

Figure S1 Kaplan-Meier curves for overall survival (OS) of NSCLC patients according to *ALK* positivity (mean OS: *ALK* Rearrangements negative = 14.81 months; Mean OS *ALK* Rearrangements positive = 16.65 months). Survival time is presented in months; p values are related to Log-rank test results.

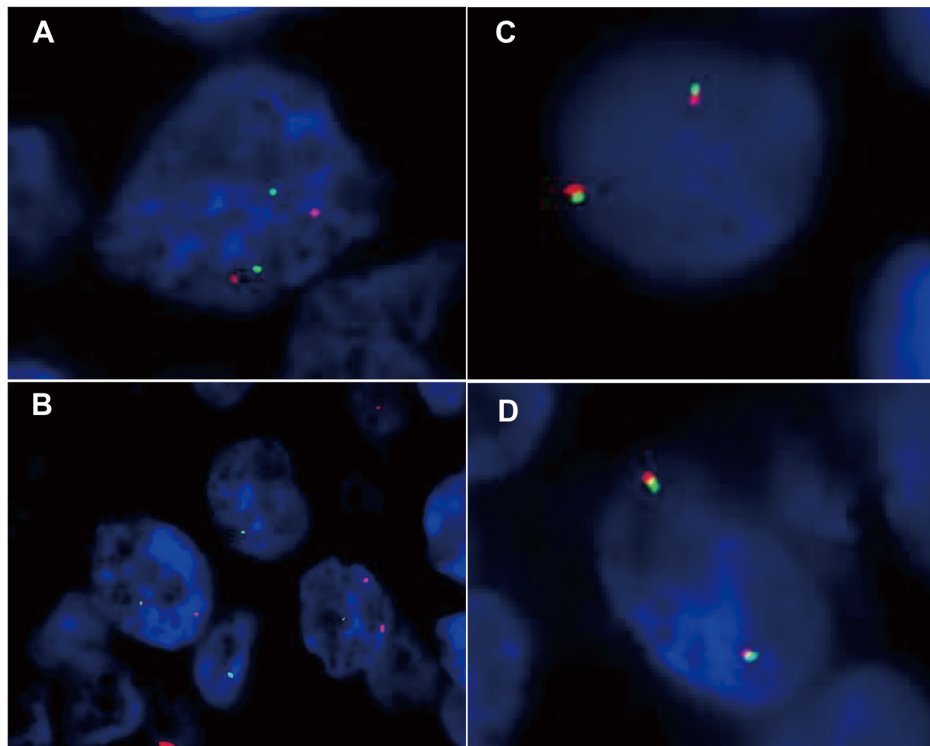


Figure S2 Representation of the fluorescence *in situ* hybridization (FISH) for (A) *RET* (n = 1) and (B) *ROS1* (n = 1) rearrangements (results obtained by the NanoString platform). These results obtained by FISH were considered “inconclusive” (low visualization of hybridization signal). Negative controls (breast tissue) for (C) *RET* and (D) *ROS1* rearrangements were also represented. All experiments were repeated twice.

