5 PSME4 RFL1 SOK2 SLC35E3 SRFS5 TBCK TNK1 UBR2 YLPM1
AB1 AGF1G1 ARHGAP22 BB59 CASD1 CEACAM2 CPEB4 DLEU2 ENKP2 FILIP1G GPAT2CH2 HSPA4 KNMC58 LINC01101 MAP2K6 MRP1L3 NAIN3 PATL2 PLEKHG2 PSPC1 RFTN1 SEC11C SLC35F5 SRFS6 TBL1X TNIP2 UBR3 YPEL2
AB3 AGO4 ARHGAP22 BBX CASK CELF2 CPED1 DLG2 ENKP2 FKBP1A GPAT2CH2 HUWE1 KNMC5 LINC01124 MAP3K1 MRP1L4 NKAOP1 PAWR PLEKHG1 PTPB2 RFK3 SEC13 SLC37A1 SERF7 TBL1XK1 TNK5 UBR4 YPEL3
ABU4M1 AGPAT3 ARHGAP3 BCAC3 CASP1 CELSR1 CRANL1 DLGAP4 ENTPD1 FKBP5 GNLN1 KNM6A LINC01215 MAP3K5 MRP127 NGC7 PAIS PLEKH2 PIGL1 RP7 SEC14L1 SLC8B1 TBK21 TNPO1 UBR5 YVHAB
ABR AGPAT5 ARHGAP4 BCAC4 CASP3 CEMIP2 CPNE5 DMD EP400 FL1 GPCPD1 IBTK KDN7A LINC01278 MAP3K8 MRP1L NGLXNK PAXX PLEKHM2 PTK2 RGCC SEC31A SLC3B11 SSBP2 TBKAS1 TNK5CA UBR7 YVHAB
ABRACL AGTPBP1 ARHGAP4 BC111A C8FAZT2 CEP104 CPQ DMTF1 EPB41 FLNA GPD2 ID3 HGBR82 LINC01324 MAP4 MRP14O NLK PBX3 PLEKH01 PTK2B RGS1 SEC61A1 SLC38A9 SSBP4 TCEA1 TNK5CB UBRXN1 YVHAB
ABT1 AHYU ARHGAP5 BCL11B C8FB CEP192 CPVF2 DWA4F4 EPB41L2 FLT3 GPHN IDH2 KIAA0040 LINC01356 MAP4K1 MRP15L NLRCS PBDX1 PLIN2 PTMA RGS10 SEC61B SLC39A10 SS2H TCEA4L TNK5CB UBRXN4 ZAP70
AC004687 AH1 ARHGAP6 BCL2 C8LB CEP290 CPMF DUA1B11 EPB41L4A FMN13 GPR137B IDH3A KIAA0319 LINC01362 MAP4K3 MRP25B NFKBIA NLRP1 PBLP2 PTM5 RGS13 SEC61G SLC39A11 SSNP TC12 TN53 UBRXN7 ZBP1
AC004889 AHNAK ARHGAD4 BCL2A1 C8R1 CEP83 CRL1 DUA1C1 EPH4A PMD0 GPR150 ID5 KIAA0586 LINC01374 MAP4K32 MRP56 NMEL PCD02D PEP5 PTPN1 RGS19 SEC52 SLC44A2 SSR1 TC720 TGGARAW UCLL1 ZBTB20
AC005580 AHR ARHGODR BCL11L1 C8RA CEP83L CR2 DUA1C10 EP85 FNPB1 GPR183 IER5 KIAA1191 LINC01475 MAP4K4 MRTTA NMOU PCBP1 PLSCR1 PTPN12 RGS2 SEC63 SLC4A10 SSRA TC73 TQLIP UCL2 ZBTB24
AC005670 AICDA ARHGHEF1 BCL3 C8K7 CEP95 CRADD DUA1C3 EP515 FNDC3A GPR65 IFI16 HGFAPK15 LINC01476 MAP4K5 MRTTB NMO1 PCCA PLXNCL1 PTPN18 RHBDD1 SEC15BP21 SLC4A7 SSRA TC74 TOM1 UCGG ZBTB32
AC006369 AIDA ARHGHEF13 BCL7A CCCC106 CEP11 CREB3L2 DNASE1L3 EP5T1 FNDC3B GPM33 IFI27L2 KIAA1324 LINC01486 MAP703 MSA41 NOC3L PCDH9 PMAIP1 PTPN2 RHBDF2 SELL1 SCS0A1 ST14 TC77 TOMMT UGGT1 ZBTB38
