Supplementary Information for

Exome and whole genome sequencing of esophageal adenocarcinoma identifies recurrent driver events and mutational complexity

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Contents of this PDF file

Supplementary Note

Description of esophageal adenocarcinoma cohorts

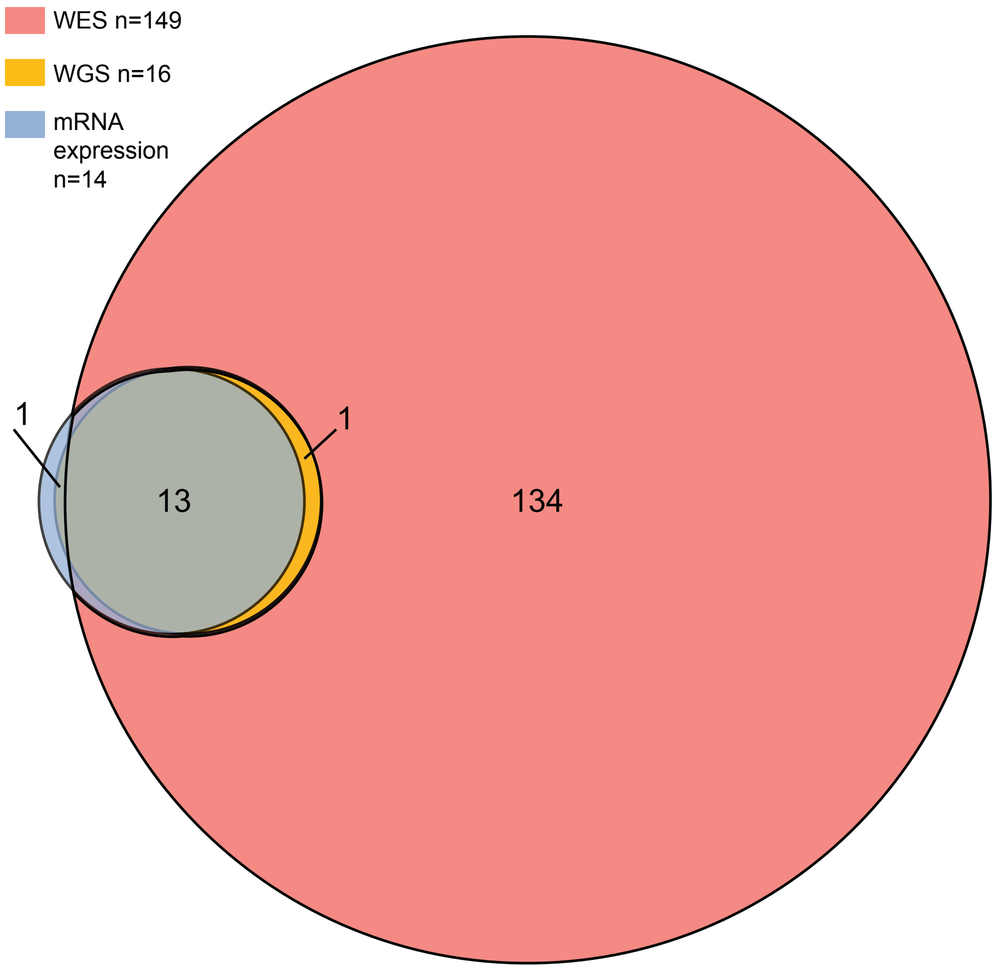
Primary esophageal adenocarcinoma samples (including tumors occurring at the gastro-esophageal junction) were selected for whole exome and whole genome sequencing from three tissue source sites: University of Pittsburgh (Pittsburgh, PA), University of Michigan (Ann Arbor, MI), and the Ontario Tissue Bank (Toronto, Canada). Patients from which specimens were acquired received no prior chemotherapy or radiation treatment prior to the surgical resection of their esophageal cancer. Samples were selected for sequencing analyses on based extraction of sufficient high-quality DNA for sequencing and upon the pathology review of the primary tumor demonstrating high estimated tumor content (estimated greater than 70%).

Tumors from all tissue source sites were collected from patients undergoing therapeutic surgical resection of their clinically localized tumor. All tumors and control samples were immediately frozen with liquid nitrogen.

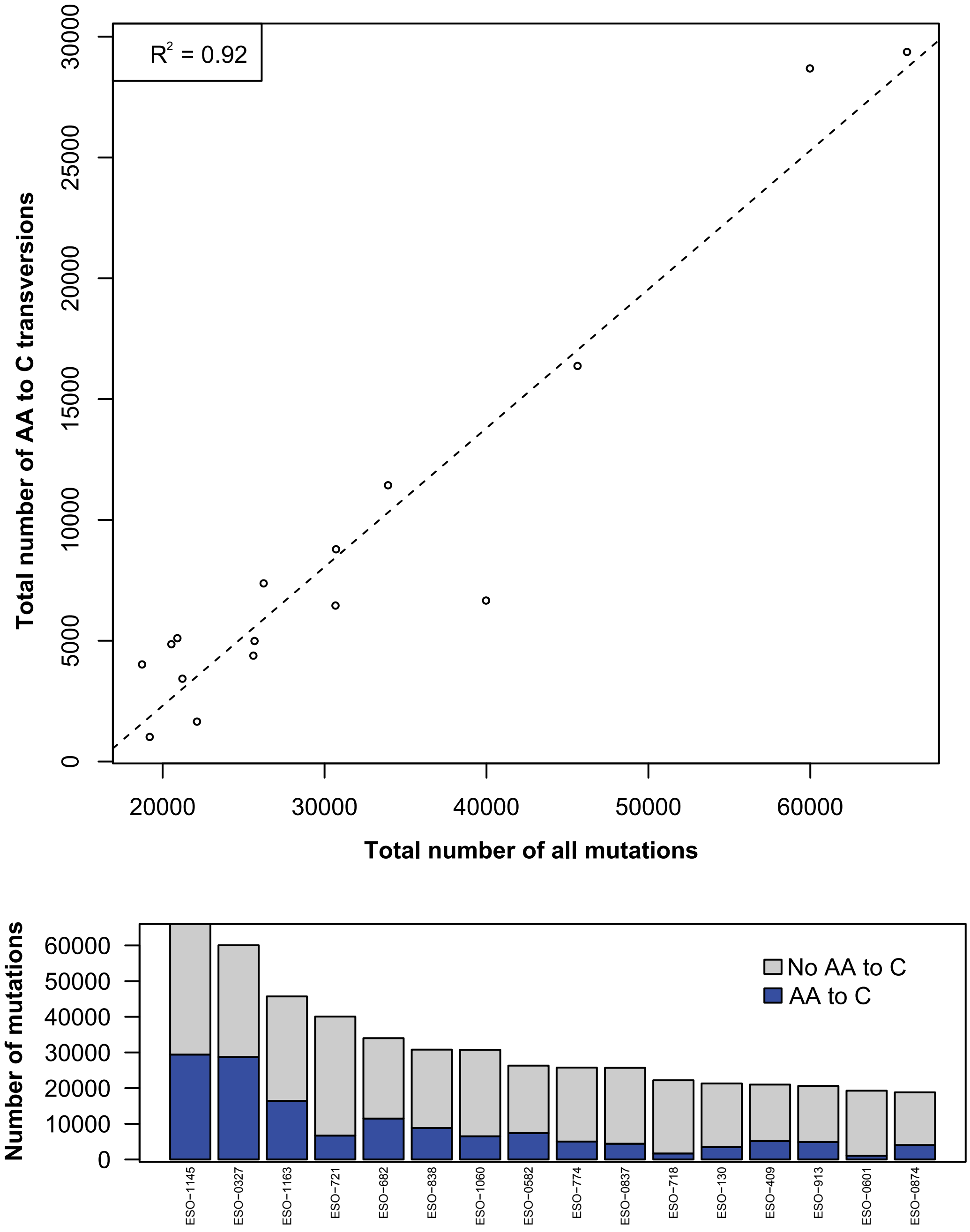
Hematoxylin and eosin stained slides were examined by a board-certified pathologist to evaluate carcinoma content of all specimens and to verify diagnosis. Patient-matched normal DNA was extracted from histologically-normal surgically resected tissue (either normal squamous esophagus or normal stomach) with no signs of dysplasia or tumor involvement upon pathology review.

All samples were obtained under approval from the institutional review boards of respective institutions and with documented informed consent of the patients. The sequencing and data release of exome sequencing of these samples was reviewed additionally by the local IRB.

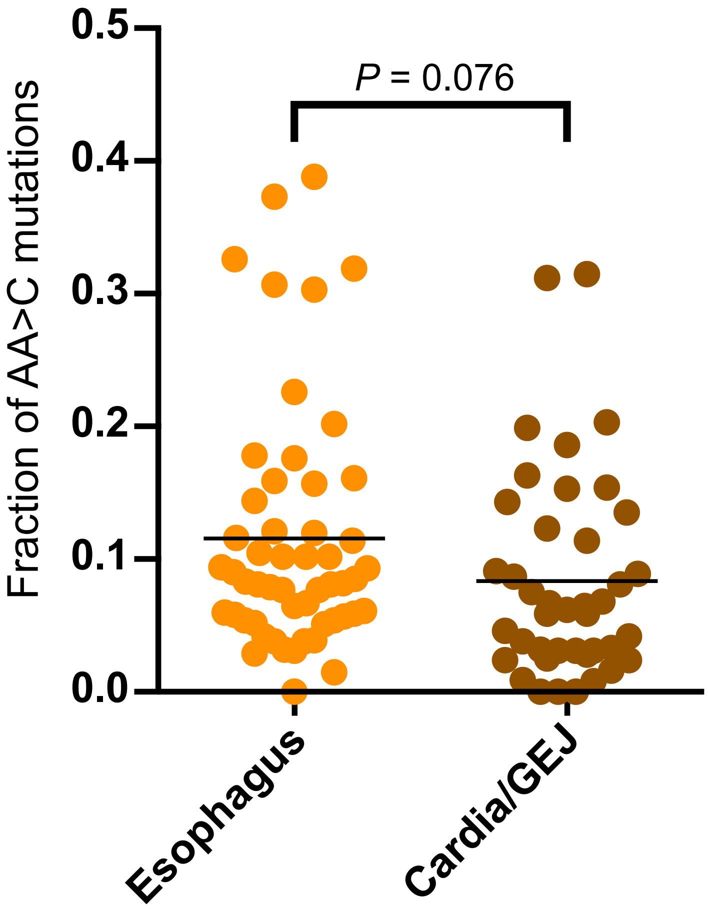
Supplemental Figure 1. Venn diagram representing EAC samples (n=150) and snalysis platforms



Supplemental Figure 2. Number of AA to C transversions is proportional to overall number of mutations