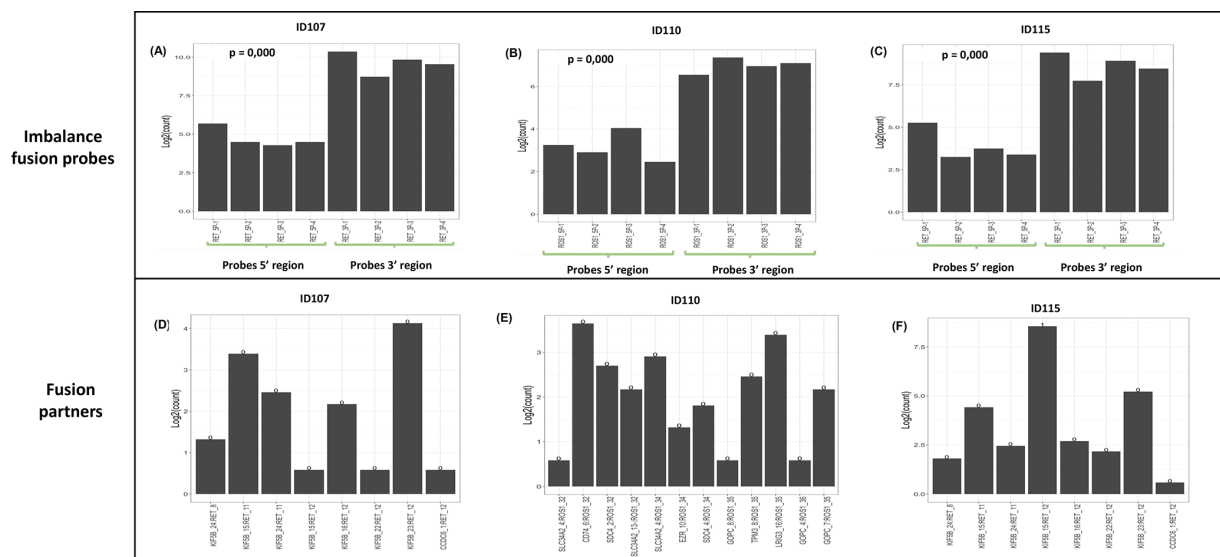


Figure S3 Representative graphs of the rearrangements obtained from the analyzed samples. The y-axis represents the significant count for imbalance probes between the 3' and 5' regions (A, B, C) and rearrangement partners (D, E, F) for the *RET* and *ROS1* genes. The x-axis represents the specific probes for 3' and 5' regions (A, B, C) and the *RET* and *ROS1* fusion partners (D, E, F). For the *RET* and *ROS1* fusion partners (D, E, F), "0" represents the absence of the specific fusion partner, and "1" represents the presence of the specific fusion partner.

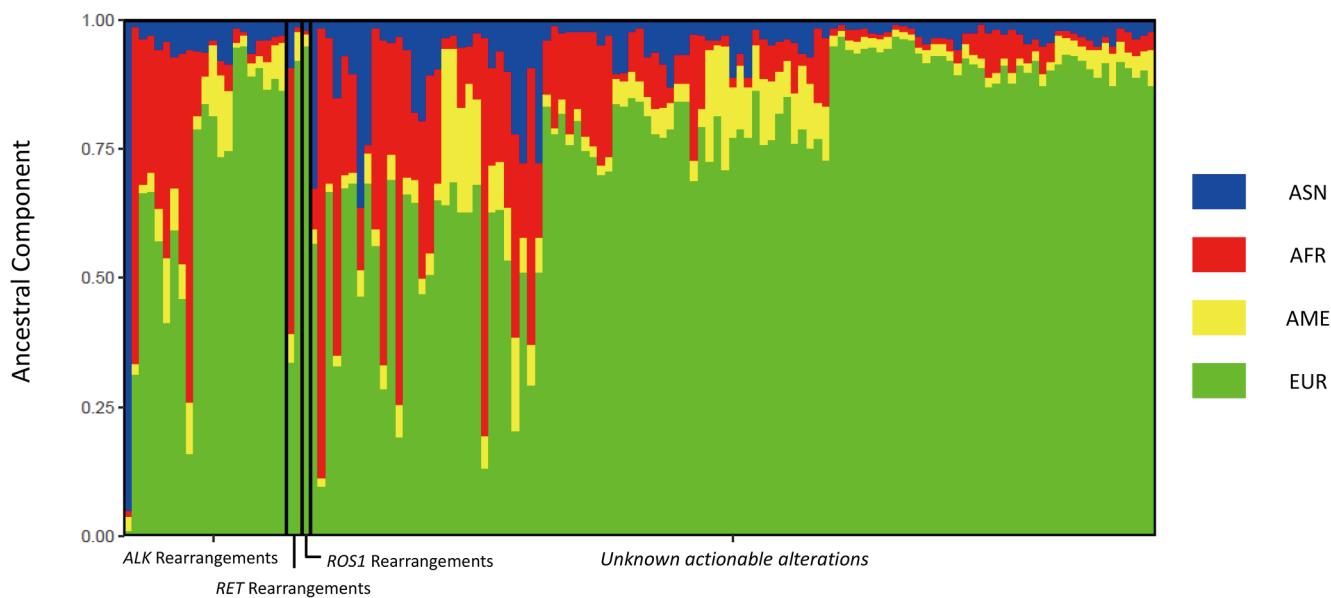


Figure S4 Genetic ancestry profiling of the Brazilian lung adenocarcinoma. Ancestry proportion of Brazilian patients (n=134) according to *ALK/RET/ROS1* positivity. The ASN (blue), AFR (red), EUR (green), AME (yellow) groups were used as reference populations. ASN, Asian ancestry; AFR, African ancestry; EUR, European ancestry; AME, Native American ancestry.