AC007364 AF1 ARHGHEF3 BDPI1 CCCC107 CER56 CREBRF DMN2 ERAW1 FNP1 GP72 IFTT1M1 KIAA1328 LINC01504 MAPK10 MSA44A NOCP3 PCD01B PMEPA1 PTPN22 RHEX SELL13 SLC66A2 STGAL1 TC7F12 TOP1 UH972 ZCCH12B
AC007368 AHM2 ARHID2 BE72 CCCC112 CFL1 CREM DMNBP EBMN FOCAD GP77 IFNAR1 LINC01517 MAPK8 MSA44E NOSP3 PCD01B4 PMF1 PTPN4 RHDA SELENOK SLC7A7 STGAL5 TCHP TOP1MT UH972 ZCCH12B
AC007381 AK9 ARID2 BE4 CCCC14 CFLAR CRP2 DMNT1 ERL1 FODN3 GRAM01B FNAR2 KIF3B HNF1B LINC01588 MAPK8P1 MSA47 NOTCH2 PCGF5 PMN2 PTPN6 RHOB SELENOM SLC3A9R1 STGAL1 TCLA TOR1AP12 ULK4 ZCCH12D
AC007384 AKAP10 ARID3A BHLHE40 CCCC141 CHAMP1 CRP3 DNP3 DHN1 GRAM01C FNNG-AS1 KIFAP3 LINC01615 MAPKAP1 M52 NOVA1 PCM1 PMS1 PTPN7 RHOBTB2 SELENOS SLC9A7 STGALNA TCL6 TOR3A UMAOD1 ZC3H7A
AC007569 AKAP11 ARID3A BHLHE41 CCCC144N CHCHD1 CTRAP DOCK10 ERLC1 FODX3 GRAP2 IFNGR1 KLF12 LINC01725 MAPKAKK MSMP MPAS3 PCDMT02 PNP PTPRE RHOC SELL SCLC01 STB5A4 TCTA TP53111 UNC50 ZCCH10
AC008014 AKAP13 ARID5B BICD1 CCCC167 CHCHD10 CTRC3 DOCK11 ERO1A FOPK1 GRB2 IFNLR1 KLF13 LINC01754 MAPK41 MSN MPAP3 PCDMT02 PNP PTPRE RHOC SELL SCLC01 STB5A4 TCTA TP53111 UNC50 ZCCH10
AC008015 AKAP17A ARH1 BICD2 CCCC168 CHCHD10 CTRC3 DOCK11 ERO1A FOPK1 GRB2 IFNLR1 KLF13 LINC01754 MAPK41 MSN MPAP3 PCDMT02 PNP PTPRE RHOC SELL SCLC01 STB5A4 TCTA TP53111 UNC50 ZCCH10
AC008555 AKAP5 ARH1 CHOD3 CCCC191 CHOD3 CGLNLRK CDD17 ES4E FPM1 GRAP2 IFNLR1 KLF13 LINC01754 MAPK41 MSN MPAP3 PCDMT02 PNP PTPRE RHOC SELL SCLC01 STB5A4 TCTA TP53111 UNC50 ZCCH10
AC008691 AKNA ARH15 BIK CCCC32 CHD4 CSC DOCKR D5E FRM05 GRINA IGFR2 KLF6 LINC01851 MAPK41 MTDH MNP1 PCKS7 POSZ PTPRG RHOC SEMA4B SMOA3 STAGE TEC TP052 UOQRC ZCCH18
AC009522 AKR1B1 ARL17A BIN2 CCCC50 CH13L2 CSMD1 DOCK3 ESR1 FR52 GRK3 IGFBP4 KLF7 LINC01945 MAPKCS MTERFA NPTN PCD04 POLD2 PTPRM RHOO SEMA7A SMOAG STAMBPL1 TEN2 TP1 USF3 ZDHHC12
AC011586 AKT2 ARL17B BIRC3 CCCC60 CH1C2 CSNK1E DOP18 ESYT2 FRY GRK5 IFNLR1 KLF8 LINC02102 MAPKCSL1 MTHFD1 NR2C1 PODE4B POLF4 PTPRO RIC1 SEPTIN10 SMOA2 STAP1 TENT5A TPK1 U501 ZDHHC14
AC012236 AKT3 ARL2 BIK CCCC66 CH1L1 CTS3 DPEP2 ETRB FRYL GSN IKZF1 KLHL14 LINC02137 MAPK1 MTHFD1 NR2C2 PODE4D POLH PTPRQ RIK3 SEPTIN7 SMOA3 STAP1 TENT5C TP23 USP12 ZDHHC20
