

List of 53 structural variations detected by DELLY, including 37 fusions.

chr1	pos1	str1	chr2	pos2	str2	gene1	transcript1	site1
chr1	24225490	0	chr1	24225990	1	CNR2	NM_001841	5'-UTR of
chr2	89077528	0	chr2	97834620	1	ANKRD3	NR_015424	5'-UTR of
chr10	69876279	0	chr10	69876818	1	MYPN	NM_032578	5'-UTR of
chr12	113655969	0	chr12	113656492	1	IQCD	NM_138451	5'-UTR of
chr13	79984564	0	chr13	79985074	1	RBM26-1	NR_038991	5'-UTR of
chr19	34117644	0	chr19	34118145	1	CHST8	NM_00112789	5'-UTR of
chr1	27803974	1	chr1	27804601	0	WASF2	NM_006990	5'-UTR of
chr2	66853813	1	chr2	66854336	0	LOC100426111	NR_110156	5'-UTR of
chr2	89077005	1	chr2	97834689	0	ANKRD3	NR_015424	5'-UTR of
chr3	113914716	1	chr3	113915224	0	DRD3	NM_00128256	5'-UTR of
chr4	1305901	1	chr4	1306418	0	MAEA	NM_00101740	Exon 2 of
chr4	6822098	1	chr4	6822622	0	KIAA023	NM_014743	5'-UTR of
chr7	100550429	1	chr7	100551331	0	MUC3A	NM_005960	Exon 2 of
chr9	71738010	1	chr9	71743545	0	TJP2	NM_00117047	5'-UTR of
chr9	71777788	1	chr9	71778389	0	TJP2	NM_00117047	5'-UTR of
chr15	73990333	1	chr15	73990965	0	CD276	NM_00102473	5'-UTR of
chr19	41303107	1	chr19	41303649	0	RAB4B-E	NR_037791	5'-UTR of
chr19	48868386	1	chr19	48868893	0	SYNGR4	NM_012451	5'-UTR of
chr16	84735776	0	chr16	84736793	0	USP10	NM_005153	Intron of
chr6	45872235	1	chr1	47804268	0	CLIC5	NM_016929	Intron of
chr6	160521753	1	chr1	64587033	0	IGF2R	NM_000876	Intron of
chr6	160521850	0	chr1	161309327	1	IGF2R	NM_000876	Intron of
chr8	104825397	1	chr3	130834933	0	RIMS2	NM_00110017	Intron of
chr9	94058283	1	chr4	80864776	1	AUH	NM_001698	Intron of
chr11	22737218	0	chr2	238252081	1	GAS2	NM_00114389	Intron of
chr11	85211483	1	chr7	107829464	0	DLG2	NM_00114269	Intron of
chr14	77657669	1	chr3	25802298	1	TMEM63	NM_020431	5'-UTR of
chr14	93525417	1	chr2	33141483	0	ITPK1	NM_00114259	Intron of
chr17	8011276	0	chr9	77754138	0	ALOXE3	NM_00116596	Intron of
chr19	466729	1	chr2	33141683	0	ODF3L2	NM_182577	Intron of
chr19	3145720	0	chr18	22759066	1	GNA15	NM_002068	Intron of
chr21	11057840	1	chr7	151970870	0	BAGE2	NM_182482	Intron of
chr21	11058592	1	chr7	151971570	0	BAGE2	NM_182482	Intron of
chr21	11061070	1	chr7	151974055	0	BAGE2	NM_182482	Intron of
chr21	11061611	0	chr7	151973858	1	BAGE2	NM_182482	Intron of
chr21	11064829	0	chr7	151977043	1	BAGE2	NM_182482	Intron of
chr21	11065650	1	chr7	151978687	0	BAGE2	NM_182482	Intron of
chr21	11066272	0	chr7	151978561	1	BAGE2	NM_182482	Intron of
chr21	11067283	0	chr7	151979484	1	BAGE2	NM_182482	Intron of
chr21	11068192	1	chr7	151981277	0	BAGE2	NM_182482	Intron of
chr21	11069441	1	chr7	151982390	0	BAGE2	NM_182482	Intron of
chr21	11070355	1	chr7	151983353	0	BAGE2	NM_182482	Intron of
chr21	11073863	0	chr7	151986009	1	BAGE2	NM_182482	Intron of
chr21	11076622	0	chr7	151988969	1	BAGE2	NM_182482	Intron of
chr21	11077444	1	chr7	152074338	0	BAGE2	NM_182482	Intron of

