Potential multi-insert clones in each patient identified by VIS correlation at different timepoints and in different cell lineages.

P1 multicopyClone

clones	Gene_chr-strand-coordinate_Counts	1	2	2	3	3	4	4	4	4	5	5	6	6	6	6	6	6	7	7	7	7	8	8
		CNA1	CEP	DDB1	MRE	KIN4	SUP1	MZF	FYN	GPA	PLC3	BTN	ATF4	HSF1	ITGA	FGD	OR7	ABCF	TBI	GGA	WIPC	EPS	SAM	NUM
1	CMAHPchr6-25004285_22954	1.0	1.0	0.8	0.8	0.5	0.5	0.7	0.7	0.7	0.6	0.6	0.7	0.9	0.9	0.5	0.3	0.2	0.0	-0.1	0.1	0.2	0.1	0.1
1	CEP128chr14+81296679_12307	1.0	1.0	0.8	0.8	0.5	0.4	0.7	0.7	0.7	0.6	0.7	0.7	0.8	0.8	0.5	0.4	0.2	0.1	-0.1	0.1	0.2	0.1	0.1
2	DCLRE1Achr10+115608313_20340	0.8	0.8	1.0	1.0	0.0	-0.1	1.0	1.0	1.0	0.9	0.7	0.8	0.7	0.7	0.8	0.7	0.7	0.8	0.7	0.4	0.2	0.4	0.5
2	MR3188chr19+18398537_12404	0.8	0.8	1.0	1.0	0.0	-0.1	1.0	1.0	1.0	0.9	0.7	0.8	0.7	0.7	0.8	0.7	0.7	0.8	0.7	0.4	0.2	0.4	0.5
3	KLH20chr1-173713069_8705	0.5	0.5	0.0	0.0	1.0	1.0	-0.2	-0.2	-0.2	-0.3	-0.1	-0.1	0.5	0.4	0.4	-0.3	-0.4	-0.4	-0.2	-0.3	0.0	-0.2	-0.3
3	SUPT3Hchr6-44902245_7442	0.5	0.4	-0.1	-0.1	1.0	1.0	-0.3	-0.2	-0.3	-0.5	-0.1	0.0	0.5	0.4	-0.4	-0.4	-0.4	-0.2	-0.2	-0.3	0.1	-0.2	-0.4
4	IKZF1chr7-50277291_4519	0.7	0.7	1.0	1.0	-0.2	-0.3	1.0	0.9	1.0	1.0	0.8	0.9	0.6	0.6	0.9	0.8	0.8	0.3	0.1	0.2	0.6	0.9	1.0
4	FYNchr6-112131278_2541	0.7	0.7	1.0	1.0	-0.2	-0.2	1.0	1.0	1.0	0.9	0.5	0.7	0.6	0.7	0.7	0.5	0.5	0.1	-0.1	0.1	0.1	0.2	0.1
4	GPATCHBchr17-42528404_1902	0.7	0.7	1.0	1.0	-0.2	-0.3	1.0	1.0	1.0	0.9	0.6	0.8	0.6	0.6	0.7	0.6	0.7	0.6	0.7	0.6	0.9	0.9	0.9
4	PLCB1chr20+45154527_1132	0.6	0.6	0.9	0.9	-0.3	-0.5	1.0	0.9	0.9	1.0	0.8	0.9	0.3	0.4	0.9	0.8	0.8	0.2	0.0	0.0	0.2	0.3	0.2
5	BTN3A3chr6-26442660_2174	0.6	0.7	0.7	0.7	-0.1	-0.2	0.8	0.5	0.6	0.8	1.0	1.0	0.2	0.2	1.0	1.0	1.0	0.1	0.1	0.2	0.4	0.3	0.2
5	ATF6chr1+161786573_1672	0.7	0.7	0.8	0.8	-0.1	0.0	0.9	0.7	0.7	0.9	1.0	1.0	0.5	0.4	1.0	1.0	1.0	0.3	0.1	0.2	0.5	0.3	0.3
6	HIF3Chr12+31988014_2844	0.9	0.8	0.7	0.7	0.5	0.5	0.6	0.6	0.6	0.3	0.2	0.5	1.0	1.0	0.2	0.0	0.0	0.0	-0.3	0.0	-0.1	0.1	0.0
6	ITGALchr16+30482288_1494	0.8	0.8	0.7	0.7	0.4	0.4	0.6	0.7	0.6	0.4	0.2	0.4	1.0	1.0	0.1	0.1	0.0	0.2	0.1	0.3	0.3	0.3	0.3
6	FGD2chr6-37056819_887	0.5	0.5	0.8	0.8	-0.4	-0.4	0.9	0.7	0.8	0.9	1.0	1.0	0.3	0.3	1.0	1.0	1.0	0.9	0.8	1.0	0.9	0.9	0.9