AC012368 ALG043P7 ARL2B BLMR1 CCCC67 CH1C2 DPEP2 ETRB FRYL GSN IKZF1 KLHL14 LINC02137 MAPK1 MTHFD1 NR2C2 PODE4D POLH PTPRQ RIK3 SEPTIN7 SMOA3 STAP1 TENT5C TP23 USP12 ZDHHC20
AC012681 ALG05039 ARL4C BLMR1 CCCC67 CH1C2 DPEP2 ETRB FRYL GSN IKZF1 KLHL14 LINC02137 MAPK1 MTHFD1 NR2C2 PODE4D POLH PTPRQ RIK3 SEPTIN7 SMOA3 STAP1 TENT5C TP23 USP12 ZDHHC20
AC018742 AL078600 ARL4D BMF CCCC88A CHP11 CTNNA1 DPM2 ETS1 FTO GSTK1 IL15 KLHL29 LINC02222 MAST4 MTR NBRF2 PODE7B POLR23 PV1 RIN3 SERINCS SMCHD1 STATS5B TESC TPR USP47 ZEB2
AC020659 AL079338 ARL8A BMP2K CCCC88B CHT11 CTSB DPH8 FTS13 GSTP1 IL18 KLHL5 LINC02228 ARB4 MTS51 NRCAM POEBA POMP PKX RINL SERPINB1 SMO1T1 STAU2 TESPA1 TP5T2 USP45 ZFAND3
AC022140 AL138963 ARL8C BMP98 CCCC91 CHT515 CTSF DPVD EVI2A FTX GTDC1 IL1R2 KLHL6 LINC02244 MB05 NKX4 NRP1 PDGFR POLJ2A1 PICARD ROPR1 SERPINB6 SMO6 STEAP1B TE72 TP11 USPNL ZFAND3
AC022325 AL139020 ARMC1C BMP19A CHT515 CTSF DPVD EVI2A FTX GTDC1 IL1R2 KLHL6 LINC02244 MB05 NKX4 NRP1 PDGFR POLJ2A1 PICARD ROPR1 SERPINB6 SMO6 STEAP1B TE72 TP11 USPNL ZFAND3
AC022516 AL161781 ARMC6C BMP92 CND02 CHT515 CTSF DRAM2 EVH5 FUS GLUCD1 IL21R4 KLRC4 LINC02361 MBN12 MYADM NRP1 PDJ4 POLJ2F PYM1 RMDN2 SERPINB9 SMOA3 STIAP2 TP0F2 TRAC UST ZFP361
AC022568 AL135604 ARMH1 BNP13L CND03 CIB1 CTS5 D5E EXOCA FJTB IL2RG KLRK1 LINC02365 MRP MYBL2 NRM PDJ6 POLJ3F QRS1L RMRP SERPINB9 SMOA3 STIAP2 TP0F2 TRAC UST ZFP361
AC0226167 AL355076 ARMH3 BOD1L1 CNGG2 CITA CUL1 D5T5 EXOCA FJTB IL2RG KLRK1 LINC02365 MRP MYBL2 NRM PDJ6 POLJ3F QRS1L RMRP SERPINB9 SMOA3 STIAP2 TP0F2 TRAC UST ZFP361
AC027097 AL365295 ARNT BPNT1 CNH CISO2 CUL3 D5TN EYAF FYK07 HJFX IL4R KMTZE LINC02414 MCCC2 MYDGF NS2 PDJUM5 PPA1 RAB11FIP1 RNASEH2B SEPTA2D SMOY3 STK17A TFRIC TRAF4 UTS2 ZH92
