

Supplementary Table 1: Summary of pathological categories from 272 samples.

Grade	Subtype	# Samples	# with fusion (%)	# with in-frame fusion
WHO grade II	astrocytomas	34	9(26.47%)	3(8.82%)
	oligodendrogliomas	21	1(4.76%)	0(0.00%)
	oligodendroastrocytomas	32	3(9.09%)	1(3.03%)
	Total	87	13(14.77%)	4(4.55%)
WHO grade III	anaplastic oligodendroastrocytomas	23	10(43.48%)	2(8.70%)
	anaplastic astrocytomas	13	5(38.46%)	4(30.77%)
	anaplastic oligodendrogliomas	11	4(36.36%)	2(18.18%)
	Total	47	19(40.43%)	8(17.02%)
WHO grade IV	primary Glioblastomas	59	34(57.63%)	18(30.51%)
	secondary Glioblastomas	20	13(61.90%)	7(33.33%)
	Total	79	47(58.75%)	25(31.25%)
Recurrent	recurrent anaplastic astrocytomas	11	5(45.45%)	2(18.18%)
	recurrent Glioblastomas	20	8(40.00%)	3(15.00%)
	recurrent astrocytomas	9	4(44.44%)	2(22.22%)
	recurrent anaplastic oligodendrogliomas	2	1(50.00%)	0(0.00%)
	recurrent anaplastic oligodendroastrocytomas	13	6(46.15%)	5(38.46%)
	recurrent oligodendroastrocytomas	4	1(25.00%)	0(0.00%)
	Total	59	25(42.37%)	12(20.34%)

Supplemental Table 2: Clinical records and data production statistics of 272 gliomas from discovery cohort

