

Supplementary table 5. Structural variants involving the IGH locus

Sample	Partner Gene				IGH Location	
	Chr	Position	Gene	Description	Chr	Position
MM2	chr11	69265894	CCND1	Upstream CCND1	chr14	106328777
MM4	chr11	68926836	CCND1	Upstream CCND1	chr14	106213471
MM54	chr11	69066683	CCND1	Upstream CCND1	chr14	106177641
MM52	chr11	69074945	CCND1	Upstream CCND1	chr14	106198580
MM56	chr11	69042227	CCND1	Upstream CCND1	chr14	106329450
MM3	chr11	69249624	CCND1	Upstream CCND1	chr14	106351905
MM1	chr11	69448178	CCND1	Upstream CCND1	chr14	106205263
MM28	chr11	69329141	CCND1	Upstream CCND1	chr14	106035720
MM25	chr11	69157963	CCND1	Upstream CCND1	chr14	106380221
MM27	chr11	69441018	CCND1	Upstream CCND1	chr14	106325867
MM29	chr11	68941330	CCND1	Upstream CCND1	chr14	106328486
MM51	chr11	68971748	CCND1	Upstream CCND1	chr14	106210831
MM50	chr11	69274620	CCND1	Upstream CCND1	chr14	106327265
MM55	chr11	69055482	CCND1	Upstream CCND1	chr14	106208357
MM57	chr11	69226380	CCND1	Upstream CCND1	chr14	106209521
MM58	chr11	68873923	CCND1	Upstream CCND1	chr14	106177107
MM53	chr11	69024193	CCND1	Upstream CCND1	chr14	106323915
MM26	chr11	68923786	CCND1	Upstream CCND1	chr14	106210920
MM11	chr6	41909759	CCND3	Intergenic space between CCND3 and TAF8	chr14	106323618
MM63	chr6	41927278	CCND3	Intergenic space between CCND3 and TAF8	chr14	106196795
MM37	chr12	4260862	CCND2	>100kb upstream CCND2	chr14	106327199
MM61	chr4	1854440	FGFR3/WHSC1	MB4-1	chr14	106323574
MM7	chr4	1865887	FGFR3/WHSC1	MB4-1	chr14	106325118
MM30	chr4	1911242	FGFR3/WHSC1	MB4-3	chr14	106208902
MM9	chr4	1873952	FGFR3/WHSC1	MB4-1	chr14	106112389
MM6	chr4	1880602	FGFR3/WHSC1	MB4-1	chr14	106324890
MM8	chr4	1878218	FGFR3/WHSC1	MB4-1	chr14	106326545
MM59	chr4	1857266	FGFR3/WHSC1	MB4-1	chr14	106113227
MM60	chr4	1857619	FGFR3/WHSC1	MB4-1	chr14	106325742
MM31	chr4	1911708	FGFR3/WHSC1	MB4-3	chr14	106325383
MM43	chr4	1873207	FGFR3/WHSC1	MB4-1	chr14	106177075
MM62	chr16	79030173	MAF	Within last intron WWOX	chr14	106791007
MM10	chr16	78663089	MAF	Within last intron WWOX	chr14	106178128
MM32	chr16	78931725	MAF	Within last intron WWOX	chr14	106112391
MM36	chr20	38501210	MAFB	Between DHX35 and MAFB	chr14	106367015
MM64	chr8	129263724	MYC	Downstream MYC, intergenic space between PVT1 and GSDMC	chr14	106067309

MM67	chr8	128887049	MYC	Downstream MYC, within PVT1 intron	chr14	106298190
MM44	chr1	17785500	RCC2	RCC2 closest upstream gene	chr14	106110571
MM33	chr16	3721137	TRAP1	Within intron of TRAP1	chr14	106326344
MM34	chr3	141121901	ZBTB38	Within intron of ZBTB38	chr14	106211420
MM35	chr1	207962297	CD46	Within intron of CD46	chr14	106112016
MM13	chr4	45261655	GABRG1/GNPDA2	Downstream of GABRG1 and upstream of GNPDA2	chr14	106259161
MM64	chr6	7921560	TXNDC5	Upstream of TXNDC5	chr14	106029433
MM12	chr12	122472355	BCL7A	Within intron of BCL7A	chr14	106326619