AC027098 AL450352 ARPC3 CACNA1 CIP1 CIP2 CIP3 CIP4 CIP5 CIP6 CIP7 CIP8 CIP9 CIP10 CIP11 CIP12 CIP13 CIP14 CIP15 CIP16 CIP17 CIP18 CIP19 CIP20 CIP21 CIP22 CIP23 CIP24 CIP25 CIP26 CIP27 CIP28 CIP29 CIP30 CIP31 CIP32 CIP33 CIP34 CIP35 CIP36 CIP37 CIP38 CIP39 CIP40 CIP41 CIP42 CIP43 CIP44 CIP45 CIP46 CIP47 CIP48 CIP49 CIP50 CIP51 CIP52 CIP53 CIP54 CIP55 CIP56 CIP57 CIP58 CIP59 CIP60 CIP61 CIP62 CIP63 CIP64 CIP65 CIP66 CIP67 CIP68 CIP69 CIP70 CIP71 CIP72 CIP73 CIP74 CIP75 CIP76 CIP77 CIP78 CIP79 CIP80 CIP81 CIP82 CIP83 CIP84 CIP85 CIP86 CIP87 CIP88 CIP89 CIP90 CIP91 CIP92 CIP93 CIP94 CIP95 CIP96 CIP97 CIP98 CIP99 CIP100 CIP101 CIP102 CIP103 CIP104 CIP105 CIP106 CIP107 CIP108 CIP109 CIP110 CIP111 CIP112 CIP113 CIP114 CIP115 CIP116 CIP117 CIP118 CIP119 CIP120 CIP121 CIP122 CIP123 CIP124 CIP125 CIP126 CIP127 CIP128 CIP129 CIP130 CIP131 CIP132 CIP133 CIP134 CIP135 CIP136 CIP137 CIP138 CIP139 CIP140 CIP141 CIP142 CIP143 CIP144 CIP145 CIP146 CIP147 CIP148 CIP149 CIP150 CIP151 CIP152 CIP153 CIP154 CIP155 CIP156 CIP157 CIP158 CIP159 CIP160 CIP161 CIP162 CIP163 CIP164 CIP165 CIP166 CIP167 CIP168 CIP169 CIP170 CIP171 CIP172 CIP173 CIP174 CIP175 CIP176 CIP177 CIP178 CIP179 CIP180 CIP181 CIP182 CIP183 CIP184 CIP185 CIP186 CIP187 CIP188 CIP189 CIP190 CIP191 CIP192 CIP193 CIP194 CIP195 CIP196 CIP197 CIP198 CIP199 CIP200 CIP201 CIP202 CIP203 CIP204 CIP205 CIP206 CIP207 CIP208 CIP209 CIP210 CIP211 CIP212 CIP213 CIP214 CIP215 CIP216 CIP217 CIP218 CIP219 CIP220 CIP221 CIP222 CIP223 CIP224 CIP225 CIP226 CIP227 CIP228 CIP229 CIP230 CIP231 CIP232 CIP233 CIP234 CIP235 CIP236 CIP237 CIP238 CIP239 CIP240 CIP241 CIP242 CIP243 CIP244 CIP245 CIP246 CIP247 CIP248 CIP249 CIP250 CIP251 CIP252 CIP253 CIP254 CIP255 CIP256 CIP257 CIP258 CIP259 CIP260 CIP261 CIP262 CIP263 CIP264 CIP265 CIP266 CIP267 CIP268 CIP269 CIP270 CIP271 CIP272 CIP273 CIP274 CIP275 CIP276 CIP277 CIP278 CIP279 CIP280 CIP281 CIP282 CIP283 CIP284 CIP285 CIP286 CIP287 CIP288 CIP289 CIP290 CIP291 CIP292 CIP293 CIP294 CIP295 CIP296 CIP297 CIP298 CIP299 CIP300 CIP301 CIP302 CIP303 CIP304 CIP305 CIP306 CIP307 CIP308 CIP309 CIP310 CIP311 CIP312 CIP313 CIP314 CIP315 CIP316 CIP317 CIP318 CIP319 CIP320 CIP321 CIP322 CIP323 CIP324 CIP325 CIP326 CIP327 CIP328 CIP329 CIP330 CIP331 CIP332 CIP333 CIP334 CIP335 CIP336 CIP337 CIP338 CIP339 CIP340 CIP341 CIP342 CIP343 CIP344 CIP345 CIP346 CIP347 CIP348 