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_171	F	37	OA	2	1	5.93	5.75	96.97	4.53	78.89	-	-	-
CGGA_235	M	25	OA	2	0	4.77	3.97	83.16	2.76	69.63	-	-	-
CGGA_236	M	47	O	2	1	4.16	3.98	95.66	3.05	76.71	-	-	-
CGGA_241	M	34	OA	2	1	6.34	6.09	96.03	4.24	69.64	-	-	-
CGGA_243	F	31	OA	2	#N/A	5.12	3.11	60.68	2.14	68.8	-	-	-
CGGA_245	F	39	rA	2	1	4.51	4.35	96.61	3.4	78.02	-	-	-
CGGA_247	M	60	AA	3	#N/A	4.27	4.17	97.63	3.1	74.46	-	-	-
CGGA_251	M	46	OA	2	1	4.03	3.92	97.19	2.89	73.73	-	-	-
CGGA_252	F	25	A	2	1	6.56	4.8	73.06	3.61	75.25	-	-	-
CGGA_254	M	38	OA	2	1	3.77	3.6	95.48	2.83	78.56	-	-	-
CGGA_256	M	39	A	2	1	5.22	4.79	91.64	3.59	74.96	-	-	-
CGGA_261	M	28	A	2	1	4.06	3.92	96.54	2.91	74.26	-	-	-
CGGA_267	M	37	A	2	1	5.19	4.76	91.68	3.4	71.41	-	-	-
CGGA_269	F	45	A	2	0	4.22	4.07	96.39	3.25	79.78	-	-	-
CGGA_272	M	51	sGBM	4	0	5.72	5.46	95.55	4.58	83.83	-	-	-
CGGA_273	F	35	OA	2	1	6.1	5.89	96.59	4.46	75.71	-	-	-
CGGA_274	F	55	pGBM	4	0	5.08	4.92	96.89	3.84	78.1	-	-	-
CGGA_276	M	44	O	2	0	6.29	5.98	95.09	4.38	73.2	-	-	-
CGGA_283	F	48	O	2	1	5.97	4.99	83.46	3.45	69.16	-	-	-
CGGA_300	F	36	A	2	1	3.22	3.05	94.8	2.35	76.89	-	-	-
CGGA_309	M	44	rGBM	4	0	7.24	4.83	66.76	3.54	73.27	-	-	-
CGGA_314	M	39	rAO	3	1	4.68	4.19	89.48	3.17	75.77	-	-	-
CGGA_318	F	42	rGBM	4	0	4.13	4.02	97.24	3.25	80.97	-	-	-
CGGA_323	F	49	O	2	0	5.63	5.46	96.93	3.97	72.63	-	-	-
CGGA_330	M	46	AOA	3	0	8.71	5.8	66.66	4.18	72	-	-	-
CGGA_333	M	41	OA	2	1	5.76	5.6	97.3	4.07	72.67	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_337	F	50	AOA	3	1	4.89	4.62	94.52	3.51	76.07	-	-	-
CGGA_374	M	38	sGBM	4	1	4.33	4.18	96.61	3.11	74.49	-	-	-
CGGA_400	F	39	rAA	3	1	4.55	3.77	82.91	2.73	72.27	-	-	-
CGGA_413	M	54	pGBM	4	0	5.12	4.93	96.35	3.67	74.38	-	-	-
CGGA_426	M	51	AA	3	0	4.14	3.98	96	3.3	82.9	-	-	-
CGGA_431	M	42	rAOA	3	1	3.4	3.11	91.7	2.33	74.74	-	-	-
CGGA_446	F	35	O	2	1	3.77	3.64	96.44	2.7	74.33	-	-	-
CGGA_448	M	65	AOA	3	0	5.5	5.24	95.3	4.24	81.02	-	-	-
CGGA_458	M	51	rOA	2	1	10.62	9.65	90.87	7.14	74.02	-	-	-
CGGA_479	F	37	OA	2	1	4.19	4.02	96.05	2.87	71.36	-	-	-
CGGA_483	F	60	pGBM	4	0	6.76	5.1	75.4	4.13	80.92	-	-	-
CGGA_485	M	32	O	2	1	3.58	3.45	96.6	2.67	77.37	-	-	-
CGGA_488	M	24	AOA	3	0	5.65	4.67	82.63	3.42	73.27	-	-	-
CGGA_490	F	38	AO	3	1	5.32	5.14	96.64	3.9	75.89	-	-	-
CGGA_491	F	37	pGBM	4	1	5.47	5.22	95.47	3.72	71.36	-	-	-
CGGA_493	F	33	A	2	0	4.64	4.42	95.22	3.31	74.83	-	-	-
CGGA_494	F	59	pGBM	4	0	4.18	3.99	95.4	2.81	70.44	-	-	-
CGGA_495	M	54	pGBM	4	0	3.82	3.68	96.4	2.97	80.73	-	-	-
CGGA_499	M	52	pGBM	4	0	6.2	6.05	97.53	4.62	76.47	-	-	-
CGGA_501	M	40	O	2	1	5.02	4.87	96.98	3.86	79.19	-	-	-
CGGA_502	M	40	A	2	1	5.82	4.3	73.88	2.98	69.31	-	-	-
CGGA_510	M	42	AO	3	1	4.15	3.96	95.39	3.09	78.02	-	-	-
CGGA_538	F	43	O	2	1	5.82	5.68	97.54	4.3	75.67	-	-	-
CGGA_541	F	36	OA	2	0	4.84	4.72	97.57	3.1	65.72	-	-	-
CGGA_543	M	43	O	2	1	5.16	4.28	82.99	2.88	67.18	-	-	-
CGGA_545	F	39	rGBM	4	1	5.77	5.61	97.25	4.41	78.62	-	-	-
CGGA_551	M	45	O	2	1	5.15	4.99	96.97	3.51	70.38	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_560	M	44	AOA	3	1	5.86	5.7	97.21	4.06	71.27	-	-	-
CGGA_564	M	48	AA	3	0	5.14	4.99	97.15	3.77	75.44	-	-	-
CGGA_565	M	51	AOA	3	0	4.98	4.79	96.04	3.42	71.45	-	-	-
CGGA_578	F	62	AOA	3	0	3.3	3.01	91.4	2.4	79.56	-	-	-
CGGA_580	M	43	OA	2	1	3.73	3.63	97.41	2.59	71.37	-	-	-
CGGA_591	F	34	AOA	3	1	5.02	4.84	96.52	3.65	75.41	-	-	-
CGGA_598	F	62	AO	3	1	4.83	4.68	96.93	3.59	76.77	-	-	-
CGGA_599	F	67	AOA	3	0	6.5	6.24	96.1	4.83	77.41	-	-	-
CGGA_601	M	36	A	2	1	4.28	4.17	97.33	2.87	68.84	-	-	-
CGGA_603	M	32	rAA	3	1	4.21	4.07	96.67	3.22	79.15	-	-	-
CGGA_604	M	46	pGBM	4	0	5.19	5.04	97.07	3.78	74.99	-	-	+
CGGA_605	M	41	rAO	3	1	8.6	7.58	88.08	6.05	79.88	-	-	-
CGGA_607	M	26	A	2	1	4.72	4.58	97.11	3.47	75.82	-	-	-
CGGA_616	M	43	AA	3	0	6.9	6.58	95.32	4.85	73.76	-	-	-
CGGA_624	F	49	rGBM	4	0	6.41	6.08	94.84	4.6	75.54	-	-	-
CGGA_630	F	30	OA	2	0	4.07	3.87	95.25	2.83	73.07	-	-	-
CGGA_633	F	57	O	2	0	6.18	5.73	95.49	3.99	69.72	-	-	-
CGGA_635	M	45	OA	2	1	3.86	3.75	97.06	2.78	74.27	-	-	-
CGGA_642	M	30	A	2	1	3.7	3.48	93.81	2.49	71.7	-	-	-
CGGA_643	M	57	AOA	3	0	6.62	6.45	97.38	4.92	76.24	-	-	-
CGGA_655	M	36	O	2	1	4.77	4.64	97.22	3.51	75.62	-	-	-
CGGA_658	M	56	pGBM	4	0	4.15	3.96	95.24	3.04	76.8	-	-	-
CGGA_659	F	51	O	2	0	6.81	6.59	96.85	4.5	68.2	-	-	-
CGGA_661	M	42	AA	3	0	5.67	5.49	96.86	4.43	80.67	+	-	-
CGGA_662	F	59	OA	2	1	3.88	3.77	97.19	2.91	77.16	-	-	-
CGGA_666	F	45	OA	2	1	3.57	3.41	95.45	2.48	72.73	-	-	-
CGGA_669	F	56	rGBM	4	0	9.95	9.49	95.35	6.42	67.68	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_671	F	37	OA	2	1	4.33	4.2	97.02	3.14	74.71	-	-	-
CGGA_675	F	23	OA	2	1	3.45	3.28	95.07	2.48	75.68	-	-	-
CGGA_676	M	60	pGBM	4	0	5.61	5.32	94.84	4.11	77.27	-	-	-
CGGA_678	M	56	rAA	3	0	5.65	5.29	93.61	4.02	75.94	-	-	-
CGGA_679	F	63	pGBM	4	0	7.12	6.78	95.32	5.65	83.26	-	-	-
CGGA_680	M	44	pGBM	4	0	3.97	3.83	96.48	3.04	79.23	-	-	-
CGGA_681	M	43	rGBM	4	0	9.71	9.21	94.84	7.27	78.86	-	-	-
CGGA_685	F	21	A	2	1	3.57	3.39	94.9	2.36	69.53	-	-	-
CGGA_689	F	37	O	2	1	3.92	3.73	95.31	2.81	75.23	-	-	-
CGGA_694	M	34	rA	2	1	3.46	3.22	93.06	2.51	77.91	-	-	-
CGGA_698	F	62	A	2	1	5.05	4.92	97.53	3.64	73.9	-	-	-
CGGA_700	F	25	pGBM	4	0	5.26	5.11	97.28	3.93	76.87	-	-	-
CGGA_704	M	37	rAOA	3	1	6.4	6.02	94.13	4.39	72.94	-	-	-
CGGA_710	M	42	pGBM	4	1	4.96	4.85	97.84	3.88	79.92	-	-	-
CGGA_715	M	44	O	2	1	4.71	4.59	97.59	3.26	70.9	-	-	-
CGGA_725	M	43	OA	2	1	4.12	4.01	97.31	2.97	73.98	-	-	-
CGGA_727	M	45	AA	3	0	5.61	5.43	96.75	4.2	77.35	-	-	-
CGGA_731	M	51	pGBM	4	0	3.6	3.34	92.94	2.66	79.7	-	-	-
CGGA_732	F	35	AA	3	0	5.33	5.1	95.64	4.1	80.32	-	-	-
CGGA_738	M	44	A	2	#N/A	3.32	3.13	94.35	2.27	72.55	-	-	-
CGGA_752	M	40	OA	2	1	4.83	4.63	95.83	3.61	78.01	-	-	-
CGGA_757	M	46	A	2	1	4.5	4.29	95.47	3.11	72.55	-	-	-
CGGA_761	M	45	pGBM	4	1	4.41	3.67	83.31	2.6	70.7	-	-	-
CGGA_762	F	40	OA	2	1	4.03	3.9	96.74	2.46	63.17	-	-	-
CGGA_766	M	32	OA	2	0	3.5	3.38	96.47	2.45	72.42	-	-	-
CGGA_773	F	50	sGBM	4	0	5.07	4.63	91.38	3.37	72.71	-	-	-
CGGA_782	M	61	pGBM	4	0	3.71	3.63	97.83	2.95	81.37	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_785	M	43	O	2	1	9.8	8.84	90.1	6.4	72.4	-	-	-
CGGA_791	M	56	AA	3	0	5.41	5.23	96.74	4.12	78.73	-	-	-
CGGA_796	M	61	A	2	0	3.77	3.52	93.41	2.62	74.49	-	-	-
CGGA_802	M	43	pGBM	4	0	5.43	5.31	97.82	4.14	77.97	-	-	-
CGGA_804	F	54	pGBM	4	0	4.15	4.02	96.98	3.15	78.31	-	-	-
CGGA_807	M	43	A	2	0	3.19	3.12	97.71	2.27	72.87	-	-	-
CGGA_808	M	39	pGBM	4	0	4.61	4.5	97.43	3.45	76.63	-	-	-
CGGA_815	F	53	OA	2	1	3.19	3.02	94.69	2.38	78.92	-	-	-
CGGA_818	M	46	A	2	1	5.05	4.83	95.66	3.53	73.11	-	-	-
CGGA_837	M	57	pGBM	4	0	4.74	4.62	97.38	3.81	82.54	-	-	-
CGGA_838	F	36	OA	2	1	5.2	4.99	95.96	3.53	70.67	-	-	-
CGGA_842	F	64	pGBM	4	0	3.16	3.06	96.73	2.52	82.52	-	+	-
CGGA_843	M	29	OA	2	1	4.8	4.6	95.79	3.33	72.44	-	-	-
CGGA_848	F	55	pGBM	4	0	8.71	8.48	97.34	6.84	80.65	-	-	-
CGGA_850	F	52	pGBM	4	0	3.53	3.45	97.82	2.86	83	-	-	-
CGGA_858	M	43	O	2	1	3.96	3.88	98	2.93	75.34	-	-	-
CGGA_859	M	57	pGBM	4	0	5.19	4.82	92.98	4.07	84.36	-	-	-
CGGA_864	M	34	OA	2	1	4.78	4.66	97.65	3.53	75.75	-	-	-
CGGA_871	M	37	O	2	0	6.98	6.65	95.32	4.34	65.33	-	-	-
CGGA_876	F	60	pGBM	4	0	4.35	4.25	97.7	3.5	82.42	-	-	-
CGGA_878	M	42	pGBM	4	0	5.14	5.03	97.88	4.16	82.7	-	-	-
CGGA_884	F	48	A	2	1	3.76	3.63	96.43	2.61	71.91	-	-	-
CGGA_892	M	35	O	2	1	4.03	3.93	97.53	2.78	70.79	-	-	-
CGGA_893	F	37	OA	2	1	5.41	5.27	97.48	3.7	70.28	-	-	-
CGGA_898	M	38	A	2	1	3.37	3.14	93.23	2.27	72.27	-	-	-
CGGA_899	M	46	sGBM	4	1	3.85	3.76	97.57	2.95	78.51	-	-	-
CGGA_902	M	55	pGBM	4	0	4.75	4.64	97.59	3.69	79.54	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_904	M	33	A	2	1	3.61	3.47	96.07	2.65	76.33	-	-	-
CGGA_905	M	46	A	2	1	3.76	3.62	96.37	2.74	75.66	-	-	-
CGGA_908	M	36	A	2	1	5.72	5.42	94.85	4.26	78.58	-	-	-
CGGA_909	F	40	OA	2	1	5.9	5.5	95.97	3.88	70.65	-	-	-
CGGA_1004	F	65	A	2	#N/A	3.6	3.5	97.14	2.5	71.58	-	-	-
CGGA_1005	F	42	A	2	1	4.37	4.07	93.27	2.92	71.76	-	-	-
CGGA_1006	M	44	pGBM	4	0	5.33	4.88	94.32	3.76	77.06	-	-	-
CGGA_1007	F	59	pGBM	4	0	3.34	3.26	97.67	2.61	80.09	-	-	-
CGGA_1008	F	56	pGBM	4	#N/A	3.33	3.26	97.78	2.68	82.26	-	-	-
CGGA_1011	F	48	pGBM	4	0	5.88	4.42	75.08	3.31	74.89	-	-	-
CGGA_1013	F	40	A	2	1	3.16	3.04	96.27	2.24	73.57	-	-	-
CGGA_1015	M	64	pGBM	4	0	3.77	3.69	97.8	2.95	79.91	-	-	-
CGGA_1020	F	39	A	2	1	3.44	3.27	95.19	2.38	72.66	-	-	-
CGGA_1022	F	64	rAA	3	0	4.38	3.65	83.23	2.78	76.33	-	-	-
CGGA_1024	M	66	pGBM	4	0	5.8	5.66	97.63	4.62	81.68	-	-	-
CGGA_1026	M	59	pGBM	4	0	4.32	4.21	97.6	2.96	70.36	-	-	-
CGGA_1027	M	38	AOA	3	1	3.75	3.43	91.66	2.57	74.95	-	-	-
CGGA_1031	F	33	A	2	1	3.34	3.16	94.69	2.41	76.22	-	-	-
CGGA_1034	M	24	AA	3	0	4.52	4.35	96.15	3.59	82.51	-	-	-
CGGA_1035	F	62	pGBM	4	0	4.84	4.71	97.3	3.87	82.07	-	-	-
CGGA_1039	M	42	pGBM	4	0	5.49	5.02	91.4	3.95	78.64	-	-	-
CGGA_1045	M	81	pGBM	4	0	4.5	4.37	97.14	3.49	79.84	-	-	-
CGGA_1046-1	M	23	A	2	1	6.52	5.78	88.75	4.15	71.75	-	-	-
CGGA_1049	M	60	pGBM	4	0	6.72	5.96	88.57	4.8	80.66	-	-	-
CGGA_1050	M	41	OA	2	1	3.69	3.5	94.81	2.44	69.82	-	-	-
CGGA_1052	M	41	OA	2	0	4.35	4.24	97.5	2.65	62.55	-	-	-
CGGA_1059	F	54	rA	2	#N/A	3.59	3.51	97.68	2.82	80.3	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_1060	M	42	rGBM	4	1	5.19	5.07	97.81	4.08	80.32	-	-	-
CGGA_1061	F	43	rAOA	3	1	4.48	4.39	97.86	3.29	74.87	-	-	-
CGGA_1068	M	29	sGBM	4	1	7.78	7.59	97.63	6.01	79.09	+	-	-
CGGA_1072	M	26	pGBM	4	0	6.97	6.8	97.52	5.34	78.52	-	-	-
CGGA_1077	M	47	pGBM	4	0	6	5.8	96.64	4.92	84.8	-	-	-
CGGA_1078	F	61	rGBM	4	0	3.66	3.57	97.52	2.61	72.97	-	-	-
CGGA_1079	M	38	AOA	3	0	4.45	4.33	97.3	3.4	78.58	-	-	-
CGGA_1081	F	30	rAA	3	0	4.92	4.8	97.57	3.46	72.06	-	-	-
CGGA_1094	F	40	rAOA	3	1	7.28	7.08	97.32	4.97	70.17	-	-	-
CGGA_1109	M	42	pGBM	4	0	6.09	5.94	97.54	4.5	75.86	-	+	-
CGGA_1113	M	34	AO	3	1	5.65	5.5	97.27	4.05	73.65	-	-	-
CGGA_1116	F	43	pGBM	4	#N/A	3.88	3.78	97.28	2.96	78.36	-	-	-
CGGA_1118	M	31	rAA	3	#N/A	4.92	4.78	97.29	3.71	77.62	-	-	-
CGGA_1119	M	52	AO	3	#N/A	4.25	4.14	97.4	3.06	73.76	-	-	-
CGGA_1124	M	49	rGBM	4	0	5.79	5.66	97.85	4.51	79.59	-	-	-
CGGA_1136	F	40	sGBM	4	1	6.37	6.07	95.33	4.95	81.49	-	-	-
CGGA_1140	F	50	rAA	3	0	4.65	4.52	97.24	3.47	76.82	-	-	-
CGGA_1145	M	42	rAA	3	0	4.53	4.4	97.28	3.45	78.36	-	-	-
CGGA_1146	M	36	AA	3	1	4.89	4.52	95.45	3.46	76.46	-	-	-
CGGA_1160	F	43	AOA	3	1	4.48	4.3	95.93	3.39	78.97	-	-	-
CGGA_1170	M	27	sGBM	4	1	3.8	3.7	97.49	2.85	77.12	-	-	-
CGGA_1171	M	42	pGBM	4	0	4.5	4.37	97.09	3.44	78.81	-	-	-
CGGA_1175	F	37	sGBM	4	1	4.92	4.78	97.24	3.73	77.98	-	-	-
CGGA_1177	M	42	rGBM	4	0	4.54	4.37	96.31	3.84	87.85	-	-	-
CGGA_1189	F	35	AOA	3	1	4.56	4.42	96.93	3.54	80.17	-	-	-
CGGA_1190	F	46	AOA	3	1	3.67	3.46	97.02	2.7	78.03	-	-	-
CGGA_1197	M	45	sGBM	4	#N/A	5.78	5.28	91.34	3.91	74.14	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_1215	M	38	rAOA	3	1	8.24	7.29	88.46	5.8	79.62	-	-	-
CGGA_1218	M	54	sGBM	4	0	6.74	6.58	97.54	4.74	72.02	-	-	-
CGGA_1227	F	47	sGBM	4	1	4.89	4.71	96.29	3.52	74.73	-	-	-
CGGA_1231	F	32	rA	2	1	6.7	6.43	96.04	4.78	74.32	-	-	-
CGGA_1234	M	33	pGBM	4	0	5.72	5.39	97.06	4.48	83.15	-	-	-
CGGA_1237	M	63	pGBM	4	0	4.81	4.7	97.64	3.45	73.42	-	-	-
CGGA_1240	M	34	pGBM	4	0	4.39	4.24	96.45	3.6	84.92	-	-	-
CGGA_1246	M	54	AO	3	#N/A	5.25	5.1	97.18	3.93	76.99	-	-	-
CGGA_1251	F	42	rAOA	3	0	6.42	6.26	97.63	5.2	83.06	-	-	-
CGGA_1263	M	51	A	2	0	6.68	6.43	96.14	4.03	62.71	-	-	-
CGGA_1271	M	18	sGBM	4	0	4.51	4.25	97.22	3.43	80.73	-	-	-
CGGA_1272	M	33	sGBM	4	0	4.59	4.5	97.92	3.39	75.47	+	-	-
CGGA_1280	M	75	AA	3	0	5.18	4.98	96.13	3.72	74.81	-	-	-
CGGA_1281	M	46	AO	3	0	4.62	4.49	97.08	3.1	69.13	-	-	-
CGGA_1284	M	74	AA	3	0	4.88	4.73	96.83	4.05	85.61	-	-	-
CGGA_1287	M	30	pGBM	4	1	4.29	4.17	97.08	3.31	79.32	-	-	-
CGGA_1292	M	18	AO	3	0	4.28	4.1	95.9	3.1	75.61	-	-	-
CGGA_1301	M	49	pGBM	4	0	3.69	3.61	97.82	2.77	76.69	-	-	-
CGGA_1307	F	26	AOA	3	1	4.62	4.44	96.15	3.64	81.88	-	-	-
CGGA_1313	M	43	pGBM	4	0	5.18	5.06	97.8	3.9	77.1	-	+	-
CGGA_1314	F	28	pGBM	4	1	5.09	4.96	97.57	4.07	81.92	-	-	-
CGGA_1324	M	42	sGBM	4	1	4.6	4.5	97.66	3.56	79.22	-	-	-
CGGA_1329	F	44	rAOA	3	1	5.98	5.79	96.92	4.79	82.72	-	-	-
CGGA_1330	M	48	A	2	1	5.18	5.04	97.4	4.02	79.7	-	-	-
CGGA_1338	F	62	pGBM	4	0	5.07	4.84	95.45	3.81	78.68	-	-	-
CGGA_1340	M	36	AOA	3	0	5.51	5.27	95.62	3.99	75.63	-	-	-
CGGA_1342	M	48	pGBM	4	0	6.31	6.03	95.48	4.84	80.29	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_1343	M	34	rGBM	4	0	5.46	5.22	95.63	4.37	83.59	-	-	-
CGGA_1374	M	22	rOA	2	1	4.62	4.46	96.65	3.5	78.45	-	-	-
CGGA_1375	F	51	sGBM	4	1	5.8	5.59	96.29	4.65	83.29	-	-	-
CGGA_1381	F	37	rGBM	4	1	4.07	3.94	96.83	3.18	80.59	-	-	-
CGGA_1384	F	40	pGBM	4	1	3.34	3.21	96.14	2.67	83.28	-	-	-
CGGA_1388	M	38	rA	2	1	4.34	4.19	96.55	3.36	80.33	-	-	-
CGGA_1394	M	38	rGBM	4	1	4.99	4.85	97.14	3.89	80.15	-	-	-
CGGA_1406	M	34	A	2	1	4.63	4.49	96.88	3.58	79.77	-	-	-
CGGA_1408	F	65	AOA	3	0	5.22	5.08	97.46	3.79	74.53	-	-	-
CGGA_1409	F	24	pGBM	4	1	4.99	4.86	97.24	3.82	78.59	-	-	-
CGGA_1411	F	41	rA	2	0	5.46	5.28	96.8	4.34	82.09	-	-	-
CGGA_1412	F	49	sGBM	4	1	4.89	4.76	97.45	3.88	81.56	-	-	-
CGGA_D02	M	44	rGBM	4	0	5.54	5.39	97.34	4.06	75.26	-	-	-
CGGA_D03	M	44	pGBM	4	0	4.58	4.4	96.1	3.52	79.93	-	-	-
CGGA_D04	M	37	A	2	1	4.72	4.47	94.7	3.49	78.04	-	-	-
CGGA_D06	F	46	rAOA	3	0	5.57	5.42	97.45	2.73	50.35	-	-	-
CGGA_D07	M	36	O	2	1	5	4.88	97.54	2.94	60.27	-	-	-
CGGA_D09	M	57	pGBM	4	0	6.21	5.98	96.25	3.85	64.45	-	-	-
CGGA_D11	F	53	AOA	3	0	7.14	6.85	95.97	5.07	73.96	-	-	-
CGGA_D14	M	27	rAOA	3	1	4.66	4.42	94.76	3.56	80.69	-	-	-
CGGA_D15	F	38	OA	2	1	4.47	4.26	95.51	3.18	74.6	-	-	-
CGGA_D16	F	59	AOA	3	0	5.95	5.79	97.33	4.74	81.87	-	-	-
CGGA_D18	M	20	AOA	3	0	4.36	4.25	97.56	3.17	74.65	-	-	-
CGGA_D20	F	40	A	2	1	3.12	3.04	97.56	2.34	76.86	-	-	-
CGGA_D21	F	37	AA	3	1	3.56	3.39	95.36	2.67	78.59	-	-	-
CGGA_D24	F	37	AOA	3	1	3.6	3.44	95.54	2.5	72.78	-	-	-
CGGA_D26	M	55	rGBM	4	0	5.12	4.9	95.54	3.93	80.19	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_D27	M	33	rAOA	3	1	6.76	6.61	97.76	5.03	76.14	-	-	+
CGGA_D29	M	36	O	2	1	4.76	4.6	96.61	3.34	72.6	-	-	-
CGGA_D32	M	61	rGBM	4	0	4.1	4.02	98.06	3.2	79.44	-	-	-
CGGA_D33	M	38	rAA	3	1	3.82	3.7	96.87	2.8	75.67	-	-	-
CGGA_D34	M	45	sGBM	4	1	5.59	5.18	92.71	4.14	79.9	-	-	-
CGGA_D36	M	58	rGBM	4	0	3.95	3.79	95.84	3.09	81.58	-	-	-
CGGA_D37	M	55	pGBM	4	0	5.64	5.21	95.22	4.05	77.86	-	-	-
CGGA_D38	F	41	rGBM	4	1	4.77	4.61	96.71	3.46	75.06	-	-	-
CGGA_D39	F	25	rA	2	1	5.42	5.11	97.17	4.21	82.33	-	-	-
CGGA_D40	M	44	rOA	2	1	7.27	7.02	96.53	4.71	67.16	-	-	-
CGGA_D44	F	18	AOA	3	0	5.35	5.04	97.15	3.56	70.69	-	-	-
CGGA_D45	M	28	rAOA	3	1	5.36	4.97	95.52	3.71	74.6	-	-	-
CGGA_D46	F	36	rAA	3	1	5.04	4.69	95.93	3.53	75.34	-	-	-
CGGA_D47	M	36	OA	2	1	5.7	5.56	97.42	4.43	79.69	-	-	-
CGGA_D48	F	18	rAOA	3	1	3.42	3.07	89.62	2.24	73.07	-	-	-
CGGA_D51	F	60	rGBM	4	0	4.98	4.74	95.19	3.83	80.74	-	-	-
CGGA_D52	M	46	AO	3	1	15.54	14.73	94.8	9.78	66.4	-	-	-
CGGA_D56	M	45	rAOA	3	1	5.31	4.92	92.6	3.58	72.67	-	-	-
CGGA_D57	M	40	pGBM	4	0	5.42	5.27	97.29	3.65	69.25	-	-	-
CGGA_D58	M	24	rAA	3	0	7.71	7.46	96.84	5.04	67.5	-	-	-
CGGA_D59	F	30	sGBM	4	1	3.89	3.79	97.44	3.04	80.23	-	-	-
CGGA_D61	M	40	AO	3	1	6.35	6.15	96.88	4.53	73.67	-	-	-
CGGA_D63	M	25	sGBM	4	1	6.54	6.04	92.47	4.38	72.55	-	-	-
CGGA_D64	M	51	sGBM	4	0	4.08	3.59	88.08	2.76	76.9	+	-	-
CGGA_J023	M	36	AO	3	1	6.35	6.17	97.22	5.04	81.67	-	-	-
CGGA_J024	F	29	rA	2	1	4.95	4.79	96.81	3.69	77.05	-	-	-
CGGA_J030	M	38	OA	2	0	4.47	4.3	96.27	3.32	77.17	-	-	-

