

What is claimed is:

1. An antibody, or a functional fragment thereof, that specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1) but does not compete with binding of E-cadherin, N-cadherin, or R-cadherin to the extracellular domain of KLRG1, for use in therapy,

which comprises a heavy chain variable region comprising three heavy chain complementarity determining regions (CDR-H1, CDR-H2 and CDR-H3), wherein said antibody, or fragment thereof comprises:

i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3).

2. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of i); wherein the heavy chain variable region comprises SEQ ID NO 4, or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO: 5, or a sequence at least 90% identical to SEQ ID NO:5.

3. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of ii); wherein the heavy chain variable region comprises SEQ ID NO:6, or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7, or a sequence at least 90% identical to SEQ ID NO:7.

4. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of iii); wherein the heavy chain variable region comprises SEQ ID NO:8, or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9, or a sequence at least 90% identical to SEQ ID NO:9.

5. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of iv); wherein the ~~the~~ heavy chain variable region comprises SEQ ID NO: 10, or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO: 11, or a sequence at least 90% identical to SEQ ID NO:11.

6. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of v); wherein the ~~the~~ heavy chain variable region comprises SEQ ID NO: 12, or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO: 13, or a sequence at least 90% identical to SEQ ID NO:13.

7. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of vi); wherein the heavy chain variable region comprises SEQ ID NO: 14, or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO: 15, or a sequence at least 90% identical to SEQ ID NO:15.

8. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of ii); wherein the heavy chain variable region comprises SEQ ID NO: 52, or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO: 53, or a sequence at least 90% identical to SEQ ID NO:53.

9. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises

the three heavy chain CDRs and the three light chain CDRs of iii); wherein the heavy chain variable region comprises SEQ ID NO: 54, or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO: 55, or a sequence at least 90% identical to SEQ ID NO:55.

10. The antibody, or a functional fragment thereof, of claim 1, wherein the antibody, or fragment thereof, comprises a chimeric antibody, or a fragment thereof.

11. The antibody of claim 1, wherein the ~~monoclonal~~ antibody, or fragment thereof, comprises a humanized antibody or a functional fragment thereof.

12. Use of an antibody, or a functional fragment thereof, that comprises:

i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3); wherein

a) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of i); wherein the heavy chain variable region comprises SEQ ID NO:4 or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO:5 or a sequence at least 90% identical to SEQ ID NO:5;

b) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:6 or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7 or a sequence at least 90% identical to SEQ ID NO:7;

c) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:8 or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9 or a sequence at least 90% identical to SEQ ID NO:9;

d) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iv); wherein the heavy chain variable region comprises SEQ ID NO:10 or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO:11 or a sequence at least 90% identical to SEQ ID NO:11;

e) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of v); wherein the heavy chain variable region comprises

SEQ ID NO:12 or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO:13 or a sequence at least 90% identical to SEQ ID NO:13;

f) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of vi); wherein the heavy chain variable region comprises SEQ ID NO:14 or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO:15 or a sequence at least 90% identical to SEQ ID NO:15;

g) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:52 or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO:53 or a sequence at least 90% identical to SEQ ID NO:53;
or

h) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:54 or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO:55 or a sequence at least 90% identical to SEQ ID NO:55

and that specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1) without interfering with binding by E-cadherin, N-cadherin, or R-cadherin to the extracellular domain of KLRG1 for the manufacture of a medicament for the treatment of a disorder associated with excess KLRG1 expressing T cells in a subject in need thereof, wherein the antibody or functional antibody fragment ~~for depleting depletes~~ excess KLRG1 expressing T cells, without releasing checkpoint inhibition, and without subsequently activating pathogenic CD8+ cytotoxic T and/or NK cells directed to self-tissues.

13. The use of claim 12, wherein the medicament is manufactured for treatment of a transplant disorder.

14. The use of claim 12, wherein the medicament is manufactured for treatment of an autoimmune disease.

15. Use of an antibody, or a functional fragment thereof, that comprises: i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3); wherein

a) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of i); wherein the heavy chain variable region comprises SEQ ID NO:4 or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO:5 or a sequence at least 90% identical to SEQ ID NO:5;

b) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:6 or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7 or a sequence at least 90% identical to SEQ ID NO:7;

c) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:8 or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9 or a sequence at least 90% identical to SEQ ID NO:9;

d) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iv); wherein the heavy chain variable region comprises