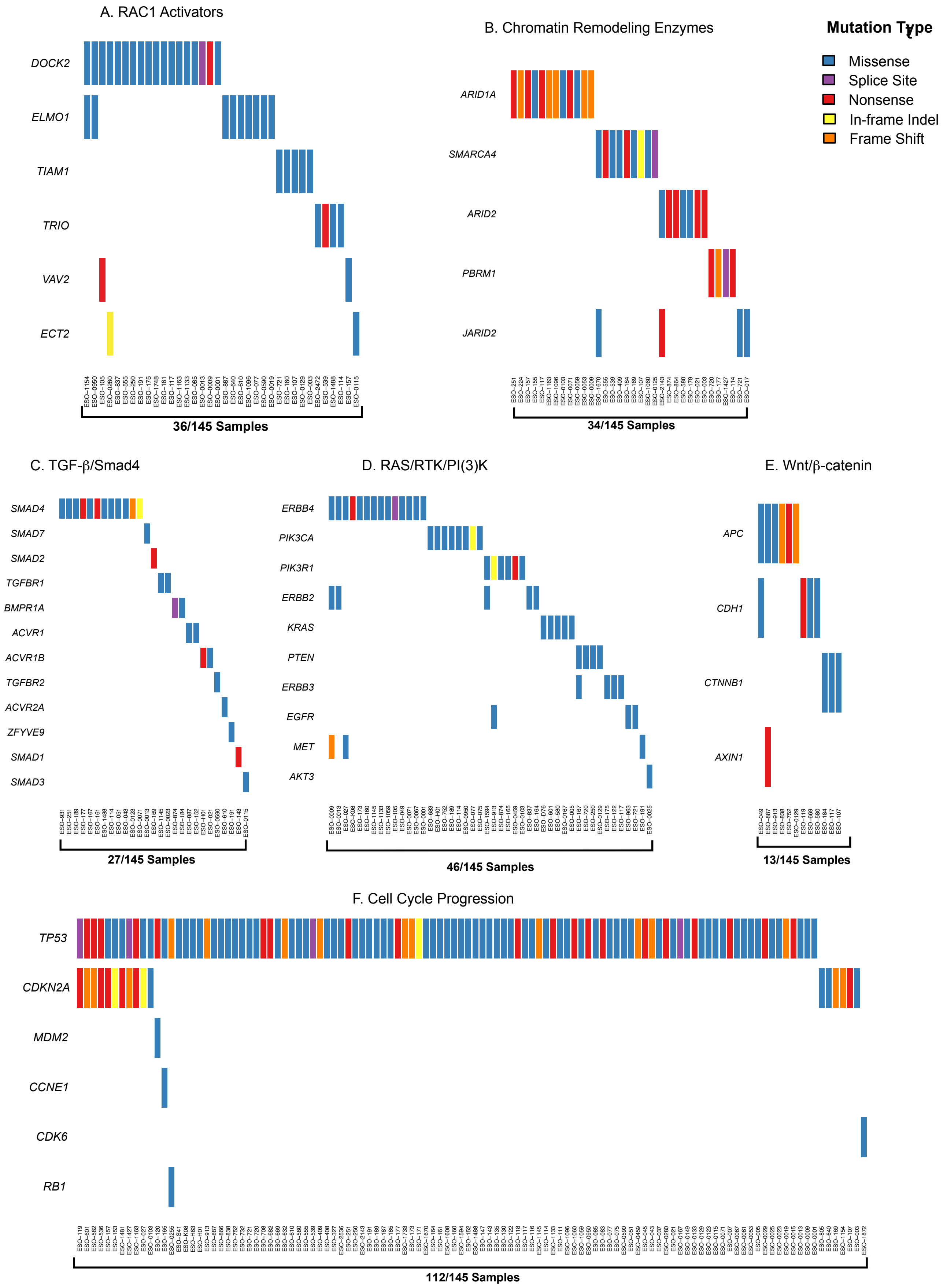


Supplemental Figure 3. Fraction of AA transversions is greater in the regions above the GEJ



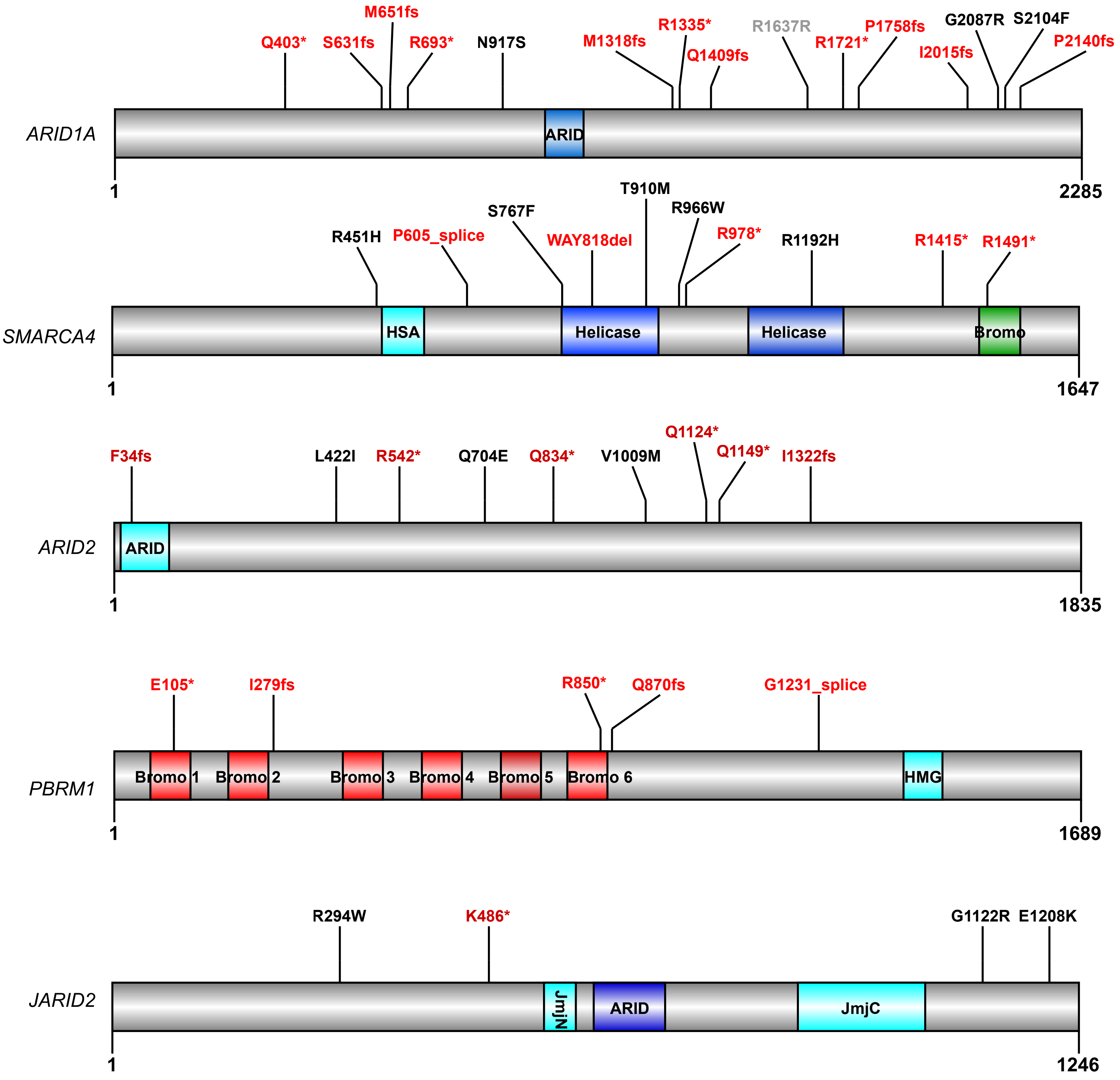
Supplemental Figure 4. EAC samples analyzed by WES were binned by region of the esophagus from which the sample was extracted, where data was available (n=95). The fraction of AA>C mutations in exons was calculated using the number of AA>C mutations over total mutations on a per sample basis. Each dot represents an individual sample. The black bar represents the median value for each bin. P-value was calculated using the Student’s t-test, paired.

Supplemental Figure 4. Overlap of protein coding modifications in known cancer signal transduction pathways.

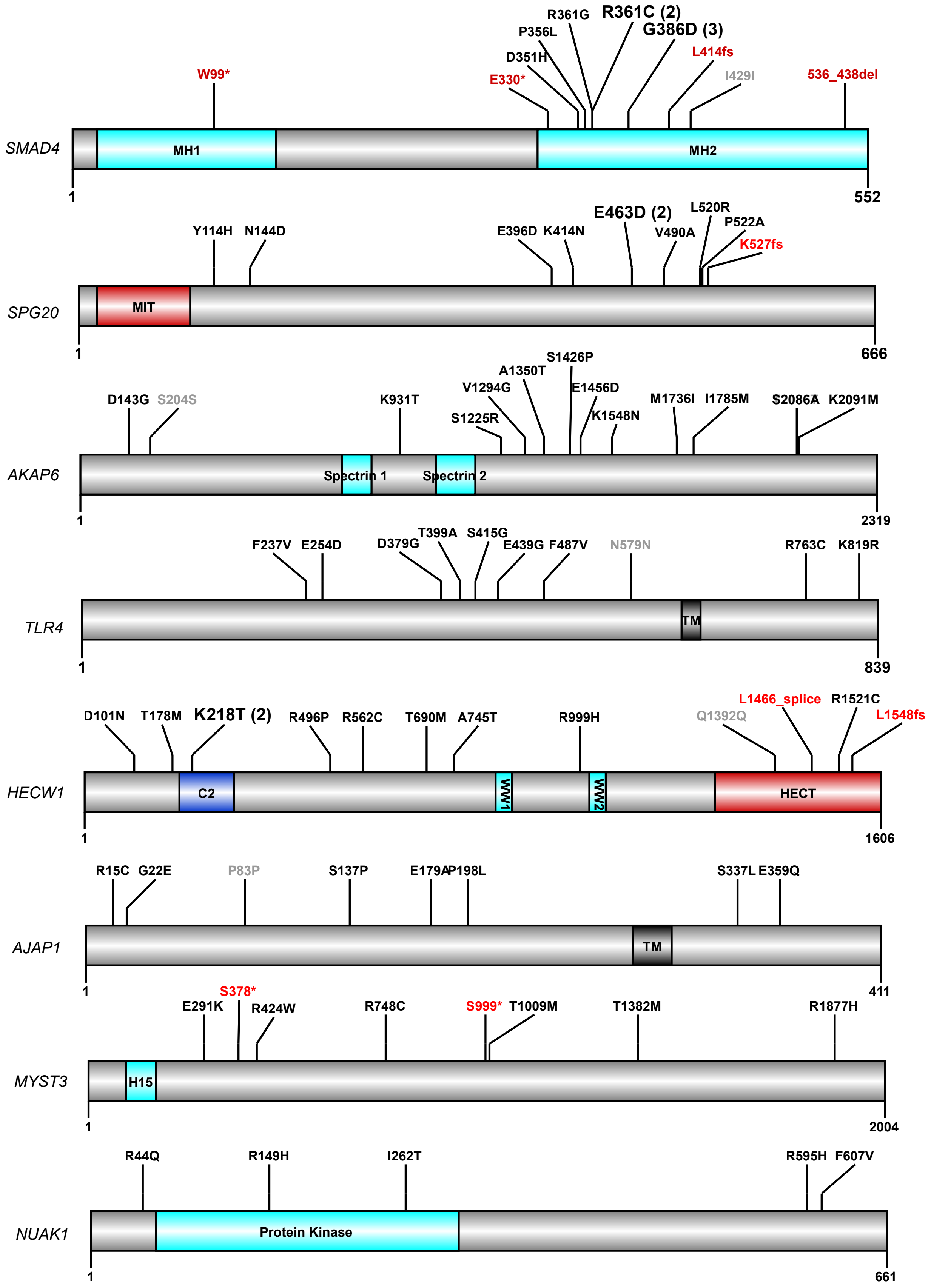


Supplemental Figure 9. Overlap of protein coding modifications in known cancer signal transduction pathways. a) RAC1 activators. b) Chromatin-remodeling enzymes. c) TGFB1(TGF-β)/SMAD4. d) KRAS/PI3K/RTK. e) WNT/CTNNB1 (β-catenin). f) Cell cycle progression.

Supplemental Figure 5. Distribution of coding mutations in chromatin remodeling enzymes.



Supplemental Figure 6. Distribution of protein coding mutations in significantly mutated genes.



Supplementary Table 1.EAC sample cohort for WGS and WES.

