Table S5. Saccer 3 coordinates of lariat junction reads*

*List of BPs detected through LJ reads from the Lariat-seq data. BP positions were determined from locations of the 3' most end of LJ reads and sequence information as described in the methods. The 'reads_at_dist_to_bp' field represents the number of LJ reads ending at various positions from the reported BP, the first in the list is zero away. The final two fields are marked 1, if the 5'SS or BP was previously annotated in the SGD annotations or by Meyer et al.[7] respectively, or 0 otherwise.

strand	chrom	5'ss	bp	reads_at_dist_to_bp	bp_seq	anno_5'ss	anno_bp
-	chrII	47146	47074	2,0,2	GTTACTAATATG	1	1
+	chrII	125155	125231	49	ATTACTAACATT	1	1
+	chrII	170677	170768	0,11	AGTACTAACGTT	1	1
-	chrIII	178213	177956	1,6	GATACTAACAAC	1	1
+	chrIV	122078	122159	19	CGTACTAACAAC	1	0
-	chrIV	215384	215274	19	TTTACTAACGAG	0	0
+	chrIV	230020	230262	122,12,5	TTTACTAACAAA	1	1
-	chrIV	239509	239421	4,9,353	AATACTAACAAT	1	1
+	chrIV	331189	331277	23	ATCACTAACCTG	0	0
+	chrIV	399362	399470	100,5,0,0,0,0,3	AATACTAACCAT	1	1
-	chrIV	715358	715267	109	TATACTAACAAA	1	1
-	chrIX	99385	99153	1,6,33	AATACTAACAAA	1	1
+	chrIX	225875	225994	2	TTTACTAATATT	0	0
+	chrIX	317018	317138	5	TTTACTAACAGG	0	1
-	chrIX	348494	348383	1,16	TTTACTAACTAT	1	1
-	chrV	166874	166787	4	ATTACTAACATC	1	1
-	chrV	248671	248563	2	CATTCTAACATT	0	0
+	chrV	362733	362835	2	AATTCTAACGCA	1	0
-	chrV	505180	505049	0,0,2	AGTACTAACCAG	0	0
-	chrVI	221414	221303	30,0,0,0,0,0,0,0,0,8	TATACTAACAGA	1	1
-	chrVII	73137	73035	10	ATTACTAACAAG	1	1
+	chrVII	249887	250015	35	GTTACTAACAGG	1	1
-	chrVII	497458	497390	0,0,5	CTTACTAACTGT	1	1
-	chrVII	1061028	1060825	10	GATACTAACTTT	0	0
+	chrVII	1084883	1085006	14	CTTACTAACTGA	1	1
+	chrVIII	129529	129617	2	AATACTAACATA	1	1
-	chrVIII	138408	138281	5,65	TGTACTAACAAC	1	1
+	chrVIII	251156	251231	0,1	GAGACTAACTTT	1	1
-	chrVIII	505516	505289	15	TTTACTAACAAG	1	1
+	chrX	73797	74179	2	TTTACTAACAAC	1	1
+	chrX	236903	237010	3	ATCACTGACATA	0	0
+	chrX	435228	435309	2	ATTACTAACTAA	1	1
+	chrX	608307	608548	32,3,3	TTTACTAACAAA	1	1

-	chrX	703054	702881	5	TTTACTAACGAG	1	1
-	chrXI	355283	355153	0,4	CATACTTACAGT	0	0
-	chrXI	430596	430520	3,5	GCTACTAACTAT	1	1
-	chrXII	327399	327294	5	TAGACTAACGTT	1	1
+	chrXII	382301	382388	6	TTTACTTACTAG	0	0
-	chrXII	707892	707769	0,0,2	CGTACTGACATT	0	0
-	chrXIII	23658	23500	3,30	TTTACTAACAGT	1	1
+	chrXIII	236592	236788	72,2,1	GCCACTAACAAT	1	1
-	chrXIII	243056	242969	0,0,4	AATACTGACAAT	0	0
+	chrXIII	424998	425114	255,10,6	TTTACTAACAAA	1	1
-	chrXIII	500151	499899	2,42	CTTACTAACAAA	1	1
-	chrXIII	721345	721232	313	AATACTAACAGC	1	1
+	chrXIV	48294	48378	10,0,3	ATTACTAACAAT	1	1
-	chrXIV	237531	237419	0,0,9	TTTACTGACCTA	0	0
-	chrXIV	380781	380701	11	ATTACTAATCTG	1	0
+	chrXIV	502164	502269	0,0,10	GATACTGACTAT	0	0
+	chrXIV	616067	616229	4,0,4	TCAACTTACTGT	0	0
-	chrXV	552874	552738	27,23,51	ATTACTAACTGG	1	1
+	chrXV	780121	780265	604,27,100	TTGACTAACACA	1	1
-	chrXVI	76223	76014	6	GTTACTAACATA	1	1
-	chrXVI	281503	281386	18	TTGACTAACACA	1	1
-	chrXVI	582701	582570	76,0,0,0,0,0,0,0,0,0,10,59	TATACTAACAAA	1	1
+	chrXVI	623578	623665	481,39,30	TATACTAACAAG	1	1
+	chrXVI	833694	833783	18	AAAACTAACAAT	1	1
+	chrXVI	943051	943174	6,0,1,0,5	CTTACTAACTGA	1	1