CIP349 CIP350 CIP351 CIP352 CIP353 CIP354 CIP355 CIP356 CIP357 CIP358 CIP359 CIP360 CIP361 CIP362 CIP363 CIP364 CIP365 CIP366 CIP367 CIP368 CIP369 CIP370 CIP371 CIP372 CIP373 CIP374 CIP375 CIP376 CIP377 CIP378 CIP379 CIP380 CIP381 CIP382 CIP383 CIP384 CIP385 CIP386 CIP387 CIP388 CIP389 CIP390 CIP391 CIP392 CIP393 CIP394 CIP395 CIP396 CIP397 CIP398 CIP399 CIP400 CIP401 CIP402 CIP403 CIP404 CIP405 CIP406 CIP407 CIP408 CIP409 CIP410 CIP411 CIP412 CIP413 CIP414 CIP415 CIP416 CIP417 CIP418 CIP419 CIP420 CIP421 CIP422 CIP423 CIP424 CIP425 CIP426 CIP427 CIP428 CIP429 CIP430 CIP431 CIP432 CIP433 CIP434 CIP435 CIP436 CIP437 CIP438 CIP439 CIP440 CIP441 CIP442 CIP443 CIP444 CIP445 CIP446 CIP447 CIP448 CIP449 CIP450 CIP451 CIP452 CIP453 CIP454 CIP455 CIP456 CIP457 CIP458 CIP459 CIP460 CIP461 CIP462 CIP463 CIP464 CIP465 CIP466 CIP467 CIP468 CIP469 CIP470 CIP471 CIP472 CIP473 CIP474 CIP475 CIP476 CIP477 CIP478 CIP479 CIP480 CIP481 CIP482 CIP483 CIP484 CIP485 CIP486 CIP487 CIP488 CIP489 CIP490 CIP491 CIP492 CIP493 CIP494 CIP495 CIP496 CIP497 CIP498 CIP499 CIP500 CIP501 CIP502 CIP503 CIP504 CIP505 CIP506 CIP507 CIP508 CIP509 CIP510 CIP511 CIP512 CIP513 CIP514 CIP515 CIP516 CIP517 CIP518 CIP519 CIP520 CIP521 CIP522 CIP523 CIP524 CIP525 CIP526 CIP527 CIP528 CIP529 CIP530 CIP531 CIP532 CIP533 CIP534 CIP535 CIP536 CIP537 CIP538 CIP539 CIP540 CIP541 CIP542 CIP543 CIP544 CIP545 CIP546 CIP547 CIP548 CIP549 CIP550 CIP551 CIP552 CIP553 CIP554 CIP555 CIP556 CIP557 CIP558 CIP559 CIP560 CIP561 CIP562 CIP563 CIP564 CIP565 CIP566 CIP567 CIP568 CIP569 CIP570 CIP571 CIP572 CIP573 CIP574 CIP575 CIP576 CIP577 CIP578 CIP579 CIP580 CIP581 CIP582 CIP583 CIP584 CIP585 CIP586 CIP587 CIP588 CIP589 CIP590 CIP591 CIP592 CIP593 CIP594 CIP595 CIP596 CIP597 CIP598 CIP599 CIP600 CIP601 CIP602 CIP603 CIP604 CIP605 CIP606 CIP607 CIP608 CIP609 CIP610 CIP611 CIP612 CIP613 CIP614 CIP615 CIP616 CIP617 CIP618 CIP619 CIP620 CIP621 CIP622 CIP623 CIP624 CIP625 CIP626 CIP627 CIP628 CIP629 CIP630 CIP631 CIP632 CIP633 CIP634 CIP635 CIP636 CIP637 CIP638 CIP639 CIP640 CIP641 CIP642 CIP643 CIP644 