SampleID	Gender	Age	Histology	Grade	IDH1 mutation	Raw base(Gb)	Clean base(Gb)	Clean rate(%)	Map base(Gb)	Map rate(%)	PTPRZ1- MET	FGFR3- TACC3	RNF213- SLC26A11
CGGA_J042	M	38	rOA	2	1	4.46	4.29	96.23	3.43	79.89	-	-	-
CGGA_J100	M	55	rGBM	4	1	4.49	4.36	96.97	3.25	74.62	-	-	-
CGGA_J130	M	40	rA	2	0	5	4.79	95.67	3.48	72.81	-	-	-
Total						681.35	651.63		498.15		4	3	2

Supplemental Table 3: 214 fusion genes identified in 272 samples by RNA-seq.

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_413	AHCYL2	TMEM178B	7	7	129037165	141170336	29	14	0.925359	N	Y	N	N	in-frame	N	N	+	+	+	-	exon5(12903706 1-129037164)	exon4(1411703 34-141180178)
CGGA_1034	AP2A2	SBF2	11	11	926088	9834255	97	16	0.8114517	N	N	N	Y	in-frame	N	N	+	-	+	+	exon1(925807- 926087)	exon11(983407 7-9834254)
CGGA_1034	AP2A2	SBF2	11	11	926088	9838571	479	14	0.954147	N	N	N	Y	in-frame	N	N	+	-	+	+	exon1(925807- 926087)	exon12(983838 5-9838570)
CGGA_D36	APEH	SHISA5	3	3	49714133	48511242	34	10	0.8628372	N	N	N	Y	in-frame	N	N	+	-	+	+	exon8(49714040 -49714132)	exon3(4851112 5-48511241)
CGGA_1175	B4GALNT3	DENND5B	12	12	569711	31605410	51	17	0.9850815	N	N	N	Y	in-frame	N	N	+	-	+	+	exon1(569541- 569710)	exon17(316048 72-31605409)
CGGA_859	BCR	LZTR1	22	22	23524426	21342299	11	6	0.7909275	N	N	Y	N	in-frame	N	N	+	+	+	-	exon1(23522550 -23524425)	exon5(2134229 7-21342406)
CGGA_1079	BIN2	CELA1	12	12	51681892	51723617	17	9	0.8071052	Y	N	Y	N	in-frame	N	N	-	-	-	+	exon3(51681890 -51681971)	exon2(5172346 6-51723616)
CGGA_1251	BRPF3	CLPSL1	6	6	36182163	35754775	80	43	0.9829611	N	N	Y	N	in-frame	N	N	+	+	+	-	exon8(36181655 -36182162)	exon2(3575477 3-35754896)
CGGA_1324	C15orf57	CBX3	15	7	40854974	26241386	2	3	0.7066071	N	N	N	N	in-frame	N	Y	-	+	-	-	exon3(40854969 -40855225)	exon1(2624132 2-26241445)
CGGA_374	CBL	FBXO2	11	1	119169250	11710891	3	5	0.8707546	N	N	N	N	in-frame	N	Y	+	-	+	+	exon15(1191690 66-119169249)	exon5(1171052 1-11710890)
CGGA_1049	CCM2	OGDH	7	7	45078025	44706335	11	5	0.9174609	N	N	Y	N	in-frame	N	N	+	+	+	-	exon2(45077850 -45078024)	exon5(4470633 3-44706449)
CGGA_1034	CD81	SPAG6	11	10	2411756	22634652	186	13	0.8975235	N	N	N	N	in-frame	N	Y	+	+	+	-	exon2(2411640- 2411755)	exon2(2263465 0-22634746)
CGGA_1324	CDK17	KCNC2	12	12	96694082	75445097	10	3	0.9343572	N	Y	N	N	in-frame	N	N	-	-	-	+	exon11(9669408 0-96694137)	exon3(7544416 8-75445096)
CGGA_1170	CDK4	TSFM	12	12	58143237	58196338	85	35	0.8473896	Y	N	N	Y	in-frame	N	N	-	+	-	-	exon3(58143235 -58143286)	exon6(5819633 6-58196638)
CGGA_413	CLASRP	SYMPK	19	19	45556435	46347458	21	8	0.9166825	N	N	N	Y	in-frame	N	N	+	-	+	+	exon5(45556354 -45556434)	exon20(463472 86-46347457)
CGGA_1060	CLSTN1	KAZN	1	1	9833330	15287180	19	7	0.9820255	N	N	N	Y	in-frame	N	N	-	+	-	-	exon18(9833328 -9833451)	exon2(1528717 8-15287370)
CGGA_1329	COG3	GPC6	13	13	46085989	94958234	16	8	0.9534272	N	Y	N	N	in-frame	N	N	+	+	+	-	exon16(4608589 8-46085988)	exon6(9495823 2-94958376)
CGGA_616	CPNE5	ANXA6	6	5	36714173	150516882	15	13	0.9736026	N	N	N	N	in-frame	N	Y	-	-	-	+	exon6(36714171 -36714353)	exon21(150516 790-150516881)
CGGA_1113	CTDSP2	XRCC6BP1	12	12	58240155	58339411	76	20	0.863824	N	N	N	Y	in-frame	N	N	-	+	-	-	exon8(58240153 -58240746)	exon2(5833940 9-58339455)
CGGA_1045	CXADR	C21orf37	21	21	18885490	18821183	18	11	0.9160158	N	N	Y	N	in-frame	N	N	+	+	+	-	exon1(18885222 -18885489)	exon4(1882118 1-18821502)
CGGA_1024	FAM117A	LGALS9	17	17	47841254	25972340	4	8	0.7062534	N	N	N	Y	in-frame	N	N	-	+	-	-	exon8(47841252 -47841517)	exon5(2597233 8-25972374)
CGGA_1251	FAM155A	COL4A1	13	13	108518030	110895081	209	117	0.9359028	N	N	Y	N	in-frame	N	N	-	-	-	+	exon3(10851802 8-108519459)	exon51(110895 020-110895080)
CGGA_309	FARP2	DTNB	2	2	242312705	25656864	38	15	0.9721039	N	N	N	Y	in-frame	N	N	+	-	+	+	exon2(24231249 7-242312704)	exon9(2565677 7-25656863)
CGGA_1313	FGFR3	TACC3	4	4	1808661	1737458	42	23	0.9699318	Y	N	Y	N	in-frame	N	N	+	+	+	-	exon17(1808554 -1808660)	exon8(1737456- 1737560)
CGGA_842	FGFR3	TACC3	4	4	1808661	1739325	79	62	0.9604375	Y	N	Y	N	in-frame	N	N	+	+	+	-	exon17(1808554 -1808660)	exon10(173932 3-1739428)
CGGA_1109	FGFR3	TACC3	4	4	1808661	1741429	1488	573	0.978299	Y	N	Y	N	in-frame	N	N	+	+	+	-	exon17(1808554 -1808660)	exon11(174142 7-1741504)
CGGA_578	FRMD4A	PFKP	10	10	13779844	3155311	10	7	0.9339032	N	N	N	Y	in-frame	N	N	-	+	-	-	exon14(1377984 2-13779929)	exon12(315530 9-3155379)
CGGA_1240	GLTP	VPS29	12	12	110318077	110934008	43	27	0.9397124	N	N	Y	N	in-frame	N	N	-	-	-	+	exon5(11031807 5-110318292)	exon3(1109338 15-110934007)
CGGA_1094	GPR162	CCDC39	12	3	6935518	180372741	10	2	0.6765751	N	N	N	N	in-frame	N	Y	+	-	+	+	exon4(6935359- 6935517)	exon14(180372 548-180372740)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_491	HUWE1	RIBC1	X	X	53672263	53453225	6	5	0.5547511	N	N	N	Y	in-frame	N	N	-	+	-	-	exon78(53672261-53672414)	exon3(53453225-53453340)
CGGA_704	IFT80	MLH1	3	3	160037548	37067128	13	14	0.9729737	N	N	N	Y	in-frame	N	N	-	+	-	-	exon12(160037546-160037726)	exon12(37067126-37067497)
CGGA_245	IL1RAP	FGF12	3	3	190338229	192078327	41	33	0.9582609	N	N	N	Y	in-frame	N	N	+	-	+	+	exon6(190338062-190338228)	exon4(192078215-192078326)
CGGA_1077	LANCL2	DNAH11	7	7	55479782	21840755	33	12	0.9469955	N	N	Y	N	in-frame	N	N	+	+	+	-	exon6(55479598-55479781)	exon63(21840753-21840892)
CGGA_1329	LHFP	SERP2	13	13	40174969	44971408	6	6	0.9530682	N	N	N	Y	in-frame	N	N	-	+	-	-	exon3(40174967-40175526)	exon3(44971406-44971849)
CGGA_1059	MARCH6	MYO10	5	5	10405789	16711354	15	7	0.9267783	N	N	N	Y	in-frame	N	N	+	-	+	+	exon16(10405668-10405788)	exon22(16711228-16711353)
CGGA_1175	MED13L	GRIP1	12	12	116675273	66800208	114	57	0.9838402	N	Y	N	N	in-frame	N	N	-	-	-	+	exon30(116675271-116675509)	exon9(66800061-66800207)
CGGA_374	MGAT5	KIAA0825	2	5	135028121	93753085	4	5	0.8994962	N	N	N	N	in-frame	N	Y	+	-	+	+	exon2(135027955-135028120)	intron7(93753070-93775684)
CGGA_1026	MLL3	CHGB	7	20	152008883	5896972	56	43	0.8757237	N	N	N	N	in-frame	N	Y	-	+	-	-	exon55(15200881-152009030)	exon2(5896970-5897017)
CGGA_578	MRPS28	ASPH	8	8	80915234	62566219	11	9	0.9395595	N	Y	N	N	in-frame	N	N	-	-	-	+	exon2(80915232-80915414)	exon22(62566125-62566218)
CGGA_274	MTAP	C9orf92	9	9	21818201	16215897	70	32	0.72412	N	N	N	Y	in-frame	N	N	+	-	+	+	exon4(21818032-21818200)	exon3(16215768-16215896)
CGGA_802	NEK6	RXRA	9	9	127089724	137320954	64	40	0.8796351	N	Y	N	N	in-frame	N	N	+	+	+	-	exon7(127089615-127089723)	exon7(137320952-137321085)
CGGA_878	NFATC3	CPNE2	16	16	68160513	57179997	62	5	0.9208133	N	N	Y	N	in-frame	N	N	+	+	+	-	exon3(68160349-68160512)	exon15(57179995-57180232)
CGGA_796	PITPNA	RAD51C	17	17	1461823	56809845	42	38	0.9838499	N	N	N	Y	in-frame	N	N	-	+	-	-	exon11(1461821-1461852)	exon8(56809843-56809904)
CGGA_1024	PLA2G6	CRYBB1	22	22	38535989	27012302	16	6	0.9843164	N	Y	N	N	in-frame	N	N	-	-	-	+	exon12(38535987-38536175)	exon5(27012102-27012301)
CGGA_1119	PLAGL2	HCK	20	20	30789722	30659465	59	34	0.6932996	N	N	N	Y	in-frame	N	N	-	+	-	-	exon2(30789720-30790094)	exon2(30659463-30659584)
CGGA_1234	PODXL	BGN	7	X	131241019	152770079	97	10	0.8790083	N	N	N	N	in-frame	N	Y	-	+	-	-	exon8(131241017-131241375)	exon2(152770077-152770326)
CGGA_1287	PTN	DGKI	7	7	136935977	137096953	25	11	0.8995343	N	N	Y	N	in-frame	N	N	-	-	-	+	exon2(136935975-136936137)	exon5(137096914-137096952)
CGGA_661	PTPRZ1	MET	7	7	121513611	116339125	12	6	0.9364792	N	N	Y	N	in-frame	N	N	+	+	+	-	exon1(121513157-121513610)	exon2(116339123-116340337)
CGGA_1068	PTPRZ1	MET	7	7	121608184	116339125	21	14	0.9444875	N	N	Y	N	in-frame	N	N	+	+	+	-	exon3(121608003-121608183)	exon2(116339123-116340337)
CGGA_D64	PTPRZ1	MET	7	7	121624171	116339125	60	10	0.9314013	N	N	Y	N	in-frame	N	N	+	+	+	-	exon8(121624019-121624170)	exon2(116339123-116340337)
CGGA_1118	PVRL2	SNTG1	19	8	45349870	51442737	29	16	0.9143789	N	N	N	N	in-frame	N	Y	+	+	+	-	exon1(45349391-45349869)	exon10(51442735-51442818)
CGGA_1272	PVRL2	SNTG1	19	8	45349870	51442737	19	13	0.9110463	N	N	N	N	in-frame	N	Y	+	+	+	-	exon1(45349391-45349869)	exon10(51442735-51442818)
CGGA_1034	RASSF7	SCUBE2	11	11	562776	9091042	1	8	0.8868921	N	N	N	Y	in-frame	N	N	+	-	+	+	exon3(5620775-562775)	exon18(9090915-9091041)
CGGA_D27	RNF213	SLC26A11	17	17	78237577	78210727	29	23	0.8917188	Y	N	Y	N	in-frame	N	N	+	+	+	-	exon2(78237371-78237576)	exon8(78210725-78210901)
CGGA_604	RNF213	SLC26A11	17	17	78237577	78210727	28	12	0.9831649	Y	N	Y	N	in-frame	N	N	+	+	+	-	exon2(78237371-78237576)	exon8(78210725-78210901)
CGGA_815	SH3GL1	CHAF1A	19	19	4364085	4422563	13	11	0.7531302	Y	N	N	Y	in-frame	N	N	-	+	-	-	exon6(4364083-4364217)	exon5(4422561-4422791)
CGGA_1094	SLC6A8	GABRA3	X	X	152960088	151337035	55	38	0.8918768	N	N	N	Y	in-frame	N	N	+	-	+	+	exon11(152959986-152960087)	exon1(151335632-151337034)
CGGA_1272	ST7	CTTNBP2	7	7	116593745	117396688	5	3	0.9788694	N	N	N	Y	in-frame	N	N	+	-	+	+	exon1(116593379-116593744)	exon12(117396607-117396687)
CGGA_1329	TCF7L1	KIF1B	2	1	85361573	10351140	14	6	0.9110896	N	N	N	N	in-frame	N	Y	+	+	+	-	exon3(85361444-85361572)	exon14(10351138-10351218)
CGGA_493	TGFB1	SAE1	19	19	41854200	47673075	6	5	0.8484431	N	N	N	Y	in-frame	N	N	-	+	-	-	exon6(41854198-41854359)	exon6(47673073-47673179)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_break_pos1	genomic_break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_1049	TPM3	ADAR	1	1	154155464	154575102	19	19	0.7751667	N	N	Y	N	in-frame	N	N	-	-	-	+	exon8(154155462-154155724)	exon14(154573515-154575101)
CGGA_1046-1	TPT1	AADAT	13	4	45914847	170999734	21	18	0.9141399	N	N	N	N	in-frame	N	Y	-	-	-	+	exon5(45914845-45914919)	exon10(170999658-170999733)
CGGA_374	TTLL11	FIBCD1	9	9	124854966	133787275	9	7	0.9704262	N	N	Y	N	in-frame	N	N	-	-	-	+	exon9(124854964-124855884)	exon3(133787177-133787274)
CGGA_1329	URI1	SLC6A20	19	3	30433571	45807233	15	8	0.9526206	N	N	N	N	in-frame	N	Y	+	-	+	+	exon1(30433144-30433570)	exon4(45807027-45807232)
CGGA_603	VEZT	CORO1C	12	12	95645847	109055934	34	23	0.9775687	N	N	N	Y	in-frame	N	N	+	-	+	+	exon2(95645714-95645846)	exon8(109055803-109055933)
CGGA_1026	VHL	BRK1	3	3	10183871	10167310	94	72	0.9550884	N	N	Y	N	in-frame	N	N	+	+	+	-	exon1(10183317-10183870)	exon2(10167308-10167391)
CGGA_564	ZC3H11A	REN	1	1	203816815	204131291	265	116	0.9332162	N	N	N	Y	in-frame	N	N	+	-	+	+	exon15(203816310-203816814)	exon9(204131139-204131290)
CGGA_1329	ZMIZ1	MAT1A	10	10	80961449	82036350	40	42	0.9854704	N	N	N	Y	in-frame	N	N	+	-	+	+	exon5(80961339-80961448)	exon4(82036130-82036349)