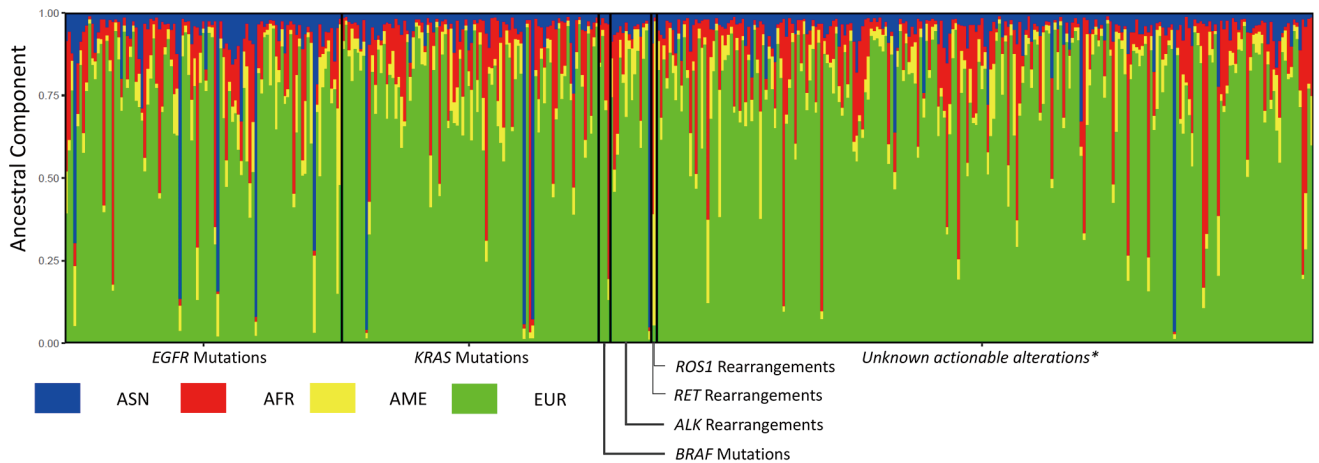


Figure S5 Genetic ancestry profiling of the Brazilian lung adenocarcinoma. Ancestry proportion of Brazilian patients (n=444) according to driver alterations. The ASN (blue), AFR (red), EUR (green), AME (yellow) groups were used as reference populations. ASN, Asian ancestry; AFR, African ancestry; EUR, European ancestry; AME, Native American ancestry.