chr21	11081547	0 chr3	25802279	1 BAGE2	NM_182482	Intron of
chr21	11083142	1 chr7	152079820	0 BAGE2	NM_182482	Intron of
chr21	11089361	1 chr7	152085825	0 BAGE2	NM_182482	Intron of
chr21	11089441	0 chr7	152085222	1 BAGE2	NM_182482	Intron of
chr21	11097380	1 chr7	152099352	0 BAGE2	NM_182482	Intron of
chr22	25156885	0 chr3	25802274	1 PIWIL3	NM_00125597	Intron of
chr22	41834849	0 chr3	25802294	1 TOB2	NM_016272	5'-UTR of
chrX	107153859	1 chr17	64220750	1 MID2	NM_052817	Intron of

Column 'fusion' shows structural variation classification.

use_dom	gene2	transcript2	site2	kinase_domain2	fusion
f	CNR2(-)	CNR2	NM_001841	5'-UTR of CNR2(-):25Kb befo	Deletion within transcript
f	ANKRD	ANKRD3	NM_001164	Intron of ANKRD36(+):1Kb aft	Transcript Fusion {ANKRD3
f	MYPN(+)	MYPN	NM_032578	5'-UTR of MYPN(+):4Kb befor	Deletion within transcript
f	IQCD(-)	IQCD	NM_138451	5'-UTR of IQCD(-):23Kb befor	Deletion within transcript
f	RBM26-	RBM26-	NR_038991	5'-UTR of RBM26-AS1(+):13K	Deletion within transcript
f	CHST8	CHST8	NM_001127	5'-UTR of CHST8(+):62Kb be	Deletion within transcript
f	WASF2	WASF2	NM_006990	5'-UTR of WASF2(-):70Kb be	Duplication within transcript
f	LOC100	LOC100	NR_110156	5'-UTR of LOC100507073(+):	Duplication within transcript
f	ANKRD	ANKRD3	NM_001164	Intron of ANKRD36(+):1Kb aft	Transcript Fusion {ANKRD3
f	DRD3(-)	DRD3	NM_001282	5'-UTR of DRD3(-):68Kb befo	Duplication within transcript
f	MAEA(+)	MAEA	NM_001017	Intron of MAEA(+):469bp afte	Duplication within transcript
f	KIAA02:	KIAA023	NM_014743	5'-UTR of KIAA0232(+):4Kb b	Duplication within transcript
f	MUC3A	MUC3A	NM_005960	Exon 2 of MUC3A(+)	Duplication within transcript
f	TJP2(+)	TJP2	NM_001170	5'-UTR of TJP2(+):84Kb befor	Duplication within transcript
f	TJP2(+)	TJP2	NM_001170	5'-UTR of TJP2(+):49Kb befor	Duplication within transcript
f	CD276(-)	CD276	NM_001024	5'-UTR of CD276(+):1Kb befo	Duplication within transcript
f	RAB4B-	RAB4B-	NR_037791	5'-UTR of RAB4B-EGLN2(+):	Duplication within transcript
f	SYNGR	SYNGR4	NM_012451	5'-UTR of SYNGR4(+):206bp	Duplication within transcript
USP10(+)	USP10	USP10	NM_005153	Intron of USP10(+):3Kb after	Antisense Fusion
CLIC5(-):	CMPK1	CMPK1	NM_016308	Intron of CMPK1(+):4Kb after	Antisense Fusion
IGF2R(+)	ROR1	ROR1	NM_005012	Intron of Kinase Domain Not	Protein Fusion: in frame {R
IGF2R(+)	SDHC	SDHC	NM_003001	Intron of SDHC(+):1Kb before	Protein Fusion: in frame {IC
RIMS2(+)	NEK11	NEK11	NM_145910	Intron of Partial Kinase Doma	Protein Fusion: in frame {N
AUH(-):1	ANTXR2	ANTXR2	NM_001286	Intron of ANTXR2(-):34Kb aft	Antisense Fusion
GAS2(+):	COL6A3	COL6A3	NM_004369	Intron of COL6A3(-):911bp aft	Antisense Fusion
DLG2(-):	NRCAM	NRCAM	NM_001193	Intron of NRCAM(-):624bp aft	Protein Fusion: in frame {D
f	TMEM6	NGLY1	NM_018297	Intron of NGLY1(-):3Kb after	Transcript Fusion {NGLY1:T
ITPK1(-):	LINC004	LINC004	NR_027099	5'-UTR of LINC00486(+):21Kt	Antisense Fusion
ALOXE3	OSTF1	OSTF1	NM_012383	Intron of OSTF1(+):2Kb after	Protein Fusion: in frame {O
ODF3L2	LINC004	LINC004	NR_027099	5'-UTR of LINC00486(+):21Kt	Antisense Fusion
GNA15(+)	ZNF521	ZNF521	NM_015461	Intron of ZNF521(-):16Kb afte	Antisense Fusion
BAGE2(-):	KMT2C	KMT2C	NM_170606	Exon 7 of KMT2C(-)	Protein Fusion: mid-exon {E
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):618bp be	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):3Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):3Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):6Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):8Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):8Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):9Kb befor	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):10Kb befo	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):11Kb befo	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):12Kb befo	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):15Kb befo	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):18Kb befo	Protein Fusion: out of frame
BAGE2(-):	KMT2C	KMT2C	NM_170606	Intron of KMT2C(-):19Kb befo	Protein Fusion: in frame {B.

