Supplementary Table 2. The blood/tumour sequence traces for the SDHA variants to allow assessment for LOH.

Tissue

contig_id	contig_srt	contig_end	region_id	attributes	go_count	overlaps	fwd_e2e	rev_e2e	total_read	fwd_read	rev_read
chr5	228171	228320	AMPL715	GENE_ID	59	6646	73	59	165	89	76
chr5	254500	254718	AMPL715	GENE_ID	135	3206	1360	1438	3206	1622	1584
chr5	224582	224757	AMPL715	GENE_ID	107	22581	28	2015	6511	4334	2177
chr5	228310	228516	AMPL715	GENE_ID	82	7185	1704	4023	7036	2367	4669
chr5	223518	223732	AMPL715	GENE_ID	94	8900	2523	4085	8900	3959	4941
chr5	233558	233769	AMPL715	GENE_ID	105	11242	4807	2907	11242	54122	5830
chr5	240532	240687	AMPL715	GENE_ID	76	26187	4759	4275	11285	61151	5134
chr5	225914	226133	AMPL715	GENE_ID	98	31342	2773	2121	11368	6059	5309
chr5	230941	231166	AMPL715	GENE_ID	135	11551	2114	5149	11551	5383	6168
chr5	251067	251289	AMPL715	GENE_ID	113	11580	6134	4293	11580	6585	4995
chr5	236522	236726	AMPL715	GENE_ID	121	12992	6166	3596	12992	6551	6441
chr5	251350	251571	AMPL715	GENE_ID	139	27813	4746	6714	13410	5456	7954
chr5	235238	235429	AMPL715	GENE_ID	114	30220	6314	5881	13417	6961	6456
chr5	251449	251651	AMPL715	GENE_ID	129	27701	7359	4631	14445	9132	5313
chr5	256397	256587	AMPL715	GENE_ID	82	14778	7828	5606	14778	8155	6623
chr5	240371	240542	AMPL715	GENE_ID	60	26689	7249	1320	16259	8615	7644
chr5	225502	225709	AMPL715	GENE_ID	127	16430	5260	9352	16430	5535	10895
chr5	224389	224592	AMPL715	GENE_ID	93	23371	7501	4077	17001	8495	8506
chr5	235426	235548	AMPL715	GENE_ID	71	30229	5585	10948	17462	5820	11642
chr5	226089	226243	AMPL715	GENE_ID	96	29423	8955	10522	20910	9258	11652

Blood

contig_id	contig_srt	contig_end	region_id	attributes	go_count	overlaps	fwd_e2e	rev_e2e	total_read	fwd_read	rev_read
chr5	228171	228320	AMPL715	GENE_ID	59	2978	30	46	124	53	71
chr5	254500	254718	AMPL715	GENE_ID	135	2975	1329	1316	2975	1529	1446
chr5	228310	228516	AMPL715	GENE_ID	82	3276	774	1600	3176	1213	1963
chr5	224582	224757	AMPL715	GENE_ID	107	14245	36	1391	5097	3595	1502
chr5	251067	251289	AMPL715	GENE_ID	113	5284	2794	2050	5284	2954	2330
chr5	233558	233769	AMPL715	GENE_ID	105	5296	2382	1661	5286	2599	2697
chr5	251449	251651	AMPL715	GENE_ID	129	16645	2780	2035	5714	3270	2444
chr5	226089	226243	AMPL715	GENE_ID	96	14289	3576	2672	6774	3702	3072
chr5	225502	225709	AMPL715	GENE_ID	127	6945	1910	4426	6945	1990	4955
chr5	223518	223732	AMPL715	GENE_ID	94	7175	2176	3037	7175	3255	3920
chr5	235426	235548	AMPL715	GENE_ID	71	20252	2538	5163	8195	2712	5483
chr5	256397	256587	AMPL715	GENE_ID	82	8628	4270	3415	8628	4485	4143
chr5	224389	234592	AMPL715	GENE_ID	93	14430	4304	811	9425	4640	4785
chr5	230941	231166	AMPL715	GENE_ID	135	9907	1869	4921	9907	4400	5507
chr5	240532	240687	AMPL715	GENE_ID	76	19864	4530	3348	10408	6018	4390
chr5	240371	240542	AMPL715	GENE_ID	60	20106	4929	371	10742	6300	4442
chr5	225914	226133	AMPL715	GENE_ID	98	17384	1982	1823	10875	5897	4978
chr5	251350	251571	AMPL715	GENE_ID	139	16850	3467	6470	11163	3873	7290
chr5	235238	235429	AMPL715	GENE_ID	114	20508	6321	5324	12619	6960	5659
chr5	236522	236726	AMPL715	GENE_ID	121	14121	6927	3651	14121	7428	6693

SDHA region coverage (depth) of Tissue is min 3206x to max 31342x, mean 19000x. SDHA region coverage of Blood is min 2975x to max 20252x, mean 12057x. For the accuracy assessment variants, we think both, Blood & Tissue, of coverage (19000x, 12057x) is enough to show sufficient accuracy.