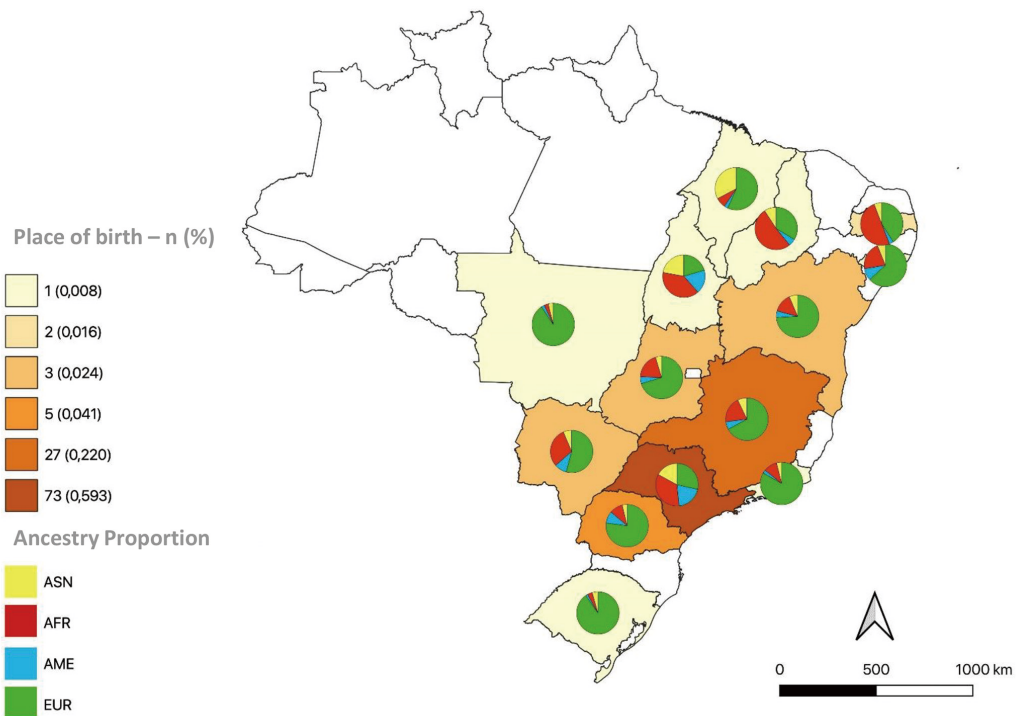


Figure S6 Geographical origin and ancestry proportions. Place of birth along with ancestry proportions of each state for *ALK*-, *RET*-, *ROS1*-positive patients and patients with unknown actionable alterations included in the present study (n=143). The ASN (yellow), AFR (red), EUR (green), AME (blue) groups were used as reference populations. ASN, Asian ancestry; AFR, African ancestry; EUR, European ancestry; AME, Native American ancestry.

Table S1 Report from Galaxy server of ratios of imbalance of ALK, RET and ROS1 in samples analyzed

	ALK ratio	RET ratio	ROS1 ratio
Horizon Commercial Control	2.59	6.19	4.76
H2228 cell line	3.54	0.33	0.50
Sample 1	6.10	0.67	0.90
Sample 2	6.66	0.70	1.02
Sample 3	5.49	0.19	0.50
Sample 4	4.56	1.06	0.14
Sample 5	6.56	0.33	0.06
Sample 6	4.07	0.76	0.48
Sample 7	2.90	0.54	0.10
Sample 8	4.87	0.60	1.88
Sample 9	1.58	0.57	1.30
Sample 10	1.92	0.18	0.72
Sample 11	8.17	0.49	1.27
Sample 12	8.55	0.13	0.83
Sample 13	2.43	0.36	1.10
Sample 14	4.30	0.24	1.25
Sample 15	6.71	1.08	1.19
Sample 16	3.07	1.19	1.10
Sample 17	3.49	0.29	1.07
Sample 18	5.96	0.17	0.51
Sample 19	5.08	0.20	1.36
Sample 20	8.12	0.49	1.27
Sample 21	2.43	0.36	1.10
Sample 22	0.39	9.85	0.13
Sample 23	0.20	7.96	0.36
Sample 24	0.52	0.64	3.02
Sample 25	0.49	1.11	0.08
Sample 26	0.88	1.00	1.08
Sample 27	1.57	1.00	0.97
Sample 28	0.28	0.27	0.75
Sample 29	0.45	0.33	0.64
Sample 30	0.33	0.85	0.33
Sample 31	0.33	0.19	0.08
Sample 32	0.24	0.70	0.20
Sample 33	0.24	0.49	0.41

Table S1 (*continued*)

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	ALK ratio	RET ratio	ROS1 ratio
Sample 34	1.70	0.58	1.05
Sample 35	0.20	0.56	0.36
Sample 36	0.05	0.12	0.05
Sample 37	0.19	0.39	0.46
Sample 38	0.23	1.39	0.35
Sample 39	0.17	0.21	0.77
Sample 40	0.09	0.36	0.05
Sample 41	0.13	0.84	0.18
Sample 42	0.53	0.30	1.62
Sample 43	0.61	0.80	0.66
Sample 44	0.32	0.23	0.16
Sample 45	0.44	0.29	0.20
Sample 46	0.41	0.44	1.18
Sample 47	0.47	1.17	0.27
Sample 48	0.52	0.54	0.21
Sample 49	0.80	0.75	0.68
Sample 50	0.11	0.27	0.08
Sample 51	0.12	0.16	0.23
Sample 52	0.56	0.58	1.78
Sample 53	0.15	0.13	0.10
Sample 54	0.20	0.21	0.11
Sample 55	0.79	1.10	0.88
Sample 56	0.37	0.56	0.60
Sample 57	0.24	1.23	1.13
Sample 58	0.34	0.87	0.03
Sample 59	0.33	0.20	0.45
Sample 60	0.33	0.28	0.10
Sample 61	0.31	0.18	0.04
Sample 62	1.78	0.57	0.12
Sample 63	0.35	0.17	1.09
Sample 64	0.46	0.28	0.35
Sample 65	0.51	1.14	1.06
Sample 66	0.41	0.28	0.20
Sample 67	0.33	0.21	0.93
Sample 68	0.35	0.49	0.76