CGGA_1046-1	ZNF197	CHMP2B	3	3	44674091	87289849	8	7	0.9050013	N	Y	N	N	in-frame	N	N	+	+	+	-	exon5(44673963-44674090)	exon2(87289847-87289939)
CGGA_1381	A2M	NOL10	12	2	9256882	10784618	161	42	0.8817214	N	N	N	N	out of frame	N	Y	-	-	-	-	exon26(9256833-9256995)	intron9(10784498-10794604)
CGGA_876	ACER3	PAK1	11	11	76637711	77034405	39	19	0.9735189	N	N	N	Y	out of frame	N	N	+	-	+	+	exon2(76637599-76637710)	exon1(77033058-77034404)
CGGA_1160	ADNP2	ITGB3BP	18	1	77867356	63920639	8	6	0.9675016	N	N	N	N	out of frame	N	Y	+	-	+	+	exon1(77866913-77867355)	exon5(63920559-63920638)
CGGA_1160	ADNP2	ITGB3BP	18	1	77867356	63955889	17	7	0.9805781	N	N	N	N	out of frame	N	Y	+	-	+	+	exon1(77866913-77867355)	exon7(63955752-63955888)
CGGA_1026	AGAP2	TSFM	12	12	58130862	58179946	91	52	0.9308048	Y	N	N	Y	out of frame	N	N	-	+	-	-	intron17(58129210-58135692)	exon3(58179944-58180073)
CGGA_603	ANO4	GALNT9	12	12	101218863	132691962	14	8	0.5749093	N	Y	N	N	out of frame	N	N	+	-	+	-	intron1(101188805-101295421)	intron5(132688235-132824460)
CGGA_1381	AVIL	VSNL1	12	2	58204601	17744679	8	4	0.5403123	N	N	N	N	out of frame	N	Y	-	+	-	+	exon15(58204597-58204708)	intron1(17722185-17773334)
CGGA_1175	B4GALNT3	DENND5B	12	12	569711	31600703	6	5	0.9854025	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(569541-569710)	exon16(31600470-31600702)
CGGA_676	BAZ2A	LRP1	12	12	57007681	57539273	348	74	0.9558675	N	N	Y	N	out of frame	N	N	-	+	-	+	intron25(57007017-57007734)	exon6(57539008-57539272)
CGGA_676	BAZ2A	METTL1	12	12	57023909	58163739	24	7	0.877482	N	N	Y	N	out of frame	N	N	-	-	-	+	intron28(57011316-57029963)	exon4(58163553-58163738)
CGGA_676	BAZ2A	METTL1	12	12	57024560	58165040	18	13	0.803968	N	N	Y	N	out of frame	N	N	-	-	-	+	intron28(57011316-57029963)	exon5(58164875-58165039)
CGGA_1175	BCAT1	FIP1L1	12	4	25101861	54245392	3	5	0.9147763	N	N	N	N	out of frame	N	Y	-	+	-	-	exon9(25101859-25102392)	exon2(54245390-54245430)
CGGA_1251	BRPF3	CLPSL1	6	6	36178305	35754775	24	11	0.9883392	N	N	Y	N	out of frame	N	N	+	+	+	-	exon6(36177991-36178304)	exon2(35754773-35754896)
CGGA_1175	C12orf5	KCNC2	12	12	4446324	75563492	87	29	0.798601	N	Y	N	N	out of frame	N	N	+	-	+	-	exon3(4446203-4446325)	intron3(75445097-75601074)
CGGA_1072	C1orf21	MIXL1	1	1	184356502	226413208	2	4	0.9459978	N	Y	N	N	out of frame	N	N	+	+	+	-	exon1(184356148-184356501)	exon2(226413206-226413512)
CGGA_884	C2CD3	SMAD9	11	13	73801858	37454012	11	6	0.9197363	N	N	N	N	out of frame	N	Y	-	-	-	+	exon12(73801856-73801980)	exon5(37453413-37454011)
CGGA_603	C2CD3	SMAD9	11	13	73801858	37454012	8	6	0.9931398	N	N	N	N	out of frame	N	Y	-	-	-	+	exon12(73801856-73801980)	exon5(37453413-37454011)
CGGA_1381	C2orf48	PRMT8	2	12	10282502	3649772	6	5	0.9640342	N	N	N	N	out of frame	N	Y	+	+	+	-	exon2(10282380-10282501)	exon2(3649770-3649956)
CGGA_616	CCDC136	FKBP9L	7	7	128445955	55755617	79	54	0.9496871	N	N	N	Y	out of frame	N	N	+	-	+	+	exon8(128445813-128445954)	exon3(55755470-55755616)
CGGA_616	CCDC136	FKBP9L	7	7	128452366	55755617	22	12	0.9410109	N	N	N	Y	out of frame	N	N	+	-	+	+	intron8(128445955-128457809)	exon3(55755470-55755616)
CGGA_616	CCDC136	FKBP9L	7	7	128453408	55757202	33	14	0.8527105	N	N	N	Y	out of frame	N	N	+	-	+	+	intron8(128445955-128457809)	intron3(55755617-55759004)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_1324	CDK17	KCNC2	12	12	96692647	75445097	14	10	0.8897734	N	Y	N	N	out of frame	N	N	-	-	-	+	exon10(9669264 5-96692760)	exon3(7544416 8-75445096)
CGGA_603	CHFR	SMARCD1	12	12	133463782	50488220	51	17	0.9678912	N	N	N	Y	out of frame	N	N	-	+	-	-	exon15(1334637 80-133463925)	exon10(504882 18-50488354)
CGGA_1313	CHST3	PTCH2	10	1	73737822	45295583	3	2	0.785235	N	N	N	N	out of frame	N	Y	+	-	+	+	intron1(7372445 2-73765491)	exon17(452955 79-45295701)
CGGA_1313	CHST3	PTCH2	10	1	73737824	45295434	16	7	0.9436951	N	N	N	N	out of frame	N	Y	+	-	+	+	intron1(7372445 2-73765491)	exon16(452952 84-45295432)
CGGA_D33	COL22A1	BMP7	8	20	139732982	55750063	29	11	0.9000251	N	N	N	N	out of frame	N	Y	-	-	-	+	exon39(1397329 80-139733034)	exon3(5574998 5-55750062)
CGGA_1251	COL4A2	FAM155A	13	13	111082955	108265736	661	4	0.7734854	N	N	Y	N	out of frame	N	N	+	-	+	-	exon10(1110828 90-111082953)	intron2(1078631 03-108518027)
CGGA_1263	COQ10A	NINJ2	12	12	56664104	721236	140	61	0.9094099	N	N	Y	N	out of frame	N	N	+	-	+	-	exon5(56663932 -56664749)	intron3(675344- 772491)
CGGA_1263	COQ10A	NINJ2	12	12	56664098	721230	92	2	0.8269454	N	N	Y	N	out of frame	N	N	+	-	+	-	exon5(56663932 -56664749)	intron3(675344- 772491)
CGGA_676	CS	STAT6	12	12	56693946	57498915	11	18	0.6163852	N	N	N	Y	out of frame	N	N	-	-	-	-	exon11(5669394 2-56694174)	intron13(574985 96-57498931)
CGGA_1094	CTC1	TMEM117	17	12	8146303	44468049	8	5	0.980174	N	N	N	N	out of frame	N	Y	-	+	-	+	exon21(8146301 -8146465)	intron3(4433814 5-44537325)
CGGA_1170	CTDSP2	SLC6A15	12	12	58240155	85270386	9	7	0.9825928	N	N	Y	N	out of frame	N	N	-	-	-	+	exon8(58240153 -58240746)	exon7(8527027 4-85270385)
CGGA_D39	CTNND1	TMEM135	11	11	57529518	86947680	64	27	0.9233243	N	Y	N	N	out of frame	N	N	+	+	+	-	exon1(57529232 -57529590)	exon5(8694767 8-86947725)
CGGA_700	CUL1	CNTNAP2	7	7	148396121	147869334	50	25	0.9721422	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(14839593 1-148396120)	exon18(147869 332-147869569)
CGGA_1045	CXADR	C21orf37	21	21	18885490	18813995	5	6	0.9034205	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(18885222 -18885489)	exon2(1881399 0-18814160)
CGGA_1079	DENND4C	ADAMTSL1	9	9	19347084	18745058	19	10	0.8701025	N	N	N	Y	out of frame	N	N	+	+	+	+	exon22(1934591 7-19347083)	intron15(187216 63-18753293)
CGGA_603	DEPDC5	ALDH18A1	22	10	32164849	97393406	8	5	0.9662598	N	N	N	N	out of frame	N	Y	+	-	+	+	exon7(32164798 -32164848)	exon13(973932 46-97393405)
CGGA_680	DGKE	CACNA1G	17	17	54940684	48682981	14	9	0.6656123	N	N	Y	N	out of frame	N	N	+	+	+	-	exon12(5493997 1-54946035)	intron21(486816 42-48683256)
CGGA_1329	DHX35	LPAR1	20	9	37652410	113638002	6	6	0.974604	N	N	N	N	out of frame	N	Y	+	-	+	+	exon17(3765233 1-37652409)	exon1(1136360 52-113638001)
CGGA_1329	DNAJC3	RNASEH2B- AS1	13	13	96416208	51478998	14	9	0.8142413	N	N	N	Y	out of frame	N	N	+	-	+	+	exon9(96416085 -96416206)	intron2(5146387 1-51484616)
CGGA_1022	EDC3	COX5A	15	15	74988221	75216111	47	26	0.9110424	N	N	Y	N	out of frame	N	N	-	-	-	+	exon8(74988219 -74988385)	exon2(7521598 7-75216110)
CGGA_878	EGFR	VSTM2A	7	7	55268106	54636824	4951	1867	0.973641	N	N	Y	N	out of frame	N	N	+	+	+	-	exon24(5526800 7-55268105)	exon5(5463670 0-54636947)
CGGA_578	ELAVL2	PLGRKT	9	9	23825804	5361888	16	6	0.9794701	N	Y	N	N	out of frame	N	N	-	-	-	+	exon7(23825802 -23826062)	exon3(5361756- 5361887)
CGGA_1094	ELK1	GPRC5A	X	12	47509320	13065018	54	37	0.9785736	N	N	N	N	out of frame	N	Y	-	+	-	-	intron5(4750087 4-47509819)	exon3(1306501 6-13065075)
CGGA_1094	ELK1	GPRC5A	X	12	47509822	13065018	40	13	0.9820164	N	N	N	N	out of frame	N	Y	-	+	-	-	exon6(47509820 -47510002)	exon3(1306501 6-13065075)
CGGA_678	EML1	EVL	14	14	100259879	100551200	11	8	0.6878078	N	N	N	Y	out of frame	N	N	+	+	+	+	exon1(10025974 3-100259879)	intron2(1005511 92-100563815)
CGGA_761	ESAM	MSANTD2	11	11	124624853	124648622	52	5	0.5819277	Y	N	N	Y	out of frame	N	N	-	-	-	-	intron3(1246246 59-124626100)	intron3(1246447 14-124669764)
CGGA_1314	ETV6	NELL2	12	12	11803094	45209919	23	13	0.9876761	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(11802786 -11803093)	exon18(452097 67-45209918)
CGGA_1292	FAM222A	MVK	12	12	110152702	110012614	34	12	0.9096144	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(11015218 5-110152701)	exon2(1100126 12-110012704)
CGGA_603	FAM222A	SIRT4	12	12	110152702	120741364	31	17	0.95175	N	Y	N	N	out of frame	N	N	+	+	+	-	exon1(11015218 5-110152701)	exon2(1207413 62-120741860)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_899	FOXP2	CAPZA2	7	7	114206015	116502706	75	32	0.8003564	N	N	N	Y	out of frame	N	N	+	+	+	+	intron5(1141784-38-114210859)	exon1(116502561-116502703)
CGGA_899	FOXP2	MET	7	7	114202653	116339125	44	19	0.9764524	N	N	N	Y	out of frame	N	N	+	+	+	-	intron5(1141784-38-114210859)	exon2(116339123-116340337)
CGGA_D32	GOLPH3	APBB1IP	5	10	32173916	26781256	26	14	0.9608038	N	N	N	N	out of frame	N	Y	-	+	-	-	exon4(32173914-32174424)	exon3(26781254-26781326)
CGGA_D03	GOLPH3	APBB1IP	5	10	32173916	26781256	26	14	0.8889296	N	N	N	N	out of frame	N	Y	-	+	-	-	exon4(32173914-32174424)	exon3(26781254-26781326)
CGGA_603	GRIP1	RNFT2	12	12	66923611	117217000	10	6	0.9720438	N	N	N	Y	out of frame	N	N	-	+	-	-	exon19(66923609-66923693)	exon7(117216998-117217152)
CGGA_1175	GRIP1	SOX5	12	12	66773060	24233533	61	20	0.9818227	N	N	N	Y	out of frame	N	N	-	-	-	-	exon5(66773058-66773215)	intron12(24048958-24366274)
CGGA_1175	IFT81	ETNK1	12	12	110630511	22795755	768	307	0.9686645	N	N	N	Y	out of frame	N	N	+	+	+	+	exon14(110630420-110630510)	intron1(22778520-22796694)
CGGA_599	IP6K2	USP19	3	3	48732523	49145961	21	10	0.938603	N	N	Y	N	out of frame	N	N	-	-	-	+	exon5(48732521-48732853)	exon1(49145477-49145960)
CGGA_1109	IQSEC1	GP1BA	3	17	13083787	4835894	7	4	0.9622963	N	N	N	N	out of frame	N	Y	-	+	-	-	intron14(12983365-13114489)	exon2(4835892-4838324)
CGGA_802	JAK1	HIVEP3	1	1	65339053	41984159	5	7	0.7746173	N	Y	N	N	out of frame	N	N	-	-	-	+	exon21(65339051-65339205)	exon3(41984071-41984158)
CGGA_1119	KIAA0430	SPR	16	2	15705449	73118476	26	13	0.8859254	N	N	N	N	out of frame	N	Y	-	+	-	-	exon10(15705447-15705590)	exon3(73118474-73119288)
CGGA_D09	KSR1	PKN3	17	9	25937224	131467582	8	5	0.9029814	N	N	N	N	out of frame	N	Y	+	+	+	-	exon18(25937091-25937223)	exon2(131467580-131467821)
CGGA_671	LAMA1	PTPRM	18	18	7079977	7573555	42	13	0.7625065	N	N	Y	N	out of frame	N	N	-	+	-	+	exon61(7079972-7080085)	intron1(7567889-7774144)
CGGA_681	LAMA1	PTPRM	18	18	7079977	7573555	25	8	0.6799715	N	N	Y	N	out of frame	N	N	-	+	-	+	exon61(7079972-7080085)	intron1(7567889-7774144)
CGGA_374	LINC00662	AP1M2	19	19	28283908	10694746	6	6	0.8074956	N	Y	N	N	out of frame	N	N	-	-	-	+	exon2(28283906-28284139)	exon11(10694588-10694745)
CGGA_1160	LMBR1L	GALNT9	12	12	49491348	132834424	58	30	0.7579476	N	N	Y	N	out of frame	N	N	-	-	-	+	exon1(49490921-49491521)	exon7(13283426-132834424)
CGGA_1375	LNK2	LHFP	13	13	28194154	39952662	9	4	0.8588507	N	N	Y	N	out of frame	N	N	-	-	-	+	intron9(28155940-28194509)	exon2(39952563-39952662)
CGGA_1375	LNK2	LHFP	13	13	28194512	39952663	33	29	0.9690522	N	N	Y	N	out of frame	N	N	-	-	-	+	exon10(28194510-28194719)	exon2(39952563-39952662)