SEQ ID NO:10 or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO:11 or a sequence at least 90% identical to SEQ ID NO:11;

e) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of v); wherein the heavy chain variable region comprises SEQ ID NO:12 or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO:13 or a sequence at least 90% identical to SEQ ID NO:13;

f) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of vi); wherein the heavy chain variable region comprises SEQ ID NO:14 or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO:15 or a sequence at least 90% identical to SEQ ID NO:15;

g) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:52 or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO:53 or a sequence at least 90% identical to SEQ ID NO:53;
or

h) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:54 or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO:55 or a sequence at least 90% identical to SEQ ID NO:55;
and that

specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1) without interfering with binding by E-cadherin, N-cadherin, or R-cadherin to the extracellular domain of KLRG1, for the manufacture of a medicament for the treatment of cancer in a subject, wherein the cancer comprises cancer cells that express KLRG1 in a subject in need thereof, and wherein the use depletes the cancer cells expressing KLRG1 without releasing checkpoint inhibition and without subsequently activating pathogenic CD8+ cytotoxic T and/or NK cells directed to self-tissues.~~by~~

~~depleting cancer cells expressing KLRG1, and without releasing checkpoint inhibition and without subsequently activating pathogenic CD8⁺ cytotoxic T and/or NK cells directed to self-tissues.~~

16. Use of an antibody, or a functional fragment thereof, that comprises

i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3); wherein

a) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of i); wherein the heavy chain variable region comprises SEQ ID NO:4 or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO:5 or a sequence at least 90% identical to SEQ ID NO:5;

b) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:6 or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7 or a sequence at least 90% identical to SEQ ID NO:7;

c) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises

SEQ ID NO:8 or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9 or a sequence at least 90% identical to SEQ ID NO:9;

d) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iv); wherein the heavy chain variable region comprises SEQ ID NO:10 or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO:11 or a sequence at least 90% identical to SEQ ID NO:11;

e) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of v); wherein the heavy chain variable region comprises SEQ ID NO:12 or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO:13 or a sequence at least 90% identical to SEQ ID NO:13;

f) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of vi); wherein the heavy chain variable region comprises SEQ ID NO:14 or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO:15 or a sequence at least 90% identical to SEQ ID NO:15;

g) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:52 or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO:53 or a sequence at least 90% identical to SEQ ID NO:53;
or

h) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:54 or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO:55 or a sequence at least 90% identical to SEQ ID NO:55;
and that

specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1) without interfering with binding by E-cadherin, N-cadherin, or R-cadherin to the extracellular domain of KLRG1, for the manufacture of a medicament for use in the treatment of cancer in a

subject undergoing checkpoint therapy, wherein the cancer comprises cancer cells that express KLRG1 in a subject in need thereof and the use depletes the cancer cells expressing KLRG1.

17. Use of an antibody, or a functional fragment thereof, that comprises

i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3); wherein

a) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of i); wherein the heavy chain variable region comprises SEQ ID NO:4 or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO:5 or a sequence at least 90% identical to SEQ ID NO:5;

b) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:6 or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7 or a sequence at least 90% identical to SEQ ID NO:7;

c) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises

SEQ ID NO:8 or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9 or a sequence at least 90% identical to SEQ ID NO:9;

d) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iv); wherein the heavy chain variable region comprises SEQ ID NO:10 or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO:11 or a sequence at least 90% identical to SEQ ID NO:11;

e) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of v); wherein the heavy chain variable region comprises SEQ ID NO:12 or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO:13 or a sequence at least 90% identical to SEQ ID NO:13;

f) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of vi); wherein the heavy chain variable region comprises SEQ ID NO:14 or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO:15 or a sequence at least 90% identical to SEQ ID NO:15;

g) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:52 or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO:53 or a sequence at least 90% identical to SEQ ID NO:53;
or

h) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:54 or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO:55 or a sequence at least 90% identical to SEQ ID NO:55;

for use in the manufacture of a medicament for the treatment of a cancer associated with excess killer cell lectin-like receptor G1 (KLRG1) expressing T cell and/or NK cells and/or cancer cells in a mixed population of cells, in a subject in need thereof, wherein the antibody or functional fragment thereof and that specifically binds to KLRG1 and depletes KLRG1 expressing T cells and/or NK cells and/or cancer cells, ~~for the manufacture of a medicament for depletes KLRG1 expressing T cells and/or NK cells and/or cancer cells in a mixed population of cells.~~

18. An antibody, or a functional fragment thereof, that specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1), and which comprises a heavy chain variable region comprising three heavy chain complementarity determining regions (CDR-~~L~~H1, CDR-~~L~~H2 and CDR-~~L~~H3), wherein said antibody, or fragment thereof comprises:

- i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);
- ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);
- iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);
- iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);
- v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or
- vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3).