Table S1 (*continued*)

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	ALK ratio	RET ratio	ROS1 ratio
Sample 69	0.37	0.31	0.89
Sample 70	0.48	0.25	0.23
Sample 71	0.40	0.12	0.06
Sample 72	0.43	0.78	0.04
Sample 73	0.71	0.67	0.19
Sample 74	1.76	0.51	1.01
Sample 75	0.70	0.67	0.13
Sample 76	0.43	0.36	0.49
Sample 77	0.79	0.52	0.50
Sample 78	0.20	0.10	1.07
Sample 79	0.20	0.42	0.32
Sample 80	0.26	0.20	1.03
Sample 81	0.55	0.70	0.09
Sample 82	0.68	0.31	0.10
Sample 83	0.19	1.03	0.06
Sample 84	0.31	0.04	0.07
Sample 85	0.19	0.82	0.09
Sample 86	0.71	0.12	0.77
Sample 87	0.97	0.90	0.86
Sample 88	0.76	0.09	2.05
Sample 89	0.82	0.89	0.95
Sample 90	0.20	1.05	0.77
Sample 91	0.80	1.00	1.05
Sample 92	1.00	1.00	1.00
Sample 93	1.08	0.93	0.50
Sample 94	1.00	1.00	1.34
Sample 95	0.50	0.62	0.54
Sample 96	0.33	0.60	0.71
Sample 97	0.94	0.58	1.13
Sample 98	1.00	1.03	0.67
Sample 99	0.46	0.79	1.49
Sample 100	0.98	0.94	0.65
Sample 101	1.56	1.03	0.71
Sample 102	0.40	0.57	0.79
Sample 103	0.50	2.29	0.81

Table S1 (*continued*)

Table S1 (continued)

	ALK ratio	RET ratio	ROS1 ratio
Sample 104	0.28	0.50	0.65
Sample 105	0.15	0.55	0.35
Sample 106	0.51	0.55	0.70
Sample 107	0.91	0.95	0.95
Sample 108	0.68	1.02	0.91
Sample 109	0.49	0.98	0.67
Sample 110	0.62	0.72	0.87
Sample 111	0.36	0.76	0.65
Sample 112	0.46	0.97	1.46
Sample 113	0.33	0.65	0.67
Sample 114	1.19	0.94	0.86
Sample 115	0.67	1.02	1.21
Sample 116	0.27	0.74	0.96
Sample 117	0.37	0.76	0.91
Sample 118	0.53	0.63	0.84
Sample 119	0.42	0.68	0.91
Sample 120	1.90	0.87	0.89
Sample 121	0.56	0.82	0.54
Sample 122	0.49	0.71	0.82
Sample 123	0.45	1.14	0.40
Sample 124	0.46	1.14	0.79
Sample 125	0.60	1.07	0.93
Sample 126	0.60	0.82	1.45
Sample 127	0.14	0.76	1.29
Sample 128	0.67	0.83	0.54
Sample 129	1.89	0.65	0.77
Sample 130	0.53	0.85	0.61
Sample 131	0.71	1.20	0.57
Sample 132	0.75	0.63	0.54
Sample 133	0.44	0.57	0.92
Sample 134	0.20	1.02	0.86

Table S2 Ancestry background categorization of Brazilian lung adenocarcinoma patients (n=444), according to tercile based on the percentage proportions for ethnic groups

Genetic Ancestry	Low	Intermediate	High
ASN	<0.028	0.028 - 0.055	>0.055
AFR	<0.027	0.027 - 0.125	>0.125
AME	<0.029	0.029 - 0.058	>0.058
EUR	<0.698	0.698 - 0.865	>0.865

Category boundaries were defined according to tercile categorization; ASN, Asian ancestry; AFR, African ancestry; EUR, European ancestry; AME, Amerindian ancestry.