Table is sorted by Sample ID (NA represents not available)

Location Key:

UM - University of Michigan, Ann Arbor, MI USA
UP - University of Pittsburgh, Pittsburgh, PA USA
ON - Ontario Tissue Bank, Toronto, ON Canada

Sample ID	Collection	Whole Genome Sequencing	Whole Exome Sequencing	Affymetrix Expression Data	Gender	Age	Ethnicity	Location	Condensed Location (used in Figure 3)	Tumor Grade	Barrett's Associated	Pathological T	Pathological N	Clinical M	Smoking Status	Pack Years	Fraction of Ap*A Mutations	Non-silent Mutation Rate per Mb (WES)
ESO-0001	UM	No	Yes	No	Male	61	Caucasian	lower	Esophagus	well	yes	3	1	0	NA	NA	0.32	7.25
ESO-0009	UM	No	Yes	No	Male	62	Caucasian	lower	Esophagus	moderately	yes	3	1	0	NA	NA	0.05	4.07
ESO-0013	UM	No	Yes	No	Male	58	Caucasian	lower	Esophagus	well	yes	3	1	0	NA	NA	0.37	9.76
ESO-0015	UM	No	Yes	No	Female	76	Caucasian	lower	Esophagus	well-moderately	yes	3	0	0	NA	NA	0.09	4.82
ESO-0019	UM	No	Yes	No	Male	63	Caucasian	mid	Esophagus	well-moderately	yes	3	1	0	NA	NA	0.33	4.58
ESO-0023	UM	No	Yes	No	Male	70	Caucasian	lower	Esophagus	moderately-poor	yes	3	1	0	NA	NA	0.12	4.23
ESO-0025	UM	No	Yes	No	Male	59	Caucasian	lower	Esophagus	poorly	yes	1	0	0	NA	NA	0.30	3.81
ESO-0029	UM	No	Yes	No	Male	76	Caucasian	lower	Esophagus	moderately-poor	yes	3	1	0	NA	NA	0.04	4.47
ESO-003	UM	No	Yes	No	Female	63	Caucasian	lower	Esophagus	well-moderately	yes	2	0	0	NA	NA	0.16	4.47
ESO-005	UM	No	Yes	No	Female	61	Caucasian	lower	Esophagus	moderately-poor	yes	3	0	0	NA	NA	0.07	2.51
ESO-0053	UM	No	Yes	No	Male	84	Caucasian	lower	Esophagus	moderately-poor	yes	2	0	0	NA	NA	0.03	4.11
ESO-0059	ON	No	Yes	No	Female	52	NA	cardia	Cardia/GEJ	moderately	NA	T2b	1	0	yes	20	0.16	2.89
ESO-0061	UM	No	Yes	No	Male	60	Caucasian	lower	Esophagus	well	yes	1	0	0	NA	NA	0.16	3.47
ESO-0067	UM	No	Yes	No	Male	68	Caucasian	cardia	Cardia/GEJ	moderately-poor	yes	3	1	1	NA	NA	0.06	4.49
ESO-007	UM	No	Yes	No	Male	60	Caucasian	mid	Esophagus	moderately	yes	4	1	0	NA	NA	0.10	4.68
ESO-0071	UM	No	Yes	No	Female	87	Caucasian	lower	Esophagus	well	yes	3	1	0	NA	NA	0.08	3.29
ESO-0079	UM	No	Yes	No	Male	74	Caucasian	lower	Esophagus	poorly	yes	3	1	0	NA	NA	0.08	3.7
ESO-0103	UM	No	Yes	No	Male	55	Caucasian	mid	Esophagus	moderately	yes	3	1	0	NA	NA	0.06	2.97
ESO-0115	UM	No	Yes	No	Male	70	Caucasian	lower	Esophagus	moderately-poor	yes	1	0	0	NA	NA	0.09	4.76
ESO-0123	UM	No	Yes	No	Male	64	Caucasian	lower	Esophagus	moderately	yes	1	1	0	NA	NA	0.06	2.02
ESO-0125	UM	No	Yes	No	Male	76	Caucasian	mid	Esophagus	poorly	no	3	1	1	NA	NA	0.03	2.99
ESO-0129	UM	No	Yes	No	Male	51	Caucasian	cardia	Cardia/GEJ	moderately-poor	no	3	0	0	NA	NA	0.02	6.63
ESO-0133	UM	No	Yes	No	Male	70	Caucasian	cardia	Cardia/GEJ	moderately	no	3	0	0	NA	NA	0.05	4.57
ESO-0149	UM	No	Yes	No	Male	74	Caucasian	lower	Esophagus	moderately	yes	1	1	0	NA	NA	0.04	3.44
ESO-0167	ON	No	Yes	No	Male	82	NA	lower	Esophagus	poorly	NA	T3	1	0	NA	NA	0.04	1.99
ESO-017	UM	No	Yes	No	Male	73	Caucasian	lower	Esophagus	moderately	yes	3	1	0	NA	NA	0.09	2.66
ESO-0176	ON	No	Yes	No	Female	52	NA	cardia	Cardia/GEJ	moderately	NA	T4	1	0	yes-former	20	0.19	1.83
ESO-021	UM	No	Yes	No	Male	60	Caucasian	lower	Esophagus	moderately	yes	3	0	0	NA	NA	0.07	3.16
ESO-0255	ON	No	Yes	No	Male	62	NA	lower	Esophagus	poorly	NA	T2a	1	0	NA	NA	0.05	2.37
ESO-027	UM	No	Yes	No	Male	54	Caucasian	lower	Esophagus	poorly	yes	3	1	0	NA	NA	0.11	2.59
ESO-0280	ON	No	Yes	No	Male	82	NA	cardia	Cardia/GEJ	well	NA	T2,NOS	1	0	yes-former	35	0.32	5.68
ESO-0292	ON	No	Yes	No	Male	52	NA	esophagus	NA	poorly	NA	T3	1	0	yes-former	35	0.03	23.6
ESO-037	UM	No	Yes	No	Male	48	Caucasian	lower	Esophagus	moderately-poor	yes	3	1	0	NA	NA	0.08	2.99
ESO-043	UM	No	Yes	No	Male	63	Caucasian	cardia	Cardia/GEJ	poorly	yes	3	1	1	NA	NA	0.09	3.48
ESO-045	UM	No	Yes	No	Female	78	Caucasian	cardia	Cardia/GEJ	poorly	yes	3	1	0	NA	NA	0.14	3.47
ESO-0459	ON	No	Yes	No	Male	67	NA	cardia	Cardia/GEJ	well	NA	T3c	1	0	yes-former	35	0.14	5.5
ESO-049	UM	No	Yes	No	Male	68	Caucasian	lower	Esophagus	poorly	yes	2	0	0	NA	NA	0.18	5.94
ESO-051	UM	No	Yes	No	Male	56	Caucasian	lower	Esophagus	moderately	yes	2	1	0	NA	NA	0.06	2.55
ESO-0590	UM	No	Yes	No	Male	56	Caucasian	mid	Esophagus	poorly	yes	1	0	0	NA	NA	0.11	3.86
ESO-075	UM	No	Yes	No	Female	79	Caucasian	lower	Esophagus	moderately	yes	3	1	0	NA	NA	0.14	4.1
ESO-077	UM	No	Yes	No	Male	82	Caucasian	lower	Esophagus	poorly	yes	3	0	1	NA	NA	0.16	4.88
ESO-081	UM	No	Yes	No	Male	60	Caucasian	lower	Esophagus	poorly	yes	T2	1	1	NA	NA	0.02	14.6
ESO-083	UM	No	Yes	No	Male	71	Caucasian	cardia	Cardia/GEJ	well	yes	3	1	1	NA	NA	0.02	3.15
ESO-085	UM	No	Yes	No	Male	78	Caucasian	upper	Esophagus	poorly	yes	3	1	0	NA	NA	0.23	5.94
ESO-0950	ON	No	Yes	No	Male	87	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	yes-former	40	0.03	4.68
ESO-105	UM	No	Yes	No	Male	65	Caucasian	lower	Esophagus	moderately	yes	1	1	0	NA	NA	0.31	9.12
ESO-1059	UP	No	Yes	No	Male	86	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	yes-former	60	0.06	7.24
ESO-1060	UP	Yes	Yes	Yes	Male	78	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	no	0	0.09	4.19
ESO-107	UM	No	Yes	No	Female	85	Caucasian	mid	Esophagus	moderately-poor	yes	3	1	0	NA	NA	0.08	3.03
ESO-1096	UP	No	Yes	No	Male	73	Caucasian	esophagus	NA	poorly	yes	T1b	1	0	no	0	0.01	4.27
ESO-111	UM	No	Yes	No	Female	83	Caucasian	lower	Esophagus	poorly	yes	3	1	0	NA	NA	0.10	3.17
ESO-1130	UP	No	Yes	No	Male	69	Caucasian	esophagus	NA	poorly	yes	T1b	0	0	yes-former	40	0.05	2.55
ESO-1133	UP	No	Yes	No	Female	71	Caucasian	esophagus	NA	poorly	no	T3	2	0	yes-former	40	0.15	4.74

ESO-114	UM	No	Yes	No	Male	78	Caucasian	lower	Esophagus	moderately	yes	3	0	0	NA	NA	0.10	10.8
ESO-1145	UP	Yes	Yes	No	Male	76	Caucasian	esophagus	NA	moderately	no	T3	1	0	no	0	0.29	5.63
ESO-1154	UP	No	Yes	No	Male	75	Caucasian	esophagus	NA	moderately	no	T3	2	0	yes-former	50	0.02	2.03
ESO-116	UM	No	Yes	No	Male	79	Caucasian	lower	Esophagus	well	yes	2	1	0	NA	NA	0.09	3.2
ESO-1163	UP	Yes	Yes	No	Male	76	Caucasian	esophagus	NA	moderately	no	T2	2	0	yes-former	20	0.18	5.03
ESO-117	UP	No	Yes	No	Male	83	Caucasian	esophagus	NA	moderately	no	T3	1	1	yes-former	60	0.05	3.21
ESO-118	UM	No	Yes	No	Male	73	Caucasian	lower	Esophagus	moderately-poor	yes	3	1	1	NA	NA	0.12	4.64
ESO-119	UM	No	Yes	No	Male	67	Caucasian	lower	Esophagus	poorly	yes	3	1	0	NA	NA	0.00	2.04
ESO-120	UM	No	Yes	No	Male	63	Caucasian	lower	Esophagus	moderately	yes	3	1	0	NA	NA	0.08	3.94
ESO-122	UM	No	Yes	No	Male	84	Caucasian	lower	Esophagus	moderately-poor	yes	2	1	0	NA	NA	0.18	6.63
ESO-130	UP	Yes	Yes	Yes	Male	76	Caucasian	esophagus	NA	moderately	yes	T2	0	0	yes-former	10	0.06	2.67
ESO-131	UM	No	Yes	No	Male	70	Caucasian	lower	Esophagus	moderately-poor	no	3	1	0	NA	NA	0.20	2.45
ESO-135	UM	No	Yes	No	Male	72	Caucasian	lower	Esophagus	poorly	no	3	0	0	NA	NA	0.06	2.3
ESO-137	UM	No	Yes	No	Male	66	Caucasian	lower	Esophagus	moderately-poor	yes	3	0	0	NA	NA	0.08	2.59
ESO-139	UM	No	Yes	No	Male	77	Caucasian	lower	Esophagus	moderately	no	3	0	0	NA	NA	0.39	6.01
ESO-141	UM	No	Yes	No	Male	52	Caucasian	lower	Esophagus	moderately-poor	no	3	1	0	NA	NA	0.05	3.28
ESO-1427	ON	No	Yes	No	Male	88	NA	cardia	Cardia/GEJ	moderately	NA	T1b	0	0	no		0.11	4.25
ESO-143	UM	No	Yes	No	Male	67	Caucasian	cardia	Cardia/GEJ	poorly	no	3	1	0	NA	NA	0.07	3.96
ESO-147	UM	No	Yes	No	Male	72	Caucasian	lower	Esophagus	moderately-poor	no	3	1	1	NA	NA	0.12	3.54
ESO-1481	ON	No	Yes	No	Male	82	NA	esophagus	NA	moderately	NA	T2,NOS	0	0	yes-former	40	0.07	3.54
ESO-1488	ON	No	Yes	No	Male	82	NA	cardia	Cardia/GEJ	moderately	NA	T1b	0	0	yes-former	NA	0.06	3.51
ESO-151	UM	No	Yes	No	Male	69	Caucasian	lower	Esophagus	poorly	yes	4	0	0	NA	NA	0.04	1.97
ESO-152	UP	No	Yes	No	Male	73	Caucasian	esophagus	NA	poorly	yes	T1b	1	0	yes-former	60	0.17	5.44
ESO-153	UM	No	Yes	No	Male	75	Caucasian	lower	Esophagus	poorly	no	2	1	0	NA	NA	0.03	3.62
ESO-155	UM	No	Yes	No	Male	81	Caucasian	cardia	Cardia/GEJ	moderately	no	2	1	0	NA	NA	0.00	2.51
ESO-157	UM	No	Yes	No	Male	87	Caucasian	cardia	Cardia/GEJ	moderately-poor	no	3	0	0	NA	NA	0.09	4.06
ESO-159	UM	No	Yes	No	Male	73	Caucasian	cardia	Cardia/GEJ	moderately	no	3	1	1	NA	NA	0.00	0.97
ESO-1594	ON	No	Yes	No	Male	62	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	no	0	0.01	3.06
ESO-160	UP	No	Yes	No	Male	69	Caucasian	esophagus	NA	poorly	no	T4a	3	0	yes-former	25	0.08	4.39
ESO-1608	ON	No	Yes	No	Male	47	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	yes-former	15	0.08	4.25
ESO-161	UM	No	Yes	No	Male	79	Caucasian	cardia	Cardia/GEJ	well-moderately	no	3	1	0	NA	NA	0.03	4.32
ESO-164	UP	No	Yes	No	Male	73	Caucasian	esophagus	NA	poorly	yes	T1b	0	0	yes-remote	NA	0.02	3.35
ESO-165	UM	No	Yes	No	Male	65	Caucasian	lower	Esophagus	moderately	yes	3	1	1	NA	NA	0.05	2.77
ESO-167	UM	No	Yes	No	Male	32	Caucasian	cardia	Cardia/GEJ	poorly	no	3	1	1	NA	NA	0.04	1.67
ESO-1670	ON	No	Yes	No	Male	72	NA	cardia	Cardia/GEJ	poorly	NA	T2,NOS	1	0	yes-former	5	0.02	4.78
ESO-169	UM	No	Yes	No	Male	59	Caucasian	cardia	Cardia/GEJ	moderately-poor	no	2	1	1	NA	NA	0.20	4.22
ESO-171	UM	No	Yes	No	Male	58	Caucasian	cardia	Cardia/GEJ	poorly	no	2	1	0	NA	NA	0.20	3.51
ESO-173	UM	No	Yes	No	Male	69	Caucasian	cardia	Cardia/GEJ	moderately	no	3	1	0	NA	NA	0.15	4.43
ESO-1733	ON	No	Yes	No	Female	77	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	yes	60	0.08	3.72
ESO-1748	ON	No	Yes	No	Male	67	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	no	0	0.00	2.39
ESO-175	UM	No	Yes	No	Male	75	Caucasian	cardia	Cardia/GEJ	poorly	no	3	1	0	NA	NA	0.31	10
ESO-177	UM	No	Yes	No	Male	64	Caucasian	cardia	Cardia/GEJ	well-moderately	yes	3	1	1	NA	NA	0.01	2.3
ESO-179	UM	No	Yes	No	Male	74	Caucasian	cardia	Cardia/GEJ	moderately-poor	yes	3	1	0	NA	NA	0.06	2.94
ESO-181	UM	No	Yes	No	Male	70	Caucasian	upper	Esophagus	poorly	no	4	1	0	NA	NA	0.03	1.84
ESO-185	UM	No	Yes	No	Male	66	Caucasian	cardia	Cardia/GEJ	moderately-poor	no	3	1	0	NA	NA	0.03	2.58
ESO-187	UM	No	Yes	No	Male	60	Caucasian	cardia	Cardia/GEJ	poorly	no	4	1	1	NA	NA	0.12	4.35
ESO-1872	ON	No	Yes	No	Male	82	NA	esophagus	NA	moderately	NA	T3	0	0	yes-former	35	0.04	3.23
ESO-189	UM	No	Yes	No	Male	65	Caucasian	lower	Esophagus	well	yes	1	0	0	NA	NA	0.06	2.17
ESO-191	UM	No	Yes	No	Male	70	Caucasian	cardia	Cardia/GEJ	poorly	no	3	1	0	NA	NA	0.07	5.37
ESO-2143	ON	No	Yes	No	Male	67	NA	cardia	Cardia/GEJ	poorly	NA	T3	1	0	yes-former	25	0.09	5.95
ESO-224	UP	No	Yes	No	Male	67	Caucasian	esophagus	NA	moderately	no	T1b	0	0	yes-former	10	0.13	4.15
ESO-2472	ON	No	Yes	No	Male	77	NA	cardia	Cardia/GEJ	poorly	NA	T3	1	0	yes-former	40	0.07	2.1
ESO-250	UP	No	Yes	No	Male	75	Caucasian	esophagus	NA	poorly	yes	T1b	0	0	yes-former	38	0.17	6.05

