

S4 Table. Annotation of processed variants detected in desmoid tumor samples

Patient ID	Processed variants	Total locus (QC-passed)	Het /Homo	Novel/Existing variants	Novel/Existing (%)	SNPs	INDELs/ Sub	Transition In SNPs	Transversion In SNPs	Ti/Tv ratio
3	82,086	846	846/0	443/403	52.3/47.7	614	232	363	251	1.45
5	91,812	832	832/0	411/421	49.3/50.7	626	206	401	225	1.78
6	98,694	1,280	1,280/0	762/518	59.5/40.5	830	450	522	308	1.69
8	242,987	4,110	4,110/0	2,593/1,514	63.1/36.9	3,128	982	1,900	1,228	1.55
9	163,985	2,140	2,140/0	1,354/786	63.3/36.7	1,513	627	973	540	1.8
15	96,373	1,465	1,465/0	966/499	65.9/34.1	983	482	599	384	1.56
16	114,154	1,977	1,977/0	1,398/579	70.7/29.3	1,245	732	758	487	1.56
18	107,933	1,824	1,824/0	1,282/542	70.3/29.7	1,173	651	588	585	1.01
19	83,290	1,065	1,065/0	605/460	56.8/43.2	770	295	470	300	1.57

Annotation-based summary was obtained using ANNOVAR. Het, heterozygous; Homo, homozygous; INDEL, insert and deletion; QC, quality control; SNP, single nucleotide polymorphism; Sub, substitution; Ti, transition; Tv, transversion.