CGGA_426	LPCAT1	DENND3	5	8	1473563	142182801	35	7	0.8388635	N	N	N	N	out of frame	N	Y	-	+	-	+	intron3(1471039-1474069)	intron13(142178624-142185296)
CGGA_676	LRP1	BAZ2A	12	12	57538883	57007681	7	8	0.9624987	N	N	Y	N	out of frame	N	N	+	-	+	-	exon5(57538753-57538882)	intron25(57007017-57007734)
CGGA_676	LRP1	BAZ2A	12	12	57539273	57007681	351	20	0.9328053	N	N	Y	N	out of frame	N	N	+	-	+	-	exon6(57539008-57539272)	intron25(57007017-57007734)
CGGA_499	LRRFIP2	GOLGA4	3	3	37116517	37401203	19	7	0.6163822	N	N	Y	N	out of frame	N	N	-	+	-	+	exon7(37116513-37116606)	intron22(37396678-37402731)
CGGA_850	MACF1	AHDC1	1	1	39550110	27885394	28	15	0.9816153	N	N	N	Y	out of frame	N	N	+	-	+	+	exon3(39549837-39550109)	exon6(27885215-27885393)
CGGA_1175	MARCH9	SLCO1B7	12	12	58149457	21216401	832	330	0.8192002	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(58148879-58149667)	intron10(21207570-21220250)
CGGA_1409	MAX	TTC7B	14	14	65560426	91161922	25	13	0.9884284	N	N	Y	N	out of frame	N	N	-	-	-	+	exon2(65560424-65560532)	exon15(91161842-91161921)
CGGA_D57	MECOM	GAP43	3	3	169098975	115439641	24	13	0.8782675	N	N	N	Y	out of frame	N	N	-	+	-	-	intron15(168861620-169381121)	exon4(115439639-115440333)
CGGA_1175	MED13L	YEATS4	12	12	116675273	69775659	2687	745	0.9411996	N	Y	N	N	out of frame	N	N	-	+	-	+	exon30(116675271-116675509)	intron6(69764755-69783924)
CGGA_272	MID1	ARHGAP6	X	X	10491132	11215116	8	7	0.8637471	N	N	Y	N	out of frame	N	N	-	-	-	+	exon8(10491130-10491226)	exon11(11215043-11215115)
CGGA_761	MSANTD2	ESAM	11	11	124648622	124624853	52	15	0.5819277	Y	N	N	Y	out of frame	N	N	-	-	-	-	intron3(124644714-124669764)	intron3(124624659-124626100)
CGGA_1324	MYO6	SENP6	6	6	76459140	76425101	15	8	0.9057436	Y	N	Y	N	out of frame	N	N	+	+	+	-	exon1(76458907-76459139)	exon24(76425099-76427993)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_676	NAB2	TAC3	12	12	57487381	57404072	121	18	0.815957	N	N	N	Y	out of frame	N	N	+	-	+	+	exon6(57487188-57487380)	exon1(57403779-57404071)
CGGA_578	NMU	LNK1	4	4	56496569	54341768	8	5	0.989379	N	N	N	Y	out of frame	N	N	-	-	-	-	exon9(56496567-56496626)	intron2(54327760-54342917)
CGGA_578	NMU	LNK1	4	4	56496569	54343494	10	6	0.9885579	N	N	N	Y	out of frame	N	N	-	-	-	-	exon9(56496567-56496626)	intron3(54343148-54344729)
CGGA_J023	NPAT	RPS11	11	19	108064684	50002769	112	67	0.9701083	N	N	N	N	out of frame	N	Y	-	+	-	-	exon16(108064682-108064743)	exon5(50002767-50002968)
CGGA_1007	NUS1	SLC25A13	6	7	117996902	95751031	32	29	0.8141455	N	N	N	N	out of frame	N	Y	+	-	+	+	exon1(117996615-117997247)	exon2(95750965-95751056)
CGGA_757	PAK4	AKT2	19	19	39616559	40762961	7	2	0.9653474	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(39616418-39616558)	exon12(40762831-40762960)
CGGA_757	PAK4	AKT2	19	19	39616559	40771258	15	16	0.9759623	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(39616418-39616558)	exon13(40771127-40771257)
CGGA_578	PAK4	NFKBIB	19	19	39616559	39395655	22	14	0.983837	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(39616418-39616558)	exon2(39395653-39395759)
CGGA_1109	PER3	CAMTA1	1	1	7863908	6880505	31	16	0.9693143	N	N	N	Y	out of frame	N	N	+	+	+	+	exon9(7863750-7863907)	intron2(6880310-6885149)
CGGA_603	PITPNM2	ACSS3	12	12	123594932	81503339	26	11	0.9887193	N	N	N	Y	out of frame	N	N	-	+	-	-	exon25(123594930-123594974)	exon2(81503337-81503482)
CGGA_578	PLGRKT	HSPBP1	9	19	5431897	55777654	13	8	0.9511153	N	N	N	N	out of frame	N	Y	-	-	-	+	exon4(5431895-5431982)	exon4(55777497-55777653)
CGGA_616	POLN	SH3BP2	4	4	2142612	2838586	62	32	0.766416	N	N	Y	N	out of frame	N	N	-	+	-	+	intron10(2133017-2158512)	exon13(2835422-2842822)
CGGA_1160	PPP1R12A	C12orf42	12	12	80328475	103716237	23	9	0.9884929	N	N	N	Y	out of frame	N	N	-	-	-	-	exon25(80328473-80328730)	intron2(103700123-103762662)
CGGA_603	PPP1R12A	OS9	12	12	80328475	58109543	102	45	0.9887159	N	N	N	Y	out of frame	N	N	-	+	-	-	exon25(80328473-80328730)	exon5(58109541-58109752)
CGGA_578	PPP6R1	MLLT3	19	9	55743407	20479063	37	16	0.7392858	N	N	N	N	out of frame	N	Y	-	-	-	+	intron6(55743350-55743440)	intron9(20456784-20620650)
CGGA_578	PPP6R1	MLLT3	19	9	55748012	20477992	26	10	0.7965757	N	N	N	N	out of frame	N	Y	-	-	-	+	exon8(55748009-55748188)	intron9(20456784-20620650)
CGGA_1381	PRMT8	LAPTM4A	12	2	3675238	20251172	187	56	0.9192414	N	N	N	N	out of frame	N	Y	+	-	+	-	intron4(3662880-3677869)	exon7(20251169-20251788)
CGGA_837	PTEN	COL17A1	10	10	89624305	105819353	72	29	0.9428049	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(89623193-89624304)	intron41(105817948-105819393)
CGGA_837	PTEN	COL17A1	10	10	89626679	105819490	29	5	0.7337664	N	N	N	Y	out of frame	N	N	+	-	+	+	intron1(89624305-89653779)	intron42(105819476-105819874)
CGGA_1381	PTPN1	CHMP4B	20	20	49127127	32436273	19	7	0.9362792	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(49126889-49127126)	exon2(32436271-32436449)
CGGA_1077	PXDC1	NFS1	6	20	3751510	34261606	30	11	0.8651512	N	N	N	N	out of frame	N	Y	-	-	-	+	exon5(3751508-3752245)	exon3(34261521-34261605)
CGGA_1197	RAB3C	CNTN5	5	11	58021947	100226848	30	18	0.9717793	N	N	N	N	out of frame	N	Y	+	+	+	-	exon3(58021827-58021946)	exon25(100226846-100229615)
CGGA_676	RBMS2	LRP1	12	12	56986178	57524059	290	99	0.7487327	N	N	N	Y	out of frame	N	N	+	+	+	+	exon14(56982922-56989979)	intron1(57522814-57532239)
CGGA_676	RDH16	R3HDM2	12	12	57348885	57663776	10	11	0.7124433	N	N	N	Y	out of frame	N	N	-	-	-	+	exon3(57348688-57348947)	exon10(57663533-57663776)
CGGA_458	RIMKLB	MICALL2	12	7	8866637	1488397	74	32	0.6279191	N	N	N	N	out of frame	N	Y	+	-	+	+	exon3(8866405-8866636)	exon15(1488254-1488396)
CGGA_D64	RIMKLB	MICALL2	12	7	8866637	1488397	41	11	0.7766348	N	N	N	N	out of frame	N	Y	+	-	+	+	exon3(8866405-8866636)	exon15(1488254-1488396)
CGGA_1175	RNFT2	MYO1A	12	12	117271746	57440328	103	33	0.9804431	N	N	Y	N	out of frame	N	N	+	-	+	-	exon8(117271595-117271745)	intron20(57437993-57440333)
CGGA_309	RPAP3	CPNE8	12	12	48091382	39111972	21	9	0.785973	N	N	N	Y	out of frame	N	N	-	-	-	-	exon14(48091378-48091501)	intron7(39096723-39117571)
CGGA_815	RRN3P2	ANK2	16	4	29093362	114095572	8	6	0.7883782	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(29089278-29095761)	exon3(114095570-114095672)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_1340	RRN3P2	ANK2	16	4	29093362	114095572	13	7	0.8399244	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_669	RRN3P2	ANK2	16	4	29093362	114095572	12	6	0.6334865	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_314	RRN3P2	ANK2	16	4	29093362	114095572	12	8	0.5679112	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_502	RRN3P2	ANK2	16	4	29093362	114095572	6	5	0.6098547	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_483	RRN3P2	ANK2	16	4	29093362	114095572	12	10	0.623076	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_773	RRN3P2	ANK2	16	4	29093362	114095572	23	16	0.7793496	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_1109	RRN3P2	ANK2	16	4	29093362	114095572	38	20	0.5891237	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_905	RRN3P2	ANK2	16	4	29093362	114095572	13	9	0.6397121	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_1411	RRN3P2	ANK2	16	4	29093362	114095572	8	5	0.6498751	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_479	RRN3P2	ANK2	16	4	29093362	114095572	3	5	0.6689171	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_565	RRN3P2	ANK2	16	4	29093362	114095572	10	8	0.7907955	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_1409	RRN3P2	ANK2	16	4	29093362	114095572	12	7	0.5757275	N	N	N	N	out of frame	N	Y	+	+	+	-	intron3(2908927 8-29095761)	exon3(1140955 70-114095672)
CGGA_D39	RTN3	TRPC6	11	11	63449250	101325832	27	17	0.8461836	N	N	N	Y	out of frame	N	N	+	-	+	+	exon1(63448920 -63449249)	exon3(1013257 47-101325831)
CGGA_D11	SCHIP1	ACOT9	3	X	159584070	23750763	175	92	0.9820946	N	N	N	N	out of frame	N	Y	+	-	+	-	exon3(15958395 0-159584069)	intron12(237491 03-23751286)
CGGA_802	SCMH1	LIMA1	1	12	41651793	50642557	14	11	0.9324933	N	N	N	N	out of frame	N	Y	-	-	-	+	exon13(4165179 1-41651921)	exon10(506424 14-50642556)
CGGA_1034	SCUBE2	ZNF195	11	11	9041997	3400269	19	10	0.944298	N	N	N	Y	out of frame	N	N	-	-	-	-	exon1(9041045- 9042743)	exon7(3400266- 3400451)
CGGA_1251	SEC61G	LANCL2	7	7	54823302	55444915	14	5	0.6737646	N	N	Y	N	out of frame	N	N	-	+	-	+	intron1(5482011 3-54823469)	intron1(5543392 2-55459483)
CGGA_1251	SEC61G	LANCL2	7	7	54823472	55438249	91	41	0.9889027	N	N	Y	N	out of frame	N	N	-	+	-	+	exon2(54823470 -54823573)	intron1(5543392 2-55459483)
CGGA_D36	SFMBT1	CCRL2	3	3	53079832	46448880	7	8	0.7636222	N	N	N	Y	out of frame	N	N	-	+	-	-	exon21(5307983 0-53080088)	exon1(4644871 9-46448992)
CGGA_1170	SFSWAP	TCP11L2	12	12	132250853	106704819	6	2	0.9836539	N	N	Y	N	out of frame	N	N	+	+	+	-	exon13(1322506 61-132250852)	exon2(1067048 17-106705009)
CGGA_D39	SIGLEC8	MBOAT7	19	19	51957032	54683165	71	31	0.861264	N	N	N	Y	out of frame	N	N	-	-	-	-	intron1(5195588 7-51957470)	intron2(5468265 8-54684487)
CGGA_1307	SLC2A8	KPNA3	9	13	130159565	50307182	6	5	0.9221255	N	N	N	N	out of frame	N	Y	+	-	+	+	exon1(13015941 5-130159564)	exon15(503070 91-50307181)
CGGA_676	SMARCC2	TSFM	12	12	56568337	58185706	51	23	0.7112387	N	N	Y	N	out of frame	N	N	-	+	-	+	intron12(565676 33-56568432)	intron4(5818094 5-58186766)
CGGA_1007	SORL1	CNTNAP2	11	7	121367757	146397921	130	40	0.8266298	N	N	N	N	out of frame	N	Y	+	+	+	+	exon6(12136757 6-121367757)	intron1(1458140 65-146471360)
CGGA_1170	SP1	TMEM132D	12	12	53777404	130304370	31	14	0.784958	N	Y	N	N	out of frame	N	N	+	-	+	-	exon3(53776036 -53777405)	intron8(1301852 43-130387803)
CGGA_374	SREBF2	EFCAB6	22	22	42267065	44152139	18	12	0.8169709	N	N	N	Y	out of frame	N	N	+	-	+	+	intron4(4226703 9-42269799)	intron27(441517 12-44161182)
CGGA_616	SRGAP3	TATDN2	3	3	9231480	10298679	22	9	0.8862027	N	N	Y	N	out of frame	N	N	-	+	-	+	intron21(916660 1-9290566)	intron2(1029129 8-10301818)
CGGA_J100	SSH2	RTN1	17	14	28022477	60074210	31	13	0.9384884	N	N	N	N	out of frame	N	Y	-	-	-	+	exon12(2802247 5-28022540)	exon6(6007400 1-60074209)
CGGA_643	SSPN	GRIN2B	12	12	26384918	14018732	18	7	0.8883299	N	N	Y	N	out of frame	N	N	+	-	+	-	exon3(26383642 -26387707)	exon12(140187 30-14019159)
CGGA_643	STAT2	CD9	12	12	56750226	6315056	10	10	0.8901583	N	Y	N	N	out of frame	N	N	-	+	-	+	exon23(5675022 3-56750361)	intron1(6309731 -6334589)