ESO-251	UP	No	Yes	No	Female	73	Caucasian	esophagus	NA	poorly	yes	T2	0	0	yes-former	NA	0.01	2.49
ESO-2536	ON	No	Yes	No	Male	57	NA	cardia	Cardia/GEJ	moderately	NA	T3	1	0	yes-former	30	0.03	3.87
ESO-327	UP	Yes	Yes	Yes	Male	57	Caucasian	esophagus	NA	poorly	no	T3	3	0	no	0	0.30	4.42
ESO-408	UP	No	Yes	No	Male	78	Caucasian	esophagus	NA	poorly	no	T3	3	0	no	0	0.04	2.26
ESO-409	UP	Yes	Yes	Yes	Male	45	Caucasian	esophagus	NA	moderately	yes	T1a	1	0	no	0	0.08	2.8
ESO-512	UP	No	Yes	No	Female	74	Caucasian	esophagus	NA	poorly	no	T2	0	0	yes-former	98	0.03	3.07
ESO-536	UP	No	Yes	No	Male	59	Caucasian	esophagus	NA	moderately	yes	T2	0	0	yes-	70	0.00	4.4
ESO-539	UP	No	Yes	No	Male	72	Caucasian	esophagus	NA	poorly	yes	T3	1	0	yes-former	160	0.06	4.84
ESO-555	UP	No	Yes	No	Male	61	Caucasian	esophagus	NA	poorly	yes	T3	2	0	no	0	0.05	2.75
ESO-580	UP	No	Yes	No	Female	71	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	no	0	0.14	2.75
ESO-582	UP	Yes	Yes	Yes	Male	53	Caucasian	esophagus	NA	poorly	no	T3	3	0	yes-current	40	0.15	2.98
ESO-601	UP	Yes	Yes	Yes	Male	76	Caucasian	esophagus	NA	moderately	yes	T1b	2	0	yes-former	20	0.03	3.5
ESO-610	UP	No	Yes	No	Male	61	Caucasian	esophagus	NA	poorly	yes	T2	0	0	yes-former	NA	0.01	2.89
ESO-632	UP	No	Yes	No	Female	69	Caucasian	esophagus	NA	moderately	yes	T2	0	0	yes-former	50	0.02	5.62
ESO-640	UP	No	Yes	No	Male	61	NA	esophagus	NA	poorly	NA	T3	1	0	NA	NA	0.01	3.33
ESO-669	UP	No	Yes	No	Male	62	Caucasian	esophagus	NA	poorly	yes	T3	1	0	yes-current	44	0.02	2.98
ESO-682	UP	Yes	Yes	Yes	Male	59	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	yes-current	120	0.11	3.79
ESO-683	UP	No	Yes	No	Male	58	Caucasian	esophagus	NA	moderately	no	T2	0	0	no	0	0.00	2.58
ESO-708	UP	No	Yes	No	Female	78	Caucasian	esophagus	NA	moderately	yes	T3	2	0	yes-former	NA	0.09	4.03
ESO-717	UP	No	Yes	No	Female	80	Caucasian	esophagus	NA	poorly	no	T3	2	0	no	0	0.02	19.7
ESO-718	UP	Yes	Yes	Yes	Male	57	Caucasian	esophagus	NA	moderately	yes	T3	2	0	yes-former	20	0.02	2.64
ESO-720	UP	No	Yes	No	Male	70	Caucasian	esophagus	NA	moderately	no	T3	3	0	yes-current	50	0.03	3.64
ESO-721	UP	Yes	Yes	Yes	Female	68	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	no	0	0.06	8.35
ESO-732	UP	No	Yes	No	Male	62	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	yes-former	44	0.19	5.03
ESO-752	UP	No	Yes	No	Male	77	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	yes-former	60	0.08	5.45
ESO-774	UP	Yes	No	Yes	Male	54	Caucasian	esophagus	NA	poorly	no	T3	3	0	yes-former	7	NA	NA
ESO-805	UP	No	Yes	No	Male	75	Caucasian	esophagus	NA	moderately	no	T3	2	0	yes-current	82	0.00	3.45
ESO-837	UP	Yes	Yes	Yes	Male	58	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	no	0	0.05	3.49
ESO-838	UP	Yes	Yes	Yes	Male	81	Caucasian	esophagus	NA	moderately	yes	T1b	0	0	no	0	0.12	3.93
ESO-859	UP	No	Yes	No	Male	81	Caucasian	esophagus	NA	poorly	no	T3	3	0	yes-former	40	0.01	50.9
ESO-864	UP	No	Yes	No	Male	69	Caucasian	esophagus	NA	moderately	yes	T2	1	0	yes-former	NA	0.00	1.54
ESO-866	UP	No	Yes	No	Male	61	Caucasian	esophagus	NA	poorly	no	T2	2	0	yes-former	5	0.13	3.31
ESO-874	UP	Yes	Yes	Yes	Male	72	Caucasian	esophagus	NA	poorly	yes	T3	2	0	no	0	0.07	2.99

ESO-887	UP	No	Yes	No	Male	84	Caucasian	esophagus	NA	well	yes	T1a	0	0	yes-former	NA	0.05	9.02
ESO-913	UP	Yes	Yes	Yes	Female	64	Caucasian	esophagus	NA	moderately	no	T3	1	0	no	0	0.09	2.86
ESO-916	UP	No	Yes	No	Male	66	Caucasian	esophagus	NA	poorly	no	T3	3	0	yes-	60	0.06	2.29
ESO-931	UP	No	Yes	No	Male	66	Caucasian	esophagus	NA	well	yes	T1b	0	0	no	0	0.03	1.34
ESO-963	UP	No	Yes	No	Male	75	Caucasian	esophagus	NA	poorly	no	T3	1	0	no	0	0.04	2.78
ESO-D76	UM	No	Yes	No	Female	57	Caucasian	cardia	Cardia/GEJ	well	NA	T2	0	0	NA	NA	0.03	2.31
ESO-H01	UM	No	Yes	No	Female	78	Caucasian	cardia	Cardia/GEJ	poorly	NA	T3	1	0	NA	NA	0.03	3.99
ESO-H63	UM	No	Yes	No	Female	66	Caucasian	cardia	Cardia/GEJ	moderately-poor	NA	T3	1	0	NA	NA	0.15	2.34
ESO-K08	UM	No	Yes	No	Female	63	Caucasian	lower	Esophagus	poorly	NA	T3	0	0	NA	NA	0.08	3.97
ESO-R61	UM	No	Yes	No	Female	60	Caucasian	cardia	Cardia/GEJ	poorly	NA	T2	2	1	NA	NA	0.03	1.63
ESO-S41	UM	No	Yes	No	Female	87	Caucasian	cardia	Cardia/GEJ	poorly	NA	T3	0	0	NA	NA	0.04	2.36

Supplementary Table 2. Coverage, mutation, and rearrangement frequencies for individual samples generated by WGS.

Table is sorted in ascending order by mutation rate.