CIP645 CIP646 CIP647 CIP648 CIP649 CIP650 CIP651 CIP652 CIP653 CIP654 CIP655 CIP656 CIP657 CIP658 CIP659 CIP660 CIP661 CIP662 CIP663 CIP664 CIP665 CIP666 CIP667 CIP668 CIP669 CIP670 CIP671 CIP672 CIP673 CIP674 CIP675 CIP676 CIP677 CIP678 CIP679 CIP680 CIP681 CIP682 CIP683 CIP684 CIP685 CIP686 CIP687 CIP688 CIP689 CIP690 CIP691 CIP692 CIP693 CIP694 CIP695 CIP696 CIP697 CIP698 CIP699 CIP700 CIP701 CIP702 CIP703 CIP704 CIP705 CIP706 CIP707 CIP708 CIP709 CIP710 CIP711 CIP712 CIP713 CIP714 CIP715 CIP716 CIP717 CIP718 CIP719 CIP720 CIP721 CIP722 CIP723 CIP724 CIP725 CIP726 CIP727 CIP728 CIP729 CIP730 CIP731 CIP732 CIP733 CIP734 CIP735 CIP736 CIP737 CIP738 CIP739 CIP740 CIP741 CIP742 CIP743 CIP744 CIP745 CIP746 CIP747 CIP748 CIP749 CIP750 CIP751 CIP752 CIP753 CIP754 CIP755 CIP756 CIP757 CIP758 CIP759 CIP760 CIP761 CIP762 CIP763 CIP764 CIP765 CIP766 CIP767 CIP768 CIP769 CIP770 CIP771 CIP772 CIP773 CIP774 CIP775 CIP776 CIP777 CIP778 CIP779 CIP780 CIP781 CIP782 CIP783 CIP784 CIP785 CIP786 CIP787 CIP788 CIP789 CIP790 CIP791 CIP792 CIP793 CIP794 CIP795 CIP796 CIP797 CIP798 CIP799 CIP800 CIP801 CIP802 CIP803 CIP804 CIP805 CIP806 CIP807 CIP808 CIP809 CIP810 CIP811 CIP812 CIP813 CIP814 CIP815 CIP816 CIP817 CIP818 CIP819 CIP820 CIP821 CIP822 CIP823 CIP824 CIP825 CIP826 CIP827 CIP828 CIP829 CIP830 CIP831 CIP832 CIP833 CIP834 CIP835 CIP836 CIP837 CIP838 CIP839 CIP840 CIP841 CIP842 CIP843 CIP844 CIP845 CIP846 CIP847 CIP848 CIP849 CIP850 CIP851 CIP852 CIP853 CIP854 CIP855 CIP856 CIP857 CIP858 CIP859 CIP860 CIP861 CIP862 CIP863 CIP864 CIP865 CIP866 CIP867 CIP868 CIP869 CIP870 CIP871 CIP872 CIP873 CIP874 CIP875 CIP876 CIP877 CIP878 CIP879 CIP880 CIP881 CIP882 CIP883 CIP884 CIP885 CIP886 CIP887 CIP888 CIP889 CIP890 CIP891 CIP892 CIP893 CIP894 CIP895 CIP896 CIP897 CIP898 CIP899 CIP900 CIP901 CIP902 CIP903 CIP904 CIP905 CIP906 CIP907 CIP908 CIP909 CIP910 CIP911 CIP912 CIP913 CIP914 CIP915 CIP916 CIP917 CIP918 CIP919 CIP920 CIP921 CIP922 CIP923 CIP924 CIP925 CIP926 CIP927 CIP928 CIP929 CIP930 CIP931 CIP932 CIP933 CIP934 CIP935 CIP936 CIP937 CIP938 CIP939 CIP940 CIP941 