SampleID	gene name1	gene name2	chromosome 1	chromosome 2	genomic_ break_pos1	genomic_ break_pos2	splitr count	span count	probability	adjacent	deletion	eversion	inversion	orf	read through	interchro mosome	gene strand1	gene strand2	genomic strand1	genomic strand2	gene_location1	gene_location2
CGGA_1024	STAU1	CABP5	20	19	47782534	48537619	13	7	0.9858678	N	N	N	N	out of frame	N	Y	-	-	-	+	intron11(47770608-47790729)	exon2(48537470-48537618)
CGGA_1024	STAU1	CABP5	20	19	47790732	48537619	55	24	0.9858678	N	N	N	N	out of frame	N	Y	-	-	-	+	exon12(47790730-47790805)	exon2(48537470-48537618)
CGGA_426	STK3	VPS13B	8	8	99837743	100396436	17	15	0.9806874	N	N	N	Y	out of frame	N	N	-	+	-	-	intron10(99787047-99895872)	exon20(100396434-100396544)
CGGA_1329	TFDP2	LMBRD1	3	6	141868025	70451769	55	20	0.9133667	N	N	N	N	out of frame	N	Y	-	-	-	+	exon13(141868023-141868385)	exon11(70451679-70451768)
CGGA_1045	TFRC	IL1RAP	3	3	195781565	190284389	15	5	0.8906788	N	N	N	Y	out of frame	N	N	-	+	-	-	intron2(195780429-195781948)	intron3(190282142-190321914)
CGGA_1094	TMEM117	CTC1	12	17	44467608	8146303	4	5	0.9732817	N	N	N	N	out of frame	N	Y	+	-	+	-	intron3(44338145-44537325)	exon21(8146301-8146465)
CGGA_1381	TOM1L2	IGSF9B	17	11	17872924	133804184	16	8	0.6400644	N	N	N	N	out of frame	N	Y	-	-	-	-	intron14(17810845-17875573)	intron13(133802108-133805509)
CGGA_1329	TRMT6	C11orf34	20	11	5930924	112126312	12	10	0.9821575	N	N	N	N	out of frame	N	Y	-	-	-	+	exon11(5930922-5931172)	exon3(112126109-112126311)
CGGA_1113	TSFM	R3HDM2	12	12	58177066	57704246	26	20	0.9563758	N	N	N	Y	out of frame	N	N	+	-	+	+	exon2(58176891-58177065)	exon22(57704045-57704245)
CGGA_323	TTC19	ADORA2B	17	17	15930016	15877993	19	13	0.9654996	Y	N	Y	N	out of frame	N	N	+	+	+	-	exon9(15929852-15930015)	exon2(15877991-15879209)
CGGA_D63	UBE3C	CNTNAP2	7	7	157024021	148106483	24	14	0.9425945	N	N	Y	N	out of frame	N	N	+	+	+	-	exon18(15702372-157024020)	exon23(148106481-148106562)
CGGA_603	VEZT	CORO1C	12	12	95656857	109055934	10	6	0.940022	N	N	N	Y	out of frame	N	N	+	-	+	+	exon4(95656680-95656856)	exon8(109055803-109055933)
CGGA_1026	VHL	BRK1	3	3	10183871	10167953	9	13	0.8144003	N	N	Y	N	out of frame	N	N	+	+	+	-	exon1(10183317-10183870)	exon3(10167951-10168873)
CGGA_1381	VSNL1	AVIL	2	12	17744677	58204132	9	3	0.9677562	N	N	N	N	out of frame	N	Y	+	-	+	-	intron1(17722185-17773334)	exon14(58204130-58204333)
CGGA_374	ZBTB17	NEB	1	2	16299534	152518793	12	10	0.9793894	N	N	N	N	out of frame	N	Y	-	-	-	-	exon14(16299532-16299619)	exon137(152518647-152518854)
CGGA_603	ZNF140	CUX2	12	12	133660146	111620521	60	26	0.781191	N	N	N	Y	out of frame	N	N	+	+	+	+	exon4(133660050-133660146)	intron1(111472044-111652001)
CGGA_D57	ZNF160	ZNF415	19	19	53606518	53625996	13	9	0.9377948	Y	N	Y	N	out of frame	N	N	-	-	-	+	exon6(53606516-53606686)	exon3(53625913-53625995)
CGGA_1034	ZNF195	SCUBE2	11	11	3400267	9078046	42	22	0.9726551	N	N	N	Y	out of frame	N	N	-	-	-	-	exon7(3400266-3400451)	intron13(9077456-9080847)
CGGA_1034	ZNF195	SCUBE2	11	11	3400268	9081155	229	111	0.9825948	N	N	N	Y	out of frame	N	N	-	-	-	-	exon7(3400266-3400451)	intron14(9080972-9081952)
CGGA_D48	ZNF564	FARSA	19	19	12662144	13039661	19	13	0.9513864	N	N	Y	N	out of frame	N	N	-	-	-	+	exon4(12662142-12662355)	exon9(13039567-13039660)
CGGA_678	ZNF564	TUT1	19	11	12662144	62349173	23	12	0.9549981	N	N	N	N	out of frame	N	Y	-	-	-	+	exon4(12662142-12662355)	exon7(62348856-62349172)
CGGA_1234	ZNF787	GPR4	19	19	56614508	46095955	43	21	0.9720027	N	Y	N	N	out of frame	N	N	-	-	-	+	exon2(56614506-56614595)	exon1(460959541-46095954)
CGGA_698	ZNF804A	PHLPP1	2	18	185463797	60497268	80	28	0.9851144	N	N	N	N	out of frame	N	Y	+	+	+	-	exon1(185463091-185463796)	exon2(60497266-60497463)
CGGA_D18	ZNF814	ZNF417	19	19	58400138	58421072	5	3	0.536504	Y	N	N	Y	out of frame	N	N	-	-	-	-	exon3(58400133-58400441)	exon1(58417140-58421481)