Individual	Tumor Coverage	Normal Coverage	Genomic Mutations	Mutations per Mb	Rearrangements
ESO-0874	38.0	40.6	18,881	7.08	170
ESO-0601	74.8	27.2	19,368	7.11	196
ESO-409	45.8	28.8	21,068	7.73	182
ESO-130	50.9	30.0	21,417	7.85	109
ESO-913	27.6	31.5	20,671	7.88	163
ESO-718	43.8	29.6	22,321	8.24	195
ESO-0837	60.2	34.8	25,779	9.53	190
ESO-0582	54.7	41.8	26,452	9.77	193
ESO-774	30.5	27.5	25,870	10.04	153
ESO-1060	68.0	27.1	30,846	11.27	402
ESO-838	80.6	22.7	30,893	11.44	147
ESO-682	38.7	30.7	34,097	12.65	114
ESO-721	43.0	30.0	40,308	14.92	360
ESO-1163	38.7	28.0	45,806	16.92	77
ESO-0327	39.5	33.4	60,213	22.24	127
ESO-1145	55.6	21.5	66,225	25.16	174
EAC samples	**44.8**	**29.8**	**26,161**	**9.9**	**172.0**

Supplemental Table 3. Mutation rates and transition-transversion ratios in regions of the genome as detected by WGS (n=16)

Table is sorted by Sample ID

Sample ID	Exon Mutation Rate (mutation/Mb)	Exon Ti:Tv Ratio	Intron Mutation Rate (mutation/Mb)	Intron Ti:Tv Ratio	IGR Mutation Rate (mutation/Mb)	IGR Ti:Tv Ratio
ESO-0327	6.60	0.90	16.05	0.54	31.49	0.47
ESO-0582	5.09	1.38	8.60	0.62	13.80	0.76
ESO-0601	8.02	2.10	8.86	1.38	13.96	1.16
ESO-0837	7.26	1.49	8.60	0.78	13.51	0.77
ESO-0874	4.71	1.40	6.33	0.96	10.20	0.82
ESO-1060	7.43	1.48	10.83	0.89	17.68	0.79
ESO-1145	10.56	0.99	19.96	0.59	37.37	0.52
ESO-1163	7.64	1.30	13.74	0.71	24.57	0.60
ESO-130	5.40	2.35	7.69	1.03	12.38	0.92
ESO-409	4.23	1.50	7.70	0.94	12.15	0.82
ESO-682	5.88	1.51	10.28	0.76	18.44	0.63
ESO-718	4.66	2.63	6.07	1.14	9.24	0.98
ESO-721	11.32	0.72	12.45	0.65	17.86	0.59
ESO-774	6.50	1.23	8.27	0.80	13.85	0.69
ESO-838	7.70	1.52	11.42	0.96	19.34	0.79
ESO-913	5.53	0.87	6.70	0.63	10.88	0.63
Median across EAC Samples	**6.55**	**1.44**	**8.73**	**0.79**	**13.91**	**0.76**

Supplementary Table 5. Predicted in-frame fusion proteins detected by dRanger

Tumor	Fusion	Fusion Sites
ESO-0327	C1orf27 exon 11 to DISC1 exon 9	chr1:186,371,326 to chr1:232,022,609
ESO-0327	HS3ST4 exon 1 to RNF213 exon 38	chr16:25,861,556 to chr17:78,331,243
ESO-0327	IGF2BP2 exon 3 to TRA2B exon 2	chr3:185,435,229 to chr3:185,644,022
ESO-0327	LAMA3 exon 12 to ZNF521 exon 4	chr18:21,364,573 to chr18:22,838,213
ESO-0582	ITPKB exon 3 to CABC1 exon 5	chr1:226,836,046 to chr1:227,167,335
ESO-0582	MICAL2 exon 3 to MICALCL exon 5	chr11:12,195,125 to chr11:12,343,815
ESO-0582	MLLT3 exon 2 to DENND1A exon 2	chr9:20,582,257 to chr9:126,603,989
ESO-0582	DNM2 exon 14 to SMARCA4 to exon 11	chr19:10,920,226 to chr19:11,110,620
ESO-0582	ITPR2 exon 6 to TMBIM4 exon 4	chr12:26,870,402 to chr12:66,542,550
ESO-0601	LEKR1 exon 6 to CCDC50 exon 6	chr3:156,656,946 to chr3:191,094,248
ESO-0837	COIL exon 4 to MSI2 exon 9	chr17:55,026,587 to chr17:55,686,932
ESO-0837	GRIK2 exon 6 to NHSL1 exon 3	chr6:102157848 to chr6:138791,528
ESO-0837	MCC exon 15 to SPOCK1 exon 2	chr5:112381747 to chr5:136723830
ESO-0874	FBXL17 exon 7 to HPSE2 exon 4	chr5:107288297 to chr10:100554400
ESO-0874	SLC30A7 exon 7 to MAP3K9	chr1:101384909 to chr14:71268480
ESO-1060	GALNT7 exon 2 to AXIN1 exon 5	chr4:174143721 to chr16:352242
ESO-1060	BCAT2 exon 3 to HSD17B14 exon 3	chr19:49307168 to chr19:49336857
ESO-1060	UNC13B exon 11 to CABIN1 exon 29	chr9:35347072 to chr22:24537512
ESO-1060	KIF13A exon 2 to DEK exon 4	chr6:17979475 to chr6:18256492
ESO-1060	MAP4K4 exon 2 to DPP10 exon 1	chr2:102356410 to chr2:115318223
ESO-1060	MAPT exon 11 to KIAA1267 exon 5	chr17:44079610 to chr17:44139887
ESO-1060	PBX1 exon 2 to MECOM exon 1	chr1:164637557 to chr3:169354157
ESO-1060	GNAL exon 5 to NPC1 to exon 1	chr18:11802335 to chr18:21161861
ESO-1060	EIF3H exon 2 to RAD21 exon 7	chr8:117723426 to chr8:117869012
ESO-1145	DOHH exon 3 to C19orf29 exon 2	chr19:3493845 to chr19:3623636
ESO-1145	MLLT3 exon 6 to KIAA1797 exon 13	chr9:20370318 to chr9:20787328
ESO-409	ANO10 exon 12 to MATR3 exon 7	chr3:43442906 to chr5:138653804
ESO-682	PLEKHM3 exon 4 to CLOCK exon 8	chr2:208805470 to chr4:56336008
ESO-682	TRIM31 exon 5 to SAP30BP exon 6	chr6:30076882 to chr17:73698121
ESO-718	ATAD5 exon 11 to ADAP2 exon 10	chr17:29192600 to chr17:29283849
ESO-718	FAM38B exon 4 to PTPN2 exon 3	chr18:10914508 to chr18:12840919
ESO-718	SYT9 exon 3 to TTC28 exon 1	chr11:7350135 to chr22:29065458
ESO-721	ADA exon 3 to ZSWIM3 exon 1	chr20:43258196 to chr20:44492697
ESO-838	CABLES1 exon 1 to TTC39C exon 1	chr18:20721977 to chr18:21599220
ESO-838	ABCA13 exon 54 to SNX30 exon 2	chr7:48565308 to chr9:115566709
ESO-913	ARL15 exon 4 to HOMER1 exon 8	chr5:53328974 to chr5:78691868
ESO-913	NPAS3 exon 5 to HUWE1 exon 6	chr14:33946315 to chr23:53673431
ESO-913	AKAP6 exon 8 to SFTA3 exon 2	chr14:33124678 to chr14:36968978

Supplementary Table 6. Mutation percentage detected by WGS.

Table is sorted in descending order by percent of mutations across all EAC samples

Fraction of mutation by WGS

	Number of Individuals	A>C	A>G	C>T	C>A	A>T	C>G
ESO-0327	1	0.54	0.24	0.07	0.06	0.08	0.02
ESO-0582	1	0.35	0.22	0.14	0.11	0.10	0.07
ESO-0601	1	0.11	0.15	0.38	0.16	0.10	0.10
ESO-0837	1	0.22	0.20	0.22	0.23	0.08	0.05
ESO-0874	1	0.27	0.22	0.23	0.15	0.09	0.05
ESO-1060	1	0.26	0.18	0.24	0.18	0.08	0.05
ESO-1145	1	0.50	0.24	0.08	0.06	0.09	0.03
ESO-1163	1	0.41	0.23	0.14	0.11	0.09	0.03
ESO-130	1	0.21	0.19	0.27	0.15	0.11	0.07
ESO-409	1	0.30	0.19	0.24	0.13	0.09	0.06
ESO-682	1	0.39	0.20	0.18	0.10	0.09	0.04
ESO-718	1	0.12	0.18	0.33	0.19	0.10	0.08
ESO-721	1	0.21	0.15	0.21	0.15	0.11	0.15
ESO-774	1	0.24	0.19	0.21	0.19	0.11	0.06
ESO-838	1	0.33	0.22	0.19	0.11	0.09	0.05
ESO-913	1	0.29	0.17	0.20	0.23	0.08	0.04
Median across all EAC Samples	**16**	**0.28**	**0.20**	**0.21**	**0.15**	**0.09**	**0.05**

Supplementary Table 8. Mutation percentage detected by WGS in exons.

Table is sorted in descending order by percent of mutations across all EAC samples

Fraction of mutation by WGS in exons

	Number of Individuals	C>T	C>A	A>C	A>G	C>G	A>T
ESO-0327	1	0.30	0.11	0.34	0.18	0.03	0.04
ESO-0582	1	0.36	0.15	0.17	0.22	0.07	0.03
ESO-0601	1	0.64	0.12	0.05	0.06	0.10	0.03
ESO-0837	1	0.46	0.24	0.07	0.14	0.04	0.04
ESO-0874	1	0.46	0.17	0.10	0.12	0.08	0.07
ESO-1060	1	0.46	0.19	0.11	0.13	0.08	0.03
ESO-1145	1	0.34	0.10	0.32	0.14	0.05	0.05
ESO-1163	1	0.44	0.15	0.21	0.11	0.05	0.04
ESO-130	1	0.60	0.13	0.09	0.07	0.09	0.02
ESO-409	1	0.56	0.11	0.11	0.10	0.07	0.05
ESO-682	1	0.54	0.15	0.15	0.09	0.04	0.03
ESO-718	1	0.61	0.15	0.06	0.10	0.04	0.04
ESO-721	1	0.35	0.18	0.09	0.06	0.22	0.10
ESO-774	1	0.42	0.19	0.13	0.12	0.08	0.05
ESO-838	1	0.47	0.13	0.20	0.12	0.06	0.02
ESO-913	1	0.40	0.34	0.08	0.08	0.05	0.06
Median across all EAC Sample	**16**	**0.46**	**0.15**	**0.11**	**0.12**	**0.06**	**0.04**

Supplementary Table 10. Mutation rates of AA>C only and all other mutations binned by expression

Table is sorted in descending order by EAC sample name

Mutation rates binned by expression (0-25% bin represents lowest expressed genes, 75-100% represents highest expressed genes)

Sample	AA>C Only - 0-25% Expression (mutations per bases covered)	AA>C Only - 25-50% Expression (mutations per bases covered)	AA>C Only - 50-75% Expression (mutations per bases covered)	AA>C Only - 75-100% Expression (mutations per bases covered)	All Other Mutations - 0-25% Expression (mutations per bases covered)	All Other Mutations - 25-50% Expression (mutations per bases covered)	All Other Mutations - 50-75% Expression (mutations per bases covered)	All Other Mutations - 75-100% Expression (mutations per bases covered)
ESO-0327	6.86E-05	3.40E-05	1.39E-05	8.87E-06	2.23E-05	1.30E-05	7.61E-06	6.94E-06
ESO-0582	1.73E-05	9.00E-06	5.60E-06	2.45E-06	1.12E-05	8.09E-06	6.43E-06	5.70E-06
ESO-0601	2.59E-06	1.80E-06	1.31E-06	1.24E-06	1.05E-05	9.62E-06	9.57E-06	7.62E-06
ESO-0837	1.13E-05	5.81E-06	3.11E-06	2.17E-06	1.21E-05	8.64E-06	7.43E-06	5.79E-06
ESO-0874	1.04E-05	6.13E-06	4.06E-06	1.61E-06	8.27E-06	6.01E-06	5.85E-06	4.68E-06
ESO-1060	1.66E-05	8.14E-06	5.64E-06	2.40E-06	1.49E-05	1.10E-05	8.86E-06	7.30E-06
ESO-130	9.30E-06	5.17E-06	2.73E-06	1.62E-06	1.09E-05	7.82E-06	6.25E-06	5.27E-06
ESO-409	1.37E-05	7.66E-06	3.30E-06	1.76E-06	1.02E-05	7.58E-06	5.73E-06	5.25E-06
ESO-682	2.81E-05	1.52E-05	8.60E-06	3.23E-06	1.44E-05	9.94E-06	7.42E-06	5.26E-06
ESO-718	3.95E-06	1.74E-06	1.19E-06	1.17E-06	8.85E-06	6.26E-06	4.95E-06	4.12E-06
ESO-721	1.67E-05	1.13E-05	5.33E-06	3.08E-06	1.56E-05	1.36E-05	9.86E-06	9.24E-06
ESO-774	1.14E-05	6.88E-06	4.12E-06	2.23E-06	1.16E-05	8.57E-06	6.39E-06	5.37E-06
ESO-838	2.18E-05	1.28E-05	6.05E-06	4.00E-06	1.46E-05	1.15E-05	8.59E-06	7.80E-06
ESO-913	1.20E-05	5.48E-06	3.50E-06	2.50E-06	8.93E-06	6.45E-06	5.94E-06	4.94E-06
Median across all EAC samples	**1.28E-05**	**7.27E-06**	**4.09E-06**	**2.32E-06**	**1.14E-05**	**8.60E-06**	**6.92E-06**	**5.53E-06**

Supplementary Table 11. Mutation strand bias comparing AA>C and all other mutations

Table is sorted in descending order by EAC sample name

Mutation rates (mutations per bases covered) binned by mutation type and strand

	AA>C Non-transcribed Strand	AA>C Transcribed Strand	All Other Mutations Non-transcribed Strand	All Other Mutations Transcribed Strand
ESO-0327	3.64E-05	3.31E-05	1.31E-05	1.28E-05
ESO-0582	9.92E-06	8.75E-06	7.94E-06	8.00E-06
ESO-0601	1.75E-06	1.87E-06	9.33E-06	9.41E-06
ESO-0837	5.75E-06	5.98E-06	8.59E-06	8.56E-06
ESO-0874	5.95E-06	5.40E-06	6.12E-06	6.14E-06
ESO-1060	9.06E-06	8.39E-06	1.07E-05	1.06E-05
ESO-1145	4.09E-05	3.73E-05	1.68E-05	1.66E-05
ESO-1163	2.30E-05	1.97E-05	1.20E-05	1.21E-05
ESO-130	5.01E-06	4.95E-06	7.69E-06	7.63E-06
ESO-409	7.17E-06	7.24E-06	7.40E-06	7.31E-06
ESO-682	1.56E-05	1.33E-05	9.28E-06	9.35E-06
ESO-718	2.25E-06	2.05E-06	6.19E-06	6.29E-06
ESO-721	1.04E-05	8.76E-06	1.21E-05	1.23E-05
ESO-774	6.65E-06	6.25E-06	8.07E-06	8.08E-06
ESO-838	1.28E-05	1.07E-05	1.06E-05	1.07E-05
ESO-913	6.65E-06	5.46E-06	6.46E-06	6.56E-06
Median across all EAC samples	**8.12E-06**	**7.82E-06**	**8.94E-06**	**8.96E-06**

Supplementary Table 12. Coverage and mutation data for individual samples generated by WES.
Table is sorted in ascending order by non-silent mutation rate.