19. An antibody, or a functional fragment thereof, that specifically binds to an extracellular domain of killer cell lectin-like receptor G1 (KLRG1) and which comprises:

~~comprises:~~

- i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);
- ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);
- iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3); wherein

a) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of i); wherein the heavy chain variable region comprises SEQ ID NO:4 or a sequence at least 90% identical to SEQ ID NO:4; and the light chain variable region comprises SEQ ID NO:5 or a sequence at least 90% identical to SEQ ID NO:5;

b) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:6 or a sequence at least 90% identical to SEQ ID NO:6; and the light chain variable region comprises SEQ ID NO:7 or a sequence at least 90% identical to SEQ ID NO:7;

c) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:8 or a sequence at least 90% identical to SEQ ID NO:8; and the light chain variable region comprises SEQ ID NO:9 or a sequence at least 90% identical to SEQ ID NO:9;

d) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iv); wherein the heavy chain variable region comprises SEQ ID NO:10 or a sequence at least 90% identical to SEQ ID NO:10; and the light chain variable region comprises SEQ ID NO:11 or a sequence at least 90% identical to SEQ ID NO:11;

e) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of v); wherein the heavy chain variable region comprises SEQ ID NO:12 or a sequence at least 90% identical to SEQ ID NO:12; and the light chain variable region comprises SEQ ID NO:13 or a sequence at least 90% identical to SEQ ID NO:13;

f) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of vi); wherein the heavy chain variable region comprises SEQ ID NO:14 or a sequence at least 90% identical to SEQ ID NO:14; and the light chain variable region comprises SEQ ID NO:15 or a sequence at least 90% identical to SEQ ID NO:15;

g) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of ii); wherein the heavy chain variable region comprises SEQ ID NO:52 or a sequence at least 90% identical to SEQ ID NO:52; and the light chain variable region comprises SEQ ID NO:53 or a sequence at least 90% identical to SEQ ID NO:53;
or

h) the three heavy chain complementarity determining regions and the three light chain complementarity determining regions of iii); wherein the heavy chain variable region comprises SEQ ID NO:54 or a sequence at least 90% identical to SEQ ID NO:54; and the light chain variable region comprises SEQ ID NO:55 or a sequence at least 90% identical to SEQ ID NO:55.

20. The antibody, or a functional fragment thereof, of claim 18, wherein the antibody, or fragment thereof, comprises a monoclonal antibody, or a fragment or derivative thereof.

21. The antibody, or a functional fragment thereof, of claim 18, wherein the antibody, or fragment thereof, comprises a chimeric antibody, or a fragment thereof.

~~22~~ 21. The antibody, or a functional fragment thereof, of claim 18, wherein the antibody, or fragment, thereof comprises a humanized antibody, or a fragment thereof.

23. A pharmaceutical composition, comprising the antibody, or a functional fragment thereof, of claim 18 and a pharmaceutically acceptable carrier.

24. A kit, comprising the antibody, or a functional fragment thereof, of claim 18 and instructions for use.

25. Use of an antibody, or a functional fragment thereof, that comprises:

i) SEQ ID NO: 16 (CDR-H1), SEQ ID NO: 17 (CDR-H2), SEQ ID NO: 18 (CDR-H3), SEQ ID NO: 19 (CRD-L1), SEQ ID NO:20 (CDR-L2), and SEQ ID NO:21 (CDR-L3);

ii) SEQ ID NO:22 (CDR-H1), SEQ ID NO:23 (CDR-H2), SEQ ID NO:24 (CDR-H3), SEQ ID NO:25 (CRD-L1), SEQ ID NO:26 (CDR-L2), and SEQ ID NO:27 (CDR-L3);

iii) SEQ ID NO:28 (CDR-H1), SEQ ID NO:29 (CDR-H2), SEQ ID NO:30 (CDR-H3), SEQ ID NO:31 (CRD-L1), SEQ ID NO:32 (CDR-L2), and SEQ ID NO:33 (CDR-L3);

iv) SEQ ID NO:34 (CDR-H1), SEQ ID NO:35 (CDR-H2), SEQ ID NO:36 (CDR-H3), SEQ ID NO:37 (CRD-L1), SEQ ID NO:38 (CDR-L2), and SEQ ID NO:39 (CDR-L3);

v) SEQ ID NO:40 (CDR-H1), SEQ ID NO:41 (CDR-H2), SEQ ID NO:42 (CDR-H3), SEQ ID NO:43 (CRD-L1), SEQ ID NO:44 (CDR-L2), and SEQ ID NO:45 (CDR-L3); or

vi) SEQ ID NO:46 (CDR-H1), SEQ ID NO:47 (CDR-H2), SEQ ID NO:48 (CDR-H3), SEQ ID NO:49 (CRD-L1), SEQ ID NO:50 (CDR-L2), and SEQ ID NO:51 (CDR-L3),

in the manufacture of a medicament for use in the treatment of a disorder associated with excess killer cell lectin-like receptor G1 (KLRG1) expressing CD8 effector T cells in a subject in need thereof, wherein the antibody, or fragment thereof, specifically binds to the extracellular domain of KLRG1 but does not compete with binding of at least one of E-cadherin, N-cadherin, or R-cadherin to the extracellular domain of KLRG1, thereby selectively depleting the KLRG1 expressing CD8 effector T cells, ~~for the manufacture of a medicament for selectively depleting KLRG1-expressing CD8-effector T cells.~~