6	OR7C1chr19-14882011_511	0.3	0.4	0.7	0.7	-0.3	-0.4	0.8	0.5	0.6	0.8	1.0	1.0	0.0	0.1	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9
6	ABCbchr9-136146694_410	0.2	0.2	0.6	0.7	-0.4	-0.4	0.8	0.5	0.6	0.8	1.0	1.0	0.0	0.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	0.9
7	PTBP3chr9-115061883_1378	0.0	0.1	0.3	0.4	-0.2	-0.2	0.3	0.1	0.7	0.2	0.3	0.3	0.0	0.2	1.0	1.0	1.0	0.9	1.0	0.9	0.8	0.8	0.8
7	GGA1chr22-38016786_1067	-0.1	-0.1	0.1	0.2	-0.3	-0.3	0.1	-0.1	0.6	0.0	0.1	0.1	-0.3	0.1	0.8	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.9
7	WIPF1chr2+175516182_957	0.1	0.1	0.3	0.4	0.0	0.0	0.2	-0.1	0.7	0.0	0.2	0.0	0.0	0.2	1.0	1.0	1.0	0.9	1.0	1.0	0.9	0.8	0.9
7	CEP57L1chr6+109451552_880	0.2	0.2	0.5	0.5	-0.2	-0.2	0.6	0.1	0.6	0.2	0.4	0.5	-0.1	0.1	0.9	1.0	0.9	0.9	0.9	1.0	0.9	0.9	0.9
8	SAMD4Bchr19-39855516_1025	0.1	0.1	0.9	0.9	-0.3	-0.4	0.9	0.2	0.9	0.3	0.3	0.3	0.1	0.3	0.9	0.9	0.9	0.8	0.8	0.8	0.9	1.0	1.0
8	NUMBchr14-73929757_1021	0.1	0.1	0.9	0.9	-0.2	-0.3	1.0	0.1	0.9	0.2	0.3	0.3	0.0	0.3	0.9	0.9	0.9	0.8	0.9	0.9	0.9	1.0	1.0

P3 multicopyClone

clones	Gene_chr-strand-coordinate_Counts	1	2	2	3	3	3	4	4	5	5	5
		NFR	SHC	HMG	ZNF	NF1	PRK	NCA	HMG	PSM	PPF	ATF7
1	NFIchr17+29625553_10123	1.0	-0.3	-0.3	-0.1	-0.2	-0.1	-0.4	-0	-0.1	-0.1	-0.2
1	SIK3chr11+116832946_8551	-0.3	1.0	1.0	-0.2	-0.2	-0.2	1.0	0.9	-0.2	-0.3	-0.3
2	HMGA2chr12+66338097_7732	-0.3	1.0	1.0	-0.2	-0.1	-0.4	1.0	0.9	-0.3	-0.3	-0.3
3	ZNF318chr6-43333206_2872	-0.1	-0.2	-0.2	1.0	0.9	1.0	-0.2	-0	0.9	0.9	0.9
3	NFIchr17+29578841_2930	-0.2	-0.2	-0.1	0.9	1.0	0.9	-0.1	-0	0.8	0.8	0.8
3	PRKRPchr7-102066577_1826	-0.1	-0.2	-0.4	1.0	0.9	1.0	-0.4	-0	1.0	1.0	0.9
4	NCAPD2chr12-6625631_2401	-0.4	1.0	1.0	-0.2	-0.1	-0.4	1.0	0.9	-0.3	-0.3	-0.3
4	HMGA2chr12+66279246_2156	-0.3	0.9	0.9	-0.3	-0.2	-0.3	0.9	1	-0.4	-0.3	-0.3
5	PSMD1chr2+232016961_1042	-0.1	-0.2	-0.3	0.9	0.8	1.0	-0.3	-0	1.0	1.0	1.0
5	PPP3Rchr2+68454944_940	-0.1	-0.3	-0.3	0.9	0.8	1.0	-0.3	-0	1.0	1.0	1.0
5	ATF7IPchr12+14546279_1675	-0.2	-0.3	-0.3	0.9	0.8	0.9	-0.3	-0	1.0	1.0	1.0

P4 MulticopyClone

clones	Gene_chr-strand-coordinate_Counts	1	1	1	1	1	1	1	2	3	3	3	4	4	5	5	5	5	5	6	6	6	7	7	8	8	8	8	8	8	9	9	9	10	10