Individual	Number of Silent Mutations	Number of Non-silent Mutations	Number of Bases Covered	Silent Mutation Rate per Mb	Non-silent Mutation Rate per Mb	MSI Status
Median across all non-MSI+ EAC samples	**36**	**106**	**29,181,146**	**1.21**	**3.62**	
ESO-859	561	1547	30,416,320	18.4	50.90	MSI
ESO-0292	223	691	29,237,901	7.63	23.6	MSI
ESO-717	248	599	30,432,219	8.15	19.70	MSI
ESO-081	159	426	29,181,146	5.45	14.60	MSI
ESO-114	100	317	29,229,856	3.42	10.8	MSS
ESO-175	74	302	30,100,720	2.46	10	MSS
ESO-0013	62	285	29,190,141	2.12	9.76	MSS
ESO-105	82	256	28,070,479	2.92	9.12	MSS
ESO-887	66	274	30,378,675	2.17	9.02	MSS
ESO-721	70	269	32,223,940	2.17	8.35	MSS
ESO-0001	52	211	29,089,996	1.79	7.25	MSS
ESO-1059	55	209	28,872,149	1.9	7.24	MSS
ESO-0129	44	193	29,091,022	1.51	6.63	MSS
ESO-122	52	199	30,026,469	1.73	6.63	MSS
ESO-250	53	183	30,238,434	1.75	6.05	MSS
ESO-139	46	173	28,776,263	1.6	6.01	MSS
ESO-2143	55	176	29,570,674	1.86	5.95	MSS
ESO-049	64	169	28,440,320	2.25	5.94	MSS
ESO-085	35	172	28,954,489	1.21	5.94	MSS
ESO-0280	45	165	29,033,184	1.55	5.68	MSS
ESO-1145	48	181	32,160,678	1.49	5.63	MSS
ESO-632	35	161	28,657,780	1.22	5.62	MSS
ESO-0459	52	162	29,450,851	1.77	5.5	MSS
ESO-752	46	166	30,458,745	1.51	5.45	MSS
ESO-152	34	154	28,322,571	1.2	5.44	MSS
ESO-191	56	161	29,986,592	1.87	5.37	MSS
ESO-1163	55	162	32,185,326	1.71	5.03	MSS
ESO-732	47	145	28,816,220	1.63	5.03	MSS
ESO-077	40	139	28,464,574	1.41	4.88	Not tested
ESO-539	50	139	28,718,223	1.74	4.84	Not tested
ESO-0015	48	138	28,639,588	1.68	4.82	Not tested
ESO-1670	46	141	29,485,158	1.56	4.78	Not tested
ESO-0115	50	136	28,559,059	1.75	4.76	Not tested
ESO-1133	48	137	28,914,943	1.66	4.74	Not tested
ESO-007	42	135	28,859,535	1.46	4.68	Not tested
ESO-0950	42	139	29,687,400	1.41	4.68	Not tested
ESO-118	36	138	29,740,488	1.21	4.64	Not tested
ESO-0019	33	133	29,062,137	1.14	4.58	Not tested
ESO-0133	45	131	28,640,995	1.57	4.57	Not tested
ESO-0067	49	130	28,928,517	1.69	4.49	Not tested
ESO-0029	44	129	28,851,689	1.53	4.47	Not tested
ESO-003	28	130	29,052,530	0.96	4.47	Not tested
ESO-173	40	132	29,799,728	1.34	4.43	Not tested
ESO-327	40	127	28,707,000	1.39	4.42	Not tested
ESO-536	35	128	29,068,849	1.2	4.4	Not tested
ESO-160	44	127	28,910,732	1.52	4.39	Not tested
ESO-187	48	132	30,324,881	1.58	4.35	Not tested
ESO-161	46	129	29,829,453	1.54	4.32	Not tested
ESO-1096	38	124	29,024,683	1.31	4.27	Not tested
ESO-1427	44	125	29,392,277	1.5	4.25	Not tested
ESO-1608	36	126	29,648,357	1.21	4.25	Not tested
ESO-0023	54	122	28,842,053	1.87	4.23	Not tested
ESO-169	37	127	30,065,118	1.23	4.22	Not tested
ESO-1060	29	135	32,249,110	0.9	4.19	Not tested
ESO-224	27	119	28,646,977	0.94	4.15	Not tested
ESO-0053	37	117	28,436,782	1.3	4.11	Not tested
ESO-075	39	120	29,269,289	1.33	4.1	Not tested
ESO-0009	50	117	28,730,034	1.74	4.07	Not tested
ESO-157	41	122	30,019,981	1.37	4.06	Not tested
ESO-708	39	117	29,015,629	1.34	4.03	Not tested
ESO-H01	55	116	29,098,022	1.89	3.99	Not tested
ESO-K08	29	114	28,724,346	1.01	3.97	Not tested
ESO-143	41	105	26,531,638	1.55	3.96	Not tested
ESO-120	40	122	30,934,434	1.29	3.94	Not tested
ESO-838	37	127	32,314,481	1.14	3.93	Not tested
ESO-2536	37	114	29,431,317	1.26	3.87	Not tested
ESO-0590	47	113	29,238,051	1.61	3.86	Not tested
ESO-0025	32	110	28,837,501	1.11	3.81	Not tested
ESO-682	49	122	32,228,720	1.52	3.79	Not tested
ESO-1733	33	109	29,305,993	1.13	3.72	Not tested
ESO-0079	29	108	29,207,368	0.99	3.7	Not tested
ESO-720	43	105	28,875,001	1.49	3.64	Not tested

ESO-153	39	108	29,870,147	1.31	3.62	Not tested
ESO-147	35	106	29,952,104	1.17	3.54	Not tested
ESO-1481	30	104	29,348,610	1.02	3.54	Not tested
ESO-1488	35	104	29,593,720	1.18	3.51	Not tested
ESO-171	38	105	29,951,051	1.27	3.51	Not tested
ESO-601	32	107	30,550,561	1.05	3.5	Not tested
ESO-837	41	101	28,932,488	1.42	3.49	Not tested
ESO-043	35	100	28,762,448	1.22	3.48	Not tested
ESO-0061	19	100	28,805,968	0.66	3.47	Not tested
ESO-045	27	101	29,084,292	0.93	3.47	Not tested
ESO-805	23	99	28,661,282	0.8	3.45	Not tested
ESO-0149	40	101	29,341,479	1.36	3.44	Not tested
ESO-164	35	97	28,932,564	1.21	3.35	Not tested
ESO-640	36	96	28,853,285	1.25	3.33	Not tested
ESO-866	27	96	29,013,096	0.93	3.31	Not tested
ESO-0071	25	94	28,544,425	0.88	3.29	Not tested
ESO-141	40	97	29,568,169	1.35	3.28	Not tested
ESO-1872	36	97	30,075,238	1.2	3.23	Not tested
ESO-117	26	92	28,644,724	0.91	3.21	Not tested
ESO-116	32	93	29,034,121	1.1	3.2	Not tested
ESO-111	19	92	28,995,825	0.66	3.17	Not tested
ESO-021	36	89	28,169,577	1.28	3.16	Not tested
ESO-083	25	89	28,281,863	0.88	3.15	Not tested
ESO-512	35	93	30,321,715	1.15	3.07	Not tested
ESO-1594	24	91	29,779,442	0.81	3.06	Not tested
ESO-107	21	89	29,365,873	0.72	3.03	Not tested
ESO-0125	34	87	29,108,707	1.17	2.99	Not tested
ESO-037	23	87	29,054,025	0.79	2.99	Not tested
ESO-874	26	85	28,471,136	0.91	2.99	Not tested
ESO-582	30	86	28,822,389	1.04	2.98	Not tested
ESO-669	35	86	28,869,301	1.21	2.98	Not tested
ESO-0103	42	86	28,954,842	1.45	2.97	Not tested
ESO-179	35	89	30,272,103	1.16	2.94	Not tested
ESO-0059	32	85	29,446,242	1.09	2.89	Not tested
ESO-610	24	83	28,671,259	0.84	2.89	Not tested
ESO-913	33	91	31,846,688	1.04	2.86	Not tested
ESO-409	25	90	32,127,439	0.78	2.8	Not tested
ESO-963	16	80	28,822,030	0.56	2.78	Not tested
ESO-165	38	84	30,328,818	1.25	2.77	Not tested
ESO-555	34	79	28,693,623	1.18	2.75	Not tested
ESO-580	23	80	29,047,025	0.79	2.75	Not tested
ESO-130	28	86	32,162,052	0.87	2.67	Not tested
ESO-017	25	75	28,230,222	0.89	2.66	Not tested
ESO-718	26	85	32,207,725	0.81	2.64	Not tested
ESO-027	30	75	28,988,391	1.03	2.59	Not tested
ESO-137	38	76	29,374,433	1.29	2.59	Not tested
ESO-185	38	77	29,858,070	1.27	2.58	Not tested
ESO-683	16	74	28,645,413	0.56	2.58	Not tested
ESO-051	30	74	29,035,081	1.03	2.55	Not tested
ESO-1130	21	74	29,076,176	0.72	2.55	Not tested
ESO-005	21	73	29,046,694	0.72	2.51	Not tested
ESO-155	28	75	29,899,585	0.94	2.51	Not tested
ESO-251	19	76	30,508,096	0.62	2.49	Not tested
ESO-131	19	73	29,851,412	0.64	2.45	Not tested
ESO-1748	23	70	29,292,060	0.79	2.39	Not tested
ESO-0255	17	70	29,557,486	0.58	2.37	Not tested
ESO-S41	27	69	29,213,879	0.92	2.36	Not tested
ESO-H63	17	68	29,041,986	0.59	2.34	Not tested
ESO-D76	29	66	28,590,218	1.01	2.31	Not tested
ESO-135	26	68	29,545,496	0.88	2.3	Not tested
ESO-177	37	69	29,957,069	1.24	2.3	Not tested
ESO-916	18	66	28,780,436	0.63	2.29	Not tested
ESO-408	31	65	28,703,759	1.08	2.26	Not tested
ESO-189	23	65	29,985,637	0.77	2.17	Not tested
ESO-2472	27	62	29,558,796	0.91	2.1	Not tested
ESO-119	18	61	29,972,420	0.6	2.04	Not tested
ESO-1154	16	59	29,009,658	0.55	2.03	Not tested
ESO-0123	33	59	29,236,815	1.13	2.02	Not tested
ESO-0167	14	59	29,577,207	0.47	1.99	Not tested
ESO-151	11	59	29,912,975	0.37	1.97	Not tested
ESO-184	19	53	28,876,057	0.66	1.84	Not tested
ESO-0176	10	54	29,493,886	0.34	1.83	Not tested
ESO-167	18	50	29,924,615	0.6	1.67	Not tested
ESO-R61	9	47	28,807,957	0.31	1.63	Not tested
ESO-864	19	47	30,524,876	0.62	1.54	Not tested
ESO-931	22	38	28,432,200	0.77	1.34	Not tested
ESO-159	9	29	29,990,384	0.3	0.97	Not tested