Supplemental Table 4: Clinical records and data production statistics of 192 gliomas from validation cohort

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_109	M	22	sGBM	4	-	-	-
CGGA_134	M	53	O	2	-	-	-
CGGA_181	F	35	sGBM	4	-	-	-
CGGA_267	M	37	A	2	-	-	-
CGGA_331	F	27	AA	3	-	-	-
CGGA_334	F	35	AA	3	-	-	-
CGGA_353	F	60	AA	3	-	-	-
CGGA_354	M	63	AA	3	-	-	-
CGGA_356	M	30	O	2	-	-	-
CGGA_385	F	41	OA	2	-	-	-
CGGA_405	M	59	AA	3	-	-	-
CGGA_410	F	71	AA	3	-	-	-
CGGA_412	F	43	AA	3	-	-	-
CGGA_414	M	28	AO	3	-	-	-
CGGA_438	M	54	AOA	3	-	-	-
CGGA_443	M	29	OA	2	-	-	-
CGGA_461	M	37	A	2	-	-	-
CGGA_462	M	38	sGBM	4	-	-	-
CGGA_470	F	38	AOA	3	+	-	-
CGGA_471	M	45	AOA	3	-	-	-
CGGA_476	F	37	AA	3	-	-	-
CGGA_481	F	61	AO	3	-	-	-
CGGA_498	M	38	AOA	3	-	-	-
CGGA_508	F	18	AO	3	-	-	-
CGGA_511	M	32	O	2	-	-	-
CGGA_513	F	44	AOA	3	-	-	-
CGGA_516	F	43	O	2	-	-	-
CGGA_521	M	32	AA	3	-	-	-
CGGA_525	M	61	GBM	4	-	-	-
CGGA_550	M	38	OA	2	-	-	-
CGGA_558	M	34	AO	3	-	-	-
CGGA_562	F	62	AOA	3	-	-	-
CGGA_566	M	41	A	2	-	-	-

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_571	M	39	A	2	-	-	-
CGGA_576	M	46	OA	2	-	-	-
CGGA_583	F	37	A	2	-	-	-
CGGA_586	F	41	OA	2	-	-	-
CGGA_590	M	37	A	2	-	-	+
CGGA_592	M	47	A	2	-	-	-
CGGA_595	F	52	A	2	-	-	-
CGGA_598	F	62	AO	3	-	-	-
CGGA_600	M	42	OA	2	-	-	-
CGGA_602	F	33	OA	2	-	-	-
CGGA_614	M	28	OA	2	-	-	-
CGGA_626	M	21	A	2	-	-	-
CGGA_632	M	30	sGBM	4	-	-	-
CGGA_638	M	42	O	2	-	-	-
CGGA_639	M	48	O	2	-	-	-
CGGA_641	F	52	O	2	-	-	-
CGGA_648	F	49	A	2	-	-	-
CGGA_663	F	38	A	2	-	-	-
CGGA_672	M	23	O	2	-	-	-
CGGA_673	M	54	A	2	-	-	-
CGGA_677	F	30	O	2	-	-	-
CGGA_686	M	51	GBM	4	-	-	-
CGGA_687	F	30	AO	3	-	-	-
CGGA_688	M	19	A	2	-	-	-
CGGA_690	M	58	AO	3	-	-	-
CGGA_697	M	38	OA	2	-	-	-
CGGA_706	M	36	OA	2	-	-	-
CGGA_707	F	40	OA	2	-	-	-
CGGA_716	F	34	AA	3	-	-	-
CGGA_721	M	45	OA	2	-	-	-
CGGA_727	M	45	AA	3	-	-	-
CGGA_732	F	35	AA	3	-	-	-
CGGA_733	M	25	OA	2	-	-	-
CGGA_736	M	38	A	2	-	-	-

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_740	M	31	OA	2	-	-	-
CGGA_743	M	30	A	2	-	-	-
CGGA_746	M	45	A	2	-	-	-
CGGA_747	M	29	GBM	4	-	-	-
CGGA_757	M	46	A	2	-	-	-
CGGA_759	M	30	GBM	4	-	-	-
CGGA_760	F	34	O	2	-	-	-
CGGA_767	M	36	A	2	-	-	-
CGGA_768	M	28	AA	3	-	-	-
CGGA_786	M	59	OA	2	-	-	-
CGGA_787	M	38	OA	2	-	-	-
CGGA_789	M	51	GBM	4	-	-	-
CGGA_791	M	56	AA	3	-	-	-
CGGA_792	F	35	A	2	-	-	-
CGGA_796	M	61	A	2	-	-	-
CGGA_797	F	39	OA	2	-	-	-
CGGA_805	M	46	OA	2	-	-	-
CGGA_812	M	27	O	2	-	-	-
CGGA_813	F	37	AOA	3	-	-	-
CGGA_816	F	54	AOA	3	-	+	-
CGGA_817	M	44	AOA	3	-	-	-
CGGA_820	M	39	AOA	3	-	-	-
CGGA_822	M	46	sGBM	4	-	-	-
CGGA_829	F	44	AOA	3	-	-	-
CGGA_835	M	31	O	2	-	-	-
CGGA_841	M	56	AO	3	-	-	-
CGGA_845	F	43	AOA	3	-	-	-
CGGA_847	M	46	AO	3	-	-	-
CGGA_852	M	41	AA	3	-	-	-
CGGA_855	M	37	AOA	3	-	-	-
CGGA_856	M	54	O	2	-	-	-
CGGA_857	M	54	AOA	3	-	-	-
CGGA_861	M	30	AOA	3	-	-	-
CGGA_865	M	60	AOA	3	-	-	-

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_877	M	38	AOA	3	-	-	-
CGGA_895	M	30	AOA	3	-	-	-
CGGA_900	M	38	A	2	-	-	-
CGGA_904	M	33	A	2	-	-	-
CGGA_907	M	63	GBM	4	-	-	-
CGGA_1002	F	45	AA	3	-	-	-
CGGA_1010	M	47	A	2	-	-	-
CGGA_1014	M	43	A	2	-	-	-
CGGA_1017	F	30	GBM	4	-	-	-
CGGA_1019	M	62	GBM	4	+	-	-
CGGA_1021	M	61	OA	2	-	-	-
CGGA_1023	F	58	GBM	4	-	-	-
CGGA_1028	F	42	GBM	4	-	-	-
CGGA_1029	F	28	A	2	-	-	-
CGGA_1036	M	43	GBM	4	-	-	-
CGGA_1037	M	46	A	2	-	-	-
CGGA_1038	M	50	A	2	-	-	-
CGGA_1041	M	60	GBM	4	-	-	-
CGGA_1053	F	63	GBM	4	-	-	-
CGGA_1055	M	43	A	3	-	-	-
CGGA_1058	M	34	A	2	-	-	-
CGGA_1066	F	34	A	2	-	-	-
CGGA_1070	M	38	GBM	4	-	-	-
CGGA_1071	M	42	A	2	-	-	-
CGGA_1073	F	42	GBM	4	-	-	-
CGGA_1074	M	50	GBM	4	-	-	-
CGGA_1075	M	72	GBM	4	-	-	-
CGGA_1083	M	60	GBM	4	-	-	-
CGGA_1084	F	68	A	2	-	-	-
CGGA_1086	F	65	GBM	4	-	-	-
CGGA_1091	F	51	GBM	4	-	-	-
CGGA_1092	M	51	A	2	-	-	-
CGGA_1095	M	29	GBM	4	-	-	-
CGGA_1101	F	35	O	2	-	-	-

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_1103	F	35	GBM	4	-	-	-
CGGA_1105	M	29	sGBM	4	-	-	-
CGGA_1114	M	53	GBM	4	-	-	-
CGGA_1123	F	49	A	2	-	-	-
CGGA_1126	M	46	AO	3	-	-	-
CGGA_1127	M	35	O	2	-	-	-
CGGA_1128	M	60	AO	3	-	-	-
CGGA_1129	M	36	sGBM	4	+	-	-
CGGA_1133	F	41	A	2	-	-	-
CGGA_1135	M	42	GBM	4	-	-	-
CGGA_1138	M	56	GBM	4	-	-	-
CGGA_1139	F	54	GBM	4	-	-	-
CGGA_1147	M	36	A	2	-	-	-
CGGA_1155	M	43	AA	3	-	-	-
CGGA_1157	M	64	A	2	-	-	-
CGGA_1159	M	51	O	2	-	-	-
CGGA_1168	F	54	O	2	-	-	-
CGGA_1172	F	37	GBM	4	-	-	-
CGGA_1180	F	49	GBM	4	-	-	-
CGGA_1183	F	26	AA	3	-	-	-
CGGA_1188	F	31	sGBM	4	-	-	-
CGGA_1196	M	49	GBM	4	-	-	-
CGGA_1209	F	38	A	2	-	-	-
CGGA_1214	F	50	GBM	4	-	-	-
CGGA_1216	M	45	GBM	4	-	-	-
CGGA_1219	F	58	GBM	4	-	-	-
CGGA_1220	F	58	GBM	4	-	+	-
CGGA_1221	M	65	GBM	4	-	-	-
CGGA_1224	M	58	GBM	4	-	-	-
CGGA_1230	M	46	sGBM	4	-	-	-
CGGA_1258	M	43	GBM	4	-	-	-
CGGA_1270	F	61	GBM	4	-	-	-
CGGA_1275	M	71	GBM	4	-	-	-
CGGA_1278	M	58	AO	3	-	-	-