CIP942 CIP943 CIP944 CIP945 CIP946 CIP947 CIP948 CIP949 CIP950 CIP951 CIP952 CIP953 CIP954 CIP955 CIP956 CIP957 CIP958 CIP959 CIP960 CIP961 CIP962 CIP963 CIP964 CIP965 CIP966 CIP967 CIP968 CIP969 CIP970 CIP971 CIP972 CIP973 CIP974 CIP975 CIP976 CIP977 CIP978 CIP979 CIP980 CIP981 CIP982 CIP983 CIP984 CIP985 CIP986 CIP987 CIP988 CIP989 CIP990 CIP991 CIP992 CIP993 CIP994 CIP995 CIP996 CIP997 CIP998 CIP999 CIP1000 CIP1001 CIP1002 CIP1003 CIP1004 CIP1005 CIP1006 CIP1007 CIP1008 CIP1009 CIP1010 CIP1011 CIP1012 CIP1013 CIP1014 CIP1015 CIP1016 CIP1017 CIP1018 CIP1019 CIP1020 CIP1021 CIP1022 CIP1023 CIP1024 CIP1025 CIP1026 CIP1027 CIP1028 CIP1029 CIP1030 CIP1031 CIP1032 CIP1033 CIP1034 CIP1035 CIP1036 CIP1037 CIP1038 CIP1039 CIP1040 CIP1041 CIP1042 CIP1043 CIP1044 CIP1045 CIP1046 CIP1047 CIP1048 CIP1049 CIP1050 CIP1051 CIP1052 CIP1053 CIP1054 CIP1055 CIP1056 CIP1057 CIP1058 CIP1059 CIP1060 CIP1061 CIP1062 CIP1063 CIP1064 CIP1065 CIP1066 CIP1067 CIP1068 CIP1069 CIP1070 CIP1071 CIP1072 CIP1073 CIP1074 CIP1075 CIP1076 CIP1077 CIP1078 CIP1079 CIP1080 CIP1081 CIP1082 CIP1083 CIP1084 CIP1085 CIP1086 CIP1087 CIP1088 CIP1089 CIP1090 CIP1091 CIP1092 CIP1093 CIP1094 CIP1095 CIP1096 CIP1097 CIP1098 CIP1099 CIP1100 CIP1101 CIP1102 CIP1103 CIP1104 CIP1105 CIP1106 CIP1107 CIP1108 CIP1109 CIP1110 CIP1111 CIP1112 CIP1113 CIP1114 CIP1115 CIP1116 CIP1117 CIP1118 CIP1119 CIP1120 CIP1121 CIP1122 CIP1123 CIP1124 CIP1125 CIP1126 CIP1127 CIP1128 CIP1129 CIP1130 CIP1131 CIP1132 CIP1133 CIP1134 CIP1135 CIP1136 CIP1137 CIP1138 CIP1139 CIP1140 CIP1141 CIP1142 CIP1143 CIP1144 CIP1145 CIP1146 CIP1147 CIP1148 CIP1149 CIP1150 CIP1151 CIP1152 CIP1153 CIP1154 CIP1155 CIP1156 CIP1157 CIP1158 CIP1159 CIP1160 CIP1161 CIP1162 CIP1163 CIP1164 CIP1165 CIP1166 CIP1167 CIP1168 CIP1169 CIP1170 CIP1171 CIP1172 CIP1173 CIP1174 CIP1175 CIP1176 CIP1177 CIP1178 CIP1179 CIP1180 CIP1181 CIP1182 CIP1183 CIP1184 CIP1185 CIP1186 CIP1187 CIP1188 CIP1189 CIP1190 CIP1191 CIP1192 CIP1193 CIP1194 CIP1195 CIP1196 CIP1197 CIP1198 CIP1199 CIP1200 CIP1201 CIP1202 CIP1203 CIP1204 CIP1205 CIP1206 CIP1207 CIP1208 