Supplementary Table 13. Comparison of coding-region mutations detected by both WGS and WES

Table is sorted in descending order by percentage of mutations detected by both platforms

Sample ID	Total Number Mutations Detected by WES	Number of Total Mutations Detected by WES and Validated by WGS	Percentage of Total Mutations Detected by WES and Validated by WGS	Total Number of Ap*A>C Mutations Detected by WES	Number of Ap*A>C Mutations Detected by WES and Validated by WGS	Percentage of Ap*A>C Mutations Detected by WES and Validated by WGS
Total	***2585***	***2200***	***85%***	***313***	***294***	***94%***
ESO-838	179	168	94%	21	21	100%
ESO-721	357	323	91%	23	23	100%
ESO-130	125	112	90%	7	7	100%
ESO-1145	245	217	89%	71	68	96%
ESO-1060	172	147	86%	16	15	94%
ESO-601	155	132	85%	4	4	100%
ESO-718	128	107	84%	3	3	100%
ESO-837	150	125	83%	8	6	75%
ESO-1163	230	190	83%	41	39	95%
ESO-327	172	142	83%	52	46	89%
ESO-682	180	147	82%	20	19	95%
ESO-409	124	100	81%	10	9	90%
ESO-874	118	95	81%	8	7	88%
ESO-582	121	97	80%	18	17	94%
ESO-913	129	98	76%	11	10	91%

Supplementary Table 16. Protein-coding mutations in EAC identified previously in the COSMIC Database. Mutated genes in EAC detected by WES that have greater than two mutation equivalents in the COSMIC database

Table is sorted in descending order by number of site mutations in COSMIC.

Gene	Protein Coding Change	Number of Site Mutations in COSMIC
KRAS	p.G12D	17389
KRAS	p.G12S	17110
KRAS	p.G12S	17110
TP53	p.R248Q	1140
TP53	p.R248Q	1140
TP53	p.R248Q	1140
TP53	p.R248Q	1140
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R248W	1105
TP53	p.R273H	1029
TP53	p.R249W	1029
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R273C	1019
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
TP53	p.R175H	827
PIK3CA	p.E545Q	763
PIK3CA	p.E545K	763
PIK3CA	p.E545K	763
TP53	p.G245C	573
TP53	p.G245S	573
TP53	p.G245D	549
TP53	p.R282W	512

TP53	p.R282W	512
TP53	p.R282W	512
TP53	p.R282W	512
TP53	p.G244D	494
TP53	p.G244V	494
PIK3CA	p.E542K	391
PIK3CA	p.E542K	391
PIK3CA	p.E542K	391
PIK3CA	p.E542K	391
CTNNB1	p.S33C	382
CTNNB1	p.S37F	379
CTNNB1	p.S37F	379
TP53	p.C238Y	299
TP53	p.C176W	289
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.R213*	262
TP53	p.C176F	258
TP53	p.C176F	258
TP53	p.M237I	251
TP53	p.R158H	245
TP53	p.P278S	244
TP53	p.R196*	241
TP53	p.R196*	241
TP53	p.P278R	227
TP53	p.S241F	216
TP53	p.R280K	216
TP53	p.H193R	200
TP53	p.H193R	200
TP53	p.C135F	193
TP53	p.C135F	193
TP53	p.C135Y	193
TP53	p.H193Y	187
TP53	p.S215R	183
TP53	p.C242W	183
TP53	p.I195F	178
TP53	p.V216M	173
TP53	p.C275*	168
TP53	p.P152L	164
TP53	p.C275F	150
TP53	p.K132R	149
TP53	p.V172D	147
APC	p.E1554fs	137
TP53	p.E258A	135
TP53	p.L252del	126
TP53	p.E271K	111
TP53	p.R306*	110
TP53	p.R306*	110
TP53	p.R306*	110

TP53	p.I255F	104
TP53	p.Y205C	103
TP53	p.H214R	99
TP53	p.H214R	99
CDKN2A	p.R80*	97
CDKN2A	p.R80*	97
CDKN2A	p.R80*	97
CDKN2A	p.R80*	97
CDKN2A	p.R58*	96
FBXW7	p.R465C	82
TP53	p.I162N	80
TP53	p.F134S	79
TP53	p.Y126D	66
TP53	p.L130V	62
TP53	p.R342*	61
TP53	p.R342*	61
TP53	p.R342*	61
ERBB2	p.G776V	55
TP53	p.G187_splice	47
CDKN2A	p.D84N	34
PTEN	p.K6N	29
APC	p.E1461fs	27
TP53	p.T125_splice	26
TP53	p.A307_splice	22
TP53	p.P98fs	21
PTEN	p.G251V	21
TP53	p.P72fs	20
TP53	p.C124fs	20
PTEN	p.D331H	20
CDKN2A	p.Y44fs	16
PIK3R1	p.T576M	15
TP53	p.Q100*	15
CDKN2A	p.P75fs	14
CDKN2A	p.E120*	14
CDKN2A	p.A76fs	13
TP53	p.Q104*	13
TP53	p.S33_splice	13
TP53	p.Q104*	13
CDKN2A	p.SYGR43del	12
SMAD4	p.D351H	12
PTEN	p.K66N	12
CDKN2A	p.Y44fs	11
TP53	p.E349*	10
CDKN2A	p.D125fs	9
PIK3R1	p.Y452C	9
PIK3CA	p.E110del	8
TP53	p.R335fs	8
CDKN2A	p.A21P	8
TP53	p.P89fs	7
KRAS	p.K117N	7
TP53	p.P34fs	6
TP53	p.N29fs	6
TP53	p.P77fs	6

SMAD4	p.R361C	6
SMAD4	p.G386D	6
SMAD4	p.G386D	6
SMAD4	p.G386D	6
SMAD4	p.R361C	6
FBXW7	p.R278*	6
SMAD4	p.R361G	6
CDKN2A	p.TA18del	5
RUNX1	p.G143_splice	5
SMAD4	p.E330*	5
SMAD4	p.536_538LDE>Q	4
CDKN2A	p.R128fs	4
PREX2	p.S565L	4
CDKN2A	p.G23V	4
ERBB2	p.D769Y	3
ERBB2	p.D769Y	3
TP53	p.L43fs	2
FGFR2	p.C382R	2
PAX5	p.D193N	2
SMAD4	p.P356L	2
SERPINA6	p.R282Q	2
RASL10B	p.V52M	2
WT1	p.V448M	2
LGR6	p.S299L	2
ARID1A	p.R1335*	2
CDH1	p.D254N	2
TNFAIP3	p.K213Q	2

Supplemental Table 17. Statistically significant protein-coding mutations in EAC generated by WES using COSMIC territory. Significance is defined as FDR q-value < 0.1.

Table is sorted in ascending order by FDR q-value.

Gene	Number of Mutations in EAC within a Respective Gene	Number of Unique Mutated Sites in COSMIC	Number of EAC Mutations Overlapping COSMIC Sites	FDR q-value
TP53	107	988	107	0.00E+00
SMAD4	12	184	11	7.00E-10
CDKN2A	19	321	18	7.51E-10
PIK3CA	8	206	8	3.18E-09
KRAS	5	56	5	6.70E-07
OR4A16	6	1	2	3.00E-04
ANO3	4	3	2	2.30E-03
ERBB2	5	50	3	5.50E-03
ITGA4	6	7	2	9.90E-03
CTNNB1	3	108	3	4.30E-02

Supplementary Table 18. Significantly enriched gene ontology (GO) processes across mutated genes identified by WES. GO enrichment analysis was performed on 8,356 genes with at least one non-silent mutation ranked by mutation significance using the GOrilla tool.

Table is sorted in ascending order by FDR q-value.