BAGE2(-);NGLY1 NM_018297 Intron of NGLY1(-):3Kb after ε Protein Fusion: out of frame
 BAGE2(-);KMT2C NM_170606 Intron of KMT2C(-):24Kb befo Protein Fusion: in frame {B
 BAGE2(-);KMT2C NM_170606 Intron of KMT2C(-):30Kb befo Protein Fusion: in frame {B
 BAGE2(-);KMT2C NM_170606 Intron of KMT2C(-):29Kb befo Protein Fusion: in frame {K
 BAGE2(-);KMT2C NM_170606 Intron of KMT2C(-):33Kb after Protein Fusion: in frame {B
 PIWIL3(-);NGLY1 NM_018297 Intron of NGLY1(-):3Kb after ε Protein Fusion: in frame {N
 f TOB2(-);NGLY1 NM_018297 Intron of NGLY1(-):3Kb after ε Transcript Fusion {NGLY1:T
 MID2(+);APOH NM_000042 Intron of APOH(-):858bp befo Protein Fusion: in frame {A

6BP2:ANKRD36}

6:ANKRD36BP2}

: mid-exon

: mid-exon

OR1:IGF2R}
3F2R:SDHC}
EK11:RIMS2}

LG2:NRCAM}
MEM63C}

STF1:ALOXE3}

3AGE2:KMT2C}
: {BAGE2:KMT2C}
: {BAGE2:KMT2C}
: {KMT2C:BAGE2}
: {KMT2C:BAGE2}
: {BAGE2:KMT2C}
: {KMT2C:BAGE2}
: {KMT2C:BAGE2}
: {BAGE2:KMT2C}
: {BAGE2:KMT2C}
: {BAGE2:KMT2C}
: {KMT2C:BAGE2}
: {KMT2C:BAGE2}
AGE2:KMT2C}

: {NGLY1:BAGE2}
AGE2:KMT2C}
AGE2:KMT2C}
MT2C:BAGE2}
AGE2:KMT2C}
GLY1:PIWIL3}
`OB2}
POH:MID2}