

Table S2 Excision events with footprints in A123-0

Insertion Position	Imperfect Aligned Spanners	Aligned Sequences that support
Chr1:39904180..39904182	2	Chr1:39904177..39904187: CCAT TA GATCA INDEL in A123-0: - T . .
Chr1:28490065..28490067	2	Chr1:28490062..28490072: TAG TTA TAGCC A -
Chr1:27292708..27292710	2	Chr1:27292705..27292715: TTAT TA TGGCG A -
Chr1:32658455..32658457	2	Chr1:32658452..32658462: TTAT TTA TGGGC A -
Chr2:9438880..9438882	2	Chr2:9438877..9438887: CTAT TTA GGGAA G - - .
Chr2:7838215..7838217	3	Chr2:7838212..7838222: GCC TTA TGGAC A -
Chr3:28577818..28577820	2	Chr3:28577815..28577825: CCC TA ATGGCC A -
Chr3:8760869..8760871	5	Chr3:8760866..8760876: GGAT TA GAGCA G -
Chr4:21249876..21249878	2	Chr4:21249873..21249883: TCAT TA GAAGA G - - . .
Chr6:24738718..24738720	8	Chr6:24738715..24738722: CTG - - - TA AGA . . GGCC
Chr7:19446275..19446277	2	Chr7:19446272..19446282: ATAT TA AGCGCC G -
Chr7:25542894..25542896	2	Chr7:25542891..25542901: ACAT TA ATGGCC A -
Chr9:12538485..12538487	3	Chr9:12538482..12538492: TAAT TTA GAGCA G -

TSDs are in bold.