GO Term	Description	FDR q-value	Enrichment	Total Number of Genes	Total Number of Genes Associated with a GO Term	Number of Genes in the Top of Input List	Number of Genes in the Intersection
GO:0022610	biological adhesion	1.56E-17	2.37	7844	497	920	138
GO:0007155	cell adhesion	7.82E-18	2.37	7844	497	920	138
GO:0007156	homophilic cell adhesion	8.56E-12	3.55	7844	123	915	51
GO:0016337	cell-cell adhesion	3.22E-11	2.61	7844	242	919	74
GO:0040011	locomotion	6.00E-07	1.93	7844	505	814	101
GO:0007411	axon guidance	4.85E-06	2.44	7844	209	814	53
GO:0003008	system process	1.32E-05	1.87	7844	476	819	93
GO:0006935	chemotaxis	3.26E-05	2.17	7844	271	814	61
GO:0042330	taxis	2.90E-05	2.17	7844	271	814	61
GO:0090343	positive regulation of cell aging	5.89E-05	3,922.00	7844	2	2	2
GO:0048856	anatomical structure development	1.25E-04	1.67	7844	1129	471	113
GO:0007268	synaptic transmission	1.42E-04	2.08	7844	236	945	59
GO:0007409	axonogenesis	1.56E-04	3.78	7844	62	737	22
GO:0048812	neuron projection morphogenesis	1.87E-04	3.32	7844	83	740	26
GO:0006928	cellular component movement	2.46E-04	2.07	7844	432	526	60
GO:2000108	positive regulation of leukocyte apoptotic process	3.20E-04	1,961.00	7844	4	2	2
GO:0006337	nucleosome disassembly	3.45E-04	230.71	7844	6	17	3
GO:0032986	protein-DNA complex disassembly	3.26E-04	230.71	7844	6	17	3
GO:0021955	central nervous system neuron axonogenesis	3.81E-04	15.67	7844	7	429	6
GO:0050877	neurological system process	4.52E-04	1.92	7844	318	833	65
GO:0032502	developmental process	5.06E-04	1.33	7844	1811	838	257
GO:0032501	multicellular organismal process	6.71E-04	1.47	7844	1252	659	155
GO:0048731	system development	6.51E-04	1.89	7844	363	767	67
GO:0021952	central nervous system projection neuron axonogenesis	6.34E-04	18.28	7844	5	429	5
GO:0016043	cellular component organization	6.91E-04	1.37	7844	1484	825	214
GO:0090399	replicative senescence	8.02E-04	1,307.33	7844	6	2	2
GO:0071840	cellular component organization or biogenesis	1.45E-03	1.36	7844	1499	825	214
GO:0048869	cellular developmental process	1.57E-03	1.63	7844	874	552	100
GO:0006936	muscle contraction	1.70E-03	3.01	7844	77	811	24
GO:0050808	synapse organization	1.89E-03	3.24	7844	59	863	21
GO:0090342	regulation of cell aging	1.98E-03	871.56	7844	9	2	2
GO:0090398	cellular senescence	1.91E-03	871.56	7844	9	2	2
GO:0030198	extracellular matrix organization	3.23E-03	3.05	7844	93	635	23
GO:0043062	extracellular structure organization	3.76E-03	3.02	7844	94	635	23
GO:0048858	cell projection morphogenesis	4.02E-03	2.76	7844	100	740	26
GO:0030199	collagen fibril organization	3.92E-03	5.67	7844	20	692	10
GO:0007600	sensory perception	4.20E-03	2.11	7844	221	707	42
GO:0048870	cell motility	4.10E-03	1.81	7844	313	859	62
GO:0048513	organ development	4.16E-03	1.67	7844	457	833	81
GO:0008637	apoptotic mitochondrial changes	4.56E-03	560.29	7844	14	2	2
GO:0032990	cell part morphogenesis	4.92E-03	2.65	7844	108	740	27
GO:0032963	collagen metabolic process	4.92E-03	7.06	7844	14	635	8
GO:2000106	regulation of leukocyte apoptotic process	6.12E-03	490.25	7844	16	2	2
GO:0032989	cellular component morphogenesis	8.71E-03	2.16	7844	177	740	36
GO:0023052	signaling	1.03E-02	1.66	7844	355	969	73
GO:0030155	regulation of cell adhesion	1.14E-02	2.16	7844	135	967	36
GO:0007569	cell aging	1.14E-02	356.55	7844	22	2	2
GO:0034728	nucleosome organization	1.16E-02	31.72	7844	43	23	4
GO:0030308	negative regulation of cell growth	1.24E-02	70.24	7844	67	5	3
GO:0042391	regulation of membrane potential	1.24E-02	2.71	7844	64	995	22
GO:0040008	regulation of growth	1.35E-02	23.04	7844	227	6	4
GO:0071158	positive regulation of cell cycle arrest	1.38E-02	313.76	7844	25	2	2
GO:0071824	protein-DNA complex subunit organization	1.37E-02	29.66	7844	46	23	4
GO:0009605	response to external stimulus	1.43E-02	1.59	7844	509	814	84
GO:0030030	cell projection organization	1.54E-02	1.91	7844	224	825	45
GO:0051276	chromosome organization	1.59E-02	7	7844	289	31	8
GO:0035507	regulation of myosin-light-chain-phosphatase activity	1.65E-02	137.61	7844	2	57	2
GO:0055082	cellular chemical homeostasis	1.68E-02	1.81	7844	218	995	50
GO:0003012	muscle system process	1.66E-02	2.58	7844	90	811	24
GO:0097105	presynaptic membrane assembly	1.84E-02	7.3	7844	8	806	6
GO:0034623	cellular macromolecular complex disassembly	1.84E-02	57.68	7844	24	17	3
GO:0032984	macromolecular complex disassembly	1.81E-02	57.68	7844	24	17	3
GO:0006873	cellular ion homeostasis	1.83E-02	1.84	7844	201	995	47
GO:0002309	T cell proliferation involved in immune response	1.81E-02	7,844.00	7844	1	1	1
GO:0019725	cellular homeostasis	1.86E-02	1.74	7844	254	995	56
GO:0007610	behavior	1.88E-02	1.85	7844	196	995	46
GO:0044259	multicellular organismal macromolecule metabolic process	1.86E-02	5.81	7844	17	635	8
GO:0042542	response to hydrogen peroxide	1.96E-02	10.54	7844	31	144	6
GO:0045926	negative regulation of growth	2.02E-02	54.1	7844	87	5	3
GO:0051899	membrane depolarization	2.01E-02	3.66	7844	33	845	13
GO:0001508	regulation of action potential	2.16E-02	4.26	7844	19	969	10
GO:0034220	ion transmembrane transport	2.29E-02	2.19	7844	112	993	31
GO:0007416	synapse assembly	2.34E-02	3.58	7844	33	863	13
GO:0007154	cell communication	2.42E-02	1.55	7844	440	969	84
GO:0000302	response to reactive oxygen species	2.39E-02	7.93	7844	43	161	7
GO:0016477	cell migration	2.38E-02	1.75	7844	283	856	54
GO:0034621	cellular macromolecular complex subunit organization	2.37E-02	9.37	7844	186	27	6
GO:0019220	regulation of phosphate metabolic process	2.39E-02	8.93	7844	439	12	6
GO:0051174	regulation of phosphorus metabolic process	2.36E-02	8.93	7844	439	12	6
GO:0009653	anatomical structure morphogenesis	2.37E-02	1.52	7844	566	830	91
GO:2000602	regulation of interphase of mitotic cell cycle	2.44E-02	201.13	7844	39	2	2
GO:0006338	chromatin remodeling	2.50E-02	22.49	7844	45	31	4
GO:2000774	positive regulation of cellular senescence	2.78E-02	3,922.00	7844	1	2	1
GO:0034393	positive regulation of smooth muscle cell apoptotic process	2.75E-02	3,922.00	7844	1	2	1
GO:0070828	heterochromatin organization	2.72E-02	3,922.00	7844	1	2	1
GO:0035986	senescence-associated heterochromatin focus assembly	2.69E-02	3,922.00	7844	1	2	1
GO:0031507	heterochromatin assembly	2.66E-02	3,922.00	7844	1	2	1
GO:0031401	positive regulation of protein modification process	2.68E-02	17.15	7844	305	6	4
GO:0042098	T cell proliferation	2.67E-02	174.31	7844	10	9	2
GO:0007267	cell-cell signaling	2.69E-02	1.61	7844	345	958	68
GO:0050690	regulation of defense response to virus by virus	2.66E-02	149.41	7844	7	15	2
GO:0007005	mitochondrion organization	2.72E-02	182.42	7844	43	2	2
GO:0050923	regulation of negative chemotaxis	2.71E-02	10.03	7844	4	782	4
GO:0043666	regulation of phosphoprotein phosphatase activity	2.74E-02	37.53	7844	11	57	3
GO:0097090	presynaptic membrane organization	3.05E-02	6.49	7844	9	806	6

GO:0006979	response to oxidative stress	3.21E-02	4.97	7844	98	161	10
GO:0042493	response to drug	3.18E-02	2.13	7844	149	792	32
GO:0033088	negative regulation of immature T cell proliferation in thymus	3.16E-02	76.16	7844	2	103	2
GO:0033087	negative regulation of immature T cell proliferation	3.13E-02	76.16	7844	2	103	2
GO:0007369	gastrulation	3.54E-02	156.88	7844	20	5	2
GO:0050793	regulation of developmental process	3.51E-02	1.86	7844	671	276	44
GO:0032270	positive regulation of cellular protein metabolic process	3.50E-02	15.56	7844	336	6	4
GO:0050954	sensory perception of mechanical stimulus	3.48E-02	3.01	7844	59	707	16
GO:2000772	regulation of cellular senescence	3.56E-02	118.85	7844	6	22	2
GO:0006811	ion transport	3.62E-02	1.56	7844	369	994	73
GO:0001558	regulation of cell growth	3.70E-02	6.3	7844	126	79	8
GO:0051966	regulation of synaptic transmission, glutamatergic	3.66E-02	4.26	7844	18	921	9
GO:0045893	positive regulation of transcription, DNA-dependent	3.63E-02	14.43	7844	435	5	4
GO:0007399	nervous system development	3.62E-02	2	7844	169	767	33
GO:0016568	chromatin modification	3.63E-02	8.21	7844	185	31	6
GO:0010661	positive regulation of muscle cell apoptotic process	3.60E-02	67.04	7844	2	117	2
GO:0050801	ion homeostasis	3.95E-02	1.71	7844	230	995	50
GO:0006941	striated muscle contraction	4.02E-02	4.53	7844	24	650	9
GO:0006983	ER overload response	4.00E-02	3,922.00	7844	2	1	1
GO:0070230	positive regulation of lymphocyte apoptotic process	3.96E-02	3,922.00	7844	2	1	1
GO:0070234	positive regulation of T cell apoptotic process	3.93E-02	3,922.00	7844	2	1	1
GO:0070245	positive regulation of thymocyte apoptotic process	3.90E-02	3,922.00	7844	2	1	1
GO:0051097	negative regulation of helicase activity	3.86E-02	3,922.00	7844	2	1	1
GO:0090403	oxidative stress-induced premature senescence	3.83E-02	3,922.00	7844	2	1	1
GO:0051254	positive regulation of RNA metabolic process	3.84E-02	13.79	7844	455	5	4
GO:0042766	nucleosome mobilization	3.82E-02	1,961.00	7844	1	4	1
GO:0042221	response to chemical stimulus	4.10E-02	1.56	7844	1187	309	73
GO:0001932	regulation of protein phosphorylation	4.28E-02	14.21	7844	368	6	4
GO:0051247	positive regulation of protein metabolic process	4.25E-02	14.21	7844	368	6	4
GO:0045056	transcytosis	4.30E-02	14.8	7844	3	530	3
GO:0016339	calcium-dependent cell-cell adhesion	4.28E-02	3.86	7844	23	883	10
GO:0010628	positive regulation of gene expression	4.34E-02	13.13	7844	478	5	4
GO:0090068	positive regulation of cell cycle process	4.39E-02	126.52	7844	62	2	2
GO:0072131	kidney mesenchyme morphogenesis	4.48E-02	1,568.80	7844	1	5	1
GO:0072134	nephrogenic mesenchyme morphogenesis	4.44E-02	1,568.80	7844	1	5	1
GO:0072133	metanephric mesenchyme morphogenesis	4.41E-02	1,568.80	7844	1	5	1
GO:0048733	sebaceous gland development	4.38E-02	1,568.80	7844	1	5	1
GO:0006210	thymine catabolic process	4.45E-02	49.33	7844	2	159	2
GO:0006212	uracil catabolic process	4.42E-02	49.33	7844	2	159	2
GO:0019859	thymine metabolic process	4.39E-02	49.33	7844	2	159	2
GO:0019860	uracil metabolic process	4.35E-02	49.33	7844	2	159	2
GO:0034332	adherens junction organization	4.43E-02	3.65	7844	30	789	11
GO:0010769	regulation of cell morphogenesis involved in differentiation	4.50E-02	2.31	7844	101	806	24
GO:0010557	positive regulation of macromolecule biosynthetic process	4.53E-02	12.86	7844	488	5	4
GO:2000026	regulation of multicellular organismal development	4.53E-02	1.97	7844	508	274	35
GO:0042592	homeostatic process	4.52E-02	1.5	7844	432	995	82
GO:0050817	coagulation	4.67E-02	2.72	7844	226	230	18
GO:0007596	blood coagulation	4.63E-02	2.72	7844	226	230	18
GO:0008306	associative learning	4.60E-02	3.47	7844	25	995	11
GO:0031344	regulation of cell projection organization	4.71E-02	2.12	7844	133	806	29
GO:0042325	regulation of phosphorylation	4.68E-02	13.34	7844	392	6	4
GO:0048666	neuron development	4.66E-02	3.36	7844	55	552	13
GO:0010604	positive regulation of macromolecule metabolic process	4.64E-02	8.09	7844	808	6	5
GO:0071842	cellular component organization at cellular level	4.64E-02	2.6	7844	1206	45	18
GO:2000653	regulation of genetic imprinting	4.62E-02	1,307.33	7844	1	6	1
GO:0044029	hypomethylation of CpG island	4.59E-02	1,307.33	7844	1	6	1
GO:0044028	DNA hypomethylation	4.56E-02	1,307.33	7844	1	6	1
GO:0007265	Ras protein signal transduction	4.57E-02	115.35	7844	68	2	2
GO:0048017	inositol lipid-mediated signaling	4.58E-02	7.99	7844	43	137	6
GO:0048015	phosphatidylinositol-mediated signaling	4.55E-02	7.99	7844	43	137	6
GO:0008037	cell recognition	4.54E-02	2.92	7844	49	823	15
GO:0008038	neuron recognition	4.51E-02	3.81	7844	25	823	10
GO:0031325	positive regulation of cellular metabolic process	4.48E-02	7.95	7844	822	6	5
GO:0007599	hemostasis	4.52E-02	2.69	7844	228	230	18
GO:0006357	regulation of transcription from RNA polymerase II promoter	4.51E-02	12.55	7844	500	5	4
GO:0002209	behavioral defense response	4.61E-02	6.73	7844	7	833	5
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	4.60E-02	12.3	7844	510	5	4
GO:0032700	negative regulation of interleukin-17 production	4.58E-02	68.81	7844	4	57	2
GO:0007050	cell cycle arrest	4.69E-02	108.94	7844	72	2	2
GO:0071841	cellular component organization or biogenesis at cellular level	4.84E-02	2.57	7844	1221	45	18
GO:0051173	positive regulation of nitrogen compound metabolic process	4.83E-02	12.09	7844	519	5	4
GO:2000177	regulation of neural precursor cell proliferation	4.86E-02	4.72	7844	22	604	8
GO:0060134	prepulse inhibition	4.87E-02	7.01	7844	8	699	5
GO:0006996	organelle organization	4.89E-02	3.1	7844	786	45	14
GO:0007612	learning	4.93E-02	2.82	7844	42	995	15
GO:0007611	learning or memory	5.03E-02	2.76	7844	80	604	17
GO:0033555	multicellular organismal response to stress	5.04E-02	5.4	7844	19	535	7
GO:0048583	regulation of response to stimulus	5.05E-02	4.17	7844	996	17	9
GO:0034330	cell junction organization	5.09E-02	2.31	7844	99	789	23
GO:0046651	lymphocyte proliferation	5.12E-02	96.84	7844	18	9	2
GO:0007568	aging	5.13E-02	101.87	7844	77	2	2