Sample ID	Gender	Age	Histology	Grade	PTPRZ1-MET	FGFR3-TACC3	RNF213-SLC26A11
CGGA_1280	M	75	AA	3	-	-	-
CGGA_1283	M	18	sGBM	4	-	-	-
CGGA_1284	M	74	AA	3	-	-	-
CGGA_1285	F	59	sGBM	4	-	-	-
CGGA_1299	M	54	GBM	4	-	-	-
CGGA_1320	M	19	GBM	4	-	-	-
CGGA_1326	M	45	GBM	4	-	-	-
CGGA_1332	F	55	GBM	4	-	-	-
CGGA_1333	F	29	GBM	4	-	-	-
CGGA_1346	F	58	sGBM	4	-	-	-
CGGA_1370	M	44	sGBM	4	-	-	-
CGGA_1393	M	42	sGBM	4	-	+	-
CGGA_1397	M	40	sGBM	4	+	-	-
CGGA_1450	M	37	sGBM	4	-	-	-
CGGA_1460	M	51	sGBM	4	-	-	-
CGGA_1475	M	38	sGBM	4	+	-	-
CGGA_1495	F	48	sGBM	4	-	-	-
CGGA_D28	M	25	A	2	-	-	-
CGGA_D30	M	70	GBM	4	-	-	-
CGGA_D35	F	68	GBM	4	-	-	-
CGGA_D42	M	63	A	2	-	-	-
CGGA_D59	F	30	sGBM	4	-	-	-
CGGA_N2	#N/A	#N/A	normal	#N/A	-	-	-
Total					5	3	1

Supplemental Table 5: Primer sequences used for fusion gene validation by PCR.

SampleID	Fusion Gene	Forward Primer	Reverse Primer	Product Size(bp)
CGGA_413	AHCYL2-TMEM178B	GCTGACCAGAAGCAAGAATTCAA	CGGGTCTGGATTTAGGGTAGTTG	679
CGGA_1034	AP2A2-SBF2	GATGCCGGCCGTGTCCAAG	GTCCCAGCCTTCCTCCAAACAG	336
CGGA_1034	AP2A2-SBF2	GATGCCGGCCGTGTCCAAG	GTCCCAGCCTTCCTCCAAACAG	520
CGGA_D36	APEH-SHISA	AACATGGGCCTGTTTATGAGGAT	GTAAGGTGGTGGGTACTGCATTG	701
CGGA_1175	B4GALNT3-DENND5B	GTGGTGTCTGTGGGGCTCTG	AAACGGTTAGCAAAGACCTCTCG	516
CGGA_859	BCR-LZTR1	ACCAGCCCTACCAGAGCATCTAC	TTGTCCACATGTCATTCAACCTG	666
CGGA_1079	BIN2-CELA1	CCTTCATCATCTGCCACAGAAGT	TGTAAGCAGAGACCTGGGTGAAG	592
CGGA_1251	BRPF3-CLPSL1	CTGGAGAATGGCGAGGACCATG	GTAGGGAGGAGAGCAGGTGGAG	466
CGGA_1324	C15orf57-CBX3	CGCTGACTCTACAGCCACAAGAT	AGGATCAAGACCTCTGGCAAATC	682
CGGA_374	CBL-FBXO2	TCTATCACCGAGAGCAGCACCT	GCTCTCATCGTGGGTGAACTCC	678
CGGA_1049	CCM2-OGDH	AAGAAAGCCCATGAGAAGGTGAC	CGCTGTAGGAACTCCTCAAACCT	409
CGGA_1034	CD81-SPAG6	TCAATTTCTGTTCTGGCTGGCT	TCGATGTTTTGGGGTCTAGTCGC	211
CGGA_1324	CDK17-KCNC2	ATGGGATCAGATGGTGAGAGTGA	AAACCACACCACACACTCCTT	486
CGGA_1170	CDK4-TSFM	CCTGGTGTTTGAGCATGTAGACC	GATGGAGGGATGGTGACAGATT	704
CGGA_413	CLASRP-SYMPK	AGCGGAGACGGGAGTATTATGAA	CTTGAGTGTGGAGTCCGAGTCAT	707
CGGA_1329	COG3-GPC6	TCATGGAATGTGGTATCCTACGG	GATTGTTGATCTGGTTGGTGAGC	491
CGGA_616	CPNE5-ANXA6	TACATCAAAGGAGGGACCCAGAT	AACTTCACTACGGCCAGCATT	669
CGGA_1113	CTDSP2-XRCC6BP1	TTCCTCCTCTTGTTCGCTCCG	TGAGCACGCCAAATGTCTGATGT	627
CGGA_1251	FAM155A-COL4A1	CAGGAGGTGAGGAGCAAGCATC	CCTCAGGTCCTTGCAATCCAGG	427
CGGA_309	FARP2-DTNB	CGAGGTGTTTTCTTCACTCATGG	TCCTCCTTCAGCAACTTCATCAG	514
CGGA_1313	FGFR3-TACC3	TGAGGCCTTGTTTGACCGAGTCTAC	TGATCTTCCCCAGTTCCAGGTTCTT	668
CGGA_842	FGFR3-TACC3	TGAGGCCTTGTTTGACCGAGTCTAC	TGATCTTCCCCAGTTCCAGGTTCTT	476
CGGA_1109	FGFR3-TACC3	TGAGGCCTTGTTTGACCGAGTCTAC	TGATCTTCCCCAGTTCCAGGTTCTT	371
CGGA_578	FRMD4A-PFKP	ACATGAGCATCGTGGAGTCTCTC	AGGTGTCGGTGATAGTGTTCCAGG	676
CGGA_1240	GLTP-VPS29	CTGGCCGAACACTTGCTGAAG	TGTGTGTGTGTCCCGAGATAAGA	443
CGGA_1094	GPR162-CCDC39	TGAGCTTCTTCTCCCTCAAGTCG	CATGGTCCTGATATGCCGTTCTA	507
CGGA_491	HUWE1-RIBC1	CTTCGATGGAATACTGGCAGATG	GAAGAATCGGTTTTGTCGCTCTT	418

SampleID	Fusion Gene	Forward Primer	Reverse Primer	Product Size(bp)
CGGA_704	IFT80-MLH1	CTTTAGCTCAGCAAGGAACACCA	GCAGAAATGCATCAAGCTTCTGT	687
CGGA_245	IL1RAP-FGF12	GTTTCAATTCCCCCATGAACTC	ATTGAGTCCCAGAAACCAAGCTC	629
CGGA_1077	LANCL2-DNAH11	TGACAGAAATGGTGAAACCCAGT	TTCGGTTAGTGGAATGGAAACCT	482
CGGA_1329	LHFP-SERP2	AATCTGGGCTTTGCTGTCTTTTC	ACGATGAAGTGATCAGGGAACAA	540
CGGA_1059	MARCH6-MYO10	GCATTGGCTAGTGGAATGGTAT	ACTCTCCGAGCAATCTGACCTCT	675
CGGA_1175	MED13L-GRIP1	GGAGGATTGTCACTCCAACCTCT	CGGAACCTTTCTTGCTCATCTGAA	443
CGGA_374	MGAT5-KIAA0825	ATGCTTCTGCACTTTACCATCCA	CCAACAACAGATTGAGCAAAACC	614
CGGA_1026	MLL3-CHGB	AAACTCAGCACCACGAAAACAAA	TCTTCTCAGAATGGCGTGTCTTC	614
CGGA_578	MRPS28-ASPH	GTGGATCCGAAAGTGGTAGTTCC	GTTCTCCTGTGGGTCCATCTTCT	511
CGGA_274	MTAP-C9orf92	GCCGTGAAGATTGGAATAATTGG	GTTGCATCCTCTTTCCAACACAG	472
CGGA_802	NEK6-RXRA	GAGCTGAACATTGTGCTGGAGTT	GGAGTCAGGGTTAAAGAGGACGA	504
CGGA_878	NFATC3-CPNE2	TGACATCCCTCTCAAAACAAGGA	AACTCTCGAAAGGGAACGAACTG	630
CGGA_796	PITPNA-RAD51C	GAAGCGACATGGTGCTGCTCAAG	TAATTCTTCCTCTGGGTCTCGTGA	222
CGGA_1024	PLA2G6-CRYBB1	GATGGATGTCACCGACTACAAGG	CCTTCTCCAGGATGAACATCTCC	638
CGGA_1119	PLAGL2-HCK	GGGAGGCTTTCTCAATAACATGG	GGTGTGTTGCTGTTGTGGCTATT	454
CGGA_1234	PODXL-BGN	CAGCGGCAGGGAGGAAGAG	TGTCGTTGTTCTGCAGGTCCAG	589
CGGA_1287	PTN-DGKI	CAAACCATGAAGACCCAGAGATG	TACCCTTGAGTCCGTCTTTCTC	520
CGGA_661	PTPRZ1-MET	CCGTCTGGAAATGCGAATCCTAAA	CAGGCCCAGTCTTGACTCAGCAA	347
CGGA_1068	PTPRZ1-MET	CCGTCTGGAAATGCGAATCCTAAA	CAGGCCCAGTCTTGACTCAGCAA	382
CGGA_D64	PTPRZ1-MET	CCGTCTGGAAATGCGAATCCTAAA	CAGGCCCAGTCTTGACTCAGCAA	1217
CGGA_1118	PVRL2-SNTG1	AGAGCAGAACAGGGAGGCTAGAG	ACATACTGAGAGAAGCGCGAATG	431
CGGA_1272	PVRL2-SNTG1	AGAGCAGAACAGGGAGGCTAGAG	ACATACTGAGAGAAGCGCGAATG	431
CGGA_1034	RASSF7-SCUBE2	GAGCTCAGGGTGACAGAGGAAT	TGTGCATCTTGACTGTGGATGG	570
CGGA_D27	RNF213-SLC26A11	GACTCCTGCTCTTGCTTCTGGAT	GGGCAGACTTGGGGATGTAGTAG	628
CGGA_604	RNF213-SLC26A11	GACTCCTGCTCTTGCTTCTGGAT	GGGCAGACTTGGGGATGTAGTAG	628
CGGA_815	SH3GL1-CHAF1A	CTGGCAGAGGTGAAGGACTCC	GGGCCTGTGGAGTCTTTGGTT	451
CGGA_1094	SLC6A8-GABRA3	GCCTCCTACTACTTCCGTTTCCA	TGACATATGTGGCCCAATAGACC	589
CGGA_1272	ST7-CTTNBP2	AATCATCCCGGCAGACACCAAG	GCTGCGATTTTCAAGAGGTGCC	595

SampleID	Fusion Gene	Forward Primer	Reverse Primer	Product Size(bp)
CGGA_1329	TCF7L1-KIF1B	ACTATTTGCGCCGAAGTGAGAAGG	AGGAGTCTTCTCTCGCTCAGCTC	653
CGGA_493	TGFB1-SAE1	GGCCAGATCCTGTCCAAGCTG	AAATCCCTCCAACCACCGCAC	522
CGGA_1049	TPM3-ADAR	GTTGGTGAGTTCCGGTATTTTCAG	GGAAAGGCAATCAACACCTCTCT	613
CGGA_1046-1	TPT1-AADAT	AGTTTCAGGCTCGTGCTAAGCTA	TTCCTTTTTGCGTTCACTGGTTA	432
CGGA_374	TTLL11-FIBCD1	GAACACCCAGGTCCTTCAGCG	TGCAGTGCCGGAATAGTCAGC	511
CGGA_1329	URI1-SLC6A20	CTGGTTCAGGACTCACACGCC	AATCGTCTCCACCAGCACGATG	497
CGGA_603	VEZT-CORO1C	GGAGTTTGACGAAGAGGTGGTTT	ATGCTGGTGTCAGGGTCATAGAA	678
CGGA_1026	VHL-BRK1	GAGTACGGCCCTGAAGAAGACG	CCCATGTGGCCTGTGTTGTGTA	441
CGGA_564	ZC3H11A-REN	AGGAGCAAGAAGCTCCTCCACTA	ATTGGACGAACCAGTGTCAAAGA	597
CGGA_1329	ZMIZ1-MAT1A	AGCAGACTTGAGTCCTGGTCCTT	GCGGTCTACCTTGGTGTAGTCCT	654
CGGA_1046-1	ZNF197-CHMP2B	CCGCATCCTCCTACTGACCTAGT	AGAAGGTGGTTCTGTCTTGAGCA	655