CIP1209 CIP1210 CIP1211 CIP1212 CIP1213 CIP1214 CIP1215 CIP1216 CIP1217 CIP1218 CIP1219 CIP1220 CIP1221 CIP1222 CIP1223 CIP1224 CIP1225 CIP1226 CIP1227 CIP1228 CIP1229 CIP1230 CIP1231 CIP1232 CIP1233 CIP1234 CIP1235 CIP1236 CIP1237 CIP1238 CIP1239 CIP1240 CIP1241 CIP1242 CIP1243 CIP1244 CIP1245 CIP1246 CIP1247 CIP1248 CIP1249 CIP1250 CIP1251 CIP1252 CIP1253 CIP1254 CIP1255 CIP1256 CIP1257 CIP1258 CIP1259 CIP1260 CIP1261 CIP1262 CIP1263 CIP1264 CIP1265 CIP1266 CIP1267 CIP1268 CIP1269 CIP1270 CIP1271 CIP1272 CIP1273 CIP1274 CIP1275 CIP1276 CIP1277 CIP1278 CIP1279 CIP1280 CIP1281 CIP1282 CIP1283 CIP1284 CIP1285 CIP1286 CIP1287 CIP1288 CIP1289 CIP1290 CIP1291 CIP1292 CIP1293 CIP1294 CIP1295 CIP1296 CIP1297 CIP1298 CIP1299 CIP1300 CIP1301 CIP1302 CIP1303 CIP1304 CIP1305 CIP1306 CIP1307 CIP1308 CIP1309 CIP1310 CIP1311 CIP1312 CIP1313 CIP1314 CIP1315 CIP1316 CIP1317 CIP1318 CIP1319 CIP1320 CIP1321 CIP1322 CIP1323 CIP1324 CIP1325 CIP1326 CIP1327 CIP1328 CIP1329 CIP1330 CIP1331 CIP1332 CIP1333 CIP1334 CIP1335 CIP1336 CIP1337 CIP1338 CIP1339 CIP1340 CIP1341 CIP1342 CIP1343 CIP1344 CIP1345 CIP1346 CIP1347 CIP1348 CIP1349 CIP1350 CIP1351 CIP1352 CIP1353 CIP1354 CIP1355 CIP1356 CIP1357 CIP1358 CIP1359 CIP1360 CIP1361 CIP1362 CIP1363 CIP1364 CIP1365 CIP1366 CIP1367 CIP1368 CIP1369 CIP1370 CIP1371 CIP1372 CIP1373 CIP1374 CIP1375 CIP1376 CIP1377 CIP1378 CIP1379 CIP1380 CIP1381 CIP1382 CIP1383 CIP1384 CIP1385 CIP1386 CIP1387 CIP1388 CIP1389 CIP1390 CIP1391 CIP1392 CIP1393 CIP1394 CIP1395 CIP1396 CIP1397 CIP1398 CIP1399 CIP1400 CIP1401 CIP1402 CIP1403 CIP1404 CIP1405 CIP1406 CIP1407 CIP1408 CIP1409 CIP1410 CIP1411 CIP1412 CIP1413 CIP1414 CIP1415 CIP1416 CIP1417 CIP1418 CIP1419 CIP1420 CIP1421 CIP1422 CIP1423 CIP1424 CIP1425 CIP1426 CIP1427 CIP1428 CIP1429 CIP1430 CIP1431 CIP1432 CIP1433 CIP1434 CIP1435 CIP1436 CIP1437 CIP1438 CIP1439 CIP1440 CIP1441 CIP1442 CIP1443 CIP1444 CIP1445 CIP1446 CIP1447 CIP1448 CIP1449 CIP1450 CIP1451 CIP1452 CIP1453 CIP1454 CIP1455 CIP1456 CIP1457 CIP1458 CIP1459 CIP1460 CIP1461 CIP1462 CIP1463 CIP1464 CIP1465 CIP1466 CIP1467 C