		HMG	DNM	PCN	SAE	IKF2	CDI	HMG	EIF	BAD	CAR	BAD	ARE	SNR	PTK	LIN	SPH	TIAF	TAF	HMG	DNM	HMG	AAM	MED	CDU	SMR	VAN	ANO	HMG	HMG	TTC	ARL	ARL	A2chr12+66295717_991
1	HMGA2chr12+66241632_25333	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	0.1	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.5	-0.2	-0.2	-0.4	-0.3	-0.2	0.0	0.2	0.2	0.8	0.7
1	DNM2chr19+10913399_25287	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	-0.1	0.2	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	-0.2	-0.2	-0.4	-0.3	-0.2	0.0	0.2	0.2	0.8	0.7
1	PCNTchr21+47761155_24620	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	-0.1	0.2	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.6	-0.3	-0.3	-0.5	-0.4	-0.3	0.0	0.2	0.2	0.8	0.7
1	SCAlchr9-127815197_23938	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.0	-0.1	-0.1	-0.1	0.1	0.1	0.5	0.4	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.6	-0.2	-0.2	-0.3	-0.3	-0.2	0.0	0.1	0.1	0.8	0.7
1	SAE1chr19-47654263_23695	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	-0.1	0.2	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.5	-0.2	-0.2	-0.4	-0.3	-0.2	0.0	0.2	0.2	0.8	0.7
1	KF28Rchr3+185531758_22723	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	-0.1	0.2	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.5	-0.2	-0.2	-0.4	-0.3	-0.2	0.0	0.2	0.2	0.8	0.7
1	C20orf194chr20+3306493_17239	1.0	1.0	1.0	1.0	1.0	1.0	0.0	0.1	-0.1	-0.1	-0.1	0.2	0.2	0.5	0.5	0.6	0.6	0.3	0.2	0.3	0.5	0.5	-0.3	-0.3	-0.4	-0.4	-0.3	0.0	0.2	0.2	0.8	0.8
2	HMGA2chr12+66241676_14237	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.9	-0.1	-0.1	-0.2	0.0	0.0	0.8	0.8	0.8	0.7	0.7	0.5	0.5	0.5	0.3	0.3	-0.2	-0.3	-0.5	-0.4	0.6	0.3	0.5	0.4	0.5
2	KIFC1chr6+33376261_10490	0.1	0.1	0.1	0.0	0.1	0.1	0.9	1.0	0.1	0.0	0.0	0.3	0.2	0.8	0.8	0.8	0.6	0.6	0.2	0.2	0.1	0.0	0.0	-0.4	-0.3	-0.4	-0.4	0.5	0.5	-0.4	0.5	0.5
3	RAD52chr12+1048229_6526	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	1.0	1.0	0.9	-0.1	-0.2	-0.2	-0.2	-0.2	-0.2	-0.3	-0.3	-0.4	-0.3	-0.3	-0.3	-0.2	-0.2	-0.4	-0.3	-0.1	-0.3	-0.1	-0.1	-0.3	-0.2
3	CARD8chr19+48751246_5976	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	0.0	1.0	1.0	-0.1	-0.2	-0.2	-0.2	-0.2	-0.2	-0.3	-0.4	-0.3	-0.3	-0.3	-0.2	-0.2	-0.4	-0.2	-0.2	-0.3	-0.1	-0.1	-0.3	-0.2
3	RAD52chr12+1048218_1468	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.2	0.0	0.9	1.0	1.0	-0.2	-0.2	-0.3	-0.3	-0.3	-0.3	-0.3	-0.4	-0.3	-0.3	-0.3	-0.2	-0.3	-0.9	-0.3	-0.2	-0.3	-0.1	-0.1	-0.3	-0.2
4	ARID1Achr1+27060375_6017	0.1	0.2	0.1	0.1	0.2	0.2	0.2	0.0	0.3	-0.1	-0.1	-0.2	1.0	1.0	0.3	0.3	0.3	0.3	-0.3	-0.4	-0.4	-0.3	-0.2	-0.4	-0.3	-0.7	-0.3	-0.5	-0.4	-0.3	-0.3	0.1	0.2
4	SNRNP27chr2+70123728_4065	0.2	0.2	0.2	0.1	0.2	0.2	0.2	0.0	0.2	-0.2	-0.2	-0.2	1.0	1.0	0.3	0.3	0.3	0.3	-0.3	-0.3	-0.4	-0.3	-0.2	-0.4	-0.3	-0.1	-0.3	-0.5	-0.4	-0.2	-0.2	0.1	0.2
5	PTK2chr8-141779229_5797	0.5	0.5	0.5	0.5	0.5	0.5	0.8	0.8	-0.2	-0.2	-0.3	0.3	1.0	1.0	1.0	0.9	0.9	0.8	0.4	0.3	0.4	0.3	0.3	-0.5	-0.3	-0.4	-0.5	-0.6	0.4	0.3	0.3	0.8	0.7
5	LINC00221chr14+107160930_5655	0.5	0.5	0.4	0.4	0.5	0.5	0.5	0.8	0.8	-0.2	-0.2	-0.3	0.3	0.3	1.0	1.0	0.9	0.9	0.9	0.4	0.3	0.4	0.4	0.3	-0.4	-0.2	-0.3	-0.4	-0.4	0.3	0.3	0.8	0.7
5	SEH1Lchr18-12975963_4633	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.8	0.8	-0.2	-0.2	-0.3	0.3	0.3	1.0	1.0	0.9	1.0	0.9	0.4	0.3	0.4	0.4	0.3	-0.4	-0.4	-0.3	0.3	0.3	0.3	0.8	0.7
5	TMMOCchr3-119223601_3242	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.7	0.6	-0.2	-0.2	-0.3	0.3	0.3	0.9	0.9	1.0	0.9	0.8	0.4	0.4	0.5	0.6	0.6	-0.4	-0.2	-0.4	-0.4	-0.4	0.2	0.2	0.8	0.7
5	TMEM125chr1+43710494_1555	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.7	0.6	-0.3	-0.2	-0.3	0.3	0.3	0.9	0.9	0.9	0.9	1.0	0.4	0.4	0.5	0.6	0.6	-0.4	-0.3	-0.9	-0.5	-0.5	0.2	0.2	0.2	0.9	0.7
6	HMGA2chr12+66304255_4944	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.2	-0.3	-0.3	-0.3	-0.3	0.4	0.4	0.4	0.4	1.0	1.0	0.9	0.7	0.7	-0.3	-0.2	-0.2	-0.4	-0.3	0.7	0.5	0.4	0.5	0.5
6	DYNLRb1chr18+46694767_4066	0.2	0.2	0.2	0.2	0.2	0.2	0.5	0.2	0.4	-0.4	-0.4	-0.3	0.3	0.3	0.4	0.4	0.4	1.0	1.0	0.9	0.7	0.7	-0.3	-0.2	-0.6	-0.3	-0.3	0.8	0.5	0.4	0.4	0.4
6	HMGA2chr12+66288561_3569	0.3	0.3	0.3	0.3	0.3	0.3	0.3	0.5	0.1	-0.3	-0.3	-0.3	-0.4	-0.4	0.4	0.4	0.4	0.5	0.5	0.9	0.9	1.0	0.8	0.8	-0.2	-0.2	-1.0	-0.3	-0.2	0.5	0.2	0.2	0.5	0.4
7	HMGA2chr12+66285086_3199	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.3	0.0	-0.3	-0.3	-0.3	-0.3	-0.3	0.4	0.4	0.4	0.6	0.6	0.7	0.7	0.8	1.0	1.0	-0.3	0.0	0.0	-0.4	-0.2	0.3	0.0	-0.1	0.6	0.4
7	FAM129Cchr19-17661479_2333	0.5	0.5	0.6	0.6	0.5	0.5	0.5	0.3	0.0	-0.3	-0.3	-0.2	-0.2	-0.3	0.4	0.4	0.4	0.6	0.6	0.7	0.7	0.8	1.0	1.0	-0.3	0.0	0.0	-0.4	-0.2	0.2	0.0	0.0	0.5	0.4
8	MED12Lchr3+151075441_2712	-0.2	-0.2	-0.3	-0.2	-0.2	-0.2	-0.3	-0.3	-0.4	-0.2	-0.2	-0.2	-0.4	-0.4	-0.5	-0.4	-0.3	-0.4	-0.4	-0.3	-0.3	-0.2	-0.3	-0.2	1.0	1.0	1.0	1.0	1.0	-0.3	-0.3	-0.4	-0.4	-0.3
8	CDLGALT1chr19-17676000_2611	-0.2	-0.2	-0.3	-0.2	-0.2	-0.2	-0.3	-0.2	-0.3	-0.2	-0.3	-0.3	-0.3	-0.3	-0.3	-0.2	-0.3	-0.2	-0.3	-0.2	-0.3	-0.3	-0.3	-0.2	1.0	1.0	1.0	1.0	1.0	-0.3	-0.5	-0.6	-0.3	-0.4
8	SMIMBchr4+154061591_2156	-0.4	-0.4	-0.5	-0.3	-0.4	-0.5	-0.4	-0.3	-0.4	-0.4	-0.4	-0.4	-0.9	-0.7	-0.1	-0.4	-0.3	-0.4	-0.4	0.8	-0.2	-0.6	1.0	1.0	1.0	1.0	1.0	1.0	1.0	-0.5	-0.4	-0.5	-0.4	0.9
8	VANGL2chr1+160415618_763	-0.3	-0.3	-0.4	-0.3	-0.3	-0.3	-0.4	-0.5	-0.4	-0.3	-0.2	-0.3	-0.3	-0.3	-0.5	-0.4	-0.4	-0.4	-0.3	-0.3	-0.4	-0.4	1.0	1.0	1.0	1.0	1.0	1.0	1.0	-0.4	-0.5	-0.7	-0.5	-0.3
8	ANKA1Lchr10+81946831_619	-0.2	-0.2	-0.3	-0.2	-0.2	-0.2	-0.3	-0.4	-0.4	-0.1	-0.2	-0.2	-0.5	-0.6	-0.4	-0.3	-0.2	-0.5	-0.3	-0.2	-0.2	-0.2	1.0	1.0	1.0	1.0	1.0	-0.4	-0.4	-0.3	-0.5	-0.4	-0.4	-0.3
9	HMGA2chr12+66303366_3829	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	0.5	-0.3	-0.3	-0.3	-0.4	-0.4	0.4	0.3	0.3	0.2	0.2	0.7	0.8	0.5	0.3	0.2	-0.3	-0.3	-0.5	-0.4	-0.4	1.0	0.9	0.8	0.3	0.5
9	HMGA2chr12+66287312_2266	0.2	0.2	0.2	0.1	0.2	0.2	0.2	0.3	0.5	-0.1	-0.1	-0.1	-0.3	-0.2	0.3	0.3	0.3	0.2	0.2	0.5	0.5	0.2	0.0	0.0	-0.3	-0.5	-0.4	-0.5	-0.4	0.9	1.0	1.0	0.4	0.6
9	TTC28chr22+28642780_1582	0.2	0.2	0.2	0.1	0.2	0.2	0.2	0.3	0.4	-0.1	-0.1	-0.1	-0.3	-0.2	0.3	0.3	0.3	0.2	0.2	0.4	0.4	0.2	-0.1	0.1	-0.4	-0.6	-0.5	-0.7	-0.5	-0.8	-1.0	-1.0	0.3	0.6
10	RABL6chr9-139707884_1051	0.8	0.8	0.8	0.8	0.8	0.8	0.8	0.5	0.5	-0.3	-0.3	-0.3	-0.3	-0.3	0.1	0.8	0.8	0.8	0.8	0.4	0.5	0.6	0.5	0.4	-0.3	-0.4	-0.5	-0.5	-0.3	0.3	0.4	0.3	1.0	0.9
10	HMGA2chr12+66295717_991	0.7	0.7	0.7	0.7	0.7	0.7	0.8	0.4	0.5	-0.2	-0.2	-0.2	-0.2	-0.2	0.7	0.7	0.7	0.7	0.7	0.5	0.4	0.4	0.4	0.4	-0.3	-0.4	-0.9	-0.3	-0.4	0.5	0.6	0.6	0.9	1.0

P6 multicopyClone

| clones | Gene_chr-strand-coordinate_Counts | 1 | 1 | 1 | 1 | 1 | 1 | 1